

Genes changed in expression in BLR-OX in the same direction in all 3 replicates with an average of >1.5-fold change, arranged in order of spot confidence

SPOTNUMBER	BLOCK	NAME	AG ID	BLR-OX (1)	Co-0 (1)	BLR-OX (2)	Co-0 (2)	BLR-OX (3)	Co-0 (3)	Mean Ratio (BLR-OX:Co-0)	Spot Confidence
3912	7	expressed protein similar to hypothetical protein GB:CA80917.Gi:7267605 from [Arabidopsis thaliana]	At1g01430	1787.80183	1147.219	1552.76854	1034.998	2896.35392	1655.476	1.602733601	0.803712
261	1	trypsin inhibitor, putative similar to SPIP26780 Trypsin inhibitor 2 precursor (MTI-2) [Sinapis alba]	At2g43520	2623.64804	1356.269	2447.05036	1903.594	1752.37643	1232.123	1.547397015	0.778414
13777	22	expressed protein weak similarity to SPIP35809 Phosphatidylcholine transfer protein (PC-TP) [Rattus norvegicus]	At1g64720	5778.65146	4729.678	3573.64263	2901.194	5432.67396	2605.493	1.512884545	0.76076
143	1	band 7 family protein strong similarity to hypersensitive-induced response protein [Zea mays] Gi:7716466; contains Pfam profile PF01145: SPFH domain / Band 7 family	At1g69840	934.878854	463.826	433.947088	365.051	1183.55169	682.818	1.645881681	0.743728
5783	9	expressed protein similar to unknown protein [Pisum sativum]	At5g220	789.76987	559.846	560.420118	483.709	888.793804	460.651	1.501018393	0.736992
247	1	thioredoxin family protein contains Pfam profile: PF00085 Thioredoxin; similar to ESTs gJ46281, gb R83933, gb N65879, emb F14466, gb N96726, gb AA042340, and emb Z18150	At1g08570	1353.88436	662.757	1128.70825	799.401	936.390775	737.109	1.575035001	0.735816
11720	19	UDP-glucose transferase (UGT5752) similar to UDP-glucose:indole-3-acetate beta-D-glucosyltransferase [Arabidopsis thaliana]; identical to cDNA UDP-glucosyltransferase (UGT75B2) Gi:13661274	At1g05560	985.290944	765.769	852.45289	673.083	2681.85157	861.069	1.889242905	0.72891
23208	36	MER1-5 protein (MER1-5) / endo-xyloglucan transferase / xyloglucan endo-1,4-beta-D-glucanase (SENA) identical to endo-xyloglucan transferase gi:944810, SPIP24806 MER1-5 protein precursor (Endo-xyloglucan transferase) [Xyloglucan endo-1,4-beta-D-glucanase] [Arabidopsis thaliana]	At4g30270	1472.93189	555.304	1890.03039	564.614	3446.82975	447.573	4.567020224	0.72864
29856	46	expressed protein	At5g56550	953.785661	467.624	805.732384	579.965	2182.90695	1098.222	1.805531167	0.728376
13384	21	alkaline alpha galactosidase, putative similar to alkaline alpha galactosidase II [Cucumis melo] Gi:29838631; contains Pfam profile PF05691: Raffinose synthase or seed imbibition protein Sip1	At3g57520	1275.32972	747.599	1160.01461	514.271	1283.00576	1123.011	1.701339916	0.7209
23377	36	ripening-responsive protein, putative similar to ripening regulated protein DDTFR18 [Lycopersicon esculentum] Gi:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family	At5g65380	892.259659	638.703	891.633662	729.42	626.72106	308.31	1.55071222	0.72036
251	1	yippee family protein similar to mgd-1 [Mus musculus] Gi:10441648, Yippee protein [Drosophila melanogaster] Gi:5713279; contains Pfam profile PF03226: Yippee putative zinc-binding protein	At2g40110	769.61837	374.016	603.829645	533.64	937.675344	601.399	1.582800619	0.71728
3038	5	26S proteasome regulatory subunit, putative (RPN9) similar to 26S proteasome subunit p40.5 [Homo sapiens] gi 3618343 db BAAS33214	At4g19006	1072.05668	623.653	803.869745	572.546	1417.85042	565.897	1.876171324	0.71253
11064	18	methylcrotonyl-CoA carboxylase alpha chain, mitochondrial / 3-methylcrotonyl-CoA carboxylase 1 (MCCA) nearly identical to SP Q42523 Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor (EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCase alpha subunit) (3-methylcrotonyl-CoA:carbon diox	At1g03090	110.623123	429.567	700.803189	352	3579.37332	1203.481	2.361654827	0.712356
18415	29	sinapoylglucose:malate sinapoyltransferase (SNG1) similar to serine carboxypeptidase 1 precursor (SP:P37890) [Oryza sativa]; contains Pfam profile PF00450: Serine carboxypeptidase; identical to cDNA sinapoylglucose:malate sinapoyltransferase (SNG1) Gi:8699618	At2g22990	4085.189	2704	2941.75071	1695.299	4667.97208	1862.184	1.917584609	0.711822
767	2	expressed protein	At1g50010	9712.49188	4642.268	7498.23309	6179.574	3226.09639	5026.816	1.732003388	0.70345
2815	5	sinapoylglucose:malate sinapoyltransferase (SNG1) similar to serine carboxypeptidase 1 precursor (SP:P37890) [Oryza sativa]; contains Pfam profile PF00450: Serine carboxypeptidase; identical to cDNA sinapoylglucose:malate sinapoyltransferase (SNG1) Gi:8699618	At2g22990	5398.73235	3458.197	3257.97392	2537.054	3825.25791	2175.012	1.534675553	0.693696
4203	7	serine carboxypeptidase S10 family protein contains Pfam profile: PF00450 serine carboxypeptidase; similar to serine carboxypeptidase 1 precursor (SP:P37890) [Oryza sativa]	At3g12230	2776.2309	1719.291	1840.89122	1297.522	2964.02162	1506.091	1.667183616	0.68904
13379	21	stictosidine synthase family protein similar to stictosidine synthase [Rauvolfia serpentina][SP15324]	At3g57020	1033.37886	687.06	607.430641	503.934	1121.54599	422.16	1.788707045	0.68904
18180	28	expressed protein similar to hypothetical protein GB:CA80917.Gi:7267605 from [Arabidopsis thaliana]	At1g01431	3364.08697	1830.95	2369.03522	1743.529	3672.4817	1682.677	1.903980553	0.688344
14032	22	trypsin inhibitor, putative similar to SPIP26780 Trypsin inhibitor 2 precursor (MTI-2) [Sinapis alba]	At2g43521	3465.72434	1873.31	2429.35368	1790.431	3767.31092	1721.287	1.908170305	0.68714
24315	38	expressed protein weak similarity to SPIP35809 Phosphatidylcholine transfer protein (PC-TP) [Rattus norvegicus]	At1g74960	3567.36171	1915.67	2489.67215	1837.332	3862.14015	1759.898	1.912360057	0.681304
19018	30	zinc finger (B-box type) family protein similar to zinc finger protein Gi:3618316 from [Oryza sativa]	At1g78600	1324.91289	1124.333	1727.28459	1456.649	1702.24939	675.64	1.627884801	0.68034
14659	23	asparagine synthetase 1 [glutamine-hydrolyzing] / glutamine-dependent asparagine synthetase 1 (ASN1) identical to SPI P49078 Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4) (Glutamine- dependent asparagine synthetase) [Arabidopsis thaliana]	At3g47340	1266.23944	777.959	1643.81796	1443.662	3379.26308	799.412	2.331157781	0.67983
11918	19	ABC transporter family protein similar to PDR5-like ABC transporter Gi:1514643 [Spirodela polytricha]	At2g26910	1151.06161	957.544	1331.99403	960.898	1786.05976	913.899	1.514208158	0.679272
2796	5	UDP-glucuronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase	At2g15490	656.863125	339.012	416.069391	246.699	667.222	767.00909	1.67265894	0.679252
28144	45	polyubiquitin (UBQ4) identical to Gi:17677	At5g20620	10704.5534	7731.081	9451.38114	7623.174	10895.6897	5629.167	1.513311976	0.689249
27282	42	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative similar to endo-xyloglucan transferase Gi:2244732 from [Cossypium hirsutum]	At5g65730	1070.29724	769.445	1416.30991	780.267	1646.2892	1065.555	1.583721976	0.685364
22655	35	bZIP transcription factor family protein similar to seed storage protein opaque-2[bZIP family]Gi:168428 from Zea mays; contains Pfam profile PF00170: bZIP transcription factor; identical to cDNA bZIP protein BZ02H3 Gi:10954098	At5g28770	763.301483	376.854	781.707687	273.982	742.346675	668.329	1.996447438	0.68521
28563	44	copper transporter 1 (COPT1) nearly identical to SPI Q39065 Copper transporter 1 (COPT1) [Arabidopsis thaliana]	At5g59030	826.422216	702.949	812.083521	663.591	763.877119	281.286	1.705027132	0.663872
15283	24	expressed protein	At3g27770	395.281354	304.093	973.10221	696.513	1153.14679	618.696	1.520269932	0.66339
25923	40	chaperone protein dnaJ-related similar to Chaperone protein dnaJ (SP:Q9WVZ3) [Thermotoga maritima]	At5g43260	528.72638	449.406	748.030409	561.464	754.241823	325.448	1.608778507	0.658416
22572	35	pectinesterase family protein contains Pfam profile: PF01095 pectinesterase	At4g33220	955.217817	691.288	721.054807	589.872	685.08749	340.709	1.538318815	0.657888
18068	28	alpha-glucosidase 1 (AGLU1) identical to alpha-glucosidase 1 [Arabidopsis thaliana] Gi:2323344	At5g11720	1126.01333	633.312	1204.73069	690.89	832.977841	410.758	1.84987238	0.657888
8444	13	importin alpha-1 subunit, putative similar to importin alpha-1 subunit [Karyopherin alpha-1 subunit, KAP alpha] [Arabidopsis thaliana] SWISS-PROT:Q96321	At1g32880	1117.83218	660.835	1114.45882	683.742	727.509185	453.906	1.641420208	0.65772
17151	27	zinc finger (CCHH-type) family protein contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar) and Pfam domain, PF00023: Ankyrin repeat	At2g40140	3845.94522	1852.075	4059.06325	2057.915	3265.53442	1333.214	2.166115211	0.657443
21322	33	nodulin family protein similar to nodulin-like protein [Arabidopsis thaliana] Gi:3329368, nodulin-specific protein Nj70 [Lotus japonicus] Gi:3329368	At1g51420	2839.33543	1674.732	2729.70309	1659.574	3226.09639	5026.816	1.6527366	0.65736
9639	15	raffinose synthase family protein / seed imbibition protein, putative (din10) similar to seed imbibition protein GB:AAA32975.Gi:167100 from [Hordeum vulgare]; contains nonconsensus AT donor splice site at intron 1; contains Pfam profile PF05691: Raffinose synthase or seed imbibition protein Sip1; identical to cDNA see At5g20250	At5g20250	3425.05727	1433.546	3228.69654	735.179	7815.1468	5532.069	2.731664712	0.65736
13322	21	glycolipid transfer protein-related contains weak similarity to Glycolipid transfer protein (GLTP) (Swiss-Prot:P17403) [Ussu scrofa]	At3g21260	877.663223	512.159	897.580085	682.184	858.984687	396.788	1.7161414697	0.6561
6014	10	wound-responsive protein, putative similar to wound-responsive protein 14.05 (Gi:16506638) [Castanea sativa]	At1g77310	4025.0686	2583.169	3413.43337	2548.594	3432.41495	1992.317	1.540120888	0.653883
7854	13	12-oxophytodienoate reductase, putative similar to OPR1 [Gi:3882355] and OPR2 [Gi:3882356]	At1g18020	2821.39995	1819.391	1602.53398	1018.547	2975.52294	1339.871	1.781614984	0.64989
5043	8	homeodomain protein (BELLRINGER) several homeodomain proteins;	At5g02030	1997.31154	633.566	2116.11884	540.4	3408.33392	946.186	3.556837127	0.649194
5461	9	trypsin inhibitor, putative similar to SPIP26780 Trypsin inhibitor 2 precursor (MTI-2) [Sinapis alba]	At2g43510	616.755282	425.664	658.437313	505.848	1171.86273	200.919	2.861029648	0.648
26220	41	CBL-interacting protein kinase 3 (CIKP3) identical to CBL-interacting protein kinase 3 [Arabidopsis thaliana] gi 9280638 gb AAF86507	At2g26980	802.937645	449.692	560.38347	322.618	1524.53354	814.292	1.798245101	0.64792
3836	6	glycosyl hydrolase family 3 protein	At5g49360	2157.03913	629.007	1057.0803	381.654	3101.16737	1940.799	2.598964415	0.645606
1931	3	asparagine synthetase 2 (ASN2) identical to asparagine synthetase (ASN2) [Arabidopsis thaliana] Gi:3859536	At5g65010	2723.47645	1608.764	2191.69992	1841.95	7634.68665	2981.252	1.814559866	0.64328
7040	27	UbiE/COQ5 methyltransferase family protein low similarity to SPI Q05197 Phosphatidylethanolamine N-methyltransferase (EC 2.1.1.17) [Rhodospseudomonas sphaeroides] [Rhodobacter sphaeroides]; contains Pfam profile PF01209: methyltransferase, UbiE/COQ5 family	At1g69526	1608.70751	708.456	1481.00356	1057.31	917.274826	647.485	1.696041525	0.642936
