

**Supplementary Fig. 1.** Expression level of all *Arabidopsis* MYB transcription factors altered during drought stress, heat shock or a combination of drought stress and heat shock. RNA isolation and Affymetrix chip analysis were performed as described in Experimental Procedures. Cont, control; D, drought stress; H, heat shock; D+H, a combination of drought stress and heat shock.

Table 1: Transcripts elevated during a combination of drought and heat shock compared to control unstressed plants	Affymetrix number	log₂ fold increase
heat shock protein 18 ;supported by full-length cDNA: Ceres:97197.	247691 at	10.7
heat shock protein 17.6A	250351_at	10.4
heat shock protein 21	253884_at	9.4
Arabidopsis mitochondrion-localized small heat shock protein (AtHSP23.6-mito); supported by cDNA: gi_1669865_gb_U72958.1_ATU72958 heat shock protein 17.6-II :supported by full-length cDNA: Ceres:2281.	254059_at 250296 at	9.3 9.3
late embryogenesis abundant protein LEA like ; supported by CDNA: gi 15293004 gb AY050936.1	250648 at	8.9
putative metal-binding protein highly similar to GB:AAD09511; supported by cDNA: gi_15450582_gb_AY052659.1_	264729_at	8.8
heat shock protein 17; supported by cDNA: gi_15294149_gb_AF410266.1_AF410266	252515_at	8.4
nonspecific lipid-transfer protein precursor - like nonspecific lipid-transfer protein precursor, Brassica napus, EMBL:AF101038;supported by fi 17.6 kDa heat shock protein (AA 1-156) identical to GI:4376161 from (Arabidopsis thaliana) (Nucleic Acids Res. 17 (19), 7995 (1989))	247718_at 260978 at	8 7.7
unknown protein similar to polen cat protein GB:CAA63531 from [Brassica oleracea]; supported by CDNA: gi 1435127 gb AY037243.1	258498 at	7.7
senescence-associated protein (SAG29) ;supported by full-length cDNA: Ceres:38843.	245982_at	7.6
heat shock protein, putative similar to heat shock protein GI:19617 from [Medicago sativa]; supported by full-length cDNA: Ceres:32795.	262911_s_at	7.3
hypothetical protein chloroplast-localized small heat shock protein, putative similar to chloroplast-localized small heat shock protein GI:6601536 from [Funaria hyc	244931_at	7.2 7.1
heat shock protein 22.0; supported by cDNA: gi 511795 gb U11501.1 ATU11501	255811 at	6.7
mitochondrial heat shock 22 kd protein-like ; supported by full-length cDNA: Ceres: 268536.	248434_at	6.7
putative major latex protein major latex protein type 1 - Arabidopsis thaliana, EMBL:X91960; supported by cDNA: gi_13605713_gb_AF36183	_	6.6
putative protein similar to unknown protein (emb]CAB62340.1),supported by full-length cDNA: Ceres:103870.	248505_at	6.5
putative small heat shock protein ;supported by full-length cDNA: Ceres:25828. putative ascorbate peroxidase strong similarity to ascorbate peroxidase GB:CAA56340	266294_at 258695 at	6.4 6.4
nonspecific lipid-transfer protein precursor - like nonspecific lipid-transfer protein precursor, Brassica napus, EMBL:AF101038;supported by fi		6.4
heat shock protein 70 identical to heat shock protein 70 GB:CAA05547 GI:3962377 [Arabidopsis thaliana]; supported by cDNA: gi_15809831_	_	6.1
SRG1-like protein Strong homology to SRG1 protein, a new member of the Fe(II)/ascorbate oxidase superfamily, Similar to SRG1 protein [Ar	_	6
late embryogenesis-abundant protein, putative similar to late embryogenesis-abundant protein GI:17828 from [Brassica napus];supported by dehydrin RAB18-like protein (sp P30185); supported by cDNA: gi 16226664 gb AF428458.1 AF428458	262128_at 247095 at	6 5.8
unknown protein EST gh/ATTS0295 comes from this gene;supported by full-length cDNA: Ceres:20380.	264580 at	5.7
putative phytochrome-associated protein 3 similar to GB:AAC99771; supported by cDNA: gi_3929585_gb_AF100166.1_AF100166		5.7
unknown protein ; supported by cDNA: gi_13265448_gb_AF324676.2_AF324676	263881_at	5.7
peptidylprolyl isomerase unknown protein ; supported by cDNA: gi 15028356 gb AY045981.1	248657_at 266462 at	5.7 5.5
unitiowin protein , supported by CDrwix, gg 1002030_gg 10040901.1	2600402_at 260062_at	5.5 5.4
hypothetical protein predicted by genscan; supported by cDNA: gi_15451109_gb_AY054635.1_	266098_at	5.3
putative NPK1-related MAP kinase similar to GB:BAA21855 from [Arabidopsis thaliana]	265216_at	5.3
heat shock protein DnaJ, putative similar to heat shock protein DnaJ GI:5020005 from [Rhodothermus marinus] putative protein predicted protein	262307_at 254823 at	5.3 5.3
elongation factor 18 alpha-subunit (emb CAB64729.1)	250304 at	5.3
heat shock protein 101 (HSP101) identical to heat shock protein 101 GI:6715468 GB:AAF26423 from [Arabidopsis thaliana]	260248_at	5.2
unknown protein similar to At14a protein GB:AAD26355 GI:4589123 [Arabidopsis thaliana]; supported by cDNA: gi_16226582_gb_AF428437	256603_at	5.2
putative protein	250624_at	5.1
protein phosphatase 2C - like ABA induced protein phosphatase 2C, Fagus sylvatica, EMBL:FSY277743; supported by cDNA: gi_15809791_ serine protease-like protein serine protease OMI - Homo sapiens, EMBL:AF020760	247723_at 246733 at	5.1 5.1
heat-shock protein ; supported by cDNA: gi_166769 gb_M62984.1_ATHHSP83	248332_at	5
mannan endo-1,4-beta-mannosidase	247097_at	5
hypothetical protein predicted by genemark.hmm	262268_at	5
hypothetical protein putative protein CDPK substrate protein 1, Mesembryanthemum crystallinum, EMBL:AF219972;supported by full-length cDNA: Ceres:13378.	265228_s_at 246724_at	4.9 4.9
similar to 14KD proline-rich protein DC2.15 precursor (sp P14009); similar to ESTs emb Z17709 and emb Z47685 similar to hybrid proline-rich	_	4.8
putative AVR9 elicitor response protein similar to GB:AAC69935; supported by cDNA: gi_14488077_gb_AF389287.1_AF389287	264583_at	4.8
ethylene-responsive transcriptional coactivator, putative similar to GB:ADD46402 from [Lycopersicon esculentum] (Plant J. 18 (6), 589-600 (1	258133_at	4.7
unknown protein ; supported by cDNA: gi_13605890_gb_AF367344.1_AF367344 NADH dehydrogenase subunit 7	250784_at 244925 at	4.7 4.7
unknown protein ; supported by cDNA: gi_3883121_gb_AF082299.1_AF082299	264005 at	4.6
unknown protein identical to LEA-like protein GB:CAA10352 from [Arabidopsis thaliana]	258347_at	4.6
hypothetical protein	254597_at	4.6
receptor protein kinase like protein lectin receptor-like serine/threonine kinase lecRK1, Arabidopsis thaliana, PIR2:S68589 1.4-alpha-qlucan branching enzyme protein soform SBE2.2 precursor	253819_at 250906_at	4.6 4.6
heat shock transcription factor-like protein	249117 at	4.6
protein phosphatase 2C, putative similar to GB:CAB90633 from [Fagus sylvatica];supported by full-length cDNA: Ceres:118185.		4.5
putative chloroplast protein import component similar to P. sativum Tic20 chloroplast protein import component, GenBank accession number	255430_at	4.5
putative protein various predicted proteins, Arabidopsis thaliana maturase	253576_at	4.5 4.5
unknown protein ; supported by cDNA: gi 14532707 gb AY039978.1	244926_s_at 267080 at	4.5
homeodomain transcription factor (ATHB-7) identical to SP:P46897; supported by cDNA: gi_15027938_gb_AY045826.1_	266327_at	4.4
hypothetical protein	263504_s_at	4.4
methionine/cystathionine gamma lyase, putative similar to methionine gamma-lyase GB:CAA04124.1 GI:2330856 from [Trichomonas vaginal	261957_at	4.4 4.4
Arm repeat containing protein - like arm repeat containing protein homolog, Arabidopsis thaliana, EMBL:AL133314 putative protein predicted proteins, Arabidopsis thaliana	251407_at 249624 at	4.4
NADH dehydrogenase subunit 5 (nad5) (trans-splicing part 2 of 2)	257337_at	4.4
hypothetical protein	266014_s_at	4.3
putative RNA-binding protein contains Pfam profile: PF00076 RNA recognition motif, (a.k.a. RRM, RBD, or RNP domain); similar to ras-GTP <sub>4</sub> brother binding brother and the state of the sta		4.3
hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 144447. NADH dehydrogenase subunit 9	246582_at 244943 at	4.3 4.3
hypothetical protein	266045_s_at	4.2
putative endochitinase	260561_at	4.2
putative GTP-binding protein similar to GTP-binding protein GB:AAB53256 [Arabidopsis thaliana]	259913_at	4.2
hypothetical protein predicted by genscan+ putative protein intracellular protein Ma11 mouse, PIP://40127; supported by cDNA; aj. 14/488068, db. 453802821, 45380282	255891_at 249403_at	4.2
putative protein intracellular protein Mg11, mouse, PIR:I49127; supported by cDNA: gi_14488068_gb_AF389282.1_AF389282 70kD heat shock protein ;supported by full-length cDNA: Ceres:98979.	249403_at 265675_at	4.2 4.1

phytochrome E	254680_at	4.1
low-temperature-induced 65 kD protein (sp[Qd980)	248352_at	4.1
RuBisCO subunit binding-protein beta subunit precursor; chaperonin, 60 kDa cvtochrome c oxidase subunit 2	248021_at 244950 at	4.1 4.1
putative transcriptional regulator similar to homeotic gene regulator (brahma protein); contains Pfam profile PF00176 SNF2 and others N-term	258559 at	4.1
unknown protein	262940 at	4
hypothetical protein predicted by genemark.hmm	261065 at	4
putative heat shock protein ;supported by full-length cDNA: Ceres:25528.	263374_at	3.9
early light-induced protein identical to early light-induced protein GB:AAB88391 from [Arabidopsis thaliana]; supported by full-length cDNA: Ce	258321_at	3.9
CTP synthase like protein CTP synthase, Methanococcus jannaschii,PIR2:E64446	254490_at	3.9
hypothetical protein	254414_at	3.9
putative protein similar to unknown protein (pir  T03813)	247293_at	3.9
	257338_s_at	3.9
	266550_s_at	3.8
hypothetical protein predicted by genemark.hmm We related transmission for the print, a write a write of the related transmission factor mixto Cl/455966 from Matirzhinum mainel	264217_at 261431 at	3.8 3.8
Myb-related transcription factor mixta, putative similar to Myb-related transcription factor mixta GI:485866 from [Antirrhinum majus] hypothetical protein predicted by genemark.hmm	259463 at	3.8
hypothetical protein predicted by genefinder	258827 at	3.8
unknown protein ; supported by cDNA: g[_13358195_gb_AF325003.2_AF325003	256114 at	3.8
Expressed protein ; supported by full-length cDNA: Ceres:270232	254263 at	3.8
putative protein Arabidopsis thaliana nap gene, PID:e1234813;supported by full-length cDNA: Ceres:38344.	253872_at	3.8
putative protein similar to unknown protein (pir  T05035)	248959_at	3.8
hypothetical protein	257320_at	3.8
potassium transporter, putative similar to potassium transporter GI:2654088 from [Arabidopsis thaliana]	264338_at	3.7
	263509_s_at	3.7
unknown protein ;supported by full-length cDNA: Ceres:96702.	260357_at	3.7
hypothetical protein predicted by genefinder, similar to seed maturation protein PM28 GB:AAD30427 from [Glycine max]	257853_at	3.7
DNA-binding protein - like DNA-binding protein R kappa B, Homo sapiens, PIR:S52863 putative protein similar to unknown protein (gb/AAC73025.1); supported by cDNA: gi 14532515 gb AY039882.1	252546_at 250825 at	3.7 3.7
DNA excision repair cross-complementing protein; similar to human Xeroderma pigmentosum group B DNA repair protein (gb AAC49987.1);		3.7
receptor-like protein kinase	247197 at	3.7
hypothetical protein	244901 at	3.7
hypothetical protein predicted by genscan	266028 at	3.6
unknown protein	264483_at	3.6
hypothetical protein contains similarity to lipid transfer protein GI:498038 from (Senecio odorus)	264146_at	3.6
unknown protein ;supported by full-length cDNA: Ceres:25894.	264094_at	3.6
	263502_s_at	3.6
putative galactinol synthase ;supported by full-length cDNA: Ceres:124236.	263320_at	3.6
hypothetical protein predicted by genscan+	261857_at	3.6
putative protein various predicted proteins, Arabidopsis thaliana	250955_at	3.6
putative protein predicted proteins, Arabidopsis thaliana putative protein similar to unknown protein (gb AAD21732.1)	250036_at 249850 at	3.6 3.6
unknown protein (supported by full-length cDNA: Ceres:534.	249830_at 248218 at	3.6
putative protein nospecific lipid-transfer protein precursor, Brassica napus, EMBL:AF101038	247713 at	3.6
serine/threonine protein kinase-like protein several serine/threonine protein kinases - different species; supported by cDNA: gi 15215663 gb	246922 at	3.6
	245627 at	3.6
	244953 s at	3.6
cytochrome c oxidase subunit 1	257333_at	3.6
unknown protein ;supported by full-length cDNA: Ceres:100283.	265907_at	3.5
	265091_s_at	3.5
hypothetical protein predicted by genemark.hmm	264562_at	3.5
aldehyde dehydrogenase homolog, putative similar to aldehyde dehydrogenase homolog GI:913941 from [Brassica napus]; supported by cDI	263157_at	3.5
unknown protein predicted by genscan+, multiple est matches	258935_at	3.5
hypothetical protein predicted by genmark	258120_at	3.5 3.5
hypothetical protein transcription factor-like protein ;supported by full-length cDNA: Ceres:114015.	257759_at 250688_at	3.5
unknown protein ; supported by cDNA: gi_15451043_gb_AY054602.1_	248223_at	3.5
serine/threonine kinase, putative similar to serine/threonine kinase GI:2632252 from [Sorghum bicolor]; supported by cDNA: gi 14486385 gt		3.5
NADH dehydrogenase subunit 4L	244902 at	3.5
putative protein predicted proteins, Arabidopsis thaliana	250359_at	3.5
putative 3-phosphoinositide-dependent protein kinase-1 similar to 3-phosphoinositide-dependent protein kinase-1 GB:AAD37165 [Arabidopsis	258964_at	3.4
hypothetical protein	266044_s_at	3.4
putative glucosyltransferase	265499_at	3.4
flavin-containing monooxygenase, putative similar to flavin-containing monooxygenase GB:AAA21178 GI:349534 from [Oryctolagus cuniculu	265119_at	3.4
Myb-related transcription factor, putative similar to GB:AAF66727 from [Petunia x hybrida] (Plant Cell 11 (8), 1433-1444 (1999)); supported b	260140_at	3.4
putative protein auxin-induced protein 10A -Glycine max,PID:g255579	254809_at	3.4
glycine-rich cell wall protein-like glycine-rich protein 1.0 precursor, Phaseolus vulgaris, PIR1:S01821; supported by cDNA: gi_14030676_gb putative protein cellulose synthase catalytic subunit, Arabidopsis thaliana, gb:AF027173;supported by full-length cDNA: Ceres:112955.	254667_at	3.4
lysine-ketoglutarate reductase/saccharopine; supported by cDNA; gi_2052507	254189_at 253373_at	3.4 3.4
putative protein predicted protein, Arabidopsis thaliana	253344_at	3.4
low-molecular-weight heat shock protein - like cytosolic class I small heat-shock protein HSP17.5, Castanea sativa, EMBL:CSA9880	249575_at	3.4
cytochrome c biogenesis orf203 Protein sequence is in conflict with the conceptual translation	244919 at	3.4
putative endochitinase	260560_at	3.3
putative protein various predicted proteins	252246_at	3.3
putative protein hypothetical protein At2g37870 - Arabidopsis thaliana, EMBL:AC007661;supported by full-length cDNA: Ceres:5920.	251928_at	3.3
DREB2A (dbj BAA33794.1) ; supported by cDNA: gi_3738229_dbj_AB007790.1_AB007790	250781_at	3.3
putative protein nucleoid DNA-binding protein cnd41, chloroplast, common tobacco, PIR:T01996; supported by cDNA: gi_15809849_gb_AY0	249626_at	3.3
drought-induced protein like	245523_at	3.3
hypothetical protein predicted by genemark.hmm	245243_at	3.3
	244954_s_at 259075 at	3.3 3.3
putative N2,N2-dimethylguanosine tRNA methyltransferase similar to N2,N2-dimethylguanosine tRNA methyltransferase GB:CAA20101 GI:6 putative protein several hypothetical proteins - Arabidopsis thaliana	259075_at 252151 at	3.3 3.2
aspartic protease, putative similar to aspartic protease GI:1326164 from [Brassica napus]	264741_at	3.2
	_ou	0.2

glucose-6-phosphate/phosphate-translocator precursor, putative similar to glucose-6-phosphate/phosphate-translocator precursor GI:299759	264400_at	3.2
unknown protein contains similarity to xenotropic and polytropic retrovirus receptor GB:4759334	262649_at	3.2
branched-chain alpha keto-acid dehydrogenase, putative similar to branched-chain alpha keto-acid dehydrogenase GB:AAC69851 GI:38222	260900 s at	3.2
hypothetical protein	256384 at	3.2
hypothetical protein predicted by genscan+	256285_at	3.2
low-temperature-induced protein 78 (sp Q06738); supported by cDNA: gi_348691_gb_L22567.1_ATHCOR78A	248337_at	3.2
pectinacetylesterase precursor, putative similar to pectinacetylesterase precursor GI:1431629 from [Vigna radiata]	246403 at	3.2
nodulin-like protein	267044 at	3.2
unknown protein contains a domain related to disease resistance genes and a proline-rich domain	265536 at	3.1
putative beta-ketoacyl-CoA synthase Strong similarity to beta-keto-Coa synthase gb/U37088 from Simmondsia chinensis	264318 at	3.1
putative SecA-type chloroplast protein transport factor Similar to gbJX82404 chloroplast SecA protein from Pisum sativum	262491 at	3.1
unknown protein predicted by genefinder; similar to GP 2194125	260565 at	3.1
unknown protein ;supported by full-length cDNA: Ceres:13102.	260005 at	3.1
CDC48 - like protein transitional endoplasmic reticulum ATPase, Arabidopsis thaliana, PIR:S60112	251975 at	3.1
putative protein contains similarity to phytocyanin/early nodulin-like protein	248236 at	3.1
putative protein predicted proteins, Arabidopsis thaliana and Drosophila melanogaster	246897 at	3.1
hypothetical protein	265242 at	3
unknown protein ; supported by cDNA: gi_13877764_gb_AF370145.1_AF370145	264989 at	3
receptor-like protein glossy1 (gl1), putative similar to receptor-like protein glossy1 (gl1) GI:1209703 from (Arabidopsis thaliana)	264147_at	3
transformer-SR ribonucleoprotein, putative similar to GB:Y09506 from [Nicotiana tabacum] (Plant Mol. Biol. 35 (3), 261-269 (1997)); supporte	261081_at	3
hypothetical protein similar to hypothetical protein GB:AAD20673 GI:4432823 from [Arabidopsis thaliana]	260951_at	3
unknown protein ; supported by cDNA: gi_16604686_gb_AY059788.1_	260361_at	3
hypothetical protein	259570_at	3
HSC70-interacting protein, putative similar to HSC70-INTERACTING PROTEIN GB:P50502 from [Homo sapiens]	258187_at	3
RNA helicase - like protein Cdc28p, Schizosaccharomyces pombe, PID:G1439562	254675_at	3
delta-1-pyrroline-5-carboxylate synthetase	251775_s_at	3
imbibition protein homolog probable imbibition protein - Brassica oleracea, PIR:S45033; supported by cDNA: gi_15292676_gb_AY050772.1_	251642_at	3
unknown protein	249870_at	3
heat shock transcription factor	248936_at	3
unknown protein	248752_at	3
putative protein similar to unknown protein (gb AAF16660.1);supported by full-length cDNA: Ceres:15457.	248759_at	3
ubiquinolcytochrome-c reductase-like protein ubiquinolcytochrome-c reductase (EC 1.10.2.2) - Arabidopsis thaliana, PIR:T05357	246944_at	3
Expressed protein ; supported by full-length cDNA: Ceres: 59.	246125_at	3
step II splicing factor, putative similar to step II splicing factor SLU7 GB:AAD13774 GI:4249705 (Homo sapiens)	264633_at	2.9
unknown protein similar to hypothetical protein GB:AAF24564 GI:6692099 from [Arabidopsis thaliana]; supported by cDNA: gi_15810166_gb_	262347_at	2.9
unknown protein ;supported by cDNA: gi_15809941_gb_AY054239.1_	259057_at	2.9
unknown protein ; supported by full-length cDNA: Ceres: 118261.	258879_at	2.9
Myb-family transcription factor, putative contains Pfam profile: PF00249: Myb-like DNA-binding domain	256198_at	2.9
putative calcium-binding EF-hand protein ; supported by cDNA: gi_10862967_dbj_AB039924.1_AB039924	255795_at	2.9
82.09 and 30.80) similar to alternative splicing factor ASF	255472_at	2.9
alpha-amylase - like protein alpha-amylase, Vigna mungo, PIR2:S10514;supported by full-length cDNA: Ceres:3059.	254101_at	2.9
unknown protein ; supported by cDNA: gj_15450646_gb_AY052691.1_ DCA like carbia author and the 24 MUR densitie for factor family DCAL. Archidensis the lines. ENRLy A 1224967	250826_at	2.9
RGA-like protein putative member of the VHIID domain transcription factor family RGAL - Arabidopsis thaliana, EMBL:AJ224957 extra surgery and the application of the surgery and the surgery a	246432_at	2.9
anthocyanin2, putative similar to anthocyanin2 (An2) GI:7673088 from [Petunia integrifolia]; supported by cDNA: gi_3941507_gb_AF062908.	245628_at	2.9
putative protein similarity to UVB-resistance protein UVR8, Arabidopsis thaliana, PIR:T50662~Contains Regulator of chromosome condensat	245210_at	2.9 2.9
hypothetical protein	257323_at	2.9
hypothetical protein predicted by genscan and genefinder 6 bew binding 570 transporting refers identical to PIPS 20295; supported by cDNA: ci. 600963, cb. 11/2001 1. ATU/2001	266590_at 266555 at	2.8
G-box binding bZIP transcription factor identical to PIR:S20885; supported by cDNA: gi_600862_gb_U17891.1_ATU17891 predicted protein	266012 s at	2.8
unknown protein similar to putative DNA dependent ATPase and helicase	264805 at	2.8
putative xylan endohydrolase similar to GB:AAD27896 to endoxylanases gi[1255238 (Thermoanaerobacterium thermosulfurigenes), gi[1813£	_	2.8
parative system citotory protected by genefinder	263975 at	2.8
FtsH protease, putative similar to zinc dependent protease GI:7650138 from [Arabidopsis thaliana]	262626 at	2.8
muth homologue-1 identical to muth homologue-1 GI3550982 from [Arabidopsis thailana]; supported by cDNA: gi_3820619_gb_AF099970.	262129 at	2.8
putative two-component phosphorelay mediator similar to two-component phosphorelay mediators (ATHP1-3) GB:BAA37111	259329 at	2.8
putative protein phosphatase-2C similar to protein phosphatase-2C GB:AAC36699 from [Mesembryanthemum crystallinum]; supported by cD	258901 at	2.8
putative cinnamoyl-CoA reductase highly similar to F4P9.37;supported by full-length cDNA: Ceres:11254.	255787_at	2.8
unknown protein similar to hypothetical protein GI:6016718 from (Arabidopsis thaliana)	255739 at	2.8
stress-induced protein sti1 -like protein stress-induced protein sti1 -Glycine max,PID:g872116	254839 at	2.8
cytochrome P450-like protein cytochrome P450 CYP94A1 - Vicia sativa,PIR2:T08014	252368 at	2.8
dehydrin-like protein dehydrin Xero2 - Arabiodopsis thaliana, EMBL:U19536	252137 at	2.8
AP2 domain transcription factor-like protein	248389 at	2.8
putative glucosyltransferase ;supported by full-length cDNA: Ceres:153418.	266532 at	2.7
protein kinase-like protein	247026 at	2.7
histone H1 ;supported by full-length cDNA: Ceres:112970.	265817_at	2.7
putative heat shock protein ; supported by cDNA: gi 15450722 gb AY053403.1	263483 at	2.7
CCAAT-binding factor B subunit, putative similar to CCAAT-binding factor B subunit GI:1173617 [Brassica napus]; supported by cDNA: gi_14	263158_at	2.7
unknown protein ; supported by full-length cDNA: Ceres: 39741.	262204_at	2.7
putative cytochrome P450 similar to cytochrome P450 89A2 GB:Q42602 [Arabidopsis thaliana]; supported by cDNA: gi_15983413_gb_AF424	259058_at	2.7
putative DnaJ protein Pfam HMM hit: DnaJ, prokaryotic heat shock protein	258984_at	2.7
copper amine oxidase like protein (fragment2) copper amine oxidase - Cicer arietinum,PID:e1335964	254833_s_at	2.7
Expressed protein ; supported by full-length cDNA: Ceres: 20948.	254278_at	2.7
putative protein hypothetical proteins	252525_at	2.7
homeobox-leucine zipper protein ATHB-12 ;supported by full-length cDNA: Ceres:32615.	251272_at	2.7
putative protein strong similarity to unknown protein (gb AAF31728.1); supported by cDNA: gi_15292740_gb_AY050804.1_	249917_at	2.7
unknown protein ; supported by cDNA: gi_14030678_gb_AF375430.1_AF375430	248969_at	2.7
Ran binding protein 1 homolog - like Ran binding protein 1 homolog, Arabidopsis thaliana, EMBL:ATU62742	247771_at	2.7
unknown protein contains similarity to phytochrome interacting factor 3 GI:3929586 from [Arabidopsis thaliana]; supported by cDNA: gi_14334	245748_at	2.7
hypothetical protein	244906_at	2.7
putative ATP-dependent RNA helicase	267627_at	2.6
unknown protein	266757_at	2.6
hypothetical protein	265229_s_at	2.6
putative SF2/ASF splicing modulator, Srp30 similar to GB:CAB42558	264255_at	2.6

jacalin, putative similar to jacalin GI:289164 from [Artocarpus heterophyllus]	262357_at	2.6
unknown protein contains similarity to eukaryotic initiation factor 4B GI:6739515 from [Triticum aestivum]; supported by cDNA: gi_14335083_(	261827_at	2.6
hypothetical protein similar to putative MYB family transcription factor GB:AAD17429 GI:4335752 from [Arabidopsis thaliana]	260999 at	2.6
NAM-like protein similar to NAM (no apical meristem) GB:CAA63101 from [Petunia x hybrida]	260203_at	2.6
unknown protein similar to SPL1-related proteins: GB:CAB56771, GB:CAB56770, GB:CAB56773 [Arabidopsis thaliana]	259971 at	2.6
hypothetical protein similar to hypothetical protein GB:AAF02805 [Arabidopsis thaliana]	258944 at	2.6
heat shock transcription factor HSF1, putative similar to GB:S52641 from [Arabidopsis thaliana] (Plant Mol. Biol. 26, 353-362 (1994)); support	258139 at	2.6
hypothetical protein predicted by genemark.hmm	256999 at	2.6
seven in absentia-like protein similar to SINA1p GB:CAB40577 from [Vitis vinifera]; supported by cDNA: gi_16323493_gb_AY059135.1_	256789_at	2.6
hypothetical protein	255723 at	2.6
putative protein hypothetical protein, Synechocystis sp., PIR2:S76701	254642 at	2.6
putative protein nybative DNA binding protein - Arabidosis thaliana, TREMBL:ATAC2339 3; supported by cDNA: gi 16649060 gb AY0599(	_	2.6
pediate proteins particles into binding potential adaptation and an adaptation and an adaptation of the pediate proteins and adaptation of the pediate proteins and adaptation of the pediate		2.6
kinase like protein RING3 protein, Homo sapiens, EMBL:X96670; supported by CDNA; gi 16604680 gb_AY059785.1_	250191 at	2.0
kindse inke protein Kindse protein, nonin sapiens, Linds. Xadord, supported by conk. gr_10004000_gv_K1034703.1_ glucose-fic-phosphate dehydrogenase	249372 at	2.6
	_	2.0
putative protein contains similarity to cyclin	248988_at	
putative protein	246285_at	2.6
lipoamide dehydrogenase, putative	262650_at	2.5
hypothetical protein	266039_s_at	2.5
unknown protein ; supported by cDNA: gi_15810470_gb_AY056274.1_	265484_at	2.5
hypothetical protein contains Pfam profile: PF01363 FYVE zinc finger; supported by full-length cDNA: Ceres: 15739.	265035_at	2.5
lactoylglutathione lyase-like protein Similar to protein gb Z74962 from Brassica oleracea which is similar to bacterial YRN1 and HEAHIO prote	264372_at	2.5
putative gigantea protein strong similarity to GB:CAB56039 from [Arabidopsis thaliana]; supported by cDNA: gi_6002679_gb_AF105064.1_AF	264211_at	2.5
putative ADP-glucose pyrophosphorylase large subunit	263544_at	2.5
hypothetical protein predicted by genemark.hmm	263127_at	2.5
hypothetical protein similar to hypothetical protein GB:AAD50003 GI:5734738 from [Arabidopsis thaliana]; supported by full-length cDNA: Cere	_	2.5
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:19976.	262369_at	2.5
unknown protein ; supported by cDNA: gi_13937194_gb_AF372951.1_AF372951	262164_at	2.5
unknown protein ;supported by full-length cDNA: Ceres:35675.	262050_at	2.5
unknown protein	260585_at	2.5
hypothetical protein similar to GB:CAB55886 [Homo sapiens], GB:BAA09774 [Homo sapiens], GB:CAA87778 [Caenorhabditis elegans]	259759_at	2.5
cathepsin B-like cysteine protease, putative similar to cathepsin B-like cysteine proteinase GI:609175 from [Nicotiana rustica]	259441_at	2.5
putative aminotransferase similar to beta-alanine-pyruvate aminotransferase GB:BAA19549 [Rattus norvegicus], alanine-glyoxylate aminotra	258983_at	2.5
putative disease resistance protein similar to putative disease resistance protein GB:AAF01514 from clone F9F8	258894_at	2.5
late-embryogenesis abundant protein, putative similar to GI:4102692 from [Glycine max]	256464 at	2.5
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:37923.	255900 at	2.5
expressed protein supported by cDNA: Ceres:13917.	254574 at	2.5
putative protein ; supported by cDNA: gi_14517539_gb_AY039605.1_	252134 at	2.5
dehydrin Xero2;supported by cDNA: gi_15809983_gb_AY054260.1_	252102 at	2.5
heat shock protein 70 (Hsc70-5); supported by cDNA: gi_6746589_gb_AF217458.1_AF217458	250502 at	2.5
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	250050 at	2.5
putative protein predicted protein, Arabidopsis thaliana acetyl-CoA synthetase-like protein	250050_at 249869_at	2.5 2.5
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acetyl-CoA synthetase-like protein         Fdr1 Cen - like protein Fdr1, Oryza sativa, EMBL:AF159883         unknown protein         ribosomal protein 116         hypothetical protein         putative tropinone reductase         unknown protein : supported by cDNA: gi_14334955_gb_AY035151.1_         hypothetical protein Similar to Nicotiana tumor-related protein (gb/2643)         unknown protein         hypothetical protein protein protein protein phosphatase 2C (AIP2C-HA) GB:A4003119 [Arabidopsis thaliana] (Plant Mol. Biol. 3         unknown protein         disulfide isomerase-related protein, putative similar to GB:AAB50217 from [Homo sapiens]         protein phosphatase 2C (AIP2C-HA) GB:A4003119 [Arabidopsis thaliana] (Plant Mol. Biol. 3         unknown protein         hypothetical protein similar to In-1 (phosphate induced protein) GB:BAA3810 [Nicotiana tabacum]; supported by full-length cDI         (1-4)-beta-mannan endohydrolase precursor, putative similar to (1-4)-beta-mannan endohydrolase precursor GI:9836826 from [Lycopersicon phi-1-like protein similar to hypothetical protein GB:CAB43801; Supported by CDN4: Ceres: 10820.         unknown protein similar to hypothetical protein GB:CAB43803; supported by CDN4: Ceres: 10821.         unknown protein similar to hypothetical protein GB:CAB43803; supported by CDN4: gi_15146402; supported by CDN4: gi_15183         hypothetical protein similar to Hove GB:CAB43803; supported by CDN4: gi_15146402; supported by CDN4: gi_1518637_gb_AY048289.1_ <t< td=""><td>249869_at 247511_at 247340_at 247340_at 257321_at 266278_at 26629_at 264661_at 264156_at 264102_at 264102_at 259718_at 259922_at 259718_at 259616_at 259616_at 259616_at 259616_at 259616_at 259616_at 259616_at 259616_at 25065_at 256983_at 256983_at 256983_at 25692_at 25109_at 251084_at 251084_at 250930_at 250930_at 250930_at 250930_at 250930_at 250930_at 250930_at 250930_at 250930_at 250930_at 249977_at 249614_at 249215_at 248763_at 248763_at 248774_at 248228_at</td><td><math display="block">\begin{array}{c} 2.5\\ 2.5\\ 2.5\\ 2.5\\ 2.5\\ 2.4\\ 2.4\\ 2.4\\ 2.4\\ 2.4\\ 2.4\\ 2.4\\ 2.4</math></td></t<>	249869_at 247511_at 247340_at 247340_at 257321_at 266278_at 26629_at 264661_at 264156_at 264102_at 264102_at 259718_at 259922_at 259718_at 259616_at 259616_at 259616_at 259616_at 259616_at 259616_at 259616_at 259616_at 25065_at 256983_at 256983_at 256983_at 25692_at 25109_at 251084_at 251084_at 250930_at 250930_at 250930_at 250930_at 250930_at 250930_at 250930_at 250930_at 250930_at 250930_at 249977_at 249614_at 249215_at 248763_at 248763_at 248774_at 248228_at	$\begin{array}{c} 2.5\\ 2.5\\ 2.5\\ 2.5\\ 2.5\\ 2.4\\ 2.4\\ 2.4\\ 2.4\\ 2.4\\ 2.4\\ 2.4\\ 2.4$
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<pre>idetty/CoA synthetase-like protein Fdr1 Cen - like protein Fdr1, Oryza sativa, EMBL:AF159883 unknown protein ribosomal protein 116 hypothetical protein i supported by cDNA: gi_14334955_gb_AY035151.1_ hypothetical protein protein similar to Nicotiana tumor-related protein (gb)24453) unknown protein hypothetical protein protein protein common comm</pre>	249869_at 247511_at 247340_at 247340_at 257321_at 266278_at 266629_at 264661_at 264166_at 264102_at 264166_at 264107_at 259922_at 2599718_at 2599718_at 259616_at 25942_at 259616_at 25942_at 25965_at 256983_at 256983_at 256983_at 253050_at 253050_at 253047_at 251084_at 251084_at 250987_at 250987_at 250987_at 250987_at 250987_at 250987_at 250987_at 250987_at 250987_at 250987_at 249977_at 249666_at 249977_at 249774_at 248763_at 247384_at	$\begin{array}{c} 2.5\\ 2.5\\ 2.5\\ 2.5\\ 2.5\\ 2.4\\ 2.4\\ 2.4\\ 2.4\\ 2.4\\ 2.4\\ 2.4\\ 2.4$

putative RNA-binding protein;supported by cDNA: gi_6650522_gb_AF101056.1_AF101056		
putative rank-binding protein , supported by contra. gi_0000022_gb_Ai 101000.1_Ai 101000	265266_at	2.3
gamma glutamyl hydrolase, putative similar to gamma glutamyl hydrolase GI:1680711 from [Glycine max]; supported by full-length cDNA: Cei	264300_at	2.3
unknown protein ;supported by full-length cDNA: Ceres:3807.	261154 at	2.3
hypothetical protein similar to dehydrogenase-like protein GI:9279732 from [Arabidopsis thaliana]	260688 at	2.3
putative heat-shock protein similar to heat-shock protein precursor GB:S49340 [Secale cereale]; contains Pfam profile: Heat shock hsp90 pro	259248 at	2.3
putative short-chain type dehydrogenase/reductase similar to short-chain type dehydrogenase/reductase GB:Q08632 [Picea abies]; supported		2.3
unknown protein ; supported by cDNA: gi 13937210 gb AF372960.1 AF372960	258400 at	2.3
CDPK-related kinase identical to GB:2AAD38059 from [Arabidopsis thaliana]	257024 at	2.3
beta-amylase, putative similar to beta-amylase GB:CAB58423 [Arabidopsis thaliana]; supported by cDNA: gi 14194172 gb AF367293.1 AF		2.3
unknown protein ;supported by full-length cDNA: Ceres:36434.	256061 at	2.3
UDP-glucose glucose glucos transferase, putative similar to UDP-glucose glucosyltransferase GI:3928543 from [Arabidopsis thaliana]; supported by	255943 at	2.3
putative fibrillin ; supported by full-length cDNA: Ceres: 1461.	255364 s at	2.3
putative protein Mei2-like protein, Arabidopsis thaliana, gb.D86122	254679 at	2.3
putative protein wolf-in Chomolog 1, Schizosaccharomyces pombe, PATCHX:G2055413	254526 at	2.3
trehalose-6-phosphate phosphatase - like protein trehalose-6-phosphatase (AtTPPA), PID:g2944178	254321 at	2.3
abscisic acid responsive elements-binding factor(ABF3) identical to abscisic acid responsive elements-binding factor (ABF3) identical to abscisic acid responsive elements-binding fact	—	2.3
putative sugar transporter protein sugar transporter. Arabidopsis thaliana, db xref=PID:q1495273	253188 at	2.3
putative social danisporter protein social danisporter, national danismo da concerning responses and an anti-	253111 at	2.3
putative protein guidanie audio non protein protein protein and protein and participation (Contra), i nacino reference and protein pro	253092 at	2.3
hypothetical protein	253020_at	2.3
putative protein activating signal cointegrator 1 - Homo sapiens, EMBL:AF168418; supported by full-length cDNA: Ceres:13265.	252424 at	2.3
putative protein adviraing signal connegrator r - none sapiens, Empl. Ar rooms, sapported by tainengin converse cores, rooms, putative protein	250956 at	2.3
cysteine proteinase inhibitor-like protein ;supported by full-length cDNA: Ceres:27304.	250811 at	2.3
putative protein storing similarity to unknown protein (mblCAB62118.1)	250786_at	2.3
putative protein strong similarity to unknown protein (SIS)AC98056.1)	250237 at	2.3
Fish proteins subrig similarly to minimum protein (gp/processor GI:4325041 from [Nicotiana tabacum]	250162 at	2.3
putative protein mD10. Mus musculus, EMBL:AB028860; supported by cDNA; gi 15450366 gb AY052284.1	249613 at	2.3
putative protein minifar, was indexended, Linder. Advocation supported by full-length cDNA: Ceres:96.	249015_at 249174 at	2.3
unknown protein (supported by full-length CDNA: Ceres:25275.	248709 at	2.3
annown protein , supported by full-rength (DrvA. Ceres.25215. permease	248558_at	2.3
homogentisate 1,2-dioxygenase ;supported by full-length cDNA: Ceres:6599.		2.3
nonogenisade 1,2-oloxygenise ; soupported by ininengin convi. Ceres.0399. protein phosphatase 2C ABI2 (PP2C) (spl004719)	248193_at 247957 at	2.3
	_	2.3
putative protein similar to unknown protein (dbj BAA96220.1); supported by full-length cDNA: Ceres: 16835.	247295_at	2.3 2.3
atfp6-like protein AP2 domain containing protein AP2 domain containing protein RAP2.4 - Arabidopsis thaliana, EMBL:AF003097	247128_at	2.3
	246939_at	2.3
HSP100/ClpB, putative similar to HSP100/ClpB GI:9651530 [Phaseolus lunatus]	246554_at	2.3
allergen like protein	245463_at	2.3
ATP synthase subunit 9 NAM / UC2 like protein pageone Archidencie thaliano, PID:e2790102; supported by cDNA; ci. 15012320, cb. AV0564421	257339_s_at 253132_at	2.3
NAM / CUC2 -like protein nap gene, Arabidopsis thaliana, PID:g2780192; supported by cDNA: gi_15912330_gb_AY056443.1_ hypothetical protein predicted by genefinder; supported by cDNA: gi_16323181_gb_AY057695.1_	267248 at	2.2
nypoliteirca protein preucied by generinder, apported by Certix. g_1022010_00_nto 0503	267035 at	2.2
unknown protein ; supported by cDNA; gj _5010737_gb_AY045670.1_	266984 at	2.2
unknown protein	266874 at	2.2
putative thiamin biosynthesis protein	266673 at	2.2
unknown protein	266628 at	2.2
hypothetical protein	266013_s_at	2.2
hypothetical protein predicted by genscan	265902 at	2.2
nyperiorial predicted by general		
putative WD-40 repeat protein similar to TUP1(GB:AF079369); supported by cDNA; gi 13605894 gb AF367346.1 AF367346	_	
putative WD-40 repeat protein similar to TUP1(GB:AF079369); supported by cDNA: gi_13605894_gb_AF367346.1_AF367346 hypothetical protein	265259_at	2.2
hypothetical protein	265259_at 265233_s_at	2.2 2.2
hypothetical protein hypothetical protein	265259_at 265233_s_at 265238_s_at	2.2 2.2 2.2
hypothetical protein hypothetical protein ribosomal protein identical to ribosomal protein GI:806279 from [Arabidopsis thaliana]	265259_at 265233_s_at 265238_s_at 265032_at	2.2 2.2 2.2 2.2
hypothetical protein hypothetical protein ribosomal protein identical to ribosomal protein GI:806279 from [Arabidopsis thaliana] stress related protein, putative similar to stress related protein GI:5802955 from [Vitis riparia];supported by full-length cDNA: Ceres:14043.	265259_at 265233_s_at 265238_s_at 265032_at 264968_at	2.2 2.2 2.2 2.2 2.2 2.2
hypothetical protein hypothetical protein ribosomal protein identical to ribosomal protein GI:806279 from [Arabidopsis thaliana] stress related protein, putative similar to stress related protein GI:5802955 from [Vitis riparia];supported by full-length cDNA: Ceres:14043. hypothetical protein similar to membrane associated salt inducible protein isolog; similar to F21B7.16 and F21B7.18	265259_at 265233_s_at 265238_s_at 265032_at 264968_at 264819_at	2.2 2.2 2.2 2.2 2.2 2.2 2.2
hypothetical protein hypothetical protein ribosomal protein identical to ribosomal protein GI:806279 from [Arabidopsis thaliana] stress related protein, putative similar to stress related protein GI:5802955 from [Vitis riparia];supported by full-length cDNA: Ceres:14043. hypothetical protein similar to membrane associated salt inducible protein isolog; similar to F21B7.16 and F21B7.18 hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:25383.	265259_at 265233_s_at 265238_s_at 265032_at 264968_at 264819_at 264186_at	2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2
hypothetical protein hypothetical protein ribosomal protein identical to ribosomal protein GI:806279 from [Arabidopsis thaliana] stress related protein, putative similar to stress related protein GI:5802955 from [Vitis riparia];supported by full-length cDNA: Ceres:14043. hypothetical protein similar to membrane associated salt inducible protein isolog; similar to F21B7.16 and F21B7.18 hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:25383. unknown protein ;supported by full-length cDNA: Ceres:151404.	265259_at 265233_s_at 265238_s_at 265032_at 264968_at 264819_at 264186_at 264086_at	2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2
hypothetical protein hypothetical protein ribosomal protein identical to ribosomal protein GI:806279 from [Arabidopsis thaliana] stress related protein, putative similar to stress related protein GI:5802955 from [Vitis riparia];supported by full-length cDNA: Ceres:14043. hypothetical protein similar to membrane associated salt inducible protein isolog; similar to F21B7.16 and F21B7.18 hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:25383. unknown protein ;supported by full-length cDNA: Ceres:151404. hypothetical protein predicted by genscan	265259_at 265233_s_at 265238_s_at 265032_at 264968_at 264968_at 264186_at 264086_at 263471_at	2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2
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outer membrane lipoprotein - like outer membrane lipoprotein, Citrobacter freundii, PIR:I40710;supported by full-length cDNA: Ceres:17098.	247851_at	2.2
cysteine proteinase AALP identical to AALP protein GI:7230640 from [Arabidopsis thaliana]; similar to barley aleurain; supported by full-length	247627 at	2.2
putative protein MtN19, Medicago truncatula, EMBL:MTY15367	247488 at	2.2
putative protein similar to unknown protein (pir  T09249); supported by cDNA: gi_15081693_gb_AY048239.1_	247061 at	2.2
Lon protease homolog 2 precursor almost identical to Lon protease homolog 2 mitochondrial precursor SP:P93655, GI:1848290 from [Arabic	246850 at	2.2
pyrroline-5-carboxylate reductase ;supported by full-length cDNA: Ceres:36386.	246594 at	2.2
hypothetical protein	244903 at	2.2
unknown protein similar to GP/2262147/AC002330	267628 at	2.1
putative heat shock transcription factor	266841 at	2.1
unknown protein	266503 at	2.1
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AP2 domain transcription factor	263823_s_at	2.1
FisH protease, putative contains similarity to chloroplast FisH protease G1:5804782 from [Nicotiana tabacum]	262937_at	2.1
unknown protein ESTs gb H37032, gb R6425, gb Z34651, gb N37268, gb AA713172 and gb Z34241 come from this gene; supported by full-le	262600_at	2.1
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:21663.	262047_at	2.1
unknown protein	261558_at	2.1
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unknown protein similar to unknown protein GB:AAC32238 (Arabidopsis thaliana)	259169_at	2.1
putative disease resistance protein similar to putative disease resistance protein GB:AAF01514 from clone F9F8	258893_at	2.1
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:101876.	258878_at	2.1
hypothetical protein similar to hypothetical proteins GB:AAC35225, GB:AAD22358, GB:AAD22682 [Arabidopsis thaliana]	258817_at	2.1
unknown protein similar to GB:AAD10646 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:117342.	258812_at	2.1
hypothetical protein predicted by genscan	258696_at	2.1
hypothetical protein predicted by genscan+; supported by cDNA: gi_15810242_gb_AY056160.1_	258374_at	2.1
unknown protein	257239 at	2.1
purple acid phosphatase, putative similar to purple acid phosphatase GB:CAA06921 [lpomoea batatas]	257087 at	2.1
beta-fructofuranosidase, putative similar to beta-fructofuranosidase 1 GB:S37212 from [Arabidopsis thaliana]	256779 at	2.1
hypothetical protein predicted by genemark.hmm	256653 at	2.1
unknown protein ; supported by cDNA: gi_14194136_gb_AF367274.1_AF367274	256343 at	2.1
26S proteasome regulatory subunit S12, putative nearly identical to 26S proteasome regulatory subunit S12 (MOV34 ) SP:O24412 [Arabidop	256249 at	2.1
calreticulin (crt1) identical to calreticulin (crt1) GI:2052379 [Arabidopsis thaliana]; supported by cDNA: gi 2052378 gb U66343.1 ATU66343	256216 at	2.1
GBF2, Goot binding factor ; supported by full-length cDNA: Ceres:16533.	255625 at	2.1
putative protein several hypothetical proteins - Arabidopsis thaliana	254872 at	2.1
putative protein	254778 at	2.1
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myb-related protein M4, isupported by full-length cDNA: Ceres:33333.	254413_at	2.1
putative major latex protein major latex protein type 1 - Arabidopsis thaliana, EMBL:X91960;supported by full-length cDNA: Ceres:108949.	254225_at	2.1
hsp 70-like protein heat shock 70 protein - Spinacia oleracea, PID:g2654208	254148_at	2.1
pumilio-like protein abdominal segment formation protein pumilio - fruitfly, PIR2:A46221; supported by cDNA: gi_13430771_gb_AF360298.1	254045_at	2.1
SOF1 protein-like protein SOF1 (involved in rRNA processing) protein-yeast; supported by cDNA: gi_13937178_gb_AF372943.1_AF372943	253777_at	2.1
putative protein ; supported by cDNA: gi_11177136_dbj_AB050977.1_AB050977	253610_at	2.1
cinnamoyl-CoA reductase - like protein cinnamoyl-CoA reductase, Saccharum officinarum, gb:AJ231134; supported by full-length cDNA: Cer	253638_at	2.1
glucose-1-phosphate adenylyltransferase (APL3);supported by cDNA: gi_16648984_gb_AY059862.1_	252888_at	2.1
protein kinase - like protein Raf protein kinase homolog CTR1 - Arabidopsis thaliana,PIR2:A45178	252469_at	2.1
aquaporin MIP - like protein aquaporin 2, Samanea saman, AF067185; supported by full-length cDNA: Ceres: 11929.	251858_at	2.1
putative protein several hypothetical proteins - Arabidopsis thaliana	251211_s_at	2.1
putative protein several hypothetical proteins - different bacteria	251137_at	2.1
calnexin homolog	250625_at	2.1
diacylglycerol kinase (ATDGK1) ; supported by cDNA: gi_1374771_dbj_D63787.1_ATHATDGK1	250556_at	2.1
serine/threonine protein kinase -like protein probable serine/threonine protein kinase SNFL3, sorghum, PIR:T14822; supported by cDNA: gi_!	250408_at	2.1
NAM (no apical meristem)-like protein ; supported by cDNA: gi_14326464_gb_AF385685.1_AF385685	249944_at	2.1
ATP-dependent Clp protease ATP-binding subunit (ClpD), ERD1 protein precursor identical to ERD1 protein GI:497629, SP:P42762 from [Ar	248487_at	2.1
dehydrodolichyl diphosphate - like protein dehydrodolichyl diphosphate, Arabidopsis thaliana, EMBL:ATH277136	247780_at	2.1
unknown protein	247350 at	2.1
	247330_at	
acyl-CoA oxidase (gb AAC13497.1); supported by cDNA: gi_3044211_gb_AF057043.1_AF057043	247330_at 247176_at	2.1
acyl-CoA oxidase (gb AAC13497.1) ; supported by cDNA: gi_3044211_gb_AF057043.1_AF057043 putative protein myosin heavy chain, chicken, PIR:S24348;supported by full-length cDNA: Ceres:147806.	247176_at	2.1 2.1
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putative protein myosin heavy chain, chicken, PIR:S24348;supported by full-length cDNA: Ceres:147806.	247176_at 246796_at	2.1
putative protein myosin heavy chain, chicken, PIR:S24348;supported by full-length cDNA: Ceres:147806. luminal binding protein ; supported by cDNA: gi_1303694_dbj_D84414.1_ATHBIPA	247176_at 246796_at 245956_s_at	2.1 2.1
putative protein myosin heavy chain, chicken, PIR:S24348;supported by full-length cDNA: Ceres:147806. luminal binding protein ; supported by cDNA: gi_1303694_dbj_D84414.1_ATHBIPA transcriptional adaptor like protein ; supported by cDNA: gi_15215639_gb_AY050348.1_	247176_at 246796_at 245956_s_at 245288_at	2.1 2.1 2.1
putative protein myosin heavy chain, chicken, PIR:S24348;supported by full-length cDNA: Ceres:147806. luminal binding protein ; supported by cDNA: gi_1303694_dbj_D84414.1_ATHBIPA transcriptional adaptor like protein ; supported by cDNA: gi_15215639_gb_AY050348.1_ putative protein disulfide-isomerase	247176_at 246796_at 245956_s_at 245288_at 245175_at	2.1 2.1 2.1 2.1
putative protein myosin heavy chain, chicken, PIR:S24348;supported by full-length cDNA: Ceres:147806. luminal binding protein ; supported by cDNA: gi_1303694_dbj_D84414.1_ATHBIPA transcriptional adaptor like protein ; supported by cDNA: gi_15215639_gb_AY050348.1_ putative protein disulfide-isomerase unknown protein Location of EST gbIN95878 putative protein disulfide isomerase ; supported by cDNA: gi_15810003_gb_AY054270.1_	247176_at 246796_at 245956_s_at 245288_at 245175_at 264167_at 267605_at	2.1 2.1 2.1 2.1 2.1 2.1 2
putative protein myosin heavy chain, chicken, PIR:S24348;supported by full-length cDNA: Ceres:147806. luminal binding protein ; supported by cDNA: gi_1303694_dbj_D84414.1_ATHBIPA transcriptional adaptor like protein ; supported by cDNA: gi_15215639_gb_AY050348.1_ putative protein disulfide-isomerase unknown protein Location of EST gb N95878	247176_at 246796_at 245956_s_at 245288_at 245175_at 264167_at 267605_at 267512_at	2.1 2.1 2.1 2.1 2.1 2.1 2
putative protein myosin heavy chain, chicken, PIR:S24348;supported by full-length cDNA: Ceres:147806. luminal binding protein ; supported by cDNA: gi_1303694_dbj_D84414.1_ATHBIPA transcriptional adaptor like protein ; supported by cDNA: gi_15215639_gb_AY050348.1_ putative protein disulfide-isomerase unknown protein Location of EST gb N95878 putative protein disulfide isomerase ; supported by cDNA: gi_15810003_gb_AY054270.1_ hypothetical protein predicted by genscan and genefinder; supported by cDNA: gi_4837732_gb_AF085354.1_AF085354 putative potassium transporter	247176_at 246796_at 245956_s_at 245288_at 245175_at 264167_at 267605_at 267512_at 267423_at	2.1 2.1 2.1 2.1 2.1 2.1 2 2 2 2
putative protein myosin heavy chain, chicken, PIR:S24348;supported by full-length cDNA: Ceres:147806. luminal binding protein ; supported by cDNA: gi_1303694_dbj_D84414.1_ATHBIPA transcriptional adaptor like protein ; supported by cDNA: gi_15215639_gb_AY050348.1_ putative protein disulfide-isomerase unknown protein Location of EST gb N95878 putative protein disulfide isomerase ; supported by cDNA: gi_15810003_gb_AY054270.1_ hypothetical protein predicted by genscan and genefinder; supported by cDNA: gi_4837732_gb_AF085354.1_AF085354 putative protein predicted by genscan	247176_at 246796_at 245996_s_at 245288_at 245175_at 264167_at 267605_at 267512_at 267423_at 267268_at	2.1 2.1 2.1 2.1 2.1 2 2 2 2 2 2
putative protein myosin heavy chain, chicken, PIR:S24348;supported by full-length cDNA: Ceres:147806. luminal binding protein ; supported by cDNA: gi_1303694_dbj_D84414.1_ATHBIPA transcriptional adaptor like protein ; supported by cDNA: gi_15215639_gb_AY050348.1_ putative protein disulfide-isomerase unknown protein Location of EST gb N95878 putative protein disulfide isomerase ; supported by cDNA: gi_15810003_gb_AY054270.1_ hypothetical protein predicted by genscan and genefinder; supported by cDNA: gi_4837732_gb_AF085354.1_AF085354 putative protein predicted by genscan putative casein kinase I	247176_at 246796_at 245956_s_at 245288_at 245175_at 264167_at 267605_at 267512_at 267512_at 267268_at 26768_at 266651_at	2.1 2.1 2.1 2.1 2.1 2 2 2 2 2 2 2 2 2
putative protein myosin heavy chain, chicken, PIR:S24348;supported by full-length cDNA: Ceres:147806. luminal binding protein ; supported by cDNA: gi_1303694_dbj_D84414.1_ATHBIPA transcriptional adaptor like protein ; supported by cDNA: gi_15215639_gb_AY050348.1_ putative protein disulfide-isomerase unknown protein Location of EST gbIN95878 putative protein disulfide isomerase ; supported by cDNA: gi_15810003_gb_AY054270.1_ hypothetical protein predicted by genscan and genefinder; supported by cDNA: gi_4837732_gb_AF085354.1_AF085354 putative casein kinase I putative casein kinase I putative pumilio/Mpt5 family RNA-binding protein	247176_at 246796_at 245956_s_at 245288_at 245175_at 264167_at 267605_at 267512_at 267512_at 26752_at 26752_at 26628_at 266288_s_at	2.1 2.1 2.1 2.1 2.1 2 2 2 2 2 2 2 2 2 2
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putative protein myosin heavy chain, chicken, PIR:S24348;supported by full-length cDNA: Ceres:147806. luminal binding protein ; supported by cDNA: gi_1303694_dbj_D84414.1_ATHBIPA transcriptional adaptor like protein ; supported by cDNA: gi_15215639_gb_AY050348.1_ putative protein disulfide-isomerase unknown protein Location of EST gbJN95878 putative protein disulfide isomerase ; supported by cDNA: gi_15810003_gb_AY054270.1_ hypothetical protein predicted by genscan and genefinder; supported by cDNA: gi_4837732_gb_AF085354.1_AF085354 putative casein kinase I putative putative putative putative fortein supported by genscan putative potein issupported by full-length cDNA: Ceres:13385. putative acyl-CoA synthetase ; supported by cDNA: gi_15450592_gb_AY052664.1_ putative protein RIO1 protein, Saccharomyces cerevisiae, PIR:S61006;supported by full-length cDNA: Ceres:42141.	247176_at 246796_at 245956_s_at 245288_at 245175_at 264167_at 267605_at 267512_at 267423_at 267268_at 266268_s_at 266288_s_at 263147_at 263811_at 263532_s_at	2.1 2.1 2.1 2.1 2 2 2 2 2 2 2 2 2 2 2 2
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putative protein myosin heavy chain, chicken, PIR:S24348;supported by full-length cDNA: Ceres:147806. luminal binding protein ; supported by cDNA: gi_1303694_dbj_D84414.1_ATHBIPA transcriptional adaptor like protein ; supported by cDNA: gi_15215639_gb_AY050348.1_ putative protein disulfide-isomerase unknown protein Location of EST gb N95878 putative protein disulfide isomerase ; supported by cDNA: gi_15810003_gb_AY054270.1_ hypothetical protein predicted by genscan and genefinder; supported by cDNA: gi_4837732_gb_AF085354.1_AF085354 putative potasium transporter hypothetical protein predicted by genscan putative casein kinase I putative casein kinase I putative aphilio//Mpt5 family RNA-binding protein hypothetical protein ; supported by cDNA: Ceres:13385. putative acyl-CoA synthetase ; supported by cDNA: gi_15450592_gb_AY052664.1_ putative protein RIO1 protein, Saccharomyces cerevisiae, PIR:S61006;supported by full-length cDNA: Ceres:42141. bZIP transcription factor (POSF21) identical to GB:Q04088; supported by cDNA: gi_15982853_gb_AY057534.1_ putative zinc-binding protein similar to zinc-binding protein (gi]3249068)	247176_at 246796_at 245268_at 245288_at 245288_at 264167_at 267605_at 267512_at 267512_at 267268_at 2662651_at 266288_s_at 266147_at 266288_s_at 263147_at 263321_at 263532_s_at 263259_at	2.1 2.1 2.1 2.1 2 2 2 2 2 2 2 2 2 2 2 2
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putative protein myosin heavy chain, chicken, PIR:S24348;supported by full-length cDNA: Ceres:147806. luminal binding protein ; supported by cDNA: gi_1303694_dbj_D84414.1_ATHBIPA transcriptional adaptor like protein ; supported by cDNA: gi_15215639_gb_AY050348.1_ putative protein disulfide-isomerase unknown protein Location of EST gb N95878 putative protein disulfide isomerase ; supported by cDNA: gi_15810003_gb_AY054270.1_ hypothetical protein predicted by genscan and genefinder; supported by cDNA: gi_4837732_gb_AF085354.1_AF085354 putative potassium transporter hypothetical protein predicted by genscan putative potassium transporter hypothetical protein predicted by genscan putative casein kinase I putative casein kinase I putative protein isupported by full-length cDNA: Ceres:13385. putative protein RIO1 protein, Saccharomyces cerevisiae, PIR:S61006; supported by full-length cDNA: Ceres:42141. bZIP transcription factor (POSF21) identical to GB:Q04088; supported by cDNA: gi_15982853_gb_AY057534.1_ putative zinc-binding protein similar to zinc-binding protein (gi]3249068) unknown protein putative cytochrome P450 monoxygenase strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana];supported by full-length cD hypothetical protein similar to hypothetical GB:QA4085 GI:26868770 from (Arabidopsis thaliana];supported by full-length cD hypothetical protein similar to hypothetical protein GB:AA74053 GI:2398533 from [Arabidopsis thaliana];supported by full-length cD hypothetical protein contains similarity to PP2 lectin polypeptide GI:410436 from [Cucurbita maxima]; supported by cDNA: gi_1529268_gb_A	247176_at 246796_at 245956_s_at 245288_at 245288_at 267175_at 2674167_at 267605_at 267512_at 267268_at 266288_s_at 266288_s_at 265147_at 263811_at 263811_at 263253_at 263253_at 262259_at 262280_at 262780_at 262298_at 262061_at	2.1 2.1 2.1 2.1 2 2 2 2 2 2 2 2 2 2 2 2
putative protein myosin heavy chain, chicken, PIR:S24348;supported by full-length cDNA: Ceres:147806. luminal binding protein ; supported by cDNA: gi_1303694_dbj_D84414.1_ATHBIPA transcriptional adaptor like protein ; supported by cDNA: gi_15215639_gb_AY050348.1_ putative protein disulfide-isomerase unknown protein Location of EST gb N95878 putative protein disulfide isomerase ; supported by cDNA: gi_15810003_gb_AY054270.1_ hypothetical protein predicted by genscan and genefinder; supported by cDNA: gi_4837732_gb_AF085354.1_AF085354 putative potassium transporter hypothetical protein predicted by genscan putative casein kinase I putative portein new for the predicted by genscan putative casein kinase I putative protein RIO1 protein, Supported by cDNA: Ceres:13385. putative protein RIO1 protein, Saccharomyces cerevisiae, PIR:S61006;supported by full-length cDNA: Ceres:42141. bzIP transcription factor (POSF21) identical to GB:Q04088; supported by cDNA: gi_15982853_gb_AY057534.1_ putative cytochrome P450 monooxygenase strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana) transcription factor, putative similar to transcription factor GB:CAA74053 GI:23985373 from (Arabidopsis thaliana); supported by full-length cDNA; gi_15292968, gb_A gibberellin 3 beta-hydroxylase, putative similar to gibberellin 3 beta-hydroxylase GI:3982753 from (Arabidopsis thaliana); supported by cDNA; gi_15292988, gb_A gibberellin 3 beta-hydroxylase, putative similar to gibberellin 3 beta-hydroxylase GI:3982753 from (Arabidopsis thaliana); supported by cDNA; gi_15292988, gb_A gibberellin 3 beta-hydroxylase, putative similar to gibberellin 3 beta-hydroxylase GI:3982753 from (Arabidopsis thaliana); supported by cDNA; gi_15292988, gb_A gibberellin 3 beta-hydroxylase, putative similar to gibberellin 3 beta-hydroxylase GI:3982753 from (Arabidopsis thaliana); supported by cDNA; gi_15292988, gb_A gibberellin 3 beta-hydroxylase, putative similar to gibberellin 3 beta-hydroxylase GI:3982753 from (Arabidopsis tha	247176_at 246796_at 245956_s_at 245288_at 245175_at 267165_at 267512_at 267512_at 26752_at 26768_at 266651_at 26688_s_at 265147_at 263811_at 263825_at 263253_at 263253_at 263259_at 262280_at 262280_at 26208_at 26208_at 26208_at 26208_at 26208_at 26208_at 26208_at 26208_at 26208_at	2.1 2.1 2.1 2.1 2 2 2 2 2 2 2 2 2 2 2 2
putative protein myosin heavy chain, chicken, PIR:S24348;supported by full-length cDNA: Ceres:147806. luminal binding protein ; supported by cDNA: gi_1303694_dbj_D84414.1_ATHBIPA transcriptional adaptor like protein ; supported by cDNA: gi_15215639_gb_AY050348.1_ putative protein disulfide-isomerase unknown protein Location of EST gb N95878 putative protein disulfide isomerase ; supported by cDNA: gi_15810003_gb_AY054270.1_ hypothetical protein predicted by genscan and genefinder; supported by cDNA: gi_4837732_gb_AF085354.1_AF085354 putative potassium transporter hypothetical protein predicted by genscan putative potasin disulfide isomerase ; unknown protein predicted by genscan putative casein kinase I putative potein isupported by full-length cDNA: Ceres:13385. putative acyl-CoA synthetase ; supported by CDNA: gi_15450592_gb_AY052664.1_ putative protein flot protein, Saccharomyces cerevisiae, PIR:S61006;supported by full-length cDNA: Ceres:42141. bZIP transcription factor (POSF21) identical to GB:Q04088; supported by cDNA: gi_15982853_gb_AY057534.1_ putative cytochrome P450 monooxygenase strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana] transcription factor, putative similar to zinc-binding protein GB:CAA74053 GI:2398533 from [Arabidopsis thaliana];supported by full-length cD hypothetical protein similar to Transcription factor GB:CAA74053 GI:2398533 from [Arabidopsis thaliana];supported by full-length cD hypothetical protein similar to Transcription factor GB:CAA74053 GI:2398533 from [Arabidopsis thaliana];supported by full-length cD hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:28026.	247176_at 246796_at 245956_s_at 245288_at 245175_at 264167_at 267605_at 267512_at 267512_at 267268_at 266268_s_at 266288_s_at 263253_at 263253_at 263259_at 263259_at 263222_at 262298_at 262061_at 262768_at 260622_at	2.1 2.1 2.1 2.1 2.1 2 2 2 2 2 2 2 2 2 2
putative protein myosin heavy chain, chicken, PIR:S24348;supported by full-length cDNA: Ceres:147806. luminal binding protein ; supported by cDNA: gi_1303694_dbj_D84414.1_ATHBIPA transcriptional adaptor like protein ; supported by cDNA: gi_15215639_gb_AY050348.1_ putative protein disulfide-isomerase unknown protein Location of EST gb N95878 putative protein disulfide isomerase ; supported by cDNA: gi_15810003_gb_AY054270.1_ hypothetical protein predicted by genscan and genefinder; supported by cDNA: gi_4837732_gb_AF085354.1_AF085354 putative potassium transporter hypothetical protein predicted by genscan putative potassium transporter hypothetical protein predicted by genscan putative casein kinase I putative casein kinase I putative casein kinase I putative acsein kinase I putative acsein kinase I putative acyl-CoA synthetase ; supported by CDNA: gi_15450592_gb_AY052664.1_ putative arc-binding protein, Saccharomyces cerevisiae, PIR:S61006;supported by full-length cDNA: Ceres:42141. bZIP transcription factor (POSF21) identical to GB:Qu4088; supported by cDNA: gi_15982853_gb_AY057534.1_ putative zinc-binding protein similar to zinc-binding protein (gi]3249068) unknown protein putative cytochrome P450 monooxygenaes strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of th hypothetical protein similar to Transcription factor GB:CAA74053 GI:2398533 from [Arabidopsis thaliana]; transcription factor, putative similar to Transcription factor GB:CAA74053 GI:2398533 from [Arabidopsis thaliana]; transcription factor, putative similar to P2 electin polypeptide GI:410436 from [Cucurbita maxima]; supported by cDNA: gi_15292968_gb_A gibberellin 3 beta-hydroxylase, putative similar to gibberellin 3 beta-hydroxylase GI:3982753 from [Arabidopsis thaliana]; supported by cDNA: hypothetical protein predicted by genscan+	247176_at 246796_at 245956_s_at 245288_at 245288_at 264167_at 267405_at 267423_at 267423_at 267268_at 2662651_at 26628_s_at 265147_at 263485_at 263253_at 263253_at 263259_at 263259_at 262260_at 262098_at 262098_at 262061_at 260594_at	2.1 2.1 2.1 2.1 2.1 2 2 2 2 2 2 2 2 2 2
putative protein myosin heavy chain, chicken, PIR:S24348;supported by full-length cDNA: Ceres:147806. luminal binding protein ; supported by cDNA: gi_1303694_dbj_D84414.1_ATHBIPA transcriptional adaptor like protein ; supported by cDNA: gi_15215639_gb_AY050348.1_ putative protein disulfide-isomerase unknown protein Location of EST gb N95878 putative protein disulfide isomerase ; supported by cDNA: gi_15810003_gb_AY054270.1_ hypothetical protein predicted by genscan and genefinder; supported by cDNA: gi_4837732_gb_AF085354.1_AF085354 putative potassium transporter hypothetical protein predicted by genscan putative potasin disulfide isomerase ; unknown protein predicted by genscan putative casein kinase I putative potein isupported by full-length cDNA: Ceres:13385. putative acyl-CoA synthetase ; supported by CDNA: gi_15450592_gb_AY052664.1_ putative protein flot protein, Saccharomyces cerevisiae, PIR:S61006;supported by full-length cDNA: Ceres:42141. bZIP transcription factor (POSF21) identical to GB:Q04088; supported by cDNA: gi_15982853_gb_AY057534.1_ putative cytochrome P450 monooxygenase strong similarity to gb X97864 cytochrome P450 from Arabidopsis thaliana] transcription factor, putative similar to zinc-binding protein GB:CAA74053 GI:2398533 from [Arabidopsis thaliana];supported by full-length cD hypothetical protein similar to Transcription factor GB:CAA74053 GI:2398533 from [Arabidopsis thaliana];supported by full-length cD hypothetical protein similar to Transcription factor GB:CAA74053 GI:2398533 from [Arabidopsis thaliana];supported by full-length cD hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:28026.	247176_at 246796_at 245956_s_at 245288_at 245288_at 267605_at 267605_at 267512_at 267268_at 266288_s_at 266288_s_at 266288_s_at 266311_at 26332_s_at 263253_at 263253_at 263259_at 263260_at 262780_at 262280_at 262061_at 262061_at 261768_at 260622_at 260622_at 260624_at 263794_at	2.1 2.1 2.1 2.1 2.1 2 2 2 2 2 2 2 2 2 2

metalloprotease, putative similar to metalloprotease 1 GB:AAC67244 from [Homo sapiens]		
110	257033 at	2
mitochondrial chaperonin hsp60 identical to mitochondrial chaperonin hsp60 GB:Z11547 [Arabidopsis thaliana] (Plant Mol. Biol. 18 (5), 873-8	256905 at	2
major latex protein, putative similar to major latex protein type1 GB:CAA63026 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:		2
isoamyase-like protein probable isoamyase (EC 3.2.1.68) sul - Zea mays, P(Z:T0132)	255070 at	2
	_	
putative protein (fragment) ATP(GTP)-binding protein, Homo sapiens, AJ010842;supported by full-length cDNA: Ceres:6952.	254375_at	2
ADP,ATP carrier-like protein ADP,ATP carrier protein-rice, PIR2:S33630;supported by full-length cDNA: Ceres:42036.	253776_at	2
putative protein kinase serine/threonine protein kinase, Arabidopsis thaliana, PID:D1006875; supported by cDNA: gi_14334745_gb_AY03504	_	2
nucellin -like protein nucellin - Hordeum vulgare,PIR:G2290202;supported by full-length cDNA: Ceres:24738.	253331_at	2
putative protein ;supported by full-length cDNA: Ceres:8161.	253322_at	2
cinnamyl alcohol dehydrogenase - like protein cinnamyl alcohol dehydrogenase, Populus deltoides, PATCHX:G288753; supported by cDNA:	253277_at	2
hypothetical protein	252432 at	2
ABC-type transport protein-like protein AbcA, Dictyostelium discoideum, DDU66526	252379 at	2
putative protein various predicted proteins; supported by full-length cDNA: Ceres:6508.	252281 at	2
translation releasing factor RF-1 - like protein translation releasing factor RF-1, Synechocystis sp., PIR:S76914	251193 at	2
putative protein ; supported by full-length cDNA: Ceres:7731.	251010 at	2
putative protein salt-inducible protein, membrane-associated, common tobacco, PIR:T02047; supported by cDNA: qi 15810430 qb AY0562	_	
	250856_at	2
putative protein	250158_at	2
glutathione S-transferase-like protein ;supported by cDNA: gi_11096011_gb_AF288189.1_AF288189	250083_at	2
putative protein similar to unknown protein (pir  T04732)	249113_at	2
spermidine synthase ;supported by full-length cDNA: Ceres:33021.	248248_at	2
putative protein contains similarity to protein kinase	247918_at	2
putative protein predicted protein, Arabidopsis thalina; supported by cDNA: gi_13899116_gb_AF370553.1_AF370553	247507 at	2
RNA helicase ; supported by cDNA: gi 14517481 gb AY039576.1	247465 at	2
putative protein similar to unknown protein (pir  T01257)	247386 at	2
lysosomal Pro-X carboxypeptidase	247156 at	2
putative protein contains similarity to unknown protein (sp Q10058);supported by full-length cDNA: Ceres:108335.	246985 at	2
lethal leaf-spot 1 homolog LIS1	_	
	246335_at	2
PPR-repeat protein, putative contains multiple PPR domains: PF01535: PPR repeat	246313_at	2
putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:32958.	245905_at	2
chaperonin precursor, putative similar to chaperonin precursor GI:806807 from [Pisum sativum]	245876_at	2
Dr4(protease inhibitor) identical to Dr4 GI:469114 from [Arabidopsis thaliana]; supported by cDNA: gi_13877842_gb_AF370184.1_AF370184	245736_at	2
cytochrome c biogenesis orf452	244951_s_at	2
hypothetical protein	244921_s_at	2
hypothetical protein	244924_at	2
hypothetical protein	257332 at	2
cyclic nucleotide gated channel (CNGC4) like protein Arabidopsis thaliana cyclic nucleotide gated channel (CNGC4),PID:g4378659	255599 at	1.9
putative small heat shock protein ;supported by full-length cDNA: Ceres:99763.	267336 at	1.9
Expressed protein ; supported by full-length cDNA: Ceres: 123915.	267036 at	1.9
putative nonspecific lipid-transfer protein ;supported by full-length cDNA: Ceres:18328.	266415 at	1.9
putative glycine-rich protein ; supported by cDNA: gi_15215617 gb_AY050337.1_	265511 at	1.9
hypothetical protein	265195 at	1.9
	_	1.9
	_	
hypothetical protein contains similarity to glycogenin GI:165512 from [Orycotalagus cuniculus]	264476_at	1.9
hypothetical protein Similar to hypothetical protein SPAC2F7.14c gi 1052797 from Schizosaccharomyces pombe cosmid gb Z50142	264357_at	1.9
unknown protein	263515_at	1.9
unknown protein	263513_at	1.9
cytoplasmic aconitate hydratase	263348_at	1.9
dynamin-like protein	263278_at	1.9
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:94743.	263151_at	1.9
hypothetical protein similar to putative disease resistance protein GB:CAB40943 GI:4586107 from [Arabidopsis thaliana]	262326_at	1.9
ABC transporter protein, putative similar to ABC transporter protein GB:AAF31030 GI:6899653 from [Leishmania major]	262005_at	1.9
hypothetical protein contains similarity to spastin protein orthologue GB:CAB60143 GI:6273572 from [Mus musculus]		1.9
	261689 at	
hypothetical protein predicted by genemark.hmm	_	
hypothetical protein predicted by genemark.hmm unknown protein contains similarity to set protein GI:338038 from [Homo sapiens]:supported by full-length cDNA: Ceres:27467.	261524_at	1.9
unknown protein contains similarity to set protein GI:338038 from [Homo sapiens];supported by full-length cDNA: Ceres:27467.		1.9 1.9
unknown protein contains similarity to set protein GI:338038 from [Homo sapiens];supported by full-length cDNA: Ceres:27467. Ca2+-dependent membrane-binding protein annexin idenctical to GB:AAD34236 from [Arabidopsis thaliana];supported by full-length cDNA: C	261524_at 261406_at 261285_at	1.9 1.9 1.9
unknown protein contains similarity to set protein GI:338038 from [Homo sapiens];supported by full-length cDNA: Ceres:27467. Ca2+-dependent membrane-binding protein annexin idenctical to GB:AAD34236 from [Arabidopsis thaliana];supported by full-length cDNA: C phosphoethanolamine N-methyltransferase, putative similar to GB:AAF61950 from [Spinacia oleracea]; supported by cDNA: gi_16226648_gt	261524_at 261406_at 261285_at 261309_at	1.9 1.9 1.9 1.9
unknown protein contains similarity to set protein GI:338038 from [Homo sapiens];supported by full-length cDNA: Ceres:27467. Ca2+-dependent membrane-binding protein annexin idenctical to GB:AAD34236 from [Arabidopsis thaliana];supported by full-length cDNA: C phosphoethanolamine N-methyltransferase, putative similar to GB:AAF61950 from [Spinacia oleracea]; supported by cDNA: gi_16226648_gt hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:19486.	261524_at 261406_at 261285_at 261309_at 260875_at	1.9 1.9 1.9 1.9 1.9
unknown protein contains similarity to set protein GI:338038 from [Homo sapiens];supported by full-length cDNA: Ceres:27467. Ca2+-dependent membrane-binding protein annexin idenctical to GB:AAD34236 from [Arabidopsis thaliana];supported by full-length cDNA: C phosphoethanolamine N-methyltransferase, putative similar to GB:AAF61950 from [Spinacia oleracea]; supported by cDNA: gi_16226648_gt hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:19486. MYB-related protein identical to GB:CAA90748 GI:1263093 from [Arabidopsis thaliana]	261524_at 261406_at 261285_at 261309_at 260875_at 260784_at	1.9 1.9 1.9 1.9 1.9 1.9
unknown protein contains similarity to set protein GI:338038 from [Homo sapiens];supported by full-length cDNA: Ceres:27467. Ca2+-dependent membrane-binding protein annexin idenctical to CB:AAD34236 from [Arabidopsis thaliana];supported by full-length cDNA: C phosphoethanolamine N-methyltransferase, putative similar to GB:AAF61950 from [Spinacia oleracea]; supported by cDNA: gi_16226648_gt hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:19486. MYB-related protein identical to GB:CAA90748 GI:1263093 from [Arabidopsis thaliana] unknown protein ;supported by full-length cDNA: Ceres:18355.	261524_at 261406_at 261285_at 261309_at 260875_at 260784_at 259342_at	1.9 1.9 1.9 1.9 1.9 1.9 1.9
unknown protein contains similarity to set protein GI:338038 from [Homo sapiens];supported by full-length cDNA: Ceres:27467. Ca2+-dependent membrane-binding protein annexin idenctical to GB:AAD34236 from [Arabidopsis thaliana];supported by full-length cDNA: C phosphoethanolamine N-methyltransferase, putative similar to GB:AAF61950 from [Spinacia oleracea]; supported by cDNA: gi_16226648_gt hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:19486. MYB-related protein identical to GB:CAA90748 GI:1263093 from [Arabidopsis thaliana] unknown protein ;supported by full-length cDNA: Ceres:18355.	261524_at 261406_at 261285_at 261309_at 260875_at 260784_at 259342_at 259318_at	1.9 1.9 1.9 1.9 1.9 1.9 1.9 1.9
unknown protein contains similarity to set protein GI:338038 from [Homo sapiens];supported by full-length cDNA: Ceres:27467. Ca2+-dependent membrane-binding protein annexin idenctical to GB:AAD34236 from [Arabidopsis thaliana];supported by full-length cDNA: C phosphoethanolamine N-methyltransferase, putative similar to GB:AAF61950 from [Spinacia oleracea]; supported by cDNA: gi_16226648_gt hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:19486. MYB-related protein identical to GB:CAA90748 GI:1263093 from [Arabidopsis thaliana] unknown protein ;supported by full-length cDNA: Ceres:18355. unknown protein similar to HYP1 GB:CAA55187 from [Arabidopsis thaliana] unknown protein similar to possible apospory-associated protein C GB:Q40784 [Pennisetum ciliare];supported by full-length cDNA: Ceres:415	261524_at 261406_at 261285_at 261309_at 260875_at 260784_at 259342_at 259318_at 259186_at	1.9 1.9 1.9 1.9 1.9 1.9 1.9 1.9
unknown protein contains similarity to set protein GI:338038 from [Homo sapiens];supported by full-length cDNA: Ceres:27467. Ca2+-dependent membrane-binding protein annexin idenctical to GB:AAD34236 from [Arabidopsis thaliana];supported by full-length cDNA: C phosphoethanolamine N-methyltransferase, putative similar to GB:AAF61950 from [Spinacia oleracea]; supported by cDNA: gi_16226648_gt hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:19486. MYB-related protein identical to GB:CAA90748 GI:1263093 from [Arabidopsis thaliana] unknown protein isimilar to HYP1 GB:CAA5187 from [Arabidopsis thaliana] unknown protein similar to HYP1 GB:CAA5187 from [Arabidopsis thaliana] unknown protein similar to possible apospory-associated protein C GB:Q40784 [Pennisetum ciliare];supported by full-length cDNA: Ceres:1415 putative serine carboxypeptidase precursor identical to serine carboxypeptidase precursor GB:P32826 [Arabidopsis thaliana] up to residue 51	261524_at 261406_at 261285_at 261309_at 260875_at 260784_at 259342_at 259318_at	1.9 1.9 1.9 1.9 1.9 1.9 1.9 1.9
unknown protein contains similarity to set protein GI:338038 from [Homo sapiens];supported by full-length cDNA: Ceres:27467. Ca2+-dependent membrane-binding protein annexin idenctical to CB:AAD34236 from [Arabidopsis thaliana];supported by full-length cDNA: C phosphoethanolamine N-methyltransferase, putative similar to GB:AAD34236 from [Spinacia oleracea]; supported by cDNA: gi_16226648_gt hypothetical protein identical to GB:CAA90748 GI:1263093 from [Arabidopsis thaliana] unknown protein is supported by full-length cDNA: Ceres:13355. unknown protein similar to HYP1 GB:CAA55187 from [Arabidopsis thaliana] unknown protein similar to possible apospory-associated protein C GB:Q40784 [Pennisetum ciliare];supported by full-length cDNA: Ceres:41: putative arTPase (ISW2-like) similar to ISW2 (ATPase component of a two subunit chromatin remodeling complex) GB:6324879 [Saccharom]	261524_at 261406_at 261285_at 261309_at 260875_at 260784_at 259342_at 259318_at 259318_at 259318_at 25970_at 258904_at	1.9 1.9 1.9 1.9 1.9 1.9 1.9 1.9 1.9
unknown protein contains similarity to set protein GI:338038 from [Homo sapiens];supported by full-length cDNA: Ceres:27467. Ca2+-dependent membrane-binding protein annexin idenctical to GB:AAD34236 from [Arabidopsis thaliana];supported by full-length cDNA: C phosphoethanolamine N-methyltransferase, putative similar to GB:AAF61950 from [Spinacia oleracea]; supported by cDNA: gi_16226648_gt hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:19486. MYB-related protein identical to GB:CAA90748 GI:1263093 from [Arabidopsis thaliana] unknown protein isimilar to HYP1 GB:CAA5187 from [Arabidopsis thaliana] unknown protein similar to HYP1 GB:CAA5187 from [Arabidopsis thaliana] unknown protein similar to possible apospory-associated protein C GB:Q40784 [Pennisetum ciliare];supported by full-length cDNA: Ceres:1415 putative serine carboxypeptidase precursor identical to serine carboxypeptidase precursor GB:P32826 [Arabidopsis thaliana] up to residue 51	261524_at 261406_at 261285_at 261309_at 260875_at 260784_at 259342_at 259318_at 259186_at 258970_at	1.9 1.9 1.9 1.9 1.9 1.9 1.9 1.9 1.9
unknown protein contains similarity to set protein GI:338038 from [Homo sapiens];supported by full-length cDNA: Ceres:27467. Ca2+-dependent membrane-binding protein annexin idenctical to CB:AAD34236 from [Arabidopsis thaliana];supported by full-length cDNA: C phosphoethanolamine N-methyltransferase, putative similar to GB:AAD34236 from [Spinacia oleracea]; supported by cDNA: gi_16226648_gt hypothetical protein identical to GB:CAA90748 GI:1263093 from [Arabidopsis thaliana] unknown protein is supported by full-length cDNA: Ceres:13355. unknown protein similar to HYP1 GB:CAA55187 from [Arabidopsis thaliana] unknown protein similar to possible apospory-associated protein C GB:Q40784 [Pennisetum ciliare];supported by full-length cDNA: Ceres:41: putative arTPase (ISW2-like) similar to ISW2 (ATPase component of a two subunit chromatin remodeling complex) GB:6324879 [Saccharom]	261524_at 261406_at 261285_at 261309_at 260875_at 260784_at 259342_at 259318_at 259318_at 259318_at 25970_at 258904_at	1.9 1.9 1.9 1.9 1.9 1.9 1.9 1.9 1.9
unknown protein contains similarity to set protein GI:338038 from [Homo sapiens];supported by full-length cDNA: Ceres:27467. Ca2+-dependent membrane-binding protein annexin idenctical to GB:AAD34236 from [Arabidopsis thaliana];supported by full-length cDNA: C phosphoethanolamine N-methyltransferase, putative similar to GB:AAF61950 from [Spinacia oleracea]; supported by cDNA: gi_16226648_gt hypothetical protein identical to GB:CAA90748 GI:1263093 from [Arabidopsis thaliana] unknown protein identical to GB:CAA90748 GI:1263093 from [Arabidopsis thaliana] unknown protein isimilar to HYP1 GB:CAA55187 from [Arabidopsis thaliana] unknown protein similar to HYP1 GB:CAA55187 from [Arabidopsis thaliana] unknown protein isimilar to possible apospory-associated protein C GB:Q40784 [Pennisetum ciliare];supported by full-length cDNA: Ceres:41: putative ATPase (ISW2-like) similar to ISW2 (ATPase component of a two subunit chromatin remodeling complex) GB:6324879 [Saccharomy unknown protein ; supported by cDNA: gi_15292900_gb_AY050884.1_	261524_at 261285_at 261309_at 260875_at 260875_at 259342_at 259342_at 259318_at 259386_at 258970_at 258904_at 258838_at	1.9 1.9 1.9 1.9 1.9 1.9 1.9 1.9 1.9 1.9
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putative protein contains similarity to RNA-binding protein; supported by full-length cDNA: Ceres:265530.	248869_at	1.9
DnaJ protein-like ;supported by full-length cDNA: Ceres:14006.	248739_at	1.9
putative protein contains similarity to 5 -nucleotidase	248628_at	1.9
putative protein similar to unknown protein (pir  T09559); supported by cDNA: gi_15810212_gb_AY056121.1_	248310_at	1.9
unknown protein ;supported by full-length cDNA: Ceres:114955.	248299_at	1.9
putative protein contains similarity to nuclear movement protein nudC;supported by full-length cDNA: Ceres:38105.	248258_at	1.9
putative protein similar to unknown protein (emb CAB76911.1)	247938_at	1.9
plasma membrane ATPase 3 (proton pump) (splP20431);supported by cDNA: gi_15982712_gb_AY056780.1_	247902_at	1.9
SKP1 interacting partner 1 (SKIP1) identical to SKP1 interacting partner 1 GI:10716947 from [Arabidopsis thaliana]; supported by full-length c[	247863_at	1.9
putative protein predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_15983810_gb_AY056811.1_	247590_at	1.9
receptor-like protein kinase ; supported by cDNA: gi_16974576_gb_AY060554.1_	247357_at	1.9
nuclear protein-like	247271_at	1.9
poly(A)-binding protein II-like ; supported by cDNA: gi_14423493_gb_AF386984.1_AF386984	247173_at	1.9
putative protein auxin-independent growth promoter - Nicotiana tabacum, PIR:A44226	246516_at	1.9
14-3-3 protein GF14upsilon (grf5) identical to 14-3-3 protein GF14 upsilon GI:2232148 from [Arabidopsis thaliana] ; supported by cDNA: gi_14	246489_at	1.9
hypothetical protein	246232_at	1.9
heat shock transcription factor HSF4 ; supported by cDNA: gi_1619920_gb_U68017.1_ATU68017	246214_at	1.9
aminopeptidase-like protein ; supported by cDNA: gi_13430673_gb_AF360249.1_AF360249	246219_at	1.9
polyubiquitin (UBQ4) identical to GI:17677	245989_s_at	1.9
putative protein protein phosphatase-1 regulatory subunit 7 alpha2 - Homo sapiens, EMBL:AF067136;supported by full-length cDNA: Ceres:	245938_at	1.9
putative protein ;supported by full-length cDNA: Ceres:29990.	245699_at	1.9
unknown protein	245678_at	1.9
putative protein	245418_at	1.9
Expressed protein ; supported by cDNA: gi_5764394_gb_AF159587.1_AF159587	245256_at	1.9
putative Na+/Ca2+ antiporter ;supported by cDNA: gi_6492236_gb_AF109178.1_AF109178	245127_at	1.9
unknown protein	266652_at	1.8
hypothetical protein	265227_s_at	1.8
putative phytochrome A similar to GB:AAA21351; supported by cDNA: gi_14517371_gb_AY039520.1_	264508_at	1.8
unknown protein ;supported by full-length cDNA: Ceres:93312.	262607_at	1.8
hypothetical protein predicted by genemark.hmm	262407_at	1.8
xylosidase, putative similar to xylosidase GI:2102655 from [Aspergillus niger]	262181_at	1.8
hypothetical protein predicted by genemark.hmm	262130_at	1.8
hypthetical protein contains similarity to spliceosome associated protein SAP 145 GI:1173904 from [Homo sapiens]	261872_s_at	1.8
abscisic acid responsive elements-binding factor identical to abscisic acid responsive elements-binding factor GB:AAF27179 GI:6739274 from	261613_at	1.8
unknown protein ;supported by full-length cDNA: Ceres:6937.	261485_at	1.8
protein kinase, putative (fragment) similar to GB:BAA94509 from [Populus nigra]	261436_at	1.8
protein kinase, putative similar to many predicted protein kinases	261368_at	1.8
putative GTP-binding protein similar to NGP-1 GB:Q13823 from (Homo sapiens)	261314_at	1.8
unknown protein	261064_at	1.8
hypothetical protein predicted by genemark.hmm	261086_at	1.8
RING finger protein, putative similar to GB:BAA78677 from [Homo sapiens]	260690_at	1.8
unknown protein	260273_at	1.8
hypothetical protein similar to hypothetical proteins: GB:AAD21751, GB:AAC33230 [Arabidopsis thaliana]	260262_at	1.8
unknown protein ;supported by full-length cDNA: Ceres:270659.	260025_at	1.8
nucellin-like protein similar to nucellin GB:AAB96882 [Hordeum vulgare] (nucellin: similar to aspartic protease and its specific expression in nu	259733_at	1.8
CONSTANS family zinc finger protein, putative contains Pfam profile: PF01760: CONSTANS family zinc finger; supported by cDNA: gi_1433	259595_at	1.8
hypothetical protein	259534_at	1.8
protein phosphatase 2C (PP2C) identical to protein phosphatase 2C (PP2C) GB:P49598 [Arabidopsis thaliana]	259231_at	1.8
unknown protein similar to hypothetical protein GB:AAC23643 [Arabidopsis thaliana]	259232_at	1.8
unknown protein similar to hypothetical proteins GB:P73627, GB:Q55884, GB:P73121 [Synechocystis sp.]; supported by full-length cDNA: Ct	259226_at	1.8
unknown protein similar to CGI-86 protein GB:AAD34081 [Homo sapiens], HMM hit: Alcohol/other dehydrogenases, short chain type	259051_at	1.8
putative glucose acyltransferase similar to glucose acyltransferase GB:AAD01263 [Solanum berthaultii]; also similar to serine carboxypeptida:	258923_at	1.8
putative O-linked GlcNAc transferase similar to O-linked GlcNAc transferase GB:AAB63465 [Caenorhabditis elegans]	258575_at	1.8
cytochrome P450, putative similar to cytochrome P450 GB:O65784 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 262802.	257634_s_at	1.8
chaperonin, putative similar to CHAPERONIN CPN60-2, MITOCHONDRIAL PRECURSOR GB:Q05046 from [Cucurbita maxima]; supported t	257608_at	1.8
9-cis-epoxycarotenoid dioxygenase, putative similar to 9-cis-epoxycarotenoid dioxygenase GB:AAF26356 [Phaseolus vulgaris]; supported by	257280_at	1.8
RNA-binding protein, putative contains Pfam profile: PF00806 Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain	257122_at	1.8
putative 3-hydroxybutyryl-CoA dehydrogenase similar to 3-HYDROXYBUTYRYL-COA DEHYDROGENASE GB:Q45223 from [Bradyrhizobiun		1.8
unknown protein ; supported by cDNA: gi_14334837_gb_AY035092.1_	256310_at	1.8
hypothetical protein predicted by genscan+	256089_at	1.8
amino acid permease I identical to amino acid permease I GI:22641 from [Arabidopsis thaliana]; supported by cDNA: gi_404018_gb_L16240.	256022_at	1.8
hypothetical protein contains Pfam profile: PF00612 IQ calmodulin-binding motif	255783_at	1.8
cathepsin B-like cysteine protease, putative similar to cathepsin B-like cysteine proteinase GI:609175 from [Nicotiana rustica]; contains an un		1.8
polycomb group - like protein similar to A. thaliana homeotic protein curlyleaf, GenBank accession number Y10580; supported by cDNA: gi_4	255590_at	1.8
	255590_at 255510_at	
putative ribosomal protein L19 similar to L19 from several species; supported by cDNA: gi_14423511_gb_AF386993.1_AF386993		1.8
coded for by A. thaliana cDNA T75804 similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91)	255510_at 255520_at 255474_at	1.8 1.8
	255510_at 255520_at	
coded for by A. thaliana cDNA T75804 similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91)	255510_at 255520_at 255474_at	1.8
coded for by A. thaliana cDNA T75804 similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) putative pre-mRNA splicing factor similar to yeast pre-mRNA splicing factors; supported by cDNA: gi_16604550_gb_AY059720.1_	255510_at 255520_at 255474_at 255382_at	1.8 1.8
coded for by A. thaliana cDNA T75804 similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) putative pre-mRNA splicing factor similar to yeast pre-mRNA splicing factors; supported by cDNA: gi_16604550_gb_AY059720.1_ putative ABC transporter similar to Guillardia theta ABC transporter, GenBank accession number AF041468; supported by cDNA: gi_155291 UV-damaged DNA binding factor - like protein XPE UV-damaged DNA binding factor, Mus musculus, BAA84699 putative protein anthocyanin rhamnosyltransferase -Petunia x hybrida, PID:g454253	255510_at 255520_at 255474_at 255382_at 255305_at 255226_at 255032_at	1.8 1.8 1.8 1.8 1.8
coded for by A. thaliana cDNA T75804 similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) putative pre-mRNA splicing factor similar to yeast pre-mRNA splicing factors; supported by cDNA: gi_16604550_gb_AY059720.1_ putative ABC transporter similar to Guillardia theta ABC transporter, GenBank accession number AF041468; supported by cDNA: gi_155291 UV-damaged DNA binding factor - like protein XPE UV-damaged DNA binding factor, Mus musculus, BAA84699 putative protein anthocyanin rhamnosyltransferase -Petunia x hybrida, PID:g454253 putative protein hypothetical protein F7H19.70 - Arabidopsis thaliana, PID:e1310057	255510_at 255520_at 255474_at 255382_at 255305_at 255226_at 255032_at 2554848_at	1.8 1.8 1.8 1.8 1.8 1.8
coded for by A. thaliana cDNA T75804 similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) putative pre-mRNA splicing factor similar to yeast pre-mRNA splicing factors; supported by cDNA: gi_16604550_gb_AY059720.1_ putative ABC transporter similar to Guillardia theta ABC transporter, GenBank accession number AF041468; supported by cDNA: gi_155291 UV-damaged DNA binding factor - like protein XPE UV-damaged DNA binding factor, Mus musculus, BAA84699 putative protein anthocyanin rhannosyltransferase -Petunia x hybrida, PID:g454253 putative protein hypothetical protein F7H19.70 - Arabidopsis thaliana, PID:e1310057 putative protein ; supported by cDNA: gi_16323185_gb_AY057697.1_	255510_at 255520_at 255474_at 255382_at 255305_at 255226_at 255226_at 255032_at 255032_at 254848_at	1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8
coded for by A. thaliana cDNA T75804 similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) putative pre-mRNA splicing factor similar to yeast pre-mRNA splicing factors; supported by cDNA: gi_16604550_gb_AY059720.1_ putative ABC transporter similar to Guillardia theta ABC transporter, GenBank accession number AF041468; supported by cDNA: gi_155291 UV-damaged DNA binding factor - like protein XPE UV-damaged DNA binding factor, Mus musculus, BAA84699 putative protein anthocyanin rhamnosyltransferase -Petunia x hybrida, PID:g454253 putative protein hypothetical protein F7H19.70 - Arabidopsis thaliana, PID:e1310057 putative protein ; supported by cDNA: gi_16323185_gb_AY057697.1_ potassium channel protein AKT3 ; supported by cDNA: gi_1100897_gb_U40154.1_ATU40154	255510_at 255520_at 255474_at 255305_at 25526_at 255032_at 255032_at 254848_at 254764_at 254305_at	1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8
coded for by A. thaliana cDNA T75804 similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) putative pre-mRNA splicing factor similar to yeast pre-mRNA splicing factors; supported by cDNA: gi_16604550_gb_AY059720.1_ putative ABC transporter similar to Guillardia theta ABC transporter, GenBank accession number AF041468; supported by cDNA: gi_155291 UV-damaged DNA binding factor - like protein XPE UV-damaged DNA binding factor, Mus musculus, BAA84699 putative protein anthocyanin rhamnosyltransferase -Petunia x hybrida, PID:e1310057 putative protein hypothetical protein F7H19.70 - Arabidopsis thaliana, PID:e1310057 putative protein is supported by cDNA: gi_16323185_gb_AY057697.1_ potassium channel protein AKT3 ; supported by cDNA: gi_1100897_gb_U40154.1_ATU40154 putative serine/threonine kinase MAP3K delta-1 protein kinase, Arabidopsis thaliana,PID:g2253010; supported by cDNA: gi_15810436_gb_A	255510_at 255520_at 255474_at 255382_at 255382_at 255226_at 255226_at 255032_at 254848_at 254764_at 254305_at 254269_at	1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8
coded for by A. thaliana cDNA T75804 similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) putative pre-mRNA splicing factor similar to yeast pre-mRNA splicing factors; supported by cDNA: gi_16604550_gb_AY059720.1_ putative ABC transporter similar to Guillardia theta ABC transporter, GenBank accession number AF041468; supported by cDNA: gi_155291 UV-damaged DNA binding factor - like protein XPE UV-damaged DNA binding factor, Mus musculus, BAA84699 putative protein anthocyanin rhamnosyltransferase -Petunia x hybrida, PID:g454253 putative protein hypothetical protein F7H19.70 - Arabidopsis thaliana, PID:e1310057 putative protein ; supported by cDNA: gi_16323185_gb_AY057697.1_ potassium channel protein AKT3 ; supported by cDNA: gi_1100897_gb_U40154.1_ATU40154 putative serine/threonine kinase MAP3K delta-1 protein kinase, Arabidopsis thaliana,PID:g2253010; supported by cDNA: gi_15810436_gb_A transcriptional activator CBF1-like protein strong similarity to transcriptional activator CBF1, Arabidopsis thaliana00	255510_at 255520_at 255474_at 255382_at 255305_at 255206_at 255206_at 255032_at 254848_at 254764_at 254305_at 254269_at 254269_at	1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8
coded for by A. thaliana cDNA T75804 similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) putative pre-mRNA splicing factor similar to yeast pre-mRNA splicing factors; supported by cDNA: gi_16604550_gb_AY059720.1_ putative ABC transporter similar to Guillardia theta ABC transporter, GenBank accession number AF041468; supported by cDNA: gi_155291 UV-damaged DNA binding factor - like protein XPE UV-damaged DNA binding factor, Mus musculus, BAA84699 putative protein anthocyanin rhannosyltransferase -Petunia x hybrida, PID:g454253 putative protein hypothetical protein F7H19.70 - Arabidopsis thaliana, PID:e1310057 putative protein ; supported by cDNA: gi_16323185_gb_AY057697.1_ potassium channel protein AKT3 ; supported by cDNA: gi_1100897_gb_U40154.1_ATU40154 putative cBrine/threonine kinase MAP3K delta-1 protein kinase, Arabidopsis thaliana,PID:g2253010; supported by cDNA: gi_15810436_gb_A transcriptional activator CBF1-like protein strong similarity to transcriptional activator CBF1, Arabidopsis thaliana00 protein phosphatase ABI1 ; supported by cDNA: gi_14334799_gb_AY035073.1_	255510_at 255520_at 255474_at 255382_at 255382_at 255226_at 255226_at 255032_at 254848_at 254764_at 254305_at 254269_at	1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8
coded for by A. thaliana cDNA T75804 similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) putative pre-mRNA splicing factor similar to yeast pre-mRNA splicing factors; supported by cDNA: gi_16604550_gb_AY059720.1_ putative ABC transporter similar to Guillardia theta ABC transporter, GenBank accession number AF041468; supported by cDNA: gi_155291 UV-damaged DNA binding factor - like protein XPE UV-damaged DNA binding factor, Mus musculus, BAA84699 putative protein anthocyanin rhannosyltransferase -Petunia x hybrida, PID:9454253 putative protein hypothetical protein F7H19.70 - Arabidopsis thaliana, PID:91310057 putative protein ; supported by cDNA: gi_16323185_gb_AY057697.1_ potassium channel protein AKT3 ; supported by cDNA: gi_1100897_gb_U40154.1_ATU40154 putative serine/threonine kinase MAP3K delta-1 protein kinase, Arabidopsis thaliana,PID:92253010; supported by cDNA: gi_15810436_gb_A transcriptional activator CBF1-like protein similarity to transcriptional activator CBF1, Arabidopsis thaliana00 protein phosphatase ABI1 ; supported by cDNA: gi_14334799_gb_AY05973.1_ AIM1 protein ; supported by cDNA: gi_1648890_gb_AY059815.1_	255510_at 255520_at 255474_at 255382_at 255305_at 255226_at 255032_at 254764_at 254764_at 254269_at 254066_at 253959_at	1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8
coded for by A. thaliana cDNA T75804 similar to ATPases associated with various cellular activites (Pfan: AAA.hmm, score: 230.91) putative pre-mRNA splicing factor similar to yeast pre-mRNA splicing factors; supported by cDNA: gi_16604550_gb_AY059720.1_ putative ABC transporter similar to Guillardia theta ABC transporter, GenBank accession number AF041468; supported by cDNA: gi_155291 UV-damaged DNA binding factor - like protein XPE UV-damaged DNA binding factor, Mus musculus, BAA84699 putative protein anthocyanin rhamnosyltransferase -Petunia x hybrida, PID:e1310057 putative protein hypothetical protein F7H19.70 - Arabidopsis thaliana, PID:e1310057 putative protein is supported by cDNA: gi_16323185_gb_AY057697.1_ potassium channel protein AKT3 ; supported by cDNA: gi_1100897_gb_U40154.1_ATU40154 putative serine/threonine kinase MAP3K delta-1 protein kinase, Arabidopsis thaliana,PID:g2253010; supported by cDNA: gi_15810436_gb_A transcriptional activator CBF1-like protein strong similarity to transcriptional activator CBF1, Arabidopsis thaliana00 protein phosphatase ABI1 ; supported by cDNA: gi_14334799_gb_AY035073.1_ AIM1 protein ; supported by cDNA: gi_1648890_gb_AY059815.1_ protein phosphatase 2C - like protein protein phosphatase 2C, Schizosaccharomyces pombe, PIR2:S54297; supported by cDNA: gi_162096!	255510_at 255520_at 255320_at 255382_at 255305_at 255226_at 255032_at 254848_at 254764_at 254305_at 254269_at 254966_at 253994_at 253759_at 253453_at	1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8
coded for by A. thaliana cDNA T75804 similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) putative pre-mRNA splicing factor similar to yeast pre-mRNA splicing factors; supported by cDNA: gi_16604550_gb_AY059720.1_ putative ABC transporter similar to Guillardia theta ABC transporter, GenBank accession number AF041468; supported by cDNA: gi_155291 UV-damaged DNA binding factor - like protein XPE UV-damaged DNA binding factor, Mus musculus, BAA84699 putative protein anthocyanin rhamnosyltransferase -Petunia x hybrida, PID:g454253 putative protein hypothetical protein F7H19.70 - Arabidopsis thaliana, PID:g454253 putative protein i, supported by cDNA: gi_16323185_gb_AY057697.1_ potassium channel protein AKT3 ; supported by cDNA: gi_1100897 gb_U40154.1_ATU40154 putative serine/threonine kinase MAP3K delta-1 protein kinase, Arabidopsis thaliana, PID:g2253010; supported by cDNA: gi_15810436_gb_A transcriptional activator CBF1-like protein strong similarity to transcriptional activator CBF1, Arabidopsis thaliana00 protein phosphatase ABI1 ; supported by cDNA: gi_1648890_gb_AY055815.1_ protein phosphatase 2C - like protein phosphatase 2C, Schizosaccharomyces pombe, PIR2:S54297; supported by cDNA: gi_162096! putative protein kinase protein kinase, Spinacia oleracea, PIR2:S42867	255510_at 255520_at 255474_at 255382_at 255382_at 255226_at 255226_at 255032_at 254764_at 254764_at 254305_at 254269_at 253994_at 253759_at 253353_at	1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8
coded for by A. thaliana cDNA T75804 similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) putative pre-mRNA splicing factor similar to yeast pre-mRNA splicing factors; supported by cDNA: gi_16604550_gb_AY059720.1_ putative ABC transporter similar to Guillardia theta ABC transporter, GenBank accession number AF041468; supported by cDNA: gi_155291 UV-damaged DNA binding factor - like protein XPE UV-damaged DNA binding factor, Mus musculus, BAA84699 putative protein anthocyanin rhamnosyltransferase -Petunia x hybrida, PID:g454253 putative protein hypothetical protein F7H19.70 - Arabidopsis thaliana, PID:e1310057 putative protein i, supported by cDNA: gi_16323185_gb_AY057697.1_ potassium channel protein AKT3; supported by cDNA: gi_1100897_gb_U40154.1_ATU40154 putative serine/threonine kinase MAP3K delta-1 protein kinase, Arabidopsis thaliana,PID:g2253010; supported by cDNA: gi_15810436_gb_A transcriptional activator CBF1-like protein strong similarity to transcriptional activator CBF1, Arabidopsis thaliana00 protein phosphatase ABI1; supported by cDNA: gi_14334799_gb_AY035073.1_ AIM1 protein; supported by cDNA: gi_16648800_gb_AY059815.1_ protein phosphatase 2C - like protein protein phosphatase 2C, Schizosaccharomyces pombe, PIR2:S54297; supported by cDNA: gi_162096! putative protein kinase, SPinacia oleracea, PIR2:S42867 arginine decarboxylase SPE2; supported by cDNA: gi_14517491_gb_AY039581.1_	255510_at 255520_at 255474_at 255305_at 255305_at 255032_at 255032_at 254348_at 254764_at 254764_at 254269_at 254966_at 253994_at 253759_at 253359_at 253329_at	1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8
coded for by A. thaliana cDNA T75804 similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) putative pre-mRNA splicing factor similar to yeast pre-mRNA splicing factors; supported by cDNA: gi_16604550_gb_AY059720.1_ putative ABC transporter similar to Guillardia theta ABC transporter, GenBank accession number AF041468; supported by cDNA: gi_155291 UV-damaged DNA binding factor - like protein XPE UV-damaged DNA binding factor, Mus musculus, BAA84699 putative protein anthocyanin rhannosyltransferase -Petunia x hybrida, PID:g454253 putative protein hypothetical protein F7H19.70 - Arabidopsis thaliana, PID:e1310057 putative protein i, supported by cDNA: gi_16323185_gb_AY057697.1_ potassium channel protein AKT3 ; supported by cDNA: gi_1100897_gb_U40154.1_ATU40154 putative scrine/threonine kinase MAP3K delta-1 protein kinase, Arabidopsis thaliana,PID:g2253010; supported by cDNA: gi_15810436_gb_A transcriptional activator CBF1-like protein strong similarity to transcriptional activator CBF1, Arabidopsis thaliana00 protein phosphatase ABI1 ; supported by cDNA: gi_14334799_gb_AY035073.1_ AIM1 protein ; supported by cDNA: gi_16648890_gb_AY059815.1_ protein kinase protein kinase, Spinacia oleracea, PIR2:S42867 arginine decarboxylase SPE2 ; supported by cDNA: gi_14517491_gb_AY039581.1_ putative protein crp1-hcf111 allele,encoding a chloroplast protein -Zea mays,PID:g3289002	255510_at 255520_at 255474_at 255302_at 255302_at 255032_at 254848_at 254764_at 254764_at 254269_at 254066_at 253994_at 253359_at 253359_at 253359_at 253303_at 253303_at	$\begin{array}{c} 1.8\\ 1.8\\ 1.8\\ 1.8\\ 1.8\\ 1.8\\ 1.8\\ 1.8\\$
coded for by A. thaliana cDNA T75804 similar to ATPases associated with various cellular activites (Pfan: AAA.hmm, score: 230.91) putative pre-mRNA splicing factor similar to yeast pre-mRNA splicing factors; supported by cDNA: gi_16604550_gb_AY059720.1_ putative ABC transporter similar to Guillardia theta ABC transporter, GenBank accession number AF041468; supported by cDNA: gi_155291 UV-damaged DNA binding factor - like protein XPE UV-damaged DNA binding factor, Mus musculus, BAA84699 putative protein anthocyanin rhamnosyltransferase -Petunia x hybrida, PID:e1310057 putative protein hypothetical protein F7H19.70 - Arabidopsis thaliana, PID:e1310057 putative protein is supported by cDNA: gi_16323185_gb_AY057697.1_ potassium channel protein AKT3 ; supported by cDNA: gi_1100897_gb_U40154.1_ATU40154 putative serine/threonine kinase MAP3K delta-1 protein kinase, Arabidopsis thaliana,PID:g2253010; supported by cDNA: gi_15810436_gb_A transcriptional activator CBF1-like protein strong similarity to transcriptional activator CBF1, Arabidopsis thaliana00 protein phosphatase ABI1 ; supported by cDNA: gi_14334799_gb_AY035073.1_ AIM1 protein ; supported by cDNA: gi_1648890_gb_AY059815.1_ protein phosphatase 2C - like protein protein phosphatase 2C, Schizosaccharomyces pombe, PIR2:S54297; supported by cDNA: gi_162096! putative protein kinase protein kinase, Spinacia oleracea, PIR2:S42867 arginine decarboxylase SPE2 ; supported by cDNA: gi_14517491_gb_AY039581.1_ putative protein crp1-hcf111 allele,encoding a chloroplast protein -Zea mays,PID:g3289002 putative protein	255510_at 255520_at 255474_at 255305_at 255305_at 255226_at 255032_at 254848_at 254764_at 254764_at 254764_at 254766_at 253495_at 253994_at 253759_at 253359_at 253359_at 253203_at 253203_at 253203_at 253209_at	1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8
coded for by A. thaliana cDNA T75804 similar to ATPases associated with various cellular activites (Pfan: AAA.hmm, score: 230.91) putative pre-mRNA splicing factor similar to yeast pre-mRNA splicing factors; supported by cDNA: gi_16604550_gb_AY059720.1_ putative ABC transporter similar to Guillardia theta ABC transporter, GenBank accession number AF041468; supported by cDNA: gi_155291 UV-damaged DNA binding factor - like protein XPE UV-damaged DNA binding factor, Mus musculus, BAA84699 putative protein anthocyanin rhannosyltransferase -Petunia x hybrida, PID:g454253 putative protein hypothetical protein F7H19.70 - Arabidopsis thaliana, PID:e1310057 putative protein i, supported by cDNA: gi_16323185_gb_AY057697.1_ potassium channel protein AKT3 ; supported by cDNA: gi_1100897_gb_U40154.1_ATU40154 putative scrine/threonine kinase MAP3K delta-1 protein kinase, Arabidopsis thaliana,PID:g2253010; supported by cDNA: gi_15810436_gb_A transcriptional activator CBF1-like protein strong similarity to transcriptional activator CBF1, Arabidopsis thaliana00 protein phosphatase ABI1 ; supported by cDNA: gi_14334799_gb_AY059815.1_ protein phosphatase 2C - like protein protein phosphatase 2C, Schizosaccharomyces pombe, PIR2:S54297; supported by cDNA: gi_162096! putative protein kinase, Spinacia oleracea, PIR2:S42867 arginine decarboxylase SPE2 ; supported by CDNA: gi_14517491_gb_AY039581.1_ putative protein crp1-hcf111 allele,encoding a chloroplast protein -Zea mays,PID:g3289002	255510_at 255520_at 255474_at 255302_at 255302_at 255032_at 254848_at 254764_at 254764_at 254269_at 254066_at 253994_at 253359_at 253359_at 253359_at 253303_at 253303_at	$\begin{array}{c} 1.8\\ 1.8\\ 1.8\\ 1.8\\ 1.8\\ 1.8\\ 1.8\\ 1.8\\$

ribonuclease II-like protein ribonuclease II family protein, Deinococcus radiodurans, PIR:C75571	251040_at	1.8
polyubiquitin (UBQ3) identical to GI:928809; supported by full-length cDNA: Ceres: 20908.	250935_at	1.8
putative protein strong similarity to unknown protein (emb CAB87679.1)	250326 at	1.8
putative protein similar to unknown protein (emb CAB69839.1)	250257 at	1.8
putative protein similar to unknown protein (pir  S77419); supported by cDNA: gi 15912216 gb AY056386.1	250259 at	1.8
disease resistance protein-like non-consensus TT donor splice site at exon 1	249320_at	1.8
N-carbamyl-L-amino acid amidohydrolase-like protein	249103_at	1.8
WD-repeat protein-like	249066 at	1.8
ornithine aminotransferase	248879 at	1.8
ATP-dependent Clp protease ATP-binding subunit (ClpC1) almost identical to ClpC GI:2921158 from [Arabidopsis thaliana]	248480 at	1.8
putative protein similar to unknown protein (pir  S42136)	248357 at	1.8
Fish protease, putative similar to ATP-dependent metalloprotease FtsH1 GI:3600100 from [Mus musculus]	248303 at	1.8
unknown protein ; supported by full-length cDNA: Ceres:21044.	247990 at	1.8
putative protein ;supported by full-length cDNA: Ceres:3086.	247748 at	1.8
putative protein gcpE protein, Chlamydia muridarum, PIR:C81715	247637 at	1.8
pseudo-response regulator 1, supported by cDNA: gi 7576353 dbj_AB041530.1_AB041530	247525 at	1.8
autophagorttosis protein - ike autophagocytosis protein AUT1, Saccharomyces cerevisiae, PIR:S45130;supported by full-length cDNA: Cere		1.8
autopragocytosis protein rate autopragocytosis protein Aor r, Saccharonyces cerevisiae, r in	247487 at	1.8
putative protein embryo-specific protein 3, Arabidopsis thaliana, PIR:T48490	247459 at	1.8
	247288 at	1.8
non-phototropic hypocotyl 3 (gb[AAF05914.1); supported by cDNA: gi_6224711_gb_AF180390.1_AF180390		1.8
unknown protein	246957_at	
	246962_s_at	1.8
putative protein predicted protein, Oryza sativa	246892_at	1.8
putative protein pyruvate water dikinase, Archaeoglobus fulgidus, PIR-F69338	246829_at	1.8
	246756_at	1.8
Carboxylesterase-like protein sterol esterase - Rattus norvegicus, EMBL:Z22803	246524_at	1.8
putative protein	246343_at	1.8
putative protein predicted protein, Drosophila melanogaster	246139_at	1.8
calcium-dependent protein kinase ; supported by cDNA: gi_836941_gb_U20624.1_ATU20624	246044_at	1.8
hypothetical protein similar to hypothetical protein GB:CAB77775 GI:7269775 from [Arabidopsis thaliana]	245789_at	1.8
hypothetical protein	245477_at	1.8
apetala2 domain TINY like protein	245445_at	1.8
HSP like protein ; supported by cDNA: gi_15293148_gb_AY051008.1_	245293_at	1.8
putative protein similarity to proteins of unknown function from human and mouse	245180_at	1.8
hypothetical protein	244904_at	1.8
	244920_s_at	1.8
hypothetical protein	257318_at	1.8
putative salt-inducible protein	257395_at	1.8
putative kinesin heavy chain	263751_at	1.7
	267644_s_at	1.7
unknown protein ;supported by cDNA: gi_15293114_gb_AY050991.1_	267602_at	1.7
putative DNA binding protein ; supported by cDNA: gi_11908071_gb_AF326883.1_AF326883	267538_at	1.7
unknown protein	266839_at	1.7
putative zinc transporter ;supported by full-length cDNA: Ceres:207558.	266718_at	1.7
putative helicase ; supported by cDNA: gi_15027926_gb_AY045820.1_	266679_at	1.7
putative phospholipid cytidylyltransferase	266359_at	1.7
putative pumilio/Mpt5 family RNA-binding protein	266284_at	1.7
unknown protein	266185_at	1.7
contains similarity to S. cerevisiae ADR1 gene (PID:g924931); supported by cDNA: gi_13605528_gb_AF361590.1_AF361590	265908_at	1.7
unknown protein predicted by genscan; supported by cDNA: gi_16930416_gb_AF419562.1_AF419562	265664_at	1.7
unknown protein	265139_at	1.7
alcohol dehydrogenase identical to alcohol dehydrogenase GI:469467 from (Arabidopsis thaliana); supported by full-length cDNA: Ceres: 403	264953_at	1.7
putative DNA-binding protein, Myb Identical to A. thaliana Myb-like protein (gb D58424); supported by cDNA: gi_1747309_dbj_D58424.1_D5	264709_at	1.7
hypothetical protein predicted by genefinder	264618_at	1.7
putative aspartic proteinase similar to GB:AAC49730;supported by full-length cDNA: Ceres:8972.	264344_at	1.7
hypothetical protein contains non-consensus donor splice site AT at exon 4 and acceptor splice site at exon5;Contains similarity to serine/thre	264331_at	1.7
starch branching enzyme II	263912_at	1.7
putative tetracycline transporter protein	263574_at	1.7
unknown protein	263545_at	1.7
unknown protein ;supported by full-length cDNA: Ceres:31655.	263517_at	1.7
cold-regulated protein cor15a precursor;supported by cDNA: gi_14532457_gb_AY039853.1_	263497_at	1.7
	263503_s_at	1.7
putative RING zinc finger protein ; supported by cDNA: gi_13265496_gb_AF324691.2_AF324691	263325_at	1.7
putative glutamate/aspartate-binding peptide Belongs to the PF 01027 Uncharacterized protein family UPF0005 with 7 transmembrane domai	263164_at	1.7
unknown protein ESTs gb R30529, gb Z48463, gb Z48467, gb AA597369 and gb AA394772 come from this gene; supported by cDNA: gi_16	262574_at	1.7
alaninetRNA ligase, putative similar to alaninetRNA ligase GB:S32671 from [Arabidopsis thaliana]	262468_at	1.7
endoplasmic reticulum-type calcium-transporting ATPase 4 identical to GB:AAD29957 from [Arabidopsis thaliana] (Plant Physiol. 120 (1999) I		1.7
ribokinase, putative similar to GB:AAD00536 from [Pyrobaculum aerophilum]	261136_at	1.7
transcription factor scarecrow-like 14, putative similar to GB:AAD24412 from [Arabidopsis thaliana] (Plant J. 18 (1), 111-119 (1999))	261062_at	1.7
unknown protein ;supported by full-length cDNA: Ceres:114093.	260793_at	1.7
hypothetical protein predicted by genemark.hmm	260647_at	1.7
unknown protein contains similarity to tub homolog GI:2072160 from [Homo sapiens]; supported by cDNA: gi_13877766_gb_AF370146.1_AF	260588_at	1.7
unknown protein	260580_at	1.7
unknown protein ;supported by full-length cDNA: Ceres:27109.	260444_at	1.7
putative carnitine/acylcarnitine translocase similar to carnitine/acylcarnitine translocase GB:CAB55356 [Homo sapiens]; supported by full-lengt	260163_at	1.7
hypothetical protein predicted by genscan	260087_at	1.7
unknown protein	259934_at	1.7
myb-related transcription factor (cpm10), putative similar to myb-related transcription factor (cpm10) GB:U33915 GI:1002795 from [Craterosti	259618_at	1.7
unknown protein predicted by genefinder, multiple est matches;supported by full-length cDNA: Ceres:7073.	258939_at	1.7
unknown protein ;supported by full-length cDNA: Ceres:13305.	258455_at	1.7
PP1/PP2A phosphatases pleiotropic regulator PRL2 identical to GB:Q39190 from [Arabidopsis thaliana]; supported by cDNA: gi_15809827_g		1.7
	258380_at	1.7
protein kinase, putative similar to serine/threonine protein kinase GB:NP_032667 from [Mus musculus]	258380_at 258186_s_at	1.7
protein kinase, putative similar to serine/threonine protein kinase GB:NP_032667 from [Mus musculus] unknown protein ;supported by cDNA: gi_14423467_gb_AF386971.1_AF386971	_	

unknown protein ;supported by full-length cDNA: Ceres:124193.	257672_at	1.7
unknown protein ;supported by cDNA: gi_15146182_gb_AY049232.1_	257154_at	1.7
unknown protein	257092_at	1.7
	256902_s_at	1.7
unknown protein ;supported by full-length cDNA: Ceres:3056. deoxyguanosine kinase, putative similar to deoxyguanosine kinase [Homo sapiens] GI:1480198;supported by full-length cDNA: Ceres:3878.	256441_at 256341 at	1.7 1.7
decxyguariser kinase, pulative similar to decxyguarisme kinase (i nono sapiens) Gr. Hoo iso, supported by runnengin convert. Ceres. Soro. hypothetical protein predicted by genemark.hmm	255929 at	1.7
AtKAP alpha similar to AtKAP, GenBank accession number U69533; supported by cDNA; gi 14326480 gb AF385693.1 AF385693	255507 at	1.7
ferredoxinNADP+ reductase - like protein ferredoxinNADP+ reductase, Pisum sativum, PIR:T06773;supported by full-length cDNA: Ceres:	255230_at	1.7
putative translation initiation factor IF-2 translation initiation factor IF-2 - Haemophilus influenzae, PIR2:E64114	254904_at	1.7
putative protein tripeptidyl-peptidase II, Homo sapiens, Pir:S54376	254433_at	1.7
putative protein predicted protein, Arabidopsis thaliana, PATCHX:G2494119;supported by full-length cDNA: Ceres:106883.	254427_at	1.7
putative beta-glucosidase beta-glucosidase BGQ60 precursor - barley, PIR2:A57512; supported by cDNA: gi_15982821_gb_AY057518.1_	253841_at	1.7
Expressed protein ; supported by cDNA: gi_13358221_gb_AF325032.2_AF325032 putative protein predicted protein, Arabidopsis thaliana; supported by cDNA: gi_15451175_gb_AY054668.1_	253293_at 253062_at	1.7 1.7
cinamy alcohol denyed protein, Alabudopsa trainaina, supported by Conk. g_ 1945 17 5_g0_A1054000.1_	253002_at 253017 at	1.7
putative protein unknown mRNA, Homo sapiens, AF091072	252968 at	1.7
carboxypeptidase precursor-like protein carboxypeptidase Y-like protein, Arabidopsis thaliana, EMBL:M81130; supported by cDNA: gi 15215	_	1.7
putative protein several hypothetical proteins	252496_at	1.7
putative protein predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_14532663_gb_AY039956.1_	252467_at	1.7
putative protein probable transcription regulator protein - Sorghum bicolor, PIR2:T03446; supported by full-length cDNA: Ceres:34151.	252323_at	1.7
hypothetical protein ; supported by cDNA: gi_13877826_gb_AF370176.1_KF370176	251964_at	1.7
fructokinase – like protein fructokinase, Lycopersicon esculentum, EMBL:LEU62329	251935_at	1.7 1.7
putative protein arm repeat containing protein, Brassica napus, AF024625 putative protein hypothetical proteins - Arabidopsis thaliana; supported by cDNA: gi 14334587 gb AY034967.1	251862_at 251356 at	1.7
parame protected protected protected protected protected by contred by contred by contred of <u>_go_</u>	251146 at	1.7
putative protein predicted protein, Arabidopsis thaliana	250877 at	1.7
signal recognition particle 54CP protein precursor ; supported by cDNA: gi_15293130_gb_AY050999.1_	250884_at	1.7
DnaJ-like protein ; supported by cDNA: gi_15810414_gb_AY056246.1_	250755_at	1.7
	250736_s_at	1.7
serine/threonine-protein kinase	250527_at	1.7
putative protein predicted proteins, Arabidopsis thaliana and Drosophila melanogaster	250516_at	1.7
putative protein unnamed ORF cDNA FLJ10872, Homo sapiens, EMBLAK001734; supported by cDNA: gi_14532679_gb_AY039964.1_	250402_at	1.7
transporter-like protein ;supported by full-length cDNA: Ceres:27439. unknown protein	250252_at 250104 at	1.7 1.7
ankyrin repeat protein EMB506 ; supported by cDNA: gi_5911311_gb_AF026167.1_AF026167	249404 at	1.7
putative protein contains similarity to unknown protein (db)[BAA76827.1); supported by cDNA; gi 14532601 gb AY039925.1	249181 at	1.7
putative protein similar to unknown protein (gb[AAD2005, 1)	248668 at	1.7
pyrophosphate-dependent phosphofructo-1-kinase-like protein; supported by cDNA: gi_14532861_gb_AY040055.1_	247983_at	1.7
putative protein predicted proteins, Homo sapiens and Drosophila melanogaster	247847_at	1.7
serine/threonine protein kinase ; supported by cDNA: gi_13249118_gb_AF295665.1_AF295665	247820_at	1.7
quinone oxidoreductase - like protein quinone oxidoreductase homolog, Vigna unguiculata, PIR:T11672;supported by full-length cDNA: Cere	_	1.7
calnexin - like protein calnexin homolog, Arabidopsis thaliana, EMBL:AT08315;supported by full-length cDNA: Ceres:2869.	247494_at	1.7
ABC transporter protein 1-like ; supported by cDNA: gi_15912314_gb_AY056435.1_ putative protein strong similarity to unknown protein (pir  T04718); supported by cDNA: gi_15529177_gb_AY052213.1_	247222_at 247013_at	1.7 1.7
RuvB DNA helicase-like protein ; supported by cDNA; gi 16974567 gb AY061754.1	247013_at 247014 at	1.7
RING finger-like protein RING-H2 finger protein RHG1 - Arabidopsis thaliana, EMBL:AF079183	246968 at	1.7
putative protein GTP-binding proteins at the N-terminus	246775 at	1.7
splicing factor-like protein	246257_at	1.7
putative protein HCNP, Homo sapiens, EMBL:AF226051	245917_at	1.7
sucrose-phosphate synthase -like protein sucrose-phosphate synthase isoform 1, Citrus unshiu, PIR:S72648	245904_at	1.7
hypothetical protein similar to putative ubiquitin GI:4415931 from [Arabidopsis thaliana]; supported by cDNA: gi_14334681_gb_AY035014.1_	245821_at	1.7
hypothetical protein predicted by genemark.hmm putative phosphatidylinositol-4-phosphate 5-kinase ; supported by cDNA: gi 13925628 gb AF260903.1 AF260903	245659_at 267081_at	1.7 1.7
putative prospirated with store and the second store of the second	248495 at	1.7
putative protein similar to unknown protein (emb(CABS1351.1)	250309 at	1.6
hypothetical protein envelope-like, Glycine max., PIR:T08898	252700_at	1.6
similar to late embryogenesis abundant proteins ; supported by cDNA: gi_14423503_gb_AF386989.1_AF386989	267263_at	1.6
unknown protein ;supported by cDNA: gi_15451173_gb_AY054667.1_	267180_at	1.6
putative alcohol dehydrogenase ; supported by cDNA: gi_16604706_gb_AY059798.1_	267181_at	1.6
	267106_s_at	1.6
hypothetical protein The first 3 exons is identical to that of GB:AJ224957. This gene appears to be a truncated version of that in GB:AJ224957 with the elegantical foreign.	266466_at	1.6
putative elongation factor unknown protein ;supported by cDNA: gi_16604650_gb_AY059770.1_	266407_at 266121_at	1.6 1.6
	266036_s_at	1.6
	266042 s at	1.6
putative senescence-associated protein 5 contains a transmembrane 4 family signature; rare (GC) splice donor consensus found instead of ((	265935_at	1.6
unknown protein	265900_at	1.6
putative SEC1 family transport protein similar to SLY1 proteins and vesicle transport proteins; supported by cDNA: gi_15215769_gb_AY0504	265822_at	1.6
putative arginine/serine-rich splicing factor	265449_at	1.6
putative inorganic pyrophosphatase ;supported by full-length cDNA: Ceres:8068. hypothetical protein	265339_at 265230 s at	1.6 1.6
putative senescence-associated protein 12 ;supported by full-length cDNA: Ceres:40806.	265230_s_at 264787 at	1.6
hypothetical protein similar to receptor-like protein riz (supported by namerigin convc. Ceres-Houdou. hypothetical protein similar to receptor-like protein kinase GI:7529754 from [Arabidopsis thaliana]	264479_at	1.6
	264354_s_at	1.6
hypothetical protein Contains similarity to transcription initiation factor IIE, alpha subunit gb/X63468 from Homo sapiens; supported by cDNA:	264368_at	1.6
beta-glucosidase, putative similar to beta-glucosidase GI:5030906 from [Polygonum tinctorium]	264270_at	1.6
putative ABC transporter related to multi drug resistance proteins and P-glycoproteins	263865_at	1.6
hypothetical protein predicted by genscan	263864_at	1.6
putative WD-40 repeat protein unknown protein similar to cell differentiation protein GB:AAC36682 from (Homo sapiens)	263824_at 263685 at	1.6 1.6
	263564_s_at	1.6
aldehyde oxidase identical to GP/3172044:gnl:PID:d1029570:AB010080; supported by cDNA; gi 5672671 dbj AB016622.1 AB016622	263570_at	1.6
		-

nypothetical protein	263510_s_at	1.6
putative myo-inositol 1-phosphate synthase ; supported by cDNA: gi_15450746_gb_AY053415.1_	263433_at	1.6
hypothetical protein predicted by genscan and genefinder; supported by cDNA: gi_16649128_gb_AY059934.1_	263265_at	1.6
zinc finger protein, putative similar to zinc finger protein GI:3618316 from [Oryza sativa];supported by full-length cDNA: Ceres:34830.	263128_at	1.6
Inknown protein similar to hypothetical protein GB:AAF27089 GI:6730668 from (Arabidopsis thaliana)	263014_at	1.6
putative ATP-dependent RNA helicase similar to GB:AAB88651, similar to human U5 snRNP-specific 200kD protein, gil3255965 and yeast p	_	1.6
unknown protein strong similarity to gb/Y09533 involved in starch metabolism from Solanum tuberosum and contains a PF 01366 Pyruvate p	_	1.6
reat shock protein, putative contains Pfam profile: PF00011 Hsp20/alpha crystallin family.supported by full-length cDNA: Ceres:21735.	262629_at	1.6
H-transporting ATPase protein, putative similar to H-transporting ATPase chain E GB:CAB43050 GI:4850294 from [Arabidopsis thaliana]	262354_at	1.6
unknown protein Similar to gb U04299 mannosyl-oligosaccharide alpha-1,2-mannosidase from Mus musculus. ESTs gb R84145 and gb AA3 unathaliagi practice proteins and the second state of the second state of the second state of the second state of	_	1.6
ypothetical protein predicted by genemark.hmm AP2 domain containing protein, putative similar to AP2 domain containing protein GI:2281649 from [Arabidopsis thaliana];supported by full-le	262238_at	1.6
splicing factor Prp8, putative similar to splicing factor Prp8 GI:3661610 from [Homo sapiens]	e 262197_at 262068 at	1.6 1.6
spicing raction ripo, putative similar to specify action ripo draction for more repeating type 2 peroxiredoxin, putative similar to type 2 peroxiredoxin Gl:4928472 from [Brassica rapa subsp. pekinensis];supported by full-length cDI		1.6
ype z provincedani, potativi similar to type z provincedani costar z more provincedani provinced	_	1.6
ranscriptional regulator, putative similar to transcriptional regulator G1:4836767 from [Zea mays]	261837 s at	1.6
TP-dependent Clp protease proteolytic subunit (ClpR1) identical to ClpP5 GB:BA&2069 (E5360595 from [Arabidopsis thaliana];supporte		1.6
no superiodi negli protesse protessi sabarini (negri ro dei negli se de la constructiva di constanti si superiodi negli se de la constructiva di constructiva		1.6
sportential protein i sonanti sommerky o zino mgor protein sin robor to om tory population partang, opported by rain engli obra i conce	261272 at	1.6
ypothetical protein predicted by genemark.hmm	261176 at	1.6
ypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:98874.	261124 at	1.6
have protein supported by full-length CDNA: Ceres:40419.	261144 s at	1.6
ropinone reductase-I, putative similar to GB:L20473 from [Datura stramonium] (Proc. Natl. Acad. Sci. U.S.A. 90, 9591-9595 (1993)); support		1.6
box protein family contains similarity to F-box protein FBX3 GI:6103643 from [Homo sapiens]	260949 at	1.6
nknown protein ; supported by cDNA: gi 15450710 gb AY052723.1	260794 at	1.6
hypothetical protein contains similarity to guanine nucleotide exchange factor, eIF-2B, delta subunit GI:529428 from [Mus musculus]	260756 at	1.6
ypothetical protein identical to hypothetical protein GB:AAF81322 GI:8920600 from (Arabidopsis thaliana)	260700 at	1.6
/jvoxalase I, putative similar to GB:Y13239 from [Brassica juncea] (Plant J. 17 (4), 385-395 (1999))	260619 at	1.6
inknown protein similar to putative cytoskeletal protein GI:1732517 from [Arabidopsis thaliana]; supported by cDNA: gi_1732516_gb_U62745		1.6
nypothetical protein predicted by genscan+, contains Viral RNA helicase domain	260283 at	1.6
utative heat shock protein similar to GB:CAB03279 from [Caenorhabditis elegans]	260251 at	1.6
putative SET protein, phospatase 2A inhibitor similar to SET protein, phospatase 2A inhibitor GB:Q01105 [Homo sapiens] (role in the mecha	_	1.6
utative ATPase contains Pfam profile: PF00004 ATPases associated with various cellular activities (AAA)	260089 at	1.6
utative serine/threonine-protein kinase similar to SERINE/THREONINE-PROTEIN KINASE ASK1 GB:P43291 from [Arabidopsis thaliana];su		1.6
ypothetical protein ; supported by cDNA: gi 13937176 gb AF372942.1 AF372942	259545 at	1.6
ypothetical protein ; supported by cDNA: gi_15081631_gb_AY048208.1_	259516_at	1.6
xpressed protein ; supported by cDNA: gi_14532525_gb_AY039887.1_	259416 at	1.6
eta-glucosidase identical to beta-glucosidase GB:AAC31962 [Arabidopsis thaliana]; supported by cDNA: gi 3420934 gb AF082157.1 AF0	£ 259173 at	1.6
nknown protein	259047_at	1.6
putative uridylate kinase similar to uridylate kinase GB:CAB13524 [Bacillus subtilis], GB:P74457 [Synechocystis PCC6803]; supported by cD	258885_at	1.6
utative exportin1 (XPO1) protein similar to GB:CAB56597	258868_at	1.6
putative RNA helicase similar to RNA helicase involved in rRNA processing GB:6321267 from [Saccharomyces cerevisiae]c, ontains DEAD a	258701_at	1.6
nknown protein	258635_at	1.6
nknown protein ;supported by full-length cDNA: Ceres:39933.	258348_at	1.6
utative casein kinase I similar to casein kinase I GB:CAA55396 from [Arabidopsis thaliana]; supported by cDNA: gi_15809823_gb_AY05417	258300_at	1.6
cid phosphatase type 5 identical to GB:CAB63938 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:113666.	258158_at	1.6
utative myc-like DNA-binding protein similar to GB:AAB72192 from [Arabidopsis thaliana]	257990_at	1.6
nknown protein ;supported by full-length cDNA: Ceres:34773.	257789_at	1.6
cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450	257628_at	1.6
ubiquitin-specific protease 14 (UBP14), putative similar to ubiquitin-specific protease 14 GI:11993473 [Arabidopsis thaliana]	257085_at	1.6
GTPase, putative contains Pfam profile: PF01926 GTPase of unknown function	256274_at	1.6
ypothetical protein predicted by genemark.hmm	256208_at	1.6
utative protein	256027_at	1.6
ypothetical protein ;supported by full-length cDNA: Ceres:37204.	255980_at	1.6
nknown protein ;supported by full-length cDNA: Ceres:23788.	255957_at	1.6
368 RNA helicase, putative similar to p68 RNA helicase (Schizosaccharomyces pombe) GI:173419	255749_at	1.6
redicted OR23 protein of unknown function	255469_at	1.6
ypothetical protein ;supported by full-length cDNA: Ceres:40589.	254683_at	1.6
butative NADPH quinone oxidoreductase Pig3 Homo sapiens, PID:G2754812;supported by full-length cDNA: Ceres:4621.	254393_at	1.6
putative protein zinc finger protein, Arabidopsis thaliana, PID:g2340088; supported by cDNA: gi_15982926_gb_AY057571.1_	254210_at	1.6
utative protein ; supported by cDNA: gi_13991647_gb_AF359388.1_AF359388	254043_at	1.6
ypothetical protein ;supported by full-length cDNA: Ceres:113230.	253689_at	1.6
outative protein putative ATPase - Haematobia irritans,PID:g525318;supported by full-length cDNA: Ceres:4.	253630_at	1.6
utative protein ; supported by cDNA: gi_13605598_gb_AF361625.1_AF361625	253388_at	1.6
VYB-like protein myb-related protein Y49, Arabidopsis thaliana, PIR:S58292	253219_at	1.6
outative protein F56F10.1, Caenorhabditis elegans, PATX:01688051	253079_s_at	1.6
eta-galactosidase like protein ; supported by cDNA: gi_15810492_gb_AY056285.1_	253090_at	1.6
utative protein ; supported by cDNA: gi 13605658_gb_AF361810.1_AF361810	252856_at	1.6
avanone 3-hydroxylase (FH3) ;supported by full-length cDNA: Ceres:36653.	252123_at	1.6
outative protein predicted proteins, Arabidopsis thaliana	251894_at	1.6
spliceosomal - like protein spliceosomal protein SAP 130, Homo sapiens, EMBL:HSAJ1443	251837_s_at	1.6
alpha-galactosidase-like protein alpha galactosidase - Phaseolus vulgaris, PIR:T10860	251729_at	1.6
putative protein HIRA interacting protein 4 (dnaJ-like) - Homo sapiens, EMBL:AJ001309;supported by full-length cDNA: Ceres:37292.	251182_at	1.6
ankyrin - like protein ankyrin G119, Homo sapiens, EMBL:HSU43965	250998_at	1.6
nistone deacetylase -like protein histone deacetylase, HD2-p39, nucleolar, Zea mays, PIR:T04141	250912_at	1.6
lucuronosyl transferase-like protein	250750_at	1.6
orting nexin-like protein	250714_at	1.6
ABA-responsive protein - like ABA-responsive protein, Hordeum vulgare, EMBL:AF026538	250279_at	1.6
igma-like factor (gb AAC97954.1); supported by cDNA: gi_3983259_gb_AF101075.1_AF101075	250255_at	1.6
putative protein CGI-67, Homo sapiens, EMBL:AF151825	250175_at	1.6
BCS1 - like protein h-bcs1, Homo sapiens, EMBL:AF026849; supported by cDNA: gi_15810570_gb_AY056324.1_	250062_at	1.6
putative protein similar to unknown protein (gb AAF00631.1);supported by full-length cDNA: Ceres:10299.	250028_at	1.6
rolylcarboxypeptidase-like protein ;supported by full-length cDNA: Ceres:122449.	249860 at	1.6