29962	45	serine carboxypeptidase S10 family protein similar to serine carboxypeptidase 1 precursor (SP:P37890) [Oryza sativa]	At2g20000	3099.55744	2281.431	2983.53886	2045.557	2347.01627	1084.925	1.642392258	0.642936
29215	45	xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase / endo-xyloglucan transferase (TCH4) identical to xyloglucan endotransglycosylase TCH4 protein Gi:886116	At5g75660	486.388482	186.933	705.078176	250.232	1814.01923	1263.888	2.284969009	0.642005
9042	14	pyridoxamine 5-phosphate oxidase-related contains weak similarity to Pyridoxamine 5-phosphate oxidase (EC 1.4.3.5) (PNP/PMP oxidase) (PNPOx). (Swiss-Prot:P28225) [Shigella flexneri]	At5g49970	868.588983	764.514	677.917745	596.381	848.37617	254.988	1.866657792	0.639821
27738	43	glutathione S-transferase-related contains weak hit to Pfam profile PF00043: Glutathione S-transferase, C-terminal domain	At4g19880	1322.62508	1030.956	1816.56857	1602.899	1337.73086	601.011	1.547338063	0.638664
25005	39	cytochrome P450, putative similar to GB:Q05407 from [Catharanthus roseus]	At3g14690	3411.44163	2466.579	3114.7228	2416.425	3480.86979	1371.652	1.736588841	0.63648
23654	37	ACT domain-containing protein contains Pfam ACT domain PF01842	At2g39570	547.189315	311.386	586.720134	266.541	557.954367	317.346	1.905565778	0.63597
25128	39	monoxygenase, putative (MO1) similar to Gi:3426062	At4g15760	1479.21241	864.126	2302.10869	1345.038	1117.17474	743.609	1.641908964	0.63495
7793	12	thioesterase family protein contains Pfam profile PF03061: thioesterase family protein	At1g35250	1424.72633	950.977	1076.10663	658.437	993.025202	699.994	1.517041917	0.63495
5550	9	nitrilase 2 (NIT2) identical to SPI P32962 Nitrilase 2 (EC 3.5.5.1) [Arabidopsis thaliana]	At3g44300	6358.29049	5388.119	5582.12357	4930.994	5720.70807	2614.229	1.502336489	0.63468
13062	21	expressed protein similar to TollB protein precursor (SP:Q9ZDM5) [Rickettsia prowazekii]; ESTs gb N96028, gb F14286, gb T20680, gb F14443, gb AA657300 and gb N65244 come from this gene	At1g21680	2892.84943	1900.774	1354.90178	956.867	2643.44028	1226.645	1.697642008	0.63427
29962	47	expressed protein contains Pfam profile PF04749: Protein of unknown function, DUF614	At1g25275	5657.93926	2326.916</						

23616	37 serine carboxypeptidase S10 family protein similar to serine carboxypeptidase I precursor (SP:P37890) [Oryza sativa]	At2g23010	2219.22613	1714.013	1558.14294	1089.417	1655.6482	776.794	1.618798308	0.54675
17720	28 kelch repeat-containing F-box family protein similar to SP QBER30 Kelch-related protein 1 (Sarcosin) [Rattus norvegicus]; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain	At1g80440	1633.70874	799.598	1404.23224	695.271	1358.92933	930.799	1.840937714	0.543576
20757	32 beta-galactosidase, putative / lactase, putative similar to beta-galactosidase precursor GI:3869280 from [Carica papaya]	At5g56870	1105.20055	282.977	625.728798	158.689	797.939839	353.94	3.367727681	0.54264
9464	15 broad-spectrum mildew resistance RPW8 family protein contains Pfam PF05659: Arabidopsis broad-spectrum mildew resistance protein RPW8	At3g50480	360.167339	287.909	339.943569	213.493	1154.47672	619.095	1.569350423	0.539616
7603	12 no apical meristem (NAM) family protein (RD26) contains Pfam PF02365: No apical meristem (NAM) domain; Arabidopsis thaliana nap gene, PID:e1234813; identical to cDNA RD26 mRNA for NAM-like protein GI:15375403	At4g27410	481.018166	226.394	403.5362	241.324	1187.5456	787.157	1.768507455	0.537516
19112	30 autophagy 8e (APG8e) identical to autophagy 8e [Arabidopsis thaliana] GI:19912159; contains Pfam profile PF02991: Microtubule associated protein 1A/1B, light chain 3	At2g45170	3948.08497	1914.459	3520.42119	1728.483	3589.19418	2378.754	1.869297057	0.536844
7090	11 acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative strong similarity to Acetoacetyl-coenzyme A thiolase (E.C. 2.3.1.9) [Raphanus sativus] GI:1542941; contains InterPro accession IPR002155: Thiolase	At5g48230	9105.54671	6615.708	9928.00169	6688.256	9930.33164	5592.62	1.508959201	0.536256
5078	6 DnaJ heat shock N-terminal domain-containing protein similar to SP P30725 Chaperone protein dnaJ Clostridium acetobutylicum; contains Pfam profile PF00226: DnaJ domain	At5g16650	920.516655	549.733	841.125712	496.199	2114.84954	1656.558	1.548719559	0.535952
8825	2 metalloprotease family protein similar to metalloprotease putative / endo-xyloglucan transferase, putative / endo-xyloglucan transferase, putative (XTR4) identical to N-terminal partial sequence of xyloglucan endotransglycosylase-related protein XTR4 GI:1244754 from [Arabidopsis thaliana]; similar to endoxyloglucan transferase [Arabidopsis thaliana] GI:1244754 from [Arabidopsis thaliana]	At1g19510	1596.99575	916.524	2537.63241	1541.72	4948.5391	753.343	3.215255964	0.485289
16210	25 CER1 protein, putative (WAX2) similar to maize glossy1 homolog GI:2213643 from [Oryza sativa]; contains Pfam profile PF01598: Sterol desaturase	At5g7800	589.737919	436.21	476.88498	336.251	395.676021	206.007	1.599866527	0.525888
16458	26 auxin-responsive protein, putative similar to small auxin-up regulated protein SAUR (GI:3043536) [Raphanus sativus]	At2g21210	3059.90993	2400.28	2294.50995	1361.066	5561.07103	2381.446	1.765265773	0.524477
19045	30 hypothetical protein	At2g18200	485.523199	332.983	503.782508	449.31	399.989533	206.195	1.506399487	0.522144
10575	17 CBS domain-containing protein low similarity to SP Q9MYP4 5'-AMP-activated protein kinase, gamma-3 subunit (AMPK gamma-3 chain) (AMPK gamma3) [Sus scrofa]; contains Pfam profile PF00571: CBS domain	At1g80090	608.623334	410.415	485.739288	310.224	716.525401	428.664	1.573415737	0.521264
1856	3 NAD-dependent epimerase/dehydratase family protein similar to sugar epimerase BimG from Streptomyces verticillus GI:9937230; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family	At5g28840	1705.07158	1129.764	1832.47509	1384.063	3840.62325	1753.779	1.674374477	0.5214
30422	47 auxin-responsive GH3 family protein similar to auxin-responsive GH3 product [Glycine max] GI:18591; contains Pfam profile PF03321: GH3 auxin-responsive promoter	At5g13370	703.037575	459.113	309.642623	223.267	80.360234	224.832	2.263108296	0.520828
26958	42 jacalin lectin family protein similar to SP Q9SAV1 Myrosinase binding protein-like At1g52030 [Arabidopsis thaliana]; contains Pfam profile: PF01419 jacalin-like lectin domain	At3g16450	5265.292658	3223.773	3956.07158	2886.038	4635.42692	2485.196	1.623082755	0.518868
19859	31 asparagine synthetase 1 [glutamine-hydrolyzing] / glutamine-dependent asparagine synthetase 1 (ASN1) identical to SP P49078 Asparagine synthetase [glutamine-hydrolyzing] [EC 6.3.5.4] [Glutamine- dependent asparagine synthetase] (Arabidopsis thaliana)	At3g47340	467.39397	229.677	1138.86274	363.042	2087.82618	251.607	4.48999301	0.516516
28616	45 no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; similar to NAC domain containing protein NAM GB:AAD17313 GI:4325282 from [Arabidopsis thaliana]	At1g01720	1770.37531	1473.838	2360.17554	1886.714	1994.4135	736.52	1.720011192	0.515592
29365	42 expressed protein	At3g19600	625.628443	403.134	630.426027	542.109	447.485584	213.921	1.602543437	0.514796
9509	14 glycine-rich protein (GRP3S) identical to cDNA glycine-rich protein 3 short isoform (GRP3S) GI:4206766	At2g05380	1625.01959	11608.79	19018.8094	14729.65	22993.2763	11367.69	1.5654895516	0.511758
8647	14 gibberellin-responsive protein, putative similar to SP P4689 Gibberellin-regulated protein 1 precursor (Arabidopsis thaliana); contains Pfam profile PF02704: Gibberellin regulated protein	At2g18420	1057.91695	633.314	793.422077	330.877	7259.93477	753.934	4.5659288	0.50949
18034	28 PQ-loop repeat family protein / transmembrane family protein similar to SP Q10482 Seven transmembrane protein 1 [Schizosaccharomyces pombe]; contains Pfam profile PF04193: PQ loop repeat	At4g36850	501.480129	235.461	352.387719	216.48	657.870305	358.637	1.863983296	0.508956
30661	48 cytochrome P450, putative similar to SP-Q42569 from [Arabidopsis thaliana]	At1g55940	407.874483	294.335	411.931619	214.958	589.57236	198.995	2.088587738	0.5031
28560	44 expressed protein	At5g58650	357.609994	308.912	440.540416	281.895	558.471906	281.798	1.567413985	0.502824
16701	26 expressed protein	At4g27040	526.340167	458.305	412.291719	358.861	1756.02601	548.857	1.832254275	0.500976
29704	46 expressed protein	At4g28080	2882.50989	2039.285	1681.74155	1171.269	2740.74791	1469.623	1.57141724	0.50049
26951	42 2-oxoisovalerate dehydrogenase / 3-methyl-2-oxobutanoate dehydrogenase / branched-chain alpha-keto acid dehydrogenase E1 beta subunit (DIN4) identical to branched chain alpha-keto acid dehydrogenase E1 beta subunit [Arabidopsis thaliana] GI:7021286	At3g13450	852.767889	542.894	1126.64007	851.199	942.310513	487.554	1.609304662	0.49662
13215	21 sinapoylglucosyl:malate sinapoyltransferase (SNG1) similar to serine carboxypeptidase I precursor (SP:P37890) [Oryza sativa]; contains Pfam profile PF00450: Serine carboxypeptidase; identical to cDNA sinapoylglucosyl:malate sinapoyltransferase (SNG1) GI:8699618	At2g22990	4727.50061	3288.406	3052.85896	2231.705	5543.61904	2696.614	1.620448761	0.494286
19842	31 cytochrome P450 family protein contains Pfam profile: PF00067 cytochrome P450	At3g28740	1948.39578	1355.407	429.514358	290.052	532.469184	176.831	1.976497567	0.493228
23827	37 integral membrane family protein contains TIGRFAM TIGR01569: plant integral membrane protein TIGR01569; contains Pfam PF04535: Domain of unknown function (DUF588)	At4g15610	1596.99575	916.524	2537.63241	1541.72	4948.5391	753.343	3.215255964	0.485289
16063	25 expressed protein	At4g29050	4001.74107	1703.996	3897.2192	1590.37	4708.83912	3853.931	2.007014386	0.4842716
23835	37 expressed protein	At4g18740	311.151039	235.378	297.515553	198.571	441.761727	156.103	1.883380368	0.489168
13750	22 expressed protein similar to PGPS/D12 [Petunia x hybrida] GI:4105794; contains Pfam profile PF04749: Protein of unknown function, DUF614	At1g52200	640.665542	290.882	256.532714	157.974	522.615325	426.776	1.68365026	0.485112
29083	45 catalase 2 identical to catalase 2 SP-P25819, GI:17865693 from [Arabidopsis thaliana]	At4g35090	3341.16332	2392.986	2266.62135	1832.177	3628.38487	1650.253	1.610678359	0.483807
8916	14 UDP-glucuronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase	At4g34135	1117.30488	803.638	977.613015	816.577	3149.57684	1020.532	1.891242683	0.482856
1525	3 WRKY family transcription factor	At2g30250	447.30101	289.577	546.162723	274.967	576.682677	316.847	1.783673898	0.47712
13977	22 hydrolase, alpha/beta fold family protein low similarity to 3-oxoadipate enol-lactone hydrolase [Pseudomonas sp. B13] GI:17736948, B-ketoadipate enol-lactone hydrolase [Bradyrhizobium japonicum] GI:2239060; contains Pfam profile:PF00561 abhydrolase/alpha/beta hydrolase fold	At3g24420	302.286434	267.16	392.623271	335.09	607.63604	187.542	1.847725218	0.472685
12855	20 glutamate dehydrogenase 2 (GDH2) identical to glutamate dehydrogenase 2 (GDH 2) [Arabidopsis thaliana] SWISS-PROT:Q38946	At5g07440	3403.08079	1891.486	4092.93332	2626.374	5715.37392	2574.548	1.958916873	0.471707
17967	28 major latex protein-related / MLP-related low similarity to major latex protein [Papaver somniferum] GI:2940601; contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family	At4g14060	1882.7776	827.188	326.956084	242.282	1673.64866	1007.612	1.762202956	0.47073
20031	31 NADP-dependent oxidoreductase, putative strong similarity to probable NADP-dependent oxidoreductase (zeta-crySTALLIN homolog) P1 [SP Q39172]GI:886430, Arabidopsis thaliana	At5g16980	1698.63063	1203.975	1799.39469	1346.834	2344.18527	754.096	1.930318696	0.46215
9599	15 arginase, putative similar to Swiss-Prot P46637 arginase (EC 3.5.3.1) [Arabidopsis thaliana]	At4g08870	351.727354	217.176	480.012748	263.89	480.012748	169.303	1.59185154	0.461336
24028	37 no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; contains similarity to NAC-domain protein	At5g63790	2459.29669	1768.805	2794.274	2441.158	3585.37166	1332.859	1.744170418	0.459648
1107	2 villin, putative similar to villin 2 (VLN2) [Arabidopsis thaliana] GI:3415115, villin 3 (VLN3) [Arabidopsis thaliana] GI:3415117; contains Pfam profiles PF00626: Gelsolin repeat, PF02209: Villin headpiece domain	At4g30160	2998.03746	1838.975	2274.20734	2042.05	2388.26886	1256.566	1.548198727	0.45864
4701	8 integral membrane protein, putative strong similarity to integral membrane protein GI:1209756 from [Beta vulgaris]; contains Pfam profile PF00083: major facilitator superfamily protein	At1g75220	371.320825	280.851	237.052283	157.326	970.818453	494.454	1.597433685	0.458755
6345	10 expressed protein	At5g01280	275.14607	222.294	340.233561	267.169	281.825709	102.195	1.75631983	0.457884
6431	10 26S proteasome regulatory subunit, putative (RPN9) contains similarity to 26S proteasome subunit p40.5 GI:3618343 from [Homo sapiens]	At5g45620	3773.09139	2160.17	3908.15443	2364.345	5128.658	1324.07	2.424340819	0.454674
23977	37 serine protease inhibitor, potato inhibitor 1-type family protein similar to SP P24076 Glu S.griseus protease inhibitor (BGIA) [Momordica charantia]; contains Pfam profile PF00280: Potato inhibitor I family	At5g43570	337.278519	178.679	515.343935	245.868	1205.27389	118.804	4.709567618	0.452709
1519	24 calcium-transporting ATPase 4, plasma membrane-type / Ca2+-ATPase, isoform 4 (ACA4) identical to SP Q22218 Calcium-transporting ATPase 4, plasma membrane-type (EC 3.6.3.8) (Ca2+)-ATPase isoform 4 (Arabidopsis thaliana)	At2g41560	192.19977	160.194	634.167938	385.475	840.213077	450.361	1.570206671	0.451704
4292	1 expressed protein contains Pfam PF05421: Protein of unknown function (DUF751)	At4g16410	3138.19404	2127.783	2157.76133	1849.897	4777.5563	2437.021	1.533898802	0.451269
16397	26 expressed protein contains Pfam profile: PF00561 alpha/beta hydrolase fold	At1g73750	266.90286	221.55	453.82586	306.23	344.47266	149.997	1.661071567	0.449862
23615	37 sinapoylglucosyl:malate sinapoyltransferase (SNG1) similar to serine carboxypeptidase I precursor (SP:P37890) [Oryza sativa]; contains Pfam profile PF00450: Serine carboxypeptidase; identical to cDNA sinapoylglucosyl:malate sinapoyltransferase (SNG1) GI:8699618	At2g22990	4727.50061	3288.406	3052.85896	2231.705	5543.61904	2696.614	1.620448761	0.449286
1222	2 metalloendopeptidase identical to chloroplast processing enzyme metalloendopeptidase [Arabidopsis thaliana] gi 2227039 g :886430	At5g16980	1698.63063	1203.975	1799.39469	1346.834	2344.18527	754.096	1.930318696	0.46215
10371	16 MA3 domain-containing protein low similarity to programmed cell death 4 protein [Gallus gallus] GI:12958564; contains Pfam profile PF02847: MA3 domain	At5g63190	282.490814	222.888	425.368839	308.637	830.606647	439.573	1.511732801	0.443111
17007	27 AP2 domain-containing protein RAP2.12 (RAP2.12) identical to AP2 domain containing protein GI:2281649 from [Arabidopsis thaliana]	At1g53910	9939.20029	5701.513	9052.98485	5221.677	8509.22008	4206.881	1.833226287	0.43282
16082	25 senescence-associated protein (SEN1) identical to senescence-associated protein GI:1046270 from [Arabidopsis thaliana]	At4g35770	1619.12941	532.436	2529.72031	1262.767	3030.33876	1823.453	2.235389202	0.42768
2147	4 zinc finger (C3HC4-type RING finger) family protein contains Pfam PF00097: Zinc finger, C3HC4-type (RING finger) domain; similar to RING-H2 finger protein RHA3a (GI:3790573) [Arabidopsis thaliana]; similar to ReMembr-R-H2 protein JR700 (GI:6942147) [Arabidopsis thaliana]	At2g17730	308.399033	220.022	360.196781	253.407	889.758664	455.032	1.593495967	0.42435
24134	38 expressed protein	At1g36640	525.304823	314.184	290.499984	237.34	304.733507	148.833	1.647811369	0.420036
10014	16 cytochrome P450 family protein	At2g45560	830.47482	674.413	866.672069	687.117	1274.76019	605.184	1.533040509	0.41888
13860	22 protein phosphatase 2C, putative / PP2C, putative	At2g25070	926.889159	796.283	926.928202	765.436	4095.28538	1062.742	2.076169664	0.418656
4730	8 glycine-rich protein	At2g05540	1613.71952	1076.313	1011.26639	816.128	3507.71377	1439.974	1.7247874	0.41624
2368	4 xyloglucan/xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative (XTR7) almost identical to xyloglucan endotransglycosylase-related protein XTR7 GI:1244760 from [Arabidopsis thaliana], one amino acid difference	At4g14130	281.026572	187.022	233.958063	149.863	722.432768	481.665	1.521271049	0.413899
14553	23 kelch repeat-containing F-box family protein contains F-box domain Pfam:PF00646 and Kelch motif Pfam:PF01344	At3g98210	451.271795	413.45	347.1335	305.028	415.16167592	169.55	1.537185194	0.413849
11761	19 proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family	At1g22570	460.559411	273.783	343.691155	156.559	758.808949	429.133	1.871851706	0.411348
22790	36 expressed protein	At1g13245	2381.87472	1554.505	3464.5213	1934.383	1832.80528	863.746	1.815066255	0.4004
30114	47 serine carboxypeptidase S10 family protein similar to serine carboxypeptidase I precursor (SP:P37890) [Oryza sativa]	At2g22920	3879.00245	2734.365	3100.55463	2327.008	3346.39008	1877.564	1.511112355	0.396198
19164	30 expressed protein	At3g20340</								

4042	7	expressed protein	
6180	10	leucine-rich repeat family protein	
17618	28	expressed protein	
16921	27	leucine-rich repeat protein kinase, putative similar to light repressible receptor protein kinase, gij2129635; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069	
1133	2	G-box binding factor 1 (GBF1) identical to G-box binding factor 1 SP:P42774 from [Arabidopsis thaliana]; contains Pfam profile: PF00170 bZIP transcription factor	
30386	47	expressed protein	
1227	2	disease resistance protein (TIR-NBS-LRR class), putative (RPS4) domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein. Identical to RPS4 (GI:11357255). False intron created at intron 2 to escape a frameshift in the BAC sequence.	
26208	44	expressed protein	
30325	47	UDP-glucuronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase ;similar to UDP-glucose:sinapate glucosyltransferase GI:9794913 from [Brassica napus]	
4437	7	UDP-glucuronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00069	
1563	3	UDP-glucuronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase	
28594	44	thioesterase family protein contains Pfam profile PF03061: thioesterase family protein	
27408	43	GDSL-motif lipase/hydrolase family protein similar to lipase GI:1145627 from [Arabidopsis thaliana]; contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif	
21214	33	zinc finger (C3HC4-type RING finger) family protein zinc finger protein, Arabidopsis thaliana, gb:L76926	
780	2	MATE efflux family protein contains TIGRfam profile: TIGR00797: MATE efflux family protein, Pfam profile PF01554: Uncharacterized membrane protein family	
11139	18	expressed protein similar to putative non-LTR retroelement reverse transcriptase GB:AAD21515 GI:4510429 from [Arabidopsis thaliana]; expression supported by MPSS	
8446	13	MATE efflux family protein similar to ripening regulated protein DDTFR18 [Lycopersicon esculentum] GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family	
5486	9	expressed protein identical to unknown protein GB:AAF30301 from [Arabidopsis thaliana]	
26698	42	myb family transcription factor (MYB58) contains PFAM profile: myb DNA binding domain PF00249	
4922	8	expressed protein	
19234	30	glycosyl hydrolase family 1 protein contains Pfam PF00232: Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to Cyanogenic Beta-Glucosidase (GI:1311386)(pdb:1CBG) [Trifolium Repens]; identical beta-galactosidase GI:10834547	
5901	10	expressed protein	
9540	15	hypothetical protein	
16714	26	expressed protein	
22152	35	phytochrome kinase substrate-related contains weak similarity to Swiss-Prot:Q9SW11 phytochrome kinase substrate 1 [Arabidopsis thaliana]	
23935	37	myb family transcription factor similar to CCA1 [Arabidopsis thaliana] GI:4090569; contains Pfam profile PF00249: Myb-like DNA-binding domain	
30576	48	branched-chain amino acid aminotransferase 2 / branched-chain amino acid transaminase 2 (BCAT2) identical to SPIQ9M439 Branched-chain amino acid aminotransferase 2, chloroplast precursor (EC 2.6.1.42) [Atbcat-2] (Arabidopsis thaliana); contains Pfam profile: PF01063 aminotransferase class IV	
11820	19	expressed protein	
256	1	nucleotidyltransferase family protein contains Pfam profile: PF01909 nucleotidyltransferase domain	
2782	5	expressed protein	
10360	16	haloacid dehalogenase-like hydrolase family protein low similarity to SPIP53078 SSM1 protein (Saccharomyces cerevisiae); contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase	
17478	27	expressed protein	
22503	35	expressed protein contains Pfam profile PF04520: Protein of unknown function, DUF584	
17127	27	hypothetical protein	
18014	28	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed storage/LTP family domain PF00234	
14449	23	MADS-box protein (AGL60) contains Pfam profile: PF00319 SRF-type transcription factor (DNA-binding and dimerisation domain)	
17030	27	expressed protein contains Pfam profile PF03140: Plant protein of unknown function	
28	1	L-allo-threonine aldolase-related similar to L-allo-threonine aldolase (EC 4.1.2.-) (L-allo-TA) (L-allo-threonine acetaldehyde-lyase) (SP:O07051) (Aeromonas jandaei); similar to ESTs gb R30517, gb T42772, gb R90493, and gb R90493	
25885	40	hydrolase, alpha/beta fold family protein low similarity to hydrolase [Terrabacter sp. DBF63] GI:14196240; contains Pfam profile PF00561: hydrolase, alpha/beta fold family	
16271	29	phytochrome and flowering time regulatory protein (PFT1) PMID: 12815435	
18169	28	peptidylcan-binding LysM domain-containing protein contains Pfam profile PF01476: LysM domain	
23501	37	F-box family protein contains F-box domain Pfam:PF00646	
23064	36	hypothetical protein	
1004	2	cytochrome P450 71A21, putative (CYP71A21) identical to Cytochrome P450 71A21 (SP:Q9STL2) [Arabidopsis thaliana]	
9706	15	expressed protein similar to unknown protein (pir T05871)	
1293	2	phosphate-responsive protein, putative similar to phi-1 (phosphate-induced gene) [Nicotiana tabacum] GI:3759184; contains Pfam profile PF04674: Phosphate-induced protein 1 conserved region	
15370	24	expressed protein	
2184	4	nodulin-related contains 14 transmembrane domains; supported by tandem duplication of nodulin -related protein (TIGR_Ath1:At2g34350) [Arabidopsis thaliana]	