	249622_at	1.6
	249433_at	1.6
	249316_s_at 249218 at	1.6 1.6
	249115 at	1.6
	248952 at	1.6
	248906_at	1.6
	248834_at	1.6
	248067_at	1.6
	248016_at	1.6
	247891_at	1.6
	247466_at 247186 at	1.6 1.6
	247139 at	1.6
	246581 at	1.6
	246533_at	1.6
putative protein AAA family protein Bor, Drosophila melanogaster, EMBL:AF227209	246461_at	1.6
	246076_at	1.6
	246055_at	1.6
	245998_at 245787 at	1.6 1.6
	245668 at	1.6
	245483 at	1.6
	245427_at	1.6
putative protein various predicted proteins, Arabidopsis thaliana	254457_at	1.5
	253285_at	1.5
	267314_at	1.5
	267196_at	1.5 1.5
	267095_at 266932_s_at	1.5
	266702 at	1.5
	266362_at	1.5
putative PCI domain protein proteasome, COP9-complex and eIF3-domain protein; members of multi-protein complexes; supported by full-ler	266310_at	1.5
	266315_at	1.5
	266188_at	1.5
	266127_s_at	1.5
	265990_at 265760 at	1.5 1.5
	265425_at	1.5
	265359 at	1.5
	265079_at	1.5
	265037_at	1.5
putative protein kinase, ADK1 dual specificity kinase 1; Location of ESTs 184A2XP 3 , gb AA651408 and est 184A2T7, gb H37603. 99%+ idc 2		1.5
	265011_at	1.5
	264927_at 264894 at	1.5 1.5
	264772 at	1.5
	264776 at	1.5
	264683_at	1.5
	264597_at	1.5
	264524_at	1.5
	264486_at 264458 at	1.5 1.5
	264402 at	1.5
	264224 at	1.5
putative rubisco subunit binding-protein alpha subunit supported by full-length cDNA: Ceres:25773.	264069_at	1.5
	264045_at	1.5
	264002_at	1.5
	264019_at 263972 at	1.5 1.5
	263986 at	1.5
	263921_at	1.5
	263870_at	1.5
subtilisin-like serine protease AIR3 almost identical to subtilisin-like protease AIR3 GI:4218991 from [Arabidopsis thaliana], missing 18 aa at (	263406_at	1.5
	263200_at	1.5
	263150_at	1.5
	263116_s_at 263083 at	1.5 1.5
mak16-likke protein-related similar to MAK16 PROTEIN GB:P10962 GI:127112 from [Saccharomyces cerevisiae] (Proc. Natl. Acad. Sci. U.S.,		1.5
	262964 at	1.5
putative inosine-5-monophosphate dehydrogenase strong similarity to gb/L34684 inosine monophosphate dehydrogenase (IMPDH) from Arat	262754_at	1.5
	262570_at	1.5
	262521_at	1.5
	262275_at 262118 at	1.5 1.5
	262080 at	1.5
	261896 at	1.5
hypothetical protein predicted by genemark.hmm	261762_at	1.5
hypothetical protein contains similarity to cockayne syndrome complementation group A protein GB:U28413 GI:975301 from (Homo sapiens) 2		1.5
	261625_at	1.5
	261538_at	1.5
	261250_at 261219_at	1.5 1.5
	a	

subtilisin-like serine protease similar to subtilisin-type protease precursor GI:14150446 from [Glycine max];supported by full-length cDNA: Cer unknown protein	261224_at 261168 at	1.5 1.5
homeodomain protein BELL1, putative similar to GB:AAB05099 from [Arabidopsis thaliana] (Cell 83 (5), 735-742 (1995));supported by full-ler	_	1.5
	260995 at	1.5
Inknown protein similar to unknown protein GB:AAF18609 GI:6598419 from [Arabidopsis thaliana]	260884 at	1.5
inknown protein sinimal to dirknown protein GL-AAT 10009 GL0390419 Irolin [Atabidopsis trailaita]	260862 at	1.5
	_	
valyI-IRNA synthetase, putative similar to valyI tRNA synthetase GB:AAB49704 GI:1890130 from [Arabidopsis thaliana]; supported by cDNA: Diaco lite barandemain protein similar to valyI tRNA synthetase GB:AAB49704 GI:1890130 from [Arabidopsis thaliana]; supported by cDNA:	_	1.5
Ring3-like bromodomain protein similar to Ring3 GB:BAA25416 GI:3041763 from [Mus musculus], contains Pfam profile:PF00439 Bromodon DUP UID State of the second state		1.5
RING-H2 finger protein RHA3a, putative similar to RING-H2 finger protein RHA3a GI.3790573 from [Arabidopsis thaliana]; supported by cDN		1.5
protein phosphatase 2C, putative similar to protein phosphatase 2C GI:3242077 from (Arabidopsis thaliana)	260712_at	1.5
Expressed protein ; supported by full-length cDNA: Ceres: 13270.	260670_at	1.5
ypothetical protein contains Pfam profile: PF01535 Domain of unknown function	260331_at	1.5
putative sulfate transporter contains Pfam profile: PF00916 sulfate transporter family;supported by full-length cDNA: Ceres:120095.	260302_at	1.5
Inknown protein supported by cDNA: Ceres:35985; supported by cDNA: gi_13877918_gb_AF370222.1_AF370222	259739_at	1.5
protein kinase, putative similar to GI:7573596 from [Populus nigra]	259670_at	1.5
ATP-dependent RNA helicase, putative similar to ATP-dependent RNA helicase [Schizosaccharomyces pombe] GI:218533; supported by cD	259597_at	1.5
lpha subunit of F-actin capping protein supported by full-length cDNA: Ceres:33531.	259111 at	1.5
hypothetical protein predicted by genscan+; supported by full-length cDNA: Ceres:19154.	259037 at	1.5
Autator-like transposase similar to MURA transposase of maize Mutator transposon	258789_at	1.5
putative 2,3-bisphosphoglycerate-independent phosphoglycerate mutase similar to 2,3-bisphosphoglycerate-independent phosphoglycerate r		1.5
utative tRNA pseudouridine synthase similar to tRNA pseudouridine synthase A GB:P07649 [Escherichia coli]	258538 at	1.5
neutral invertase, putative similar to neutral invertase GB:CAA76145 from [Dacuss carota] (Physiol. Plantarum (1999) 107, 159-165)	258507 at	1.5
	_	1.5
typothetical protein predicted by genemark.hmm	257864_at	
mitogen activated protein kinase kinase, putative similar to mitogen activated protein kinase kinase GB:AAC32599 from [Oryza sativa]	257801_at	1.5
Inknown protein	257685_at	1.5
Inknown protein contains Pfam profile:PF00439 bromodomain:Bromodomain	257146_at	1.5
inknown protein ;supported by cDNA: gi_15081754_gb_AY048270.1_	257153_at	1.5
cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450; supported by full-length cDNA: Ceres: 149380.	257129_at	1.5
zinc finger protein, putative similar to Cys2/His2-type zinc finger protein 2 GB:BAA85107 from [Arabidopsis thaliana]; supported by cDNA: gi_		1.5
Anthocyanin 5-aromatic acyltransferase, putative similar to Anthocyanin 5-aromatic acyltransferase GB:BAA74428 from [Gentiana triflora]	256924_at	1.5
unknown protein contains similarity to plastid protein GB:AAB80660 from [Arabidopsis thaliana], contains Pfam profile: PF00076 RNA recogn	256805_at	1.5
far-red impaired response protein, putative similar to GB:far-red impaired response protein GB:AAD51282 from [Arabidopsis thaliana] (Genes	256820 at	1.5
hypothetical protein predicted by genemark.hmm	256613 at	1.5
recombination signal sequence recognition protein, putative similar to recombination signal sequence recognition protein (SSRP1) SP:Q0894		1.5
hypothetical protein predicted by genemark.hmm	256573 at	1.5
geranylgeranyl transferase type II beta subunit, putative similar to geranylgeranyl transferase type II beta subunit SP:P53611 [Homo sapiens	256276 at	1.5
gerangigerangi utalistetase type in octa subuliti, putatre sinima te gerangigerangi utalistetase type in octa subuliti or in oso n ( nonio sapiens) Inknown protein	256229 at	1.5
utative protein contains similarity to pseudouridine synthases; supported by cDNA: gi 13430549 gb AF360187.1 AF360187	255985 at	1.5
vipothetical protein protein predicted by generation and an experimental statement by convertige to the statement of the stat	255994 at	1.5
	_	
ypothetical protein predicted by genscan and genefinder; similar to EGADJ5081/YBR228W	255866_at	1.5
ypothetical protein similar to putative phloem transcription factor GI:7630279 from [Apium graveolens]	255725_at	1.5
utative myb-related DNA-binding protein	255614_at	1.5
iypothetical protein ;supported by cDNA: gi_14517493_gb_AY039582.1_	255557_at	1.5
putative protein similar to plant nucleic acid-binding proteins;supported by full-length cDNA: Ceres:6568.	255496_at	1.5
auxin-binding protein 1 precursor ;supported by full-length cDNA: Ceres:34126.	255412_at	1.5
putative protein proteins of this bac	255087_at	1.5
putative trehalose-6-phosphate phosphatase (AtTPPA) trehalose-6-phosphate phosphatase - Arabidopsis thaliana, PID:g2944178; supported	254806_at	1.5
DAG-like protein DAG precursor, Antirrhinum majus, MNOS:S71747	254493_at	1.5
putative protein pmt2 methyltransferase - Schizosaccharomyces pombe,PID:e1362538	254079_at	1.5
hypothetical protein	253782 at	1.5
lycine-rich protein glycine-rich cell wall structural protein - garden petunia,Pir2:A26099	253619 at	1.5
outative protein hypothetical protein - Synechocystis sp. (strain PCC 6803),PIR2:S76076	253585 at	1.5
redicted protein ; supported by cDNA: gi_15292824 gb_AY050846.1_	253524 at	1.5
utifilipid biosynthesis protein SQD1 ; supported by cDNA: gi_14190482 gb_AF380641.1_AF380641	253386 at	1.5
union biosyntilesis protein formamidase, Methylophilus methylotrophus, PIR2:S74213; supported by cDNA; gi 14334653 gb AY035000.1		
	253048_at	1.5
hosphoenolpyruvate carboxykinase (ATP) -like protein; supported by cDNA: gi_13937136_gb_AF372922.1_AF372922	253041_at	1.5
ypothetical protein several hypothetical proteins - Arabidopsis thaliana	252473_s_at	1.5
putative protein predicted proteins, Arabidopsis thaliana	252402_s_at	1.5
erine palmitoyltransferase-like protein	252331_s_at	1.5
putative protein pir7a protein - Oryza sativa, PIR:s47086;supported by full-length cDNA: Ceres:30104.	252168_at	1.5
putative protein predicted protein, Arabidopsis thaliana	252016_at	1.5
putative protein GTP-binding regulatory protein beta chain, Dictyostelium discoideum, PIR:A47370; supported by cDNA: gi_13430701_gb_AF	251888_at	1.5
putative protein MSP58 - nucleolar protein, Mus musculus, EMBL:AF015309; supported by cDNA: gi_17063177_gb_AY062111.1_	251866_at	1.5
Ipha-soluble NSF attachment protein ; supported by cDNA: gi_6013203_gb_AF177989.1_AF177989	251721_s_at	1.5
utative protein several hypothetical proteins - Arabidopsis thaliana;supported by full-length cDNA: Ceres:112338.	251530 at	1.5
guarnosa promoter binding protein-like 12	251450 at	1.5
quanticour protein thioesterase precursor - like palmitoyl-protein thioesterase precursor, Mus musculus, EMBL:AF071025; supported by full-ler		1.5
pamingy-protein intersetase precursor interpatingy-protein intersetase precursor, most musculas, curber and roze, supported by characteristic serine/threeonine-protein kinase-like protein serine/threeonine kinase UNC51.2 - Mus musculus, EMBL:AF145922; supported by CDNA: gi 143		1.5
aldose reductase-like protein aldose reductase - Hordeum vulgare, EMBL:Z48360	251275_at 251100 at	1.5
putative protein hypothetical protein T6H20.90 - Arabidopsis thaliana, EMBL:AL096859; supported by cDNA: gi_16648747_gb_AY058150.1_ utative protein hypothetical protein T6H20.90 - Arabidopsis thaliana, EMBL:AL096859; supported by cDNA: gi_16648747_gb_AY058150.1_	_	1.5
utative protein; supported by cDNA: gj_14190430_gb_AF378893.1_AF378893	250970_at	1.5
putative protein ABI3-interacting protein, Arabidopsis thaliana, EMBL:ATH251086; supported by cDNA: gi_14532637_gb_AY039943.1_	250971_at	1.5
butative protein	250946_at	1.5
	250899_at	1.5
putative protein ; supported by cDNA: gi_1019903_gb_U37587.1_ATU37587	250863_at	1.5
putative protein ; supported by cDNA: gi_1019903_gb_U37587.1_ATU37587		1.5
butative protein ; supported by cDNA: gi_1019903_gb_U37587.1_ATU37587 F1F0-ATPase inhibitor - like protein F1F0-ATPase inhibitor protein, OsIF1-1, Oryza sativa, EMBL:AB029059; supported by full-length cDNA:	250529_at	
butative protein ; supported by cDNA: gi_1019903_gb_U37587.1_ATU37587 F1F0-ATPase inhibitor - like protein F1F0-ATPase inhibitor protein, OsIF1-1, Oryza sativa, EMBL:AB029059; supported by full-length cDNA: RNA helicase-like protein		1.5
outative protein ; supported by cDNA: gi_1019903_gb_U37587.1_ATU37587 F1F0-ATPase inhibitor - like protein F1F0-ATPase inhibitor protein, OsIF1-1, Oryza sativa, EMBL:AB029059; supported by full-length cDNA: RNA helicase-like protein putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:403.	250332_at	1.5 1.5
butative protein ; supported by cDNA: gi_1019903_gb_U37587.1_ATU37587 F1F0-ATPase inhibitor - like protein F1F0-ATPase inhibitor protein, OsIF1-1, Oryza sativa, EMBL:AB029059; supported by full-length cDNA: RNA helicase-like protein putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:403. ranslocon Tic40-like protein ; supported by cDNA: gi_16226312_gb_AF428299.1_AF428299	250332_at 250080_at	1.5
putative protein ; supported by cDNA: gi_1019903_gb_U37587.1_ATU37587 F1F0-ATPase inhibitor - like protein F1F0-ATPase inhibitor protein, OsIF1-1, Oryza sativa, EMBL:AB029059; supported by full-length cDNA: RNA helicase-like protein putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:403. ranslocon Tic40-like protein ; supported by cDNA: gi_16226312_gb_AF428299, 1_AF428299 putative protein strong similarity to unknown protein (gb AAD21756.1); supported by cDNA: gi_15146184_gb_AY049233.1_ although this cDN	250332_at 250080_at 249703_at	1.5 1.5
putative protein ; supported by cDNA: gi_1019903_gb_U37587.1_ATU37587 F1F0-ATPase inhibitor - like protein F1F0-ATPase inhibitor protein, OsIF1-1, Oryza sativa, EMBL:AB029059; supported by full-length cDNA: RNA helicase-like protein putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:403. ranslocon Tic40-like protein ; supported by cDNA: gi_16226312_gb_AF428299.1_AF428299 jutative protein strong similarity to unknown protein (gb[AAD21756.1); supported by cDNA: gi_15146184_gb_AY049233.1_ although this cDN receptor serine/threonine protein kinase -like receptor serine/threonine kinase PR5K, Arabidopsis thaliana, EMBL:AT48698	250332_at 250080_at 249703_at 249552_s_at	1.5 1.5 1.5
putative protein ; supported by cDNA: gi_1019903_gb_U37587.1_ATU37587 F1F0-ATPase inhibitor - like protein F1F0-ATPase inhibitor protein, OsIF1-1, Oryza sativa, EMBL:AB029059; supported by full-length cDNA: RNA helicase-like protein putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:403. ranslocon Tic40-like protein ; supported by cDNA: gi_16226312_gb_AF428299.1_AF428299 putative protein strong similarity to unknown protein (gb AD21756.1); supported by cDNA: gi_15146184_gb_AY049233.1_ although this cDN receptor serine/threonine protein kinase -like receptor serine/threonine kinase PR5K, Arabidopsis thaliana, EMBL:AT48698 unknown protein ;supported by full-length cDNA: Ceres:101366.	250332_at 250080_at 249703_at 249552_s_at 249456_at	1.5 1.5 1.5 1.5
putative protein ; supported by cDNA: gi_1019903_gb_U37587.1_ATU37587 F1F0-ATPase inhibitor - like protein F1F0-ATPase inhibitor protein, OsIF1-1, Oryza sativa, EMBL:AB029059; supported by full-length cDNA: RNA helicase-like protein putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:403. ranslocon Tic40-like protein ; supported by cDNA: gi_16226312_gb_AF428299.1_AF428299 jutative protein strong similarity to unknown protein (gb[AAD21756.1); supported by cDNA: gi_15146184_gb_AY049233.1_ although this cDN receptor serine/threonine protein kinase -like receptor serine/threonine kinase PR5K, Arabidopsis thaliana, EMBL:AT48698	250332_at 250080_at 249703_at 249552_s_at	1.5 1.5 1.5

cytosolic malate dehydrogenase ;supported by full-length cDNA: Ceres:40174.	249147_at	1.5
putative protein strong similarity to unknown protein (pir  T05325); supported by cDNA: gi_13605502_gb_AF361577.1_AF361577	249011_at	1.5
GTP-binding protein-like; root hair defective 3 protein-like	248985_at	1.5
putative protein contains similarity to unknown protein (pirl T39016);supported by full-length cDNA: Ceres: 15623.	248757_at	1.5
putative protein contains similarity to CCAAT-box-binding trancription factor; supported by cDNA: gi_14326579_gb_AF385744.1_AF385744	248764_at	1.5
putative protein contains similarity to L-isoaspartyl protein carboxyl methyltransferase	248544_at	1.5 1.5
putative protein contains similarity to unknown protein (pir  T05510) putative protein contains similarity to unknown protein (pir  T26512)	248499_at 248463 at	1.5
unknown protein (summarky to unknown protein (pii)) (2012) unknown protein (supported by full-length CDNA: Ceres:92267.	248445_at	1.5
putative protein similar to unknown protein (ref/NP_014050.1)	248308 at	1.5
putative protein strong similarity to unknown protein (pir T04825); supported by cDNA: gi_14596222_gb_AY042899.1_	248115 at	1.5
ubiquitin-specific protease 23 (UBP23), putative similar to GI:11993486; supported by cDNA: gi_11993485_gb_AF302671.1_AF302671	247838_at	1.5
contains similarity to phosphoesterase	247854_at	1.5
oxysterol-binding protein - like oxysterol-binding protein, Mus musculus, EMBL:AB017026; supported by cDNA: gi_15450785_gb_AY054473	247677_at	1.5
pseudo-response regulator - like pseudo-response regulator 1 APRR1, Arabidopsis thaliana, EMBL:AB041530; supported by cDNA: gi_1028	247668_at	1.5
glucosidase II alpha subunit	247298_at	1.5
putative protein similar to unknown protein (emb CAB77570.1)	247323_at	1.5
putative protein strong similarity to unknown protein (emb[CAB62118.1)	247032_at	1.5
PHD finger protein - like PHD finger protein 3, Homo sapiens, EMBL:AF091622 dehydration-induced protein RD22 ; supported by cDNA: gi_16974545_gb_AY060560.1_	246893_at 246908 at	1.5 1.5
putative protein protein At2g40060 - Arabidopsis thaliana, EMBL:AF002109;supported by full-length cDNA: Ceres:93427.	246305 at	1.5
TINY-like protein ; supported by cDNA: gi_16323158_gb_AY057683.1_	246222 at	1.5
protein kinase tousled i supported by cDNA: gi_433051_gb_L23985.1_ATHTGPA	246134 at	1.5
putative protein BEM46 bem1/bud5 suppressor, Schizosaccharomyces pombe, bem1/bud5 suppressor, EMBL:SP29892;supported by full-ler	246090 at	1.5
hyoscyamine 6-dioxygenase hydroxylase, putative similar to hyoscyamine 6-dioxygenase hydroxylase GB:P24397 from [Hyoscyamus niger];	245756 at	1.5
AMP-binding protein	245621 at	1.5
putative protein	245588_at	1.5
SEN1 like protein	245529_at	1.5
acyl-CoA oxidase like protein ; supported by cDNA: gi_3044213_gb_AF057044.1_AF057044	245249_at	1.5
phytochelatin synthetase-like protein gene_id:K17E7.120;supported by full-length cDNA: Ceres:98007.	245228_at	1.5
unknown protein	245054_at	1.5
hypothetical protein	244918_at	1.5
hypothetical protein	257324_at	1.5
putative RING3 protein	257352_at	1.5
hypothetical protein predicted by genscan	257444_at	1.5
hypothetical protein	259535_at	1.5
hypothetical protein contains non-consensus GA donor splice site at exon 2	251298_at	1.5
	245227_s_at	1.4
putative protein ;supported by full-length cDNA: Ceres:32357.	253229_at	1.4
Escherichia coli /REF=J04423 /DEF=E coli bioB gene biotin synthetase corresponding to nucleotides 2772-3004 of J04423 /LEN=1114 (-5, -F)		1.4 1.4
unknown protein ;supported by full-length cDNA: Ceres:35441. putative DNA2-NAM7 helicase family protein	267483_at 267489 s at	1.4
putative DIP-galactose-4-epimerase	267429 at	1.4
unknown protein ;supported by full-length cDNA: Ceres:9398.	267364 at	1.4
unknown protein	267312 at	1.4
	267335 s at	1.4
hypothetical protein predicted by genscan	267130 at	1.4
putative small nuclear ribonucleoprotein Prp4p	267102 at	1.4
putative RNA-binding protein ; supported by cDNA: gi_16612301_gb_AF439844.1_AF439844	267050_at	1.4
plasma membrane proton ATPase (PMA) identical to GB:M24107; supported by cDNA: gi_166745_gb_M24107.1_ATHHATPA	266939_at	1.4
remorin identical to GB:M25268, a non-specific DNA binding protein; may be involved in intercellular communication; supported by cDNA: gi	266897_at	1.4
unknown protein	266763_at	1.4
hypothetical protein predicted by genscan	266707_at	1.4
hypothetical protein predicted by genscan and genefinder	266589_at	1.4
Expressed protein ; supported by full-length cDNA: Ceres: 34622.	266537_at	1.4
unknown protein	266090_at	1.4
chloroplast single subunit DNA-dependent RNA polymerase identical to GB:Y08722	265991_at	1.4
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:21954.	265912_at	1.4
unknown protein	265810_at	1.4
hypothetical protein hypothetical protein predicted by genscan and genefinder, contains a Bem1/NCF1/PI3K domain (prosite:QDOC50195)	265519_at 265535 at	1.4 1.4
Expressed protein is supported by cDNA: gi 14335135 gb AY037247.1	265474 at	1.4
Lanessed billet in supported by control grandous in a grand bill bill bill bill bill bill bill bil	265452 at	1.4
pEARLI 4 protein Same as GB: L43081; supported by cDNA: gi_871781_gb_L43081.1_ATHPEARA	265440_at	1.4
hypothetical protein predicted by genefinder	265310 at	1.4
	265235 s at	1.4
putative auxin-induced protein ;supported by full-length cDNA: Ceres:155143.	265182 at	1.4
G-box binding factor, GBF4 Identical to Arabidopsis thaliana G-box-binding factor 4, gb U01823;supported by full-length cDNA: Ceres:36980.	265040 at	1.4
unknown protein ; supported by cDNA: gi_14517457_gb_AY039564.1_	264987_at	1.4
hypothetical protein contains similarity to light-induced DNA-binding protein(CG-1) GI:587503 from [Petroselinum crispum]	264999_at	1.4
F-box protein family, AtFBL5 contains similarity to F-box protein FBL2 GI:6063090 from [Homo sapiens]; supported by full-length cDNA: Cere:	264957_at	1.4
unknown protein	264878_at	1.4
putative protochlorophyllide reductase similar to protochlorophyllide reductase precusor; similar to ESTs gb R30630, gb T46162, emb Z2672{	264839_at	1.4
hypothetical protein predicted by genscan	264806_at	1.4
hypothetical protein predicted by genemark.hmm	264540_at	1.4
CTP synthase-like protein similar to ctp synthase (spIP17812IPYRG_HUMAN); similar to ESTs gbJAA660762, gbJAA220982, dbJJAU008137, brother better the sentence of the synthase (spIP17812IPYRG_HUMAN); similar to ESTs gbJAA600762, gbJAA220982, dbJJAU008137, brother better the sentence of the synthase (spIP17812IPYRG_HUMAN); similar to ESTs gbJAA600762, gbJAA220982, dbJJAU008137, brother better the sentence of the synthase (spIP17812IPYRG_HUMAN); similar to ESTs gbJAA600762, gbJAA220982, dbJJAU008137, brother better the sentence of the synthase (spIP17812IPYRG_HUMAN); similar to ESTs gbJAA600762, gbJAA220982, dbJJAU008137, brother better the sentence of the synthase (spIP17812IPYRG_HUMAN); similar to ESTs gbJAA600762, gbJAA220982, dbJJAU008137, brother better the sentence of the synthase (spIP17812IPYRG_HUMAN); similar to ESTs gbJAA600762, gbJAA220982, dbJJAU008137, brother better the sentence of the synthase (spIP17812IPYRG_HUMAN); similar to ESTs gbJAA600762, gbJAA220982, dbJJAU008137, brother better the synthase (spIP17812IPYRG_HUMAN); similar to ESTs gbJAA600762, gbJAA220982, dbJJAU008137, brother better the synthase (spIP17812IPYRG_HUMAN); similar to ESTs gbJAA600762, gbJAA220982, dbJJAU008137, brother better the synthase (spIP17812IPYRG_HUMAN); similar to ESTs gbJAA600762, gbJAA220982, dbJJAU008137, brother better the synthase (spIP17812IPYRG_HUMAN); similar to ESTs gbJAA600762, gbJAA220982, dbJJAU008137, brother better the synthase (spIP17812IPYRG_HUMAN); similar to ESTs gbJAA600762, gbJAA220982, dbJJAU008137, brother better the synthase (spIP17812IPYRG_HUMAN); similar to ESTs gbJAA600762, gbJAA220982, dbJJAU008137, brother better the synthase (spIP17812IPYRG_HUMAN); similar to ESTs gbJAA600762, gbJAA200981, brother better the synthase (spIP17812IPYRG_HUMAN); similar to ESTs gbJAA600762, gbJAA220982, dbJAA20098137, brother better the synthase (spIP17812IPYRG_HUMAN); similar to ESTs gbJAA6000762, gbJAA20008137, brother better the synthase (spIP17812IPYRG_HUMAN); similar to ESTs gbJAA60000000, gbJAA20008137, br	264529_at	1.4
hypothetical protein similar to transcriptional repressor NF-X1 in Homo sapiens (sp[Q12986[NFX1_HUMAN); similar to EST gb[T21002 brothetical protein similar to transcriptional repressor NF-X1 in Homo sapiens (sp[Q12986[NFX1_HUMAN); similar to EST gb[T21002	264460_at	1.4
hypothetical protein similar to hypothetical protein GI:7378617 from [Arabidopsis thaliana]	264310_at	1.4
gamma glutamyl hydrolase, putative similar to gamma glutamyl hydrolase Gl:1680711 from [Glycine max]; supported by cDNA: gi_3169655_	264250_at	1.4
unknown protein contains similarity to tryparedoxin GI:3851498 from [Crithidia fasciculata];supported by full-length cDNA: Ceres:34936. unknown protein contains similarity to splicing factor required for vegetative and meiotic growth GI:2959374 from [Schizosaccharomyces por	264219_at 264221_s_at	1.4 1.4
putative peroxidase ;supported by full-length cDNA: Ceres:113695.	∠u+∠∠ı_S_dl	1.4
	264001 at	1 /
putative cryptochrome 2 apoprotein Match to Arabidopsis photolysase (PHH1) gene (gb/X99061) and cryptochrome 2 apoprotein (CRY2) (gb/	264001_at 263669_at	1.4 1.4

transcription factor ZAP1 identical to GP:1064883:X92976	263626_at	1.4
hypothetical protein unknown protein ; supported by cDNA: gi 15810174 gb AY056101.1	263505_s_at 263333 at	1.4 1.4
putative protein kinase contains a protein kinase domain profile (PDOC00100); supported by cDNA: gi 13605880 gb AF367339.1 AF367339		1.4
hypothetical protein predicted by genscan and genefinder	263101 s at	1.4
NADP-isocitrate dehydrogenase, putative similar to NADP-isocitrate dehydrogenase GI:5764653 from [Citrus limon]; supported by cDNA: gi_	262962_at	1.4
polyamine oxidase, putative similar to polyamine oxidase SP:O64411 [Zea mays (Maize)]; supported by cDNA: gi_13877614_gb_AF370508.	262933_at	1.4
unknown protein contains similarity to helicase GI:914852 from [Homo sapiens]	262906_at	1.4
putative heat-shock protein strong similarity to gb/Z70314 heat-shock protein from Arabidopsis thaliana and is a member of the PF/00012 Hsp hypothetical protein identical to hypothetical protein GB:AAD50051 GI:5734786 from [Arabidopsis thaliana]; supported by cDNA: gi 15081691	262814_at 262419 at	1.4 1.4
putative cyclin similar to cyclin GB:4502627 from [Homo sapiens];supported by full-length cDNA: Ceres:33877.	262296 at	1.4
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:116121.	262111 at	1.4
unknown protein contains similarity to peroxin-2 GI:6103008 from [Pichia pastoris]; supported by full-length cDNA: Ceres:96370.	262114_at	1.4
transcriptional regulator, putative similar to transcriptional regulator GI:4836767 [Zea mays]	261891_at	1.4
scarecrow-like protein similar to SCARECROW GB:AAB06318 GI:1497987 from [Arabidopsis thaliana]; supported by cDNA: gi_14334475_gb	261860_at	1.4
receptor-like kinase, putative similar to receptor-like kinase GI:1783311 from [Brassica oleracea]	261819_at	1.4
ferrodoxin NADP oxidoreductase, putative similar to ferrodoxin NADP oxidoreductase GB:X99419 GI:1480346 from [Pisum sativum]supporte vacuolar assembly protein vps41 GI:1835787 from [Lycopersicon esculentum]	261806_at	1.4 1.4
hypothetical protein contains similarity to Na+/H+ antiporter GI:1655701 from [Xenopus laevis]	261783_at 261398 at	1.4
26S proteasome regulatory subunit, putative similar to GB:AAC04490 from [Arabidopsis thaliana]	261174 at	1.4
DYW7 protein identical to DYW7 protein of unknown function GB:CAA06829 from [Arabidopsis thaliana] (Plant Mol. Biol. 42 (4), 603-613 (201	261133 at	1.4
hypothetical protein predicted by genscan+; supported by full-length cDNA: Ceres: 107992.	260981_at	1.4
chloroplast inner envelope protein, putative similar to chloroplast inner envelope protein GB:CAA92823 GI:1495768 from [Pisum sativum]	260815_at	1.4
splicing factor, putative similar to human splicing factor GB:CAA59494 GI:899298 from [Homo sapiens]	260779_at	1.4
fructokinase (Frk1), putative similar to fructokinase (Frk1) GI:2102690 from (Lycopersicon esculentum)	260343_at	1.4
hypothetical protein similar to hypothetical protein GB:AAC00595 [Arabidopsis thaliana] hypothetical protein similar to hypothetical protein GB:CAB37532 from [Arabidopsis thaliana], predicted by genscan+;supported by full-length	260194_at 260127 at	1.4 1.4
Provenced a protein similaria or riportenda protein do consider tom pratinopasi animana, proteine da protein subprise tay dimensional F-box protein FKF1/ADO3, AtF9X2a identical to FKF1 GIS960305 and Adagio 3 GI:13487072 from [Arabidopsis thaliana]	259990 s at	1.4
hypothetical protein ;supported by full-length cDNA: Ceres:110945.	259862 at	1.4
beta-1,3-glucanase precursor, putative similar to GI:4097948 from [Oryza sativa] (Gene 223 (1-2), 311-320 (1998))	259823_at	1.4
unknown protein	259767_s_at	1.4
GRAB1-like protein similar to GRAB1 protein GB:CAA09371, a novel member of the NAC domain family; supported by full-length cDNA: Cere	_	1.4
unknown protein	259489_at	1.4
unknown protein ; supported by cDNA: gi_16930412_gb_AF419560.1_AF419560 methionine aminopeptidase I (MAP1), putative similar to methionine aminopeptidase I (MAP1) GI:975722 from [Saccharomyces cerevisiae]; ;	259418_at	1.4 1.4
hypothetical protein predicted by genscan:supported by full-length cDNA: Ceres:18207.	259363_at	1.4
putative mRNA capping enzyme, RNA guanylyltransferase contains similarly to mRNA capping enzyme GB:BAA25198 from [Homo sapiens]	259202 at	1.4
transcription initiation factor IIB (TFIIB) identical to AtTFIIB2 GB:CAA84309 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:3895(	259155 at	1.4
digalactosyldiacylglycerol synthase identical to digalactosyldiacylglycerol synthase GB:AAD42378 [Arabidopsis thaliana]; supported by cDNA:	259070_at	1.4
unknown protein	259052_at	1.4
unknown protein	258949_at	1.4
hydroxyacylglutathione hydrolase cytoplasmic (glyoxalase II) (GLX II) identical to hydroxyacylglutathione hydrolase cytoplasmic (glyoxalase I hydroxyacylglutathione hydrolase cytoplasmic (glyoxalase I ) (GLX II) identical to hydroxyacylglutathione hydrolase cytoplasmic (glyoxalase I )	258775_at	1.4
hypothetical protein predicted by genscan; supported by cDNA: gi_15982780_gb_AY057497.1_ putative cytochrome P450 similar to GB:Q05047 from [Catharanthus roseus]	258660_at 258114 at	1.4 1.4
hypothetical protein predicted by genmark;supported by full-length cDNA: Ceres:19279.	258091 at	1.4
unknown protein ; supported by cDNA: gi 14334819 gb_AY035083.1_	258093 at	1.4
ethylene-insensitive 3 (EIN3) identical to GB:AAC49749 from [Arabidopsis thaliana]		1.4
seed maturation protein, putative similar to seed maturation protein (PM36) GB:AAD51624 [Glycine max]; supported by full-length cDNA: Cen	257888_at	1.4
SNF1 related protein kinase (ATSRPK1) identical to SNF1 related protein kinase (ATSRPK1) GB:AB027153 [Arabidopsis thaliana]; supported	257771_at	1.4
unknown protein	257719_at	1.4
monodehydroascorbate reductase similar to cytosolic monodehydroascorbate reductase GB:BAA77214 [Oryza sativa]; supported by cDNA: g Expressed protein ; supported by full-length cDNA: Ceres: 93242.	257227_at 257193 at	1.4 1.4
RNA helicase, putative similar to RNA helicase GB:CAA09195 from [Arabidopsis thaliana]; supported by cDNA: gi_15215677_gb_AY050367	257023 at	1.4
hypothetical protein predicted by genscan+	256823 at	1.4
unknown protein contains similarity to phospholipase a-2-activating protein SP:P27612 from [Mus musculus]; supported by cDNA: gi_152942(	256657_at	1.4
unknown protein ;supported by full-length cDNA: Ceres:38478.	256663_at	1.4
unknown protein	256542_at	1.4
unknown protein similar to N-term half of NAC domain protein NAM [Arabidopsis thaliana] GI:4325282; supported by full-length cDNA: Ceres:2 transcription factor HBP-1B-like nearly identical to transcription factor HBP-1B SP:P43273 [Arabidopsis thaliana (Mouse-ear cress)]; supporte	256300_at 256269_at	1.4 1.4
unknown protein	256258 at	1.4
DNA polymerase A family protein, putative contains Pfam profile: PF00476: DNA polymerase family A	256204 at	1.4
hypothetical protein similar to putative glutamine dependent NAD+ synthetase GB:074940 GI:8928216 from [Schizosaccharomyces pombe]	256148_at	1.4
unknown protein	256106_at	1.4
unknown protein	256041_at	1.4
putative protein embryonic abundant protein EMB20, white spruce, PIR:T09241	255859_at	1.4
putative protein hypothetical protein	255664_at 255611 at	1.4 1.4
nyponencial protein putative CHP-rich zinc finger protein similar to several A. thaliana CHP-rich proteins	255546 at	1.4
hypothetical protein identical to T10M13.21; supported by CDNA; gi_15293058, gb_AY050963.1_	255509 at	1.4
predicted protein of unknown function similar to P. falciparum O1 protein, GenBank accession number AF030694	255495_at	1.4
4-coumarateCoA ligase - like protein 4-coumarateCoA ligase 4CL, Arabidopsis thaliana, PIR:S57784	255263_at	1.4
subtilisin-like serine protease contains similarity to subtilisin-like protease AIR3 GI:4218991 from [Arabidopsis thaliana]	254979_at	1.4
putative transcriptional regulator	254992_at	1.4
3-hydroxyisobutyryl-coenzyme A hydrolase - like protein 3-hydroxyisobutyryl-coenzyme A hydrolase, Homo sapiens, U66669;supported by fu vacuolar sorting receptor-like protein BP-80 vacuolar sorting receptor, Pisum sativum, PATCHX:G1737222	254776_at 254500 at	1.4 1.4
auxin response factor 9 (ARF9) ; supported by cDNA: gi 4580574 gb AF082176.1 AF082176	254500_at 254194 at	1.4
nucleosome assembly protein I-like protein; supported by cDNA: gi_15450807 gb_AY054484.1_	253996_at	1.4
pyrophosphate-dependent phosphofructo-1-kinase pyrophosphate-dependent phosphofructo-1-kinase, Prunus armeniaca, U93272; supporte	253987_at	1.4
putative protein hypothetical protein YOR261c, yeast, PIR2:S67158;supported by full-length cDNA: Ceres:36616.	253969_at	1.4
translation initiation factor; supported by full-length cDNA: Ceres: 5206.	253900_at	1.4
signal recognition particle receptor-like protein signal recognition particle receptor - Homo sapiens, PIR2:A29440 putative protein tetratricopeptide repeat protein - Homo sapiens, PID:g1688074; supported by full-length cDNA: Ceres: 12573.	253625_at 253633_at	1.4 1.4
putative protein tetratricopeptide repeat protein - Homo sapiens,PID:g1688074;supported by full-length cDNA: Ceres: 12573. putative protein KIAA0800 protein, Homo sapiens, EMBL:AB018343	253633_at 253560_at	1.4 1.4
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predicted protein cation transport protein ChaC, Escherichia coli, PIR2:G64868;supported by full-length cDNA: Ceres:39740.	253522_at	1.4
putative protein various predicted proteins	253432_at	1.4
putative poly(A) polymerase polynucleotide adenylyltransferase (EC 2.7.7.19) class I - bovine, PIR2:S17875	253399_at	1.4
hypothetical protein	253294_at	1.4
putative protein B subunit of propionyl-CoA carboxylase, Mycobacterium tuberculosis, PATCHX:E290075; supported by cDNA: gi_14423377_ hyrothetical protein is supported by full learch oDNA: Coreci15167	_	1.4
hypothetical protein ;supported by full-length cDNA: Ceres:115167. putative protein various predicted proteins, Arabidopsis thaliana	253232_at	1.4
putative protein 70K peroxisomal membrane protein, Rattus norvegicus ,PIR2:A35723; supported by cDNA: gi 15320528 gb AF378120.1 /	252901_at 252830 at	1.4 1.4
plative protein 70K peroxisorian memorane protein, Ratus norvegicus, <i>iniz.Asor.</i> 72, supported by CDIVA. gr 1320322, <u>upported by CDIVA</u> disease resistance protein RPP13-like protein disease resistance protein RPP8 - Arabidopsis thaliana, EMBL:AF089710; supported by CDIVA	252485 at	1.4
putative protein ; supported by cDNA; gi 14334983, gb_AY035165.1	252391 at	1.4
Expressed protein ; supported by full-length cDNA: Ceres: 151603.	252365 at	1.4
putative protein hypothetical protein F16F14.2 - Arabidopsis thaliana, EMBL:AC007047	252142 at	1.4
putative protein mybaneous protein, Arabidopsis thaliana	251753 at	1.4
putative protein PBK1 protein, Homo sapiens, EMBL:HSA7398	251538 at	1.4
putative protein ETHIONINE AMINOPEPTIDASE 2 (EC 3.4.11.18) - Mus musculus,EMBL:AB003144;supported by full-length cDNA: Ceres:1	251444 at	1.4
dynamin-like protein 4 (ADL4) ; supported by cDNA: gi_6651400_gb_AF180733.1_AF180733	251429 at	1.4
ABC transporter-like protein glutathione-conjugate transporter AtMRP4 - Arabidopsis thaliana, EMBL:AJ002584	251227 at	1.4
putative protein hypothetical protein At2g28380 - Arabidopsis thaliana, EMBL:AC006283	251233 at	1.4
putative protein ZCF61, Arabidopsis thaliana, EMBL:AB028228; supported by cDNA: gi 15810464 gb AY056271.1	251156 at	1.4
putative protein predicted protein, Arabidopsis thaliana	251145_at	1.4
putative protein various predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_13878024_gb_AF370275.1_AF370275	250937_at	1.4
putative protein;supported by cDNA: gi_14326524_gb_AF385716.1_AF385716	250896_at	1.4
putative protein NAC2, Arabidopsis thaliana, EMBL:AF201456; supported by cDNA: gi_6456750_gb_AF201456.1_AF201456	250849_at	1.4
unknown protein	250822_at	1.4
cleft lip and palate associated transmembrane protein-like	250522_at	1.4
putative protein similar to unknown protein (pir  T27191);supported by full-length cDNA: Ceres:249722.	250532_at	1.4
putative protein rjs protein, Mus musculus, PIR:T14317;supported by full-length cDNA: Ceres:266544.	250382_at	1.4
putative protein various predicted proteins, Drosophila melanogaster, Caenhorhabditis elegans, Homo sapiens; supported by full-length cDN/	250384_at	1.4
protein kinase precursor - like receptor-like protein kinase 5 precursor, Arabidopsis thaliana, SWISSPROT:RLK5_ARATH	250284_at	1.4
pescadillo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadillo, Homo sapiens, EMBL:U78310	250192_at	1.4
isocitrate dehydrogenase - like protein isocitrate dehydrogenase, Nicotiana tabacum, pir:T04356	250197_at	1.4
potassium-dependent sodium-calcium exchanger - like protein cone sodium-calcium potassium exchanger (NCKX), Homo sapiens, EMBL:AF	250053_at	1.4
kinase associated protein phosphatase ; supported by cDNA: gi_15027992 gb_AY045853.1_	249924_at	1.4
unknown protein ; supported by cDNA: gi_9695278_dbj_AB046717.1_AB046717	249840_at	1.4
putative protein contains similarity to two-component response regulator protein; supported by cDNA: gi_10281005_dbj_AB046955.1_AB0469	249741_at	1.4
putative protein GTP-binding proteins - different species	249434_at	1.4
putative protein similar to unknown protein (pir  T30561)	249240_at	1.4 1.4
putative protein similar to unknown protein (sp P42251); supported by cDNA: gi_13430795_gb_AF360310.1_AF360310 putative protein similar to unknown protein (pir  T02918); supported by full-length cDNA: Ceres: 26596.	249201_at 249122 at	1.4
ATP dependent copper transporter ; supported by cDNA: gi_14194134_gb_AF367273.1_AF367273	249122_at 249027_at	1.4
An experience opper language is apported by consequence in the start of a start of the start of	248817 at	1.4
unknown protein	248743 at	1.4
putative protein contains similarity to CONSTANS homologs	248744 at	1.4
ADPG pyrophosphorylase small subunit (b AAC39441.1) supported by cDNA: gi_15146247_gb_AY049265.1_	248687 at	1.4
putative protein similar to unknown protein (sp[O15736)	248543 at	1.4
DEAD-box protein abstrakt	248442 at	1.4
cleavage and polyadenylation specificity factor subunit	248418 at	1.4
prolyl tRNA synthetase	248339 at	1.4
unknown protein ; supported by cDNA: gi_15810027_gb_AY054282.1_	248289_at	1.4
cyclic nucleotide-regulated ion channel (emb CAA76178.1); supported by cDNA: gi_13877752_gb_AF370139.1_AF370139	248250_at	1.4
flavonol 3-O-glucosyltransferase-like	248185_at	1.4
pyruvate decarboxylase (gb AAB16855.1)	248138_at	1.4
trigger factor-like protein	248094_at	1.4
putative protein contains similarity to actin	247997_at	1.4
putative protein similar to unknown protein (gb AAF04433.1);supported by full-length cDNA: Ceres:156439.	247944_at	1.4
unknown protein	247859_at	1.4
ABC transporter homolog PnATH - like PnATHABC transporter homolog, Populus nigra, EMBL:AB041505	247593_at	1.4
putative protein Atu, Drosophila melanogaster, EMBL:DMU75467	247565_at	1.4
RNA-binding protein - like RNA-binding protein, Nicotiana sylvestris, PIR:S46286; supported by cDNA: gi_16974555_gb_AY060565.1_	247575_at	1.4
pyrophosphate-dependent phosphofructo-1-kinase - like protein pyrophosphate-dependent phosphofructo-1-kinase, Prunus armeniaca, EMB	247534_at	1.4
ARF1-binding protein ; supported by cDNA: gi_2245393_gb_U89771.1 ATU89771	247468_at	1.4
proteasome regulatory subunit-like ; supported by cDNA: gi_17063180_gb_AY062113.1_	247257_at	1.4
trehalose-6-phosphate phosphatase DNA binding protein TGA1a homolog ;supported by full-length cDNA: Ceres:31032.	247228_at 247199_at	1.4
2-oxoglutarate dehydrogenase, E1 component	_	1.4 1.4
unknown protein	247155_at 247063 at	1.4
anthranilate N-hydroxycinnamoyl/benzoyttransferase-like protein ;supported by full-length cDNA: Ceres:32856.	247038 at	1.4
antinamide reniginosystemanogrado attiva	_	1.4
famesylated protein ATFP6-like protein famesylated protein ATFP6 - Arabidopsis thaliana, EMBL:U64909	246000 at	1.4
	246909_at 246429_at	1.4
putative protein hnRNP A/B related protein - Felis catus. EMBL:AF153444: supported by cDNA: oi 14194148 ob AF367280 1 AF367280	246429_at	
putative protein hnRNP A/B related protein - Felis catus, EMBL:AF153444; supported by cDNA: gi_14194148_gb_AF367280.1_AF367280 putative protein	246429_at 246292_at	1.4
putative protein hnRNP A/B related protein - Felis catus, EMBL:AF153444; supported by cDNA: gi_14194148_gb_AF367280.1_AF367280 putative protein putative protein ;supported by full-length cDNA: Ceres:13475.	246429_at	1.4 1.4
putative protein supported by full-length cDNA: Ceres:13475.	246429_at 246292_at 246283_at 246225_at	1.4
putative protein putative protein ;supported by full-length cDNA: Ceres:13475. putative protein hypothetical protein F2A19.120 - Arabidopsis thaliana, PIR:T47944	246429_at 246292_at 246283_at	
putative protein supported by full-length cDNA: Ceres:13475.	246429_at 246292_at 246283_at 246225_at 246173_s_at	1.4 1.4
putative protein putative protein ;supported by full-length cDNA: Ceres:13475. putative protein hypothetical protein F2A19.120 - Arabidopsis thaliana, PIR:T47944 putative protein CD2 cytoplasmic domain binding protein - Homo sapiens, EMBL:AF104222;supported by full-length cDNA: Ceres:13887.	246429_at 246292_at 246283_at 246225_at 246173_s_at 245887_at	1.4 1.4 1.4
putative protein putative protein ;supported by full-length cDNA: Ceres:13475. putative protein hypothetical protein F2A19.120 - Arabidopsis thaliana, PIR:T47944 putative protein CD2 cytoplasmic domain binding protein - Homo sapiens, EMBL:AF104222;supported by full-length cDNA: Ceres:13887. ferredoxin-dependent glutamate synthase ; supported by cDNA: gi_3869250_gb_U39287.1_ATU39287	246429_at 246292_at 246283_at 246225_at 246173_s_at 245887_at 245701_at	1.4 1.4 1.4 1.4
putative protein putative protein ;supported by full-length cDNA: Ceres:13475. putative protein hypothetical protein F2A19.120 - Arabidopsis thaliana, PIR:T47944 putative protein CD2 cytoplasmic domain binding protein - Homo sapiens, EMBL:AF104222;supported by full-length cDNA: Ceres:13887. ferredoxin-dependent glutamate synthase ; supported by cDNA: gi_3869250_gb_U39287.1_ATU39287 RNA-binding protein-like	246429_at 246292_at 246283_at 246225_at 246173_s_at 245887_at 245701_at 245714_at	1.4 1.4 1.4 1.4 1.4
putative protein putative protein ;supported by full-length cDNA: Ceres:13475. putative protein hypothetical protein F2A19.120 - Arabidopsis thaliana, PIR:T47944 putative protein CD2 cytoplasmic domain binding protein - Homo sapiens, EMBL:AF104222;supported by full-length cDNA: Ceres:13887. ferredoxin-dependent glutamate synthase ; supported by cDNA: gi_3869250_gb_U39287.1_ATU39287 RNA-binding protein-like pyruvate,orthophosphate dikinase	246429_at 246292_at 246283_at 246225_at 246173_s_at 245887_at 245701_at 245714_at 245528_at	1.4 1.4 1.4 1.4 1.4 1.4
putative protein putative protein ;supported by full-length cDNA: Ceres:13475. putative protein hypothetical protein F2A19.120 - Arabidopsis thaliana, PIR:T47944 putative protein CD2 cytoplasmic domain binding protein - Homo sapiens, EMBL:AF104222;supported by full-length cDNA: Ceres:13887. ferredoxin-dependent glutamate synthase ; supported by cDNA: gi_3869250_gb_U39287.1_ATU39287 RNA-binding protein-like pyruvate, orthophosphate dikinase ATP-dependent Clp protease proteolytic subunit (ClpR4), putative similar to ATP-dependent Clp protease proteolytic subunit GI:7264063 fror	246429_at 246292_at 246283_at 246225_at 246773_s_at 245887_at 245701_at 245701_at 245714_at 245528_at 245400_at	1.4 1.4 1.4 1.4 1.4 1.4 1.4
putative protein putative protein ;supported by full-length cDNA: Ceres:13475. putative protein hypothetical protein F2A19.120 - Arabidopsis thaliana, PIR:T47944 putative protein CD2 cytoplasmic domain binding protein - Homo sapiens, EMBL:AF104222;supported by full-length cDNA: Ceres:13887. ferredoxin-dependent glutamate synthase ; supported by cDNA: gi_3869250_gb_U39287.1_ATU39287 RNA-binding protein-like pyruvate,orthophosphate dikinase ATP-dependent Clp protease proteolytic subunit (ClpR4), putative similar to ATP-dependent Clp protease proteolytic subunit GI:7264063 fror putative protein similarity to ALR - Homo sapiens~contains EST gb:Aa39558600	246429_at 246292_at 246225_at 246225_at 246173_s_at 245701_at 245701_at 245714_at 245528_at 24500_at 245237_at	1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4
putative protein isupported by full-length cDNA: Ceres:13475. putative protein hypothetical protein F2A19.120 - Arabidopsis thaliana, PIR:T47944 putative protein CD2 cytoplasmic domain binding protein - Homo sapiens, EMBL:AF104222;supported by full-length cDNA: Ceres:13887. ferredoxin-dependent glutamate synthase ; supported by cDNA: gi_3869250_gb_U39287.1_ATU39287 RNA-binding protein-like pyruvate, orthophosphate dikinase ATP-dependent Clp protease proteolytic subunit (ClpR4), putative similar to ATP-dependent Clp protease proteolytic subunit GI:7264063 fror putative protein similarity to ALR - Homo sapiens-contains EST gb:Aa39558600 small nuclear ribonucleoprotein U1A identical to GB:Z49991; supported by cDNA: gi_15450590_gb_AY052663.1_ unknown protein ; supported by cDNA: gi_16930450_gb_AF419579.1_AF419579 putative xylulose kinase	246429_at 246292_at 246283_at 246225_at 24673_s_at 245887_at 245701_at 245714_at 245528_at 245237_at 245237_at 245124_at 245124_at 245119_at 263773_at	1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4
putative protein putative protein ;supported by full-length cDNA: Ceres:13475. putative protein hypothetical protein F2A19.120 - Arabidopsis thaliana, PIR:T47944 putative protein hypothetical protein F2A19.120 - Arabidopsis thaliana, PIR:T47944 putative protein CD2 cytoplasmic domain binding protein - Homo sapiens, EMBL:AF104222;supported by full-length cDNA: Ceres:13887. ferredoxin-dependent glutamate synthase ; supported by cDNA: gi_3869250_gb_U39287.1_ATU39287 RNA-binding protein-like pyruvate,orthophosphate dikinase ATP-dependent Clp protease proteolytic subunit (ClpR4), putative similar to ATP-dependent Clp protease proteolytic subunit GI:7264063 fror putative protein similarity to ALR - Homo sapiens~contains EST gb:Aa39558600 small nuclear ribonucleoprotein U1A identical to GB:Z49991; supported by cDNA: gi_15450590_gb_AY052663.1_ unknown protein ; supported by cDNA: gi_16930450_gb_AF419579.1_AF419579	246429_at 246292_at 246283_at 246225_at 246173_s_at 245701_at 245701_at 245714_at 245528_at 245400_at 245400_at 245237_at 245124_at 245119_at	1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4

unknown protein ; supported by cDNA: gi_15450835_gb_AY054498.1_	261127_at	1.3
hypothetical protein ; supported by cDNA: gi_12659317 gb_AF331066.1_AF331066	259512 at	
hypothetical protein predicted by genscan; similar to SPIQ09298/YQO9 CAEEL	267632 at	
putative RING zinc finger protein	267581 at	
hypothetical protein predicted by genscan	267508 at	
unknown protein	267073_at	
unknown protein 'supported by full-length cDNA: Ceres:39666.	266848 at	
anitom protein , adoptined by full-length CDNA: Ceres:34564.	266822 at	
putative amino acid acetyltransferase	266826 at	
unknown protein ; supported by cDNa: gi_14030738_gb_AF375460.1_AF375460	266617 at	
	_	
putative splicing factor ;supported by full-length cDNA: Ceres:16224.	266534_at	
ferredoxin-dependent glutamate synthase (GLU2)	266365_at	
unknown protein	266389_s_a	
putative ubiquitin activating enzyme	266333_at	
unknown protein	266189_at	
unknown protein ;supported by full-length cDNA: Ceres:39558.	266170_at	
unknown protein	265807_at	
Expressed protein ; supported by full-length cDNA: Ceres: 157460.	265770_at	
putative MYB family transcription factor	265700_at	
putative glucan synthase	265729_at	1.3
putative cellular apoptosis susceptibility protein	265453_at	1.3
putative chloroplast outer membrane protein	265412_at	1.3
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:25903.	265100_at	1.3
branched-chain alpha-keto acid decarboxylase E1 beta subunit similar to Bovine branched chain alpha-keto acid dehydrogenase (BCKDHE	3) I 265070_at	1.3
Rubisco subunit binding-protein beta subunit identical to chaperonin 60 beta precursor GB:JT0901 from [Arabidopsis thaliana]; supported b	yc 265076_at	1.3
unknown protein Contains similarity to pre-mRNA processing protein PRP39 gb L29224 from S. cerevisiae. ESTs gb R64908 and gb T881	58 265036_at	1.3
myrosinase binding protein, putative similar to myrosinase binding protein GI:1711295 from [Brassica napus]	265053 at	1.3
hypothetical protein predicted by genemark.hmm	264913 at	1.3
unknown protein similar to unknown protein GB:AAD20911;supported by full-length cDNA: Ceres:30006.	264835 at	
putative ligand-gated ion channel protein Similar to Arabidopsis putative ion-channel PID:g2262157 (gb]AC002329); supported by cDNA: g		
unknown protein	264563_s_a	
unknown protein ; supported by cDNA: gi_13430435_gb_AF360130.1_AF360130	264548 at	
unknown protein similar to salt-inducible protein (gi)375717); similar to ESTs gb]R30192 and gb]AA651017	264452 at	
hypothetical protein predicted by genefinder; supported by cDNA; gi 15983441 gb AF424595.1 AF424595	264408 at	
unknown protein similarity to stromal cell-derived factor 2, Mus musculus, PIR2:JC5105; contains EST gb:T22533, AA067386, Z18160;sup		
unitoring isoamylase Similar to gij1652733 glycogen operon protein GlgX from Synechocystis sp. genome splD90908. ESTs gb 136690, gl	· –	
hypothetical protein predicted by genemark.hmm	264268_at	
hypothetical protein predicted by genscan+	264142_at	
unknown protein ;supported by full-length cDNA: Ceres:41712.	263978_at	
putative homeodomain transcription factor; supported by cDNA: gi_13877516_gb_AF353094.1_AF353094	263956_at	
unknown protein ;supported by full-length cDNA: Ceres:20834.	263755_at	
hypothetical protein predicted by genefinder; supported by full-length cDNA: Ceres:119045.	263538_at	
hypothetical protein predicted by genscan	263488_at	
putative RING zinc finger protein	263424_at	
putative nonsense-mediated mRNA decay protein ; supported by cDNA: gi_15810402_gb_AY056240.1_	263334_at	
putative glyoxalase II	263243_at	
hypothetical protein predicted by genefinder; supported by cDNA: gi_14423545_gb_AF387010.1_AF387010	263075_at	
lipase, putative contains Pfam profile: PF00657 Lipase/Acylhydrolase with GDSL-like motif; supported by cDNA: gi_13937188_gb_AF3729	_	
TPR-repeat protein contains multiple TPR domains: Pfam profile: PF00515	262691_at	
hypothetical protein similar to GB:P49967 signal recognition particle 54 kDa subunit (Srp54-1) from [Arabidopsis thaliana].;supported by full	-le 262601_at	1.3
hypothetical protein similar to hypothetical protein GB:AAD50049 GI:5734784 from [Arabidopsis thaliana]	262459_at	1.3
unknown protein Similar to gb AF151884 CGI-126 protein from Homo sapiens. EST gb Z18048 comes from this gene; supported by full-len	gtl 262298_at	1.3
unknown protein ; supported by cDNA: gi_16648825_gb_AY058190.1_	262232_at	1.3
Avr9 elicitor response protein, putative similar to Avr9 elicitor response protein GI:4138265 from [Nicotiana tabacum]	262188_at	1.3
peptide transporter, putative similar to peptide transporter GI:2655098 from [Hordeum vulgare]	261937_at	1.3
ribosomal protein L7, putative similar to ribosomal protein L7 GB:AAA03081 GI:307388 from [Homo sapiens]	261911_at	1.3
Expressed protein ; supported by full-length cDNA: Ceres: 39481.	261858_at	1.3
unknown protein ; supported by cDNA: gi_15451153_gb_AY054657.1_	261795_at	1.3
unknown protein similar to hypothetical protein GB:CAA20583 GI:3549672 from [Arabidopsis thaliana]	261682_at	1.3
unknown protein	261295_at	1.3
unknown protein ;supported by full-length cDNA: Ceres:158528.	261253_at	
unknown protein ;supported by full-length cDNA: Ceres:6672.	261153_at	1.3
GSH-dependent dehydroascorbate reductase 1, putative similar to GB:BAA90672 from [Oryza sativa]; supported by full-length cDNA: Cere		
unknown protein ; supported by cDNA: gi 16974626 gb AY060591.1	260989 at	
hypothetical protein similar to hypothetical protein GB:AAB67625 GI:2342727 from [Arabidopsis thaliana]; supported by full-length cDNA: C		
unknown protein ; supported by cDNA: gi 15028086 gb AY045900.1	260832 at	
storage protein, putative similar to GB:CAA53781 from [Dioscorea cayenensis] (Plant Mol. Biol. 28 (3), 369-380 (1995)); supported by cDN		
poly(A)-specific ribonuclease, putative similar to GB:CAA06683 from [Homo sapiens]	260593 at	
unknown protein	260436 at	
unknown protein identical to most of OBP32pep protein (fragment) GB:S71212 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres	_	
unknown protein ; supported by cDNA: gi 13878054 gb AF370290.1 AF370290	260157 at	
putative RNA-binding protein contains Pfam profile: PF0076 RNA recognition motif. (aka RRM, RBD, or RNP domain); similar to putative		
unknown protein	259993 at	
putative protein kinase C-terminal region similar to MAP3K delta-1 protein kinase GB:CAA74591 [Arabidopsis thaliana]; contains Pfam prof		
leucine-rich repeat transmembrane protein kinase 1, putative similar to GI:3360289 from [Zea mays] (Plant Mol. Biol. 37 (5), 749-761 (1998)		
putative UDP-glucose:glycoprotein glucosyltransferase similar to UDP-glucose:glycoprotein glucosyltransferase precursor GB:200332 [Drc		
transfactor, putative similar to GI:4519671 from [Nicotiana tabacum]	259930_at 259832 at	
unknown protein	259832_at	
unknown protein	259689 x a	
unknown protein ; supported by cDNA: gi_15293080_gb_AY050974.1_	259669_x_a	
spindly (gibberellin signal transduction protein) identical to spindly GB:AAC49446 [Arabidopsis thaliana]; supported by cDNA: gi 1589777	_	
homeobox-leucine zipper protein HAT5 (HD-ZIP protein 5) (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (H unknown protein ;supported by full-length cDNA: Ceres:801.	D-2 259165_at 259055_at	
analoni, protein joopportee by fair longer borne of the out of the	200000_dl	1.5

unknown protein ;supported by full-length cDNA: Ceres:105296.	258990_at	1.3
putative ribosome recycling factor similar to ribosome recycling factor gene (RRF) GB:BAA76865 [Thermus thermophilus]	258996_at	1.3
hypothetical protein predicted by genscan+	258946_at	1.3
hypothetical protein predicted by genscan unknown protein	258844_at 258687 at	1.3 1.3
acetyl-coA dehydrogenase, putative similar to acetyl-coenzyme A dehydrogenase GB:NP_031408 from [Mus musculus]	258524 at	1.3
hypothetical protein	258533 at	1.3
expressed protein supported by cDNA: qi:14194102	258444 at	1.3
putative protein kinase similar to mitogen activated protein kinase kinase GB:AAC32599 from [Oryza sativa]; supported by full-length cDNA: C	258456_at	1.3
putative protein disulfide isomerase similar to protein disulfide isomerase GB:AAD55566 from [Volvox carteri f. nagariensis]	258329_at	1.3
putative ethylene-inducible protein similar to ethylene-inducible protein GB:M88254 from [Hevea brasiliensis]; supported by cDNA: gi_410395	258336_at	1.3
unknown protein	258263_at	1.3
hypothetical protein contains Pfam profile: PF01055 Glycosyl hydrolases family 31; supported by cDNA: gi_16648902_gb_AY059821.1_	258109_at	1.3
putative MAP kinase similar to GB:AAD52659 from [Oryza sativa]	258119_at	1.3
putative cytochrome P450 similar to GB:Q05047 from [Catharanthus roseus]; supported by cDNA: gi_15292786_gb_AY050827.1_ FtsH protease, putative contains similarity to cell division protein FtsH GI:1652085 from [Synechocystis sp. PCC 6803]	258094_at 258048 at	1.3 1.3
hypothetical protein predicted by genemark	257948 at	1.3
Expressed protein ; supported by cDNA: gi_16604419_gb_AY058108.1_	257914 at	1.3
protein phosphatase-2c, putative similar to protein phosphatase-2c GB:AAC35951 [Mesembryanthemum crystallinum]; contains Pfam profile:		1.3
	257857_s_at	1.3
unknown protein	257803_at	1.3
unknown protein	257717_at	1.3
unknown protein contains Pfam profile: PF00515 tetratricopeptide repeat domain (TPR domain);supported by full-length cDNA: Ceres:23733.	257730_at	1.3
unknown protein contains Pfam profiles: PF01388 ARID DNA binding domain, PF00505 HMG (high mobility group) box;supported by full-lenc		1.3
hemolysin-like protein similar to hemolysin C GB:Q54318 [Brachyspira hyodysenteriae]	257178_at	1.3
Expressed protein ; supported by cDNA: gi_15215805_gb_AY050432.1_ unknown protein contains PF00612 IQ:IQ calmodulin-binding motif	257007_at 256822 at	1.3 1.3
hypothetical protein predicted by genemark.hmm	256792 at	1.3
protein kinase, putative contains Pfam profile: PF00069: Eukaryotic protein kinase domain	256529_at	1.3
unknown protein ;supported by full-length cDNA: Ceres:33407.	256440 at	1.3
lipid transfer protein, putative similar to lipid transfer protein GI:9279661 from [Arabidopsis thaliana]; supported by cDNA: gi 15028044 gb A	256145 at	1.3
unknown protein ; supported by cDNA: gi_14532715_gb_AY039982.1_	256074_at	1.3
ubiquitin, putative similar to ubiquitin GI:10177083 from [Arabidopsis thaliana]; supported by cDNA: gi_16974595_gb_AY060574.1_	256071_at	1.3
ABC transporter, putative similar to ABC transporter GI:10280532 from [Homo sapiens]	255889_at	1.3
putative WD repeat membrane protein ; supported by cDNA: gi_15912316_gb_AY056436.1_	255711_at	1.3
Shaggy related protein kinase tetha ; supported by CDNA: gi_17063157_gb_AY062099.1	255635_at	1.3
	255600_s_at	1.3
putative NAM-like protein hypothetical protein similar to C. elegans protein B0414.8, GenBank accession number 2088768	255585_at 255560_at	1.3 1.3
coded for by A. thaliana CDNA T04215 similar to epoxide hydrolases	255525 at	1.3
hypothetical protein	255526 at	1.3
putative protein	255527 at	1.3
, putative cullin-like 1 protein similar to O. sativa cullin-like proteins; supported by cDNA: gi_15028160_gb_AY046030.1_		1.3
putative host response protein pir7a protein - rice, PIR2:S47086	255025_at	1.3
polyubiquitin-like protein polyubiquitin 6 - red alga (Gracilaria verrucosa), PIR2:S53719	254822_at	1.3
putative protein phospho-N-acetylmuramoyl-pentapeptide-transferase, Haemophilus influenzae, Pir2:A64185	254662_at	1.3
initiation factor-2Bepsilon-like protein initiation factor-2Be, Rattus norvegicus, PATCHX:G924597	254664_at	1.3
putative protein RNase L inhibitor-like protein RNase L inhibitor (clone 8), Homo sapiens	254645_at	1.3 1.3
hypothetical protein	254615_at 254501 at	1.3
hypothetical protein	254502 at	1.3
3-hydroxyisobutyrate dehydrogenase -like protein 3-hydroxyisobutyrate dehydrogenase, Rattus norvegicus, Pir:A32867;supported by full-len		1.3
putative protein hypothetical protein, chr.4, Arabidopsis thaliana, PATCHX:G2392763	254350 at	1.3
predicted protein PVPR3 protein, Phaesolis vulgaris, PATCHX:G169363;supported by full-length cDNA: Ceres:13832.	254276_at	1.3
NADPH-ferrihemoprotein reductase ATR1 ; supported by cDNA: gi_15451215_gb_AY054688.1_	254127_at	1.3
grpE like protein ;supported by full-length cDNA: Ceres:35284.	253949_at	1.3
putative protein met-10+ protein, Neurospora crassa, PIR2:S46697	253912_at	1.3
hypothetical protein	253888_at	1.3
putative DNA-binding protein AP2 domain containing protein RAP2.4 - Arabidopsis thaliana, PID:g2281633 putative protein predicted protein. Arabidopsis thaliana; supported by cDNA: gi 15293152 gb AY051010.1	253799_at 253739_at	1.3 1.3
X-Pro dipeptidase - like protein (riagment) X-Pro dipeptidase, Horo sapiens, PIR2:A32454	253704 at	1.3
NADPH-ferrihemoprotein reductase (ATR2)	253664 at	1.3
Expressed protein ; supported by full-length cDNA: Ceres: 7876.	253549 at	1.3
putative protein tomato leucine zipper-containing protein - Lycopersicon esculentum, PIR2:S21495	253531_at	1.3
predicted protein predicted protein on BAC T06B20; Arabidopsis thaliana chromosome II; PATCHX:G1946371	253501_at	1.3
putative protein prolyl 4-hydroxylase alpha(II)-subunit, Mus musculus, PIR2:I49135;supported by full-length cDNA: Ceres:2306.	253321_at	1.3
protein kinase - like protein protein kinase, 41K, Arabidopsis thaliana,PIR2:S71172; supported by cDNA: gi_15451087_gb_AY054624.1_	253264_at	1.3
L-ascorbate peroxidase ;supported by full-length cDNA: Ceres:21896.		1.3
putative ubiquitin-dependent proteolytic protein ubiquitin fusion-degradation protein - Mus musculus, PID:g1654348; supported by cDNA: gi_	253223_at	
	252931_at	1.3
starch phosphorylase H (cytosolic form) - like protein starch phosphorylase H, cytosolic isoform, Vicia faba, PIR:T12091; supported by cDNA	252931_at 252468_at	1.3
starch phosphorylase H (cytosolic form) - like protein starch phosphorylase H, cytosolic isoform, Vicia faba, PIR:T12091; supported by cDNA putative protein br-1 protein (NITRIC OXIDE SYNTHASE) - Helix pomatia, PID:e234055	252931_at 252468_at 252410_at	1.3 1.3
starch phosphorylase H (cytosolic form) - like protein starch phosphorylase H, cytosolic isoform, Vicia faba, PIR:T12091; supported by cDNA putative protein br-1 protein (NITRIC OXIDE SYNTHASE) - Helix pomatia,PID:e234055 putative transcription factor MYB94 ; supported by cDNA: gi_3941527_gb_AF062918.1_AF062918	252931_at 252468_at 252410_at 252408_at	1.3 1.3 1.3
starch phosphorylase H (cytosolic form) - like protein starch phosphorylase H, cytosolic isoform, Vicia faba, PIR:T12091; supported by cDNA putative protein br-1 protein (NITRIC OXIDE SYNTHASE) - Helix pomatia, PID:e234055	252931_at 252468_at 252410_at	1.3 1.3
starch phosphorylase H (cytosolic form) - like protein starch phosphorylase H, cytosolic isoform, Vicia faba, PIR:T12091; supported by cDNA putative protein br-1 protein (NITRIC OXIDE SYNTHASE) - Helix pomatia,PID:e234055 putative transcription factor MYB94 ; supported by cDNA: gi_3941527_gb_AF062918.1_AF062918 hypothetical protein	252931_at 252468_at 252410_at 252408_at 252362_at	1.3 1.3 1.3 1.3
starch phosphorylase H (cytosolic form) - like protein starch phosphorylase H, cytosolic isoform, Vicia faba, PIR:T12091; supported by cDNA putative protein br-1 protein (NITRIC OXIDE SYNTHASE) - Helix pomatia,PID:e234055 putative transcription factor MYB94 ; supported by cDNA: gi_3941527_gb_AF062918.1_AF062918 hypothetical protein putative protein CRP1 protein, Zea mays, gb:AAC25599 putative protein lea32, Arabidopsis thaliana, EMBL:ATH131342;supported by full-length cDNA: Ceres:35969. U1 snRNP 70K protein ; supported by cDNA: gi_14532499_gb_AY039874.1_	252931_at 252468_at 252410_at 252408_at 252362_at 252305_at 252229_at 252182_at	1.3 1.3 1.3 1.3 1.3 1.3 1.3
starch phosphorylase H (cytosolic form) - like protein starch phosphorylase H, cytosolic isoform, Vicia faba, PIR:T12091; supported by cDNA putative protein br-1 protein (NITRIC OXIDE SYNTHASE) - Helix pomatia,PID:e234055 putative transcription factor MYB94 ; supported by cDNA: gi_3941527_gb_AF062918.1_AF062918 hypothetical protein putative protein CRP1 protein, Zea mays, gb:AAC25599 putative protein lea32, Arabidopsis thaliana, EMBL:ATH131342; supported by full-length cDNA: Ceres:35969. U1 snRNP 70K protein ; supported by cDNA: gi_14532499_gb_AY039874.1_ putative protein hypothetical protein F16F14.4 - Arabidopsis thaliana: EMBL:AC007047; supported by cDNA: gi_14423521_gb_AF386998.1_/	252931_at 252468_at 252410_at 252408_at 252362_at 252305_at 25229_at 25229_at 25229_at 252297_at	1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3
starch phosphorylase H (cytosolic form) - like protein starch phosphorylase H, cytosolic isoform, Vicia faba, PIR:T12091; supported by cDNA putative protein br-1 protein (NITRIC OXIDE SYNTHASE) - Helix pomatia,PID:e234055 putative transcription factor MYB94 ; supported by cDNA: gi_3941527_gb_AF062918.1_AF062918 hypothetical protein putative protein CRP1 protein, Zea mays, gb:AAC25599 putative protein lea32, Arabidopsis thaliana, EMBL:ATH131342;supported by full-length cDNA: Ceres:35969. U1 snRNP 70K protein ; supported by cDNA: gj_14532499_gb_AY039874.1_ putative protein hymothetical protein F16F14.4 - Arabidopsis thaliana: EMBL:AC007047; supported by cDNA: gj_14423521_gb_AF386998.1_/ mucin -like protein hemomucin, Drosophila melanogaster, EMBL:DM42014;supported by full-length cDNA: Ceres:34197.	252931_at 252468_at 252410_at 252408_at 252305_at 252305_at 252229_at 252182_at 25207_at 252117_at	1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3
starch phosphorylase H (cytosolic form) - like protein starch phosphorylase H, cytosolic isoform, Vicia faba, PIR:T12091; supported by cDNA putative protein br-1 protein (NITRIC OXIDE SYNTHASE) - Helix pomatia,PID:e234055 putative transcription factor MYB94 ; supported by cDNA: gi_3941527_gb_AF062918.1_AF062918 hypothetical protein putative protein CRP1 protein, Zea mays, gb:AAC25599 putative protein lea32, Arabidopsis thaliana, EMBL:ATH131342;supported by full-length cDNA: Ceres:35969. U1 snRNP 70K protein ; supported by cDNA: gi_14532499_gb_AY038874.1_ putative protein hypothetical protein F16F14.4 - Arabidopsis thaliana: EMBL:AC007047; supported by cDNA: gi_14423521_gb_AF386998.1_/ mucin -like protein hemomucin, Drosophila melanogaster, EMBL:DM42014;supported by full-length cDNA: Ceres:34197. receptor-protein kinase-like protein receptor-like protein kinase, Catharanthus roseus, PIR:T10060; supported by cDNA: gi_14334759_gb_AY	252931_at 252468_at 252410_at 252408_at 252305_at 252305_at 252229_at 252182_at 252097_at 25207_at 252076_at	1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3
starch phosphorylase H (cytosolic form) - like protein starch phosphorylase H, cytosolic isoform, Vicia faba, PIR:T12091; supported by cDNA putative protein br-1 protein (NITRIC OXIDE SYNTHASE) - Helix pomatia,PID:e234055 putative transcription factor MYB94 ; supported by cDNA: gi_3941527_gb_AF062918.1_AF062918 hypothetical protein putative protein CRP1 protein, Zea mays, gb:AAC25599 putative protein lea32, Arabidopsis thaliana, EMBL:ATH131342; supported by full-length cDNA: Ceres:35969. U1 snRNP 70K protein ; supported by cDNA: gi_14532499_gb_AY039874.1_ putative protein hypothetical protein F16F14.4 - Arabidopsis thaliana: EMBL:AC007047; supported by cDNA: gi_14423521_gb_AF386998.1_/ mucin -like protein hemomucin, Drosophila melanogaster, EMBL:DM42014; supported by full-length cDNA: Ceres:34197. receptor-protein kinase-like protein receptor-like protein kinase, Catharanthus roseus, PIR:T10060; supported by cDNA: gi_14334759_gb_A\ putative protein predicted protein, Arabidopsis thaliana	252931_at 252468_at 252410_at 252408_at 252362_at 252305_at 252229_at 252182_at 252097_at 252017_at 252017_at 252066_at 251937_at	1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3
starch phosphorylase H (cytosolic form) - like protein starch phosphorylase H, cytosolic isoform, Vicia faba, PIR:T12091; supported by cDNA putative protein br-1 protein (NITRIC OXIDE SYNTHASE) - Helix pomatia,PID:e234055 putative transcription factor MYB94 ; supported by cDNA: gi_3941527_gb_AF062918.1_AF062918 hypothetical protein putative protein CRP1 protein, Zea mays, gb:AAC25599 putative protein lea32, Arabidopsis thaliana, EMBL:ATH131342; supported by full-length cDNA: Ceres:35969. U1 snRNP 70K protein ; supported by cDNA: gi_14532499_gb_AY039874.1_ putative protein hemomucin, Drosophila melanogaster, EMBL:DM42014; supported by full-length cDNA: Ceres:34197. receptor-protein kinase-like protein receptor-like protein kinase, Catharanthus roseus, PIR:T10060; supported by cDNA: gi_14334759_gb_A) putative protein predicted proteins, Arabidopsis thaliana	252931_at 252468_at 252410_at 252408_at 252305_at 252305_at 252229_at 252182_at 252182_at 252097_at 252117_at 252066_at 251937_at 251951_s_at	1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3
starch phosphorylase H (cytosolic form) - like protein starch phosphorylase H, cytosolic isoform, Vicia faba, PIR:T12091; supported by cDNA putative protein br-1 protein (NITRIC OXIDE SYNTHASE) - Helix pomatia,PID:e234055 putative transcription factor MYB94 ; supported by cDNA: gi_3941527_gb_AF062918.1_AF062918 hypothetical protein putative protein CRP1 protein, Zea mays, gb:AAC25599 putative protein lea32, Arabidopsis thaliana, EMBL:ATH131342; supported by full-length cDNA: Ceres:35969. U1 snRNP 70K protein ; supported by cDNA: gi_14532499_gb_AY039874.1_ putative protein hemomucin, Drosophila melanogaster, EMBL:DM42014; supported by full-length cDNA: Ceres:34197. receptor-protein kinase-like protein receptor-like protein kinase, Catharanthus roseus, PIR:T10060; supported by cDNA: gi_14334759_gb_A) putative protein predicted protein, Arabidopsis thaliana	252931_at 252468_at 252410_at 252408_at 252362_at 252305_at 252229_at 252182_at 252097_at 252017_at 252017_at 252066_at 251937_at	1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3

hypothetical protein	251614_at 1.	.3
putative protein ferritin 1 precursor - Arabidopsis thaliana, EMBL:X94248	251347_at 1.	
putative protein putative protein BcDNA.GH03694 - Drosophila melanogaster, EMBL:AF181626	251316_s_at 1.	
putative protein putative protein F26O13.260 - Arabidopsis thaliana, EMBL:AL133452	251333_at 1.	
ARGININE/SERINE-RICH SPLICING FACTOR RSP31; supported by cDNA: gi_16612267_gb_AF439831.1_AF439831	251242_at 1.	
putative protein phytochrome-associated protein 3 (PAP3) - Arabidopsis thaliana, EMBL:AF088280	251245_at 1.	
ATP-dependent RNA helicase-like protein ATP-dependent RNA helicase (EC 3.6) - Homo sapiens, PIR:JC5785	251265_at 1.	
putative protein predicted protein, Arabidopsis thaliana; supported by cDNA: gi_14334781_gb_AY035064.1_ putative protein hypothetical proteins - Arabidopsis thaliana	251153_at 1. 251078_at 1.	
putative protein histone H2A, garden pea, PIR:JQ1183; supported by full-length cDNA: Ceres: 1553.	251078_at 1. 251011 at 1.	
putative protein various predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres: 98672.	250931 at 1.	
putative protein various similarity to unknown protein (gb AAF19567.1)	250809 at 1.	
SET-domain protein-like ; supported by cDNA; gi 13517742 gb AF344444.1 AF344444	250817 at 1.	
arginine-tRNA-protein transferase 1 homolog; supported by cDNA: gi 3806097 gb AF079100.1 AF079100	250754_at 1.	
ankyrin-like protein	250761 at 1.	
cell division related protein-like	250711 at 1.	
splicing factor 3a ; supported by cDNA: gi_14532639_gb_AY039944.1_	250715_at 1.	.3
putative protein similar to unknown protein (gb AAF32477.1);supported by full-length cDNA: Ceres:117588.	250737_at 1.	.3
diadenosine 5,5-P1,P4-tetraphosphate hydrolase-like protein ; supported by cDNA: gi_13937174_gb_AF372941.1_AF372941	250705_at 1.	.3
alpha-hydroxynitrile lyase-like protein alpha-hydroxynitrile lyase HNL4 - Manihot esculenta, EMBL:AJ223281; supported by cDNA: gi_		
putative protein NLI-interacting factor isoform T1, Gallus gallus, EMBL:AF189773;supported by full-length cDNA: Ceres:151766.	250298_at 1.	
CCAAT box binding factor/ transcription factor Hap2a	250320_at 1.	
unknown protein	250232_at 1.	
unknown protein ; supported by cDNA: gi_15215581_gb_AY050319.1_	250211_at 1.	
putative protein amino acid transport protein, Arabidopsis thaliana, EMBL:U39783 Expressed protein ; supported by cDNA: gi 16648944 gb AY059842.1	250161_at 1.	
GTP-binding protein obg -like GTP-binding protein obg, Bacillus subtilis, PIR:B32804	250134_at 1. 249993 at 1.	
squamosa promoter binding protein-like 7; supported by cDNA: gi 13605911 gb AF367355.1 AF367355	249995_at 1. 249960 at 1.	
alkaline/neutral invertase ; supported by cDNA: gi_15912342_gb_AY056449.1_	249898_at 1.	
putative protein 5 -AMP-ACTIVATED PROTEIN KINASE, BETA-1 SUBUNIT, pig, SWISSPROT:AAKB_PIG; supported by cDNA: gi_1		
40S ribosomal protein S9-like 40S ribosomal protein S9 - Chlamydomonas sp.,EMBL:AU066528;supported by full-length cDNA: Ceres		
protein import receptor TOM20, mitochondrial-like	249322 at 1.	
GAMM1 protein-like ; supported by cDNA: gi 15146291 gb AY049287.1	249238 at 1.	.3
unknown protein	249019_at 1.	.3
putative protein strong similarity to unknown protein (pir  T05077);supported by full-length cDNA: Ceres:111998.	248871_at 1.	.3
Lon protease homolog 1 precursor identical to Lon protease homolog 1 mitochondrial precursor SP:O64948 from [Arabidopsis thaliana	a] 248818_at 1.	.3
unknown protein	248771_at 1.	
unknown protein	248694_at 1.	
putative protein strong similarity to unknown protein (pir  T09376)	248630_at 1.	
putative protein contains similarity to unknown protein (pir  T01052)	248616_at 1.	
ATP-dependent Clp protease ATP-binding subunit ClpX2, putative similar to CLP protease regulatory subunit CLPX GI:2674203 from		
putative protein contains similarity to salt-inducible protein Notchless protein homolog	248547_at 1. 248326 at 1.	
O-methyltransferase ;supported by full-length cDNA: Ceres:33790.	248320_at 1.	
putative protein similar to unknown protein (pir  T05472);supported by full-length cDNA: Ceres:30073.	248148 at 1.	
DNA topoisomerase I (sp P30181)	248099 at 1.	
putative protein similar to unknown protein (ref]NP_004583.1); supported by cDNA: gi_14532719_gb_AY039984.1_	248106 at 1.	
HEAT SHOCK PROTEIN 81-2 (HSP81-2) (splP55737)	248045 at 1.	
transcription factor-like; similar to CH6 and COP9 complex subunit 6; supported by cDNA: gi_15809662_gb_AY048692.1_	248009_at 1.	.3
unknown protein	247992_at 1.	.3
profilin-like protein ; supported by full-length cDNA: Ceres: 102364.	247964_at 1.	.3
Expressed protein ; supported by full-length cDNA: Ceres: 99033.	247792_at 1.	
putative protein predicted proteins, Arabidopsis thaliana	247698_at 1.	
aspartyl aminopeptidase - like protein aspartyl aminopeptidase, Homo sapiens, EMBL:AF005050;supported by full-length cDNA: Cere		
putative protein supported by cDNA: Ceres: 146274.	247491_at 1.	
peroxisomal Ca-dependent solute carrier - like protein peroxisomal Ca-dependent solute carrier, Oryctolagus cuniculus, EMBL:AF004	161; su 247498_at 1. 247393_at 1.	
unknown protein putative protein similar to unknown protein (pir  T00246)	247393_at 1. 247277_at 1.	
putative protein similar to unknown protein (pl/102-107) putative protein similar to unknown protein (pl/AB71479.1)	247062_at 1.	
putative protein contains similarity to MYB-like DNA-binding protein; supported by cDNA: gi 14532517 gb AY039883.1	247012_at 1.	
unknown protein ;supported by full-length cDNA: Ceres:8440.	246953 at 1.	
putative protein	246926_at 1.	
acid phosphatase-like protein purple acid phosphatase - Ipomoea batatas, EMBL:AJ006224; supported by cDNA: gi_15292756_gb_A	Y0508' 246636_at 1.	.3
putative protein ;supported by full-length cDNA: Ceres:38281.	246612_at 1.	.3
putative protein SART-1 protein - Homo sapiens, PIR:T00034	246447_at 1.	.3
unknown protein	246286_at 1.	
hypothetical protein ;supported by full-length cDNA: Ceres:108940.	246196_at 1.	
G-box-binding factor 1; supported by cDNA: gi_15450987_gb_AY054574.1_	246211_at 1.	
IPP transferase - like protein tRNA delta(2)-isopentenylpyrophosphate transferase (IPP transferase), Pseudomonas putida, EMBL:AF(	_	
putative protein VAC8 protein, Saccharomyces cerevisiae, PIR:S50446 24 kDa vacuolar protein - like 24 kDa vacuolar protein VP24, Ipomoea batatas, EMBL:AB025531	246062_at 1. 245991 at 1.	
pinoresinol-lariciresinol reductase, putative similar to pinoresinol-lariciresinol reductase GB:AAF63508 GI:7542583 from [Thuja plicata	—	
hypothetical protein predicted by genemark.hmm	245724 at 1.	
Expressed protein supported by cDNA: gi_11762135_gb_AF324994.1_AF324994	245684_at 1.	
Expressed protein ;supported by cDNA: gi:14423333	245521_at 1.	
hypothetical protein	245481_at 1.	
Expressed protein ; supported by full-length cDNA: Ceres: 16319.	245373_s_at 1.	
casein kinase I ; supported by cDNA: gi_15450524_gb_AY052364.1_	245294_at 1.	
hypothetical protein ; supported by cDNA: gi_16323154_gb_AY057681.1_	245272_at 1.	
photolyase/blue-light receptor (PHR2) ;supported by full-length cDNA: Ceres:34800.	245150_at 1.	
cytochrome c biogenesis onf206	244945_at 1.	
unknown protein	258783_at 1.	
unknown protein	256013_at 1.	.s

putative protein contains similarity to (pir  T14814)	248901_at	1.3
unknown protein ;supported by full-length cDNA: Ceres:106330.	259153_at	1.2
NAM-like protein (no apical meristem) similar to NAM GB:CAA63101 [Petunia x hybrida]; supported by full-length cDNA: Ceres: 119460.	258813 at	1.2
hypothetical protein predicted by genscan+	257073 at	1.2
unknown protein ;supported by full-length cDNA: Ceres:35578.	267504 at	1.2
unknown protein ; supported by cDNA: gi_15450620_gb_AY052678.1_	267468 at	1.2
putative receptor-like protein kinase	267477 at	1.2
putative protein kinase contains a protein kinase domain profile (PDOC00100); supported by cDNA: gi_2852448_dbj_D88207.1_D88207	267486 at	1.2
putative phosphoribosyl pyrophosphate synthetase	267365 at	1.2
putative isoamylase	267356 at	1.2
putative acetone-cyanohydrin lyase	267127 at	1.2
putative MYB family transcription factor	267141 at	1.2
hypothetical protein predicted by genscan	266962 at	1.2
nyponetical protein protein unknown protein	266934_at	1.2
		1.2
unknown protein E hav gentein femily, AERXE agateing similarity to E hav gratein ERLA Ch6040000 from (Pattus pages)	266855_at	
F-box protein family, AtFBX5 contains similarity to F-box protein FBL2 GI:6010699 from [Rattus norvegicus]	266815_at	1.2
unknown protein ;supported by full-length cDNA: Ceres:26655.	266657_at	1.2
putative zinc-finger protein (B-box zinc finger domain)	266514_at	1.2
hypothetical protein	266304_at	1.2
hypothetical protein predicted by genscan and genefinder; supported by cDNA: gi_13605570_gb_AF361611.1_AF361611	266182_at	1.2
putative helicase ; supported by cDNA: gi_16648974_gb_AY059857.1_	266122_at	1.2
putative alcohol dehydrogenase	266087_at	1.2
unknown protein ;supported by full-length cDNA: Ceres:40538.	266093_at	1.2
putative methionyl-tRNA synthetase ; supported by cDNA: gi_14334467_gb_AY034925.1_	266057_at	1.2
unknown protein unusual splice site at second intron; GA instead of conserved GT at donor site	266060_at	1.2
hypothetical protein predicted by genscan and genefinder	265957_at	1.2
Expressed protein ; supported by full-length cDNA: Ceres: 465.	265913_at	1.2
unknown protein ;supported by cDNA: gi_14334541_gb_AY035175.1_	265739_at	1.2
unknown protein	265707_at	1.2
proline iminopeptidase identical to GP:1710151:U72711; supported by cDNA: gi_15450388_gb_AY052295.1_	265575_at	1.2
hypothetical protein predicted by genscan and grail	265429_at	1.2
unknown protein ;supported by full-length cDNA: Ceres:39669.	265388_s_at	1.2
unknown protein ESTs gb H76594 and gb H76252 come from this gene	265217_s_at	1.2
RNA polymerase subunit identical to RNA polymerase subunit GI:514324 from [Arabidopsis thaliana]; supported by cDNA: gi_14423463 gb_	264924 at	1.2
unknown protein	264890 at	1.2
putative plastid RNA polymerase sigma-subunit similar to GB:BAA22427 and EST gb N65838; supported by cDNA: gi_2353172_gb_AF01554	264781 at	1.2
hypothetical protein predicted by genscan; supported by cDNA: gi 15450913 gb AY054537.1	264447 at	1.2
putative glutathione S-transferase TSI-1 similar to glutathione S-transferase TSI-1 (gil2190992); similar to ESTs gb/R29860, emb/Z29757, an	264436 at	1.2
unknown protein ; supported by cDNA: gi_15081790_gb_AY048288.1_	264265 at	1.2
hypothetical protein predicted by genscan and genefinder;supported by full-length cDNA: Ceres:17483.	264111 at	1.2
plastid division protein (FtsZ) identical to AF089738; supported by cDNA: gi 15292820 gb_AY050844.1_	263906 at	1.2
RNA helicase, putative similar to RNA helicase GI:3776015 from [Arabidopsis thaliana]; supported by cDNA: gi 15983391 gb AF424570.1	263679 at	1.2
unknown protein Location of ESTs 108M1417, gb[T41823 and 108M14XP 3, gb[AA395002; supported by cDNA: gi 14335101 gb AY03725	263692 at	1.2
utative protein kinase/endoribonuclease ; supported by cDNA: gi_13194577 gb_AF308596.1_AF308596	263076 at	1.2
splicing factor, putative similar to RSZp21 protein GB:CAA05351 (25282643 from [Arabidopsis thaliana] (Plant Mol. Biol. 39 (4), 761-773 (19	263035 at	1.2
spinning instant, putative similar to receipt i protein GL. SPARSSOT GL. 2022 49 inom [Plablicipsis dialitanta] (i lant work biol. 50 (4), 151-115 (15 conserved hypothetical protein	263037 at	1.2
Expressed protein ; supported by full-length cDNA: Ceres: 18244.	262746 at	1.2
unknown protein ESta gblR90323, gblR90338, gblZ5504 and gblA4651448 come from this gene	262576 at	1.2
unition protein ESTS golfsouss, golfsouss, golfsouss, golfsouss (golfsouss)	262532 at	1.2
	_	
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:111951.	262453_at	1.2
receptor protein kinase, putative similar to receptor protein kinase GI:389566 from [Arabidopsis thaliana]	262360_at	1.2
26S proteasome ATPase subunit, putative similar to 26S proteasome ATPase subunit GI:1395190 from [Spinacia oleracea];supported by full benefit direction and include the reported to home.		1.2
hypothetical protein predicted by genemark.hmm	262221_at	1.2
betaine aldehyde dehydrogenase, putative similar to betaine aldehyde dehydrogenase GI:2388709 from [Amaranthus hypochondriacus];supp	262173_at	1.2
hypothetical protein predicted by genemark.hmm	262142_at	1.2
glycosyl transferase, putative similar to Pfam profile: PF00534 Glycosyl transferases group 1	262155_at	1.2
putative heat-shock protein contains Pfam profile: PF00012 Heat shock hsp70 proteins; similar to heat-shock proteins GB:CAA94389, GB:AA		1.2
S-ribonuclease binding protein SBP1, putative similar to S-ribonuclease binding protein SBP1 GI:6760451 from [Petunia hybrida]; supported t	_	1.2
HD-Zip protein identical to HD-Zip protein GB:CAA71854 GI:2145358 from [Arabidopsis thaliana]	261800_at	1.2
hypothetical protein similar to putative protease GI:4415912 from [Arabidopsis thaliana]; supported by cDNA: gi_11993876_gb_AF329505.1_/	261757_at	1.2
hypothetical protein similar to hypothetical protein GB:AAD22292 GI:6598654 from [Arabidopsis thaliana]	261681_at	1.2
LIM domain protein, putative similar to LIM domain protein PLIM-2 GB:AAD15745 GI:4321401 from [Helianthus annuus]	261559_at	1.2
unknown protein	261424_at	1.2
CMP-KDO synthetase, putative similar to GB:CAB89846 from [Zea mays]	261373_at	1.2
unknown protein ; supported by full-length cDNA: Ceres: 117183.	261269_at	1.2
hypothetical protein predicted by genemark.hmm	261177_at	1.2
unknown protein ; supported by cDNA: gi_14334841_gb_AY035094.1_	261107_at	1.2
transcriptional activator RF2a, putative similar to transcriptional activator RF2a GB:AF005492 GI:2253277 from [Oryza sativa]; supported by fi	260953_at	1.2
hypothetical protein predicted by genemark.hmm	260872_at	1.2
unknown protein	260824_at	1.2
peptide transporter PTR2-B, putative similar to SP:P46032 from [Arabidopsis thaliana]	260693_at	1.2
putative ATP-dependent RNA helicase ; supported by cDNA: gi_16323191_gb_AY057700.1_	260532_at	1.2
hypothetical protein similar to CCAAT-box-binding transcription factor GB:NP_005751 [Homo sapiens], GB:P53569 [Mus musculus]	260425_at	1.2
putative protein kinase similar to protein kinase APK1A GB:Q06548 [Arabidopsis thaliana]; contains Pfam profile: PF00069 Eukaryotic protein	260415_at	1.2
unknown protein contains a region similar to uridine kinase GB:AAF09747 from [Deinococcus radiodurans]	260372_at	1.2
unknown protein	260374_at	1.2
putative U3 small nucleolar ribonucleoprotein protein identical to putative U3 small nucleolar ribonucleoprotein protein GB:AAF07373 (Arabido	_	1.2
unknown protein	260162_at	1.2
putative protein kinase Pfam HMM hit: Eukaryotic protein kinase domain	260036_at	1.2
putative trehalose-6-phosphate synthase similar to trehalose-6-phosphate synthase GB:CAA69879 [Arabidopsis thaliana]; supported by cDN/	260010_at	1.2
	259937_s_at	1.2
unknown protein	259945_at	1.2
putative 3 -5 exoribonuclease similar to ribonuclease II RNB family protein GB:CAB16367 [Schizosaccharomyces pombe]; Pfam HMM hit: Va	259704_at	1.2

unknown protein ;supported by full-length cDNA: Ceres:25703.	259639_at	1.2
bZIP protein, putative similar to GI:600855 from [Arabidopsis thaliana] (Plant Physiol. 109 (2), 723 (1995)); supported by cDNA: gi_15450	410 259610_at	1.2
hypothetical protein similar to hypothetical protein GI:6598642 from [Arabidopsis thaliana]	259392_at	1.2
protein phosphatase 2A 65 kDa regulatory subunit identical to protein phosphatase 2A 65 kDa regulatory subunit GB:X82002 [Arabidopsi	s th 259408_at	1.2
putative lectin contains Pfam profile: PF01419 jacalin-like lectin domain; similar to jasmonate inducible protein GB:Y11483 (Brassica napu	s), 259381_s_at	1.2
hypothetical protein predicted by genefinder	259249_at	1.2
RNA helicase, DRH1 identical to RNA helicase DRH1 GB:BAA28347 [Arabidopsis thaliana]; supported by cDNA: gi_15215693_gb_AY05	037 259194_at	1.2
lysyl-tRNA synthetase identical to lysyl-tRNA synthetase; LysRS GB:AAD17333 [Arabidopsis thaliana]; supported by cDNA: gi_4325323_	b_/ 259069_at	1.2
F-box protein family, AtFBL12 contains similarity to F-box protein FBL6 GI:6456737 from [Homo sapiens]	259067_at	1.2
unknown protein similar to putative guanine nucleotide binding protein GB:CAB08769 [Schizosaccharomyces pombe]; supported by cDNA	.: gi 258994_at	1.2
putative RNA helicase similar to RNA helicase (DRH1) GB:BAA28347 [Arabidopsis thaliana]; Pfam HMM hits: WW/rsp5/WWP domain co	ntai 258910_at	1.2
unknown protein similar to RNA helicase GB:AAF03534	258863_at	1.2
unknown protein predicted by genscan, multiple est matches; supported by cDNA: gi_15027888_gb_AY045801.1_	258801_at	1.2
putative bZIP transcription factor contains Pfam profile: PF00170 bZIP transcription factor; contains similarity to TGACG-sequence specifi	DI 258759_at	1.2
putative histone H2B similar to histone H2B-3 GB:CAA12231 from [Lycopersicon esculentum]	258707_at	1.2
putative RING zinc finger protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger); supported by full-length cDNA: 0	ere 258714_at	1.2
putative GTPase activating protein contains Pfam profile: PF01412 Putative GTP-ase activating protein for Arf	258689_at	1.2
hypothetical protein contains Pfam profile: PF01535 domain of unknown function	258573_at	1.2
importin alpha identical to GB:AAC27644 from [Arabidopsis thaliana] (Plant Cell (1996) 8(8), 1337-1352);supported by full-length cDNA: (	ere 258531_at	1.2
putative WD-repeat protein contains Pfam profile: PF00400 WD domain, G-beta repeat (7 copies)	258268_at	1.2
unknown protein ;supported by full-length cDNA: Ceres:15577.	258188_at	1.2
putative sucrose cleavage protein similar to GB:S51376 from [Solanum tuberosum]supported by full-length cDNA: Ceres:40179.	257970 at	1.2
unknown protein ; supported by full-length cDNA: Ceres: 33530.	257703 at	1.2
protein kinase, putative similar to PROTEIN KINASE APK1A GB:Q06548 from [Arabidopsis thaliana]	257016 at	1.2
glutamine:fructose-6-phosphate amidotransferase, putative similar to glutamine:fructose-6-phosphate amidotransferase 2 GB:BAA74729	_	1.2
alpha-glucan phosphorylase, putative similar to alpha-glucan phosphorylase, L isozyme 1 precursor GB:P04045 from [Solanum tuberosu		1.2
unknown protein similar to CW14 GB:BAA87958 from [Arabidopsis thaliana]; supported by cDNA: gi 15450961 gb AY054561.1	256747 at	1.2
unknown protein ;supported by full-length cDNA: Ceres:13928.	256724 at	1.2
putative protein ;supported by full-length cDNA: Ceres:114734.	256676 at	1.2
unknown protein	256480 at	1.2
GTP-binding protein, putative similar to GTP-binding protein NGB [Homo sapiens] GI:4191616	256207 at	1.2
putative PRP19-like spliceosomal protein WD-40 repeat protein	255830 at	1.2
hypothetical protein supported by full-length cDNA: Ceres:25253.	255586 at	1.2
putative thioredoxin ; supported by cDNA; gi 16648848 gb AY058202.1	255279 at	1.2
UDP-galactose 4-epimerase - like protein UDP-galactose 4-epimerase, Cyamopsis tetragonoloba, AJ005082;supported by full-length cDI	_	1.2
putative protein 24 kDa seed maturation protein - Glycine max.PID:q4102690;supported by full-length cDNA; Ceres:23536.	254920 at	1.2
hypothetical protein supported by full-length cDNA: Ceres:151415.	254844 at	1.2
ethylene-regulated transcript 2 (ERT2)	254434 at	1.2
putative protein various predicted proteins, Arabidopsis thaliana	254179 at	1.2
putative protein various predicted proteins, Arabidopsis tranana putative protein protein induced upon wounding - Arabidopsis thaliana, PID:e257749;supported by full-length cDNA: Ceres:34176.	254179_at 254157 at	1.2
putative protein immunophilin FKBP46 - Spodoptera frugiperda (fall armyworm),PIR2:A55320; supported by cDNA: gi_15982871_gb_AY(	_	1.2
putative APG protein proline-rich protein APG - Arabidopsis thaliana, EMBL:X60377;supported by full-length cDNA: Ceres:2574.	253946_at	1.2
putative protein hypothetical protein - Schizosaccharomyces pombe, PID:e1295810	253803_at	1.2
pyrophosphate-dependent phosphofructo-1-kinase-like protein pyrophosphate-dependent phosphofructo-1-kinase - Prunus armeniaca (a		1.2
putative protein RING-finger protein - Lotus japonicus,PIR2:S49446; supported by cDNA: gi_15983461_gb_AF424605.1_AF424605	253539_at	1.2
putative protein norbin, Rattus norvegicus, PIR2:JC5812	253456_at	1.2
putative protein predicted protein, Arabidopsis thaliana, gb:AC002337	253431_at	1.2
glycine hydroxymethyltransferase (EC 2.1.2.1) - like protein glycine hydroxymethyltransferase, Pisum sativum, PIR2:A42906; supported t		1.2
putative protein beta transducin-like protein, Podospora anserina, gb:L28125; supported by cDNA: gi_11141604_gb_AF277458.1_AF277	_	1.2
putative protein peptidyl-prolyl cis-trans isomerase, Schizosaccharomyces pombe, gb:SPBC16H5	253415_at	1.2
2-dehydro-3-deoxyphosphoheptonate aldolase ;supported by full-length cDNA: Ceres:37432.	253333_at	1.2
putative protein protein phosphatase Wip1, Homo sapiens, PID:g2218063;supported by full-length cDNA: Ceres:40123.	253323_at	1.2
Expressed protein ; supported by full-length cDNA: Ceres: 9341.	253292_at	1.2
putative protein membrane-associated salt-inducible protein, Nicotiana tabacum, PIR:T02047	253209_at	1.2
WD-40 repeat protein (MSI3) ; supported by cDNA: gi_2394232_gb_AF016848.1_AF016848	253175_at	1.2
putative protein various predicted proteins, Arabidopsis thaliana	252903_at	1.2
putative protein KIAA0274 protein, Homo sapiens, SWISSPROT:Y274_HUMAN	252737_at	1.2
dnaJ protein homolog atj3 ;supported by full-length cDNA: Ceres:40976.	252670_at	1.2
putative protein hypothetical protein At2g28360 - Arabidopsis thaliana, EMBL:AAD20690	252613_at	1.2
putative RNA-binding protein various putative RNA binding proteins	252453_at	1.2
putative protein finger protein SIG1, Saccharomyces cerevisiae, PIR2:A56015;supported by full-length cDNA: Ceres:122162.	252371_at	1.2
aldehyde dehydrogenase (NAD+)-like protein aldehyde dehydrogenase (NAD+) 2A precursor (mitochondrial), Nicotiana tabacum; suppor	_	1.2
hypothetical protein ; supported by cDNA: gi_13507562_gb_AF360347.1_AF360347	252276_at	1.2
CASEIN KINASE II, ALPHA CHAIN 2 (CK II) ; supported by cDNA: gi_391604_dbj_D10247.1_ATHCK2B	252192_at	1.2
putative protein various predicted proteins, C. elegans, Homo sapiens and yeast; supported by full-length cDNA: Ceres:36721.	252064_at	1.2
mucin -like protein hemomucin, Drosophila melanogaster, EMBL:DM42014; supported by cDNA: gi_13430723_gb_AF360274.1_AF3602		1.2
MAP kinase ; supported by cDNA: gi_14194094_gb_AF367253.1_AF367253	252079_at	1.2
putative protein various predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:4829.	252023_at	1.2
putative protein KIAA0122 gene , Homo sapiens, EMBL:HSDKG02	251873_at	1.2
putative protein contains alternative donor splice site TT at exon 2, hypothetical protein C14A4.1 - Caenorhabditis elegans, PIR:T19243; s	·· —	1.2
putative protein crp1 protein, involved in post-transcriptional control of chloroplast gene expression - Zea mays, PIR:T01685	251496_at	1.2
putative protein CGI-136 protein - Homo sapiens, EMBL:AF151894; supported by cDNA: gi_14190486_gb_AF380643.1_AF380643	251492_at	1.2
putative protein RING finger protein AO7, Mus musculus, EMBL:AF171060	251403_at	1.2
putative protein various predicted proteins, Arabidopsis thaliana	251416_at	1.2
putative protein CGI-94 protein, Homo sapiens, EMBL:AF151852;supported by full-length cDNA: Ceres:13387.	251371_at	1.2
auxin response factor-like protein auxin response factor 9 - Arabidopsis thaliana, PIR:T08917; supported by cDNA: gi_16604602_gb_AY(	_	1.2
cytochrome p450 (CYP78A9) ;supported by full-length cDNA: Ceres:29661.	251301_at	1.2
putative zinc-finger protein zinc-finger protein - Schizosaccharomyces pombe, PIR:T41264	251253_at	1.2
putative protein putative protein F15G16.70 - Arabidopsis thaliana, EMBL:AL132959; supported by cDNA: gi_15810023_gb_AY054280.1		1.2
hypothetical protein RNA polymerase II CTD phosphatase (CTDP1), Homo sapiens, EMBL:AF154115	251134_at	1.2
F-box protein family, AtFBL3 contains similarity to leucine-rich repeats containing F-box protein FBL3 GI:5919219 from [Homo sapiens]	251104_at	1.2
putative protein Hsp70 binding protein HspBP1 - Homo sapiens, EMBL:AF093420	251022_at	1.2
putative protein predicted protein, Arabidopsis thaliana; supported by cDNA: gi_13430449_gb_AF360137.1_AF360137	251015_at	1.2

putative protein ;supported by cDNA: gi_14423557_gb_AF387016.1_AF387016	250897 at	1.2
myotubularin - like protein myotubularin, Homo sapiens, EMBL:U46024	250833 at	1.2
putative protein similar to unknown protein (dbj BAA90353.1)	250830 at	1.2
tetrahydrofolylpolyglutamate synthase-like protein	250757 at	1.2
putative protein similar to unknown protein (splP36540)	250726_at	1.2
putative amidase	250627_at	1.2
putative protein condensin subunit SMC4, Drosophila melanogaster, EMBL:AF186472	250559_at	1.2
RNA binding protein - like rna binding protein, Schizosaccharomyces pombe, PIR:T39586	250436_at	1.2
putative protein HSPC184, Homo sapiens, EMBL:AF151018; supported by cDNA: gi_14335059_gb_AY037209.1_	250401_at	1.2
putative protein predicted protein, Arabidopsis thaliana	250355_at	1.2
alpha-N-acetylglucosaminidase	250245_at	1.2
polynucleotide phosphorylase	250196_at	1.2
low density lipoprotein B-like protein	250112_at	1.2
transcription factor (gb AAD53095.1); supported by cDNA: gi_5823312_gb_AF175990.1_AF175990	250103_at	1.2
zinc finger protein-like ; supported by full-length cDNA: Ceres: 16392.	249888_s_at	1.2
squalene monooxygenase	249774_at	1.2
nuclear pore protein -like nuclear pore protein gp210 precursor, rat, PIR:S04921	249354_at	1.2 1.2
Expressed protein ; supported by full-length cDNA: Ceres: 121432. unknown protein ;supported by full-length cDNA: Ceres:36901.	249026_at 248966 at	1.2
Expressed protein ; supported by full-length cDNA: Ceres: 13184.	248813_at	1.2
VAMP (vesicle-associated methane protein)-associated protein-like ;supported by full-length cDNA: Ceres:14236.	248796 at	1.2
putative protein similar to unknown protein (db)[BAA90625.1)	248805 at	1.2
regulator of chromosome condensation (cell cycle regulatory protein) like	248693 at	1.2
mitotic checkpoint protein-like	248579 at	1.2
ubiquitin activating enzyme ;supported by full-length cDNA: Ceres:26820.	248523 s at	1.2
arginine-aspartate-rich RNA binding protein-like ; supported by cDNA: gi_1699050_gb_U78867.1_ATU78867	248403 at	1.2
peroxidase	248382_at	1.2
putative protein strong similarity to unknown protein (dbj/BAA78737.1);supported by full-length cDNA: Ceres:150246.	248399_at	1.2
non phototropic hypocotyl 1-like ; supported by cDNA: gi_5391441_gb_AF053941.2_AF053941	247853_at	1.2
putative protein B2 protein, Daucus carota, PIR:S32124	247500_at	1.2
auxin response factor - like protein auxin response factor 9, Arabidopsis thaliana, PIR:T08917	247508_at	1.2
putative protein	247422_at	1.2
putative protein contains similarity to protein kinase	247309_at	1.2
2-oxoglutarate/malate translocator ; supported by cDNA: gi_15028072_gb_AY045893.1_	247286_at	1.2
G protein-coupled receptor-like protein ; supported by cDNA: gi_15451139_gb_AY054650.1_	247175_at	1.2
amino acid transporter protein-like	247120_at	1.2
protein kinase, 41K (EC 2.7.1) (pir  S71172) ; supported by cDNA: gi_166818_gb_L05562.1_ATHPROKINB	247043_at	1.2
MAP protein kinase ; supported by cDNA: gi_13430659_gb_AF3602421_AF360242	247044_at	1.2 1.2
putative protein strong similarity to unknown protein (ref NP_005638.1); supported by cDNA: gi_16323187_gb_AY057698.1_ putative protein	247002_at	1.2
CRS2-like protein CRS2 - Zea mays, EMBL:AF225708	246846_at 246492 at	1.2
putative protein Tat-SF1 - Homes apiens, EMBL:U76992	246499 at	1.2
amino acid permease putative contains Pfam profile: PF00324: Amino acid permease	246259 at	1.2
amino acid permease, putative contains Pfam profile: PF00324: Amino acid permease	246260 at	1.2
putative protein predicted proteins - Arabidopsis thaliana	246110 at	1.2
vegetative storage protein Vsp1 ;supported by full-length cDNA: Ceres:32606.	245928_s_at	1.2
putative subunit of TOC complex chloroplast gene Toc64 - Pisum sativum, EMBL:AF179282	245879 at	1.2
lysophospholipase homolog, putative similar to lysophospholipase homolog GI:2801536 from [Oryza sativa]; supported by cDNA: gi_1502821	245734_at	1.2
proline-rich protein, putative similar to proline-rich protein GI:3242079 from [Capsicum annuum]; supported by cDNA: gi_14334847_gb_AY03	245749_at	1.2
tRNA-glutamine synthetase, putative similar to tRNA-glutamine synthetase GI:2995454 from [Lupinus luteus]	245631_at	1.2
glucosyltransferase like protein	245624_at	1.2
hypothetical protein	245482_at	1.2
LET1 like protein	245496_at	1.2
G2484-1 protein	245415_at	1.2
unknown protein similar to glycoprotein SP Q16186 G100_HUMAN; supported by cDNA: gi_13926226_gb_AF372873.1_AF372873	245045_at	1.2
hypothetical protein	244928_s_at	1.2
NADH dehydrogenase subunit 4	244929_at	1.2
putative protein strong similarity to unknown protein (pir  T08938) putative protein various predicted proteins, Arabidopsis thaliana	248226_at 246899_at	1.2 1.2
hypothetical protein various predicted by genemark, hum, supported by cDNA: gi 13605620 gb AF361636.1 AF361636	262965_at	1.1
unknown protein	250066 at	1.1
unknown protein	267642 at	1.1
putative protein kinase contains a protein kinase domain profile (PDOC00100)	267550 at	1.1
unknown protein	267518_at	1.1
unknown protein	267406_at	1.1
unknown protein	267373_at	1.1
G protein alpha subunit 1 (GPA1) identical to GB:M32887; supported by cDNA: gi_14326501_gb_AF385704.1_AF385704	267375_at	1.1
Expressed protein ; supported by full-length cDNA: Ceres: 114879.	267309_at	1.1
similar to late embryogenesis abundant proteins ; supported by full-length cDNA: Ceres: 2450.	067040 of	1.1
unknown protein ;supported by full-length cDNA: Ceres:2337.	267212_at	1.1
hypothetical protein predicted by genscan	267078_at	
	267078_at 267020_at	1.1
hypothetical protein predicted by genscan	267078_at 267020_at 266903_at	1.1
hypothetical protein predicted by genscan unknown protein	267078_at 267020_at 266903_at 266732_at	1.1 1.1
hypothetical protein predicted by genscan unknown protein putative CCCH-type zinc finger protein ;supported by full-length cDNA: Ceres:101255.	267078_at 267020_at 266903_at 266732_at 266695_at	1.1 1.1 1.1
hypothetical protein predicted by genscan unknown protein putative CCCH-type zinc finger protein ;supported by full-length cDNA: Ceres:101255. putative cinnamoyl CoA reductase ;supported by full-length cDNA: Ceres:14133.	267078_at 267020_at 266903_at 266732_at 266695_at 266578_at	1.1 1.1 1.1 1.1
hypothetical protein predicted by genscan unknown protein putative CCCH-type zinc finger protein ;supported by full-length cDNA: Ceres:101255. putative cinnamoyl CoA reductase ;supported by full-length cDNA: Ceres:14133. putative preprotein translocase SECY protein Identical to GB:U37247; targeted to the thylakoid membrane; the protein has a chloroplast targe	267078_at 267020_at 266903_at 266732_at 266695_at 266578_at 266018_at	1.1 1.1 1.1 1.1 1.1
hypothetical protein predicted by genscan unknown protein putative CCCH-type zinc finger protein ;supported by full-length cDNA: Ceres:101255. putative cinnamoyl CoA reductase ;supported by full-length cDNA: Ceres:14133. putative preprotein translocase SECY protein Identical to GB:U37247; targeted to the thylakoid membrane; the protein has a chloroplast targe putative cytochrome P450 identical to GB:D78604; supported by cDNA: gi_15450907_gb_AY054534.1_	267078_at 267020_at 266903_at 266732_at 266695_at 266578_at 266018_at 266000_at	1.1 1.1 1.1 1.1 1.1 1.1
hypothetical protein predicted by genscan unknown protein putative CCCH-type zinc finger protein ;supported by full-length cDNA: Ceres:101255. putative cinnamoyl CoA reductase ;supported by full-length cDNA: Ceres:14133. putative preprotein translocase SECY protein Identical to GB:U37247; targeted to the thylakoid membrane; the protein has a chloroplast targe putative cytochrome P450 identical to GB:D78604; supported by cDNA: gi_15450907_gb_AY054534.1_ putative spliceosome associated protein ;supported by full-length cDNA: Ceres:38968.	267078_at 267020_at 266903_at 266952_at 266695_at 266578_at 266018_at 266018_at 266000_at 265930_at	1.1 1.1 1.1 1.1 1.1 1.1 1.1
hypothetical protein predicted by genscan unknown protein putative CCCH-type zinc finger protein ;supported by full-length cDNA: Ceres:101255. putative cinnamoyl CoA reductase ;supported by full-length cDNA: Ceres:14133. putative preprotein translocase SECY protein Identical to GB:U37247; targeted to the thylakoid membrane; the protein has a chloroplast targu putative cytochrome P450 identical to GB:D78604; supported by cDNA: gi_15450907_gb_AY054534.1_ putative spliceosome associated protein ;supported by full-length cDNA: Ceres:38968. putative nucleosome assembly protein	267078_at 267020_at 266903_at 266695_at 266578_at 266018_at 266018_at 26600_at 266930_at 265930_at	1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1
hypothetical protein predicted by genscan unknown protein putative CCCH-type zinc finger protein ;supported by full-length cDNA: Ceres:101255. putative cinnamoyl CoA reductase ;supported by full-length cDNA: Ceres:14133. putative preprotein translocase SECY protein Identical to GB:U37247; targeted to the thylakoid membrane; the protein has a chloroplast targi putative cytochrome P450 identical to GB:D78604; supported by cDNA: gi_15450907_gb_AY054534.1_ putative spliceosome associated protein ;supported by full-length cDNA: Ceres:38968. putative nucleosome assembly protein hypothetical protein predicted by genefinder	267078_at 267020_at 266903_at 266952_at 26695_at 26695_at 266958_at 266018_at 266900_at 265930_at 265940_at 265985_at	1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1
hypothetical protein predicted by genscan unknown protein putative CCCH-type zinc finger protein ;supported by full-length cDNA: Ceres:101255. putative cinnamoyl CoA reductase ;supported by full-length cDNA: Ceres:14133. putative preprotein translocase SECY protein Identical to GB:U37247; targeted to the thylakoid membrane; the protein has a chloroplast targu putative cytochrome P450 identical to GB:D78604; supported by cDNA: gi_15450907_gb_AY054534.1_ putative spliceosome associated protein ;supported by full-length cDNA: Ceres:38968. putative nucleosome assembly protein hypothetical protein predicted by genefinder putative acyl-CoA oxidase possibly a peroxisomal component	267078_at 267020_at 266903_at 266732_at 266695_at 266695_at 266018_at 266000_at 265930_at 265940_at 265940_at 265843_at	1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1
hypothetical protein predicted by genscan unknown protein putative CCCH-type zinc finger protein ;supported by full-length cDNA: Ceres:101255. putative cinnamoyl CoA reductase ;supported by full-length cDNA: Ceres:14133. putative preprotein translocase SECY protein Identical to GB:U37247; targeted to the thylakoid membrane; the protein has a chloroplast targi putative cytochrome P450 identical to GB:D78604; supported by cDNA: gi_15450907_gb_AY054534.1_ putative spliceosome associated protein ;supported by full-length cDNA: Ceres:38968. putative nucleosome assembly protein hypothetical protein predicted by genefinder	267078_at 267020_at 266903_at 266952_at 26695_at 26695_at 266958_at 266018_at 266900_at 265930_at 265940_at 265985_at	1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1

Expressed protein ; supported by full-length cDNA: Ceres: 16367.	265627_at	1.1
unknown protein predicted by genefinder	265344_at	1.1
unknown protein	265273_at	1.1
hypothetical protein predicted by genscan and genefinder	265276_at	1.1
hypothetical protein	265232_s_at	1.1
unknown protein	265201_at	1.1
integral membrane protein, putative similar to integral membrane protein GI:1209755 from [Beta vulgaris]	264992_at	1.1
U2 snRNP auxiliary factor, large subunit, putative similar to GI:3850823 from (Nicotiana plumbaginifolia) (J. Biol. Chem. 273 (51), 34603-346		1.1
Expressed protein ; supported by full-length cDNA: Ceres: 31252.	264726_at	1.1
hypothetical protein similar to hypothetical protein GI:4455225 from [Arabidopsis thaliana]; supported by cDNA: gi_15293160_gb_AY051014.	264701_at	1.1
unknown protein	264712_at	1.1
hypothetical protein similar to hypothetical protein GB:S51583	264515_at	1.1
unknown protein EST gb/N65787 comes from this gene	264437_at	1.1
multi-drug resistance protein Strong similarity to MRP-like ABC transporter gb/U92650 from A. thaliana and canalicular multi-drug resistance protein Strong similarity to trabalage 6 phosphote outbace CI:207700 from K/Inverse location and canalicular multi-drug resistance protein Strong similarity to trabalage 6 phosphote outbace CI:207700 from K/Inverse location and canalicular multi-drug resistance protein Strong similarity to MRP-like ABC transporter gb/U92650 from A. thaliana and canalicular multi-drug resistance protein Strong similarity to MRP-like ABC transporter gb/U92650 from A. thaliana and canalicular multi-drug resistance protein Strong similarity to MRP-like ABC transporter gb/U92650 from A. thaliana and canalicular multi-drug resistance protein Strong similarity to MRP-like ABC transporter gb/U92650 from A. thaliana and canalicular multi-drug resistance protein Strong similarity to MRP-like ABC transporter gb/U92650 from A. thaliana and canalicular multi-drug resistance protein Strong similarity to MRP-like ABC transporter gb/U92650 from A. thaliana and canalicular multi-drug resistance protein Strong similarity to MRP-like ABC transporter gb/U92650 from A. thaliana and canalicular multi-drug resistance protein Strong similarity to MRP-like ABC transporter gb/U92650 from A. thaliana and canalicular multi-drug resistance protein Strong similarity to MRP-like ABC transporter gb/U92650 from A. thaliana and canalicular multi-drug resistance protein Strong similarity to MRP-like ABC transporter gb/U92650 from A. thaliana and canalicular multi-drug resistance protein Strong similarity to MRP-like ABC transporter gb/U92650 from A. thaliana and canalicular multi-drug resistance protein Strong similarity to MRP-like ABC transporter gb/U92650 from A. thaliana and canalicular multi-drug resistance protein Strong similarity to MRP-like ABC transporter gb/U92650 from A. thaliana and canalicular multi-drug similarity to MRP-like ABC transporter gb/U92650 from A. thaliana and canalicular multi-drug similarity to	264330_at	1.1
trehalose-6-phosphate synthase, putative similar to trehalose-6-phosphate synthase GI:297792 from [Kluyveromyces lactis] heme activated protein, putative similar to heme activated protein GI:6289057 from (Arabidopsis thaliana); supported by full-length cDNA: Ce	264246_at 264190 at	1.1 1.1
unknown protein ; supported by cDNA: gi 15450510 gb_AY052357.1_	263787 at	1.1
hypothetical protein predicted by genscan; supported by full-length cDNA: Ceres:25127.	263589 at	1.1
nyponana na promon promote by general apponent by an engli brit cerector transmission and transmission apponent by an engli brit cerector transmission apponent being a cerector transmission a	263459 at	1.1
putative acetolactate synthase	263460 at	1.1
	263184_at	1.1
hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 148082.	263196 at	1.1
RSH3 (RelA/SpoT homolog) identical to RSH3 (RelA/SpoT homolog) GI:7141308 from [Arabidopsis thaliana]; supported by cDNA: gi 714130	263159 at	1.1
glucosyltransferase, putative similar to beta-(1-3)-glucosyl transferase GB:AAC62210 GI:3687658 from [Bradyrhizobium japonicum	263031_at	1.1
DNA-binding protein similar to cellular nucleic acid binding protein GB:CAA45345 GI:50471 from [Mus musculus]; supported by full-length cDI	262948_at	1.1
hypothetical protein predicted by genemark.hmm	262897_at	1.1
hypothetical protein predicted by genemark.hmm	262901_at	1.1
unknown protein ; supported by cDNA: gi_14596044_gb_AY042810.1_	262845_at	1.1
cysteine proteinase XCP2 identical to papain-type cysteine endopeptidase XCP2 GI:6708183 from [Arabidopsis thaliana]	262796_at	1.1
somatic embryogenesis receptor-like kinase, putative similar to somatic embryogenesis receptor-like kinase GI:2224910 from [Daucus carota	262563_at	1.1
Expressed protein ; supported by full-length cDNA: Ceres: 6612.	262512_at	1.1
unknown protein ; supported by full-length cDNA: Ceres:3744.	262496_at	1.1
hypothetical protein predicted by genscan; supported by cDNA: gi_14334811_gb_AY035079.1_	262503_at	1.1 1.1
unknown protein ;supported by full-length cDNA: Ceres:3024. unknown protein ;supported by full-length cDNA: Ceres:101924.	262171_at 261948 at	1.1
hypothetical protein supported by hambar barber octors for 524.	261701 at	1.1
2-isopropylmalate synthase, putative similar to 2-isopropylmalate synthase GB:AF004165 GI:2213881 from [Lycopersicon pennellii]	261668 at	1.1
uknown protein contains similarity to actin-related protein GB:BAr4577 GI:4218064 from [Homo sapiens], supported by full-length cDNA: C	261672 at	1.1
unknown protein contains similarity to formin binding protein GB:AAC34811 GI:3550080 from [Homo sapiens]	261604 at	1.1
unknown protein similar to MAP3K-like protein kinase GB:CAB16796 GI:4006878 from [Arabidopsis thaliana]; supported by full-length cDNA: (	261609 at	1.1
fucosyltransferase c3 protein, putative similar to fucosyltransferase c3 protein GB:CAB52254 GI:5702039 from [Vigna radiata]; supported by	261612_at	1.1
Expressed protein ; supported by full-length cDNA: Ceres: 5811.	261535_at	1.1
ethylene-responsive element binding factor, putative similar to ethylene-responsive element binding factor GI:8809573 from [Nicotiana sylves	261470_at	1.1
Eukaryotic peptide chain release factor subunit 1 (ERF1) identical to Eukaryotic peptide chain release factor subunit 1 (ERF1) SP:P35614 ((In 2	261204_s_at	1.1
peroxisomal targeting signal type 2 receptor ; supported by cDNA: gi_15215675_gb_AY050366.1_	261207_at	1.1
unknown protein	261179_at	1.1
bZIP transcription factor ATB2, putative similar to GB:CAA18838 from [Arabidopsis thaliana]	261114_at	1.1
	261059_at	1.1
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:34178. glyoxalase II, putative similar to GI:1644427 from (Arabidopsis thaliana); supported by cDNA: gi_15450394_gb_AY052298.1_	261026_at 260986 at	1.1 1.1
	260786_s_at	1.1
unknown protein contains similarity to apoptotic cell clearance receptor PtdSerR GI:11037740 from [Mus musculus]	260798 at	1.1
heat shock transcription factor HSF8, putative similar to heat shock transcription factor HSF8 GB:S25481 from (Lycopersicon peruvianum)	260701 at	1.1
membrane-associated salt-inducible protein isolog	260465_at	1.1
putative lipase similar to lipase GB:CAA74737 from [Drosophila melanogaster]; supported by cDNA: gi_15293100_gb_AY050984.1_	260393_at	1.1
putative protease IV similar to protease IV GB:AAA57008 from [Escherichia coli]; supported by cDNA: gi_6690269_gb_AF114385.1_AF11438	260336_at	1.1
receptor protein kinase, putative similar to receptor protein kinase GI:1389566 from (Arabidopsis thaliana); supported by cDNA: gi_4204848_	260345_at	1.1
putative phosphoribosylformylglycinamidine synthase similar to GB:KIAA0361 from [Homo sapiens]	260250_at	1.1
hypothetical protein predicted by genefinder	260264_at	1.1
putative lipase similar to monoglyceride lipase GB:NP_035974 from [Mus musculus];supported by full-length cDNA: Ceres:36954.	260153_at	1.1
unknown protein ; supported by cDNA: gi_15982810_gb_AY057512.1_	259819_at	1.1
hypothetical protein predicted by genscan+; supported by cDNA: gi_15028380_gb_AY045993.1_	259754_at	1.1
lysophospholipase isolog, putative similar to lysophospholipase isolog GI:1931639 from (Arabidopsis thaliana),supported by full-length cDNA	259708_at	1.1
DNA-directed RNA polymerase identical to DNA-directed RNA polymerase, mitochondrial precursor GB:P92969 [Arabidopsis thaliana] putative DNA-binding protein predicted by genscan, multiple est matches; Pfam HMM hit: helix-loop-helix DNA-binding domain; supported by	259672_at 259645 at	1.1 1.1
hypothetical protein	259582_at	1.1
hypothetical protein ; supported by cDNA: gi_1518449_gb_U43340.1_ATU43340	259517 at	1.1
unknown protein	259422 at	1.1
hypothetical protein contains similarity to 1-phosphatidylinositol-4-phosphate 5-kinase(AtPIP5K1) GI:3702691 from [Arabidopsis thaliana]	259426 at	1.1
unknown protein	259356 at	1.1
unknown protein ;supported by cDNA: gi_15724287_gb_AF412084.1_AF412084		1.1
O-acetylserine (thiol) lyase identical to O-acetylserine (thiol) lyase GB:BAA21628 [Arabidopsis thaliana]; supported by cDNA: gi_2281779_dbj	259172_at	1.1
	259138_s_at	1.1
unknown protein ; supported by cDNA: gi_16226859_gb_AF428353.1_AF428353	258731_at	1.1
putative histidyl tRNA synthetase similar to histidyl tRNA synthetase GB:NP_032240 [Mus musculus]	258601_at	1.1
transfactor, putative similar to transfactor GB:BAA75684 from [Nicotiana tabacum]	258626_at	1.1
unknown protein ; supported by cDNA: gi_15450690_gb_AY052713.1_	258565_at	1.1
fatty acid multifunctional protein (AtMFP2) identical to fatty acid multifunctional protein (AtMFP2) GB:AF123254 [Arabidopsis thaliana] (fatty acid multifunctional protein (AtMFP2) GB:AF123554 [Arabidopsis thaliana] (fatty acid multifunctional protein (AtMFP2) (fatty acid multifunctional protein (AtMFP2) (fatty acid multifunctional protein (AtMFP2) (fatty acid multifunctional protein (fatty acid multifunctional	258555_at	1.1
UDP-glucose:sterol glucosyltransferase UDP-glucose:sterol glucosyltransferase GB:Z83833 [Arabidopsis thaliana]; supported by cDNA: gi_1{	258556_at	1.1
	258449_s_at	1.1
Expressed protein ; supported by full-length cDNA: Ceres: 18951. putative leucine-rich repeat transmembrane protein kinase similar to leucine-rich repeat transmembrane protein kinase 1 GB:AAC27894 from	258397_at 258357 at	1.1 1.1
unknown protein similar to hypothetical protein GB:CAB36798 from [Arabidopsis thaliana]	258361_at	1.1
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DNA-binding protein contains AP2 domain, identical to AP2 domain containing protein RAP2.2 from GB:AAC49768 from [Arabidopsis thalian:	258366_at	1.1
putative cytochrome P450 similar to GB:Q05047 from [Catharanthus roseus]	258113_at	1.1
putative hydrolase predicted by genemark.hmm; contains Pfam profile: PF00857 isochorismatase familysupported by full-length cDNA: Ceres	258052_at	1.1
calmodulin-binding protein, putative contains Pfam profile: PF00612 IQ calmodulin-binding motif (3 copies)	257883_at	1.1
hypothetical protein predicted by genemark.hmm	257773_at	1.1
1,4-alpha-glucan branching enzyme, putative similar to GB:NP_000149 from [Homo sapiens], contains Pfam profile: PF00128 Alpha amylase	257667_at	1.1
unknown protein	257268_at	1.1
lysyl-tRNA synthetase, putative similar to GB:P73443 from [Synechocystis PCC6803], contains Pfam profile: PF00152 tRNA synthetases clas	256963_at	1.1
unknown protein	256927_at	1.1
O-acetylserine(thiol) lyase, putative similar to O-acetylserine(thiol) lyase GB:CAA71798 from [Brassica juncea]	256930 at	1.1
hypothetical protein contains similarity to flavanone-3-hydroxylase GB:Q05965 from [Matthiola incana], contains Pfam profile: PF00671 Iron//	256892 at	1.1
DEAD box helicase protein, putative similar to DEAD box helicase protein GB:NP_006764 from [Homo sapiens], contains Pfam profile: PF00	256797 at	1.1
casein kinase, putative similar to casein kinase 1 GB:NP_001883 from [Homo sapiens]	256783 at	1.1
unknown protein	256734 at	1.1
plastid protein, putative similar to GI:2246378 from [Arabidopsis thaliana] (Proc. Natl. Acad. Sci. U.S.A. 94 (23), 12722-12727 (1997))	256466 at	1.1
unknown protein	256271 at	1.1
MYB-family transcription factor, putative contains Pfam profile: PF00249 Myb-like DNA-binding domain;supported by full-length cDNA: Ceres	256255 at	1.1
hypothetical protein contains similarity to peptidyl-prolyl cis-trans isomerase E GI:4406227 from [Homo sapiens]; supported by cDNA: gi 1498	256068 at	1.1
carbamoylphosphate synthetase, putative similar to carbamoylphosphate synthetase GI:6552726 from [Medicago sativa]; supported by cDN/	256002 at	1.1
putative small nuclear ribonucleoprotein U2B ;supported by full-length cDNA: Ceres:34995.	255871 at	1.1
putative steroid dehydrogenase ; supported by cDNA: gi_16226672_gb_AF428460.1_AF428460	255797 at	1.1
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:111757.	255784 at	1.1
	255668 s at	1.1
putative glycosylasparaginase	255684 at	1.1
putative protein similar to nucleolin protein; supported by cDNA: gi 13605915 gb AF367357.1 AF367357	255598 at	1.1
hypothetical protein	255604 at	1.1
putative GTP pyrophosphokinase similar to bacterial GTP pyrophosphokinases (ReIA) similar to B. subtilis ReIA (EC 2.7.6.5), GenBank acce	255522 at	1.1
tryptophan synthase alpha 1-like protein similar to A. thaliana tryptophan synthase alpha chain (EC 4.2.1.20), GenBank accession number U	255487 at	1.1
hypothetical protein similar to A. thaliana hypothetical protein F6E13.15, GenBank accession number 3212859	255465 at	1.1
putative protein phosphatase regulatory subunit	255421 at	1.1
putative protein hypothetical protein, Arabidopsis thaliana	255224 at	1.1
hypothetical protein	255026 at	1.1
lipase-like protein monoglyceride lipase - Mus musculus, PID:e1184892;supported by full-length cDNA: Ceres:6822.	255010 at	1.1
	254984 s at	1.1
COP1 like protein photomorphogenesis repressor COP1 - Arabidopsis thaliana, PIR2:T01112	254966 at	1.1
putative protein	254646 at	1.1
putative protein	254547_at	1.1
putative protein hypothetical protein - Caenorhabditis elegans, SPTREMBL:Q17527; supported by cDNA: gi_14326565_gb_AF385737.1_AF3	254479_at	1.1
DNA-directed RNA polymerase (EC 2.7.7.6) II second largest chain	254368_at	1.1
putative protein probable membrane protein YFR005c, Saccharomyces cerevisiae, PIR2:S56260	254353_s_at	1.1
nifU-like protein nifU protein homolog YPL135w, Saccharomyces cerevisiae, PIR2:S69049;supported by full-length cDNA: Ceres:8156.	254357_at	1.1
HSP associated protein like p48, Homo sapiens, PATCHX:G904032;supported by full-length cDNA: Ceres:35786.	254275_at	1.1
serine/threonine kinase-like protein serine/threonine kinase - Sorghum bicolor,PID:e1184911; supported by cDNA: gi_14532685_gb_AY039!	254167_at	1.1
putative proteasome regulatory subunit KIAA0107 gene, Homo sapiens, D14663;supported by full-length cDNA: Ceres:38927.	254086_at	1.1
protein-methionine-S-oxide reductase ;supported by full-length cDNA: Ceres:36536.	254099_at	1.1
putative phosphatidylserine decarboxylase phosphatidylserine decarboxylase (EC 4.1.1.65) 2 - yeast, Pir2:S64484	254035_at	1.1
putative aconitase Pumpkin mRNA for aconitase, Cucurbita sp.,PID:g868003; supported by cDNA: gi_15215803_gb_AY050431.1_	253954_at	1.1
UDP rhamnoseanthocyanidin-3-glucoside rhamnosyltransferase - like protein UDP rhamnoseanthocyanidin-3-glucoside rhamnosyltransfer is subsitive antisis bursthe facility of the subset to the subsitive region of the subsitive subsitive region of the subsitive subsit		1.1
putative protein hypothetical chloroplast protein RF19, Guillardia theta, PIR2:S73274;supported by full-length cDNA: Ceres:32397. putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:19314.	253857_at 253789 at	1.1 1.1
early auxin-inducible protein 11 (IAA11); supported by cDNA: gi_972924_gb_U18413.1_ATU18413	253769_at 253791 at	1.1
Any additional protein and (Action), supported by Conversion (1977) and (1977	253751_at	1.1
nyponetical protein ; supported by full-length cDNA: Ceres:12759.	253752 at	1.1
putative protein ; supported by full-length cDNA: Ceres: 142647.	253687 at	1.1
putative protein ; supported by full-length cDNA: Ceres: 32848.	253640 at	1.1
	253596 s at	1.1
hypothetical protein ; supported by full-length cDNA: Ceres:151518.	253520_at	
nypoliteitaa protein rappoliteita by tainengan constructiona. Celes, 1910-19. putative protein crp1 protein, 2ea mays, 214393	253320_at 253495 at	1.1 1.1
putative protein rule protein, zea mays, z 14593 putative protein mixed-lineage protein kinase, Homo sapiens, PIR:A53800		
putative protein mixed-imeage protein kinase, nomo sapiens, PIR.A53800 putative protein	253473_at 253343 at	1.1 1.1
putative protein hemolysin, 38K, Synechocystis sp., Pir2:S75595	253345_at 253351 at	1.1
putative protein nemorysm, son, synethocysus sp., Fil2.575595	_	
DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain	253143_at 253133 at	1.1
putative protein zinc finger protein, Arabidopsis thaliana, gb:L76926	253135_at 253105 at	1.1
Expressed protein : supported by full-length cDNA: Ceres: 147351.	252946 at	1.1 1.1
	252940_at 252475 s at	1.1
putative protein profeine transport helper PTH - Candida albicans, EMBL:Y18210	252475_s_at	1.1
putative protein prome participant protection of the participant of th		1.1
putative popular of the popular popular popular product - Homo sapiens, PID: 1013904; supported by CDNA: gi_14532611_gb_AY039930.1_	252353 at	1.1
	252344 s at	1.1
RNA-directed RNA polymerase RNA-directed RNA polymerase	252261 at	1.1
putative protein hypothetical protein - Schizosacchargoryces pombe, EMBL:CAB11710.1	252264 at	1.1
NAC2-like protein NAC2 - Arabidopsis thaliana, EMBL:AF201456; supported by cDNA: gi 16604578 gb AY059734.1	252278 at	1.1
crooked neck-like protein crooked neck protein (CRN) - Drosophila melanogaster, SWISSPROT:CRN_DROME; supported by cDNA: gi_1525	252100_at	1.1
hypothetical protein	252086_at	1.1
monodehydroascorbate reductase (NADH) - like protein monodehydroascorbate reductase (NADH), Lycoperison esculentum, PIR:T06407;st	_	1.1
RNA helicase -like protein RNA helicase, Mus musculus, PIR:149731; supported by cDNA: gi_15982880_gb_AY057548.1_	251989_at	1.1
putative protein peroxisomal Ca-dependent solute carrier - Oryctolagus cuniculus, EMBL:AF004161	251915_at	1.1
putative protein	251917_at	1.1
putative protein MULTICOPY SUPPRESSOR OF RAS1 - Schizosaccharomyces pombe, EMBL:D78582;supported by full-length cDNA: Cere		1.1
zinc finger-like protein several zinc finger proteins - Arabidopsis thaliana	251586_at	1.1
putative protein paladin - Mus musculus, EMBL:MMPAL	251296_at	1.1
putative protein phosphoprotein phosphatase (EC 3.1.3.16) 1A-alpha - Homo sapiens, PIR:S22423; supported by full-length cDNA: Ceres:20(	251259_at	1.1

hypothetical protein ; supported by cDNA: gi_15292666_gb_AY050767.1_	251083_at	1.1
putative protein KIAA1303 protein - Homo sapiens, EMBL:AB037724	251056 at	1.1
cytochrom P450 - like protein cytochrome P450 77A30, Glycine max., PIR:T05948;supported by full-length cDNA: Ceres:7867.	250859 at	1.1
ubiquitin activating enzyme 2 (UBA2) identical to gi:1703477	250729 at	1.1
transcription factor HBP-1b (gb)AAD24395.1)	250655 at	1.1
	_	
DR1-like protein TATA-binding protein-associated phosphoprotein Dr1 - Arabidopsis shaliana, EMBL:D38110supported by full-length cDNA: (		1.1
dihydropyrimidinase ; supported by cDNA: gi_13878036_gb_AF370281.1_AF370281	250318_at	1.1
putative protein mRNA, Moritella marina, EMBL:AB025342	250276_at	1.1
putative protein ;supported by full-length cDNA: Ceres:37090.	250290_at	1.1
putative protein apospory-associated protein C, Chlamydomonas reinhardtii, EMBL:AF195243; supported by full-length cDNA: Ceres:93845.	250186_at	1.1
putative protein COP9 complex subunit 3, Mus musculus, EMBL:AF071313;supported by full-length cDNA: Ceres:121028.	250188 at	1.1
putative protein mRNA (orf04), Arabidopsis thaliana, EMBL:ATORF04	250045 at	1.1
disease resistance protein - like downy mildew resistance protein RPP5, Arabidopsis thaliana, EMBL:AF180942	250064 at	1.1
putative protein similar to unknown protein (pir  T09939);supported by full-length cDNA: Ceres:23754.	250013 at	1.1
casein kinase-like protein	250021 at	1.1
	_	1.1
eukaryotic cap-binding protein (gb AAC17220.1); supported by cDNA: gi_3108208_gb_AF028809.1_AF028809	250033_at	
putative protein similar to unknown protein (gb AAD20392.1)	249825_at	1.1
MtN3-like protein ;supported by cDNA: gi_3747110_gb_AF095641.1_AF095641	249800_at	1.1
putative protein contains similarity to integral membrane protein	249759_at	1.1
NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K cha	249627_at	1.1
unknown protein	249315_at	1.1
unknown protein	249273 at	1.1
putative protein contains similarity to glutathione-S-transferase/glutaredoxin;supported by full-length cDNA: Ceres:4645.	249233 at	1.1
putative protein similar to unknown protein (pir  T26506); supported by cDNA: gi_16649056_gb_AY059898.1_	249165 at	1.1
putative protein contains similarity to unknown protein (pir  T00959); supported by cDNA; gi 15450893 gb AY054527.1	249079 at	1.1
DNA-directed RNA polymerase subunit	248984_at	1.1
putative protein contains similarity to maturase-related protein	248815_at	1.1
unknown protein	248786_at	1.1
unknown protein ;supported by full-length cDNA: Ceres:31667.	248710_at	1.1
putative protein contains similarity to peptidase	248426_at	1.1
selenium-binding protein-like	248315_at	1.1
developmental protein SINA (seven in absentia)	248256_at	1.1
unknown protein	248243 at	1.1
E2, ubiquitin-conjugating enzyme, putative ;supported by full-length cDNA: Ceres:10022.	247999 at	1.1
WD-repeat protein-like ;supported by full-length cDNA: Ceres:109499.	248000 at	1.1
peroxisomal targeting signal type 1 receptor	248010 at	1.1
putative protein fibrinogen-binding protein, Staphylococcus aureus, PIR:S41539	247849 at	1.1
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protein kinase 6 - like protein kinase 6, Glycine max, PIR:S29851; supported by cDNA: gi_17063197_gb_AY062096.1_	247750_at	1.1
Expressed protein ; supported by full-length cDNA: Ceres: 11699.	247657_at	1.1
unknown protein ;supported by cDNA: gi_15809801_gb_AY054168.1_	247446_at	1.1
unknown protein ; supported by full-length cDNA: Ceres: 11054.	247355_at	1.1
putative protein strong similarity to unknown protein (emb CAB89363.1)	247265_at	1.1
histone acetyltransferase	247238_at	1.1
unknown protein	247241 at	1.1
putative protein contains similarity to RING3 protein	247147_at	1.1
dimethyladenosine transferase-like protein	247089_at	1.1
SKP1 interacting partner 2 (SKIP2) identical to SKP1 interacting partner 2 GI:10716949 from [Arabidopsis thaliana]	247033 at	1.1
case in kinase li alpha subunit ; supported by cDNA; igi 391602 dbi D10246.1 ATHCK2A	247000 at	1.1
putative protein UBIQUINONE BIOSYNTHESIS PROTEIN AARF - Providencia stuartii, EMBL:AF002165	246973_at	1.1
serine-rich protein ;supported by full-length cDNA: Ceres:99323.	246917_at	1.1
cytochrome P450 GA3 ; supported by cDNA: gi_3342248_gb_AF047719.1_AF047719	246864_at	1.1
chaperonin gamma chain - like protein chaperonin containing TCP-1 complex gamma chain, African clawed frog, PIR:S54210; supported by	246830_at	1.1
long-chain-fatty-acidCoA ligase-like protein long-chain-fatty-acidCoA ligase - Brassica napus, EMBL:Z72152	246789_at	1.1
putative protein ;supported by full-length cDNA: Ceres:232091.	246645_at	1.1
epsilon-adaptin, putative similar to epsilon-adaptin GI:5689377 from [Homo sapiens]	246634 at	1.1
putative protein HR21spA protein involved in DNA double-strand break repair - Mus musculus, EMBL:X98293	246500 at	1.1
TOM (target of myb1) -like protein TOM1, Mus musculus, EMBL:MUS6972;supported by full-length cDNA: Ceres:1330.	246421 at	1.1
Cu2+transporting ATPase-like protein	246276 at	1.1
putative protein	246234_at	1.1
putative protein predicted proteins, Arabidopsis thaliana and others		1.1
	246180_at	
RAN1 small Ras-like GTP-binding nuclear protein (Ran-1) ;supported by full-length cDNA: Ceres:9480.	246153_s_at	1.1
putative protein predicted proteins - Arabidopsis thaliana	246112_at	1.1
protein phosphatase 2A regulatory subunit B-like protein protein phosphatase 2A 62 kDa B regulatory subunit, Arabidopsis thaliana, TREME		1.1
Pspzf zinc finger protein - like DNA binding zinc finger protein (Pspzf), Pisum sativum, EMBL:AB018422	246012_at	1.1
putative protein ;supported by full-length cDNA: Ceres:120101.	245948_at	1.1
predicted protein		1.1
putative protein	245913 at	1.1
putative protein DNA-binding protein - Triticum aestivum, EMBL:AF091837;supported by full-length cDNA: Ceres:249741.	245913_at 245881 at	1.1
	245881_at	
	245881_at 245888_at	11
SIR2-family protein sirtuin type 4 (SIRT4) - Homo sapiens, EMBL:AF083109; supported by cDNA: gi_15028032_gb_AY045873.1_	245881_at 245888_at 245895_at	1.1
SIR2-family protein sirtuin type 4 (SIRT4) - Homo sapiens, EMBL:AF083109; supported by cDNA: gi_15028032_gb_AY045873.1_ GTL1 - like protein GTL1, Arabidopsis thaliana, EMBL:ATAJ3215; supported by cDNA: gi_14423451_gb_AF386963.1_AF386963	245881_at 245888_at 245895_at 245861_at	1.1
SIR2-family protein sirtuin type 4 (SIRT4) - Homo sapiens, EMBL:AF083109; supported by cDNA: gi_15028032_gb_AY045873.1_ GTL1 - like protein GTL1, Arabidopsis thaliana, EMBL:ATAJ3215; supported by cDNA: gi_14423451_gb_AF386963.1_AF386963 hypothetical protein contains similarity to cockayne syndrome complementation group A protein GB:U28413 GI:975301 from [Homo sapiens]	245881_at 245888_at 245895_at 245861_at 245764_s_at	1.1 1.1
SIR2-family protein sirtuin type 4 (SIRT4) - Homo sapiens, EMBL:AF083109; supported by cDNA: gi_15028032_gb_AY045873.1_ GTL1 - like protein GTL1, Arabidopsis thaliana, EMBL:ATAJ3215; supported by cDNA: gi_14423451_gb_AF386963.1_AF386963 hypothetical protein contains similarity to cockayne syndrome complementation group A protein GB:U28413 GI:975301 from [Homo sapiens] prolin-rich protein, putative similar to prolin-rich protein GI:21045 from [Phaseolus vulgaris]	245881_at 245888_at 245895_at 245861_at 245764_s_at 245688_at	1.1 1.1 1.1
SIR2-family protein sirtuin type 4 (SIRT4) - Homo sapiens, EMBL:AF083109; supported by cDNA: gi_15028032_gb_AY045873.1_ GTL1 - like protein GTL1, Arabidopsis thaliana, EMBL:ATAJ3215; supported by cDNA: gi_14423451_gb_AF386963.1_AF386963 hypothetical protein contains similarity to cockayne syndrome complementation group A protein GB:U28413 GI:975301 from [Homo sapiens] prolin-rich protein, putative similar to prolin-rich protein GI:21045 from [Phaseolus vulgaris] hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_16648668_gb_AY058110.1_	245881_at 245888_at 245895_at 245861_at 245764_s_at 245688_at 245629_at	1.1 1.1 1.1 1.1
SIR2-family protein sirtuin type 4 (SIRT4) - Homo sapiens, EMBL:AF083109; supported by cDNA: gi_15028032_gb_AY045873.1_ GTL1 - like protein GTL1, Arabidopsis thaliana, EMBL:ATAJ3215; supported by cDNA: gi_14423451_gb_AF386963.1_AF386963 hypothetical protein contains similarity to cockayne syndrome complementation group A protein GB:U28413 GI:975301 from [Homo sapiens] prolin-rich protein, putative similar to prolin-rich protein GI:21045 from [Phaseolus vulgaris] hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_16648668_gb_AY058110.1_ SYBL1 like protein	245881_at 245888_at 245895_at 245861_at 245764_s_at 245688_at 245629_at 245513_at	1.1 1.1 1.1 1.1 1.1
SIR2-family protein sirtuin type 4 (SIRT4) - Homo sapiens, EMBL:AF083109; supported by cDNA: gi_15028032_gb_AY045873.1_ GTL1 - like protein GTL1, Arabidopsis thaliana, EMBL:ATAJ3215; supported by cDNA: gi_14423451_gb_AF386963.1_AF386963 hypothetical protein contains similarity to cockayne syndrome complementation group A protein GB:U28413 GI:975301 from [Homo sapiens] prolin-rich protein, putative similar to prolin-rich protein GI:21045 from [Phaseolus vulgaris] hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_16648668_gb_AY058110.1_ SYBL1 like protein DEF (CLA1) protein ; supported by cDNA: gi_14334451_gb_AY034917.1_	245881_at 245888_at 245895_at 245861_at 245764_s_at 245688_at 245629_at 245513_at 245281_at	1.1 1.1 1.1 1.1 1.1 1.1
SIR2-family protein sirtuin type 4 (SIRT4) - Homo sapiens, EMBL:AF083109; supported by cDNA: gi_15028032_gb_AY045873.1_ GTL1 - like protein GTL1, Arabidopsis thaliana, EMBL:ATAJ3215; supported by cDNA: gi_14423451_gb_AF386963.1_AF386963 hypothetical protein contains similarity to cockayne syndrome complementation group A protein GB:U28413 GI:975301 from [Homo sapiens] prolin-rich protein, putative similar to prolin-rich protein GI:21045 from [Phaseolus vulgaris] hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_16648668_gb_AY058110.1_ SYBL1 like protein	245881_at 245888_at 245895_at 245861_at 245764_s_at 245688_at 245629_at 245513_at	1.1 1.1 1.1 1.1 1.1
SIR2-family protein sirtuin type 4 (SIRT4) - Homo sapiens, EMBL:AF083109; supported by cDNA: gi_15028032_gb_AY045873.1_ GTL1 - like protein GTL1, Arabidopsis thaliana, EMBL:ATAJ3215; supported by cDNA: gi_14423451_gb_AF386963.1_AF386963 hypothetical protein contains similarity to cockayne syndrome complementation group A protein GB:U28413 GI:975301 from [Homo sapiens] prolin-rich protein, putative similar to prolin-rich protein GI:21045 from [Phaseolus vulgaris] hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_16648668_gb_AY058110.1_ SYBL1 like protein DEF (CLA1) protein ; supported by cDNA: gi_14334451_gb_AY034917.1_	245881_at 245888_at 245895_at 245861_at 245764_s_at 245688_at 245629_at 245513_at 245281_at	1.1 1.1 1.1 1.1 1.1 1.1
SIR2-family protein sirtuin type 4 (SIRT4) - Homo sapiens, EMBL:AF083109; supported by cDNA: gi_15028032_gb_AY045873.1_ GTL1 - like protein GTL1, Arabidopsis thaliana, EMBL:ATAJ3215; supported by cDNA: gi_14423451_gb_AF386963.1_AF386963 hypothetical protein contains similarity to cockayne syndrome complementation group A protein GB:U28413 GI:975301 from [Homo sapiens] prolin-rich protein, putative similar to prolin-rich protein GI:21045 from [Phaseolus vulgaris] hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_16648668_gb_AY058110.1_ SYBL1 like protein DEF (CLA1) protein ; supported by cDNA: gi_14334451_gb_AY034917.1_ hypothetical protein ; supported by cDNA: gi_16226250_gb_AF428283.1_AF428283 unknown protein	245881_at 245888_at 245895_at 245861_at 245764_s_at 245688_at 245629_at 245513_at 245281_at 245269_at 245269_at 257477_at	1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1
SIR2-family protein sirtuin type 4 (SIRT4) - Homo sapiens, EMBL:AF083109; supported by cDNA: gi_15028032_gb_AY045873.1_ GTL1 - like protein GTL1, Arabidopsis thaliana, EMBL:ATAJ3215; supported by cDNA: gi_14423451_gb_AF386963.1_AF386963 hypothetical protein contains similarity to cockayne syndrome complementation group A protein GB:U28413 GI:975301 from [Homo sapiens] prolin-rich protein predicted by genemark.hmm; supported by cDNA: gi_16648668_gb_AY058110.1_ SYBL1 like protein DEF (CLA1) protein ; supported by cDNA: gi_14334451_gb_AY034917.1_ hypothetical protein ; supported by cDNA: gi_16226250_gb_AF428283.1_AF428283 unknown protein RIBOSOMAL PROTEIN, putative similar to 30S RIBOSOMAL PROTEIN S1 GB:P46228 from [Synechococcus sp.]	245881_at 245888_at 245895_at 245861_at 245764_s_at 245688_at 245629_at 245513_at 245281_at 245289_at 257477_at 261507_at	1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1
SIR2-family protein sirtuin type 4 (SIRT4) - Homo sapiens, EMBL:AF083109; supported by cDNA: gi_15028032_gb_AY045873.1_ GTL1 - like protein GTL1, Arabidopsis thaliana, EMBL:ATAJ3215; supported by cDNA: gi_14423451_gb_AF386963.1_AF386963 hypothetical protein contains similarity to cockayne syndrome complementation group A protein GB:U28413 GI:975301 from [Homo sapiens] prolin-rich protein protein protein to prolin-rich protein GI:21045 from [Phaseolus vulgaris] hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_16648668_gb_AY058110.1_ SYBL1 like protein DEF (CLA1) protein ; supported by cDNA: gi_14334451_gb_AY034917.1_ hypothetical protein ; supported by cDNA: gi_16226250_gb_AF428283.1_AF428283 unknown protein RIBOSOMAL PROTEIN, putative similar to 30S RIBOSOMAL PROTEIN S1 GB:P46228 from [Synechococcus sp.] FKBP-type peptidyl-prolyl cis-trans isomerases, putative contains Pfam profile: PF00254 FKBP-type peptidyl-prolyl cis-trans isomerases	245881_at 245888_at 245805_at 245861_at 245764_s_at 245629_at 245629_at 245213_at 245281_at 245269_at 245269_at 257477_at 261507_at 258175_at	1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1
SIR2-family protein sirtuin type 4 (SIRT4) - Homo sapiens, EMBL:AF083109; supported by cDNA: gi_15028032_gb_AY045873.1_ GTL1 - like protein GTL1, Arabidopsis thaliana, EMBL:ATAJ3215; supported by cDNA: gi_14423451_gb_AF386963.1_AF386963 hypothetical protein contains similarity to cockayne syndrome complementation group A protein GB:U28413 GI:975301 from [Homo sapiens] prolin-rich protein protein contains similarity to cockayne syndrome complementation group A protein GB:U28413 GI:975301 from [Homo sapiens] prolin-rich protein protein predicted by genemark.hmm; supported by cDNA: gi_16648668_gb_AY058110.1_ SYBL1 like protein DEF (CLA1) protein ; supported by cDNA: gi_14334451_gb_AY034917.1_ hypothetical protein ; supported by cDNA: gi_16226250_gb_AF428283.1_AF428283 unknown protein RIBOSOMAL PROTEIN, putative similar to 30S RIBOSOMAL PROTEIN S1 GB:P46228 from [Synechococcus sp.] FKBP-type peptidyl-prolyl cis-trans isomerases, putative contains Pfam profile: PF00254 FKBP-type peptidyl-prolyl cis-trans isomerases	245881_at 245888_at 245861_at 245861_at 245661_at 245629_at 245513_at 2452629_at 245263_at 245269_at 257477_at 261507_at 258175_at 256230_at	1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1
SIR2-family protein sirtuin type 4 (SIRT4) - Homo sapiens, EMBL:AF083109; supported by cDNA: gi_15028032_gb_AY045873.1_ GTL1 - like protein GTL1, Arabidopsis thaliana, EMBL:ATAJ3215; supported by cDNA: gi_14423451_gb_AF386963.1_AF386963 hypothetical protein contains similar to prolin-rich protein GI:21045 from [Phaseolus vulgaris] hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_16648668_gb_AY058110.1_ SYBL1 like protein DEF (CLA1) protein ; supported by cDNA: gi_14334451_gb_AY034917.1_ hypothetical protein ; supported by cDNA: gi_16226250_gb_AF428283.1_AF428283 unknown protein RIBOSOMAL PROTEIN, putative similar to 30S RIBOSOMAL PROTEIN S1 GB:P46228 from [Synechococcus sp.] FKBP-type peptidyl-prolyl cis-trans isomerases, putative contains Pfam profile: PF00254 FKBP-type peptidyl-prolyl cis-trans isomerases putative protein various predicted proteins, Arabidopsis thaliana	245881_at 245888_at 245861_at 245661_at 245664_s_at 245629_at 245513_at 245269_at 245269_at 257477_at 261507_at 258175_at 256230_at 250194_at	1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1
SIR2-family protein sirtuin type 4 (SIRT4) - Homo sapiens, EMBL:AF083109; supported by cDNA: gi_15028032_gb_AY045873.1_ GTL1 - like protein GTL1, Arabidopsis thaliana, EMBL:ATAJ3215; supported by cDNA: gi_14423451_gb_AF386963.1_AF386963 hypothetical protein contains similarity to cockayne syndrome complementation group A protein GB:U28413 GI:975301 from [Homo sapiens] prolin-rich protein, putative similar to prolin-rich protein GI:21045 from [Phaseolus vulgaris] hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_16648668_gb_AY058110.1_ SYBL1 like protein DEF (CLA1) protein ; supported by cDNA: gi_1626250_gb_AF428283.1_AF428283 unknown protein RIBOSOMAL PROTEIN, putative similar to 30S RIBOSOMAL PROTEIN S1 GB:P46228 from [Synechococccus sp.] FKBP-type peptidyl-prolyl cis-trans isomerases, putative contains Pfam profile: PF00254 FKBP-type peptidyl-prolyl cis-trans isomerases FKBP-type peptidyl-prolyl cis-trans isomerases, putative contains Pfam profile: PF00254 FKBP-type peptidyl-prolyl cis-trans isomerases putative protein predicted proteins, Arabidopsis thaliana putative protein predicted proteins, Arabidopsis thaliana, D.melanogaster, C.elegans and S.pombe	245881_at 245888_at 245895_at 245861_at 245764_s_at 245629_at 245513_at 245281_at 245281_at 245269_at 257477_at 261507_at 256175_at 256230_at 250194_at 246714_at	1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1
SIR2-family protein sirtuin type 4 (SIRT4) - Homo sapiens, EMBL:AF083109; supported by cDNA: gi_15028032_gb_AY045873.1_ GTL1 - like protein GTL1, Arabidopsis thaliana, EMBL:ATAJ3215; supported by cDNA: gi_14423451_gb_AF386963.1_AF386963 hypothetical protein contains similarity to cockayne syndrome complementation group A protein GB:U28413 GI:975301 from [Homo sapiens] prolin-rich protein, putative similar to prolin-rich protein GI:21045 from [Phaseolus vulgaris] hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_16648668_gb_AY058110.1_ SYBL1 like protein DEF (CLA1) protein ; supported by cDNA: gi_14334451_gb_AY034917.1_ hypothetical protein ; supported by cDNA: gi_16226250_gb_AF428283.1_AF428283 unknown protein RIBOSOMAL PROTEIN, putative similar to 30S RIBOSOMAL PROTEIN S1 GB:P46228 from [Synechococcus sp.] FKBP-type peptidyl-prolyl cis-trans isomerases, putative contains Pfam profile: PF00254 FKBP-type peptidyl-prolyl cis-trans isomerases putative protein various predicted proteins, Arabidopsis thaliana	245881_at 245888_at 245861_at 245661_at 245664_s_at 245629_at 245513_at 245269_at 245269_at 257477_at 261507_at 258175_at 256230_at 250194_at	1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1