11003	17	ankyrin repeat family protein contains Pfam domain, PF00023: Ankyrin repeat	
14867	23	hypothetical protein	
16698	28	RNA recognition motif (RRM)-containing protein low similarity to tumor-rejection antigen SART3 [Mus musculus] GI:7637845; contains INTERPRO:IPR000504 RNA-binding region RNP-1 (RNA recognition motif) domain	
12001	22	transcription elongation factor-related low similarity to transcription elongation factor TFIIS.h [Mus musculus] GI:3288547	
22649	35	ACT domain-containing protein contains Pfam ACT domain PF01842	
551	1	protein kinase family protein contains Pfam kinase domain, Pfam:PF00069	
19615	31	pseudouridine synthase family protein low similarity to SPIP23851 Ribosomal large subunit pseudouridine synthase C (EC 4.2.1.70) (Pseudouridylylase) [Escherichia coli]; contains Pfam profile PF00849: RNA pseudouridylylase synthase	
17870	28	lipid-binding serum glycoprotein family protein similar to SPIP17213 Bactericidal permeability-increasing protein precursor (BPI) (Homo sapiens); contains Pfam profile PF02886: LBP / BPI / CETP family, C-terminal domain	
914	14	peroxidase, putative identical to peroxidase ATP24a [Arabidopsis thaliana] gi 1990313 emb CAA72484	
1015	1	carbonic anhydrase family protein / carbonate dehydratase family protein similar to SPIP46512 Carbonic anhydrase 1 (EC 4.2.1.1) (Carbonate dehydratase 1) [Flaveria linearis]; contains Pfam profile PF00484: Carbonic anhydrase	
20589	32	MATE efflux family protein similar to ripening regulated protein DDTFR18 [Lycopersicon esculentum] GI:12231296; contains Pfam profile PF01554: MatE	
20476	32	glycosyl hydrolase family 17 protein similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from [Nicotiana tabacum]	
13547	21	squalene monoxygenase 1,2 / squalene epoxidase 1,2 (SQEP1,2) identical to SPI065402	
427058	42	hypothetical protein	
21221	33	late embryogenesis abundant domain-containing protein / LEA domain-containing protein similar to LEA protein [Cicer arietinum] GI:2909420; contains Pfam profile PF02987: Late embryogenesis abundant protein	
17540	27	miRNA gene Arabidopsis thaliana miR390f stem-loop	
17141	27	UDP-glucuronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase	
2054	4	protein kinase family protein contains Serine/Threonine protein kinases active-site signature, PROSITE:PS00108	
1275	2	ethylene insensitive 3 family protein contains Pfam profile: PF04873 ethylene insensitive 3	
10676	17	acyl-[acyl-carrier-protein] desaturase, putative / stearyl-ACP desaturase, putative similar to Acyl-[acyl-carrier protein] desaturase from Spinacia oleracea SPIP28645, Cucumis sativus SPIP32061, Ricinus communis SPIP22337; contains Pfam profile PF03405 Fatty acid desaturase	
7726	12	hypothetical protein	
13987	22	hypothetical protein contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287	
8030	13	UDP-glucuronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase	
20732	32	ABC transporter family protein contains Pfam profile: PF00005 ABC transporter; similar to multidrug-resistant protein CjMDR1 GI:14715462 from [Coptis japonica]	
12865	2	miRNA gene Arabidopsis thaliana miR395e stem-loop	
2949	5	hypothetical protein predicted protein, Arabidopsis thaliana	
20365	32	expressed protein	
29620	46	yippee family protein similar to mdg1-1 [Mus musculus] GI:10441648, Yippee protein [Drosophila melanogaster] GI:5713279; contains Pfam profile PF03226: Yippee putative zinc-binding protein	
1873	3	hypothetical protein similar to unknown protein (emb CAB86921.1)	
2183	4	expressed protein	
4772	8	leucine-rich repeat protein kinase, putative similar to light repressible receptor protein kinase [Arabidopsis thaliana] gi 1321686 emb CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00069	
14839	23	floral homeotic protein PISTILLATA (PI) contains Pfam profiles PF01486: K-box region and PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain)	
20497	32	receptor protein kinase-related similar to light repressible receptor protein kinase GI:1321686 from [Arabidopsis thaliana]	
16559	26	F-box family protein contains F-box domain Pfam:PF00646	
29479	46	expressed protein	
11129	18	S-adenosyl-L-methionine:carboxyl methyltransferase family protein similar to defense-related protein cjs 1 [Brassica carinata]GI:14009292[Mol Plant Pathol (2001) 2(3):159-169]	
28303	41	auxin-responsive protein-related similar to indole-3-acetic acid induced protein arg7 (SP:P32295) [Vigna radiata]	
25920	40	hypothetical protein	
14814	23	expressed protein - expression supported by MPSS	
11374	18	expressed protein contains Pfam domain PF05003: protein of unknown function (DUF668); expression supported by MPSS	
28142	44	hypothetical protein	
20277	32	MATE efflux family protein similar to ripening regulated protein DDTFR18 [Lycopersicon esculentum] GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family; contains 12 transmembrane domains, PMID: 11852613	
22551	35	F-box family protein contains F-box domain Pfam:PF00646	
9856	16	DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain	
10600	17	expressed protein	
9016	14	no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; NAC domain protein NAM, Arabidopsis thaliana, gb:AAD17313	
16291	28	expressed protein	
23994	37	ankyrin repeat family protein contains ankyrin repeat domains, Pfam:PF00023	
16659	26	subtilase family protein contains similarity to subtilase; SP1 GI:9957714 from [Oryza sativa]	
11156	18	calcium-binding EF-hand family protein contains Pfam profile: PF00036 EF hand	
16364	26	glutathione S-transferase, putative similar to glutathione S-transferase GB:AAF29773 GI:6856103 from [Gossypium hirsutum]	
7458	12	F-box family protein contains F-box domain Pfam:PF00646	

At1g68945	261.445935	157.519	307.13786	194.681	227.20989	99.16	1.84292233	0.0285
At3g26500	154.578679	101.428	96.5337762	61.341	287.310385	139.566	1.71878199	0.027885
At1g27510	142.068977	124.584	135.950341	101.604	251.422876	122.879	1.508163122	0.027495
At1g05700	192.703537	130.074	199.621046	154.116	179.039595	102.65	1.506972689	0.025872
At4g36730	200.358457	152.574	212.410955	189.838	1335.41121	607.551	1.543372789	0.02432
At4g35430	305.476965	263.299	201.799171	104.451	147.407865	81.415	1.634254204	0.0243
At5g42520	220.251408	113.827	171.179552	146.234	358.287444	171.268	1.732507467	0.02405
At2g44010	215.492887	119.051	180.546922	139.013	133.867315	95.045	1.505760614	0.023667
At4g15490	191.831827	160.39	118.2327	118.2327	184.5229495	95.271	2.156380394	0.023187
At5g20050	238.968901	130.655	181.415303	139.823	325.610326	156.765	1.734510329	0.022914
At2g43840	204.050616	123.849	149.302706	130.509	288.320719	130.916	1.664637551	0.02128
At1g35290	307.70809	191.945	209.687901	132.043	119.522621	70.289	1.630526173	0.019684
At1g53940	280.260759	133.49	145.134473	108.856	164.837173	61.815	2.033126681	0.019536
At4g10160	511.843202	400.304	317.652729	273.187	212.320852	64.378	1.913151218	0.01887
At1g66760	281.051172	143.285	164.868249	141.866	236.370947	143.964	1.588499873	0.015708
At1g47320	129.178507	92.626	91.4907886	60.552	119.007144	59.386	1.63651002	0.014664
At1g33090	152.404241	130.642	199.527038	179.303	173.979673	60.843	1.712952935	0.01386
At3g06080	274.671181	162.311	109.130888	53.519	316.193592	209.634	1.746556824	0.01326
At1g16490	85.8514021	71.223	106.635959	63.672	345.426766	192.774	1.571352196	0.012546
At3g56230	127.103588	101.428	149.549677	100.548	202.529642	100.038	1.592894654	0.010759
At3g60140	163.883947	109.178	270.11293	182.171	375.652833	15.071	9.303118767	0.010248
At1g19530	132.099505	61.514	58.1736101	40.551	420.62932	72.298	3.133347384	0.01005
At4g19280	86.6159987	58.634	97.5152866	63.312	248.216609	95.777	1.869691751	0.009776
At4g30790	137.501909	84.735	152.744366	135.939	117.297822	43.269	1.819083461	0.008526
At1g18810	183.998299	142.503	1008.25175	56.505	78.2555943	64.938	6.779951779	0.008432
At5g17300	96.4047125	65.593	198.014938	89.288	110.21723	54.052	1.908849215	0.008424
At1g10070	151.817047	36.508	146.573278	33.886	1110.14776	71.997	7.96776554	0.008424
At1g59590	187.83485	94.422	135.980614	98.473	185.373777	158.312	1.513714745	0.00774
At2g40520	100.034836	43.817	100.980847	91.272	89.3239165	41.571	1.846031459	0.006663
At2g07670	120.879705	69.833	68.9804151	57.438	329.165055	195.317	1.574380394	0.006432
At5g59490	60.9783818	43.231	73.978757	80.86	163.723745	63.497	1.573325178	0.00598
At5g44575	199.579809	70.997	138.093411	83.727	163.888965	31.875	3.200679215	0.005883
At4g04630	69.4889583	51.703	76.4717678	62.846	845.693628	377.844	1.599674297	0.005625
At2g30430	98.0304604	81.705	109.309345	68.07	617.056898	257.673	1.733458562	0.00546
At4g30880	379.733001	254.416	104.695171	268.073	156.968932	44.475	2.184656396	0.005328
At1g72350	87.2716457	26.72	204.158938	142.159	1116.83041	429.967	2.433254901	0.004648
At1g65985	110.050299	65.886	146.372515	75.835	334.416735	138.344	2.005914144	0.0043
At1g08630	99.8883053	30.275	112.623536	59.297	640.486358	41.41	6.888542509	0.00414
At5g19850	122.308653	107.091	251.972515	215.736	192.209002	46.647	2.143522653	0.00363
At1g25540	228.661445	165.151	102.955021	59.584	1495.5926	928.896	1.574177453	0.003621
At5g73510	152.894335	121.988	110.201967	83.868	177.480793	94.295	1.60352526	0.003528
At1g49810	108.350751	90.053	183.023005	136.61	104.718122	9.024	4.715779561	0.002714
At3g19610	162.325582	137.48	168.856432	99.025	148.385209	90.139	1.51069782	0.002695
At3g48320	150.635171	89.772	89.7110044	48.133	85.4166008	71.3	1.57992624	0.00198
At5g54150	70.0365787	49.577	72.3991371	34.368	530.61759	301.602	1.759533013	0.00196
At1g35140	133.531661	52.713	83.4411288	48.618	135.613751	87.895	1.930783017	0.001848
At4g14990	144.702261	129.615	135.889793	115.168	2097.92953	744.454	1.704801785	0.00182
At2g34355	99.2112668	65.204	75.7611288	53.593	206.786691	94.714	1.706155061	0.00175
At5g54620</								

18395	29 xyloglucan fucosyltransferase, putative (FUT4) identical to SPIQ9SJ2 Probable fucosyltransferase 4 (EC 2.4.1.-) (AifUT4) (Arabidopsis thaliana); similar to SPIQ9SWH5 Galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) (Xyloglucan alpha-(1,2)-fucosyltransferase) (AifUT1) (Arabidopsis thaliana)	At2g15390	1133.21368	1555.81	1075.49637	1449.85	481.521499	1120.857	0.633258309	0.635008
17421	27 3-isopropylmalate dehydrogenase, chloroplast, putative, strong similarity to SPIP29102 3-isopropylmalate dehydrogenase, chloroplast precursor (Brassica napus)	At5g14200	1476.25291	1960.594	1084.7777	1594.785	505.536542	1272.971	0.610098799	0.63495
23354	36 pectinesterase family protein contains Pfam profile: PF01095 pectinesterase	At5g55590	1619.49949	1921.911	364.020847	651.356	566.655618	1229.065	0.620854301	0.6336
18990	30 AP2 domain-containing transcription factor, putative	At1g71130	1414.91979	2321.514	642.796881	1003.692	752.829416	1481.759	0.657713293	0.63063
29019	45 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to pEARLI 1 (Accession No. L43080): an Arabidopsis member of a conserved gene family (PGF95-099), Plant Physiol. 109 (4), 1497 (1995); contains Pfam protease inhibitor/seed storage/LTP family domain PF00234	At4g12500	1375.60842	2216.844	1760.79297	3688.234	1304.93827	1798.645	0.607815197	0.62118