MYB - like protein cM4 myb transcription factor, Arabidopsis thaliana, gb:S58280; supported by cDNA: gi_14423389_gb_AF386932.1_AF386		
mind - like protein ewithing transcription racio, Arabidopsis transmark, gb.000200, supported by cbind. gi_14420005_gb_Ar 300302.1_Ar 300	255250_at	1
putative protein merozoite surface antigen 2, Plasmodium falciparum, PIR:A45637	252112_at	1
1-D-deoxyxylulose 5-phosphate synthase - like protein 1-D-deoxyxylulose 5-phosphate synthase, Lycopersicon esculentum, EMBL:AF14381	250362 at	1
unknown protein	248005 at	1
hypothetical protein predicted by genscan; similar to GP 2623296 AC002409	267608 at	1
putative CCCH-type zinc finger protein also an ankyrin-repeat protein; supported by cDNA: gi_14335105_gb_AY037232.1_	267534 at	1
26S proteasome regulatory subunit	267543 at	1
putative cytochrome P450	267500 s at	1
unknown protein ; supported by full-length cDNA: Ceres:36855.	267503 at	1
putative lipse; supported by full-length CDNA: Ceres: 207043.	267496_at	1
hypothetical protein predicted by genefinder and genscan	267473_at	1
Expressed protein ; supported by full-length cDNA: Ceres: 269036.	267462_at	1
hypothetical protein	267378_at	1
hypothetical protein predicted by grail and genscan	267396_at	1
putative alcohol dehydrogenase	267168_at	1
hypothetical protein predicted by genscan	266901_at	1
putative protein kinase contains a protein kinase domain profile (PDOC00100)	266911_at	1
unknown protein	266871_at	1
FtsH protease, putative contains similarity to YME1 GI:295582, a member of the ftsH-SEC18-PAS1-CDC48 family of putative ATPase-encod	266842_at	1
hypothetical protein predicted by genefinder and genscan; supported by cDNA: gi_14532607_gb_AY039928.1_	266734_at	1
unknown protein ; supported by cDNA: gi_16604341_gb_AY058069.1_	266557_at	1
hypothetical protein predicted by genscan and genefinder	266574_at	1
unknown protein ; supported by cDNA: gi 16612316 gb AF439849.1 AF439849	266480 at	1
putative carboxyphosphonoenolpyruvate mutase	266438_at	1
putative proline-rich protein	266283 at	1
putative RNA-binding protein; supported by cDNA: gi 16226862 gb AF428354.1 AF428354	266240 at	1
unknown protein ; supported by cDNA: gi_13358176_gb_AF324984.2_AF324984	266207 at	1
putative C2H2-type zinc finger protein	266110 at	1
putative alpha-carboxyltransferase ; supported by cDNA: gi_6851090 gb_AF056969.1_AF056969	266099 at	1
unknown protein	266005_at	1
unknown protein ;supported by full-length cDNA: Ceres:9001.	265961 at	1
unknown protein	265974 at	1
•	_	
recA, putative similar to GB:CAA39098 GI:48781 recA from [Legionella pneumophila]	265941_s_at	1
		1
unknown protein ;supported by full-length cDNA: Ceres:104853.	265867_at	1
unknown protein	265793_at	1
hypothetical protein predicted by genscan	265697_at	1
putative C2H2-type zinc finger protein likely a nucleic acid binding protein; supported by cDNA: gi_4585204_gb_AF095588.1_AF095588	265662_at	1
putative nitrilase ;supported by full-length cDNA: Ceres:20875.	265642_at	1
50S ribosomal protein L4 ;supported by full-length cDNA: Ceres:156843.	265594_at	1
putative D-amino acid dehydrogenase	265318_at	1
hypothetical protein predicted by genscan; supported by full-length cDNA: Ceres:13277.	265285_at	1
hypothetical protein predicted by genscan	265141_at	1
hypothetical protein predicted by genscan	265092_at	1
hypothetical protein predicted by genemark.hmm	264935 at	1
putative glycosylation enzyme ; supported by cDNA: gi_15292806_gb_AY050837.1_	264844 at	1
hypothetical protein predicted by genscan+	264750 at	1
	264660 at	1
		1
putative glutamyl-tRNA reductase 2 precursor similar to GB:P49294 and to A. thaliana HEMA2 (gb/U27118) putative U2 small puckear ribonucleoprotein A (U2 SNRNP-A) Identical to A thaliana U2 SnRNP-specific A protein (gb/X69137) ESTs gb/AT		•
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<sup>1</sup> putative <sup>1</sup> U2 small nuclear ribonucleoprotein A (U2 SNRNP-A) Identical to A. thaliana U2 SnRNP-specific A protein (gb)X69137). ESTs gb AT unknown protein ; supported by cDNA; gi_13430645_gb_AF360235.1_AF360235 hypothetical protein predicted by genemark.hmm hypothetical protein predicted by genemark.hmm hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_15081627_gb_AY048206.1_ unknown protein is predicted by genemark.hmm; supported by cDNA: gi_15081627_gb_AY048206.1_ unknown protein predicted by genemark.hmm; supported by cDNA: gi_15081627_gb_AY048206.1_ unknown protein predicted by genemark.hmm; supported by cDNA: gi_7209639_dbj_A8029916.1_A8029916 putative ABC transporter related to multi drug resistance proteins and P-glycoproteins hypothetical protein predicted by genesan putative RNA polymerase sigma-70 factor ; supported by full-length cDNA: Ceres:34470. putative NADPH dependent mannose 6-phosphate reductase ; supported by full-length cDNA: Geres: 21730. hypothetical protein predicted by genesan and genefinder; supported by full-length cDNA: Geres: 21730. hypothetical protein redicted by genesan and genefinder; supported by full-length cDNA: Geres: 21730. hypothetical protein redicted by genesan and genefinder; supported by GIN-ag _Gi _AY04200.1_ F-box protein ORE9, AIFBL7 identical to F-box containing protein ORE9 GI:15420162 from [Arabidopsis thaliana] putative importin (nuclear transport factor ) protein unknown protein ; supported by full-length cDNA: Ceres:264189. Unknown protein ; supported by full-length cDNA: Ce	264615_at 264491_at 264491_at 264491_at 264493_at 264098_at 263904_at 263904_at 263846_at 263756_s_at 263756_s_at 263755_s_at 263755_s_at 263375_s_at 263375_s_at 263375_s_at 263305_at 263305_at 263023_at 263023_at 263010_at 262947_at 262947_at 262881_at 262831_at 262794_at 262794_at 262794_at 262794_at 262794_at 262794_at 262794_at 262794_at	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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<sup>1</sup> putative <sup>1</sup> U2 small nuclear ribonucleoprotein A (U2 SNRNP-A) Identical to A. thaliana U2 SnRNP-specific A <sup>2</sup> protein (gb)X69137). ESTs gb)AT unknown protein ; supported by cDNA: gi_13430645_gb_AF360235.1_AF360235 hypothetical protein predicted by genemark.hmm hypothetical protein predicted by genemark.hmm hypothetical protein is upported by full-length cDNA: Ceres: 39286. spermidine synthase, putative similar to spermidine synthase GI:4138109 from [Lycopersicon esculentum]; supported by cDNA: gi_14030636 hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_15081627_gb_AY048206.1_ unknown protein putative ABC transporter related to multi drug resistance proteins and P-glycoproteins hypothetical protein predicted by genscan putative RNA polymerase sigma-70 factor ; supported by cDNA: gi_7209639_dbj_AB029916.1_AB029916 putative NADPH dependent manose 6-phosphate reductase ; supported by full-length cDNA: Ceres: 21730. hypothetical protein redicted by genscan and genefinder; supported by CNI-3 gi_14596224_gb_AY042900.1_ F-box protein ORE9, AtFBL7 identical to F-box containing protein ORE9 GI:15420162 from [Arabidopsis thaliana] putative RNA-binding protein ; supported by full-length cDNA: Ceres:4595. Expressed protein ; supported by full-length cDNA: Ceres:21223. unknown protein ; supported by full-length cDNA: Ceres:21223. unknown protein ; supported by full-length cDNA: Ceres:2421. AF436824.1_AF436824.1_AF436824 similar to glucose inibilited division protein A from prokaryotes unknown protein ; supported by full-length cDNA: Ceres:9435. hypothetical protein predicted by genemark.hmm hypothetical protein predicted by genemark.hmm	264615_at 264439_at 264491_at 264443_at 264443_at 264098_at 264011_at 26304_at 26304_at 263756_at 263756_at 263756_at 263756_at 263375_at 263375_at 263375_at 263375_at 263375_at 263375_at 263300_at 263050_at 263050_at 263050_at 26300_at 263050_at 26300_at 263050_at 263023_at 26300_at 263023_at 263023_at 263023_at 262024_at 262881_at 262881_at 262794_at 262794_at 262668_at 26262_at	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
<sup>1</sup> putative <sup>1</sup> U2 small nuclear ribonucleoprotein A (U2 SNRNP-A) Identical to A. thaliana U2 SnRNP-specific A protein (gb)X69137). ESTs gb)AT unknown protein ; supported by cDNA: gi_13430645_gb_AF360235.1_AF360235 Hypothetical protein predicted by genemark.hmm hypothetical protein predicted by genemark.hmm Expressed protein ; supported by full-length cDNA: Ceres: 39286. spermidine synthase, putative similar to spermidine synthase GI:4138109 from [Lycopersicon esculentum]; supported by cDNA: gi_14030635 hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_15081627_gb_AY048206.1_ unknown protein putative ABC transporter related to multi drug resistance proteins and P-glycoproteins hypothetical protein predicted by genscan putative RNA polymerase sigma-70 factor ; supported by cDNA: gi_7209639_dbj_AB029916.1_AB029916 putative NADPH dependent manose 6-phosphate reductase ; supported by full-length cDNA: Ceres: 21730. hypothetical protein predicted by genscan and genefinder; supported by cDNA: gi_14596224_gb_AY042900.1_ F-box protein ORE9, AIFBL7 identical to F-box containing protein ORE9 GI:15420162 from [Arabidopsis thaliana] putative importin (nuclear transport factor) protein putative protein jsupported by full-length cDNA: Ceres:264189. unknown protein ; supported by full-length cDNA: Ceres:2123. unknown protein ; supported by full-length cDNA: Ceres:9455. Expressed protein ; supported by full-length cDNA: Ceres:9456. unknown protein ; supported by full-length cDNA: Ceres:9458. hypothetical protein predicted by genemark.hmm hypothetical protein predicted by genemark.hmm hypothetical protein protein Supported by full-length cDNA: Ceres:2458. Expressed protein ; supported by full-length cDNA: Ceres:2458. hypothetical protein ; supported by full-length cDNA: Ceres:9458. hypothetical protein predicted by genemark.hmm hypot	264615_at 264439_at 264491_at 264443_at 264443_at 264098_at 264011_at 26304_at 26304_at 263756_at 263756_at 263756_at 263756_at 263375_at 263375_at 263375_at 263375_at 263375_at 263375_at 263300_at 263050_at 263050_at 263050_at 26300_at 263050_at 26300_at 263050_at 263023_at 26300_at 263023_at 263023_at 263023_at 262024_at 262881_at 262881_at 262794_at 262794_at 262668_at 26262_at	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
<sup>1</sup> putative <sup>1</sup> U2 small nuclear ribonucleoprotein A (U2 SNRNP-A) Identical to A. thaliana U2 SNRNP <sup>2</sup> -specific A <sup>2</sup> protein (gb)X69137). ESTs gb)AT unknown protein ; supported by cDNA: gi_13430645_gb_AF360235.1_AF360235 hypothetical protein predicted by genemark.hmm hypothetical protein is predicted by genemark.hmm texpressed protein ; supported by full-length cDNA: Ceres: 39286. spermidine synthase, putative similar to spermidine synthase GI:4138109 from [Lycopersicon esculentum]; supported by cDNA: gi_14030636 hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_15081627_gb_AY048206.1_ unknown protein putative ABC transporter related to multi drug resistance proteins and P-glycoproteins hypothetical protein predicted by genscan putative RNA polymerase sigma-70 factor ; supported by cDNA: gi_7209639_db]_AB029916.1_AB029916 putative NADPH dependent mannose 6-phosphate reductase ; supported by full-length cDNA: Ceres: 21730. hypothetical protein redicted by genscan and genefinder; supported by cDNA: gi_14596224_gb_AY042900.1_ F-box protein ORE9, AIFBL7 identical to F-box containing protein ORE9 GI:15420162 from [Arabidopsis thaliana] putative RNA-binding protein supported by full-length cDNA: Ceres:4595. Expressed protein ; supported by full-length cDNA: Ceres:21223. unknown protein ; supported by full-length cDNA: Ceres:21223. unknown protein ; supported by full-length cDNA: Ceres:2431. AF436824.1_AF436824.1_AF436824 similar to glucose inhibited division protein A from prokaryotes unknown protein ; supported by full-length cDNA: Ceres:9435. hypothetical protein predicted by genemark.hmm hypothetical protein predicted by genemark.hmm	264615_at 264439_at 264491_at 264443_at 264443_at 264098_at 264011_at 26304_at 26304_at 263756_at 263756_at 263756_at 263756_at 263375_at 263375_at 263375_at 263375_at 263375_at 263375_at 263300_at 263050_at 263050_at 263050_at 26300_at 263050_at 26300_at 263050_at 263023_at 26300_at 263023_at 263023_at 263023_at 262024_at 262881_at 262881_at 262794_at 262794_at 262668_at 26262_at	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

putative translation initiation factor IF2 Except for first 311 amino acids, 41% identical to translation initiation factor IF2 [Bacillus subtilis] (gi 12	262483 at	1
	262504 at	1
	_	1
unknown protein Similar to gb/X84260 POS5 gene product from Saccharomyces cerevisiae. EST gb/W43879 comes from this gene; supporte		
	262478_at	1
unknown protein ;supported by full-length cDNA: Ceres:150507.	262071_at	1
SAR DNA binding protein, putative similar to SAR DNA binding protein GB:BAA31260 GI:3288883 from [Oryza sativa]; supported by full-leng	262094 at	1
hypothetical protein identical to hypothetical protein GB:AAD55482 (Arabidopsis thaliana)	262052 at	1
	261974 at	1
	261921_at	1
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:108306.	261823_at	1
BTG1 binding factor 1, putative similar to BTG1 binding factor 1 GI:6016012 from [Homo sapiens]	261841_at	1
unknown protein	261774 at	1
hypothetical protein similar to hypothetical protein GB:AAF22892 GI:6664310 from [Arabidopsis thaliana]; supported by cDNA: gi 15294161	_	1
	261663 at	1
	261667_at	1
DNA-binding protein PcMYB1, putative similar to DNA-binding protein PcMYB1 GB:U67133 GI:2224898 from [Petroselinum crispum];support	261637_at	1
hypothetical protein similar to guanine nucleotide exchange factor-like protein GB:CAB82690 GI:7329696 from [Arabidopsis thaliana]	261621 at	1
	261547 at	1
	261552_at	1
	261518_at	1
unknown protein ;supported by full-length cDNA: Ceres:920.	261377_at	1
unknown protein ;supported by full-length cDNA: Ceres:23407.	261403 at	1
putative NPK1-related protein kinase 2 predicted by genemark.hmm	261312 at	1
	261277_at	1
	261248_at	1
	261192_at	1
unknown protein	261112_at	1
sec14 cytosolic factor, putative similar to SP:P24859 from [Kluyveromyces lactis]	261116 at	1
	261040_at	1
	260927 at	1
	_	
	260923_at	1
unknown protein	260817_at	1
putative U1 small nuclear ribonucleoprotein 70 kDa	260533 at	1
putative salt-inducible protein	260523_at	1
	260442 at	1
	_	
	260398_at	1
	260396_at	1
putative serine/threonine kinase similar to serine/threonine kinase GB:AAB68776 [Arabidopsis thaliana]; supported by cDNA: gi_2352083_gb_	260339_at	1
putative aminopeptidase similar to aminopeptidase N (alpha-aminoacylpeptide hydrolase) GB:P04825 [Escherichia coli]; contains Pfam profile	260295_at	1
putative protein kinase Pfam HMM hit: Eukaryotic protein kinase domain; C-term region is similar to C-term region of chicken protein kinase P	260191 at	1
	260099 at	1
	_	1
	260055_at	
	260029_at	1
cell division control protein, putative similar to SP:P40986 from [Saccharomyces cerevisiae]	259960_at	1
unknown protein	259943_at	1
unknown protein similar to LIGATIN GB:Q61211 from (Mus musculus), contains PAS domain Sensory-box	259948 at	1
putative phenylalanyl-tRNA synthetase beta-subunit; PheHB similar to phenylalanyl-tRNA synthetase beta-subunit (PheHB) GB:5032011 [Hor	_	1
	259812_at	1
	259769_at	1
hypothetical protein predicted by genscan+, similar to aminomethyltransferase GB:CAA20175 from [Streptomyces coelicolor A3(2)]	259715_at	1
putative cleavage and polyadenylation specificity factor similar to cleavage and polyadenylation specificity factor 73 kDa subunit GB:AAF0022	259717_at	1
hypothetical protein contains similarity to myosin heavy chain cardiac muscle specific isoform 1 GI:7416982 from (Argopecten irradians); supp	259659 at	1
	259532 at	1
	259470_at	1
	259438_at	1
hypothetical protein predicted by genemark.hmm	259397_at	1
unknown protein similar to hect domain and RLD 2 GB:NP_004658 [Homo sapiens]	259334 at	1
putative adenylylsulfate kinase similar to GB:S47640 [Arabidopsis thaliana]	259339_at	1
	259311_at	1
	259277_at	1
	259292_at	1
unknown protein similar to zinc finger protein GB:BAA33206 [Oryza sativa]	259244_at	1
unknown protein predicted by genefinder, multiple est matches	259245_at	1
hypothetical protein predicted by genscan 2		1
	259246 s at	1
	259246_s_at 259122_at	
	259122_at	1
	259122_at 259092_at	1
hypothetical protein similar to hypothetical protein GB:AAB72157 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:1132.	259122_at 259092_at 259012_at	1
hypothetical protein similar to hypothetical protein GB:AAB72157 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:1132.	259122_at 259092_at	
hypothetical protein similar to hypothetical protein GB:AAB72157 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:1132. putative DnaJ protein Pfam HMM hit: DnaJ, prokaryotic heat shock protein	259122_at 259092_at 259012_at	1
hypothetical protein similar to hypothetical protein GB:AAB72157 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:1132. putative DnaJ protein Pfam HMM hit: DnaJ, prokaryotic heat shock protein hypothetical protein similar to hypothetical protein GB:AAC17075 [Arabidopsis thaliana]; supported by cDNA: gi_15810358_gb_AY056218.1_	259122_at 259092_at 259012_at 258909_at 258804_at	1 1 1
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hypothetical protein similar to hypothetical protein GB:AAB72157 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:1132. putative DnaJ protein Pfam HMM hit: DnaJ, prokaryotic heat shock protein hypothetical protein similar to hypothetical protein GB:AAC17075 [Arabidopsis thaliana]; supported by cDNA: gi_15810358_gb_AY056218.1_ putative alpha-L-arabinofuranosidase contains similarity to alpha-L-arabinofuranosidase A precursor GB:P42254 [Aspergillus niger]; supported hypothetical protein similar to hypothetical protein GB:AAF23212 GI:6671952 from (Arabidopsis thaliana) IAA-amino acid hydrolase (ILR1) identical to IAA-amino acid hydrolase (ILR1) GB:U23794 [Arabidopsis thaliana]; supported by full-length cDN	259122_at 259092_at 259012_at 258909_at 258804_at 258774_at 258756_at 258610_at	1 1 1 1 1
hypothetical protein similar to hypothetical protein GB:AAB72157 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:1132. putative DnaJ protein Pfam HMM hit: DnaJ, prokaryotic heat shock protein hypothetical protein similar to hypothetical protein GB:AAC17075 [Arabidopsis thaliana]; supported by cDNA: gi_15810358_gb_AY056218.1_ putative alpha-L-arabinofuranosidase contains similarity to alpha-L-arabinofuranosidase A precursor GB:P42254 [Aspergillus niger]; supported hypothetical protein similar to hypothetical protein GB:AAF23212 GI:6671952 from (Arabidopsis thaliana) IAA-amino acid hydrolase (ILR1) identical to IAA-amino acid hydrolase (ILR1) GB:U23794 [Arabidopsis thaliana]; supported by full-length cDN Rab escort protein, putative similar to choroideremia-like Rab escort protein GB:2NP_001812 from [Homo sapiens]	259122_at 259092_at 259012_at 258099_at 258804_at 258774_at 258756_at 258610_at 258536_at	1 1 1 1 1 1
hypothetical protein similar to hypothetical protein GB:AAB72157 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:1132. putative DnaJ protein Pfam HMM hit: DnaJ, prokaryotic heat shock protein hypothetical protein similar to hypothetical protein GB:AAC17075 [Arabidopsis thaliana]; supported by cDNA: gi_15810358_gb_AY056218.1_ putative alpha-L-arabinofuranosidase contains similarity to alpha-L-arabinofuranosidase A precursor GB:P42254 [Aspergillus niger]; supported hypothetical protein similar to hypothetical protein GB:AAF23212 GI:6671952 from (Arabidopsis thaliana) IAA-amino acid hydrolase (ILR1) identical to IAA-amino acid hydrolase (ILR1) CB:U23794 [Arabidopsis thaliana]; supported by full-length cDN Rab escort protein, putative similar to choroideremia-like Rab escort protein GB:2NP_001812 from [Homo sapiens] hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_14334461_gb_AY034922.1_	259122_at 259092_at 259012_at 258909_at 258804_at 258774_at 258756_at 258610_at 258536_at 258536_at	1 1 1 1 1 1 1
hypothetical protein similar to hypothetical protein GB:AAB72157 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:1132. putative DnaJ protein Pfam HMM hit: DnaJ, prokaryotic heat shock protein hypothetical protein similar to hypothetical protein GB:AAC17075 [Arabidopsis thaliana]; supported by cDNA: gi_15810358_gb_AY056218.1_ putative alpha-L-arabinofuranosidase contains similarity to alpha-L-arabinofuranosidase A precursor GB:P42254 [Aspergillus niger]; supported hypothetical protein similar to hypothetical protein GB:AAF23212 GI:6671952 from (Arabidopsis thaliana) IAA-amino acid hydrolase (ILR1) identical to IAA-amino acid hydrolase (ILR1) CB:U23794 [Arabidopsis thaliana]; supported by full-length cDN Rab escort protein, putative similar to choroideremia-like Rab escort protein GB:2NP_001812 from [Homo sapiens] hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_14334461_gb_AY034922.1_	259122_at 259092_at 259012_at 258099_at 258804_at 258774_at 258756_at 258610_at 258536_at	1 1 1 1 1 1
hypothetical protein similar to hypothetical protein GB:AAB72157 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:1132. putative DnaJ protein Pfam HMM hit: DnaJ, prokaryotic heat shock protein hypothetical protein similar to hypothetical protein GB:AAC17075 [Arabidopsis thaliana]; supported by cDNA: gi_15810358_gb_AY056218.1_ putative alpha-L-arabinofuranosidase contains similarity to alpha-L-arabinofuranosidase A precursor GB:P42254 [Aspergillus niger]; supported hypothetical protein similar to hypothetical protein GB:AAF23212 GI:6671952 from (Arabidopsis thaliana) IAA-amino acid hydrolase (ILR1) identical to IAA-amino acid hydrolase (ILR1) GB:U23794 [Arabidopsis thaliana]; supported by full-length cDN Rab escort protein, putative similar to choroideremia-like Rab escort protein GB:2NP_001812 from [Homo sajens] hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_14334461_gb_AY034922.1_ 14-3-3 protein GF14nu (grf7) identical to 14-3-3 protein GF14 nu GI:1531631 from [Arabidopsis thaliana]; supported by full-length cDNA: Cere	259122_at 259092_at 259092_at 258909_at 258804_at 258774_at 258756_at 258510_at 258526_at 258522_at 258489_at	1 1 1 1 1 1 1
hypothetical protein Similar to hypothetical protein GB:AAB72157 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:1132. putative DnaJ protein Pfam HMM hit: DnaJ, prokaryotic heat shock protein hypothetical protein similar to hypothetical protein GB:AAC17075 [Arabidopsis thaliana]; supported by cDNA: gi_15810358_gb_AY056218.1_ putative alpha-L-arabinofuranosidase contains similarity to alpha-L-arabinofuranosidase A precursor GB:P42254 [Aspergillus niger]; supported hypothetical protein similar to hypothetical protein GB:AAF23212 GI:6671952 from (Arabidopsis thaliana) IAA-amino acid hydrolase (ILR1) identical to IAA-amino acid hydrolase (ILR1) GB:U23794 [Arabidopsis thaliana]; hypothetical protein putative similar to choroideremia-like Rab escort protein GB:2NP_001812 from [Homo sapiens] hypothetical protein GP14 nu (grf7) identical to 14-3-3 protein GF14 nu GI:1531631 from [Arabidopsis thaliana]; supported by full-length cDNA: Cere cell division protein FtsH-like protein similar to cell division protein FtsH GB:AAP35665 from [Thermotoga maritima]; supported by full-length cl	259122_at 259092_at 259092_at 258909_at 258804_at 258774_at 258756_at 258610_at 258526_at 258522_at 258499_at 258499_at	1 1 1 1 1 1 1 1
hypothetical protein similar to hypothetical protein GB:AAB72157 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:1132. putative DnaJ protein Pfam HMM hit: DnaJ, prokaryotic heat shock protein hypothetical protein similar to hypothetical protein GB:AAC17075 [Arabidopsis thaliana]; supported by cDNA: gi_15810358 _gb_AY056218.1_ putative alpha-L-arabinofuranosidase contains similarity to alpha-L-arabinofuranosidase A precursor GB:P42254 [Aspergillus niger]; supported hypothetical protein similar to hypothetical protein GB:AAF23212 GI:6671952 from (Arabidopsis thaliana) IAA-amino acid hydrolase (ILR1) identical to IAA-amino acid hydrolase (ILR1) GB:U23794 [Arabidopsis thaliana]; hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_14334461 _gb_AY034922.1_ 14-3-3 protein GF14nu (grf7) identical to 14-3-3 protein GF14 nu GI:1531631 from [Arabidopsis thaliana]; supported by full-length cDNA: Cere cell division protein FtsH-like protein similar to cell division protein FtsH GB:AAF23656 from [Thermotoga maritima]; supported by full-length cDNA: Ceres:116257.	259122_at 259022_at 258009_at 258804_at 25874_at 258756_at 258676_at 258676_at 258636_at 258636_at 258536_at 258492_at 258492_at	1 1 1 1 1 1 1 1 1
hypothetical protein Similar to hypothetical protein GB:AAB72157 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:1132. putative DnaJ protein Pfam HMM hit: DnaJ, prokaryotic heat shock protein hypothetical protein similar to hypothetical protein GB:AAC17075 [Arabidopsis thaliana]; supported by cDNA: gi_15810358_gb_AY056218.1_ putative alpha-L-arabinofuranosidase contains similarity to alpha-L-arabinofuranosidase A precursor GB:P42254 [Aspergillus niger]; supported hypothetical protein similar to hypothetical protein GB:AAF23212 GI:6671952 from (Arabidopsis thaliana) IAA-amino acid hydrolase (ILR1) identical to IAA-amino acid hydrolase (ILR1) GB:U23794 [Arabidopsis thaliana] HA-amino acid hydrolase (ILR1) identical to IAA-amino acid hydrolase (ILR1) GB:U23794 [Arabidopsis thaliana]; hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_14334461_gb_AY034922.1_ 14-3-3 protein GF14nu (grf7) identical to 14-3-3 protein GF14 nu GI:1531631 from [Arabidopsis thaliana]; supported by full-length cDNA: Cere cell division protein FtsH-like protein similar to cell division protein FtsH GB:AAD35665 from [Thermotoga maritima]; supported by full-length cl 0GB:Q39219 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:116257. ubiquitin-specific protease 25 (UBP25) similar to GI:11993490; supported by cDNA: gi_11993489_gb_AF302673.1_AF302673	259122_at 259092_at 258909_at 258909_at 258804_at 258774_at 258756_at 258610_at 258526_at 258522_at 2584549_at 258449_at 258452_at	1 1 1 1 1 1 1 1 1 1
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hypothetical protein Similar to hypothetical protein GB:AAB72157 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:1132. putative DnaJ protein Pfam HMM hit: DnaJ, prokaryotic heat shock protein hypothetical protein similar to hypothetical protein GB:AAC17075 [Arabidopsis thaliana]; supported by cDNA: gi_15810358_gb_AY056218.1_ putative alpha-L-arabinofuranosidase contains similarity to alpha-L-arabinofuranosidase A precursor GB:P42254 [Aspergillus niger]; supported hypothetical protein similar to hypothetical protein GB:AAF23212 GI:6671952 from (Arabidopsis thaliana) IAA-amino acid hydrolase (ILR1) identical to IAA-amino acid hydrolase (ILR1) GB:U23794 [Arabidopsis thaliana]; Na amino acid hydrolase (ILR1) identical to IAA-amino acid hydrolase (ILR1) GB:U23794 [Arabidopsis thaliana]; Nypothetical protein predicted by genemark.hmm; supported by cDNA: gi_14334461_gb_AY034922.1_ 14-3-3 protein GF14nu (grf7) identical to 14-3-3 protein GF14 nu GI:1531631 from [Arabidopsis thaliana]; supported by full-length cDNA: Cere cell division protein FtsH-like protein similar to cell division protein FtsH GB:AAD35665 from [Thermotoga maritima]; supported by full-length cl alternative oxidase 1a precursor identical to GB:Q39219 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:116257. ubiquitin-specific protease 25 (UBP25) similar to GI:11993490; supported by cDNA: gi_11993489_gb_AF302673.1_AF302673 hypothetical protein predicted by genemark.hmm	259122_at 259092_at 258909_at 258909_at 258804_at 258774_at 258756_at 258610_at 258526_at 258522_at 2584549_at 258449_at 258452_at	1 1 1 1 1 1 1 1 1 1
hypothetical protein Similar to hypothetical protein GB:AAB72157 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:1132. putative DnaJ protein Pfam HMM hit: DnaJ, prokaryotic heat shock protein hypothetical protein similar to hypothetical protein GB:AAC17075 [Arabidopsis thaliana]; supported by cDNA: gi_15810358_gb_AY056218.1_ putative alpha-L-arabinofuranosidase contains similarity to alpha-L-arabinofuranosidase A precursor GB:P42254 [Aspergillus niger]; supported hypothetical protein similar to hypothetical protein GB:AAF23212 GI:6671952 from (Arabidopsis thaliana) IAA-amino acid hydrolase (ILR1) identical to IAA-amino acid hydrolase (ILR1) GB:U23794 [Arabidopsis thaliana]; hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_14334461_gb_AY034922.1_ 14-3-3 protein GF14nu (grf7) identical to 14-3-3 protein GF14 nu GI:1531631 from [Arabidopsis thaliana]; supported by full-length cDNA: Cere cell division protein FtsH-like protein similar to cell division protein FtsH GB:AAD35665 from [Thermotoga maritima]; supported by full-length cDNA: Ceres: 116257. ubiquitin-specific protease 25 (UBP25) similar to GI:11993490; supported by cDNA: gi_11993489_gb_AF302673.1_AF302673 hypothetical protein predicted by genemark.hmm unknown protein contains Pfam profile: PF00076 RNA recognition motif	259122_at 259092_at 259012_at 258004_at 258804_at 258774_at 258756_at 258610_at 258536_at 258522_at 258489_at 258452_at 258472_at 258372_at	1 1 1 1 1 1 1 1 1 1 1 1
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hypothetical protein Similar to hypothetical protein GB:AAB72157 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:1132. putative DnaJ protein Pfam HMM hit: DnaJ, prokaryotic heat shock protein hypothetical protein Similar to hypothetical protein GB:AAC17075 [Arabidopsis thaliana]; supported by cDNA: gi_15810358_gb_AY056218.1_ putative alpha-L-arabinofuranosidase contains similarity to alpha-L-arabinofuranosidase A precursor GB:P42254 [Aspergillus niger]; supported hypothetical protein similar to hypothetical protein GB:AAC23212 GI:6671952 from (Arabidopsis thaliana) IAA-amino acid hydrolase (ILR1) identical to IAA-amino acid hydrolase (ILR1) GB:U23794 [Arabidopsis thaliana]; hypothetical protein prediced by generark.hmm; supported by cDNA: gi_14334461 gb_AY034922.1_ 14-3-3 protein GFI4nu (grf7) identical to 14-3-3 protein GF14 nu GI:1531631 from [Arabidopsis thaliana]; supported by full-length cDNA: Cere cell division protein FtsH-like protein similar to cell division protein FtsH GB:AAD5665 from [Thermotoga maritima]; supported by full-length cl alternative oxidase 1a precursor identical to GB:Q39219 from [Arabidopsis thaliana]; supported by full-length cl alternative oxidase 1a precursor identical to GB:Q39219 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:116257. ubiquitin-specific protease 25 (UBP25) similar to GI:11993490; supported by cDNA: gi_11993489_gb_AF302673.1_AF302673 hypothetical protein predicted by genemark.hmm unknown protein contains Pfam profile: PF00076 RNA recognition motif putative pectinesterase similar to pectinesterase precursor GB:Q43043 [Petunia integrifolia]; contains Pfam profile: PF01095 pectinesterase; hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_15028198_gb_AY045922.1_	259122_at 259022_at 258909_at 258909_at 258804_at 258774_at 258756_at 258536_at 258536_at 258522_at 258459_at 258459_at 258452_at 258452_at 258452_at 258452_at 258259_at 25829_at 258206_at	1 1 1 1 1 1 1 1 1 1 1 1 1
hypothetical protein Similar to hypothetical protein GB:AAB72157 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:1132. putative DnaJ protein Pfam HMM hit: DnaJ, prokaryotic heat shock protein hypothetical protein Similar to hypothetical protein GB:AAC17075 [Arabidopsis thaliana]; supported by cDNA: gi_15810358_gb_AY056218.1_ putative alpha-L-arabinofuranosidase contains similarity to alpha-L-arabinofuranosidase A precursor GB:P42254 [Aspergillus niger]; supported hypothetical protein similar to hypothetical protein GB:AAF23212 GI:6671952 from (Arabidopsis thaliana) IAA-amino acid hydrolase (ILR1) identical to IAA-amino acid hydrolase (ILR1) GB:U23794 [Arabidopsis thaliana]; hypothetical protein putative similar to choroideremia-like Rab escort protein GB:2NP_001812 from [Homo sapiens] hypothetical protein off4nu (grf7) identical to 14.3-3 protein GF14 nu G[1531631 from [Arabidopsis thaliana]; supported by full-length cDNA: Cere cell division protein FtsH-like protein similar to cell division protein FtsH GB:AAD35665 from [Thermotoga maritima]; supported by full-length cDNA: Cere cell division protein FtsH-like protein similar to GB:Q39219 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:116257. ubiquitin-specific protease 25 (UBP25) similar to GI:11993490; supported by cDNA: gi_11993489_gb_AF302673.1_AF302673 hypothetical protein protein contains Pfam profile: PF00076 RNA recognition motif putative pectinesterase similar to pectinesterase precursor GB:Q43043 [Petunia integrifolia]; contains Pfam profile: PF01095 pectinesterase; supported by contains Pfam profile: PF00076 RNA recognition motif	259122_at 259022_at 258909_at 258909_at 258804_at 258774_at 258756_at 258536_at 258536_at 258522_at 258459_at 258459_at 258452_at 258452_at 258452_at 258452_at 258259_at 25829_at 258206_at	1 1 1 1 1 1 1 1 1 1 1 1

Expressed protein ; supported by full-length cDNA: Ceres: 26411.	258092_at	1
unknown protein ;supported by full-length cDNA: Ceres:141813.	258078_at	1
unknown protein similar to MRP-like ABC transporter GB:AAC49791 from [Arabidopsis thaliana]	258033_at	1
Expressed protein ; supported by full-length cDNA: Ceres: 12996.	258041_at	1
hypothetical protein predicted by genemark.hmm	258051_at	1
putative cell differentiation protein similar to cell differentiation protein, Rcd1p GB:CAB16251 from [Schizosaccharomyces pombe]; supported	257984_at	1
hypothetical protein contains Pfam profiles: PF00415 regulator of chromosome condensation (RCC1), PF01363 FYVE zinc finger	257921_at	1
E2, ubiquitin-conjugating enzyme, putative similar to ubiquitin conjugating enzyme GB:CAA51706 [Saccharomyces cerevisiae] (Nature 365 (f	257893_at	1
unknown protein contains Pfam profile:PF01435 Peptidase family M48;supported by full-length cDNA: Ceres:156849.	257791_at	1
hypothetical protein contains Pfam profile:PF00534 Glycosyl transferases group 1	257797_at	1
nucleolar protein, putative nucleolar protein GB:NP_006383 from [Homo sapiens], (Mol. Cell. Biol. 17 (12), 7088-7098 (1997))	257694_at	1
CTP-synthetase, putative similar to CTP synthetase GB:U49350 GI:1515356 (Mus musculus)	257702_at	1
unknown protein contains Pfam profile: PF00400 2 WD domains, G-beta repeats	257684_s_at	1
Expressed protein ; supported by full-length cDNA: Ceres: 32454.	257659_at	1
cytochrome P450 monooxygenase (CYP71B4) identical to cytochrome P450 monooxygenase (CYP71B4) GB:D78603 [Arabidopsis thaliana]	257635_at	1
unknown protein ; supported by cDNA: gi_15294249_gb_AF410316.1_AF410316	257253_at	1
hypothetical protein contains Pfam profile: PF01535 domain of unknown function	257188_at	1
unknown protein	257019_at	1
protein kinase, putative contains similarity to serine/threonine-protein kinase homolog GB:Q61136 from [Mus musculus], contains Pfam profile	256995_at	1
subtilisin-like serine protease, putative contains similarity to cucumisin-like serine protease GI:3176874 from [Arabidopsis thaliana]	256997_at	1
unknown protein	256928_at	1
hypothetical protein contains similarity to transporter proteins	256697_at	1
unknown protein	256422_at	1
hypothetical protein	256387_at	1
unknown protein	256173_at	1
hypothetical protein contains similarity to nuclear DNA helicase II GI:577738 from [Bos taurus]	256140_at	1
ethylene-responsive RNA helicase, putative similar to ethylene-responsive RNA helicase GI:5669638 from [Lycopersicon esculentum]	256152_at	1
guanine nucleotide regulatory protein, putative similar to guanine nucleotide regulatory protein GI:3461880 from [Mus musculus]	256119_at	1
MAP kinase, putative similar to MAP3K delta-1 protein kinase GI:2253010 from [Arabidopsis thaliana]	256121_at	1
calcium dependent protein kinase, putative similar to calcium dependent protein kinase GI:587499 from [Oryza sativa]	255936_at	1
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_13877978_gb_AF370252.1_AF370252	255939_at	1
putative protein	255639_at	1
putative acetyltransferase similar to Digitalis lanata lanatoside 15 -O-acetyltransferase, GenBank accession number AJ011567	255607_at	1
putative SecA-type chloroplast protein transport factor non-consensus GA donor splice site at exon 4	255540_at	1
coded for by A. thaliana cDNA T46835 similar to several small proteins (~100 aa) that are induced by heat, auxin, ethylene and wounding suc	255479_at	1
putative chloroplast outer envelope 86-like protein similar to P. sativum outer envelope 86 protein OEP86, GenBank accession number Z315	255482_at	1
hypothetical protein similar to A. thaliana hypothetical protein F15K9.11, GenBank accession number AC005278	255452_at	1
hypothetical protein ;supported by full-length cDNA: Ceres:6957.	255456_at	1
hypothetical protein	255348_at	1
hypothetical protein	255062_at	1
Arabidopsis thaliana flavin-type blue-light photoreceptor (SW:Q43125) (Pfam: PF00875, Score=765.2, E=2.6e-226, N=1); supported by cDN	255068_at	1
AX110P -like protein AX110P -Daucus carota, PID:g285739; supported by full-length cDNA: Ceres:19582.	255047_at	1
putative protein beta-transducin repeats containing protein - Homo sapiens,PID:e1284220	254913_at	1
Expressed protein ; supported by full-length cDNA: Ceres: 24475.	254846_at	1
hypothetical protein	254779_at	1
DnaJ-like protein DnaJ-like protein, Phaseolus vulgaris, U77935; supported by cDNA: gi_6691126_gb_AF214107.1_AF214107	254688_at	1
N-acetylornithine deacetylase-like protein, fragment N-acetylornithine deacetylase (AOdD) - Dictyostelium discoideum, PID:G763048	254690_at	1
putative protein W15DMY32F, W25DMY32F	254657_s_at	1
hypothetical protein ; supported by full-length cDNA: Ceres: 14794.	254626_at	1
hypothetical protein ;supported by full-length cDNA: Ceres:40232.	254503_at	1
putative protein transcription initiation factor IID beta chain, fruit fly, Pir2:B49453; supported by cDNA: gi_15293300_gb_AY051084.1_	254463_at	1
putative protein CRP1, Zea mays, PID:g3289002	254483_at	1
putative protein predicted protein, Caenorhabditis elegans, PIR2:S44608; supported by cDNA: gi_13241745_gb_AF327068.1_AF327068	254449_at	1
phosphatase like protein phosphoprotein phosphatase (EC 3.1.3.16) PPT - rat	254211_at	1
hypothetical protein	254178_at	1
putative protein ; supported by cDNA: gi_15810434_gb_AY056256.1_	254169_at	1
CER2 ;supported by full-length cDNA: Ceres:33382.	254122_at	1
proton pump interactor non-consensus GA donor splice site at exon 5	253868_at	1
pelota (PEL1)	253882_at	1
putative protein WREBP-1, Nicotiana tabacum, EMBL:AB017693	253784_at	1
26S proteasome subunit 4-like protein Drosophila melanogaster 26S proteasome subunit 4 ATPase, PID:g1066065; supported by cDNA: gi_	253755_at	1
gamma-glutamyltransferase-like protein gamma-glutamyltransferase - Arabidopsis thaliana,PIR2:S58286	253708_at	1
putative protein	253577_at	1
ubiquitin-specific protease 24 (UBP24), putative similar to GI:11993488; ubiquitin carboxyl-terminal hydrolase, Mus musculus, PID:D101289;	253552_at	1
kinase binding protein - like Skb1 protein homolog, Homo sapiens, PIR2:T03842	253558_at	1
predicted protein DAN26, Homo sapiens, PID:E285308	253565_at	1
putative protein microtubule-associated protein 1B (MAP1B), Homo sapiens, L06237	253497_at	1
putative protein RNA-binding protein LAH1, Saccharomyces cerevisiae,PIR2:B48600; supported by cDNA: gi_15810396_gb_AY056237.1_	253396_at	1
gamma-VPE (vacuolar processing enzyme);supported by cDNA: gi_13877794_gb_AF370160.1_AF370160	253358_at	1
putative protein Caenorhabditis elegans cosmid, gene T16G1.11,PID:e1349366; supported by cDNA: gi_14335023_gb_AY037191.1_	253336_at	1
putative protein aminotransferase (AspC family), Aquifex aeolicus, PIR2:D70479; supported by cDNA: gi_15912290_gb_AY056423.1_		1
putative protein protein kinase APK1, Arabidopsis thaliana, PIR2:S28615; supported by cDNA: gi 16612248 gb AF439824.1 AF439824	253308_at	1
putative protein probable membrane protein YBL019w, yeast, PIR2:S45753	253308_at 253184_at 253126_at	1
	253308_at 253184_at	
putative protein probable membrane protein YBL019w, yeast, PIR2:S45753	253308_at 253184_at 253126_at	1
putative protein probable membrane protein YBL019w, yeast, PIR2:S45753 heat shock protein 70 like protein dnaK-type molecular chaperone PHSP1 -Pisum sativum,PID:g20835	253308_at 253184_at 253126_at 253013_at	1 1
putative protein probable membrane protein YBL019w, yeast, PIR2:S45753 heat shock protein 70 like protein dnaK-type molecular chaperone PHSP1 -Pisum sativum,PID:g20835 putative protein	253308_at 253184_at 253126_at 253013_at 253022_at	1 1 1
putative protein probable membrane protein YBL019w, yeast, PIR2:S45753 heat shock protein 70 like protein dnaK-type molecular chaperone PHSP1 -Pisum sativum,PID:g20835 putative protein putative protein ubiquitin fusion degradation protein - Schizosaccharomyces pombe, PID:e1132723	253308_at 253184_at 253126_at 253013_at 253022_at 252947_at	1 1 1 1
putative protein probable membrane protein YBL019w, yeast, PIR2:S45753 heat shock protein 70 like protein dnaK-type molecular chaperone PHSP1 -Pisum sativum,PID:g20835 putative protein putative protein ubiquitin fusion degradation protein - Schizosaccharomyces pombe, PID:e1132723 isovaleryI-CoA-dehydrogenase precursor (IVD) :supported by full-length cDNA: Ceres:33674.	253308_at 253184_at 253126_at 253013_at 253022_at 252947_at 252570_at	1 1 1 1
putative protein probable membrane protein YBL019w, yeast, PIR2:S45753 heat shock protein 70 like protein dnaK-type molecular chaperone PHSP1 -Pisum sativum,PID:g20835 putative protein putative protein ubiquitin fusion degradation protein - Schizosaccharomyces pombe, PID:e1132723 isovaleryI-CoA-dehydrogenase precursor (IVD) ;supported by full-length cDNA: Ceres:33674. glucosyltransferase-like protein UDP-glucose glucosyltransferase - Arabidopsis thaliana, EMBL:AB016819;supported by full-length cDNA: Ce	253308_at 253184_at 253126_at 253013_at 253022_at 252947_at 252570_at 252482_at	1 1 1 1 1
putative protein probable membrane protein YBL019w, yeast, PIR2:S45753 heat shock protein 70 like protein dnaK-type molecular chaperone PHSP1 -Pisum sativum,PID:g20835 putative protein putative protein ubiquitin fusion degradation protein - Schizosaccharomyces pombe, PID:e1132723 isovaleryI-CoA-dehydrogenase precursor (IVD) ;supported by full-length cDNA: Ceres:33674. glucosyltransferase-like protein UDP-glucose glucosyltransferase - Arabidopsis thaliana, EMBL:AB016819;supported by full-length cDNA: Ce FtsH protease, putative contains similarity to FtsH protease GI:13183728 from [Medicago sativa]	253308_at 253184_at 253126_at 253013_at 253022_at 252947_at 252570_at 2522482_at 2522449_at	1 1 1 1 1 1
putative protein probable membrane protein YBL019w, yeast, PIR2:S45753 heat shock protein 70 like protein dnaK-type molecular chaperone PHSP1 -Pisum sativum,PID:g20835 putative protein putative protein ubiquitin fusion degradation protein - Schizosaccharomyces pombe, PID:e1132723 isovaleryI-CoA-dehydrogenase precursor (IVD) ;supported by full-length cDNA: Ceres:33674. glucosyltransferase-like protein UDP-glucose glucosyltransferase - Arabidopsis thaliana, EMBL:AB016819;supported by full-length cDNA: Ce FtsH protease, putative contains similarity to FtsH protease GI:13183728 from [Medicago sativa] putative protein PrMC3 - Pinus radiata,PID:g4154352	253308_at 253184_at 253126_at 253013_at 253022_at 252947_at 252570_at 252482_at 252449_at 252315_at	1 1 1 1 1 1 1
putative protein probable membrane protein YBL019w, yeast, PIR2:S45753 heat shock protein 70 like protein dnaK-type molecular chaperone PHSP1 -Pisum sativum,PID:g20835 putative protein putative protein ubiquitin fusion degradation protein - Schizosaccharomyces pombe, PID:e1132723 isovaleryI-CoA-dehydrogenase precursor (IVD) ;supported by full-length cDNA: Ceres:33674. glucosyltransferase-like protein UDP-glucose glucosyltransferase - Arabidopsis thaliana, EMBL:AB016819;supported by full-length cDNA: Ce FtsH protease, putative contains similarity to FtsH protease GI:13183728 from [Medicago sativa] putative protein N7 protein - Medicago truncatula, EMBL:CAA76808;supported by full-length cDNA: Ceres:99337.	253308_at 253184_at 253126_at 253013_at 253022_at 252947_at 252947_at 252482_at 252449_at 252315_at 252336_at	1 1 1 1 1 1 1

putative protein predicted protein, Arabidopsis thaliana	252113_at 1
putative protein predicted protein, Oryza sativa, EMBL:AP000367;supported by full-length cDNA: Ceres:1514.	252093_at 1
putative protein 150-kD protein cluA - Dictyostelium discoideum,PID:g2281117 transporter-like protein oligopeptide transporter (LeOPT1) - Lycopersicon esculentum, EMBL:AF016713	252031_at 1 251916 at 1
protein kinase like protein protein kinase APK1, Arabidopsis thaliana, PIR:S28615;supported by full-length cDNA: Ceres:150889.	251922 at 1
hypothetical protein ;supported by full-length cDNA: Ceres:101230.	251925 at 1
Expressed protein ; supported by full-length cDNA: Ceres: 120919.	251845 at 1
	251757_at 1
putative protein predicted protein, Arabidopsis thaliana; supported by cDNA: gi_14596046_gb_AY042811.1_	251741_at 1
PROBABLE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 8 ; supported by cDNA: gi_2789659_gb_AF040102.1_AF040	_
putative protein several hypothetical proteins - different plant species; supported by cDNA: gi_16604698_gb_AY059794.1_	251713_at 1
translation initiation factor 3 -like protein mammary tumor-associated protein INT6 - Homo sapiens, EMBL:U94174; supported by cDNA: gi_1	_
putative protein predicted protein, Arabidopsis thaliana; supported by full-length cDNA; Ceres:114412.	251554_at 1
putative protein putative proteins - Arabidopsis thaliana; supported by cDNA: gi_16604381_gb_AY058089.1_ protein synthesis initiation factor - like eukaryotic protein synthesis initiation factor, Homo sapiens, EMBL:AF104913	251467_at 1 251431 at 1
dividro dipico linate synthase precursor; supported by full-length cDNA: Ceres:37907.	251392 at 1
	251331_s_at 1
putative protein DNAJ PROTEIN - Synechococcus PCC7942, EMBL:D29968; supported by cDNA: gi 16648711 gb AY058132.1	251263 at 1
mRNA capping enzyme - like protein mRNA capping enzyme (HCE), Homo sapiens, EMBL:AF025654	251136_at 1
putative protein unknown protein At2g37660 - Arabidopsis thaliana, EMBL:AC004684; supported by cDNA: gi_15294289_gb_AF410336.1_A	251038_at 1
putative protein In2, Zea mays, EMBL:X58573;supported by full-length cDNA: Ceres:13224.	250967_at 1
putative protein	250928_at 1
putative protein predicted proteins, Arabidopsis thaliana; supported by CDNA: gi_15215621_gb_AY050339.1_	250883_at 1
I-box binding factor - like protein I-box binding factor (LeMYBI gene), Lycopersicon esculentum, EMBL:LES243339;supported by full-length c putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:34592.	250858_at 1 250861 at 1
AtPH1-like protein ;supported by full-length cDNA: Ceres:109246.	250861_at 1 250748_at 1
eukaryotic translation initiation factor 3 subunit-like protein	250758_at 1
transcription factor HBP-1b homolog (spIP43273) ; supported by cDNA: gi 217826 dbj D10042.1 ATHAHBP1B	250671 at 1
putative protein SF16 protein, pollen specific - Helianthus annuus, PIR:T13992	250613 at 1
splicing factor-like protein ; supported by cDNA: gi_15451045_gb_AY054603.1_	250457_at 1
bromodomain protein - like bromodomain protein (BRDT), Homo sapiens, EMBL:AF019085	250424_at 1
beta-adaptin-like protein A ; supported by cDNA: gi_7385050_gb_AF216385.1_AF216385	250352_at 1
	250268_s_at 1
putative protein GCN4-complementing protein, Arabidopsis thaliana, EMBL:AJ130878	250285_at 1
unknown protein	250238_at 1
putative protein protein kinase MSK-3 - like protein kinase MSK-3, A.medicago, PIR:S37642	250179_at 1 250141_at 1
unknown protein ; supported by cDNA: gi_14423559_gb_AF387017.1_AF387017	250141_at 1
putative protein	250092_at 1
UDP-glucose pyrophosphorylase ; supported by cDNA: gi 13430663 gb AF360244.1 AF360244	250074 at 1
putative protein non-consensus GC donor splice site at exon 1, unknown (C40) protein, Homo sapiens, EMBL:AF103798	250042_at 1
triacylglycerol lipase-like protein triacylglycerol lipase (EC 3.1.1.3) precursor 1 - Rhizomucor miehei, PIR:A34959	249999_at 1
putative protein similar to unknown protein (dbj BAA91724.1)	249844_at 1
putative protein contains similarity to remorin;supported by full-length cDNA: Ceres:28686.	249797_at 1
putative protein crp1, Zea mays, PIR:T01685	249464_at 1
unknown protein ; supported by cDNA: gi_15081800_gb_AY048293.1_	249308_at 1
putative protein similar to unknown protein (emb[CAB66408.1);supported by full-length cDNA: Ceres:106836.	249231_at 1
U2 snRNP auxiliary factor, small subunit ; supported by cDNA: gi_15723292_gb_AF409140.1_AF409140 putative protein contains similarity to RNA-binding protein; supported by cDNA: gi_15215747_gb_AY050403.1_	249164_at 1 248905_at 1
casein kinase II beta chain; supported by cDNA; gi_468263 gb_L22563.1_ATHCKIB	248826 at 1
eukaryotic release factor 1 homolog (gb/AAA91169.1) ; supported by cDNA; gi 15215862 gb AY050462.1	248749 at 1
putative protein strong similarity to unknown protein (emb[CAB71043.1); supported by cDNA: gi 15810326 gb AY056202.1	248721_at 1
putative protein similar to unknown protein (gb AAF31026.1)	248648_at 1
unknown protein ;supported by full-length cDNA: Ceres:147765.	248592_at 1
putative protein contains similarity to unknown protein (dbj BAA90946.1)	248601_at 1
putative protein strong similarity to unknown protein (gb AAD25781.1)	248497_at 1
putative protein similar to unknown protein (pir  T31651);supported by full-length cDNA: Ceres:32353.	248492_at 1
putative protein contains similarity to iron-containing superoxide dismutase;supported by full-length cDNA: Ceres:126592. arginine/serine-rich splicing factor RSP41 homolog; supported by cDNA: gi_13877816_gb_AF370171.1_AF370171	248493_at 1 248369_at 1
ang minersementar spinong radio (C) + ( minorog , supported by converging radio ( ), ( ), ( ), ( ), ( ), ( ), ( ), ( )	248294 at 1
	248255 at 1
putative protein contains similarity to unknown protein (gb]AAC64884.1)	248124 at 1
chaperone GrpE-like protein ;supported by full-length cDNA: Ceres:20790.	248101 at 1
putative protein contains similarity to cytochrome oxidase assembly factor	248049_at 1
putative protein contains similarity to phosphatidylinositol/phosphatidylcholine transfer protein	247995_at 1
putative protein similar to unknown protein (gb AAD55473.1);supported by full-length cDNA: Ceres:7233.	247931_at 1
putative protein similar to unknown protein (ref NP_004732.1);supported by full-length cDNA: Ceres:11265.	247942_at 1
protein carboxyl methylase-like	247926_at 1
putative protein similar to unknown protein (emb CAB79781.1);supported by full-length cDNA: Ceres:31005. ABC transporter-like protein ; supported by cDNA: qi 9964120 qb AF287699.1 AF287699	247835_at 1 247806 at 1
NADP-dependent malate dehydrogenase (supported by full-length CDNA: Ceres:25200.	247813 at 1
light harvesting pigment - like protein LEDI-3 protein, Lithospermum erythrorhizon, EMBL:D45900	247783 at 1
cyclophilin ROC7 supported by full-length cDNA: Ceres:25325.	247791_at 1
RNA helicase - like protein RNA helicase, Homo sapiens, EMBL:Z70200	247564_at 1
putative protein predicted protein, Arabidopsis thaliana; supported by cDNA: gi_14517559_gb_AY039615.1_	247574_at 1
putative protein many predicted proteins from Arabidopsis thaliana;supported by full-length cDNA: Ceres:38421.	247550_at 1
putative protein rhoGAP, Homo sapiens, EMBL:Z23024; supported by full-length cDNA: Ceres: 152557.	247545_at 1
putative protein various predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:14414.	247461_at 1
MYB96 transcription factor-like protein ; supported by cDNA: gi_5823334_gb_AF176001.1_AF176001	247455_at 1
putative protein similar to unknown protein (pir  S76033) putative protein contains similarity to FtsH	247390_at 1 247235 at 1
putative protein contains similarity to rish putative protein similar to unknown protein (dbj BAA75199.1)	247187_at 1
oligopeptidase A; supported by cDNA: gj / 5028226 gb _AY045936.1_	247152_at 1

putative protein similar to unknown protein (sp P55606); supported by cDNA: gi_14190422_gb_AF378889.1_AF378889	247077_at 1
eukaryotic translation initiation factor - like protein eukaryotic translation initiation factor 3, Nicotiana tabacum, EMBL:Y11996; supp	ported by c 246865_s_at 1
voltage-dependent anion-selective channel protein hsr2 ;supported by full-length cDNA: Ceres:1417.	246546_at 1
Exportin1 (XPO1) protein ; supported by cDNA: gi_15810122_gb_AY056126.1_	246424_at 1
hypothetical protein ; supported by full-length cDNA: Ceres: 8960.	246291_at 1
putative protein sequence in GenBank Accession Number AC002330	246298_at 1
Expressed protein ; supported by full-length cDNA: Ceres: 37542.	246193_at 1
putative protein	246111_at 1
putative protein predicted proteins, Homo sapiens	246066_at 1
putative protein FH protein interacting protein FIP1, Arabidopsis thaliana, EMBL:AF174428;supported by full-length cDNA: Ceres:	19508. 246034_at 1
putative protein HERC2 - Homo sapiens, EMBL:AF071172	245851_at 1
hypothetical protein contains similarity to maleless protein (mle) GI:157905 from [Drosophila melanogaster]	245863_s_at 1
hypothetical protein	245868_at 1
receptor serine/threonine kinase PR5K, putative similar to receptor serine/threonine kinase PR5K GI:1235680 from [Arabidopsis th	haliana] 245760_s_at 1
Expressed protein ; supported by cDNA: gi_13877886_gb_AF370206.1_AF370206	245261_at 1
putative dihydrodipicolinate synthase ;supported by full-length cDNA: Ceres:26817.	245145 at 1
putative beta-1,3-glucanase ;supported by full-length cDNA: Ceres:95083.	245039 <sup>-</sup> at 1
hypothetical protein	257319 <sup>-</sup> at 1
hypothetical protein	257336 at 1
hypothetical protein similar to polyketide hydroxylases from several bacterial species	257410_at 1
unknown protein	257519 <sup>-</sup> at 1
unknown protein	256505 at 1
hypothetical protein predicted by genscan	264047 at 0.9
RNA-directed RNA polymerase, putative similar to RNA-directed RNA polymerase GB:CAA09697 GI:4138282 [Nicotiana tabacum	_
unknown protein	260620 at 0.9
putative long-chain acyl-CoA synthetase similar to malonyl CoA synthetase GB:AAF28840 from [Bradyrhizobium japonicum];support	
hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 33269.	257601 at 0.9
putative protein vsf-1 protein, Lycopersicon esculentum, PIR2:S52203; supported by cDNA: gi 15100048 gb AF401297.1 AF401	
phosphatidylinositol-4-phosphate 5-kinase-like protein phosphatidylinositol-4-phosphate 5-kinase AtPIPSK1 - Arabidopsis thaliana	
Arabidopsis thaliana /REF=U37281.1 /DEF=actin-2 mRNA, complete cds /LEN=1637 (_5, _M, _3 represent transcript regions 5 pr	
photomorphogenesis repressor (COP1) identical to GB:L24437; supported by CDNA: gi 402684 gb L24437.1 ATHCOP1A	267640 at 0.9
unknown protein similar to hypothetical protein PIRIS76698[supported by cDNA: gi 15809963 gb AY054250.1	267562 at 0.9
unknown protein ; supported by cDNA: gi 13430537 gb AF360181.1 AF360181	267513 at 0.9
putative tyrosyl-RNA synthetase	267446_s_at 0.9
putative U5 small nuclear ribonucleoprotein, an RNA helicase	267454 at 0.9
putative of small holical holicopide and the function of the proteins supported by cDNA: gi 12963360 gb AF327524.1 AF327524	267405 at 0.9
putative related to microbial divalent calon tolerance proteins, supported by cDiva. gr_1290500_g0_Al 32/324.1_Al 32/324	267415 at 0.9
diacylglycerol O-acyltransferase ; supported by cDNA: gi 15450799 gb AY054480.1	267280 at 0.9
putative WRKY-type DNA binding protein ; supported by cDNA: gi_15450739_gb_A1054460.1_	267260_at 0.9 267246 at 0.9
putative write special supported by convertige source and a support of the second state of the second stat	267256_s_at 0.9
Expressed protein ; supported by full-length cDNA: Ceres: 24003.	267211 at 0.9
unknown protein ; supported by cDNA: gi 14194142 gb AF367277.1 AF367277	267211_at 0.9
putative spliceosome associated protein ; supported by cDNA: gi_15450714_gb_AY052725.1_	267062 at 0.9
unknown protein	267052_at 0.9
unknown protein	267015 at 0.9
putative dolichyl-phosphate beta-glucosyltransferase ; supported by cDNA: gi 15810210 gb AY056120.1	266986 at 0.9
putative dolichymphosphale belangidoosyntaniserase, supported by CDNA. gr_15010210_gb_A1050120.1_ putative katanin ;supported by full-length cDNA: Ceres:119620.	266905 at 0.9
unknown protein ;supported by full-length cDNA: Ceres:9000.	_
putative poly(A) polymerase ; supported by cDNA: gi_14532699_gb_AY039974.1_	266924_at 0.9 266659_at 0.9
unknown protein unknown protein	
	266621_at 0.9
eukaryotic translation initiation factor 3 delta subunit ; supported by cDNA: gi_1036802_gb_U36765.1_ATU36765	266554_s_at 0.9
putative GTP-binding protein	266471_at 0.9
putative ligand-gated ion channel subunit ; supported by cDNA: gi_5759099_gb_AF170494.1_AF170494	266337_at 0.9
chloroplast membrane protein (ALBINO3) identical to GB:U89272;supported by full-length cDNA: Ceres:31457.	266224_at 0.9
unknown protein	266192_at 0.9
cytochrome p450, putative similar to cytochrome p450 GI:438242 from [Solanum melongena]; supported by cDNA: gi_14334809_0	
putative vacuolar protein sorting-associated protein; supported by cDNA: gi_15081710_gb_AY048248.1_	266096_at 0.9
putative NADP-dependent glyceraldehyde-3-phosphate dehydrogenase ; supported by cDNA: gi_14335051_gb_AY037205.1_	265998_at 0.9
unknown protein ;supported by full-length cDNA: Ceres:98881.	265959_at 0.9
unknown protein ;supported by full-length cDNA: Ceres:12261.	265911_at 0.9
hypothetical protein predicted by genscan	265879_at 0.9
unknown protein	265779_at 0.9
unknown protein ; supported by cDNA: gi_15450376_gb_AY052289.1_	265657_at 0.9
putative cAMP-dependent protein kinase	265581_at 0.9
putative microtubule-associated protein ;supported by full-length cDNA: Ceres:3416.	265510_at 0.9
unknown protein similarity to ubiquitin family of proteins; supported by cDNA: gi_16930424_gb_AF419566.1_AF419566	265461_at 0.9
hypothetical protein predicted by genscan; supported by full-length cDNA: Ceres: 32660.	265402_at 0.9
putative AAA-type ATPase similar to 26S proteosome regulatory subunit 8; supported by cDNA: gi_15450827_gb_AY054494.1_	265340_at 0.9
putative MYB family transcription factor	265301_s_at 0.9
beta-fructosidase nearly identical to beta-fructosidase GB:CAA67560 GI:1429209 (Arabidopsis thaliana); supported by cDNA: gi_1	
carboxyphosphonoenolpyruvate mutase, putative similar to carboxyphosphonoenolpyruvate mutase GI:47149 from [Streptomyces	,
unknown protein ; supported by cDNA: gi_13926184_gb_AF370567.1AF370567	264958_at 0.9
auxin-induced protein, putative similar to auxin-induced atb2 GI:6562980 from [Arabidopsis thaliana]; supported by cDNA: gi_6562	
hypothetical protein similar to hypothetical protein GB:014360	264818_at 0.9
unknown protein similar to ESTs gb/T22270 and gb/T76886	264797_at 0.9
putative protein kinase similar to MAP3K delta-1 protein kinase (Y14199); supported by cDNA; gi_11127924_gb_AF305913.1_AF3	_
putative leucyl-tRNA synthetase Strong similarity to S. pombe leucyl-tRNA synthetase (gb]Z73100)	264705_at 0.9
cysteine protease XBCP3 identical to papain-like cysteine peptidase XBCP3 GI:14600257 from [Arabidopsis thaliana]	264687_at 0.9
allyl alcohol dehydrogenase, putative similar to allyl alcohol dehydrogenase GI:9758497 from [Arabidopsis thaliana]; supported by	
putative sensory transduction histidine kinase similar to GB:AAD21777; similar to ESTs gb AA712891 and gb AA042438; supported	
unknown protein similar to EST gb/AA598098;supported by full-length cDNA: Ceres:23916.	264467_at 0.9
putative mitogen-activated protein kinase, MAP Kinase 1 similar to ESTs gb T41567 and gb R30629; supported by cDNA: gi_4641	136_dbj_D1 264405_at 0.9

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unincom problem         28625         at         28628         at         286288         at         28628		264335_s_at	0.9
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unknown protein Similar to hypothetical protein C342 2 gi 172800 thron L elegani Somile gi 252220 24172 170 comes from the part of the second part		_	
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putable fifth adenytiminatese Similar to RNA deinythenaterea gb/1532 from Lapina aba. EST gb/AZ1197 comes from the ge withown protein : supported by CDNA, gj. 1543972; gb. 705779.1. unknown protein : supported by CDNA, gj. 1543972; gb. 705779.1. Unknown protein : supported by CDNA, gj. 1543972; gb. 705779.1. Unknown protein : supported by CDNA, gj. 1543972; gb. 705779.1. Unknown protein : unknown in unknown in unknown protein : unaported by CNN gj. 15810332, gg. AVG56207.1. Unknown protein : unaported by CNN gj. 15810332, gg. AVG56207.1. Unknown protein : unaported by CNN gj. 15810332, gg. AVG56207.1. Unknown protein : unaported by CNN gj. 15810332, gg. AVG56207.1. Unknown protein : unaported by CNN gg. 15810332, gg. AVG56207.1. Unknown protein : unaported by CNN gg. 15810332, gg. AVG56207.1. Unknown protein : unaported by CNN gg. 15810332, gg. AVG56207.1. Unknown protein : unaported by CNN gg. 15810332, gg. AVG56207.1. Unknown protein : unaported by CNN gg. 15810332, gg. AVG56207.1. Unknown protein : unaported by CNN gg. 15810332, gg. AVG56207.1. Unknown protein : unaported by Unknown Gg. CNN GGN GGN GGN GGN GGN GGN GGN GGN GGN		_	
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unknown protein : supported by cDNA: g1.1546/072, gb, AV052704.1		_	
enclase (zhospho-Cycycene) supported by constant supported by CDNA ( <u>1</u> : 5300886 <u>0</u> , AV7050651. Supported by the predicted by gencaris. supported by CDNA ( <u>1</u> : 5300886 <u>0</u> , <u>A</u> V7050651. Supported by CDNA ( <u>1</u> : 5300886 <u>1</u> ) Supported by CDNA ( <u>1</u> : 1570876 <u>1</u> ) Supported by CDNA ( <u>1</u> : 1570876 <u>1</u> ) Supported by CDNA ( <u>1</u> : 15708776 <u>1</u> ) Supported by CDNA ( <u>1</u> : 15708777, <u>1</u> ) Supported by CDNA ( <u>1</u> : 15708777, <u>1</u> ) Supported by CDNA ( <u>1</u> : 157087776 <u>1</u> ) Supported by CDNA ( <u>1</u> : 15708777, <u>1</u> ) Supported by CDNA ( <u>1</u> : 157087777, <u>1</u> ) Su		_	
hypothetical protein prediced by general: supported by cDNA: gl_16648980.gb_AY059865.123883.3 et 0.9 24888.3 et 0.4 24888.4 et 0.4 248		_	
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unknown protein         20080-4, jit         20080-4, j		_	
glyclam-cin RNA binding protein 7.Maranike spling exists based on EST evidence. form 1 splice atle is A.Q. from 2 splice at			
14-3 protein GF14mu (gmt) demical to GF14 mu (G1350102, SP 06829 from (Aabidopsis thaliana) supported by Vulk-gt, 154508.       20344 at       0.9         12-3 protein GF14mu (gmt) demical a XIP transcription factor basic domin signature (PDOC0039); supported by VDNA: gt, 154003.       20339 at       0.9         12-3 protein GF14mu (gmt) demical a XIP transcription factor basic domina signature (PDOC0039); supported by VDNA: gt, 154003.       20339 at       0.9         12-3 protein GF14mu (gmt) demical and protein GFA7410 from (Protea americans); supported by CDNA; gt, 1540744.       20330 at       0.9         12-3 protein GF14mu (gmt) demical and genericans-supported by Laboration (GNAMF).       20320 at       0.9       20330 at       0.9         12-3 protein GF14mu (gmt) demical and genericans-supported by Laboration (GNAMF).       20320 at       0.9       20337 at       0.9         12-3 protein GF14mu (gmt) demical and genericans-supported by Laboration (GNAMF).       20337 at       0.9		_	
unknown protein : supported by cDNA gl [1581030] gb AV056207.1         223326 at 0.9           putative metryfinantias sem-idde/by deprotein factor MPRPT / 0[12823220); similar to ESTs emb[F1643 and db]AU062661         22520 at 0.9           putative metryfinantias sem-idde/by deprotein and protein factor MPRPT / 0[12823220); similar to ESTs emb[F1643 and db]AU062661         22520 at 0.9           protein protein protein by deprotein and protein factor MPRPT / 0[12823220); similar to ESTs emb[F1643 and db]AU062661         22520 at 0.9           protein and protein by deprotein and protein factor MPRPT / 0[12832220]; similar to ESTs emb[F1643 and db]AU062661         225288, at 0.9           protein and protein by deprotein and protein factor MPRPT / 0[12832224]; br 00 FTB contain marking to DAN-bid (protein factor protein factor group and protein by deprotein protein deprotein by deprotein protein deprotein protein deprotein by deprotein protein deprotein by deprotein protein by deprotein protein deprotein by deprotein protein deprotein by deprotein deprotein by deprotein deprotein by deprotein by deprotein by deprotein by deprotein by de		_	0.9
putative pre-rRNA spokensk terminate spikeling starter hPRP17 (g)[2282220); similar to ESTs emb]F16435 and ds]AU062661 22825 at 0.0 ptypethetical protein predicted by generant- putative ignominate devingenges component of the private devingenges complex E3, contains PF[0001 0 helix-loop-helix DNA-binding flavarinos 3-hydroxylase, putative isimilar to flavarinos 3-hydroxylase (g)[2271 0 from [Presea americani]; supported by CDNA; g][228222, at 0.0 ptypethetical protein contains similar to binding protein (PMN19] G12224980 from [Qvas studie]; supported by CDNA; g][128232, at 0.0 ptypethetical protein contains similar to binding protein (PMN19] G12224896 from [Qvas studie]; supported by CDNA; g][128232, at 0.0 ptypethetical protein contains similar to binding protein (PMN19] G12224896 from [Avabidopsis thaliana]; supported by CDNA; g][128232, at 0.0 ptypethetical protein contains similar to binding protein (PMN19] G12224896 from [Avabidopsis thaliana]; supported by CDNA; g][12822, g][2282,	putative bZIP transcription factor contains a bZIP transcription factor basic domain signature (PDOC00036); supported by cDNA: gi_1545083:	263414_at	0.9
putative pre-mRNA spitong factor similar to bigining factor PPPT 7 (g)228322(); similar to ESTs emP[F1633 and bijkU0626301 202307 at 0.9 potative lipomical dehydrogenese component of the proveste deny functional supported by CDNA; g]:1300744, 23153 at 0.9 minutes 3, Piptone and the proveste deny functional supported by CDNA; g]:1300744, 23153 at 0.9 minutes 4, Piptone and the proveste deny functional supported by CDNA; g]:1300744, 232307, at 0.9 minutes 4, Piptone and the proveste deny functional supported by CDNA; g]:1300744, 0.9 minutes 4, Piptone and the proveste deny functional supported by CDNA; g]:1300744, 232307, at 0.9 minutes 4, Piptone and the proveste deny functional supported by CDNA; g]:1300744, 232307, at 0.9 minutes 4, Piptone and the proveste deny functional supported by CDNA; g]:1300744, 22 22234, at 0.9 minutes 4, Piptone and the proveste deny functional supported by CDNA; g]:1300744, 22 22234, at 0.9 minutes 4, Piptone and the proveste deny functional supported by CDNA; g]:1300747, 2 222329, at 0.9 minutes 4, Piptone and the proveste deny functional supported by CDNA; g]:1300747, 2 22234, at 0.9 minutes 4, Piptone and the proveste deny functional supported by CDNA; g]:1300747, 2 22234, at 0.9 minutes 4, Piptone and the proveste deny functional supported by CDNA; g]:1300707, at 0.2023, at 0.9 minutes 4, Piptone and the proveste dense for provestice proveste deny functional supported by CDNA; g]:1300707, at 0.2023, at 0.9 minutes 4, Piptone and the proveste dense for provestice by CDNA; g]:1300707, at 0.2023, at 0.9 minutes 4, Piptone and the proveste dense for provestice and piptone and the provestice	unknown protein ; supported by cDNA: gi_15810336_gb_AY056207.1_	263326_at	0.9
hypothetical protein predicted by generant         28320_att         28320_att         28320_att         28320_att         28330_att	putative methylmalonate semi-aldehyde dehydrogenase	263275_at	0.9
julative lipiamide dehydrogensies component of the pruvate dehydrogensee complex E3, contains FP(D010 helic-toop-leks VA: gl_130754 fixanore 3-%/textorpress (sime solution to fixanore 3-%/textorpress (sime amonicans); supported by CDNA: gl_1375827_1 282381, at 0.9 282381, at 0.9 282382, at 0.9 28	putative pre-mRNA splicing factor similar to splicing factor hPRP17 (gi 3283220); similar to ESTs emb F15435 and dbj AUO62661	263261_at	0.9
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DegP protease contains similarity to degP GI:2623992 from [Bradyrhizobium japonicum]       259048_at       0.9			
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unknown proton reteminus similar to unknown protein GD. AAD20015 [Arabitopsis trailand], supported by full-length CDIVA. Celes. 30329. 208921_81 0.9		_	
	uninitian proton a terminus similar to uninitian proton OB.200250 to [Alabidopsis trailaria], supported by full-feligiti (DNA, Offes, 30329.	200021_at	0.9

putative RHO GDP-dissociation inhibitor 1 similar to RHO GDP-dissociation inhibitor 1 GB:P19803 [Bos taurus]; supported by full-length cDNA	258637 at	0.9
putative transitional endoplasmic reticulum ATPase identical to cell division cycle protein 48 (CDC48) homolog GB:P54609 (EMBO J. 14 (22)	258649 at	0.9
	_	
putative mudrA protein similar to mudrA protein GB:S59141 [Zea mays]	258550_at	0.9
hypothetical protein similar to receptor protein kinases: GB:CAB43834, GB:S71277 [Arabidopsis thaliana]	258557_at	0.9
hypothetical protein similar to hypothetical protein GB:CAB57979 from [Lycopersicon esculentum]	258406 at	0.9
unknown protein contains GMC oxidoreductase domain; supported by cDNA: gi 13605691 gb AF361827.1 AF361827	258299 at	0.9
unknown protein	258202 at	0.9
	_	0.9
putative GTP pyrophosphokinase similar to GTP PYROPHOSPHOKINASE GB:087331 from [Corynebacterium glutamicum]; supported by cC	258207_at	
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:20484.	258161_at	0.9
hypothetical protein predicted by genemark.hmm	258126_at	0.9
unknown protein contains Pfam profile: PF01738 dienelactone hydrolase family; supported by cDNA: gi 13899072 gb AF370531.1 AF3705	258108 at	0.9
unknown protein	258015 at	0.9
·	257972 at	0.9
		0.9
gda-1, putative similar to gda-1 GB:CAA74993 from [Pisum sativum];supported by full-length cDNA: Ceres:3049.	257790_at	
chorismate mutase identical to chorismate mutase GB:Z26519 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:39613.	257746_at	0.9
hypothetical protein predicted by genemark.hmm	257721_at	0.9
unknown protein contains Pfam profile: PF00400 WD domain, G-beta repeat; supported by cDNA: gi 15081810 gb AY048298.1	257661 at	0.9
unknown protein	257594 at	0.9
unknown protein	257611 at	0.9
hypothetical protein predicted by genscan+	257208 at	0.9
	_	
exonuclease, putative contains Pfam profile: PF00929 exonuclease;supported by full-length cDNA: Ceres:39883.	257211_at	0.9
RING zinc finger protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)	257081_at	0.9
unknown protein similar to unknown protein GB:AAD43153 from [Arabidopsis thaliana]	256944_at	0.9
unknown protein similar to alpha galactosidase GB:AAA73963 [Glycine max}	256866 at	0.9
unknown protein ; supported by cDNA: gi 13899104 gb AF370547.1 AF370547	256683 at	0.9
hypothetical protein predicted by genscan+	256605 at	0.9
	_	
unknown protein supported by full-length cDNA: Ceres:42677.	256543_at	0.9
unknown protein	256534_at	0.9
NADPH oxidoreductase, putative similar to GI:1708420 from [Arabidopsis thaliana] (J. Biol. Chem. 270 (44), 26224-26231 (1995)); supported	256454_at	0.9
unknown protein ;supported by full-length cDNA: Ceres:10857.	256301 at	0.9
NADP-specific glutatamate dehydrogenase, putative similar to NADP-specific glutatamate dehydrogenase (NADP-GDH) SP:P28724 [Giardia	256174 at	0.9
ubiquitin-specific protease 6 (UBP6), putative similar to GI:11993465; supported by full-length cDNA: Ceres:116145.	256179 at	0.9
	_	0.9
glycine hydroxymethyltransferase, putative similar to glycine hydroxymethyltransferase GI:438246 from [Solanum tuberosum]	255946_at	
unknown protein	255963_at	0.9
hypothetical protein similar to RING3-like bromodomain protein GI:3033386 from [Arabidopsis thaliana]; supported by cDNA: gi_15810438_gt	255906_at	0.9
putative CONSTANS-like B-box zinc finger protein	255839_at	0.9
Expressed protein ; supported by full-length cDNA: Ceres: 39479.	255671 at	0.9
putative potassium/H+ antiporter	255686 at	0.9
Expressed protein ; supported by full-length cDNA: Ceres: 36229.	255602 at	0.9
	_	
hypothetical protein	255615_at	0.9
hypothetical protein	255593_at	0.9
putative zinc finger protein identical to T10M13.22 ; supported by cDNA: gi_14334911_gb_AY035129.1_	255508_at	0.9
putative symbiosis-related protein ;supported by full-length cDNA: Ceres:119712.	255283 at	0.9
F-box protein family, AtFBW2 contains similarity to N7 protein GI:3273101 from [Medicago truncatula]:supported by full-length cDNA: Ceres:1	255066 at	0.9
putative protein	255077 at	0.9
	_	0.9
putative protein predicted protein W02G9.1 Caenorhabditis elegans cosmid W02G9, PID:g3165571; supported by cDNA: gi_15450340_gb_A	254863_at	
hypothetical protein ;supported by cDNA: gi_16648694_gb_AY058123.1_	254814_at	0.9
putative protein predicted protein, Saccaromyces cerevisiae;supported by full-length cDNA: Ceres:33190.	254830_at	0.9
putative protein G9A protein, Mus musculus, AF109906; supported by cDNA: gi_13517758_gb_AF344452.1_AF344452	254745_at	0.9
putative protein IFA-binding protein, Arabidopsis thaliana, AF004556	254724 at	0.9
methionyl-tRNA synthetase - like protein methionyl-tRNA synthetase, Oryza sativa, AF040700	254734 at	0.9
putative protein kinase ; supported by cDNA: gi_13249122 gb_AF295667.1_AF295667	254636 at	0.9
hypothetical protein	_	0.9
	254455_at	
putative protein	254417_at	0.9
Expressed protein ; supported by full-length cDNA: Ceres: 16643.		0.9
ODD disculations and such stars like protein ODD disculations and such stars. Associate a DATOLIV, F040004, such as to do to full loss other	254388_at	
CDP-diacylglycerol synthetase-like protein CDP-diacylglycerol synthetase, Arabidopsis thaliana, PATCHX:E218681;supported by full-length (		0.9
	254360_at	
putative Ap2 domain protein DNA-binding protein Pti6 - Lycopersicon esculentum,PID:g2213785; supported by cDNA: gi_15982736_gb_AY0	254360_at 254235_at	0.9 0.9
putative Ap2 domain protein DNA-binding protein Pti6 - Lycopersicon esculentum, PID:g2213785; supported by cDNA: gi_15982736_gb_AY0 putative protein hypothetical protein, Synechocystis sp., PIR:S76577; supported by full-length cDNA: Ceres:30708.	254360_at 254235_at 254187_at	0.9 0.9 0.9
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putative protein ;supported by full-length cDNA: Ceres:125922.	252945_at	0.9
putative protein	252909_at	0.9
putative protein ;supported by full-length cDNA: Ceres:5968.	252880_at	0.9
GTP-binding - like protein GTP-binding protein DRG, Xenopus laevis, SWISS-PROT:P43690; supported by cDNA: gi_14334721_gb_AY035C myo-inositol-1-phosphate synthase ;supported by full-length cDNA: Ceres:1978.	252883_at 252863 at	0.9 0.9
putative protein predicted protein, Drosophila melanogaster, EMBL:AE003789	252738 at	0.9
hypothetical protein ; supported by full-length cDNA: Ceres: 281.	252723 at	0.9
hypothetical protein SPOP protein, Homo sapiens, EMBL:HSJ000644	252701 at	0.9
putative protein predicted protein, C.elegans, PIR:T24538	252680_at	0.9
putative protein KIAA0073, Homo sapiens, EMBL:HSORF006	252644_at	0.9
serine threonine-protein kinase-like protein Ca2+ calmodulin-dependent protein kinase - Rattus norvegicus, PIR:A57156; supported by cDNA	252616_at	0.9
putative protein tRNA nucleotidyltransferase, Methanobacterium thermoautotrophicum, PIR:A69191	252508_at	0.9
betaine aldehyde dehydrogenase-like protein betaine aldehyde dehydrogenase - Amaranthus hypochondriacus, PID:g2388710; supported by Expressed protein ; supported by full-length cDNA: Ceres: 26537.	252354_at 252366 at	0.9 0.9
	252291 s at	0.9
putative protein hypothetical protein L1648.04 - Leishmania major, EMBL:LMFL1648	252139 at	0.9
epoxide hydrolase-like protein epoxide hydrolase homolog - Glycine max, PIR:T07145; supported by cDNA: gi_13937212_gb_AF372961.1_/	252095_at	0.9
putative protein hin1 protein -Nicotiana tabacum, PID:e259431; supported by full-length cDNA: Ceres:92178.	252058_at	0.9
splicing factor - like protein splicing factor, arginine/serine-rich 7, Homo sapiens, PIR:A57198	251943_at	0.9
putative protein KIAA0544 protein, Homo sapiens, EMBL:AB011116;supported by full-length cDNA: Ceres:110247.	251959_at	0.9
sigma factor SigC ; supported by cDNA: gi_2353174_gb_AF015544.1_AF015544	251929_at	0.9 0.9
pasticcino 1 ; supported by cDNA: gi_15810452_gb_AY056265.1_ putative protein proteophosphoglycan, Leishmania major, PIR:T46707supported by full-length cDNA: Ceres:6954.	251932_at 251859 at	0.9
putative protein unamed sequence, Homo sapiens, EMBL:AK001088; supported by rainong metangenesis cores.	251828_at	0.9
putative protein predicted proteins, Arabidopsis thaliana	251749 at	0.9
putative protein TATA-binding protein-binding protein, ABT1 - Mus musculus, EMBL:AB021860	251690_at	0.9
hypothetical protein	251650_at	0.9
dnaJ-like protein DNAJ protein - Schizosaccharomyces pombe, PIR:T39697;supported by full-length cDNA: Ceres:120719.	251622_at	0.9
putative protein ;supported by full-length cDNA: Ceres:29384., Ceres:101256.	251558_at	0.9
ATP-dependent RNA helicase-like protein ATP-dependent RNA helicase - Xenopus laevis, PIR:S13654;supported by full-length cDNA: Cere:	_	0.9 0.9
putative protein RanBP7/importin 7 - Homo sapiens, EMBL:AF098799 putative protein polyamine oxidase (EC 1.5.3.11) precursor - Zea mays plasmid pCR2.1;supported by full-length cDNA: Ceres:16421.	251495_at 251505 at	0.9
actin - like protein actin 3, Drosophila melanogaster, PIR-A03000;supported by full-length CDNA: Ceres:38396.	251340 at	0.9
putative protein ISOPENICILLIN N EPIMERASE - Streptomyces clavuligerus, EMBL:M3324;supported by full-length cDNA: Ceres:27922.	251260 at	0.9
putative protein hypothetical protein BAA87851.1 - Oryza sativa, EMBL:AP000816	251267_at	0.9
cyclophylin -like protein CDC28/cdc2-like kinase associating arginine-serine cyclophilin, Homo sapiens, PIR:JC5314	251177_at	0.9
putative protein putative hydrolase At2g32150 - Arabidopsis thaliana, EMBL:AC006223;supported by full-length cDNA: Ceres:36724.	251028_at	0.9
ubiquitin-specific protease 12 (UBP12) almost identical to ubiquitin-specific protease 12 GI:11993471 [Arabidopsis thaliana], one amino acid u Mai Difference in the protein Mai Difference in Arabidopsis thaliana EMDL 1984202	250693_at	0.9
Mei2-like protein Mei2-like protein - Arabidopsis thaliana, EMBL:D86122 myosin heavy chain-like protein ; supported by cDNA: gi_1732514_gb_U62744.1_ATU62744	250617_at 250548 at	0.9 0.9
microbody NAD-dependent malate dehydrogenase; supported by cDNA: gi 14335145 gb AY037252.1	250498 at	0.9
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putative protein prdeicted proteins, Schizosaccharomyces pombe	250281_at 250293_s_at	0.9 0.9 0.9
putative protein prdeicted proteins, Schizosaccharomyces pombe	250281_at	0.9
putative protein prdeicted proteins, Schizosaccharomyces pombe auxin reponsive - like protein Nt-gh3 deduced protein, Nicotiana tabacum, EMBL:AF123503 putative protein similar to unknown protein (emb CAB86638.1) putative protein similar to unknown protein (ref NP_057085.1);supported by full-length cDNA: Ceres:38057.	250281_at 250293_s_at 250202_at 250222_at	0.9 0.9 0.9 0.9
putative protein prdeicted proteins, Schizosaccharomyces pombe auxin reponsive – like protein Nt-gh3 deduced protein, Nicotiana tabacum, EMBL:AF123503 putative protein similar to unknown protein (mb)CAB86638.1) putative protein similar to unknown protein (refINP_057085.1);supported by full-length cDNA: Ceres:38057. putative protein various predicted proteins, Arabidopsis thaliana	250281_at 250293_s_at 250202_at 250222_at 250144_at	0.9 0.9 0.9 0.9 0.9
putative protein prdeicted proteins, Schizosaccharomyces pombe auxin reponsive - like protein Nt-gh3 deduced protein, Nicotiana tabacum, EMBL:AF123503 putative protein similar to unknown protein (emb CAB86638.1) putative protein similar to unknown protein (ref NP_057085.1);supported by full-length cDNA: Ceres:38057. putative protein various predicted proteins, Arabidopsis thaliana APG5 (autophagy 5)-like protein	250281_at 250293_s_at 250202_at 250222_at 250144_at 250088_at	0.9 0.9 0.9 0.9 0.9 0.9
putative protein prdeicted proteins, Schizosaccharomyces pombe auxin reponsive - like protein Nt-gh3 deduced protein, Nicotiana tabacum, EMBL:AF123503 putative protein similar to unknown protein (emb[CAB86638.1) putative protein similar to unknown protein (ref NP_057085.1);supported by full-length cDNA: Ceres:38057. putative protein various predicted proteins, Arabidopsis thaliana APG5 (autophagy 5)-like protein chromo domain protein polycomb-like protein, Daucus carota, PIR:T14294; supported by cDNA: gi_15625406_gb_AF387639.1_AF387639	250281_at 250293_s_at 250202_at 250222_at 250144_at 250088_at 250060_at	0.9 0.9 0.9 0.9 0.9 0.9 0.9
putative protein prdeicted proteins, Schizosaccharomyces pombe auxin reponsive - like protein Nt-gh3 deduced protein, Nicotiana tabacum, EMBL:AF123503 putative protein similar to unknown protein (emb]CAB86638.1) putative protein similar to unknown protein (ref]NP_057085.1);supported by full-length cDNA: Ceres:38057. putative protein various predicted proteins, Arabidopsis thaliana APG5 (autophagy 5)-like protein chromo domain protein polycomb-like protein, Daucus carota, PIR:T14294; supported by cDNA: gi_15625406_gb_AF387639.1_AF387639 MAP kinase -like protein ATMPK9, Arabidopsis thaliana, EMBL:AB038694	250281_at 250293_s_at 250202_at 250222_at 250144_at 250088_at 250060_at 249964_at	0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9
putative protein prdeicted proteins, Schizosaccharomyces pombe auxin reponsive - like protein Nt-gh3 deduced protein, Nicotiana tabacum, EMBL:AF123503 putative protein similar to unknown protein (emb[CAB86638.1) putative protein similar to unknown protein (ref NP_057085.1);supported by full-length cDNA: Ceres:38057. putative protein various predicted proteins, Arabidopsis thaliana APG5 (autophagy 5)-like protein chromo domain protein polycomb-like protein, Daucus carota, PIR:T14294; supported by cDNA: gi_15625406_gb_AF387639.1_AF387639	250281_at 250293_s_at 250202_at 250222_at 250144_at 250088_at 250060_at	0.9 0.9 0.9 0.9 0.9 0.9 0.9
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putative protein prdeicted proteins, Schizosaccharomyces pombe auxin reponsive - like protein Nt-gh3 deduced protein, Nicotiana tabacum, EMBL:AF123503 putative protein similar to unknown protein (emb[CAB86638.1) putative protein similar to unknown protein (ref NP_057085.1);supported by full-length cDNA: Ceres:38057. putative protein various predicted proteins, Arabidopsis thaliana APG5 (autophagy 5)-like protein chromo domain protein polycomb-like protein, Daucus carota, PIR:T14294; supported by cDNA: gi_15625406_gb_AF387639.1_AF387639 MAP kinase -like protein ATMPK9, Arabidopsis thaliana, EMBL:AB038694 putative protein similar to unknown protein (ref NP_015265.1); supported by cDNA: gi_12007446_gb_AF322255.1_AF322255 putative protein similar to unknown protein (ref NP_015265.1); supported by cDNA: gi_12007446_gb_AF322255.1_AF322255 putative protein similar to unknown protein (pir  C72413) serine palmitoyltransferase ; supported by cDNA: gi_15292790_gb_AY050829.1_ nucleolar protein-like	250281_at 250293_s_at 250202_at 250222_at 250144_at 250080_at 249964_at 249964_at 249864_at 249849_at 249799_at 249672_at	0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9
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putative protein prdeicted proteins, Schizosaccharomyce's pombe auxin reponsive - like protein NL-gh3 deduced protein, Nicotiana tabacum, EMBL:AF123503 putative protein similar to unknown protein (mb)CA886638.1) putative protein various predicted proteins, Arabidopsis thaliana APG5 (autophagy 5)-like protein chromo domain protein (polycomb-like protein, Daucus carota, PIR:T14294; supported by cDNA: gi_15625406_gb_AF387639.1_AF387639 MAP kinase - like protein ATMPK9, Arabidopsis thaliana, EMBL:AB038694 putative protein similar to unknown protein (refINP_015265.1); supported by cDNA: gi_12007446_gb_AF322255.1_AF322255 putative protein similar to unknown protein (refINP_015265.1); supported by cDNA: gi_12007446_gb_AF322255.1_AF322255 putative protein similar to unknown protein (refINP_015265.1); supported by cDNA: gi_12007446_gb_AF322255.1_AF322255 putative protein similar to unknown protein (refINP_015265.1); supported by cDNA: gi_15292790_gb_AY050829.1_ nucleolar protein-like putative protein unnamed ORF, Horno sapiens, EMBL:BNA245479 RING finger -like protein RING-H2 zinc finger protein ATL 4, Arabidopsis thaliana, EMBL:AF132014 urophorphylin III methylase (gbIAA892676.1); supported by cDNA: gi_1146164_gb_L47479.1_ATHUPM1R unknown protein MAP kinase; supported by cDNA: gi_15983508_gb_AF424629 [_FA44629 FISH protease, putative similar to FISH protease GI:13183728 from (Medicago sativa] brain and reproductive organ-expressed protein-like 1-aminocy(topropane-1-catox)ylate oxidase; supported by cDNA: gi_15983808_gb_AY056810.1_ nuclear cap-binding protein; CBP20 (gb)AAD29697.1) non-consensus AT donor splice site at exon 4, AC acceptor splice site at exon 5; supp putative protein strong similarity to unknown protein (gb]AAC61825.1); supported by cDNA: gi_15081732_gb_AY048259.1_ unknown protein culini; supported by cDNA: Gi_13605826_gb_AF367312.1_AF367312 heat shock protein 70 (gb]AAF27639.1) ; supported by cDNA: gi_6746591_gb_AF217459.1_AF217459 histone acetyltransferase ; supported by cDNA:	250281_at 250293_s_at 250202_at 25022_at 250144_at 250088_at 250060_at 249964_at 249964_at 249864_at 249872_at 249672_at 249672_at 249611_at 249672_at 249612_at 249308_at 249325_at 249313_at 249244_at 249128_at 249128_at 24976_at 24976_at 248976_at 248976_at 248976_at 248976_at 248976_at 248976_at 248976_at 248976_at 248976_at 248976_at 248976_at 248368_at 248368_at 248368_at 248368_at 248368_at 248378_at 248378_at 248300_at 248301_at 248301_at 24820_at 248301_at 248220_at 24835_at 248311_at 248301_at 248301_at 248220_at 24835_at 24835_at 248318_at	0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9
putative protein prdeinced proteins, Schizosaccharomyce's pombe auxin reponsive - like protein Nt-gh3 deduced protein, Nicotiana tabacum, EMBL:AF123503 putative protein similar to unknown protein (mb)CA886638.1) putative protein various predicted proteins, Arabidopsis thaliana APG5 (autophagy 5)-like protein chromo domain protein polycomb-like protein, Daucus carota, PIR:114294; supported by cDNA: gi_15625406_gb_AF387639.1_AF387639 MAP kinase - like protein TMPK9, Arabidopsis thaliana, EMBL:A8038694 putative protein similar to unknown protein (refINP_015265.1); supported by cDNA: gi_12007446_gb_AF322255.1_AF322255 putative protein similar to unknown protein (refINP_015265.1); supported by cDNA: gi_12007446_gb_AF322255.1_AF322255 putative protein similar to unknown protein (refINP_015265.1); supported by cDNA: gi_12007446_gb_AF322255.1_AF322255 putative protein similar to unknown protein (refINP_015265.1); supported by cDNA: gi_12007446_gb_AF322255.1_AF322255 putative protein similar to unknown protein (refINP_015265.1); supported by cDNA: gi_12007446_gb_AF322255.1_AF322255 putative protein similar to unknown protein (refINP_015265.1); supported by cDNA: gi_12007446_gb_AF32014 urobolar protein-like putative protein similar to unknown protein (refINP_015265.1); supported by cDNA: gi_1146164_gb_L47479.1_ATHUPM1R unclooar protein SINA similar to TISH protease (SI:13183728 from [Medicago sativa] brain and reproductive organ-expressed protein-like 1-aminocyclopropane-1-carboxylate oxidase : supported by cDNA: gi_15983808_gb_AY056810.1_ nuclear cap-binding protein. CBP20 (gb)AAD29807.1) non-consensus AT donor splice site at exon 5; supp putative protein strong similar to Inknown protein (gb]AAC61825.1); supported by cDNA: gi_15081732_gb_AY048259.1_ unknown protein cullin supported by full-length cDNA: Ceres:101723. receptor-like protein singa portein JCBP20 (gb)AAD29807.1) non-consensus AT donor splice site at exon 5; supp putative protein by full-length cDNA: Ceres:10172. receptor-like protein	250281_at 250293_s_at 250202_at 250202_at 250144_at 250088_at 250060_at 249964_at 249964_at 249964_at 249979_at 249672_at 249672_at 249672_at 249672_at 249398_at 249325_at 249325_at 249325_at 249325_at 249326_at 249326_at 24936_at 248976_at 248976_at 248976_at 248976_at 248976_at 248976_at 248976_at 248976_at 248976_at 248368_at 248698_at 248698_at 248698_at 248698_at 248698_at 2483788_at 2483788_at 2483788_at 24837888_at 2483788888888888888888888888888888888888	0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9
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putative protein prdeinced proteins, Schizosaccharomyce's pombe auxin reponsive - like protein Nt-gh3 deduced protein, Nicotiana tabacum, EMBL:AF123503 putative protein similar to unknown protein (mb)CA886638.1) putative protein various predicted proteins, Arabidopsis thaliana APG5 (autophagy 5)-like protein chromo domain protein polycomb-like protein, Daucus carota, PIR:114294; supported by cDNA: gi_15625406_gb_AF387639.1_AF387639 MAP kinase - like protein TMPK9, Arabidopsis thaliana, EMBL:A8038694 putative protein similar to unknown protein (refINP_015265.1); supported by cDNA: gi_12007446_gb_AF322255.1_AF322255 putative protein similar to unknown protein (refINP_015265.1); supported by cDNA: gi_12007446_gb_AF322255.1_AF322255 putative protein similar to unknown protein (refINP_015265.1); supported by cDNA: gi_12007446_gb_AF322255.1_AF322255 putative protein similar to unknown protein (refINP_015265.1); supported by cDNA: gi_12007446_gb_AF322255.1_AF322255 putative protein similar to unknown protein (refINP_015265.1); supported by cDNA: gi_12007446_gb_AF322255.1_AF322255 putative protein similar to unknown protein (refINP_015265.1); supported by cDNA: gi_12007446_gb_AF32014 urobolar protein-like putative protein similar to unknown protein (refINP_015265.1); supported by cDNA: gi_1146164_gb_L47479.1_ATHUPM1R unclooar protein SINA similar to TISH protease (SI:13183728 from [Medicago sativa] brain and reproductive organ-expressed protein-like 1-aminocyclopropane-1-carboxylate oxidase : supported by cDNA: gi_15983808_gb_AY056810.1_ nuclear cap-binding protein. CBP20 (gb)AAD29807.1) non-consensus AT donor splice site at exon 5; supp putative protein strong similar to Inknown protein (gb]AAC61825.1); supported by cDNA: gi_15081732_gb_AY048259.1_ unknown protein cullin supported by full-length cDNA: Ceres:101723. receptor-like protein singa portein JCBP20 (gb)AAD29807.1) non-consensus AT donor splice site at exon 5; supp putative protein by full-length cDNA: Ceres:10172. receptor-like protein	250281_at 250293_s_at 250202_at 250202_at 250144_at 250088_at 250060_at 249964_at 249964_at 249964_at 249979_at 249672_at 249672_at 249672_at 249672_at 249398_at 249325_at 249325_at 249325_at 249325_at 249326_at 249326_at 24936_at 248976_at 248976_at 248976_at 248976_at 248976_at 248976_at 248976_at 248976_at 248362_at 248698_at 248698_at 248698_at 248698_at 248362_at 248378_at 24837	0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9
putative protein prideided proteins. Schizosaccharomycise pombei auxin reponsive - like protein NL-gh3 deduced protein, Nicotiana tabacum, EMBL:AF123503 putative protein similar to unknown protein (erhl)CAB86638.1) putative protein various predicted proteins, Arabidopsis thaliana APG5 (autophagy 5)-like protein chromo domain protein inpolycomb-like proteins, Arabidopsis thaliana, EMBL:AB038694 putative protein similar to unknown protein (erhl)P_057065.1); supported by cDNA: gj_15625406_gb_AF387639.1_AF387639 MAP kinase - like protein ATMPK9, Arabidopsis thaliana, EMBL:AB038694 putative protein similar to unknown protein (refl)NP_015265.1); supported by cDNA: gj_12007446_gb_AF322255.1_AF322255 putative protein similar to unknown protein (refl)NP_015265.1); supported by cDNA: gj_12007446_gb_AF322255.1_AF322255 putative protein similar to unknown protein (refl)NP_015265.1); supported by cDNA: gj_12007446_gb_AF322255.1_AF322255 putative protein innamed ORF, Homo sapiens, EMBL:AB038694 putative protein innamed ORF, Homo sapiens, EMBL:AB038694 putative protein INRO-H2 zinc finger protein ATL4, Arabidopsis thaliana, EMBL:AF132014 urophorphyrin III methylase (gb AAB92676.1) ; supported by cDNA: gj_1146164_gb_L47479.1_ATHUPM1R unknown protein MAP kinase ; supported by cDNA: gj_15883508_gb_AF424629.1_AF424629 FISH protease, putative similar to FISH protease GI:13183728 from [Medicago sativa] brain and reproductive organ-expressed protein-like 1-aminocyclopropane-1-carboxylate oxidase : supported by cDNA: gj_15983808_gb_AY048259.1_ unknown protein CMAP kinase ; supported by cDNA: gj_13605826_gb_AF367312.1_AF367312 heat shock protein 73 (gb/AAF27633.1); supported by cDNA: gj_13605826_gb_AF367312.1_AF367312 heat shock protein 73 (gb/AAF27633.1); supported by cDNA: gj_13605826_gb_AF367312.1_AF367312 heat shock protein 73 (gb/AAF27633.1); supported by full-length cDNA: Ceres:129386. nucleatide-binding protein ; supported by cDNA: gj_13605826_gb_AF367312.1_AF367312 heat shock protein 7300427653.1); supported by full-length cDN	250281_at 250293_s_at 250202_at 250202_at 250144_at 250028_at 250060_at 249964_at 249964_at 249864_at 249864_at 249879_at 249672_at 249611_at 249615_at 249305_at 249305_at 249313_at 249239_at 249313_at 249236_at 249316_at 249244_at 24936_at 249926_at 249926_at 248966_at 248966_at 248966_at 248506_at 248376_at 248376_at 248300_at 248301_at 248200_at 248235_at 248118_at 24801_at 248031_at 248031_at	0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9

branched-chain amino acid aminotransferase-like protein	247886 at	0.9
26S proteasome AAA-ATPase subunit RPT3 (gb)AAF22523.1)	247810 at	0.9
putative protein MNUDC protein, Homo sapiens, EMBL:AF100760	247777 at	0.9
thymidylate kinase - like protein thymidylate kinase, Arabidopsis thaliana, EMBL:AF081570;supported by full-length cDNA: Ceres:155539.	247735 at	0.9
putative protein transcriptional repressor NOT4-N, Homo sapiens, EMBL:AF180475	247669 at	0.9
putative protein contains similarity to DNA-binding protein;supported by full-length cDNA: Ceres:112281.	247430 at	0.9
putative protein predicted proteins, Arabidopsis thaliana	247395 at	0.9
1-deoxy-D-xylulose 5-phosphate reductoisomerase (DXR) ;supported by full-length cDNA: Ceres:117626.	247401 at	0.9
topoisomerase-like protein ;supported by full-length cDNA; Ceres:19433.	247374_at	0.9
putative protein similar to unknown protein (splP54122)	247385_at	0.9
putative protein contains similarity to RNA-binding protein	247276_at	0.9
cdc2-like protein kinase ; supported by cDNA; gi_13430443_gb_AF360134.1_AF360134	247220_at	0.9
WD repeat protein-like ;supported by full-length cDNA: Ceres:11277.	247106_at	0.9
unknown protein ; supported by cDNA: gi_14488062_gb_AF389279.1_AF389279	247046_at	0.9
putative protein Leaf protein, Pharbitis nil, EMBL:D85101	246901_at	0.9
putative protein ;supported by full-length cDNA: Ceres:108509.	246840_at	0.9
glycine hydroxymethyltransferase - like protein glycine hydroxymethyltransferase, Solanum tuberosum, EMBL:Z25863; supported by cDNA: ç	246800_at	0.9
putative protein many predicted proteins, Arabidopsis thaliana	246808_at	0.9
putative protein hypothetical proteins - different species	246768_at	0.9
putative protein hypothetical protein F22F7.12 - Arabidopsis thaliana, EMBL:AC009606	246732_at	0.9
putative protein hypothetical protein F14P3.15 - Arabidopsis thaliana, EMBL:AC009755	246564_at	0.9
N2,N2-dimethylguanine tRNA methyltransferase-like protein several N2,N2-dimethylguanine tRNA methyltransferases	246521_at	0.9
serine/threonine-specific protein kinase-like protein serine/threonine-specific protein kinase NPK15 - Nicotiana tabacum;supported by full-leng	246529_at	0.9
valinetRNA ligase-like protein several bacterial valinetRNA ligases	246509_at	0.9
Inositol 1,3,4-Trisphosphate 5/6 kinase ;supported by full-length cDNA: Ceres:30653.	246451_at	0.9
putative protein predicted protein, Drosophila melanogaster, EMBL:AE003450	246469_at	0.9
putative protein cisplatin resistance-associated overexpressed protein - Homo sapiens, EMBL:AB034205; supported by cDNA: gi_15450598_	246436_at	0.9
S-locus protein, putative similar to S-locus protein 5 GI:6069485 from [Brassica rapa]	246322_at	0.9
high mobility group protein 2-like ; supported by cDNA: gi_15912190_gb_AY056373.1_	246311_at	0.9
G-protein, putative contains Pfam profile: PF00503: G-protein alpha subunit	246312_at	0.9
unknown protein	246261 at	0.9
cytochrome P450, putative contains Pfam profile: PF00067: Cytochrome P450; supported by cDNA: gi 15912336 gb AY056446.1	246268 at	0.9
T-complex protein 1, beta subunit T-COMPLEX PROTEIN 1, BETA SUBUNIT, Homo sapiens, EMBL:AF026293, supported by full-length cDN		0.9
26S proteasome AAA-ATPase subunit RPT6a - like protein 26S proteasome AAA-ATPase subunit RPT6a, Arabidopsis thaliana, EMBL:AF12		0.9
putative protein predicted proteins, H. sapiens, D. melanogaster and others	246094 at	0.9
	246038 s at	0.9
putative protein serine-arginine-rich splicing regulatory protein SRRP86, Rattus norvegicus, EMBL:AF234765	246039 at	0.9
putative protein predicted proteins, Arabidopsis thaliana and others	246052 at	0.9
putative protein farmesyl cysteine arboxyl methyltransferase, Rattus norvegicus, EMBL:AF075595	246053 at	0.9
putative protein realistic of proteins, Arabidospis thaliana and Synacchocystis sp.	246057_at	0.9
putative protein predicted proteins, Arabidopsis thaliana	246058 at	0.9
rev interacting protein mis3 - like rev interacting protein mis3, Schizosaccharomyces pombe, PIR:T39981;supported by full-length cDNA: Cer	_	0.9
putative protein medicate protein mieracung protein mieracung, conzosaciationyces pointe, rich 1950, supported by charge and the putative protein predicted proteins, Arabidopsis thaliana; supported by cDNA; gi 13877640, gb AF3705211 AF370521	246010 at	0.9
	245803 at	0.9
cysteine proteinase RD21A identical to thiol protease RD21A SP:P43297 from [Arabidopsis thaliana]	_	
unknown protein contains similarity to calmodulin GI:166304 from [Achtya klebsiana]; supported by cDNA; gi_13358218_gb_AF325029.2_AF; calcium jiai binding carbon units of the contained of the contained by cDNA; gi_13358218_gb_AF325029.2_AF;	_	0.9
calcium lipid binding protein - like GC donor splice site at exon 3; supported by cDNA: gi_16604592_gb_AY059741.1_	245702_at	0.9
Expressed protein ; supported by cDNA: gi_535587_gb_L36113.1_ATHATJ	245686_at	0.9
mitochondrial protein (AtJ1), putative similar to mitochondrial protein (AtJ1) GI:564030 from [Arabidopsis thaliana]; supported by cDNA: gi_56	245670_at	0.9
Expressed protein supported by cDNA: Ceres:30129; supported by cDNA: gi:15028002	245602_at	0.9
hypothetical protein	245501_at	0.9
galactokinase like protein	245478_at	0.9
enoyl-CoA hydratase	245446_at	0.9
hypothetical protein	245431_at	0.9
trehalose-6-phosphate synthase like protein ;supported by full-length cDNA: Ceres:95947.	245348_at	0.9
hypothetical protein ;supported by full-length CDNA: Ceres:38042.	245330_at	0.9
scarecrow-like 13 (SCL13) ; supported by cDNA: gi_16930432_gb_AF419570.1_AF419570	245247_at	0.9
	245218_s_at	0.9
putative protein similarity to cDNA clones from human and mouse	245178_at	0.9
mitochondrial chaperonin (HSP60)	245164_at	0.9
putative receptor-like protein kinase	245130_at	0.9
4-alpha-glucanotransferase	245094_at	0.9
transcription factor IIB (TFIIB) identical to GB:P48512; contains a transcription factor TFIIB repeat signature (PDOC00624), supported by full-le		0.9
hypothetical protein predicted by genscan; similar to SPIP34568 YNV5_CAEEL;supported by full-length cDNA: Ceres:8256.	245062_at	0.9
cytochrome c biogenesis orf382 Protein sequence is in conflict with the conceptual translation	244912_at	0.9
hypothetical protein	257322_at	0.9
unknown protein	249100_at	0.9
putative ATP-dependent RNA helicase similar to gb L13612 DEAD-box protein (dbp45A) from Drosophila melanogaster and is a member of P	262706_at	0.8
putative NAK-like ser/thr protein kinase similar to A. thaliana NAK ser/thr protein kinase, GenBank accession number P43293	255559_at	0.8
	249319_s_at	0.8
putative protein contains similarity to phosphatidylinositol/phosphatidylcholine transfer protein	248808_at	0.8
unknown protein	247273_at	0.8
putative protein hypothetical proteins - Arabidopsis thaliana	246493_at	0.8
putative protein	246088_at	0.8
Arabidopsis thaliana /REF=U37281 /DEF=actin-2 mRNA, complete cds /LEN=1637 (-5, -M, -3 represent transcript regions 5 prime, Middle, a C	-	0.8
unknown protein ;supported by cDNA: gi_11907565_gb_AF123315.1_AF123315	267557_at	0.8
citrate synthase similar to GB:X17528, 10 possible frameshifts in that submission.;supported by full-length cDNA: Ceres:16528.	267368_at	0.8
hypothetical protein predicted by genefinder and genscan	267347_at	0.8
ABC transporter (AtMRP2) identical to GB:AF014960; transports glutathione conjugates; supported by cDNA: gi_2909780_gb_AF020288.1_A	267319_at	0.8
ubiquitin activating enzyme 1 (UBA1) identical to GB:U80808	267301_at	0.8
putative casein kinase II catalytic (alpha) subunit ;supported by full-length cDNA: Ceres:38084.	267257_at	0.8
unknown protein	267269_at	0.8
hypothetical protein predicted by grail; supported by full-length cDNA: Ceres: 35095.	267152_at	0.8
unknown protein	267163_at	0.8

unknown protein ; supported by full-length cDNA: Ceres: 16625.	267060_at	0.8
unknown protein	267071_at	0.8
hypothetical protein predicted by genscan	267031 at	0.8
unknown protein	267017 at	0.8
F-box protein LKP2/ADO2, AtFBX2c identical to Adagio 2 GI:13487070 from [Arabidopsis thaliana]	266935 at	0.8
unknown protein ;supported by full-length cDNA: Ceres:35872.	266806 at	0.8
unknown protein	266818 at	0.8
putative cytochrome P450	266778 at	0.8
predicted by genscan	266796 at	0.8
copia-like retroelement pol polyprotein ; supported by cDNA: gi_15028176_gb_AY045911.1_	266698_at	0.8
uptative N-acetyl-gamma-glutamyl-phosphate reductase; supported by cDNA; gj_16604367, gb_AY058082.1_	266704_at	0.8
putative reactive gamma-gutatiny-prospirate reactives, supported by Colver, g_10004307_g0_n1000002.1_ unknown protein ;supported by full-length CDNA: Ceres:13821.	266635 at	0.8
unknown protein "supported by full-length converties. 1902.1.	-	0.8
	266523_at	0.8
putative phospholipid cytidylyltransferase	266399_at	
unknown protein ; supported by full-length cDNA: Ceres: 948.	266228_at	0.8
putative RING zinc finger ankyrin protein ; supported by cDNA: gi_13926221_gb_AF370581.1_AF370581	266229_at	0.8
putative glutathione S-transferase ; supported by cDNA: gi_15450462 gb_AY052332.1_	266181_at	0.8
putative protein phosphatase 2C ; supported by cDNA: gi_14517519_gb_AY039595.1_	265886_at	0.8
CDC27/NUC2-like protein TPR-repeat protein	265585_at	0.8
hypothetical protein predicted by genscan; supported by cDNA; gi_15292678_gb_AY050773.1_	265512_at	0.8
unknown protein ; supported by full-length cDNA: Ceres: 122665.	265457_at	0.8
unknown protein predicted by genscan; supported by cDNA: gi_16323050_gb_AY057629.1_	265291_at	0.8
putative spermidine synthase	265172_at	0.8
unknown protein ; supported by cDNA: gi_15912334_gb_AY056445.1_	265150_at	0.8
hypothetical protein similar to RING-H2 finger protein RHC1a GB:AAC69854 GI:3790583 from [Arabidopsis thaliana]; supported by cDNA: gi_	265077_at	0.8
unknown protein	265098_at	0.8
unknown protein ; supported by cDNA: gi_1669598_dbj_D88746.1_D88746	265059_at	0.8
RNA binding protein, putative similar to RNA binding protein(RZ-1) GI:1435061 from [Nicotiana sylvestris]; supported by full-length cDNA: Cer	264921_at	0.8
putative presenilin similar to presenilin GB:AAD23630;supported by full-length cDNA: Ceres:43026.	264807_at	0.8
unknown protein location of EST emb F15151	264722_at	0.8
hypothetical protein contains similarity to arginine/serine-rich protein GI:6601502 from [Arabidopsis thaliana]	264715_at	0.8
unknown protein EST gb R64758 comes from this gene; supported by cDNA: gi_15450400_gb_AY052301.1_	264676_at	0.8
uracil phosphoribosyltransferase, putative similar to uracil phosphoribosyltransferase 1 GB:AAD28199 GI:4704662 from [Arabidopsis thaliana	264561_at	0.8
unknown protein similar to hypothetical protein HYP1 gb Z97338 from A. thaliana	264389_at	0.8
putative topoisomerase strong similarity to GB:CAA72903 from [Arabidopsis thaliana]; supported by cDNA: gi_14334597_gb_AY034972.1_	264206_at	0.8
unknown protein ; supported by cDNA: gi_15810005_gb_AY054271.1_	264166_at	0.8
hypothetical protein predicted by genemark.hmm; supported by cDNA: Ceres: 11408 (cDNA not full-length)	264141_at	0.8
putative beta-galactosidase	264078_at	0.8
hypothetical protein predicted by genefinder	263938_at	0.8
hypothetical protein ;supported by full-length cDNA: Ceres:123727.	263946_at	0.8
putative auxin-responsive protein ; supported by cDNA: gi_15292854_gb_AY050861.1_	263786_at	0.8
putative plasma membrane proton ATPase	263791_at	0.8
putative aspartate kinase-homoserine dehydrogenase almost identical to gb/X71364 gene for aspartate kinase homoserine dehydrogenase fr	263696 at	0.8
putative casein kinase I similar to GB:CAA55395	263657_at	0.8
putative RNA-binding protein ; supported by full-length cDNA: Ceres:803.	263356_at	0.8
unknown protein ; supported by cDNA: gi_15027886_gb_AY045800.1_	263331 at	0.8
Ca2+-dependent lipid-binding protein, putative similar to Ca2+-dependent lipid-binding protein (CLB1) GI:2789434 from (Lycopersicon escule	263205 at	0.8
MAP kinase (ATMPK7) identical to GB:Q39027; MAP-mitogen activated protein kinase; supported by cDNA: gi 457405 dbj D21843.1 ATH/	263065 at	0.8
unknown protein ;supported by full-length cDNA: Ceres:13758.	262955 at	0.8
ATP-dependent Clp protease proteolytic subunit (ClpP6) identical to ATP-dependent Clp protease proteolytic subunit GI:2827888 from [Arabic		0.8
putative clathrin-coat assembly protein similar to gb/L26291 clathrin-associated protein unc-101 from Caenorhabditis elegans and is a membe	262787 at	0.8
hypothetical protein	262741 at	0.8
unknown protein ESTs gb T04357 and gb AA595092 come from this gene; supported by full-length cDNA: Ceres: 114103.	262710 at	0.8
unknown protein	262673 at	0.8
unknown protein similar to elongation factor G SP:P34811 [Glycine max (Soybean)]; supported by cDNA: gi_14532623_gb_AY039936.1_	262645_at	0.8
initiation factor 5A-4 identical to initiation factor 5A-4 GB:AAD39281 GI:5080771 from (Arabidopsis thaliana); supported by cDNA: gi_1240778	262615 at	0.8
hypothetical protein Strong similarity to gb X95263 Periodic tryptophan protein 2 gene (PWP2) from Homo sapiens and contains 6 WD40, G-I	262584_at	0.8
unknown protein Similar to gb AJ005073 Alix (ALG-2-interacting protein X) from Mus musculus. ESTs gb R90133, gb Z17944 and gb AA6054		0.8
NAM(no apical meristem) protein, putative similar to NAM protein GI:6066595 from (Petunia hybrida); supported by cDNA: gi 13605664 gb	262514 at	0.8
unknown protein Contains PF[00646 F-box domain. ESTs gb]Z37267, gb]R90412, gb]Z37268 and gb]T88189 come from this gene; supported		0.8
	262430_s_at	0.8
putative U2 snRNP auxiliary factor Strong similarity to gb/Y18349 U2 snRNP auxiliary factor, small subunit from Oryza sativa. ESTs gb/AA58	262295 at	0.8
Niemann-Pick C disease protein-like protein similar to Niemann-Pick C disease protein GB:AAB63982 GI:2276463 from [Homo sapiens]	262264 at	0.8
deaminase, putative similar to cytidine/deoxycytidylate deaminase family protein GB:AAF73539 GI:8163170 from [Chlamydia muridarum]	262274_at	0.8
unknown protein ; supported by cDNA: gi 15294195 gb AF410289.1 AF410289	262175 at	0.8
hypothetical protein contains similarity to far-red impaired response protein GI:5764395 from [Arabidopsis thaliana]	262150_at	0.8
hypothetical protein predicted by genscan+; supported by cDNA: (i) 6520211 (db) AB028226 (AB028226)	262078 at	0.8
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:3454.	262095 at	0.8
unknown protein	262035_at	0.8
proteasome regulatory subunit, putative similar to 26S proteasome regulatory complex subunit p30 GB:AAF08395 GI:6434966 from [Drosop	261955_at	0.8
proteisone regulatory subulat, putative similar to 200 proteasone regulatory complex subulat pool 22.44 00000 G.0404000 nom [Diosop unknown protein]	261885 at	0.8
CR4-associated factor, putative\0CCR4-associated factor, putative similar to CCR4-ASSOCIATED FACTOR 1 GB:Q60809 from [Mus musc		0.8
unknown protein contains similarity to autocrine motility factor receptor GI:5931955 from [Homo sapiens]	261904 at	0.8
unknown protein identical to unknown protein GB:AAC32929 GI:3395758 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:12	261745_at	0.8
unknown protein isupported by full-length cDNA: Ceres:33310.	261677_at	0.8
hypothetical protein contains similarity to ribulose-1,5 bisphosphate carboxylase GB:L34291 GI:508550 from [Pisum sativum]	261654_at	0.8
unknown protein ; supported by cDNA: gi 12083293 gb AF332443.1 AF332443	261626 at	0.8
RIBOSOMAL PROTEIN, supported by cDNA. gr_1203293_g0_AF332443.1_AF332443 RIBOSOMAL PROTEIN, putative similar to 30S RIBOSOMAL PROTEIN S1 GB:P46228 from [Synechococcus sp.]; supported by cDNA: gi 1	261626_at 261522 at	0.8
Expressed protein ; supported by cDNA: gi_13877958_gb_AF370242.1_AF370242	261322_at 261388 at	0.8
hypothetical protein contains similarity to peroxisome membrane protein PEX2 GI:2623264 from [Mus musculus]; supported by full-length cDN	261366_at	0.8
proton pump interactor, putative similar to GB:CAB43882 from [Arabidopsis thaliana]	261365_at	0.8
unknown protein unknown protein supported by full length cDNA: Ceres 727	261366_at	0.8 0.8
unknown protein ;supported by full-length cDNA: Ceres:727.	261336_at	0.8

unknown protein ; supported by cDNA: gi_14596146_gb_AY042861.1_	261337_at 0	0.8
dihydroxyacetone kinase, putative similar to GB:U09771 from [Citrobacter freundii]	261294_at (	0.8
hypothetical protein predicted by genemark.hmm	261301_at (	0.8
unknown protein ; supported by cDNA: gi_13605832_gb_AF367315.1_AF367315		0.8
		0.8
TATA binding protein-associated factor, putative similar to GB:CAA74021 from [Arabidopsis thaliana]; supported by cDNA: gi_15293056_gb_		0.8
disease resistance protein, putative similar to GB:AAC15780 from [Lycopersicon pimpinellifolium] (Cell 84 (3), 451-459 (1996))	—	0.8
developmentally regulated GTP-binding protein identical to GB:AAB67830 from (Arabidopsis thaliana) (Plant Mol. Biol. 39 (1), 75-82 (1999));		0.8
glyoxalase II isozyme, putative similar to glyoxalase II isozyme GB:AAC49865 GI:2570338 from [Arabidopsis thaliana]; supported by full-lengt		0.8
scarecrow-like 1 identical to scarecrow-like 1 GB:AAF21043 GI:6644390 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:10!		0.8
19S proteosome subunit 9, putative similar to 19S proteosome subunit 9 GB:AAC34120 GI:3450889 from [Arabidopsis thaliana];supported by		0.8
unknown protein ; supported by cDNA: gi_16604612_gb_AY059751.1_	_	0.8
myb-related DNA-binding protein, putative similar to GB:U67132 from [Petroselinum crispum] (Plant J. 11 (5), 1079-1093 (1997))	-	0.8
unknown protein ; supported by cDNA: gi_15810124_gb_AY056127.1_		0.8
hypothetical protein predicted by genemark.hmm		0.8
unknown protein ; supported by cDNA: gi_13605638_gb_AF361800.1_AF361800	_	0.8
RNA-binding protein, putative similar to GB:AAF29078 from [Homo sapiens];supported by full-length cDNA: Ceres:10976.	—	0.8
hypothetical protein ; supported by cDNA: gi_15292844_gb_AY050856.1_		0.8
phosphatidylinositol-4-phosphate 5-kinase isolog	_	0.8
putative alpha-amylase similar to alpha-amylase GB:AAA91884 [Solanum tuberosum]; supported by cDNA: gi_15215737_gb_AY050398.1_		0.8
unknown protein	_	0.8
unknown protein similar to hypothetical proteins GB:AAD39276 [Arabidopsis thaliana], GB:CAB53491 [Oryza sativa];supported by full-length	_	0.8
putative lipoxygenase similar to 13-lipoxygenase GB:CAA65269 [Solanum tuberosum]	—	0.8 0.8
putative G protein-coupled receptor similar to G protein-coupled receptor 69A GB:NP_006046 from [Homo sapiens] unknown protein ;supported by full-length cDNA: Ceres:269548.		0.8
Initiowin protein supported by directing to the Cores.20046. hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:38940.		0.8
nyponetical protein predicted by geneminaer, sopported by numeright conc. Ceres.Josetto. DNA-directed RNA polymerase subunit, putative similar to GI:67:23961 from [Schizosaccharomyces pombe]	_	0.8
putative nuclear matrix constituent protein 1 (NMCP1) similar to nuclear matrix constituent protein 1 (NMCP1) GB:BAA20407 [Daucus carota]	—	0.8
putative notate in mark constance in profile: Pf01388 ARID DNA binding domain		0.8
hypothetical protein ; supported by full-length cDNA: Ceres:147838.	—	0.8
putative RNA-binding protein contains Pfam profile: PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain); supported by cDN/		0.8
putative P-type transporting ATPase similar to ATPase II GB:AAD34706 [Homo sapiens]		0.8
putative ranslation initiation factor IF-2 similar to translation initiation factor IF-2 GB:P39730 [Saccharomyces cerevisiae]	_	0.8
putative phorbol ester / diacylgiverol binding protein Pfam HMM hit: Phorbol esters / diacylgiverol binding domain		0.8
protein kinase, putative similar to protein kinase GI:2852447 from (Arabidopsis thaliana)	—	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 20443.		0.8
unknown protein ; supported by cDNA: gi 14423507 gb AF386991.1 AF386991		0.8
protein serine/threonine kinase, putative similar to protein serine/threonine kinase GI:7248457 from [Lophopyrum elongatum]; supported by c	—	0.8
GTP-binding protein(RAB11D), putative similar to RAB11D GI:1370148 from [Lotus japonicus]; supported by cDNA: gi_12083263_gb_AF332		0.8
protein phosphatase 2A regulatory subunit, putative similar to protein phosphatase 2A regulatory subunit GI:683502 from [Arabidopsis thaliar	_	0.8
unknown protein ;supported by full-length cDNA: Ceres:7124.	259306_at (	0.8
Expressed protein ; supported by cDNA: gi_15081629_gb_AY048207.1_	259310_s_at (	0.8
26S proteasome AAA-ATPase subunit RPT5a identical to GB:AAF22525 from [Arabidopsis thaliana]; supported by cDNA: gi_5669046_gb_Af	259114_at (	0.8
unknown protein similar to unknown protein GB:BAA24863 [Homo sapiens], unknown protein GB:BAA20831 [Homo sapiens], unknown prote	259118_at (	0.8
unknown protein similar to hypothetical protein GB:BAA29429 [Pyrococcus horikoshii];supported by full-length cDNA: Ceres:100279.	259053 at 0	0.8
hypothetical protein similar to Ku70-binding protein GB:AAD31085 [Homo sapiens]; supported by cDNA: gi 13877934 gb AF370230.1 AF37		0.0
		0.8
hypothetical protein	259056_at 0	
putative GTP-binding protein similar to GTP-binding protein GB:BAA02108 [Pisum sativum], HMM hit: Ras family (contains ATP/GTP binding	259056_at ( 259059_at ( 259061_at (	0.8 0.8 0.8
putative GTP-binding protein similar to GTP-binding protein GB:BAA02108 [Pisum sativum], HMM hit: Ras family (contains ATP/GTP binding unknown protein predicted by genscan; est match; supported by full-length cDNA: Ceres:3820.	259056_at () 259059_at () 259061_at () 259038_at ()	0.8 0.8 0.8 0.8
putative GTP-binding protein similar to GTP-binding protein GB:BAA02108 [Pisum sativum], HMM hit: Ras family (contains ATP/GTP binding unknown protein predicted by genscan; est match; supported by full-length cDNA: Ceres:3820. unknown protein similar to unknown proteins GB:AAD24625 [Arabidopsis thaliana], GB:AAC73026 [Arabidopsis thaliana]	259056_at ( 259059_at ( 259061_at ( 259038_at ( 258933_at (	0.8 0.8 0.8 0.8 0.8
putative GTP-binding protein similar to GTP-binding protein GB:BAA02108 [Pisum sativum], HMM hit: Ras family (contains ATP/GTP binding unknown protein predicted by genscan; est match; supported by full-length cDNA: Ceres:3820. unknown protein similar to unknown proteins GB:AAD24625 [Arabidopsis thaliana], GB:AAC73026 [Arabidopsis thaliana] hypothetical protein similar to symbiosis related proteins: GB:AAB53650 [Laccaria bicolor], GB:P87068 [Laccaria bicolor]; supported by full-ler	259056_at () 259059_at () 259061_at () 259038_at () 258933_at () 258880_at ()	0.8 0.8 0.8 0.8 0.8 0.8
putative GTP-binding protein similar to GTP-binding protein GB:BAA02108 [Pisum sativum], HMM hit: Ras family (contains ATP/GTP binding unknown protein predicted by genscan; est match;supported by full-length cDNA: Ceres:3820. unknown protein similar to unknown proteins GB:AAD24625 [Arabidopsis thaliana], GB:AAC73026 [Arabidopsis thaliana] hypothetical protein similar to symbiosis related proteins: GB:AAB53650 [Laccaria bicolor], GB:P87068 [Laccaria bicolor];supported by full-length putative helicase similar to C-terminal half of transcription-repair coupling factor (TRCF) GB:Q55750 [Synechocystis PCC6803]; contains Pfan	259056_at ( 259059_at ( 259061_at ( 259038_at ( 258933_at ( 258880_at ( 258861_at (	0.8 0.8 0.8 0.8 0.8 0.8 0.8
putative GTP-binding protein similar to GTP-binding protein GB:BAA02108 [Pisum sativum], HMM hit: Ras family (contains ATP/GTP binding unknown protein predicted by genscan; est match;supported by full-length cDNA: Ceres:3820. unknown protein similar to unknown proteins GB:AA024625 [Arabidopsis Haliana], GB:AAC73026 [Arabidopsis thaliana] hypothetical protein similar to symbiosis related proteins: GB:AAB53650 [Laccaria bicolor], GB:P87068 [Laccaria bicolor];supported by full-ler putative helicase similar to C-terminal half of transcription-repair coupling factor (TRCF) GB:Q55750 [Synechocystis PCC6803]; contains Pfar putative 26S proteosome regulatory subunit	259056_at ( 259059_at ( 259061_at ( 258038_at ( 258933_at ( 258880_at ( 258861_at ( 258871_at (	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
putative GTP-binding protein similar to GTP-binding protein GB:BAA02108 [Pisum sativum], HMM hit: Ras family (contains ATP/GTP binding unknown protein predicted by genscan; est match;supported by full-length cDNA: Ceres:3820. unknown protein similar to unknown proteins GB:AAD24625 [Arabidopsis thaliana], GB:AAC73026 [Arabidopsis thaliana] hypothetical protein similar to symbiosis related proteins: GB:AAB53650 [Laccaria bicolor], GB:P87068 [Laccaria bicolor];supported by full-ler putative helicase similar to C-terminal half of transcription-repair coupling factor (TRCF) GB:Q55750 [Synechocystis PCC6803]; contains Pfan putative 26S proteosome regulatory subunit unknown protein ;supported by full-length cDNA: Ceres:320.	259056_at ( 259059_at ( 259061_at ( 258038_at ( 258833_at ( 258880_at ( 258861_at ( 258871_at ( 258771_at (	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
putative GTP-binding protein similar to GTP-binding protein GB:BAA02108 [Pisum sativum], HMM hit: Ras family (contains ATP/GTP binding unknown protein predicted by genscan; est match;supported by full-length cDNA: Ceres:3820. unknown protein similar to unknown proteins GB:AAD24625 [Arabidopsis thaliana], GB:AAC73026 [Arabidopsis thaliana] hypothetical protein similar to symbiosis related proteins: GB:AAB53650 [Laccaria bicolor], GB:P87068 [Laccaria bicolor];supported by full-ler putative helicase similar to C-terminal half of transcription-repair coupling factor (TRCF) GB:Q55750 [Synechocystis PCC6803]; contains Pfan putative 26S proteosome regulatory subunit unknown protein ;supported by full-length cDNA: Ceres:320. putative ubiquitin carboxyl-terminal hydrolase similar to ubiquitin carboxyl-terminal hydrolase GB:AAF01440 [Schizosaccharomyces pombe]	259056_at ( 259059_at ( 259061_at ( 259038_at ( 258933_at ( 258830_at ( 258861_at ( 258871_at ( 258771_at ( 258770_at (	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
putative GTP-binding protein similar to GTP-binding protein GB:BAA02108 [Pisum sativum], HMM hit: Ras family (contains ATP/GTP binding unknown protein predicted by genscan; est match;supported by full-length cDNA: Ceres:3820. unknown protein similar to unknown proteins GB:AA024625 [Arabidopsis thaliana], GB:AAC73026 [Arabidopsis thaliana] hypothetical protein similar to symbiosis related proteins: GB:AAB53650 [Laccaria bicolor];supported by full-length putative helicase similar to C-terminal half of transcription-repair coupling factor (TRCF) GB:Q55750 [Synechocystis PCC6803]; contains Pfan putative 26S proteosome regulatory subunit unknown protein ;supported by full-length cDNA: Ceres:320. putative ubiquitin carboxyl-terminal hydrolase similar to ubiquitin carboxyl-terminal hydrolase GB:AAF01440 [Schizosaccharomyces pombe] unknown protein ; supported by full-length cDNA: Ceres: 28024.	259056_at ( 259059_at ( 259061_at ( 259038_at ( 2588380_at ( 258880_at ( 258871_at ( 258871_at ( 258771_at ( 258780_at ( 258780_at ( 258780_at (	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
putative GTP-binding protein similar to GTP-binding protein GB:BAA02108 [Pisum sativum], HMM hit: Ras family (contains ATP/GTP binding unknown protein predicted by genscan; est match;supported by full-length cDNA: Ceres:3820. unknown protein similar to unknown proteins GB:AA024625 [Arabidopsis thaliana], GB:AAC73026 [Arabidopsis thaliana] hypothetical protein similar to symbiosis related proteins: GB:AAB53650 [Laccaria bicolor], GB:P87068 [Laccaria bicolor];supported by full-leng putative helicase similar to C-terminal half of transcription-repair coupling factor (TRCF) GB:Q55750 [Synechocystis PCC6803]; contains Pfan putative Aelicase similar to C-terminal half of transcription-repair coupling factor (TRCF) GB:Q55750 [Synechocystis PCC6803]; contains Pfan putative 26S proteosome regulatory subunit unknown protein ;supported by full-length cDNA: Ceres:320. putative ubiquitin carboxyl-terminal hydrolase similar to ubiquitin carboxyl-terminal hydrolase GB:AAF01440 [Schizosaccharomyces pombe] unknown protein ;supported by full-length cDNA: Ceres: 28024. unknown protein similar to a region of DNAJ domain-containing protein MCJ GB:AAD38506; supported by full-length cDNA: Ceres: 5219.	259056_at ( 259059_at ( 259061_at ( 259038_at ( 258933_at ( 258830_at ( 258871_at ( 258771_at ( 25971_at ( 25	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
putative GTP-binding protein similar to GTP-binding protein GB:BAA02108 [Pisum sativum], HMM hit: Ras family (contains ATP/GTP binding unknown protein predicted by genscan; est match;supported by full-length cDNA: Ceres:3820. unknown protein similar to unknown proteins GB:AA024025 [Arabidopsis thaliana], GB:AAC73026 [Arabidopsis thaliana] hypothetical protein similar to symbiosis related proteins: GB:AAB53650 [Laccaria bicolor], GB:P87068 [Laccaria bicolor];supported by full-ler putative helicase similar to C-terminal half of transcription-repair coupling factor (TRCF) GB:Q55750 [Synechocystis PCC6803]; contains Pfan putative helicase similar to C-terminal half of transcription-repair coupling factor (TRCF) GB:Q55750 [Synechocystis PCC6803]; contains Pfan putative biquitin carboxyl-terminal hydrolase similar to ubiquitin carboxyl-terminal hydrolase GB:AAF01440 [Schizosaccharomyces pombe] unknown protein ; supported by full-length cDNA: Ceres: 28024. unknown protein ; supported by full-length cDNA: Ceres: 28024. unknown protein ; supported by cDNA: domain-containing protein MCJ GB:AAD38506; supported by full-length cDNA: Ceres: 5219. unknown protein ; supported by cDNA: gj_15983478_gb_AF424614.1_AF424614	259056_at ( 259056_at ( 259061_at ( 259038_at ( 258933_at ( 258830_at ( 258861_at ( 258871_at ( 258871_at ( 258771_at ( 258774_at ( 258747_at ( 258747_at ( 258747_at (	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
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putative GTP-binding protein similar to GTP-binding protein GB:BAA02108 [Pisum sativum], HMM hit: Ras family (contains ATP/GTP binding unknown protein similar to symbiosis related proteins: GB:AAB23650 [Laccaria bicolor], GB:P87068 [Laccaria bicolor]; supported by full-leng putative helicase similar to C-terminal half of transcription-repair coupling factor (TRCF) GB:Q55750 [Synechocystis PCC6803]; contains Pfar putative 265 proteosome regulatory subunit unknown protein ; supported by full-length cDNA: Ceres: 320. putative ubiquitin carboxyl-terminal hydrolases similar to a region of DNA1 domain-containing protein MCJ GB:AAD38506; supported by full-length cDNA: Ceres: 28024. unknown protein ; supported by GNA: g_15983478, gb_AF242614 (LacCafia) (LacCaf	259056_at (259056_at (259056_at (2590659_at (2590659_at (259061_at (2558731_at (2558771_at (2558771_at (2558747_at (2558747_at (2558747_at (2558747_at (2558747_at (2558747_at (2558745_at (255824_at (255824_at (2557863_at (255785_at (2557863_at (255785_at (2557878_at (2557878_at (2557878_at (2557878_at (2557878_at (2557878_at (2557149_at (2557149_at (2557149_at (2557149_at (2557149_at (255611_at (2556851_at (2556851_at (2556851_at (255661_at (255679_at (255650_at (255661_at (255610_at (255610_at (255661_at (255661_at (255610_at (255601_at (255610_at (255610_at (255610_at (255610_at (255610_at (255610_at (255610_at (255610_at (2556100_at (2556000_at (2556100_at (2556000_at (2556100_at (255600000000000000000000000000000000000	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8

AT-hook DNA-binding protein (AHP1) almost identical to GB:CAA10857; supported by cDNA: gi_14326503_gb_AF385705.1_AF385705	255792 at	0.8
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unknown protein ;supported by full-length cDNA: Ceres:121070.	255766_at	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 36326.	255670_at	0.8
probable plasma membrane intrinsic protein 1c; supported by cDNA: gi_2373400_dbj_D85192.1_D85192	255674_at	0.8
putative protein	255651 at	0.8
predicted protein of unknown function	255544_at	0.8
	255556 at	
	_	0.8
hypothetical protein similar to A. thaliana hypothetical protein from chromosome III, GenBank accession number 3068704	255492_at	0.8
putative WD-repeat protein similar to L. erythrorhizon LEC14B, GenBank accession number Q40153	255468 at	0.8
	255428 at	0.8
	_	
hypothetical protein	255171_at	0.8
putative protein oxysterol-binding protein - Oryctolagus cuniculus (domestic rabbit),PIR2:A34404	255151_at	0.8
inositol 1,3,4-trisphosphate 5/6-kinase-like protein inositol 1,3,4-trisphosphate 5/6-kinase (EC 2.7) - Arabidopsis thaliana, PIR2:JC5401; si	255132 at	0.8
hypothetical protein supported by full-length cDNA: Ceres:41730.	254721 at	0.8
	_	
hypothetical protein	254727_at	0.8
putative protein WERBP-1 - Nicotiana tabacum, EMBL:AB017693;supported by full-length cDNA: Ceres:38327.	254682_at	0.8
putative protein	254594 at	0.8
putative protein heat shock protein dnaJ homolog, yeast, PIR2:A33618	254458 at	0.8
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putative protein ; supported by cDNA: gi_15028268_gb_AY046049.1_	254376_at	0.8
symbiosis-related like protein symbiosis-related protein, Laccaria bicolor,PATX:G2072023;supported by full-length cDNA: Ceres:14759.	254346_at	0.8
hypothetical protein ;supported by full-length cDNA: Ceres:29391.	254299 at	0.8
putative protein chS-Rex-b - Gallus gallus (chicken),gb:L10333;supported by full-length cDNA: Ceres:39185.	254227 at	0.8
	_	
tyrosine transaminase like protein tyrosine transaminase (EC 2.6.1.5) - rat, EMBL:X02741; supported by cDNA: gi_15076852_gb_AF268090	254232_at	0.8
putative protein similarity Human mRNA for KIAA0156 gen - Homo sapiens, PID:d1010577	254147_at	0.8
protein kinase (AFC2);supported by cDNA: gi_601788_gb_U16177.1_ATU16177	254131 at	0.8
putative protein apoptosis gene MA3, Suberites domuncula, Y15421; supported by cDNA: gi_17063162_gb_AY062102.1_	254089 at	0.8
	_	
putative protein cell death suppressor protein lls1, Zea mays, T04133; supported by cDNA: gi_15810258_gb_AY056168.1_	254021_at	0.8
P-glycoprotein-2 (pgp2)	254034_at	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 9546.	254041 at	0.8
putative protein ;supported by full-length cDNA: Ceres:15410.	253992 at	0.8
putative aspartate-tRNA ligase aspartate-tRNA ligase (EC 6.1.1.12) -Methanobacterium thermoautotrophicum, GB:AE000809	253935_at	0.8
aspartatetRNA ligase - like protein aspartyl tRNA synthetase, Drosophila melanogaster, EMBL:AF113612	253561_at	0.8
L-ascorbate peroxidase - like protein various L-ascorbate peroxidases	253477 at	0.8
F-box protein family, AtFBL15 contains similarity to F-box protein FBL2 GI:6063090 from [Homo sapiens]	253369 at	0.8
	_	
	253335_at	0.8
putative protein	253349_at	0.8
putative protein TEB4 protein, Homo sapiens, PID:G2331104	253267 at	0.8
putative protein hypothetical protein slr2121, Synechocystis sp., PIR2:S75497; supported by full-length cDNA: Ceres:8686.	253273 at	0.8
homeodomain - like protein several homeodomain transcription factors; supported by cDNA: gi_15081750_gb_AY048268.1_	253131_at	0.8
putative protein predicted protein A_TM017A05.4 Arabidopsis thalianaBAC TM017A05, PID:g2435512	253109_at	0.8
putative protein F35D11.3, Caenorhabditis elegans, PATX:G868225	253081 at	0.8
putative protein gene T10 protein - mouse, PIR2:S37488; supported by cDNA: gi 15451201 gb AY054681.1	252981 at	0.8
	_	
putative protein Niemann-Pick C disease protein - Homo sapiens, PID:g2276463	252985_at	0.8
putative protein;supported by cDNA: gi_13878068_gb_AF370297.1_AF370297	252974_at	0.8
2-dehydro-3-deoxyphosphoheptonate aldolase; supported by cDNA: gi 166687 gb M74819.1 ATHDHS1	252831 at	0.8
amine oxidase -like protein amine oxidase, Canavalia lineata, EMBL:AF172681	252698 at	0.8
	252625 at	0.8
	_	
	252527_at	0.8
GTPase activating -like protein GTPase activating protein gyp7, Yarrowia lipolytica, EMBL:YLGYP7	252310_at	0.8
putative protein putative protein - Drosophila melanogaster, EMBL:AF132172	252239 at	0.8
protein kinase SPK-2 ;supported by full-length cDNA: Ceres:3988.	252166 at	0.8
putative protein	252185 at	0.8
	_	
	252099_at	0.8
putative protein NADH dehydrogenase subunit 1, Lymantria dispar albescens, EMBL:AF075286;supported by full-length cDNA: Ceres:36750	252091_at	0.8
mucin-like protein hemomucin, Drosophila melanogaster, EMBL:DM42014;supported by full-length cDNA: Ceres:38547.	252092 at	0.8
	252069_s_at	0.8
putative protein putative protein risk and the second state and the		
	252042_at	0.8
putative protein various predicted proteins, Arabidopsis thaliana	252018_at	0.8
TATA box binding protein (TBP) associated factor (TAF) -like protein TAF-172, Homo sapiens, EMBL:AF038362	251876_at	0.8
putative protein	251892_at	0.8
putative protein	251893_at	0.8
Expressed protein ; supported by cDNA: gi_15451129_gb_AY054645.1_	251848_at	0.8
	251786_at	0.8
transcriptional coactivator - like protein hMBF1alpha, Homo sapiens, EMBL:AB002282;supported by full-length cDNA: Ceres:112835.	251551 at	0.8
putative protein phytochrome-associated protein 3 - Arabidopsis thaliana, EMBL:AF088280		0.8
receptor-like protein kinase receptor-like protein kinase (RKS2) - Arabidopsis thaliana, EMBL:AF084036	251500_at	0.8
putative protein chloroplast Cpn21 protein - Arabidopsis thaliana, EMBL:ATH010818;supported by full-length cDNA: Ceres:35721.	251425_at	0.8
CaLB protein	251351 s at	0.8
putative protein several hypothetical proteins - Arabidopsis thaliana; supported by cDNA: gi 16648920 gb AY059830.1	251314_at	0.8
putative protein PrMC3, Pinus radiata, EMBL:AF110333	251200_at	0.8
hypothetical protein ; supported by full-length cDNA: Ceres: 4524.	251151_at	0.8
putative protein SqdX protein, Synechococcus PCC7942, EMBL:SP45308; supported by cDNA: gi_15028316_gb_AY045961.1_	251143_at	0.8
DP-2 transcription factor - like transcription factor DP-2, Homo sapiens, PIR:A57381	251052 at	0.8
putative protein thyroid receptor interacting protein 12, Homo sapiens, EMBL:D28476	250988 at	0.8
	_	
unknown protein ;supported by full-length cDNA: Ceres:150381.	250792_at	0.8
putative protein heparanase precursor, Homo sapiens, EMBL:AF155510	250604_at	0.8
WD-repeat protein-like ; supported by cDNA: gi_15450909_gb_AY054535.1_	250539_at	0.8
putative protein predicted proteins, Arabidopsis thaliana	250486 at	0.8
embryogenic callus protein - like embryogenic callus protein 181, Daucus carota, PIR:T14282;supported by full-length cDNA: Ceres:266771.	250494_at	0.8
	_	
	250470_at	0.8
putative protein predicted proteins, Homo sapiens, Drosophila melanogaster, Caenorhabditis elegans	250377_at	0.8
	250273 at	0.8
acetolactate synthase-like protein	250111_at	0.8
aotoratia ognatao mile proton	200111_at	0.0

2-hydroxyphytanoyl-CoA lyase-like protein	250094_at	0.8
unknown protein ; supported by cDNA: gi 14334891 gb AY035119.1	250073 at	0.8
Cu/Zn superoxide dismutase-like protein	250016 at	0.8
putative protein contains similarity to transcription regulator; supported by cDNA: gi_13877644_gb_AF370523.1_AF370523	250035_at	0.8
putative protein nuclear FMRP interacting protein 1 NUFIP1, Homo sapiens, EMBL:AF159548	250009_at	0.8
hypothetical protein	249990_at	0.8
putative protein predicted proteins, Arabidopsis thaliana	249974_at	0.8
putative protein predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_15983814_gb_AY056813.1_	249961_at	0.8
histone deacetylase-like protein non-consensus AT donor splice site at exon 3, AC acceptor splice site at exon 4	249901_at	0.8
Expressed protein ; supported by cDNA: gi_15529239_gb_AY052244.1_	249839_at	0.8
putative protein similar to unknown protein (gb AAD12714.1)	249845_at	0.8
cation-transporting ATPase	249846_at	0.8
putative protein contains similarity to general transcription factor IIIC, polypeptide 5	249735_at	0.8
putative protein contains similarity to ribosomal protein 30S subunit; supported by cDNA: gi_13877770_gb_AF370148.1_AF370148	249742_at	0.8
putative protein DNA-binding protein CCA1, Arabidopsis thaliana, PIR:T02684	249606_at	0.8
calmodulin 1 (CAM1) ; supported by cDNA: gi_15081766_gb_AY048276.1_	249582_at	0.8
cysteine-tRNA ligase -like protein cysteine-tRNA ligase, Arabidopsis thaliana, PIR:T47747	249537_at	0.8
putative protein KIAA0409 protein, Homo sapiens, EMBL:AB007869	249360_at	0.8
homeotic protein BEL1 homolog; supported by cDNA: gi_15146192_gb_AY049237.1_	249309_at	0.8
putative protein similar to unknown protein (dbj BAA84809.1);supported by full-length cDNA: Ceres:27758.	249229_at	0.8
maize crp1 protein-like	249247_at	0.8
COP8 (constitutive photomorphogenic) homolog ;supported by full-length cDNA: Ceres:31282.	249175_at	0.8
putative protein contains similarity to chloroplast nucleoid DNA-binding protein	249130_at	0.8
protein transport protein SEC23 ; supported by cDNA: gi_15810472_gb_AY056275.1_	249106_at	0.8
putative protein contains similarity to unknown protein (gb AAD17413.1);supported by full-length cDNA: Ceres:27195.	249064_at	0.8
berberine bridge enzyme-like protein	249047_at	0.8
regulatory protein NPR1-like; transcription factor inhibitor I kappa B-like	248981_at	0.8
putative protein similar to unknown protein (pir  T27174); supported by full-length cDNA: Ceres: 15222.	248884_at	0.8
putative protein contains similarity to kinase	248850_at	0.8
putative protein contains similarity to salt-inducible protein	248854_at	0.8
photoreceptor-interacting protein-like	248772_at	0.8
putative protein contains similarity to transcription or splicing factor; supported by cDNA: gi_13877738_gb_AF370132.1_AF370132	248452_at	0.8
unknown protein	248453_at	0.8
receptor protein kinase-like	248454_at	0.8
aldo/keto reductase-like protein	248242_at	0.8
putative protein similar to unknown protein (pir  C71422);supported by full-length cDNA: Ceres:819.	247988_at	0.8
apospory-associated protein C	247929_at	0.8
SNF1 related protein kinase-like protein ; supported by cDNA: gi_14334389_gb_AY034100.1_	247867_at	0.8
putative protein predicted proteins, Drosophila melanogaster and Arabidopsis thaliana	247841_at	0.8
beta-1,3 glucanase - like protein beta-1,3 glucanase, Populus alba x Populus tremula, EMBL:AF230109	247845_at	0.8
putative protein various predicted proteins from different species;supported by full-length cDNA: Ceres:36809.	247787_at	0.8
putative protein	247630_at	0.8
putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:34861.	247496_at	0.8
Mei2-like protein Mei2-like protein, Arabidopsis thaliana, EMBL:D86122; supported by cDNA: gi_2443328_dbj_D86122.1_D86122	247506_at	0.8
cdc2-like protein kinase-like protein supported by full-length cDNA: Ceres: 22817.	247334_at	0.8
beta-ureidopropionase	247275_at	0.8
putative protein similar to unknown protein (ref NP_014115.1);supported by full-length cDNA: Ceres:14033.	247249_at	0.8
putative protein contains similarity to unknown protein (gb AAF44992.1); supported by cDNA: gi_15028246_gb_AY046038.1_	247256_at	0.8
putative protein contains similarity to unknown protein (gb AAF47170.1);supported by full-length cDNA: Ceres:13188.	247209_at	0.8
Expressed protein ; supported by cDNA: gi_15983431_gb_AF424590.1_AF424590	247178_at	0.8
3-hydroxyisobutyryl-coenzyme A hydrolase ; supported by cDNA: gi_8572759_gb_AF276301.1_AF276301	247117_at	0.8
	246809_s_at	0.8
replication factor C - like replication factor C 38K chain, Homo sapiens, PIR:T09573	246738_at	0.8
putative protein YTM1 - Homo sapiens, EMBL:AF242546	246559_at	0.8
ubiquitin-fusion degradation protein-like ubiquitin-fusion degradation protein - Homo sapiens, EMBL:AF043117; supported by cDNA: gi_1521	246541_at	0.8
putative protein	246245_at	0.8
RNA-binding like protein non-consensus TA donor splice site at exon 6; supported by cDNA: gi_15081786_gb_AY048286.1_	246207_at	0.8
step II splicing factor - like protein ; supported by cDNA: gi_15912280_gb_AY056418.1_	246221_at	0.8
ABI3-interacting protein 2 ;supported by full-length cDNA: Ceres:30983.	246189_at 246160 at	0.8
putative protein predicted protein, Oryza sativa; supported by cDNA: gi_15081722_gb_AY048254.1_ subtilisin-like protein subtilisin/kexin isozyme SKI-1 precursor - Rattus norvegicus, EMBL:AF094821	_	0.8
	245960_at	0.8
unknown protein similar to unknown protein GB:AAC36170 GI:3608137 from [Arabidopsis thaliana]; supported by CDNA: gi_11044956, emb	245796_at	0.8
S-ribonuclease binding protein SBP1, putative similar to S-ribonuclease binding protein SBP1 Gi:3760451 from [Petunia hybrida]; supported	245781_at	0.8
aldehyde dehydrogenase, putative similar to aldehyde dehydrogenase GI:2351120 from [Synechococcus PCC7942]; supported by full-length	245742_at	0.8
unknown protein	245687_at	0.8
unknown protein similar to putative Tub family protein GI:3738302 from [Arabidopsis thaliana]	245633_at	0.8
hypothetical protein RNA polymerase II fifth largest subunit like protein	245618_at	0.8
hypothetical protein	245569_at 245502_at	0.8 0.8
hypothetical protein	245430 at	0.8
auxin-responsive protein IAA1 ;supported by full-length cDNA: Ceres:33860.	245450_at 245397 at	0.8
auximesponsive protein raw i, supported by runnengin constructions ceres.socous indole-3 acetate beta-glucosyltransferase like protein ;supported by full-length cDNA; Ceres:35383.	245352 at	0.8
Expressed protein ; supported by cDNA: gi 14334421 gb AY034902.1	245352_at 245280_at	0.8
phytoene dehydrogenase precursor (phytoene desaturase) ; supported by cDNA: gi_14532765 gb_AY040007.1_	245280_at 245284_at	0.8
hypothetical protein ; supported by cDNA: gi_15450995_gb_AY054578.1_	245295 at	0.8
syntaxin ; supported by cDNA: gi 2149379 gb U85036.1 ATU85036	245295_at 245278_at	0.8
	245276_at 245187_s_at	0.8
F12A21.17 similar to signal recognition particle 72AD grj3902124 F12A21.19 unknown protein; similar to ESTs gb/Al996033.1, and dbj/AV563431.1	245187_5_at 245188 at	0.8
	245186_at 245131_s_at	0.8
putative TGACG-sequence-specific bZIP DNA-binding protein	245151_5_at	0.8
ubiquitin-specific protease 5 (UBP5), putative similar to GI:6648604; supported by cDNA: gi_6648603_gb_AF048705.1_AF048705	245092_at 245100 at	0.8
ubiquini specinic protesse 5 (Cbr 5), putative sininar to 5:0040004, supported by CbrAc, g_004000_g0_Al 040705, r_Al 040705 putative cytochrome P450	245075_at	0.8
putative cyclonionie i 430 putative cyclin ;supported by full-length cDNA: Ceres:22595.	245043_at	0.8
		0.0

ribosomal protein L22	244985_at 0.8
hypothetical protein Contains similarity to hypothetical protein gb U95973 from A. thaliana	257422_at 0.8
hypothetical protein predicted by genescan+	258375_at 0.8
unknown protein similar to far-red impaired response protein GB:AAD51282 [Arabidopsis thaliana]; supported by cDNA: gi_13	
putative protein polygalacturonase(EC 3.2.1.15) precursor - Erwinia carotovora,PID:g42330	253326_at 0.8 253037 at 0.8
putative protein other predicted Arabidopsis thaliana proteins amine oxidase, putative similar to amine oxidase GB:AAD49420 GI:5733089 [Canavalia lineata]	262667 at 0.7
proteasome, 30 kda subunit (ec 3.4.99.46) (multicatalytic endopeptidase complex 30 kda subunit). >gp[166830]gb]aaa16326.	
hypothetical protein predicted by genscan+	259884 at 0.7
eukaryotic translation initiation factor 4E, putative similar to SP:023252 from [Arabidopsis thaliana]	259776_s_at 0.7
hypothetical protein predicted by genscan	259295 at 0.7
hypothetical protein ; supported by cDNA: gi_14194138_gb_AF367275.1_AF367275	258553 at 0.7
hypothetical protein predicted by genemark.hmm	258506 at 0.7
unknown protein	255865_at 0.7
putative protein several hypothetical proteins - Arabidopsis thaliana; supported by cDNA: gi_16604614_gb_AY059752.1_	251313_at 0.7
unknown protein	249679_at 0.7
putative protein	245718_at 0.7
Arabidopsis thaliana /REF=U37281 /DEF=actin-2 mRNA, complete cds /LEN=1637 (-5, -M, -3 represent transcript regions 5 p	
putative RING zinc finger protein ; supported by cDNA: gi_16648813_gb_AY058184.1_	267539_at 0.7
unknown protein	267430_at 0.7
beta-ketoacyl-CoA synthase (FIDDLEHEAD) identical to GBAJ010713; contains a chalcone and stilbene synthase active site	
Expressed protein ; supported by full-length cDNA: Ceres: 40603.	267114_at 0.7
unknown protein	267072_at 0.7 266889 at 0.7
hypothetical protein predicted by genscan; supported by cDNA: gi_15146245_gb_AY049264.1_ putative embryo-abundant protein contains a bZIP transcription factor basic domain signature (PDOC00036)	266889_at 0.7 266798 at 0.7
unknown protein	266758 at 0.7
hypothetical protein predicted by genefinder and genscan; supported by cDNA: gi_15724241_gb_AF412061.1_AF412061	266608 at 0.7
putative tubby protein	266515 at 0.7
phosphoprotein phosphatase, type 1 catalytic subunit identical to GB:X64328; supported by cDNA: gi 166571 gb M93408.1	
unknown protein ;supported by full-length cDNA: Ceres:33700.	266259 at 0.7
unknown protein	266193 at 0.7
ATP-dependent RNA helicase identical to GB:CAA09207, contains a DEAD/DEAH box family ATP-dependent helicas signatu	re 266076_at 0.7
phytochrome B Identical to GB:X17342	266065_at 0.7
putative signal recognition particle receptor beta subunit ;supported by full-length cDNA: Ceres:14084.	266073_at 0.7
subtilisin-like serine protease, putative contains similarity to cucumisin-like serine protease GI:3176874 from [Arabidopsis thal	liana] 266022_at 0.7
putative glutamate/ornithine acetyltransferase ;supported by full-length cDNA: Ceres:121873.	265965_at 0.7
putative casein kinase I ;supported by full-length cDNA: Ceres:2312.	265942_at 0.7
unknown protein ;supported by full-length cDNA: Ceres:19157.	265866_at 0.7
unknown protein ;supported by full-length cDNA: Ceres:121540.	265871_at 0.7
putative DnaJ protein	265850_at 0.7
putative stress protein unknown protein predicted by genscan	265761_at 0.7 265691 at 0.7
putative protein kinase contains a protein kinase domain profile (PDOC00100); supported by cDNA: gi 15028152 gb AY046(	
unknown protein similar to ovarian tumor protein; supported by CDNA: gi 16604333 gb AY058065.1	265630 at 0.7
26S proteasome subunit 4 ;supported by full-length cDNA: Ceres:36815.	265595 at 0.7
hypothetical protein predicted by genscan	
ferredoxinnitrite reductase ; supported by cDNA: gi_15010613_gb_AY045608.1_	265475_at 0.7
unknown protein	265330_at 0.7
hypothetical protein predicted by genefinder; supported by full-length cDNA: Ceres: 91902.	265258_at 0.7
putative RNA methyltransferase	265274_at 0.7
putative amine oxidase	265244_at 0.7
unknown protein ; supported by cDNA: gi_15146299_gb_AY049291.1_	265190_at 0.7
similar to flavin-binding monooxygenase-like protein (Z71258); similar to ESTs gb R30018 and gb H36886 similar to flavin-con	-
hypothetical protein ; supported by cDNA: gi_14334789_gb_AY035068.1_ HD-Zip protein, putative similar to HD-Zip protein GI:2145356 from [Arabidopsis thaliana]; supported by cDNA: gi 16974580	265074_at 0.7 qb AY060556.' 265060 at 0.7
putative glucanase	gb_AY060556. 265060_at 0.7 264875 at 0.7
putative glucanase putative glycine-rich, zinc-finger DNA-binding protein genomic copy of EST T76328 cold-shock signature from position 22 to	
unknown protein	264696 at 0.7
hypothetical protein predicted by genscan	264689_at 0.7
putative K+ channel, beta subunit similar to GB:AAA87294;supported by full-length cDNA: Ceres:23300.	264607 at 0.7
putative acetyl-CoA acyltransferase Strong similarity to Cucumis acetyl-CoA acyltransferase (gb D70895);supported by full-ler	ngth cDNA: Cer∉ 264608_at 0.7
putative vacuolar sorting protein 35	264622_at 0.7
hypothetical protein predicted by genemark.hmm	264471_at 0.7
hypothetical protein contains similarity to F-box protein Fbx7 GI:6164624 from [Homo sapiens]	264336_at 0.7
unknown protein Contains similarity to tetratricopeptide repeat protein gb U46571 from home sapiens. EST gb Z47802 and gb	· _
hypothetical protein predicted by genemark.hmm	264299_s_at 0.7
unknown protein	264257_at 0.7
putative sucrose transport protein, SUC2 strong similarity to GB:S38196 sucrose transport protein SUC2 from [Arabidopsis th	
putative myb-related transcription factor Similar to myb-related transcription factor (THM27) gb X95296 from Solanum lycoper hypothetical protein contains similarity to toluene tolerance protein Ttg2A GI:4336798 from [Pseudomonas putida]; supported	
unknown protein	by cDNA: gi_13 264165_at 0.7 264128 at 0.7
replicase, putative similar to replicase GI:166841 from [Arabidopsis thaliana]; supported by cDNA: gi_15292902_gb_AY0508{	
unknown protein similar to putative CREB-binding protein GI:7025854 from [Arabidopsis thaliana]; supported by cDNA: gi_10222002_g0_Ar00000	
putative kinesin light chain	264084_at 0.7
unknown protein	264031_at 0.7
putative ATP-dependent RNA helicase A	263936_at 0.7
putative farnesylated protein ;supported by full-length cDNA: Ceres:19570.	263866_at 0.7
hypothetical protein predicted by genscan; supported by full-length cDNA: Ceres: 38737.	263808_at 0.7
putative GDSL-motif lipase/hydrolase similar to APG proteins; pFAM domain PF00657;supported by full-length cDNA: Ceres:3	—
unknown protein ;supported by full-length cDNA: Ceres:35274.	263802_at 0.7
putative phosphatidylinositol/phosphatidylcholine transfer protein	263749_at 0.7
putative kinesin heavy chain ; supported by cDNA: gi_14532683_gb_AY039966.1_ putative pre-mRNA splicing factor PRP19 similar to GB:AAB80652; supported by cDNA: gi 14532631 gb AY039940.1	263762_at 0.7 263666 at 0.7
ארע אין	263666_at 0.7

putative 1-aminocyclopropane-1-carboxylate oxidase Similar to Arabidopsis 2A6 (gb X83096). EST gb T76913 comes from this gene; support	263668_at	0.7
unknown protein predicted by genefinder putative receptor-like protein kinase	263643_at 263590 at	0.7 0.7
putative receptor line protein kinase hypothetical protein similar to hypothetical protein GB:AAC27412	263404 s at	0.7
putative protein kinase contains a protein kinase domain profile (PDOC00100);supported by full-length cDNA: Ceres:13257.	263419 at	0.7
En/Spm-like transposon protein related to En/Spm transposon family of maize	263352_at	0.7
unknown protein similar to ribonuclease inhibitors; supported by cDNA: gi_15810394_gb_AY056236.1_	263212_at	0.7
hypothetical protein putative acetyl-CoA carboxylase (partial) dbj BAA07012; similar to ESTs gb AW144916.1, gb Al993440.1, gb T14234, gb	263192_at	0.7
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_16604353_gb_AY058075.1_	263162_at	0.7
putative peroxisome assembly factor-2 Belongs to PF[00004 ATPases associated with various cellular activities	263170_at	0.7
cytochrome P450, putative similar to cytochrome P450 GI:4176420 from (Arabidopsis thaliana)	263120_at	0.7
putative mitotic control protein dis3; supported by cDNA: gi_15982744_gb_AY057479.1_ exonuclease, putative similar to 5 -3 exonuclease GI:1894792 from [Mus musculus]; supported by cDNA: gi_11875625 gb_AF286718.1 AF	263077_at 262961 at	0.7 0.7
hypothetical protein predicted by generark.hmm	262859 at	0.7
gama-tocopherol methyltransferase almost identical to gamma-tocopherol methyltransferase GI:4106538 from [Arabidopsis thaliana];suppor	262875 at	0.7
nucleoporin, putative similar to nuclear pore complex protein (NUP155) SP:075694 [Homo sapiens (Human)]	262890 at	0.7
unknown protein Location of ESTs OAO242 5 end, gb Z30466 and OAO242 3 end, gb Z30467	262853_at	0.7
unknown protein Location of ESTs 152C14T7 , gb T88012, 173P7T7 , gb H36502 and 107E18T7 , gb T22775;supported by full-length cDNA	262803_at	0.7
putative cytochrome P450 monooxygenase identical to gb D78605 cytochrome P450 monooxygenase from Arabidopsis thaliana and is a mer	262826_at	0.7
putative ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase highly similar to ribulose-1,5 bisphosphate carb	262648_at	0.7
putative pattern formation protein EMB30 highly similar to GB:Q42510; supported by cDNA: gi_1209630_gb_U36432.1_ATU36432 4-hydroxyphenylpyruvate dioxygenase (HPD) identical to 4-hydroxyphenylpyruvate dioxygenase (HPD) SP:P93836 [Arabidopsis thaliana (Mo	262614_at	0.7 0.7
oxidoreductase, putative contains Pfam profile: PF00671 Iron/Ascorbate oxidoreductase family; supported by cDNA: gi 13878118 gb AF37(	262635_at 262638_at	0.7
ubiquitin-specific protesse 15 (UBP15) almost identical to ubiquitin-specific protesse 15 (CI:1993475 [Arabidopsis Haliana], 7 amino acid diff	262523 at	0.7
unknown protein Contains similarity to gb/AJ000644 SPOP (speckle-type POZ protein) from Homo sapiens and contains a PF/00651 BTB/PC	262495 at	0.7
serine/threonine kinase, putative similar to serine/threonine kinase GB:Y12530 GI:2181187 from [Brassica oleracea]; supported by cDNA: gi_	262458_at	0.7
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:230.	262397_at	0.7
alpha-xylosidase precursor identical to alpha-xylosidase precursor GB:AAD05539 GI:4163997 from [Arabidopsis thaliana]; supported by cDN/	262230_at	0.7
leaf development protein Argonaute identical to GB:AAC18440 from (Arabidopsis thaliana); supported by cDNA: gi_2149639_gb_U91995.1_4	262246_at	0.7
GTPase, putative similar to GTPase GI:1524359 from [Synechocystis PCC6803]	262189_at	0.7
phosphoribosylanthranilate transferase, putative similar to phosphoribosylanthranilate transferase GI:1396053 from [Pisum sativum] chloroplast drought-induced stress protein GI:2582821 from [Solanum tuberosu	261935_at 261751 at	0.7 0.7
hypothetical protein predicted by genemark.hmm	261628 at	0.7
putative lipse similar to hypothetical protein GB:AAF24946 GI:6693020 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:11{	261646 at	0.7
unknown protein ;supported by full-length cDNA: Ceres:8976.	261566 at	0.7
unknown protein	261540_at	0.7
unknown protein contains DNA-J domain; supported by cDNA: gi_15028270_gb_AY046050.1_	261458_at	0.7
unknown protein ;supported by full-length cDNA: Ceres:120232.	261413_at	0.7
homeodomain transcription factor, putative similar to homeodomain transcription factor (AGL30) GI:3461830 from [Arabidopsis thaliana]	261423_at	0.7
hypothetical protein predicted by genemark.hmm	261383_at	0.7
unknown protein ; supported by cDNA: gi_15912328_gb_AY056442.1_ aminoacylase, putative similar to aminoacylase I GI:1844 from [Sus scrofa]	261354_at 261326 s at	0.7 0.7
		0.7
	261189 at	0.7
hypothetical protein predicted by genemark.hmm	261189_at 261173 at	0.7 0.7
hypothetical protein predicted by genemark.hmm unknown protein ; supported by full-length cDNA: Ceres: 13391. hypothetical protein contains similarity to transcription factor TFIID GB:U57693 GI:1373376 from (Homo sapiens); supported by cDNA: gi_158	261173_at 261038_at 261041_at	0.7 0.7 0.7
hypothetical protein predicted by genemark.hmm unknown protein ; supported by full-length cDNA: Ceres: 13391. hypothetical protein contains similarity to transcription factor TFIID GB:U57693 GI:1373376 from (Homo sapiens); supported by cDNA: gi_15£ hypothetical protein similar to unknown protein GB:AAF32477 GI:6957733 from [Arabidopsis thaliana]	261173_at 261038_at 261041_at 261043_at	0.7 0.7 0.7 0.7
hypothetical protein predicted by genemark.hmm unknown protein ; supported by full-length cDNA: Ceres: 13391. hypothetical protein contains similarity to transcription factor TFIID GB:U57693 GI:1373376 from (Homo sapiens); supported by cDNA: gi_15£ hypothetical protein similar to unknown protein GB:AAF32477 GI:6957733 from [Arabidopsis thaliana] flavonol 3-o-glucosyltransferase, putative similar to flavonol 3-o-glucosyltransferase GB:Q40287 from [Manihot esculenta]	261173_at 261038_at 261041_at 261043_at 261048_at	0.7 0.7 0.7 0.7 0.7
hypothetical protein predicted by genemark.hmm unknown protein ; supported by full-length cDNA: Ceres: 13391. hypothetical protein contains similarity to transcription factor TFIID GB:U57693 GI:1373376 from (Homo sapiens); supported by cDNA: gi_15£ hypothetical protein similar to unknown protein GB:AAF32477 GI:6957733 from [Arabidopsis thaliana] flavonol 3-o-glucosyltransferase, putative similar to flavonol 3-o-glucosyltransferase GB:Q40287 from [Manihot esculenta] hypothetical protein similar to Pto kinase interactor 1 GB:AAC61805 GI:3668069 from [Lycopersicon esculentum]	261173_at 261038_at 261041_at 261043_at 261048_at 260924_at	0.7 0.7 0.7 0.7 0.7 0.7
hypothetical protein predicted by genemark.hmm unknown protein ; supported by full-length cDNA: Ceres: 13391. hypothetical protein contains similarity to transcription factor TFIID GB:U57693 GI:1373376 from (Homo sapiens); supported by cDNA: gi_15E hypothetical protein similar to unknown protein GB:AAF32477 GI:6957733 from [Arabidopsis thaliana] flavonol 3-o-glucosyltransferase, putative similar to flavonol 3-o-glucosyltransferase GB:Q40287 from [Manihot esculenta] hypothetical protein similar to Pto kinase interactor 1 GB:AAC61805 GI:3668069 from [Lycopersicon esculentum] hypothetical protein predicted by genscan+	261173_at 261038_at 261041_at 261043_at 261048_at 260924_at 260963_at	0.7 0.7 0.7 0.7 0.7 0.7 0.7
hypothetical protein predicted by genemark.hmm unknown protein ; supported by full-length cDNA: Ceres: 13391. hypothetical protein contains similarity to transcription factor TFIID GB:U57693 GI:1373376 from (Homo sapiens); supported by cDNA: gi_15E hypothetical protein similar to unknown protein GB:AAF32477 GI:6957733 from [Arabidopsis thaliana] flavonol 3-o-glucosyltransferase, putative similar to flavonol 3-o-glucosyltransferase GB:Q40287 from [Manihot esculenta] hypothetical protein similar to Pto kinase interactor 1 GB:AAC61805 GI:3668069 from [Lycopersicon esculentum] hypothetical protein predicted by genscan+ translation elongation factor EF-1 alpha identical to GB:AAB07881 from [Arabidopsis thaliana] (Mol. Gen. Genet. 219 (1-2), 106-112 (1989))	261173_at 261038_at 261041_at 261043_at 261048_at 260924_at 260663_at 260677_at	0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7
hypothetical protein predicted by genemark.hmm unknown protein ; supported by full-length cDNA: Ceres: 13391. hypothetical protein contains similarity to transcription factor TFIID GB:U57693 GI:1373376 from (Homo sapiens); supported by cDNA: gi_15E hypothetical protein similar to unknown protein GB:AAF32477 GI:6957733 from [Arabidopsis thaliana] flavonol 3-o-glucosyltransferase, putative similar to flavonol 3-o-glucosyltransferase GB:Q40287 from [Manihot esculenta] hypothetical protein similar to Pto kinase interactor 1 GB:AAC61805 GI:3668069 from [Lycopersicon esculentum] hypothetical protein predicted by genscan+	261173_at 261038_at 261041_at 261043_at 261048_at 260924_at 260963_at	0.7 0.7 0.7 0.7 0.7 0.7 0.7
hypothetical protein predicted by genemark.hmm unknown protein ; supported by full-length cDNA: Ceres: 13391. hypothetical protein contains similarity to transcription factor TFIID GB:U57693 GI:1373376 from (Homo sapiens); supported by cDNA: gi_15£ hypothetical protein similar to unknown protein GB:AAF32477 GI:6957733 from [Arabidopsis thaliana] flavonol 3-o-glucosyltransferase, putative similar to flavonol 3-o-glucosyltransferase GB:Q40287 from [Manihot esculenta] hypothetical protein similar to Pto kinase interactor 1 GB:AAC61805 GI:3668069 from [Lycopersicon esculentum] hypothetical protein predicted by genscan+ translation elongation factor EF-1 alpha identical to GB:AAB07881 from [Arabidopsis thaliana] (Mol. Gen. Genet. 219 (1-2), 106-112 (1989)) putative SF16 protein {Helianthus annuus}	261173_at 261038_at 261041_at 261043_at 261048_at 260924_at 260623_at 260677_at 260610_at	0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7
hypothetical protein predicted by genemark.hmm unknown protein ; supported by full-length cDNA: Ceres: 13391. hypothetical protein contains similarity to transcription factor TFIID GB:U57693 GI:1373376 from (Homo sapiens); supported by cDNA: gi_15E hypothetical protein similar to unknown protein GB:AAF32477 GI:6957733 from [Arabidopsis thaliana] flavonol 3-o-glucosyltransferase, putative similar to flavonol 3-o-glucosyltransferase GB:Q40287 from [Manihot esculenta] hypothetical protein similar to Pto kinase interactor 1 GB:AAC61805 GI:3668069 from [Lycopersicon esculentum] hypothetical protein predicted by genscan+ translation elongation factor EF-1 alpha identical to GB:AAB07881 from [Arabidopsis thaliana] (Mol. Gen. Genet. 219 (1-2), 106-112 (1989)) putative SF16 protein {Helianthus annuus} putative AP2 domain transcription factor pFAM domain (PF00847); supported by full-length cDNA: Ceres: 41462. unknown protein putative N-terminal acetyltransferase similar to N-TERMINAL ACETYLTRANSFERASE GB:P12945 from (Saccharomyces cerevisiae)	261173_at 261038_at 261041_at 261043_at 261048_at 260924_at 260663_at 260677_at 260610_at 260498_at 260375_at 260282_at	0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7
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hypothetical protein predicted by genemark.hmm unknown protein ; supported by full-length cDNA: Ceres: 13391. hypothetical protein contains similarity to transcription factor TFIID GB:U57693 GI:1373376 from (Homo sapiens); supported by cDNA: gi_15E hypothetical protein similar to unknown protein GB:AAF32477 GI:6957733 from [Arabidopsis thaliana] flavonol 3-o-glucosyltransferase, putative similar to flavonol 3-o-glucosyltransferase GB:Q40287 from [Manihot esculenta] hypothetical protein similar to to kinase interactor 1 GB:AAC61805 GI:3668069 from [Lycopersicon esculentum] hypothetical protein similar to Pto kinase interactor 1 GB:AAC61805 GI:3668069 from [Lycopersicon esculentum] hypothetical protein factor EF-1 alpha identical to GB:AAB07881 from [Arabidopsis thaliana] (Mol. Gen. Genet. 219 (1-2), 106-112 (1989)) putative SF16 protein {Helianthus annuus} putative SF16 protein [Helianthus annuus} putative AP2 domain transcription factor pFAM domain (PF00847); supported by full-length cDNA: Ceres: 41462. unknown protein putative N-terminal acetyltransferase similar to N-TERMINAL ACETYLTRANSFERASE GB:P12945 from (Saccharomyces cerevisiae) unknown protein contains zinc finger, C3HC4 type (RING finger) domain ethylene-response protein, ETR1 identical to GB:P49333 from [Arabidopsis thaliana] (Science 262 (5133), 539-544 (1993)) hypothetical protein C-term similar to C-term of apoptosis inhibitor GB:AAC70265 [Lymantria dispar nucleopolyhedrovirus]; supported by cDN. putative heat shock transcription factor cotains Pfam profile: PF00447 HSF-type DNA-binding domain; N-terminal portion similar to heat sho putative chlorophyll A-B binding protein similar to chlorophyll A-B binding protein GB:P12470 [Nicotiana plumbaginifolia]; contains Pfam profile	261173_at 261038_at 261041_at 261043_at 260048_at 260663_at 260663_at 260677_at 260677_at 260670_at 260498_at 260375_at 260282_at 260168_at 260133_at 260942_at 259992_at 259970_at	0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7
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hypothetical protein oredicted by genemark.hmm unknown protein ; supported by full-length cDNA: Ceres: 13391. hypothetical protein contains similarity to transcription factor TFIDI GB:U57693 GI:1373376 from (Homo sapiens); supported by cDNA: gi_15E hypothetical protein similar to unknown protein GB:AAF32477 GI:6957733 from [Arabidopsis thaliana] flavonol 3-o-glucosyltransferase, putative similar to flavonol 3-o-glucosyltransferase GB:Q40287 from [Manihot esculenta] hypothetical protein nerdicted by genscan+ translation elongation factor EF-1 alpha identical to GB:AA601805 GI:3668069 from [Lycopersioon esculentum] hypothetical protein in redicted by genscan+ translation elongation factor EF-1 alpha identical to GB:AAB07881 from [Arabidopsis thaliana] (Mol. Gen. Genet. 219 (1-2), 106-112 (1989)) putative SF16 protein (Helianthus annuus} putative SF16 protein (Helianthus annuus) putative SF16 protein (Helianthus annuus) putative SF16 protein (Elexin GE:CHC4 type (RING finger) domain ethylene-response protein, ETR1 identical to GB:P43933 from [Arabidopsis thaliana] (Science 262 (5133), 539-544 (1993)) hypothetical protein c-term similar to C-term of apoptosis inhibitor GB:AAC70265 [Lymantria dispar nucleopolyhedrovirus]; supported by cDN. putative heat shock transcription factor contains Pfam profile: PF00447 HSF-type DNA-binding domain; N-terminal portion similar to heat sho putative chorphyll A-B binding protein similar to Chorophyll A-B binding protein GB:P12470 (Nicotiana plumbaginfolia]; contains Pfam profile zinc finger protein, nutative similar to CH3N5001 from [Zea mays] (Cell 93 (4), 593-603 (1998)); supported by full-length cDNA: Ceres:40167. putative exportin, IRNA (nuclear export receptor for tRNAs) GB:6005954 [Homo unknown protein ; supported by full-length cDNA: Ceres:3231. putative aported protein contains similarity to Nacers:3773. hypothetical protein endel predicida to residues 14-204 of 20S proteasome beta subunit PBC2 deB:AAC32069 [AraBidopsis unknown protein ; supported by full-length cDNA: Cer	261173_at 261038_at 261041_at 261043_at 261048_at 260063_at 260663_at 260677_at 260677_at 260610_at 260428_at 260168_at 260188_at 260188_at 260188_at 260188_at 260188_at 2609292_at 259970_at 259970_at 259970_at 259970_at 259712_at 259712_at 259712_at 259475_at 259475_at 259277_at 25927_at 25927_at 25927_at 25927_at 25927_at 259216_at 259216_at 259216_at 259216_at 259216_at 259216_at 259216_at 259216_at 259216_at 25927_at 259216_at 25927_at 259216_at 25927_at 258848_at	0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7
<ul> <li>hypothetical protein predicted by genemark.hmm</li> <li>unknown protein ; supported by full-length cDNA: Ceres: 13391.</li> <li>hypothetical protein contains similarity to transcription factor TFIID GB.U57693 GI:1373376 from (Homo sapiens); supported by cDNA: gi_15E</li> <li>hypothetical protein similar to unknown protein GB:AAF32477 GI:8957733 from [Arabidopsis thaliana]</li> <li>flavonol 3oglucosyltransferase GB:040287 from [Manihot esculenta]</li> <li>hypothetical protein predicted by genscan+</li> <li>translation elongation factor EF-1 alpha identical to GB:AAA61805 GI:3668069 from [Lycopersicon esculentum]</li> <li>hypothetical protein predicted by genscan+</li> <li>translation elongation factor EF-1 alpha identical to GB:AAB07881 from [Arabidopsis thaliana] (Mol. Gen. Genet. 219 (1-2), 106-112 (1989))</li> <li>putative SF16 protein (Helianthus annuus)</li> <li>putative SF2 domain transcription factor pFAM domain (PF00847); supported by full-length cDNA: Ceres: 41462.</li> <li>unknown protein contains zinc finger, C3HC4 type (RING finger) domain</li> <li>ethylene-response protein, ETR1 identical to GB:P49333 from [Arabidopsis thaliana] (Science 262 (513), 539-544 (1993))</li> <li>hypothetical protein C-term of appotosis inhibitor GB:AAC70265 [Lymantria dispar nucleopolyhedrovirus]; supported by cDN.</li> <li>putative has thook transcription factor contains Pfam profile: PF00447 HSF-type DNA-binding domain; N-terminal portion similar to has binding protein similar to Charge protein, putative similar to Chlorophyll A-B binding protein similar to apportein similar to chlorophyll A-B binding protein similar to Science 262 (513), 539-544 (1993))</li> <li>hypothetical protein supported by full-length cDNA: Ceres:2017.</li> <li>putative exportin, putative similar to kynurenine aminotransferase GB: S42737 [Raitus norvegicus], similar to sapartate aminotransferase GB:</li> <li>putative exportin, nuclear export receptor for tRNAs) similar to exportin, RNA (nuclear export receptor for tRNAs) GB:0005954 [Ho</li></ul>	261173_at 261038_at 261041_at 261043_at 261048_at 260063_at 260663_at 260677_at 260677_at 260610_at 26042_at 260188_at 260188_at 260188_at 260188_at 260188_at 260188_at 2609292_at 259970_at 259970_at 259970_at 2599712_at 259712_at 259712_at 259475_at 259475_at 259475_at 259475_at 259478_at 259277_at 259468_at 259277_at 259148_at 259148_at 259974_at 258966_at 258966_at 258970_at 258970_at 258970_at 258970_at 258970_at 258970_at 258970_at 258970_at 258970_at 258970_at 258970_at 258970_at 258970_at 258970_at 258970_at 25870_at 25870_at 25870_at 25870_at 25870_at 25870_at 25866_at 25870_at 25870_at 25870_at 25870_at 25870_at 25870_at	0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7
hybothetical protein predicted by genemark.hmm unknown protein ; supported by full-length cDNA: Ceres: 13391. hypothetical protein similar to unknown protein GB:AAF32477 GI:B957733 from [Arabidopsis thaliana] flavon01 3-oglucosyltransferase, putative similar to flavon01 3-oglucosyltransferase GB:Q40287 from [Manihot esculenta] hypothetical protein similar to Pto kinase interactor 1 GB:AAF32477 GI:B957733 from [Arabidopsis thaliana] flavon01 3-oglucosyltransferase, putative similar to flavon01 3-oglucosyltransferase GB:Q40287 from [Manihot esculenta] hypothetical protein predicted by genscan+ translation elongation factor EF-1 alpha identical to GB:AAB07881 from [Arabidopsis thaliana] (Mol. Gen. Genet. 219 (1-2), 106-112 (1989)) putative SF16 protein (Helianthus annuus) putative SF16 protein (Helianthus annuus) putative AP2 domain transcription factor pFAM domain (PF00847); supported by full-length cDNA: Ceres: 41462. unknown protein putative N-terminal acetyltransferase similar to N-TERMINAL ACETYLTRANSFERASE GB:P129265 from (Saccharomyces cerevisiae) unknown protein contains zinc finger, C3H04 type (RING finger) domain ethylene-response protein, ETR1 identical to GB:P49333 from [Arabidopsis thaliana] (Science 282 (5133), 539-544 (1993)) hypothetical protein C-term similar to C-term of apoptosis inhibitor GB:AAC70265 [Lymantria dispar nucleopolyhedrovirus]; supported by cDN putative heat shock transcription factor contains Pfam profile: PF00447 HSF-type DNA-binding domain; N-terminal pinotinal; no heat sho putative exportin, IRNA (nuclear export receptor for tRNAs) similar to exportin, GB:P12470 [Nicotiana plumbaginfolia]; contains Pfam profile: putative exportin, IRNA (nuclear export receptor for tRNAs) similar to exportin, tRNA (nuclear export receptor for tRNAs) GB:6005954 [Homo unknown protein ; supported by full-length cDNA: Ceres:3273. putative acytorin, tRNA (nuclear export receptor for tRNAs) similar to exportin, tRNA (nuclear export apoptosis similarits) to hepatocellular acrinoma-associated antigen 59	261173_at 261038_at 261041_at 261043_at 261043_at 260063_at 260063_at 260067_at 260077_at 260010_at 260042_at 260133_at 260042_at 260922_at 259970_at 259970_at 259970_at 259970_at 259712_at 259712_at 259712_at 259275_at 25927_at 25927_at 25927_at 25927_at 25927_at 259216_at 258216_at 2	0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7

Expressed protein ; supported by cDNA: gi_15081712_gb_AY048249.1_	258458_at	0.7
unknown protein ;supported by full-length cDNA: Ceres:38468.	258435_at	0.7
hypothetical protein predicted by genscan+	258355 at	0.7
unknown protein	258316_at	0.7
unknown protein ; supported by cDNA: gi_15293102_gb_AY050985.1_	258256_at	0.7
unknown protein similar to serine/threonine kinase receptor associated protein GB:NP_035629 [Mus musculus], unr-interacting protein GB:N	258272_at	0.7
unknown protein ; supported by cDNA: gi_13358213_gb_AF325024.2_AF325024	258223_at	0.7
phosphoprotein phosphatase, putative similar to phosphoprotein phosphatase GB:AAB18613 from [Mus musculus]	258215_at	0.7
Expressed protein ; supported by full-length cDNA: Ceres: 41430.	258153_at	0.7
Expressed protein ; supported by cDNA: gi_15810370_gb_AY056224.1_	258124_at	0.7
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:25758.	258104_at	0.7
putative cytochrome P450 similar to GB:Q05047 from [Catharanthus roseus]; supported by cDNA: gi_15529168_gb_AY052208.1_	258063_at	0.7
putative tyrosine phosphatase similar to GB:AAF08382 from [Drosophila melanogaster]	258007_at	0.7
abscisic acid responsive elements-binding factor almost identical (one amino acid) to GB:AAF27182 from [Arabidopsis thaliana]; supported by	258026_at	0.7
unknown protein similar to ER6 protein GB:AAD46412 [Lycopersicon esculentum]; contains Pfam profile: PF00582 universal stress protein fai	257892_at	0.7
hypothetical protein contains Pfam profile: PF01535 domain of unknown function	257838_at	0.7
RING zinc finger protein, putative contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)	257826_at	0.7
transcriptional regulator protein, putative similar to ATAN11 GB:AAC18912 [Arabidopsis thaliana] (Genes Dev. 11 (11), 1422-1434 (1997)); c	257833_at	0.7
PRT1 identical to GB:CAA11891 from [Arabidopsis thaliana] (Proc. Natl. Acad. Sci. U.S.A. (1998) 95(14), 7904-7908); supported by full-length	257598_at	0.7
hypothetical protein	257209_at	0.7
hypothetical protein predicted by genscan+	257044_at	0.7
hypothetical protein predicted by genemark.hmm	257000_at	0.7
glycolate oxidase, putative similar to GB:999542 from [Spinacia oleracea] (J. Biol. Chem. 264 (6), 3624-3628 (1989)), contains Pfam profile: I	257004_s_at	0.7
unknown protein	256932_at	0.7
hypothetical protein ; supported by cDNA: gi_15293218_gb_AY051043.1_	256881_at	0.7
auxin-independent growth promoter, putative similar to GB:A44226 from [Nicotiana tabacum] (Science 258 (5086), 1350-1353 (1992))	256706_at	0.7
ATP-dependent Clp protease proteolytic subunit (ClpP3) identical to ATP-dependent Clp protease (nClpP3) GI:5360591 (Arabidopsis thaliana)	256411_at	0.7
unknown protein ; supported by full-length cDNA: Ceres: 38207.	256353_at	0.7
protein kinase, putative contains Pfam profile: PF00069 Eukaryotic protein kinase domain	256291_at	0.7
unknown protein	256284_at	0.7
ankyrin-like protein contains Pfam profile: PF00023 Ank repeat; supported by full-length cDNA: Ceres: 153785.	256233_at	0.7
electron transport flavoprotein, putative similar to electron transport flavoprotein [Homo sapiens] GI:182251	256209_at	0.7
hypothetical protein	256210_at	0.7
unknown protein	256220_at	0.7
unknown protein ; supported by cDNA: gi_16209716_gb_AY057619.1_	256161_at	0.7
hypothetical protein predicted by genemark.hmm	256078_at	0.7
unknown protein ; supported by cDNA: gi_15146333_gb_AY049308.1_	256034_at	0.7
unknown protein ;supported by full-length cDNA: Ceres:38751.	256017_at	0.7
glycyl tRNA synthetase, putative similar to glycyl tRNA synthetase GI:577711 from [Homo sapiens];supported by full-length cDNA: Ceres:296	256000_at	0.7
transcription factor identical to transcription factor GI:304113 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:33016.	255953_at	0.7
unknown protein similar to putative prolyl 4-hydroxylase, alpha subunit GI:6598804 from [Arabidopsis thaliana]; supported by full-length cDNA	255883_at	0.7
hypothetical protein contains Pfam profile: PF01416 tRNA pseudouridine synthase; supported by cDNA: gi_14334543_gb_AY035176.1_	255887_at	0.7
hypothetical protein contains similarity to PF01535 PPR repeat; supported by cDNA: gi_15450346_gb_AY052274.1_	255888_at	0.7
putative pseudouridine synthase	255864_at	0.7
hypothetical protein predicted by genscan	255870_at	0.7
putative proline-rich protein ;supported by full-length cDNA: Ceres:33482.	255704_at	0.7
predicted protein of unknown function ; supported by cDNA: gi_15809916_gb_AY054226.1_	255710_at	0.7
putative RNA helicase similar to ATP-dependent RNA helicases	255688_at	0.7
predicted protein of unknown function ; supported by cDNA: gi_16648930_gb_AY059835.1_	255638_at	0.7
predicted protein of unknown function ; supported by cDNA: gi_15810532_gb_AY056305.1_	255332_at	0.7
U3 snoRNP-associated -like protein U3 snoRNP-associated 55-kDa protein, Homo sapiens, gb:NP_004695	255225_at	0.7
putative protein hypothetical protein ssr1391 - Synechocystis sp. (strain PCC 6803), PIR2:S75571; supported by cDNA: gi_14190426_gb_AF:	255131_at	0.7
putative protein (fragment) glutamine-rich tetratricopeptide repeat (TPR) containing protein (SGT) - Rattus norvegicus, PID:e1285298	255133_at	0.7
putative protein RNA helicase -Mus musculus,PIR2:I84741	255053_at	0.7
isoleucine-tRNA ligase - like protein isoleucinetRNA ligase, Homo sapiens, PIR2:I59314	255020_at	0.7
putative protein conserved hypothetical protein yqeH -Bacillus subtilis,PIR2:D69951; supported by cDNA: gi_15293098_gb_AY050983.1_	254991_at	0.7
predicted protein of unknown function	254936_at	0.7
putative protein ; supported by full-length cDNA: Ceres: 93362.	254957_at	0.7
putative protein single strand DNA-binding protein - Vibrio cholerae, PIR2:T01928	254963_at	0.7
putative protein Fly Fas-associated factor (FFAF), Drosophila melanogaster, AB013610; supported by cDNA: gi_14596000_gb_AY042788.1_	254891_at	0.7
putative protein several hypothetical proteins - Arabidopsis thaliana	254800_at	0.7
putative protein hypothetical protein sll1769 - Synechocystis sp,PID:d1018406;supported by full-length cDNA: Ceres:18082.	254760_at	0.7
hypothetical protein ; supported by full-length cDNA: Ceres: 38412.	254691_at	0.7
putative protein ; supported by cDNA: gi_14190356_gb_AF378856.1_AF378856	254580_at	0.7
potassium transporter-like protein putative potassium transporter AtKT2p & AtKT1p, Arabidopsis thaliana, Patchx:G2384669 & Patchx:G2384	254520_at	0.7
putative protein retinoblastoma binding protein 2, Homo sapiens, PIR:178879	254464_at	0.7
	254283_s_at	0.7
putative protein	254140_at	0.7
argininosuccinate synthase -like protein argininosuccinate synthase, Aquifex aeolicus, PIR2:B70398	254134_at	0.7
hypothetical protein ;supported by full-length cDNA: Ceres:149683.	254100_at	0.7
putative protein several hypothetical proteins - Arabidopsis thaliana	254061_at	0.7
putative protein	253942_at	0.7
protein phosphatase homolog (PPH1)	253834_at	0.7
protein kinase ADK1-like protein protein kinase ADK1-Arabidopsis thaliana;supported by full-length cDNA: Ceres:113439.	253770_at	0.7
putative protein predicted protein, Arabidopsis thaliana	253783_at	0.7
	253764_s_at	0.7
Expressed protein supported by cDNA: gi_15983772_gb_AY056792.1_	253758_at	0.7
putative protein putative NADH oxidoreductase complex I subunit - Caenonhabditis elegans,PID:g5019819	253712_at	0.7
putative protein, fragment prolidase - Suberites domuncula,PID:e1289868	253719_at	0.7
nucleotide pyrophosphatase - like protein nucleotide pyrophosphatase homolog, Oryza sativa, gb:T03293; supported by cDNA: gi_13877570	253698_at	0.7
mRNA cleavage factor subunit - like protein mRNA cleavage factor I 25 kDa subunit, Homo sapiens, AJ001810;supported by full-length cDN/	253672_at	0.7
putative protein heat shock protein 101 - Triticum aestivum,PID:g4558484	253614_at	0.7
putative protein 2-acylglycerophosphoethanolamine acyltransferase - Aquifex aeolicus,PIR2:E70476	253624_at	0.7

putative protein predicted protein, Arabidopsis thaliana;supported by full-length cDNA: Ceres:154912.	253636_at	0.7
putative protein SP8 binding protein, Cucumis sativus, PIR2:JC6203	253603_at	0.7
hypothetical protein	253572 at	0.7
putative protein LipB gene, Prochlorothrix hollandica, PID:G1399931; supported by cDNA: gi_15887051_dbj_AB072390.1_AB072390	253553 at	0.7
Expressed protein ; supported by full-length cDNA: Ceres: 40692.	253485_at	0.7
enoyl-CoA hydratase - like protein enoyl-CoA hydratase, Prunus armeniaca, U93271	253492 at	0.7
putative protein gene C42D8.3, Caenorhabditis elegans, PID:G1293846	253469 at	0.7
putative protein tom-1B protein, Gallus gallus	253418 at	0.7
hypothetical protein ; supported by cDNA: gi_15028324_gb_AY045965.1_	253391 at	0.7
putative aldehyde dehydrogenase aldehyde dehydrogenase (NAD+), Rattus norvegicus, PIR2:A41028; supported by cDNA: gi_15451105_gt	253237_at	0.7
putative squalene synthase non-consensus GC donor splice site at exon 3, squalene synthase 2 (SQS2), Arabidopsis thaliana; supported by	253206 at	0.7
invertase - like protein mRNA, Lilium longiflorum, gb:D21823; supported by cDNA: gi 15215775 gb AY050417.1	253224 at	0.7
putative protein various predicted proteins	253071 at	0.7
glycosyltransferase like protein alpha-1,3-mannosyl-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (EC 2.4.1.101) I - rat,PIR2:JC207	253035_at	0.7
gypostrationas incertain apra to maintory gypostration sou that to actigate animy addictable (Lo Little) in taking a source of the source of t	252960 at	0.7
beta-Dglucan exohydrolase - like protein beta-D-glucan exohydrolase, Nicotiana tabacum, TREMBL:AB017502_1	252445 at	0.7
putative protein various predicted proteins, Arabidopsis thaliana	252355 at	0.7
putative protein various proteins, rutaniouspas uraliana putative protein GTP-binding protein beta chain homolog, Nicotiana tabacum, PIR:T16970;supported by full-length cDNA: Ceres:33776.	252252 at	0.7
putative protein or romaning protein rotation including involuting involuting additional addition, rinch rosho, supported by full-englished by constraints and the protein various predicted proteins. Arabidopsis thaliana	252245_at	0.7
		0.7
putative protein transcribed gene of unknown function, Arabidopsis thaliana, EMBL/ATH132745	252226_at	
F-box protein family, AtFBL16 contains similarity to SKP1 interacting partner 2 GI:10716949 from [Arabidopsis thaliana]	252242_at	0.7
putative protein UDP-glucose:(glucosyl) LPS alpha1,3-glucosyltransferase WaaO, E.coli, EMBL:AF019746	252179_at	0.7
putative protein saposin precursor - Homo sapiens, PIR:SAHUP:supported by full-length cDNA: Ceres:93651.	252075_at	0.7
plastid division protein FtsZ-like FtsZ protein, Gentiana lutea, EMBL:AF205859; supported by cDNA: gi_14488049_gb_AF384167.1_AF3841	252001_at	0.7
serine protein kinase - like serine protein kinase SRPK1, Homo sapiens, PIR:S45337; supported by cDNA: gi_15010661_gb_AY045632.1_	252026_at	0.7
putative protein zinc finger protein GCS1 - Saccharomyces cerevisiae, HR:S47006	251905_at	0.7
putative protein hin1 protein, Nicotiana tabacum, PIR:T03265;supported by full-length cDNA: Ceres:1678.	251879_at	0.7
SKP1 interacting partner 5 (SKIP5)	251867_at	0.7
Expressed protein ; supported by full-length cDNA: Ceres: 102807.	251813_at	0.7
P-glycoprotein - like P-glycoprotein (pmdr1), Solanum tuberosum, EMBLU52079	251781_at	0.7
putative protein neuronal glutamine transporter - Rattus norvegicus, EMBL:AF075704	251722_at	0.7
N2,N2-dimethylguanosine tRNA methyltransferases-like protein several N2,N2-dimethylguanosine tRNA methyltransferases	251730_at	0.7
putative protein leucine-rich receptor-like protein kinase - Malus domestica, EMBL:AF053127	251714_at	0.7
putative protein several hypothetical proteins - Arabidopsis thaliana	251525_at	0.7
putative protein mitochondrial RNA splicing protein MRS2 - Saccharomyces cerevisiae, PIR:S62064; supported by cDNA: gi_16209701_gb_/	251508_at	0.7
putative protein weak homology with predicted proteins, Arabidopsis thaliana	251391_at	0.7
putative protein carbonyl reductase (NADPH) - Rattus norvegicus, PIR:JC5285; supported by cDNA: gi_15028054_gb_AY045884.1_	251309_at	0.7
putative protein PGP237-11, Petunia x hybrida, EMBL:AF049930	251198_at	0.7
heat shock protein 40-like heat shock protein 40 - Mus musculus, EMBL:AB028272; supported by full-length cDNA: Ceres:114622.	251089_at	0.7
putative protein RING-H2 finger protein RHA3a - Arabidopsis thaliana, EMBL:AF078824	251066_at	0.7
importin alpha - like protein importin alpha, Oryza sativa, EMBL:AB006788	250977_at	0.7
rna binding protein - like rna binding protein, Schizosaccharomyces pombe, PIR:T41166;supported by full-length cDNA: Ceres:3774.	250845_at	0.7
disease resistance - like protein rpp8, Arabidopsis thaliana, EMBL:AF089711; supported by cDNA: gi_15292720_gb_AY050794.1_	250829_at	0.7
E2, ubiquitin-conjugating enzyme, putative contains similarity to ubiquitin conjugating enzyme; supported by full-length cDNA: Ceres:41386.	250814_at	0.7
putative protein similar to unknown protein (pir  T00468)	250713_at	0.7
putative protein similar to unknown protein (ref NP_055701.1);supported by full-length cDNA: Ceres:15229.	250703_at	0.7
putative protein strong similarity to unknown protein (gb AAF23201.1); supported by cDNA: gi_15293220_gb_AY051044.1_	250692_at	0.7
putative protein p100 co-activator - Mus musculus, EMBL:AB021491	250626_at	0.7
myc-like protein myc-like regulatory R gene product - Phyllostachys acuta, EMBL:U11448	250569_at	0.7
putative protein contains similarity to unknown protein (gb AAF72944.1)	250525_at	0.7
ribsomal protein - like chloroplast ribosomal protein L17, Nicotiana tabacum, PIR:T01744;supported by full-length cDNA: Ceres:22697.	250495_at	0.7
ACTIN 2/7 (sp[P53492) ; supported by cDNA: gi_1049306_gb_U37281.1_ATU37281	250458_s_at	0.7
putative protein predicted protein, Arabidopsis thaliana	250274_at	0.7
putative protein mRNA, Moritella marina, EMBL:AB025342	250275_at	0.7
putative protein ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I, Spinacia oleracea chloroplast, pir:T0	250170_at	0.7
early nodule-specific protein - like early nodule-specific protein, Medicago truncatula, EMBL:AF064775	250180_at	0.7
cinnamoyl CoA reductase - like protein cinnamoyl CoA reductase, Populus tremuloides, EMBL:AF217958;supported by full-length cDNA: Cer	250149_at	0.7
putative protein similar to unknown protein (pir  T01798)	250113_at	0.7
unknown protein	250084_at	0.7
galactose-1-phosphate uridyl transferase-like protein ;supported by full-length cDNA: Ceres:34699.	250029_at	0.7
putative protein predicted proteins, Arabidopsis thaliana	250005_at	0.7
FAR1 - like protein far-red impaired response protein (FAR1), Arabidopsis thaliana, EMBL:AF159587	249953_at	0.7
putative protein similar to unknown protein (gb AAD55417.1)	249723_at	0.7
40S ribosomal protein S3 ; supported by full-length cDNA: Ceres: 10394.	249700_at	0.7
contains similarity to DnaJ protein	249616_s_at	0.7
5-oxoprolinase -like protein 5-oxoprolinase (ATP-hydrolyzing) (EC 3.5.2.9) - rat, PIR:T42756	249585_at	0.7
v-SNARE AtVTI1a	249453 at	0.7
unknown protein	249294_at	0.7
putative protein strong similarity to unknown protein (pir  T13026)	249303_at	0.7
unknown protein ;supported by full-length cDNA: Ceres:1558.	249204_at	0.7
unknown protein	249210_at	0.7
squamosa promoter binding protein-like 2 (emb CAB56576.1)		0.7
cyclin-dependent protein kinase-like protein ; supported by cDNA: gi_15983484_gb_AF424617.1_AF424617	249050_at	0.7
disease resistance protein-like	248845_at	0.7
xylulose kinase ;supported by cDNA: gi_15292818_gb_AY050843.1_		0.7
methionine S-methyltransferase (gb AAD49574.1); supported by cDNA: gi_5733428_gb_AF137380.1_AF137380	248576_at	0.7
putative protein contains similarity to pyridoxamine 5-phosphate oxidase;supported by full-length cDNA: Ceres:6244.	248560_at	0.7
putative protein contains similarity to unknown protein (pir  T05571)	248533_at	0.7
putative protein strong similarity to unknown protein (gb/AAC72128.1); supported by cDNA: gi_15810202_gb_AY056116.1_	248553_at	0.7
HCF106 (gb/AAD32652.1) ; supported by cDNA: gi_4894913_gb_AF139188.1_AF139188	248338_at	0.7
putative protein similar to unknown protein (gb AAD38661.1); supported by cDNA: gi_13430647_gb_AF360236.1_AF360236	248305_at	0.7
unknown protein	248293_at	0.7
putative protein contains similarity to zinc finger protein	248265_at	0.7
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putative protein similar to unknown protein (gb AAB63610.1)	248213_at	0.7
putative protein similar to unknown protein (gb AAF16663.1)	248142_at	0.7
putative protein similar to unknown protein (pir  T04913)	248093_at	0.7
pyruvate kinase ;supported by full-length cDNA: Ceres:31580.	247989_at	0.7
putative protein similar to unknown protein (gb AAD38255.1)	247889_at	0.7
elongin - like protein elongin C, Drosophila melanogaster, PIR:JC5794; supported by cDNA: gi_15028384_gb_AY045995.1_	247721_at	0.7
1-aminocyclopropane-1-carboxylate oxidase - like protein 1-aminocyclopropane-1-carboxylate oxidase kidney bean, PIR:T10818; supported	247679_at	0.7
replication protein A1 - like probable replication protein A1, Oryza sativa, EMBL:AF009179;supported by full-length cDNA: Ceres:40850.	247608_at	0.7
ribulose-5-phosphate-3-epimerase ; supported by cDNA: gi_15027996_gb_AY045855.1_	247523_at	0.7
putative protein strong similarity to unknown protein (gb AAD55296.1)	247429_at	0.7
dehydrogenase ; supported by cDNA: gi_15383743_gb_AY039787.1_	247436_at	0.7
histone deacetylase ;supported by full-length cDNA: Ceres:5511.	247371_at	0.7
putative protein contains similarity to NAC-domain protein;supported by full-length cDNA: Ceres:6637.	247351_at	0.7
unknown protein	247300_at	0.7
putative protein contains similarity to splicing factor	247325_at	0.7
beta-xylosidase	247266_at	0.7
50S ribosomal protein L17 ;supported by full-length cDNA: Ceres:2806.	247247_at	0.7
putative protein strong similarity to unknown protein (emb]CAB89401.1); supported by cDNA: gi_14030730_gb_AF375456.1_AF375456	247193_at	0.7
NifS-like aminotranfserase ; supported by cDNA: gi_15292880_gb_AY050874.1_	247164_at	0.7
unknown protein	247112_at	0.7
ATP-dependent RNA helicase-like ; supported by cDNA: gi_16649120_gb_AY059930.1_	247119_at	0.7
protein phosphatase 2C-like protein	247126_at	0.7
GTP-binding protein-like putative protein contains similarity to ATP binding protein associated with cell differentiation;supported by full-length cDNA: Ceres:2489.	247098_at	0.7 0.7
	247075_at 247045 at	0.7
putative protein similar to unknown protein (pir  T38383); supported by cDNA: gi_15810344_gb_AY056211.1_ cvtochrome P450-like protein CYTOCHROME P450 71B1 - Thlaspi arvense, EMBL:L24438	247045_at 246947 at	0.7
endopeptidase - like protein O-sialoglycoprotein endopeptidase, Methanococcus jannaschii, pir:A64441;supported by full-length cDNA: Ceres		0.7
endopentase - interpretento-statogroup dem endopentase, international anazonii, pri Adverti rsappried by international control control putative protein various predicted proteins, Arabidopsis thaliana, Caenorhabditis elegans and Drosophila melanogaster; supported by CDNA:	246843 at	0.7
putative protein venous predicted proteins, Arabidopis inflamana, caenomadutis elegans and prosophila melanogaster, supported by conve. putative protein predicted proteins, Arabidopis inflama	246820 at	0.7
putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:40501.	246611 at	0.7
cold and ABA inducible protein kin1 (supported by full-length cDMA) Ceres:2270.	246481 s at	0.7
cellulose synthase catalytic subunit (IRX3) ; supported by cDN4: gi 4886755 gb AF088917.1 AF088917	246425 at	0.7
glutaredoxin, putative similar to glutaredoxin Gl:1732424 from [Ricinus communis]	246384 at	0.7
guatacovin, polario similario guatacovino in concernante a substancia da subst	246300 at	0.7
acyl-coA dehydrogenase Mus musculus glutaryI-CoA dehydrogenase precursor encoded by GenBank Accession Number U18992;supported	246304 at	0.7
hydroxynitrile lyase like protein	246272 at	0.7
BEL1-like homeobox 2 protein (BLH2); supported by cDNA: gi 15215856 gb AY050459.1	246209 at	0.7
putative protein DIM1 protein, Homo sapiens, EMBL:AF023611; supported by full-length cDNA: Ceres: 12591.	246006 at	0.7
putative protein ; supported by cDNA: gj_4103242_gb_AF022368.1_AF022368	245971 at	0.7
HOMEOBOX PROTEIN KNOTTED-1 LIKE 4 (KNAT4)	245901 at	0.7
alkaline/neutral invertase, putative similar to alkaline/neutral invertase GI:9758657 from [Arabidopsis thaliana]	245681 at	0.7
putative protein	245422 at	0.7
hypothetical protein	245374 at	0.7
putative methionine aminopeptidase ;supported by full-length cDNA: Ceres:37621.	245144 at	0.7
RNA polymerase beta subunit-1	244998_at	0.7
ribosomal protein S3	244984 at	0.7
hypothetical protein	244958_at	0.7
hypothetical protein	244959_s_at	0.7
hypothetical protein	244927_at	0.7
	257325_at	0.7
hypothetical protein		
hypothetical protein hypothetical protein predicted by genemark.hmm	257487_at	0.7
	257487_at 257553_at	0.7 0.7
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hypothetical protein predicted by genemark.hmm unknown protein contains Pfam profile:PF00400 WD domain, G-beta repeat hypothetical protein similar to putative protein GB:CAB52443 [Arabidopsis thaliana] hypothetical protein contains similarity to glucosidase I GI:2344809 from [Homo sapiens] hypothetical protein predicted by genscan putative RING zinc finger protein contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger);supported by full-length cDNA: Cere	257553_at 259285_at 264228_at 263521_at 262167_at	0.7 0.7 0.6
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hypothetical protein predicted by genemark.hmm unknown protein contains Pfam profile:PF00400 WD domain, G-beta repeat hypothetical protein similar to putative protein GB:CAB52443 [Arabidopsis thaliana] hypothetical protein contains similarity to glucosidase I GI:2344809 from [Homo sapiens] hypothetical protein predicted by genscan putative RING zinc finger protein contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger);supported by full-length cDNA: Cere protein serine/threonine phosphatase alpha, putative similar to protein serine/threonine phosphatase alpha GB:AAC69437 GI:3811109 from [ unknown protein transcription factor, putative similar to SP:088060 from [Streptomyces coelicolor]	257553_at 259285_at 264228_at 263521_at 262167_at 261743_s_at 261060_at 259929_at	0.7 0.7 0.6 0.6 0.6 0.6 0.6 0.6
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hypothetical protein predicted by genemark.hmm unknown protein contains Pfam profile:PF00400 WD domain, G-beta repeat hypothetical protein similar to putative ortoein CB:CAB52443 [Arabidopsis thaliana] hypothetical protein predicted by genscan putative RING zinc finger protein contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger);supported by full-length cDNA: Cere protein serine/threonine phosphatase alpha, putative similar to protein serine/threonine phosphatase alpha GB:AAC69437 GI:3811109 from [ unknown protein transcription factor, putative similar to SP:O88060 from [Streptomyces coelicolor] hypothetical protein predicted gene T10G3.5, Caenorhabditis elegans, PATCHX:E308128; supported by cDNA: gi_16604600_gb_AY059745.1_ putative protein predicted gene T10G3.5, Caenorhabditis elegans, PATCHX:E308128; supported by cDNA: gi_16604600_gb_AY059745.1_ putative protein similar to unknown protein (db)[BAA91806.1); supported by full-length cDNA: Ceres:13930. putative protein similar to unknown protein (db)[BAA91806.1); supported by cDNA: gi_13877730_gb_AF370128.1_AF370128 putative protein similar to unknown protein (db)[BAA93030.1) putative protein predicted proteins, prosophila melanogaster, Caenorhabditis elegans and Arabidopsis thaliana J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represent transcript regions 5 prime and 3 prime respectively) X303453 Bacteriophage P1 cer ecombinase protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively) Escherichia coli /REEF=J04423 /DEF=E coli bioD gene dethiobiotin synthetase corresponding to nucleotides 5024-5244 of J04423 /LEN=776 (- Arabidopsis thaliana /REF=U37281 /DEF=actin-2 mRNA, complete cds /LEN=1637 (-5, -M, -3 represent transcript regions 5 prime, Middle, av Arabidopsis thaliana /REF=U37281 /DEF=actin-2 mRNA, complete cds /LEN=1637 (-5, -M, -3 represent transcript regions 5 prime, Middle, av Arabidopsis thaliana regretin kinase domain profile (PDOC00100) Expressed protein sinase contains a protein kinase domain p	257553_at 259285_at 2692285_at 263228_at 263221_at 261767_at 261767_at 259929_at 257189_at 25929_at 257189_at 253468_at 249092_at 247042_at 249092_at 247142_at 249092_at 247742_at 2476750_at FFX-CreX-5_a X-r2-Ec-bioD-5_i (-Athal-Actin-5_ (-Athal-Actin-5_at 267612_at 267612_at 267371_at 26736_at 26736_at 26736_at 26736_at 266938_at	0.7 0.6
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hypothetical protein predicted by genemark.hmm unknown protein contains Pfam profile:PF00400 WD domain, G-beta repeat hypothetical protein similar to putative ortoein CB:CAB52443 [Arabidopsis thaliana] hypothetical protein predicted by genscan putative RING zinc finger protein contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger);supported by full-length cDNA: Cere protein serine/threonine phosphatase alpha, putative similar to protein serine/threonine phosphatase alpha GB:AAC69437 GI:3811109 from [ unknown protein transcription factor, putative similar to SP:O88060 from [Streptomyces coelicolor] hypothetical protein predicted gene T10G3.5, Caenorhabditis elegans, PATCHX:E308128; supported by cDNA: gi_16604600_gb_AY059745.1_ putative protein predicted gene T10G3.5, Caenorhabditis elegans, PATCHX:E308128; supported by cDNA: gi_16604600_gb_AY059745.1_ putative protein similar to unknown protein (db)[BAA91806.1); supported by full-length cDNA: Ceres:13930. putative protein similar to unknown protein (db)[BAA91806.1); supported by cDNA: gi_13877730_gb_AF370128.1_AF370128 putative protein similar to unknown protein (db)[BAA93030.1) putative protein predicted proteins, prosophila melanogaster, Caenorhabditis elegans and Arabidopsis thaliana J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represent transcript regions 5 prime and 3 prime respectively) X303453 Bacteriophage P1 cer ecombinase protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively) Escherichia coli /REEF=J04423 /DEF=E coli bioD gene dethiobiotin synthetase corresponding to nucleotides 5024-5244 of J04423 /LEN=776 (- Arabidopsis thaliana /REF=U37281 /DEF=actin-2 mRNA, complete cds /LEN=1637 (-5, -M, -3 represent transcript regions 5 prime, Middle, av Arabidopsis thaliana /REF=U37281 /DEF=actin-2 mRNA, complete cds /LEN=1637 (-5, -M, -3 represent transcript regions 5 prime, Middle, av Arabidopsis thaliana regretare to GPi52127[pnl]PID]e34073[325639 and GP]2242677[gnl]PID]D1021664]AB002366 putative nitrate	257553_at 259285_at 2692285_at 263228_at 263221_at 261767_at 261767_at 259929_at 257189_at 25929_at 257189_at 253468_at 249092_at 247042_at 249092_at 247142_at 249092_at 247742_at 2476750_at FFX-CreX-5_a X-r2-Ec-bioD-5_i (-Athal-Actin-5_ (-Athal-Actin-5_at 267612_at 267612_at 267371_at 26736_at 26736_at 26736_at 26736_at 266938_at	0.7 0.6
hypothetical protein predicted by genemark.hmm unknown protein contains Pfam profile:PF00400 WD domain, G-beta repeat hypothetical protein similar to putative protein GB:CAB52443 [Arabidopsis thaliana] hypothetical protein contains similarity to glucosidase I GI:2344809 from [Homo sapiens] hypothetical protein contains similarity to glucosidase I GI:2344809 from [Homo sapiens] hypothetical protein incluins protein contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger):supported by full-length cDNA: Cere protein genine/threonine phosphatase alpha, putative similar to protein serine/threonine phosphatase alpha GB:AAC69437 GI:3811109 from [ unknown protein transcription factor, putative similar to SP:088060 from [Streptomyces coelicolor] hypothetical protein predicted gene T10G3.5, Caenorhabditis elegans, PATCHX:E308128; supported by cDNA: gi_16604600_gb_AY059745.1_ putative protein various predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres:13930. putative protein various predicted proteins, Prosophila melanogaster, Caenorhabditis elegans and Arabidopsis thaliana J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represent transcript regions 5 prime and 3 prime respectively) X03453 Bacteriophage P1 cre recombinase protein (-6 and -3 represent transcript regions 5 prime and 3 prime respectively) X03453 bacteriophage P1 cre recombinase protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively) X03453 bacteriophage P1 cre recombinase protein (-6 and -3 represent transcript regions 5 prime and 3 prime respectively) X03453 bacteriophage P1 cre recombinase protein corresponding to nucleotides 4257-4573 of J04423 /LEN=777 (-5 and -3 represent transcript regions 5 prime and 3 prime respectively) X03453 Bacteriophage P1 cre recombinase domain profile (PDCC00100) Expressed protein similar to GP[522127]gn] PID[e349073]Z35639 and GP[2224677]gn] PID[d1021664 AB002366 putative nitrate transporter putative protein kinase contain s protein kinase domain prof	257553_at 259285_at 263228_at 263221_at 263221_at 261743_s_at 261743_s_at 259329_at 257189_at 253468_at 251005_at 249092_at 247142_at 246750_at FFX-GRX-5_a X-r2-Ec-bioD-5_i K-r2-Ec-bioD-5_i X-r	0.7 0.6

Expressed protein ; supported by full-length cDNA: Ceres: 9670.	266641_at	0.6
hypothetical protein predicted by genefinder; supported by cDNA: gi_14532491_gb_AY039870.1_	266536_at	0.6
putative ligand-gated ion channel subunit ; supported by cDNA: gi_6644387_gb_AF210701.1_AF210701 putative transport of the support of the sup	266338_at	0.6
putative tropinone reductase putative tropinone reductase ;supported by full-length cDNA: Ceres:1637.	266280_at 266291 at	0.6 0.6
putative dopinoir reductase ,supported by full-regimentation ceres. Ceres. 607.	266299 at	0.6
gratatione bloem-specific lectin	266235 at	0.6
putative ABC transporter	266158 at	0.6
hypothetical protein predicted by genscan	266114_at	0.6
protease inhibitor II ; supported by cDNA: gi_15293090_gb_AY050979.1_	266118 at	0.6
putative mitochondrial carrier protein	266109 at	0.6
putative protein kinase contains a protein kinase domain profile (PDOC00100); supported by cDNA: gi 14335115 gb AY037237.1	265772 at	0.6
putative ABC1 protein identical to EGAD/110384/118464supported by full-length cDNA: Ceres:141861.	265721 at	0.6
putative CCR4-associated factor ; supported by cDNA: gi_15293024_gb_AY050946.1_	265676_at	0.6
putative beta-1,3-glucanase ;supported by full-length cDNA: Ceres:1126.	265648_at	0.6
hypothetical protein predicted by genefinder; supported by full-length cDNA: Ceres: 32664.	265628_at	0.6
unknown protein	265583_at	0.6
hypothetical protein ; supported by cDNA: gi_13442982_gb_AY026065.1_	265483_at	0.6
unknown protein predicted by genscan	265495_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:250015.	265458_at	0.6
putative Na+/H+ antiporter	265252_at	0.6
putative transcription factor	265218_at	0.6
hypothetical protein predicted by genecan:supported by full-length cDNA: Ceres:37455.	265192_at	0.6
putative zinc finger protein similar to zinc finger protein, 207 GB:4508017 from [Homo sapiens], similar to ESTs gb]N38677 and gb]H77073;si		0.6
unknown protein similar to ESTs gb R30049 and gb T46176;supported by full-length cDNA: Ceres:102343. T-complex chaperonin protein , epsilon subunit identical to GB:004450, similar to ESTs gb R29812, emb Z38124, gb AA297087, gb R29812,	265101_at 265010 at	0.6 0.6
unknown protein supported by cDNA: Ceres: 103034, cDNA may not be full-length in this case.; supported by cDNA: gi 15982865 gb AY05	264990 at	0.6
E-box protein family. At EBX3 contains similarity to stamina pistibilidide Gi4101570, the pea ortholog of Fim and UFC from [Pisum sativum];su	264955 at	0.6
receptor-like kinase, putative similar to somency to stamma presented actor of the control of th	264930_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:99231.	264848 at	0.6
unknown protein similar to beta-galactoside alpha-2,3-sial/transferase (pir/IJC5251)	264793 at	0.6
unknown protein similar to ESTs gb/T20593 and emb/Z35049	264796 at	0.6
unknown protein	264698 at	0.6
putative elongation factor similar to GB:AAC67357	264664 at	0.6
auxin-resistance protein AXR1 E1 ubiquitin-like activating enzyme; identical to GB:P42744; supported by cDNA: gi_15215701_gb_AY050379	264585_at	0.6
unknown protein Location of EST gb Z34586 and gb Z34166; supported by cDNA: gi_15529271_gb_AY052260.1_	264509_at	0.6
hypothetical protein predicted by genemark.hmm	264475_s_at	0.6
unknown protein similar to daunorubicin C-13 (U77891); similar to oxidoreductase in MRPL44-MTF1 intergenic protein (sp Q05016 YM71_YE	264468_at	0.6
fumarylacetoacetate hydrolase-like protein similar to fumarylacetoacetate hydrolase, gb L41670 from Emericella nidulans	264396_at	0.6
coatomer alpha subunit, putative similar to coatomer alpha subunit GI:4567286 from [Arabidopsis thaliana]	264309_at	0.6
vacuolar-type H+-translocating inorganic pyrophosphatase identical to vacuolar-type H+-translocating inorganic pyrophosphatase GI:6901678	_	0.6
unknown protein	264218_at	0.6
hypothetical protein predicted by genemark.htmm	264236_at	0.6
CRK1 protein, putative similar to CRK1 protein GI:7671528 from [Beta vulgaris]; supported by cDNA: gi_13877618_gb_AF370510.1_AF3705 here the first enchance for protein GI:7671528 from [Beta vulgaris]; supported by cDNA: gi_13877618_gb_AF370510.1_AF3705		0.6
hypothetical protein contains Pfam profile: PF01535 PPR repeat	264177_at	0.6
Mago Nashi-like protein similar to Mago Nashi, Genbank Accession Number U03559;supported by full-length cDNA: Ceres:35733.	264152_at	0.6
unknown protein	264063_at 264041 at	0.6 0.6
MADS-box protein (AGL3) ; supported by cDNA: gi_1737494_gb_U81369.1_ATU81369 putative shikimate kinase precursor	263897_at	0.6
SKP1 interacting partner 6 (SKIP6), putative similar to SKP1 interacting partner 6 GI:10716957 from [Arabidopsis thaliana]	263898 at	0.6
Expressed protein ; supported by cDNA: gi 15027870 gb AY045792.1	263763 at	0.6
unknown protein ESTs gb]T20589, gb]T04648, gb]A597906, gb]T04111, gb]R84180, gb]R65428, gb]T44439, gb]T76570, gb]R90004, gb]T4	263709 at	0.6
hypothetical protein Similar to Babesia aldo-keto reductase (gb/l99122	263678 at	0.6
unknown protein	263613_at	0.6
putative homeodomain transcription factor ;supported by cDNA: gi_15983780_gb_AY056796.1_	263557_at	0.6
putative Rieske iron-sulfur protein ;supported by full-length cDNA: Ceres:29774.	263533_at	0.6
phosphoenolpyruvate carboxylase	263491_at	0.6
putative glucosyltransferase ; supported by cDNA: gi_15810476_gb_AY056277.1_	263477_at	0.6
cyclophilin-like protein ;supported by full-length cDNA: Ceres:124189.	263288_at	0.6
putative GTP-binding protein Similar to WO8E3.3 gi]3880615 putative GTP-binding protein from C. elegans cosmid gb]Z92773. EST gb]AA59	263224_at	0.6
unknown protein	263171_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:157730.	262982_at	0.6
hypothetical protein ;supported by full-length cDNA: Ceres:30113.	262929_at	0.6
pyruvate dehydrogenase e1 alpha subunit, putative similar to pyruvate dehydrogenase e1 alpha subunit GI:473168 from [Solanum tuberosun di utblica Subassi alpha subunit, putative similar to pyruvate dehydrogenase e1 alpha subunit GI:473168 from [Solanum tuberosun di utblica Subassi alpha subunit, putative similar to pyruvate dehydrogenase e1 alpha subunit GI:473168 from [Solanum tuberosun di utblica Subassi alpha subunit, putative similar to pyruvate dehydrogenase e1 alpha subunit GI:473168 from [Solanum tuberosun di utblica Subassi alpha subunit, putative similar to pyruvate dehydrogenase e1 alpha subunit GI:473168 from [Solanum tuberosun di utblica Subassi alpha subunit, putative similar to pyruvate dehydrogenase e1 alpha subunit GI:473168 from [Solanum tuberosun di utblica Subassi alpha subunit, putative similar to pyruvate dehydrogenase e1 alpha subunit GI:473168 from [Solanum tuberosun di utblica Subassi alpha subunit, putative similar to pyruvate dehydrogenase e1 alpha subunit GI:473168 from [Solanum tuberosun di utblica Subassi alpha subunit, putative similar to pyruvate dehydrogenase e1 alpha subunit GI:473168 from [Solanum tuberosun di utblica Subassi alpha subunit, putative similar to pyruvate dehydrogenase e1 alpha subunit di utblica subunit di ut	262908_at	0.6
glutathione S-transferase, putative similar tosimilar to glutathione S-transferase GB:AAF29773 GI:6856103 from (Gossypium hirsutum); supp	262916_at	0.6
putative protein predicted protein, Caenorhabditis elegans, AL033514 purple acid phosphatase, putative contains Pfam profile: PF02227 Purple acid phosphatase	262869_s_at 262830 at	0.6 0.6
unknown protein ; supported by cDNA: gi_16612297_gb_AF439842.1_AF439842	262849 at	0.6
lipase, putative contains Pfam profile: PF0057 Lipase/Acvhytoclase with GDSL-like motif	262736 at	0.6
hypothetical protein	262738_at	0.6
vacuolor sorting protein 35, putative similar to vacuolar sorting protein 35 GB:AAF02778 GI:6049847 [Homo sapiens]	262695 at	0.6
PPR-repeat protein contains multiple PPR repeats Pfam Profile: PF01535	262690 at	0.6
unknown protein ;supported by full-length cDNA: Ceres:153154.	262641_at	0.6
unknown protein ESTs gb H37295 and gb R64895 come from this gene;supported by full-length cDNA: Ceres:13543.	262592_at	0.6
hypothetical protein similar to hypothetical protein GB:AAF24586 GI:6692121 from [Arabidopsis thaliana]	262549_at	0.6
hypothetical protein predicted by genscan+; supported by cDNA: gi_14517529_gb_AY039600.1_	262248_at	0.6
	262253_s_at	0.6
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_16209708_gb_AY057616.1_	262223_at	0.6
dynamin-like protein similar to dynamin GB:AAA37324 GI:487857 from [Mus musculus]; supported by cDNA: gi_15146178_gb_AY049230.1_	262077_at	0.6
hypothetical protein contains similarity to helicase-like protein NHL GI:6969265 from [Homo sapiens]	262066_at	0.6
putative DnaJ protein contains Pfam profile: PF00226 DnaJ, prokaryotic heat shock protein; similar to hypothetical protein GB:AAD55462 (Ar	262053_at	0.6
10-formyltetrahydrofolate synthetase identical to 10-formyltetrahydrofolate synthetase (Arabidopsis thaliana) GI:5921663; supported by cDNA		0.6
DNA damage repair protein, putative similar to DNA damage repair protein GB:P42698 from [Arabidopsis thaliana]; supported by cDNA: gi_1	261808_at	0.6

prolyl endopeptidase, putative similar to prolyl endopeptidase GI:6561876 from [Mus musculus]	261770_at	0.6
hypothetical protein predicted by genemark.hmm ADP-glucose pyrophosphorylase, putative similar to ADP-glucose pyrophosphorylase GB:X78900 GI:556623 from [Beta vulgaris]	261632_at 261642 at	0.6 0.6
April spudues propriosition ytake, patalwe similar to April spudues propriosition set of Arrosof 61.50025 from [Leta vagans] hypothetical protein predicted by genemark.hmm;supported by full-length CDNA: Ceres:2686.	261610 at	0.6
unknown protein	261469_at	0.6
L-ascorbate peroxidase identical to GB:CAA42168 from [Arabidopsis thaliana] (Plant Mol. Biol. 18 (4), 691-701 (1992)); supported by full-leng	261412_at	0.6
unknown protein ; supported by cDNA: gi_15292702_gb_AY050785.1_	261293_at	0.6 0.6
unknown protein ;supported by full-length cDNA: Ceres:39874. transcription factor MYC7E, putative similar to transcription factor MYC7E GB:AAD15818 GI:4321762 from [Zea mays]	261155_at 261050 at	0.6
hypothetical protein predicted by genemark.hmm	261053_at	0.6
beta-glucosidase, putative similar to beta-glucosidase GB:L41869 GI:804655 from [Hordeum vulgare];supported by full-length cDNA: Ceres:1	261016_at	0.6
unknown protein contains similarity to peptidyl-prolyl cis/trans isomerase GB:AAC62692 GI:3599386 from [Cenarchaeum symbiosum];support	261018_at	0.6
hypothetical protein contains similarity to vacuolating cytotoxin (vacA) GI:6634155 from [Helicobacter pylori] hypothetical protein predicted by genemark.hmm	260938_at 260922 at	0.6 0.6
hypothetical protein predicted by general kinim	260899 at	0.6
hypothetical protein contains similarity to transcriptional regulator protein GB:X68061 GI:57911 from [Mus musculus]; supported by full-length	260894_at	0.6
ER lumen protein retaining receptor identical to SP:P35402 from (Arabidopsis thaliana)	260897_at	0.6
histone H1, putative similar to histone H1-1 GB:CAA44312 GI:16314 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:24648 unknown protein	260830_at 260718 at	0.6 0.6
hypothetical protein predicted by genscan+	260641 at	0.6
unknown protein	260596_at	0.6
serine acetyltransferase identical to GB:CAA84371 from [Arabidopsis thaliana] (Eur. J. Biochem. 227 (1-2), 500-509 (1995)); supported by CL	260602_at	0.6
Expressed protein ; supported by cDNA: gi_13605678_gb_AF361820.1_AF361820 hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:40765.	260500_at 260479_at	0.6 0.6
Ser/Th kinase ; supported by full-length cDNA: Ceres:10245.	260480 at	0.6
hypothetical protein predicted by genefinder; supported by cDNA: gi_15450969_gb_AY054565.1_	260413_at	0.6
unknown protein ; supported by cDNA: gi_13937138_gb_AF372923.1_AF372923	260358_at	0.6
hypothetical protein predicted by genscan+; supported by cDNA: gi_14335049_gb_AY037204.1_ putative RING zinc finger protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)	260310_at 260330_at	0.6 0.6
hypothetical protein similar to putative protein GB:CAA18164 [Arabidopsis thaliana]; supported by cDNA: gi_13878144_gb_AF370335.1_AF3	260243 at	0.6
unknown protein	260069_at	0.6
unknown protein contains Pfam profile: PF00561 alpha/beta hydrolase fold; supported by cDNA: gi_16930504_gb_AF419606.1_AF419606	260048_at	0.6
hydrophilic protein, putative similar to GI:198573 from [Mus musculus] (Gene 107, 345-346 (1992)) hydroxypyruvate reductase (HPR) identical to hydroxypyruvate reductase (HPR) GB:D85339 [Arabidopsis thaliana] (Plant Cell Physiol 1997 A	260020_at 260014 at	0.6 0.6
hypothetical protein predicted by genscan+	259938 at	0.6
putative ribophorin I (dolichyl-diphosphooligosaccharide-protein glycosyltransferase) similar to ribophorin I (dolichyl-diphosphooligosaccharide	259883_at	0.6
leucine-rich receptor-like protein kinase, putative similar to GI:3641252 from [Malus x domestica] (Plant Mol. Biol. 40 (6), 945-957 (1999))	259848_at	0.6 0.6
Expressed protein ; supported by full-length cDNA: Ceres: 30602. putative replication factor C similar to replication factor C GB:P40937 [Homo sapiens]	259789_at 259732 at	0.6
putative DNA-binding protein similarity to short region of heat shock transcription factors: GB:CAB10177, GB:AAC31792, GB:CAA16745, GB		0.6
unknown protein	259651_at	0.6
hypothetical protein	259633_at	0.6 0.6
hypothetical protein hypothetical protein	259551_at 259564 at	0.6
unknown protein similar to putative cis-Golgi SNARE protein GI:2583133 from [Arabidopsis thaliana]; supported by cDNA: gi_12083259_gb_A	259498_at	0.6
unknown protein ; supported by cDNA: gi_15028126_gb_AY046013.1_	259501_at	0.6
unknown protein similar to putative MYB family transcription factor GI:4335752 from [Arabidopsis thaliana] putative aminopeptidase similar to X-prolyl aminopeptidase GB:NP_006514 from [Homo sapiens]	259423_at	0.6 0.6
putative animopepidase similar to x-proly animopepidase GB.rvr_000314 from [rom sapiens] putative nodulin similar to nodulin GB:AAA91034 from [Medicago sativa];supported by full-length cDNA: Ceres:16718.	259296_at 259308 at	0.6
putative porin similar to outer mitochondrial membrane porin (voltage-dependent anion-selective channel protein) (VDAC) (POM 34) GB:P420	259270_at	0.6
putative polypyrimidine tract-binding protein similar to polypyrimidine tract-binding proteins from rat, mouse and human; supported by cDNA:	259280_at	0.6
unknown protein est hit, predicted by genscan unknown protein ;supported by full-length cDNA: Ceres:22512.	259190_at 259192 at	0.6 0.6
putative auxin-independent growth promoter similar to auxin-independent growth promoter GB:A44226 [Nicotiana tabacum];supported by full-	259132_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:32811.	259039_at	0.6
putative D-ribulose-5-phosphate 3-epimerase similar to D-ribulose-5-phosphate 3-epimerase GB:AAF01048 [Oryza sativa]; contains non-cons		0.6
unknown protein contains Pfam profile: PF00498 Forkhead-associated (FHA) domain (putative nuclear protein) unknown protein similar to hypothetical protein KIAA0188 GB: Q14693 from [Homo sapiens]	258822_s_at 258721 at	0.6 0.6
E2, ubiquitin-conjugating enzyme 11 (UBC11) identical to gi:12643427, SP:P35134;supported by full-length cDNA: Ceres:21455.	258678_at	0.6
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:34682.	258640_at	0.6
unknown protein contains Pfam profile: PF01965 ThiJ PfpI family	258622_at	0.6
unknown protein phospholipase D, putative similar to phospholipase D GB:BAA32278 from [Candida albicans]	258478_at	0.6
	258430_at 258359_s_at	0.6 0.6
	258259_s_at	0.6
unknown protein	258238_at	0.6
Snf1-related protein kinase KIN11 (AKIN11) identical to protein kinase AKin11 GI:1729444 [Arabidopsis thaliana] unknown protein ; supported by cDNA: gi 13605520 gb AF361586.1 AF361586	258221_at 258165 at	0.6 0.6
	258152_at	0.6
putative UDP-glucose glucosyltransferase similar to GB:Q40284 from [Manihot esculenta]	257940_at	0.6
hypothetical protein predicted by generative publication publication predicted by generative publication publications and pub	257923_at	0.6
putative protein peroxidase - Lycopersicon esculentum, PIR:S32768 unknown protein contains Pfam profile: PF01535 domain of unknown function (2 copies)	257890_s_at 257827 at	0.6 0.6
unknown protein ; supported by full-length cDNA: Ceres:120050.	257770_at	0.6
unknown protein C-term similar to phosphatidylcholine transfer protein GB:AAF08345 [Homo sapiens]; supported by cDNA: gi_15810256_gb_	257772_at	0.6
RING zinc finger protein, putative contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger); supported by cDNA: gi_14326492_	257215_at	0.6
Expressed protein ; supported by full-length cDNA: Ceres: 6801. lipid transfer protein, putative similar to GB:AAB47967 from [Hordeum vulgare], contains Pfam profile: PF00279 Plant lipid transfer protein far	257169_at 257066 at	0.6 0.6
hypothetical protein predicted by genemark.hmm; supported by cDNA; gi_15146180_gb_AY049231.1_	257000_at 257006_at	0.6
hypothetical protein predicted by genemark.hmm	256624_at	0.6
hypothetical protein ;supported by full-length cDNA: Ceres:38428.	256568_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:20812. hypothetical protein contains similarity to glucose-repressible alcohol dehydrogenase transcriptional effector GI:3859723 from (Candida albica	256523_at 256491_at	0.6 0.6
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Expressed protein ; supported by full-length CDNA: Ceres: 2009.         284628_at         06           UV-damaged DNA-binding protein - NRG, Arabidogas thaliana, PIC2: S21901         284508_at         06           UV-damaged DNA-binding protein - NRG, Arabidogas thaliana, DL/020184; supported by CDNA: g1_1546542_gb_A7312         284282         06           garma glutamy(cysteine synthetase : supported by CDNA: g1_1512188_gb_AY066572.1         284270_at         06           protein proteins - NRD, Control (TRH1) Injt-Arabidopsis thaliana, DL/020184; supported by CDNA: g1_151218_gb_AY066572.1         284128_dL         05           protein proteins - NRD, Control (TRH1) Injt-Arabidopsis thaliana, DL/020184; supported by CDNA: g1_151218_gb_AY03604.1         284128_dL         06           protein proteins - NRD, Control (TRS), plattive similation and the unquint-specific proteins - NRD, Control (TRS), plattive proteins - NRD, Control (TRS), plattive proteins - NRD, Control (TRS), Schooland - 280909_at         06           putative protein virul - Schooland - 280907_grupprotein by full-length CDNA: Ceres:112720.         283928_dL         06           putative protein Virul - Schooland - 2815078.supported by full-length CDNA: Ceres:11270.         283928_dL         06           putative protein Virul - Schooland - 2815078.supported by full-length CDNA: Ceres:11270.         283928_dL         06           putative protein Virul - Schooland - 281624_grup, VIRul - 281634_GRUp, VIRUL - 281634_GRU			
public protein proline-irch protein APG, Arabidopsis thaliana, PHZ-S21961         254490         at         254490         at         0           UV-damaged DNA-binding protein: Ike damage-specific DNA binding policy and binding binding.         254271         254270         0         0           gamma glutamy/stellen synthesis : supported by CNN: g1 [591248_g0_AV056721_         254270         0         0           publicy proteins and roles : guoported by CNN: g1 [591248_g0_AV056721_         254271_d.         0         0           publicy proteins and roles proteins (TRH1) high-affinity polassium transport protein (LPT). Arabidopsis thaliana, EMBL-AC04165         254712_d.         0         0           publicy proteins and roles proteid by cohenis. Arabidopsis bhaliana         254078_d.         0         0         0         0         0         0         0         254712_d.         0 <td></td> <td>_</td> <td></td>		_	
UV-damaged DNA-binding protein - like damage-specific DNA binding protein 1, Homo sepiens, PIR2:138006         25442, et         0.6           putative MADS box protein MADS-box protein AGL14, Arabidopsis haliana, JL20184; supported by cDNA: gi_1155422, gi         0.6           putative protein supported by cDNA: gi_15912188, gip_AV056372.1_         254270, at         0.6           putative protein control (TRH1) (high-fittin) polasis turn transport protein kingsis haliana; KMLLACOUGH by CDNA: gi_14517337, gip_AV056372.1_         254230, at         0.6           putative protein control (TRH1) (high-fittin) contassiun transport protein kingsis haliana; supported by CDLA: gi_14517337, gip_AV039604.1_         254004, at         0.6           arginy-HRNA synthetase         254004, at         0.6         254004, at         0.6           putative protein (UN3) Schizosaccharomyces pombe, G1381578; supported by full-length cDNA: Ceres: 112720.         25397, at         0.6           putative protein upportein by full-length cDNA: Ceres: 11590.         25340, at         0.6           putative protein upportein by full-length cDNA: Ceres: 117720.         25347, at         0.6           SETINE CARRENCYPEPTIONAS: Contrasting SERESSCS supported by full-length cDNA: Ceres: 7471.         25342, at         0.6           synaptote-rise supported by full-length cDNA: Ceres: 117720.         25342, at         0.6           SETINE CARRENCYPEPTIONAS: Cares: 14361.         753164.         253462, at		_	
putative vAADS Box / AGL protein MADE box protein AGL14, Arabidopsis thaliana, gb.U20184; supported by cDNA: gi_1151248.gb_AV056721.1         254270_at         0.6           putative potassum transport protein (TRH1) ligh-affinity potassum transport protein KUP1, Arabidopsis thaliana, EbLAC000165         254214_at         0.6           polytenythranderse like protein par-hydroxybencose polyrenythranderses (EC 25.1.6) percursor- yeas(Saccharomyces cervise)E, E 25428_at         0.6           polytenythranderse like protein par-hydroxybencose to hydroxythranderses (EC 25.1.6) percursor- yeas(Saccharomyces cervise)E, E 254050_st         0.6           putative protein various prediction proteins, XPA100505 thaliana         254050_st         0.6           putative protein various prediction protein XPA110500         253928_att         0.6           putative protein UV31, Schizosaccharomyces pombe, G1381578.supported by full-length cDNA: Ceres:112720.         253929_att         0.6           putative protein supported by full-length cDNA: Ceres:11590.         253923_att         0.6           putative protein supported by full-length cDNA: Ceres:11720.         253923_att         0.6           SteNIAC CARADVYEPETTIDASE         254042_att         0.6         25442_att         0.6           putative protein supported by full-length cDNA: Ceres:11590.         25342_att         0.6         25342_att         0.6           putative protein supported by full-length cDNA: Ceres:11720.         25342_att </td <td></td> <td>_</td> <td></td>		_	
jamma glutamyloysteine synthetase : supported by cDNX: g1 [591218: gb, AV056372.1_ 1 2 4 2 4 4 6 6 by premyltansferase like protein para-hydroxybenzoate polypremyltransferase (EC 2.5.1.) precursor - yeast (Saccharomyces cerevisiae). E 254230, at 0.6 by proteines proteines 1900 (EPI6), buttave sentiliar to ubiquita-specific protease 16 GU1993X77 [Arabidopsis haliana]. Supported by CC 25478, at 0.6 by proteines protein : supported by CDNX: g1.4517537_gb, AY039604.1_ 254078, at 0.6 putative protein : supported by CDNX: g1.451753.upported by t0.4518.1578.supported by t0.4518.1578.1578.supported by t0.4518.1578.supported by t0.4518.1578.supported by t0.4518.1578.supported by t0.4518.1578.1578.supported by t0.4518.1578.1578.1578.1578.1578.1578.1578.1			
putative protein         24214 at         0.6           optymeryitransferse like protein grar-hydroxybraceta polyrenyitransferse (E.S. 5.1.) precursor -yeast (Saccharomyces cerevisiae). E         25423.         0.6           ublquitti-specific protease 16 (UBP16), putative similar to ublquitti-specific protease 16 GL:11993477 [Arabidopsis thaliana]: supported by CD         254128.         0.6           uptative protein various predictopsis thaliana         254004.         0.6           putative protein various predictopsis thaliana         254004.         0.6           putative protein VU31, Schizosecharomyces pombe, G1381576; supported by full-length cDNA: Ceres: 112720.         253987.         0.6           putative protein         253897.         0.6         253897.         0.6           putative protein         253897.         0.6         253897.         0.6           putative protein         253897.         0.6         25382.         0.6           putative protein SV71 protein - Saccharomyces cervisiae. PIR2:54290, supported by full-length CDA: Ceres: 11590.         25382.         0.6         25382.         0.6         25382.         0.6         25382.         0.6         25382.         0.6         25382.         0.6         25382.         0.6         25382.         0.6         25382.         0.6         25382.         0.6         253842.         0		_	
pobprenytransferase like protein para-hydroxyberzoate pobyrenytransferase (EC 2.51.) precursor - yeat (Sacharomyces cerevisiae). E         24472. at         0.6           putative protein crotease 16 (DHP6), putative specific protease 16 GL:11993477 [Arabidopsis thaliana]; supported by CDA: gi_14517537.gb, AY039604.1_         254072. at         0.6           arginyi-HRNA synthetase         254072. at         0.6         254072. at         0.6           putative protein         Scharobace         254072. at         0.6         254072. at         0.6           putative protein         Disphoprotein phosphatese (PPX-1)         253392. at         0.6           putative protein         Supported by full-ength CDNA: Ceres: 11590.         253872. at         0.6           putative protein         Supported by full-ength CDNA: Ceres: 17471.         253542. at         0.6           SERINE CARBOXYPEPTIDASE II - like protein serine-type carboxypeptidase, Hordcum vulgar. PIR2: 544191; supported by cDNA: gi_1522 (S3462. at         0.6           synaptobrevin-like protein synaptobrevin-like protein, Mus musculus.supported by full-ength CDNA: Ceres: 11540         253462. at         0.6           putative protein is supported by full-ength CDNA: Ceres: 11540         253462. at         0.6         253462. at         0.6           putative protein is supported by full-ength CDNA: Ceres: 11540         25342. at         0.6         253462. at         0.6			
ubiquith-specific protease 16 (UBP16), putative similar to ubiquith-specific protease 16 GL:11993477 [Arabidopsis thaliana]: supported by cD         254162, at         0.6           hypothetical protein         supported proteins, Arabidopsis thaliana         254000, at         0.6           argini-KRAN synthetase         254000, at         0.6         253992, at         0.6           putative protein         253972, at         0.6         253972, at         0.6           putative protein         253972, at         0.6         253972, at         0.6           putative protein         253972, at         0.6         253987, at         0.6           putative protein         253972, at         0.6         253987, at         0.6           putative protein         253972, at         0.6         253982, at         0.6           putative protein         Seacharomyces correvisiae, PIR2:SX5290, supported by full-length cDNA: Ceres: 11590.         253982, at         0.6           putative protein         Seacharomyces correvisiae, PIR2:SX5290, supported by full-length cDNA: Ceres: 11530.         253462, at         0.6           synaphoterin-like protein full-length cDNA: Ceres: 11732.         253462, at         0.6         253462, at         0.6           synaphoterin-like protein full-length cDNA: Ceres: 11732.         253462, at         0.6         <		_	
putative protein various predicted proteins. Arabidopsis thaliana         244078 at         0.6           arginyl-RNA synthetase         254007 at         0.6           putative protein         254007 at         0.6           putative protein         253090 at         0.6           putative protein         Supported by full-length CDA: Ceres: 11590.         253092 at         0.6           putative protein         Supported by CDNA: gl 1300745 gb Ar301841 (A730184         253402 at         0.6           SERINE CARBOYTEPTIDASE Muster initia protein senine-kyte carboxpeptidase, Hordeum vulgare, PIR2:544191; supported by cDNA: gl 1522 35300 at         253402 at         0.6           synapbotem-inke protein initiana: supported by cDNA: gl 1502745 gb Ar301844         253402 at         0.6           synapbotem-inke protein supported by cDNA: gl 1502745 gb Ar301844         253402 at         0.6           putative protein stroported by cDNA: gl 1502745 gb Ar301844         253402 at         0.6           putative protein stroported by cDNA: gl 1302745 gb		_	
hypothetical protein:         supported by cDNA: gi_14517537_gb_AY039604.1_         254004_at         6.6           putative protein         253907_at         0.6           putative protein         253907_at         0.6           putative protein         253907_at         0.6           putative protein         253987_at         0.6           putative protein         25397_at         0.6           SERINE CARGADYPEPTIDASE         253987_at         0.6           SPRINE CARGADYPEPTIDASE         1.186 protein serine-type carboxyeptidase, Hordeum vulgare, PIR2:54191; supported by cDNA: gi_152         253402_at         0.6           putative protein ATACG8, Arabidopsis malana: supported by cDNA: gi_15226862_gb_AY050775.1_         253462_at         0.6           putative protein i supported by full-length cDNA: Ceres:14733         253462_at         0.6           putative protein i supported by full-length cDNA: Ceres:2404         253422_at         0.6           putative protein at AraCG8, Arabidopsis malana: supported by cDNA: gi_15226862_gb_AY050775.1_         253462_at         0.6		_	
ariginyLiPNA synthetase         254004         ail         0.6           putative protein         253959         0.6           putative protein         253957.ail         0.6           putative protein         253957.ail         0.6           putative protein         253957.ail         0.6           putative protein         25392.ail         0.6           putative protein         25392.ail         0.6           putative protein         25392.ail         0.6           putative protein         32007.ail         0.6           protein         32007.ail         0.6           putative protein         32007.ail         0.6           protein         32007.ail         0.6           synaptotevinike protein supported by full-lengt oDNA: Ceres: 11772.         253462.ail           synaptotevinike protein ATACAB, Arabidopsis thalana: supported by CDNA: gl 1522/200.2 gb _V105077.5		_	
putative protein         253959, at         0.6           putative protein         253972, at         0.6           phosphorotein phosphatase (PPX-1)         253972, at         0.6           putative protein         253975, at         0.6           SERINE CARBOXYPEPTIDASE II - like protein seine-type carboxypeptidase, Hordeum vulgare, PIR2:S44191; supported by CDNA: g1.05276, dt. 7.3576, at         253462, at         0.6           synaptobrevin-like protein synaptobrevin-like protein, supported by full-length cDNA: Gress.11543.         253462, at         0.6           putative protein is supported by full-length cDNA: Gress.149861         253462, at         0.6         253342, at         0.6           putative protein is supported by full-length cDNA: Gress.14365.         253342, at         0.6         253342, at         0.6           Expressed protein synaported by full-length cDNA: Gress.14385.         25334, at         0.6         253341, at         0.6         253342, at         0.6         253342, at         0.6         253			
putative protein Uv31, Schizosaccharomyces pombe, G1381578;supported by full-length cDNA: Ceres:112720.         253972_at         0.6           putative protein         253987_at         0.6           putative protein         253987_at         0.6           putative protein         Supported by full-length cDNA: Ceres:11790.         253887_at         0.6           putative protein         Supported by full-length cDNA: Ceres:11772.         253735_at         0.6           SERINE CARGXYPEPTDASE II - like protein sontexpopetidase, Hordeum vulgare, PIR2:S44191; supported by cDNA: g1_3605745_gb_A7381854         253452_at         0.6           synaptotervin-like protein singapototevin-like protein, Mus musculus.supported by full-length cDNA: Ceres:41543.         253452_at         0.6           putative protein and protein, Mus musculus.supported by full-length cDNA: Ceres:41543.         253452_at         0.6           putative protein storph dronology to Tic22 - Pisoum sativum, PID:3769671         253452_at         0.6           Putative protein in supported by full-length CDNA: Geres:14355.         253374_at         0.6           Expressed protein in supported by full-length CDNA: Geres:14385.         253374_at         0.6           putative protein forsph dronology to Tic22 - Pisum sativum, PID:3769671         253482_at         0.6           putative protein fundamitylinositoi-phosphatase's Schutage         25347_at         0.6 </td <td></td> <td>_</td> <td></td>		_	
phosphortein phosphatase (PFX-1)25392, at0.6putative protein25392, at0.6putative protein25392, at0.6putative protein3600, 2532, at0.6putative protein3600, 2532, at0.6putative protein3600, 2532, at0.6putative proteinSupported by full-length cDNA: Ceres:117732.253462, at0.6SERINE CARBOXPETTIDASE II - like protein seme-type carboxypeptidase, Hordeum vulgare, PIR2:544191; supported by cDNA; gj.1521, 25360, at0.6hypothetical proteinsupported by cDNA; gj.15282828, gd.250775.1253452, at0.6putative protein3100, 25346, gd.253828, gd.253775.1253452, at0.6putative proteinDCD28/dcd2+like kinase associating arginine-serine cyclophilin, Homo sapiens, PIR2:JC531425342, at0.6putative proteinDCD28/dcd2+like kinase associating arginine-serine cyclophilin, Homo sapiens, PIR2:JC531425337, at0.6putative proteinDCD28/dcd2+like kinase associating arginine-serine cyclophilin, Homo sapiens, PIR2:JC531425337, at0.6putative protein Into DCD28/dcd2+like kinase associating arginine-serine cyclophilin, Homo sapiens, PIR2:JC531425332, at0.6putative protein human (H326)PLS311, supported by cDNA: gj.1532(3025, 1, AF360225253324, at0.6putative protein Human (H326)PLS314, at0.625347, at0.6putative protein protein Assophatative hybriditike/holine transfer protein SEC14, Yarrowiki Biophilice, PIR2:S4345, supported by cDNA: gj.25328, gd.25324, at0.6protein-tyrosine-phosp		_	
putative protein         253897_at         0.6           putative protein         Supported by full-length cDNA: Ceres:11590.         253823_at         0.6           putative protein         Supported by full-length cDNA: Ceres:117732.         253785_at         0.6           SERINE CARBOX/YEEFTIDASE II - like protein serine-type carboxypeptidase, Hordeum vulgare, PIR2:S44191; supported by cDNA: gj_1521         253600_at         0.6           synaptobrevin-like protein synaptote by full-length cDNA: Ceres:14385         25342_at         0.6           putative protein SNAPTOP domology to Tic22 - Pisum sativum, PID:g3769671         25384_at         0.6           putative protein synaptote by full-length cDNA: Ceres:14385         25314_at         0.6           putative protein synaptote by full-length cDNA: Ceres:14385         25317_at		_	
putative protein         253823_at         0.6           putative protein         Saccharomyces cerevisae.PR2:552500;supported by full-length cDNA: Ceres:7471.         25342_at         0.6           hypothetical protein         Supported by full-length cDNA: Ceres:11773.         253462_at         0.6           SERINE CARBOXYPEPTIDASE II - like protein senine-type carboxypeptidase. Hordeum vulgare, PIR2:S44191; supported by cDNA: g1522         253462_at         0.6           hypothetical protein         synaptotervin-like protein synaptotervin-like protein. Mus musculus;supported by full-length cDNA: Ceres:41543.         253462_at         0.6           putative protein         synaptotervin-like protein synaptotervin-like protein. Supported by full-length cDNA: Ceres:29664.         253422_at         0.6           putative protein         CCC28/dc22/lek kinase associating arginine-serine cyclophilin, Homo sapiens, PIR2:JC5314         253422_at         0.6           hypothetical protein         Supported by full-length cDNA: Ceres: 14385.         253314_at         0.6           cinamy-actord by full-length cDNA: Ceres: 14385.         253324_at         0.6           putative protein Human (H326) mRNA, Homo sapiens, gb:U06631         253324_at         0.6           SEC14 - like protein phosphatidylinosito-phosphatigb/choline transfer protein SEC14, Yarrowiai lipotylice, PIR2:A53745, supported by full-length cDNA: Ceres:1430.         252847_at         0.6 <td< td=""><td></td><td>_</td><td></td></td<>		_	
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SERINE CARBOXYPEPTIDASE II. like protein serine-type carboxypeptidase, Hordeum vulgare, PIR2:S44191; supported by cDNA: g1_522253462_at0.6hypothetical protein synaptobrevin-like protein, Mus musculus, supported by full-length cDNA: Ceres:41543.253462_at0.6putative protein Styported by full-length cDNA: ceres:29964.253422_at0.6putative protein is supported by full-length cDNA: Ceres:29964.253342_at0.6Expressed protein Stoported by full-length cDNA: Ceres:29964.253341_at0.6Expressed protein is supported by full-length cDNA: Ceres:29964.253341_at0.6Expressed protein is supported by full-length cDNA: Ceres:14385.253314_at0.6Expressed protein is supported by full-length cDNA: Ceres:14385.253314_at0.6Expressed protein is supported by full-length cDNA: Ceres:14385.253242_at0.6putative trotein Human (H320) mRNA, Homo sapiens, gi-U06631252847_at0.6putative trotein stop horben by ophtaldy cholone transfer protein SEC14. Yarrowia lipolytica, PIR2:S43745; supported by cDNA: g22884_at0.6putative trotein stop horben tady.chonosphatidy/choline transfer protein SEC14. Yarrowia lipolytica, PIR2:S43745; supported by cDNA: g22847_at0.6vacular sorting protein sis protein cortein-tyrosine-phosphatase-like protein protein-tyrosine-phosphatase - Scitzosaccharomyces pombe, PIRA55446252847_at0.6vacular sorting protein Shomodogi vacular sorting protein Shomodogi supported by CDNA: g1_1582390_gLAY057573.1_251936_at0.6vacular sorting protein Tyropheted by CDNA: g1_1582390_gLAY057573.1_251936_at0.6vative protein		_	
hypothetical protein ; supported by cDNA: gL 13605745 gb, AF361854 1_AF361854253452 at0.6synaptobrevin-like protein ATAC98, Arabidopsis thaliana; supported by full-length cDNA: Ceres:41543.253465 at0.6putative protein ATAC98, Arabidopsis thaliana; supported by cDNA: gL 15292602 gb, AY050775.1_253465 at0.6putative protein in CDC28/dc2-like kinase associating arginine-serine cyclophilin, Homo sapiens, PIR2;JC5314253422 at0.6Tic22 - like protein storog homology to Tic22 - Pisum sativum, PID:g3769671253314 at0.6hypothetical protein253312 at0.6Expressed protein ; supported by full-length cDNA: Ceres: 14385.253324_ at0.6Expressed protein Human (H226) mRNA, Homo sapiens, gb:U06631253176_ at0.6SEC14 - like protein phosphatidylinositol-phosphatidylcholine transfer protein SEC14. Varrowia lipolytica, PIR2;S43745; supported by cDNA: 225844_ at0.6putative transposase hypothetical protein a maize transposable element Ac - Zea mays, PIR:T02916252847_ at0.6putative transposase hypothetical protein a maize transposable element Ac - Zea mays, PIR:T02916252847_ at0.6putative protein hypothetical protein a s-thomo sapiens, EMBL:AF191298252150_ at0.6putative protein hypothetical protein - Synechocystis sp., EMBL:D09003;supported by full-length cDNA: Ceres:37834.251936_ at0.6putative protein rprotein CYTCO/HROME P450 9782. GJ, Ceneso, ap., AF360220251804_ at0.6putative protein rprotein hypothetical protein - Synechocystis sp., EMBL:D0903;supported by full-length cDNA: Ceres:37834.25119_ at0.6put		_	
putative protein ATAC98, Arabidopsis thalians; supported by DNA: gi_15292682_gb_AY050775.1_253462_at0.6putative protein Supported by full-length cDNA: Ceres:29964.25342_at0.6putative protein CDC28/cdc2-like kinase associating arginine-serine cyclophilin, Homo sapiens, PIR2:JC5314253381_at0.6Tic22 - like protein strong homology to Tic22 - Pisum sativum, PIC:93769671253324_at0.6kpyothetical protein253314_at0.6Expressed protein : supported by full-length cDNA: Ceres: 14385.253374_at0.6cinnamy-latcohol dehydrogenase ELI3-1 : supported by cDNA: gi_13430625_gb_AF360225.1_AF36022525983_at0.6SEC14 - like protein phosphatitylinosito-phosphatidylcholine transfer protein SEC14, Yarrowia lipolytica, PIR2:S43745; supported by cDNA: 252884_at0.6vptative transposase hy plothetical protein a, maze transposable element Ac - Zea mays, PIR:To2916252847_at0.6vptative transposase hy plothetical protein a, maze transposable element Ac - Zea mays, PIR:To2916252847_at0.6vacuolar sorting protein 'synechocystis sp., EMBL:D90903:supported by full-length cDNA: Ceres:266414.25215_at0.6vptative protein hypothetical protein crYTO-CHROME P450 PPS2, Glycine max, gb:O48921251986_at0.6putative protein firs7D inding protein AS - Homo sapiens, EMBL:AF191298251191_at0.6putative protein hypothetical protein crYTO-CHROME P450 PPS2, Glycine max, gb:O48921_QrV50775.1_25180_at0.6putative protein hypothetical protein S- Homo sapiens, EMBL:AF09342_0s.supported by full-length cDNA: Ceres:37834.251191_at0.6putative prote			0.6
putative protein253422_at0.6putative protein25342_at0.6putative protein253242_at0.6fitte253381_at0.6hypothetical protein253381_at0.6hypothetical protein253314_at0.6Expressed protein253314_at0.6putative protein253314_at0.6putative protein253314_at0.6putative protein253314_at0.6putative protein1:supported by full-length cDNA: Ceres: 14385.253324_at0.6252983_at0.6putative protein1:supported by full-length cDNA: Ceres: 14375.252983_at0.6252847_at0.6putative transposase hypothetical protein a, maize transposable element Ac. Zea mays, PIR:T02916252847_at0.6252847_at0.6hypothetical protein supported by full-length cDNA: Ceres: 124275.252321_at0.6252647_at0.6vacuolar sorting protein 35 homolog vacuolar sorting protein 35 - Homo sapiens, EMBL:AF191298252150_at0.625160_at0.6putative protein reprotein reprotein reprotein protein 25.25180_at0.625187_at0.6putative protein 1970 binding protein 35.FMBL:AF03420;supported by full-length cDNA: Ceres:37834.251919_at0.6251867_at0.6putative protein reprotein	synaptobrevin-like protein synaptobrevin-like protein, Mus musculus;supported by full-length cDNA: Ceres:41543.	253462_at	0.6
putative protein CDC28/cdc2-like kinase associating arginine-serine cyclophilin, Homo sapiens, PIR2;JC531425349_at0.6Tic22 - like protein strong homology to Tic22 - Pisum sativum, PID;33769671253381_at0.6Expressed protein ; supported by full-length cDNA: Ceres: 14385.253324_at0.6Dutative protein Human (H326) mRNA, Homo sapiens, gb;U066312533725388_at0.6SEC14 - like protein phosphatidylionistio-lphosphatidylcholine transfer protein SEC14, Yarowia lipolytica, PIR2:S43745; supported by cDNA:252884_at0.6putative protein phosphatase-like protein n, amaze transposable element Ac - Zea mays, PIR:T02916252847_at0.6protein-tyrosine-phosphatase-like protein protein 35 - Homo sapiens, EMBL:AF19129825216_at0.6vacuolar sorting protein 35 homolog vacuolar sorting protein 35 - Homo sapiens, EMBL:AF19129825216_at0.6putative protein hypothetical protein - Synechocystis sp., EMBL:D90903:supported by full-length cDNA: Ceres:26614.25216_at0.6putative protein hypothetical protein Saponted by cDNA: gj_15862303_pAY057573.1_25198_at0.6putative protein hypothetical protein Saponted by cDNA: gj_15862303_pAY057573.1_25187_at0.6putative protein hypothetical protein Saponted by cDNA: gj_13859943_gb_AF084570.1_AF08457025187_at0.6putative protein hypothetical protein 2, Homo sapiens, FIR2-JS9525180_at0.6putative protein hypothetical protein 1,3-jeancho sapiens, PRIC-2093525186_at0.6putative protein hypothetical protein 2, Homo sapiens, PRIC-2093525180_at0.6putative protein hypothetical p	putative protein ATAC98, Arabidopsis thaliana; supported by cDNA: gi_15292682 gb_AY050775.1_	253465_at	0.6
Tic22 like protein strong homology to Tic22 -Pisum sativum, PID:g376967125381_at0.6hypothetical protein253314_at0.6Expressed protein ; supported by full-length cDNA: Ceres: 14385.253176_at0.6cinnamy-lackohol dehydrogenase ELI3-1 ; supported by cDNA: gj_13430625_gb_AF360225.1_AF36022525276_at0.6SEC14 - like protein phosphatidylinositol-phosphatidylicholine transfer protein SEC14, Yarrowia lipolytica, PIR2:S43745; supported by cDNA:252884_at0.6protein-tyrosine-phosphatidylinositol-phosphatidylicholine transfer protein SEC14, Yarrowia lipolytica, PIR2:S43745; supported by cDNA:252847_at0.6protein-tyrosine-phosphatidylinositol-phosphatidylicholine transfer protein SEC14, Yarrowia lipolytica, PIR2:S43745; supported by cDNA:252847_at0.6protein-tyrosine-phosphatidylicholine transfer protein SEC14, Yarrowia lipolytica, PIR2:S43745; supported by cDNA:252847_at0.6vacuolar sorting protein 35 homolog vacuolar sorting protein 35 - Homo sapiens, EMBL:AF191298252162_at0.6vacuolar sorting protein CPTOCHROME P450 9782, Glycine max, gb:O4892125199_at0.6putative protein rhspTP rotein, Zaa mays, PIR:T01685; supported by full-length cDNA: Ceres:2647.125199_at0.6FKBP12 interacting protein (FIP37); supported by cDNA: gj_3859943_gb_AF084570_AP084570_AP08457025187_at0.6putative protein nextopshate synthase, FibeLi20462 to25187_at0.6putative protein nextopshate synthase, EX935525187_at0.6putative protein nextopshate synthase, PR:A2597025186_at0.6putative protein inknown protein A2240800 - Ar	putative protein ;supported by full-length cDNA: Ceres:29964.	253422_at	0.6
hypothetical protein25314_at0.6Expressed protein253314_at0.6putative protein Human (H326) mRNA, Homo sapiens, gb:U06631253176_at0.6cinnamy-lacohol dehydrogenase ELI3-1 ; supported by cDNA: gj_13430625_gb_AF360225_1_AF360225252883_at0.6SEC14 - like protein phosphatidylinositol-phosphatidylcholine transfer protein SEC14, Yarrowia lipolytica, PIR2:S43745; supported by cDNA:252884_at0.6putative transposase hypothetical protein a, maize transposable element Ac - Zea mays, PIR-T02916252847_at0.6putative transposase hypothetical protein a, maize transposable element Ac - Zea mays, PIR-T02916252847_at0.6vacuolar sorting protein 35 homolog vacuolar sorting protein 35 - Homo sapiens, EMBL:AF191298252150_at0.6vacuolar sorting protein 750 PR2, Glycine max, gb:Vo4892125160_at0.6putative protein crp1 protein, Zea mays, PIR:T01685; supported by cDNA: gj_15982930_gb_AY057573.1_251936_at0.6putative protein trp1 protein, Zea mays, PIR:T01685; supported by cDNA: gj_15982930_gb_AY057573.1_251819_at0.6putative protein theracting protein HspBP1 - Homo sapiens, EMBL:AF093420;supported by full-length cDNA: Ceres:37834.2511919_at0.6pbsphatidylglycerophosphate synthase - like protein phosphatidylglycerophosphate synthase, Pseudomonas fluorescens, EMBL:L29642 co251819_at0.6putative protein exostose-related protein 2, Homo sapiens, PIR:JC5935251802_at0.6251802_at0.6putative protein invitowing the synthase - like protein phosphatidylglycerophosphate synthase, Pseudomonas fluorescens, EMBL:L29642 co25181		253429_at	0.6
Expressed protein ; supported by full-length cDNA: Ceres: 14385.253324_at0.6putative protein Human (H326) mRNA, Homo sapiens, gb:U06631253176_at0.6cinnamy-lachold dehytogenase ELI-31 : supported by cDNA: gi_13430625_gb_AF360225.1_AF360225252983_at0.6SEC14 - like protein phosphatidylinositol-phosphatidylcholine transfer protein SEC14, Yarrowia lipolytica, PIR2:S43745; supported by cDNA:252847_at0.6protein-Tyrosine-phosphatase-like protein protein-Tyrosine-phosphatase - Schizosaccharomyces pombe, PIR:A55446252647_at0.6hypothetical protein ; supported by full-length cDNA: Ceres:124275.252321_at0.6vacuolar sorting protein 35 homolog vacuolar sorting protein 35 - Homo sapiens, EMBL:AF191298252150_at0.6vacuolar sorting protein 35 homolog vacuolar sorting protein 35 - Homo sapiens, EMBL:AF191298252150_at0.6vative protein hypothetical protein - Synechocysits sp. LEMBL:D09003; supported by full-length cDNA: Ceres:266414.25212_at0.6cytochrom P450-like protein CYTOCHROME P450 97B2, Glycine max., gb:O48921251969_at0.6putative protein crytorien HspBP1 - Homo sapiens, EMBL:AF0912302_supported by full-length cDNA: Ceres:37834.251919_at0.6FKBP12 interacting protein (HSP37) ; supported by cDNA: gi_15820303_gb_AY057573.1_251867_at0.6potabihtidylglycerophosphate synthase - like protein probable beta-1; s-glucanase, Triticum aestivum, PIR:T06268; supported by full-length cDNA: Ceres:25842.25180_at0.6putative protein explored in At2g40800 - Arabidopsis thaliana, EMBL:AC007660251685_at0.6putative protein introtein involuti	Tic22 -like protein strong homology to Tic22 -Pisum sativum, PID:g3769671	253381 at	0.6
putative protein Human (H326) mRNA, Homo sapiens, gb:U06631253176_at0.6cinnamy-lacohol dehydrogenase ELI3-1 ; supported by cDNA: gi_13430625_gb_AF360225_1AF360225252840.6SEC14 - like protein phosphatidy/insitol-phosphatidy/choine transfer protein SEC14, Yarrowia lipolytica, PIR2:S43745; supported by cDNA:25284 at0.6putative transposase hypothetical protein a, maize transposable element Ac - Zea mays, PIR:T02916252847_at0.6protein-hyrosine-phosphatase-like protein protein-tyrosine-phosphatase - Schizosaccharomyces pombe, PIR:A55446252647_at0.6vacuolar sorting protein 35 homolog vacuolar sorting protein 35 - Homo sapiens, EMBL:AF191298252150_at0.6vacuolar sorting protein 7950 like protein cYTOCHROME P480 97B2, Glyoine max, gb:O48921251966_gt251867_atputative protein rup P450 like protein CYTOCHROME P480 97B2, Glyoine max, gb:O48921251966_gt0.6putative protein rup protein AspBP1 - Homo sapiens, EMBL:AF093420;supported by full-length cDNA: Ceres:37834.251916_gt0.6putative protein rup protein HspBP1 - Homo sapiens, EMBL:AF093420;supported by full-length cDNA: Ceres:37834.25187_gt0.6posphatidylg/lycerophosphate synthase - like protein phosphatidy/glycerophosphate synthase, Pseudomonas fluorescens, EMBL:129642 co251847_gt0.6putative protein express - like protein ny probab beta-1.3-glucanase. Tritcum aestivum, PIR:T06268; supported by full-length cDNA: Ceres:2582.25180_gt0.6putative protein unknown protein Al2940800 - Arabidopsis thaliana, EMBL:AC007660251687_gt0.6putative protein nuknown protein Al2940800 - Arabidopsis thaliana, EMBL:AC007660	hypothetical protein	253314_at	0.6
cinnamyl-alcohol dehydrogenase ELI3-1 ; supported by cDNA: gi_13430625_gb_AF360225_1_AF360225252983_at0.6SEC14 - like protein phosphatidylinositol-phosphatidylcholine transfer protein SEC14, Yarrowia lipolytica, PIR2:S43745; supported by cDNA:252844_at0.6protein-tyrosine-phosphatase-like protein a, mater transposabe hore hore transposabe hor	Expressed protein ; supported by full-length cDNA: Ceres: 14385.	253324_at	0.6
SEC14 - like protein phosphatidylinositol-phosphatidylcholine transfer protein SEC14, Yarrowia lipolytica, PIR2:S43745; supported by cDNA:252847_at0.6putative transposase hypothetical protein a, maize transposable element Ac - Zea mays, PIR:T02916252847_at0.6protein-tyrosine-phosphatase-like protein protein-strosine-phosphatase - Schizosaccharomyces pombe, PIR:A55446252647_at0.6hypothetical protein 35 homolog vacuolar sorting protein 35 - Homo sapiens, EMBL:AF191298252150_at0.6vacuolar sorting protein 35 homolog vacuolar sorting protein 35 - Homo sapiens, EMBL:AF191298252160_at0.6putative protein hypothetical protein -Synechocystis sp., EMBL:D90903;supported by full-length cDNA: Ceres:266414.25122_at0.6cytochrom P450 -like protein Cr1P rotein, Zea mays, PIR:T01685; supported by cDNA: gi_15982930_gb_AY057573.1_251936_at0.6putative protein hsp70 binding protein HspBP1 - Homo sapiens, EMBL:AF093420;supported by full-length cDNA: Ceres:37834.251919_at0.6FKBP12 interacting protein (FIP37) ; supported by cDNA: gi_3659943_gb_AF084570251887_at0.6E2, ubiquitin-conjugating enzyme 14 (UBC14) UbcA73; identical to gi:2129757, X46565; supported by full-length cDNA: Ceres:25382.251802_at0.6putative protein exotose-related protein 2. Homo sapiens, PIR:JC593525164_at0.6putative protein unknown protein At2g40800 - Arabidopsis thaliana, EMBL:AC007660251885_at0.6putative protein nuknown protein At2g40800 - Arabidopsis thaliana, EMBL:AC007660251685_at0.6putative protein nuknown protein At2g40800 - Arabidopsis thaliana, EMBL:AC004665251542_at <t< td=""><td>putative protein Human (H326) mRNA, Homo sapiens, gb:U06631</td><td>253176_at</td><td>0.6</td></t<>	putative protein Human (H326) mRNA, Homo sapiens, gb:U06631	253176_at	0.6
putative transposase hypothetical protein a, maize transposable element Ac - Zea mays, PIR:T02916252847_at0.6protein-tyrosine-phosphatase-like protein protein-tyrosine-phosphatase - Schizosaccharomyces pombe, PIR:A55446252647_at0.6hypothetical protein : supported by full-length cDNA: Ceres: 124275.252321_at0.6vacuolar sorting protein 35 homolog vacuolar sorting protein 35 - Homo sapiens, EMBL:AF191298252150_at0.6putative protein hypothetical protein - Synechocystis sp., EMBL:D09003;supported by full-length cDNA: Ceres:266414.252122_at0.6Cytochrom P450 -like protein CYTOCHROME P450 97B2, Glycine max, gb:O48921251969_at0.6putative protein fprotein, Zea mays, PIR:T01686; supported by cDNA: gi_15982930_gb_AY057573.1_251936_at0.6putative protein Hsp70 binding protein Hsp8P1 - Homo sapiens, EMBL:AF093420; supported by full-length cDNA: Ceres:37834.251919_at0.6FKBP12 interacting protein (FIP37) ; supported by cDNA: gi_385943_gb_AF084570251867_at0.6potein expose-related protein in probable beta-1,3-glucanase - like protein probabil beta-1,3-glucanase, Triticum aestivum, PIR:T06268; supported by full-length cDNA: Ceres: 8880.251804_at0.6putative protein unknown protein Al2940800 - Arabidopsis thaliana, EMBL:AC007660251685_at0.6putative protein in protein Al2940800 - Arabidopsis thaliana, EMBL:AC007660251685_at0.6putative protein nuknown protein Al2940800 - Arabidopsis thaliana, EMBL:AC007660251685_at0.6putative protein protein-tyrosine kinase, Dickyostelium discoideum, PIR:A53570251542_at0.61-acylcerol-3-phosp	cinnamyl-alcohol dehydrogenase ELI3-1;supported by cDNA: gi_13430625_gb_AF360225.1_AF360225	252983_at	0.6
protein-tyrosine-phosphatase-like protein protein tyrosine-phosphatase - Schizosaccharomyces pombe, PIR:A55446252647_at0.6hypothetical protein 35 homolog vacuolar sorting protein 35 - Homo sapiens, EMBL:AF191298252150_at0.6vacuolar sorting protein 35 homolog vacuolar sorting protein 35 - Homo sapiens, EMBL:AF191298252150_at0.6putative protein hypothetical protein - Synechocystis sp., EMBL:D90903;supported by full-length cDNA: Ceres:266414.252122_at0.6Cytochrom P450 -like protein CYTOCHROME P450 97B2, Glycine max., gb:O48921251969_at0.6putative protein trp1 protein. Zea mays, PIR:T01685, supported by cDNA: gi_1582930_gb_AY057573.1_251936_at0.6putative protein thsp70 binding protein HspBP1 - Homo sapiens, EMBL:AF093420;supported by full-length cDNA: Ceres:37834.251919_at0.6phosphatidylglycerophosphate synthase - like protein phosphatidylglycerophosphate synthase, Pseudomonas fluorescens, EMBL:L29642 co25180_at0.6E2, ubiquitin-conjugating enzyme 14 (UBC14) UbcAT3; identical to gi:2129757, S46656; supported by full-length cDNA: Ceres:25382.25180_at0.6putative protein unknown protein Al2940800 - Arabidopsis thaliana, EMBL:AC007660251685_at0.6putative protein strictosidine synthase - like protein 1.acylcerol-3-phosphate acyltransferase - like protein 1.acylcerol-3-phosphate synthase, Prassica napus, Z49860;supported by full-leng25169_at0.6putative protein introsine kinase - Like protein 1.acylcerol-3-phosphate acyltransferase subunit A (FTA) ; supported by cDNA: gi_1342697_gb_AF064542.1_AF06454225164_at0.6putative protein introsine kinase - Like protein serine/threonine-specifi	SEC14 - like protein phosphatidylinositol-phosphatidylcholine transfer protein SEC14, Yarrowia lipolytica, PIR2:S43745; supported by cDNA:		0.6
hypothetical protein 'supported by full-length cDNA: Ceres:124275.252321_at0.6vacuolar sorting protein 35 homolog vacuolar sorting protein 35 - Homo sapiens, EMBL:AF191298252150_at0.6putative protein hypothetical protein - Synechocystis sp., EMBL:D0903;supported by full-length cDNA: Ceres:266414.252122_at0.6Cytochrom P450_like protein CYTOCHROME P450 97B2, Glycine max., gb:048921251969_at0.6putative protein crp1 protein, Zea mays, PIR:T01865; supported by cDNA: gi_15822930_gb_AY057573.1_251969_at0.6putative protein trp1 protein, Zea mays, PIR:T01865; supported by cDNA: gi_15822930_gb_AY057573.1_25187_at0.6putative protein trp1 protein, Zea mays, PIR:T01865; supported by cDNA: gi_15822930_gb_AY0657573.1_25187_at0.6phosphatidylglycerophosphate synthase - like protein phosphatidylglycerophosphate synthase, Pseudomonas fluorescens, EMBL:L29642 co25180_at0.6E2, ubiquitin-conjugating enzyme 14 (UBC14) UbcAT3; identical to gi:2129757, S46656; supported by full-length cDNA: Ceres:25382.251804_at0.6putative protein unknown protein At2g40800 - Arabidopsis thaliana, EMBL:AC007660251685_at0.6putative protein unknown protein At2g40800 - Arabidopsis thaliana, EMBL:AC007660251659_at0.6putative protein strictosidine synthase - like protein serine/threonine-specific protein kinase NAK, Arabidopsis thaliana, PIR:S3832625159_at0.6putative protein protein-tyrosine kinase. Dictyostelium discoideum, PIR:AS677025164_at0.6putative protein protein-tyrosine kinase. Dictyostelium discoideum, PIR:AS6770251542_at0.6farmesyltransf	putative transposase hypothetical protein a, maize transposable element Ac - Zea mays, PIR:T02916	252847_at	0.6
vacuolar sorting protein 35 homolog vacuolar sorting protein 35 - Homo sapiens, EMBL:AF191298252150_at0.6putative protein hypothetical protein - Synechocystis sp., EMBL:D90903;supported by full-length cDNA: Ceres:266414.252122_at0.6Cytochrom P450 - like protein CYTOCHROME P450 97B2, Glycine max., gb:O48921251969_at0.6putative protein crj 1 protein, Zea mays, PIR:T01685; supported by cDNA: gi_15982930_gb_AY057573.1_251936_at0.6putative protein Hsp70 binding protein HspBP1 - Homo sapiens, EMBL:AF093420; supported by full-length cDNA: Ceres:37834.251919_at0.6FKBP12 interacting protein (FIP37) ; supported by cDNA: gi_3859943_gb_AP084570.1_AF084570251887_at0.6phosphatidylglycerophosphate synthase - like protein phosphatidylglycerophosphate synthase, Pseudomonas fluorescens, EMBL:L29642 co251819_at0.6c2, ubiquitin-conjugating enzyme 14 (UBC14) UbcAT3; identical to gi:2129757, S46656; supported by full-length cDNA: Ceres:25382.251804_at0.6putative protein exostose-related protein 2, Homo sapiens, PIR:JC5935251764_at0.6putative protein unknown protein At2g40800 - Arabidopsis thaliana, EMBL:AC007660251685_at0.6putative protein nuknown protein At2g40800 - Arabidopsis thaliana, EMBL:AC007660251596_at0.6putative protein protein-tyrosine kinase, Dictyostelium discoideum, PIR:A5670251596_at0.61-acylcerol-3-phosphate acyltransferase - like protein 1-acylcerol-3-phosphate acyltransferase, Brassica napus, Z49860; supported by full-leng251596_at0.6putative protein protein-tyrosine kinase, Dictyostelium discoideum, PIR:A3670251542_at0.6<			
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nypometical protein 251148_at 0.6	• • •	_	
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putative protein CGI-77 protein, Homo sapiens, EMBL:AF151836;supported by full-length cDNA: Ceres:153131.	251149 at	0.6
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putative protein symplekin - Homo sapiens, EMBL:HSSYMPLEK	251115_at	0.6
putative protein ;supported by full-length cDNA: Ceres:35934.	251094_at	0.6
putative protein ;supported by full-length cDNA: Ceres:158771.	251008 at	0.6
putative protein various predicted proteins, Arabidopsis thaliana	250879 at	0.6
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putative protein contains similarity to unknown protein (pir  D70614); supported by cDNA: gi_14334951_gb_AY035149.1_	250824_at	0.6
eukaryotic translation initiation factor 2 alpha subunit-like protein ; supported by cDNA: gi_13358180_gb_AF324988.2_AF324988	250779_at	0.6
gamma-tubulin interacting protein-like	250686 at	0.6
unknown protein ; supported by cDNA: gi 15451037 gb AY054599.1	250599_at	0.6
RNA helicase (emb CAA09212.1);supported by cDNA: gi_14334881_gb_AY035114.1_	250538_at	0.6
15.9 kDa subunit of RNA polymerase II (gb AAB95261.1) ;supported by full-length cDNA: Ceres:21208.	250510_at	0.6
unknown protein ; supported by cDNA: gi_15983383_gb_AF424566.1_AF424566	250459 at	0.6
putative protein	250481 at	0.6
cytochrome P450 - like protein cytochrome P450, Helianthus tuberosus, EMBL:HTCYP81L	250423_s_at	0.6
putative protein yIIC, Enterococcus faecalis, EMBL:EFU94707	250394_at	0.6
putative protein contains similarity to unknown protein (gb AAF03441.1)	250218_at	0.6
putative protein de novo DNA methyltransferase 3, Danio rerio, EMBL:AF135438	250139_at	0.6
rRNA methylase - like protein rRNA methylase SpoU, Aquifex aeolicus, PIR:H70443	250137_at	0.6
putative protein similar to unknown protein (gb AAF02163.1);supported by full-length cDNA: Ceres:115644.	250127_at	0.6
putative protein unnamed ORF, Mus musculus, EMBL:AB041577; supported by cDNA: gi_11494361_gb_AF280057.1_AF280057	249998_at	0.6
E1, ubiquitin-like activating enzyme ECR1 identical to gi:2952433; supported by cDNA: gi_15215793_gb_AY050426.1_	249926 at	0.6
Ruv DNA-helicase-like protein ;supported by full-length cDNA: Ceres:113109.	249938 at	0.6
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protease-like protein	249914_at	0.6
serine protein kinase-like protein ;supported by full-length cDNA: Ceres:10218.	249859_at	0.6
protein kinase-like	249678_at	0.6
putative protein tyrosine aminotransferase-like; also similar to nicotianamine aminotransferase	249688_at	0.6
putative protein tropomyosin gene 1, isoform 9D, D.melanogaster, EMBL:DMTRO13	249628_at	0.6
putative protein similar to unknown protein (sp P54493)	249510_at	0.6
putative protein DNA DAMAGE-RESPONSIVE PROTEIN 48, Saccharomyces cerevisiae, EMBL:SCDDR48A; supported by cDNA: gi 16604	249416 at	0.6
unknown protein ; supported by cDNA: gi_12006359_gb_AF281154.1_AF281154	249326 at	0.6
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ubiquitin-like protein ; supported by cDNA: gi_13899064_gb_AF370527.1_AF370527	249217_at	0.6
putative protein similar to unknown protein (gb AAF18661.1);supported by full-length cDNA: Ceres:7878.	249199_at	0.6
20S proteasome subunit PAF1 (gb AAC32062.1); supported by full-length cDNA: Ceres: 12455.	249161 at	0.6
E2, ubiquitin-conjugating enzyme 18 (UBC18) identical to gi:2801448; supported by cDNA: gi_16648721_gb_AY058137.1_	249183 at	0.6
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unknown protein ;supported by full-length cDNA: Ceres:114691.	248881_at	0.6
calcium sensor protein, calcineurin-like ; supported by cDNA: gi_15866278_gb_AF411958.1_AF411958	248827_at	0.6
40S ribosomal protein S19 ; supported by cDNA: gi_15028320_gb_AY045963.1_	248800 at	0.6
protein kinase (EC 2.7.1.37) 5 (pir JN0505) ; supported by cDNA: gi 15809918 gb AY054227.1	248720 at	0.6
	_	0.6
SCARECROW gene regulator-like ; supported by cDNA: gi_8132288_gb_AF153443.1_AF153443	248689_at	
putative protein strong similarity to unknown protein (pir  T09371)	248631_at	0.6
putative protein strong similarity to unknown protein (gb AAD32890.1)	248574_at	0.6
putative protein contains similarity to alpha/beta hydrolase; supported by cDNA: gi 13877626 gb AF370514.1 AF370514	248531 at	0.6
	_	
Expressed protein ; supported by cDNA: gi_13878180_gb_AF370353.1_AF370353	248532_at	0.6
putative protein contains similarity to squamosa promoter binding protein;supported by full-length cDNA: Ceres:113229.	248524_s_at	0.6
calcium-binding transporter-like protein	248485_at	0.6
RAR1 (gb AAF18433.1) non-consensus GT acceptor splice site at exon 2; supported by full-length cDNA: Ceres: 99615.	248379_at	0.6
	248263 at	
pectinesterase ; supported by cDNA: gi_15293286_gb_AY051077.1_	_	0.6
membrane related protein-like ;supported by full-length cDNA: Ceres:37644.	248199_at	0.6
	248199_at	
membrane related protein-like ;supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_1632317	248199_at 248153_at	0.6
membrane related protein-like ;supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_1632317 translation initiation factor-like protein	248199_at 248153_at 248146_at	0.6 0.6 0.6
membrane related protein-like ;supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_163231; translation initiation factor-like protein putative protein contains similarity to NRK-related kinase	248199_at 248153_at 248146_at 248060_at	0.6 0.6 0.6 0.6
membrane related protein-like ;supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_1632317 translation initiation factor-like protein putative protein contains similarity to NRK-related kinase selenium-binding protein-like	248199_at 248153_at 248146_at 248060_at 248075_at	0.6 0.6 0.6 0.6 0.6
membrane related protein-like ;supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_1632317 translation initiation factor-like protein putative protein contains similarity to NRK-related kinase selenium-binding protein-like beta-amylase ; supported by cDNA: gi_15027954_gb_AY045834.1_	248199_at 248153_at 248146_at 248060_at 248075_at 248029_at	0.6 0.6 0.6 0.6 0.6 0.6
membrane related protein-like ;supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_1632317 translation initiation factor-like protein putative protein contains similarity to NRK-related kinase selenium-binding protein-like	248199_at 248153_at 248146_at 248060_at 248075_at	0.6 0.6 0.6 0.6 0.6
membrane related protein-like ;supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_1632317 translation initiation factor-like protein putative protein contains similarity to NRK-related kinase selenium-binding protein-like beta-amylase ; supported by cDNA: gi_15027954_gb_AY045834.1_ heat shock protein (emb CAA72514.1)	248199_at 248153_at 248146_at 248060_at 248075_at 248029_at	0.6 0.6 0.6 0.6 0.6 0.6
membrane related protein-like ;supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_163231; translation initiation factor-like protein putative protein contains similarity to NRK-related kinase selenium-binding protein-like beta-amylase ; supported by cDNA: gi_15027954_gb_AY045834.1_ heat shock protein (emb CAA72514.1) beta-1,3-glucanase-like protein	248199_at 248153_at 248146_at 248060_at 248075_at 248029_at 248043_s_at 247963_at	0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6
membrane related protein-like ;supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_1632317 translation initiation factor-like protein putative protein contains similarity to NRK-related kinase selenium-binding protein-like beta-amylase ; supported by cDNA: gi_15027954_gb_AY045834.1_ heat shock protein (emb]CAA72514.1) beta-1,3-glucanase-like protein N-myristoyl transferase ;supported by full-length cDNA: Ceres:36525.	248199_at 248153_at 248146_at 248060_at 248075_at 248029_at 248043_s_at 247963_at 247960_at	0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6
membrane related protein-like ;supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_1632317 translation initiation factor-like protein putative protein contains similarity to NRK-related kinase selenium-binding protein-like beta-amylase ; supported by cDNA: gi_15027954_gb_AY045834.1_ heat shock protein (emb[CAA72514.1) beta-1,3-glucanase-like protein N-myristoyl transferase ; supported by full-length cDNA: Ceres:36525. Expressed protein	248199_at 248153_at 248146_at 248060_at 248029_at 248043_s_at 247960_at 247960_at 247924_at	0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6
membrane related protein-like ;supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_1632317 translation initiation factor-like protein putative protein contains similarity to NRK-related kinase selenium-binding protein-like beta-amylase ; supported by cDNA: gi_15027954_gb_AY045834.1_ heat shock protein (emb CAA72514.1) beta-1,3-glucanase-like protein N-myristoyl transferase ;supported by full-length cDNA: Ceres:36525. Expressed protein similar to unknown protein (pir  S75584) ;supported by full-length cDNA: Ceres:3488.	248199_at 248153_at 248166_at 248060_at 248075_at 248043_s_at 247963_at 247963_at 247960_at 247924_at 247816_at	0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6
membrane related protein-like ;supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_163231; translation initiation factor-like protein putative protein contains similarity to NRK-related kinase selenium-binding protein-like beta-amylase ; supported by cDNA: gi_15027954_gb_AY045834.1_ heat shock protein (emb CAA72514.1) beta-1,3-glucanase-like protein N-myristoyl transferase ;supported by full-length cDNA: Ceres:36525. Expressed protein similar to unknown protein (pirl S75584) ;supported by full-length cDNA: Ceres:3488. phytochelatin synthetase - like protein putative phytochelatin synthetase, Arabidopsis thaliana, EMBL:ATH6787;supported by full-length cDNA;	248199_at 248153_at 248166_at 248060_at 248075_at 248029_at 248043_s_at 247963_at 247960_at 247924_at 247924_at 247816_at 247552_at	0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6
membrane related protein-like ;supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_163231; translation initiation factor-like protein putative protein contains similarity to NRK-related kinase selenium-binding protein-like beta-amylase ; supported by cDNA: gi_15027954_gb_AY045834.1_ heat shock protein (emb CAA72514.1) beta-1,3-glucanase-like protein N-myristoyl transferase ;supported by full-length cDNA: Ceres:36525. Expressed protein similar to unknown protein (pirl S75584) ;supported by full-length cDNA: Ceres:3488. phytochelatin synthetase - like protein putative phytochelatin synthetase, Arabidopsis thaliana, EMBL:ATH6787;supported by full-length cDNA;	248199_at 248153_at 248166_at 248060_at 248075_at 248029_at 248043_s_at 247963_at 247960_at 247924_at 247924_at 247816_at 247552_at	0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6
membrane related protein-like ;supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_1632317 translation initiation factor-like protein putative protein contains similarity to NRK-related kinase selenium-binding protein-like beta-amylase ; supported by cDNA: gi_15027954_gb_AY045834.1_ heat shock protein (emb]CAA72514.1) beta-1,3-glucanase-like protein N-myristoyl transferase ;supported by full-length cDNA: Ceres:36525. Expressed protein similar to unknown protein (pir  S75584) ;supported by full-length cDNA: Ceres:3488. phytochelatin synthetase - like protein putative phytochelatin synthetase, Arabidopsis thaliana, EMBL:ATH6787;supported by full-length cDNA: putative protein various predicted proteins from different species; supported by cDNA: gi_15912286_gb_AY056421.1_	248199_at 248153_at 248060_at 248060_at 248075_at 248029_at 247963_at 247960_at 247924_at 247924_at 2478255_at	0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6
membrane related protein-like ;supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_1632317 translation initiation factor-like protein putative protein contains similarity to NRK-related kinase selenium-binding protein-like beta-amylase ; supported by cDNA: gi_15027954_gb_AY045834.1_ heat shock protein (emb CAA72514.1) beta-1,3-glucanase-like protein N-myristoyl transferase ;supported by full-length cDNA: Ceres:36525. Expressed protein similar to unknown protein (pirl S75584) ;supported by full-length cDNA: Ceres:3488. phytochelatin synthetase - like protein putative phytochelatin synthetase, Arabidopsis thaliana, EMBL:ATH6787;supported by full-length cDN/ putative protein predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 38273.	248199_at 248153_at 248165_at 248060_at 248075_at 248029_at 247963_at 247963_at 247924_at 2477552_at 247555_at 24743_at	0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6
membrane related protein-like ;supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_1632317 translation initiation factor-like protein putative protein contains similarity to NRK-related kinase selenium-binding protein-like beta-amylase ; supported by cDNA: gi_15027954_gb_AY045834.1_ heat shock protein (emb[CAA72514.1) beta-1,3-glucanase-like protein N-myristoyl transferase ; supported by full-length cDNA: Ceres:36525. Expressed protein similar to unknown protein (pir] S75584) ;supported by full-length cDNA: Ceres:3488. phytochelatin synthetase - like protein putative phytochelatin synthetase, Arabidopsis thaliana, EMBL:ATH6787;supported by full-length cDN, putative protein various predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_15912286_gb_AY056421.1_ putative protein predicted proteins, Arabidopsis thaliana; putative protein predicted proteins, Arabidopsis thaliana	248199_at 248153_at 248153_at 248060_at 248075_at 248043_s_at 247963_at 247960_at 247924_at 247924_at 247552_at 247555_at 24743_at 247398_at	0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6
membrane related protein-like ;supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_163231; translation initiation factor-like protein putative protein contains similarity to NRK-related kinase selenium-binding protein-like beta-amylase ; supported by cDNA: gi_15027954_gb_AY045834.1_ heat shock protein (emb CAA72514.1) beta-1,3-glucanase-like protein N-myristoyl transferase ;supported by full-length cDNA: Ceres:36525. Expressed protein similar to unknown protein (pirl S75584) ;supported by full-length cDNA: Ceres:3488. phytochelatin synthetase - like protein putative phytochelatin synthetase, Arabidopsis thaliana, EMBL:ATH6787;supported by full-length cDN, putative protein redicted proteins, Arabidopsis thaliana; supported by cDNA: gi_15912286_gb_AY056421.1_ putative protein predicted protein, Arabidopsis thaliana putative protein predicted proteins similarity to kinase	248199_at 248153_at 248060_at 248075_at 248043_s_at 247963_at 247963_at 247960_at 247924_at 247952_at 247555_at 247555_at 24743_at 247398_at 247368_at	0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6
membrane related protein-like ;supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_1632317 translation initiation factor-like protein putative protein contains similarity to NRK-related kinase selenium-binding protein-like beta-amylase ; supported by cDNA: gi_15027954_gb_AY045834.1_ heat shock protein (emb[CAA72514.1) beta-1,3-glucanase-like protein N-myristoyl transferase ; supported by full-length cDNA: Ceres:36525. Expressed protein similar to unknown protein (pir] S75584) ;supported by full-length cDNA: Ceres:3488. phytochelatin synthetase - like protein putative phytochelatin synthetase, Arabidopsis thaliana, EMBL:ATH6787;supported by full-length cDN, putative protein various predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_15912286_gb_AY056421.1_ putative protein predicted proteins, Arabidopsis thaliana; putative protein predicted proteins, Arabidopsis thaliana	248199_at 248153_at 248153_at 248060_at 248075_at 248043_s_at 247963_at 247960_at 247924_at 247924_at 247552_at 247555_at 24743_at 247398_at	0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6
membrane related protein-like ;supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_1632317 translation initiation factor-like protein putative protein contains similarity to NRK-related kinase selenium-binding protein-like beta-amylase ; supported by cDNA: gi_15027954_gb_AY045834.1_ heat shock protein (emb CAA72514.1) beta-1,3-glucanase-like protein N-myristoyl transferase ;supported by full-length cDNA: Ceres:36525. Expressed protein similar to unknown protein (pir][S75584) ;supported by full-length cDNA: Ceres:3488. phytochelatin synthetase - like protein protein by full-length cDNA: Ceres:3488. phytochelatin synthetase - like protein sfrom different species; supported by cDNA: gi_15912286_gb_AY056421.1_ putative protein predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 38273. putative protein predicted protein, Arabidopsis thaliana putative protein contains similarity to kinase histidinol dehydrogenase ;supported by full-length cDNA: Ceres:40175.	248199_at 248195_at 24805_at 248060_at 248075_at 248029_at 247960_at 247960_at 247924_at 247924_at 2477826_at 247555_at 247555_at 247443_at 247398_at 247308_at 247303_at	0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6
membrane related protein-like ;supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_1632317 translation initiation factor-like protein putative protein contains similarity to NRK-related kinase selenium-binding protein-like beta-amylase ; supported by cDNA: gi_15027954_gb_AY045834.1_ heat shock protein (emb CAA72514.1) beta-1,3-glucanase-like protein N-myristoyl transferase ;supported by full-length cDNA: Ceres:36525. Expressed protein similar to unknown protein (pirl S75584) ;supported by full-length cDNA: Ceres:3488. phytochelatin synthetase - like protein putative phytochelatin synthetase, Arabidopsis thaliana, EMBL:ATH6787;supported by full-length cDN/ putative protein predicted proteins, from different species; supported by cDNA: Geres: 38273. putative protein predicted protein, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 1000, full-length cDNA: Ceres: 1000, full-length cDNA: Ceres: 1000, full-length cDNA: Geres: 1000, ful	248199_at 248153_at 248153_at 248060_at 248075_at 248029_at 247963_at 247960_at 247924_at 2477816_at 247552_at 247555_at 247443_at 247368_at 247303_at 247307_at	0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6 0.6
membrane related protein-like ;supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_1632317 translation initiation factor-like protein putative protein contains similarity to NRK-related kinase selenium-binding protein-like beta-amylase ; supported by cDNA: gi_15027954_gb_AY045834.1_ heat shock protein (emb[CAA72514.1) beta-1,3-glucanase-like protein N-myristoyl transferase ; supported by full-length cDNA: Ceres:36525. Expressed protein similar to unknown protein (pirl S75584) ;supported by full-length cDNA: Ceres:3488. phytochelatin synthetase - like proteins in putative phytochelatin synthetase, Arabidopsis thaliana, EMBL:ATH6787;supported by full-length cDN, putative protein various predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_15912286_gb_AY056421.1_ putative protein contains similarity to kinase histidinol dehydrogenase ;supported by full-length cDNA: Ceres:40175. UVB-resistance protein UVR8 (gb]AAD43920.1) ; supported by cDNA: gi_5478529_gb_AF130441.1_AF130441 putative protein strong similarity to unknown protein (gb AAF01562.1)	248199_at 248153_at 248153_at 248060_at 248075_at 248029_at 247963_at 247963_at 247964_at 247924_at 247816_at 247552_at 2474555_at 24743_at 247308_at 247308_at 247307_at 247312_at	0.6 0.6
membrane related protein-like ;supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_163231; translation initiation factor-like protein putative protein contains similarity to NRK-related kinase selenium-binding protein-like beta-amylase ; supported by cDNA: gi_15027954_gb_AY045834.1_ heat shock protein (emb CAA72514.1) beta-1,3-glucanase-like protein N-myristoyl transferase ;supported by full-length cDNA: Ceres:36525. Expressed protein similar to unknown protein (pirl S75584) ;supported by full-length cDNA: Ceres:3488. phytochelatin synthetase - like protein putative phytochelatin synthetase, Arabidopsis thaliana, EMBL:ATH6787;supported by full-length cDNA; putative protein predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_15912286_gb_AY056421.1_ putative protein predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 38273. putative protein predicted proteins, Arabidopsis thaliana putative protein predicted proteins, Arabidopsis thaliana; putative protein predicted proteins, Arabidopsis thaliana putative protein contains similarity to kinase histidinol dehydrogenase; supported by full-length cDNA: Ceres:40175. UVB-resistance protein UVR8 (gb AAD43920.1); supported by cDNA: gi_5478529_gb_AF130441.1_AF130441 putative protein strong similarity to unknown protein (gb AAF01562.1) fructose-bisphosphatase-like protein ; supported by full-length cDNA: Ceres:1888.	248199_at 248153_at 24805_at 248075_at 248075_at 248043_s_at 247963_at 247960_at 247960_at 247924_at 247752_at 247555_at 247555_at 247308_at 247308_at 247303_at 247307_at 247278_at	0.6 0.6
membrane related protein-like ;supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_1632317 translation initiation factor-like protein putative protein contains similarity to NRK-related kinase selenium-binding protein-like beta-amylase ; supported by cDNA: gi_15027954_gb_AY045834.1_ heat shock protein (emb CAA72514.1) beta-1,3-glucanase-like protein N-myristoyl transferase ;supported by full-length cDNA: Ceres:36525. Expressed protein similar to unknown protein (pir][S75584) ;supported by full-length cDNA: Ceres:3488. phytochelatin synthetase - like protein putative phytochelatin synthetase, Arabidopsis thaliana, EMBL:ATH6787;supported by full-length cDNA: putative protein predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_15912286_gb_AY056421.1_ putative protein predicted protein, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 38273. putative protein predicted protein, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 38273. putative protein predicted protein, Arabidopsis thaliana histidinol dehydrogenase ;supported by full-length cDNA: Ceres:40175. UVB-resistance protein UVR8 (gb AAD43920.1) ; supported by cDNA: gi_5478529_gb_AF130441.1_AF130441 putative protein strong similarity to unknown protein (gb AAF01562.1) fructose-bisphosphatase-like protein ;supported by full-length cDNA: Ceres:1888. auxin-independent growth promoter-like protein	248199_at 248195_at 248153_at 248060_at 248075_at 248029_at 247963_at 247960_at 247924_at 247924_at 2477816_at 247555_at 247433_at 247308_at 247303_at 247307_at 247312_at 247237_at	0.6 0.6
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membrane related protein-like ; supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_163231; translation initiation factor-like protein putative protein contains similarity to NRK-related kinase selenium-binding protein-like beta-amylase ; supported by cDNA: gi_15027954_gb_AY045834.1_ heat shock protein (emb[CAA72514.1) beta-1,3-glucanase-like protein N-myristoyl transferase ; supported by full-length cDNA: Ceres:36525. Expressed protein similar to unknown protein (pir][S75584) ; supported by full-length cDNA: Ceres:3488. phytochelatin synthetase - like protein putative phytochelatin synthetase, Arabidopsis thaliana, EMBL:ATH6787; supported by full-length cDNA putative protein predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 3487. putative protein predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 38273. putative protein predicted proteins, Arabidopsis thaliana putative protein predicted protein, Arabidopsis thaliana; supported by cDNA: gi_5478529_gb_AF130441.1_AF130441 UVB-resistance protein UVR8 (gb]AAD43920.1); supported by cDNA: gi_5478529_gb_AF130441.1_AF130441 putative protein protein ceredicting supported by full-length cDNA: Ceres:1888. auxin-independent growth promoter-like protein 4-alpha-glucanotransferase ; supported by cDNA: gi_14334479_gb_AY037231.1_ unknown protein unknown protein ; supported by cDNA: gi_14334479_gb_AY034931.1_ 3-dehydroguinate synthase-like protein ; supported by full-length cDNA: Ceres:117923. selenium-binding protein-like succinate dehydrogeneae flavoprotein alpha subunit (emb[CAA05025.1) ; supported by cDNA: gi_15010745_gb_AY045674.1_ formi-like protein putative protein similar to unknown protein (gb]AAD25674.1) putative protein similar to unknown protein [gb]AAD25674.1) putative protein similar to unknown protein [gb]AAD25674.1) putative protein isopnicillin N epimerase, Streptomyces clavuligerus, EMBL:	248199_at 248193_at 248153_at 248060_at 248075_at 248029_at 247963_at 247963_at 247960_at 247924_at 2477824_at 24778255_at 24778255_at 2477433_at 247303_at 247303_at 247307_at 247312_at 247237_at 247216_at 247216_at 247216_at 247166_at 247166_at 247114_at 247138_at 247100_at 246955_at 246955_at 246955_at 246955_at 246955_at 246955_at	0.6 0.6
membrane related protein-like ; supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_163231; translation initiation factor-like protein putative protein contains similarity to NRK-related kinase selenium-binding protein-like beta-amylase ; supported by cDNA: gi_15027954_gb_AY045834.1_ heat shock protein (emb[CAA72514.1) beta1.3;giucanase-like protein N-myristoyl transferase ; supported by full-length cDNA: Ceres:36525. Expressed protein similar to unknown protein (pir][S75584) ; supported by full-length cDNA: Ceres:3488. phytochelatin synthetase - like protein putative phytochelatin synthetase, Arabidopsis thaliana, EMBL:ATH6787; supported by full-length cDNA: putative protein predicted proteins, frabidopsis thaliana; supported by full-length cDNA: Ceres:3488. phytochelatin synthetase - like protein putative phytochelatin synthetase, Arabidopsis thaliana, EMBL:ATH6787; supported by full-length cDNA: putative protein predicted proteins, Arabidopsis thaliana; putative protein predicted proteins, Arabidopsis thaliana; putative protein predicted proteins, Arabidopsis thaliana putative protein predicted proteins, Arabidopsis thaliana putative protein predicted proteins, Arabidopsis thaliana putative protein predicted proteins, Supported by CDNA: Geres:40175. UVB-resistance protein UVR8 (gb]AAD43920.1); supported by CDNA: Gi_5478529_gb_AF130441.1_AF130441 putative protein strong similarity to unknown protein (gb]AAF01562.1) fructose-bisphosphatase-like protein supported by cDNA: gi_1433479_gb_AY037231.1_ unknown protein unknown protein supported by cDNA: gi_1433479_gb_AY034931.1_ 3-dehydroginate synthase-like protein (gb]AAD25674.1) putative protein similar to unknown protein (gb]AAD25674.1] putative protein similar to unknown protein (gb]AAD25674.1] putative protein similar to unknown protein (gb]AAD25674.1] putative protein similar to unknown protein Ispense flavgorotein alpha subunit (emb]CAA05025.1);	248199_at 248195_at 248153_at 248055_at 248075_at 248029_at 247960_at 247960_at 247960_at 247924_at 247924_at 247525_at 247555_at 247555_at 247443_at 247307_at 247307_at 247307_at 247312_at 247216_at 247766_at 247716_at 247710_at 247710_at 247706_at 247100_at 247060_at 246958_at 246958_at 246964_at 246831_at 246748_at	$egin{array}{cccc} 0.6\\ 0.6\\ 0.6\\ 0.6\\ 0.6\\ 0.6\\ 0.6\\ 0.6\\$
membrane related protein-like :supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_163231; translation initiation factor-like protein putative protein contains similarity to NRK-related kinase selenium-binding protein-like beta-amylase : supported by cDNA: gi_15027954_gb_AY045834.1_ heat shock protein (emb[CAA72514.1) beta-1.3; gtucanase-like protein N-myristoyl transferase :supported by full-length cDNA: Ceres:36525. Expressed protein (similar to unknown protein (pir][S75584] ;supported by full-length cDNA: Ceres:3488. phytochelatin synthetase - like protein putative phytochelatin synthetase, Arabidopsis thaliana, EMBL:ATH6787;supported by full-length cDNA: putative protein various predicted proteins from different species; supported by DNA: gi_1592286_gb_AY056421.1_ putative protein predicted proteins from different species; supported by DNA: gi_15912286_gb_AY056421.1_ putative protein predicted proteins from different species; supported by DNA: gi_1691287. UVB-resistance protein uravious predicted protein (binase histidinol dehydrogenase :supported by full-length cDNA: Ceres:40175. UVB-resistance protein UVR8 (gb]AAD43920.1) ; supported by cDNA: gi_5478529_gb_AF130441.1_AF130441 putative protein strong similarity to unknown protein (gb]AAF01652.1) fructose-bisphosphatase-like protein :supported by full-length cDNA: Ceres:1888. auxin-independent growth promoter-like protein 4-alpha-glucanotransferase ; supported by full-length cDNA: Ceres:117923. selenium-binding protein-like protein alpha subunit (emb]CAA05025.1) ; supported by cDNA: gi_15010745_gb_AY045674.1_ formin-like protein ing protein-like protein alpha subunit (emb]CAA05025.1) ; supported by cDNA: gi_15010745_gb_AY045674.1_ formin-like protein ing protein-like protein alpha subunit (emb]CAA05025.1) ; supported by cDNA: gi_15010745_gb_AY045674.1_ putative protein insportein for Unknown protein (gb]AAD25674.1) putative protein isminiar to	248199_at 248199_at 248153_at 248075_at 248075_at 248029_at 247960_at 247960_at 247960_at 247924_at 2477816_at 247552_at 247552_at 247443_at 247308_at 247308_at 247303_at 247307_at 247312_at 247216_at 247278_at 247278_at 247216_at 247114_at 24716_at 247114_at 247100_at 247060_at 246995_at 246958_at 246632_at 246762_at 246759_at	$egin{array}{cccc} 0.6\\ 0.6\\ 0.6\\ 0.6\\ 0.6\\ 0.6\\ 0.6\\ 0.6\\$
membrane related protein-like ; supported by full-length cDNA: Ceres:37644. cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_163231; translation initiation factor-like protein putative protein contains similarity to NRK-related kinase selenium-binding protein-like beta-amylase ; supported by cDNA: gi_15027954_gb_AY045834.1_ heat shock protein (emb[CAA72514.1) beta1.3;glucanase-like protein N-myristoyl transferase ; supported by full-length cDNA: Ceres:36525. Expressed protein similar to unknown protein (pir][S75584) ; supported by full-length cDNA: Ceres:3488. phytochelatin synthetase - like protein putative phytochelatin synthetase, Arabidopsis thaliana, EMBL:ATH6787; supported by full-length cDNA: putative protein predicted proteins, frabidopsis thaliana; supported by full-length cDNA: Ceres:3488. phytochelatin synthetase - like protein putative phytochelatin synthetase, Arabidopsis thaliana, EMBL:ATH6787; supported by full-length cDNA: putative protein predicted proteins, Arabidopsis thaliana; putative protein predicted proteins, Arabidopsis thaliana; putative protein predicted protein, Arabidopsis thaliana putative protein predicted proteins, Arabidopsis thaliana putative protein predicted protein, Supported by CDNA: Geres:40175. UVB-resistance protein UVR8 (gb]AAD43920.1); supported by CDNA: Gi_5478529_gb_AF130441.1_AF130441 putative protein strong similarity to unknown protein (gb]AAF01562.1) fructose-bisphosphatase-like protein = supported by cDNA: gi_1433479_gb_AY037231.1_ unknown protein unknown protein supported by cDNA: gi_1433479_gb_AY034931.1_ 3-dehydroginate synthase-like protein ; supported by full-length cDNA: Ceres:117923. selenium-binding protein-like succinate dehydrogenase flavoprotein alpha subunit (emb]CAA05025.1) ; supported by cDNA: gi_15010745_gb_AY045674.1_ formin-like protein - Zea mays, PIR:T01685 hexose transporter - like protein in cunknown protein (gb]AAD25674.1) putative protein isopenicIllin N epimerase,	248199_at 248195_at 248153_at 248055_at 248075_at 248029_at 247960_at 247960_at 247960_at 247924_at 247924_at 247525_at 247555_at 247555_at 247443_at 247307_at 247307_at 247307_at 247312_at 247216_at 247766_at 247716_at 247710_at 247710_at 247706_at 247100_at 247060_at 246958_at 246958_at 246964_at 246831_at 246748_at	$egin{array}{cccc} 0.6\\ 0.6\\ 0.6\\ 0.6\\ 0.6\\ 0.6\\ 0.6\\ 0.6\\$