16490	29 expressed protein contains Pfam profile PF04862: Protein of unknown function, DUF642	At3g08030	1116.28772	1547.955	857.604251	1180.465	421.532348	974.096	0.626792046	0.61776
6153	10 seven in absentia (SINA) family protein low similarity to SPIP21461 Developmental protein seven in absentia (Drosophila melanogaster); contains Pfam profile PF03145: Seven in absentia protein family	At3g13672	465.840953	544.613	482.844151	910.893	250.61667	444.479	0.649760963	0.61776
6624	11 aspartate aminotransferase, cytoplasmic isozyme 2 / transaminase A (ASP4) identical to aspartate aminotransferase, cytoplasmic isozyme 2 SP-P46646 [Arabidopsis thaliana]	At1g62800	474.876865	558.403	533.006342	1020.786	310.781063	644.018	0.620528426	0.613008
4419	7 sulfate transporter identical to sulfate transporter [Arabidopsis thaliana] GI:2114104	At5g10190	94.947621	695.219	847.366	385.244	1304.87429	135.84	0.612	0.55880441
17251	27 60S acidic ribosomal protein P2 (RPP2D) acidic ribosomal protein P2, maize, PIR-S54179	At3g44590	794.830887	1208.689	387.56435	617.719	710.500506	1235.704	0.620022855	0.604824
11400	18 expressed protein	At3g45160	587.668299	787.865	177.310805	340.514	356.235845	989.931	0.54215806	0.601524
5042	8 lipid transfer protein, putative similar to lipid transfer protein 6 from Arabidopsis thaliana [gi:8571927]; contains Pfam protease inhibitor/seed storage/LTP family domain PF00234	At5g01870	313.114771	523.68	384.653279	689.26	383.778812	703.904	0.567064714	0.598752
26134	41 glycosyl hydrolase family 1 protein contains Pfam PF00232: Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to beta-glucosidase 1 (GI:12043529) [Arabidopsis thaliana]	At1g66280	697.145308	840.614	303.892183	494.949	321.599915	670.335	0.641025182	0.598347
11824	19 aspartate aminotransferase, cytoplasmic isozyme 2 / transaminase A (ASP4) identical to aspartate aminotransferase, cytoplasmic isozyme 2 SP-P46646 [Arabidopsis thaliana]	At1g62800	596.458033	827.563	840.932915	1758.586	299.875652	752.502	0.532477366	0.595056
9572	15 expressed protein contains Pfam profile PF04862: Protein of unknown function, DUF642	At4g32460	342.853123	539.991	398.665296	651.109	513.540868	721.42	0.653019209	0.59211
23669	37 expressed protein	At2g46000	1097.70286	1435.249	1008.94487	2120.533	407.092806	865.308	0.570358262	0.588468
25092	39 expressed protein contains Pfam profile PF04396: Protein of unknown function, DUF537	At3g61100	2283.83891	3001.513	1880.64399	2961.003	1120.5439	2054.866	0.647115257	0.58608
18763	29 expressed protein	At5g36800	1323.03794	2477.41	1315.94729	2188.039	641.603912	1699.99	0.504294922	0.585316
13375	21 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed storage/LTP family domain PF00234	At3g53980	371.93155	1747.509	463.706159	3619.41	380.622046	1311.665	0.212220496	0.585174
12897	23 eukaryotic translation initiation factor 3 subunit 9 / eIF-3 eta / eIF3 (TIF3B1) nearly identical to SPIQ9CS21 Eukaryotic translation initiation factor 3 subunit 9 (eIF-3 eta) (eIF3 p110) (eIF3b) [Arabidopsis thaliana]	At5g27340	3927.36952	6253.568	3066.92711	4871.49	1643.12845	3905.036	0.595197708	0.58473
9216	15 nicotianamine synthase, putative similar to nicotianamine synthase [Lyocopersicon esculentum]GI:47538011, nicotianamine synthase 2 [Hordeum vulgare]GI:4894912	At1g56430	494.173889	915.084	503.299719	854.625	323.799997	736.022	0.522958859	0.582309
11507	18 GDSL-motif lipase/hydrolase family protein low similarity to family II lipases EXL3 GI:15054386, EXL1 GI:15054382 from [Arabidopsis thaliana]; contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase	At4g30140	1067.23399	1726.25	374.31874	972.999	180.91387	1015.806	0.393681134	0.581856
5022	8 peptidyl-prolyl cis-trans isomerase / cyclophilin (CYP1) / rotamase identical to cyclophilin (CYP1) gi 992643 gb AAV5512; similar to peptidyl-prolyl cis-trans isomerase, PPIase (cyclophilin, cyclosporin A-binding protein) [Catharanthus roseus] SWISS-PROT:Q39613	At4g34870	2204.44894	3128.739	2313.53946	3141.263	2847.46608	5394.925	0.656294993	0.578676
9277	15 plant defensin-fusion protein, putative (PDF2.1) plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be); contains a gamma-thionin family signature (PDOCO0725)	At2g02120	908.955662	1859.646	213.800366	672.713	657.994019	2998.762	0.342006284	0.5742
30329	47 drought-responsive protein / drought-induced protein (Di21) identical to GI:469112; contains Pf03242 Late embryogenesis abundant protein domain	At4g15910	1253.79177	2738.148	1572.84329	2381.044	290.64449	636.892	0.524938218	0.5733
4681	8 expressed protein	At1g67865	351.031063	635.47	186.729162	325.996	413.053782	1402.153	0.473259073	0.56848
10260	16 amino acid permease 2 (AAP2) identical to amine acid permease AAP2 [Arabidopsis thaliana] GI:510236	At5g09220	418.864325	589.08	396.139818	905.74	463.378771	897.368	0.554929877	0.5568
27815	43 expressed protein contains Pfam profile PF04654: Protein of unknown function, DUF599	At5g10580	539.729057	864.711	614.339188	1521.279	232.473941	544.776	0.493676743	0.55593
13352	21 GDSL-motif lipase, putative similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from [Arabidopsis thaliana]; contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase	At3g43570	808.171056	1092.098	854.790376	1499.623	241.880366	484.504	0.603059145	0.55593
13372	30 expressed protein	At5g15960	502.501569	742.333	688.623537	1030.969	331.242976	510.159	0.652304121	0.53341
18717	29 nuclear matrix protein-related low similarity to nuclear matrix protein p84 [Homo sapiens] GI:550058	At5g09860	2369.3051	3190.201	2178.33664	3150.468	1110.03684	2371.137	0.634006246	0.5544
11885	19 expressed protein	At2g07724	587.185922	728.83	661.682989	1217.21	277.50395	603.244	0.603093739	0.5544
29679	46 NLI interacting factor (NIF) family protein contains Pfam profile PF03031: NLI interacting factor	At4g18140	951.397309	1356.064	817.067554	1317.567	670.417015	1455.117	0.594150523	0.552188
24556	38 serine carboxypeptidase S10 family protein similar to Serine carboxypeptidase II chains A and B (SP-P08819) (EC 3.4.16.6) [Triticum aestivum (Wheat)]; carboxypeptidase D - Triticum aestivum, PIR-A29639	At5g08260	359.578005	574.992	483.094308	568.647	235.632784	483.467	0.654097837	0.544896
11452	18 kinesin-like protein A, putative kinesin like protein A, Arabidopsis thaliana, gb:Q07970	At4g05190	357.99397	555.141	205.734772	271.04	349.831559	637.589	0.650868666	0.543348
18582	29 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam profile: PF00234 protease inhibitor/seed storage/LTP family	At3g57310	1808.29053	2433.132	1164.49036	2419.208	873.539696	1603.555	0.589766141	0.53856
11196	18 thaumatin-like protein, putative / pathogenesis-related protein, putative strong similarity to SPIP05699 Thaumatin-like protein precursor [Arabidopsis thaliana], pathogenesis-related group 5 protein [Brassica rapa] GI:2749943; contains Pfam profile: PF00314 thaumatin family	At1g73620	743.990799	766.03	241.085079	696.227	250.864099	762.172	0.362205464	0.537342
3652	6 hypothetical protein	At4g07740	743.145418	909.828	698.061014	1530.925	515.225447	867.483	0.622234174	0.5248
20951	33 protease inhibitor, putative (DR4) identical to DR4 GI:469114 from [Arabidopsis thaliana]; contains Pfam profile PF00197: Trypsin and protease inhibitor	At1g73330	927.28597	1533.271	346.785461	567.672	585.418981	926.99	0.615731202	0.521985
13871	22 osmotin-like protein, putative similar to SPIQ41350 Osmotin-like protein precursor (Lyocopersicon esculentum); contains Pfam profile PF00314: Thaumatin family	At2g28790	543.733531	1105.398	473.787487	780.278	314.010031	725.105	0.510717277	0.521848
12897	20 glycosyl hydrolase family 1 protein contains Pfam PF00232: Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; identical to thioglucosidase (GI:871992) [Arabidopsis thaliana]; similar to myrosinase precursor (EC 3.2.3.1)(Sinigrinase) (Thioglucosidase) SPIP37702 from [Arabidopsis thaliana]	At5g25980	598.31055	1080.771	593.624716	4871.49	1643.12845	3905.036	0.595197708	0.52085
3108	5 hydroxyproline-rich glycoprotein family protein	At5g05860	1051.94982	1265.282	145.49298	648.969	444.458703	1246.374	0.470740814	0.51901
4177	7 prokaryotic nuclear pore complex protein	At3g02120	492.188765	701.509	392.898922	576.932	390.15217	681.096	0.6251819506	0.51448
29306	46 cell division control protein, putative cdc2Msf [Medicago sativa] gi 1806146 emb CAA65982	At1g20930	455.830838	713.948	378.692516	600.455	243.746392	482.075	0.591586735	0.511839
23745	37 phosphoenolpyruvate carboxylase-related / PEP carboxylase-related identical to phosphoenolpyruvate carboxylase [Arabidopsis thaliana] GP:26800701 over first 45 residues	At3g42628	978.856405	1397.72	544.480134	895.105	352.786273	904.453	0.566221615	0.51128
23775	37 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed storage/LTP family domain PF00234	At3g53980	289.973533	1284.963	305.750042	1803.251	263.229361	703.665	0.256435028	0.51051
20273	32 expressed protein	At1g64370	883.111618	1173.42	1276.21205	1971.714	627.853048	1280.71	0.630031167	0.510048
9619	15 inositol-3-phosphate synthase, putative / myo-inositol-1-phosphate synthase, putative / MI-1-P synthase, putative very strong similarity to SPIQ38862 Myo-inositol-1-phosphate synthase isozyme 2 (EC 5.5.1.4) (MI-1-P synthase 2) (IPS 2) [Arabidopsis thaliana]; identical to SPI QNLX12 Probable inositol-3-phosphate synth [Arabidopsis thaliana]	At5g10170	291.392854	425.977	282.275055	396.159	272.821357	507.596	0.644688259	0.503644
14054	22 hypothetical protein weak similarity to SPIQ13200 26 proteasome non-ATPase regulatory subunit S2 (26S proteasome subunit p97) (Tumor necrosis factor type 1 receptor associated protein 2) (Homo sapiens)	At4g08140	361.339588	553.448	505.884151	750.272	247.552674	549.457	0.592256533	0.50184
8667	14 expressed protein contains similarity to anther-specific protein GI:1448935 from [Brassica rapa]	At2g28355	375.209785	507.529	286.354059	477.929	351.926457	573.296	0.650769545	0.495936
23595	37 xyloglucan fucosyltransferase, putative (FUT4) identical to SPIQ9SJ2 Probable fucosyltransferase 4 (EC 2.4.1.-) (AifUT4) (Arabidopsis thaliana); similar to SPIQ9SWH5 Galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) (Xyloglucan alpha-(1,2)-fucosyltransferase) (AifUT1) [Arabidopsis thaliana]	At2g15390	586.769859	861.373	640.0324	932.297	343.761302	817.683	0.59604109	0.487078
18717	29 nuclear matrix protein-related low similarity to nuclear matrix protein p84 [Homo sapiens] GI:550058	At5g10220	470.345986	920.834	560.561927	870.642	233.106947	417.703	0.634006246	0.48552
22637	35 chaperonin, putative similar to SWISS-PROT:P78371- T-complex protein 1, beta subunit (TCP-1-beta) [Homo sapiens]; contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family	At5g20890	433.034002	647.133	484.149113	734.535	209.906358	513.743	0.57895445	0.48074
6762	11 glycosyl hydrolase family protein 17 similar to endo-1,3-beta-glucosidase precursor SP-P52409 from [Triticum aestivum]; C terminal homology only	At2g43660	616.220497	847.724	614.6884	910.958	363.55768	888.53	0.603616897	0.472857
13442	21 pectate lyase family protein similar to pectate lyase 2 GP:6606534 from [Musa acuminata]	At4g22090	572.25899	763.364	483.608964	669.344	173.268315	446.826	0.6199806	0.4698