bystin, putative similar to bystin GI:1160618 from [Homo sapiens]	246575_at	0.6
putative protein hypothetical protein T2E12.2 - Arabidopsis thaliana, EMBL:AC015986	246495_at	0.6
syntaxin homologue ;supported by full-length cDNA: Ceres:8257.	246453_at	0.6
unknown protein contains similarity to beta-1,4 mannosyltransferase GI:60970470 from [Homo sapiens]	246351_at	0.6
putative protein predicted protein BAA88548.1- Oryza sativa, EMBL:AP000969;supported by full-length cDNA: Ceres:18436.	246318_at 246288_at	0.6 0.6
unknown protein tubulin-like protein	246278 at	0.6
uuuinimee protein putative protein predicted protein, Haemophilus influenzae	246169 at	0.6
DNA binding protein ACBF - like DNA binding protein ACBF, Nicotiana tabacum, PIR:T03934	246064 at	0.6
putative protein predicted proteins, Drosophila melanagoster and Homo sapiens; supported by cDNA: gi 13605552 gb AF361602.1 AF361	246045 at	0.6
putative protein KED, Nicotiana tabacum, EMBL:AB009883	246059 at	0.6
putative protein predicted proteins from various species;supported by full-length cDNA: Ceres:10217.	246017_at	0.6
putative protein predicted proteins, Arabidopsis thaliana and Oryza sativa; supported by full-length cDNA: Ceres: 254744.	246019_at	0.6
ascorbate oxidase-like protein ascorbate oxidase - Brassica juncea, EMBL:AF206721	246021_at	0.6
leucine-rich repeat protein ; supported by cDNA: gi_13358181_gb_AF324989.2_AF324989	246029_at	0.6
putative protein outer membrane protein (IAP75) - Pisum sativum, L36858; supported by cDNA: gi_13430585_gb_AF360205.1_AF360205	245914_at	0.6
hypothetical protein predicted by genemark.hmm	245770_at	0.6
hypothetical protein contains similarity to glucosidase II beta-subunit GI:5452942 from [Mus musculus]	245727_at	0.6 0.6
SNF1 like protein kinase ; supported by cDNA: gi_13249502_gb_AY007221.1_ phosphatase like protein	245563_at 245557_at	0.6
hypothetical ince protein	245517 at	0.6
F-box protein family, AtFBL4 contains similarity to grr1 GI:2407790 from [Glycine max]; supported by full-length cDNA: Ceres:100411.	245344 at	0.6
nuclear antigen homolog supported by full-length cDNA: Ceres: 118826.	245350 at	0.6
UFD1 like protein ; supported by full-length cDNA: Ceres: 207652.	245313 at	0.6
Expressed protein ; supported by full-length cDNA: Ceres: 30227.	245319_at	0.6
Expressed protein ; supported by full-length cDNA: Ceres: 307.	245321_at	0.6
calcium-dependent protein kinase-like protein strong similarity to calcium-dependent protein kinase 19, Arabidopsis thaliana, PIR:S71778~Cc	245156_at	0.6
unknown protein	245134_s_at	0.6
putative cytochrome P450 ; supported by cDNA: gi_15810181_gb_AY056105.1_	245101_at	0.6
PSII 43 KDa protein	245003_at	0.6
orf153b orf153b	244923_s_at	0.6
unknown protein putative protein similarity to NCA2 protein, veast, PIR:S54389~Contains Homeobox domain signature and profile AA305-328	257459_at 245206 at	0.6 0.6
putative protein similarity to took protein yeas, inc. 394367-011ains Homeobox domain signature and profile AA303-326 unknown protein (supported by full-length CDNA; Ceres:6967.	265284 at	0.0
unknown protein contains similarity to guarine nucleotide exchange factor GI:4220427 from [Homo sapiens]; supported by cDNA: gi 158113€	-	0.5
putative replication factor Similar to gb/M87339 replication factor C, 37-kDa subunit from Homo sapiens and is a member of PF/00004 ATPas		0.5
hypothetical protein contains similarity to phosphatidyl-inositol-glycan protein GI:303615 from [Homo sapiens]	261835 at	0.5
unknown protein ;supported by full-length cDNA: Ceres:21241.	260868_at	0.5
putative splicing factor	260606_at	0.5
putative protein kinase contains Pfam profile: PF00069 Eukaryotic protein kinase domain	260206_at	0.5
hypothetical protein contains Pfam profile: PF00515 TPR Domain (5 copies)	259973_at	0.5
putative small nuclear ribonucleoprotein (Sm-D1) similar to small nuclear ribonucleoprotein (Sm-D1) GB:AAD15345 [Arabidopsis thaliana];sur	_	0.5
unknown protein ; supported by cDNA: gi_15027906_gb_AY045810.1_	257989_at	0.5
hypothetical protein use sure statis cartains similarity to expected a rate of TEAD10 Cl/0407060 from Ulano caria cloure and hy full length a DNA. Cou	256172_at	0.5
unknown protein contains similarity to apoptosis-related protein TFAR19 GI:2407068 from [Homo sapiens];supported by full-length cDNA: Cer putative protein hypothetical protein T29E15.27 - Arabidopsis thaliana,PID:g3738334	256001_at 253586 s at	0.5 0.5
DNA topoisomerase like- protein Bacillus subtilis DNA Topoisomerase I; PID:G520753	253566 at	0.5
ubiquitin-specific protesses 3 (UBP3) identical to Gi:2347098; supported by CDNA: gi 2347097 gb U76845.1 ATU76845	252832 at	0.5
cell division cycle protein 23 homolog cell division cycle protein 23 - Homo sapiens, PID:g3283051	252349 at	0.5
putative protein putative protein At2g25690 - Arabidopsis thaliana, EMBL:AC006053;supported by full-length cDNA: Ceres:40080.	251169_at	0.5
putative protein Ube-1a, Mus musculus, EMBL:AB030503	250880_at	0.5
putative protein similar to unknown protein (emb CAB62355.1)	249329_at	0.5
histone acetyltransferase HAT B	247972_at	0.5
glycine-rich RNA-binding protein - like glycine-rich RNA-binding protein (GRRBP2), Euphorbia esula, TREMBL:AF031933; supported by full-le		0.5
hypothetical protein contains similarity to virulence regulator GI:9106522 from [Xylella fastidiosa]	245751_s_at	0.5
	FFX-CreX-3_a	0.5
Arabidopsis thaliana /REF=U84969 /DEF=ubiquitin (UBQ11) gene, complete cds /LEN=1140 (_5, _M, _3 represent transcript regions 5 primex		0.5
unknown protein ; supported by cDNA: gi_13605814_gb_AF367306.1_AF367306 E2, ubiquitin-conjugating enzyme 2 (UBC2) identical to gi:2689242, SP:P42745; supported by cDNA: gi_12083309 gb_AF332451.1_AF3324	267558_at 267484_at	0.5 0.5
CPDK-related protein kinase CDPK-relation dependent protein kinase; supported by CDA: gj 5020365 gb AF153351.1 AF153351	267082_at	0.5
mitochondrial ribosomal protein S14	266955 at	0.5
hypothetical protein predicted by grail;supported by full-length cDNA: Ceres:142426.	266847 at	0.5
putative NADH dehydrogenase (ubiquinone oxidoreductase)	266835 at	0.5
putative nucleotide-binding protein ;supported by full-length cDNA: Ceres:33511.	266801_at	0.5
unknown protein	266771_s_at	0.5
putative squamosa-promoter binding protein	266748_at	0.5
hypothetical protein predicted by genscan; supported by cDNA: gi_15294291_gb_AF410337.1_AF410337	266660_at	0.5
unknown protein ; supported by cDNA: gi_16604658_gb_AY059774.1_	266519_at	0.5
unknown protein ;supported by full-length cDNA: Ceres:12017.	266448_s_at	0.5
putative nonspecific lipid-transfer protein ;supported by cDNA: gi_15146309_gb_AY049296.1_ unknown protein	266421_at 266424 at	0.5 0.5
putative cytochrome P450	266321 at	0.5
hypothetical protein predicted by genscan	266080 at	0.5
unknown protein ; supported by cDNA: gi_15450955_gb_AY054558.1_	265799_at	0.5
putative membrane transporter	265759_at	0.5
putative WRKY DNA-binding protein ; supported by cDNA: gi_13506736_gb_AF224701.1_AF224701	265718_at	0.5
unknown protein ; supported by cDNA: gi_15028290_gb_AY045948.1_		0.5
aquaporin (plasma membrane intrinsic protein 2C) water channel protein in plasma membrane; supported by full-length cDNA: Ceres:11998.	265444_s_at	0.5
	265107_s_at	0.5
unknown protein similar to putative tyrosine phosphatase GB:AAF81798 GI:8926334 from [Oryza sativa]; supported by full-length cDNA: Cere	265073_at	0.5
hypothetical protein contains similarity to ABC transporter protein GI:6626257 from [Methanobacterium thermoautotrophicum]	265061_at	0.5
unknown protein ;supported by full-length cDNA: Ceres: 13008.	264984_at	0.5
putative calmodulin-domain protein kinase CPK6 (calmodulin-domain protein kinase isoform 6, accession U31835); supported by cDNA: gi_1	264851_at	0.5

putative indole-3-acetate beta-glucosyltransferase similar to GB:AAB64022; supported by cDNA: gi_14423541_gb_AF387008.1_AF387008		
	264873_at 0	).5
hypothetical protein predicted by genemark.hmm	264731 at 0	).5
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi 14532671 gb AY039960.1		.5
unknown protein Contains similarity to Bos beta-mannosidase (gb[U46067); supported by cDNA: gi 15028222 gb AY045934.1	—	).5
hypothetical protein contains similarity to Nicotiana tabacum membrane-associated salt-inducible protein (GB:U08285);supported by full-lengt		).5
putative 60S ribosomal protein L17 similar to GB:P51413 from [Arabidopsis thaliana]; similar to ESTs gb[L33542 and gb]AA660016;supported	_	).5
	_	).5
putative heat-shock protein similar to CB:AAD39315;supported by full-length cDNA: Ceres:37036.	—	
hypothetical protein predicted by genemark.hmm		).5
putative chromodomain-helicase-DNA-binding protein similarity to Mi-2, Homo sapiens, GB:X86691; supported by cDNA: gi_6318929_gb_AF	_	).5
putative translation initiation factor eIF-2, gamma subunit similar to gb U37354 from S. pombe. ESTs gb T41979, gb N37284 and gb N37529	_	).5
hypothetical protein similar to hypothetical protein GI:2894569 from [Arabidopsis thaliana]; supported by cDNA: gi_15028186_gb_AY045916.	264289_at 0	).5
hypothetical protein contains similarity to chloroplast membrane-associated protein IM30 GI:169106 from [Pisum sativum]; supported by full-lei	264158_at 0	).5
hypothetical protein predicted by genscan	264171 at 0	).5
unknown protein similar to FUS5 protein of the COP9 complex, GB:AAC25563;supported by full-length cDNA: Ceres:40042.	_	).5
mercaptopyruvate sulfurtransferase (Mst1/Rdh1) identical to mercaptopyruvate sulfurtransferase GI:6009981 and thiosulfate sulfurtransferase	—	).5
	_	0.5
translin-like protein; supported by cDNA: gj_14596008_gb_AY042792.1		
putative vacuolar proton-ATPase subunit; supported by cDNA: gi_15450750_gb_AY053417.1_		0.5
putative cap-binding protein; supported by cDNA: gi_15192737_gb_AF272891.1_AF272891		.5
putative DNA-directed RNA polymerase II subunit	_	).5
putative steroid binding protein ;supported by full-length cDNA: Ceres:10261.	263534_at 0	).5
molybdopterin synthase (CNX2) ;supported by full-length cDNA: Ceres:33192.	263472_at 0	).5
putative ATP-dependent RNA helicase	263435 at 0	).5
transcription initiation factor, putative similar to transcription initiation factor iif, beta subunit GB:CAA22523 GI:4049502 from [Schizosaccharo		).5
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi 15146253 gb AY049268.1	_	.5
unknown protein ;supported by full-length cDNA: Ceres:21947.		).5
auxin response factor 1 identical to auxin response factor 1 Gi:2245378 from [Arabidopsis thaliana]; supported by cDNA; gi 2245377 gb U8;	_	).5
lipase, putative contains Pfam profile: PF00657 Lipase/Acylhydrolase with GDSL-like motif; supported by cDNA: gi_15027914_gb_AY045814	_	).5
unknown protein ESTs gb F15498, gb H37515, gb T41906, gb T22448, gb W43356 and gb T20739 come from this gene; supported by full-ler		).5
sterol glucosyltransferase, putative similar to sterol glucosyltransferase GI:4731867 from [Dictyostelium discoideum]		).5
unknown protein similar to hypothetical protein GB:AAD41412 GI:5263310 from (Arabidopsis thaliana); supported by cDNA: gi_13265575_gb	262502_at 0	).5
serpin, putative similar to serpin GB:X95277 GI:1197576 from (Hordeum vulgare)	262440 at 0	).5
Expressed protein ; supported by full-length cDNA: Ceres: 97474.		).5
unknown protein		).5
unknown protein contains similarity to 1-aminocyclopropane-1-carboxylate deaminases	_	).5
	—	
hypothetical protein predicted by genscan+		).5
hypothetical protein contains similarity to protien kinase C (PRKC) GI:155789 from [Aplysia californica]		).5
hypothetical protein contains similarity to nodule-specific protein NIj70 GI:3329366 from [Lotus japonicus]		0.5
Expressed protein ; supported by full-length cDNA: Ceres: 12159.	262056_at 0	).5
hypothetical protein predicted by genemark.hmm	261909_at 0	).5
adenine nucleotide translocase, putative similar to adenine nucleotide translocase GI:6469340 from [Arabidopsis thaliana]; supported by full-le	261767 s at 0	).5
hypothetical protein predicted by genemark.hmm		).5
unknown protein similar to putative esterase GB:AAD17422 GI:4335745 from [Arabidopsis thaliana]		).5
		).5
NAC domain protein, putative similar to NAC domain protein NAM GB:AAD17313 GI:432528 from [Arabidopsis thaliana];supported by full-le		
		).5
hypothetical protein	261553_at 0	).5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf	261553_at 0 261513_at 0	).5 ).5
	261553_at 0 261513_at 0	).5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf	261553_at 0 261513_at 0 261519_at 0	).5 ).5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/	261553_at 0 261513_at 0 261519_at 0 261418_at 0	).5 ).5 ).5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm	261553_at         0           261513_at         0           261519_at         0           261418_at         0           261322_at         0	).5 ).5 ).5 ).5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein	261553_at         0           261513_at         0           261519_at         0           261418_at         0           261322_at         0           261299_at         0	).5 ).5 ).5 ).5 ).5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein unknown protein ;supported by full-length cDNA: Ceres:6332.	261553_at         0           261513_at         0           261519_at         0           261418_at         0           261322_at         0           261299_at         0           261225_at         0	).5 ).5 ).5 ).5 ).5 ).5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein ; supported by full-length cDNA: Ceres:6332. unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_	261553_at         0           261513_at         0           261519_at         0           261418_at         0           26132_at         0           26132_at         0           26125_at         0           261225_at         0           261209_at         0	).5 ).5 ).5 ).5 ).5 ).5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF0069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein supported by full-length cDNA: Ceres:6332. unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica)	261553_at         0           261513_at         0           261519_at         0           261418_at         0           261322_at         0           261225_at         0           261225_at         0           261209_at         0           261209_at         0           261209_at         0           261209_at         0           261209_at         0           261209_at         0	).5 ).5 ).5 ).5 ).5 ).5 ).5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein unknown protein ; supported by full-length cDNA: Ceres:6332. unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein	261553_at         0           261513_at         0           261519_at         0           261418_at         0           261322_at         0           261225_at         0           261225_at         0           26129_at         0           26129_at         0           26129_at         0           26129_at         0           26129_at         0           26175_at         0	).5 ).5 ).5 ).5 ).5 ).5 ).5 ).5 ).5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein unknown protein ; supported by full-length cDNA: Ceres:6332. unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein hypothetical protein contains similarity to RNA helicase (HRH1) GB:D50487 GI:1742909 from [Homo sapiens]	261553_at         0           261513_at         0           261519_at         0           261418_at         0           26129_at         0           261225_at         0           261209_at         0           26127_at         0           26129_at         0           26129_at         0           26129_at         0           26129_at         0           26139_at         0           261075_at         0           261008_at         0	).5 ).5 ).5 ).5 ).5 ).5 ).5 ).5 ).5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein unknown protein ; supported by full-length cDNA: Ceres:6332. unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein hypothetical protein contains similarity to RNA helicase (HRH1) GB:D50487 GI:1742909 from [Homo sapiens] transmembrane protein, putative similar to TRANSMEMBRANE PROTEIN TMP21 GB:Q63584 from [Rattus norvegicus]	261553_at         0           261513_at         0           261519_at         0           261418_at         0           26132_at         0           261425_at         0           261225_at         0           261209_at         0           261205_at         0           261205_at         0           261075_at         0           26108_at         0           260852_at         0	0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein ; supported by full-length cDNA: Ceres:6332. unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein hypothetical protein contains similarity to RNA helicase (HRH1) GB:D50487 GI:1742909 from [Homo sapiens] transmembrane protein, putative similar to TRANSMEMBRANE PROTEIN TMP21 GB:Q63584 from [Rattus norvegicus] protein kinase interactor, putative similar to Pto kinase interactor GB:1AAC61805 GI:3668069 from [Lycopersicon esculentum]; supported by	261553_at         0           261513_at         0           261519_at         0           261418_at         0           261422_at         0           261225_at         0           261225_at         0           261225_at         0           26125_at         0           26109_at         0           26109_at         0           261075_at         0           260852_at         0           260855_at         0	).5 ).5 ).5 ).5 ).5 ).5 ).5 ).5 ).5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein unknown protein ; supported by full-length cDNA: Ceres:6332. unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein hypothetical protein contains similarity to RNA helicase (HRH1) GB:D50487 GI:1742909 from [Homo sapiens] transmembrane protein, putative similar to TRANSMEMBRANE PROTEIN TMP21 GB:Q63584 from [Rattus norvegicus]	261553_at         0           261513_at         0           261519_at         0           261418_at         0           261422_at         0           261225_at         0           261225_at         0           261225_at         0           26125_at         0           26109_at         0           26109_at         0           261075_at         0           260852_at         0           260855_at         0	0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein ; supported by full-length cDNA: Ceres:6332. unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein hypothetical protein contains similarity to RNA helicase (HRH1) GB:D50487 GI:1742909 from [Homo sapiens] transmembrane protein, putative similar to TRANSMEMBRANE PROTEIN TMP21 GB:Q63584 from [Rattus norvegicus] protein kinase interactor, putative similar to Pto kinase interactor GB:1AAC61805 GI:3668069 from [Lycopersicon esculentum]; supported by	261553_at         0           261513_at         0           261519_at         0           261418_at         0           261422_at         0           261225_at         0           261225_at         0           261209_at         0           261008_at         0           261008_at         0           260835_at         0           260746_at         0	0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein unknown protein ; supported by full-length cDNA: Ceres:6332. unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein hypothetical protein contains similarity to RNA helicase (HRH1) GB:D50487 GI:1742909 from [Homo sapiens] transmembrane protein, putative similar to TRANSMEMBRANE PROTEIN TMP21 GB:Q63584 from [Rattus norvegicus] protein kinase interactor, putative similar to glutathione transferase GI:2853219 from [Carica papaya]; supported by full-length cDNA: Ceres: 3	261553_at         0           261513_at         0           261519_at         0           261418_at         0           261299_at         0           261225_at         0           261322_at         0           261225_at         0           26139_at         0           26129_at         0           26139_at         0           26108_at         0           26108_at         0           260852_at         0           260746_at         0           260714_at         0	0.5 0.5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein ; supported by full-length cDNA: Ceres:6332. unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein hypothetical protein contains similarity to RNA helicase (HRH1) GB:D50487 GI:1742909 from [Homo sapiens] transmembrane protein, putative similar to TRANSMEMBRANE PROTEIN TMP21 GB:Q63584 from [Rattus norvegicus] protein kinase interactor, putative similar to Pto kinase interactor GB:1AAC61805 GI:368069 from [Lycopersicon esculentum]; supported by glutathione transferase, putative similar to SP:P34803 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 26943. unknown protein ; supported by full-length cDNA: Ceres:41461.	261553_at         0           261513_at         0           261519_at         0           261418_at         0           26122_at         0           261225_at         0           26129_at         0           26129_at         0           26129_at         0           26129_at         0           261075_at         0           26108_at         0           260852_at         0           260746_at         0           260746_at         0           260665_at         0	0.5 0.5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein ; supported by full-length cDNA: Ceres:6332. unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein hypothetical protein contains similarity to RNA helicase (HRH1) GB:D50487 GI:1742909 from [Homo sapiens] transmembrane protein, putative similar to TRANSMEMBRANE PROTEIN TMP21 GB:Q63584 from [Rattus norvegicus] protein kinase interactor, putative similar to Pto kinase interactor GB:1AAC61805 GI:3668069 from [Lycopersicon esculentum]; supported by glutathione transferase, putative similar to pto kinase interactor GB:1AAC61805 GI:3668069 from [Lycopersicon esculentum]; supported by glutathione transferase, putative similar to glutathione transferase GI:2853219 from [Carica papaya]; supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:26943. unknown protein	261553_at         0           261553_at         0           261519_at         0           261418_at         0           261418_at         0           261322_at         0           261225_at         0           261225_at         0           26109_at         0           261075_at         0           26108_at         0           26108_at         0           260852_at         0           260835_at         0           260746_at         0           26065_at         0           26065_at         0	0.5 0.5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein unknown protein ; supported by full-length cDNA: Ceres:6332. unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein hypothetical protein contains similarity to RNA helicase (HRH1) GB:D50487 GI:1742909 from [Homo sapiens] transmembrane protein, putative similar to Pto kinase interactor GB:1AAC61805 GI:3668069 from [Lycopersicon esculentum]; supported by glutathione transferase, putative similar to glutathione transferase GI:2853219 from [Carica papaya]; supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres: 26943. unknown protein putative WD-40 repeat protein	261553_at         0           261513_at         0           261519_at         0           261418_at         0           261418_at         0           261422_at         0           261225_at         0           261225_at         0           26109_at         0           261075_at         0           261008_at         0           260852_at         0           260746_at         0           260665_at         0           2606526_at         0           260526_at         0	0.5 0.5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein i ; supported by full-length cDNA: Ceres:6332. unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein hypothetical protein contains similarity to RNA helicase (HRH1) GB:D50487 GI:1742909 from [Homo sapiens] transmembrane protein, putative similar to TRANSMEMBRANE PROTEIN TMP21 GB:Q63584 from [Rattus norvegicus] protein kinase interactor, putative similar to glutathione transferase GI:2853219 from [Carica papaya]; supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres: 3 chaperonin Supported by cDNA: gi_2570339_gb_U90928.1_ATU90928	261553_at         0           261513_at         0           261519_at         0           261418_at         0           261422_at         0           261225_at         0           261209_at         0           261209_at         0           261008_at         0           261008_at         0           260746_at         0           260746_at         0           260665_at         0           260665_at         0           260526_at         0           260526_at         0	0.5 0.5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein hypothetical protein contains similarity to RNA helicase (HRH1) GB:D50487 GI:1742909 from [Homo sapiens] transmembrane protein, putative similar to TRANSMEMBRANE PROTEIN TMP21 GB:Q63584 from [Rattus norvegicus] protein kinase interactor, putative similar to 9to kinase interactor GB:1AAC61805 GI:3668069 from [Lycopersicon esculentum]; supported by glutathione transferase, putative similar to glutathione transferase GI:2853219 from [Carica papaya]; supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres: 26943. unknown protein putative WD-40 repeat protein	261553_at         0           261513_at         0           261519_at         0           261418_at         0           261299_at         0           261225_at         0           261322_at         0           261225_at         0           261322_at         0           26129_at         0           26139_at         0           26108_at         0           260852_at         0           260746_at         0           260746_at         0           260526_at         0           260526_at         0           260526_at         0           260526_at         0           260546_at         0           260526_at         0           260546_at         0	0.5 0.5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein unknown protein ; supported by full-length cDNA: Ceres:6332. unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein hypothetical protein contains similarity to RNA helicase (HRH1) GB:D50487 GI:1742909 from [Homo sapiens] transmembrane protein, putative similar to TRANSMEMBRANE PROTEIN TMP21 GB:Q63584 from [Rattus norvegicus] protein kinase interactor, putative similar to Pto kinase interactor GB:1AAC61805 GI:368068 from [Lycopersicon esculentum]; supported by glutathione transferase, putative similar to Dto kinase interactor GB:1AAC61805 GI:368068 from [Lycopersicon esculentum]; supported by glutathione transferase, putative similar to glutathione transferase GI:2853219 from [Carica papaya]; supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P348893 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 26943. unknown protein putative WD-40 repeat protein putative glyoxalase II ; supported by cDNA: gi_2570339_gb_U90928.1_ATU90928 unknown protein hypothetical protein predicted by genscan+	261553_at         0           261553_at         0           261519_at         0           261418_at         0           261322_at         0           261225_at         0           26125_at         0           26125_at         0           26108_at         0           261075_at         0           260835_at         0           260746_at         0           260652_at         0           260652_at         0           260526_at         0           260552_at         0           260552_at         0           260552_at         0           260552_at         0           260455_at         0	0.5 0.5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein unknown protein ; supported by full-length cDNA: Ceres:6332. unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein hypothetical protein contains similarity to RNA helicase (HRH1) GB:D50487 GI:1742909 from [Homo sapiens] transmembrane protein, putative similar to Pto kinase interactor GB:1AAC61805 GI:3668069 from [Lycopersicon esculentum]; supported by glutathione transferase, putative similar to Pto kinase interactor GB:1AAC61805 GI:3668069 from [Lycopersicon esculentum]; supported by glutathione transferase, putative similar to glutathione transferase GI:2853219 from [Carica papaya]; supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres: 26943. unknown protein putative WD-40 repeat protein putative WD-40 repeat protein putative glyoxalase II ; supported by cDNA: gi_2570339_gb_U90928.1_ATU90928 unknown protein hypothetical protein predicted by genscan+ putative RING zinc finger protein Pfam HMM hit: zinc finger, C3HC4 type (RING finger)	261553_at         0           261513_at         0           261519_at         0           261418_at         0           261418_at         0           261422_at         0           261225_at         0           261225_at         0           261008_at         0           261075_at         0           260835_at         0           260746_at         0           260652at         0           260520_at         0           260520_at         0           260520_at         0           260652at         0           260520_at         0           260552_at         0           260552_at         0           260552_at         0           260446_at         0           260455_at         0           260455_at         0           260455_at         0	0.5 0.5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein i ; supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein , putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein , putative similar to to RNA helicase (HRH1) GB:D50487 GI:1742909 from [Homo sapiens] transmembrane protein, putative similar to TRANSMEMBRANE PROTEIN TMP21 GB:Q63584 from [Rattus norvegicus] protein kinase interactor, putative similar to glutathione transferase GI:2853219 from [Carica papaya]; supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres: 26943. unknown protein putative WD-40 repeat protein putative WD-40 repeat protein putative RVD-40 repeat protein putative RVD-40 repeat protein Pram HMM hit: zinc finger, C3HC4 type (RING finger) GMP synthase similar to GMP synthase GB:6323873 [Saccharomyces cerevisiae]	261553_at         0           261513_at         0           261519_at         0           261418_at         0           261429_at         0           261225_at         0           261209_at         0           261008_at         0           261008_at         0           260746_at         0           260746_at         0           260652_at         0           260526_at         0           260526_at         0           260552_at         0           260446_at         0           260445_at         0           26024_at         0	0.5 $0.5$
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein unknown protein ; supported by full-length cDNA: Ceres:6332. unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein hypothetical protein contains similarity to RNA helicase (HRH1) GB:D50487 GI:1742909 from [Homo sapiens] transmembrane protein, putative similar to Pto kinase interactor GB:1AAC61805 GI:3668069 from [Lycopersicon esculentum]; supported by glutathione transferase, putative similar to Pto kinase interactor GB:1AAC61805 GI:3668069 from [Lycopersicon esculentum]; supported by glutathione transferase, putative similar to glutathione transferase GI:2853219 from [Carica papaya]; supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres: 26943. unknown protein putative WD-40 repeat protein putative WD-40 repeat protein putative glyoxalase II ; supported by cDNA: gi_2570339_gb_U90928.1_ATU90928 unknown protein hypothetical protein predicted by genscan+ putative RING zinc finger protein Pfam HMM hit: zinc finger, C3HC4 type (RING finger)	261553_at         0           261513_at         0           261519_at         0           261418_at         0           261429_at         0           261225_at         0           261209_at         0           261008_at         0           261008_at         0           260746_at         0           260746_at         0           260652_at         0           260526_at         0           260526_at         0           260552_at         0           260446_at         0           260445_at         0           26024_at         0	0.5 0.5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein i ; supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein , putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein , putative similar to to RNA helicase (HRH1) GB:D50487 GI:1742909 from [Homo sapiens] transmembrane protein, putative similar to TRANSMEMBRANE PROTEIN TMP21 GB:Q63584 from [Rattus norvegicus] protein kinase interactor, putative similar to glutathione transferase GI:2853219 from [Carica papaya]; supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres: 26943. unknown protein putative WD-40 repeat protein putative WD-40 repeat protein putative RVD-40 repeat protein putative RVD-40 repeat protein Pram HMM hit: zinc finger, C3HC4 type (RING finger) GMP synthase similar to GMP synthase GB:6323873 [Saccharomyces cerevisiae]	261553_at         0           261513_at         0           261519_at         0           261418_at         0           261229_at         0           261225_at         0           261225_at         0           261008_at         0           26108_at         0           26108_at         0           260746_at         0           260746_at         0           26052_at         0           260652_at         0           26026_at         0           26026_at         0           260446_at         0           260445_at         0           260244_at         0           260445_at         0           260445_at         0           260445_at         0           260445_at         0           260445_at         0           26024_at         0           26024_at         0	0.5 $0.5$
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein hypothetical protein contains similarity to RNA helicase (HRH1) GB:D50487 GI:1742909 from [Homo sapiens] transmembrane protein, putative similar to TRANSMEMBRANE PROTEIN TMP21 GB:Q63584 from [Rattus norvegicus] protein kinase interactor, putative similar to Pto kinase interactor GB:1AAC61805 GI:3668069 from [Lycopersicon esculentum]; supported by glutathione transferase, putative similar to glutathione transferase GI:2853219 from [Carica papaya]; supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres: 26943. unknown protein putative WD-40 repeat protein putative WD-40 repeat protein putative glyoxalase II ; supported by cDNA: gi_2570339_gb_U90928.1_ATU90928 unknown protein hypothetical protein predicted by genscan+ putative RING zinc finger protein Pfam HMM hit: zinc finger, C3HC4 type (RING finger) GMP synthase similar to GMP synthase GB:6323873 [Saccharomyces cerevisiae] putative RNA-binding protein similar to RNA-binding protein GB:S46286 from [Nicotiana sylvestris]	261553_at         0           261553_at         0           261519_at         0           261418_at         0           261322_at         0           261225_at         0           261225_at         0           261225_at         0           26109_at         0           261075_at         0           260835_at         0           260746_at         0           260652_at         0           260552_at         0           260552_at         0           260552_at         0           260552_at         0           260455_at         0           260446_at         0           260455_at         0           260455_at         0           260321_at         0           260245_at         0           260245_at         0           269864_at         0	0.5 $0.5$
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein unknown protein ; supported by full-length cDNA: Ceres:6332. unknown protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein, putative similar to to NA helicase (HRH1) GB:D50487 GI:1742909 from [Homo sapiens] transmembrane protein, putative similar to TRANSMEMBRANE PROTEIN TMP21 GB:Q63584 from [Rattus norvegicus] protein kinase interactor, putative similar to Pto kinase interactor GB:1AAC61805 GI:3668069 from [Lycopersicon esculentum]; supported by glutathione transferase, putative similar to glutathione transferase GI:2853219 from [Carica papaya]; supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 26943. unknown protein putative WD-40 repeat protein putative WD-40 repeat protein putative glyoxalase II ; supported by cDNA: gi_2570339_gb_U90928.1_ATU90928 unknown protein putative RING zinc finger protein Pfam HMM hit: zinc finger, C3HC4 type (RING finger) GMP synthase similar to GMP synthase GB:6323873 [Saccharomyces cerevisiae] putative RING zinc finger protein Pfam HMM hit: zinc finger, C3HC4 type (RING finger) GMP synthase similar to RNA-binding protein GB:S46286 from [Nicotiana sylvestris] hypothetical protein predicted by genscan+ putative RING zinc finger protein Pfam HMM hit: zinc finger, C3HC4 type (ZING finger) GMP synthase similar to RNA-binding protein GB:S46286 from [Nicotiana s	261553_at         0           261513_at         0           261519_at         0           261418_at         0           261418_at         0           261418_at         0           261429_at         0           261225_at         0           26120_at         0           26108_at         0           261075_at         0           260752_at         0           260746_at         0           260652at         0           260526_at         0           260552_at         0           260552_at         0           260552_at         0           260552_at         0           260552_at         0           260446_at         0           260455_at         0           260455_at         0           260294_at         0           260294_at         0           259864_at         0	0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to TRANSMEMBRANE PROTEIN TMP21 GB:Q63584 from [Rattus norvegicus] protein kinase interactor, putative similar to TRANSMEMBRANE PROTEIN TMP21 GB:Q63584 from [Rattus norvegicus] protein kinase interactor, putative similar to Pto kinase interactor GB:1AAC61805 GI:3668069 from [Lycopersicon esculentum]; supported by glutathione transferase, putative similar to glutathione transferase GI:2853219 from [Carica papaya]; supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres: 3 chaperonin protein ; supported by cDNA: gi_2570339_gb_U90928.1_ATU90928 unknown protein putative glyoxalase II ; supported by cDNA: gi_2570339_gb_U90928.1_ATU90928 unknown protein hypothetical protein predicted by genscan+ putative RING zinc finger protein PMM hit: zinc finger, C3HC4 type (RING finger) GMP synthase similar to GMP synthase GB:6323873 [Saccharomyces cerevisiae] putative RNA-binding protein similar to RNA-binding protein GB:S46286 from [Nicotiana sylvestris] hypothetical protein predicted by genscan; supported by CDNA: gi_1563957 [Arabidopsis thaliana]; supported by cDNA: gi_16648960_gb_AY059850.1_ hypothetical protein similar to casein kinase I GB:CAA853595 [Arabidopsis thaliana]; supported by cDNA: gi_16648960_gb_AY059850.1_ hypothetical protein similar to nodule inception protein GB:CAB61243 [Lotus japonicus]	261553_at         0           261513_at         0           261519_at         0           261418_at         0           261418_at         0           261429_at         0           261225_at         0           261008_at         0           261075_at         0           261075_at         0           260746_at         0           260746_at         0           26052_at         0           26052_at         0           26052_at         0           260552_at         0           260552_at         0           260445_at         0           260245_at         0           260245_at         0           260245_at         0           26024_at         0           26024_at         0           26024_at         0           259864_at         0           259888_at         0	0.5 0.5.5 0.
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]: supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein ; unknown protein predicted by genscan+ putative glyoxalase II ; supported by cDNA: gi_2570339_gb_U90928.1_ATU90928 unknown protein ; unknown protein predicted by genscan+ putative glyoxalase II ; unknown protein predicted by genscan+ putative RNA-binding protein GB:32873 [Saccharomyces cerevisiae] putative RNA-binding protein similar to casein kinase I	261553_at         0           261513_at         0           261519_at         0           261418_at         0           26129_at         0           26122_at         0           261225_at         0           261209_at         0           261008_at         0           261075_at         0           260746_at         0           260714_at         0           260552_at         0           260526_at         0           260526_at         0           260526_at         0           260521_at         0           260245_at         0           259864_at         0           259804_at         0	0.5 0.5.5 0.
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_A hypothetical protein predicted by genemark.hmm unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein ; putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein ; putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein ; putative similar to TRANSMEMBRANE PROTEIN TMP21 GB:Q63584 from [Rattus norvegicus] protein kinase interactor, putative similar to TRANSMEMBRANE PROTEIN TMP21 GB:Q63584 from [Rattus norvegicus] protein kinase interactor, putative similar to Pto kinase interactor GB:1AAC681085 GI:3668069 from [Lycopersicon esculentum]; supported by glutathione transferase, putative similar to glutathione transferase GI:2853219 from [Carica papaya]; supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres: 26943. unknown protein putative WD-40 repeat protein putative WD-40 repeat protein putative glyoxalase II ; supported by cDNA: gi_2570339_gb_U90928.1_ATU90928 unknown protein predicted by genscan+ putative RING zinc finger protein Pfam HMM hit: zinc finger, C3HC4 type (RING finger) GMP synthase similar to GNP synthase GB:G323873 [Saccharomyces cerevisiae] putative RING zinc finger protein Pfam HMM hit: zinc finger, C3HC4 type (AING finger) GMP synthase I similar to casein kinase I GB:CAA55395 [Arabidopsis thaliana]; supported by cDNA: gi_16648960_gb_AY059850.1_ hypothetical protein similar to nodule inception	261553_at         0           261553_at         0           261519_at         0           261519_at         0           261418_at         0           261322_at         0           261299_at         0           26125_at         0           26109_at         0           261075_at         0           260835_at         0           260746_at         0           260652_at         0           260552_at         0           260552_at         0           260552_at         0           260552_at         0           260455_at         0           260446_at         0           260245_at         0           260321_at         0           260845_at         0           269864_at         0           259886_at         0           259884_at         0           259884_at         0           259884_at         0	0.5 0.5.5 0.
unknown protein is supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein is supported by full-length cDNA: Ceres:6332. unknown protein is supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein in putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein in putative similar to nomeodomain protein GI:7239157 from (Malus domestica) unknown protein in putative similar to TRANSMEIMBRANE PROTEIN TMP21 GB:Q63584 from [Rattus norvegicus] protein kinase interactor, putative similar to TRANSMEIMBRANE PROTEIN TMP21 GB:Q63584 from [Rattus norvegicus] protein kinase interactor. putative similar to Pto kinase interactor GB:1AAC61805 GI:3668069 from [Lycopersicon esculentum]; supported by glutathione transferase, putative similar to 19th interasferase GI:2853219 from [Carica papaya]; supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:26943. unknown protein putative glyoxalase II ; supported by cDNA: gi_2570339_gb_U90928.1_ATU90928 unknown protein hypothetical protein predicted by genscan+ putative RING zinc finger protein Pfam HMM hit: zinc finger, C3HC4 type (RING finger) GMP synthase similar to GMP synthase GB:6323873 [Saccharomyces cerevisiae] putative RNA-binding protein similar to RNA-binding protein GB:546286 from [Nicotiana sylvestris] hypothetical protein predicted by genscan+ putative RNA-binding protein similar to RNA-binding protein GB:546286 from [Nicotiana sylvestris] hypothetical protein predicted by genscan, supported by cDNA: gi_15081613_gb_AY059850.1_ hypothetical protein similar to nodule inception protein GB:CA861243 [Lotus japonicus] cytosolic factor, putative similar to GI:8079585 from [Saccharo	261553_at         0           261513_at         0           261519_at         0           261418_at         0           261418_at         0           261422_at         0           261225_at         0           261225_at         0           26129_at         0           26125_at         0           26108_at         0           261075_at         0           260746_at         0           260652at         0           260652at         0           260526_at         0           260526_at         0           260526_at         0           260446_at         0           260452_at         0           260446_at         0           260425_at         0           260446_at         0           260294_at         0           259886_at         0           259884_at         0           259884_at         0           259884_at         0           259875_at         0           259878_at         0	0.5 $0.5$
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_/ hypothetical protein predicted by genemark.hmm unknown protein unknown protein ; supported by cDNA: Gi_15450466_gb_AY052334.1_ homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein hypothetical protein contains similarity to RNA helicase (HRH1) GB:D50487 GI:1742909 from [Homo sapiens] transmembrane protein, putative similar to TRANSMEMBRANE PROTEIN TMP21 GB:Q63584 from [Rattus norvegicus] protein kinase interactor, putative similar to Pto kinase interactor GB:1AAC61805 GI:3668069 from [Lycopersicon esculentum]; supported by glutathione transferase, putative similar to Pto kinase interactor GB:1AAC61805 GI:3668069 from [Lycopersicon esculentum]; supported by glutattione transferase, putative similar to glutatione transferase GI:2863219 from [Carico apaya]; supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:26943. unknown protein putative WD-40 repeat protein putative WD-40 repeat protein putative glyoxalase II ; supported by cDNA: gi_2570339_gb_U90928.1_ATU90928 unknown protein putative RING zinc finger protein Pfam HMM hit: zinc finger, C3HC4 type (RING finger) GMP synthase similar to GMP synthase GB:6323873 [Saccharomyces cerevisiae] putative RNA-binding protein similar to RNA-binding protein GB:S46286 from [Nicotiana sylvestris] hypothetical protein inredicted by genscan; supported by cDNA: gi_15292714_gb_AY05791.1_ putative casein kinase I similar to casein kinase I GB:CAA55395 [Arabidopsis thaliana]; supported by cDNA: gi_16648960_gb_AY059850.1_ hypothetical protein similar to GB:A807956 from [Saccharomyces cerevisiae]; supported b	261553_at         0           261513_at         0           261519_at         0           261418_at         0           261418_at         0           261418_at         0           261429_at         0           261225_at         0           26125_at         0           261075_at         0           261075_at         0           260746_at         0           260746_at         0           260552_at         0           260552_at         0           260552_at         0           260552_at         0           260552_at         0           260446_at         0           260252_at         0           260252_at         0           260252_at         0           260245_at         0           260244_at         0           259864_at         0           259888_at         0           259888_at         0           259884_at         0           259884_at         0           259788_at         0           259783_at         0	0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5
unknown protein contains Pfam profile:PF00660 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_ mitochondrial ribosomal protein, putative similar to BS:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_ hypothetical protein predicted by genemark.hmm unknown protein ; supported by full-length cDNA: Ceres:6332. unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_ homeodomain protein ; putative similar to TRANSMEMBRANE PROTEIN TMP21 GB:263584 from [Ratus norvegicus] protein kinase interactor, putative similar to TRANSMEMBRANE PROTEIN TMP21 GB:263584 from [Ratus norvegicus] protein kinase interactor, putative similar to glutathione transferase GI:2853219 from [Carica papaya]; supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 26943. unknown protein putative WD-40 repeat protein putative glyoxalase II ; supported by cDNA: gi_2570339_gb_U90928.1_ATU90928 unknown protein hypothetical protein predicted by genscan+ putative RING zinc finger protein Pfam HMM hit: zinc finger, C3HC4 type (RING finger) GMP synthase similar to GMP synthase GB:6323873 [Saccharomyces cerevisiae] putative RING zinc finger protein FMIHM hit: zinc finger, C3HC4 type (RING finger) GMP synthase similar to GMP synthase GB:6323873 [Saccharomyces cerevisiae] putative RINA-binding protein is Milar to RNA-binding protein GB:S46286 from [Nicotiana sylvestris] hypothetical protein predicted by genscan+ putative RING zinc finger protein Pfam HMM hit: zinc finger, C3HC4 type (AING finger) GMP synthase similar to GR:07956 from [Saccharomyces cerevisiae] puta	261553_at         0           261553_at         0           261513_at         0           261519_at         0           261418_at         0           261322_at         0           261299_at         0           26125_at         0           26125_at         0           26125_at         0           261139_at         0           26108_at         0           260085_at         0           260746_at         0           260652_at         0           260652_at         0           260652_at         0           260552_at         0           260552_at         0           260455_at         0           260455_at         0           260245_at         0           260245_at         0           260245_at         0           259864_at         0           25988_at         0           25988_at         0           25988_at         0           25988_at         0           259763_at         0           25960_at         0	0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5
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unknown protein contains Pfam profile:PF00660 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1	261553_at         0           261513_at         0           261519_at         0           261418_at         0           261322_at         0           261425_at         0           261225_at         0           26125_at         0           261008_at         0           261075_at         0           260746_at         0           260652_at         0           260652_at         0           260526_at         0           260526_at         0           260526_at         0           260526_at         0           260446_at         0           260455_at         0           260446_at         0           260294_at         0           260294_at         0           259865_at         0           259888_at         0           259763_at         0           259763_at         0           259459_at         0           259459_at         0           259519_at         0           259419_at         0	0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5
unknown protein contains Pfam profile:PF00860 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pf unknown protein ; supported by cDNA: gi_14532543_gb_47039896.1_ mitochondrial ribosomal protein, predicted by genemark.hmm unknown protein ; supported by full-length cDNA: Ceres:6332. unknown protein ; supported by full-length cDNA: Ceres:6332. unknown protein ; supported by cDNA: gi_15450466_gb_47052334.1_ homeodomain protein ontains similarity to RNA helicase (HRH1) GB:D50487 GI:1742909 from [Homo sapiens] transmembrane protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica) unknown protein hypothetical protein contains similarity to RNA helicase (HRH1) GB:D50487 GI:1742909 from [Homo sapiens] transmembrane protein, putative similar to TRANSMEMBRANE PROTEIN TMP21 GB:063584 from [Rattus norvegicus] protein kinase interactor, putative similar to Pto kinase interactor GB:1AAC61805 GI:3668069 from [Lycopersicon esculentum]: supported by glutathione transferase, putative similar to glutathione transferase GI:2853219 from [Carica papaya]: supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres: 3 chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres: 3 unknown protein putative @V-04 orepeat protein putative @V-04 orepeat protein putative @NO-40 repeat protein putative RNA-20 repeat protein Pfam HMM hit: zinc finger, C3HC4 type (RING finger) GMP synthase similar to GMP synthase GB:6323873 [Saccharomyces cerevisiae] putative RNA-binding protein similar to RNA-binding protein GB:S46286 from [Nicotiana sylvestris] hypothetical protein predicted by genscan+ putative RNA-binding protein similar to RA-binding protein GB:CAA6539571_d_b_A'Y05791.1_ putative case kinase 1 GMP synthase GB:6323873 [Saccharomyces cerevisiae] supported by cDNA: gi_16648960_gb_A'Y059850.1_ hypothetical protein predicted by genscan; supported by cDNA	261553_at         0           261513_at         0           261519_at         0           261418_at         0           261418_at         0           261422_at         0           261225_at         0           26125_at         0           261008_at         0           261075_at         0           260746_at         0           260746_at         0           260522_at         0           260652_at         0           260526_at         0           260552_at         0           260552_at         0           260552_at         0           260452_at         0           260552_at         0           260252_at         0           260252_at         0           260455_at         0           26024_at         0           26024_at         0           259888_at         0           259888_at         0           259888_at         0           25978_at         0           259763_at         0           259519_at         0           259540_at <td>0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5</td>	0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5
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metallothionein-like protein similar to metallothionein GB:JQ2128 [Glycine max]; supported by cDNA: gi_14335167_gb_AY037263.1_	259008_at 0.5
unknown protein similar to unknown protein GB:BAA83351 [Oryza sativa]; supported by cDNA: gi_14334835_gb_AY035091.1_	258992_at 0.5
putative aspartate kinase similar to aspartate kinase GB:CAA67376 (Arabidopsis thaliana); supported by full-length cDNA: Ceres: 6203	
unknown protein contains Pfam profile: PF00514 armadillo/beta-catenin-like repeats (4 copies);supported by full-length cDNA: Ceres:34	
hypothetical protein predicted by genefinder; supported by full-length cDNA: Ceres:40090.	258856 at 0.5
putative integral membrane protein contains Pfam profile: PF00892 Integral membrane protein	258831 at 0.5
putative 40S ribosomal protein identical to p40 protein homolog GB:AAB67866 [Arabidopsis thaliana]; similar to 40S ribosomal protein	_
putative T-complex protein 1, theta subunit (TCP-1-Theta) similar to T-complex protein 1, theta subunit (TCP-1-Theta) GB:P42932 [Mu	
putative GTP-binding protein (ATFP8) identical to ATFP8 GB:AD00111 [Arabidopsis thaliana]; supported by CDNA; gi 4097556 gb L	
hypothetical protein predicted by genscan; supported by cDNA: gi_14517382_gb_AY039526.1_	258749_at 0.5
unknown protein	258628_at 0.5
L-allo-threonine aldolase, putative similar to L-ALLO-THREONINE ALDOLASE GB:007051 from [Aeromonas jandaei]; supported by fu	
unknown protein	258542_at 0.5
unknown protein ;supported by cDNA: gi_13878146_gb_AF370336.1_AF370336	258518_at 0.5
DAG protein, putative similar to DAG PROTEIN GB:Q38732 from [Antirrhinum majus]	258526_at 0.5
Expressed protein ; supported by cDNA: gi_15293078_gb_AY050973.1_	258417_at 0.5
hypothetical protein predicted by genscan+; supported by cDNA: gi 15028188 gb AY045917.1	258403 at 0.5
unknown protein	258345 at 0.5
hypothetical protein similar to putative transposase of transposable element Ac GB:CAA25635 [Zea mays]	258246 s at 0.5
hypothetical protein predicted by genemark.hmm	258211 at 0.5
ribonucleoside-diphosphate reductase small chain almost identical to ribonucleoside-diphosphate reductase small chain GB:P50651 fro	_
unknown protein ; supported by cDNA: gi_15983782 gb_AY056797.1_	258061 at 0.5
hypothetical protein predicted by generark	258034 at 0.5
unknown protein ;supported by full-length cDNA: Ceres:39041.	258039 at 0.5
Dof zinc finger protein identical to GB:BAA33197 from [Arabidopsis thaliana]; supported by cDNA; gi 15027980 gb AY045847.1	_
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:42922.	257937_at 0.5
unknown protein	257879_at 0.5
uridylate kinase, putative similar to UMP-kinase GB:CAB38122 from [Lactococcus lactis]; supported by cDNA: gi_15292788_gb_AY05	
hypothetical protein predicted by genemark.hmm	257724_at 0.5
unknown protein ;supported by cDNA: gi_15292984_gb_AY050926.1_	257705_at 0.5
RNA-binding protein contains Pfam profile: PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	257266_at 0.5
unknown protein similar to DAG protein (required for chloroplast differentiation and palisade development) GB:Q38732 [Antirrhinum ma	jus]; si 257218_at 0.5
Tic22, putative similar to Tic22 GB:AAC64606 from [Pisum sativum]	257199_at 0.5
unknown protein contains Pfam profile: PF01188 Mandelate racemase/muconate lactonizing enzyme family; supported by cDNA: gi 13	87812 257067 at 0.5
hypothetical protein predicted by genemark.hmm, contains Pfam profile:PF00400 WD domain, G-beta repeat	256967 at 0.5
aminotransferase, putative similar to aminotransferase GB:CAA19897 from [Streptomyces coelicolor A3(2)]; supported by cDNA: gi 14	
unknown protein	256754 at 0.5
unknown protein	256658 at 0.5
At14a-1 protein identical to At14a protein GB:AAD26355 GI:4589123 [Arabidopsis thaliana] [Gene 230 (1), 33-40 (1999)]	256601 s at 0.5
A training in the international of A training in the protein of the protein of the protein and the protein of t	256483 at 0.5
	_
unknown protein	_
putative clathrin heavy chain similar to clathrin heavy chain GB:AAC49294 [Glycine max]	
Sm-like protein contains Pfam profile: PF01423: Sm protein; supported by full-length cDNA: Ceres: 23170.	256333_at 0.5
arginine N-methyltransferase 3, putative similar to arginine N-methyltransferase 3 GB:AAC40158 [Rattus norvegicus]	256288_at 0.5
betaine aldehyde dehydrogenase, putative similar to betaine aldehyde dehydrogenase (BADH) GI:1813537 [Spinacia oleracea]	256246_at 0.5
phosphoinositide specific phospholipase (AtPLC2) identical to phosphoinositide specific phospholipase (AtPLC2) GI:857374 [Arabidops	sis thal 256156_at 0.5
hypothetical protein contains Pfam profile: PF01084 ribosomal protein S18	256043_at 0.5
unknown protein	256049_at 0.5
putative protein kinase contains a protein kinase domain profile (PDOC00100); supported by cDNA: gi_13448034_gb_AF339146.1_AF	339146 255872_at 0.5
putative potassium transporter ; supported by cDNA: gi_2384670_gb_AF012657.1_AF012657	255829_at 0.5
putative malate oxidoreductase	255683_at 0.5
putative tetrahydrofolate synthase similar to other dehydrogenase/cyclohydrolase domains	255685_s_at 0.5
putative ABC transporter	255594 at 0.5
predicted protein of unknown function similar to bacterial tolB proteins but unclear if T7B11.13 is involved in viral transport	255543 at 0.5
Expressed protein ; supported by cDNA: gi 5059351 gb AF154574.1 AF154574	255512 at 0.5
F-box protein family, AtFBL20 contains similarity to N7 protein GI:3273101 from [Medicago truncatula];supported by full-length cDNA: (	
hypothetical protein	255021_at 0.5
putative protein phosphatase like protein - Arabidopsis thaliana, PIR2:T05589;supported by full-length cDNA: Ceres:152712.	254918 at 0.5
kinase-like protein protein kinase rck, Mus musculus, PIR2:148733; supported by cDNA: gi 14532759 gb AY040004.1	254560_at 0.5
resistence protein - like downy mildew resistance protein RPP5, Arabidopsis thaliana, PATX:G2109275	254585 at 0.5
small GTP-binding protein - like GTP-binding protein RHA1, Arabidopsis thaliana, PIR2:S23727; supported by cDNA: gi 15450604 gb	
putative protein hypothetical protein YPL065w yeast, PIR2:S60925	_
receptor like protein (fragment) ES43 protein, barley, PIR2:S44281	254342_at 0.5
putative protein putative protein F6118_70 - Arabidopsis thaliana, PATX:E1283548;supported by full-length cDNA: Ceres:121159.	254121_at 0.5
transcriptional activator CBF1 CRT CRE binding factor 1 involved in low-temperature-responsive gene expression00; supported by cDI	
putative protein ;supported by full-length cDNA: Ceres:14312.	254010_at 0.5
putative protein transcription termination factor nusB, Synechocystis sp., PIR2:S76233; supported by full-length cDNA: Ceres:943.	254011_at 0.5
fimbrin-like protein (ATFIM1);supported by cDNA: gi_2905892_gb_U66424.1_ATU66424	253956_at 0.5
putative protein ENOD20 gene, Medicago truncatula, X99467;supported by full-length cDNA: Ceres:33380.	253875_at 0.5
putative protein MSP1 protein, Saccharomyces cerevisia, PIR2:A49506;supported by full-length cDNA: Ceres:142160.	253861_at 0.5
putative protein KIAA0210 gene, Homo sapiens, gb:D86965; supported by cDNA: gi_5032257_gb_AF126057.2_AF126057	253647_at 0.5
transcription factor-like protein Arabidopsis thaliana auxin response factor 4 (ARF4) - Arabidopsis thaliana, PID:g4102598; supported b	oy cDN 253662_at 0.5
putative protein predicted proetein, Arabidopsis thaliana	253555_at 0.5
putaive DNA-binding protein DNA-binding protein WRKY3 - Petroselinum crispum, PIR2:S72445;supported by full-length cDNA: Ceres	
monogalactosyldiacylglycerol synthase - like protein monogalactosyldiacylglycerol synthase, Cucumis sativus, PID:g1805254; supporte	
aspartate aminotransferase ;supported by full-length cDNA: Ceres:33414. Ceres:103854.	253481 at 0.5
protein kinase AME3; supported by cDNA: gi_64213_dbj_D45355.1_ATHPKAME3C	253395_at 0.5
homeobox gene ATH1	253411 at 0.5
putative protein AT.1.24, Arabidopsis thaliana, gb:U63815;supported by full-length cDNA: Ceres:4868.	253382_at 0.5
putative protein ABC-type transport protein sll1623 -Synechocystis,PIR2:S74812	
Putative Protein ABC-type transport protein sin 623 -Synechocystis, PIR2.574612 Putative S-phase-specific ribosomal protein	253328 of 0.5
	253328_at 0.5
	253248_at 0.5
putative protein ;supported by full-length cDNA: Ceres:21838.	253248_at 0.5 253171_at 0.5
	253248_at 0.5

putative protein CRP1, Zea mays, gb:AF073522;supported by full-length cDNA: Ceres:5482. putative protein permease 1 - Mesembryanthemum crystallinum,PID:g3202040		
putative protein permease 1 - Mesembryanthemum crystallinum,PID:g3202040	253116_at	0.5
	253021_at	0.5
hypothetical protein	253025_at	0.5
putative protein hypothetical protein HI0722 (pepQ 5 region) -E.coli,PID:g1790283;supported by full-length cDNA: Ceres:18344.	253007_at	0.5
xyloglucan endo-transglycosylase ; supported by cDNA: gi_15810248_gb_AY056163.1_	252607_at	0.5
nuclear receptor binding factor-like protein nuclear receptor binding factor-1 NRBF-1 - Rattus norvegicus, EMBL:AB015724;supported by full-	_	0.5
putative protein	252552_at	0.5
putative protein Na+-dependent inorganic phosphate corransporter, Rattus norvegicus, U07609FUNC 99	252444_at	0.5
RNA-binding protein-like protein various RNA-binding proteins;supported by full-length cDNA: Ceres:9763.	252464_at	0.5 0.5
flavonol synthase - like protein SRG1 protein, Arabidopsis thaliana, PIR:S44261; supported by full-length cDNA: Ceres: 25787.	252213_at	0.5
putative protein APRIL protein, Homo sapiens, EMBL:HSAPRIL_1 putative protein	252174_at 251869 at	0.5
putative protein various Arabidopsis thaliana predicted proteins	251853 at	0.5
serine/threeoine-specific protein kinase-like serine/threeoine-specific protein kinase NAK, Arabidopsis thaliana, PIR:S38326	251789 at	0.5
putative protein strictosidine synthase (EC 4.3.3.2) - Rauvolfa mannii (fragment), supported by full-length cDNA: Ceres:98698.	251658 at	0.5
putative protein DYSKERIN (NUCLEOLAR PROTEIN NAP57) - Rattus norvegicus, EMBL:Z34922; supported by cDNA: gi 8901185 gb AF2		0.5
putative protein Bet1 homolog - Rattus norvegicus, EMBL:RN42755; supported by cDNA: gi_14030602_gb_AF368175.1_AF368175	251579 at	0.5
putative protein F-box protein Fbl2 - Homo sapiens, EMBL:AF174589;supported by full-length cDNA: Ceres:35534.	251532 at	0.5
hypothetical protein	251463_at	0.5
putative protein hypothetical protein At2g46420 - Arabidopsis thaliana, EMBL:AC006526	251274_at	0.5
putative protein various predicted proteins; supported by full-length cDNA: Ceres:105564.	251138_at	0.5
putative protein putative protein F4P12.100 - Arabidopsis thaliana, EMBL:AL132966; supported by cDNA: gi_15810368_gb_AY056223.1_	251055_at	0.5
protein kinase ATN1-like protein protein kinase ATN1 (EC 2.7.1) - Arabidopsis thaliana, PIR:S61766	251063_at	0.5
Expressed protein ; supported by full-length cDNA: Ceres: 12197.	250921_at	0.5
monodehydroascorbate reductase (NADH) - like protein monodehydroascorbate reductase (NADH), cucumber, PIR:JU0182;supported by ful	_	0.5
putative protein similar to unknown protein (emb]CAB88266.1);supported by full-length cDNA: Ceres:157058.	250643_at	0.5
DnaJ homologue (gb AAB91418.1 ) ; supported by cDNA: gi_2689719_gb_AF037168.1_AF037168	250672_at	0.5
unknown protein	250602_s_at 250540 at	0.5 0.5
unknown protein ; supported by cDNA: gi_16648868_gb_AY059804.1_ putative protein 110K5.11, unknown protein, Sorghum bicolor, EMBL:AF124045; supported by cDNA: gi_13605727 gb_AF361845.1 AF3618		0.5
plative protein intervent in alteriowing protein, softman blocking, and and a starter an	250264 at	0.5
peptide transporter - like protein peptide transporter Hordeum vulgare, EMBL:AF023472	250261 at	0.5
cobalamin biosynthesis protein	250243 at	0.5
putative protein various unknown or predicted proteins, Arabidopsis thaliana	250178 at	0.5
putative protein contains similarity to unknown protein (emb CAB89315.1); supported by cDNA: gi 15451067 gb AY054614.1	249863 at	0.5
putative protein contains similarity to ABA-repsonsive protein	249823_s_at	0.5
iron superoxide dismutase 3 (gb AAC24834.1) ;supported by full-length cDNA: Ceres:26637.	249826_at	0.5
putative protein contains similarity to polyA polymerase	249821_at	0.5
putative protein contains similarity to unknown protein (emb CAB87908.1);supported by full-length cDNA: Ceres:152842.	249793_at	0.5
26S proteasome, non-ATPase regulatory subunit ;supported by full-length cDNA: Ceres:23276.	249796_at	0.5
putative protein similar to unknown protein (emb CAB62460.1).supported by full-length cDNA: Ceres:5684.	249751_at	0.5
putative protein CG14881, Drosophila melanogaster, EMBL:AE003713;supported by full-length cDNA: Ceres:9887.	249612_at	0.5
receptor protein kinase - like protein receptor serine/threonine kinase PR5K, Arabidopsis thaliana, EMBL:AT48698	249486_at	0.5 0.5
thioredoxin ; supported by full-length cDNA: Ceres: 7791. glutathione transferase AtGST 10 (emb CAA10457.1) ; supported by cDNA: gi 15451157 gb AY054659.1	249385_at 249291 at	0.5
gutative protein similar to unknown protein (ab)AAF19669.1)	249253 at	0.5
alcohol dehydrogenase (EC 1.1.1) class III (pri][371244) ;supported by full-length cDNA: Ceres:33315.	249077 at	0.5
putative protein contains similarity to heat shock transcription factor	249000 at	0.5
putative protein strong similarity to unknown protein (piri/T04533);supported by full-length cDNA: Ceres:18140.	248883 at	0.5
unknown protein	248785_at	0.5
DNA-binding protein-like	248788_at	0.5
putative protein similar to unknown protein (emb CAB78730.1)	248751_at	0.5
sodium-dicarboxylate cotransporter-like ;supported by full-length cDNA: Ceres:107593.	248756_at	0.5
RNA-binding protein-like ;supported by full-length cDNA: Ceres:1876.	248758_at	0.5
	248737 at	
unknown protein		0.5
unknown protein	248745_at	0.5
unknown protein putative protein contains similarity to unknown protein (dbj BAA91655.1)	248745_at 248612_at	0.5 0.5
unknown protein putative protein contains similarity to unknown protein (dbj BAA91655.1) adenylate kinase  ;supported by full-length cDNA: Ceres:21741.	248745_at 248612_at 248506_at	0.5 0.5 0.5
unknown protein putative protein contains similarity to unknown protein (dbj BAA91655.1) adenylate kinase ;supported by full-length cDNA: Ceres:21741. unknown protein	248745_at 248612_at 248506_at 248471_at	0.5 0.5 0.5 0.5
unknown protein putative protein contains similarity to unknown protein (dbj BAA91655.1) adenylate kinase ;supported by full-length cDNA: Ceres:21741. unknown protein putative protein similar to unknown protein (gb AAF03497.1)	248745_at 248612_at 248506_at 248471_at 248410_at	0.5 0.5 0.5 0.5 0.5
unknown protein putative protein contains similarity to unknown protein (dbj BAA91655.1) adenylate kinase ;supported by full-length cDNA: Ceres:21741. unknown protein putative protein similar to unknown protein (gb AAF03497.1) unknown protein	248745_at 248612_at 248506_at 248471_at 248410_at 248394_at	0.5 0.5 0.5 0.5 0.5 0.5
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unknown protein putative protein contains similarity to unknown protein (dbj/BAA91655.1) adenylate kinase ;supported by full-length cDNA: Ceres:21741. unknown protein putative protein similar to unknown protein (gb/AAF03497.1) unknown protein putative protein similar to unknown protein (pir  S77462); supported by cDNA: gi_15081647_gb_AY048216.1_ putative protein similar to unknown protein (gb/AAF34839.1); supported by cDNA: gi_13926341_gb_AF372918.1_AF372918 ubiquitin-like protein Similar to unknown protein (gb/AAF34839.1); supported by cDNA: gi_14326341_gb_AF372918.1_AF372918 ubiquitin-like protein FtsZ chloroplast homolog precursor (sp[Q42545) ; supported by cDNA: gi_14334637_gb_AY034992.1_ molybdopterin synthase sulphurylase (gb AAD18050.1) ; supported by cDNA: gi_4337039_gb_AF124159.1_AF124159	248745_at 248612_at 248506_at 248471_at 248410_at 248394_at 248287_at 248230_at 248103_at 248105_at 248105_at	0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5
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hypothetical protein predicted by genemark.hmm	246576_at	0.5
formate dehydrogenase (FDH) ;supported by full-length cDNA: Ceres:7530.	246595_at	0.5
putative protein hypothetical proteins - Arabidopsis thaliana	246497_at	0.5
putative protein predicted proteins - Arabidopsis thaliana; supported by full-length cDNA: Ceres:34944.	246452_at	0.5
Expressed protein ; supported by full-length cDNA: Ceres: 16205.	246454_at	0.5
spindle pole body protein-like spindle pole body protein - Homo sapiens, EMBL:AF042379; supported by cDNA: gi_14532825_gb_AY040037	7 246428_at	0.5
root cap 1 (RCP1) ;supported by full-length cDNA: Ceres:10216.	246434_at	0.5
putative protein serine kinase SRPK2, Homo sapiens, EMBL:AC005070	246334 at	0.5
putative protein	246237_at	0.5
SOH1 - like protein SOH1, Saccharomyces cerevisiae, PIR:S47895	246140_at	0.5
chloroplast Cpn21 protein ; supported by cDNA: gi_14334611_gb_AY034979.1_	246003_at	0.5
putative protein predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_15810384_gb_AY056231.1_	245972_at	0.5
putative protein predicted proteins - different species	245936_at	0.5
putative protein ER66 - Lycopersicon esculentum, EMBL:AF096260	245910_at	0.5
salt-inducible protein homolog	245597_at	0.5
PRL1 protein ;supported by full-length cDNA: Ceres:123113.	245358_at	0.5
Expressed protein ; supported by full-length cDNA: Ceres: 42223.	245333_at	0.5
hypothetical protein ; supported by full-length cDNA: Ceres: 91870.	245303_at	0.5
putative dimethyladenosine transferase ; supported by cDNA: gi_14532649_gb_AY039949.1_	245122_at	0.5
cytochrome B6	244976_at	0.5
hypothetical protein predicted by genscan	257374_at	0.5
En/Spm-like transposon protein related to En/Spm transposon family of maize	267353_at	0.5
putative protein various predicted proteins, Arabidopsis thaliana	254997_s_at	0.5
putative protein other hypothetical proteins - Arabidopsis thaliana	254965_at	0.5

Table 2: Transcripts elevated in cells during heat shock compared to unstressed plants	Affymetrix number	log₂ fold increase
Arabidopsis mitochondrion-localized small heat shock protein (AtHSP23.6-mito); supported by cDNA: gi_1669865 gb U72958.1 ATU72958	254059 at	10.1
heat shock protein 18 ;supported by full-length cDNA: Ceres:97197.	247691 at	9.8
heat shock protein 17.6A	250351 at	8.8
heat shock protein 17.6-II ;supported by full-length cDNA: Ceres:2281.	250296 at	8.7
heat shock protein 17 ; supported by cDNA: gi_15294149_gb_AF410266.1_AF410266	252515 at	7.4
mitochondrial heat shock 22 kd protein-like; supported by full-length cDNA: Ceres: 268536.	248434_at	7.4
heat shock protein, putative similar to heat shock protein GI:19617 from [Medicago sativa]; supported by full-length cDNA: Ceres:32795.	262911_s_at	7.1
putative small heat shock protein ;supported by full-length cDNA: Ceres:25828.	266294_at	6.7
17.6 kDa heat shock protein (AA 1-156) identical to GI:4376161 from (Arabidopsis thaliana) (Nucleic Acids Res. 17 (19), 7995 (1989))	260978_at	6.7
hypothetical protein	244931_at	6.6
heat shock protein 101 (HSP101) identical to heat shock protein 101 GI:6715468 GB:AAF26423 from [Arabidopsis thaliana]	260248_at	5.3
peptidylprolyl isomerase	248657_at	5.2
heat shock protein 22.0 ; supported by cDNA: gi_511795_gb_U11501.1_ATU11501	255811_at	5.1
expressed protein supported by cDNA: Ceres:13917.	254574_at	5.1
putative ascorbate peroxidase strong similarity to ascorbate peroxidase GB:CAA56340	258695_at	5
heat shock protein 21	253884_at	5
NADH dehydrogenase subunit 7	244925_at	5
maturase	244926_s_at	4.9
elongation factor 1B alpha-subunit (emb CAB64729.1)	250304_at	4.8
putative major latex protein major latex protein type 1 - Arabidopsis thaliana, EMBL:X91960; supported by cDNA: gi_13605713_gb_AF361838.1_AF	254234_at	4.7
NADH dehydrogenase subunit 5 (nad5) (trans-splicing part 2 of 2)	257337_at	4.7
hypothetical protein	266045_s_at	4.6
cytochrome c oxidase subunit 2	244950_at	4.6
heat shock protein 70 identical to heat shock protein 70 GB:CAA05547 GI:3962377 [Arabidopsis thaliana]; supported by cDNA: gi_15809831_gb_AY		4.5
NADH dehydrogenase subunit 6	244953_s_at	4.5
hypothetical protein	265228_s_at	4.4
hypothetical protein	263509_s_at	4.4
NADH dehydrogenase subunit 9	244943_at	4.3
putative protein similar to unknown protein (pir  T05035)	248959_at	4.1
heat-shock protein ; supported by cDNA: gi_166769_gb_M62984.1_ATHHSP83	248332_at	4.1
ubiquinolcytochrome-c reductase-like protein ubiquinolcytochrome-c reductase (EC 1.10.2.2) - Arabidopsis thaliana, PIR:T05357	246944_at	4.1
NADH dehydrogenase subunit 5 (nad5) (trans-splicing part 1 of 2)	257338_s_at	
putative protein predicted proteins - Arabidopsis thaliana	246178_s_at	
hypothetical protein	244901_at	4
hypothetical protein	266014_s_at	
hypothetical protein	263502_s_at	
putative protein ;supported by full-length cDNA: Ceres:16476.	251012_at	3.9
NADH dehydrogenase subunit 4L	244902_at	3.9
cytochrome c oxidase subunit 1	257333_at	3.9
protein kinase-like protein	247026_at	3.9

Expressed protein ; supported by full-length cDNA: Ceres:270232	254263 at	3.7
putative chloroplast protein import component similar to P. sativum Tic20 chloroplast protein import component, GenBank accession number AF095		3.6
putative GTP-binding protein similar to GTP-binding protein GB:AAB53256 [Arabidopsis thaliana]	259913 at	3.5
cytochrome c biogenesis orf203 Protein sequence is in conflict with the conceptual translation	244919 at	3.5
hypothetical protein	257323 at	3.5
	266044 s at	3.4
putative protein similar to unknown protein (pir  T03813)	247293 at	3.4
hypothetical protein	244906 at	3.4
hypothetical protein	257321 at	3.4
unknown protein	263515 at	3.3
	265670 s at	3.2
ethylene-responsive transcriptional coactivator, putative similar to GB:AAD46402 from [Lycopersicon esculentum] (Plant J. 18 (6), 589-600 (1999));		3.2
receptor like protein kinase receptor like protein kinase LRK1 - Arabidopsis thaliana, EMBL:ATLECGENE	252574 at	3.2
cytochrome P450-like protein cytochrome P450 CYP94A1 - Vicia sativa,PIR2:T08014	252368_at	3.2
hypothetical protein	246769 at	3.2
	266012_s_at	3.2 3.1
putative protein auxin-induced protein 10A -Glycine max,PID:g255579	254809 at	3.1
hypothetical protein predicted by genscan+	256285 at	3.1 3.1
Expressed protein ; supported by full-length cDNA: Ceres: 38545.	253737 at	3
heat shock transcription factor -like protein heat shock transcription factor HSF1, Arabidopsis thaliana, PIR:S52641	250910_at	3
hypothetical protein Similar to Nicotiana tumor-related protein (gb/26453)	264661_at	2.9
putative two-component phosphorelay mediator similar to two-component phosphorelay mediators (ATHP1-3) GB:BAA37110, GB:BAA37111, GB:B		2.9
unknown protein	257239_at	2.9
transcriptional activator CBF1 CRT CRE binding factor 1 involved in low-temperature-responsive gene expression00; supported by cDNA: gi_18990		2.9
hypothetical protein	244942_at	2.9
putative protein similar to unknown protein (gb AAC73025.1); supported by cDNA: gi_14532515_gb_AY039882.1_	250825_at	2.9
putative protein predicted protein, Arabidopsis thaliana	254289_at	2.8
late embryogenesis abundant protein, putative similar to late embryogenesis abundant protein GI:1350540 from [Picea glauca]	264758_at	2.8
hypothetical protein similar to hypothetical protein GB:AAD50003 GI:5734738 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:3759		2.8
putative short-chain type dehydrogenase/reductase similar to short-chain type dehydrogenase/reductase GB:Q08632 [Picea abies]; supported by cD		2.8
putative jasmonic acid regulatory protein similar to jasmonic acid 2 GB:AAF04915 from [Lycopersicon esculentum]; supported by full-length cDNA: Ce		2.8
stress-induced protein sti1 -like protein stress-induced protein sti1 -Glycine max,PID:g872116	254839_at	2.8
hypothetical protein	244903_at	2.8
putative small heat shock protein ;supported by full-length cDNA: Ceres:99763.	267336_at	2.7
unknown protein EST gb ATTS0295 comes from this gene;supported by full-length cDNA: Ceres:20380.	264580_at	2.7
RING-H2 zinc finger protein ATL5, putative similar to RING-H2 zinc finger protein ATL5 GI:4928401 from [Arabidopsis thaliana]	261927_at	2.7
putative DNA-binding protein ; supported by cDNA: gi_15028172_gb_AY045909.1_	255568_at	2.7
hypothetical protein predicted by genemark.hmm	245243_at	2.7
	244944_s_at	2.7
hypothetical protein	244904_at	2.7
•	257339_s_at	2.7
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_16648713_gb_AY058133.1_	261539_at	2.6

subtilisin-like serine protease contains similarity to subtilisin-like protease AIR3 GI:4218991 from [Arabidopsis thaliana] hypothetical protein putative heat shock protein ;supported by full-length cDNA: Ceres:25528. transformer-SR ribonucleoprotein, putative similar to GB:Y09506 from [Nicotiana tabacum] (Plant Mol. Biol. 35 (3), 261-269 (1997)); supported by cI hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:24933. putative protein similar to unknown protein (pir  T07711);supported by full-length cDNA: Ceres:23920. putative protein similar to unknown protein (mb CAB89402.1) unknown protein ; supported by cDNA: gi_15450380_gb_AY052291.1_ putative galactinol synthase ;supported by full-length cDNA: Ceres:124236. unknown protein ;supported by full-length cDNA: Ceres:124236. putative protein RING-H2 zinc finger protein ATL4 - Arabidopsis thaliana, EMBL:AF132014;supported by full-length cDNA: Ceres:3137. AP2 domain transcription factor-like protein NADH dehydrogenase subunit 3 Protein sequence is in conflict with the conceptual translation 70kD heat shock protein ;supported by full-length cDNA: Ceres:98979. hypothetical protein	253104_at 249575_at 265227_s_at 265229_s_at 265230_s_at 244921_s_at 254979_at 265242_at 263374_at 260744_at 247431_at 247431_at 260316_at 262947_at 262947_at 252751_at 248389_at 244920_s_at 265238_s_at 265238_s_at 263510_s_at 261470_at	2.6 2.6 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.4 2.4 2.4 2.4 2.4 2.4 2.3 2.3 2.3 2.3 2.3 2.2 2.2 2.2 2.2 2.2
putative protein similar to unknown protein (pir  T05226);supported by full-length cDNA: Ceres:96. hypothetical protein	249174_at 257318_at	2.2 2.2
putative RING zinc finger protein	265853_at	2.2
hypothetical protein predicted by genscan and genefinder	266590_at	2.1
hypothetical protein	266039_s_at	2.1
hypothetical protein	265233_s_at	2.1
hypothetical protein	265235_s_at	2.1
unknown protein	263467_at	2.1
putative calmodulin similar to calmodulin GB:CAA56517 [Leishmania tarentolae]; Pfam HMM hit: EF hand;supported by full-length cDNA: Ceres:300{		2.1 2.1
unknown protein very similar to unknown protein GB:AAC39468 from [Arabidopsis thaliana]; supported by cDNA: gi_14335087_gb_AY037223.1_ hypothetical protein	258402_at 254731_at	2.1
putative protein EREBP-3 homolog, Stylosanthes hamata, EMBL:U91982; supported by cDNA: gi 15010555 gb AY045579.1	252214 at	2.1
putative protein predicted proteins, Arabidopsis thaliana	251951 s at	2.1
hypothetical protein predicted by genemark.hmm	264217 at	2.1
TINY-like transcription factor Contains similarity to transcription factor (TINY) isolog T02004.22 gb/2062174 from A. thaliana BAC gb/AC001645;sup		2
hypothetical protein	263503 s at	2
unknown protein ;supported by full-length cDNA: Ceres:35218.	256522_at	2

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DnaJ protein, putative contains Pfam profile: PF00226: DnaJ domain; supported by full-length cDNA: Ceres:25796.	256221_at	2
hypothetical protein predicted by genscan+	255891_at	2
glycine-rich cell wall protein-like glycine-rich protein 1.0 precursor, Phaseolus vulgaris, PIR1:S01821; supported by cDNA: gi_14030676_gb_AF3754		2
putative protein hypothetical protein F1N19.27 - Arabidopsis thaliana, EMBL:AC009519	251292_at	2
conglutin gamma - like protein conglutin gamma precursor, Lupinus angustifolius, PIR:S21426; supported by cDNA: gi_15010797_gb_AY045700.1_		2
putative protein predicted proteins, Homo sapiens and Drosophila melanogaster	247847_at	2
protein phosphatase 2C - like ABA induced protein phosphatase 2C, Fagus sylvatica, EMBL:FSY277743; supported by cDNA: gi_15809791_gb_AY	247723_at	2
pyrroline-5-carboxylate reductase ;supported by full-length cDNA: Ceres:36386.	246594_at	2
hypothetical protein	257332_at	2
Expressed protein ; supported by full-length cDNA: Ceres: 123915.	267036 at	1.9
unknown protein ; supported by cDNA: gi_15010737_gb_AY045670.1_	266984 at	1.9
hypothetical protein	266042 s at	1.9
putative beta-1,3-glucanase ;supported by full-length cDNA: Ceres:1126.	265648 at	1.9
putative glycine-rich protein ; supported by cDNA: gi 15215617 gb AY050337.1	265511 at	1.9
unknown protein ;supported by full-length cDNA: Ceres:34827.	265387 at	1.9
H+-transporting ATPase protein, putative similar to H+-transporting ATPase chain E GB:CAB43050 GI:4850294 from [Arabidopsis thaliana]	262354 at	1.9
hypothetical protein similar to hypothetical protein GB:AAD45997 GI:5668770 from (Arabidopsis thaliana)	262322 at	1.9
unknown protein ;supported by full-length cDNA: Ceres:6937.	261485 at	1.9
bZIP transcription factor ATB2, putative similar to GB:CAA18838 from [Arabidopsis thaliana]	261114 at	1.9
unknown protein ;supported by full-length cDNA: Ceres:13102.	260005 at	1.9
chaperonin 60 beta, putative very similar to GB:JT0901 from [Arabidopsis thaliana] (Gene 111 (2), 175-181 (1992))	256983 at	1.9
82.09 and 30.80) similar to alternative splicing factor ASF	255472 at	1.9
putative protein Arabidopsis thaliana nap gene, PID:e1234813; supported by full-length cDNA: Ceres: 38344.	253872_at	1.9
Expressed protein ; supported by full-length cDNA: Ceres: 147351.	252946 at	1.9
hypothetical protein ; supported by cDNA: gi 13877826 gb AF370176.1 AF370176	251964 at	1.9
protein kinase-like protein Pto kinase interactor 1 - Lycopersicon esculentum, EMBL:U28007; supported by cDNA: gi_15451117_gb_AY054639.1_	251494 at	1.9
putative protein chloroplast Cpn21 protein - Arabidopsis thaliana, EMBL:ATH010818;supported by full-length cDNA: Ceres:35721.	251425 at	1.9
	250493 at	1.9
putative protein various predicted proteins, Arabidopsis thaliana		
potassium-dependent sodium-calcium exchanger - like protein cone sodium-calcium potassium exchanger (NCKX), Homo sapiens, EMBL:AF17798		1.9
arabinogalactan-protein (gb AAC77823.1) ;supported by full-length cDNA: Ceres:25423.	247279_at	1.9
unknown protein ;supported by full-length cDNA: Ceres:124621.	247139_at	1.9
Expressed protein ; supported by full-length cDNA: Ceres: 59.	246125_at	1.9
SYBL1 like protein	245513_at	1.9
	244951_s_at	1.9
hypothetical protein	244918_at	1.9
unknown protein ;supported by full-length cDNA: Ceres:35441.	267483_at	1.8
putative senescence-associated protein 12 ;supported by full-length cDNA: Ceres:40806.	264787_at	1.8
Expressed protein ; supported by full-length cDNA: Ceres: 31252.	264726_at	1.8
unknown protein similar to Lambda-PRL2 Arabidopsis thaliana cDNA clone GB:R30041	264354_s_at	1.8
putative SF2/ASF splicing modulator, Srp30 similar to GB:CAB42558	264255_at	1.8
hypothetical protein predicted by genefinder	260522_x_at	1.8
unknown protein ;supported by full-length cDNA: Ceres:114376.	259977_at	1.8
	—	

unknown protein	257670_at	1.8
AP2 domain containing protein RAP2, putative similar to AP2 domain containing protein RAP2.4 GI:2281633 from [Arabidopsis thaliana]; supported		1.8
DRE CRT-binding protein DREB1C involved in low-temperature-responsive gene expression00; supported by cDNA: gi_3738227_dbj_AB007789.1_		1.8
peroxidase ATP17a -like protein peroxidase ATP17a -A.thaliana,PID:e252638;supported by full-length cDNA: Ceres:32346.	253332_at	1.8
putative protein cim1 induced allergen, Glycine max, EMBL:U03860;supported by full-length cDNA: Ceres:27534.	252563_at	1.8
putative protein MEL-26, Caenorhabditis elegans, U67737; supported by cDNA: gi_14532781_gb_AY040015.1_	252367_at	1.8
putative protein P58 protein, Bos primigenius taurus, PIR:A56534;supported by full-length cDNA: Ceres:146009.	250930_at	1.8
pectin methylesterase-like	248807_at	1.8
unknown protein	247393_at	1.8
unknown protein ; supported by cDNA: gi_13877834_gb_AF370180.1_AF370180	247177_at	1.8
seed imbitition protein-like seed imbitition protein Sip1 - Hordeum vulgare, EMBL:M77475	246114_at	1.8
blue copper binding protein ;supported by full-length cDNA: Ceres:7767.	246099_at	1.8
cytochrome c biogenesis orf206	244945_at	1.8
hypothetical protein	257324_at	1.8
hypothetical protein predicted by genemark.hmm	261514_at	1.8
similar to gibberellin-regulated proteins	266613_at	1.7
hypothetical protein	263505_s_at	1.7
hypothetical protein predicted be genemark.hmm	262336_at	1.7
protein kinase, putative (fragment) similar to GB:BAA94509 from [Populus nigra]	261436_at	1.7
hypothetical protein predicted by genemark.hmm	261065_at	1.7
unknown protein	259812_at	1.7
HSC70-interacting protein, putative similar to HSC70-INTERACTING PROTEIN GB:P50502 from [Homo sapiens]	258187_at	1.7
9-cis-epoxycarotenoid dioxygenase, putative similar to 9-cis-epoxycarotenoid dioxygenase GB:AAF26356 [Phaseolus vulgaris]; supported by cDNA:	257280_at	1.7
zinc finger protein, putative similar to Cys2/His2-type zinc finger protein 2 GB:BAA85107 from [Arabidopsis thaliana]; supported by cDNA: gi 15028/		1.7
putative symbiosis-related protein ;supported by full-length cDNA: Ceres:119712.	255283 at	1.7
Expressed protein ; supported by full-length cDNA: Ceres: 24475.	254846 at	1.7
hypothetical protein	254414 at	1.7
putative protein activating signal cointegrator 1 - Homo sapiens, EMBL:AF168418; supported by full-length cDNA: Ceres:13265.	252424 at	1.7
putative protein ;supported by full-length cDNA: Ceres:1198.	250098 at	1.7
integral membrane protein-like	248392 at	1.7
profilin-like protein ; supported by full-length cDNA: Ceres: 102364.	247964 at	1.7
Expressed protein ; supported by full-length cDNA: Ceres: 11699.	247657 at	1.7
phosphoglycerate kinase, putative similar to phosphoglycerate kinase GI:155584 from [Zymomonas mobilis]	246393 at	1.7
putative protein predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 32958.	245905 at	1.7
putative ATP-dependent RNA helicase	267627 at	1.7
putative zinc finger protein	255094 at	1.7
	267335 s at	1.6
putative beta-alanine-pyruvate aminotransferase ;supported by full-length cDNA: Ceres:147543.	267035 at	1.6
putative calcium binding protein ;supported by full-length cDNA: Ceres:31535.	266447_at	1.6
	266013 s at	1.6
	265232 s at	1.6
unknown protein ;supported by full-length cDNA: Ceres:36437.	265184 at	1.6

step II splicing factor, putative similar to step II splicing factor SLU7 GB:AAD13774 GI:4249705 (Homo sapiens)	264633 at	1.6
hypothetical protein predicted by genemark.hmm	261655 at	1.6
disulfide isomerase-related protein, putative similar to GB:AAB50217 from [Homo sapiens]	261167_at	1.6
putative heat-shock protein similar to heat-shock protein precursor GB:S49340 [Secale cereale]; contains Pfam profile: Heat shock hsp90 proteins	259248 at	1.6
germin-like protein similar to germin precursor GB:P26759 (Triticum aestivum); contains Pfam profile: PF01072 germin family	258746 at	1.6
hypothetical protein similar to germin precursor GB. 20739 (Thicdin aestivum), contains Fram profile. FF01072 germin family hypothetical protein supported by full-length cDNA: Ceres:41730.	254721_at	1.6
	_	1.6
putative protein hypothetical protein YPL065w yeast, PIR2:S60925	254422_at	
Expressed protein ; supported by full-length cDNA: Ceres: 9341.	253292_at	1.6
CDC48 - like protein transitional endoplasmic reticulum ATPase, Arabidopsis thaliana, PIR:S60112	251975_at	1.6
putative protein similar to unknown protein (gb AAD21732.1)	249850_at	1.6
U2 snRNP auxiliary factor, small subunit ; supported by cDNA: gi_15723292_gb_AF409140.1_AF409140	249164_at	1.6
unknown protein	248774_at	1.6
putative protein similar to unknown protein (pir  T06016); supported by cDNA: gi_10880504_gb_AF195895.1_AF195895	247965_at	1.6
outer membrane lipoprotein - like outer membrane lipoprotein, Citrobacter freundii, PIR:I40710; supported by full-length cDNA: Ceres:17098.	247851_at	1.6
Ran binding protein 1 homolog - like Ran binding protein 1 homolog, Arabidopsis thaliana, EMBL:ATU62742	247771_at	1.6
putative protein hypothetical protein T26J14.6 - Arabidopsis thaliana, EMBL:AC011915; supported by cDNA: gi_13358202_gb_AF325010.2_AF3250		1.6
	245956_s_at	1.6
dormancy-associated protein, putative similar to dormancy-associated protein GI:2995990 from [Arabidopsis thaliana]; supported by cDNA: gi_1433		1.6
phytochelatin synthetase-like protein gene_id:K17E7.120;supported by full-length cDNA: Ceres:98007.	245228_at	1.6
hypothetical protein	244959_s_at	1.6
hypothetical protein contains similarity to cyclin-dependent kinase inhibitor GB:AAC34660 GI:3550262 from [Arabidopsis thaliana]	257483_at	1.6
hypothetical protein predicted by genscan; supported by cDNA: gi_15146245_gb_AY049264.1_	266889_at	1.5
putative fatty acid elongase	265918_at	1.5
putative CCAAT-box binding trancription factor	265466 at	1.5
putative gigantea protein strong similarity to GB:CAB56039 from [Arabidopsis thaliana]; supported by cDNA: gi_6002679_gb_AF105064.1_AF10506	264211 at	1.5
putative aquaporin (tonoplast intrinsic protein gamma) ;supported by full-length cDNA: Ceres:36633.	263867 at	1.5
putative RNA helicase Contains DEAD-box subfamily ATP-dependent helicases protein motif	262851 at	1.5
hypothetical protein predicted by genemark.hmm	260872 at	1.5
hypothetical protein similar to GB:AAB61488 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:34864.	260411 at	1.5
unknown protein	260276 at	1.5
bZIP transcription factor, putative contains Pfam profile: PF00170: bZIP transcription factor; supported by cDNA: gi_15028322_gb_AY045964.1_	259626 at	1.5
hypothetical protein predicted by genefinder; supported by full-length cDNA: Ceres:40090.	258856 at	1.5
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:108820.	257985 at	1.5
major latex protein, putative similar to major latex protein type1 GB:CAA63026 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 8841.	256880 at	1.5
calreticulin (crt1) identical to calreticulin (crt1) GI:2052379 [Arabidopsis thaliana]; supported by cDNA: gi_2052378_gb_U66343.1_ATU66343	256216 at	1.5
predicted protein of unknown function similar to bacterial tolB proteins but unclear if T7B11.13 is involved in viral transport	255543 at	1.5
	_	1.5
trehalose-6-phosphate phosphatase - like protein trehalose-6-phosphate phosphatase (AtTPPA), PID:g2944178	254321_at	1.5 1.5
Expressed protein ; supported by full-length cDNA: Ceres: 28506.	254190_at	
putative protein various predicted proteins, Arabidopsis thaliana	254078_at	1.5
putative DNA-binding protein AP2 domain containing protein RAP2.4 - Arabidopsis thaliana, PID:g2281633	253799_at	1.5
putative protein	253317_at	1.5
putative protein ;supported by full-length cDNA: Ceres:8161.	253322_at	1.5

anthranilate phosphoribosyltransferase-like protein anthranilate phosphoribosyltransferase - Pisum sativum, PIR:T06460; supported by cDNA: gi_14		1.5
putative protein hypothetical protein T6H20.90 - Arabidopsis thaliana, EMBL:AL096859; supported by cDNA: gi_16648747_gb_AY058150.1_	251039_at	1.5
putative protein similar to unknown protein (gb AAF02153.1)	248167_at	1.5
50S ribosomal protein L17 ;supported by full-length cDNA: Ceres:2806.	247247_at	1.5
unknown protein ;supported by full-length cDNA: Ceres:108595.	247189 at	1.5
Cys2/His2-type zinc finger protein 1 (dbj BAA85108.1)	246993 at	1.5
putative protein hypothetical protein T2E12.2 - Arabidopsis thaliana, EMBL:AC015986	246495 at	1.5
heat shock transcription factor HSF4 ; supported by cDNA: gi_1619920_gb_U68017.1_ATU68017	246214 at	1.5
Expressed protein ; supported by full-length cDNA: Ceres: 103171.	246018 at	1.5
predicted protein	245913 at	1.5
putative protein ;supported by full-length cDNA: Ceres:42742.	245906 at	1.5
calcineurin B-like protein 1 ; supported by cDNA: gi_3309081_gb_AF076251.1_AF076251	245251 at	1.5
	267518 at	1.5
unknown protein	_	
hypothetical protein predicted by genscan and genefinder, contains a Bem1/NCF1/PI3K domain (prosite:QDOC50195)	265535_at	1.4
putative MYB family transcription factor	265301_s_at	1.4
unknown protein Contains similarity to Rhodococcus amidase (gb D16207). ESTs gb T20504,gb H36650,gb N97423,gb H36595 come from this gen		1.4
cyclophilin (CYP2) Same as GB: AF020434;supported by full-length cDNA: Ceres:35643.	264019_at	1.4
unknown protein	263296_at	1.4
splicing factor, putative similar to RSZp21 protein GB:CAA05351 GI:2582643 from [Arabidopsis thaliana] (Plant Mol. Biol. 39 (4), 761-773 (1999)); si		1.4
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:2030.	262159_at	1.4
peptide transporter, putative similar to peptide transporter GI:2655098 from [Hordeum vulgare]	261937_at	1.4
auxin-induced protein IAA5, putative similar to auxin-induced protein IAA5 GI:972913 from [Arabidopsis thaliana]	261766_at	1.4
unknown protein similar to hypothetical protein GB:AAF25972 GI:6714276 from [Arabidopsis thaliana]	261702_at	1.4
unknown protein ; supported by cDNA: gi_12083293_gb_AF332443.1_AF332443	261626_at	1.4
Expressed protein ; supported by full-length cDNA: Ceres: 5811.	261535 at	1.4
chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:26943.	260714 at	1.4
ferredoxin precusor isolog ;supported by full-length cDNA: Ceres:20637.	260481 at	1.4
protein phosphatase 2C (PP2C) identical to protein phosphatase 2C (PP2C) GB:P49598 [Arabidopsis thaliana]	259231_at	1.4
unknown protein ; supported by full-length cDNA: Ceres: 28024.	258747 at	1.4
neutral invertase, putative similar to neutral invertase GB:CAA76145 from [Daucus carota] (Physiol. Plantarum (1999) 107, 159-165)	258507 at	1.4
ethylene responsive element binding factor 4 (AtERF4) identical to GB:BAA32421 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:2	_	1.4
hypothetical protein predicted by genemark.hmm	256653 at	1.4
unknown protein ;supported by full-length cDNA: Ceres:38478.	256663 at	1.4
transcriptional activator CBF1-like protein strong similarity to transcriptional activator CBF1, Arabidopsis thaliana00	254066 at	1.4
putative protein ; supported by full-length cDNA: Ceres: 35749.	253919 at	1.4
		1.4
putaive DNA-binding protein DNA-binding protein WRKY3 - Petroselinum crispum, PIR2:S72445;supported by full-length cDNA: Ceres:11953.	253535_at	
putative protein several hypothetical proteins - Arabidopsis thaliana	252475_s_at	1.4
hypothetical protein	252432_at	1.4
wax synthase-like protein wax synthase - Simmondsia chinensis, PID:g5020219	252084_at	1.4
putative protein DNAJ PROTEIN - Synechococcus PCC7942, EMBL:D29968; supported by cDNA: gi_16648711_gb_AY058132.1_	251263_at	1.4
DREB2A (dbj BAA33794.1) ; supported by cDNA: gi_3738229_dbj_AB007790.1_AB007790	250781_at	1.4
putative protein similar to unknown protein (emb CAB87627.1)	250018_at	1.4

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Expressed protein ; supported by full-length cDNA: Ceres: 18973.	248904_at	1.4
unknown protein ;supported by full-length cDNA: Ceres:31667.	248710_at	1.4
thioredoxin-like 3 ; supported by cDNA: gi_4973259_gb_AF144389.1_AF144389	247524_at	1.4
unknown protein ; supported by full-length cDNA: Ceres: 11054.	247355_at	1.4
putative protein similar to unknown protein (dbj BAA96220.1); supported by full-length cDNA: Ceres: 16835.	247295_at	1.4
WD repeat protein-like ;supported by full-length cDNA: Ceres:11277.	247106_at	1.4
casein kinase II alpha subunit ; supported by cDNA: gi_391602_dbj_D10246.1_ATHCK2A	247000_at	1.4
putative protein FH protein interacting protein FIP1, Arabidopsis thaliana, EMBL:AF174428; supported by full-length cDNA: Ceres: 19508.	246034_at	1.4
HSP like protein ; supported by cDNA: gi_15293148_gb_AY051008.1_	245293_at	1.4
hypothetical protein	244927_at	1.4
orf153b orf153b	244923_s_at	1.4
hypothetical protein	257325_at	1.4
Escherichia coli /REF=J04423 /DEF=E coli bioB gene biotin synthetase corresponding to nucleotides 2772-3004 of J04423 /LEN=1114 (-5, -M, -3 re	X-r2-Ec-bioB-	1.3
unknown protein	267073_at	1.3
putative bHLH transcription factor	266456_at	1.3
unknown protein	266188_at	1.3
unknown protein ;supported by full-length cDNA: Ceres:123225.	265626_at	1.3
putative microtubule-associated protein ;supported by full-length cDNA: Ceres:3416.	265510_at	1.3
hypothetical protein predicted by genscan and genefinder	265276_at	1.3
Unknown protein ; supported by full-length cDNA: Ceres: 28033.	264898_at	1.3
hypothetical protein predicted by genemark.hmm	264739_at	1.3
unknown protein similarity to stromal cell-derived factor 2, Mus musculus, PIR2:JC5105; contains EST gb:T22533, AA067386, Z18160;supported by	264382_at	1.3
unknown protein similar to hypothetical protein HYP1 gb Z97338 from A. thaliana	264389_at	1.3
heat-shock protein, putative similar to heat-shock protein GI:472939 from [Helianthus annuus]; supported by full-length cDNA: Ceres:97415.	263150_at	1.3
hypothetical protein similar to putative protease GI:4415912 from [Arabidopsis thaliana]; supported by cDNA: gi 11993876 gb AF329505.1 AF3295	261757_at	1.3
NAC domain protein, putative similar to NAC domain protein NAM GB:AAD17313 GI:4325282 from [Arabidopsis thaliana]; supported by full-length cI		1.3
hypothetical protein predicted by genemark.hmm	260656 at	1.3
F-box protein FKF1/ADO3, AtFBX2a identical to FKF1 GI:6960305 and Adagio 3 GI:13487072 from [Arabidopsis thaliana]	259990 s at	1.3
putative RNA-binding protein contains Pfam profile: PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain); supported by cDNA: gi 14		1.3
AP2-containing DNA-binding protein contains Pfam profile: PF00847 AP2 domain	259793 at	1.3
putative DNA-binding protein similarity to short region of heat shock transcription factors: GB:CAB10177, GB:AAC31792, GB:CAA16745, GB:CAA16	259711 at	1.3
hypothetical protein contains bromodomain, predicted by genscan; supported by cDNA: gi_16323116_gb_AY057662.1_	259164 at	1.3
rotamase FKBP (ROF1) identical to rotamase FKBP (ROF1) GB:U49453 [Arabidopsis thaliana] (Mol. Gen. Genet. 252 (5), 510-517 (1996)); support		1.3
unknown protein similar to At14a protein GB:AAD26355 GI:4589123 [Arabidopsis thaliana]; supported by cDNA: gi 16226582 gb AF428437.1 AF4		1.3
hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 126401.	256413 at	1.3
unknown protein ;supported by full-length cDNA: Ceres:13451.	256223 at	1.3
unknown protein ;supported by full-length cDNA: Ceres:94739.	256067 at	1.3
GBF2, G-box binding factor ;supported by full-length cDNA: Ceres:16533.	255625 at	1.3
Expressed protein ; supported by cDNA: gi_4741922_gb_AF130849.1_AF130849	255511 at	1.3
protein phosphatase type 1 PP1BG ;supported by full-length cDNA: Ceres:20905.	254923 at	1.3
putative protein hypothetical protein F7H19.70 - Arabidopsis thaliana, PID:e1310057	254848 at	1.3
	254833 s at	1.3
opper amine oxidase like protein (nagmentz) opper amine oxidase - older anetinum, i D.e 1000804	207000_3_al	1.5

putative protein hypothetical protein, chr.4, Arabidopsis thaliana, PATCHX:G2392763	254350_at	1.3
putative protein ; supported by full-length cDNA: Ceres: 37881.	253464_at	1.3
putative protein ;supported by full-length cDNA: Ceres:29964.	253422_at	1.3
senescence-associated protein sen1 identical to senescence-associated protein GI:1046270 from [Arabidopsis thaliana] ;supported by full-length cDI	253161_at	1.3
putative protein physical impedance induced protein, Zea mays, gb:AF001635	253113_at	1.3
putative protein various predicted proteins, Arabidopsis thaliana	252903_at	1.3
putative protein arm repeat containing protein ARC1 -Brassica napus,PID:g2558938	252045_at	1.3
putative protein zinc finger transcription factor (PEI1), Arabidopsis thaliana, EMBL:AF050463; supported by cDNA: gi_15810486_gb_AY056282.1_	251745_at	1.3
putative protein ;supported by full-length cDNA: Ceres:35934.	251094_at	1.3
putative protein putative proteins - Arabidopsis thaliana; supported by cDNA: gi_15292802_gb_AY050835.1_	251084_at	1.3
putative protein predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 2344.	250399_at	1.3
PGPD14 protein ;supported by full-length cDNA: Ceres:41666.	249862_at	1.3
unknown protein ;supported by full-length cDNA: Ceres:25275.	248709_at	1.3
xylosidase	248622_at	1.3
unknown protein	247992_at	1.3
calnexin - like protein calnexin homolog, Arabidopsis thaliana, EMBL:AT08315;supported by full-length cDNA: Ceres:2869.	247494_at	1.3
nitrate transporter NTL1 - like protein nitrate transporter NTL1, Arabidopsis thaliana, EMBL:AF073361	247447_at	1.3
putative protein contains similarity to pathogenesis-related protein; supported by full-length cDNA: Ceres:2152.	247074_at	1.3
putative protein predicted protein, Arabidopsis thaliana	246584_at	1.3
putative protein ;supported by full-length cDNA: Ceres:13475.	246225_at	1.3
prolin-rich protein, putative similar to prolin-rich protein GI:21045 from [Phaseolus vulgaris]	245688_at	1.3
putative WRKY-type DNA-binding protein ; supported by cDNA: gi_13506742_gb_AF224704.1_AF224704	245051_at	1.3
aquaporin MIP - like protein aquaporin 2, Samanea saman, AF067185; supported by full-length cDNA: Ceres: 11929.	251858_at	1.3
hypothetical protein predicted by grail	260275_at	1.2
Expressed protein ; supported by full-length cDNA: Ceres: 7152.	266658_at	1.2
hypothetical protein predicted by genefinder and genscan; supported by cDNA: gi_15724241_gb_AF412061.1_AF412061	266608_at	1.2
putative tropinone reductase	266280_at	1.2
protease inhibitor II ; supported by cDNA: gi_15293090_gb_AY050979.1_	266118_at	1.2
hypothetical protein predicted by genefinder; supported by full-length cDNA: Ceres: 32664.	265628_at	1.2
unknown protein	265330_at	1.2
	265237_s_at	1.2
putative prohibitin 2 B-cell receptor associated protein; supported by full-length cDNA: Ceres: 6208.	265037_at	1.2
putative 10kd chaperonin strongly similar to GB:P34893;supported by full-length cDNA: Ceres:21053.	264895_at	1.2
unknown protein	264617_at	1.2
unknown protein ; supported by cDNA: gi_13265448_gb_AF324676.2_AF324676	263881_at	1.2
hypothetical protein predicted by genemark.hmm	262901_at	1.2
unknown protein ;supported by full-length cDNA: Ceres:93312.	262607_at	1.2
unknown protein ;supported by full-length cDNA: Ceres:8932.	262313_at	1.2
putative RING zinc finger protein contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger); supported by full-length cDNA: Ceres: 9668:	262167_at	1.2
Expressed protein ; supported by full-length cDNA: Ceres: 40238.	261756_at	1.2
hypothetical protein predicted by genemark.hmm	261524_at	1.2
Expressed protein ; supported by cDNA: gi_13926326_gb_AF372912.1_AF372912	261272_at	1.2

hypothetical protein similar to putative MYB family transcription factor GB:AAD17429 GI:4335752 from [Arabidopsis thaliana]	260999_at	1.2
hypothetical protein contains similarity to guanine nucleotide exchange factor, eIF-2B, delta subunit GI:529428 from [Mus musculus]	260756_at	1.2
Expressed protein ; supported by full-length cDNA: Ceres: 21834.	260768_at	1.2
putative sulfate transporter contains Pfam profile: PF00916 sulfate transporter family;supported by full-length cDNA: Ceres:120095.	260302_at	1.2
putative protein kinase contains Pfam profile: PF00069 Eukaryotic protein kinase domain	260206_at	1.2
unknown protein ;supported by full-length cDNA: Ceres:270659.	260025_at	1.2
unknown protein	259942_at	1.2
RING-H2 zinc finger protein ATL3, putative similar to GI:4928397 from [Arabidopsis thaliana] (Plant Mol. Biol. 40 (4), 579-590 (1999))	259854 at	1.2
unknown protein Pfam HMM hit: EF hand	259137 at	1.2
unknown protein ; supported by full-length cDNA: Ceres: 118261.	258879 at	1.2
putative beta-1,3-glucanase similar to beta-1,3-glucanase GB:S12402 [Nicotiana sp], GB:CAA03908 [Citrus sinensis], GB:S44364 [Lycopersicon es		1.2
unknown protein	258699 at	1.2
putative shikimate kinase similar to shikimate kinase precursor GB:CAA45121 [Lycopersicon esculentum]	258281 at	1.2
unknown protein ; supported by cDNA: gi_15529233_gb_AY052241.1_	258225 at	1.2
unknown protein	256763 at	1.2
Sm-like protein contains Pfam profile: PF01423: Sm protein; supported by full-length cDNA: Ceres: 23170.	256333 at	1.2
Expressed protein ; supported by full-length cDNA: Ceres: 31945.	256159 at	1.2
putative protein contains similarity to pseudouridine synthases; supported by cDNA: gi 13430549 gb AF360187.1 AF360187	255985 at	1.2
		1.2
mitochondrial inner membrane translocase component, putative similar to mitochondrial inner membrane translocase component Tim17a GI:437852		
Expressed protein ; supported by cDNA: gi_15010591_gb_AY045597.1_	255793_at	1.2
putative protein hypothetical proteins Arabidopsis thaliana; supported by full-length cDNA: Ceres: 12923.	254787_at	1.2
putative protein AR411 - Arabidopsis thaliana (thale cress), PID:g1669603; supported by cDNA: gi_13507100_gb_AF272748.1_AF272748	254231_at	1.2
putative DNA-binding protein DNA-binding protein WRKY3 - Petroselinum crispum, PIR2:S72445; supported by full-length cDNA: Ceres:112528.	254159_at	1.2
hypothetical protein ;supported by cDNA: gi_15028324_gb_AY045965.1_	253391_at	1.2
RING-H2 finger protein RHA3b ;supported by full-length cDNA: Ceres:31493.	253140_at	1.2
putative protein various predicted proteins, Arabidopsis thaliana	252901_at	1.2
putative protein ; supported by full-length cDNA: Ceres: 40302.	252234_at	1.2
hypothetical protein ;supported by full-length cDNA: Ceres:101230.	251925_at	1.2
putative protein MtN24, Medicago truncatula, EMBL:MTY15290;supported by full-length cDNA: Ceres:6434.	251795_at	1.2
putative protein ;supported by cDNA: gi_14326524_gb_AF385716.1_AF385716	250896_at	1.2
(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase -like protein beta-hydroxyacyl-ACP dehydratase precursor, Toxoplasma gondii, EMBL:AF06	250470_at	1.2
separation anxiety protein - like separation anxiety protein, Drosophila melanogaster, EMBL:AF225902	250390_at	1.2
putative protein prdeicted proteins, Schizosaccharomyces pombe	250281 at	1.2
chloroplast GrpE protein ; supported by cDNA: gi_13878046_gb_AF370286.1_AF370286	250061 at	1.2
acetyl-CoA synthetase-like protein	249869 at	1.2
thaumatin-like protein thaumatin-like protein - Arabidopsis thaliana, PIR:S71175	249439 at	1.2
RING finger -like protein RING-H2 zinc finger protein ATL4, Arabidopsis thaliana, EMBL:AF132014	249398 at	1.2
putative protein contains similarity to bZIP transcription factor; supported by full-length cDNA: Ceres:43004.	248606 at	1.2
unknown protein ;supported by full-length cDNA: Ceres:92267.	248445 at	1.2
putative protein similar to unknown protein (gb/AAB68039.1);supported by full-length cDNA: Ceres:1076.	248432 at	1.2
putative protein similar to unknown protein (gb/AAB08039.1),supponed by full-length CDNA. Ceres. 1070.	247459 at	1.2
		1.2
MYB96 transcription factor-like protein ; supported by cDNA: gi_5823334_gb_AF176001.1_AF176001	247455_at	1.2

putative protein contains similarity to unknown protein (gb AAC17084.1); supported by cDNA: gi 14596230 gb AY042903.1	247047 at	1.2
glutaredoxin, putative similar to glutaredoxin GI:1732424 from [Ricinus communis]	246384 at	1.2
hypothetical protein ;supported by full-length cDNA: Ceres:38657.	245893 at	1.2
hypothetical protein similar to hypothetical protein GB:CAB77775 GI:7269775 from [Arabidopsis thaliana]	245789 at	1.2
putative protein contains EST gb:T4504800	245229 at	1.2
hypothetical protein	257336 at	1.2
unknown protein	267406_at	1.1
putative anthocyanin 5-aromatic acyltransferase ; supported by cDNA: gi_13937225_gb_AF372968.1_AF372968	267337 at	1.1
unknown protein ;supported by full-length cDNA: Ceres:9284.	267261_at	1.1
unknown protein ; supported by full-length cDNA: Ceres: 28529.	267178_at	1.1
similar to MIo proteins from H. vulgare ; supported by cDNA: gi_14091593_gb_AF369573.1_AF369573	266992_at	1.1
putative zinc transporter ;supported by full-length cDNA: Ceres:207558.	266718_at	1.1
hypothetical protein predicted by genscan	266707_at	1.1
unknown protein	266005_at	1.1
unknown protein ;supported by full-length cDNA: Ceres:19338.	265895_at	1.1
putative auxin-regulated protein	265806_at	1.1
unknown protein ; supported by cDNA: gi_13877764_gb_AF370145.1_AF370145	264989_at	1.1
unknown protein	264909_at	1.1
putative elongation factor similar to GB:AAC67357	264664_at	1.1
	264488_s_at	1.1
hypothetical protein predicted by genscan+	264491_at	1.1
hypothetical protein similar to transcriptional repressor NF-X1 in Homo sapiens (sp Q12986 NFX1_HUMAN); similar to EST gb T21002	264460_at	1.1
unknown protein similar to EST gb AA598098;supported by full-length cDNA: Ceres:23916.	264467_at	1.1
hypothetical protein contains non-consensus donor splice site AT at exon 4 and acceptor splice site at exon5;Contains similarity to serine/threonine p		1.1
symbiosis-related protein, putative similar to symbiosis-related protein GI:2072022 from [Laccaria bicolor]; supported by full-length cDNA: Ceres:191	_	1.1
putative mitochondrial dicarboxylate carrier protein ;supported by full-length cDNA: Ceres:20723.	264000_at	1.1
glycine-rich RNA binding protein 7 Alternative splicing exists based on EST evidence, form 1 splice site is AG, form 2 splice site is AT	263548_at	1.1
putative heat shock protein ; supported by cDNA: gi_15450722_gb_AY053403.1_	263483_at	1.1
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:94743.	263151_at	1.1
putative glutamate/aspartate-binding peptide Belongs to the PF 01027 Uncharacterized protein family UPF0005 with 7 transmembrane domains	263164_at	1.1
DNA-binding protein similar to cellular nucleic acid binding protein GB:CAA45345 GI:50471 from [Mus musculus]; supported by full-length cDNA: Ce	_	1.1
hypothetical protein predicted by genscan+	262719_at	1.1
hypothetical protein similar to hypothetical protein GB:AAD50049 GI:5734784 from [Arabidopsis thaliana]	262459_at	1.1
transcription factor, putative similar to Transcription factor GB:CAA74053 GI:2398533 from [Arabidopsis thaliana]; supported by full-length cDNA: Ce		1.1
hypothetical protein predicted by genscan+	262067_at	1.1
methionine/cystathionine gamma lyase, putative similar to methionine gamma-lyase GB:CAA04124.1 GI:2330885 from [Trichomonas vaginalis]; sup		1.1
type 2 peroxiredoxin, putative similar to type 2 peroxiredoxin GI:4928472 from [Brassica rapa subsp. pekinensis]; supported by full-length cDNA: Cer		1.1
chloroplast drought-induced stress protein, putative similar to chloroplast drought-induced stress protein GI:2582821 from [Solanum tuberosum]; sup		1.1
unknown protein	261558_at	1.1
AP2 domain containing protein, putative similar to AP2 domain containing protein RAP2.5 GI:2281635 from (Arabidopsis thaliana); supported by cDI		1.1
defensin AMP1, putative similar to PIR:S66219 from [Clitoria ternatea]	261135_at	1.1
ribokinase, putative similar to GB:AAD00536 from [Pyrobaculum aerophilum]	261136_at	1.1

hypothetical protein predicted by genscan+, contains Viral RNA helicase domain	260283_at	1.1
unknown protein similar to putative protein GB:CAB38899 [Arabidopsis thaliana]	260055_at	1.1
unknown protein ; supported by cDNA: gi_15809819_gb_AY054177.1_	259792_at	1.1
CONSTANS family zinc finger protein, putative contains Pfam profile: PF01760: CONSTANS family zinc finger; supported by cDNA: gi_14335053_g	259595_at	1.1
hypothetical protein	259570_at	1.1
unknown protein similar to zinc finger protein GB:BAA33206 [Oryza sativa]	259244_at	1.1
RNA helicase, DRH1 identical to RNA helicase DRH1 GB:BAA28347 [Arabidopsis thaliana]; supported by cDNA: gi_15215693_gb_AY050375.1_	259194_at	1.1
unknown protein similar to CGI-86 protein GB:AAD34081 [Homo sapiens], HMM hit: Alcohol/other dehydrogenases, short chain type	259051 at	1.1
unknown protein ; supported by cDNA: gi_15809941_gb_AY054239.1_	259057_at	1.1
NAM-like protein (no apical meristem) similar to NAM GB:CAA63101 [Petunia x hybrida]; supported by full-length cDNA: Ceres: 119460.	258813_at	1.1
putative auxin-resistance protein, AXR1 similar to GB:P42744 from [Arabidopsis thaliana]	258073_at	1.1
hypothetical protein predicted by genemark.hmm	257724_at	1.1
Expressed protein ; supported by full-length cDNA: Ceres: 262289.	257312_at	1.1
unknown protein ;supported by cDNA: gi_15081754_gb_AY048270.1_	257153_at	1.1
unknown protein ;supported by cDNA: gi_15146182_gb_AY049232.1_	257154_at	1.1
unknown protein	256940_at	1.1
hypothetical protein predicted by genefinder, similar to GP 1301832 gnl PID e239862 Z71287	256715_at	1.1
plastid protein, putative similar to GI:2246378 from [Arabidopsis thaliana] (Proc. Natl. Acad. Sci. U.S.A. 94 (23), 12722-12727 (1997))	256466_at	1.1
putative small nuclear ribonucleoprotein U2B ;supported by full-length cDNA: Ceres:34995.	255871_at	1.1
unknown protein similar to unknown protein GI:6714347 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:103226.	255733_at	1.1
putative hypoersensitive response protein similar to N. tabacum hin1, GenBank accession number Y07563; supported by full-length cDNA: Ceres:29	255577_at	1.1
putative protein	255134_at	1.1
zinc-finger protein Lsd1 ;supported by full-length cDNA: Ceres:38456.	254477_at	1.1
protein-methionine-S-oxide reductase ;supported by full-length cDNA: Ceres:36536.	254099_at	1.1
putative ribosomal protein ribosomal protein L31, Nicotiana glutinosa, U23784;supported by full-length cDNA: Ceres:14013.	254012_at	1.1
glycine-rich protein like glycine-rich protein 5 - Arabidopsis thaliana, PIR2: JQ1064; supported by full-length cDNA: Ceres: 33435.	253754_at	1.1
putative protein (fragment)	253238_at	1.1
putative protein	252539_at	1.1
response reactor 2 (ATRR2) ;supported by cDNA: gi_3273197_dbj_AB010916.1_AB010916	252374_at	1.1
putative protein	251917_at	1.1
putative protein leucine zipper-EF-hand containing transmembrane protein 1 - Mus musculus, EMBL:AF061026	251432_at	1.1
putative protein RING finger protein AO7, Mus musculus, EMBL:AF171060	251403_at	1.1
putative protein several protein kinases - different species	251068_at	1.1
I-box binding factor - like protein I-box binding factor (LeMYBI gene), Lycopersicon esculentum, EMBL:LES243339; supported by full-length cDNA: C		1.1
putative protein	250158_at	1.1
hypothetical protein	249990_at	1.1
CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED (TCH2) ;supported by full-length cDNA: Ceres:25475.	249583_at	1.1
protein kinase - like protein protein kinase ATN1, Arabidopsis thaliana, PIR:S61766	249361_at	1.1
2-oxoglutarate/malate translocator ;supported by cDNA: gi_15028072_gb_AY045893.1_	247286_at	1.1
COP1-interacting protein CIP8 ; supported by cDNA: gi_5929905_gb_AF162150.1_AF162150	247219_at	1.1
hypothetical protein ;supported by full-length cDNA: Ceres:96001.	246442_at	1.1
hypothetical protein contains similarity to cockayne syndrome complementation group A protein GB:U28413 GI:975301 from [Homo sapiens]	245764_s_at	1.1

hypothetical protein predicted by genemark.hmm	245659_at	1.1
Expressed protein ; supported by cDNA: gi_13877886_gb_AF370206.1_AF370206	245261_at	1.1
Expressed protein ; supported by cDNA: gi_15810220_gb_AY056149.1_	264512_at	1.1
hypothetical protein	257317_at	1.1
hypothetical protein predicted by genemark.hmm	260935_at	1
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:101876.	258878_at	1
UDP-glucose glucosyltransferase, putative similar to UDP-glucose glucosyltransferase GI:3928543 from [Arabidopsis thaliana]; supported by cDNA:	255943_at	1
unknown protein similar to GP 2262147 AC002330	267628_at	1
Expressed protein ; supported by full-length cDNA: Ceres: 27620.	267591_at	1
putative small nuclear ribonucleoprotein Prp4p	267102_at	1
Expressed protein ; supported by full-length cDNA: Ceres: 42237.	266886_at	1
unknown protein ;supported by full-length cDNA: Ceres:35872.	266806_at	1
putative non-LTR retroelement reverse transcriptase	266786_at	1
putative protein kinase contains a protein kinase domain profile (PDOC00100)	266749_at	1
hypothetical protein predicted by genefinder	266545_at	1
unknown protein	266189_at	1
putative microtubule-associated protein ; supported by cDNA: gi_15724331_gb_AF412106.1_AF412106	266106_at	1
putative senescence-associated protein 5 contains a transmembrane 4 family signature; rare (GC) splice donor consensus found instead of (GT) at i	265935_at	1
hypothetical protein predicted by genscan	265849_at	1
predicted by genscan and genefinder ;supported by full-length cDNA: Ceres:120459.	265732_at	1
putative arginine/serine-rich splicing factor	265449_at	1
unknown protein	265451_at	1
putative WD-40 repeat protein similar to TUP1(GB:AF079369); supported by cDNA: gi_13605894_gb_AF367346.1_AF367346	265259_at	1
carboxyphosphonoenolpyruvate mutase, putative similar to carboxyphosphonoenolpyruvate mutase GI:47149 from [Streptomyces hygroscopicus];si	264954_at	1
hypothetical protein ;supported by full-length cDNA: Ceres:250028.	264870_at	1
gamma glutamyl hydrolase, putative similar to gamma glutamyl hydrolase GI:1680711 from [Glycine max]; supported by full-length cDNA: Ceres:413	264300_at	1
hypothetical protein ;supported by full-length cDNA: Ceres:123727.	263946_at	1
unknown protein ;supported by full-length cDNA: Ceres:12251.	263931_at	1
putative cis-Golgi SNARE protein ;supported by full-length cDNA: Ceres:2416.	263839_at	1
putative acetolactate synthase	263460_at	1
hypothetical protein predicted by genefinder; supported by cDNA: gi_14423545_gb_AF387010.1_AF387010	263075_at	1
hypothetical protein ;supported by full-length cDNA: Ceres:30113.	262929_at	1
FtsH protease, putative contains similarity to chloroplast FtsH protease GI:5804782 from [Nicotiana tabacum]	262937_at	1
membrane related protein CP5, putative similar to membrane related protein CP5 GI:4741929 from [Arabidopsis thaliana]; supported by cDNA: gi_4	262884_at	1
unknown protein similar to pectinesterase GB:X85216 GI:732912 [Phaseolus vulgaris];supported by full-length cDNA: Ceres:33355.	262844_at	1
unknown protein Location of ESTs 152C14T7, gb T88012, 173P7T7, gb H36502 and 107E18T7, gb T22775; supported by full-length cDNA: Ceres	262803_at	1
unknown protein	262677_at	1
Expressed protein ; supported by full-length cDNA: Ceres: 17598.	262226_at	1
putative ubiquinol-cytochrome c reductase similar to ubiquinol-cytochrome c reductase GB:P48504 from [Solanum tuberosum]; supported by cDNA:	262206_at	1
mRNA export protein, putative similar to mRNA export protein GB:AAC28126 GI:1903456 from [Homo sapiens]; supported by full-length cDNA: Cere		1
unknown protein	261545_at	1
actin capping protein beta-2, putative similar to actin capping protein beta-2 GB:U07826 GI:565063 from [Gallus gallus]	261512_at	1

unknown protein ; supported by cDNA: gi_15292702_gb_AY050785.1_ unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_ flavonol 3-o-glucosyltransferase, putative similar to flavonol 3-o-glucosyltransferase GB:Q40287 from [Manihot esculenta] unknown protein ; supported by cDNA: gi_15028364_gb_AY045985.1_ F-box protein family contains similarity to F-box protein FBX3 GI:6103643 from [Homo sapiens] RNA recognition motif-containing protein SEB-4 similar to RNA recognition motif-containing protein SEB-4 GI:8895698 from [Xenopus laevis]; suppor putative protein kinase similar to protein kinase APK1A GB:Q06548 [Arabidopsis thaliana]; contains Pfam profile: PF00069 Eukaryotic protein kinase hypothetical protein predicted by genscan+; supported by cDNA: gi_14335049_gb_AY037204.1_ hypothetical protein similar to putative protein GB:CAA18164 [Arabidopsis thaliana]; supported by cDNA: gi_13878144_gb_AF370335.1_AF370335 unknown protein 60S ribosomal protein L18A, putative similar to GI:3128228 from [Arabidopsis thaliana] (Nature 402 (6763), 761-768 (1999)); supported by full-length hypothetical protein ; supported by full-length cDNA: Ceres:147838. unknown protein putative thioredoxin similar to protein disulfide isomerase precursor GB:P29828 [Medicago sativa]; Pfam HMM hit: Thioredoxins hypothetical protein contains similarity to myosin heavy chain cardiac muscle specific isoform 1 GI:7416982 from (Argopecten irradians); supported b hypothetical protein predicted by genscan; supported by full-length cDNA: Ceres:18207.	260310_at 260243_at 260155_at 260026_at 259976_at 259934_at 259757_at	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
unknown protein ;supported by full-length cDNA: Ceres:102038. putative D-ribulose-5-phosphate 3-epimerase similar to D-ribulose-5-phosphate 3-epimerase GB:AAF01048 [Oryza sativa]; contains non-consensus E2, ubiquitin-conjugating enzyme 11 (UBC11) identical to gi:12643427, SP:P35134;supported by full-length cDNA: Ceres:21455. unknown protein ;supported by full-length cDNA: Ceres:35949. hypothetical protein similar to receptor protein kinases: GB:CAB43834, GB:S71277 [Arabidopsis thaliana] unknown protein ethylene responsive element binding factor, putative similar to GB:BAA32420 from [Arabidopsis thaliana], contains Pfam profile: PF00847 P2 domai DNA-binding protein, putative similar to GB:AAF32491 from [Triticum aestivum] (Mol. Cell. Biol. 19 (12), 8113-8122 (1999)) prohibitin, putative similar to prohibitin GB:AAC49691 from [Arabidopsis thaliana] (Plant Mol. Biol. (1997) 33 (4), 753-756);supported by full-length cI unknown protein ; supported by cDNA: gi_14194136_gb_AF367274.1_AF367274	259184_at 258999_at 258678_at 258608_at 258557_at 258364_at 258282_at 257675_at 257291_at 257149_at	1 1 1 1 1 1 1 1 1 1 1
unknown protein ; supported by cDNA: gi_13358195_gb_AF325003.2_AF325003	256114_at	1 1 1 1 1 1 1 1 1 1 1 1

hypothetical protein SOF1 protein-like protein SOF1 (involved in rRNA processing) protein-yeast; supported by cDNA: gi_13937178_gb_AF372943.1_AF372943 glycine-rich protein glycine-rich cell wall structural protein - garden petunia,Pir2:A26099 ribosomal protein L11 homolog several ribosomal proteins L11;supported by full-length cDNA: Ceres:95636.	253796_at 253777_at 253619_at 253138_at	1 1 1 1
putative protein hypothetical protein HI0722 (pepQ 5 region) -E.coli, PID:g1790283;supported by full-length cDNA: Ceres:18344.	253007 at	1
Expressed protein ; supported by cDNA: gi_15451093_gb_AY054627.1_	253001 at	1
putative protein NADH dehydrogenase subunit 1, Lymantria dispar albescens, EMBL:AF075286;supported by full-length cDNA: Ceres:36750.	252091 at	1
putative protein various predicted proteins, C. elegans, Homo sapiens and yeast; supported by full-length cDNA: Ceres:36721.	252064 at	1
putative protein validus proteins, Nicotiana tabacum, PIR:T03265;supported by full-length cDNA: Ceres:1678.	251879 at	1
putative protein fill protein, Nicotiana tabacum, Fill 19209, supported by full-length CDIVA. Ceres. 1970. putative protein GTP-binding regulatory protein beta chain, Dictyostelium discoideum, PIR:A47370; supported by cDNA: gi_13430701_gb_AF36026		1
beta-1,3-glucanase - like protein probable beta-1,3-glucanase, Triticum aestivum, PIR:T06268; supported by full-length cDNA: Ceres: 8980.	251804_at	1
putative protein CND41, chloroplast nucleoid DNA binding protein - Nicotiana tabacum, EMBL:D26015; supported by cDNA: gi_15983375_gb_AF42		1
RING-H2 zinc finger protein ATL4 ; supported by cDNA: gi_4928398_gb_AF132014.1_AF132014	251507_at 251412_at	1
putative protein HIRA interacting protein 4 (dnaJ-like) - Homo sapiens, EMBL:AJ001309;supported by full-length cDNA: Ceres:37292.	251412_at 251182_at	1
putative protein Myb-related transcriptional activator mybSt1, Solanum tuberosum, EMBL:S74753	251132_at	1
	250965 at	1
putative protein various predicted proteins, Arabidopsis thaliana		
Expressed protein ; supported by full-length cDNA: Ceres: 12197.	250921_at	1 1
putative protein	250572_at	
putative protein HSPC184, Homo sapiens, EMBL:AF151018; supported by cDNA: gi_14335059_gb_AY037209.1_	250401_at	1
GASA4 ; supported by cDNA: gi_950098_gb_U15683.1_ATU15683	250109_at	1
	249975_s_at	1
NAM (no apical meristem)-like protein ; supported by cDNA: gi_14326464_gb_AF385685.1_AF385685	249944_at	1
putative protein similar to unknown protein (gb AAF19669.1)	249253_at	1
unknown protein	249134_at	1
GDSL-motif lipase/hydrolase-like protein ;supported by full-length cDNA: Ceres:18389.	248912_at	1
putative protein contains similarity to S-ribonuclease binding protein	248819_at	1
putative protein strong similarity to unknown protein (pir  T09376)	248630_at	1
putative protein strong similarity to unknown protein (gb AAB95234.1)	248502_at	1
protein translocation complex Sec61 gamma chain (pir  T05513) ; supported by cDNA: gi_13877812_gb_AF370169.1_AF370169	248512_at	1
HCF106 (gb AAD32652.1) ; supported by cDNA: gi_4894913_gb_AF139188.1_AF139188	248338_at	1
homogentisate 1,2-dioxygenase ;supported by full-length cDNA: Ceres:6599.	248193_at	1
putative protein similar to unknown protein (gb AAD50013.1)	248140_at	1
unknown protein ;supported by full-length cDNA: Ceres:21044.	247990_at	1
Expressed protein ; supported by full-length cDNA: Ceres: 22388.	247865_at	1
beta-1,3 glucanase - like protein beta-1,3 glucanase, Populus alba x Populus tremula, EMBL:AF230109	247845_at	1
pseudo-response regulator 1 ;supported by cDNA: gi_7576353_dbj_AB041530.1_AB041530	247525_at	1
putative protein contains similarity to NAC-domain protein; supported by full-length cDNA: Ceres: 6637.	247351_at	1
putative protein contains similarity to unknown protein (pir  T05568)	247182_at	1
putative protein contains similarity to unknown protein (sp Q10058);supported by full-length cDNA: Ceres:108335.	246985_at	1
hypothetical protein predicted by genemark.hmm	246630_at	1
putative protein predicted protein At2g41010 - Arabidopsis thaliana, EMBL:AC004261;supported by full-length cDNA: Ceres:39584.	246289_at	1
putative protein ; supported by cDNA: gi_11245493_gb_AF319540.1_AF319540	246212_at	1

putative protein phi-1 - Nicotiana tabacum, EMBL:AB018441;supported by full-length cDNA: Ceres:38576.	245885 at	1
disease resistance protein RPS4, putative similar to disease resistance protein RPS4 GI:9759605 from [Arabidopsis thaliana]	245826 at	1
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:124269.	245840 at	1
RNA-binding glycine-rich protein, putative similar to RNA-binding glycine-rich protein (RGP-1a) GI:436789 from [Nicotiana sylvestris]	245778 at	1
hypothetical protein predicted by genemark.hmm	245662 at	1
Expressed protein ; supported by full-length cDNA: Ceres: 6580.	245336_at	1
putative protein disulfide-isomerase	245175 at	1
photolyase/blue-light receptor (PHR2) ;supported by full-length cDNA: Ceres:34800.	245150_at	1
	244928 s at	1
NADH dehydrogenase subunit 4	244929 at	1
hypothetical protein predicted by genscan	257404 at	1
putative mitochondrial carrier protein Graves disease mitochondrial solute carrier protein- bovine, PIR2:S26596	254018 at	1
putative interior contains similarity to unknown protein (emb/CAB87908.1);supported by full-length cDNA: Ceres:152842.	249793 at	1
putative protein contains similarly to unknown protein (emperator soor 1), supported by full-length cDNA. Ceres. 192042. putative uridylate kinase similar to uridylate kinase GB:CAB13524 [Bacillus subtilis], GB:P74457 [Synechocystis PCC6803]; supported by cDNA: gi_		0.9
putative undylate kinase similar to undylate kinase ob.orb 19924 [bacinds sublins], ob.i 74497 [bynechocysiis 1 000000], supported by cDNA: gi_ putative protein ; supported by cDNA: gi_13991647_gb_AF359388.1_AF359388	254043 at	0.9
putative protein proline transport helper PTH1 - Candida albicans, EMBL:Y18210	252426 at	0.9
putative protein kinase	267624 at	0.9
putative protein kinase protein kinase domain profile (PDOC00100)	267564 at	0.9
unknown protein	267523 at	0.9
E2, ubiquitin-conjugating enzyme 2 (UBC2) identical to gi:2689242, SP:P42745; supported by cDNA: gi_12083309 gb AF332451.1 AF332451	267484_at	0.9
putative related to microbial divalent cation tolerance proteins ; supported by cDNA: gi_12063360_gb_AF327524.1_AF327524	267405 at	0.9
putative related to microbial divalent cation tolerance proteins, supported by cDNA. gi_1290300_gb_Ar327324.1_Ar327324	267246 at	0.9
	267069 at	0.9
unknown protein	267009_at 267017_at	0.9
unknown protein		
unknown protein ; supported by full-length cDNA: Ceres: 41621.	266587_at	0.9
phosphoprotein phosphatase, type 1 catalytic subunit identical to GB:X64328; supported by cDNA: gi_166571_gb_M93408.1_ATH1PPHA	266238_at	0.9 0.9
unknown protein ;supported by cDNA: gi_15028290_gb_AY045948.1_ pEARLI 4 protein Same as GB: L43081; supported by cDNA: gi_871781_gb_L43081.1_ATHPEARA	265481_at 265440 at	0.9
unknown protein Contains similarity to hypothetical mitochondrial import receptor subunit gb Z98597 from S. pombe. ESTs gb[T45575 and gb]Z2643		0.9
	265041_at 265032_at	0.9
ribosomal protein identical to ribosomal protein GI:806279 from [Arabidopsis thaliana]	264665 at	0.9
unknown protein ESTs gb H37208,gb H36853 come from this gene		0.9
allyl alcohol dehydrogenase, putative similar to allyl alcohol dehydrogenase GI:9758497 from [Arabidopsis thaliana]; supported by cDNA: gi_143351		
unknown protein Similar to Glycine SRC2 (gb AB000130). ESTs gb H76869,gb T21700,gb ATTS5089 come from this gene; supported by cDNA: gi_		0.9
putative zinc transporter Similar to Arabidopsis Fe(II) transport protein (gb/U27590)	264574_at	0.9
putative calcium-binding protein, calreticulin similar to GB:AAA80652;supported by full-length cDNA: Ceres:27210.	264260_at	0.9
putative rubisco subunit binding-protein alpha subunit ;supported by full-length cDNA: Ceres:25773.	264069_at	0.9
hypothetical protein predicted by genefinder	263938_at	0.9
putative glycine-rich RNA-binding protein	263608_at	0.9
putative non-LTR retroelement reverse transcriptase	263559_at	0.9
putative protein kinase contains a protein kinase domain profile (PDOC00100)	263461_at	0.9
cyclophilin-like protein ;supported by full-length cDNA: Ceres:124189.	263288_at	0.9
Expressed protein ; supported by full-length cDNA: Ceres: 264189.	263209_at	0.9

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hypothetical protein predicted by genemark.hmm	262897_at	0.9
unknown protein ;supported by full-length cDNA: Ceres:17521.	262801_at	0.9 0.9
alpha-xylosidase precursor identical to alpha-xylosidase precursor GB:AAD05539 GI:4163997 from [Arabidopsis thaliana]; supported by cDNA: gi_1!		
AP2 domain containing protein, putative similar to AP2 domain containing protein GI:2281649 from [Arabidopsis thaliana]; supported by full-length cE		0.9
unknown protein; supported by full-length cDNA: Ceres: 39741.	262204_at	0.9
unknown protein ; supported by cDNA: gi_13937194_gb_AF372951.1_AF372951	262164_at	0.9
AP2 domain containing protein, putative similar to AP2 domain containing protein GI:2281633 from [Arabidopsis thaliana]; supported by cDNA: gi_1;	_	0.9
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:116121.	262111_at	0.9
hypothetical protein contains similarity to PP2 lectin polypeptide GI:410436 from [Cucurbita maxima]; supported by cDNA: gi_15292968_gb_AY0509		0.9
gibberellin 3 beta-hydroxylase, putative similar to gibberellin 3 beta-hydroxylase GI:3982753 from [Arabidopsis thaliana]; supported by cDNA: gi_194		0.9
unknown protein identical to unknown protein GB:AAC32929 GI:3395758 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:123625.	261745_at	0.9
protein kinase identical to protein kinase GI:2852447 from [Arabidopsis thaliana]; supported by cDNA: gi_2852446_dbj_D88206.1_D88206	261526_at	0.9
ornithine carbamoyltransferase precursor identical to SP:O50039 from [Arabidopsis thaliana]; supported by cDNA: gi_2764517_emb_AJ000476.1_A		0.9
transmembrane protein, putative similar to TRANSMEMBRANE PROTEIN TMP21 GB:Q63584 from [Rattus norvegicus]	260852_at	0.9
unknown protein ;supported by full-length cDNA: Ceres:123140.	260666_at	0.9
hypothetical protein contains Pfam profile: PF01965 ThiJ/PfpI family;supported by full-length cDNA: Ceres:101735.	260616_at	0.9
unknown protein similar to hypothetical protein GB:AAD12705 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:40506.	260179_at	0.9
unknown protein similar to Pi starvation-induced protein GB:BAA06151 from [Nicotiana tabacum]; supported by full-length cDNA: Ceres: 37751.	260176_at	0.9
Expressed protein ; supported by full-length cDNA: Ceres: 8189.	260100_at	0.9
nucellin-like protein similar to nucellin GB:AAB96882 [Hordeum vulgare] (nucellin: similar to aspartic protease and its specific expression in nucellar (	259733_at	0.9
unknown protein similar to hypothetical protein GB:P34661 [Caenorhabditis elegans]	259675_at	0.9
hypothetical protein	259551_at	0.9
putative small nuclear ribonucleoprotein (Sm-D1) similar to small nuclear ribonucleoprotein (Sm-D1) GB:AAD15345 [Arabidopsis thaliana]; supported		0.9
putative cytochrome P450 similar to cytochrome P450 89A2 GB:Q42602 [Arabidopsis thaliana]; supported by cDNA: gi_15983413_gb_AF424581.1_	259058_at	0.9
unknown protein similar to hypothetical protein GB:AAC17612 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:251012.	259015_at	0.9
unknown protein predicted by genefinder, multiple est matches;supported by full-length cDNA: Ceres:7073.	258939_at	0.9
unknown protein similar to a region of DNAJ domain-containing protein MCJ GB:AAD38506; supported by full-length cDNA: Ceres: 5219.	258716_at	0.9
putative protein kinase contains Pfam profile: PF00069 Eukaryotic protein kinase domain (2 copies); supported by cDNA: gi_14581444_gb_AY02675	258683_at	0.9
Expressed protein ; supported by full-length cDNA: Ceres: 1232.	258493_at	0.9
hypothetical protein predicted by genscan+	258391 at	0.9
Expressed protein ; supported by cDNA: gi 15810370 gb AY056224.1	258124 at	0.9
unknown protein ; supported by cDNA: gi_15010765_gb_AY045684.1_	257894 at	0.9
MutT-like protein contains Pfam profile: PF00293 Bacterial mutT protein	257830 at	0.9
unknown protein ; supported by cDNA: gi_15292984_gb_AY050926.1_	257705 at	0.9
unknown protein	257611_at	0.9
blue copper protein, putative similar to uclacyanin I GB:AAC32038 from [Arabidopsis thaliana] (Protein Sci (1996) 5(11):2175-83); supported by full-le		0.9
hypothetical protein	256583 at	0.9
hypothetical protein predicted by genefinder and genscan; supported by full-length cDNA: Ceres: 15024.	255824 at	0.9
hypothetical protein	255723 at	0.9
Expressed protein ; supported by full-length cDNA: Ceres: 29072.	255536 at	0.9
AtKAP alpha similar to AtKAP, GenBank accession number U69533; supported by cDNA: gi 14326480_gb AF385693.1_AF385693	255507 at	0.9
RMA1 RING zinc finger protein identical to RMA1 gi:3164222; supported by cDNA: gi 3164221 dbj AB008518.1 AB008518	255381 at	0.9
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score=526.5, E=1.9e-154, N=3 ;supported by full-length cDNA: Ceres:3001.	255257 at	0.9
hypothetical protein	255021 at	0.9
putative protein hypothetical protein F16G20.230 - Arabidopsis thaliana, PIR2:T05391; supported by full-length cDNA: Ceres: 17771.	254921_at	0.9
hypothetical protein	254727 at	0.9
putative protein inositol polyphosphate 5-phosphatase, Homo sapiens, PATCHX:G1019103; supported by cDNA: gi_10444262_gb_AF289634.1_		0.9
Expressed protein ; supported by full-length cDNA: Ceres: 42850.	254609 at	0.9
DAG-like protein DAG precursor, Antirrhinum majus, MNOS:S71747	254493 at	0.9
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fatty acid hydroxylase - like protein fatty acid hydroxylase Fah1p, Arabidopsis thaliana, PID:g2736147; supported by cDNA: gi_14994242_gb_AY		0.9
hypothetical protein ;supported by full-length cDNA: Ceres:29155.	254161_at	0.9
putative protein ;supported by full-length cDNA: Ceres:5367.	253981_at	0.9
putative protein hypothetical chloroplast protein RF19, Guillardia theta, PIR2:S73274;supported by full-length cDNA: Ceres:32397.	253857_at	0.9
putative protein	253802_at	0.9
ADP,ATP carrier-like protein ADP,ATP carrier protein-rice, PIR2:S33630;supported by full-length cDNA: Ceres:42036.	253776_at	0.9
putative protein predicted protein, Arabidopsis thaliana;supported by full-length cDNA: Ceres:154912.	253636_at	0.9
putative protein LipB gene, Prochlorothrix hollandica, PID:G1399931; supported by cDNA: gi_15887051_dbj_AB072390.1_AB072390	253553_at	0.9
synaptobrevin-like protein synaptobrevin-like protein, Mus musculus;supported by full-length cDNA: Ceres:41543.	253462_at	0.9
putative protein protein phosphatase Wip1, Homo sapiens, PID:g2218063;supported by full-length cDNA: Ceres:40123.	253323_at	0.9
bZIP transcription factor ATB2	253245_at	0.9
putative protein SPOP, Homo sapiens, AJ000644;supported by full-length cDNA: Ceres:122670.	253061_at	0.9
putative protein ;supported by cDNA: gi_13878068_gb_AF370297.1_AF370297	252974_at	0.9
glycine-rich protein (clone AtGRP8) ;supported by cDNA: gi_166838_gb_L00649.1_ATHRBPB	252885_at	0.9
hypothetical protein ; supported by full-length cDNA: Ceres: 281.	252723_at	0.9
RNA-binding protein-like protein various RNA-binding proteins; supported by full-length cDNA: Ceres: 9763.	252464_at	0.9
serine palmitoyltransferase-like protein	252331_s_at	0.9
putative protein	252155_at	0.9
thioredoxin -like protein cop c2, Coprinus comatus, EMBL:CCO24279;supported by full-length cDNA: Ceres:260075.	251985_at	0.9
putative protein amino acid selective channel protein - Hordeum vulgare, EMBL:AJ011921	251208_at	0.9
putative protein S1R protein - Homo sapiens, EMBL:AF113127	251163_at	0.9
putative protein various predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_13878024_gb_AF370275.1_AF370275	250937_at	0.9
AMP-binding protein	250114_s_at	0.9
translocon Tic40-like protein ; supported by cDNA: gi_16226312_gb_AF428299.1_AF428299	250080_at	0.9
Cu/Zn superoxide dismutase-like protein	250016_at	0.9
putative protein rsc43, Dictyostelium discoideum, EMBL:AF011338;supported by full-length cDNA: Ceres:6084.	249984_at	0.9
putative protein similar to unknown protein (pir  C72413)	249849_at	0.9
putative protein predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 11539.	249377_at	0.9
unknown protein ;supported by full-length cDNA: Ceres:23293.	249177 at	0.9
ATP synthase delta chain, mitochondrial precursor (splQ96252); supported by cDNA: gi_1655483_dbj_D88376.1_D88376	248825 at	0.9
putative protein similar to unknown protein (gb AAF16660.1);supported by full-length cDNA: Ceres:15457.	248759 at	0.9
putative protein similar to unknown protein (pir  H71431);supported by full-length cDNA: Ceres:31680.	248763 at	0.9
unknown protein	248771 at	0.9
unknown protein ;supported by full-length cDNA: Ceres:27885.	248491_at	0.9
putative protein similar to unknown protein (emb CAB62440.1)	248016 at	0.9

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putative protein non-consensus CG donor splice site at exon 1, GA donor splice site at exon 3, similar to unknown protein (pir  T04268);supported by		0.9
putative protein similar to unknown protein (gb AAF04433.1);supported by full-length cDNA: Ceres:156439.	247944_at	0.9
putative protein contains similarity to unknown protein (pir  T08554); supported by full-length cDNA: Ceres: 266884.	247945_at	0.9
nonspecific lipid-transfer protein precursor - like nonspecific lipid-transfer protein precursor, Brassica napus, EMBL:AF101038;supported by full-leng		0.9
putative protein COP1-interacting protein CIP8, Arabidopsis thaliana, EMBL:AF162150; supported by cDNA: gi_15450686_gb_AY052711.1_	247708_at	0.9
mipC protein - like (aquaporin) mipC protein, common ice plant, PIR:T12440;supported by full-length cDNA: Ceres:33231.	247586_at	0.9
putative protein strong similarity to unknown protein (emb CAB89350.1)	247240_at	0.9
protein phosphatase 2C-like protein	247126_at	0.9
putative protein various predicted bacterial rRNA methylases	246852_at	0.9
	246153_s_at	0.9
putative protein BEM46 bem1/bud5 suppressor, Schizosaccharomyces pombe, bem1/bud5 suppressor, EMBL:SP29892;supported by full-length cD		0.9
Expressed protein ;supported by cDNA: Ceres:30129; supported by cDNA: gi:15028002	245602_at	0.9
putative protein	245418_at	0.9
Expressed protein ; supported by full-length cDNA: Ceres: 42223.	245333_at	0.9
scarecrow-like 13 (SCL13) ; supported by cDNA: gi_16930432_gb_AF419570.1_AF419570	245247_at	0.9
putative protein similarity to cDNA clones from human and mouse	245178_at	0.9
putative dimethyladenosine transferase ; supported by cDNA: gi_14532649_gb_AY039949.1_	245122_at	0.9
unknown protein	245106_at	0.9
putative AP2 domain transcription factor	245078_at	0.9
hypothetical protein	245000_at	0.9
hypothetical protein	257322_at	0.9
protein phosphatase 2C, putative similar to GB:CAB90633 from [Fagus sylvatica]; supported by full-length cDNA: Ceres:118185.	261077_at	0.8
hypothetical protein predicted by genscan	259917_at	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 22461.	256743_at	0.8
unknown protein ; supported by cDNA: gi 14532715 gb AY039982.1	256074 at	0.8
putative protein endothelin converting enzyme, Bos primigenius taurus, PIR2:146078	253256 at	0.8
putative protein disulfide isomerase; supported by cDNA: gi 15810003 gb AY054270.1	267605 at	0.8
putative WRKY-type DNA binding protein	267028 at	0.8
hypothetical protein predicted by genefinder; supported by full-length cDNA: Ceres: 29146.	267003 at	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 9670.	266641 at	0.8
	266533 s at	0.8
unknown protein ;supported by full-length cDNA: Ceres:33700.	266259 at	0.8
protease inhibitor II identical to GB:X69139, contains a gamma-thionin family signature (PDOC00725); supported by cDNA: gi_13878184 gb_AF37(		0.8
unknown protein	265987 at	0.8
hypothetical protein predicted by genscan	265898 at	0.8
RING-H2 finger protein RHA2b identical to GP/AF078823; supported by cDNA: gi_3790570_gb_AF078823.1_AF078823	265740 at	0.8
unknown protein	265637 at	0.8
hypothetical protein predicted by genscan; supported by cDNA: gi 15292678 gb AY050773.1	265512 at	0.8
unknown protein ;supported by full-length cDNA: Ceres:250015.	265458 at	0.8
	265444 s at	0.8
hypothetical protein predicted by genefinder; supported by full-length cDNA: Ceres: 15103.	265442 at	0.8
lipoic acid synthase (LIP1) ; supported by cDNA: gi_14334939_gb_AY035143.1_	265392_at	0.8
ipole delle stitules (Lin 1), supported by eDita. gi_1+00+505_gb_A10001+0.1_	200002_01	0.0

hypothetical protein265195_atputative presenilin similar to presenilin GB:AAD23630;supported by full-length cDNA: Ceres:43026.264807_atExpressed protein ; supported by full-length cDNA: Ceres: 22723.264441_atExpressed protein ; supported by full-length cDNA: Ceres: 39286.264443 at	0.8 0.8 0.8 0.8 0.8
Expressed protein ; supported by full-length cDNA: Ceres: 22723. 264441_at	0.8 0.8 0.8
	0.8 0.8
	0.8
postsynaptic protein CRIPT, putative similar to postsynaptic protein CRIPT GI:3098551 from [Rattus norvegicus]; supported by full-length cDNA: Ce 264399_at	
HSP100/ClpB, putative similar to HSP100/ClpB GI:9651530 [Phaseolus lunatus] 264402_at	0.8
hypothetical protein Similar to hypothetical protein SPAC2F7.14c gi 1052797 from Schizosaccharomyces pombe cosmid gb Z50142 264357_at	0.8
unknown protein Strong similarity to gb/D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb/H37281, gb/T441 264365 s	
hypothetical protein similar to hypothetical protein GI:2894569 from [Arabidopsis thaliana]; supported by cDNA: gi 15028186 gb AY045916.1 264289 at	0.8
gamma glutamyl hydrolase, putative similar to gamma glutamyl hydrolase GI:1680711 from [Glycine max]; supported by cDNA: gi_3169655 gb AF( 264250 at	0.8
beta-glucosidase, putative similar to beta-glucosidase GI:5030906 from [Polygonum tinctorium] 264270 at	0.8
receptor-like protein glossy1 (gl1), putative similar to receptor-like protein glossy1 (gl1) GI:1209703 from (Arabidopsis thaliana) 264147 at	0.8
Mago Nashi-like protein similar to Mago Nashi, Genbank Accession Number U03559;supported by full-length cDNA: Ceres:35733. 264152 at	0.8
Expressed protein ; supported by cDNA: gi_15450487_gb_AY052345.1_ 263923_at	0.8
putative farnesylated protein ;supported by full-length cDNA: Ceres:19570. 263866_at	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 29157. 263840_at	0.8
unknown protein; supported by cDNA: gi_14423471_gb_AF386973.1_AF386973 263785_at	0.8
hypothetical protein identical to hypothetical protein GB:AAD21690 GI:4512621 from (Arabidopsis thaliana) 263702_at	0.8
unknown protein 263613_at	0.8
hypothetical protein predicted by genefinder; supported by full-length cDNA: Ceres: 32729. 263567_at	0.8
hypothetical protein predicted by genscan 263471_at	0.8
unknown protein ;supported by full-length cDNA: Ceres:39169. 263371_at	0.8
hypothetical protein predicted by genscan and genefinder; supported by cDNA: gi_16649128_gb_AY059934.1_ 263265_at	0.8
beta-Amyrin Synthase, putative similar to beta-Amyrin Synthase GI:3688600 from [Panax ginseng] 263124_at	0.8
polyamine oxidase, putative similar to polyamine oxidase SP:O64411 [Zea mays (Maize)]; supported by cDNA: gi_13877614_gb_AF370508.1_AF3; 262933_at	0.8
hypothetical protein predicted by genemark.hmm 262918_at	0.8
unknown protein ; supported by cDNA: gi_14596044_gb_AY042810.1_ 262845_at	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 18244. 262746_at	0.8
unknown protein ; supported by cDNA: gi_15724323_gb_AF412102.1_AF412102 262685_at	0.8
heat shock protein, putative contains Pfam profile: PF00011 Hsp20/alpha crystallin family;supported by full-length cDNA: Ceres:21735. 262629_at	0.8
hypothetical protein Strong similarity to gi 4734005 F3L12.7 hypothetical protein from Arabidopsis thaliana BAC gb AC007178; supported by cDNA: (262569_at	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 109156. 262558_at	0.8
hypothetical protein predicted by genscan; supported by cDNA: gi_14334811_gb_AY035079.1_ 262503_at	0.8
unknown protein Similar to gb AF151884 CGI-126 protein from Homo sapiens. EST gb Z18048 comes from this gene; supported by full-length cDNA 262298_at	0.8
scarecrow-like 3 identical to GB:AAD24404 GI:4580515 from [Arabidopsis thaliana] (Plant J. 18 (1), 111-119 (1999)); supported by cDNA: gi_15810 261866_at	0.8
transcription factor, putative similar to transcription factor GB:CAA74050 GI:2398525 from [Arabidopsis thaliana] 261803_at	0.8
unknown protein 261295_at	0.8
calreticulin, putative similar to GB:AAF06346 from [Vitis vinifera] 261248_at	0.8
hypothetical protein predicted by genemark.hmm 261086_at	0.8
unknown protein ;supported by full-length cDNA: Ceres:37370. 261033_at	0.8
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_13430817_gb_AF360321.1_AF360321 260927_at	0.8
scarecrow-like 1 identical to scarecrow-like 1 GB:AAF21043 GI:6644390 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:109490. 260878_at	0.8

coded for by A. thaliana cDNA R64991 ;supported by full-length cDNA: Ceres:19543.	255477_at	0.8
auxin-binding protein 1 precursor ;supported by full-length cDNA: Ceres:34126.	255412_at	0.8
putative M-type thioredoxin similar to A. thaliana protein F21B7.7, GenBank accession number AC002560;supported by full-length cDNA: Ceres:10		0.8
putative protein Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence, gene T30B22.22, PID:g2529679	255028_at	0.8
putative protein 24 kDa seed maturation protein - Glycine max, PID:g4102690; supported by full-length cDNA: Ceres:23536.	254920_at	0.8
putative protein	254794_at	0.8
putative protein hypothetical protein sll1769 - Synechocystis sp,PID:d1018406;supported by full-length cDNA: Ceres:18082.	254760_at	0.8
potassium transporter-like protein putative potassium transporter AtKT2p & AtKT1p, Arabidopsis thaliana, Patchx:G2384669 & Patchx:G2384671	254520_at	0.8
hypothetical protein ;supported by cDNA: gi_15028392_gb_AY045999.1_	254481_at	0.8
ethylene-regulated transcript 2 (ERT2)	254434_at	0.8
hypothetical protein ;supported by full-length cDNA: Ceres:36892.	254424_at	0.8
hsp 70-like protein heat shock 70 protein - Spinacia oleracea,PID:g2654208	254148_at	0.8
putative mitochondrial uncoupling protein mitochondrial uncoupling protein, Arabidopsis thaliana (thale cress), PATX:E1316826; supported by full-le	254120_at	0.8
superoxide dismutase (EC 1.15.1.1) (Fe)(fragment) ;supported by full-length cDNA: Ceres:32935.	254098_at	0.8
nucleosome assembly protein I-like protein ; supported by cDNA: gi_15450807_gb_AY054484.1_	253996_at	0.8
translation initiation factor ; supported by full-length cDNA: Ceres: 5206.	253900_at	0.8
hypothetical protein	253888 at	0.8
glycine-rich protein glycine-rich cell wall structural protein - Petunia x hybrida, Pir2: A26099; supported by full-length cDNA: Ceres: 115209.	253629 at	0.8
hypothetical protein; supported by cDNA: gi 14335143 gb AY037251.1	253596 s at	0.8
predicted protein ; supported by cDNA: gi 15292824 gb AY050846.1	253524 at	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 40692.	253485 at	0.8
Expressed protein ; supported by cDNA: gi 16648998 gb AY059869.1	253342 at	0.8
hypothetical protein ;supported by full-length cDNA: Ceres:115167.	253232 at	0.8
putative protein predicted protein, Arabidopsis thaliana;supported by full-length cDNA: Ceres:1368.	253183_at	0.8
putative protein	253004 at	0.8
putative thaumatin-like protein thaumatin-like protein(TL1) - Arabidopsis thaliana, PID:g4105697	252949 at	0.8
disease resistance response like protein disease resistance response protein 206-d - Pisum sativum, PID:g508844	252951 at	0.8
putative protein AP2 domain containing protein RAP2.4, Arabidopsis thaliana	252859 at	0.8
		0.8
putative protein ; supported by cDNA: gi_14517539_gb_AY039605.1_	252134 at	0.8
mucin-like protein hemomucin, Drosophila melanogaster, EMBL:DM42014;supported by full-length cDNA: Ceres:38547.	252092_at	0.8
putative protein several hypothetical proteins - Arabidopsis thaliana; supported by full-length cDNA: Ceres:112338.	251530 at	0.8
DNA-binding WRKY - like protein AR411 protein, Arabidopsis thaliana, EMBL:ATD748; supported by full-length cDNA: Ceres: 100465.	251553 at	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 17055.	251446 at	0.8
		0.8
hypothetical protein	251414 at	0.8
putative protein weak homology with predicted proteins, Arabidopsis thaliana	251391_at	0.8
putative protein transcription factor Pti6 - Lycopersicon esculentum, PIR:T07728;supported by full-length cDNA: Ceres:100688.	251282 at	0.8
putative protein PrMC3, Pinus radiata, EMBL:AF110333	251200 at	0.8
putative protein predicted protein, Caenorhabditis elegans;supported by full-length cDNA: Ceres:20404.	251117_at	0.8
light-inducible protein ATLS1	251098_at	0.8
ferritin 1 precursor ;supported by full-length cDNA: Ceres:1100.	251109 at	0.8
	201100_at	0.0

putative protein hypothetical protein T18N14.110 - Arabidopsis thaliana, PIR:T46069; supported by cDNA: gi_15912284_gb_AY056420.1_	251074_at	0.8
hypothetical protein	251026_at	0.8
histone deacetylase -like protein histone deacetylase, HD2-p39, nucleolar, Zea mays, PIR:T04141	250912_at	0.8
AtPH1-like protein ;supported by full-length cDNA: Ceres:109246.	250748_at	0.8
thioredoxin-like ; supported by cDNA: gi_4973263_gb_AF144391.1_AF144391	250649_at	0.8
putative amidase	250627_at	0.8
diacylglycerol kinase (ATDGK1) ; supported by cDNA: gi_1374771_dbj_D63787.1_ATHATDGK1	250556_at	0.8
putative protein	250562 at	0.8
ribsomal protein - like chloroplast ribosomal protein L17, Nicotiana tabacum, PIR:T01744; supported by full-length cDNA: Ceres:22697.	250495 at	0.8
heat shock protein 70 (Hsc70-5); supported by cDNA: gi_6746589 gb_AF217458.1_AF217458	250502 at	0.8
lysophospholipase - like protein lysophospholipase homolog LPL1, Oryza sativa, EMBL:AF039531;supported by full-length cDNA: Ceres:15284.	250335 at	0.8
putative protein similar to unknown protein (emb CAB69839.1)	250257_at	0.8
squalene monooxygenase 1,2 (squalene epoxidase 1,2) (se 1,2) (sp O65402)	249775 at	0.8
putative protein contains similarity to 40S ribosomal protein S10; supported by cDNA: gi 14335121 gb AY037240.1	249310 at	0.8
putative protein contains similarity to unknown protein (dbj/BAA76827.1); supported by cDNA: gi_14532601_gb_AY039925.1_	249181_at	0.8
unknown protein ; supported by cDNA: gi_13926304_gb_AF372903.1_AF372903	248975 at	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 28462.	248762 at	0.8
gibberellin 20-oxidase-like protein	248443 at	0.8
ubiquitin-like protein SMT3-like ; supported by full-length cDNA: Ceres: 13697.	248103 at	0.8
unknown protein	248050 at	0.8
putative protein similar to unknown protein (pir  C71422);supported by full-length cDNA: Ceres:819.	247988 at	0.8
putative protein (supported by full-length cDNA: Ceres:3086.	247748_at	0.8
nonspecific lipid-transfer protein precursor - like nonspecific lipid-transfer protein precursor, Brassica napus, EMBL:AF101038;supported by full-leng		0.8
Expressed protein ; supported by full-length cDNA: Ceres: 30313.	247716_at 247434_at	0.8
	_	
putative protein predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 38273.	247443_at	0.8
putative protein predicted proteins, Oryza sativa, Arabidopsis thaliana and yeast	247396_at	0.8
protein kinase ; supported by cDNA: gi_16974578_gb_AY060555.1_	247384_at	0.8
putative protein similar to unknown protein (pir  T01257)	247386_at	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 35683.	247305_at	0.8
putative protein similar to unknown protein (emb CAB89373.1); supported by cDNA: gi_14334413_gb_AY034898.1_	247285_at	0.8
putative protein contains similarity to ribonucleoprotein F	247121_at	0.8
putative protein predicted proteins, Arabidopsis thaliana and Drosophila melanogaster	246897_at	0.8
nucleic acid binding protein - like nucleic acid binding protein, Oryza sativa, PIR:T02745;supported by full-length cDNA: Ceres:32443.	246856_at	0.8
hexose transporter - like protein hexose transporter HT2, Lycopersicon esculentum, EMBL:LES132224; supported by cDNA: gi_15010579_gb_AY04		0.8
mevalonate kinase supported by full-length cDNA: Ceres:1045.	246778_at	0.8
putative protein	246644_at	0.8
hypothetical protein	246479_at	0.8
cytochrome P450 like protein ; supported by cDNA: gi_4176419_dbj_AB008097.1_AB008097	246216_at	0.8
putative protein centrosomal Nek2-associated protein 1, Homo sapiens, EMBL:AF049105; supported by cDNA: gi_13877754_gb_AF370140.1_AF3		0.8
AKIN beta1 ; supported by full-length cDNA: Ceres: 41668.	246028_at	0.8
chloroplast Cpn21 protein ; supported by cDNA: gi_14334611_gb_AY034979.1_	246003_at	0.8
water stress-induced protein, putative similar to water stress-induced protein GI:454879 from [Oryza sativa]; supported by cDNA: gi_15215761_gb_/	245627_at	0.8

hypothetical protein ;supported by full-length cDNA: Ceres:2505.	245388_at	0.8
putative protein ; supported by cDNA: gi_13926241_gb_AF372879.1_AF372879	245309_at	0.8
hypothetical protein ; supported by cDNA: gi_15451033_gb_AY054597.1_	245297_at	0.8
putative protein similarity to proteins of unknown function from human and mouse	245180_at	0.8
putative flavonol reductase	245141_at	0.8
hypothetical protein	244922_s_at	0.8
putative protein various predicted proteins, Arabidopsis thaliana	254179_at	0.8
putative protein	250481 at	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 124835.	245369 at	0.8
similar to axi 1 protein from Nicotiana tabacum	267393 at	0.7
unknown protein	258687 at	0.7
putative protein nucleoid DNA-binding protein cnd41, chloroplast, common tobacco, PIR:T01996; supported by cDNA: gi_15809849_gb_AY054192.	249626 at	0.7
putative protein strong similarity to unknown protein (pir  T04808)	248091 at	0.7
Expressed protein ; supported by full-length cDNA: Ceres: 30472.	267555 at	0.7
putative auxin-regulated protein ;supported by full-length cDNA: Ceres:1711.	267461 at	0.7
unknown protein ; supported by full-length cDNA: Ceres: 37787.	267278 at	0.7
putative spliceosome associated protein ; supported by cDNA: gi_15450714_gb_AY052725.1_	267062 at	0.7
	266834_s_at	0.7
Expressed protein ; supported by full-length cDNA: Ceres: 124634.	266808_at	0.7
unknown protein	266620_at	0.7
Expressed protein ; supported by cDNA: gi_15215834_gb_AY050447.1_	266583 at	0.7
putative small nuclear ribonucleoprotein E ; supported by full-length cDNA: Ceres: 4850.	266579 at	0.7
putative auxin-regulated protein	266322 at	0.7
hypothetical protein predicted by genscan and genefinder; supported by cDNA: gi_13605570_gb_AF361611.1_AF361611	266182 at	0.7
unknown protein	265900 at	0.7
unknown protein ;supported by full-length cDNA: Ceres:19157.	265866 at	0.7
predicted protein	265802 at	0.7
putative elongation factor beta-1 ;supported by full-length cDNA: Ceres:35337.	265816 s at	0.7
putative ferredoxin ; supported by full-length cDNA: Ceres: 26333.	265649 at	0.7
unknown protein	265620 at	0.7
unknown protein	265417 at	0.7
putative sugar transporter	265424 at	0.7
putative ADP-ribosylation factor ;supported by full-length cDNA: Ceres:5695.	265337_at	0.7
putative D-amino acid dehydrogenase	265318 at	0.7
unknown protein ;supported by full-length cDNA: Ceres:6967.	265284 at	0.7
unknown protein ; supported by cDNA: gi_15912334_gb_AY056445.1_	265150 at	0.7
hypothetical protein predicted by genemark.hmm	264693 at	0.7
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:2118.	264636 at	0.7
unknown protein Location of EST gb/Z34586 and gb/Z34166; supported by cDNA: gi 15529271 gb AY052260.1	264509 at	0.7
hypothetical protein predicted by grail	264379_at	0.7
potassium transporter, putative similar to potassium transporter GI:2654088 from [Arabidopsis thaliana]	264338_at	0.7
Expressed protein ; supported by full-length cDNA: Ceres: 13607.	264304_at	0.7

unknown protein	264254 at	0.7
actin depolymerizing factor 6 ;supported by full-length cDNA: Ceres:255294.	264089 at	0.7
putative fructose bisphosphate aldolase ;supported by full-length cDNA: Ceres:13024.	263921 at	0.7
SKP1 interacting partner 6 (SKIP6), putative similar to SKP1 interacting partner 6 GI:10716957 from [Arabidopsis thaliana]	263898 at	0.7
Expressed protein ; supported by full-length cDNA: Ceres: 15689.	263712 at	0.7
putative steroid binding protein ;supported by full-length cDNA: Ceres:10261.	263534 at	0.7
hypothetical protein predicted by genscan	263465 at	0.7
unknown protein	263023 at	0.7
RNA polymerase II subunit, putative similar to RNA polymerase II subunit hRPB17 GI:854177 from [Homo sapiens]; supported by full-length cDNA: (		0.7
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi 15146253 gb AY049268.1	262957_s_at	0.7
linker histone protein, putative contains Pfam profile:PF00538 linker histone H1 and H5 family;supported by full-length cDNA: Ceres:10525.	262840 at	0.7
putative contains r and prome. I roosso inker historie rr and ris family, supported by full-length cDrA. Ceres. 1925.		0.7
	262714 s at	0.7
unknown protein Similar to gb/3224339 suffer focus protein 5 (suffsb) norm form sapiens, supported by full-length cDNA: Ceres: 13543.	262592 at	0.7
hypothetical protein similar to GB:P49967 signal recognition particle 54 kDa subunit (Srp54-1) from [Arabidopsis thaliana].;supported by full-length c[		0.7
hypothetical protein predicted by genscan+; supported by cDNA: gi_15293248_gb_AY051058.1_	262571 at	0.7
unknown protein ESTs gb R30529, gb Z48463, gb Z48467, gb AA597369 and gb AA394772 come from this gene; supported by cDNA: gi 1620967		0.7
unknown protein ESTs gb/rs0029, gb/240403, gb/240407, gb/AA597309 and gb/AA594772 come from this gene, supported by cDNA. gi_1020907; unknown protein EST gb/r21171 comes from this gene	262489 at	0.7
unknown protein Contains similarity to gb/AJ000644 SPOP (speckle-type POZ protein) from Homo sapiens and contains a PF/00651 BTB/POZ dom		0.7
ribosomal protein S9, putative similar to ribosomal protein S9 GI:5456946 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 25038;		0.7
unknown protein ; supported by cDNA: gi_15294195_gb_AF410289.1_AF410289	262175_at	0.7 0.7
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_13605648_gb_AF361805.1_AF361805	262065_at	0.7
unknown protein ;supported by full-length cDNA: Ceres:35811.	262049_at	
unknown protein ;supported by full-length cDNA: Ceres:101924.	261948_at	0.7
adenine nucleotide translocase, putative similar to adenine nucleotide translocase GI:6469340 from [Arabidopsis thaliana]; supported by full-length c		0.7
small nuclear ribonucleoprotein, putative similar to small nuclear ribonucleoprotein GI:600749 from [Homo sapiens]; supported by full-length cDNA: (		0.7
protein kinase, putative identical to bHLH protein GB:CAA67885 GI:1465368 from [Arabidopsis thaliana]; supported by cDNA: gi_14335047_gb_AY(		0.7
unknown protein similar to putative esterase GB:AAD17422 GI:4335745 from [Arabidopsis thaliana]	261607_at	0.7
serine/threonine kinase, putative similar to serine/threonine kinase GB:CAA73067.1 GI:2632252 from [Sorghum bicolor]; supported by cDNA: gi_14-		0.7
endoplasmic reticulum-type calcium-transporting ATPase 4 identical to GB:AAD29957 from [Arabidopsis thaliana] (Plant Physiol. 120 (1999) In press		0.7
unknown protein ;supported by full-length cDNA: Ceres:727.	261336_at	0.7
		0.7
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_14334897_gb_AY035122.1_	260968_at	0.7
hypothetical protein predicted by genemark.hmm	260946_at	0.7
hypothetical protein predicted by genemark.hmm	260760_at	0.7
hypothetical protein predicted by genefinder	260605_at	0.7
putative chloroplast protein CP12; supported by full-length cDNA: Ceres: 95662.	260529_at	0.7
unknown protein ;supported by full-length cDNA: Ceres:27109.	260444_at	0.7
putative glucosyltransferase similar to glucosyltransferase GB:AAB36653 from [Nicotiana tabacum]	260379_at	0.7
Eukaryotic initiation factor 5A, putative similar to eukaryotic initiation factor 5A (2) (Nicotiana plumbaginifolia) GI:19702; supported by full-length cD		0.7
E2, ubiquitin-conjugating enzyme, putative similar to putative protein GB:CAB43411 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:582		0.7
hypothetical protein similar to vanilloid receptor-like protein GB:AAD26363 from [Homo sapiens]supported by full-length cDNA: Ceres:21959.	260129_at	0.7

putative trypsin inhibitor similar to trypsin inhibitor propeptide GB:AAB68964 [Brassica oleracea]; contains Pfam profile: PF00197 Trypsin and proteation	260101 at	0.7
putative DNA-binding protein contains Pfam profile: PF01388 ARID DNA binding domain	259967 at	0.7
putative RING zinc finger protein contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger); supported by full-length cDNA: Ceres: 274		0.7
3-hydroxy-3-methylglutaryl CoA reductase (AA 1-592) identical to hydroxy methylglutaryl CoA reductase (AA 1-592) GB:X15032 (Plant Mol. Biol. 13		0.7
zinc finger protein, putative similar to GI:3170601 from [Zea mays] (Cell 93 (4), 593-603 (1998));supported by full-length cDNA: Ceres:40167.	259932 at	0.7
unknown protein	259943 at	0.7
predicted protein ; supported by cDNA: gi_13358245_gb_AF325060.2_AF325060	259889 at	0.7
beta-1,3-glucanase precursor, putative similar to GI:4097948 from [Oryza sativa] (Gene 223 (1-2), 311-320 (1998))	259823 at	0.7
unknown protein ;supported by full-length cDNA: Ceres:141685.	259591 at	0.7
hypothetical protein ; supported by cDNA: gi 1518449 gb U43340.1 ATU43340	259517 at	0.7
hypothetical protein preedicted by genemark.hmm	259490 at	0.7
dioxygenase, putative similar to dioxygenase GI:1666096 from [Marah macrocarpus]	259445 at	0.7
methionine aminopeptidase I (MAP1), putative similar to methionine aminopeptidase I (MAP1) GI:975722 from [Saccharomyces cerevisiae]; support		0.7
putative nodulin similar to nodulin GB:AAA91034 from [Medicago sativa]; supported by full-length cDNA: Ceres:16718.	259308 at	0.7
putative RING-H2 zinc finger protein ATL6 similar to GB:AAD33584 from [Arabidopsis thaliana]; supported by cDNA: gi 4928402 gb AF132016.1 /		0.7
O-acetylserine (thiol) lyase identical to O-acetylserine (thiol) lyase GB:BAA21628 [Arabidopsis thaliana]; supported by cDNA: gi_4926402_gb_Ai 162010.1_F		0.7
unknown protein similar to hin1 GB:CAA68848 [Nicotiana tabacum]; supported by cDNA: gi 9502173 gb AF264698.1 AF264698		0.7
putative ubiquinol-cytochrome C reductase complex ubiquinone-binding protein (QP-C) similar to ubiquinol-cytochrome C reductase complex ubiquinol-	259071_at	0.7
		0.7
low temperature and salt responsive protein LTI6A identical to low temperature and salt responsive protein LTI6A GB:AAC97512 from [Arabidopsis t		
putative histone H2B similar to histone H2B-3 GB:CAA12231 from [Lycopersicon esculentum]	258707_at	0.7
unknown protein ; supported by cDNA: gi_15983478_gb_AF424614.1_AF424614	258647_at	0.7
unknown protein	258654_at	0.7
disease resistance gene (RPM1) identical to disease resistance gene (RPM1) GB:X87851 [Arabidopsis thaliana]	258544_at	0.7
unknown protein ;supported by full-length cDNA: Ceres:8978.	258562_at	0.7
putative RAD23 similar to RAD23 protein GB:CAB51544 from [Lycopersicon esculentum]; supported by cDNA: gi_14517453_gb_AY039562.1_	258499_at	0.7
alternative oxidase 1a precursor identical to GB:Q39219 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:116257.	258452_at	0.7
unknown protein similar to pop3 peptide GB:AAC26526 from [Populus balsamifera subsp. trichocarpa X Populus deltoides]; supported by full-length c		0.7
unknown protein ;supported by full-length cDNA: Ceres:112601.	258432_at	0.7
hypothetical protein	258262_at	0.7
	258246_s_at	0.7
putative GTP pyrophosphokinase similar to GTP PYROPHOSPHOKINASE GB:087331 from [Corynebacterium glutamicum]; supported by cDNA: gi		0.7
unknown protein ;supported by full-length cDNA: Ceres:15577.	258188_at	0.7
Expressed protein ; supported by full-length cDNA: Ceres: 26411.	258092_at	0.7
putative peroxiredoxin similar to peroxiredoxin Q GB:BAA90524 from [Sedum lineare]; supported by cDNA: gi_15081742_gb_AY048264.1_	258087_at	0.7
putative myc-like DNA-binding protein similar to GB:AAB72192 from [Arabidopsis thaliana]	257990_at	0.7
cell elongation protein, Dwarf1 identical to GB:S71189 from [Arabidopsis thaliana]; supported by cDNA: gi_516042_gb_U12400.1_ATU12400	257938_at	0.7
hypothetical protein predicted by genemark	257948_at	0.7
Expressed protein ; supported by cDNA: gi_16604419_gb_AY058108.1_	257914_at	0.7
1,4-alpha-glucan branching enzyme, putative similar to GB:NP_000149 from [Homo sapiens], contains Pfam profile: PF00128 Alpha amylase	257667_at	0.7
	257634_s_at	0.7
unknown protein	257596_at	0.7
RING zinc finger protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)	257081_at	0.7

purple acid phosphatase, putative similar to purple acid phosphatase GB:CAA06921 [Ipomoea batatas]	257087 at	0.7
putative 3-hydroxybutyryl-CoA dehydrogenase similar to 3-HYDROXYBUTYRYL-COA DEHYDROGENASE GB:Q45223 from [Bradyrhizobium japon]		0.7
dem-like protein similar to dem GB:CAA73973 from [Lycopersicon esculentum] (Plant Cell (1998) 10, 1-12)	257029 at	0.7
	256375 at	0.7
unknown protein	_	0.7
GTPase, putative contains Pfam profile: PF01926 GTPase of unknown function	256274_at	
unknown protein ; supported by full-length cDNA: Ceres: 38389.	256238_at	0.7
unknown protein similar to hypothetical protein GI:1469227 from [Brassica oleracea];supported by full-length cDNA: Ceres:94809.	256191_at	0.7
unknown protein	256046_at	0.7
plastid protein identical to GB:Z86094; supported by full-length cDNA: Ceres: 8717.	255791_at	0.7
Expressed protein ; supported by full-length cDNA: Ceres: 36326.	255670_at	0.7
predicted protein of unknown function similar to P. falciparum O1 protein, GenBank accession number AF030694	255495_at	0.7
putative pre-mRNA splicing factor similar to yeast pre-mRNA splicing factors; supported by cDNA: gi_16604550_gb_AY059720.1_	255382_at	0.7
putative DNA-directed RNA polymerase subunit similar to A. fulgidus DNA-directed RNA polymerase subunit M, GenBank accession number AE001		0.7
hypothetical protein	255155_at	0.7
AX110P -like protein AX110P -Daucus carota, PID:g285739; supported by full-length cDNA: Ceres: 19582.	255047_at	0.7
putative protein ; supported by full-length cDNA: Ceres: 142381.	254999_at	0.7
Ribosomal protein L7Ae -like various L7Ae ribosomal proteins; supported by full-length cDNA: Ceres: 33381.	254831_at	0.7
putative protein	254778_at	0.7
DnaJ-like protein DnaJ-like protein, Phaseolus vulgaris, U77935; supported by cDNA: gi_6691126_gb_AF214107.1_AF214107	254688_at	0.7
putative protein predicted protein, Arabidopsis thaliana	254402 at	0.7
putative protein SF16 protein, Helianthus annuus, PID:g560150	254293 at	0.7
putative protein hypothetical protein T8K22.16, Arabidopsis thalianachromosome II BAC T8K22, PATX:G3184285; supported by cDNA: gi_1661229	254132 at	0.7
putative protein	253959 at	0.7
mRNA cleavage factor subunit - like protein mRNA cleavage factor I 25 kDa subunit, Homo sapiens, AJ001810; supported by full-length cDNA: Cere		0.7
hypothetical protein ;supported by full-length cDNA: Ceres:249769.	253643 at	0.7
snRNP Sm protein F - like Sm protein F, Homo sapiens, PIR:S55053; supported by full-length cDNA: Ceres: 37087.	253668 at	0.7
putative protein ;supported by full-length cDNA: Ceres:32848.	253640 at	0.7
predicted protein cation transport protein ChaC, Escherichia coli, PIR2:G64868;supported by full-length cDNA: Ceres:39740.	253522 at	0.7
putative protein predicted protein, Arabidopsis thaliana, PATCHX:G2252634	253475 at	0.7
2-dehydro-3-deoxyphosphoheptonate aldolase ;supported by full-length cDNA: Ceres:37432.	253333 at	0.7
DNA-directed RNA polymerase (EC 2.7.6) Il largest chain	253133 at	0.7
	253099 s at	0.7
putative protein predicted protein, Arabidopsis thaliana; supported by full-length cDNA: Ceres:33704.	253043 at	0.7
cytochrome P450 - like protein cytochrome P450, Glycyrrhiza echinata, AB001379;supported by full-length cDNA: Ceres:253698.	253046 at	0.7
hypothetical protein	253020 at	0.7
cysteine proteinase RD19A identical to thiol protease SP:P43296, GI:435618 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:3713		0.7
protein kinase-like protein protein kinase - Solanum berthaultii, EMBL:X97980	252646 at	0.7
nuclear receptor binding factor-like protein nuclear receptor binding factor-1 NRBF-1 - Rattus norvegicus, EMBL:AB015724; supported by full-length	252540_at 252542 at	0.7
	_	
scarecrow-like protein scarecrow-like 11 - Arabidopsis thaliana, EMBL:AF036307;supported by full-length cDNA: Ceres:35201.	252483_at	0.7
putative protein several hypothetical proteins	252496_at	0.7
putative protein PIT1 - Arabidopsis thaliana, GB: AF130849	252422_at	0.7
putative protein hypothetical protein - Arabidopsis thaliana, EMBL:CAB38293;supported by full-length cDNA: Ceres:17840.	252220_at	0.7

putative protein	252186 at	0.7
putative protein predicted protein, Oryza sativa, EMBL:AP000367;supported by full-length cDNA: Ceres:1514.	252093 at	0.7
expressed protein supported by cDNA: gi:15450891	252048 at	0.7
ribosomal protein L17 -like protein ribosomal protein L17, chloroplast, Nicotiana tabacum, PIR:T01744;supported by full-length cDNA: Ceres:25166.		0.7
putative protein lateral root primordia (LRP1) - Arabidopsis thaliana, EMBL:AT24702; supported by cDNA: gi_15450614_gb_AY052675.1_	251900 at	0.7
putative protein hypothetical protein SPBC19C2.12 - Schizosaccharomyces pombe, PIR:T39803;supported by full-length cDNA: Ceres:92264.	251483 at	0.7
putative protein hypothetical protein At2g45900 - Arabidopsis thaliana, EMBL:AC004665	251368_at	0.7
putative protein hypothetical protein At2g46330 - Arabidopsis thaliana, EMBL:AC006526;supported by full-length cDNA: Ceres:11394.	251281_at	0.7
putative protein nypothetical protein Azg40000 - Alabidopsis inaliana, EMBE. Acouse20, supported by fail-length cDNA. Ceres. (1994).	251201_at	0.7
putative protein putative proteins - uncrent species, supported by eDNA. gr_1+517+15_gb_A10550+0.1_	251194 at	0.7
putative protein hypothetical proteins - Arabidopsis thaliana	251078_at	0.7
ribonuclease II-like protein ribonuclease II family protein, Deinococcus radiodurans, PIR:C75571	251040 at	0.7
putative protein ; supported by cDNA: gi_14190430_gb_AF378893.1_AF378893	250970 at	0.7
polyubiquitin (UBQ3) identical to GI:928809; supported by full-length cDNA: Ceres: 20908.	250970_at 250935_at	0.7
putative protein ; supported by full-length cDNA: Ceres: 270908.	250955_at	0.7
putative protein ; supported by cDNA: gi_2160689_gb_U73526.1_ATU73526	250925_at	0.7
helicase-like transcription factor-like protein	250900_at 250807 at	0.7
putative protein similar to unknown protein (pir  T02514);supported by full-length cDNA: Ceres:117347.	250807_at 250777 at	0.7
	_	0.7
putative protein contains similarity to RNA-binding protein;supported by full-length cDNA: Ceres:36764. diadenosine 5,5-P1,P4-tetraphosphate hydrolase-like protein; supported by cDNA: gi 13937174 gb AF372941.1 AF372941	250721_at 250705_at	0.7
calnexin homolog	250705_at 250625_at	0.7
putative protein 110K5.11, unknown protein, Sorghum bicolor, EMBL:AF124045; supported by cDNA: gi_13605727_gb_AF361845.1_AF361845	250625_at 250409 at	0.7
putative protein predicted protein, Arabidopsis thaliana	250145_at 250155_at	0.7 0.7
putative protein predicted proteins, Arabidopsis thaliana		
APG5 (autophagy 5)-like protein	250088_at	0.7
auxin-induced protein-like	250012_x_at	0.7
putative protein ;supported by full-length cDNA: Ceres:154134.	249954_at	0.7
kinase associated protein phosphatase ; supported by cDNA: gi_15027992_gb_AY045853.1_	249924_at	0.7
unknown protein	249872_at	0.7
MtN3-like protein ; supported by cDNA: gi_3747110_gb_AF095641.1_AF095641	249800_at	0.7
prohibitin (gb AAC49691.1) ;supported by full-length cDNA: Ceres:37298.	249344_at	0.7
urophorphyrin III methylase (gb AAB92676.1); supported by cDNA: gi_1146164_gb_L47479.1_ATHUPM1R	249325_at	0.7
putative protein similar to unknown protein (gb AAF24581.1)	249258_at	0.7
GAMM1 protein-like ; supported by cDNA: gi_15146291_gb_AY049287.1_	249238_at	0.7
putative protein strong similarity to unknown protein (gb AAF24960.1)	249133_at	0.7
unknown protein ;supported by full-length cDNA: Ceres:36901.	248966_at	0.7
putative protein similar to unknown protein (pir  T05524);supported by full-length cDNA: Ceres:767.	248952_at	0.7
putative protein similar to unknown protein (sp P74035); supported by cDNA: gi_15292692_gb_AY050780.1_	248906_at	0.7
putative protein contains similarity to unknown protein (pir  T39016);supported by full-length cDNA: Ceres:15623.	248757_at	0.7
unknown protein ;supported by full-length cDNA: Ceres:116332.	248646_at	0.7
putative protein contains similarity to pyridoxamine 5-phosphate oxidase; supported by full-length cDNA: Ceres:6244.	248560_at	0.7
putative protein contains similarity to L-isoaspartyl protein carboxyl methyltransferase	248544_at	0.7

putative protein contains similarity to squamosa promoter binding protein; supported by full-length cDNA: Ceres: 113229.	248524_s_at	0.7
putative protein similar to unknown protein (pir  S77462); supported by cDNA: gi_15081647_gb_AY048216.1_	248287_at	0.7
GTPase activator protein of Rab-like small GTPases-like protein ; supported by cDNA: gi_14517421_gb_AY039546.1_	248222_at	0.7
putative protein contains similarity to phytocyanin/early nodulin-like protein	248236_at	0.7
putative protein various predicted proteins from different species; supported by full-length cDNA: Ceres: 36809.	247787_at	0.7
cyclophilin ROC7 ;supported by full-length cDNA: Ceres:25325.	247791_at	0.7
putative protein predicted protein, Arabidopsis thaliana; supported by cDNA: gi_14517559_gb_AY039615.1_	247574_at	0.7
putative protein	247547_at	0.7
putative protein contains similarity to kinase	247368_at	0.7
nucleotide diphosphate kinase Ia (emb CAB58230.1); supported by cDNA: gi_3063660_gb_AF058391.1_AF058391	247376_at	0.7
DNA topoisomerase III	247301_at	0.7
immunophilin (gb AAB57847.1) ;supported by full-length cDNA: Ceres:10243.	247281_at	0.7
putative protein similar to unknown protein (dbj BAA75199.1)	247187_at	0.7
lysosomal Pro-X carboxypeptidase	247156_at	0.7
putative protein similar to unknown protein (pir  T05276); supported by cDNA: gi_15292834_gb_AY050851.1_	247049_at	0.7
putative protein hypothetical protein - Ricinus communis, EMBL:Z81012;supported by full-length cDNA: Ceres:1351.	246919 at	0.7
Expressed protein ; supported by full-length cDNA: Ceres: 30174.	246842 at	0.7
putative protein ;supported by full-length cDNA: Ceres:232091.	246645_at	0.7
14-3-3 protein GF14upsilon (grf5) identical to 14-3-3 protein GF14 upsilon GI:2232148 from [Arabidopsis thaliana]; supported by cDNA: gi_1433453		0.7
aminopeptidase-like protein ; supported by cDNA: gi 13430673 gb AF360249.1 AF360249	246219 at	0.7
putative protein hypothetical protein F2A19.120 - Arabidopsis thaliana, PIR:T47944	246173 s at	0.7
putative protein ;supported by full-length cDNA: Ceres:39563.	245981 at	0.7
putative protein predicted proteins - Arabidopsis thaliana; supported by full-length cDNA: Ceres:2537.	245984 at	0.7
putative protein protein phosphatase-1 regulatory subunit 7 alpha2 - Homo sapiens, EMBL:AF067136; supported by full-length cDNA: Ceres:110392		0.7
GTL1 - like protein GTL1, Arabidopsis thaliana, EMBL:ATAJ3215; supported by cDNA: gi_14423451 gb_AF386963.1 AF386963		0.7
hypothetical protein	245868 at	0.7
S-ribonuclease binding protein SBP1, putative similar to S-ribonuclease binding protein SBP1 GI:6760451 from [Petunia hybrida]; supported by cDN		0.7
hypothetical protein predicted by genscan+; supported by cDNA: gi_16323183_gb_AY057696.1_	245776 at	0.7
Expressed protein ; supported by cDNA: gi 11762135 gb AF324994.1 AF324994	245684 at	0.7
carnitine racemase like protein ;supported by full-length cDNA: Ceres:28978.	245359 at	0.7
hypothetical protein ;supported by full-length cDNA: Ceres:42815.	245361 at	0.7
ethylene responsive element binding factor-like protein (AtERF6); supported by cDNA: gi_3298497_dbj_AB013301.1_AB013301	245250 at	0.7
unknown protein ;supported by full-length cDNA: Ceres:23203.	245143 at	0.7
PSII L protein	245022 at	0.7
hypothetical protein	244958 at	0.7
unknown protein	257477 at	0.7
unknown protein	257519 at	0.7
Yippee-like protein similar to Yippee putative zinc binding protein GB:AAD47882 [Homo sapiens]	257522 at	0.7
putative microfibril-associated protein	255093 s at	0.7
unknown protein similar to unknown protein GB:AAD24850;supported by full-length cDNA: Ceres:3900.	263179 at	0.6
hypothetical protein similar to putative beta-1,3-glucanase GB:AAD26909 GI:4662638 from [Arabidopsis thaliana]	261004 at	0.6
putative cell division control protein cdc2 similar to protein kinase (EC 2.7.1.37) cdc2 GB:A36074 [Mus musculus] (protein kinase cdc2);supported by		0.6

	257969_at	0.6
	254502_at	0.6
	249535_at	0.6
	247675_at	0.6
Escherichia coli /REF=J04423 /DEF=E coli bioC protein corresponding to nucleotides 4257-4573 of J04423 /LEN=777 (-5 and -3 represent transcriptX		0.6
Arabidopsis thaliana /REF=U84969 /DEF=ubiquitin (UBQ11) gene, complete cds /LEN=1140 (_5, _M, _3 represent transcript regions 5 prime, MiddK-	-Athal-Ubq_5	0.6
	267596_s_at	0.6
	267553_s_at	0.6
	267504_at	0.6
	267510_at	0.6
	267524_at	0.6
	267435_at	0.6
	267379_at	0.6
	267364_at	0.6
	267323_at	0.6
	267309_at	0.6
	267280_at	0.6
	267199_at	0.6
	267104_at	0.6
	267116_at	0.6
	267072_at	0.6
	267018_at	0.6
	266904_at	0.6
	266916_at	0.6
		0.6
	266684_at	0.6
	266695_at	0.6
	266657_at	0.6
	266673_at	0.6
	266514_at	0.6
	266428_at	0.6
	266285_at	0.6
	266172_at	0.6
	266072_at	0.6
	266001_at	0.6
	265739_at	0.6
	265668_at	0.6
	265517_at	0.6
	265035_at	0.6
	264894_at	0.6
	264854_at	0.6
unknown protein location of EST gb T45083 and gb R65542; supported by cDNA: gi_15215601_gb_AY050329.1_	264728_at	0.6

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	264561_at	0.6
CTP synthase-like protein similar to ctp synthase (sp P17812 PYRG_HUMAN); similar to ESTs gb AA660762, gb AA220982, dbj AU008137, gb AI0		0.6
	264445_at	0.6
putative nuclear transport factor similar to nuclear transport factor 2 (NTF2) from [Oryza sativa], GB:BAA81910; similar to ESTs gb T21347, gb N96;		0.6
	264452_at	0.6
putative mitogen-activated protein kinase, MAP Kinase 1 similar to ESTs gb T41567 and gb R30629; supported by cDNA: gi_464136_dbj_D14713.1		0.6
	264171_at	0.6
	264146_at	0.6
	264045_at	0.6
	263862_at	0.6
	263829_at	0.6
	263831_at	0.6
cysteine proteinase similar to cysteine proteinase RD19A (thiol protease) GI:435618, SP:P43296 from [Arabidopsis thaliana]; supported by full-length	263757_at	0.6
hypothetical protein predicted by genefinder; supported by cDNA: gi_13265516_gb_AF324697.2_AF324697	263759_at	0.6
unknown protein ; supported by full-length cDNA: Ceres: 34035.	263631_at	0.6
hypothetical protein predicted by genscan and genefinder;supported by full-length cDNA: Ceres:7520.	263637_at	0.6
CONSTANS-like B-box zinc finger protein ;supported by full-length cDNA: Ceres:17434.	263537_at	0.6
unknown protein	263438 at	0.6
hypothetical protein	263442 at	0.6
unknown protein ; supported by full-length cDNA: Ceres: 552.	263420 at	0.6
unknown protein Similar to gb/U51990 pre-mRNA-splicing factor hPrp18 from Homo sapiens. ESTs gb/T46391 and gb/AA721815 come from this gei 2	263116 s at	0.6
	263064 at	0.6
trehalose 6-phosphate synthase, putative similar to trehalose 6-phosphate synthase GB:CAA09463 GI:3647365 from [Yarrowia lipolytica]	263019 at	0.6
hypothetical protein predicted by genemark.hmm	262992 at	0.6
	262965 at	0.6
	262600 at	0.6
	262505 at	0.6
	262399 at	0.6
	262338 at	0.6
E2, ubiquitin-conjugating enzyme, putative similar to ubiquitin-conjugating enzyme GB:P35135 from [Lycopersicon esculentum]; supported by cDNA		0.6
	262296 at	0.6
	262171_at	0.6
	262182 at	0.6
	262160 at	0.6
	262114 at	0.6
	262068 at	0.6
	262014 at	0.6
	261911_at	0.6
ethylene responsive element binding factor 3 (AtERF3) identical to GB:080339 GI:7531109 from [Arabidopsis thaliana]; supported by cDNA: gi 343		0.6
	261793 at	0.6
	261723 at	0.6
	261597 at	0.6
	201007_at	0.0

<ul> <li>unknown protein contains similarity to SNA dependent reverse transcriptase GI:292063 from [Spraguae Jophi]</li> <li>26:1426_21</li> <li>unknown protein contains similarity to SS ribosomal protein L32; supported by full-length cDNA: Ceres:27467.</li> <li>26:1406_21</li> <li>Control SNA Ceres 3200</li> <li>VSNARE protein AVT1b, putative similar to GB:AF24062 from [Arabidopsis thaliana]; supported by GNA: Ceres:3767.</li> <li>26:1406_21</li> <li>Control SNARE protein AVT1b, putative similar to GB:AF24062 from [Cartina coll; supported by GNA: Ceres:3760.</li> <li>26:193_1</li> <li>Control T1: Spraguae JOP (Cartina Control SNAR) (Cartina Cartina Coll) Supported by GNA: Ceres:3760.</li> <li>26:0967_21</li> <li>Control SNARE protein AVT1b, putative similar to GB:L20473 from [Datura stramonium] (Proc. Natl. Acad. Sci. U.S.A. 90, 9591-9595 (1993)); supported by GNA: Ceres:32648.</li> <li>26:0967_21</li> <li>Control SNARE protein simplard to Yull-ength CDNA: Ceres:114920.</li> <li>26:0763_21</li> <li>Control SNARE protein simplard to Yull-ength CDNA: Ceres:14920.</li> <li>26:0763_21</li> <li>Control SNARE protein simplard to Yull-ength CDNA: Ceres:4084.</li> <li>26:0661_21</li> <li>Control SNARE protein SNARE Protein Prodicted by Guenark hmm</li> <li>26:0671_21</li> <li>26:0671_21</li></ul>	hypothetical protein predicted by genemark.hmm	261500 at	0.6
unknown protein contains similarity to set protein Gl:338038 from [Horno sapiens]:supported by full-length cDNA: Ceres: 27467.261406_at0.6v=SNARE protein AVIT1b, putative similar to GB:AAF24082 from [Arabidopsis thaliana]: supported by cDNA: gi_6690275_gb_AF114751.1_AF114261276_at0.6v=SNARE protein AVIT1b, putative similar to GB:AAF24082 from [Arabidopsis thaliana]: supported by cDNA: gi_6690275_gb_AF114751.1_AF114261276_at0.6v=SNARE protein AVIT1b, putative similar to GB:AAF24082 from [Calitra stramonium] (Proc. Natl. Acad. Sci. U.S.A. 90, 9591-9695 (1993)); supported by cDNA: Ceres:7490.260690_at0.6unknown protein contains similarity to transaldolase GB:P30144 from [Escherichia coli]; supported by full-ength cDNA: Ceres:7404.2606773_at0.6unknown protein similar to hypothetical protein G1:770340 from (Arabidopsis thaliana]; supported by full-ength cDNA: Ceres:7404.260775_at0.6hypothetical protein predicted by genemark.hmm260775_at0.60.6hypothetical protein predicted by genemark.hmm260775_at0.6hypothetical protein predicted by genemark.hmm260775_at0.6hypothetical protein predicted by genemark.hmm260775_at0.6hypothetical protein protein polypeptide F260684_at0.6unknown protein similar to bardite protein fieldscheal protein fieldscheal protein fieldscheal protein fieldscheal protein fieldscheal protein fieldscheal protein polypeptide F2606418_atunknown proteinfieldschall protein fieldscheal protein fieldsche			
unknown protein similar to 50S ribosomal protein 123; supported by full-length cDNA: Ceres: 10780			
<ul> <li>v-SNARE protein AVT11b, putative similar to GB:AAF24062 from [Arabidopsis thaliana]; supported by cDNA: gi_6690275_gb_AF114751.1_AF1147 261276_at</li> <li>0.6</li> <li>tropinnoe reductase1, putative similar to GB:L20473 from [Datura stramonium] (Proc. Natl. Acad. Sci. U. S.A. 90, 9591-9586 (1993); supported by c. 261084_at</li> <li>0.6</li> <li>histone H1, putative similar to histone H1-1 GB:CAA44312 G1:16314 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 7590.</li> <li>260780_at</li> <li>0.6</li> <li>unknown protein similar to protein GE:770304 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 24648.</li> <li>260780_at</li> <li>0.6</li> <li>unknown protein similar to protein GE:770304 from (Arabidopsis thaliana); supported by full-length cDNA: Ceres: 24648.</li> <li>260766_at</li> <li>0.6</li> <li>hypothetical protein predicted by genemark.hmm</li> <li>hypothetical protein predicted by genemark.hmm</li> <li>putative simal rubutive cytoskeletal protein G1:7722517 from [Arabidopsis thaliana]; supported by cDNA: gi_1732516_gb_U62745.1_AT1</li> <li>260674_at</li> <li>0.6</li> <li>unknown protein ismilar to unavoid 4 sulfotransferase GB:P52837 from [Flaveria chloraefolia]; supported by full-length cDNA: Ceres: 24084.</li> <li>260418_ast</li> <li>0.6</li> <li>unknown protein outative cytoskeletal protein G1:74291 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 24084.</li> <li>260475_at</li> <li>0.6</li> <li>putative favorol sulfotransferase similar to flavonol 4 -sulfotransferase GB:P52837 from [Flaveria chloraefolia]; supported by full-length cDNA: Ceres: 2485.</li> <li>260474_ast</li> <li>260474_ast</li></ul>			
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	sterol-C5-desaturase identical to GB:AAD12944 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:7564.	258484_at	0.6

expressed protein supported by cDNA: gi:14194102	258444 at	0.6
hypothetical protein similar to hypothetical protein GB:CAB57979 from [Lycopersicon esculentum]	258406 at	0.6
Expressed protein ; supported by full-length cDNA: Ceres: 29124.	258297 at	0.6
protein kinase, putative similar to GB:BAA24694 from [Arabidopsis thaliana] (Plant Cell Physiol. 38 (3), 248-258 (1997)); supported by full-length cDN	258132 at	0.6
Expressed protein ; supported by full-length cDNA: Ceres: 7103.	258105 at	0.6
hypothetical protein predicted by genmark;supported by full-length cDNA: Ceres:19279.	258091 at	0.6
light regulated protein, putative similar to light regulated protein precursor GB:Q03200 [Oryza sativa] (Plant Mol. Biol. 22 (1), 165-170 (1993)), ccr pr		0.6
hypothetical protein predicted by genemark.hmm	257780 at	0.6
hypothetical protein predicted by genemark.hmm	257728 at	0.6
unknown protein contains Pfam profiles: PF01388 ARID DNA binding domain, PF00505 HMG (high mobility group) box;supported by full-length cDN		0.6
Expressed protein ; supported by full-length cDNA: Ceres: 642.	257609 at	0.6
unknown protein similar to symbiosis-related proteins; supported by full-length cDNA: Ceres:2186.	257293 at	0.6
unknown protein similar to DAG protein (required for chloroplast differentiation and palisade development) GB:Q38732 [Antirrhinum majus]; supporte		0.6
unknown protein ; supported by cDNA: gi_14190488_gb_AF380644.1_AF380644	256799 at	0.6
unknown protein contains Pfam profile: PF01165 ribosomal protein S21; supported by cDNA: gi_14532553_gb_AY039901.1_	256753 at	0.6
DREB2B transcription factor identical to dehydration response element binding transcription factor DREB2B GB:BAA33795 [Arabidopsis thaliana]; su		0.6
hypothetical protein	256387 at	0.6
unknown protein similar to N-term half of NAC domain protein NAM [Arabidopsis thaliana] GI:4325282;supported by full-length cDNA: Ceres:21634.	256300 at	0.6
unknown protein ; supported by cDNA: gi_14334837_gb_AY035092.1_	256310 at	0.6
unknown protein ; supported by cDNA: gi_15982827_gb_AY057521.1_	256270 at	0.6
unknown protein ; supported by full-length cDNA: Ceres: 11684.	256231 at	0.6
Expressed protein ; supported by full-length cDNA: Ceres: 25069.	256063 at	0.6
unknown protein similar to putative prolyl 4-hydroxylase, alpha subunit GI:6598804 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres		0.6
putative protein kinase contains a protein kinase domain profile (PDOC00100); supported by cDNA: gi_13448034_gb_AF339146.1_AF339146	255872 at	0.6
putative protein kinase contains a protein kinase domain profile (PDOC00100)	255844 at	0.6
putative protein vesicle-associated membrane protein 7B, Arabidopsisthaliana, AF025333	255803 at	0.6
hypothetical protein predicted by genemark.hmm	255759 at	0.6
putative protein predicted protein, Arabidopsis thaliana and various predicted ATP dependent RNA helicases	255600 s at	0.6
putative protein various predicted proteins; supported by cDNA: gi 15809939 gb AY054238.1	255221 at	0.6
putative protein hypothetical protein ssr1391 - Synechocystis sp. (strain PCC 6803), PIR2:S75571; supported by cDNA: gi 14190426 gb AF378891	255131 at	0.6
MEKK1/MAP kinase kinase kinase ; supported by cDNA: gi_1255447_dbj_D50468.1_ATHATMEKK1	255095_at	0.6
Expressed protein ; supported by full-length cDNA: Ceres: 11425.	254953_at	0.6
RING-H2 finger protein RHA1b ;supported by full-length cDNA: Ceres:37097.	254919 at	0.6
putative protein zinc finger protein ZNF216 - Mus musculus, PID:g3643807;supported by full-length cDNA: Ceres:45.	254861 at	0.6
ribosomal protein L13a like protein ribosomal protein L13a -Lupinus luteus, PID:e1237871; supported by cDNA: gi_15529277_gb_AY052263.1_	254763 at	0.6
putative protein ; supported by cDNA: gi_16323185_gb_AY057697.1_	254764 at	0.6
putative protein phospho-N-acetylmuramoyl-pentapeptide-transferase, Haemophilus influenzae, Pir2:A64185	254662 at	0.6
putative NADPH quinone oxidoreductase Pig3 Homo sapiens, PID:G2754812;supported by full-length cDNA: Ceres:4621.	254393 at	0.6
heat shock protein - like heat shock protein 17, Triticum aestivum, PIR1:HHWT17;supported by full-length cDNA: Ceres:23223.	254384_at	0.6
Ribosomal protein L7Ae - like NHP2/RS6 FAMILY PROTEIN, Homo sapiens, PID:g4826860	254355_at	0.6
nifU-like protein nifU protein homolog YPL135w, Saccharomyces cerevisiae, PIR2:S69049;supported by full-length cDNA: Ceres:8156.	254357_at	0.6
Expressed protein ; supported by full-length cDNA: Ceres: 38360.	254279_at	0.6

	hypothetical protein	254258 at	0.6
	putative protein hypothetical protein, Synechocystis sp., PIR:S76577;supported by full-length cDNA: Ceres:30708.	254187 at	0.6
	Expressed protein ; supported by full-length cDNA: Ceres: 37704.	254208 at	0.6
	butative protein other Arabidopsis putative proteins	254051 at	0.6
	grpE like protein ;supported by full-length cDNA: Ceres:35284.	253949 at	0.6
	GH3 like protein GH3 protein, Glycine max., PIR2:S17433	253908 at	0.6
	putative protein stem-specific protein - Nicotiana tabacum,PID:g20037;supported by full-length cDNA: Ceres:35207.	253874 at	0.6
	putative protein stemspecific protein - Micoliana tabacum, 10.920037, supported by full-length CDNA. Ceres. 33207.		0.6
	Expressed protein ; supported by full-length cDNA: Ceres: 31814.	253823_at 253825_at	0.6
	butative protein ;supported by full-length cDNA: Ceres: 10077.	253814 at	0.6
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	putative protein putative NADH oxidoreductase complex I subunit - Caenorhabditis elegans,PID:g5019819	253712_at	0.6
	ribosomal protein S15a homolog ribosomal protein S15a - Brassica napus,PIR2:S20945; supported by full-length cDNA: Ceres: 18105.	253726_at	0.6
	hypothetical protein ;supported by full-length cDNA: Ceres:117732.	253642_at	0.6
	nypothetical protein ;supported by full-length cDNA: Ceres:31287.	253546_at	0.6
	Expressed protein ; supported by cDNA: gi_13926316_gb_AF372908.1_AF372908	253482_at	0.6
	putative protein	253455_at	0.6
	nucellin -like protein nucellin - Hordeum vulgare, PIR:G2290202; supported by full-length cDNA: Ceres:24738.	253331_at	0.6
	putative protein auxin-induced protein, Helianthus annuus, gb:AF030301; supported by cDNA: gi_15215697_gb_AY050377.1_	253307_at	0.6
	predicted protein	253281_at	0.6
	putative protein hydroxyproline-rich glycoprotein precursor, Nicotiana tabacum, PIR2:S06733; supported by cDNA: gi_15724315_gb_AF412098.1_A		0.6
	amine oxidase -like protein amine oxidase, Canavalia lineata, EMBL:AF172681	252698_at	0.6
	dnaJ protein homolog atj3 ;supported by full-length cDNA: Ceres:40976.	252670_at	0.6
	putative protein tRNA intron endonuclease - Arabidopsis thaliana, EMBL:AB036339; supported by cDNA: gi_6635255_dbj_AB036339.1_AB036339	252593_at	0.6
	putative protein CDP-alcohol phosphatidyltransferase - Schizosaccharomyces pombe, EMBL:CAB16578	252540_at	0.6
	ABC-type transport protein-like protein AbcA, Dictyostelium discoideum, DDU66526	252379_at	0.6
	Expressed protein ; supported by cDNA: gi_14326548_gb_AF385728.1_AF385728	252390_at	0.6
	Expressed protein ; supported by full-length cDNA: Ceres: 26537.	252366_at	0.6
	RNA-directed RNA polymerase RNA-directed RNA polymerase	252261_at	0.6
	mucin -like protein hemomucin, Drosophila melanogaster, EMBL:DM42014;supported by full-length cDNA: Ceres:34197.	252117_at	0.6
	putative protein hypothetical protein F10M6.70 - Arabidopsis thaliana, PIR3: T05399; supported by cDNA: gi_15293266_gb_AY051067.1_	252040_at	0.6
	putative protein predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 108517.	251957_at	0.6
	putative protein patatin, Solanum tuberosum, PIR2:A29810	251839_at	0.6
	E2, ubiquitin-conjugating enzyme 14 (UBC14) UbcAT3; identical to gi:2129757, S46656; supported by full-length cDNA: Ceres:25382.	251802_at	0.6
t	ranscription factor L2 ;supported by full-length cDNA: Ceres:105441.	251758_at	0.6
	putative protein several hypothetical proteins - Arabidopsis thaliana	251525_at	0.6
	putative protein hypothetical proteins - Arabidopsis thaliana; supported by cDNA: gi_14334587_gb_AY034967.1_	251356_at	0.6
	Sar1-like GTP binding protein small GTP-binding protein Bsar1a - Brassica campestris, EMBL:U55035	251217_at	0.6
	alpha galactosyltransferase-like protein alpha galactosyltransferase - Trigonella foenum-graecum, EMBL:TFO245478; supported by cDNA: gi_1598;	251192_at	0.6
	putative protein salt-inducible protein, membrane-associated, common tobacco, PIR:T02047; supported by cDNA: gi_15810430_gb_AY056254.1_	250856_at	0.6
	putative protein strong similarity to unknown protein (gb AAF19572.1); supported by cDNA: gi_16649096_gb_AY059918.1_	250819_at	0.6
	putative protein strong similarity to unknown protein (pir  T12704)	250745_at	0.6
	cytochrome P450 90A1 (sp Q42569) ; supported by full-length cDNA: Ceres: 36334.	250752_at	0.6
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putative protein similar to unknown protein (pir  T00468)	250713_at	0.6
harpin-induced protein-like ; supported by cDNA: gi 9502175 gb AF264699.1 AF264699	250676 at	0.6
RNA binding protein - like rna binding protein, Schizosaccharomyces pombe, PIR:T39586	250436 at	0.6
putative protein various predicted proteins, Drosophila melanogaster, Caenhorhabditis elegans, Homo sapiens; supported by full-length cDNA: Cere	250384 at	0.6
Expressed protein ; supported by full-length cDNA: Ceres: 13951.	250225 at	0.6
putative protein similar to unknown protein (gb AAF02163.1);supported by full-length cDNA: Ceres:115644.	250127 at	0.6
unknown protein	250017 at	0.6
eukaryotic cap-binding protein (gb AAC17220.1); supported by cDNA: gi_3108208_gb_AF028809.1_AF028809	250033 at	0.6
6-phosphogluconolactonase-like protein ;supported by full-length cDNA: Ceres:21890.	249733 at	0.6
thaumatin-like protein	249748 at	0.6
unknown protein	249726 at	0.6
Expressed protein ; supported by cDNA: gi_14190358_gb_AF378857.1_AF378857	249650 at	0.6
40S ribosomal protein S9-like 40S ribosomal protein S9 - Chlamydomonas sp., EMBL: AU066528; supported by full-length cDNA: Ceres: 41408.	249427_at	0.6
putative protein predicted protein, Arabidopsis thaliana; supported by full-length cDNA: Ceres:26524.	249379 at	0.6
putative protein contains similarity to metallothionein-I gene transcription activator	249335 at	0.6
putative protein similar to unknown protein (gb AAF16660.1);supported by full-length cDNA: Ceres:4267.	249234 at	0.6
ubiquitin-like protein ; supported by cDNA: gi 13899064 gb AF370527.1 AF370527	249217 at	0.6
Rab-type small GTP-binding protein-like ; supported by full-length cDNA: Ceres: 102017.	248914 at	0.6
putative protein similar to unknown protein (gb/AAC61815.1);supported by full-length cDNA: Ceres:254442.	248868 at	0.6
putative protein contains similarity to maturase-related protein	248815 at	0.6
Bax inhibitor-1 like ;supported by full-length cDNA: Ceres:36400.	248833 at	0.6
putative protein similar to unknown protein (gb AAF30317.1);supported by full-length cDNA: Ceres:101665.	248586 at	0.6
ATP-dependent Clp protease ATP-binding subunit (ClpC1) almost identical to ClpC GI:2921158 from [Arabidopsis thaliana]	248480 at	0.6
putative protein contains similarity to iron-containing superoxide dismutase; supported by full-length cDNA: Ceres: 126592.	248493_at	0.6
putative protein similar to unknown protein (gb AAD29711.1)	248437 at	0.6
putative protein contains similarity to transcription or splicing factor; supported by cDNA: gi_13877738_gb_AF370132.1_AF370132	248452_at	0.6
unknown protein	248415_at	0.6
putative protein similar to unknown protein (pir  T34137)	248266_at	0.6
cytochrome b5 (dbj/BAA74839.1) ;supported by full-length cDNA: Ceres:31303.	248217_at	0.6
putative protein contains similarity to RNA-binding protein; supported by full-length cDNA: Ceres: 14044.	248173_at	0.6
50S ribosomal protein L24, chloroplast precursor ;supported by full-length cDNA: Ceres:27973.	248174_at	0.6
30S ribosomal protein S16 ; supported by full-length cDNA: Ceres: 20539.	247935_at	0.6
unknown protein	247950_at	0.6
putative protein ; supported by full-length cDNA: Ceres: 36602.	247801_at	0.6
elongin - like protein elongin C, Drosophila melanogaster, PIR: JC5794; supported by cDNA: gi_15028384_gb_AY045995.1_	247721_at	0.6
thymidylate kinase - like protein thymidylate kinase, Arabidopsis thaliana, EMBL:AF081570;supported by full-length cDNA: Ceres:155539.	247735_at	0.6
putative protein supported by cDNA: Ceres: 146274.	247491_at	0.6
putative protein predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_13877822_gb_AF370174.1_AF370174	247407_at	0.6
expressed protein similar to unknown protein (gb AAF03448.1); supported by full-length cDNA: Ceres: 97900.	247258_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:25419.	247149_at	0.6
putative protein strong similarity to unknown protein (pir  T04718); supported by cDNA: gi_15529177_gb_AY052213.1_	247013_at	0.6
transcription factor-like protein light-induced protein CPRF-2 - Petroselinum crispum, PIR:S16321	246962_s_at	0.6

nutetive protein source transmombrane demain emban resenter. Mus museulus, EMPLAE051008/sourceted by full length sDNA: Coros/06808	246702 of	0.6
putative protein seven transmembrane domain orphan receptor, Mus musculus, EMBL:AF051098;supported by full-length cDNA: Ceres:96808.	246793_at 246737_at	0.6 0.6
putative protein		0.6
CRS2-like protein CRS2 - Zea mays, EMBL:AF225708	246492_at	
arginine/serine-rich protein, putative similar to arginine/serine-rich protein GI:6601502 from [Arabidopsis thaliana]; supported by cDNA: gi_15027956		0.6
SOH1 - like protein SOH1, Saccharomyces cerevisiae, PIR:S47895	246140_at	0.6
putative protein predicted protein, Arabidopsis thaliana;supported by full-length cDNA: Ceres:32193.	246154_at	0.6
putative protein DIM1 protein, Homo sapiens, EMBL:AF023611; supported by full-length cDNA: Ceres: 12591.	246006_at	0.6
Expressed protein ; supported by full-length cDNA: Ceres: 31366.	246007_at	0.6
elongation factor 1B alpha-subunit ;supported by full-length cDNA: Ceres:26936.	245949_at	0.6
hypothetical protein	245501_at	0.6
dynein light chain like protein	245525_at	0.6
allergen like protein	245463_at	0.6
Expressed protein ; supported by full-length cDNA: Ceres: 5455.	245334_at	0.6
DEF (CLA1) protein ; supported by cDNA: gi_14334451_gb_AY034917.1_	245281_at	0.6
	245227_s_at	0.6
	245134_s_at	0.6
PSII component	245021_at	0.6
PSII cytochrome b559	244964_at	0.6
cytochrome c biogenesis orf382 Protein sequence is in conflict with the conceptual translation	244912_at	0.6
hypothetical protein	257334_at	0.6
unknown protein	257495_at	0.6
putative protein hypothetical protein, Synechocystis sp., PIR2:S76637	254715_at	0.6
putative protein predicted protein, Arabidopsis thaliana	246586_at	0.6
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:4845.	265333_at	0.5
HD-Zip protein identical to HD-Zip protein GB:CAA71854 GI:2145358 from [Arabidopsis thaliana]	261800_at	0.5
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi 15451209 gb AY054685.1	260987 at	0.5
unknown protein similar to brahma associated protein GB:AAC28455 (Drosophila melanogaster), SWI SNF-related matrix-associated actin-depende	258974 at	0.5
hypothetical protein predicted by genscan+	257073_at	0.5
putative protein hypothetical protein F9F8.14 - Arabidopsis thaliana, EMBL:AC009991	251348 at	0.5
	FFX-BioDn-5	0.5
Escherichia coli /REF=J04423 /DEF=E coli bioD gene dethiobiotin synthetase corresponding to nucleotides 5024-5244 of J04423 /LEN=676 (-5 and		0.5
Arabidopsis thaliana /REF=U84969 /DEF=ubiquitin (UBQ11) gene, complete cds /LEN=1140 ( 5, M, 3 represent transcript regions 5 prime, Middl		0.5
putative phosphoribosyl pyrophosphate synthetase	267365 at	0.5
putative isoamylase	267356 at	0.5
putative RING zinc finger protein ;supported by full-length cDNA: Ceres:17402.	267297 at	0.5
Expressed protein ; supported by full-length cDNA: Ceres: 14468.	267259 at	0.5
unknown protein ; supported by cDNA: gi 14335015 gb AY037187.1	266982 at	0.5
hypothetical protein predicted by genscan	266901 at	0.5
F-box protein family, AtFBX5 contains similarity to F-box protein FBL2 GI:6010699 from [Rattus norvegicus]	266815 at	0.5
putative RNA-binding protein	266715_at	0.5
putative CCCH-type zinc finger protein identical to GB:U81238;supported by full-length cDNA: Ceres:39893.	266656 at	0.5
unknown protein ; supported by cDNA: gi_16226795 gb_AF428334.1_AF428334	266468_at	0.5
	200700_u	0.0

	266421_at	0.5
	266366_at	0.5
	266331_at	0.5
	266319_s_at	0.5
	266247_at	0.5
Expressed protein ; supported by full-length cDNA: Ceres: 112146.	266264_at	0.5
unknown protein ;supported by cDNA: gi_13358176_gb_AF324984.2_AF324984	266207_at	0.5
unknown protein	266192_at	0.5
unknown protein	266193_at	0.5
putative alcohol dehydrogenase	266087_at	0.5
putative small nuclear ribonucleoprotein E ;supported by full-length cDNA: Ceres:24619.	266074_at	0.5
putative preprotein translocase SECY protein Identical to GB:U37247; targeted to the thylakoid membrane; the protein has a chloroplast targeting si	266018_at	0.5
putative spliceosome associated protein ;supported by full-length cDNA: Ceres:38968.	265930_at	0.5
ubiquitin-like (UBQ7), putative similar to GI:304119	265825_at	0.5
Expressed protein ; supported by full-length cDNA: Ceres: 157460.	265770_at	0.5
12-oxophytodienoate-10,11-reductase ; supported by cDNA: gi_15294261_gb_AF410322.1_AF410322	265530_at	0.5
putative photosystem I reaction center subunit IV ;supported by full-length cDNA: Ceres:27629.	265287 at	0.5
hypothetical protein predicted by genefinder; supported by full-length cDNA: Ceres: 91902.	265258_at	0.5
unknown protein ; supported by full-length cDNA: Ceres: 14111.	265281_at	0.5
unknown protein	265142_at	0.5
unknown protein ; supported by full-length cDNA: Ceres: 12055.	265149_at	0.5
putative zinc finger protein similar to zinc finger protein, 207 GB:4508017 from [Homo sapiens], similar to ESTs gb[N38677 and gb[H77073; supporte	265129_at	0.5
NBS/LRR disease resistance protein, putative similar to NBS/LRR disease resistance protein GB:AAC26125 GI:3309619 from [Arabidopsis thaliana 2	265109_s_at	0.5
unknown protein similar to small zinc finger-like protein GI:5107149 from [Oryza sativa]; supported by full-length cDNA: Ceres: 21075.	265006_at	0.5
unknown protein similar to hypothetical protein GB:AAD11584;supported by full-length cDNA: Ceres:123030.	264836_at	0.5
unknown protein location of EST gb H36530, gb AA395402, and gb T43793	264772_at	0.5
unknown protein similar to putative glycosyl transferase GI:7268597 from [Arabidopsis thaliana]; supported by cDNA: gi_13878002_gb_AF370264.1	264704_at	0.5
putative chloroplast 50S ribosomal protein, L6 Similar to Mycobacterium RIpF (gb Z84395). ESTs gb T75785,gb R30580,gb T04698 come from this	264575_at	0.5
unknown protein similar to multiple exostoses type II protein EXT2.I (U72263); similar to ESTs dbj[D39982, gb]L37635, and dbj]C28418	264493_at	0.5
putative glutathione S-transferase TSI-1 similar to glutathione S-transferase (sp Q03666 GTX4_TOBAC); similar to EST gb H36275; supported by cE	264435_at	0.5
	264336_at	0.5
unknown protein ESTs gb/T04610, gb/N38459, gb/T45174, gb/R30481 and gb/N64971 come from this gene; supported by full-length cDNA: Ceres:9	264264_at	0.5
unknown protein contains similarity to tryparedoxin GI:3851498 from [Crithidia fasciculata]; supported by full-length cDNA: Ceres:34936.	264219 at	0.5
putative cyclin-dependent kinase regulatory subunit ;supported by full-length cDNA: Ceres:5750.	264070_at	0.5
putative cyclin D	264043_at	0.5
unknown protein	264054_at	0.5
putative triosephosphate isomerase ;supported by full-length cDNA: Ceres:39351.	264018 at	0.5
Expressed protein ; supported by full-length cDNA: Ceres: 20090.	264023_at	0.5
putative WD-40 repeat protein	263824 at	0.5
	263665_at	0.5
	263638_at	0.5
putative fatty acid elongase ;supported by full-length cDNA: Ceres:115769.	263443_at	0.5
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putative glyoxalase II263243_atl0.5Expressed protein ; supported by full-length cDNA: Ceres: 27081.263182_atl0.5jasmonate inducible protein, putative similar to jasmonate inducible protein GI:9279638 from [Arabidopsis thaliana]263174_atl0.5putative peroxisome assembly factor-2 Belongs to PF[00004 ATPases associated with various cellular activities2638170_atl0.5ATP-dependent Clp protease proteolytic subunit (ClpP6) identical to ATP-dependent Clp protease proteolytic subunit (ClpP6) identical to ATP-dependent Clp protease proteolytic subunit GI:2827888 from [Arabidopsis I262823_atl0.5hypothetical protein ; supported by full-length cDNA: Ceres: 2663.262618_atl0.5unknown protein262182_atl0.5hypothetical protein Similar to gil4377403 Polypeptide Deformylase from Chlamydia pneumoniae genome gblAE001687; supported by cDNA: cj_115262673_atl0.5unknown protein EST gblAA586241 comes from this gene262488_atl0.5unknown protein supported by full-length cDNA: Ceres: 37444.262480_atl0.5threonine synthase, putative similar to Niemann-Pick C disease protein (B:AAB63982 GI:2276463 from [Homo sapiens]262264_atl0.5Niemann-Pick C disease protein-like protein similar to Niemann-Pick C disease protein (Clp2399 GI:3851670 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 1981.261904_atl0.5Jal-like protein contains similarit to brine GI:3821670 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 1981.261904_atl0.5unknown protein ropticic dby genscan+; supported by full-length cDNA: Ceres: 1981.261904_atl0.5<
jasmonate inducible protein, putative similar to jasmonate inducible protein GI:9279638 from [Arabidopsis thaliana] 263174_at 0.5 putative peroxisome assembly factor-2 Belongs to PF[00004 ATPases associated with various cellular activities 261170_at 0.5 ATP-dependent Clp protease proteolytic subunit (ClpP6) identical to ATP-dependent Clp protease proteolytic subunit GI:2827888 from [Arabidopsis   262823_at 0.5 ATP-dependent Clp protease proteolytic subunit (ClPF6) identical to ATP-dependent Clp protease proteolytic subunit GI:2827888 from [Arabidopsis   262823_at 0.5 hypothetical protein supported by full-length cDNA: Ceres:2663. 262678_at 0.5 unknown protein Similar to gil4377403 Polypeptide Deformylase from Chlamydia pneumoniae genome gb AE001687; supported by cDNA: gi_112 262573_at 0.5 unknown protein is upported by full-length cDNA: Ceres:37444. 262496_at 0.5 Expressed protein, supported by full-length cDNA: Ceres:37444. 262380_at 0.5 Expressed protein , supported by full-length cDNA: Ceres: 97474. 262380_at 0.5 Expressed protein , putative similar to Isimann-Pick C disease protein GB:AAB63982 GI:2276463 from [Homo sapiens] 262264_at 0.5 Unknown protein ; supported by full-length cDNA: Ceres: 97474. 262380_at 0.5 DNA binding protein, putative similar to IB:BAA23142 GI:2850438 from [Oryza sativa]; supported by cDNA: gi_15912302_gb_AY056429. 262247_at 0.5 Unknown protein is supported by full-length cDNA: Ceres: 1981. 26198_at 0.5 unknown protein is supported by full-length cDNA: Ceres: 1981. 26198_at 0.5 unknown protein is supported by full-length cDNA: Ceres: 2087. 26190_at 0.5 unknown protein is miliar to IB:BAA23142 GI:2850438 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 4150. 26190_at 0.5 unknown protein is supported by full-length cDNA: Ceres: 13871. 26190_at 0.5 unknown protein is supported by full-length cDNA: Ceres: 13871. 26190_at 0.5 thioredoxin h, putative similar to Indire XAP22236 GI:6651245 from [Lycopersicon esculentum] 261864_s at 0.5 tunknown protein ;
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unknown protein contains similarity to autocrine motility factor receptor GI:5931955 from [Homo sapiens]261904_at0.5pirin-like protein similar to pirin GB:AAF22236 GI:6651245 from [Lycopersicon esculentum]261876_at0.5thioredoxin h, putative similar to thioredoxin h GI:4928460 from [Hevea brasiliensis];supported by full-length cDNA: Ceres:2054.261821_at0.5unknown protein ;supported by full-length cDNA: Ceres:113571.261843_at0.5unknown protein261843_at0.5hypothetical protein contains similarity to preprotein translocase GB:AAF28359 GI:6760455 from [Mus musculus]261664_s_at0.5unknown protein ;supported by full-length cDNA: Ceres:33310.261677_at0.5
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thioredoxin h, putative similar to thioredoxin h GI:4928460 from [Hevea brasiliensis];supported by full-length cDNA: Ceres:2054.261821_at0.5unknown protein ;supported by full-length cDNA: Ceres:113571.261822_at0.5unknown protein261843_at0.5hypothetical protein contains similarity to preprotein translocase GB:AAF28359 GI:6760455 from [Mus musculus]261664_s_at0.5unknown protein ;supported by full-length cDNA: Ceres:33310.261677_at0.5
unknown protein ;supported by full-length cDNA: Ceres:113571.261822_at0.5unknown protein261843_at0.5hypothetical protein contains similarity to preprotein translocase GB:AAF28359 GI:6760455 from [Mus musculus]261664_s_at0.5unknown protein ;supported by full-length cDNA: Ceres:33310.261677_at0.5
unknown protein       261843_at       0.5         hypothetical protein contains similarity to preprotein translocase GB:AAF28359 GI:6760455 from [Mus musculus]       261664_s_at       0.5         unknown protein ;supported by full-length cDNA: Ceres:33310.       261677_at       0.5
hypothetical protein contains similarity to preprotein translocase GB:AAF28359 GI:6760455 from [Mus musculus] 261664_s_at 0.5 unknown protein ;supported by full-length cDNA: Ceres:33310. 261677_at 0.5
unknown protein ;supported by full-length cDNA: Ceres:33310.
nypothetical protein contains similarity to cockayne syndrome complementation group A protein GB.020415 GI.975301 from (Homo sapiens) 201044_S at 0.5
putative lipase similar to hypothetical protein GB:AAF24946 GI:6693020 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:118034. 261646 at 0.5
ribosomal protein L9, putative similar to RIBOSOMAL PROTEIN L9 GB:P49209 from [Arabidopsis thaliana] 261620 s_at 0.5
unknown protein 29, putative similar to RIBOSOWAL PROTEIN 29 GB.P49209 from [Arabidopsis thailana] 201020_s_at 0.5 261572_at 0.5
peroxidase ATP4a identical to GB:CAA67309 GI:1429213 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 39968. 261518 at 0.5
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:9495. 261487_at 0.5
unknown protein 201407_at 0.5 261422 at 0.5
unknown protein similar to YGL010w-like protein GI:2982301 from [Picea mariana]; supported by cDNA: gi 15809883 gb AY054209.1 261379 at 0.5
dihydroxyacetone kinase, putative similar to GB:U09771 from [Citrobacter freundii] 261294 at 0.5
hypothetical protein predicted by genemark.hmm 261301_at 0.5
unknown protein ; supported by cDNA: gi_15450636_gb_AY052686.1_ 261193_at 0.5
uridine diphosphate glucose epimerase identical to GB:CAA90941 from [Arabidopsis thaliana] (Arch. Biochem. Biophys. 327 (1), 27-34 (1996)); supple 261211_at 0.5
unknown protein ;supported by full-length cDNA: Ceres:33426.
unknown protein identical to SP:050061 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:12704. 261078 at 0.5
hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 12/04. 260983 at 0.5
peroxisomal targeting signal type 2 receptor almost identical to peroxisomal targeting signal type 2 receptor GB:AAD27848 GI:4689316 from [Arabid: 260844 at 0.5

unknown protein ; supported by cDNA: gi 16604612 gb AY059751.1	260747 at	0.5
Expressed protein ; supported by cDNA: gi_10004012_gb_A1039731.1_	260650 at	0.5
		0.5
putative MYB family transcription factor similar to GB:AAD33584 from [Arabidopsis thaliana] (Plant Mol. Biol. 40 (4), 579-590 (1999)); supported by (		
glyoxalase I, putative similar to GB:Y13239 from [Brassica juncea] (Plant J. 17 (4), 385-395 (1999))	260619_at	0.5
unknown protein contains similarity to tub homolog GI:2072160 from [Homo sapiens]; supported by cDNA: gi_13877766_gb_AF370146.1_AF370146		0.5
60S ribosomal protein L38	260538_at	0.5
unknown protein ; supported by full-length cDNA: Ceres: 2381.	260442_at	0.5
hypothetical protein predicted by genscan+, similar to adenosine kinase (EC 2.7.1.20) GB:S52758 from [Leishmania donovani]; supported by full-len		0.5
receptor protein kinase, putative similar to receptor protein kinase GI:1389566 from (Arabidopsis thaliana); supported by cDNA: gi_4204848_gb_U5		0.5
unknown protein similar to putative protein GB:CAA20468 [Arabidopsis thaliana]	260314_at	0.5
putative ribosomal protein similar to ribosomal protein L33B GB:NP_014877 from [Saccharomyces cerevisiae]; supported by full-length cDNA: Ceres		0.5
GAST1-like protein similar to GAST1 protein precursor GB:P27057 [Lycopersicon esculentum] (induced by gibberellins, inhibited by ABA Plant J 19		0.5
leucine-rich repeat transmembrane protein kinase 1, putative similar to GI:3360289 from [Zea mays] (Plant Mol. Biol. 37 (5), 749-761 (1998))	259958_at	0.5
GRAB1-like protein similar to GRAB1 protein GB:CAA09371, a novel member of the NAC domain family; supported by full-length cDNA: Ceres: 3647		0.5
replication factor, putative similar to GI:4972952 from [Mus musculus] (Mamm. Genome (2000) In press)	259690_at	0.5
hypothetical protein ; supported by cDNA: gi_15081631_gb_AY048208.1_	259516_at	0.5
unknown protein ;supported by full-length cDNA: Ceres:17287.	259267_at	0.5
putative cell division related protein similar to GIsA (required for asymmetric cell division) GB:AAD26632 [Volvox carteri f. nagariensis]	259284_at	0.5
hypothetical protein predicted by genefinder	259249_at	0.5
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:9503.	259253_at	0.5
unknown protein similar to putative protein GB:CAB40986 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:5170.	259093_at	0.5
unknown protein ;supported by cDNA: gi_14334501_gb_AY034942.1_	259103_at	0.5
putative RING zinc finger protein contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger)	258758_at	0.5
unknown protein ;supported by full-length cDNA: Ceres:38495.	258606_at	0.5
unknown protein	258542_at	0.5
unknown protein ;supported by full-length cDNA: Ceres:9391.	258511_at	0.5
unknown protein ;supported by full-length cDNA: Ceres:13305.	258455_at	0.5
hypothetical protein predicted by genemark.hmm	258211_at	0.5
Expressed protein ; supported by full-length cDNA: Ceres: 15880.	258135_at	0.5
hypothetical protein predicted genemark;supported by full-length cDNA: Ceres:255040.	258021_at	0.5
unknown protein ;supported by full-length cDNA: Ceres:92314.	257925_at	0.5
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:104278.	257751_at	0.5
hypothetical protein contains Pfam profile: PF01535 domain of unknown function (3 copies)	257765_at	0.5
unknown protein contains Pfam profile: PF00515 tetratricopeptide repeat domain (TPR domain);supported by full-length cDNA: Ceres:23733.	257730_at	0.5
hypothetical protein predicted by genemark.hmm	257741_at	0.5
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_16323108_gb_AY057658.1_	257707_at	0.5
putative HLH DNA-binding protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain; supported by full-length cDNA: Ceres: 24788	257642_at	0.5
oligouridylate binding protein, putative similar to GB:CAB75429 from [Nicotiana plumbaginifolia], contains Pfam profiles: PF00076 RNA recognition r	257002_at	0.5
unknown protein	256927_at	0.5
hypothetical protein similar to DNA-directed RNA polymerase II 19 KD polypeptide (subunit 5) GB:P46279 [Glycine max]; supported by full-length cDI	256837_at	0.5
unknown protein ; supported by full-length cDNA: Ceres: 33058.	256680_at	0.5
hypothetical protein ;supported by full-length cDNA: Ceres:38428.	256568_at	0.5

hypothetical protein	256518 at	0.5
	256493 at	0.5
	256452_at	0.5
	256426 at	0.5
	256353 at	0.5
	256267 at	0.5
	—	0.5
	256041_at	
	256034_at	0.5
	256016_at	0.5
	255877_at	0.5
	255819_s_at	0.5
	255830_at	0.5
	255749_at	0.5
	255698_at	0.5
	255659_at	0.5
	255607_at	0.5
	255520_at	0.5
	255364_s_at	0.5
	255288_at	0.5
ferredoxinNADP+ reductase - like protein ferredoxinNADP+ reductase, Pisum sativum, PIR:T06773; supported by full-length cDNA: Ceres:33486.		0.5
	255185_at	0.5
	254372_at	0.5
	254378_at	0.5
	254346_at	0.5
	254049_at	0.5
	253958_at	0.5
	253952_at	0.5
	253865_at	0.5
	253614_at	0.5
	253607_at	0.5
	253574_at	0.5
	253558_at	0.5
putative poly(A) polymerase polynucleotide adenylyltransferase (EC 2.7.7.19) class I - bovine, PIR2:S17875	253399_at	0.5
putative protein predicted protein, Caenorhabditis elegans, gb:Z70780;supported by full-length cDNA: Ceres:8739.	253385_at	0.5
putative protein hypothetical protein slr2121, Synechocystis sp., PIR2:S75497;supported by full-length cDNA: Ceres:8686.	253273_at	0.5
putative protein ;supported by full-length cDNA: Ceres:8286.	253072_at	0.5
Expressed protein ; supported by full-length cDNA: Ceres: 39781.	252979_at	0.5
cinnamyl-alcohol dehydrogenase ELI3-1 ;supported by cDNA: gi_13430625_gb_AF360225.1_AF360225	252983_at	0.5
putative protein other predicted proteins Arabidopsis thaliana; supported by full-length cDNA: Ceres: 123929.; supported by cDNA: gi_15810308_gb_/2	252975_s_at	0.5
	252976_s_at	0.5
putative protein	252918_at	0.5
hypothetical protein	252612_at	0.5
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R12D like protein R12D protein - Herdeum vulgere RIR2:660284	050240 of	0 5
B12D-like protein B12D protein - Hordeum vulgare,PIR2:S60284 hypothetical protein	252348_at 252362 at	0.5 0.5
	252302_at 252327 at	0.5
MTN3-like protein MtN3 gene product - Medicago truncatula,PID:e1169583; supported by cDNA: gi_13605687_gb_AF361825.1_AF361825 putative protein predicted protein, Arabidopsis thaliana	2522527_at 252250 at	0.5
cyclin D3-like protein Nicotiana tabacum NtcycD3-1 - Nicotiana tabacum, EMBL:AB015222;supported by full-length cDNA: Ceres:36056.	252250_at 252189_at	0.5
		0.5 0.5
putative protein predicted protein, Arabidopsis thaliana	252204_at	
zinc finger protein zinc finger protein ID1, Zea mays, EMBL:AF058757	252175_at	0.5
U1 snRNP 70K protein ; supported by cDNA: gi_14532499_gb_AY039874.1_	252182_at	0.5
putative disease resistance protein	252126_at	0.5
putative protein ;supported by full-length cDNA: Ceres:118329.	252036_at	0.5
hypothetical protein predicted protein, Arabidopsis thaliana	252000_at	0.5
splicing factor - like protein splicing factor, arginine/serine-rich 7, Homo sapiens, PIR:A57198	251943_at	0.5
plasma membrane intrinsic protein 2a ;supported by full-length cDNA: Ceres:38965.	251962_at	0.5
RING finger - like protein DNA-binding Mel-18 protein, Homo sapiens, PIR:JN0717supported by full-length cDNA: Ceres:20931.	251897_at	0.5
pectate lyase - like protein pectate lyase, Musa acuminata, X92943	251864_at	0.5
protein kinase C inhibitor-like protein protein kinase C inhibitor - Zea mays, PIR:S45368; supported by full-length cDNA: Ceres: 28847.	251707_at	0.5
hypothetical protein	251650_at	0.5
hypothetical protein	251632_at	0.5
imbibition protein homolog probable imbibition protein - Brassica oleracea, PIR:S45033; supported by cDNA: gi_15292676_gb_AY050772.1_	251642_at	0.5
putative protein ;supported by full-length cDNA: Ceres:29384., Ceres:101256.	251558_at	0.5
putative DNA-binding protein DNA-binding protein (dbp) - Arabidopsis thaliana, EMBL:ATDNABP;supported by full-length cDNA: Ceres:40796.	251306_at	0.5
putative protein paladin - Mus musculus, EMBL:MMPAL	251296_at	0.5
putative protein hypothetical protein - Synechocystis sp. (strain PCC 6803), PIR:S75899; supported by cDNA: gi_16648774_gb_AY058164.1_	251243_at	0.5
putative protein glycosyl transferase lgtC - Neisseria gonorrhoeae, EMBL:AF208062	251225_at	0.5
small nuclear ribonucleoprotein-like protein small nuclear ribonucleoprotein chain D2 - Homo sapiens, PIR:138861; supported by full-length cDNA: Ce	_	0.5
putative protein ; supported by full-length cDNA: Ceres: 39035.	250925_at	0.5
F1F0-ATPase inhibitor - like protein F1F0-ATPase inhibitor protein, OsIF1-1, Oryza sativa, EMBL:AB029059; supported by full-length cDNA: Ceres:		0.5
harpin-induced protein-like	250724_at	0.5
putative protein similar to unknown protein (gb AAF32477.1);supported by full-length cDNA: Ceres:117588.	250737_at	0.5
putative protein similar to unknown protein (ref NP_055701.1);supported by full-length cDNA: Ceres:15229.	250703_at	0.5
putative protein similar to unknown protein (pir  T27191);supported by full-length cDNA: Ceres:249722.	250532_at	0.5
unknown protein ; supported by full-length cDNA: Ceres: 37422.	250454_at	0.5
14-3-3 protein GF14lambda (grf6/AFT1) identical to 14-3-3 GF14lambda GI:1345595 from [Arabidopsis thaliana]; supported by cDNA: gi_14335137_		0.5
membrane translocase - like protein inner mitochondrial membrane translocase Tim17b, Homo sapiens, EMBL:AF034790; supported by full-length c		0.5
NADH dehydrogenase (ubiquinone) ;supported by full-length cDNA: Ceres:13161.	250334_at	0.5
ABA-responsive protein - like ABA-responsive protein, Hordeum vulgare, EMBL:AF026538	250279_at	0.5
putative protein contains similarity to N-acetyltransferase; supported by full-length cDNA: Ceres: 30545.	250226_at	0.5
putative protein various predicted proteins, Arabidopsis thaliana	250183_at	0.5
putative protein similar to unknown protein (gb AAF26981.1)	250119_at	0.5
putative protein; similar to unknown protein (gb AAF26969.1)	250076_at	0.5
putative protein COLD-INDUCIBLE RNA-BINDING PROTEIN, Homo sapiens, SWISSPROT:CIRP_HUMAN	249966_at	0.5
E1, ubiquitin-like activating enzyme ECR1 identical to gi:2952433; supported by cDNA: gi_15215793_gb_AY050426.1_	249926_at	0.5

photosystem II stability/assembly factor HCF136 (sp O82660); supported by cDNA: gi 15010779 gb AY045691.1	249875 at	0.5
squalene monooxygenase	249774_at	0.5
putative protein contains similarity to ribosomal protein 30S subunit; supported by cDNA: gi_13877770_gb_AF370148.1_AF370148	249742_at	0.5
peroxidase ATP26a	249392_at	0.5
putative protein similar to unknown protein (emb CAB62355.1);supported by full-length cDNA: Ceres:94968.	249330_at	0.5
unknown protein	249313_at	0.5
putative protein contains similarity to glutathione-S-transferase/glutaredoxin;supported by full-length cDNA: Ceres:4645.	249233_at	0.5
putative protein similar to unknown protein (sp P37707);supported by full-length cDNA: Ceres:6903.	249237 at	0.5
beta-ketoacyl-CoA synthase ; supported by cDNA: gi 14334713 gb AY035030.1	249123 at	0.5
Expressed protein ; supported by full-length cDNA: Ceres: 121432.	249026 at	0.5
regulatory protein NPR1-like; transcription factor inhibitor I kappa B-like	248981_at	0.5
ras-related GTP-binding protein RHA1 (sp P31582) ;supported by full-length cDNA: Ceres:37862.	248983 at	0.5
DNA-directed RNA polymerase subunit	248984 at	0.5
calcium sensor protein, calcineurin-like; supported by cDNA: gi_15866278 gb_AF411958.1 AF411958	248827 at	0.5
60S acidic ribosomal protein P1-like protein ;supported by full-length cDNA: Ceres:14401.	248768_at	0.5
NADH dehydrogenase 10.5K chain-like protein ; supported by full-length cDNA: Ceres: 39633.	248746 at	0.5
Expressed protein ; supported by full-length cDNA: Ceres: 12974.	248665 at	0.5
putative protein contains similarity to unknown protein (dbj/BAA90946.1)	248601 at	0.5
putative protein contains similarity to unknown protein (pir T05510)	248499 at	0.5
putative protein similar to unknown protein (pir  T04431);supported by full-length cDNA: Ceres:26264.	248329 at	0.5
putative protein similar to unknown protein (pir  T02893)	248302 at	0.5
FtsH protease, putative similar to ATP-dependent metalloprotease FtsH1 GI:3600100 from [Mus musculus]	248303 at	0.5
unknown protein ; supported by full-length cDNA: Ceres: 106913.	248219_at	0.5
pyruvate decarboxylase (gb AAB16855.1)	248138 at	0.5
putative protein similar to unknown protein (pir  T05472);supported by full-length cDNA: Ceres:30073.	248148 at	0.5
Expressed protein ; supported by full-length cDNA: Ceres: 39314.	247899 at	0.5
CONSTANS-like B-box zinc finger protein-like ;supported by full-length cDNA: Ceres:6639.	247921_at	0.5
Expressed protein	247924 at	0.5
beta 1-3 glucanase - like protein beta 1-3 glucanase, Vitis vinifera, EMBL:VVI277900	247826 at	0.5
putative protein various predicted proteins, Arabidopsis thaliana	247563 at	0.5
RNA helicase ; supported by cDNA: gi_14517481_gb_AY039576.1_	247465 at	0.5
putative protein contains similarity to nonspecific lipid-transfer protein; supported by full-length cDNA: Ceres: 98459.	247268 at	0.5
nuclear protein-like	247271 at	0.5
putative protein strong similarity to unknown protein (emb[CAB89363.1)	247265 at	0.5
putative protein contains similarity to auxin-independent growth promoter	247186 at	0.5
putative protein contains similarity to NADH dehydrogenase chain CI-18; supported by full-length cDNA: Ceres: 28455.	247011 at	0.5
putative protein hypothetical proteins - different species	246768 at	0.5
ribosomal protein S21 - like ribosomal protein S21, Zea mays, PIR:T03945;supported by full-length cDNA: Ceres:93174.	246747 at	0.5
bcnt-like protein ; supported by full-length cDNA: Ceres: 9811.	246674 at	0.5
cold and ABA inducible protein kin1 ;supported by full-length cDNA: Ceres:2270.	246481 s at	0.5
hypothetical protein ; supported by full-length cDNA: Ceres: 8960.	246291_at	0.5
sugar transporter like protein	246238_at	0.5
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hypothetical protein ;supported by full-length cDNA: Ceres:108940.	246196_at	0.5
putative protein predicted proteins from various species; supported by full-length cDNA: Ceres: 17786.	246156_at	0.5
ribosomal protein L7Ae-like NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG - Homo sapiens, EMBL:D50420; supported by full-length cDNA: C	246070_at	0.5
hypothetical protein ; supported by full-length cDNA: Ceres: 38847.	246074_at	0.5
putative protein farnesyl cysteine carboxyl methyltransferase, Rattus norvegicus, EMBL:AF075595	246053_at	0.5
polyubiquitin (UBQ4) identical to GI:17677	245989_s_at	0.5
putative protein predicted protein, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 29453.	245999_at	0.5
germin-like protein ; supported by cDNA: gi_14517363_gb_AY039516.1_	246004_at	0.5
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:7343.	245761_at	0.5
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:20991.	245666_at	0.5
RNA polymerase II fifth largest subunit like protein	245569_at	0.5
hypothetical protein ;supported by full-length cDNA: Ceres:38042.	245330_at	0.5
unknown protein ; supported by cDNA: gi_16930450_gb_AF419579.1_AF419579	245119_at	0.5
PSII cytochrome b559	244963_at	0.5
ribosomal protein L33	244968_at	0.5
cytochrome B6	244976_at	0.5

Table 3: Transcripts elevated in cells during drought stress compared to unstressed plants	Affymetrix	log₂ fold
	number	increase
late embryogenesis abundant protein LEA like ; supported by cDNA: gi_15293004_gb_AY050936.1_ senescence-associated protein (SAG29) ;supported by full-length cDNA: Ceres:38843.	250648_at 245982_at	8.6 7.8
uknown protein similar to pollen coat protein GB:CAA63531 from [Brassica oleracea]; supported by cDNA: gi_14335127_gb_AY037243.1_	258498_at	7.5
late embryogenesis-abundant protein, putative similar to late embryogenesis-abundant protein GI:17828 from [Brassica napus]; supported by full-len		5.9
putative sucrose synthetase similar to several plant sugar synthetases similar to P. sativum second sugar synthetase, GenBank accession number / nonspecific lipid-transfer protein precursor - like nonspecific lipid-transfer protein precursor, Brassica napus, EMBL:AF101038; supported by full-leng		5.9 5.9
Myb-related transcription factor, putative similar to GB:AR66727 from [Petunia x hybrida] (Plant Cell 11 (8), 1433-1444 (1999)); supported by CDNA		5.8
	265091_s_at	5.6
nonspecific lipid-transfer protein precursor - like nonspecific lipid-transfer protein precursor, Brassica napus, EMBL/AF101038;supported by full-leng homodemonit transpecific protein (ATUR 7) (dottional to SED/69027); upported by PDM.oid 14007029, eb AV0459054		5.6
homeodomain transcription factor (ATHB-7) identical to SP:P46897; supported by cDNA: gi_15027938_gb_AY045826.1_ putative metal-binding protein highly similar to GB:AAD09511; supported by cDNA: gi 15450582 gb AY052659.1	266327_at 264729_at	5.3 5.3
putative protein predicted protein	254823_at	5.3
1,4-alpha-glucan branching enzyme protein soform SBE2.2 precursor	250906_at 255056 at	5.3
putative protein helix-loop-helix protein DEL -Antirrhinum majus,PIR2:A42220 dihydroflavonol 4-reductase	255056_at 249215_at	5.2 5.2
dehydrin RAB18-like protein (sp P30185) ; supported by cDNA: gi_16226664_gb_AF428458.1_AF428458	247095_at	5.2
unknown protein similar to At14a protein GB:AAD26355 GI:4589123 [Arabidopsis thaliana]; supported by cDNA: gi_16226582_gb_AF428437.1_AF4		5
putative protein putative protein - Arabidopsis thaliana, EMBL:AL078465.1;supported by full-length cDNA: Ceres:121300. putative protein similar to unknown protein (emb CAB62340.1);supported by full-length cDNA: Ceres:103870.	252319_at 248505_at	5 5
hypothetical protein contains Pfam profile: PF01535 domain of unknown function (contains 3 copies)	260062_at	5
unknown protein ; supported by cDNA: gi_15028356_gb_AY045981.1_	266462_at	4.9
hypothetical protein predicted by genscan; supported by cDNA: gi_15451109_gb_AY054635.1_ putative AVR9 elicitor response protein similar to GB:AAC69935; supported by cDNA: gi_14488077_gb_AF389287.1_AF389287	266098_at 264583 at	4.9 4.9
putative phytochrome-associated protein 3 similar to GB:AAC99771; supported by CDNA; gi 3929585 gb AF100166.1 AF100166	264510 at	4.9
En/Spm-like transposon protein, putative similar to En/Spm-like transposon protein GI:2739374 from [Arabidopsis thaliana]	262448_at	4.9
hypothetical protein predicted by genefinder	260540_at	4.9 4.9
putative protein predicted protein, Arabidopsis thaliana flavanone 3-hydroxylase (FH3) ;supported by full-length cDNA: Ceres:36653.	253344_at 252123 at	4.9
hypothetical protein	251637_at	4.9
mannan endo-1,4-beta-mannosidase	247097_at	4.9
putative NPK1-related MAP kinase similar to GB:BAA21855 from [Arabidopsis thaliana] putative ADP-glucose pyrophosphorylase large subunit	265216_at 263544 at	4.8 4.8
putative per groups proprior province and a second and a second province and a second pr	251668_at	4.8
Arm repeat containing protein - like arm repeat containing protein homolog, Arabidopsis thaliana, EMBL:AL133314	251407_at	4.8
MAP kinase kinase 3 (ATMKK3) 10.01.01.11; supported by cDNA: gi_3219268_dbj_AB015314.1_AB015314 unknown protein ; supported by cDNA: gi 14532707 gb AY039978.1	249351_at	4.8
unkitowin protein , supported by CDFxx, gg_resozy our _gg_resozy	267080_at 263230_at	4.7 4.7
glucosyltransferase like protein	245624_at	4.7
putative Ras-like GTP-binding protein contains Pfam profile: PF00071 Ras family	258652_at	4.6
heat shock protein 70 identical to heat shock protein 70 GB:CAA05547 GI:3962377 [Arabidopsis thaliana]; supported by cDNA: gi_15809831_gb_AY gibberellin-regulated protein GASA3 precursor ; supported by cDNA: gi_15450402_gb_AY052302.1_	255048 at	4.6 4.6
anthocyanidin synthase - like protein putative leucoanthocyanidin dioxygenase, Arabidopsis thaliana, PID:g1575699	254283_s_at	4.6
low-temperature-induced protein 78 (splQ06738); supported by cDNA; gi_348691_gb_L22567.1_ATHCOR78A	248337_at	4.6
hypothetical protein similar to hypothetical protein GI:4539438 from [Arabidopsis thaliana] SRG1-like protein Strong homology to SRG1 protein, a new member of the Fe(II)/ascorbate oxidase superfamily, Similar to SRG1 protein [Arabidop:	261233_at 262482 at	4.6 4.5
putative protein contains similarity to chalcone-flavonone isomerase (chalcone isomerase)supported by full-length cDNA: Ceres:40439.	250794_at	4.5
unknown protein similar to hypothetical protein GB:AAF24564 GI:6692099 from [Arabidopsis thaliana]; supported by CDNA: gi_15810166_gb_AY056	_	4.4
putative protein hypothetical protein At2g37870 - Arabidopsis thaliana, EMBL:AC007661;supported by full-length cDNA: Ceres:5920. flavonol 3-O-olucosyltransferase-like	251928_at 248185 at	4.4 4.4
DNA gyrase subunit B - like protein	245719_at	4.4
hypothetical protein predicted by genemark.hmm	256999_at	4.3
Anthocyanin 5-aromatic acyltransferase, putative similar to Anthocyanin 5-aromatic acyltransferase GB:BAA74428 from [Gentiana triflora] delta-1-pyrroline-5-carboxylate synthetase	256924_at 251775 s at	4.3 4.3
DNA excision repair cross-complementing protein; similar to human Xeroderma pigmentosum group B DNA repair protein (gb AAC49987.1); suppor		4.3
bHLH transcription factor	248867_at	4.3
unknown protein ;supported by cDNA: gi_15451043_gb_AY054602.1_ unknown protein	248223_at 262940 at	4.3 4.2
hypothetical protein predicted by genscan	263871_at	4.2
lipoamide dehydrogenase, putative	262650_at	4.2
putative transcriptional regulator similar to homeotic gene regulator (brahma protein); contains Pfam profile PF00176 SNF2 and others N-terminal do unknown protein identical to LEA-like protein GB:CAA10352 from [Arabidopsis thaliana]	258559_at 258347_at	4.2 4.2
unktiowin protein indentica to LEA-like protein 50-2044 10322 from [Atabudopis transmark] putative protein similar to unknown protein (gb AAC73025.1); supported by CDNA: gj_14532515_gb_AY039882.1_	250825_at	4.2
low-temperature-induced 65 kD protein (splQ04980)	248352_at	4.2
RuBisCO subunit binding-protein beta subunit precursor; chaperonin, 60 kDa	248021_at	4.2
receptor-like protein kinase putative protein CDPK substrate protein 1, Mesembryanthemum crystallinum, EMBL:AF219972;supported by full-length cDNA: Ceres:13378.	247197_at 246724 at	4.2 4.2
hypothetical protein predicted by genscan; supported by cDNA: gi_15010703 gb_AY045653.1_	267341_at	4.1
putative glucosyltransferase	265499_at	4.1
protein phosphatase 2C, putative similar to GB:CAB90633 from [Fagus sylvatica];supported by full-length cDNA: Ceres:118185. B regulatory subunit of protein phosphatase 2A, putative similar to B regulatory subunit of protein phosphatase 2A GI:2160694 from (Arabidopsis th	261077_at 259359_at	4.1 4.1
by obtained protein process process process and a process of the process process process process and the process of the proces	253145_at	4.1
putative protein various predicted proteins, Arabidopsis thaliana	250955_at	4.1
putative protein intracellular protein Mg11, mouse, PIR:I49127; supported by cDNA: gi_14488068_gb_AF389282.1_AF389282 hypothetical protein predicted by genefinder	249403_at 257436_s_at	4.1 4.1
oxidase, putative similar to oxidase GB:AAA32870 GI:166876 from (Arabidopsis thaliana);supported by full-length cDNA: Ceres:152458.	260706_at	4.1
phytochrome E	254680_at	4
glucose-1-phosphate adenylyltransferase (APL3); supported by cDNA: gi_16648984_gb_AY059862.1_	252888_at	4
glutathione S-transferase-like protein ; supported by cDNA: gi_11096011_gb_AF288189.1_AF288189 protein phosphatase 2C - like ABA induced protein phosphatase 2C, Fagus sylvatica, EMBL:FSY277743; supported by cDNA: gi_15809791 gb_AY	250083_at 247723 at	4 4
unknown protein ; supported by cDNA: gi_13265448_gb_AF324676.2_AF324676	263881_at	3.9
unknown protein ; supported by cDNA: gi_15983443_gb_AF424596.1_AF424596	258624_at	3.9
unknown protein ; supported by cDNA: gj_13358195_gb_AF325003.2_AF325003 dehydrin Xero2  ; supported by cDNA: gj  15809983  gb  AY054260.1	256114_at 252102 at	3.9 3.9
Expressed protein ; supported by cDNA: gi_14517386_gb_AY039528.1_	245283_at	3.9
	_	

nodulin-like protein unknown protein :supported by full-length cDNA: Ceres:100283.	267044_at	3.8
putative RNA helicase A 3 end of this gene is located at the beginning of F10A8, GB:AAD14515	265907_at 265731_at	3.8 3.8
glucose-6-phosphate/phosphate-translocator precursor, putative similar to glucose-6-phosphate/phosphate-translocator precursor GI:2997591 from		3.8
methionine/cystathionine gamma lyase, putative similar to methionine gamma-lyase GB:CAA04124.1 GI:2330885 from [Trichomonas vaginalis]; sup		3.8
branched-chain alpha keto-acid dehydrogenase, putative similar to branched-chain alpha keto-acid dehydrogenase GB:AAC69851 GI:3822223 from 2		3.8
putative RNA-binding protein contains Pfam profile: PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain); similar to ras-GTPase-acti		3.8
unknown protein contains Pfam profile: PF00430 ATP synthase B/B CF(0); supported by cDNA: gi_15810372_gb_AY056225.1_	257732_at 254289_at	3.8 3.8
putative protein predicted protein, Arabidopsis thaliana putative major latex protein major latex protein type 1 - Arabidopsis thaliana, EMBL:X91960; supported by cDNA: gi 13605713 gb AF361838.1 AF	_	3.8
putative protein cellulose synthase catalytic subunit (Ath-A). Arabidopsis thaliana; gb:AF027173	254186 at	3.8
putative protein predicted proteins, Arabidopsis thaliana and Oryza sativa	249952_at	3.8
phospholipase D ;supported by cDNA: gi_15284210_gb_U84568.2_ATU84568	267536_at	3.7
putative glutathione S-transferase ; supported by CDNA: gi_11096003_gb_AF288185.1_AF288185	266270_at	3.7
flavin-containing monooxygenase, putative similar to flavin-containing monooxygenase GB:AAA21178 GI:349534 from [Oryctolagus cuniculus]; supp mutM homologue-1 identical to mutM homologue-1 GI:3550982 from [Arabidopsis thaliana]; supported by cDNA: gi 3820619 gb AF099970.1 AF05		3.7 3.7
indum nonologue i denitica lo indum nonologue i Gilosobosc non prasidopsis trananaj, supported by conve, gi_socoto s_go_ki osservi. T_ki os unknown protein	259322 at	3.7
putative N2,N2-dimethylguanosine tRNA methyltransferase similar to N2,N2-dimethylguanosine tRNA methyltransferase GB:CAA20101 GI:6901242	_	3.7
signal recognition particle receptor beta subunit-like protein	250768_at	3.7
F5A9.19 unknown protein; similar to ESTs dbj AV529799.1, dbj[AV524005.1	245645_at	3.7
drought-induced protein like	245523_at	3.7 3.6
hypothetical protein predicted by genscan+ hypothetical protein similar to membrane associated salt inducible protein isolog; similar to F21B7.18 and F21B7.21	267397_at 264816_at	3.6
putative 3-methylcrotonyl-CoA carboxylase ESTs gbl/135836, gbl/A651295 and gbl/AA721862 come from this gene; supported by cDNA: gi 53370€		3.6
cinnamoyl CoA reductase, putative similar to cinnamoyl CoA reductase GB:AAF43141 GI:7239228 from [Populus tremuloides]; supported by full-len		3.6
hypothetical protein predicted by genemark.hmm	259463_at	3.6
unknown protein ; supported by cDNA: gi_13605890_gb_AF367344.1_AF367344	250784_at	3.6
heat shock transcription factor receptor-like protein kinase precursor - like receptor-like protein kinase precursor, Madagascar periwinkle, PIR:T10060	248936_at 247686_at	3.6 3.6
pectinace/vieter protein minace precursor inter receptor interpretation to many protein activity and a statistical protei	246403 at	3.6
putative TPR repeat nuclear phosphoprotein TPR repeat protein	265522 at	3.5
hypothetical protein similar to Human XE169 protein (gi]3033385); similar to EST gb T88128	264528_at	3.5
unknown protein ;supported by full-length cDNA: Ceres:25894.	264094_at	3.5
	263157_at	3.5
Myb-related transcription factor mixta, putative similar to Myb-related transcription factor mixta GI:485866 from [Antirrhinum majus] hypothetical protein	261431_at 259568_at	3.5 3.5
unknown protein similar to hypothetical 77.0 KD protein in HES1-SEC63 intergenic region GB:Q08647 [Saccharomyces cerevisiae]	259082 at	3.5
unknown protein ; supported by cDNA: gi_16930484_gb_AF419596.1_AF419596	256323_at	3.5
TMV resistance protein N-like TMV resistance protein N, Nicotiana glutinosa, PIR2:A54810	254586_at	3.5
hypothetical protein ; supported by cDNA: gi_14334435_gb_AY034909.1_	251262_at	3.5
flavonoid 3-hydroxylase - like protein flavonoid 3-hydroxylase Ht1, Petunia x hybrida, EMBL:AF155332; supported by cDNA: gi_10334803_gb_AF2'	-	3.5
hypothetical protein contains similarity to DNA polymerase III, epsilon subunit GI:8163241 from [Chlamydia muridarum] anthocyanin2, putative similar to anthocyanin2 (An2) GI:7673088 from [Petunia integrifolia]; supported by cDNA: gi 3941507 gb AF062908.1 AF0(	245743_at 245628_at	3.5 3.5
hypothetical protein predicted by genscan	264065 at	3.4
putative SecA-type chloroplast protein transport factor Similar to gb X82404 chloroplast SecA protein from Pisum sativum	262491_at	3.4
sec14 cytosolic factor, putative similar to SP:P24859 from [Kluyveromyces lactis]; supported by cDNA: gi_15810424_gb_AY056251.1_	261151_at	3.4
hypothetical protein predicted by genemark.hmm	260823_at	3.4
unknown protein ;supported by full-length cDNA: Ceres:96702. hypothetical protein	260357_at 257759_at	3.4 3.4
nyponetical protein serine/threnine-specific kinase lecRK1 precursor,lectin receptor-like	251479_at	3.4
putative protein strong similarity to unknown protein (gb]AAC98056.1)	250237_at	3.4
chalcone synthase (naringenin-chalcone synthase) (testa 4 protein) (splP13114) ;supported by full-length cDNA: Ceres:38370.	250207_at	3.4
serine/threonine protein kinase-like protein several serine/threonine protein kinases - different species; supported by cDNA: gi_15215663_gb_AY050		3.4
protein kinase, putative similar to SERINE/THREONINE-PROTEIN KINASE CTR1 GB:Q05609 from [Arabidopsis thaliana]	258509_at	3.3
Expressed protein ; supported by cDNA: gi_14532529_gb_AY039889.1_ 2 putative aldehyde dehydrogenase ; supported by cDNA: gi_14334931_gb_AY035139.1_	266550_s_at 265188_at	3.3 3.3
unknown protein ; supported by cDNA: gi 16604686 gb AY059788.1	260361 at	3.3
putative 3-phosphoinositide-dependent protein kinase-1 similar to 3-phosphoinositide-dependent protein kinase-1 GB:AAD37165 [Arabidopsis thaliar	258964_at	3.3
	256601_s_at	3.3
hypothetical protein predicted by genemark.hmm	255929_at	3.3
hypothetical protein RNA helicase - like protein Cdc28p, Schizosaccharomyces pombe, PID:G1439562	255687_at 254675_at	3.3 3.3
NAM / CUC2 -like protein nap gene, Arabidopsis thaliana, PID:g2780192; supported by cDNA: gi 15912330 gb AY056443.1	253132 at	3.3
putative protein strong similarity to unknown protein (gb AAF31728.1); supported by cDNA: gi_15292740_gb_AY050804.1_	249917_at	3.3
unknown protein ;supported by cDNA: gi_14030678_gb_AF375430.1_AF375430	248969_at	3.3
serine/threonine kinase, putative similar to serine/threonine kinase GI:2632252 from [Sorghum bicolor]; supported by cDNA: gi_14486385_gb_AY03		3.3
water stress-induced protein, putative similar to water stress-induced protein GI:454879 from [Oryza sativa]; supported by cDNA: gi_15215761_gb_/ putative protein various hypothetical proteins from Arabidopsis thaliana	245627_at 254917 at	3.3 3.3
beta-VPE nearly identical to beta-VPE GB:BAA09615 6[1:805364 [Arabidopsis thaliana]; supported by cDNA; gi 14194096 gb AF367254.1 AF367		3.2
putative endochitinase	260561_at	3.2
putative calcium-binding EF-hand protein ; supported by cDNA: gi_10862967_dbj_AB039924.1_AB039924	255795_at	3.2
homeobox-leucine zipper protein ATHB-12 ;supported by full-length cDNA: Ceres:32615.	251272_at	3.2
putative protein similar to unknown protein (gb/AAF23188.1)	250728_at	3.2
ABC transporter -like protein TAP-like ABC transporter, Rattus norvegicus, EMBL:AB027520 heat shock transcription factor-like protein	249487_at 249117_at	3.2 3.2
	267256_s_at	3.1
unknown protein ;supported by cDNA: gi_15810470_gb_AY056274.1_	265484_at	3.1
phenylalanine ammonia lyase (PAL1) ; supported by cDNA: gi_15028192_gb_AY045919.1_	263845_at	3.1
hypothetical protein similar to hypothetical proteins: GB:AAD21751, GB:AAC33230 [Arabidopsis thaliana]	260262_at	3.1
seven in absentia-like protein similar to SINA1p GB:CAB40577 from [Vitis vinifera]; supported by cDNA: gi_16323493_gb_AY059135.1_ putative protein predicted proteins, Arabidopsis thaliana	256789_at 252782_at	3.1 3.1
putative protein various predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:6263.	252762_at 251206_at	3.1
alcohol dehydrogenase identical to alcohol dehydrogenase GI:469467 from (Arabidopsis thaliana); supported by full-length cDNA: Ceres: 4033.	264953_at	3
hypothetical protein predicted by genscan	264831_at	3
hypothetical protein predicted by genemark.hmm	264217_at	3
putative acyl-CoA synthetase ; supported by cDNA: gi_15450592_gb_AY052664.1_ putative aminotransferase similar to beta-alanine-pyruvate aminotransferase GB:BAA19549 [Rattus norvegicus], alanine-glyoxylate aminotransferas	263811_at 258983_at	3 3
	_00000_at	0

RNA-binding protein, putative contains Pfam profile: PF00806 Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain) (8 cor	257122_at	3
hypothetical protein predicted by genscan+	256379_at	3
unknown protein contains Pfam profile: PF00917 MATH domain; supported by cDNA: gi_12083245_gb_AF332419.1_AF332419	256021_at	3
major intrinsic protein (MIP) - like nodulin-26, Glycine max., PIR2:JQ2285; supported by full-length cDNA: Ceres: 36655.	254971_at	3
CTP synthase like protein CTP synthase, Methanococcus jannaschii,PIR2:E64446	254490_at	3
phenylalanine ammonia-lyase ;supported by full-length cDNA: Ceres:110886.	251984_at	3
putative protein hypothetical proteins - different species	249656_at	3
hypothetical protein predicted by genemark.hmm	264562_at	2.9
lysine-ketoglutarate reductase/saccharopine; supported by cDNA: gi_2052507	253373_at	2.9
putative protein contains similarity to nucleolar protein	247130_at	2.9
PSII T protein	244973_at	2.9
putative serine/threonine protein kinase ;supported by full-length cDNA: Ceres:18783.	267599_at	2.8
putative putative sister-chromatide cohesion protein member of stromalin protein family;supported by full-length cDNA: Ceres:11935.	266484_at	2.8
hypothetical protein predicted by genscan	266028_at	2.8
histone H1 ;supported by full-length cDNA: Ceres:112970.	265817_at	2.8
putative O-GlcNAc transferase similar to Rattus O-GlcNAc transferase (gb U76557)	264568_at	2.8
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_11908125_gb_AF326910.1_AF326910	264102_at	2.8
3-hydroxyisobutyryl-coenzyme A hydrolase, putative similar to 3-hydroxyisobutyryl-coenzyme A hydrolase GB:AAC52114 GI:3320120 [Homo sapier		2.8
unknown protein ; supported by cDNA: gi_16648825_gb_AY058190.1_	262232_at	2.8
polygalacturonase -like protein polygalacturonase, muskmelon, PIR:T08213; supported by cDNA: gi_15215708_gb_AY050383.1_	252781_at	2.8
protein kinase - like protein Pto kinase interactor 1 (Pti1), Lycopersicon esculentum, EMBL:SL28007; supported by full-length cDNA: Ceres:105458.	249588_at	2.8
putative protein contains similarity to phytocyanin/early nodulin-like protein	248236_at	2.8
unknown protein contains similarity to phytochrome interacting factor 3 GI:3929586 from [Arabidopsis thaliana]; supported by cDNA: gi_14334499_gl		2.8
hypothetical protein	258672_at	2.8
putative protein crp1 protein - Zea mays, PIR:T01685	249436_at	2.8
unknown protein EST gb/ATTS0295 comes from this gene;supported by full-length cDNA: Ceres:20380.	264580_at	2.7
hypothetical protein similar to unknown protein GI:4585976 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:94828.	262942_at	2.7
unknown protein	260420_at	2.7
putative protein kinase C-terminal region similar to MAP3K delta-1 protein kinase GB:CAA74591 [Arabidopsis thaliana]; contains Pfam profile: PF00C		2.7
unknown protein ; supported by cDNA: gi_16974549_gb_AY060562.1_	259756_at	2.7
unknown protein ; supported by cDNA: gi_13937210_gb_AF372960.1_AF372960	258400_at	2.7
cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450	257628_at	2.7
putative protein ;supported by full-length cDNA: Ceres:114734.	256676_at	2.7
putative protein hypothetical protein, Arabidopsis, PID:E353139; supported by cDNA: gi_13430803_gb_AF360314.1_AF360314	253089_at	2.7
phytochrome C (sp P14714)	249666_at	2.7
putative protein predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_15810554_gb_AY056316.1_	249614_at	2.7
kinesin -like protein Krm protein, L.japonicus, EMBL:LJGLN1	249629_at	2.7
plasma membrane ATPase 3 (proton pump) (sp[P20431); supported by cDNA: gi_15982712_gb_AY056780.1_	247902_at	2.7
putative protein MtN19, Medicago truncatula, EMBL:MTY15367	247488_at	2.7
putative protein similarity to predicted proteins, Arabidopsis thaliana	245179_at	2.7
unknown protein	245076_at	2.7
putative glucosyltransferase supported by full-length cDNA: Ceres:153418.	266532_at	2.6
unknown protein ; supported by cDNA: gi_13877764_gb_AF370145.1_AF370145	264989_at	2.6
unknown protein	263513_at	2.6
hypothetical protein contains similarity to ABC transporter GI:6626257 from [Methanobacterium thermoautotrophicum]	261969_at	2.6
unknown protein similar to SPL1-related proteins: GB:CAB56771, GB:CAB567770, GB:CAB56773 [Arabidopsis thaliana]	259971_at	2.6
protein phosphatase 2C (AIP2C-HA) identical to protein phosphatase 2C (AIP2C-HA) GB: AJ003119 [Arabidopsis thaliana] (Plant Mol. Biol. 38 (5), 8		2.6
early light-induced protein identical to early light-induced protein GB:AAB883391 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:14/		2.6
HSC70-interacting protein, putative similar to HSC70-INTERACTING PROTEIN GB:P50502 from [Homo sapiens]	258187_at	2.6
putative cinnamoyl-CoA reductase highly similar to F4P9.37;supported by full-length cDNA: Ceres:11254. putative protein membrane-associated salt-inducible protein, Nicotiana tabacum; supported by cDNA: gi 15810160 gb AY056145.1	255787_at	2.6 2.6
putative protein memoralerassociated asseminduate protein, includina abademin, supported by carve, gr_156 of ord_ga_r 1000 res. [ fatty acid elongase - like protein KCS1 fatty acid elongase - ketoacyt-CCA synthase 1, Arabidopsis thaliana, EMBL:AF053345	254581_at 250891_at	2.6
nau adu elongase - inte protein rost integradu elongase stretuacyrook syminase i, riaduopsis integratiana, Lind Costa Sketo-acyl CoA thiolase 2 (gb/AAC17877.1); supported by cDNA; gi 3192892, gb AF062590.1 AF062590	248625 at	2.6
3-reto-edy-cod initiate 2 (glyane rran, r), supported by conv. gr_3192092_gu_Artio2390.1_Artio2390.	248025_at 247828_at	2.6
petidylprolyl isomerase (cyclophilin)-like ; supported by cDNA: gi 17063169 gb AY062106.1	246980 at	2.6
hypothetical protein predicted by genemark.html; supported by full-length cDNA: Ceres: 14447.	246582 at	2.6
UDP glucose:flavonoid 3-o-glucosyltransferase -like protein UDP glucose:flavonoid 3-o-glucosyltransferase, Vitis vinifera, EMBL:AF000372	246468 at	2.6
GA-like protein putative member of the VHIID domain transcription factor family RGAL - Arabidopsis thaliana, EMBLA/L224957	246432 at	2.6
sucrose-phosphate synthase-like protein sucrose-phosphate synthase (EC 2.4.1.14) isoform 1 - Citrus unshiu, EMBL:AB005023; supported by cDN/		2.6
	245094_at	2.6
hypothetical protein	245477_at	2.5
putative cinnamoyl CoA reductase ;supported by full-length cDNA: Ceres:14133.	266578 at	2.5
unknown protein	266503_at	2.5
putative pectinesterase ; supported by full-length cDNA: Ceres: 25729.	266488 at	2.5
unknown protein ; supported by cDNA: gi 14334955 gb AY035151.1	265629 at	2.5
hypothetical protein similar to receptor-like protein kinase GI:7529754 from [Arabidopsis thaliana]	264479 at	2.5
unknown protein	263296 at	2.5
FtsH protease, putative similar to zinc dependent protease GI:7650138 from [Arabidopsis thaliana]	262626 at	2.5
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:19976.	262369_at	2.5
unknown protein	258425_at	2.5
glucose-6-phosphate 1-dehydrogenase, putative similar to glucose-6-phosphate 1-dehydrogenase GB:CAB52674 from [Arabidopsis thaliana] (Plan	257144_at	2.5
hypothetical protein	255449_at	2.5
putative protein	253343_at	2.5
putative sugar transporter protein sugar transporter, Arabidopsis thaliana, db_xref=PID:g1495273	253188_at	2.5
Spot 3 protein and vacuolar sorting receptor homolog/AtELP1 ; supported by cDNA: gi_15081792_gb_AY048289.1_	252027_at	2.5
imbibition protein homolog probable imbibition protein - Brassica oleracea, PIR:S45033; supported by cDNA: gi_15292676_gb_AY050772.1_	251642_at	2.5
putative protein	251490_at	2.5
putative protein kinesin light chain - Plectonema boryanum, EMBL:U78597;supported by full-length cDNA: Ceres:118233.	251030_at	2.5
transcription factor-like protein ;supported by full-length cDNA: Ceres:114015.	250688_at	2.5
putative protein similar to unknown protein (sp P37707);supported by full-length cDNA: Ceres:6903.	249237_at	2.5
unknown protein	248158_at	2.5
ribosomal protein L36	244980_at	2.5
protein kinase - like protein wall-associated kinase 4, Arabidopsis thaliana, AJ009695;supported by full-length cDNA: Ceres:13355.	251600_at	2.5
	267644_s_at	2.4
ferredoxin-dependent glutamate synthase (GLU2)	266365_at	2.4
unknown protein ; supported by cDNA: gj-14517457_gb_4Y039564.1_	264987_at	2.4
stress related protein, putative similar to stress related protein GI:5802955 from [Vitis riparia]; supported by full-length cDNA: Ceres: 14043.	264968_at	2.4

aspartic protease, putative similar to aspartic protease GI:1326164 from [Brassica napus]	264741_at	2.4
	264338_at	2.4
•	264156_at	2.4
	263570_at	2.4
	263253_at	2.4
	263259_at	2.4
CCAAT-binding factor B subunit, putative similar to CCAAT-binding factor B subunit GI:1173617 [Brassica napus]; supported by cDNA: gi_1442343{ hypothetical protein predicted by genemark.hmm	263156_at 263127_at	2.4 2.4
unknown protein strong similarity to gb/Y09533 involved in starch metabolism from Solanum tuberosum and contains a PF/01326 Pyruvate phospha		2.4 2.4
	262357 at	2.4
	262164 at	2.4
unknown protein contains similarity to eukaryotic initiation factor 4B GI:6739515 from [Triticum aestivum]; supported by cDNA: gi 14335083 gb AY(		2.4
	260794 at	2.4
unknown protein predicted by genefinder; similar to GP 2194125	260565_at	2.4
hypothetical protein ; supported by cDNA: gi_15081631_gb_AY048208.1_	259516_at	2.4
	259403_at	2.4
putative serine/threonine protein kinase similar to serine/threonine-specific kinase GB:S68589 [Arabidopsis thaliana]; Pfam HMM hits: putative serine		2.4
	258901_at	2.4
	257056_at	2.4
	254377_at	2.4
	254189_at 252525 at	2.4 2.4
	251896 at	2.4
	251753 at	2.4
	251332 at	2.4
	251010_at	2.4
putative protein contains similarity to remorin; supported by full-length cDNA: Ceres: 28686.	249797_at	2.4
putative protein similar to unknown protein (pir  T26506); supported by cDNA: gi_16649056_gb_AY059898.1_	249165_at	2.4
	247340_at	2.4
	247222_at	2.4
	246946_at	2.4
	246554_at	2.4
	246036_at	2.4 2.4
	245736_at 245025 at	2.4
	243025_at 244981_at	2.4
	256329 at	2.3
	267268 at	2.3
putative glucosyl transferase an EST matching the 5 end of this gene (GB:AA605508) was originally described as polyadenylated (GB:AA006321) a 2		2.3
lactoylglutathione lyase-like protein Similar to protein gb Z74962 from Brassica oleracea which is similar to bacterial YRN1 and HEAHIO proteins. Et		2.3
hypothetical protein contains similarity to lipid transfer protein GI:498038 from (Senecio odorus)	264146_at	2.3
	263031_at	2.3
	262860_at	2.3
ferrodoxin NADP oxidoreductase, putative similar to ferrodoxin NADP oxidoreductase GB:X99419 GI:1480346 from [Pisum sativum]supported by ful		2.3
Ca2+-dependent membrane-binding protein annexin idenctical to GB:AAD34236 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:2	_	2.3
•	260585_at 259718 at	2.3 2.3
•	259570 at	2.3
	258264 at	2.3
leucine-rich repeat disease resistance protein, putative, 5 partial similar to NL0C GB:AAD13302 from [Lycopersicon esculentum] (Mol. Plant Microb		2.3
	255070 at	2.3
UDP rhamnoseanthocyanidin-3-glucoside rhamnosyltransferase - like protein UDP rhamnoseanthocyanidin-3-glucoside rhamnosyltransferase, P 2		2.3
predicted protein	253254_at	2.3
starch phosphorylase H (cytosolic form) - like protein starch phosphorylase H, cytosolic isoform, Vicia faba, PIR:T12091; supported by cDNA: gi_15	252468_at	2.3
	250956_at	2.3
	250556_at	2.3
	249372_at	2.3
ATP-dependent Clp protease ATP-binding subunit (ClpD), ERD1 protein precursor identical to ERD1 protein GI:497629, SP:P42762 from [Arabidop: understand for the subunit environment for the subunit (ClpD), ERD1 protein precursor identical to ERD1 protein GI:497629, SP:P42762 from [Arabidop: understand for the subunit environment for the subunit for t	248487_at 247508 at	2.3
	247508_at 246796_at	2.3 2.3
	246790_at 246282_at	2.3
	246232 at	2.3
	244972 at	2.3
ribosomal protein L14	244982_at	2.3
AMP-binding protein, putative similar to AMP-binding protein GB:CAA96521 from [Brassica napus] (Plant Mol. Biol. (1997) 33 (5), 911-922)	257196_at	2.2
unknown protein	266874_at	2.2
	266555_at	2.2
	265902_at	2.2
	265596_at	2.2
myrosinase-binding protein homolog, putative almost identical to myrosinase-binding protein homolog GI:2997767 from [Arabidopsis thaliana]; suppr2 ukrawu protein supprise in the super su		2.2 2.2
	264985_at 264633 at	2.2
	263384 at	2.2
dTDP-glucose 4.6-dehydratase putative similar to dTDP-glucose 4.6-dehydratase Gl:5921157 from [Streptomyces avernitilis]; supported by cDNA:		2.2
	61872 s at	2.2
		2.2
	261113_at	
putative O-linked GlcNAc transferase similar to O-linked GlcNAc transferase GB:AAB63465 [Caenorhabditis elegans]	261113_at 261065_at	2.2
	261065_at 258575_at	2.2
ethylene-responsive transcriptional coactivator, putative similar to GB:AAD46402 from [Lycopersicon esculentum] (Plant J. 18 (6), 589-600 (1999));s	261065_at 258575_at 258133_at	2.2 2.2
putative sucrose cleavage protein similar to GB:S51376 from [Solanum tuberosum]supported by full-length cDNA: Ceres:40179.	261065_at 258575_at 258133_at 257970_at	2.2 2.2 2.2
putative sucrose cleavage protein similar to GB:S51376 from [Solanum tuberosum]supported by full-length cDNA: Ceres:40179. dynamin-like protein similar to phragmoplastin GB:CAB56619 from [Nicotiana tabacum]	261065_at 258575_at 258133_at 257970_at 257045_at	2.2 2.2 2.2 2.2
putative sucrose cleavage protein similar to GB:S51376 from [Solanum tuberosum]supported by full-length cDNA: Ceres:40179. dynamin-like protein similar to phragmoplastin GB:CAB56619 from [Nicotiana tabacum] hypothetical protein	261065_at 258575_at 258133_at 257970_at 257045_at 256384_at	2.2 2.2 2.2 2.2 2.2 2.2
putative sucrose cleavage protein similar to GB:S51376 from [Solanum tuberosum]supported by full-length cDNA: Ceres:40179. dynamin-like protein similar to phragmoplastin GB:CAB56619 from [Nicotiana tabacum] hypothetical protein 26S proteasome regulatory subunit S12, putative nearly identical to 26S proteasome regulatory subunit S12 (MOV34 ) SP:024412 [Arabidopsis thal	261065_at 258575_at 258133_at 257970_at 257045_at 256384_at 256249_at	2.2 2.2 2.2 2.2 2.2 2.2 2.2
putative sucrose cleavage protein similar to GB:S51376 from [Solanum tuberosum]supported by full-length cDNA: Ceres:40179. dynamin-like protein similar to phragmoplastin GB:CAB56619 from [Nicotiana tabacum] hypothetical protein 26S proteasome regulatory subunit S12, putative nearly identical to 26S proteasome regulatory subunit S12 (MOV34 ) SP:O24412 [Arabidopsis thal putative protein	261065_at 258575_at 258133_at 257970_at 257045_at 256384_at 256249_at 254807_at	2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2
putative sucrose cleavage protein similar to GB:S51376 from [Solanum tuberosum]supported by full-length cDNA: Ceres:40179. dynamin-like protein similar to phragmoplastin GB:CAB56619 from [Nicotiana tabacum] hypothetical protein 26S proteasome regulatory subunit S12, putative nearly identical to 26S proteasome regulatory subunit S12 (MOV34 ) SP:O24412 [Arabidopsis thal putative protein putative protein Mei2-like protein, Arabidopsis thaliana, gb:D86122	261065_at 258575_at 258133_at 257970_at 257045_at 256384_at 256249_at	2.2 2.2 2.2 2.2 2.2 2.2 2.2
putative sucrose cleavage protein similar to GB:S51376 from [Solanum tuberosum]supported by full-length cDNA: Ceres:40179. dynamin-like protein similar to phragmoplastin GB:CAB56619 from [Nicotiana tabacum] hypothetical protein 265 proteasome regulatory subunit S12, putative nearly identical to 26S proteasome regulatory subunit S12 (MOV34 ) SP:O24412 [Arabidopsis thal putative protein putative protein Mei2-like protein, Arabidopsis thaliana, gb:D86122 putative protein hypothetical protein, Synechocystis sp., PIR2:S76701	261065_at 258575_at 258133_at 257970_at 257045_at 256384_at 256249_at 256249_at 254807_at	2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2

protein phosphatase 2C - like protein protein phosphatase 2C, Schizosaccharomyces pombe, PIR2:S54297; supported by cDNA: gi 16209697 gb	253453 at	2.2
abscisic acid responsive elements-binding factor(ABF3) identical to abscisic acid responsive elements-binding factor (ABF3) GI:6739280 from [Arabi		2.2
ABC transporter-like protein glutathione-conjugate transporter AtMRP4 - Arabidopsis thaliana, EMBL:AJ002584	251227_at	2.2
heat shock protein 70 (Hsc70-5) ; supported by cDNA: gi_6746589_gb_AF217458.1_AF217458	250502_at	2.2
putative protein similar to unknown protein (gb AAD21732.1)	249850 at	2.2
sigma-like factor (emb CAA77213.1)	249769 at	2.2
putative protein nucleoid DNA-binding protein cnd41, chloroplast, common tobacco, PIR:T01996; supported by cDNA: gi 15809849 gb AY054192.		2.2
putative protein similar to unknown protein (pir  T05035)	248959_at	2.2
prematurely terminated mRNA decay factor-like protein	248816_at	2.2
spermidine synthase ;supported by full-length cDNA: Ceres:33021.	248248 at	2.2
	247918 at	2.2
	247593_at	2.2
receptor-like protein kinase ; supported by cDNA: gi_16974576_gb_AY060554.1_	247357_at	2.2
sucrose-UDP glucosyltransferase	245998 at	2.2
hypothetical protein predicted by genemark.hmm	245724 at	2.2
	_	
	260773_at	2.2
putative protein auxin-induced protein 10A -Glycine max,PID:g255579	254809_at	2.2
unknown protein	257476 at	2.1
putative DNA2-NAM7 helicase family protein 2	267489 s at	2.1
	266673 at	2.1
	_	
	265664_at	2.1
hypothetical protein contains Pfam profile: PF01363 FYVE zinc finger; supported by full-length cDNA: Ceres: 15739.	265035_at	2.1
receptor-like protein glossy1 (gl1), putative similar to receptor-like protein glossy1 (gl1) GI:1209703 from (Arabidopsis thaliana)	264147 at	2.1
	263912 at	2.1
unknown protein	263870 at	2.1
putative aspartate kinase-homoserine dehydrogenase almost identical to gb X71364 gene for aspartate kinase homoserine dehydrogenase from Ara		2.1
transcription factor ZAP1 identical to GP:1064883:X92976	263626_at	2.1
putative tetracycline transporter protein	263574 at	2.1
	263083 at	2.1
	262050_at	2.1
DYW7 protein identical to DYW7 protein of unknown function GB:CAA06829 from [Arabidopsis thaliana] (Plant Mol. Biol. 42 (4), 603-613 (2000))	261133_at	2.1
unknown protein	260995 at	2.1
	260878 at	2.1
		2.1
	260670_at	
putative P-type transporting ATPase similar to ATPase II GB:AAD34706 [Homo sapiens]	259910_at	2.1
hypothetical protein similar to hypothetical protein GB:AAB72157 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:1132.	259012 at	2.1
	258277 at	2.1
	258119 at	2.1
	_	
	256902_s_at	2.1
hypothetical protein	255621_at	2.1
putative fibrillin; supported by full-length cDNA: Ceres: 1461. 2	255364 s at	2.1
	253841 at	2.1
	_	2.1
	253407_at	
	253081_at	2.1
putative protein KIAA0274 protein, Homo sapiens, SWISSPROT:Y274_HUMAN	252737_at	2.1
putative protein various predicted proteins	252246 at	2.1
	251644 at	2.1
	_	
putative protein several hypothetical proteins - different bacteria	251137_at	2.1
polyubiquitin (UBQ3) identical to GI:928809; supported by full-length cDNA: Ceres: 20908.	250935_at	2.1
DREB2A (dbj BAA33794.1);supported by cDNA: gi_3738229_dbj_AB007790.1_AB007790	250781_at	2.1
tetrahydrofolylpolyglutamate synthase-like protein	250757 at	2.1
ubiquitin-specific protease 12 (UBP12) almost identical to ubiquitin-specific protease 12 GI:11993471 [Arabidopsis thaliana], one amino acid differen		2.1
putative protein	250158_at	2.1
ubiquitin C-terminal hydrolase-like protein ;supported by full-length cDNA: Ceres:8635.	250126_at	2.1
NAM (no apical meristem)-like protein; supported by cDNA: gi 14326464 gb AF385685.1 AF385685	249944 at	2.1
	249074 at	2.1
		2.1
	248480_at	
	248218_at	2.1
protein phosphatase 2C ABI2 (PP2C) (sp 004719)	247957_at	2.1
Fdr1 Cen - like protein Fdr1, Oryza sativa, EMBL:AF159883	247511_at	2.1
	247032_at	2.1
AP2 domain containing protein AP2 domain containing protein RAP2.4 - Arabidopsis thaliana, EMBL:AF003097	246939 at	2.1
glycine hydroxymethyltransferase - like protein glycine hydroxymethyltransferase, Solanum tuberosum, EMBL:Z25863; supported by cDNA: gi_1433		2.1
putative protein auxin-independent growth promoter - Nicotiana tabacum, PIR:A44226	246516_at	2.1
AtPP -like protein AtPP protein, Brassica napus, EMBL:BNA245479; supported by cDNA: gi 15293070 gb AY050969.1	246340 s at	2.1
putative protein	246285 at	2.1
hypothetical protein similar to putative ubiquitin GI:4415931 from [Arabidopsis thaliana]; supported by cDNA: gi 14334681 gb AY035014.1	245821 at	2.1
trehalose-6-phosphate synthase like protein ;supported by full-length cDNA: Ceres:95947.	245348_at	2.1
putative protein ATP/GTP nucleotide-binding protein, Leishmania infantum, EMBL:LIIMNBA; supported by cDNA: gi_14423543_gb_AF387009.1_AF	247521_at	2.1
putative ubiquitin fusion-degradation protein	266776_at	2
	251522 at	2
	257395 at	2
	267498_at	2
putative UDP-galactose-4-epimerase	267429_at	2
putative receptor-like protein kinase, ERECTA identical to GB:U47029 and GB:D83257; contains a protein kinase domain profile (PDOC00100); con	267376_at	2
ABC transporter (AtMRP2) identical to GB:AF014960; transports glutathione conjugates; supported by cDNA: gi 2909780 gb AF020288.1 AF0202		2
	267248 at	2
	266405_at	2
putative mitochondrial translation elongation factor G 2	266127_s_at	2
	265822 at	2
similar to flavin-binding monoxygenase-like protein (Z71258); similar to ESTs gb/R30018 and gb/H36886 similar to flavin-containing monoxygenase-like protein (Z71258); similar to ESTs gb/R30018 and gb/H36886 similar to flavin-containing monoxygenase-like protein (Z71258); similar to ESTs gb/R30018 and gb/H36886 similar to flavin-containing monoxygenase-like protein (Z71258); similar to ESTs gb/R30018 and gb/H36886 similar to flavin-containing monoxygenase-like protein (Z71258); similar to ESTs gb/R30018 and gb/H36886 similar to flavin-containing monoxygenase-like protein (Z71258); similar to ESTs gb/R30018 and gb/H36886 similar to flavin-containing monoxygenase-like protein (Z71258); similar to ESTs gb/R30018 and gb/H36886 similar to flavin-containing monoxygenase-like protein (Z71258); similar to ESTs gb/R30018 and gb/H36886 similar to flavin-containing monoxygenase-like protein (Z71258); similar to ESTs gb/R30018 and gb/H36886 similar to flavin-containing monoxygenase-like protein (Z71258); similar to ESTs gb/R30018 and gb/H36886 similar to flavin-containing monoxygenase-like protein (Z71258); similar to ESTs gb/R30018 and gb/H36886 similar to flavin-containing monoxygenase-like protein (Z71258); similar to ESTs gb/R30018 and gb/H36886 similar to flavin-containing monoxygenase-like protein (Z71258); similar to ESTs gb/R30018 and gb/H36886 similar to flavin-containing monoxygenase-like protein (Z71258); similar to ESTs gb/R30018 and gb/H36886 similar to flavin-containing monoxygenase-like protein (Z71258); similar to ESTs gb/R30018 and gb/R3001		2
hypothetical protein predicted by genemark.hmm	264748_at	2
putative isoamylase Similar to gi 1652733 glycogen operon protein GlgX from Synechocystis sp. genome gb D90908. ESTs gb H36690, gb AA7124		2
putative protein phosphatase 2C ;supported by full-length cDNA: Ceres:22316.	263711_at	2
unknown protein	263545 at	2
	263433 at	
putative myo-inositol 1-phosphate synthase ; supported by cDNA: gi_15450776_gb_270603415.1_		2
unknown protein ESTs gb H37032, gb R6425, gb Z34651, gb N37268, gb AA713172 and gb Z34241 come from this gene;supported by full-length cl	∠o∠o∪u_at	2