19305	30 beta-expansin, putative (XPB3) similar to soybean pollen allergen (cim1) protein - soybean, PIR2:S48032; beta-expansin gene family, PMID:11641069	At4g28250	624.878674	788.971	642.208931	911.365	177.010678	455.978	0.62829874	0.463884
27422	43 flavin-containing monooxygenase family protein / FMO family protein similar to flavin-containing monooxygenase GB:AAA21178 GI:349534 SPIP32417 from [Oryctolagus cuniculus]; contains Pfam profile PF00743 Flavin-binding monooxygenase-like	At1g62560	511.252799	862.439	506.408366	1058.972	201.718522	405.229	0.522931755	0.446959
21199	33 meprin and TRAF homology domain-containing protein / MATH domain-containing protein weak similarity to ubiquitin-specific protease 12 [Arabidopsis thaliana] GI:11993471; contains Pfam profile PF00917: MATH domain	At4g01390	516.512949	878.815	532.496466	906.883	216.556012	471.764	0.54464826	0.4437
26713	42 ubiquitin extension protein, putative / 40S ribosomal protein S27A (RPS27aA) strong similarity to ubiquitin extension protein (UBQ5) GB:AAA32906 GI:166934 from (Arabidopsis thaliana)	At1g23410	377.971417	590.929	412.843022	686.467	155.824573	376.35	0.551688869	0.442953
18575	29 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed storage/LTP family domain PF00234	At3g53980	331.807663	1741.057	301.812847	2860.952	214.056979	728.039	0.196696901	0.431172
20098	31 expressed protein system 1; expression supported by MPSS	At5g05730	456.323911	656.154	454.201893	715.897	194.404934	353.037	0.626856128	0.430582
15183	24 glycine cleavage system H protein, mitochondrial, putative similar to SPIQ39732 Glycine cleavage system H protein, mitochondrial precursor (Flaveria anomala); contains Pfam profile PF01597: Glycine cleavage H-protein	At2g35120	258.833077	409.671	633.62083	1137.631	311.855937	402.629	0.629612529	0.42987
27149	42 phenylalanine ammonia-lyase 3 (PAL3) nearly identical to SPIP45725	At5g04230	339.548149	439.663	343.687968	538.039	687.935448	975.996	0.656957708	0.4284
29188	45 senescence-associated protein-related similar to senescence-associated protein SAC102 (GI:22331931) [Arabidopsis thaliana];	At5g47060	165.309685	315.566	215.851021	434.021	187.198565	229.833	0.611892701	0.42484
28135	44 Ulp1 protease family protein contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain; similar to At5g28270, At2g05450, At1g45090, At2g16180, At2g06750	At2g12100	373.587927	997.279	230.927403	353.465	31			

15014	24 lysine and histidine specific transporter, putative similar to lysine and histidine specific transporter GI:2576361 from [Arabidopsis thaliana]; contains Pfam profile PF01490: Transmembrane amino acid transporter protein	At1g24400	79.9889368	124.85	109.275884	180.913	59.0262403	128.955	0.567477412	0.00966
9912	16 phosphoglycerate/bisphosphoglycerate mutase family protein similar to SPIP31217 Phosphoglycerate mutase 1 (EC 5.4.2.1) [Escherichia coli O157:H7]; contains Pfam profile PF00300: phosphoglycerate mutase family	At1g78050	50.6559521	69.412	31.3621246	132.688	43.0773819	84.601	0.491776492	0.0096
15551	24 actin-related protein, putative (ARPB) strong similarity to actin-related protein 8A (ARPB) [Arabidopsis thaliana] GI:21427473; contains Pfam profile PF00022: Actin; supporting cDNA gi 21427470 gb AF507916.1	At5g56180	218.014935	272.876	243.280731	273.006	35.1885219	144.774	0.64437644	0.00957
15316	24 pectate lyase family protein similar to pectate lyase 2 GP:6606534 from [Musa acuminata]	At3g53190	77.8604905	133.296	160.789245	260.618	53.205474	159.786	0.511350176	0.009177
6986	11 zinc finger protein-related similar to lateral root primordium 1 (LRP1) [Arabidopsis thaliana] GI:882341; contains Pfam profile PF05142: Domain of unknown function (DUF702), TIGR01624: LRP1 C-terminal domain, TIGR01623: putative zinc finger domain, LRP1 type	At4g36260	57.8862521	68.025	35.5112366	106.854	32.7039228	71.288	0.547349166	0.009072
6646	11 disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.	At1g72860	39.2853428	70.368	67.2031869	94.542	46.4053014	80.171	0.615980712	0.008892
7086	11 forkhead-associated domain-containing protein / FHA domain-containing protein	At5g47790	59.9344806	93.966	66.0591537	94.096	40.9041309	98.363	0.585240097	0.00884
24599	38 kinesin motor protein-related non-consensus AT donor splice site at exon 12, non-consensus AC acceptor splice site at exon 13	At5g27000	125.652132	157.286	133.115751	188.077	23.5308984	68.363	0.615391224	0.008184
1896	10 leucine-rich repeat family protein similar to recessor from [Petunia integrifolia]; contains protein kinase domain, Pfam:PF00069; contains leucine-rich repeats, Pfam:PF00560	At1g16080	38.9353244	175.229	107.623572	175.229	30.4293572	90.182	0.581609332	0.008162
22923	36 methyladenine glycosylase family protein similar to SPIJ05100 DNA-3-methyladenine glycosylase I (EC 3.2.2.20) (3-methyladenine-DNA glycosylase I, constitutive) [Escherichia coli]; contains Pfam profile PF03352: Methyladenine glycosylase	At1g90850	149.813731	197.331	227.809196	309.33	30.3966477	113.401	0.57564136	0.007808
20847	33 cyclin, putative similar to cyclin A2 [Lycopersicon esculentum] GI:5420276, cyclin [Medicago sativa] GI:1050559; contains Pfam profiles PF01034: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain	At1g15570	196.372336	322.28	201.053478	293.256	44.7805179	122.918	0.553075792	0.007626
7535	12 basic helix-loop-helix (bHLH) protein, putative very strong similarity to PIF3 like basic Helix Loop Helix Protein 2 (PIL2) [Arabidopsis thaliana] GI:22535494	At3g62090	36.2969615	81.652	53.4604483	70.28	94.2271337	130.192	0.642988525	0.00759
30366	47 WRKY family transcription factor identical to WRKY DNA-binding protein 18 (WRKY18) GI:13506730 from [Arabidopsis thaliana]	At4g31805	189.944044	295.707	93.2689795	143.731	53.9848753	92.271	0.625440282	0.007524
14799	23 ankyrin repeat family protein contains ankyrin repeat domains, Pfam:PF00023	At5g02620	181.266615	255.695	163.961627	192.828	27.8563771	85.679	0.62811404	0.007473
22358	35 ribonuclease P family-related similar to Ribonuclease P protein subunit p29 (EC 3.1.26.5) (hPOP4) (Swiss-Prot:O95707) [Homo sapiens]	At2g43190	126.569823	140.725	126.13683	158.733	24.1552522	90.262	0.653890981	0.00708
15811	25 transport protein-related contains Pfam PF05911: Plant protein of unknown function (DUF869) profile; weak similarity to Intracellular protein transport protein USO1 (Swiss-Prot:P25386) [Saccharomyces cerevisiae]	At2g23360	61.7890248	138.126	119.80322	142.906	41.9598278	94.608	0.624660583	0.006837
9034	14 CHP-rich zinc finger protein, putative contains similarity to CHP-rich zinc finger protein	At5g46660	308.289936	367.956	71.0925811	97.676	65.8408463	293.528	0.596664657	0.006624
20139	31 expressed protein	At5g67350	147.682085	304.365	113.753229	160.95	19.4458543	83.513	0.474941091	0.0066
19550	31 prenylated rab acceptor (PRA1) family protein weak similarity to prenylated Rab acceptor 1 (PRA1) [Homo sapiens] GI:4877285; contains Pfam profile PF03208: Prenyated rab acceptor (PRA1)	At1g17700	102.59432	140.242	101.772747	136.596	39.1453234	99.276	0.623941315	0.00648
11733	19 expressed protein contains Pfam profile PF04520: Protein of unknown function, DUF584	At1g10700	101.31113	173.516	78.4570956	145.586	63.5946163	76.657	0.548494932	0.006394
25327	39 amino acid transporter 4, putative (AAP4) identical to amino acid transporter GI:608671 from [Arabidopsis thaliana];	At5g63850	123.441328	154.909	101.857195	192.899	21.8500391	72.649	0.54188635	0.006272
24835	39 cytochrome P450 family protein similar to Cytochrome P450 90A1 (SP:Q42569) [Arabidopsis thaliana]	At1g65670	802.646722	1019.197	286.115055	343.317	32.7781515	92.183	0.65882999	0.00616
27444	43 CLE26, putative CLAVATA3/ESR-Related 26 (CLE26)	At1g69970	122.09046	154.473	88.0507222	113.509	23.7222515	89.903	0.609982792	0.006138
20711	32 calmodulin-binding protein-related has weak similarity to calmodulin-binding proteins	At5g39380	325.092897	410.248	279.994955	391.366	20.5943371	54.865	0.627741321	0.00568
27431	43 zinc finger (C2H2 type) family protein contains Pfam domain, PF00096: Zinc finger, C2H2 type	At1g66140	125.098094	261.386	107.68093	149.955	27.7759627	89.86	0.50192872	0.005544
20201	32 cyclin, putative similar to SPIQ40671 G2/mitotic-specific cyclin 2 (B-like cyclin) (CYCOS2) [Oryza sativa]; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain	At1g20590	96.5940266	159.653	65.1620915	105.929	27.633691	108.108	0.491928486	0.005376
21036	33 DNA-binding family protein / AT-hook protein 1 (AHP1) identical to AT-hook protein 1 [Arabidopsis thaliana] gi 2598227 emb CAA10857	At2g33620	192.761294	312.447	236.687403	260.438	36.8751627	128.085	0.604547327	0.005368
24733	39 expressed protein similar to hypothetical protein GB:AA071979	At1g10820	182.862415	238.826	220.030407	275.344	22.7572786	90.837	0.605103944	0.005313
20760	38 haloacid dehalogenase-like hydrolase family protein low similarity to SPIP53078 SSM1 protein [Saccharomyces cerevisiae]; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase	At5g59480	262.895204	346.488	346.183171	404.445	23.9676186	68.945	0.65410757	0.005293
23382	36 ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023	At5g65860	185.876466	274.115	275.020482	404.686	38.4629572	97.739	0.587149377	0.005106
7061	11 pentapeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat	At5g37570	42.5111618	72.455	57.2462076	92.419	40.3901058	65.513	0.60166881	0.005096
15521	24 cysteine proteinase, putative / thiol protease, putative similar to cysteine proteinase RD21A precursor (thiol protease) GI:435619, SP:P43297 from [Arabidopsis thaliana]	At5g43060	79.0017228	120.664	164.34244	189.231	25.281054	105.357	0.58718741	0.005088
24986	39 C2 domain-containing protein similar to cold-regulated gene SRC2 [glycine max] GI:2055230; contains Pfam profile PF00168: C2 domain	At3g05440	178.776654	203.739	194.783602	248.09	29.3966224	101.694	0.650560338	0.00507
26990	42 hypothetical protein similar to At2g04970, At2g15200, At1g32830, At2g14140, At4g03990, At5g34895, At3g47270, At2g02200	At3g30450	64.3368348	114.247	126.038042	140.773	20.8087755	79.606	0.573287793	0.00504
2363	4 high mobility group (HMG1/2) family protein similar to SPIP40618 High mobility group protein HMG2A (Gallus gallus); contains Pfam profile PF00505: HMG (high mobility group) box	At4g11080	103.325906	143.882	73.7327803	117.464	25.6439498	142.706	0.508510865	0.005031
18663	29 auxin-responsive AUX/IAA family protein similar to SPIQ38826 Auxin-responsive protein IAA8, SPIQ38827 Auxin-responsive protein IAA9 from Arabidopsis thaliana; contains Pfam profile: PF02309: AUX/IAA family	At4g29080	115.670895	162.14	105.110838	167.446	23.5366798	92.202	0.532134701	0.005016
25960	40 haloacid dehalogenase-like hydrolase family protein low similarity to SPIP53078 SSM1 protein [Saccharomyces cerevisiae]; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase	At5g59480	129.180646	172.087	245.904996	346.369	25.5367306	80.417	0.59272513	0.00494
30011	47 mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein contains Pfam profile PF00924: Mechanosensitive ion channel	At1g53470	283.186035	401.892	269.716183	322.129	11.4394656	43.385	0.629186596	0.00494