26S proteasome ATPase subunit, putative similar to 26S proteasome ATPase subunit GI:1395190 from [Spinacia oleracea]; supported by full-length 2		2
homeobox transcription factor Hox7, putative similar to homeobox transcription factor Hox7 GI:19486 from [Lycopersicon peruvianum]	261494_at	2
hypothetical protein predicted by genemark.hmm	261176_at	2
hypothetical protein predicted by genemark.hmm	261177_at	2
putative endochitinase	260560_at	2 2
putative two-component phosphorelay mediator similar to two-component phosphorelay mediators (ATHP1-3) GB:BAA37110, GB:BAA37111, GB:B. putative disease resistance protein similar to putative disease resistance protein GB:AAF01514 from clone F9F8	259329_at 258893_at	2
putative disease resistance protein similar to putative disease resistance protein GB:AF01514 from clone F9F8	258894 at	2
putative phospholipase D similar to phospholipase D1 GB:AAC78487 [Brassica oleracea], GB:Q38882 [Arabidopsis thaliana]; supported by cDNA: g		2
hypothetical protein	258245 at	2
heat shock transcription factor HSF1, putative similar to GB:S52641 from [Arabidopsis thaliana] (Plant Mol. Biol. 26, 353-362 (1994)); supported by (		2
unknown protein contains Pfam profiles: PF00036 EF hand (2 copies); supported by cDNA: gi_14334439_gb_AY034911.1_	257677_at	2
UDP-glucose glucosyltransferase, putative similar to UDP-glucose glucosyltransferase GI:3928543 from [Arabidopsis thaliana]; supported by cDNA:	255943_at	2
putative NAM-like protein	255585_at	2
hypothetical protein similar to C. elegans protein B0414.8, GenBank accession number 2088768	255560_at	2
5-adenylylsulfate reductase supported by full-length cDNA: Ceres:40330.	255284_at	2
putative ABC transporter similar to Guillardia theta ABC transporter, GenBank accession number AF041468; supported by cDNA: gi_15529142_gb_	_	2
putative microfibril-associated protein putative protein anthocyanin rhamnosyltransferase -Petunia x hybrida, PID:g454253	255093_s_at 255032_at	2 2
putative protein manifolyamin manifolyamin manifolyamin manifold and a straining a	254225 at	2
	253785 s at	2
glycine-rich protein glycine-rich cell wall structural protein - garden petunia, Pir2:A26099	253619 at	2
putative protein phospholipase D, Arabidopsis thaliana, gb:U84568; supported by cDNA: gi_11761141 dbj_AB031047.1 AB031047	253120 at	2
beta-galactosidase like protein ; supported by cDNA: gi_15810492_gb_AY056285.1_	253090_at	2
phosphoenolpyruvate carboxykinase (ATP) -like protein ; supported by cDNA: gi_13937136_gb_AF372922.1_AF372922	253041_at	2
Expressed protein ; supported by full-length cDNA: Ceres: 151603.	252365_at	2
putative protein	250946_at	2
serine/threonine-protein kinase	250527_at	2
putative protein predicted proteins, Arabidopsis thaliana and Drosophila melanogaster	250516_at	2
putative protein unnamed ORF cDNA FLJ10872, Homo sapiens, EMBL:AK001734; supported by cDNA: gi_14532679_gb_AY039964.1_ putative protein similar to unknown protein (gbIAAF00631.1);supported by full-length cDNA: Ceres:10299.	250402_at 250028_at	2 2
producerboxypeptidase-like protein (supported by full-length cDNA: Ceres:122449.	249860 at	2
tryptophan synthase beta chain	249515 at	2
	249316 s at	2
unknown protein ;supported by full-length cDNA: Ceres:253359.	248228 at	2
HEAT SHOCK PROTEIN 81-2 (HSP81-2) (sp P55737)	248045_at	2
ARF1-binding protein ; supported by cDNA: gi_2245393_gb_U89771.1_ATU89771	247468_at	2
putative protein similar to unknown protein (emb CAB77570.1)	247323_at	2
putative protein predicted proteins, Arabidopsis thaliana and Drosophila melanogaster	246897_at	2
putative protein predicted protein, Drosophila melanogaster	246139_at	2
calcium-dependent protein kinase ; supported by cDNA: gi_836941_gb_U20624.1_ATU20624	246044_at	2 2
unknown protein proline-rich protein, putative similar to proline-rich protein GI:3242079 from [Capsicum annuum]; supported by cDNA: gi 14334847 gb AY035097.1	245787_at	2
prometricit protein, putatve similar to prometricit protein GL3242019 from [Capacitan annuum], supported by CDNA. gr_14334347_gg_A103393.1	245528 at	2
putative beta-amylase ;supported by full-length cDNA: Ceres:36882.	245346 at	2
transcriptional adaptor like protein ; supported by cDNA: gi 15215639 gb AY050348.1	245288 at	2
putative protein similarity to UVB-resistance protein UVR8, Arabidopsis thaliana, PIR:T50662~Contains Regulator of chromosome condensation (RC	245210_at	2
ribosomal protein L22	244985_at	2
NADH dehydrogenase 49KDa protein	244937_at	2
putative RING zinc finger protein	267581_at	1.9
E2, ubiquitin-conjugating enzyme, putative	267456_at	1.9
putative alcohol dehydrogenase Expressed protein ; supported by full-length cDNA: Ceres: 34622.	267168_at 266537_at	1.9 1.9
Expressed protein , supported by fun-length CDNX. Ceres. 34022.	266278_at	1.9
putative peptide/amino acid transporter	266108 at	1.9
NADC homolog identical to GPJ1216074 gnl PID e225599 F20096;supported by full-length cDNA: Ceres:2877.	265738 at	1.9
unknown protein ; supported by full-length cDNA: Ceres: 122665.	265457_at	1.9
unknown protein predicted by genefinder	265344_at	1.9
similar to flavin-containing monooxygenase (sp P36366); similar to ESTs gb R30018, gb H36886, gb N37822, and gb T88100 similar to flavin-contai	265121_at	1.9
putative senescence-associated protein 12 ;supported by full-length cDNA: Ceres:40806.	264787_at	1.9
hypothetical protein contains similarity to glycogenin GI:165512 from [Oryctolagus cuniculus]	264476_at	1.9
putative ABC transporter related to multi drug resistance proteins and P-glycoproteins	263865_at	1.9
putative kinesin heavy chain unknown protein ;supported by full-length cDNA: Ceres:31655.	263751_at 263517_at	1.9 1.9
cold-regulated protein cor15a precursor; supported by cDNA: gi 14532457 gb AY039853.1	263517_at 263497_at	1.9
ent-kauren synthase, putative similar to ent-kaurene synthase Gl:3056725 from [Arabidopsis thaliana]; supported by cDNA: gi 3056724 gb AF034		1.9
unknown protein Location of est 278F3T7 (dplAA650690)	262521 at	1.9
amp-binding protein, putative similar to amp-binding protein GI:1903033 from [Brassica napus]; supported by cDNA: gi_15215765_gb_AY050412.1_		1.9
abscisic acid responsive elements-binding factor identical to abscisic acid responsive elements-binding factor GB:AAF27179 GI:6739274 from [Arabi	261613_at	1.9
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_15451209_gb_AY054685.1_	260987_at	1.9
MYB-related protein identical to GB:CAA90748 GI:1263093 from [Arabidopsis thaliana]	260784_at	1.9
phosphoenolpyruvate carboxylase 1, putative similar to phosphoenolpyruvate carboxylase 1 GI:2266947 from [Gossypium hirsutum]; supported by c	_	1.9
hypothetical protein similar to CCAAT-box-binding transcription factor GB:NP_005751 [Homo sapiens], GB:P53569 [Mus musculus]	260425_at	1.9
unknown protein putative ATPase contains Pfam profile: PF00004 ATPases associated with various cellular activities (AAA)	260162_at 260089_at	1.9 1.9
putative A rease contains relating noise, revolver An rease associated with various central advintes (AAA) feebly-like protein similar to feebly protein GBLS70648 [Lycopersicon esculentum] (tomato knockout developed into small fragile plants)	260069_at	1.9
hypothetical protein predicted by generant	259899 at	1.9
unknown protein ; supported by gonoath 12_gb_AF419560.1_AF419560	259418_at	1.9
unknown protein similar to hypothetical proteins GB:P73627, GB:Q55884, GB:P73121 [Synechocystis sp.]; supported by full-length cDNA: Ceres: 9{		1.9
putative histidyl tRNA synthetase similar to histidyl tRNA synthetase GB:NP_032240 [Mus musculus]	258601_at	1.9
putative leucine-rich repeat transmembrane protein kinase similar to leucine-rich repeat transmembrane protein kinase 1 GB:AAC27894 from [Zea m		1.9
putative casein kinase I similar to casein kinase I GB:CAA55396 from [Arabidopsis thaliana]; supported by cDNA: gi_15809823_gb_AY054179.1_	258300_at	1.9
	258186_s_at	1.9
UDP-glucose:indole-3-acetate beta-D-glucosyltransferase, putative similar to UDP-glucose:indole-3-acetate beta-D-glucosyltransferase GB:AAB584		1.9
putative cytochrome P450 similar to GB:005047 from [Catharanthus roseus]; supported by cDNA: gi_15292786_gb_AY050827.1_ putative A_ourparterize CoA liagos _ algost identical (1 aming a cid difference) is GB:AADV702 from Larbidgesis italiansi: supported by cDNA: gi_5	258094_at	1.9
putative 4-coumarate:CoA ligase 2 almost identical (1 amino acid difference) to GB:AAD47192 from [Arabidopsis thaliana]; supported by cDNA: gi_5 unknown protein	258047_at 257612_at	1.9 1.9
	u	

unknown protein contains Pfam profile:PF00439 bromodomain:Bromodomain	257146_at	1.9
CDPK-related kinase identical to GB:2AAD38059 from [Arabidopsis thaliana]	257024_at	1.9
hypothetical protein contains similarity to flavanone-3-hydroxylase GB:Q05965 from [Matthiola incana], contains Pfam profile: PF00671 Iron/Ascorba		1.9
hypothetical protein predicted by genscan+	256823_at	1.9
unknown protein	256577_at	1.9
hypothetical protein predicted by genscan+	256089_at	1.9
unknown protein ;supported by full-length cDNA: Ceres:36434.	256061_at	1.9
putative potassium/H+ antiporter	255686_at	1.9
putative ribosomal protein L19 similar to L19 from several species; supported by cDNA: gi_14423511_gb_F386993.1_AF386993	255520_at	1.9
UV-damaged DNA binding factor - like protein XPE UV-damaged DNA binding factor, Mus musculus, BAA84699	255226_at	1.9
	254833_s_at	1.9
3-hydroxyisobutyryl-coenzyme A hydrolase - like protein 3-hydroxyisobutyryl-coenzyme A hydrolase, Homo sapiens, U66669;supported by full-lengt		1.9
	254741_s_at	1.9
cytochrome P450 cytochrome P450, Arabidopsis thaliana; supported by cDNA: gi_15293092_gb_AY050980.1_	254562_at	1.9
putative protein zinc finger protein, Arabidopsis thaliana, PID:g2340088; supported by cDNA: gi_15982926_gb_AY057571.1_	254210_at	1.9
putative protein ; supported by cDNA: gi_11177136_dbj_AB050977.1_AB050977	253610_at	1.9
	253079_s_at	1.9
formamidase - like protein formamidase, Methylophilus methylotrophus, PIR2:S74213; supported by cDNA: gi_14334653_gb_AY035000.1_	253048_at	1.9
putative protein predicted protein. Arabidopsis thaliana	252016_at	1.9
putative protein predicted protein. Arabidopsis thaliana	251937_at	1.9
protein kinase -like protein protein kinase APK1, Arabidopsis thaliana, PIR:S28615;supported by full-length cDNA: Ceres:150889.	251922_at	1.9
putative protein leucine zipper-EF-hand containing transmembrane protein 1 - Mus musculus, EMBL:AF061026	251432_at	1.9
putative protein different MAP kinases	251165_at	1.9
ferritin 1 precursor ;supported by full-length cDNA: Ceres:1100.	251109_at	1.9
putative protein ABI3-interacting protein, Arabidopsis thaliana, EMBL:ATH251086; supported by cDNA: gi_14532637_gb_AY039943.1_	250971_at	1.9
sorting nextin-like protein	250714_at	1.9
putative protein similar to unknown protein (gb/AAF19552.1)	250303_at	1.9 1.9
transporter-like protein ;supported by full-length cDNA: Ceres:27439. kinase - like protein RING3 protein, Homo sapiens, EMBL:X96670; supported by cDNA: gi 16604680 gb AY059785.1	250252_at	1.9
	250191_at	
putative protein predicted protein, Arabidopsis thaliana putative protein similar to unknown protein (gb AAC80581.1)	250050_at	1.9
	249908_at 249869 at	1.9 1.9
acetyl-CoA synthetase-like protein	249009_at 249759_at	1.9
putative protein contains similarity to integral membrane protein	249759_at 249622 at	1.9
putative protein disease resistance protein-like non-consensus TT donor splice site at exon 1	249022_at 249320 at	1.9
usease resistance proteinnine non-consensus in dono spine sue at exon n N-carbamyl-L-amino acid amidohydrolase-like protein	249320_at 249103_at	1.9
	249103_at 248766 at	1.9
putative protein strong similarity to unknown protein (pir  E71441); supported by cDNA: gi_16974604_gb_AY060580.1_ putative protein contains similarity to unknown protein (gb AAF49898.1); supported by cDNA: gi_15724227_gb_AF412054.1_AF412054	248700_at 248549_at	1.9
putative protein contains similarity to nuclear movement protein nudC; supported by curve, gr (174421, gu = 144204, gu = 144204) putative protein contains similarity to nuclear movement protein nudC; supported by full-length cDNA: Ceres:38105.	248349_at 248258 at	1.9
Determinanty and the analysis of the set of	248200 at	1.9
Grinering and an	248200_at 248082_at	1.9
pyrophosphate-dependent phosphofructo-1-kinase-like protein ; supported by cDNA: gi_14532861_gb_AY040055.1_	240002_at 247983_at	1.9
propriez proteinase AALP identical to AALP protein GI:7230640 from [Arabidopsis thaliana]; similar to barley aleurain; supported by full-length cDNA:		1.9
succinate dehydrogenase flavoprotein alpha subunit (emb[CAA05025.1); supported by CDNA; gi_15010745_gb_AY045674.1	247060 at	1.9
atural resistance-associated macrophage protein ; supported by CDM: gi 6468013 gb AF202540.1 AF202540	247001_at	1.9
putative protein pyruvate water dikinase, Archaeoglobus fulgidus, PIR:F69338	246829 at	1.9
putative protein 68 kDa protein - Cicer arietinum, EMBL:AJ276420	246555 at	1.9
putative protein	246343 at	1.9
centromere protein homolog	245575 at	1.9
unknown protein	245028 at	1.9
RNA polymerase beta subunit-1	244998 at	1.9
PSI P700 apoprotein A1	245007 at	1.9
ferredoxin-NADP+ reductase - like protein ferredoxinNADP+ reductase, Mus musculus, PIR2:S60028	253479 at	1.8
unknown protein ; supported by cDNA; gi 15293114 gb AY050991.1	267602 at	1.8
hypothetical protein predicted by genscan; similar to GPI2623296/AC002409	267608 at	1.8
unknown protein	267518 at	1.8
putative alcohol dehydrogenase ; supported by cDNA: gi_16604706_gb_AY059798.1_	267181_at	1.8
putative PCI domain protein proteasome, COP9-complex and eIF3-domain protein; members of multi-protein complexes; supported by full-length cD	266310 at	1.8
cytochrome p450, putative similar to cytochrome p450 GI:438242 from [Solanum melongena]; supported by cDNA: gi_14334809_gb_AY035078.1_	266155_at	1.8
contains similarity to S. cerevisiae ADR1 gene (PID:g924931); supported by cDNA: gi_13605528_gb_AF361590.1_AF361590	265908_at	1.8
Expressed protein ; supported by full-length cDNA: Ceres: 465.	265913_at	1.8
unknown protein	265707_at	1.8
unknown protein ;supported by full-length cDNA: Ceres:41585.	265717_at	1.8
hypothetical protein predicted by genscan and genefinder, contains a Bem1/NCF1/PI3K domain (prosite:QDOC50195)	265535_at	1.8
NBS/LRR disease resistance protein, putative similar to NBS/LRR disease resistance protein GB:AAC26125 GI:3309619 from [Arabidopsis thaliana]		1.8
myrosinase binding protein, putative similar to myrosinase binding protein GI:1711295 from [Brassica napus]	265053_at	1.8
putative calmodulin-domain protein kinase CPK6 (calmodulin-domain protein kinase isoform 6, accession U31835); supported by cDNA: gi_122009{		1.8
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:25383.	264186_at	1.8
unknown protein	263972_at	1.8
hypothetical protein predicted by genefinder	263780_at	1.8
unknown protein similar to cell differentiation protein GB:AAC36682 from (Homo sapiens)	263685_at	1.8
	263532_s_at	1.8
cytoplasmic aconitate hydratase	263348_at	1.8
putative galactinol synthase ;supported by full-length cDNA: Ceres:124236.	263320_at	1.8
UDP-galactose 4-epimerase-like protein similar to proteins from many bacterial species including [Bacillus subtilis] and [Methanobacterium thermoau authority the second		1.8
putative protein kinase Strong similarity to gb X71057 protein kinase from Nicotaina tabacum and contains PF]00069 eukaryotic protein kinase doma contains at the strong similarity to gb X71057 protein kinase from Nicotaina tabacum and contains PF]00069 eukaryotic protein kinase doma contains euk		1.8
math3-like protein-related similar to MAK16 PROTEIN GB:P10962 GI:127112 from [Saccharomyces cerevisiae] (Proc. Natl. Acad. Sci. U.S.A. 85 (1	_	1.8
unknown protein EST gb/H77143 comes from this gene; supported by cDNA: gi_15293206_gb_AY051037.1_ bwortheride location splitter to hysteriation Dir ACE/SER0116 from (Arbitranic Hollowshi supported by cDNA: gi_	262570_at	1.8
hypothetical protein similar to hypothetical protein GB:AAF24581 GI:6692116 from [Arabidopsis thaliana]; supported by cDNA: gi_15724299_gb_AF4		1.8
ATP-dependent Clp protease proteolytic subunit (ClpR1) identical to nClpP5 GB:BAA82069 GI:5360595 from [Arabidopsis thaliana]; supported by full putative GTP-binding protein similar to NGP-1 GB:Q13823 from (Homo sapiens)		1.8
transcription factor TINY, putative similar to NGP-1 GB:Q13823 from (Homo sapiens)	261314_at 261059_at	1.8 1.8
transcription ractor first, putative similar to transcription ractor first GB-CAR04539 GL 22000 non (Prabiologis transmis), supported by full-length hypothetical protein similar to Pto kinase interactor 1 GB-AAC61805 GL 3668009 from [Lycopersicon esculentum]	261059_at 260924_at	1.8
inponiencal protein similar to rio kniase interactor i GB.AACO DOS GL3000009 into interactori scutenturing putative heme oxygenase similar to heme oxygenase GB.AACO2017 (Arabidopsis thaliana];supported by full-length cDNA: Ceres:101223.	260924_at 260396 at	1.8
putative nene dxygenase similar to neme dxygenase G5.AAD22101 [Analousis liainata],supported by luinengui CDVA. Ceres. 101223. putative heat shock protein similar to GB:CAB03279 from [Caenorhabditis elegans]	260396_at 260251_at	1.8
putative precision know protein similar to do zozoozz / similar politika protein know politika politika protein know politika	2600251_at 260036 at	1.8
unknown protein jsupported by full-length cDNA: Ceres: 13102.	260005_at	1.8
		-

	nown protein contains non-consensus GG donor splice site at exon2; modeled to est match.;supported by full-length cDNA: Ceres:124169.	260007_at	1.8
	othetical protein similar to GB:CAB55886 [Homo sapiens], GB:BAA09774 [Homo sapiens], GB:CAA87778 [Caenorhabditis elegans]	259759_at	1.8
	nown protein	259644_at	1.8
	ein kinase, putative similar to GI:7573596 from [Populus nigra]	259670_at	1.8
	sin-like protein contains Pfam profile: PF00658 Poly-adenylate binding protein, unique domain.; supported by cDNA: gi_15081708_gb_AY04824		1.8
	tive lectin contains Pfam profile: PF01419 jacalin-like lectin domain; similar to jasmonate inducible protein GB:Y11483 (Brassica napus), myrosii nown protein ;supported by full-length cDNA: Ceres:18355.	259381_s_at 259342 at	1.8 1.8
	town protein supported by functionengin concerns 10000.	259342_at 259169_at	1.8
	isom protein similar to unation protein source outputs inflation of the second statement of the second		1.8
	gives have being being being and the second grade being	258696 at	1.8
	othetical protein predicted by genemark.hmm	258525 at	1.8
	tive protein disulfide isomerase similar to protein disulfide isomerase GB:AAD55566 from [Volvox carteri f. nagariensis]	258329 at	1.8
hypo	othetical protein contains Pfam profile: PF01055 Glycosyl hydrolases family 31; supported by cDNA: gi_16648902_gb_AY059821.1_	258109_at	1.8
unkr	nown protein contains an RNase_PH domain; supported by full-length cDNA: Ceres:104182.	257857_s_at	1.8
	mase FKBP (ROF1) identical to rotamase FKBP (ROF1) GB:U49453 [Arabidopsis thaliana] (Mol. Gen. Genet. 252 (5), 510-517 (1996)); support	_	1.8
	A-binding protein, putative similar to GB:AAF32491 from [Triticum aestivum] (Mol. Cell. Biol. 19 (12), 8113-8122 (1999))	257291_at	1.8
	nooxygenase, putatve contains Pfam profile: PF01360 Monooxygenase	257240_at	1.8
	ole acid phosphatase, putative similar to purple acid phosphatase GB:CAA06921 [Ipomoea batatas]	257087_at	1.8
	thetical protein predicted by genscan+	257073_at 257044_at	1.8 1.8
	othetical protein predicted by genscan+ a-amylase, putative similar to beta-amylase GB:CAB58423 [Arabidopsis thaliana]; supported by cDNA: gi 14194172 gb AF367293.1 AF36729;		1.8
	thetical protein predicted by generark.htm; supported by cDNA: g16930516 gb_AF419612.1_AF419612	256858_at	1.8
	-family transcription factor, putative contains Pfam profile: PF00249: Myb-like DNA-binding domain	256198 at	1.8
	I transfer protein, putative similar to lipid transfer protein GI:9279661 from [Arabidopsis thaliana]; supported by cDNA: gi 15028044 gb AY0458;		1.8
trans	scription factor identical to transcription factor GI:304113 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:33016.	255953_at	1.8
	othetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:37923.	255900_at	1.8
	tive protein	255527_at	1.8
	ative WD-repeat protein similar to L. erythrorhizon LEC14B, GenBank accession number Q40153	255468_at	1.8
•	icted protein of unknown function	255418_at	1.8
	tive methyltransferase	254994_at	1.8
	/1 receptor kinase like protein CLAVATA1 receptor kinase, Arabidopsis th., PATX:G2160756	254515_at	1.8
	ative protein tripeptidyl-peptidase II, Homo sapiens, Pir:S54376	254433_at 254416 at	1.8 1.8
	ptor-like serine/threonine protein kinase ARK3 I26 protein :supported by full-length cDNA: Ceres:36866.	254343_at	1.8
	ressed protect is supported by full-tength CDNA: Ceres: 20948.	254278_at	1.8
	ibilo-like protein addominal segment formation protein pumilio - fruitfly, PIR2:A46221; supported by cDNA: gi_13430771_gb_AF360298.1_AF360		1.8
		253764 s at	1.8
	1 protein ; supported by cDNA: gi_16648890_gb_AY059815.1_	253759_at	1.8
sigr	al recognition particle receptor-like protein signal recognition particle receptor - Homo sapiens,PIR2:A29440	253625_at	1.8
puta	ative protein probable transcription regulator protein - Sorghum bicolor,PIR2:T03446;supported by full-length cDNA: Ceres:34151.	252323_at	1.8
	ydrin-like protein dehydrin Xero2 - Arabiodopsis thaliana, EMBL:U19536	252137_at	1.8
	ative protein various predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:4829.	252023_at	1.8
	iccino 1; supported by cDNA: gi_15810452_gb_4V056265.1_	251932_at	1.8
	G finger - like protein DNA-binding Mel-18 protein, Homo sapiens, PIR: JN0717supported by full-length cDNA: Ceres:20931.	251897_at	1.8
	C transporter-like protein putative multi resistance protein mrp - Arabidopsis thaliana, EMBL:ATMRPPROT	251503_at 250960_at	1.8 1.8
•	tive protein density lipoprotein B-like protein	250900_at 250112_at	1.8
	lown protecting supported by cDNA: gi 15912298 gb AY056427.1	249886_at	1.8
	rin repeat rotein EMB506; supported by cDNA: gi_5011311_gb_AF026167.1_AF026167	249404_at	1.8
	ase resistance protein-like	248848 at	1.8
	tive protein contains similarity to unknown protein (gb AAF56975.1)	248458_at	1.8
heat	shock protein (emb CAA72514.1)	248043_s_at	1.8
unkr	nown protein ;supported by full-length cDNA: Ceres:21044.	247990_at	1.8
	-galactosidase (emb CAB64746.1)	247348_at	1.8
	tive protein similar to unknown protein (sp P55606); supported by cDNA: gi_14190422_gb_AF378889.1_AF378889	247077_at	1.8
	tive protein protein At2g40060 - Arabidopsis thaliana, EMBL:AF002109;supported by full-length cDNA: Ceres:93427.	246305_at	1.8
•	tive protein	246247_at	1.8
	opeptidase-like protein ; supported by cDNA: gi_13430673_gb_AF360249.1_AF360249 /-like protein ; supported by cDNA: gi_16323158_gb_AY057683.1_	246219_at 246222_at	1.8 1.8
		245989_s_at	1.8
	thetical protein	245482 at	1.8
	ase resistance RPP5 like protein	245451_at	1.8
	tive protein	245427_at	1.8
•	ase alpha subunit	245024_at	1.8
	somal protein S11	244979_at	1.8
	tive cytochrome P450	267567_at	1.7
	amate-4-hydroxylase molecular marker C4H (GB:U71080); supported by cDNA: gi_1773288_gb_U71081.1_ATU71081	267470_at	1.7
		267335_s_at	1.7
	ar to late embryogenesis abundant proteins ; supported by full-length cDNA: Ceres: 2450.	267212_at	1.7
•	tive cytochrome P450 nown protein	266995_at 266757_at	1.7 1.7
	tive arginine N-methyltransferase	266757_at 266687_at	1.7
	winase (ATHXK2); supported by cDNA: gi 1899024 gb U28215.1 ATU28215	266702 at	1.7
	tive glutathione S-transferase : supported by cDNA: gi 14423533 gb AF387004.1 AF387004	266267 at	1.7
		266036_s_at	1.7
		265388_s_at	1.7
	tive MYB family transcription factor; supported by cDNA: gi_1020156_gb_U26937.1_ATU26937	265359_at	1.7
	tive RNA-binding protein ; supported by cDNA: gi_6650522_gb_AF101056.1_AF101056	265266_at	1.7
	nown protein	265273_at	1.7
	othetical protein contains similarity to zinc finger protein rts2 GB:U16133 GI:563244 from [Saccharomyces cerevisiae]; supported by cDNA: gi_13		1.7
	tive protein kinase, ADK1 dual specificity kinase 1; Location of ESTs 184A2XP 3, gb]AA651408 and est 184A2T7, gb]H37603, 99%+ identity w		1.7
puta	ative phosphoglucomutase similar to GB:AAD13031 and GB:AAC50049, location of ESTs gb/W43354, gb/N37499 and gb/N96251; supported by	_	1.7
puta puta		264776 at	1.7
puta puta unkr	nown protein location of EST gb T46445		
puta puta unkr hypo	nown protein location of EST gb T46445 othetical protein contains similarity to nuclear protein GI:1236985 from [Homo sapiens]; supported by cDNA: gi_14423425_gb_AF386950.1_AF38	264486_at	1.7
puta puta unkr hypo puta	nown protein location of EST gb T46445 othetical protein contains similarity to nuclear protein GI:1236985 from [Homo sapiens]; supported by cDNA: gi_14423425_gb_AF386950.1_AF3i tive beta-galactosidase	264486_at 264078_at	1.7
puta puta unkr hypo puta puta	nown protein location of EST gb T46445 othetical protein contains similarity to nuclear protein GI:1236985 from [Homo sapiens]; supported by cDNA: gi_14423425_gb_AF386950.1_AF38	264486_at	

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hypothetical proton similar to https://www.commission.com/sci.post.post.post.post.post.post.post.post	unknown protein ;supported by full-length cDNA: Ceres:21223.	263110_at	1.7
palate healthook protein summary on granularity to glp/27014 head-thook potent from Autabogsis Palanian and is a member of the PT[00121 Head Pote) 202017, at 100000000000000000000000000000000000	NADP-isocitrate dehydrogenase, putative similar to NADP-isocitrate dehydrogenase GI:5764653 from [Citrus limon]; supported by cDNA: gi_127443	262962_at	1.7
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sionage protein, pulative similar to GBCAAS378 from [Discores expensing (Plant Not) Ibil. 28 (3), 369-380 (1995)); supported by CDNA: gL, 158 20056, at 17. prophene is pass minor to mark prevent the PV1606 Th/1PV1 tramins, supported by Uhl-length CDNA: Ceres: 3034. Discore is passed to mark prevent the PV1606 Th/1PV1 tramins, supported by Uhl-length CDNA: Ceres: 3034. Discore is passed to mark prevent by CDNA: gL, 2593917, gb, AF331068, J, AF331068 Discore is passed by CDNA: gL, 2593917, gb, AF331068, J, AF331068 Discore is passed by CDNA: gL, 2593917, gb, AF331068, J, AF331068 Discore is passed by CDNA: gL, 2593917, gb, AF331068, J, AF331068 Discore is passed by CDNA: gL, 2593917, gb, AF331068, J, AF331068 Discore is passed by CDNA: gL, 2593917, gb, AF331068, J, AF331068 Discore is passed by CDNA: gL, 2593917, gb, AF331068, J, AF331068 Discore is passed by CDNA: gL, 2593917, gb, AF331068, J, AF331068 Discore is passed by CDNA: gL, 25959, at 17. Discore is passed by CDNA: gL, 25950, at 17. Discore is passed by CDNA: gL, 25050, at 17. Discore is passe	hypothetical protein predicted by genemark.hmm	260647_at	1.7
<ul> <li>hypothetical protein contains PBm profile FP01965 Thui/PBn family-supported by full-ength CDNA. Cores: 10715.</li> <li>20016 J. T. Junkowski PBM profile FP01965 Thui/PBn family-supported by full-ength CDNA. Cores: 20054.</li> <li>200173 J. T. Zapaterki Team profile FP01965 Phase component of a two subout chromatin emodeling complexes poneling C125833. supported by CDNA. gp. 125877.</li> <li>200174 J. T. Zapaterki Team Profile FP01960 WD domain.</li> <li>200183 J. T. Zapaterki Team Profile FP00400 WD domain. G-beta repeat ("copies)</li> <li>200183 J. T. Zapaterki Team Profile FP00400 WD domain. G-beta repeat ("copies)</li> <li>200183 J. T. Zapaterki Team Profile FP00400 WD domain. G-beta repeat ("copies)</li> <li>200183 J. T. Zapaterki Team Profile FP00400 WD domain. G-beta repeat ("copies)</li> <li>200183 J. T. Zapaterki Team Profile FP00400 WD domain. G-beta repeat ("copies)</li> <li>200184 J. Zapaterki Team Profile FP00400 WD domain. G-beta repeat ("copies)</li> <li>200184 J. Zapaterki Team Profile FP00400 WD domain. G-beta repeat ("copies)</li> <li>200184 J. Zapaterki Team Profile FP00400 WD domain.</li> <li>200184 J. Zapaterki Team Profile FP00400 WD domain.</li> <li>200184 J. Zapaterki Team Profile FP00400 WD domain.</li> <li>200184 J. Zapaterki Team Profile FP00470 WD domain.</li> <li>200184 J. Z</li></ul>			1.7
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putative protein GTP-binding proteins - different species249434_at1.7putative protein strong similarity to unknown protein (pir][T05325); supported by cDNA: gi_13605502_gb_AF361577.1_AF361577249011_at1.7putative protein similar to unknown protein (sp P74035); supported by cDNA: gi_15292692_gb_AY050780.1_248986_at1.7Dnal protein-like ; supported by full-length cDNA: Ceres:14006.248579_at1.7putative protein similar to unknown protein (pir [T09559); supported by cDNA: gi_15810212_gb_AY056121.1_248306_at1.7PP2A regulatory subunit ; supported by full-length cDNA: Ceres:19116.248300_at1.7putative protein similar to unknown protein (pir [T05643)248065_at1.7putative protein kinase ; supported by cDNA: gi_1551039576.1_24705512.1_24705_atprotein kinase ; supported by cDNA: gi_15451139_gb_AY054650.1_247384_at1.7putative protein kinase ; supported by cDNA: gi_16974578_gb_AY060555.1_247384_at1.7g rotein-coupled receptor-like protein ; supported by cDNA: gi_15451139_gb_AY054650.1_247364_at1.7putative similar to enknown protein (pir [T05643]24705_at1.7protein kinase ; supported by cDNA: gi_16974578_gb_AY060555.1_247384_at1.7G rotein-coupled receptor-like protein ; supported by cDNA: gi_15451139_gb_AY054650.1_24705_at1.7putative similar to enknown protein (pir [T05643]24705_at1.7putative protein Leaf protein, pharbitis nil, EMBL:D8510124630_at1.7g rotein-coupled receptor-like protein ; supported by cDNA: gi_15451139_gb_AY054650.1_247364_	putative protein contains similarity to unknown protein (emb CAB89315.1); supported by cDNA: gi_15451067_gb_AY054614.1_	249863_at	1.7
putative protein strong similarity to unknown protein (pir  T05325); supported by cDNA: gi_13605502_gb_AF361577.1_AF361577         249011_at         1.7           putative protein contains similarity to cyclin         248988_at         1.7           putative protein contains similarity to cyclin         248906_at         1.7           putative protein similar to unknown protein (sp P74035); supported by cDNA: gi_15292692_gb_AY050780.1_         248906_at         1.7           DnaJ protein-like ; supported by full-length cDNA: Ceres:14006.         248779_at         1.7           mitotic checkpoint protein-like         248579_at         1.7           putative protein similar to unknown protein (pir  T09559); supported by cDNA: gi_15810212_gb_AY056121.1_         248300_at         1.7           PP2A regulatory suburit ; supported by full-length cDNA: Ceres:19116.         248300_at         1.7           putative protein similar to unknown protein (pir  T09563)         248663_at         1.7           putative protein         241517481_gb_AY039576.1_         24765_at         1.7           RNA helicase ; supported by cDNA: gi_14517481_gb_AY039576.1_         247384_at         1.7           protein kinase ; supported by cDNA: gi_15451139_gb_AY054650.1_         247384_at         1.7           putative protein cere forcein, Pharbitis nil, EMBL:D85101         24702_at         1.7           epsilon-adaptin, putative similar to epsilo	putative protein DNA DAMAGE-RESPONSIVE PROTEIN 48, Saccharomyces cerevisiae, EMBL:SCDDR48A; supported by cDNA: gi_16604363_gb	249416_at	1.7
putative protein contains similarity to cyclin248988_at1.7putative protein similar to unknown protein (sp P74035); supported by cDNA: gi_15292692_gb_AY050780.1_248906_at1.7DnaJ protein-like ; supported by full-length cDNA: Ceres:14006.248739_at1.7mitotic checkpoint protein-like248310_at1.7putative protein similar to unknown protein (pir  T09559); supported by cDNA: gi_15810212_gb_AY056121.1_248379_at1.7PP2A regulatory subunit ; supported by full-length cDNA: Ceres:19116.248300_at1.7putative protein similar to unknown protein (pir  T05643)248065_at1.7putative proteingi_14517481_gb_AY039576.1_24765_at1.7RNA helicase ; supported by cDNA: gi_15451139_gb_AY054650.1_247384_at1.7protein-kinase ; supported by cDNA: gi_15451139_gb_AY054650.1_247775_at1.7putative protein kinase ; supported by cDNA: gi_164578_gb_AY064650.1_24634_at1.7epsilon-adaptin, putative similar to epsilon-adaptin Gl:5689377 from [Homo sapiens]24634_at1.7		_	1.7
putative protein similar to unknown protein (sp P74035); supported by cDNA: gi_15292692_gb_AY050780.1_         248906_at         1.7           DnaJ protein-like ; supported by full-length cDNA: Ceres:14006.         248739_at         1.7           mitotic checkpoint protein-like         248579_at         1.7           putative protein similar to unknown protein (pir [T09559); supported by cDNA: gi_15810212_gb_AY056121.1_         248300_at         1.7           PP2A regulatory subunit ; supported by full-length cDNA: Ceres:19116.         248006_at         1.7           putative protein similar to unknown protein (pir [T05643)         248065_at         1.7           putative protein         2481065_at         1.7           putative protein         248065_at         1.7           putative protein         24762_at         1.7           protein kinase ; supported by cDNA: gi_14517481_gb_AY039576.1_         247645_at         1.7           protein-coupled receptor-like protein ; supported by cDNA: gi_15451139_gb_AY054650.1_         247175_at         1.			1.7
DnaJ protein-like ;supported by full-length cDNA: Ceres:14006.         248739_at         1.7           mitotic checkpoint protein-like         248579_at         1.7           putative protein similar to unknown protein (pir  T09559); supported by cDNA: gi_15810212_gb_AY056121.1_         248310_at         1.7           PP2A regulatory subunit ;supported by full-length cDNA: Ceres:19116.         248005_at         1.7           putative protein similar to unknown protein (pir  T05643)         247629_at         1.7           putative protein         247629_at         1.7           RNA helicase ; supported by cDNA: gi_14517481_gb_AY039576.1_         247629_at         1.7           protein-coupled receptor-like protein ; supported by cDNA: gi_15451139_gb_AY054650.1_         247384_at         1.7           putative protein Leaf protein, putative similar to epsilon-adaptin Gl:5689377 from [Homo sapiens]         246034_at         1.7			
mitotic checkpoint protein-like         248579 at         1.7           putative protein similar to unknown protein (pir  T09559); supported by cDNA: gi_15810212_gb_AY056121.1_         248310_at         1.7           PP2A regulatory subunit ; supported by full-length cDNA: Ceres:19116.         248300_at         1.7           putative protein similar to unknown protein (pir  T05643)         248065_at         1.7           putative protein         247629_at         1.7           RNA helicase ; supported by cDNA: gi_14517481_gb_AY039576.1_         247629_at         1.7           protein kinase ; supported by cDNA: gi_16974578_gb_AY060555.1_         247384_at         1.7           G protein-coupled receptor-like protein ; supported by cDNA: gi_15451139_gb_AY054650.1_         24702_at         1.7           utative protein Leaf protein, plarbitis nil, EMBL:D85101         24634_at         1.7           epsilon-adaptin, putative similar to epsilon-adaptin Gl:5689377 from [Homo sapiens]         246634_at         1.7		_	
putative protein similar to unknown protein (pir  T09559); supported by cDNA: gi_15810212_gb_AY056121.1_         248310_at         1.7           PP2A regulatory subunit ; supported by full-length cDNA: Ceres:19116.         248300_at         1.7           putative protein similar to unknown protein (pir  T09559); supported by cDNA: Ceres:19116.         248065_at         1.7           putative protein         248065_at         1.7           RNA helicase ; supported by cDNA: gi_14517481_gb_AY039576.1_         24765_at         1.7           protein kinase ; supported by cDNA: gi_15974578_gb_AY060555.1_         247384_at         1.7           G protein-coupled receptor-like protein ; supported by cDNA: gi_15451139_gb_AY054650.1_         24702_at         1.7           uputative protein Leaf protein, pirabits nil, EMBL:D85101         246034_at         1.7           epsilon-adaptin, putative similar to epsilon-adaptin Gl:5689377 from [Homo sapiens]         24634_at         1.7		_	
PP2A regulatory subunit ;supported by full-length cDNA: Ceres:19116.         248300_at         1.7           putative protein similar to unknown protein (pir [T05643)         248065_at         1.7           putative protein similar to unknown protein (pir [T05643)         248065_at         1.7           putative protein RNA helicase; supported by cDNA: gi_14517481_gb_AY039576.1_         24765_at         1.7           protein kinase; supported by cDNA: gi_16974578_gb_AY06055.1_         247465_at         1.7           G protein-coupled receptor-like protein; supported by cDNA: gi_15451139_gb_AY054650.1_         247175_at         1.7           putative protein Leaf protein, Phatbits inil, EMBL:D85101         246934_at         1.7           epsilon-adaptin, putative similar to epsilon-adaptin GI:5689377 from [Homo sapiens]         246634_at         1.7			
putative protein similar to unknown protein (pir [T05643)         248065_at         1.7           putative protein         247629_at         1.7           RNA helicase ; supported by cDNA: gi_14517481_gb_AY039576.1_         247629_at         1.7           protein kinase ; supported by cDNA: gi_16974578_gb_AY060555.1_         247384_at         1.7           G protein-coupled receptor-like protein ; supported by cDNA: gi_15451139_gb_AY054650.1_         247175_at         1.7           utative protein Leaf protein, pharbitis nil, EMBL:085101         246031_at         1.7           epsilon-adaptin, putative similar to epsilon-adaptin GI:5689377 from [Homo sapiens]         24634_at         1.7 <td></td> <td>_</td> <td></td>		_	
putative protein         247629 at         1.7           RNA helicase ; supported by cDNA: gi_14517481_gb_AY039576.1_         247465_at         1.7           protein kinase ; supported by cDNA: gi_16974578_gb_AY060555.1_         247384_at         1.7           G protein-coupled receptor-like protein ; supported by cDNA: gi_15451139_gb_AY054650.1_         247175_at         1.7           utative protein Leaf protein, pharbitis nil, EMBL:D85101         246901_at         1.7           epsilon-adaptin, putative similar to epsilon-adaptin GI:5689377 from [Homo sapiens]         246634_at         1.7		_	1.7
RNA helicase ; supported by cDNA: gi_14517481_gb_AY039576.1_         247465_at         1.7           protein kinase ; supported by cDNA: gi_16974578_gb_AY060555.1_         247384_at         1.7           G protein-coupled receptor-like protein ; supported by cDNA: gi_15451139_gb_AY054650.1_         247175_at         1.7           utative protein Leaf protein, Pharbitis nil, EMBL:D85101         246901_at         1.7           epsilon-adaptin, putative similar to epsilon-adaptin GI:5689377 from [Homo sapiens]         246634_at         1.7			1.7
protein kinase ; supported by cDNA: gi_16974578_gb_AY060555.1_         247384_at         1.7           G protein-coupled receptor-like protein ; supported by cDNA: gi_15451139_gb_AY054650.1_         247175_at         1.7           putative protein Leaf protein, Pharbitis nil, EMBL:D85101         246901_at         1.7           epsilon-adaptin, putative similar to epsilon-adaptin GI:5689377 from [Homo sapiens]         24634_at         1.7			1.7
G protein-coupled receptor-like protein ; supported by cDNA: gi_15451139_gb_AY054650.1247175_at1.7putative protein Leaf protein, Pharbitis nil, EMBL:D85101246901_at1.7epsilon-adaptin, putative similar to epsilon-adaptin GI:5689377 from [Homo sapiens]246634_at1.7			1.7
epsilon-adaptin, putative similar to epsilon-adaptin GI:5689377 from [Homo sapiens] 246634_at 1.7	G protein-coupled receptor-like protein ; supported by cDNA: gi_15451139_gb_AY054650.1_		1.7
			1.7
PPR-repeat protein, putative contains multiple PPR domains: PF01535: PPR repeat 246313_at 1.7			1.7
	PPR-repeat protein, putative contains multiple PPR domains: PPU1535: PPR repeat	∠40313_at	1.7

putative protein predicted proteins, Arabidopsis thaliana and others	246180_at	1.7
luminal binding protein ; supported by cDNA: gi_1303694_dbj_D84414.1_ATHBIPA sucrose-phosphate synthase -like protein sucrose-phosphate synthase isoform 1, Citrus unshiu, PIR:S72648	245956_s_at 245904 at	1.7 1.7
sucrose-priospinate synthesis are protein sucrose-priospinate synthase isoloninin, citicus unsind, FIR.372046 allergen like protein	245904_at 245463 at	1.7
putative protein disulfide-isomerase	245175_at	1.7
unknown protein	245054_at	1.7
cytochrome b6-f complex, subunit V	244966_at	1.7
putative protein strong similarity to unknown protein (gb AAF16763.1) putative protein various predicted proteins, Arabidopsis thaliana	249086_at 246899_at	1.6 1.6
photomorphogenesis repressor (COP1) identical to GB:L24437; supported by cDNA: gi 402684 gb L24437.1 ATHCOP1A	267640 at	1.6
unknown protein ; supported by full-length cDNA: Ceres:36855.	267503_at	1.6
putative U5 small nuclear ribonucleoprotein, an RNA helicase	267454_at	1.6
putative potassium transporter Expressed protein ; supported by cDNA: gi 14334701 gb AY035024.1	267423_at 266802_at	1.6 1.6
Laplessed protein, supported by Christian (g) (+354701_g0_A105024.1_	266748 at	1.6
unknown protein	266628_at	1.6
putative phospholipid cytidylyltransferase	266359_at	1.6
putative pumilio/Mpt5 family RNA-binding protein	266288_s_at	1.6
unknown protein ;supported by full-length cDNA: Ceres:39558. putative calmodulin-binding protein ; supported by cDNA: gi_15983494_gb_AF424622.1_AF424622	266170_at 266019_at	1.6 1.6
putative prolylcarboxypeptidase	265990 at	1.6
unknown protein ;supported by full-length cDNA: Ceres:98881.	265959_at	1.6
similar to flavin-binding monooxygenase (Z71258); similar to ESTs gb R30018, gb T23015, and gb T88100 contains similarity to flavin-containing mono-		1.6
unknown protein hypothetical protein predicted by genemark.hmm	264563_s_at 264472_at	1.6 1.6
hypothetical protein Contains similarity to transcription initiation factor IIE, alpha subunit gb/X63468 from Homo sapiens; supported by cDNA; gi 158		1.6
putative homeodomain transcription factor ; supported by cDNA: gi 13877516 gb AF353094.1 AF353094	263956_at	1.6
enolase (2-phospho-D-glycerate hydroylase); supported by cDNA: gi_15809969_gb_AY054253.1_	263924_at	1.6
phosphoenolpyruvate carboxylase	263491_at	1.6
RSH3 (ReIA/SpoT homolog) identical to RSH3 (ReIA/SpoT homolog) GI:7141308 from [Arabidopsis thaliana]; supported by cDNA: gi_7141307_gb_/ dynamin, putative similar to dynamin-1 SP:P21575 [Rattus norvegicus (Rat)]; supported by full-length cDNA: Ceres:12880.	263159_at 262837 at	1.6 1.6
dynamin, putative similar to dynamini - 05.72.1073 (Katus norvegicus (Katij),supported by iun-lengin conve. Ceres, 1266). hypothetical protein predicted by genscan	262766 at	1.6
putative cytochrome P450 monooxygenase strong similarity to gb/X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00		1.6
putative cytochrome P450 similar to gb AF069494 cytochrome P450 from Sinapis alba and is a member of the PF 00067 Cytochrome P450 family. E	262717_s_at	1.6
putative pattern formation protein EMB30 highly similar to GB:Q42510; supported by cDNA: gi_1209630_gb_U36432.1_ATU36432	262614_at	1.6
CCAAT-binding factor B subunit homolog, putative similar to CCAAT-binding factor B subunit homolog GI:1173615 from (Brassica napus); supporter hypothetical protein similar to putative disease resistance protein GB:CAB40943 GI:4586107 from [Arabidopsis thaliana]	_	1.6 1.6
nyponetical protein similar to putative disease esistance protein do czadowa di 4300 tor indir (Arabidopsis tranana) unknown protein identical to unknown protein GB:AAD55492 (Arabidopsis thaliana)	262326_at 262289_at	1.6
hypothetical protein predicted by genemark.hmm	262238_at	1.6
unknown protein ; supported by cDNA: gi_15215759_gb_AY050409.1_	261863_at	1.6
phosphoethanolamine N-methyltransferase, putative similar to GB:AAF61950 from [Spinacia oleracea]; supported by cDNA: gi_16226648_gb_AF42		1.6
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:98874.	261124_at 261112_at	1.6 1.6
unknown protein homeodomain protein BELL1, putative similar to GB:AAB05099 from [Arabidopsis thaliana] (Cell 83 (5), 735-742 (1995));supported by full-length cD		1.6
hypothetical protein predicted by genemark.hmm	260922 at	1.6
unknown protein ;supported by full-length cDNA: Ceres:21241.	260868_at	1.6
putative urease similar to urease GB:225714 [Canavalia ensiformis]	260189_at	1.6
NAM-like protein similar to NAM (no apical meristem) GB:CAA63101 from [Petunia x hybrida] subtitue troplane 6 heraphate subthase similar to trabelace 6 heraphate subthase CB:CAA60270 (Arabidapsis balancia to appendix to trabelace 6 heraphate subthase)	260203_at	1.6 1.6
putative trehalose-6-phosphate synthase similar to trehalose-6-phosphate synthase GB:CAA69879 [Arabidopsis thaliana]; supported by cDNA: gi_15 unknown protein ;supported by full-length cDNA: Ceres:19761.	259895 at	1.6
Expressed protein ; supported by full-length cDNA: Ceres: 30602.	259789_at	1.6
GRAB1-like protein similar to GRAB1 protein GB:CAA09371, a novel member of the NAC domain family;supported by full-length cDNA: Ceres:3647		1.6
unknown protein ; supported by cDNA: gi_15028084_gb_AY045899.1_	259230_at	1.6
unknown protein similar to possible apospory-associated protein C GB:Q40784 [Pennisetum ciliare];supported by full-length cDNA: Ceres:41354. digalactosyldiacylglycerol synthase identical to digalactosyldiacylglycerol synthase GB:AAD42378 [Arabidopsis thaliana]; supported by cDNA: gi 535	259186_at	1.6 1.6
ugalactus/inlacy/groteiors/minase deminate to ugalactus/inlacy/groteiors/inlace co-Anderson (maintaina), supported by control, g_ou- putative MAP3K epsilon protein kinase similar to MAP3K epsilon protein kinase GB:CAA12272 [Arabidopsis thaliana], GB:CAA54520 [Brassica nap		1.6
unknown protein	258362_at	1.6
kinesin-like protein similar to kinesin heavy chain member 2 GB:NP_032468 from [Mus musculus]; supported by cDNA: gi_15450500_gb_AY052352	_	1.6
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:116381.	257855_at	1.6
unknown protein Expressed protein ; supported by cDNA: gi 15215805 gb AY050432.1	257084_at 257007_at	1.6 1.6
UDP-glucose dehydrogenase, putative UDP-glucose 6-dehydrogenase (UDPGDH) GB:Q96558 from [Glycine max];supported by full-length cDNA: (		1.6
Eukaryotic translation initiation factor 5, putative Eukaryotic translation initiation factor 5 [Zea mays] GI:4160402; supported by cDNA: gi_15810338_	· · · · <u> </u>	1.6
unknown protein	256451_s_at	1.6
unknown protein ;supported by full-length cDNA: Ceres:33407.	256440_at	1.6
guanine nucleotide regulatory protein, putative similar to guanine nucleotide regulatory protein GI:3461880 from [Mus musculus] putative myb-related DNA-binding protein	256119_at 255614_at	1.6 1.6
hypothetical protein	255588 at	1.6
putative protein LEA protein , Cicer arietinum, AJ224518	254716_at	1.6
putative protein (fragment) ATP(GTP)-binding protein, Homo sapiens, AJ010842;supported by full-length cDNA: Ceres:6952.	254375_at	1.6
potassium channel protein AKT3 ; supported by cDNA: gi_1100897_gb_U40154.1_ATU40154 nucleosome assembly protein I-like protein ; supported by cDNA: gi_15450807 gb_AY054484.1	254305_at	1.6
pyrophosphate-dependent phosphofructo-1-kinase pyrophosphate-dependent phosphofructo-1-kinase, Prunus armeniaca, U93272; supported by CE	253996_at 253987_at	1.6 1.6
265 proteasome subunit 4-like protein Drosophila melanogaster 265 proteasome subunit 4 ATPase, PID:g1066065; supported by cDNA: gi 143346		1.6
putative protein hypothetical protein T29E15.27 - Arabidopsis thaliana,PID:g3738334	253586_s_at	1.6
putative protein ; supported by cDNA: gi_14334555_gb_AY035182.1_	253424_at	1.6
Expressed protein ; supported by CDNA: gi_13358221_gb_AF325032 2_AF325032	253293_at	1.6
putative aldehyde dehydrogenase aldehyde dehydrogenase (NAD+), Rattus norvegicus, PIR2:A41028; supported by cDNA: gi_15451105_gb_AY05 MYB-like protein myb-related protein Y49, Arabidopsis thaliana, PIR:S58292	253237_at 253219_at	1.6 1.6
Mi Delike protein intro-related protein 199, Radiopsis Inaliana, Firk-30632 dhaJ-like protein CAJ1 protein, Saccharomyces cerevisiae, PIR2:S48085	252935 at	1.6
putative protein Human (H326) translated mRNA - Homo sapiens, EMBL:HS06631	252587_at	1.6
putative protein predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_14532663_gb_AY039956.1_	252467_at	1.6
putative protein putative hydrolyse - Arabidopsis thaliana, PID:g4191785	252423_at	1.6
putative protein activating signal cointegrator 1 - Homo sapiens, EMBL:AF168418; supported by full-length cDNA: Ceres:13265. putative protein KIAA0226 gene product - Homo sapiens,PID:d1013904; supported by cDNA: gi 14532611 gb AY039930.1	252424_at 252353_at	1.6 1.6
	2522555_at 252291_s_at	1.6
vacuolar sorting protein 35 homolog vacuolar sorting protein 35 - Homo sapiens, EMBL:AF191298	252150_at	1.6

beta-ketoacyl-ACP reductase - like protein beta-ketoacyl-ACP reductase, Cuphea lanceolata, EMBL:X64566 PROBABLE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 8 ; supported by cDNA: gi 2789659 gb AF040102.1 AF040102		
PROBABLE FUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBLINIT 8 supported by CDNA of 2789659 ob AE040102.1 AE040102	251780 s at	1.6
	251738 at	1.6
putative protein DOC4, Mus musculus, AF059485	251594 at	1.6
putative protein putative protein BcDNA.GH03694 - Drosophila melanogaster, EMBL:AF181626	251316 s at	1.6
tubulin gamma-1 chain	251331 s at	1.6
putative protein predicted protein, Arabidopsis thaliana	251145 at	1.6
ankyrin - like protein ankyrin G119, Homo sapiens, EMBL:HSU43965	250998 at	1.6
glucuronosyl transferase-like protein	250750 at	1.6
elongation factor 1B alpha-subunit (emb[CAB64729.1)	250304 at	1.6
ABA-responsive protein - like ABA-responsive protein, Hordeum vulgare, EMBL:AF026538	250279 at	1.6
chaperonin 60 alpha chain - like protein chaperonin 60 alpha chain precursor, garden pea, PIR:T06518	249977 at	1.6
squamosa promoter binding protein-like 7; supported by cDNA: gi 13605911 gb AF367355.1 AF367355	249960 at	1.6
putative protein predicted protein, Drosophila melanogaster	249528_at	1.6
putative protein contains similarity to CONSTANS homologs	248744_at	1.6
putative protein similar to unknown protein (gb/AAD20092.1)	248668_at	1.6
putative protein similar to unknown protein (ref NP_014050.1)	248308_at	1.6
putative protein similar to unknown protein (pir  T02891);supported by full-length cDNA: Ceres:112574.	248271_at	1.6
E2, ubiquitin-conjugating enzyme, putative ;supported by full-length cDNA: Ceres:10022.	247999 at	1.6
phosphatidylserine decarboxylase	247940_at	1.6
GTP binding protein-like	247891_at	1.6
ubiquitin-specific protease 23 (UBP23), putative similar to GI:11993486; supported by cDNA: gi_11993485_gb_AF302671.1_AF302671	247838_at	1.6
1-aminocyclopropane-1-carboxylate oxidase - like protein 1-aminocyclopropane-1-carboxylate oxidase kidney bean, PIR:T10818; supported by cDN	1 247679_at	1.6
putative protein gcpE protein, Chlamydia muridarum, PIR:C81715	247637_at	1.6
putative protein Atu, Drosophila melanogaster, EMBL:DMU75467	247565_at	1.6
peroxisomal Ca-dependent solute carrier - like protein peroxisomal Ca-dependent solute carrier, Oryctolagus cuniculus, EMBL:AF004161; supporter	c 247498_at	1.6
putative protein predicted protein, Arabidopsis thalina; supported by cDNA: gi_13899116_gb_AF370553.1_AF370553	247507_at	1.6
putative protein similar to unknown protein (pir  T01257)	247386_at	1.6
ABC transporter-like	247232_at	1.6
annexin ;supported by full-length cDNA: Ceres:1728.	247210_at	1.6
NifS-like aminotranfserase ; supported by cDNA: gi_15292880_gb_AY050874.1_	247164_at	1.6
zeaxanthin epoxidase precursor ; supported by cDNA: gi_10444087_gb_AF281655.1_AF281655	247025_at	1.6
putative protein UBIQUINONE BIOSYNTHESIS PROTEIN AARF - Providencia stuartii, EMBL:AF002165(N-terminus) and to Esterase STE1 - Metai	r 246976_s_at	1.6
protein phosphatase - like protein phosphatase-2C, Mesembryanthemum crystallinum, EMBL:AF075581; supported by full-length cDNA: Ceres:2334	4 246756_at	1.6
hypothetical protein ; supported by cDNA: gi_13605878_gb_AF367338.1_AF367338	246633_at	1.6
quinone oxidoreductase -like protein probable quinone oxidoreductase (EC 1.6.5.5) P1, Arabidopsis thaliana, PIR:S57611	246464_at	1.6
unknown protein	246286_at	1.6
Expressed protein ; supported by full-length cDNA: Ceres: 59.	246125_at	1.6
24 kDa vacuolar protein - like 24 kDa vacuolar protein VP24, Ipomoea batatas, EMBL:AB025531	245991_at	1.6
putative protein HCNP, Homo sapiens, EMBL:AF226051	245917_at	1.6
hypothetical protein contains similarity to arginine metabolism regulation protein i GI:695715 from [Saccharomyces cerevisiae]	245872_at	1.6
hypothetical protein ; supported by cDNA: gi_15451217_gb_AY054689.1_	245298_at	1.6
putative protein similarity to proteins of unknown function from human and mouse	245180_at	1.6
calcium-dependent protein kinase-like protein strong similarity to calcium-dependent protein kinase 19, Arabidopsis thaliana, PIR:S71778~Contains	245156_at	1.6
NADH dehydrogenase subunit 9	244943_at	1.6
hypothetical protein predicted by genscan	257444_at	1.6
putative beta-glucosidase	267645_at	1.5
putative translation initiation factor eIF-2B epsilon subunit	267415_at	1.5
putative vacuolar sorting receptor identical to GB:U79960; contains a calcium-binding EGF-like domain signature	267106_s_at	1.5
hypothetical protein predicted by genscan	266962_at	1.5
putative NADH dehydrogenase (ubiquinone oxidoreductase)	266835_at	1.5
putative amino acid acetyltransferase	266826_at	1.5
putative cytochrome P450	266778_at	1.5
MYB-related transcription factor (CCA1)	266719_at	1.5
unknown protein	266362_at	1.5
	266292 at	1.5
putative tropinone reductase ;supported by full-length cDNA: Ceres:14555.		
putative tropinone reductase ;supported by full-length cDNA: Ceres:14555. putative membrane channel protein ;supported by full-length cDNA: Ceres:10159.	266225_at	1.5
	_	1.5 1.5
putative membrane channel protein ;supported by full-length cDNA: Ceres:10159. putative retroelement pol polyprotein putative vacuolar protein sorting-associated protein ; supported by cDNA: gi_15081710_gb_AY048248.1_	266225_at	
putative membrane channel protein ;supported by full-length cDNA: Ceres:10159. putative retroelement pol polyprotein	266225_at 266187_at	1.5
putative membrane channel protein ;supported by full-length cDNA: Ceres:10159. putative retroelement pol polyprotein putative vacuolar protein sorting-associated protein ; supported by cDNA: gi_15081710_gb_AY048248.1_	266225_at 266187_at 266096_at 266099_at 265974_at	1.5 1.5
putative membrane channel protein ;supported by full-length cDNA: Ceres:10159. putative retroelement pol polyprotein putative vacuolar protein sorting-associated protein ; supported by cDNA: gi_15081710_gb_AY048248.1_ putative alpha-carboxyltransferase ; supported by cDNA: gi_6851090_gb_AF056969.1_AF056969 unknown protein unknown protein	266225_at 266187_at 266096_at 266099_at 265974_at 265900_at	1.5 1.5 1.5 1.5 1.5
putative membrane channel protein ;supported by full-length cDNA: Ceres:10159. putative retroelement pol polyprotein putative vacuolar protein sorting-associated protein ; supported by cDNA: gi_15081710_gb_AY048248.1_ putative alpha-carboxyltransferase ; supported by cDNA: gi_6851090_gb_AF056969.1_AF056969 unknown protein unknown protein unknown protein	266225_at 266187_at 266096_at 266099_at 265974_at 265900_at 265706_at	1.5 1.5 1.5 1.5 1.5 1.5
putative membrane channel protein ;supported by full-length cDNA: Ceres:10159. putative retroelement pol polyprotein putative vacuolar protein sorting-associated protein ; supported by cDNA: gi_15081710_gb_AY048248.1_ putative alpha-carboxyltransferase ; supported by cDNA: gi_6851090_gb_AF056969.1_AF056969 unknown protein unknown protein putative WRKY DNA-binding protein ; supported by cDNA: gi_13506736_gb_AF224701.1_AF224701	266225_at 266187_at 266096_at 266099_at 265974_at 265900_at 265706_at 265718_at	1.5 1.5 1.5 1.5 1.5 1.5 1.5
putative membrane channel protein ;supported by full-length cDNA: Ceres:10159. putative retroelement pol polyprotein putative alpha-carboxyltransferase ; supported by cDNA: gi_15081710_gb_AY048248.1_ putative alpha-carboxyltransferase ; supported by cDNA: gi_6851090_gb_AF056969.1_AF056969 unknown protein unknown protein unknown protein putative WRKY DNA-binding protein ; supported by cDNA: gi_13506736_gb_AF224701.1_AF224701 putative chloroplast outer membrane protein	266225_at 266187_at 266096_at 266099_at 265974_at 265900_at 265706_at 265718_at 265718_at	1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5
putative membrane channel protein ;supported by full-length cDNA: Ceres:10159. putative retroelement pol polyprotein putative vacuolar protein sorting-associated protein ; supported by cDNA: gi_15081710_gb_AY048248.1_ putative alpha-carboxyltransferase ; supported by cDNA: gi_6851090_gb_AF056969.1_AF056969 unknown protein unknown protein putative WRKY DNA-binding protein ; supported by cDNA: gi_13506736_gb_AF224701.1_AF224701 putative chloroplast outer membrane protein putative RNA methyltransferase	266225_at 266187_at 266096_at 266099_at 265974_at 265900_at 265706_at 265718_at 265718_at 265412_at 265274_at	1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5
putative membrane channel protein ;supported by full-length cDNA: Ceres:10159. putative retroelement pol polyprotein putative vacuolar protein sorting-associated protein ; supported by cDNA: gi_15081710_gb_AY048248.1_ putative alpha-carboxyltransferase ; supported by cDNA: gi_6851090_gb_AF056969.1_AF056969 unknown protein unknown protein putative WRKY DNA-binding protein ; supported by cDNA: gi_13506736_gb_AF224701.1_AF224701 putative chloroplast outer membrane protein putative RNA methyltransferase UDP-N-acetylglucosamine pyrophosphorylase-like protein similar to sperm associated antigen 2, GB:4507759 from [Homo sapiens], similar to ESTs	266225_at 266187_at 266096_at 266099_at 265974_at 265976_at 265706_at 265718_at 265412_at 265274_at 265274_at 265103_at	1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5
putative membrane channel protein ;supported by full-length cDNA: Ceres:10159. putative retroelement pol polyprotein putative vacuolar protein sorting-associated protein ; supported by cDNA: gi_15081710_gb_AY048248.1_ putative alpha-carboxyltransferase ; supported by cDNA: gi_6851090_gb_AF056969.1_AF056969 unknown protein unknown protein putative WRKY DNA-binding protein ; supported by cDNA: gi_13506736_gb_AF224701.1_AF224701 putative WRKY DNA-binding protein ; supported by cDNA: gi_13506736_gb_AF224701.1_AF224701 putative KINA methyltransferase UDP-N-acetylglucosamine pyrophosphorylase-like protein similar to sperm associated antigen 2, GB:4507759 from [Homo sapiens], similar to ESTs G-box binding factor, GBF4 Identical to Arabidopsis thaliana G-box-binding factor 4, gb]U01823;supported by full-length cDNA: Ceres:36980.	266225_at 266187_at 266096_at 266099_at 265974_at 2659706_at 265776_at 265718_at 265274_at 265274_at 262574_at 262574_at 2625040_at	1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5
putative membrane channel protein ;supported by full-length cDNA: Ceres:10159. putative retroelement pol polyprotein putative vacuolar protein sorting-associated protein ; supported by cDNA: gi_15081710_gb_AY048248.1_ putative alpha-carboxyltransferase ; supported by cDNA: gi_6851090_gb_AF056969.1_AF056969 unknown protein unknown protein putative WRKY DNA-binding protein ; supported by cDNA: gi_13506736_gb_AF224701.1_AF224701 putative kloroplast outer membrane protein putative RNA methyltransferase UDP-N-acetylglucosamine pyrophosphorylase-like protein similar to sperm associated antigen 2, GB:4507759 from [Homo sapiens], similar to ESTs G-box binding factor, GBF4 Identical to Arabidopsis thaliana G-box-binding factor 4, gb U01823;supported by full-length cDNA: Ceres:36980. putative 26S protease regulatory subunit 6A Similar to probable Mg-dependent ATPase (pir[S56671). ESTs gb]T46782,gb]AA04798 come from this	266225_at 266187_at 266096_at 266099_at 265974_at 265970_at 265776_at 265718_at 265718_at 265718_at 265274_at \$ 265103_at 265040_at 264057_at	1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5
putative membrane channel protein ;supported by full-length cDNA: Ceres:10159. putative retroelement pol polyprotein putative vacuolar protein sorting-associated protein ; supported by cDNA: gi_15081710_gb_AY048248.1_ putative alpha-carboxyltransferase ; supported by cDNA: gi_6851090_gb_AF056969.1_AF056969 unknown protein unknown protein putative WRKY DNA-binding protein ; supported by cDNA: gi_13506736_gb_AF224701.1_AF224701 putative chloroplast outer membrane protein putative chloroplast outer membrane protein putative RNA methyltransferase UDP-N-acetylglucosamine pyrophosphorylase-like protein similar to sperm associated antigen 2, GB:4507759 from [Homo sapiens], similar to ESTs G-box binding factor, GBF4 Identical to Arabidopsis thaliana G-box-binding factor 4, gb U01823;supported by full-length cDNA: Ceres:36980. putative glutathione S-transferase TSI-1 similar to glutathione S-transferase TSI-1 (gil2190992); similar to ESTs gb]F46782.gb]AA04798 come from this	266225_at 266187_at 266096_at 266099_at 265974_at 265976_at 265718_at 265718_at 265412_at 265413_at 265413_at 265404_at 264635_at 264436_at	1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5
putative membrane channel protein ;supported by full-length cDNA: Ceres:10159. putative retroelement pol polyprotein putative vacuolar protein sorting-associated protein ; supported by cDNA: gi_15081710_gb_AY048248.1_ putative alpha-carboxyltransferase ; supported by cDNA: gi_6851090_gb_AF056969.1_AF056969 unknown protein unknown protein putative WRKY DNA-binding protein ; supported by cDNA: gi_13506736_gb_AF224701.1_AF224701 putative chloroplast outer membrane protein putative RNA methyltransferase UDP-N-acetylglucosamine pyrophosphorylase-like protein similar to sperm associated antigen 2, GB:4507759 from [Homo sapiens], similar to ESTs G-box binding factor, GBF4 Identical to Arabidopsis thaliana G-box-binding factor 4, gb U01823;supported by full-length cDNA: Ceres:36980. putative 26S protease regulatory subunit 6A Similar to probable Mg-dependent ATPase (pir]S56671). ESTs gb T46782,gb AA04798 come from this putative glutathione ESTs gb H36966, gb R65511, gb T42324 and gb T20569 come from this gene	266225_at 266187_at 266096_at 266099_at 265974_at 265976_at 265776_at 265776_at 26574_at 265274_at 262574_at 262613_at 265040_at 264065_at 264436_at 26436_at	1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5
putative membrane channel protein ;supported by full-length cDNA: Ceres:10159. putative retroelement pol polyprotein putative vacuolar protein sorting-associated protein ; supported by cDNA: gi_15081710_gb_AY048248.1_ putative alpha-carboxyltransferase ; supported by cDNA: gi_6851090_gb_AF056969.1_AF056969 unknown protein unknown protein putative WRKY DNA-binding protein ; supported by cDNA: gi_13506736_gb_AF224701.1_AF224701 putative WRKY DNA-binding protein ; supported by cDNA: gi_13506736_gb_AF224701.1_AF224701 putative WRKY DNA-binding protein ; supported by cDNA: gi_0206736_gb_AF224701.1_AF224701 putative WRKY DNA-binding protein ; supported by cDNA: gi_0206736_gb_AF224701.1_AF224701 putative Chloroplast outer membrane protein putative Chloroplast outer membrane protein putative chloroplast outer membrane protein putative chloroplast outer membrane protein putative 20S protease regulatory subunit 6A Similar to probable Mg-dependent ATPase (pir]S56671). ESTs gb]T46782.gb]AA04798 come from this putative glutathione S-transferase TSI-1 similar to glutathione S-transferase TSI-1 (gi]2190992); similar to ESTs gb]H36966, gb]R65511, gb]T42324 and gb]T20569 come from this gene unknown protein Contains similarity to gb]Z69902 from C. elegans	266225_at 266187_at 266096_at 266099_at 265974_at 265970_at 265776_at 265718_at 265718_at 265714_at 265274_at 265040_at 26404_at 264046_at 26436_at 264362_at 264321_at	1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5
putative membrane channel protein ;supported by full-length cDNA: Ceres:10159. putative retroelement pol polyprotein putative vacuolar protein sorting-associated protein ; supported by cDNA: gi_15081710_gb_AY048248.1_ putative alpha-carboxyltransferase ; supported by cDNA: gi_6851090_gb_AF056969.1_AF056969 unknown protein unknown protein putative WRKY DNA-binding protein ; supported by cDNA: gi_13506736_gb_AF224701.1_AF224701 putative WRKY DNA-binding protein ; supported by cDNA: gi_13506736_gb_AF224701.1_AF224701 putative WRKY DNA-binding protein ; supported by cDNA: gi_13506736_gb_AF224701.1_AF224701 putative KINA methyltransferase UDP-N-acetylglucosamine pyrophosphorylase-like protein similar to sperm associated antigen 2, GB:4507759 from [Homo sapiens], similar to ESTs G-box binding factor, GBF4 Identical to Arabidopsis thaliana G-box-binding factor 4, gb]U01823;supported by full-length cDNA: Ceres:36980. putative 26S protease regulatory subunit 6A Similar to probable Mg-dependent ATPase (pir[S56671). ESTs gb]R46782,gb]AA04798 come from this putative glutathione S-transferase TSI-1 similar to glutathione S-transferase TSI-1 (gi 2190992); similar to ESTs gb]R29860, emb]Z29757, and emb] unknown protein ESTs gb]H30966, gb]R45511, gb]T42324 and gb]T20569 come from this gene unknown protein Similarity to gb]Z69902 from C. elegans hypothetical protein similar to hypothetical protein GI:7378617 from [Arabidopsis thaliana]	266225_at 266187_at 266096_at 266099_at 265974_at 265976_at 265776_at 265778_at 265718_at 265412_at 265412_at 265404_at 265404_at 264436_at 264436_at 264321_at 264310_at	1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5
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putative membrane channel protein ;supported by full-length cDNA: Ceres:10159. putative retroelement pol polyprotein putative vacuolar protein sorting-associated protein ; supported by cDNA: gi_15081710_gb_AY048248.1_ putative alpha-carboxyltransferase ; supported by cDNA: gi_6851090_gb_AF056969.1_AF056969 unknown protein unknown protein putative WRKY DNA-binding protein ; supported by cDNA: gi_13506736_gb_AF224701.1_AF224701 putative chloroplast outer membrane protein putative RNA methyltransferase UDP-N-acetylglucosamine pyrophosphorylase-like protein similar to sperm associated antigen 2, GB:4507759 from [Homo sapiens], similar to ESTs G-box binding factor, GBF4 Identical to Arabidopsis thaliana G-box-binding factor 4, gb[U01823;supported by full-length cDNA: Ceres:36980. putative 26S protease regulatory subunit 6A Similar to probable Mg-dependent ATPase (pir]S56671). ESTs gb]T46782,gb]AA04798 come from this putative glutathione S-transferase TSI-1 similar to gb]T42524 and gb]T20569 come from this gene unknown protein Contains similarity to gb]Z69902 from C. elegans hypothetical protein similar to hypothetical protein GI:7378617 from [Arabidopsis thaliana] unknown protein contains similarity to typaredoxin GI:3351498 from [Crithidia fasciculata]:supported by full-length cDNA: Ceres:34936. hypothetical protein predicted by genscan and genefinder:supported by full-length cDNA: Ceres:17483.	266225_at 266187_at 266096_at 266099_at 265974_at 265976_at 265706_at 265718_at 265718_at 26574_at 265274_at 265040_at 264040_at 264057_at 264436_at 264362_at 264321_at 264310_at 264219_at 26411_at	$\begin{array}{c} 1.5\\ 1.5\\ 1.5\\ 1.5\\ 1.5\\ 1.5\\ 1.5\\ 1.5\\$
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ABC transporter protein, putative similar to ABC transporter protein GB:AAF31030 GI:6899653 from [Leishmania major]	262005_at	1.5
vacuolar assembly protein vps41, putative similar to vacuolar assembly protein vps41 GI:1835787 from [Lycopersicon esculentur	m] 261783_at	1.5
hypothetical protein contains similarity to spastin protein orthologue GB:CAB60143 GI:6273572 from [Mus musculus]	261689_at	1.5
ARP protein, putative similar to ARP protein GB:CAA89858 GI:886434 from [Arabidopsis thaliana]	261601_at	1.5
peroxidase ATP4a identical to GB:CAA67309 GI:1429213 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 399	68. 261518_at	1.5
isochorismate synthase, putative similar to isochorismate synthase GI:3348077 from [Arabidopsis thaliana]	261428_at	1.5
hypothetical protein predicted by genscan+; supported by full-length cDNA: Ceres: 107992.	260981_at	1.5
unknown protein	260862_at	1.5
valyl-tRNA synthetase, putative similar to valyl tRNA synthetase GB:AAB49704 GI:1890130 from [Arabidopsis thaliana]; supported		1.5
hypothetical protein predicted by genscan+	260785_at	1.5
RING finger protein, putative similar to GB:BAA78677 from [Homo sapiens]	260690_at	1.5
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:28026.	260622_at	1.5
putative pre-mRNA splicing factor RNA helicase	260525_at	1.5
unknown protein	260374_at	1.5
putative serine/threonine kinase similar to serine/threonine kinase GB:AAB68776 [Arabidopsis thaliana]; supported by cDNA: gi_1		1.5
putative alanine aminotransferase similar to alanine aminotransferase GB:AAB01685 (Chlamydomonas reinhardtii); supported by		1.5
unknown protein similar to unknown protein GB:AAD21437 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:310.		1.5
hypothetical protein similar to hypothetical protein GB:CAB37532 from [Arabidopsis thaliana], predicted by genscan+;supported to the protein similar to hypothetical protein GB:CAB37532 from [Arabidopsis thaliana], predicted by genscan+;supported to the protein similar to hypothetical protein GB:CAB37532 from [Arabidopsis thaliana], predicted by genscan+;supported to the protein similar to hypothetical protein GB:CAB37532 from [Arabidopsis thaliana], predicted by genscan+;supported to the protein similar to hypothetical protein GB:CAB37532 from [Arabidopsis thaliana], predicted by genscan+;supported to the protein similar to hypothetical protein GB:CAB37532 from [Arabidopsis thaliana], predicted by genscan+;supported to the protein similar to hypothetical protein GB:CAB37532 from [Arabidopsis thaliana], predicted by genscan+;supported to the protein similar to hypothetical protein GB:CAB37532 from [Arabidopsis thaliana], predicted by genscan+;supported to the protein similar to hypothetical protein GB:CAB37532 from [Arabidopsis thaliana], predicted by genscan+;supported to the protein similar to hypothetical protein GB:CAB37532 from [Arabidopsis thaliana], predicted by genscan+;supported to hypothetical protein similar to hypot		1.5
putative nuclear matrix constituent protein 1 (NMCP1) similar to nuclear matrix constituent protein 1 (NMCP1) GB:BAA20407 [Da RNA-binding protein MEI2, putative similar to GI:6650523 from [Arabidopsis thaliana]		1.5 1.5
sphingosine-1-phosphate lyase, putative similar to sphingosine-1-phosphate lyase [Homo sapiens] GI:4160532; supported by cD	259769_at	1.5
hypothetical protein	259535 at	1.5
myb-related protein, putative similar to myb-related protein GI:2505876 from [Arabidopsis thaliana]	259432 at	1.5
hypotentical protein contains similarity to hepatocellular carcinoma-associated antiqen 59 GI:7158847 from [Homo sapiens]; supp	_	1.5
putative lectin contains Pfam profile: PF01419 jacalin-like lectin domain; similar to jasmonate inducible protein GB:Y11483 (Brass	, , , ,	1.5
unknown protein similar to hypothetical protein GB:AAC23643 [Arabidopsis thaliana]	259232 at	1.5
hypothetical protein predicted by genscan	259246 s at	1.5
unknown protein ;supported by full-length cDNA: Ceres:249634.	259188 at	1.5
unknown protein	259052_at	1.5
unknown protein ; supported by cDNA: gi_15809941_gb_AY054239.1_	259057_at	1.5
unknown protein ; supported by cDNA: gi 15292900 gb AY050884.1	258838_at	1.5
ankyrin-like protein similar to ankyrin proteins: GB:CAA48803 [Mus musculus], GB:CAA40279 [Homo sapiens], GB:AAB47551 [F	Rattus norvegicus]; / 258794_at	1.5
hypothetical protein similar to hypothetical protein GB:AAC17075 [Arabidopsis thaliana]; supported by cDNA: gi_15810358_gb_A	Y056218.1_ 258804_at	1.5
L-allo-threonine aldolase, putative similar to L-ALLO-THREONINE ALDOLASE GB:007051 from [Aeromonas jandaei];supported	by full-length cDN/ 258599_at	1.5
acetyl-coA dehydrogenase, putative similar to acetyl-coenzyme A dehydrogenase GB:NP_031408 from [Mus musculus]	258524_at	1.5
hypothetical protein predicted by genscan+; supported by cDNA: gi_15810242_gb_AY056160.1_	258374_at	1.5
putative B regulatory subunit of protein phosphatase 2A similar to GB:AAB58902 from [Arabidopsis thaliana]; supported by cDNA		1.5
putative 4-coumarate:CoA ligase 2 similar to GB:AAD47192 from [Arabidopsis thaliana]	258037_at	1.5
unknown protein	258015_at	1.5
protein phosphatase-2c, putative similar to protein phosphatase-2c GB:AAC35951 [Mesembryanthemum crystallinum]; contains		1.5
unknown protein	257719_at	1.5
unknown protein	257249_at	1.5
glutathione reductase, cytosolic identical to GB:P48641 from [Arabidopsis thaliana] (); supported by cDNA: gi_14532809_gb_AYi		1.5
mitochondrial chaperonin hsp60 identical to mitochondrial chaperonin hsp60 GB:Z11547 [Arabidopsis thaliana] (Plant Mol. Biol.		1.5
far-red impaired response protein, putative similar to GB:far-red impaired response protein GB:AAD51282 from [Arabidopsis thal alpha-glucan phosphorylase, putative similar to alpha-glucan phosphorylase, L isozyme 1 precursor GB:P04045 from [Solanum t		1.5 1.5
putative protein DNA-binding protein PD2 - Pisum sativum,PID:e275185	256675 at	1.5
recombination signal sequence recognition protein, putative similar to recombination signal sequence recognition protein (SSRP)	_	1.5
putative clathrin heavy chain similar to clathrin heavy chain (B:AAC49294 [Glycine max]	256437 s at	1.5
unknown protein ;supported by full-length cDNA: Ceres:3056.	256441 at	1.5
pinhead-like protein similar to pinhead [Arabidopsis thaliana] GI:5107374	256293 at	1.5
glutathione S-conjugate transporting ATPase (AtMRP1) identical to glutathione S-conjugate transporting ATPase (AtMRP1) [Arab		1.5
GTP-binding protein, putative similar to GTP-binding protein NGB [Homo sapiens] GI:4191616	256207_at	1.5
phosphoinositide specific phospholipase (AtPLC2) identical to phosphoinositide specific phospholipase (AtPLC2) GI:857374 [Aral	bidopsis thaliana]; s 256156_at	1.5
unknown protein	256013_at	1.5
hypothetical protein ;supported by full-length cDNA: Ceres:37204.	255980_at	1.5
hypothetical protein contains Pfam profile: PF00650 CRAL/TRIO domain	255923_at	1.5
hypothetical protein contains Pfam profile: PF00612 IQ calmodulin-binding motif	255783_at	1.5
flavonol 4 -sulfotransferase, putative similar to flavonol 4 -sulfotransferase GI:168168 from [Flaveria chloraefolia]	255773_at	1.5
82.09 and 30.80) similar to alternative splicing factor ASF	255472_at	1.5
putative cullin-like 1 protein similar to 0. sativa cullin-like proteins; supported by cDNA: gi_15028160_gb_AY046030.1_	255441_at	1.5
coded for by A. thaliana cDNA W43435 ; supported by cDNA: gi_14532463_gb_AY039856.1_	255259 at	1.5
putative transcriptional regulator		4 -
UDP-galactose 4-epimerase - like protein UDP-galactose 4-epimerase, Cyamopsis tetragonoloba, AJ005082;supported by full-le	254992_at	1.5
putative protein other hypothetical proteins - Arabidopsis thaliana	254992_at ngth cDNA: Ceres: 254952_at	1.5
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putative translation elongation factor ts elongation factor ts (tsf) RP087 - Rickettsia prowazekii, PIR2:F71717	254992_at ngth cDNA: Ceres: 254952_at 254965_at 254932_at	1.5 1.5 1.5
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putative translation elongation factor ts elongation factor ts (tsf) RP087 - Rickettsia prowazekii, PIR2:F71717 putative protein beta-transducin repeats containing protein - Homo sapiens,PID:e1284220 putative SWH1 protein SWH1 protein - yeast, PIR2:S47536 putative protein ;supported by full-length cDNA: Ceres:100165.	254992_at ngth cDNA: Ceres: 254952_at 254965_at 254932_at 254913_at 254817_at 254577_at	1.5 1.5 1.5 1.5 1.5 1.5
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putative translation elongation factor ts elongation factor ts (tsf) RP087 - Rickettsia prowazekii, PIR2:F71717 putative protein beta-transducin repeats containing protein - Homo sapiens,PID:e1284220 putative SWH1 protein SWH1 protein - yeast, PIR2:S47536 putative protein is wipported by full-length cDNA: Ceres:100165. putative protein cyclin C homolog 1, Schizosaccharomyces pombe, PATCHX:G2055413 trehalose-6-phosphate phosphatase - like protein trehalose-6-phosphate phosphatase (AtTPPA), PID:g2944178 transcriptional activator CBF1-like protein strong similarity to transcriptional activator CBF1, Arabidopsis thaliana00 putative protein hypothetical protein - Synechocystis sp. (strain PCC 6803),PIR2:S76076 putative protein hypothetical protein - Synechocystis sp. (strain PCC 6803),PIR2:S76076 putative protein kinase protein aminopeptidase, Mus musculus, U35646 calmodulin-domain protein aminopeptidase, Mus musculus, PID:d1026227 putative protein glutamic acid-rich protein precursor, Plasmodium falciparum (GARP), PIR2:A54514 putative protein various predicted protein precursor, Plasmodium falciparum (GARP), PIR2:A54514 putative protein various predicted protein grotein R kappa B, Homo sapiens, PIR:S52863 putative protein several hypothetical protein R kappa B, Homo sapiens, PIR:S52863	254992_at ngth cDNA: Ceres: 254952_at 254952_at 254932_at 254913_at 254817_at 254526_at 254526_at 254056_at 253805_at 253858_at 253858_at 253528_s_at 253359_at 253137_at 253137_at 25317_at 25319_at 25319_at 25319_at 25319_at 25319_at 25319_at 25319_at 25319_at 25319_at 25319_at 25319_at 25319_at 25319_at 253264_at	$\begin{array}{c} 1.5\\ 1.5\\ 1.5\\ 1.5\\ 1.5\\ 1.5\\ 1.5\\ 1.5\\$
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putative translation elongation factor ts elongation factor ts (tsf) RP087 - Rickettsia prowazekii, PIR2:F71717 putative protein beta-transducin repeats containing protein - Homo sapiens,PID:e1284220 putative SWH1 protein SWH1 protein - yeast, PIR2:S47536 putative protein is wipported by full-length cDNA: Ceres:100165. putative protein cyclin C homolog 1, Schizosaccharomyces pombe, PATCHX:G2055413 trehalose-6-phosphate phosphatase - like protein trehalose-6-phosphate phosphatase (AtTPPA), PID:g2944178 transcriptional activator CBF1-like protein strong similarity to transcriptional activator CBF1, Arabidopsis thaliana00 putative protein hypothetical protein - Synechocystis sp. (strain PCC 6803),PIR2:S76076 putative protein hypothetical protein - Synechocystis sp. (strain PCC 6803),PIR2:S76076 putative protein kinase protein aminopeptidase, Mus musculus, U35646 calmodulin-domain protein aminopeptidase, Mus musculus, PID:d1026227 putative protein glutamic acid-rich protein precursor, Plasmodium falciparum (GARP), PIR2:A54514 putative protein various predicted protein precursor, Plasmodium falciparum (GARP), PIR2:A54514 putative protein various predicted protein grotein R kappa B, Homo sapiens, PIR:S52863 putative protein several hypothetical protein R kappa B, Homo sapiens, PIR:S52863	254992_at ngth cDNA: Ceres: 254952_at 254952_at 254932_at 254913_at 254817_at 254526_at 254526_at 254056_at 253805_at 253858_at 253858_at 253528_s_at 253359_at 253137_at 253137_at 25317_at 25319_at 25319_at 25319_at 25319_at 25319_at 25319_at 25319_at 25319_at 25319_at 25319_at 25319_at 25319_at 25319_at 253264_at	$\begin{array}{c} 1.5\\ 1.5\\ 1.5\\ 1.5\\ 1.5\\ 1.5\\ 1.5\\ 1.5\\$

receptor-protein kinase-like protein receptor-like protein kinase, Catharanthus roseus, PIR:T10060; supported by cDNA: gi 14334759 gb AY03505		
	252066_at	1.5
putative protein arm repeat containing protein, Brassica napus, AF024625	251862_at	1.5
chalcone isomerase ;supported by full-length cDNA: Ceres:2122.	251827_at	1.5
putative protein CARBON CATABOLITE REPRESSOR PROTEIN 4 - Saccharomyces cerevisiae, SWISSPROT:CCR4_YEAST	251582 at	1.5
putative protein ETHIONINE AMINOPEPTIDASE 2 (EC 3.4.11.18) - Mus musculus, EMBL:AB003144; supported by full-length cDNA: Ceres:115696.	251444 at	1.5
putative protein predicted protein, Synechocystis sp., PIR:S74969;supported by full-length cDNA: Ceres:110188.	250865 at	1.5
putative protein predicted protein, Arabidopsis thaliana	250877 at	1.5
cysteine proteinase inhibitor-like protein ;supported by full-length cDNA: Ceres:27304.	250811 at	1.5
ankyrin-like protein	250761 at	1.5
serine/threonine protein kinase -like protein probable serine/threonine protein kinase SNFL3, sorghum, PIR:T14822; supported by cDNA: gi 928063	_	1.5
putative protein similar to unknown protein (emb[CABS1351.1)	250309 at	1.5
putative protein similar to unknown protein (emb[CAB69839.1)	250257_at	1.5
putative protein similar to unknown protein (pir  S77419); supported by cDNA: gi_15912216_gb_AY056386.1_	250259_at	1.5
Ser/Thr specific protein kinase - like protein various protein kinase, Arabidopsis thaliana;supported by full-length cDNA: Ceres:15535.	249985_at	1.5
zinc finger protein-like ; supported by full-length cDNA: Ceres: 16392.	249888_s_at	1.5
unknown protein ; supported by cDNA: gi_9695278_dbj_AB046717.1_AB046717	249840_at	1.5
NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - like protein NADH dehydrogenase (ubiquinone) (Ubiquinone) (Ubiquinone) (Ubiquinone) (Ubiquinone) (Ubiquinone) (Ubiquinone) (Ubiquinone) (Ub	249627_at	1.5
cytosolic malate dehydrogenase ;supported by full-length cDNA: Ceres:40174.	249147 at	1.5
1-aminocyclopropane-1-carboxylate oxidase ; supported by cDNA: gi 14596164 gb AY042870.1	249125 at	1.5
ATP dependent copper transporter; supported by cDNA: gi 14194134 gb AF367273.1 AF367273	249027 at	1.5
putative protein similar to unknown protein (pirl/T05524);supported by full-length cDNA: Ceres:767.	248952 at	1.5
ADPG pyrophosphorylase small subunit (ph AAC39441.1); supported by cDNA: gi 15146247 gb AY049265.1	248687 at	1.5
peptidyprolyl isomerase	_	1.5
	248657_at	
methionine S-methyltransferase (gb AAD49574.1); supported by cDNA: gi_5733428_gb_AF137380.1_AF137380	248576_at	1.5
putative protein strong similarity to unknown protein (pir] T05518)	248495_at	1.5
putative protein similar to unknown protein (pir  S42136)	248357_at	1.5
non phototropic hypocotyl 1-like ;supported by cDNA: gi_5391441_gb_AF053941.2_AF053941	247853_at	1.5
dehydrodolichyl diphosphate - like protein dehydrodolichyl diphosphate, Arabidopsis thaliana, EMBL:ATH277136	247780_at	1.5
autophagocytosis protein - like autophagocytosis protein AUT1, Saccharomyces cerevisiae, PIR:S45130;supported by full-length cDNA: Ceres:8184	247542_at	1.5
dehydrogenase; supported by cDNA: gi 15383743 gb AY039787.1	247436 at	1.5
pyruvate kinase	247338 at	1.5
putative protein contains similarity to FtsH	247235 at	1.5
proteasome regulatory subunit-like ; supported by cDNA: gi 17063180 gb AY062113.1	247257 at	1.5
putative protein strong similarity to unknown protein (pir  T04718); supported by cDNA: gi 15529177 gb AY052213.1	247013 at	1.5
	246908 at	1.5
dehydration-induced protein RD22; supported by cDNA; gi_16974545_gb_47060560.1_		
chaperonin gamma chain - like protein chaperonin containing TCP-1 complex gamma chain, African clawed frog, PIR:S54210; supported by cDNA:	_	1.5
putative protein GTP-binding proteins at the N-terminus	246775_at	1.5
putative protein predicted protein, Arabidopsis thaliana; supported by cDNA: gi_16930704_gb_AF436836.1_AF436836	246660_at	1.5
putative protein gamma-tubulin interacting protein - Xenopus laevis, EMBL:AF052663	246329_at	1.5
putative protein hnRNP A/B related protein - Felis catus, EMBL:AF153444; supported by cDNA: gi_14194148_gb_AF367280.1_AF367280	246292_at	1.5
putative protein thiamin pyrophosphokinase, Schizosaccharomyces pombe, PIR:S52350	246038_s_at	1.5
putative protein DNA-binding protein - Triticum aestivum, EMBL:AF091837;supported by full-length cDNA: Ceres:249741.	245888_at	1.5
ferredoxin-dependent glutamate synthase ; supported by cDNA: gi_3869250_gb_U39287.1_ATU39287	245701 at	1.5
AMP-binding protein	245621 at	1.5
acyl-CoA oxidase like protein ; supported by cDNA: gi_3044213_gb_AF057044.1_AF057044	245249 at	1.5
	245218_s_at	1.5
mitochondrial chaptern pricting (HSP60)	245164 at	1.5
inicosonal protein S3		
	244984_at	1.5
ATPase, putative similar to chromaffin granule ATPase II GB:AAD03352 GI:4115341 from [Bos taurus]	262275_at	1.5
putative DNA binding protein ; supported by cDNA: gi_11908071_gb_AF326883.1_AF326883	267538_at	1.4
putative protein kinase contains a protein kinase domain profile (PDOC00100); supported by cDNA: gi_2852448_dbj_D88207.1_D88207	267486_at	1.4
unknown protein	267312_at	1.4
hypothetical protein predicted by genscan	267130_at	1.4
putative AMP deaminase ; supported by cDNA: gi_15810524_gb_AY056301.1_	267095 at	1.4
putative RNA-binding protein ; supported by cDNA: gi_16612301_gb_AF439844.1_AF439844	201000_ut	1.4
	267050_at	1.4
putative ABC transporter		1.4
putative ABC transporter	267050_at	
putative ABC transporter unknown protein	267050_at 266990_at 266855_at	1.4 1.4
putative ABC transporter unknown protein putative casein kinase I	267050_at 266990_at 266855_at 266651_at	1.4 1.4 1.4
putative ABC transporter unknown protein putative casein kinase I TINY-like AP2 domain transcription factor ; supported by cDNA: gi_13878156_gb_AF370341.1_AF370341	267050_at 266990_at 266855_at 266651_at 266661_at	1.4 1.4 1.4 1.4
putative ABC transporter unknown protein putative casein kinase I TINY-like AP2 domain transcription factor; supported by cDNA: gi_13878156_gb_AF370341.1_AF370341 unknown protein; supported by cDNA: gi_14030738_gb_AF375460.1_AF375460	267050_at 266990_at 266855_at 266651_at 266661_at 266617_at	1.4 1.4 1.4 1.4 1.4
putative ABC transporter unknown protein putative casein kinase I TINY-like AP2 domain transcription factor ; supported by cDNA: gi_13878156_gb_AF370341.1_AF370341 unknown protein ; supported by cDNA: gi_14030738_gb_AF375460.1_AF375460 unknown protein	267050_at 266990_at 266855_at 266651_at 266661_at 266617_at 266185_at	1.4 1.4 1.4 1.4 1.4 1.4
putative ABC transporter unknown protein putative casein kinase I TINY-like AP2 domain transcription factor ; supported by cDNA: gi_13878156_gb_AF370341.1_AF370341 unknown protein ; supported by cDNA: gi_14030738_gb_AF375460.1_AF375460 unknown protein unknown protein	267050_at 266990_at 266855_at 266651_at 266661_at 266617_at 266185_at 266090_at	1.4 1.4 1.4 1.4 1.4 1.4 1.4
putative ABC transporter unknown protein putative casein kinase I TINY-like AP2 domain transcription factor ; supported by cDNA: gi_13878156_gb_AF370341.1_AF370341 unknown protein ; supported by cDNA: gi_14030738_gb_AF375460.1_AF375460 unknown protein unknown protein putative WD-40 repeat protein, MSI4 almost identical to GB:2599091; contains a Trp-Asp (WD-40) repeat signature; supported by cDNA: gi_2599092	267050_at 266990_at 266855_at 266661_at 266661_at 266617_at 266185_at 266090_at 266946_s_at	1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4
putative ABC transporter unknown protein putative casein kinase I TINY-like AP2 domain transcription factor ; supported by cDNA: gi_13878156_gb_AF370341.1_AF370341 unknown protein ; supported by cDNA: gi_14030738_gb_AF375460.1_AF375460 unknown protein unknown protein putative WD-40 repeat protein, MSI4 almost identical to GB:2599091; contains a Trp-Asp (WD-40) repeat signature; supported by cDNA: gi_2599092 hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:21954.	267050_at 266990_at 266855_at 266661_at 266661_at 266617_at 266185_at 266900_at 265946_s_at 265942_at	1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4
putative ABC transporter unknown protein putative casein kinase I TINY-like AP2 domain transcription factor ; supported by cDNA: gi_13878156_gb_AF370341.1_AF370341 unknown protein ; supported by cDNA: gi_14030738_gb_AF375460.1_AF375460 unknown protein unknown protein putative WD-40 repeat protein, MSI4 almost identical to GB:2599091; contains a Trp-Asp (WD-40) repeat signature; supported by cDNA: gi_2599092 hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:21954. unknown protein ;supported by full-length cDNA: Ceres:121540.	267050_at 266990_at 266855_at 266651_at 266651_at 266617_at 266185_at 266946_s_at 265946_s_at 265942_at 265971_at	1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4
putative ABC transporter unknown protein putative casein kinase I TINY-like AP2 domain transcription factor ; supported by cDNA: gi_13878156_gb_AF370341.1_AF370341 unknown protein ; supported by cDNA: gi_14030738_gb_AF375460.1_AF375460 unknown protein putative WD-40 repeat protein, MSI4 almost identical to GB:2599091; contains a Trp-Asp (WD-40) repeat signature; supported by cDNA: gi_2599092 hypothetical protein predicted by genscan.supported by full-length cDNA: Ceres:21954. unknown protein ; supported by full-length cDNA: Ceres:220875.	267050_at 266890_at 266855_at 266651_at 266651_at 266617_at 266185_at 266190_at 265946_s_at 265942_at 265871_at 265842_at	1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4
putative ABC transporter unknown protein putative casein kinase I TINY-like AP2 domain transcription factor ; supported by cDNA: gi_13878156_gb_AF370341.1_AF370341 unknown protein ; supported by cDNA: gi_14030738_gb_AF375460.1_AF375460 unknown protein unknown protein putative WD-40 repeat protein, MSI4 almost identical to GB:2599091; contains a Trp-Asp (WD-40) repeat signature; supported by cDNA: gi_2599092 hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:21954. unknown protein ;supported by full-length cDNA: Ceres:121540.	267050_at 266990_at 266855_at 266651_at 266651_at 266617_at 266185_at 266946_s_at 265946_s_at 265942_at 265971_at	1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4
putative ABC transporter unknown protein putative casein kinase I TINY-like AP2 domain transcription factor ; supported by cDNA: gi_13878156_gb_AF370341.1_AF370341 unknown protein ; supported by cDNA: gi_14030738_gb_AF375460.1_AF375460 unknown protein putative WD-40 repeat protein, MSI4 almost identical to GB:2599091; contains a Trp-Asp (WD-40) repeat signature; supported by cDNA: gi_2599092 hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:21954. unknown protein ; supported by full-length cDNA: Ceres:121540. putative nitrilase ; supported by full-length cDNA: Ceres:121540. Expressed protein ; supported by full-length cDNA: Ceres: 16367. hypothetical protein predicted by genefinder	267050_at 266855_at 266855_at 266855_at 266661_at 266661_at 266090_at 266090_at 266090_at 265946_s_at 265946_s_at 265946_t_at 265871_at 265827_at 265627_at 265310_at	1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4
putative ABC transporter unknown protein putative casein kinase I TINY-like AP2 domain transcription factor ; supported by cDNA: gi_13878156_gb_AF370341.1_AF370341 unknown protein ; supported by cDNA: gi_14030738_gb_AF375460.1_AF375460 unknown protein putative WD-40 repeat protein, MSI4 almost identical to GB:2599091; contains a Trp-Asp (WD-40) repeat signature; supported by cDNA: gi_2599092 hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:21954. unknown protein ; supported by full-length cDNA: Ceres:121540. putative nitrilase ; supported by full-length cDNA: Ceres:121540. Expressed protein ; supported by full-length cDNA: Ceres:16367. hypothetical protein predicted by genefinder	267050_at 266855_at 266855_at 266855_at 266661_at 266661_at 266090_at 266090_at 266090_at 265946_s_at 265946_s_at 265946_t_at 265871_at 265827_at 265627_at 265310_at	1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4
putative ABC transporter unknown protein putative casein kinase I TINY-like AP2 domain transcription factor ; supported by cDNA: gi_13878156_gb_AF370341.1_AF370341 unknown protein ; supported by cDNA: gi_14030738_gb_AF375460.1_AF375460 unknown protein putative WD-40 repeat protein, MSI4 almost identical to GB:2599091; contains a Trp-Asp (WD-40) repeat signature; supported by cDNA: gi_2599092 hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:21954. unknown protein ; supported by full-length cDNA: Ceres:121540. putative nitrilase ; supported by full-length cDNA: Ceres:121540. Expressed protein ; supported by full-length cDNA: Ceres:16367. hypothetical protein predicted by genefinder	267050_at 266690_at 266655_at 266651_at 266661_at 266661_at 266615_at 266090_at 265912_at 265912_at 265871_at 265842_at 265642_at 265642_at 265510_at	1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4
putative ABC transporter unknown protein putative casein kinase I TINY-like AP2 domain transcription factor ; supported by cDNA: gi_13878156_gb_AF370341.1_AF370341 unknown protein ; supported by cDNA: gi_14030738_gb_AF375460.1_AF375460 unknown protein putative WD-40 repeat protein, MSI4 almost identical to GB:2599091; contains a Trp-Asp (WD-40) repeat signature; supported by cDNA: gi_2599092 hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:21954. unknown protein ; supported by full-length cDNA: Ceres:121540. putative nitrilase ; supported by full-length cDNA: Ceres:20875. Expressed protein ; supported by full-length cDNA: Ceres: 16367. hypothetical protein predicted by genefinder unknown protein similar to putative tyrosine phosphatase GB:AAF81798 GI:8926334 from [Oryza sativa];supported by full-length cDNA: Ceres:8301.	267050_at 266690_at 266655_at 266651_at 266661_at 266661_at 266615_at 266090_at 265912_at 265912_at 265871_at 265842_at 265642_at 265642_at 265510_at	1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4
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putative ABC transporter unknown protein putative caseni knase I TINY-like AP2 domain transcription factor ; supported by cDNA: gi_13878156_gb_AF370341.1_AF370341 unknown protein ; supported by cDNA: gi_14030738_gb_AF375460.1_AF375460 unknown protein putative caseni knase I putative WD-40 repeat protein, MSI4 almost identical to GB:2599091; contains a Trp-Asp (WD-40) repeat signature; supported by cDNA: gi_2599092 hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:21954. unknown protein putative nitrilase ; supported by full-length cDNA: Ceres:121540. putative nitrilase ; supported by full-length cDNA: Ceres:121540. putative nitrilase ; supported by full-length cDNA: Ceres: 16367. hypothetical protein predicted by genefinder unknown protein is predicted by genefinder unknown protein is putative tyrosine phosphatase GB:AAF81798 GI:8926334 from [Oryza sativa];supported by full-length cDNA: Ceres:8301. putative plastid RNA polymerase sigma-subunit similar to GB:BAA22427 and EST gb N65838; supported by cDNA: gi_2353172_gb_AF015543.1_AF unknown protein location of EST gb H36530, gb AA395402, and gb T43793 5 -adenylylphosphosulfate reductase, putative similar to 5 -adenylylphosphosulfate reductase GI:1336168 from [Arabidopsis thaliana];supported by cDNA: gi_15293160_gb_AY051014.1_ unknown protein putative cinnamyl alcohol dehydrogenase similar to cinnamyl alcohol dehydrogenase, gi[1143445; supported by cDNA: gi_15983385_gb_AF424567 unknown protein inimilar to ESTs gb]N86021 and gb]N86863 hypothetical protein similar to ESTs gb]N86021 and gb]N86863 hypothetical protein similar to test-glucosidase GI:877530 from [Saccharomyces cerevisiae] beta-glucosidase, putative similar to ceeptor kinase 1 GI:2924449 from [Arabidopsis thaliana] unknown protein contains similarity to splicing factor required for vegetative and meiotic growth GI:2959374 from [Schizosaccharomyces pombe]; suf receptor kinase, putative similar to RAA helicase GI:3776015 from [Arabidopsis thaliana]; su	267050_at 266890_at 266855_at 266651_at 266651_at 266651_at 266661_at 266661_at 266671_at 265090_at 265946_s_at 265971_at 265871_at 265642_at 265672_at 265073_at 2647745_at 2647745_at 264777_at 264771_at 264797_at 264791_at 264291_at 264291_at 264291_at 264291_at 264221_s_at 264221_s_at 264211_at 264201_at 264201_at 264221_s_at 264211_at 264201_at 264292_at 263692_at	$\begin{array}{c} 1.4\\ 1.4\\ 1.4\\ 1.4\\ 1.4\\ 1.4\\ 1.4\\ 1.4\\$
putative ABC transporter unknown protein putative caseni knase I TINY-like AP2 domain transcription factor ; supported by cDNA: gi_13878156_gb_AF370341.1_AF370341 unknown protein ; supported by cDNA: gi_14030738_gb_AF375460.1_AF375460 unknown protein putative caseni knase I putative WD-40 repeat protein, MSI4 almost identical to GB:2599091; contains a Trp-Asp (WD-40) repeat signature; supported by cDNA: gi_2599092 hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:21954. unknown protein putative nitrilase ; supported by full-length cDNA: Ceres:121540. putative nitrilase ; supported by full-length cDNA: Ceres:121540. putative nitrilase ; supported by full-length cDNA: Ceres: 16367. hypothetical protein predicted by genefinder unknown protein is predicted by genefinder unknown protein is putative tyrosine phosphatase GB:AAF81798 GI:8926334 from [Oryza sativa];supported by full-length cDNA: Ceres:8301. putative plastid RNA polymerase sigma-subunit similar to GB:BAA22427 and EST gb N65838; supported by cDNA: gi_2353172_gb_AF015543.1_AF unknown protein location of EST gb H36530, gb AA395402, and gb T43793 5 -adenylylphosphosulfate reductase, putative similar to 5 -adenylylphosphosulfate reductase GI:1336168 from [Arabidopsis thaliana];supported by cDNA: gi_15293160_gb_AY051014.1_ unknown protein putative cinnamyl alcohol dehydrogenase similar to cinnamyl alcohol dehydrogenase, gi[1143445; supported by cDNA: gi_15983385_gb_AF424567 unknown protein inimilar to ESTs gb]N86021 and gb]N86863 hypothetical protein similar to ESTs gb]N86021 and gb]N86863 hypothetical protein similar to test-glucosidase GI:877530 from [Saccharomyces cerevisiae] beta-glucosidase, putative similar to ceeptor kinase 1 GI:2924449 from [Arabidopsis thaliana] unknown protein contains similarity to splicing factor required for vegetative and meiotic growth GI:2959374 from [Schizosaccharomyces pombe]; suf receptor kinase, putative similar to RAA helicase GI:3776015 from [Arabidopsis thaliana]; su	267050_at 266890_at 266855_at 266651_at 266661_at 266661_at 266615_at 266090_at 265912_at 265912_at 265912_at 265971_at 265071_at 265073_at 265073_at 264781_at 2647745_at 264770_at 2647745_at 264770_at 264797_at 264797_at 264781_at 264721_at 264291_at 264291_at 264221_s_at 264221_s_at 264221_at 264221_at 264221_at 264221_at 264221_at 264221_at	$\begin{array}{c} 1.4\\ 1.4\\ 1.4\\ 1.4\\ 1.4\\ 1.4\\ 1.4\\ 1.4\\$

plastid RNA polymerase sigma-subunit identical to plastid RNA polymerase sigma-subunit GI:2398851 from [Arabidopsis thaliana]; supported by cDN	262879 at	1.4
putative SPL1-related protein similar to GB:CAB56770, part of the SBP-box gene family that codes for transcription factors	262798 at	1.4
unknown protein ESTs gb T04357 and gb AA595092 come from this gene;supported by full-length cDNA: Ceres:114103.	262710_at	1.4
unknown protein	262677_at	1.4
late embryogenesis abundant protein (EMB8), putative similar to late embryogenesis abundant protein (EMB8) GI:1350544 from [Picea glauca]	262561 at	1.4
putative glutathione transferase One of three repeated glutathione transferases. 65% identical to glutathione transferase [Arabidopsis thaliana] (gil40		1.4
cytochrome b245 beta chain homolog RbohAp108, putative similar to cytochrome b245 beta chain homolog RbohAp108 GBT03826 G17484893 fro		1.4
unknown protein similar to hypothetical protein GB:AAF07360 from [Arabidopsis thaliana]; supported by cDNA: gi_15810007_gb_AY054272.1_	262346_at	1.4
glycosyl transferase, putative similar to Pfam profile: PF00534 Glycosyl transferases group 1	262155_at	1.4
GTP-binding protein, putative similar to GTP-binding protein GB:AAF31009 GI:6899606 from [Ureaplasma urealyticum]	262086 at	1.4
transcription factor, putative similar to Transcription factor GB:CAA74053 GI:2398533 from [Arabidopsis thaliana]; supported by full-length cDNA: Ce	262098_at	1.4
		1.4
putative DnaJ protein contains Pfam profile: PF00226 DnaJ, prokaryotic heat shock protein; similar to hypothetical protein GB:AAD55462 (Arabidope		
ribosomal protein L7, putative similar to ribosomal protein L7 GB:AAA03081 GI:307388 from [Homo sapiens]	261911_at	1.4
Expressed protein ; supported by full-length cDNA: Ceres: 39481.	261858_at	1.4
transcription factor, putative similar to transcription factor GB:CAA74050 GI:2398525 from [Arabidopsis thaliana]	261803 at	1.4
hypothetical protein predicted by genemark.hmm	261762 at	1.4
ADP-glucose pyrophosphorylase, putative similar to ADP-glucose pyrophosphorylase GB:X78900 GI:556623 from [Beta vulgaris]	_	1.4
	261642_at	
CAF protein identical to RNA helicase/RNAseIII CAF protein GB:AAF03534 GI:6102610 from [Arabidopsis thaliana]; supported by cDNA: gi_1155964		1.4
unknown protein ; supported by cDNA: gi_16604588_gb_AY059739.1_	261538_at	1.4
endoplasmic reticulum-type calcium-transporting ATPase 4 identical to GB:AAD29957 from [Arabidopsis thaliana] (Plant Physiol. 120 (1999) In press.	261433 s at	1.4
fatty acid elongase 3-ketoacyl-CoA synthase, putative similar to GB:AAC99312 from [Arabidopsis thaliana] (Plant J. (1999) In press); supported by c	261420 at	1.4
hypothetical protein contains similarity to Na+/H+ antiporter GI:1655701 from [Xenopus laevis]	261398 at	1.4
	_	
unknown protein ; supported by cDNA: gi_14596146_gb_AY042861.1_	261337_at	1.4
unknown protein ;supported by full-length cDNA: Ceres:6672.	261153_at	1.4
Expressed protein ; supported by full-length cDNA: Ceres: 41453.	260984_at	1.4
dTDP-D-glucose 4,6-dehydratase, putative similar to GI:4128133 from (Homo sapiens); supported by cDNA: gi_15081768_gb_AY048277.1_	260985_at	1.4
unknown protein ; supported by cDNA: gi_15028086_gb_AY045900.1_	260832 at	1.4
unknown protein	260598 at	1.4
unknown protein	260580_at	1.4
putative aminopeptidase similar to aminopeptidase N (alpha-aminoacylpeptide hydrolase) GB:P04825 [Escherichia coli]; contains Pfam profile: PF00	260295_at	1.4
putative phosphoribosylformylglycinamidine synthase similar to GB:KIAA0361 from [Homo sapiens]	260250 at	1.4
putative RNA-binding protein contains Pfam profile: PF00076 RNA recognition motif. (aka RRM, RBD, or RNP domain); similar to putative protein GI	260160 at	1.4
unknown protein similar to C-terminal half of myosin heavy chain: GB:BAA22067 [Cyprinus carpio], GB:P13538 [Gallus gallus], GB:P12847 [Rattus I		1.4
hypothetical protein contains Pfam profile: PF00515 TPR Domain (5 copies)	259973_at	1.4
putative catechol O-methyltransferase similar to catechol O-methyltransferase GB:CAA55358 [Vanilla planifolia]; supported by full-length cDNA: Cere	259878_at	1.4
hypothetical protein contains Pfam profile: PF00439 Bromodomain	259885_at	1.4
unknown protein supported by cDNA: Ceres:35985; supported by cDNA: gi_13877918_gb_AF370222.1_AF370222	259739 at	1.4
putative serine/threonine-protein kinase similar to SERINE/THREONINE-PROTEIN KINASE ASK1 GB:P43291 from [Arabidopsis thaliana];supportec		1.4
myb-related transcription factor (cpm10), putative similar to myb-related transcription factor (cpm10) GB:U33915 GI:1002795 from [Craterostigma pl		1.4
	_	
hypothetical protein ; supported by cDNA: gi_14532585_gb_AY039917.1_	259561_at	1.4
hypothetical protein ; supported by cDNA: gi_13937176_gb_AF372942.1_AF372942	259545_at	1.4
putative glycogen synthase similar to glycogen synthase precursor (Granule-Bound Starch Synthase II) GB:Q43093 from [Pisum sativum]; supported	259277_at	1.4
putative heat-shock protein similar to heat-shock protein precursor GB:S49340 [Secale cereale]; contains Pfam profile: Heat shock hsp90 proteins	259248 at	1.4
hypothetical protein contains bromodomain, predicted by genscan; supported by cDNA: gi 16323116 gb AY057662.1	259164 at	1.4
	_	1.4
alpha subunit of F-actin capping protein supported by full-length cDNA: Ceres:33531.	259111_at	
putative serine carboxypeptidase precursor identical to serine carboxypeptidase precursor GB:P32826 [Arabidopsis thaliana] up to residue 514	258970_at	1.4
putative UDP-glucose pyrophosphorylase similar to UDP-glucose pyrophosphorylase GB:AAB71613 from [Solanum tuberosum]; supported by cDNA	258849_at	1.4
putative ubiquitin carboxyl-terminal hydrolase similar to ubiquitin carboxyl-terminal hydrolase GB:AAF01440 [Schizosaccharomyces pombe]	258780 at	1.4
putative transitional endoplasmic reticulum ATPase identical to cell division cycle protein 48 (CDC48) homolog GB:P54609 (EMBO J. 14 (22), 5626-		1.4
hypothetical protein predicted by genscan; supported by CDNA; gi 15982780 gb AY057497.1_	258660 at	1.4
UDP-glucose:sterol glucosyltransferase UDP-glucose:sterol glucosyltransferase GB:Z83833 [Arabidopsis thaliana]; supported by cDNA: gi_1598277	_	1.4
hypothetical protein	258533_at	1.4
alternative oxidase 1a precursor identical to GB:Q39219 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:116257.	258452_at	1.4
unknown protein ;supported by full-length cDNA: Ceres:13305.	258455 at	1.4
putative coatomer complex subunit similar to subunit of coatomer complex GB:X70476 from [Homo sapiens]	258331 at	1.4
myosin heavy chain-like protein similar to myosin heavy chain GB:L03534 from [Entamoeba histolytica]	258333 at	1.4
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_15028198_gb_AY045922.1_	258206_at	1.4
hypothetical protein predicted by genemark.hmm	258126_at	1.4
putative cytochrome P450 similar to GB:Q05047 from [Catharanthus roseus]	258114_at	1.4
FtsH protease, putative contains similarity to cell division protein FtsH GI:1652085 from [Synechocystis sp. PCC 6803]	258048_at	1.4
calmodulin-binding protein, putative contains Pfam profile: PF00612 IQ calmodulin-binding motif (3 copies)	257883_at	1.4
Appointed and protein predicted by genemark. I him promet 1 00012 to composite protein (0 00000)	257864_at	1.4
RING zinc finger protein, putative contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)		
	257826_at	1.4
hypothetical protein predicted by genscan+	257708_at	1.4
root hair defective 3 (RHD3) identical to GB:AAB58375 from [Arabidopsis thaliana] (Genes Dev (1997) 11(6), 799-811)	257606_at	1.4
unknown protein ; supported by cDNA: gi_13811668_gb_AF356816.1_AF356816	256681_at	1.4
unknown protein contains similarity to phospholipase a-2-activating protein SP:P27612 from [Mus musculus]; supported by cDNA: gi 15294239 gb	256657 at	1.4
myosin identical to myosin GB:CAB61875 GI:6491702 [Arabidopsis thaliana]	256623 at	1.4
hypothetical protein	256210 at	1.4
4-coumarate:CoA ligase 1 identical to 4-coumarate:CoA ligase 1 [Arabidopsis thaliana] GI:5702184; supported by cDNA: gi_609339_gb_U18675.1_/		1.4
hypothetical protein contains similarity to nuclear DNA helicase II GI:577738 from [Bos taurus]	256140_at	1.4
hypothetical protein similar to putative glutamine dependent NAD+ synthetase GB:074940 GI:8928216 from [Schizosaccharomyces pombe]	256148_at	1.4
p68 RNA helicase, putative similar to p68 RNA helicase (Schizosaccharomyces pombe) GI:173419	255749 at	1.4
putative protein	255664 at	1.4
Expressed protein ; supported by full-length cDNA: Ceres: 39479.	255671_at	1.4
hypothetical protein	255604_at	1.4
predicted protein of unknown function	255544_at	1.4
coded for by A. thaliana cDNA T04215 similar to epoxide hydrolases	255525 at	1.4
tryptophan synthase alpha 1-like protein similar to A. thaliana tryptophan synthase alpha chain (EC 4.2.1.20), GenBank accession number U18993	200020_at	
	255487_at	1.4
	255487_at	
hypothetical protein	255487_at 255429_at	1.4
hypothetical protein	255487_at 255429_at 255348_at	1.4 1.4
putative protein glutamic acid-rich protein precursor - Plasmodium falciparum, PIR2:A54514	255487_at 255429_at 255348_at 255128_at	1.4 1.4 1.4
putative protein glutamic acid-rich protein precursor - Plasmodium falciparum, PIR2:A54514 putative zinc finger protein	255487_at 255429_at 255348_at 255128_at 255094_at	1.4 1.4 1.4 1.4
putative protein glutamic acid-rich protein precursor - Plasmodium falciparum, PIR2:A54514	255487_at 255429_at 255348_at 255128_at	1.4 1.4 1.4
putative protein glutamic acid-rich protein precursor - Plasmodium falciparum, PIR2:A54514 putative zinc finger protein	255487_at 255429_at 255348_at 255128_at 255094_at	1.4 1.4 1.4 1.4
putative protein glutamic acid-rich protein precursor - Plasmodium falciparum, PIR2:A54514 putative zinc finger protein putative protein hypothetical protein sll1775 - Synechocystis sp.,PIR2:S77106 lipase-like protein monoglyceride lipase - Mus musculus, PID.e1184892;supported by full-length cDNA: Ceres:6822.	255487_at 255429_at 255348_at 255128_at 255094_at 255008_at 255010_at	1.4 1.4 1.4 1.4 1.4 1.4
putative protein glutamic acid-rich protein precursor - Plasmodium falciparum, PIR2:A54514 putative zinc finger protein putative protein hypothetical protein sll1775 - Synechocystis sp.,PIR2:S77106 lipase-like protein monoglyceride lipase - Mus musculus, PID:e1184892;supported by full-length cDNA: Ceres:6822. putative translation initiation factor IF-2 translation initiation factor IF-2 - Haemophilus influenzae, PIR2:E64114	255487_at 255429_at 255348_at 255128_at 255094_at 255008_at 255010_at 254904_at	1.4 1.4 1.4 1.4 1.4 1.4 1.4
putative protein glutamic acid-rich protein precursor - Plasmodium falciparum, PIR2:A54514 putative zinc finger protein putative protein hypothetical protein sll1775 - Synechocystis sp.,PIR2:S77106 lipase-like protein monoglyceride lipase - Mus musculus, PID.e1184892;supported by full-length cDNA: Ceres:6822.	255487_at 255429_at 255348_at 255128_at 255094_at 255008_at 255010_at	1.4 1.4 1.4 1.4 1.4 1.4

putative protein IFA-binding protein, Arabidopsis thaliana, AF004556	254724_at	1.4
putative protein KIAA0682 protein, Homo sapiens, AB014582	254527_at	1.4
acyl-CoA synthetase - like protein acyl-CoA synthetase, Brassica napus, X94624; supported by cDNA: gi_15146195_gb_AY049239.1_	254192_at	1.4
putative protein several hypothetical proteins - Arabidopsis thaliana	254061_at	1.4
putative phosphatidylserine decarboxylase phosphatidylserine decarboxylase (EC 4.1.1.65) 2 - yeast, Pir2:S64484	254035_at	1.4
	253994_at	1.4
sucrase-like protein sucrose cleavage protein - potato, Pir2:S51376;supported by full-length cDNA: Ceres:111209.	253980_at	1.4
Avr9 elicitor response like protein Avr9 elicitor response protein - Nicotiana tabacum, PID:e1363999;supported by full-length cDNA: Ceres:149102.	253948_at	1.4
NADPH-ferrihemoprotein reductase (ATR2)	253664_at	1.4
putative protein putative ATPase - Haematobia irritans,PID:g525318;supported by full-length cDNA: Ceres:4.	253630_at	1.4
putative zinc finger protein hypothetical protein YLR387c, Saccharomyces cerevisiae, PIR2:S51474; supported by cDNA: gi_13878012_gb_AF3702	253526_at	1.4
putative protein predicted protein T10M13.8, Arabidopsis thaliana	253446_at	1.4
putative protein protein phosphatase Wip1, Homo sapiens, PID:g2218063;supported by full-length cDNA: Ceres:40123.	253323_at	1.4
protein kinase - like protein protein kinase, 41K, Arabidopsis thaliana,PIR2:S71172; supported by cDNA: gi_15451087_gb_AY054624.1_	253264_at	1.4
putative protein ;supported by full-length cDNA: Ceres:32357.	253229_at	1.4
	253042_at	1.4
glycine hydroxymethyltransferase like protein glycine hydroxymethyltransferase -Solanum tuberosum, PID:g438247; supported by full-length cDNA: C	253009_at	1.4
	252613_at	1.4
	252570_at	1.4
	252469_at	1.4
ABC-type transport protein-like protein AbcA, Dictyostelium discoideum, DDU66526	252379_at	1.4
BCS1 protein-like protein Homo sapiens h-bcs1 (BCS1) mRNA, nuclear gene encoding mitochondrial protein which is involved in the expression of f	_	1.4
CDC48 - like protein transitional endoplasmic reticulum ATPase, Arabidopsis thaliana, PIR:S60112	251975_at	1.4
	251876_at	1.4
	251887_at	1.4
putative protein GTP-binding regulatory protein beta chain, Dictyostelium discoideum, PIR:A47370; supported by cDNA: gi_13430701_gb_AF36026 putative protein MSP58 - nucleolar protein, Mus musculus, EMBL:AF015309; supported by cDNA: gi_17063177_gb_AY062111.1_	251866 at	1.4 1.4
	251600_at 251646_at	1.4
	251040_at 251253 at	1.4
	251255_at 251198_at	1.4
	251196_at 251143 at	1.4
	251145_at 251084_at	1.4
	251004_at	1.4
putative protein mation enzer, garden in too into a support as y terregarden to the objects. Too: putative protein PSB protein, Bos primigenius taurus, PIR-A56534; supported by full-length cDNA: Ceres:146009.	250930 at	1.4
putative protein ; supported by cDNA: gi 14423557 gb AF387016. A F387016	250897 at	1.4
	250711 at	1.4
	250729 at	1.4
	250598 at	1.4
	250604 at	1.4
nucleoid DNA-binding protein cnd41 - like protein nucleoid DNA-binding protein cnd41, chloroplast, common tobacco, PIR:T01996	250446 at	1.4
	250305 at	1.4
	250238 at	1.4
•	250197 at	1.4
2-hydroxyphytanoyl-CoA lyase-like protein	250094 at	1.4
	250035 at	1.4
	249866 at	1.4
	249792 at	1.4
putative protein tyrosine aminotransferase-like; also similar to nicotianamine aminotransferase	249688 at	1.4
	249454 at	1.4
putative protein similar to unknown protein (pir  T30561)	249240_at	1.4
5-3 exoribonuclease 2 ; supported by cDNA: gi_11875629_gb_AF286720.1_AF286720	249200_at	1.4
GTP-binding protein-like; root hair defective 3 protein-like	248985_at	1.4
disease resistance protein-like	248995_at	1.4
ornithine aminotransferase	248879_at	1.4
putative protein contains similarity to peptide:N-glycanase	248615_at	1.4
putative protein similar to unknown protein (sp O15736)	248543_at	1.4
DEAD-box protein abstrakt	248442_at	1.4
cleavage and polyadenylation specificity factor subunit	248418_at	1.4
SKP1 interacting partner 1 (SKIP1) identical to SKP1 interacting partner 1 GG:10716947 from [Arabidopsis thaliana]; supported by full-length cDNA: C		1.4
subtilisin-like serine protease contains similarity to prepro-cucumisin GI:807698 from [Cucumis melo]	247760_at	1.4
serine/threonine-specific protein kinase - like putative protein serine /threonine kinase, Sorghum bicolor, EMBL:SBRLK1	247684_at	1.4
carbonyl reductase - like protein inducible carbonyl reductase, Rattus norvegicus, EMBL:RND0691	247489_at	1.4
	247410_at	1.4
	247298_at 247186_at	1.4 1.4
	247166_at 247155_at	1.4 1.4
	247156 at	1.4
	247012 at	1.4
calcium-dependent protein kinase; supported by CDNA; gi 289189, gb_14771.1_ATHCALLIPR	246955 at	1.4
	246962_s_at	1.4
putative protein CG6949 - Drosophila melanogaster, EMBL:AE003739	246767 at	1.4
	246583 at	1.4
	246496 at	1.4
	246501 at	1.4
quinone oxidoreductase - like protein probable quinone oxidoreductase (EC 1.6.5.5) P1, Arabidopsis thaliana, PIR:S57612;supported by full-length (		1.4
	246173_s_at	1.4
putative protein	246111_at	1.4
RAN GTPase activating protein 2 ; supported by cDNA: gi_6708467_gb_AF214560.1_AF214560	246061_at	1.4
		1.4
chorismate synthase, putative similar to chorismate synthase GI:452796 from [Synechocystis sp.]; supported by cDNA: gi_15982823_gb_AY057519	245832_at	1.4
	245751_s_at	1.4
unknown protein	245678_at	1.4
unknown protein similar to receptor-like protein kinase GI:7529754 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:36000.	245657_at	1.4
putative protein	245588_at	1.4
disease resistance RPP5 like protein	245448_at	1.4
	245200_at	1.4
regulator of chromosome condensation (cell cycle regulatory protein) like	248693_at	1.3

unknown protein	247350_at	1.3
hypothetical protein predicted by genscan; similar to SP[Q09288]YQO9_CAEEL	267632_at	1.3
putative protein disulfide isomerase ; supported by cDNA: gi_15810003_gb_AY054270.1_	267605_at 267543 at	1.3 1.3
26S proteasome regulatory subunit hypothetical protein predicted by genscan	267543_at 267508_at	1.3
hypothetical proton protonal by general putative CCAAT-binding transcription factor subunit	267315 at	1.3
unknown protein	267269 at	1.3
putative methylenetetrahydrofolate reductase ; supported by cDNA: gi_15215809_gb_AY050434.1_	267187_s_at	1.3
putative acetone-cyanohydrin lyase	267127_at	1.3
putative phosphatidylinositol-4-phosphate 5-kinase ; supported by cDNA: gi_13925628_gb_AF260903.1_AF260903	267081_at	1.3
unknown protein ; supported by cDNA: gi_15292712_gb_AY050790.1_	266898_at	1.3
putative signal recognition particle receptor (alpha subunit); supported by cDNA: gi_15293184_gb_AY051026.1_	266867_at	1.3
unknown protein	266763_at	1.3
Expressed protein ; supported by full-length cDNA: Ceres: 17422. putative CCCH-type zinc finger protein ;supported by full-length cDNA: Ceres:101255.	266767_at 266695_at	1.3 1.3
unknown protein	266652 at	1.3
putative splicing factor ;supported by full-length cDNA: Ceres:16224.	266534 at	1.3
putative phospholipid cytidylyltransferase	266399 at	1.3
unknown protein	266389_s_at	1.3
unknown protein ;supported by cDNA: gi_16604650_gb_AY059770.1_	266121_at	1.3
unknown protein ;supported by full-length cDNA: Ceres:40538.	266093_at	1.3
putative protein kinase contains a protein kinase domain profile (PDOC00100); supported by cDNA; gi_15810412_gb_AY056245.1_	266037_at	1.3
putative NADP-dependent glyceraldehyde-3-phosphate dehydrogenase ; supported by cDNA: gi_14335051_gb_AY037205.1_	265998_at	1.3
hypothetical protein predicted by genscan and genefinder unknown protein	265957_at 265779_at	1.3 1.3
unition poetin	265729 at	1.3
putative dioxygenase ; supported by cDNA: gi 15292706 gb AY050787.1	265615 at	1.3
putative inorganic pyrophosphatase ;supported by full-length cDNA: Ceres:8068.	265339 at	1.3
succinyl-CoA ligase beta subunit ;supported by full-length cDNA: Ceres:36904.	265257_at	1.3
integral membrane protein, putative similar to integral membrane protein GI:1209755 from [Beta vulgaris]	264992_at	1.3
unknown protein ; supported by cDNA: gi_13926184_gb_AF370567.1_AF370567	264958_at	1.3
phosphatidylinositol 3-kinase, putative similar to phosphatidylinositol 3-kinase GI:736338 from [Glycine max]; supported by cDNA: gi_555699_gb_U		1.3
NBS/LRR disease resistance protein, putative similar to NBS/LRR disease resistance protein GI:3309619 from [Arabidopsis thaliana]; supported by		1.3
putative DNA-binding protein, Myb Identical to A. thaliana Myb-like protein (gb)D58424); supported by cDNA: gj_1747309_dbj_D58424,1_D58424	264709_at	1.3
tat-binding protein, putative Highly Similar to branched-chain amino acid aminotransferase; Location of EST gb[T44177 and gb]AA395381; supporte CTP synthase-like protein similar to ctp synthase (sp]P17812[PYRG HUMAN); similar to ESTs gb]AA660762, gb]AA220982, dbj]AU008137, gb]Al0!		1.3 1.3
unknown protein similar to EST gb/N96077; supported by cDNA: g1 15810035 gb AY054286.1	264407 at	1.3
putative aspartic proteinase similar to GB:AC49730;supported by full-length cDNA: Ceres:8972.	264344 at	1.3
unknown protein Contains similarity to tetratricopeptide repeat protein gb/U46571 from home sapiens. EST gb/Z47802 and gb/Z48402 come from thi		1.3
hypothetical protein similar to hypothetical protein GI:2894571 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:30230.	264287_at	1.3
unknown protein Similar to hypothetical protein C34B7.2 gb 1729503 from C. elegans cosmid gb Z83220	264197_at	1.3
unknown protein ;supported by full-length cDNA: Ceres:151404.	264086_at	1.3
putative ubiquitin fusion-degradation protein ;supported by full-length cDNA: Ceres:34470.	263756_at	1.3
hypothetical protein predicted by genscan; supported by cDNA: gi_16604630_gb_AY059760.1_	263766_at	1.3
putative receptor-like protein kinase	263590_at 263333_at	1.3 1.3
unknown protein ; supported by cDNA: gi_15810174_gb_AY056101.1_ putative nonsense-mediated mRNA decay protein ; supported by cDNA: gi_15810402_gb_AY056240.1_	263333_at 263334_at	1.3
putative GTP-binding protein Similar to WO8E3.3 gil3880615 putative GTP-binding protein from C. elegans cosmid gb/Z92773. EST gb/A4597331 or		1.3
Ca2+-dependent lipid-binding protein, putative similar to Ca2+-dependent lipid-binding protein (CLB1) GI:2789434 from (Lycopersicon esculentum)	263205 at	1.3
unknown protein Similar to gb U51990 pre-mRNA-splicing factor hPrp18 from Homo sapiens. ESTs gb T46391 and gb AA721815 come from this ger		1.3
hypothetical protein predicted by genscan and genefinder	263085_at	1.3
glutathione S-transferase, putative similar to similar to glutathione S-transferase GB:AAF29773 GI:6856103 from (Gossypium hirsutum); supported b		1.3
putative membrane-associated salt-inducible protein strong similarity to gi]3367521 F8K4.8 from Arabidopsis thaliana BAC gb]AC004392;supported I		1.3
anthranilate N-hydroxycinnamoyl/benzoyltransferase, putative similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase GB:Z84384 GI:22390E		1.3
lipase, putative contains Pfam profile: PF00657 Lipase/Acylhydrolase with GDSL-like motif; supported by cDNA: gi_13937188_gb_AF372948.1_AF; putative translation initiation factor IF2 [Except for first 311 amino acids, 41% identical to translation initiation factor IF2 [Bacillus subtilis] (gi]124209)		1.3 1.3
hypothetical protein similar to hypothetical protein GB:AD50003 GI:5734738 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:3759		1.3
hypothetical protein identical to hypothetical protein GB:AAD50051 GI:5734786 from [Arabidopsis thaliana]; supported by cDNA; gi_15081661_gb_A		1.3
serpin, putative similar to serpin GB:X95277 GI:1197576 from (Hordeum vulgare)	262440 at	1.3
hypothetical protein contains similarity to phosphatidylinositol 4-kinase 230 GI:2326227 from [Homo sapiens]	262387_s_at	1.3
betaine aldehyde dehydrogenase, putative similar to betaine aldehyde dehydrogenase GI:2388709 from [Amaranthus hypochondriacus]:supported t		1.3
beta-glucosidase, putative similar to beta-glucosidase GI:5030906 from [Polygonum tinctorium]; supported by cDNA: gi_15146265_gb_AY049274.1		1.3
putative heat-shock protein contains Pfam profile: PF0012 Heat shock hspr0 proteins; similar to heat-shock proteins GB:CAA94389, GB:AAD5546 (Section 2014) (		1.3
calcium-dependent protein kinase identical to GB:BAA04830 GI:604881 from [Arabidopsis thaliana]; supported by cDNA: gi_15293094_gb_AY0509i glutamate decarboxylase (gad), putative similar to glutamate decarboxylase (gad) GI:294111 from [Petunia hybrida]; supported by cDNA: gi_118495		1.3 1.3
glutanate declatoxytase (gad), putative similar to glutanate declatoxytase (gad) (3.254111 non (Fetunia honiza), supported by CDVA, g_11045C hypothetical protein predicted by genemark.hmm	261970_at 261909 at	1.3
4-coumarate:CoA ligase 3 identical to 4-coumarate:CoA ligase 3 GI:5702190 from [Arabidopsis thaliana]; supported by cDNA; gi 5702191 gb AF10		1.3
scarecrow-like protein similar to SCARECROW GB:AAB06318 GI:1497987 from [Arabidopsis thaliana]; supported by cDNA: gi 14334475 gb AY03-	_	1.3
ABC transporter, putative similar to ABC transporter GI:9279716 from [Arabidopsis thaliana]	261763_at	1.3
wall-associated kinase 4, putative similar to wall-associated kinase 4 GI:3355308 from [Arabidopsis thaliana]	261402_at	1.3
CMP-KDO synthetase, putative similar to GB:CAB89846 from [Zea mays]	261373_at	1.3
unknown protein similar to Glu-tRNAGIn amidotransferase subunit B GB:AAB83965; supported by cDNA: gi_11078539_gb_AF239836.1_AF239836	261307_at	1.3
unknown protein ; supported by cDNA: gi_15450835_gb_AY054498.1_ hypothetical protein contains Pfam profile: PF00534 glycosyl transferases group 1	261127_at	1.3
nyponetical protein contains Pram prome. Provosy gycosy iranserases group i sec14 cytosolic factor, putative similar to SPT24859 from [Kluyveromyces lactis]	261138_at 261116_at	1.3 1.3
sec + Gyussien factor, putative similar to or - 24009 into (Gyusyetoniyee) factor	260989 at	1.3
unknown protein similar to unknown protein GB:AAF18609 GI:6598419 from [Arabidopsis thaliana]	260884_at	1.3
unknown protein similar to putative cytoskeletal protein GI:1732517 from [Arabidopsis thaliana]; supported by cDNA: gi_1732516_gb_U62745.1_ATL		1.3
putative zinc protease member of insulinase protein family	260554_at	1.3
DHHC-type zinc finger protein, putative contains Pfam profile: PF01529: DHHC zinc finger domain	260347_at	1.3
putative protein kinase similar to C-terminal region of s-receptor kinases GB:BAA2132, GB:BAA06285 [Brassica rapa]; Pfam HMM hit: Eukaryotic putative protein kinase similar to C-terminal region of s-receptor kinases GB:BAA2132, GB:BAA06285 [Brassica rapa]; Pfam HMM hit: Eukaryotic putative protein kinases similar to C-terminal region of s-receptor kinases GB:BAA2132, GB:BAA06285 [Brassica rapa]; Pfam HMM hit: Eukaryotic putative protein kinases similar to C-terminal region of s-receptor kinases GB:BAA2132, GB:BAA06285 [Brassica rapa]; Pfam HMM hit: Eukaryotic putative protein kinases similar to C-terminal region of s-receptor kinases GB:BAA2132, GB:BAA06285 [Brassica rapa]; Pfam HMM hit: Eukaryotic putative protein kinases similar to C-terminal region of s-receptor kinases GB:BAA2132, GB:BAA06285 [Brassica rapa]; Pfam HMM hit: Eukaryotic putative protein kinases similar to C-terminal region of s-receptor kinases GB:BAA2132, GB:BAA06285 [Brassica rapa]; Pfam HMM hit: Eukaryotic putative protein kinases similar to C-terminal region of s-receptor kinases GB:BAA2132, GB:BAA06285 [Brassica rapa]; Pfam HMM hit: Eukaryotic putative protein kinases similar to C-terminal region of s-receptor kinases GB:BAA2132, GB:BAA06285 [Brassica rapa]; Pfam HMM hit: Eukaryotic putative putat		1.3
unknown protein identical to most of OBP32pep protein (fragment) GB:S71212 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:23753.	260304_at	1.3
unknown protein hypothetical protein predicted by genscan	260155_at 260087_at	1.3 1.3
putative chlorophyll A-B binding protein similar to chlorophyll A-B binding protein GB:P12470 [Nicotiana plumbaginifolia]; contains Pfam profile: PF00		1.3
cytosolic factor, putative similar to Gis07956 from [Saccharomyces cerevisiae], supported by cDNA: gi 1508113 gb AY048199.1	259804 at	1.3
	259767_s_at	1.3