22962	36 expressed protein	At2g24440	135.023713	208.671	137.717378	194.72	34.6984897	65.44	0.628192666	0.004872
2463	4 transducin family protein / WD-40 repeat family protein contains 3 WD-40 repeats (PF00400); similar to uncharacterized protein KIAA0007 (GI:1663708) [Homo sapiens] 1.2e-11	At5g11240	57.4263366	124.309	64.9995686	75.55	79.6638775	154.377	0.612783576	0.004805
21730	14 adenylylsulfate kinase, putative similar to adenylylsulfate kinase 1, chloroplast precursor (APS kinase, Adenosine-5-phosphosulfate kinase, ATP adenosine-5'-phosphosulfate 3'-phosphotransferase) [Arabidopsis thaliana] SWISS-PROT:Q43295	At3g03900	59.8842107	98.485	131.3237946	186.433	31.5946163	76.767	0.60441433	0.004416
22701	35 expressed protein contains Pfam profile PF04398: Protein of unknown function, DUF538	At5g54530	81.8564078	105.377	131.490523	180.974	22.4521162	75.119	0.600751477	0.004408
7058	11 Ca+2-binding EF hand family protein contains similarity to Ca+2-binding EF hand protein GI:2270994 from [Glycine max]	At5g29560	71.500021	95.781	46.5309213	85.886	38.8607801	71.917	0.608323939	0.004257
27038	42 F-box family protein contains Pfam:PF00646 F-box domain	At3g62230	91.6354954	122.597	85.6638674	95.638	25.281054	86.672	0.644949681	0.00392
20583	32 kinesin-like protein A (KATA)	At4g21270	125.689566	174.488	121.14483	153.67	22.2933493	86.445	0.588856064	0.00384
14055	22 nodulin MtN21 family protein similar to MtN21 GI:2598575 (root nodule development) from [Medicago truncatula]	At4g08290	66.2096536	127.699	117.433892	156.295	60.848967	107.367	0.612193586	0.003726
7068	11 disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.	At5g38340	78.6380686	99.189	35.7789213	92.375	43.1928488	90.951	0.551678448	0.003696
23168	36 F-box family protein contains F-box domain Pfam:PF00646	At4g14096	100.558926	142.611	162.61205	209.609	77.0473162	166.633	0.647764085	0.003572
25933	40 basic helix-loop-helix (bHLH) family protein contains similarity to bHLH DNA-binding protein	At5g46690	90.1241916	135.31	164.068382	279.85	32.8008325	65.418	0.58457834	0.0031
15639	25 expressed protein	At1g12180	90.9712918	119.688	88.5159836	114.194	26.1078791	81.118	0.619019271	0.003034
18015	28 dem protein-related / defective embryo and meristems protein-related identical to dem GI:2190419 from [Lycopersicon esculentum]	At4g33400	69.6269411	108.459	75.077577	113.68	31.4131684	75.178	0.634881907	0.002944
2283	11 WD-40 repeat family protein / mitotic checkpoint protein, putative contains 5 WD-40 repeats (PF00400) (1 weak); similar to testis mitotic checkpoint protein BUB3 (GB:AA02849,SP O43684) [Homo sapiens]	At3g19590	73.3447618	110.963	67.2462076	78.134	32.5101034	90.93	0.577520924	0.002904
3822	6 leucine-rich repeat transmembrane protein kinase, putative	At5g43020	57.779295	91.091	88.6769131	118.423	31.153368	78.615	0.593313871	0.00285
25932	40 AWPM-19-like membrane family protein similar to AWPM-19 [Triticum aestivum] GI:1724112; contains Pfam profile PF05512: AWPM-19-like family	At5g46530	92.706136	118.248	169.696133	192.654	20.955171	72.565	0.65120304	0.002784
19862	31 leucine-rich repeat transmembrane protein kinase, putative receptor-like protein kinase (RKL1), Arabidopsis thaliana, EMBL:AF084034	At3g50230	126.701381	143.361	97.389411	131.103	18.7303723	80.375	0.619892123	0.002728
24152	38 caldesmon-related weak similarity to Caldesmon (CDM) (Swiss-Prot:P12957) [Gallus gallus]	At1g52410	91.1606059	126.087	152.965843	179.606	4.73001695	34.048	0.571198046	0.002684
20682	32 calcium-dependent protein kinase 19 (CDPK19) identical to calcium-dependent protein kinase [Arabidopsis thaliana] gi 839642 gb AAA67655	At5g19450	84.1025069	107.181	175.825793	205.765	18.309743	57.306	0.652894584	0.002684
24819	39 expressed protein contains Pfam domain, PF04678: Protein of unknown function, DUF607	At1g57610	103.99118	140.678	125.011917	141.322	13.1529111	66.203	0.607492968	0.002655
7094	11 expressed protein	At5g51180	34.1171758	85.291	35.0396018	78.703	38.3514888	75.338	0.451427053	0.002576
6607	11 ubiquitin family protein contains Pfam profile: PF00240 ubiquitin family	At1g53930	48.1659908	92.07	38.2151702	59.955	30.367781	91.055	0.498017731	0.002508
16592	29 expressed protein	At3g09900	127.294993	186.843	132.612249	162.047	29.5698262	69.099	0.642528225	0.002394
27384	43 light stress-responsive one-helix protein (OHP2) contains similarity to photosystem II 22 kDa protein GI:6006279 from [Arabidopsis thaliana]	At1g34000	93.697014	103.751	82.219317	117.879	33.9404038	70.02	0.642892727	0.002334
27294	42 hypothetical protein / F-box domain Pfam:PF00646	At1g51500	83.607295	102.946	94.3190044	112.142	34.4031663	19.203	0.628412514	0.002322
6775	11 hypothetical protein	At3g02880	43.9401158	74.987	67.2210292	98.527	27.4151288	63.442	0.586477841	0.002268
3085	5 nucleotide-sugar transporter family protein similar to SPIQ77592 UDP N-acetylglucosamine transporter (Golgi) UDP-GlcNAc transporter (Canis familiaris), SPIP78382 CMP-sialic acid transporter (Homo sapiens); contains Pfam profile PF04142: Nucleotide-sugar transporter	At4g35335	71.5724826	99.48	56.9360167	96.265	43.1309915	94.654	0.587823515	0.00221
15868	25 hypothetical protein and genefinder; expression supported by MPSS	At2g46640	51.6474444	99.8	69.6697097	81.175	53.2322788	99.154	0.637546574	0.002187
30564	48 zinc finger (C3HC4-type RING finger) family protein / BRCT domain-containing protein contains Pfam domain, PF00533: BRCA1 C Terminus (BRCT) domain	At1g04020	110.959435	158.139	140.351204	174.793	9.59900549	72.96	0.545210451	0.002162
6829	11 F-box family protein contains F-box domain Pfam:PF00646	At3g25750	57.734373	69.535	81.6661247	106.345	19.6025594	62.676	0.636996071	0.00216
30683	48 glycosyl transferase family 20 protein / trehalose-phosphatase family protein similar to SPIQ00764 Alpha, alpha-trehalose-phosphate synthase [UDP-forming] 56 kDa subunit (EC 2.4.									

19572	31 phosphoribulokinase/uridine kinase family protein weak similarity to SP Q59190 Uridine kinase (EC 2.7.1.48) (Uridine monophosphokinase) (Cytidine monophosphokinase) (Borrelia burgdorferi); contains Pfam profile PF00485: Phosphoribulokinase / Uridine kinase family	At1g26190	130.854525	221.497	50.9891454	99.945	28.3223683	64.703	0.512891409	0.000473
1322	3 jacalin lectin family protein similar to gi:6503088 (GB:AAF4583) from [Arabidopsis thaliana] [Proc. Natl. Acad. Sci. U.S.A. 97 (1), 489-494 (2000)]; contains Pfam profile PF01419 jacalin-like lectin domain	At1g05770	65.7957296	75.463	57.2367138	111.566	80.1937878	151.905	0.637614881	0.000468
22249	35 sugar transporter family protein contains Pfam profile: PF00083 sugar (and other) transporter	At1g73220	50.2816023	79.005	53.4445147	87.116	15.6601913	25.396	0.622187518	0.000442
30183	47 sugar transporter family protein similar to sugar-porter family proteins 1 and 2 [Arabidopsis thaliana] GI:14585699, GI:14585701; contains Pfam profile PF00083: major facilitator superfamily protein	At3g05150	97.0806814	134.96	50.9190375	83.503	42.2258139	105.971	0.575860655	0.00044
22590	35 expressed protein : expression supported by MPSS	At4g39190	1331.23277	1890.812	74.6346226	120.965	42.1495233	83.424	0.608764655	0.000416
24146	38 endo-1,4-beta-glucanase, putative / cellulase, putative similar to endo-beta-1,4-glucanase GI:4972236 from [Fragaria x ananassa]	At1g48930	61.5837559	90.776	118.891818	153.895	24.3800002	63.877	0.610879035	0.000396
20076	31 myb family transcription factor contains Pfam profile: PF00249 Myb DNA binding domain	At5g41020	60.0767335	84.099	69.029213	119.892	43.2402727	97.542	0.577983081	0.000396
14607	23 phosphoesterase identical to phosphoesterase [Arabidopsis thaliana] GI:21630064; contains Pfam profile PF00645: Poly(ADP-ribose) polymerase and DNA-Ligase Zn-finger region	At3g14890	66.1486881	93.211	75.214606	90.754	13.1013634	59.825	0.58581162	0.00039
6941	11 WD-40 repeat family protein contains 6 WD-40 repeats (PF00400); similar to fizzy-related protein (GI:5813253) Drosophila melanogaster, PID:gd236419;	At4g22310	31.3232807	63.204	39.992127	63.22586	17.14241	69.812	0.5003384	0.000384
17856	28 expressed protein	At3g16330	46.3883638	69.609	59.5040065	92.001	46.8609831	84.856	0.621810285	0.000378
6790	11 protein phosphatase 2C family protein / PP2C family protein similar to protein phosphatase-2c (GI:3680412) [Mesembryanthemum crystallinum]; contains Pfam PF00481 : Protein phosphatase 2C domain	At3g09400	46.3498593	63.417	29.1186723	76.937	24.4480432	51.104	0.529248812	0.000368
21360	33 hypothetical protein	At5g32070	188.998544	268.017	153.035951	209.812	37.4360016	90.756	0.615686657	0.000336
6341	10 serine/threonine protein kinase, putative similar to serine-threonine protein kinase [Triticum aestivum] gi 2055374 gb AAB58348	At4g40010	19.8758379	60.797	57.6286806	81.769	11.161108	49.549	0.418983166	0.000322
18281	29 late embryogenesis abundant group 1 domain-containing protein / LEA group 1 domain-containing protein contains Pfam domain, PF03760: Late embryogenesis abundant (LEA) group 1	At1g32560	78.8402176	108.119	106.16883	157.665	27.7285388	64.873	0.61000298	0.000312
28299	44 SIT4 phosphatase-associated family protein contains Pfam profile: PF04499 SIT4 phosphatase-associated protein	At3g45190	37.1611748	64.892	46.07522	78.24	48.5599553	80.562	0.588107786	0.0003
19528	31 LOB domain protein 1 / lateral organ boundaries domain protein 1 (LBD1) identical to SP Q9LQR0 LOB domain protein 1 (Arabidopsis thaliana)	At1g07900	79.0092098	90.462	103.914224	148.447	24.4315479	70.164	0.640537303	0.00028
23331	36 NLI interacting factor (NIF) family protein contains Pfam profile PF03031: NLI interacting factor	At5g45700	85.1752866	180.082	78.2451786	184.547	51.0734612	222.721	0.375427182	0.00027
3015	5 beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructofuranosidase, putative similar to neutral invertase [Daucus carota] GI:4200165; contains Pfam profile PF04853: Plant neutral invertase	At4g09510	120.682905	134.51	55.4505562	88.842	14.0560268	69.735	0.574305133	0.000261
10020	16 vacuolar ATP synthase subunit G 1 (VATG1) / V-ATPase G subunit 1 (VAG1) / vacuolar proton pump G subunit 1 (VMA10) identical to SWISS-PROT:O62628 vacuolar ATP synthase subunit G 1 (V-ATPase G subunit 1, Vacuolar proton pump G subunit 1) [Arabidopsis thaliana]	At3g01390	42.6191956	63.733	20.5289631	67.786	40.8649547	96.573	0.464904662	0.00026
17209	27 DNA-binding protein similar to viroid symptom modulation protein [Lycopersicon esculentum] gi 72777 gb AAF66537	At3g12890	43.7398669	94.823	73.157577	122.736	14.4456942	76.076	0.417433352	0.000258
10311	16 pollen specific phosphatase, putative / phosphatase and tensin, putative (PTEN1) identical to phosphatase and tensin homolog [Arabidopsis thaliana] GI:21535746	At5g39400	35.8819679	51.163	68.0795354	79.868	31.3286302	100.918	0.621387894	0.00024
2942	5 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat	At3g28660	108.85131	136.284	39.8929794	65.025	20.7860945	53.569	0.600078753	0.00021
10207	16 expressed protein	At4g31010	41.050135	46.043	45.1893113	67.592	15.5674054	51.527	0.620747401	0.000208
21355	33 SSXT protein-related / glycine-rich protein contains weak hit to Pfam profile PF05030: SSXT protein (N-terminal region)	At5g28640	96.622905	220.242	100.915519	160.835	37.1432107	113.959	0.4640316	0.000204
31148	48 seed maturation family protein similar to SP P09444 Late embryogenesis abundant protein D-34 (LEA D-34) (Gossypium hirsutum); contains Pfam profile PF04927: Seed maturation protein	At5g53270	44.8567382	70.279	195.424133	226.64	37.6958021	87.878	0.643163137	0.000201
18615	29 glycosyltransferase family protein contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase	At4g09500	68.6589712	110.189	67.8915188	95.391	14.9117187	34.444	0.589248866	0.0002
24353	38 protein kinase family protein contains protein kinase domain, Pfam:PF00069	At3g14370	39.0970983	89.679	112.425959	129.639	36.5328859	58.28	0.6433472	0.000188
1744	3 protein kinase family protein contains Pfam domain, PF00069: Protein kinase domain	At4g23210	88.1893377	111.423	89.9611621	122.058	30.8255246	90.264	0.623340871	0.000177
23535	36 expressed protein	At5g55540	88.2588598	111.602	98.5382243	113.137	24.2872143	86.168	0.647886141	0.000174
23279	19 expressed protein similar to p53 inducible protein [Homo sapiens] GI:5616320	At5g18410	35.3581832	108.986	111.164017	138.419	5.36714852	63.209	0.554969711	0.000168
30523	47 regulator of chromosome condensation (RCC1) family protein similar to UVB-resistance protein UVR8 [Arabidopsis thaliana] GI:5478530; contains Pfam profile PF00415: Regulator of chromosome condensation (RCC1)	At5g68070	56.2262774	71.086	60.978757	84.985	2.5590816	57.944	0.697270284	0.00016
4404	7 lectin protein kinase family protein contains Pfam domains, PF00138: Legume lectins beta domain and PF00069: Protein kinase domain	At5g03140	75.5512867	100.48	64.4989591	94.557	90.455904	192.138	0.634762607	0.000161
5249	9 actin-related protein 4 (ARP4) nearby identical to actin-related protein 4 (ARP4) [Arabidopsis thaliana] GI:21427463; contains Pfam profile PF00022: Actin; supporting cDNA gi 21427462 gb AF507912.1	At1g18450	211.737623	239.18	53.5162159	89.589	37.2174394	99.917	0.618366946	0.000142
7043	11 harpin-induced family protein / HIN1 family protein / harpin-responsive family protein similar to harpin-induced protein hin1 (GI:1619321) [Nicotiana tabacum]	At5g22200	34.0005925	65.473	28.6964316	47.536	37.9349834	53.296	0.611588048	0.00013
10352	16 expressed protein	At5g56250	29.7971785	57.733	39.9248466	74.238	29.4667272	64.974	0.502477116	0.000126
5273	9 acetyltransferase-related low similarity to O-acetyltransferase [Cryptococcus neoformans var. neoformans] GI:17063556	At1g29890	158.145698	231.217	43.8317677	60.066	54.4096283	97.708	0.656852387	0.000126
23003	36 basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	At2g41130	70.8612179	110.931	64.714357	150.526	14.208608	39.935	0.474833751	0.000114
6506	11 D-3-phosphoglycerate dehydrogenase / 3-PGDH identical to SP O04130	At1g17745	48.9382211	57.754	33.6772781	64.38	19.656169	33.029	0.655192149	0.00011
27740	43 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat	At4g20090	29.8923703	62.525	39.9583072	69.227	187.80889	229.648	0.657067968	0.000114
19519	31 ribonuclease P family protein / Rpp14 family protein contains Pfam profile: PF01900 Rpp14 family	At1g04635	91.6900435	110.938	43.6596848	116.766	39.2051187	68.195	0.591767617	0.000112
30349	47 DNA-binding protein-related contains Pfam domain PF03479: Domain of unknown function (DUF296), found in AT-hook motifs Pfam:PF02178	At4g25320	109.070572	194.864	53.538582	67.863	21.9139582	69.541	0.554781742	0.000111
1623	3 expressed protein	At3g22415	65.2224396	98.927	37.7499088	87.185	24.2934001	114.724	0.434686004	0.000106
11940	19 expressed protein contains Pfam profile: PF05097 protein of unknown function (DUF688)	At2g34170	73.1800478	88.422	41.2776101	97.169	23.9098852	84.845	0.511410509	0.000105
6514	11 glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein similar to polygalacturonase PG1 GI:5669846, PG2 GI:5669848 from (Glycine max); contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)	At1g02460	38.172989	48.435	63.2245645	96.482	20.2025746	52.579	0.609220008	0.000104
20009	31 expressed protein similar to unknown protein (sp G3E2E8)	At5g06180	55.632666	80.142	69.860913	89.787	13.1632207	61.169	0.652481427	0.000102
13899	22 apurinic endonuclease-redox protein / DNA-(apurinic or apyrimidinic site) lyase identical to apurinic endonuclease-redox protein SP: P45951 from [Arabidopsis thaliana]	At2g41460	70.1210748	103.539	65.4664234	83.227	25.4109542	99.42	0.573145291	0.0001
6581	11 protein kinase family protein contains Pfam domain, PF00069: Protein kinase domain	At1g33770	26.5863263	56.038	32.8710374	70.314	13.1920874	51.652	0.39910878	0.000099
30888	48 hypothetical protein	At3g32394	51.5779223	97.756	50.2869599	102.97	15.8931869	35.019	0.489951683	0.000084
12078	19 leucine-rich repeat transmembrane protein kinase, putative several receptor-like protein kinases	At3g57830	77.9781433	114.894	33.231137	85.009	19.7798834	50.622	0.486782152	0.00008
15592	24 clathrin adaptor complex medium subunit family protein contains Pfam profile: PF00928 adaptor complexes medium subunit family	At4g24550	65.2716398	99.627	114.591326	139.145	38.3370554	79.929	0.652779345	0.00008
28377	44 farnesyl pyrophosphate synthetase 2 (FPS2) / FPP synthetase 2 / farnesyl diphosphate synthase 2 identical to SP Q43315 Farnesyl pyrophosphate synthetase 2 (FPP synthetase 2) [Includes: Dimethylallyltransferase (EC 2.5.1.1); Geranyltransferase (EC 2.5.1.10)] [Ara	At4g17190	73.4453014	94.746	48.8514856	80.395	16.8828976	68.491	0.546280298	0.000078
58170	10 VHS domain-containing protein / GAT domain-containing protein weak similarity to SP Q9LYJ5 ADP-ribosylation factor binding protein GGA1 [Homo sapiens]; contains Pfam profiles PF00790: VHS domain, PF03127: GAT domain	At1g06210	62.9153749	76.81	41.4241993	47.711	5.68874226	63.544	0.595438212	0.000076
12000	19 protein kinase, putative similar to viroid symptom modulation protein [Lycopersicon esculentum] gi 767277 gb AAF66637	At3g12890	47.3862736	67.247	67.2127471	80.6	29.4131176	70.331	0.652258316	0.000075
13443	21 hypothetical protein	At4g22217	29.683804	75.308	82.1648467	96.119	11.4683323	52.967	0.488502661	0.000074
3008	5 Ulp1 protease family protein contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain; similar to At1g32840, At2g06430, At2g15140, At2g04980, At2g14130, At3g44500, At2g15190, At3g47260, At5g34900, At3g29210, At2g02210, At3g32900	At4g04010	50.1746452	69.215	65.2403652	53.166	46.4176729	89.105	0.636226265	0.000072
8800	14 calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase	At3g46120	90.5691331	141.307	69.4386724	90.957	56.3498837	101.341	0.653468047	0.000068
19997	31 expressed protein	At5g02440	63.8619453	84.574	55.1701246	121.273	31.376054	92.771	0.516078719	0.000066
6666	11 eukaryotic translation initiation factor 2 family protein / eIF-2 family protein similar to SP O60841 Translation initiation factor IF-2 (Homo sapiens); contains Pfam profile PF00009: Elongation factor Tu GTP binding domain	At1g76825	28.7607642	59.523	15.3823071	62.245	31.1904823	52.847	0.440172018	0.000063
28485	44 speckle-type POZ protein-related contains Pfam PF00651 : BTB/POZ domain; contains Pfam PF00917: MATH domain; similar to Speckle-type POZ protein (SP:O43791) [Homo sapiens]	At5g19000	148.907814	213.247	63.866689	91.439	12.8992964	31.552	0.601858931	0.000059
3236	5 disease resistance protein (CC-NBS-LRR class), putative domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	At5g66910	68.2396994	89.164	64.4004649	74.647	14.8560071	47.941	0.645981093	0.000056
5816	9 peroxidase, putative similar to peroxidase [Nicotiana tabacum] gi 5381253 dbj BAAB2306	At5g58590	68.2450472	105.839	75.7611288	86.533	19.0437823	84.081	0.582270348	0.000054
11	hypothetical protein	At5g36500	33.2946757	52.715	14.637013	48.255	18.2234018	91.187	0.415727237	0.000053
21539	34 F-box family protein similar to hypothetical protein GB:AA22295 GI:4544395 from [Arabidopsis thaliana]	At1g74300	37.8403524	56.732	67.0190869	78.547	17.7303469	50.378	0.626958925	0.000052
1580	3 no apical meristem (NAM) family protein similar to NAC2 (GI:6456751) (Arabidopsis thaliana)	At3g03200	43.0705546	78.03	21.578888	149.716	26.938828	36.168	0.480310457	0.000048

12055 19 expressed protein
 15696 25 F-box protein-related contains weak hit to Pfam PF00646: F-box domain; contains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain
 24163 38 SWIM zinc finger family protein contains Pfam domain PF04434: SWIM zinc finger
 19868 31 AAA-type ATPase family protein contains Pfam profile: ATPase family PF00004
 24579 38 heavy-metal-associated domain-containing protein contains Pfam heavy-metal-associated domain PF00403: glycine-rich protein GRP22, rape, PIR:S31415; isoform contains a non-consensus TG-acceptor splice site at intron 3
 22198 35 C2 domain-containing protein low similarity to CLB1 [Lycopersicon esculentum] GI:2789434; contains Pfam profile PF00168: C2 domain
 28287 44 myosin heavy chain-related similar to Myosin heavy chain, non-muscle (Zipper protein) (Myosin II)(SP:Q99323) [Drosophila melanogaster]
 20290 32 expressed protein contains Pfam profile: PF04842 plant protein of unknown function (DUF639)
 6846 11 hypothetical protein
 3173 5 nitrate-responsive NOI protein, putative similar to nitrate-induced NOI protein [Zea mays] GI:2642213
 7240 12 endonuclease/exonuclease/phosphatase family protein similar to SPIP32019 Type II inositol-1,4,5-trisphosphate 5-phosphatase precursor (EC 3.1.3.56) (Homo sapiens); contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family
 21813 34 serine carboxypeptidase S10 family protein similar to SPIP52711 Serine carboxypeptidase II-3 precursor (EC 3.4.16.6) Hordeum vulgare; contains Pfam profile PF0450 serine carboxypeptidase
 5047 8 expressed protein
 15081 24 hypothetical protein hypothetical protein
 23131 36 DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain

At3g47720	15.5975539	32.185	23.4463071	71.655	18.9674917	60.802	0.374595981	0.000001
At1g46984	13.8691272	58.055	14.0231702	39.462	16.8829027	29.042	0.39186077	0.000001
At1g60560	30.9555239	59.674	47.8645644	70.278	8.46413234	47.269	0.45962721	0.000001
At3g50930	37.7002386	55.134	36.1995686	76.83	11.5961706	42.261	0.476450517	0.000001
At5g19090	22.777584	40.335	45.6545727	56.602	7.50328321	42.525	0.515914531	0.000001
At1g50260	39.0404111	54.587	31.7604648	64.137	16.6767119	47.494	0.520508795	0.000001
At3g30230	24.7295511	53.068	69.0690126	122.056	8.12185561	12.918	0.55353368	0.000001
At1g71240	35.6990713	58.498	31.0609793	68.931	25.1800205	41.874	0.55406647	0.000001
At3g43950	18.8693716	21.306	4.16028557	32.622	6.78161541	10.436	0.554331652	0.000001
At5g40845	44.1829084	49.373	19.8150374	43.344	14.1611841	43.452	0.559313869	0.000001
At1g47510	31.7833718	52.203	47.9872532	64.656	26.0130313	73.073	0.569007374	0.000001
At3g52020	25.0889269	38.353	22.0505229	79.81	17.7468422	22.203	0.576581715	0.000001
At5g05020	39.9923293	45.788	40.2674192	67.749	27.7862722	63.65	0.634777835	0.000001
At1g67855	28.4484495	56.915	56.3157512	62.594	22.2871636	39.1	0.656514679	0.000001
At3g59130	51.2335205	63.632	41.1469545	48.072	20.1819555	64.2	0.658486123	0.000001