unknown protein	259771_at	1.3
putative thioredoxin similar to protein disulfide isomerase precursor GB:P29828 [Medicago sativa]; Pfam HMM hit: Thioredoxins	259757_at	1.3
hypothetical protein contains similarity to invertase inhibitor GB:CAA73333 GI:2765240 from [Nicotiana tabacum]; supported by full-length cDNA: Cei	259616_at	1.3
hypothetical protein	259633_at	1.3
unknown protein	259489_at	1.3
unknown protein	259470_at	1.3
(1-4)-beta-mannan endohydrolase precursor, putative similar to (1-4)-beta-mannan endohydrolase precursor GI:9836826 from [Lycopersicon escule	_	1.3
	259408_at	1.3
unknown protein	259292_at	1.3
hypothetical protein predicted by genscan	259219_at	1.3
	259173_at	1.3
transcription initiation factor IIB (TFIIB) identical to AtTFIIB2 GB:CAA84309 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:38950.	259155_at	1.3
putative auxin-independent growth promoter similar to auxin-independent growth promoter GB:A44226 (histoitana tabacum];supported by full-length (		1.3
putative ribosomal-protein S6 kinase (ATPK19) identical to putative ribosomal-protein S6 kinase (ATPK19) GB:D42061 [Arabidopsis thaliana] (FEBS	_	1.3
unknown protein	258635_at	1.3
unknown protein	258316_at	1.3
unknown protein ;supported by full-length cDNA: Ceres:141813. unknown protein similar to CGI-18 protein GB:AAD27727 [Homo sapiens]	258078_at 258053 at	1.3 1.3
unknown protein	258055_at 258017_at	1.3
ethylene-insensitive 3 (EIN3) identical to GB:AAC49749 from [Arabidopsis thaliana]	257981_at	1.3
mitogen activated protein kinase kinase, putative similar to mitogen activated protein kinase GB:AAC32599 from [Oryza sativa]	257801_at	1.3
TP-synthetase, putative similar to CTP synthetase GB:049350 GI:1515356 (Mus musculus)	257702 at	1.3
Expressed protein i supported by full-length cDNA: Ceres: 22745.	257271 at	1.3
hemolysin-like protein similar to hemolysin C GB:Q54318 [Brachyspira hyodysenteriae]	257178 at	1.3
unknown protein	257092 at	1.3
ATPase, putative similar to spastin protein GB:CAB60141 from [Homo sapiens] (Hum. Mol. Genet. (2000) 9, 637-644)	257046 at	1.3
CLC-b chloride channel protein identical to CLC-b chloride channel protein GB:CAA96058 from [Arabidopsis thaliana] (J. Biol. Chem. 271 (52), 3363	256751 at	1.3
auxin-independent growth promoter, putative similar to GB:A44226 from [Nicotiana tabacum] (Science 258 (5086), 1350-1353 (1992))	256706_at	1.3
unknown protein	256542_at	1.3
protein kinase, putative contains Pfam profile: PF00069: Eukaryotic protein kinase domain	256366_at	1.3
unknown protein ; supported by cDNA: gi_14194136_gb_AF367274.1_AF367274	256343_at	1.3
unknown protein ;supported by full-length cDNA: Ceres:10857.	256301_at	1.3
calreticulin (crt1) identical to calreticulin (crt1) GI:2052379 [Arabidopsis thaliana]; supported by cDNA: gi_2052378_gb_U66343.1_ATU66343	256216_at	1.3
ubiquitin-specific protease 6 (UBP6), putative similar to GI:11993465;supported by full-length cDNA: Ceres:116145.	256179_at	1.3
fructose-2,6-bisphosphatase, putative similar to fructose-2,6-bisphosphatase GI:8572069 from [Arabidopsis thaliana]; supported by cDNA: gi_13096		1.3
carbamoy/phosphate synthetase, putative similar to carbamoy/phosphate synthetase GI:6552726 from [Medicago sativa]; supported by cDNA: gi_14		1.3
hypothetical protein predicted by genscan+	255891_at	1.3
hypothetical protein predicted by genscan and genefinder; similar to EGAD[50981]VBR228W	255866_at	1.3
putative steroid dehydrogenase ; supported by cDNA: gi_16226672_gb_AF428460.1_AF428460 predicted protein of unknown function	255797_at 255681_at	1.3 1.3
hypothetical protein	255573 at	1.3
nyponencial potent	255294 at	1.3
putative borgen vanaponent putative homeotic protein ; supported by cDNA: gi_15983371_gb_AF424560.1_AF424560	255277 at	1.3
predicted protein of unknown function	255181 at	1.3
putative protein proteins of this bac	255087 at	1.3
COP1 like protein photomorphogenesis repressor COP1 - Arabidopsis thaliana, PIR2:T01112	254966 at	1.3
KI domain interacting kinase 1 -like protein KI domain interacting kinase 1 - Zea mays,PID:g2735017	254870 at	1.3
hypothetical protein supported by full-length cDNA: Ceres:151415.	254844_at	1.3
putative protein phospho-N-acetylmuramoyl-pentapeptide-transferase, Haemophilus influenzae, Pir2:A64185	254662_at	1.3
initiation factor-2Bepsilon-like protein initiation factor-2Be, Rattus norvegicus, PATCHX:G924597	254664_at	1.3
	254593_s_at	1.3
putative protein gene F4P9.34 chromosome II BAC F4P9, Arabidopsis thaliana	254508_at	1.3
berberine bridge enzyme - like protein ; supported by cDNA: gi_14194126_gb_AF367269.1_AF367269	254447_at	1.3
putative protein predicted protein, Arabidopsis thaliana, PATCHX:G2494119;supported by full-length cDNA: Ceres:106883.	254427_at	1.3
gamma-glutamylcysteine synthetase; supported by cDNA: gi_15912188_gb_AY056372.1_	254270_at 254247 at	1.3
putative protein receptor protein kinase, Ipomoea trifida	_	1.3 1.3
argininosuccinate synthase -like protein argininosuccinate synthase, Aquifex aeolicus, PIR2:B70398 putative protein proliferating-cell nucleolar antigen P120 -Homo sapiens,PIR2:A48168	254134_at 253975 at	1.3
putative protein promittaining contracted at angert 120 months application application of the second s	253954_at	1.3
putative protein	253897_at	1.3
pelota (PEL1)	253882 at	1.3
SOF1 protein-like protein SOF1 (involved in rRNA processing) protein-yeast; supported by cDNA: gi 13937178 gb AF372943.1 AF372943	253777 at	1.3
putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:19314.	253789_at	1.3
putative protein ;supported by full-length cDNA: Ceres:12759.	253752_at	1.3
X-Pro dipeptidase - like protein (fragment) X-Pro dipeptidase, Homo sapiens, PIR2:A32454	253704_at	1.3
putative protein kinase serine/threonine protein kinase, Arabidopsis thaliana, PID:D1006875; supported by cDNA: gi_14334745_gb_AY035046.1_	253550_at	1.3
putative protein deubiquitinating enzyme (DUB-1), Mus musculus, PIR2:JC6133	253542_at	1.3
predicted protein predicted protein on BAC T06B20; Arabidopsis thaliana chromosome II; PATCHX:G1946371	253501_at	1.3
putative protein peptidyl-prolyl cis-trans isomerase, Schizosaccharomyces pombe, gb:SPBC16H5	253415_at	1.3
P-Protein - like protein P-Protein precursor, Solanum tuberosum, gb:Z99770; supported by cDNA: gi 14596024 gb AY042800.1		1.3
	253387_at	1.3
putative protein ; supported by cDNA: gi_13605598_gb_AF361625.1_AF361625	253388_at	4.0
putative protein ; supported by cDNA: gi_13605598_gb_AF361625.1_AF361625 gamma-VPE (vacuolar processing enzyme) ; supported by cDNA: gi_13877794_gb_AF370160.1_AF370160	253388_at 253358_at	1.3
putative protein ; supported by cDNA: gi_13605598_gb_AF361625.1_AF361625 gamma-VPE (vacuolar processing enzyme) ; supported by cDNA: gi_13877794_gb_AF370160.1_AF370160 putative protein hemolysin, 38K, Synechocystis sp., Pir2:S75595	253388_at 253358_at 253351_at	1.3
putative protein ; supported by cDNA: gi_13605598_gb_AF361625.1_AF361625 gamma-VPE (vacuolar processing enzyme) ; supported by cDNA: gi_13877794_gb_AF370160.1_AF370160 putative protein hemolysin, 38K, Synechocystis sp., Pir2:S75595 putative protein B subunit of propionyl-CoA carboxylase, Mycobacterium tuberculosis, PATCHX:E290075; supported by cDNA: gi_14423377_gb_AF	253388_at 253358_at 253351_at 253279_at	1.3 1.3
putative protein ; supported by cDNA: gi_13605598_gb_AF361625.1_AF361625 gamma-VPE (vacuolar processing enzyme) ; supported by cDNA: gi_13877794_gb_AF370160.1_AF370160 putative protein hemolysin, 38K, Synechocystis sp., Pir2:S75595 putative protein B subunit of propionyl-CoA carboxylase, Mycobacterium tuberculosis, PATCHX:E290075; supported by cDNA: gi_14423377_gb_AF Nonclathrin coat protein gamma - like protein coat protein gamma-cop, Bos primigenius	253388_at 253358_at 253351_at 253279_at 253231_at	1.3 1.3 1.3
putative protein ; supported by cDNA: gi_13605598_gb_AF361625.1_AF361625 gamma-VPE (vacuolar processing enzyme) ; supported by cDNA: gi_13877794_gb_AF370160.1_AF370160 putative protein hemolysin, 38K, Synechocystis sp., Pir2:S75595 putative protein B subunit of propionyl-CoA carboxylase, Mycobacterium tuberculosis, PATCHX:E290075; supported by cDNA: gi_14423377_gb_AF Nonclathrin coat protein gamma - like protein coat protein gamma -cop, Bos primigenius putative squalene synthase non-consensus GC donor splice site at exon 3, squalene synthase 2 (SQS2), Arabidopsis thaliana; supported by cDNA:	253388_at 253358_at 253351_at 253279_at 253231_at 253206_at	1.3 1.3 1.3 1.3
putative protein ; supported by cDNA: gi_13605598_gb_AF361625.1_AF361625 gamma-VPE (vacuolar processing enzyme) ; supported by cDNA: gi_13877794_gb_AF370160.1_AF370160 putative protein hemolysin, 38K, Synechocystis sp., Pir2:S75595 putative protein B subunit of propionyl-CoA carboxylase, Mycobacterium tuberculosis, PATCHX:E290075; supported by cDNA: gi_14423377_gb_AF Nonclathrin coat protein gamma - like protein coat protein gamma-cop, Bos primigenius putative squalene synthase non-consensus GC donor splice site at exon 3, squalene synthase 2 (SQS2), Arabidopsis thaliana; supported by cDNA: putative protein predicted proteins, Arabidopsis thaliana	253388_at 253358_at 253351_at 253279_at 253231_at 253206_at 253107_at	1.3 1.3 1.3 1.3 1.3
putative protein ; supported by cDNA: gi_13605598_gb_AF361625.1_AF361625. gamma-VPE (vacuolar processing enzyme) ; supported by cDNA: gi_13877794_gb_AF370160.1_AF370160 putative protein hemolysin, 38K, Synechocystis sp., Pir2:S75595 putative protein B subunit of propionyl-CoA carboxylase, Mycobacterium tuberculosis, PATCHX:E290075; supported by cDNA: gi_14423377_gb_AF Nonclathrin coat protein gamma - like protein coat protein gamma-cop, Bos primigenius putative squalene synthase non-consensus GC donor splice site at exon 3, squalene synthase 2 (SQS2), Arabidopsis thaliana; supported by cDNA: putative protein KIAA0776 protein, Homo sapiens, EMBL:AB018319; supported by cDNA: gi_14334491_gb_AY034937.1_	253388_at 253358_at 253351_at 253279_at 253231_at 253206_at 253107_at 252513_at	1.3 1.3 1.3 1.3 1.3 1.3
putative protein ; supported by cDNA: gi_13605598_gb_AF361625.1_AF361625 gamma-VPE (vacuolar processing enzyme) ; supported by cDNA: gi_13877794_gb_AF370160.1_AF370160 putative protein hemolysin, 38K, Synechocystis sp., Pir2:S75595 putative protein B subunit of propionyl-CoA carboxylase, Mycobacterium tuberculosis, PATCHX:E290075; supported by cDNA: gi_14423377_gb_AF Nonclathrin coat protein gamma - like protein coat protein gamma-cop, Bos primigenius putative squalene synthase non-consensus GC donor splice site at exon 3, squalene synthase 2 (SQS2), Arabidopsis thaliana; supported by cDNA: putative protein predicted proteins, Arabidopsis thaliana	253388_at 253358_at 253351_at 253279_at 253231_at 253206_at 253107_at	1.3 1.3 1.3 1.3 1.3
putative protein ; supported by cDNA: gi_13605598_gb_AF361625.1_AF361625 gamma-VPE (vacuolar processing enzyme) ; supported by cDNA: gi_13877794_gb_AF370160.1_AF370160 putative protein hemolysin, 38K, Synechocystis sp., Pir2:S75595 putative protein B subunit of propionyl-CoA carboxylase, Mycobacterium tuberculosis, PATCHX:E290075; supported by cDNA: gi_14423377_gb_AF Nonclathrin coat protein gamma - like protein coat protein gamma-cop, Bos primigenius putative squalene synthase non-consensus GC donor splice site at exon 3, squalene synthase 2 (SQS2), Arabidopsis thaliana; supported by cDNA: putative protein IRA0776 protein, Homo sapiens, EMBL:AB018319; supported by cDNA: gi_14334491_gb_AY034937.1_ FtsH protease, putative contains similarity to FtsH protease GI:13183728 from [Medicago sativa]	253388_at 253358_at 253351_at 253279_at 253206_at 253206_at 253107_at 252513_at 2522449_at 252431_at	1.3 1.3 1.3 1.3 1.3 1.3 1.3
putative protein ; supported by cDNA: gi_13605598_gb_AF361625.1_AF361625 gamma-VPE (vacuolar processing enzyme) ; supported by cDNA: gi_13877794_gb_AF370160.1_AF370160 putative protein hemolysin, 38K, Synechocystis sp., Pir2:S75595 putative protein B subunit of propionyl-CoA carboxylase, Mycobacterium tuberculosis, PATCHX:E290075; supported by cDNA: gi_14423377_gb_AF Nonclathrin coat protein gamma - like protein coat protein gamma-cop, Bos primigenius putative squalene synthase non-consensus GC donor splice site at exon 3, squalene synthase 2 (SQS2), Arabidopsis thaliana; supported by cDNA: putative protein predicted proteins, Arabidopsis thaliana putative protein KIAA0776 protein, Homo sapiens, EMBL:AB018319; supported by cDNA: gi_14334491_gb_AY034937.1_ FtsH protease, putative contains similarity to FtsH protease GI:13183728 from [Medicago sativa] putative protein	253388_at 253358_at 253351_at 253279_at 253206_at 253206_at 253107_at 252513_at 2522449_at 252431_at	1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3
putative protein '; supported by cDNA: gi_13605598_gb_AF361625.1_AF361625.1_AF361625 gamma-VPE (vacuolar processing enzyme) ; supported by cDNA: gi_13877794_gb_AF370160.1_AF370160 putative protein hemolysin, 38K, Synechocystis sp., Pir2:S75595 putative protein B subunit of propionyl-CoA carboxylase, Mycobacterium tuberculosis, PATCHX:E290075; supported by cDNA: gi_14423377_gb_AF Nonclathrin coat protein gamma - like protein coat protein gamma-cop, Bos primigenius putative protein proteiny for the subunit of proteins, Arabidopsis thaliana; supported by cDNA: gi_14334491_gb_AY034937.1_ putative protein KIAA0776 protein, Homo sapiens, EMBL:AB018319; supported by cDNA: gi_14334491_gb_AY034937.1_ FtsH protease, putative contains similarity to FtsH protease GI:13183728 from [Medicago sativa] putative protein ubiquitin-specific protease 26 (UBP26) similar to GI:11993492; RNA binding protein - Homo sapiens, EMBL:AB016089 (N-terminus), several ubiquit	253388_at 253358_at 253351_at 253279_at 253231_at 253206_at 253107_at 252431_at 252449_at 252431_at 252431_at	1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3
putative protein ; supported by cDNA: gi_13605598_gb_AF361625.1_AF361625 gamma-VPE (vacuolar processing enzyme) ; supported by cDNA: gi_13877794_gb_AF370160.1_AF370160 putative protein hemolysin, 38K, Synechocystis sp., Pir2:S75595 putative protein B subunit of propionyl-CoA carboxylase, Mycobacterium tuberculosis, PATCHX:E290075; supported by cDNA: gi_14423377_gb_AF Nonclathrin coat protein gamma - like protein coat protein gamma-cop, Bos primigenius putative squalene synthase non-consensus GC donor splice site at exon 3, squalene synthase 2 (SQS2), Arabidopsis thaliana; supported by cDNA: putative protein predicted proteins, Arabidopsis thaliana putative protein predicted protein, Homo sapiens, EMBL:AB018319; supported by cDNA: gi_14334491_gb_AY034937.1_ FtsH protease, putative contains similarity to FtsH protease GI:13183728 from [Medicago sativa] putative protein ubiquitin-specific protease 26 (UBP26) similar to GI:11993492; RNA binding protein - Homo sapiens, EMBL:AB016089 (N-terminus), several ubiquit hypothetical protein ; supported by cDNA: gi_13507562_gb_AF360347.1_AF360347 putative disease resistance protein	253388_at 253358_at 253351_at 253279_at 253279_at 253206_at 252513_at 252431_at 252449_at 252431_at 252275_at 252276_at 252276_at 252239_at	1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.3
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putative protein unknown protein At2g40800 - Arabidopsis thaliana, EMBL:AC007660	251685_at	1.3
squamosa promoter binding protein-like 12	251450_at	1.3
guanine nucleotide exchange factor - like protein guanine nucleotide exchange factor, Homo sapiens, EMBL:AF111162	251390_at	1.3
putative protein putative protein F26O13.260 - Arabidopsis thaliana, EMBL:AL133452	251333_at	1.3
ARGININE/SERINE-RICH SPLICING FACTOR RSP31 ; supported by cDNA: gi_16612267_gb_AF439831.1_AF439831	251242_at	1.3
putative protein hypothetical protein At2g28380 - Arabidopsis thaliana, EMBL:AC006283	251233_at	1.3
	251193_at	1.3
	251134_at	1.3
	251015_at	1.3
	250970_at	1.3
	250899_at	1.3
	250824_at	1.3
	250742_at	1.3
	250755_at	1.3
	250736_s_at	1.3
	250613_at	1.3
	250625_at	1.3
	250626_at 250463 at	1.3 1.3
•	250274 at	1.3
	250255 at	1.3
	250255_at	1.3
	250041 at	1.3
	249964 at	1.3
	249898 at	1.3
	249613 at	1.3
	249456 at	1.3
nuclear pore protein -like nuclear pore protein gp210 precursor, rat, PIR:S04921	249354_at	1.3
disease resistance protein-like 2	249264_s_at	1.3
maize crp1 protein-like	249247_at	1.3
unknown protein	249134_at	1.3
	249158_at	1.3
	248882_at	1.3
	248901_at	1.3
	248749_at	1.3
	248616_at	1.3
	248393_at	1.3
	248305_at	1.3
	248283_at	1.3
	248303_at	1.3
	247993_at 248005 at	1.3 1.3
	247989 at	1.3
	247820 at	1.3
	247624 at	1.3
cleavage stimulation factor 50K chain cleavage stimulation factor 50K chain Homo sapiens, PIR:A45142;supported by full-length cDNA: Ceres:1172		1.3
pyrophosphate-dependent phosphofructo-1-kinase - like protein pyrophosphate-dependent phosphofructo-1-kinase, Prunus armeniaca, EMBL:U932		1.3
quinone oxidoreductase - like protein quinone oxidoreductase homolog, Vigna unguiculata, PIR:T11672;supported by full-length cDNA: Ceres:37197		1.3
	247309 at	1.3
	247321_s_at	1.3
putative protein similar to unknown protein (dbj BAA96220.1); supported by full-length cDNA: Ceres: 16835.	247295_at	1.3
nuclear protein-like	247271_at	1.3
	247275_at	1.3
	247173_at	1.3
	247176_at	1.3
	247147_at	1.3
	247114_at	1.3
	247063_at	1.3
	247041_at	1.3
	246927_s_at	1.3
eukaryotic translation initiation factor - like protein eukaryotic translation initiation factor 3, Nicotiana tabacum, EMBL:Y11996; supported by cDNA: g2 SAR DNA-binding protein - like SAR DNA-binding protein-1, garden pea, PIR:T06377	246809 s at	1.3 1.3
	246759 at	1.3
signal recognition particle 54 kDa protein 2 (SRP54), putative similar to signal recognition particle 54 kDa protein 2 (SRP54) GI:556901 from [Lycopt		1.3
putative protein HR21spA protein involved in DNA double-strand break repair - Mus musculus, EMBL:X88293	246500 at	1.3
TOM (target of myb1) -like protein TOM1, Mus musculus, EMBL:MUS6972;supported by full-length cDNA: Ceres:1330.	246421_at	1.3
phosphoglucomutase-like protein phosphoglucomutase, chloroplast - Spinacia oleracea, EMBL:X75898; supported by cDNA: gi 16974561 gb AY0		1.3
putative protein hexamer-binding protein HEXBP - Leishmania major, PIR:A47156	246328 at	1.3
splicing factor-like protein	246257_at	1.3
ids4-like protein ids-4 protein - Hordeum vulgare, PIR:T05905;supported by full-length cDNA: Ceres:32843.	246071_at	1.3
putative protein predicted proteins from various species;supported by full-length cDNA: Ceres:10217.	246017_at	1.3
putative protein predicted proteins - different species	245936_at	1.3
putative protein protein phosphatase-1 regulatory subunit 7 alpha2 - Homo sapiens, EMBL:AF067136;supported by full-length cDNA: Ceres:110392		1.3
putative protein CD2 cytoplasmic domain binding protein - Homo sapiens, EMBL:AF104222;supported by full-length cDNA: Ceres:13887.	245887_at	1.3
unknown protein similar to unknown protein CB:AAC36170 GI:3608137 from [Arabidopsis thaliana]; supported by cDNA: gj_11044956 emb_AJ2515		1.3
hyoscyamine 6-dioxygenase hydroxylase, putative similar to hyoscyamine 6-dioxygenase hydroxylase CB:P24397 from [Hyoscyamus niger];support		1.3
lysophospholipase homolog, putative similar to lysophospholipase homolog GI:2801536 from [Oryza sativa]; supported by cDNA: gi_15028212_gb_ unknown protein		1.3
	245744_at	1.3
	245702_at 245313 at	1.3
	245313_at 245293_at	1.3 1.3
	LIVEUU al	1.3
· · · · · · · · · · · · · · · · · · ·	245237_at	
putative beta-1.3-glucanase :supported by full-length cDNA: Ceres:95083.	245237_at 245116_at	1.3
putative beta-1,3-glucanase ;supported by full-length cDNA: Ceres:95083. hypothetical protein predicted by genscan+	245237_at 245116_at 245039_at	1.3 1.3
hypothetical protein predicted by genscan+	245237_at 245116_at	1.3
hypothetical protein predicted by genscan+	245237_at 245116_at 245039_at 261463_at	1.3 1.3 1.3

unknown protein : signaportel by CNA by G1540007 (G. A-2000 FL			
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public NVS family transcription factor         265700, at 1           S50 ritionami protein L4, supported by full-anglin CDAC Const 15632.         2553           S50 ritionami protein L4, supported by CDNA Const 15632.         2553           S50 ritionami protein L4, supported by CDNA Const 15632.         2553           S50 ritionami protein L4, supported by CDNA Const 15632.         2553           S50 ritionami protein Constraint Constrate Constraint Constraint Constraint Constraint Constraint Constr			1.2
hyperbetical protein predicted by genesan         2657-28, aft         1           patient optic nucleotide and Lampotatin Siguidati for hannel protein         2556 Hosenal groutes (http://dis.WD73892), supported by cDNA: g_13805594_gb_AF387346.1_AF387346         25554.3         att           patient optic nucleotide and Lampotatin Siguidati for hannel protein         2556 Hosenal groutes (http://dis.WD73892), supported by cDNA: g_13805594.gb_AF387346.1_AF387346         25556 Hosenal groutes (http://dis.WD73892), supported by cDNA: g_13805594.gb_AF387346.1_AF387346         25556 Hosenal groutes (http://dis.WD73892), supported by cDNA: g_13805597.gb_AF387346         25566 Hosenal groutes (http://dis.WD73892), supported by cDNA: g_14242545.gb_AF387346.1_OH328742.gb_HT         25566 Hosenal groutes (http://dis.WD73891), supported by cDNA: g_14242545.gb_AF387346.1_OH328742.gb_HT         25666 Hosenal groutes (http://dis.WD73891), supported by cDNA: g_14242545.gb_AF387346.1_OH3284728, gb/AF387348, stp.HT         25666 Hosenal groutes (http://dis.WD73891, gb_AF387346.1_OH3284728, gb/AF387391), supported by cDNA: g_1437487.gb_AF387346.1_OH3284728, gb/AF387391, supported by cDNA: g_1437373, gb_AF3873450.1_GF387391, supported by cDNA: g_1437373, gb_AF387346.1_OH3289527, gb_AF3873450.1_GF38734, gb_AF3873450.1_GF38734, gb_AF3873510.1_AF3873450, gb_AF3873510.1_AF3873510, gb_AF3873510.1_AF3873510, gb_AF3873510.1_AF3873510, gb_AF3873510, gb_AF3873510, gb_AF3873510, gb_AF3873510, gb_AF3873510, gb_AF3873510, gb_AF3873510, gb_AF3873510, gb_AF			1.2
503 intesoral protein L4 :supported by full-ength CDAV: Ceres:15683.         2650 it.			1.2
putative protein indextoted and calmodulin-regulated in channel protein         26554 [iii]         1           putative PD-App zanc finger protein         26252 [iii]         1           putative PD-App zanc finger protein         26222 [iii]         1           Diractive PD-App zanc finger protein         262478 [iii]         2           Diractive PD-App zanc finder protein         24478 [iii]         24478 [iiii]           Diractive PD-App zanc finder protein         24478 [iiii]         24478 [iiii]           Diractive PD-App zanc finder protein         24478 [iiii]         24478 [iiiii]           Diractive PD-App zanc finder protein         24478 [iiiii]         24478 [iiiii]           Diractive PD-App zanc finder protein         24478 [iiiiiiiii]         24488 [iiiiii]           Diractive PD-App zanc finder protein         24488 [iiiiii]         24488 [iiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii			1.2
putatio V0-40 repeat protein imilar to TUP (1024/270280): supported by CMA: gi_13005894_gb_A730746.1_AF307346 1_AF307346 1_AF30734 1_AF			1.2
unknown protein         supported by cDNA: 0_1.680588, dbj.D88746.1.088746         280509, dt         1.           U2 arRNP auxiley factor. Impres subunt. Jointation EGN CoN4050, similar to EST spliP28912, embj238124, gb/A297087, gb/P28912, gb/H12         280504, dt         300504, dt         300500, dt         <		265259_at	1.2
T-comptor chapteronin protein , opsion Suburit contenical to GB: OxF300, similar to ESTs gb/R2812, dm/R24827, gb/R24827,		_	1.2
U2 en/RNP auxiliary factor, impe subunit, putative similar to G13850825 twon (Nicotiana plumbaghitolia) (J. Biol. Chem. 273 (5), 3400-3410; (19224922, al. 1 IRN polymerase subunit identical to RN polymerase subunit (S14324 of multicabosis thaliana) patiente protoinforophylicle inductase similar to protochlorophylicle reductase precusor: similar to ESTs gb/R30530, gb/T46162, emb/Z2072, gb/R4053, al. 1 phypothetical protein contains similarly to caltractific (S13826 from (Natabiogsis thaliana) 244683, al. 1 hypothetical protein contains similarly to caltractific (S13865 from (Natabiogsis thaliana) 244683, al. 1 hypothetical protein contains similarly to caltractific (S13865 from (Natabiogsis thaliana) 244682, al. 1 hypothetical protein contains similarly to caltractific (S13865 from (Natabiogsis thaliana) 244682, al. 1 hypothetical protein contains similarly to caltractific (S13865 from (Natabiogsis thaliana) 244692, al. 1 unincom protein Similar to Calter more alpha subunit (S147716 from (Natabiogsis thaliana) 244692, al. 1 unincom protein similar to Calter may albumy hydrolase G1:1807711 from (Gyrien may supported by full-length CDNA. Ceners 312 244502, al. 1 unincom protein ypothetical protein predicted by generank.hmm CFKK protein, putaties winnik to Calter protein (S7971528 from (Natabiogsis thaliana) 24450, al. 1 unincom protein ypothetical protein predicted by generank.hmm CFKK protein, putaties winnik to CRK protein G77971528 from (Natabiogsis thaliana) 24530, al. 1 100000000000000000000000000000000000			1.2
RNA polynerase silunit lemical to RNA polynerase subunt (E:154224 for (Arabidopsis thaliana): supported by CDNA: gl_1422463, gb_A7365 24492, at 1. patative protochlorophyllide reductase similar to protochlorophyllide reductase precusor; similar to ESTs gb/R26630, gb/T4612, emb/Z26728, gb/A 244893, at 1. abago, heap protein frame support leaders in Arabida polynosphates 5, cyhosphates G12312348 from (Arabidopsis thaliana) 244823, gt 1 24483, gt 1 24484, gt 1			1.2
<ul> <li>unknown protein</li> <li>patker protochinophylide reductase similar to protochinophylide reductase precusor, similar to ESTs gb/R30630, gb/T46162, emb/226728, gb/k</li> <li>patker protochinophylide reductase similar to protochinophylide reductase precusor, similar to ESTs gb/R30630, gb/T46162, emb/226728, gb/k</li> <li>patker protochinose, kappa Identical to A. thaliana AIK-1 (gb/X79270)</li> <li>patker protochinase, kappa Identical to A. thaliana AIK-1 (gb/X79270)</li> <li>patker protochinase contains a governe kinase domain governe binase dowain governe binase domain governe binase dowain governe bindite dowain governe binase dowain governe binase dowain govern</li></ul>			1.2
putative priorochirophylide reductase similar to protochirophylide reductase precusor: similar to ESTs goj/R30630, gbjT46162, embjZ28728, gbj4, 244837, at 1. shaggy-tike protein kinase, kappa i dentical to A. thaliana AK-1 (gbjK78279) unknown protein similar to utative using hybrophystech S-phosphatase G13212848 from (Arabidopsis thaliana) 244828, at 1. hypothetical protein contants similar to calitacin G13688162 from (Arabidopsis thaliana) 244828, at 1. hypothetical protein contants similar to calitacin Kinase domain particle (PDC00100) 244821, at 1. unknown protein similar to calitacin Kinase domain particle (PDC00100) 244821, at 1. contomer a phicanizero protein Strong similar to SRAA21351: supported by CMA (gl. 14517371, gb. AY039820 1. 244908, gl. 244908, gl. 2449008, gl. 244908, g			1.2
ehagg-wike protein kinase, kappa identical to A. thaliana AKI-1 (gb/K7272)         24485 at         1.           hypothetical protein contains similarly to caltractin (J:3688162 from (Arabidopsis thaliana)         24482 at         1.           hypothetical protein contains similarly to caltractin (J:3688162 from (Arabidopsis thaliana)         24487 at         1.           unknow protein Similar to Caltractin kinase domain and protein Kinase domain and protein Similar to Caltractin kinase domain and protein maxisupported by full-length cDNA. Ceres 1312         244302 at         1.           unknow protein in hypothetical protein productor by genemark hrm         244218, at         1.         244302 at         1.           CRK1 protein, publick protein productor by genemark hrm         244218, at         1.         244303, at         1.           CRK1 protein, publick protein brotein productor by genemark hrm         24430, at         24430, at         1.           CRK1 protein, publick protein divid-folame transform [beta vulgaris]: supported by CDNA. Ceres: 12730.         245734, at         245332, at         1.           Divide brotein protein supported by full-length CDNA. Ceres: 1202.         253742, at         1.         1.         253742, at         1.		264839_at	1.2
unknöm protein similar to putative insolio Jopyhosphale 5-phosphatase G12212484 form Arabidopsis thaliana] 26468_at 1. putative protein kinase contains similar to central solitarius (or contains similar to central solitarius (or contains similar to central solitarius) to caltractic G1288162 form (Abdobussi thaliana] 26462_1 at 1. putative protein kinase contains a protein kinase domain profile (PDC00100) 26462_1 at 1. putative protein kinase contains a protein kinase domain profile (PDC00100) 26462_1 at 1. putative protein kinase contains a maintar to GB-AAA21351_supported by CDAA.g1_4377371_g2_AY03862.0.1 centomer apha suburit, putative similar to goman kabita solution (Ci-667286 form (Arabidopsis thaliana)) 26462_1 at 1. Expressed protein 'supported by full-length cABC transporter dy GJ03600 form A thaliana and canalicular multi-drug resistance protein 'Strong Harabidopsis thaliana) 26462_1 at 1. Phypothetical protein predicted by genemark.tmm 26403_at 1. Expressed protein 'supported by full-length cDNA. Ceres: 4227. 26400_2 at 1. putative insuina to Canadi Carbon Ceres: 4227. 26400_2 at 1. putative construction (Strong Carbon Carbon Ceres: 4227. 26400_2 at 1. putative construction (Strong Carbon Carbon Ceres: 4227. 26400_2 at 1. 26403_at 1. 26404_at 1. 26404_at 1. 26404_at 1. 26404_at 1. 26404_at 1. 26404_at 1. 26		_	1.2
hypothetical protein contains semilarity to calitactin G1:3688162 from [Arabidopsis thailana]         26462, at         1.           unknown protein Similar to Caenorhabdilis unknown protein T03F1 (gb/U88160         264570, at         1.           unknown protein Similar to Caenorhabdilis unknown protein T03F1 (gb/U88160         264570, at         1.           unknown protein Similar to Caenorhabdilis unknown protein T03F1 (gb/U88160         26430, at         1.           gamma glutarw [hydrolase, putative similar to costner alpha sebund (13462786 from (Arabidopsis thailana)         26430, at         1.           gamma glutarw [hydrolase, putative similar to costner alpha sebund (13462786 from (Arabidopsis thailana)         26440, at         1.           CPK1 protein, putative similar to CRK1 protein G1:7671528 from [Beta vulgaris]: supported by cDNA: gi_13877618_gb_AF370510.         1_AF370510         264403, at         1.           Unknown protein         :supported by full-ength cDNA. Ceres: 10312         264403, at         1.         264403, at         1.           Unknown protein         :supported by full-ength cDNA. Ceres: 10312         263478, g, at         1.         263478, g, at         1.           Unknown protein         :supported by full-ength cDNA. Ceres: 10312         263378, g, at         1.         263378, g, at         1.           Unknown protein         :supported by full-ength cDNA. Ceres: 3182.         263378, g, at			1.2
pitable protein kinase contains a protein kinase domain profile (PDCc00100) 264672 at 1. putate hytochrome A similar to GB-AAA21351 supported by CDNA: gi_14517371, gb_AY039520.1 2 putate hytochrome A similar to GB-AAA21351 supported by CDNA: gi_14517371, gb_AY039520.1 2 coatomer apha subunit, putative similar to commer apha subunit G14657268 from [Arabidopsis thaliana] 26430 at 1. coatomer apha subunit, putative similar to commer apha subunit G14657268 from [Arabidopsis thaliana] CPKH proten, putative similar to CB-AAA21352 from [Beta vulganis]: supported by cDNA: gi_13877618_gb_AF370510.1_AF370510 26413, at 1. Expressed protein : supported by full-length cDNA. Ceres: 4267. 264403_at 1. Expressed protein : supported by full-length cDNA. Ceres: 4267. 264403_at 1. Putative Dnaj protein : supported by full-length cDNA. Ceres: 4267. 264403_at 1. 264403_at 1. 264404_at 1. 2644			1.2 1.2
unknown protein Similar to Caenorhabdilis unknown protein T03F1 (gb)U88160 26470.at 1. putate phytochrome A similar to Schwart 135 (gb)U88160 2650 from A. thaliana and canalicular multi-drug resistance protein is 264330, at 1. agarma glutany inytoriase, putative similar to coatomer alpha sobubit (13-652768 from (Anabiogsis thaliana) (264300, at 1. agarma glutany inytoriase, putative similar to coatomer alpha sobubit (13-652768 from (Anabiogsis thaliana) (264300, at 1. agarma glutany inytoriase, putative similar to coatomer alpha sobubit (13-652768 from (Anabiogsis thaliana) (264300, at 1. agarma glutany inytoriase, putative similar to coatomer alpha sobubit (13-652768 from (Anabiogsis thaliana) (26420, at 1. bytophetical protein predicted by genemark.hmm. 264224, at 1. bytophetical protein is supported by URI-ength cDNA. Ceres: 13312 unknown protein supported by URI-ength cDNA. Ceres: 1312 unknown protein supported by URI-ength cDNA. Ceres: 1312 263375, at 1. putative KDNAPH dependent mannose 6-phosphate reductase : supported by URI-ength CDNA. Ceres: 13102 263376, at 1. putative KDNAPH dependent mannose 6-phosphate reductase : supported by URI-ength CDNA. Ceres: 34830 263101, at 1. putative KDNAPH dependent mannose 6-phosphate reductase : supported by URI-ength CDNA. Ceres: 34830 263101, at 1. putative KDNAPH dependent mannose 6-phosphate reductase : supported by URI-ength CDNA. Ceres: 34830 263101, at 1. putative KDNAPH dependent mannose 6-phosphate reductase (Ja3818316 from (Dryza sativa) 263101, at 1. putativ			1.2
multi-drug resistance protein         26430.g. tt         1.           gamma glutamyi hydrolase, putative similar to gamma glutamyi hydrolase GI:1680711 from (Glycine max], supported by full-length cDNA: Ceres 413         26430.g. tt         1.           unknown protein         26420.g. att         1.         26420.g. att         1.           Unknown protein         26421.g. att         1.         26421.g. att         1.           EXR protein, putative similar to catomer and partitive similar to gamma glutamyi hydrolase GI:1680711 from (Glycine max], supported by full-length cDNA: Ceres: 4227.         264103.att         1.           Unknown protein ; supported by full-length cDNA: Ceres: 10312.         264403.att         1.           unknown protein ; supported by full-length cDNA: Ceres: 10312.         26376.g. att         1.           Unknown protein ; supported by full-length cDNA: Ceres: 10405.         263536.g. att         1.           Nycobhetical protein precided by genefinder: supported by full-length cDNA: Ceres: 11945.         263530.g. att         1.           Nycobhetical protein precided by genefinder: supported by full-length cDNA: Ceres: 3192.         263749.g. att         1.           Unknown protein ; supported by full-length cDNA: Genes: 3192.         26330.g. att         1.           Unknown protein ; supported by full-length cDNA: Genes: 3192.         263370.g. att         1.           Unknown protein ; supported by			1.2
coatomer alpha subunit, putative similar to catomer alpha subunit G1/4567286 from [Arabidopsis haliana]         284300_att         1.           gamma glutamy lydrolase, putative similar to gamma glutamy lydrolase G1:680711 from [Glycine max];supported by full-length cDNA: Ceres 413         28421_att         1.           CRK1 protein, putative similar to CRK1 protein G17671528 from [Beta vulgaris]; supported by cDNA: gi_13877618_gb_AF370510_1_AF370510         284193_att         1.           Lynchow protein         supported by full-length cDNA: Ceres: 1237.         28400_att         1.           unknow protein         supported by full-length cDNA: Ceres: 10312.         284063_att         1.           unknow protein         supported by full-length cDNA: Ceres: 3192.         283954_att         1.           unknow protein         supported by full-length cDNA: Ceres: 3192.         283954_att         1.           Unknow protein         supported by full-length cDNA: Ceres: 3192.         283472_att         1.           EnSym-like transpoon protein respoon favore incespoon taby full-length cDNA: Ceres: 3192.         283472_att         1.           Unknow protein         supported by cDNA: gi_13825496_g. DA F3240912_AF3240912_AF324091         283372_att         1.           Unknow protein         supported by cDNA: gi_13636496_g. DA F434891_AF336481_AF324691         283372_att         1.           Unknow protein         supported by cDNA: gi_1363649		264508_at	1.2
gamma glutamyl hydrolase, putative similar to gamma glutamyl hydrolase Gl: 1680711 from [Glycine max]:supported by full-length cDNA: Ceres: 413         284218, at 1           hypothelical protein predicted by genemark.mm         284228, at 1           CRK1 protein, putative similar to CRN1 protein G12701528 from [Beta vulgaris]; supported by cDNA: gl_13877618_gb_AF370510.1_AF370510         28428, at 1           Linknown protein         :supported by full-length cDNA: Ceres: 42267.         284103, at 1           unknown protein         :supported by full-length cDNA: Ceres: 10312.         2844003, at 1           unknown protein         :supported by full-length cDNA: Ceres: 10312.         283578, g. at 1           hypothetical protein predicted by genefinder:supported by full-length cDNA: Ceres: 119045.         283532, g. at 1           putative NADPH fundee (DNA: Q): 12805476, g. AF3246912, AF324691         283532, g. at 1           zanc finger protein:         puportein fundee (DNA: Geres: 3192.         28352, g. at 1           zanc finger protein:         puportein fundee (DNA: Geres: 3192.         28352, g. at 1           zanc finger protein:         puportein fundee (DNA: Geres: 3192.         28352, g. at 1           zanc finger protein:         puportein fundee (DNA: Geres: 3192.         28352, g. at 1           zanc finger protein:         puportein fundee (DNA: Geres: 3192.         28352, g. at 1           zanc finger protein:         puportein fundee (DNA			1.2
unknown protein         244218, att         1.           CRK1 protein, putative similar to CRK1 protein (317671528 from [Beta vulgaris]; supported by cDNA: gl_13877618_gb_AF370510.1_AF370510         244193, att           CRK1 protein, supported by Uil-length cDNA: Ceres: 42267.         244063, att         1.           unknown protein         2440063, att         1.         2440063, att         1.           unknown protein         1:supported by CDNA: gl_15450787_gb_AY054474.1_         2633748, att         2633748, att         1.           unknown protein         :supported by CDNA: gl_15450787_gb_AY054474.1_         2633748, att         1.         2633742, att         1.         263372, att         1.         2633742, att         1.         263372, att         1.         2633742, att         1.         2633742, att         1.         263374, att         2.         263372, att         1.         263376, att         1.		_	1.2
hypothetical protein predicted by genemark.hmm         24422_att         1.           CRK Protein, putative similar to CRK Protein Ci/R71528 from [Beta vulgaris]; supported by cDNA: gi_13877618_gb_AF370510.1_AF370510.         264163_att         1.           Narkown protein         244063_att         1.         264163_att         1.           Inknown protein         supported by full-length cDNA: Ceres: 1202.         264063_att         1.           Inknown protein         supported by full-length cDNA: Ceres: 1203.         2639754_att         1.           Inknown protein         supported by full-length cDNA: Ceres: 119045.         263375_att         263375_att         263375_att         263375_att         1. <t< td=""><td></td><td></td><td>1.2 1.2</td></t<>			1.2 1.2
ČRK1 protein, putative similar to CRK1 protein G1:771528 from [Beta vulgaris]: supported by cDNA: gl_13877618_gb_AF370510.1_AF370510         244163_at         1.           unknown protein         244063_at         1.         244063_at         1.           unknown protein         1:supported by full-length cDNA: Ceres: 42207.         244063_at         1.         244063_at         1.           unknown protein         :supported by CDNA: cj_15450787_gb_AY054474_1_         2639749_at         1.         2639749_at         1.           putative Phasphetidyhoshot (hropsphate reductase : supported by full-length cDNA: Ceres: 21730.         283784_g_at         1.         2633742_gt         2.         2633742_gt         2.         2.         2633742_gt         1.         2.         2633742_gt         2.         263332_gt         1.         1.         molybothetid protein protein transposon family transposon protein ransposon family to zunc finger protein a: supported by CDNA: cj_153264691_2_AF326491_2_AF326491_2_AF326491         263312_dt         2.         263312_dt         1.         hypothetical protein protein call to Ending manaposon family to zunc finger protein a: supported by CDNA: gj_13285496_dt_2_AF326491_2_AF326491_2_AF326491_2_AF326491_2_AF32695_at         2.         263312_dt         1.         hypothetical protein protein call to zunc finger protein Cills033336_dt         1.         1.         1.         1.         1.         1.         1.         1.			1.2
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putative Dnal protein supported by full-length cDNA: Ceres: 1012.         244002_att         1.           unknown protein supported by CDNA: gj 1=540787 gj b_AV054741 1_         283954 git         1.           putative NADPH dependent manose 6-phosphater deutcase : supported by full-length cDNA: Ceres: 21730.         283758_git         1.           hypothetical protein predicted by genefinder, supported by full-length cDNA: Ceres: 31905.         283472_git         1.           Enr/Spm-like transposon protein related to Enr/Spm transposon family of maize         283472_git         1.           putative RNIPM (arc finger protein : supported by full-length cDNA: Ceres: 3192.         283172_git         1.           hypothetical protein predicted by genson and genefinder         283101_g.git         1.           hypothetical protein predicted by genson and genefinder         283101_g.git         1.           unknown protein : supported by CDNA: gj.15982744_gb_AY057479.1_         283050_git         1.           conserved hypothetical protein prediction for Conserved hypothetical protein in gene supported by CDNA: gj.15982744_gb_AY057479.1_         283052_git         1.           unknown protein : supported by CDNA: gj.15982744_gb_AY057479.1_         283052_git         1.         283052_git         1.           unknown protein i: supported by CDNA: gj.15982744_gb_AY057479.1_         282646_git         1.         282640_git         1.         283052_git		264163_at	1.2
unknown protein         :supported by cDNA: g15450787_gb_AY054474.1			1.2
platiery biosphatidy/inosphatidy/inosphatidy/inosphatidy/inosphater/dic/boline transfer protein         283749_att         1.           hypothetical protein predicted by genefinder:supported by full-length cDNA: Ceres: 21730.         283783_att         1.           hypothetical protein predicted by genefinder:supported by full-length cDNA: Ceres: 31904.         283532_att         1.           En/Spm-like transposon protein related to En/Spm transposon family of maize         283352_att         1.           ztr. finger protein, platitive similar to zinc finger protein GI:3618316 from [Onyza sativa]:supported by full-length cDNA: Ceres:34830.         283129_att         1.           unknown protein         : supported by CDNA: gl_1_3265469_gb_AF3264812_AF3246811         283050_att         1.           unknown protein         : supported by CDNA: gl_1_3265469_gb_AF3268241_AF436824         283070_att         1.           unknown protein         : supported by CDNA: gl_1_15982744_gb_AY057479.1_         283077_att         1.           conserved hypothetical protein pedicted by generant.hum         28200_att         1.         28200_att         1.           unknown protein         : supported by CDNA: gl_1_3252645         1.         28200_att         1.           unknown protein         : supported by CDNA: gl_1_4536824.1_AF436824         28200_att         1.           unknown protein         : supported by CDNA: gl_1_650676			1.2
putative NADPH dependent mannose 6-phosphate reductase : supported by full-length cDNA: Ceres: 21730.         283786 g. at 1.           molydopteria predicted by genefinder: supported by full-length cDNA: Ceres: 31942.         283472 at 1.           ENSpm-like transposon protein related to EnSported by full-length cDNA: Ceres: 3192.         283472 at 1.           ENSpm-like transposon protein related to EnSported by cDNA: gi_13265496 gb_AF3246912_AF3246914_AF324691         283104 at 1.           zinc finger protein : supported by cDNA: gi_16930680_gb_AF436824.1_AF436824         283104 at 1.           unknown protein : supported by cDNA: gi_16930680_gb_AF436824.1_AF436824         283107 at 1.           conserved hypothetical protein dis 3: supported by cDNA: gi_15982744_gb_AY057479.1_         283077 at 1.           putative winkle to end to be cDNA: gi_15982744_gb_AY057479.1_         283077 at 1.           putative winkle to and the bis subunit similar to human U5 snRNP-specific 200KD protein, sij3255965 and yeat prevent?         228200_at 1.           putative winkle TD elongation factor G SP:P34811 (Glycine max (Soybean)), supported by cDNA: gi_14522623_gb_AY039936.1_         282862_at 1.           hypothetical protein similar to alonineRNA ligase GB:S32671 from [Chrus X paradis] and GB: Q411407787.         282465_at 1.           hypothetical protein similar to alonineRNA ligase GB:S32671 from [Arabidopsis thaliana]         282486_at 1.           hypothetical protein similar to dynamin GB: AAA372824 GI 473757 from [Mus musculus]; supported by cDNA: gi_15146178_gb_AY0492		_	1.2
hypothetical protein predicted by genefinder.supported by full-length CDNA: Ceres:119045.         28558_at         1.           En/Spm-like transposon protein related to En/Spm transposon family of maize         283352_at         1.           Inclimentike transposon protein related to En/Spm transposon family of maize         283312_at         1.           Inclimentike transposon protein related to En/Spm transposon family of maize         283104_at         1.           Inclimentike transposon protein related to En/Spm transposon family of maize         283104_at         1.           Inclimentike transposon protein related to En/Spm transposon family of maize         283104_at         1.           Invikown protein         283104_at         1.         283104_at         1.           Unknown protein         283104_at         1.         283077_at         1.           Unknown protein         280307_at         283077_at         1.         283077_at         1.           Unknown protein similar to GB:AAB88651, similar to thuman U5 snRNP-specific 200kD protein, gi(3255965 and yeast pre-RNF         282045_at         1.           Unknown protein similar to GB:AAB88661, similar to thuman U5 snRNP-specific 200kD protein, gi(3255965 and yeast pre-RNF         282045_at         1.           Unknown protein similar to danaine-RNA helicase similar to CB:AAC67587 from [Chruix x paradis] and GB:O41140 from [Ricin Z2500_at         282645_at         1. <td></td> <td>_</td> <td>1.2</td>		_	1.2
En/Sgm-like transposon protein related to En/Sgm transposon family of maize         263352, at         1.           Junk Tinger protein, putative SING zinc finger protein GL:3618316 from [Oryza sativa];supported by full-length cDNA: Ceres:34830.         263128, at         1.           hypothetical protein predicted by genscan and genefinder         263101, sat         1.           unknown protein         263101, sat         1.           unknown protein         263102, sat         263102, sat           putative NIKOC control protein dis 3: supported by cDNA: gi_15982744_gb_AV057479.1_         263077, at         1.           conserved hypothetical protein         putative miticic control protein gation factor G SP-P34811 [Oscien max (Sophean); supported by cDNA: gi_14532623, gb_AV039936.1         263037, at         1.           putative wincip content predicted by generark.hmm         262508, at         1.         262508, at         1.           hypothetical protein predicted by generark.hmm         262508, at         1.         262508, at         1.           hypothetical protein predicted by generark.hmm         262508, at         1.         262508, at         1.           hypothetical protein predicted by generark.hmm         262508, at         1.         262508, at         1.           hypothetical protein predicted by generark.hmm         262508, at         1.         262508, at         1.			1.2
putative protein         supported by cDNA: gi_13265496 gb_A7324691_2_AF324691         263325_et         1.           sunc finger protein         putative protein predicted by genscan and genefinder         263101_s_at         1.           unknown protein         263104_at         263104_at         263104_at         1.           unknown protein         263104_at         263104_at         263007_at         26300_at         1.         1.         1.         1.         1.         1.         1.         1.         1.         1.	molybdopterin synthase (CNX2) ;supported by full-length cDNA: Ceres:33192.	263472_at	1.2
zinc finger protein, putative similar to zinc finger protein GL3618316 from [Oryza sativa]:supported by full-length cDNA: Ceres:34830.       263128_it       1.         hypothetical protein predicted by genscan and genefinder       263101_s at       1.         unknown protein       263101_s at       1.         unknown protein       263101_s at       1.         unknown protein       263030_at       1.         putative mitotic control protein is 3: supported by cDNA: gi_15982744_gb_AY0574751_       263037_at       1.         conserved hypothetical protein       263037_at       1.       263037_at       1.         putative prophosphate-dependent RNA helicase similar to GB-AAB88651, similar to burnan U5 snRNP-specific 200kD protein, gi]3255965 and yeast pre-RNP       262645_at       1.         unknown protein EST gb/N65467 comes from this gene supported by full-length cDNA: Ceres:30239.       262568_at       1.         unknown protein       263128_if and early indenical to Ubiquitin-Conjugating Enzyme EZ [Saccharomyces cerevisiae] (gi]480374).       262468_if at       1.         hypothetical protein predicted by genemark.hmm       262468_if at       2.       262468_if at       1.         hypothetical protein predicted by genemark.hmm       262468_if at       2.       262468_if at       1.         vanknown protein       262468_if at       2.       2.       264181_if at <td></td> <td></td> <td>1.2</td>			1.2
hypothetical protein predicted by genesan and genefinder       263101_s_at       1.         unknown protein       263104_at       1.         unknown protein       263050_at       1.         unknown protein       263077_at       263077_at       1.         conserved hypothetical protein       263077_at       1.       263077_at       1.         putative prophothetical protein       263077_at       1.       263077_at       1.         putative prophothetical protein       26307_at       1.       26307_at       1.         unknown protein similar to GB-AAB88651, similar to human U5 snRNP-specific 200kD protein, gil3255965 and yeast pre-mRP       262680_at       1.         unknown protein SST gb/N68467 comes from this gene, supported by cDNA: gi_14532623_gb_AY039936.1_       262645_at       1.         unknown protein STS gb/N68467 comes from this gene, supported by cDNA: Gi_14532623_gb_AY039936.1_       262645_at       1.         unknown protein SST gb/N68467 comes from this gene, Supported by cDNA: gi_14532623_gb_AY039936.1_       262468_at       1.         unknown protein similar to tanine-RTAN ligase GB:S32671 from [Arabidopsis thaliana]       262468_at       1.         unknown protein predicin predicided by genemark.hmm       26211_at       1.         xylosidase, putative similar to tanine-RTAN ligase GB:S32677 from [Ms msucoils]: supported by cDNA: gi_15146178_		_	1.2
unknown protein263104_at1.unknown protein263063_gb_AF436824.1_AF436824263050_at1.unknown proteinsupported by cDNA: gi_15982744_gb_AY057479.1_26307_at1.conserved hypothetical protein263007_at1.putative mitolic control protein dis3 ; supported by cDNA: gi_15982744_gb_AY057479.1_26300_at1.unknown protein similar to GB:AAB88651, similar to CB:AAC67587 from [Citrus X paradis] and GB:Q41140 from [Rcin.262680_at1.unknown protein similar to tongation factor GS:PP:34811 [Glycine max; (Soybean)]; supported by cDNA: gi_14532623_gb_AY039936.1_262645_at1.unknown proteinCS:PP:34811 [Glycine max; (Soybean)]; supported by cDNA: gi_14532623_gb_AY039936.1_262582_at1.unknown proteinCS:PP:34811 [Glycine max; (Soybean)]; supported by cDNA: gi_14532623_gb_AY039936.1_262562_at1.unknown protein262463_at1.262465_at1.unknown protein262463_at1.262468_at1.unknown protein262473_gat1.262468_at1.vyboidsee, putative similar to alanineRNA ligase GB:S32671 from [Arabidopsis thaliana]26248_at1.vylosidase, putative similar to alynamin GB:AAA37324 GI:487657 from [Mus musculus]; supported by cDNA: gi_15146178_gb_AY049230.1_26207_at1.unknown protein26248_at1.1.26188_at1.unknown protein similar to alynamin GB:AAA37324 GI:487657 from [Mus musculus]; supported by cDNA: gi_15146178_gb_AY049230.1_26188_at1.unknown protein similar to alynamin GB:AAA37324 GI:			1.2
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unknown protein similar to elongation factor G SP:P34811 [Glycine max (Soybean)]: supported by cDNA: gi_14532623_gb_AY039936.1_       262645_at       1.         unknown protein EST gb]N65467 comes from this gene; supported by full-length cDNA: Ceres:30239.       262562_at       1.         putative ubiquitin-conjugating enzyme First 212 a.a. are 41% identical to Ubiquitin-Conjugating Enzyme E2 [Saccharomyces cerevisiae] (gil480374).       262537_s.at       1.         alanine-tRNA ligase, putative similar to alanine-trNA ligase GB:S32671 from [Arabidopsis thaliana]       262430_s.at       1.         unknown protein       putative similar to dynamin GB:AAA37324 GI:487857 from [Mus musculus]; supported by cDNA: gi_15146178_gb_AY049230.1_       266181_at       1.         dynamin-like protein similar to dynamin GB:AAA37324 GI:487857 from [Mus musculus]; supported by cDNA: gi_15146178_gb_AY049230.1_       261894_at       1.         unknown protein is supported by cDNA: gi_150281563 GI:3549672 from [Arabidopsis thaliana]       26189_at       1.         UDP glucose:flavonoid 3-o-glucosyltransferase, putative similar to UDP glucose:flavonoid 3-o-glucosyltransferase GB:AAB61683 GI:2564114 from [261804_at       1.         unknown protein is supported by cDNA: gi_15028128_gb_AY040923.GI:35635754_2_A5555754_2_A555754_2_A555754_2_A555754_2_A555754_2_A55575			1.2
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xylosidase, putative similar to xylosidase GI:2102655 from [Aspergillus niger]262181_at1.dynamin-like protein similar to dynamin GB:AAA37324 GI:487857 from [Mus musculus]; supported by cDNA: gi_15146178_gb_AY049230.1262077_at1.myrosinase precursor, putative261884_at1.transcriptional regulator, putative similar to transcriptional regulator GI:4836767 [Zea mays]261891_at1.UDP glucose:flavonoid 3-o-glucosyltransferase, putative similar to UDP glucose:flavonoid 3-o-glucosyltransferase GB:AAB81683 GI:2564114 from [261804_at1.unknown protein similar to hypothetical protein GB:CAA20583 GI:3549672 from [Arabidopsis thaliana]261862_at1.unknown protein ; supported by cDNA: gi_15028128_gb_AY046014.1_261804_at1.unknown protein ; supported by cDNA: gi_1502828_gb_AY046014.1_261804_at1.unknown protein ; supported by cDNA: gi_15912328_gb_AY056442.1_261354_at1.unknown protein ; supported by cDNA: gi_15912328_gb_AY056442.1_261354_at1.unknown protein ; supported by cDNA: Ceres: 117183.261206_at1.heat shock factor protein hsf8, putative predicted by genemark.hmm; supported by cDNA: gi_15028376_gb_AY045991.1_260302_at1.unknown protein260629_at1.1.putative aTP-dependent RNA helicase ; supported by cDNA: gi_16323191_gb_AY057700.1_26032_at1.putative protein kinase contains Pfam profile: PF00069 Eukaryotic protein kinase domain260419_at1.hypothetical protein contains Pfam profile: PF01535 Domain of unknown function260331_at1.hypothetical protein			1.2 1.2
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hypothetical protein predicted by genemark.hmm; supported by cDNA; gi_16041649_gb_AF355754.2_AF355754261444_at1.unknown protein contains similarity to set protein GI:338038 from [Homo sapiens]; supported by full-length cDNA: Ceres:27467.261406_at1.unknown protein ; supported by cDNA: gi_15912328_gb_AY056442.1_261354_at1.unknown protein ; supported by full-length cDNA: Ceres: 117183.261269_at1.heat shock factor protein hsf8, putative predicted by genemark.hmm; supported by cDNA: gi_15028376_gb_AY045991.1_261206_at1.unknown protein261064_at1.unknown protein261064_at1.putative ATP-dependent RNA helicase ; supported by cDNA: gi_16323191_gb_AY057700.1_260532_at1.putative alpha-amylase similar to alpha-amylase GB:AAA91884 [Solanum tuberosum]; supported by cDNA: gi_15215737_gb_AY050398.1_260419_at1.hypothetical protein isupported by full-length cDNA: Ceres:108322.260301_at1.hypothetical protein isupported by full-length cDNA: Ceres:108322.260301_at1.hypothetical protein isupported by full-length cDNA: Ceres:108322.260301_at1.hypothetical protein profile: PF01344 Kelch motif260301_at1.F-box protein KF1/ADO3, AtFBX2a identical to FKF1 GI:6960305 and Adagio 3 GI:13487072 from [Arabidopsis thaliana]259990_s_at1.			1.2 1.2
unknown protein contains similarity to set protein GI:338038 from [Homo sapiens];supported by full-length cDNA: Ceres:27467. 261406_at 1. unknown protein ; supported by cDNA: gi_15912328_gb_AY056442.1_ unknown protein ; supported by full-length cDNA: Ceres: 117183. 261269_at 1. Lot shock factor protein hsf8, putative predicted by genemark.hmm; supported by cDNA: gi_15028376_gb_AY045991.1_ 261206_at 1. unknown protein 261064_at 1. unknown protein 261064_at 1. putative ATP-dependent RNA helicase ; supported by cDNA: gi_16323191_gb_AY057700.1_ 260532_at 1. putative alpha-amylase similar to alpha-amylase GB:AAA91884 [Solanum tuberosum]; supported by cDNA: gi_15215737_gb_AY050398.1_ 260412_at 1. putative protein kinase contains Pfam profile: PF00069 Eukaryotic protein kinase domain 260419_at 1. hypothetical protein ; supported by full-length cDNA: Ceres:10332. 260301_at 1. hypothetical protein ; supported by full-length cDNA: Ceres:10322. 26031_at 1. F-box protein FKF1/ADO3, AtFBX2a identical to FKF1 GI:6960305 and Adagio 3 GI:13487072 from [Arabidopsis thaliana] 259990_s_at 1.			1.2
unknown protein ; supported by cDNA: gi_15912328_gb_AY056442.1_       261354_at       1.         unknown protein ; supported by full-length cDNA: Ceres: 117183.       261269_at       1.         heat shock factor protein hsf8, putative predicted by genemark.hmm; supported by cDNA: gi_15028376_gb_AY045991.1_       261206_at       1.         unknown protein       261064_at       1.         unknown protein       260629_at       1.         unknown protein       260632_at       1.         putative ATP-dependent RNA helicase ; supported by cDNA: gi_16323191_gb_AY057700.1_       260332_at       1.         putative alpha-amylase GB:AAA91884 [Solanum tuberosum]; supported by cDNA: gi_15215737_gb_AY050398.1_       260419_at       1.         putative protein kinase contains Pfam profile: PF00069 Eukaryotic protein kinase domain       260331_at       1.         hypothetical protein contains Pfam profile: PF01535 Domain of unknown function       26031_at       1.         hypothetical protein is supported by full-length cDNA: Ceres:108322.       260041_at       1.         hypothetical protein is profile: PF01344 Kelch motif       26021_at       1.         F-box protein FKF1/ADO3, AtFBX2a identical to FKF1 GI:6960305 and Adagio 3 GI:13487072 from [Arabidopsis thaliana]       259990_s_at       1.			1.2
heat shock factor protein hsf8, putative predicted by genemark.hmm; supported by cDNA: gi_15028376_gb_AY045991.1_       261206_at       1.         unknown protein       261064_at       1.         putative ATP-dependent RNA helicase ; supported by cDNA: gi_16323191_gb_AY057700.1_       260532_at       1.         putative alpha-amylase similar to alpha-amylase GB:AAA91884 [Solanum tuberosum]; supported by cDNA: gi_15215737_gb_AY050398.1_       260412_at       1.         putative protein kinase contains Pfam profile: PF00069 Eukaryotic protein kinase domain       260331_at       1.         hypothetical protein ; supported by full-length cDNA: Ceres:108322.       260301_at       1.         hypothetical protein profile: PF01344 Kelch motif       260021_at       1.         F-box protein KFT/ADO3, AtFBX2a identical to FKF1 GI:6960305 and Adagio 3 GI:13487072 from [Arabidopsis thaliana]       259990_s_at       1.	unknown protein ; supported by cDNA: gi_15912328_gb_AY056442.1_		1.2
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unknown protein       260629_at       1.         putative ATP-dependent RNA helicase ; supported by cDNA: gi_16323191_gb_AY057700.1_       260532_at       1.         putative alpha-amylase similar to alpha-amylase GB:AAA91884 [Solanum tuberosum]; supported by cDNA: gi_15215737_gb_AY050398.1_       260412_at       1.         putative protein kinase contains Pfam profile: PF00069 Eukaryotic protein kinase domain       260331_at       1.         hypothetical protein contains Pfam profile: PF01535 Domain of unknown function       26031_at       1.         hypothetical protein is supported by full-length cDNA: Ceres: 108322.       26001_at       1.         hypothetical protein profile: PF01344 Kelch motif       26021_at       1.         F-box protein FKF1/ADO3, AtFBX2a identical to FKF1 GI:6960305 and Adagio 3 GI:13487072 from [Arabidopsis thaliana]       259990_s_at       1.			1.2
putative ATP-dependent RNA helicase ; supported by cDNA: gi_16323191_gb_AY057700.1_       260532_at       1.         putative alpha-amylase similar to alpha-amylase GB:AAA91884 [Solanum tuberosum]; supported by cDNA: gi_15215737_gb_AY050398.1_       260412_at       1.         putative protein kinase contains Pfam profile: PF00069 Eukaryotic protein kinase domain       260419_at       1.         hypothetical protein contains Pfam profile: PF01535 Domain of unknown function       26031_at       1.         hypothetical protein ; supported by full-length cDNA: Ceres:108322.       26031_at       1.         hypothetical protein contains Pfam profile: PF01344 Kelch motif       260214_at       1.         F-box protein FKF1/ADO3, AtFBX2a identical to FKF1 GI:6960305 and Adagio 3 GI:13487072 from [Arabidopsis thaliana]       259990_s_at       1.			1.2 1.2
putative alpha-amylase similar to alpha-amylase GB:AAA91884 [Solanum tuberosum]; supported by cDNA: gi_15215737_gb_AY050398.1_       260412_at       1.         putative protein kinase contains Pfam profile: PF00069 Eukaryotic protein kinase domain       260419_at       1.         hypothetical protein contains Pfam profile: PF01535 Domain of unknown function       260331_at       1.         hypothetical protein ;supported by full-length cDNA: Ceres:108322.       260301_at       1.         hypothetical protein contains Pfam profile: PF01344 Kelch motif       260211_at       1.         F-box protein FKF1/ADO3, AtFBX2a identical to FKF1 GI:6960305 and Adagio 3 GI:13487072 from [Arabidopsis thaliana]       259990_s_at       1.			1.2
putative protein kinase contains Pfam profile: PF00069 Eukaryotic protein kinase domain       260419_at       1.         hypothetical protein contains Pfam profile: PF01535 Domain of unknown function       260331_at       1.         hypothetical protein ;supported by full-length cDNA: Ceres:108322.       260301_at       1.         hypothetical protein contains Pfam profile: PF01344 Kelch motif       260214_at       1.         F-box protein FKF1/ADO3, AtFBX2a identical to FKF1 GI:6960305 and Adagio 3 GI:13487072 from [Arabidopsis thaliana]       259990_s_at       1.			1.2
hypothetical protein ;supported by full-length cDNA: Ceres:108322.       260301_at       1.         hypothetical protein contains Pfam profile: PF01344 Kelch motif       260214_at       1.         F-box protein FKF1/ADO3, AtFBX2a identical to FKF1 GI:6960305 and Adagio 3 GI:13487072 from [Arabidopsis thaliana]       259990_s_at       1.	putative protein kinase contains Pfam profile: PF00069 Eukaryotic protein kinase domain	260419_at	1.2
hypothetical protein contains Pfam profile: PF01344 Kelch motif       260214_at       1.         F-box protein FKF1/ADO3, AtFBX2a identical to FKF1 GI:6960305 and Adagio 3 GI:13487072 from [Arabidopsis thaliana]       259990_s_at       1.			1.2
F-box protein FKF1/ADO3, AtFBX2a identical to FKF1 GI:6960305 and Adagio 3 GI:13487072 from [Arabidopsis thaliana] 259990_s_at 1.			1.2
			1.2 1.2
			1.2
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putative phenylalanyl-tRNA synthetase beta-subunit; PheHB similar to phenylalanyl-tRNA synthetase beta-subunit (PheHB) GB:5032011 [Homo sap putative ribophorin I (dolichyl-diphosphooligosaccharide-protein glycosyltransferase) similar to ribophorin I (dolichyl-diphosphooligosaccharide-protein		
	250020 3	t 1.2
beta-glucosidase, putative identical to GI:6651430 from [Arabidopsis thaliana]; supported by cDNA: gi_14532461_gb_AY039855.1_	259640_a	t 1.2
CONSTANS family zinc finger protein, putative contains Pfam profile: PF01760: CONSTANS family zinc finger; supported by cDNA: gi 14335053 g	259595 at	t 1.2
cathepsin B-like cysteine protease, putative similar to cathepsin B-like cysteine proteinase GI:609175 from [Nicotiana rustica]	259441 at	
trehalose-6-phosphate synthase, putative similar to trehalose-6-phosphate synthase GI:4468259 from [Pichia angusta]	259393_a	
hypothetical protein predicted by genscan+	259385_a	t 1.2
putative adenylylsulfate kinase similar to GB:S47640 [Arabidopsis thaliana]	259339 at	t 1.2
putative mRNA capping enzyme, RNA guanylyltransferase contains similarty to mRNA capping enzyme GB:BAA25198 from [Homo sapiens]	259202 at	
putative phosphoribosylanthranilate transferase similar to phosphoribosylanthranilate transferase GB:CAA16616 [Arabidopsis thaliana], phosphoribc		
unknown protein est hit, predicted by genscan	259190 at	t 1.2
lysyl-tRNA synthetase identical to lysyl-tRNA synthetase; LysRS GB:AAD17333 [Arabidopsis thaliana]; supported by cDNA: gi 4325323 gb AF125£	259069 at	t 1.2
	258979 at	
heat-shock protein (At-hsc70-3) identical to (At-hsc70-3) (cytosolic Hsp70) GB:CAA76606 [Arabidopsis thaliana]; supported by cDNA: gi_15292924_	_	
putative ribosome recycling factor similar to ribosome recycling factor gene (RRF) GB:BAA76865 [Thermus thermophilus]	258996_a	t 1.2
hypothetical protein similar to hypothetical protein GB:P40055 [Saccharomyces cerevisiae], Pfam HMM hit: WD domain, G-beta repeats	258965 at	t 1.2
unknown protein similar to hypothetical proteins: GB:P51281 [Chloroplast Porphyra purpurea], GB:BAA16982 [Synechocystis sp], GB:P49540 [Odor	258925 at	
	_	
	258926_s_a	
unknown protein predicted by genscan, multiple est matches; supported by full-length cDNA: Ceres: 97694.	258883_a	t 1.2
unknown protein similar to RNA helicase GB:AAF03534	258863 at	t 1.2
putative RNA helicase similar to RNA helicase involved in rRNA processing GB:6321267 from [Saccharomyces cerevisiae]c, ontains DEAD and DE/		
putative GTPase contains Pfam profile: PF01926 GTPase of unknown function	258545_a	
fatty acid multifunctional protein (AtMFP2) identical to fatty acid multifunctional protein (AtMFP2) GB:AF123254 [Arabidopsis thaliana] (fatty acid beta	258555_at	t 1.2
ubiquitin-specific protease 25 (UBP25) similar to GI:11993490; supported by cDNA: gi 11993489 gb AF302673.1 AF302673	258372 at	t 1.2
unknown protein contains RanBP1 domain;supported by full-length cDNA: Ceres:108414.	258313 at	
	258259_s_a	
unknown protein similar to unknown protein GB:AAD14522 from [Arabidopsis thaliana]	258228_a	t 1.2
FKBP-type peptidyl-prolyl cis-trans isomerases, putative contains Pfam profile: PF00254 FKBP-type peptidyl-prolyl cis-trans isomerases	258175 at	t 1.2
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:25758.	258104 at	
unknown protein	257973_a	
formin-like protein AHF1 identical to formin-like protein AHF1 GB:AAF14548 from [Arabidopsis thaliana]; supported by cDNA: gi_6503009_gb_AF174	257912_a	t 1.2
seed maturation protein, putative similar to seed maturation protein (PM36) GB:AAD51624 [Glycine max]; supported by full-length cDNA: Ceres:316{	257888 at	t 1.2
unknown protein	257803 at	
cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450	257625_a	
9-cis-epoxycarotenoid dioxygenase, putative similar to 9-cis-epoxycarotenoid dioxygenase GB:AAF26356 [Phaseolus vulgaris]; supported by cDNA:	257280_a	t 1.2
unknown protein ; supported by cDNA: gi_15294249_gb_AF410316.1_AF410316	257253 at	1.2
Expressed protein ; supported by full-length cDNA: Ceres: 93242.	257193 at	
major latex protein, putative similar to major latex protein type1 GB:CAA63026 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 8841.	256880_a	
unknown protein	256485_a	t 1.2
adenylosuccinate lyase - like protein adenylosuccinate lyase - Haemophilus influenzae	256461 s a	at 1.2
lipoxygenase, putative similar to lipoxygenase GI:1407704 from [Solanum tuberosum]; supported by cDNA: gi 289202 gb L04637.1 ATHLIPOXY		
	256321_a	
unknown protein ; supported by cDNA: gi_14334837_gb_AY035092.1_	256310_a	t 1.2
unknown protein	256271 at	t 1.2
unknown protein	256258 at	t 1.2
unknown protein	256220 at	
NADP-specific glutatamate dehydrogenase, putative similar to NADP-specific glutatamate dehydrogenase (NADP-GDH) SP:P28724 [Giardia lamblik		
55 kDa B regulatory subunit of phosphatase 2A nearly identical to 55 kDa B regulatory subunit of phosphatase 2A [Arabidopsis thaliana] GI:710330;	256187 at	t 1.2
unknown protein ;supported by full-length cDNA: Ceres:23788.	255957 at	1.2
	255668 s a	
hypothetical protein	255611_a	
cathepsin B-like cysteine protease, putative similar to cathepsin B-like cysteine proteinase GI:609175 from [Nicotiana rustica]; contains an unusually	255590_a	t 1.2
	255546 at	t 1.2
putative CHP-rich zinc finger protein similar to several A. thaliana CHP-rich proteins		
putative CHP-rich zinc finger protein similar to several A. thaliana CHP-rich proteins hypothetical protein identical to T10M13.21 ; supported by cDNA: gi_15293058_gb_AY050963.1_	255509_a	
putative CHP-rich zinc finger protein similar to several A. thaliana CHP-rich proteins hypothetical protein identical to T10M13.21 ; supported by cDNA: gi_15293058_gb_AY050963.1_ hypothetical protein ;supported by full-length cDNA: Ceres:6957.	255509_at 255456_at	
putative CHP-rich zinc finger protein similar to several A. thaliana CHP-rich proteins hypothetical protein identical to T10M13.21 ; supported by cDNA: gi_15293058_gb_AY050963.1_	255509_a	
putative CHP-rich zinc finger protein similar to several A. thaliana CHP-rich proteins hypothetical protein identical to T10M13.21; supported by cDNA: gi_15293058_gb_AY050963.1_ hypothetical protein ;supported by full-length cDNA: Ceres:6957. putative protein phosphatase regulatory subunit	255509_at 255456_at 255421_at	t 1.2
putative CHP-rich zinc finger protein similar to several A. thaliana CHP-rich proteins hypothetical protein identical to T10M13.21; supported by cDNA: gi_15293058_gb_AY050963.1_ hypothetical protein ;supported by full-length cDNA: Ceres:6957. putative protein phosphatase regulatory subunit predicted protein of unknown function; supported by cDNA: gi_15810532_gb_AY056305.1_	255509_at 255456_at 255421_at 255332_at	t 1.2 t 1.2
putative CHP-rich zinc finger protein similar to several A. thaliana CHP-rich proteins hypothetical protein identical to T10M13.21; supported by cDNA: gi_15293058_gb_AY050963.1_ hypothetical protein supported by full-length cDNA: Ceres:6957. putative protein phosphatase regulatory subunit predicted protein of unknown function; supported by cDNA: gi_15810532_gb_AY056305.1_ putative calcium dependent protein kinase	255509_at 255456_at 255421_at 255332_at 255292_s_a	t 1.2 t 1.2 at 1.2
putative CHP-rich zinc finger protein similar to several A. thaliana CHP-rich proteins hypothetical protein identical to T10M13.21 ; supported by cDNA: gi_15293058_gb_AY050963.1_ hypothetical protein supported by full-length cDNA: Ceres:6957. putative protein phosphatase regulatory subunit predicted protein of unknown function ; supported by cDNA: gi_15810532_gb_AY056305.1_ putative calcium dependent protein kinase putative calcium dopendent protein kinase putative component of vesicle-mediated transport similar to N. tabacum N-ethylmaleimide sensitive fusion protein, GenBank accession number D86	255509_ai 255456_ai 255421_ai 255332_ai 255292_s_a 255308_ai	t 1.2 t 1.2 at 1.2 t 1.2
putative CHP-rich zinc finger protein similar to several A. thaliana CHP-rich proteins hypothetical protein identical to T10M13.21; supported by cDNA: gi_15293058_gb_AY050963.1_ hypothetical protein phosphatase regulatory subunit predicted protein of unknown function; supported by cDNA: gi_15810532_gb_AY056305.1_ putative calcium dependent protein kinase putative component of vesicle-mediated transport similar to N. tabacum N-ethylmaleimide sensitive fusion protein, GenBank accession number D86 putative thioredoxin; supported by CDNA: gi_16648848_gb_AY058202.1_	255509_at 255456_at 255421_at 255332_at 255292_s_t 255308_at 255279_at	t 1.2 t 1.2 at 1.2 t 1.2 t 1.2 t 1.2
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putative CHP-rich zinc finger protein similar to several A. thaliana CHP-rich proteins hypothetical protein identical to T10M13.21; supported by cDNA: gi_15293058_gb_AY050963.1_ hypothetical protein isosported by full-length cDNA: Ceres:6957. putative protein phosphatase regulatory subunit predicted protein of unknown function ; supported by cDNA: gi_15810532_gb_AY056305.1_ putative calcium dependent protein kinase putative component of vesicle-mediated transport similar to N. tabacum N-ethylmaleimide sensitive fusion protein, GenBank accession number D86 putative protein Homo sapiens deubiquitinating enzyme UnpEL (UNP),PID:g2656141; supported by cDNA: gi_15450766_gb_AY054463.1_ putative protein a 162 kDa component of a multi-protein complex phosphorylated by Src - Mus musculus,PID:g1205976; supported by cDNA: gi_124 N-acetylomithine deacetylase-like protein, fragment N-acetylomithine deacetylase (AOdD) - Dictyostelium discoideum, PID:G763048	255509_ai 255456_ai 255421_ai 255332_ai 255292_s_i 255308_ai 255279_ai 254984_s_i 254984_s_i 254873_ai 254778_ai	t 1.2 t 1.2 at 1.2 t 1.2
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putative ubiquitin-dependent proteolytic protein ubiquitin fusion-degradation protein - Mus musculus, PID:g1654348; supported by cDNA: gi 169304		1.2
	252863 at	1.2
	252410_at	1.2
	252429_at	1.2
hypothetical protein	252400_at	1.2
aldehyde dehydrogenase (NAD+)-like protein aldehyde dehydrogenase (NAD+) 2A precursor (mitochondrial), Nicotiana tabacum; supported by cDN	252372_at	1.2
hypothetical protein	252346_at	1.2
	252321_at	1.2
	251946_at	1.2
	251935_at	1.2
	251690_at	1.2
	251494_at	1.2
	251460_at	1.2
putative protein carbonyl reductase (NADPH) - Rattus norvegicus, PIR:JC5285; supported by cDNA: gi_15028054_gb_AY045884.1_ serine/threonine-protein kinase-like protein serine/threonine kinase UNC51.2 - Mus musculus, EMBL:AF145922; supported by cDNA: gi_14334751	251309_at	1.2 1.2
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CDK5 activator-binding protein-like	250700_at	1.2
transcription factor HBP-1b (gb AAD24395.1)	250655_at	1.2
myosin heavy chain-like protein ; supported by cDNA: gi_1732514_gb_U62744.1_ATU62744	250548_at	1.2
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	248369 at	1.2
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SGP1 monomeric G-protein (emb CAB54517.1)	248132_at	1.2
pyruvate decarboxylase (gb AAB16855.1)	248138_at	1.2
DNA topoisomerase I	248109_at	1.2
	248036_at	1.2
transcription factor-like; similar to CH6 and COP9 complex subunit 6; supported by cDNA: gi_15809662_gb_AY048692.1_	248009_at	1.2
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	246595_at	1.2
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putative protein cisplatin resistance-associated overexpressed protein - Homo sapiens, EMBL:AB034205; supported by cDNA: gi_15450598_gb_AY	246426	1.2
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unknown protein         28885 git         11           desease restatunce protein         240774 git         11           publiev contein Kinsse IT catalytic (ph0)a sub.unit         240767 gitt         217768 gitt           publiev contein Kinsse IT catalytic (ph0)a sub.unit         240767 gitt         217768 gitt         11           publiev contein Kinsse IT catalytic (ph0)a sub.unit         240767 gitt         266872 gitt         11           publiev contein Kinsse IT catalytic (ph0)a sub.unit         240707 gitt         266872 gitt         11           publiev contein Kinsse IT catalytic (ph0)a sub.unit         240708 gitt         266872 gitt         11           publiev contein Kinsse IT catalytic (ph0)a sub.unit         266877 gitt         266872 gitt         11           publiev contein Kinsse IT catalytic (ph0)a sub.unit         266877 gitt         266877 gitt         11           publiev contein mole (ph0) contein Catalytic (ph0)a sub.unit         266877 gitt         11         266877 gitt         11           publiev contein mole (ph0) contein Catalytic (p			_	
putative protein predicted protein, Arabidopsis malana.supported by ML-kength cDNA: Ceres: 11412.         21565.4[m]         1.1           unknown protein : supported by (LNA: g] 15450620 gb. AV052378.1_         277.40 gt         1.1           presease proteins : supported by (LNA: g] 15450620 gb. AV052378.1_         277.50 gt         1.1           prative causin Kinase II. caught(c) (LNA: Ceres: 3004.         277.50 gt         1.1           prative causin Kinase II. caught(c) (LNA: Ceres: 3004.         277.50 gt         1.1           prative biolizes: supported by (LNA: g] 1502726 gb. AV045820.1_         266672 gt         1.1           prative biolizes: supported by (LNA: g] 1502726 gb. AV045820.1_         266672 gt         1.1           prative biolizes: supported by (LNA: gl. 15027260 gb. AV045911.1_         266667 gt         1.1           prative protein (B-tox cere forge domain)         266667 gt         1.1           prative protein (B-tox cere forge domain)         266667 gt         1.1           prative protein (B-tox cere forge domain)         266667 gt         1.1           prative exploration factor         266647 gt         1.1	·		_	1.1
desage resistance protein         2477-24, at 1.1           Expressed protein : supported by CNA: g1:1545020 gb, XY05277.1_         277.06 gt         1.1           Expressed protein : supported by CNA: g1:1545020 gb, XY05277.1_         277.07 gt         1.1           DNA: fagurine or apprimidine telly yase (ARP) definitiant to GB.X70012         277.07 gt         1.1           DNA: fagurine or apprimidine telly yase (ARP) definitiant to GB.X70012         277.07 gt         1.1           protein tells and young te	unknown protein		258356_at	1.1
unknown protein         :supported by UNA: g] :1562062, gb, AV05275.1_         277488_1         1.1           pressest proteins: supported by UNA: g] :1562075.1_         27759.2_         1.1           public casen kinses II catalytic (abina) sub.ont: supported by UNA: Gar.Y8912         27759.2_         1.1           public casen kinses II catalytic (abina) sub.ont: supported by CMA: g]. 1502757.2_         1.1         200072.1_ <td></td> <td></td> <td>_</td> <td></td>			_	
Expressed protein : supported by full-length CDNA: Ceres: 31647.         207302, at         1.1           DNA: (quurine or apprinting stubit): supported by full-length CDNA: Ceres: 3804.         207752, at         1.1           DNA: (quurine or apprinting stub): supported by full-length CDNA: Ceres: 3804.         207762, at         1.1           DNA: (quurine or apprinting stub): supported by full-length CDNA: Ceres: 3804.         207762, at         1.1           Database signed gated (an channel protein         207802, at         1.1           Digitable relevation supported by full-length CDNA: Ceres: 20766.         206662, at         1.1           putable signed gated (an channel protein         2066612, at         1.1           putable signed gated (an channel protein by full-length CDNA: Ceres: 20766.         2066612, at         1.1           putable signed gate full-length CDNA: Ceres: 20766.         2066612, at         1.1           hypothetical protein factor         2066014, at         1.1         1.1           hypothetical protein factor         2060014, at         1.1         1.1 <td< td=""><td></td><td></td><td>_</td><td></td></td<>			_	
putative casient kinase ii catalytic (alpha) subunit supported by full-ength CDNA: Ceres: 38084.         287757_at         1.1           putative ligand-galactic on channel protein         286787_at         1.1           putative ligand-galactic on channel protein         286687_at         1.1           putative ligand-galactic on channel protein         286687_at         1.1           putative ligand-galactic on channel protein         286687_at         1.1           putative transchannel protein         286687_at         1.1           putative transchannel protein         286687_at         1.1           putative transchannel protein         286687_at         1.1           putative enconcomme P450 denchand to BCJNR04. Supported by full-length cDNA: Ceres: 20820.         286407_at         1.1           putative enconcomme P450 denchand to BCJNR04. Supported by full-length cDNA: Ceres: 30815.         286507_at         1.1           putative enconcomme P450 denchand to BCJNR04. Ceres: 30815.         285507_at         1.1           putative enconcomme P450 denchand to BCJNR04. Ceres: 30815.         285507_at         1.1 <td></td> <td></td> <td>_</td> <td></td>			_	
DNA-(apuritio or apprintionic site) iyase (APP) identical to GE:X76912         227099, at         1.1           putable by dived edyndopenase         226682, at         1.1           oppi-late entrelement pol ophyroten : supported by CDNA gt. 15022176, gb_AV045911.1_         226678, at         1.1           oppi-late entrelement pol ophyroten : supported by CDNA gt. 15022176, gb_AV045911.1_         226669, at         1.1           putabre biology ophyrease : supported by CDNA gt. 1522081, gb_AV045911.1_         226669, at         1.1           putabre polytic phyrotenes : supported by CDNA gt. 1522081, gb_AV045911.1_         226664, at         1.1           putabre polytic phyrotenes : supported by CDNA gt. 1542081, gb_AV045911.1_         226664, at         1.1           hypothetical protein (Bo-Care Topic Content)         226614, at         1.1           hypothetical protein factor         226614, at         1.1           hypothetical protein         226600, at         1.1           hypothetical protein for tool GB.D76804, supported by CDNA: gt_15454007, gb_AV0340251			_	
platbe         206802_et al.           platbe         206802_et al.           platbe         206732_et al.           platbe         206673_et al.           platbe         206674_et al.           platbe         206674_et al.           platbe         206674_et al.           platbe         206677_et al.           platbe         2			_	
putative heiligand-gated in channel protein         266782, at         1.1           copia-like retroelement polyprotein; supported by CDNA; gj.15028176, gb_AY045911.1_         266689, at         1.1           copia-like retroelement polyprotein; supported by VLNA; gj.15028176, gb_AY045911.1_         266689, at         1.1           putative polyApomeraes: supported by VLNA; gj.15028176, gb_AY045911.1_         266643, g, at         1.1           putative singApomera         supported by VLNA; gj.15028176, gb_AY045911.1_         266643, g, at         1.1           putative singApomera         supported by CDNA; gj.15028176, gb_AY045911.1_         266643, g, at         1.1           putative singApomera         supported by CDNA; gj.15028176, gb_AY034925, 1_         266630, at         1.1           hypothetical protein         putative singApomera         266640, at         1.1           hypothetical protein         supported by CDNA; gj.15430467, gb_AY034925, 1_         266600, at         1.1           hypothetical protein         supported by full-length cDNA; Ceres: 36815.         26650, at         1.1           sunknown protein         supported by full-length cDNA; Ceres: 36815.         265650, at         1.1           hypothetical protein protein contains similarity to hip-ducose-regulated protein A GBAAF08413 Gl6A40083 from [Homo sepiens]; supported by cDNA; gj.265078, at         1.1           hypothetical protei				
putative indecises : supported by CDNA: g1:15027326, gb, AY045911.1_         266679, at         1.1           putative poly(A) polymerase : supported by CDNA: g1:15028176, gb, AY045911.1_         266669, at         1.1           putative favoral protein (B-box zhe finger domain)         26643, gs         1.1           putative favoral protein (B-box zhe finger domain)         26643, gs         1.1           hypothetical protein (B-box zhe finger domain)         26643, gs         1.1           putative zhranger protein (B-box zhe finger domain)         26643, gs         1.1           putative zhranger protein (B-box zhe finger domain)         26643, gs         1.1           putative zhranger protein (B-box zhe finger domain)         266407, gs         1.1           putative zhranger protein (B-box zhe finger domain)         266407, gs         1.1           putative zhranger protein (B-box zhe finger domain)         266407, gs         1.1           putative zhranger protein (B-box zhe finger domain)         266407, gs         1.1           putative zhranger protein (B-box zhe finger domain)         266407, gs         1.1           putative zhranger protein (B-box zhe finger domain)         265407, gs         1.1           putative zhranger protein (B-box zhe finger domain)         265570, gs         1.1           unknown protein         250071, gs         1.1				
putative fervord 3-0-Qlucoxyftrarfersers :supported by ful-length cDNA: Ceres:29796.         266649_st         1.1           putative fervord 3-0-Qlucoxyftrarfersers :supported by ful-length cDNA: Ceres:20796.         266450_st         1.1           putative transportin         266450_st         1.1           hypothetical protein predicted by genscan:supported by ful-length cDNA: Ceres:20820.         266450_st         1.1           putative enclosed on factor         266450_st         1.1           hypothetical protein         266450_st         1.1           putative enclosed on factor         26650_st         1.1           putative enclosed on factor         26650_st         1.1           putative enclosed on supported by ful-length cDNA: Ceres:36815.         26550_st         1.1           putative enclosed on supported by cDNA: ginst factor         265650_st         1.1           putative ligand-pate factor         265650_st         1.1           putative ligand-pate factor         265650_st         1.1           putative enclosed on tan factor         266561_st         1.1           putative enc			266679_at	1.1
putative transport         266643 e.g. at         1.1           putative transport         26653 at         1.1           putative transport         26654 e.g.         1.1           putative transport         266450 e.g.         266450 e.g.         1.1           putative transport         266440 e.g.         1.1           putative transport         266450 e.g.         266450 e.g.         1.1           putative transport         266450 e.g.         266450 e.g.         1.1           putative operation factor         266400 r.g.         1.1         266000 r.g.         1.1           putative operation Pacific definition (B.B.D78604 r.g.) (14334467 g.g.AV034925.126000 at         266900 r.g.         1.1           unknown protein         289810 at         1.1         289810 at         1.1 </td <td>copia-like retroelement pol polyprotein ; supported by cDNA: gi_15028176_gb_AY045911.1_</td> <td></td> <td>266698_at</td> <td>1.1</td>	copia-like retroelement pol polyprotein ; supported by cDNA: gi_15028176_gb_AY045911.1_		266698_at	1.1
putative transportin         26652.3.dt         1.1           hypothetical protein predicted by genscansupported by full-length cDNA: Cares 20820.         266407.st         1.1           hypothetical protein predicted by genscansupported by cDNA: gl_14334467_gb_AY034925.1_         266304_at         1.1           hypothetical protein         266407.st         1.1           hypothetical protein         266307_at         1.1           putative enclosition is supported by cDNA: gl_14334467_gb_AY034925.1_         266007_at         1.1           nuknown protein         268307_at         1.1           unknown protein         268307_at         1.3           unknown protein         268307_at         1.3           unknown protein         268407_at         1.3           unknown prote			_	
putative zinc-finger protein (B-box zinc finger domain)         266514 at         1.1           putative elongation factor         266440 s, 24         1.1           putative elongation factor         266407 zt         1.1           putative elongation factor         266407 zt         1.1           putative elongation factor         266807 zt         1.1           putative elongation factor         266807 zt         1.1           unknown protein         266807 zt         1.1           unknown protein         266807 zt         1.1           unknown protein         265870 zt         1.1           unknown protein         265971 zt         1.1           unknown protein         265980 zt         1.1           unknown protein         266308 zt         1.1           unknown protein         266371 zt         1.1           unknown protein         266380 zt         1.1           unknown protein         266380 zt         1.1           unknown protein         266491 zt         1.1           unknown protein		2		
hypothetical protein pedictical by genscan.supported by full-length cDNA: Ceres: 20820.         2664407, at         1.1           hypothetical protein         266304, at         1.1           putative englosition factor         266304, at         1.1           putative methodiny-HRNA synthetase : supported by cDNA: gl_14334467_gb_AY034925.1_         266807, at         1.1           putative methodiny-HRNA synthetase : supported by cDNA: Ceres: 3001.         266807, at         1.1           unknown protein         266807, at         1.1           unknown protein         266807, at         1.1           unknown protein         266570, at         1.1           pyothetical protein contains similarity to high-glucose-regulated protein 6 GB:AAF08813 Gl:6449083 from [Homo sapiens]; supported by cDNA: gl_27318         265201, at           unknown protein         266570, at         1.1           pyothetical protein similarity to pre-nINNA processing protein PRP39 gb L2224 from S. cerevisiae. ESTs gb[R44908 and gb]T88158, gb]N3         264482, at         1.1           pyothetical protein similarity to pre-nINNA processing protein PRP39 gb L2224 from S. cerevisiae. ESTs gb[R44908 and gb]T88158, gb]N3         264482, at         1.1           pyothetical protein similarity to pre-nINNA processing protein PRP39 gb L2224 from S. cerevisiae. ESTs gb[R44908 and gb]T84584, gb]T44131         264482, at         1.1           pyothetical protein protein Sim				
putative elongation factor         266407_att         11.1           putative elongation factor         266304_att         11.1           putative methionyl-RNA synthetase : supported by cDNA: gi_14334467_gb_AY034925.1_         266007_att         11.1           putative explorimer P450 idential to GB D78604; supported by CDNA: gi_15450907_gb_AY054534.1_         266007_att         11.1           unknown protein         266501_att         11.1         266010_att         11.1           unknown protein         266570_att         11.1         266570_att         11.1           unknown protein         266570_att         11.1         265712_att         11.1           unknown protein         266178_att         11.1         265712_att         11.1           unknown protein         266178_att         265176_att         11.1           unknown protein         269178_att         264778_att         11.1           unknown protein         269178_att         264787_att         11.1			_	
hypothelical protein         266304_att         1.1           putative enclorioni-RNA synthetase ; supported by cDNA: gl_14334467_gb_AY034925.1_         266057_att         1.1           putative exptochrome P450 identical to GED/78043, supported by cDNA: gl_15450907_gb_AY054534.1_         266561_att         1.1           unknown protein         266561_att         1.1           unknown protein         266576_att         1.1           unknown protein         266576_att         1.1           unknown protein         266506_att         1.1           unknown protein         266201_att         1.1           unknown protein         266281_att         1.1           unknown protein         266282_att         1.1           unknown protein         264789_att         1.1           unknown protein         264789_att         1.1           unknown protein         264789_att         1.1           unknown protein         264789_att         1.1           unknown protein         264778_att				
putative enchionyl-RNA synthetase : supported by cDNA: g1_14324467_gb_AY034925.1260057_at         260057_at         11.           putative enchioner P450 identical to GED/7806/01 supported by CDNA: g1_15450807_gb_AY054534.1260000_gt 11.         260000_gt 11.           unknown protein         260570_gt 11.         260570_gt 11.           Unknown protein         265710_gt 11.         265710_gt 11.           Unknown protein         26570_gt 11.         265710_gt 11.           Unknown protein         265710_gt 11.         265712_gt 11.           Unknown protein         265712_gt 11.         265701_gt 11.           Unknown protein         265712_gt 11.         265701_gt 11.           Unknown protein         265701_gt 11.         265701_gt 11.           Unknown protein         265712_gt 11.         265701_gt 11.           Unknown protein         265701_gt 11.         265701_gt 11.           Unknown protein         265701_gt 11.         265760_gt 11.           Unknown protein         26571_gt 11.         265760_gt 11.           Unknown protein         265760_gt 11.         26576				
putative cytochrome P450 identical to GB1078604; supported by cDNA: gi_1545007_gb_AV054534.1_         26600_gt_11         1.1           unknown protein         266310_gt_11         1.1           unknown protein         266510_gt_11         1.1           285 proteasome subunt 4_supported by full-length cDNA: Ceres:36815.         265507_gt_11         1.1           265207_st_11         1.1         265207_gt_11         1.1           unknown protein         265207_gt_11         1.1           unknown protein contains similarly to hgi-pucoses-reguladed protein 8 GB-AF08813 Gr644083 from [Homo sapiens]; supported by CDNA: gi_245078_gt_11         1.1           unknown protein contains similarly to hgi-pucoses-reguladed protein 8 GB-AF08813 Gr644083 from [LeoG708_gt_12]         264630_gt_11         1.1           unknown protein is supported by CDNA: gi_14360430_gb_0 AF30010_1_AF36012         264441         1.1           unknown protein is supported by CDNA: gi_1430430_gb_0 AF30010_1_AF36010_1_AF36010_1_AF3601_1_AF3601_1_AF3601_1_AF3601_1_AF3601_1_AF3601_1_AF3601_1_AF3601_1_AF3601_1_AF3601_1_AF3601_1_AF3601_1_AF3601_1_AF3601_1_AF3601_1_AF3601_1_AF360_1_AF360_1_AF360_1_AF36_1_1_AF36_1_AF36_1_AF36_1_1_AF36_1				
unknown protein         2659f.jat         1.1           unknown protein         26591.jat         1.1           unknown protein         26570.jat         1.1           265 protessome subunit 4: supported by full-length cDNA: Ceres:36815.         265570.jat         1.1           unknown protein         265201.jat         1.1           unknown protein         265271.jat         1.1           unknown protein         265479.jat         1.1           unknown protein         1.1         264587.jat         1.1           unknown protein         1.1         263774.jat				
unknown protein         265700         26570         26570			265961_at	1.1
265 proteasome subunit 4 ; supported by full-length cDNA: Ceres:36815.         265597_it         11           unknown protein         265201_st         11           hypothetical protein ESTs gb H76594 and gb H76252 come from this gene         265201_st         11           unknown protein Contains similarity to pre-mRNA processing protein PRP39 gb L29224 from S. cerevisiae. ESTs gb R64908 and gb T86158, gb N3         266036_at         11           hypothetical protein protein Contains similarity to pre-mRNA processing protein PRP39 gb L29224 from S. cerevisiae. ESTs gb R64908 and gb T86158, gb N3         266132         244789_at         11           nutnown protein is supported by cDNA: gj_12430435_gb L732613010_L75301301         244584_at         11         244584_at         11           nutnown protein similar to trabidopsis putative ion-channel PID:2262157 (gb AC002329); supported by cDNA: gj_124571348         264548_at         11           nutnown protein similar to hypothetical protein GB:551583         11         putative chormodomain-helicase-DNA-binding protein similar to hudeoporin NUP145 (sp P49687/IN145_YEAST); similar to Br352         264346_at         11           nutnown protein : supported by cDNA: gj 1269039_1.1_AB029916.1_AB029916         28346_at         11           nutnown protein : supported by cDNA: gj 126902_gb_AY056871.1_         283471_at         11           nutnown protein : supported by cDNA: gj 12610476_gb_AY056877.1_         283471_at         11      <	unknown protein		265810_at	1.1
unknown protein265201_att11unknown protein ESTs gbl/T6594 and gbl/T6252 come from this gene265217.att11unknown protein ESTs gbl/T6594 and gbl/T6252 come from this gene265217.att11unknown protein Contains similarity to pre-mRNA processing protein PRP39 gb L29224 from S. cerevisiae. ESTs gblR64098 and gbl/T88158, gbl/N3265037.att11putative vialaxanthin de-epoxidase precursor (U44133) similar to EST gbl/N37612; supported by cDNA; gj_1465734_gb_U44133, 1_ATU44133264036.att11putative vialaxanthin de-epoxidase precursor (U44133) similar to EST gbl/N37612; supported by cDNA; gj_17186264567.att11unknown protein ; supported by cDNA; gj_17340435, gb_AF360130, _AF360130264546.att11unknown protein similar to Teell receptor beta chain CDR3 (gl]3064031; similar to nucleoporin NUP145 (sp)P49687[N145_YEAST); similar to EST 2644456, att11unknown protein is supported by cDNA; gj_12706439, gbl_AR6202916263346, att11unknown protein is supported by cDNA; gj_12780438, gbl_AR6302906, gblT04111, gblR84180, gblR65428, gblT64570, gblR90004, gblT4520, gblR3002, gblR3	·		_	
unknown protein ESTs gb H76594 and gb H76252 come from this gene265217_s_at1.1unknown protein Contains similarity to high-glucose-regulated protein & GB:AAF08813 Gl:6449083 from [Homo sapiens]: supported by cDNA: gj_285078_at1.1unknown protein Contains similarity to pre-mRNA processing protein PRP39 gb L29224 from S. cerevisiae. ESTs gb]R64908 and gb]T88158, gb]N3268428_athypothetical protein predicted by genscan264428_at1.1putative viduaxnith in de-epoxidase precursor (U44133) similar to EST gb]N37612; supported by cDNA: gj_1465734_gb_U44133.1_ATU44133264799_at1.1putative viduaxnith in de-epoxidase precursor (U44133) similar to FST gb[N37612; supported by cDNA: gj_1571316264548_at1.1unknown protein : supported by cDNA: gj_1340345, gb_AF3601301_AF361030264546_at1.1unknown protein is similar to hypothetical protein GE:S1568264515_at1.1putative vidnomodomain-helicase-DNA-binding protein similar to hA22, postmase Gl:29792 from [Kluyveromyces lacts]264244_at1.1putative vidnomodomain-helicase-DNA: Gers3274263362_at1.1unknown protein : supported by cDNA: gj_16649002 gb_AY059871.1_263371_at1.1unknown protein : Supported by cDNA: gj_15810476_gb_AY056277.1_263347_at1.1unknown protein : Supported by cDNA: gj_15810476_gb_AY056277.1_263347_at1.1unknown protein : supported by cDNA: gj_15810336_gb_AY056277.1_263347_at1.1unknown protein : supported by cDNA: gj_15810336_gb_AY056277.1_263347_at1.1unknown protein : supported by cDNA: gj_15810336_gb_AY056277.1_263347_at1.1 <t< td=""><td></td><td></td><td></td><td></td></t<>				
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hypothetical protein predicted by genemark.hmm262130_at1.1hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres:116121.262111_at1.1unknown protein ; supported by cDNA: gi_6520232_dbj_AB028233.1_AB02823326208_at1.1splicing factor Prp8, putative similar to splicing factor Prp8 GI:3661610 from [Homo sapiens]26208_at1.1putative coatomer protein complex, subunit beta 2 (beta prime) similar to coatomer protein complex, subunit beta 2 (beta prime) similar to coatomer protein complex, subunit beta 2 (beta prime) GB:4758032 (Homc262051_at				
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unknown protein ; supported by cDNA: gi_6520232_dbj_AB028233.1_AB028233 262080_at 1.1 splicing factor Prp8, putative similar to splicing factor Prp8 GI:3661610 from [Homo sapiens] 262068_at 1.1 putative coatomer protein complex, subunit beta 2 (beta prime) similar to coatomer protein complex, subunit beta 2 (beta prime) similar to a coatomer protein complex, subunit beta 2 (beta prime) similar to a coatomer protein complex, subunit beta 2 (beta prime) similar to a coatomer protein complex, subunit beta 2 (beta prime) similar to a coatomer protein complex, subunit beta 2 (beta prime) similar to a coatomer protein complex, subunit beta 2 (beta prime) similar to a coatomer protein complex, subunit beta 2 (beta prime) similar to a coatomer protein complex, subunit beta 2 (beta prime) similar to a coatomer protein complex, subunit beta 2 (beta prime) similar to a coatomer protein complex, subunit beta 2 (beta prime) similar to a coatomer protein complex, subunit beta 2 (beta prime) similar to a coatomer protein complex, subunit beta 2 (beta prime) similar to a coatomer protein complex, subunit beta 2 (beta prime) similar to a coatomer protein complex, subunit beta 2 (beta prime) similar to a coatomer protein complex, subunit beta 2 (beta prime) similar to a coatomer protein complex, subunit beta 2 (beta prime) similar to a coatomer protein complex, subunit beta 2 (beta prime) similar to a coatomer protein complex, subunit beta 2 (beta prime) similar to a coatomer protein complex, subunit beta 3 (beta prime) similar to a coatomer protein complex, subunit beta 3 (beta prime) similar to a coatomer protein complex, subunit beta 4 (beta prime) similar to a coatomer protein complex, subunit beta 4 (beta prime) similar to a coatomer protein complex, subunit beta 4 (beta prime) similar to a coatomer protein complex, subunit beta 5 (beta prime) similar to a coatomer protein complex, subunit beta 5 (beta prime) similar to a coatomer protein complex, subunit beta 5 (beta prime) similar to a coatomer protein complex, subunit be				
putative coatomer protein complex, subunit beta 2 (beta prime) similar to coatomer protein complex, subunit beta 2 (beta prime) GB:4758032 (Homc 262051_at 1.1				
ubiquitin, putative similar to poly-ubiquitin GB:AAC13691 GI:3047318 from [Pyricularia grisea] 261947_at 1.1		(Homc		
	uoiquiun, putauve similar to poly-uoiquitin GB:AAC13691 GI:3047318 from [Pynculana grisea]		201947_at	1.1

ATP citrate-lyase, putative similar to ATP citrate-lyase GI:9229902 from [Ciona intestinalis];supported by full-length cDNA: Ceres:36439.	261833_at	1.1
unknown protein ; supported by cDNA: gi_15451153_gb_AY054657.1_	261795_at	1.1
unknown protein contains similarity to actin-related protein GB:BAA74577 GI:4218064 from [Homo sapiens]; supported by full-length cDNA: Ceres:38	261672_at	1.1
	261686_at	1.1
unknown protein similar to unknown protein GB:AAF24950 GI:6693024 from [Arabidopsis thaliana]; supported by cDNA: gi_13605566_gb_AF36160!	-	1.1
	261621_at	1.1
	261615_at 261560 at	1.1 1.1
acy Look integendation of the source of the		1.1
	261519 at	1.1
	261458 at	1.1
	261238 at	1.1
Eukaryotic peptide chain release factor subunit 1 (ERF1) identical to Eukaryotic peptide chain release factor subunit 1 (ERF1) SP:P35614 ((In) Plant 2	261204_s_at	1.1
GSH-dependent dehydroascorbate reductase 1, putative similar to GB:BAA90672 from [Oryza sativa]; supported by full-length cDNA: Ceres: 15122.2	261149_s_at	1.1
	261107_at	1.1
	261026_at	1.1
	261023_at	1.1
s-adenosylmethionine synthetase identical to s-adenosylmethionine synthetase GB:P23686 from [Arabidopsis thaliana]; supported by full-length cDN biotection (2):242737 fore [Arabidopsis thaliana]; supported by full-length cDN is correct and the control of the co		1.1
hypothetical protein similar to hypothetical protein GB:AAB67625 GI:2342727 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 300 chloroplast inner envelope protein, putative similar to chloroplast inner envelope protein GB:CAA92823 GI:1495768 from [Pisum sativum]	260840_at 260815_at	1.1 1.1
	260627 at	1.1
	260562 at	1.1
	260466 at	1.1
	260444_at	1.1
unknown protein ; supported by full-length cDNA: Ceres: 96657.	260356_at	1.1
putative protein kinase similar to C-terminal region of s-receptor kinase precursor GB:JQ1677 [Brassica napus]; Pfam HMM hit: Eukaryotic protein kin		1.1
putative ABC transporter contains Pfam profile: PF00005 ABC transporters; similar to TAP1 protein (transporter of processed antigen) GB:AAD5303:	-	1.1
	260273_at	1.1
	260282_at	1.1
	260137_at 260073 at	1.1
putative protein kinase contains Pfam profile: PF00069 eukaryotic protein kinase domain endoplasmic reticulum alpha-mannosidase, putative similar to GI:5579331 from [Homo sapiens]; supported by cDNA: gi 15450803 gb AY054482.1		1.1 1.1
	259939_s_at	1.1
	259872 at	1.1
	259765 at	1.1
lysophospholipase isolog, putative similar to lysophospholipase isolog GI:1931639 from (Arabidopsis thaliana);supported by full-length cDNA: Ceres	259708_at	1.1
unknown protein ;supported by full-length cDNA: Ceres:25703.	259639_at	1.1
	259426_at	1.1
	259330_at	1.1
	259334_at	1.1
	259295_at	1.1
	259296_at 259284 at	1.1 1.1
	259231_at	1.1
homeobox-leucine zipper protein HAT5 (HD-ZIP protein 5) (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein ATHB-1) identical to homeobox-leucine zipper protein ATHB-1) identical to homeobox-leucine zipper protein ATHB-1) identical to homeobox-leucine z		1.1
unknown protein similar to unknown protein GB:BAA24863 [Homo sapiens], unknown protein GB:BAA20831 [Homo sapiens], unknown protein GB:/		1.1
	259094_at	1.1
putative cytochrome P450 similar to cytochrome P450 89A2 GB:Q42602 [Arabidopsis thaliana]; supported by cDNA: gi_15983413_gb_AF424581.1_	259058_at	1.1
	258844_at	1.1
	258801_at	1.1
	258744_at	1.1
putative nonspecific lipid-transfer protein similar to nonspecific lipid-transfer protein GB:Q43019 [Prunus dulcis]; supported by full-length cDNA: Ceres unknown protein	258675_at 258593_at	1.1 1.1
	258512 at	1.1
putative stearoyl-acyl carrier protein desaturase similar to stearoyl-acyl carrier protein desaturase GB:CAA07349 from [Linum usitatissimum],support	_	1.1
	258489 at	1.1
cell division protein FtsH-like protein similar to cell division protein FtsH GB:AAD35665 from [Thermotoga maritima]; supported by full-length cDNA: C	258494_at	1.1
expressed protein supported by cDNA: gi:14194102	258444_at	1.1
	258439_at	1.1
putative selenocysteine methyltransferase similar to selenocysteine methyltransferase GB:P56707 from [Astragalus bisulcatus];supported by full-lence	_	1.1
	258299_at	1.1
	258263_at 258202 at	1.1 1.1
unktiowin proteini putative GTP pyrophosphokinase similar to GTP PYROPHOSPHOKINASE GB:087331 from [Corynebacterium glutamicum]; supported by cDNA; gi		1.1
	258188 at	1.1
	258108 at	1.1
	258007_at	1.1
hypothetical protein contains Pfam profile:PF00534 Glycosyl transferases group 1	257797_at	1.1
	257672_at	1.1
calmodulin-domain protein kinase CDPK isoform 9 identical to GB:AAB03242 from [Arabidopsis thaliana]; supported by cDNA: gi_1399264_gb_U31;		1.1
	257646_at	1.1
	257212_at 257154 at	1.1
	257154_at 257018_at	1.1 1.1
	256986 at	1.1
	256928_at	1.1
	256866_at	1.1
casein kinase, putative similar to casein kinase 1 GB:NP_001883 from [Homo sapiens]	256783_at	1.1
	256754_at	1.1
	256724_at	1.1
dTDP-glucose 4.6-dehydratase, putative similar to dTDP-glucose 4.6-dehydratase GB:AE000666 GI:6626257 from [Methanobacterium thermoautoti bursthickersteinerstitated by another provide the state of th		1.1
	256399_at	1.1
	256411_at 256300 at	1.1 1.1
	256300_at 256233_at	1.1
	256229 at	1.1
	256229_at 255876_at	1.1 1.1

putative PRP19-like spliceosomal protein WD-40 repeat protein	255830_at	1.1
predicted protein of unknown function ; supported by cDNA: gi_16648930_gb_AY059835.1_	255638_at	1.1
	255600_s_at	1.1
hypothetical protein	255615_at	1.1
GBF2, G-box binding factor ;supported by full-length cDNA: Ceres:16533.	255625_at	1.1
putative protein similar to several proteins containing a tandem repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U278 contains a short region of similarity to another Arabidopsis hypothetical protein F19K23.8 (GB:AC000375)	255473_at 255475_at	1.1 1.1
putative protein similar to A. thaliana protein F15K9.3, GenBank accession number 3850566	255466 at	1.1
putative protein similar to A. utaliaria protein 1 rotos), certaina accession inimiter operation of the state similar to P. vulgaris gibberellin 20-oxidase, GenBank accession number U70530	255437 at	1.1
putative protein hypothetical protein, Arabidopsis thaliana	255224 at	1.1
ferredoxin-NADP+ reductase - like protein ferredoxin-NADP+ reductase, Pisum sativum, PIR:T06773;supported by full-length cDNA: Ceres:33486.		1.1
putative host response protein pir7a protein - rice, PIR2:S47086	255025 at	1.1
putative protein phosphatase like protein - Arabidopsis thaliana,PIR2:T05589;supported by full-length cDNA: Ceres:152712.	254918 at	1.1
hypothetical protein	254779 at	1.1
putative protein ; supported by cDNA: gi_16323185_gb_AY057697.1_	254764_at	1.1
putative protein predicted protein, Arabidopsis thaliana, PATCHX:E327449	254701_at	1.1
putative protein	254711_at	1.1
	254657_s_at	1.1
hypothetical protein	254602_at	1.1
hypothetical protein	254501_at	1.1
	254389_s_at	1.1
cellulose synthase catalytic subunit - like protein cellulose synthase catalytic subunit (Ath-A), Arabidopsis thaliana, gb:AF027173	254185_at	1.1
auxin response factor 9 (ARF9) ; supported by cDNA: gi_4580574, gb_AF082176. https://doi.org/10.1007/10.0000000000000000000000000000	254194_at	1.1 1.1
hsp 70-like protein heat shock 70 protein - Spinacia oleracea,PID:g2654208 putative proteasome regulatory subunit KIAA0107 gene, Homo sapiens, D14663;supported by full-length cDNA: Ceres:38927.	254148_at 254086 at	1.1
	254053 s at	1.1
hypothetical protein	254067 at	1.1
choline monooxygenase - like protein choline monooxygenase precursor, Spinacia oleracea,gb:U85780	253701 at	1.1
MAP kinase kinase 2 ; supported by cDNA: gi 14326470 gb AF385688.1 AF385688	253646 at	1.1
cyclic nucleotide and calmodulin-regulated ion channel-like protein cyclic nucleotide and calmodulin-regulated ion channel - Arabidopsis thaliana, PIC		1.1
putative protein myosin heavy chain, neuronal, Rattus norvegicus, Pir1:S21801; supported by cDNA: gi 14334773 gb AY035060.1	253523 at	1.1
putative protein tomato leucine zipper-containing protein - Lycopersicon esculentum, PIR2:S21495	253531_at	1.1
putative protein gene C42D8.3, Caenorhabditis elegans, PID:G1293846	253469_at	1.1
putative protein mixed-lineage protein kinase, Homo sapiens, PIR:A53800	253473_at	1.1
putative protein ring finger protein, Hordeum vulgare	253444_at	1.1
	253362_s_at	1.1
putative protein YHR077c (NMD2,IFS1) protein -Saccharomyces cerevisiae,PID:g555939; supported by cDNA: gi_14334747_gb_AY035047.1_	253335_at	1.1
hypothetical protein	253294_at	1.1
putative protein RING-finger protein, Lotus japonicus, PIR2:S49446	253265_at	1.1
cytoplasmatic aconitate hydratase (citrate hydro-lyase)(aconitase)(EC 4.2.1.3)	253135_at	1.1
hypothetical protein	253020_at	1.1
putative protein other predicted Arabidopsis thaliana proteins	253037_at	1.1
putative protein ;supported by full-length cDNA: Ceres:125922. putative protein alpha-amino-epsilon-caprolactam racemase, Achromobacter obae, PIR2:JC1497; supported by cDNA: gi 5731258 gb AF166351.1	252945_at	1.1
putative protein 70K pervisional membrane protein, Rattus norvegicus, PIR2:A35723 supported by CDNA, gr_3731232_gu_Ar 10031.		1.1 1.1
putative protein ; supported by CDNA; gi 14334983 gb AV035165.1	252391_at	1.1
	252402 s at	1.1
betaine aldehyde dehydrogenase-like protein betaine aldehyde dehydrogenase - Amaranthus hypochondriacus,PID:g2388710; supported by cDNA:		1.1
putative protein pirsa protein - Oryza sativa, PIR:s47086;supported by full-length cDNA: Ceres:30104.	252168 at	1.1
putative protein hypothetical protein F16F14.2 - Arabidopsis thaliana, EMBL:AC007047	252142 at	1.1
sigma factor SigC ; supported by cDNA: gi_2353174_gb_AF015544.1_AF015544	251929_at	1.1
Expressed protein ; supported by full-length cDNA: Ceres: 120919.	251845_at	1.1
aquaporin MIP - like protein aquaporin 2, Samanea saman, AF067185; supported by full-length cDNA: Ceres: 11929.	251858_at	1.1
Ca-dependent solute carrier - like protein peroxisomal Ca-dependent solute carrier, Oryctolagus cuniculus, EMBL:AF004161;supported by full-length	251757_at	1.1
	251721_s_at	1.1
putative protein several hypothetical proteins - different plant species; supported by cDNA: gi_16604698_gb_AY059794.1_	251713_at	1.1
putative protein strictosidine synthase (EC 4.3.3.2) - Rauvolfia mannii (fragment)	251679_at	1.1
putative protein translation releasing factor RF-2 - Synechocystis sp., PIR:S76448	251670_at	1.1
translation initiation factor 3 -like protein mammary tumor-associated protein INT6 - Homo sapiens, EMBL:U94174; supported by cDNA: gi_145325;	_	1.1
ATP-dependent RNA helicase-like protein ATP-dependent RNA helicase - Xenopus laevis, PIR:S13654;supported by full-length cDNA: Ceres:4158.		1.1
putative protein PBK1 protein, Homo sapiens, EMBL:HSA7398 putative protein crp1 protein, involved in post-transcriptional control of chloroplast gene expression - Zea mays, PIR:T01685	251538_at 251496 at	1.1 1.1
putative protein hypothetical proteins. Arabidopsis thaliana; supported by cDNA; gi 14334587 gb AY034967.1	251490_at 251356_at	1.1
putative protein several hypothetical proteins - Arabidopsis thaliana; supported by cDNA: gi 145/17361 gb AY039515.1	251308 at	1.1
cytochrome p450 (CYP78A9) ;supported by full-length cDNA: Ceres:29661.	251301 at	1.1
putative protein several O-methyltransferases - different species;supported by full-length cDNA: Ceres:40117.	251304 at	1.1
putative protein predicted protein, Arabidopsis thaliana; supported by CDNA: gi 14334781 gb AY035064.1	251153 at	1.1
putative protein hypothetical proteins - Arabidopsis thaliana; supported by full-length cDNA: Ceres:14817.	251073 at	1.1
putative protein	250928 at	1.1
putative protein similar to unknown protein (dbj BAA90353.1)	250830_at	1.1
eukaryotic translation initiation factor 2 alpha subunit-like protein ; supported by cDNA: gi_13358180_gb_AF324988.2_AF324988	250779_at	1.1
ABC transporter-like protein ; supported by cDNA: gi_14488081_gb_AF389289.1_AF389289	250690_at	1.1
Mei2-like protein Mei2-like protein - Arabidopsis thaliana, EMBL:D86122	250617_at	1.1
putative protein condensin subunit SMC4, Drosophila melanogaster, EMBL:AF186472	250559_at	1.1
putative protein predicted proteins, Arabidopsis thaliana	250486_at	1.1
putative protein mRNA, Moritella marina, EMBLAB025342	250275_at	1.1
putative protein mRNA, Moritella marina, EMBL:AB025342	250276_at	1.1
putative protein	250179_at	1.1
putative protein various predicted proteins, Arabidopsis thaliana	250194_at	1.1
putative protein contains similarity to DNA repair protein	250105_at	1.1
anthranilate phosphoribosyltransferase, chloroplast precursor (sp Q02166); supported by cDNA: gi_15450851_gb_AY054506.1_ casein kinase-like protein	050014 -+	1.1
	250014_at	4 4
	250021_at	1.1
soluble starch synthase	250021_at 249785_at	1.1
soluble starch synthase acyl-peptide hydrolase-like	250021_at 249785_at 249690_at	1.1 1.1
soluble starch synthase acyl-peptide hydrolase-like putative protein tropomyosin gene 1, isoform 9D, D.melanogaster, EMBL:DMTRO13	250021_at 249785_at 249690_at 249628_at	1.1 1.1 1.1
soluble starch synthase acyl-peptide hydrolase-like	250021_at 249785_at 249690_at	1.1 1.1

putative protein	249506_at	1.1
GTPase activator protein of Rab-like small GTPases-like protein	249281_at	1.1
putative protein similar to unknown protein (dbj BAA84809.1);supported by full-length cDNA: Ceres:27758.	249229_at	1.1
dynamin-like protein (pir  S59558) ;supported by full-length cDNA: Ceres:42932.	249232_at	1.1
pitrilysin	249218_at	1.1
putative protein strong similarity to unknown protein (emb CAB87688.1)	248817_at	1.1
Lon protease homolog 1 precursor identical to Lon protease homolog 1 mitochondrial precursor SP:064948 from [Arabidopsis thaliana]	248818_at	1.1
putative protein contains similarity to CCAAT-box-binding trancription factor; supported by cDNA: gi_14326579_gb_AF385744.1_AF385744	248764_at	1.1
putative protein contains similarity to 5 -nucleotidase	248628_at	1.1
permease	248558_at	1.1
putative protein similar to unknown protein (pir  S75732);supported by full-length cDNA: Ceres:35710.	248537_at	1.1
putative protein strong similarity to unknown protein (dbj BAA78737.1);supported by full-length cDNA: Ceres:150246.	248399_at	1.1
cyclic nucleotide-regulated ion channel (emb CAA76178.1); supported by cDNA: gi_13877752_gb_AF370139.1_AF370139	248250_at	1.1
putative protein contains similarity to enolase-phosphatase	248234_at	1.1
homogentisate 1,2-dioxygenase ;supported by full-length cDNA: Ceres:6599.	248193_at	1.1
putative protein strong similarity to unknown protein (pir  T04825); supported by cDNA: gi_14596222_gb_AY042899.1_	248115_at	1.1
unknown protein	248067_at	1.1
putative protein contains similarity to actin	247997_at	1.1
WD-repeat protein-like ;supported by full-length cDNA: Ceres:109499.	248000_at	1.1
Ca2+-transporting ATPase-like protein (emb CAB79748.1)	247937_at	1.1
leucine zipper-containing protein leucine zipper-containing protein, Lycopersicon esculentum, PIR:S21495	247811_at	1.1
putative protein ;supported by full-length cDNA: Ceres:3086.	247748_at	1.1
putative protein myosin heavy chain, Dugesia japonica, EMBL:AB015484	247738_at	1.1
oxysterol-binding protein - like oxysterol-binding protein, Mus musculus, EMBL:AB017026; supported by cDNA: gi_15450785_gb_AY054473.1_	247677_at	1.1
putative protein transcriptional repressor NOT4-N, Homo sapiens, EMBL:AF180475	247669_at	1.1
putative protein various predicted proteins from different species; supported by cDNA: gi_15912286_gb_AY056421.1_	247555_at	1.1
RNA helicase - like protein RNA helicase, Homo sapiens, EMBL:Z70200	247564_at	1.1
snap25a ;supported by full-length cDNA: Ceres:14562.	247571_at	1.1
RNA-binding protein - like RNA-binding protein, Nicotiana sylvestris, PIR:S46286; supported by cDNA: gi_16974555_gb_AY060565.1_	247575_at	1.1
putative transcription factor MYB28 ; supported by cDNA: gi_5823328_gb_AF175998.1_AF175998	247549_at	1.1
100 kDa coactivator - like protein 100 kDa coactivator, Homp sapiens, PIR:I38968	247517_at	1.1
putative protein similar to unknown protein (pir  T00246)	247277_at	1.1
disease resistance protein-like	247065_s_at	1.1
putative protein contains similarity to unknown protein (sp Q10058);supported by full-length cDNA: Ceres:108335.	246985_at	1.1
RuvB DNA helicase-like protein ; supported by cDNA: gi_16974567_gb_AY061754.1_	247014_at	1.1
serine/threonine-specific protein kinase-like protein serine/threonine-specific protein kinase NPK15 - Nicotiana tabacum; supported by full-length cDN	246529_at	1.1
putative protein Tat-SF1 - Homo sapiens, EMBL:U76992	246499_at	1.1
cellulose synthase catalytic subunit -like protein Ath-B, cellulose synthase catalytic subunit, Arabidopsis thaliana, EMBL:AF027174	246460_at	1.1
Cu2+-transporting ATPase-like protein	246276_at	1.1
myb-related protein	246253_at	1.1
tetratricopeptide repeat protein tetratricopeptide repeat protein - Homo sapiens, EMBL:U46570	246120_at	1.1
katanin p80 subunit - like protein katanin p80 subunit, Strongylocentrotus purpuratus, EMBL:AF052433	246056_at	1.1
putative protein ; supported by cDNA: gi_4103242_gb_AF022368.1_AF022368	245971_at	1.1
putative protein ;supported by full-length cDNA: Ceres:120101.	245948_at	1.1
hypothetical protein contains similarity to maleless protein (mle) GI:157905 from [Drosophila melanogaster]	245863_s_at	1.1
hypothetical protein predicted by genemark.hmm	245844_at	1.1
tRNA-glutamine synthetase, putative similar to tRNA-glutamine synthetase GI:2995454 from [Lupinus luteus]	245631_at	1.1
galactokinase like protein	245478_at	1.1
hypothetical protein	245481_at	1.1
disease resistance RPP5 like protein (fragment)	245460_at	1.1
hypothetical protein ;supported by full-length cDNA: Ceres:13520.	245385_at	1.1
nuclear RNA binding protein A-like protein ;supported by full-length cDNA: Ceres:35156.	245387_at	1.1
	245187_s_at	1.1
putative receptor-like protein kinase	245130_at	1.1
unknown protein	245137_at	1.1
unknown protein similar to glycoprotein SP Q16186 G100_HUMAN; supported by cDNA: gi_13926226_gb_AF372873.1_AF372873	245045_at	1.1
PSII D2 protein	245002_at	1.1
RNA polymerase alpha subunit	244978_at	1.1
putative 3 -5 exoribonuclease similar to ribonuclease II RNB family protein GB:CAB16367 [Schizosaccharomyces pombe]; Pfam HMM hit: VacB and		1.1
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:39566.	256854_at	1.1
hypothetical protein	253716_at	1.1
resistance protein, putative similar to resistance protein MG23 GI:9858478 from [Glycine max]	264910_at	1
	254985_x_at	1
putative protein strong similarity to unknown protein (emb CAB16785.1)	247067_at	1
unknown protein similar to hypothetical protein PIR S76698 S76698; supported by cDNA: gi_15809963_gb_AY054250.1_	267562_at	1
unknown protein	267501_at	1
putative receptor-like protein kinase	267481_at	1
unknown protein	267406_at	1
Expressed protein ; supported by full-length cDNA: Ceres: 24003.	267211_at	1
unknown protein ; supported by cDNA: gi_15451173_gb_AY054667.1_	267180_at	1
unknown protein ; supported by full-length cDNA: Ceres: 16625.	267060_at	1
unknown protein	267014_at	1
unknown protein	267015_at	1
hypothetical protein predicted by genscan	266903_at 266839_at	1
unknown protein	_	1
		1
putative peptide chain release factor phytophytophytophytophytophytophytophyto	266751_at	1
phytochrome B Identical to GB:X17342	266065_at	1
putative potassium/proton antiporter	265936_at	1
unknown protein ; supported by cDNA: gj_15450955_gb_AY054558.1	265799_at	1
unknown protein similar to ovarian tumor protein; supported by cDNA: gi_16604333_gb_AY058065.1_ unknown protein similarity to ubiquitin family of proteins; supported by cDNA: gi_16930424_gb_AF419566.1_AF419566	265630_at 265461_at	1
unknown protein similarity to ubiquitin family of proteins, supported by CDNA: gi_16930424_gb_AF419566.1_AF419566 hypothetical protein	265461_at 265425_at	1 1
similar to mammalian MHC III region protein G9a	265425_at 265347_at	1
histidine transport protein (PTR2-B); supported by cDNA: gi 13937184 gb AF372946.1 AF372946	265347_at 265220_at	1
putative auxin-induced protein (PTR2-B); supported by cUNA: gi_1393/184_go_AF3/2946.1_AF3/2946	265220_at 265182_at	1
		1
similar to glucose 1-dehydrogenase (AB000617); similar to EST gb T88100 similar to oxidoreductase-like protein GB:CAB75763 GI:7019662 from [A 2	200107_S_a(	I

similar to 14KD proline-rich protein DC2.15 precursor (sp P14009); similar to ESTs emb Z17709 and emb Z47685 similar to hybrid proline-rich protein		
	265092_at 1	
	264999_at 1	
F-box protein family, AtFBL5 contains similarity to F-box protein FBL2 GI:6063090 from [Homo sapiens];supported by full-length cDNA: Ceres:3549. Interstitute that the second statement of the second		
	264935_at 1 264792_at 1	
hypotretical protein similar to hypotretical protein 56-C6493000 unknown protein similar to L-allo-threonine aldolase (D874300); similar to ESTs gb R30517, gb T42772, gb R90493, and gb R90493;supported by full	-	
	264516_at 1	
	264396 at 1	
	264354 s at 1	
	264367 at 1	
	264299 sat 1	
ATPase 70 kDa subunit, putative similar to ATPase 70 kDa subunit GI:558478 from [Brassica napus]; supported by full-length cDNA: Ceres:17815.	264302_at 1	1
putative SF2/ASF splicing modulator, Srp30 similar to GB:CAB42558	264255_at 1	1
hypothetical protein predicted by genemark.hmm	264268_at 1	1
	264141_at 1	
mercaptopyruvate sulfurtransferase (Mst1/Rdh1) identical to mercaptopyruvate sulfurtransferase GI:6009981 and thiosulfate sulfurtransferase GI:58:		
	264048_at 1	
	263958_at 1	
	263921_at 1 263922_s_at 1	
	263874_at 1	
	263864_at 1	
	263804_at 1	
	263743_at 1	
	263755 at 1	
	263764_at 1	
	263728_at 1	1
3-methyladenine DNA glycosylase, putative Strong similarity to GB:P29102, 3-isopropylmalate dehydrogenase (IMDH) from Brassica napus. EST gl 2	263706_s_at 1	1
putative 1-aminocyclopropane-1-carboxylate oxidase Similar to Arabidopsis 2A6 (gb X83096). EST gb T76913 comes from this gene; supported by c	263668_at 1	1
	263639_at 1	
	263452_at 1	
putative bZIP transcription factor contains a bZIP transcription factor basic domain signature (PDOC00036); supported by cDNA: gi_15450833_gb_A	-	
	263419_at 1	
	263261_at 1	
UDP-glucose:indole-3-acetate beta-D-glucosyltransferase, putative similar to UDP-glucose:indole-3-acetate beta-D-glucosyltransferase GI:2149127 burnthetical parties produced by page second by the product of the produ	-	
	263145_at 1 263122_at 1	
trehalose-6-phosphate synthase, putative similar to trehalose-6-phosphate synthase GI4468259 from [Pichia angusta]; supported by cDNA; gi 138;		
dihydrolipoamide S-acetyltransferase, putative similar to dihydrolipoamide S-acetyltransferase GI:5669871 from [Zea mays], supported by cDNA; gj		
	262934 s at 1	
	262888 at 1	
putative glycogen synthase strong similarity to gb X95759 soluble-starch-synthase precursor (SSIII) from Solanum tuberosum	262809_at 1	1
aspartate aminotransferase nearly identical to aspartate aminotransferase, cytoplasmic isozyme 2 SP:P46646 [Arabidopsis thaliana (Mouse-ear cre-	262646_at 1	1
oxidoreductase, putative contains Pfam profile: PF00671 Iron/Ascorbate oxidoreductase family; supported by cDNA: gi_13878118_gb_AF370322.1_		
putative glutathione transferase One of three repeated putative glutathione transferases. 72% identical to glutathione transferase [Arabidopsis thaliar		
	262455_at 1	
serine/threonine kinase, putative similar to serine/threonine kinase GB:Y12530 GI:2181187 from [Brassica oleracea]; supported by cDNA: gi_15810		
	262331_at 1	
	262316_at 1 262296_at 1	
unknown protein Similar to gbl/F151884 CGI-126 protein from Homo sapiens, EST gbl/218048 comes from this gene; supported by full-length cDNA		
	262281 at 1	
	262207 at 1	
	262223 at 1	
	262188 at 1	
glutathione S-transferase, putative similar to glutathione S-transferase GI:860955 from [Hyoscyamus muticus]; supported by cDNA: gi_15215607_gI2	262119_s_at 1	1
hypothetical protein contains similarity to helicase-like protein NHL GI:6969265 from [Homo sapiens]	262066_at 1	1
hypothetical protein contains similarity to PP2 lectin polypeptide GI:410436 from [Cucurbita maxima]; supported by cDNA: gi_15292968_gb_AY0509	262061_at 1	1
	261921_at 1	
	261885_at 1	
	261853_at 1	
DNA-binding protein, putative similar to helicase-like transcription factor GB:CAA86572 GI:1658307 from [Homo sapiens]; supported by cDNA: gi_14 hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres;108306.	-	
hypotretical protein prediced by generical similar, supported by luniering of Cores. Ceres. Dosoo. unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pfam pro		
RIBOSOMAL PROTEIN, putative similar to 30S RIBOSOMAL PROTEIN S1 GB:P46228 from [Synechococcus sp.]; supported by cDNA: g1 150818(		
	261524_at 1	
hypothetical protein contains similarity to zinc finger protein GI:1399465 from [Cryptosporidium parvum];supported by full-length cDNA: Ceres:20571!		
	261365 at 1	
unknown protein	261250_at 1	1
hypothetical protein predicted by genemark.hmm	261183_at 1	1
	261167_at 1	1
	261173_at 1	
	261179_at 1	
	261136_at 1	
tropinone reductase-I, putative similar to GB:L20473 from [Datura stramonium] (Proc. Natl. Acad. Sci. U.S.A. 90, 9591-9595 (1993)); supported by c burdthetical practing is millar to upknown practing. GP: A6527473 (1997) (2773) from (Arabidonsis thetingal.		
	261043_at 1	
glyoxalase II, putative similar to GI:1644427 from (Arabidopsis thaliana); supported by cDNA: gi_15450394_gb_AY052298.1_ 26S proteasome regulatory particle triple-A ATPase subunit4, putative similar to 26S proteasome regulatory particle triple-A ATPase subunit4 GI:11(	260986_at 1 260940_at 1	
	260693 at 1	
	260663_at 1	
	260673_at 1	
	260679_at 1	
	260568_at 1	
•	260536_at 1	
putative protein kinase similar to protein kinase APK1A GB:Q06548 [Arabidopsis thaliana]; contains Pfam profile: PF00069 Eukaryotic protein kinase		
receptor protein kinase, putative similar to receptor protein kinase GI:1389566 from (Arabidopsis thaliana); supported by cDNA: gi_4204848_gb_U5!	260345_at 1	I

putative alpha galactosyltransferase similar to alpha galactosyltransferase GB:CAB52246 [Trigonella foenum-graecum] (plant cell wall matrix polysac	260222_at	1
putative SET protein, phospatase 2A inhibitor similar to SET protein, phospatase 2A inhibitor GB:Q01105 [Homo sapiens] (role in the mechanism of	260235_at	1
putative phosphoglucomutase similar to phosphoglucomutase GB:AAC00601 [Arabidopsis thaliana]	260207_at	1
putative hydroxymethyltransferase similar to serine hydroxymethyltransferage GB:P50433 from [Solanum tuberosum]; supported by full-length cDNA:	260126_at	1
unknown protein ;supported by full-length cDNA: Ceres:36337.	260009_at	1
unknown protein	259942_at	1
unknown protein similar to LIGATIN GB:Q61211 from (Mus musculus), contains PAS domain Sensory-box	259948_at	1
unknown protein	259903_at	1
putative cinnamyl-alcohol dehydrogenase similar to cinnamyl-alcohol dehydrogenase GB:AAC35846 [Medicago sativa]	259911_at	1
hypothetical protein predicted by genscan	259762_at	1
	259689_x_at	1
hypothetical protein	259582_at	1
protein kinase, putative similar to protein kinase GI:2852447 from (Arabidopsis thaliana)	259541_at	1
unknown protein	259422_at	1
hypothetical protein predicted by genscan+	259444_at	1
hypothetical protein similar to hypothetical protein GI:6598642 from [Arabidopsis thaliana]	259392_at	1
hypothetical protein predicted by genemark.hmm	259397_at	1
putative SAR DNA-binding protein-1 similar to GB:AAC16330 from [Pisum sativum]; supported by cDNA: gi_11878186_gb_AF302491.1_AF302491	259311_at	1
unknown protein similar to HYP1 GB:CAA55187 from [Arabidopsis thaliana]	259318_at	1
unknown protein	259321_at	1
spindly (gibberellin signal transduction protein) identical to spindly GB:AAC49446 [Arabidopsis thaliana]; supported by cDNA: gi_1589777_gb_U621:		1
unknown protein ; supported by cDNA: gi_15724287_gb_AF412084.1_AF412084	259240_at	1
hypothetical protein predicted by genefinder	259249_at	1
unknown protein	259207_at	1
putative cell division control protein similar to cell division control protein 48, AAA family (cdc48-1) GB:AAB89948 [Archaeoglobus fulgidus]	259176_at	1
unknown protein	259191_at	1
hypothetical protein predicted by genefinder; supported by cDNA: gi_16604436_gb_AY059763.1_	259156_at	1
hypothetical protein predicted by genemark.hmm, contains Pfam profile PF01553 Acyltransferase; supported by cDNA; gi_14423461_gb_AF386968	_	1
26S proteasome AAA-ATPase subunit RPT5a identical to GB:AAF22525 from [Arabidopsis thaliana]; supported by cDNA: gi_5669046_gb_AF08157	_	1
unknown protein	259121_at	1
putative zeta-carotene desaturase precursor nearly identical to zeta-carotene desaturase precursor GB:AAA91161 [Arabidopsis thaliana];supported I		1
unknown protein similar to putative protein GB:CAB40988 [Arabidopsis thaliana]	259043_at	1
unknown protein ;supported by full-length cDNA: Ceres:801.	259055_at	1
hypothetical protein similar to Ku70-binding protein GB:AAD31085 [Homo sapiens]; supported by CDNA: gi_13877934_gb_AF370230.1_AF370230	259056_at	1
unknown protein C-terminal portion similar to mannosyltransferase GB:BAA28328 [Escherichia coli]supported by full-length cDNA: Ceres:17844.	258917_at	1
unknown protein similar to GB:AAD55296; supported by cDNA: gi_13605628_gb_AF361640.1_AF361640	258853_at	1
putative potassium transporter similar to potassium transporter GB:AAB87687 [Arabidopsis thaliana]; supported by cDNA: gi_6742168_gb_AF20762 unlocume patation is unstand by full location BDNA: constant 410/2014		1
unknown protein ; supported by full-length cDNA: Ceres: 118261.	258879_at	1
unknown protein similar to GB:AAD10646 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:117342.	258812_at	1
hypothetical protein similar to hypothetical protein GB:AAF23212 GI:6671952 from (Arabidopsis thaliana)	258756_at	1
unknown protein	258478_at	1
	258449_s_at	1
putative protein kinase similar to mitogen activated protein kinase kinase GB:AAC32599 from [Oryza sativa]:supported by full-length cDNA: Ceres:26 unknown protein kinase similar to mitogen activated protein kinase GB:CAA75001 from [Oryza sativa]:supported by full-length cDNA: Ceres:26		1 1
unknown protein similar to leucine-rich repeat protein GB:CAA76000 and GB:CAA76001 from [Arabidopsis thaliana] unknown protein contains Pfam profile: PF00076 RNA recognition motif	258390_at 258229_at	1
anknown protein contains r Jann prome: n tooror n toor recognition mou Sn1-related protein kinase KIN11 (AKIN11) identical to protein kinase KKin11 GI:1729444 [Arabidopsis thaliana]	258229_at 258221_at	1
phosphoprotein phosphatase, putative similar to phosphoprotein phosphotase GB:AB18613 from [Mus musculus]	258215 at	1
prosprioproduct in prospriates, putative similar to grosproprotein prospriates do Areb to or non truto most mesources glutamine synthetase, putative similar to Gri synthetase GB:228456 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:5507.	258160_at	1
gutanine synthease, putative similar to cytosolic chaperonin, delta-subunit GB:CAA09989 [Citycine max]; contains Pfam profile: PF00118 TCP-1/cpnf		1
	257890_s_at	1
unknown protein contains Pfam profile:PF01435 Peptidase family M48;supported by full-length cDNA: Ceres:156849.	257791 at	1
unknown protein	257717 at	1
hypothetical protein predicted by genemark.hmm	257723 at	1
		1
Unknown protein contains Ptam protile: PE()(4()) 2 WI) domains. (a-beta repeats	_	
	257684_s_at	1
cytochrome P450, putative similar to cytochrome P450 GB:O65784 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 262802.	257684_s_at 257634_s_at	1 1
cytochrome P450, putative similar to cytochrome P450 GB:O65784 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 262802. cytochrome P450 monooxygenase (CYP71B4) identical to cytochrome P450 monooxygenase (CYP71B4) GB:D78603 [Arabidopsis thaliana] (Plant	257684_s_at 257634_s_at 257635_at	1
cytochrome P450, putative similar to cytochrome P450 GB:O65784 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 262802. cytochrome P450 monooxygenase (CYP71B4) identical to cytochrome P450 monooxygenase (CYP71B4) GB:D78603 [Arabidopsis thaliana] (Plant cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450;supported by full-length cDNA: Ceres: 149380.	257684_s_at 257634_s_at 257635_at 257129_at	1 1
cytochrome P450, putative similar to cytochrome P450 GB:O65784 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 262802. cytochrome P450 monooxygenase (CYP71B4) identical to cytochrome P450 monooxygenase (CYP71B4) GB:D78603 [Arabidopsis thaliana] (Plant cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450;supported by full-length cDNA: Ceres:149380. unknown protein similar to unknown protein GB:AAD43153 from [Arabidopsis thaliana]	257684_s_at 257634_s_at 257635_at 257129_at 256944_at	1 1 1
cytochrome P450, putative similar to cytochrome P450 GB:O65784 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 262802. cytochrome P450 monooxygenase (CYP71B4) identical to cytochrome P450 monooxygenase (CYP71B4) GB:D78603 [Arabidopsis thaliana] (Plant cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450;supported by full-length cDNA: Ceres: 149380. unknown protein similar to unknown protein GB:AAD43153 from [Arabidopsis thaliana] glutamine:fructose-6-phosphate amidotransferase, putative similar to glutamine:fructose-6-phosphate amidotransferase 2 GB:BAA74729 [Mus musc	257684_s_at 257634_s_at 257635_at 257129_at 256944_at 256911_at	1 1
cytochrome P450, putative similar to cytochrome P450 GB:O65784 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 262802. cytochrome P450 monooxygenase (CYP71B4) identical to cytochrome P450 monooxygenase (CYP71B4) GB:D78603 [Arabidopsis thaliana] (Plant cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450;supported by full-length cDNA: Ceres:149380. unknown protein similar to unknown protein GB:AAD43153 from [Arabidopsis thaliana]	257684_s_at 257634_s_at 257635_at 257129_at 256944_at 256911_at	1 1 1
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cytochrome P450, putative similar to cytochrome P450 GB:O65784 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 262802. cytochrome P450 monooxygenase (CYP71B4) identical to cytochrome P450 monooxygenase (CYP71B4) GB:D78603 [Arabidopsis thaliana] (Plant cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450; supported by full-length cDNA: Ceres: 149380. unknown protein similar to unknown protein GB:AAD43153 from [Arabidopsis thaliana] glutamine:fructose-6-phosphate amidotransferase, putative similar to glutamine:fructose-6-phosphate amidotransferase 2 GB:BAA74729 [Mus musc aminotransferase, putative similar to aminotransferase GB:CAA19897 from [Streptomyces coelicolor A3(2)]; supported by cDNA: gi_14334463_gb_/ unknown protein ; supported by cDNA: gi_13899104_gb_AF370547.	257684_s_at 257634_s_at 257635_at 257129_at 256944_at 256911_at 256765_at 256683_at	1 1 1 1 1
cytochrome P450, putative similar to cytochrome P450 GB:O65784 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 262802. cytochrome P450 monooxygenase (CYP71B4) identical to cytochrome P450 monooxygenase (CYP71B4) GB:D78603 [Arabidopsis thaliana] (Plant cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450;supported by full-length cDNA: Ceres: 149380. unknown protein similar to unknown protein GB:AAD43153 from [Arabidopsis thaliana] glutamine:fructose-6-phosphate amidotransferase, putative similar to glutamine:fructose-6-phosphate amidotransferase 2 GB:BAA74729 [Mus musc aminotransferase, putative similar to aminotransferase GB:CAA19897 from [Streptomyces coelicolor A3(2)]; supported by cDNA: gi_14334463_gb_/ unknown protein ; supported by cDNA: gi_13899104_gb_AF370547.1_AF370547 hypothetical protein predicted by genemark.hmm	257684_s_at 257634_s_at 257635_at 257129_at 256944_at 256944_at 256765_at 256765_at 256683_at 256613_at	1 1 1 1 1 1
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cytochrome P450, putative similar to cytochrome P450 GB:O65784 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 262802. cytochrome P450 monooxygenase (CYP71B4) identical to cytochrome P450 monooxygenase (CYP71B4) GB:D78603 [Arabidopsis thaliana] (Plant cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450;supported by full-length cDNA: Ceres: 149380. unknown protein similar to unknown protein GB:AAD43153 from [Arabidopsis thaliana] glutamine:fructose-6-phosphate amidotransferase, putative similar to glutamine:fructose-6-phosphate amidotransferase 2 GB:BAA74729 [Mus musc aminotransferase, putative similar to aminotransferase GB:CAA19897 from [Streptomyces coelicolor A3(2)]; supported by cDNA: gi_14334463_gb_/ unknown protein ; supported by cDNA: gi_13899104_gb_AF370547.1_AF370547 hypothetical protein predicted by genemark.hmm protein kinase, putative contains Pfam profile: PF00069: Eukaryotic protein kinase domain deoxyguanosine kinase, putative similar to deoxyguanosine kinase [Homo sapiens] GI:1480198;supported by full-length cDNA: Ceres:3878.	257684_s_at 257634_s_at 257635_at 257129_at 256944_at 256911_at 256765_at 256683_at 256613_at 256629_at 256341_at	1 1 1 1 1 1 1
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choline kinase GmCK2p -like protein choline kinase GmCK2p -Glycine max,PID:g1438881;supported by full-length cDNA: Ceres:126037., Ceres:73	_	1
protein kinase - like protein KI domain interacting kinase 1 -Zea mays,PIR2:T02053	254869_at	1
flavonoid 3,5-hydroxylase -like protein flavonoid 3 ,5 -hydroxylase - Campanula medium, PID:d1003951	254834_at	1
short-chain alcohol dehydrogenase like protein short-chain alcohol dehydrogenase -Picea abies, PIR2:S34678;supported by full-length cDNA: Ceres	_	1
putative protein WERBP-1 - Nicotiana tabacum, EMBL:AB017693;supported by full-length cDNA: Ceres:38327.	254682_at	1
hypothetical protein ;supported by full-length cDNA: Ceres:40589.	254683_at	1
starch synthase-like protein bacterial and plant glycogen (starch) synthases; for example B.subtilis, PATCHX:D1020368	254659_at	1
putative protein kinase ; supported by cDNA: gi_13249122_gb_AF295667.1_AF295667	254636_at	1
putative protein	254547_at	1
hypothetical protein ;supported by full-length cDNA: Ceres:40232.	254503_at	1
UV-damaged DNA-binding protein- like damage-specific DNA binding protein 1, Homo sapiens, PIR2:138908	254452_at	1
putative protein heat shock protein dnaJ homolog, yeast, PIR2:A33618	254458_at	1
serine/threonine protein kinase like protein serine/threonine protein kinase (ARSK1 gene), Arabidopsis thaliana, PATCHX:G1066501	254341_at	1
HSP associated protein like p48, Homo sapiens, PATCHX:G904032;supported by full-length cDNA: Ceres:35786.	254275_at	1
putative fizzy-related protein fizzy-related protein, Drosophila melanogaster, PID:g2326419	254284_at	1
putative protein various predicted proteins; supported by cDNA; gj_14423555 gb_AF387015.1_AF387015.1_AF387015	254174_at	1
HSP90-like protein HSP90 homolog - Catharanthus roseus, PIR2:S39558; supported by cDNA: gi_14532541_gb_AY038895.1_	254166_at	1
brefeldin A-sensitive Golgi protein - like brefeldin A-sensitive Golgi protein LDLC, Homo sapiens, PIR2:A53542; supported by cDNA: gi_13605802_c B chiveneritien 2 (constrained a)	254087_at 254034 at	1 1
P-glycoprotein-2 (pgp2) fimbrin-like protein (ATFIM1) ; supported by cDNA: gi 2905892 gb U66424.1 ATU66424	253956 at	1
		1
ubiquitin-specific protease 24 (UBP4), putative similar to GI:11993488; ubiquitin carboxyl-terminal hydrolase, Mus musculus, PID:D101289; suppo		1
budquarespecific protein car protein car protein car mays, 214393	2533552_at 253495_at	1
sulfolipid biosynthesis protein SQD1 ; supported by cDNA: gi 14190482 gb AF380641.1 AF380641	253386 at	1
E-box protein family, AtFBL15 contains similarly to F-box protein FBL2 GI:6063090 from [Homo sapiens]	253369_at	1
putative protein FABI protein, Saccharomyces cerevisiae, PIR2:56274	253371_at	1
hypothetical protein	253288 at	1
putative protein ARI protein, Drosophila melanogaster, X98309; supported by cDNA: gi 15292860 gb AY050864.1	253236 at	1
L-ascorbate peroxidase supported by full-length cDNA: Ceres:21896.	253223 at	1
invertase - like protein mRNA, Lilium longiforum, gb:D21823; supported by cDNA; gi 15215775 gb AY050417.1	253224 at	1
phosphoserine aminotransferase ;supported by full-length cDNA: Ceres:34272.	253162 at	1
putative protein Niemann-Pick C disease protein - Homo sapiens, PID:g2276463	252985_at	1
glycine-rich protein (clone AtGRP8); supported by cDNA: gi_166838_gb_L00649.1_ATHRBPB	252885 at	1
dnaJ protein homolog atj3 ;supported by full-length cDNA: Ceres:40976.	252670 at	1
putative protein	252552 at	1
heat shock protein 17; supported by cDNA; gi 15294149 gb AF410266.1 AF410266	252515 at	1
dTDP-glucose 4-6-dehydratases-like protein dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana.PIR:S58282;supported by full-length c		1
telomere repeat-binding protein homolog telomere repeat-binding protein - Arabidopsis thaliana, SWALL:CAB50690	252504_at	1
putative RNA-binding protein various putative RNA binding proteins	252453_at	1
chloroplast NAD-dependent malate dehydrogenase ; supported by cDNA: gi_3256065_emb_Y13987.1_ATMDH	252407_at	1
putative protein predicted proteins, Arabidopsis thaliana	252359_at	1
putative protein PrMC3 - Pinus radiata,PID:g4154352	252315_at	1
putative protein lea32, Arabidopsis thaliana, EMBL:ATH131342;supported by full-length cDNA: Ceres:35969.	252229_at	1
CASEIN KINASE II, ALPHA CHAIN 2 (CK II) ; supported by cDNA: gi_391604_dbj_D10247.1_ATHCK2B	252192_at	1
putative protein hypothetical protein L1648.04 - Leishmania major, EMBL:LMFL1648	252139_at	1
putative protein	252141_at	1
hypothetical protein	252086_at	1
monodehydroascorbate reductase (NADH) - like protein monodehydroascorbate reductase (NADH), Lycoperison esculentum, PIR:T06407;supporte	252024_at	1
putative protein	251869_at	1
putative protein proteophosphoglycan, Leishmania major, PIR:T46707supported by full-length cDNA: Ceres:6954.	251859_at	1
putative protein KIAA0882 protein, Homo sapiens, EMBL:AB020689; supported by cDNA: gi_15810197_gb_AY056113.1	251829_at	1
2-oxoglutarate dehydrogenase, E1 subunit - like protein 2-oxoglutarate dehydrogenase, E1 subunit, Arabidopsis thaliana, EMBL:ART223802	251787_at	1
putative protein protein-tyrosine kinase, Dictyostellium discoideum, PIR:A35670	251542_at	1
putative protein inducible carbonyl reductase - Rattus norvegicus, EMBL:D89069	251480_at	1
dynamin-like protein 4 (ADL4) ; supported by cDNA: gi_6651400_gb_AF180733.1_AF180733	251429_at	1
putative protein Pm5 protein - Homo sapiens, PIR:S21977	251269_at	1
putative protein ABP130 protein, Homo sapiens, EMBL:AB018359	251179_at	1
putative protein various alpha amylases from diverse species; supported by cDNA: gi_16323040_gb_AY057624.1_	251110_at	1
putative protein symplekin - Homo sapiens, EMBL:HSSYMPLEK	251115_at	1
putative protein monodehydroascorbate reductase (NADH) - like protein monodehydroascorbate reductase (NADH), cucumber, PIR:JU0182;supported by full-length	250050 ot	1
	250950_at	
	250916_at	
putative protein ;supported by full-length cDNA: Ceres:257390.	250916_at 250882_at	1
putative protein ;supported by full-length cDNA: Ceres:257390. putative protein contains similarity to unknown protein	250916_at 250882_at 250656_at	1 1
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uknkom protein supported by full-ength cDNA: Ceres:36309. 244375, at pather protein singported by full-ength cDNA: Ceres:36309. 244376, at P2 domain transcription facto-take protein P24 domain transcription facto-take protein pather protein singler to unknown protein (p143314). 244397, at pather protein distribution (p243314). 244397, at pather protein distribution (p243314). 244397, at pather protein distribution (p243314). 244397, at pather protein distribution (p2433147). 244723, at pather protein distribution (p2433147). 244723, at pather protein distribution (p2433147). 244737, at KED - like protein KED. Nototana tabeoum, EMBL-AR009883, 11, supported by full-length CDNA: Ceres: 117626, 2474701, at daxylyprotein distribution to unknown protein (p14A)200312, 11, supported by full-length CDNA: Ceres: 117626, 2474701, at daxylyprotein distribution to unknown protein (p14A)200312, 11, supported by full-length CDNA: Ceres: 117626, 2474701, at daxylyprotein distribution to unknown protein (p14A)200312, 11, supported by full-length CDNA: Ceres: 117626, 247470, at pather protein similar to unknown protein (p24A)2003, supported by cDNA: g1 (533167, gb, AY057681, 1 24639, gb, at d1C-C dhoride channel protein (p14A)2003983, thaliana UDP-glucose delytdropenase-like protein to rotein (p34, 2004), 1154109, supported by cDNA: g1 (1533167, gb, AY0567681, 2 24645, at uptative protein protein distribution to 4.3 gg, 115433167, gb, AY0567681, 2 24645, at d143.		_	1
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contains similarity to phosphoesterase       247854_at         GTP-glucose 4-6-deftydratase. Ike protein GTD-glucose 4-6-deftydratase, Cicer artelinum, EMBL-CAR275318,supported by full-length CDNA. C 247720_at         GTP-binding protein rabit 1- like GTP-binding protein rabit, Arabidopsis thaliana, PIRT-12965, supported by full-length CDNA. C 247581, at         putative protein kinase-like transmembrane protein TMKL1 precursor, Arabidopsis thaliana, EMBL-ATTMKL1       247583, at         Victory Diversion FXED       247480, at         KED - like protein KED, Nootiana tabacum, EMBL-AB00883       247480, at         -teoxy-D-xylitobies S-phosphater eductosionerase (DKR), supported by full-length cDNA: Ceres: 117626.       2477346, at         utative protein similar to unknown protein (glp AD20127.1); supported by full-length cDNA: Geres: 11225.       247140, at         utative protein similar to unknown protein (glp AD20127.1); supported by full-length cDNA: gl_15823187, gb_AY057698,1_       246880, at         UDP-glucose deftydrogenase- Ratus norvegicus, EMBL-222013       246878_a, at         UDP-glucose deftydrogenase- Ratus norvegicus, EMBL-222014 from (Arabidopsis thaliana)       246820, at         UDP-glucose deftydrogenase- Ratus norvegicus, EMBL-222013       246481, at         14-3-3 protein GF14 upsilon (gr 5) identical to 14-3-3 protein GF14 upsilon (Grc5) supported by cDNA: gl_15912336, gb_AY056464.1_       246882, at         14-3-3 protein GF14 upsilon (gr 5) identical to 14-3-3 protein GF14 upsilon G/re5, supported by cDNA: gl_15912336, gb_AY0			1
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hypothetical protein245502 athypothetical protein245517 atExpressed protein ;supported by CDNA: gi:14423393245521 atdisease resistance RPP5 like protein245466 athypothetical protein supported by cDNA: gi:16323154 gb_AY057681.1_245432 atG2484-1 protein245451 athypothetical protein ; supported by cDNA: gi:16323154 gb_AY057681.1_24527 atputative dihydrodipicolinate synthase ; supported by full-length cDNA: Ceres:26817.24515 at		_	1
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disease resistance RPP5 like protein245456 athypothetical protein245430 atputative serine protease-like protein245432 atG2484-1 protein245435 athypothetical protein ; supported by cDNA: gi_16323154_gb_AY057681.1_245272 atputative dihydrodipicolinate synthase ;supported by full-length cDNA: Ceres:26817.245145 at			1
hypothetical protein245430_atputative serine protease-like protein245432_atG2484-1 protein24543_athypothetical protein ; supported by cDNA: gi_16323154_gb_AY057681.1_245472_atputative dihydrodipicolinate synthase ; supported by full-length cDNA: Ceres:26817.245145_at			1
putative serine protease-like protein     245432_at       G2484-1 protein     245415_at       hypothetical protein; supported by cDNA: gi_16323154_gb_AY057681.1_     245272_at       putative dihydrodipicolinate synthase ;supported by full-length cDNA: Ceres:26817.     245145_at			1
G2484-1 protein245415_athypothetical protein ; supported by cDNA: gi_16323154_gb_AY057681.1_245272_atputative dihydrodipicolinate synthase ;supported by full-length cDNA: Ceres:26817.245145_at			1
hypothetical protein ; supported by cDNA: gi_16323154_gb_AY057681.1_245272_atputative dihydrodipicolinate synthase ;supported by full-length cDNA: Ceres:26817.245145_at			1
putative dihydrodipicolinate synthase ;supported by full-length cDNA: Ceres:26817. 245145_at			1
			1
			1
			1
			1
-			1
			0.9 0.9
			0.9
			0.9
			0.9

peroxidase Expressed protein : supported by cDNA: gi 16200721 gb AV0576211	248382_at	0.9 0.9
Expressed protein ; supported by cDNA: gi_16209721_gb_AY057621.1_ transfactor, putative similar to GI:4519671 from [Nicotiana tabacum]	245682_at 259832_at	0.9
Arabidopsis thaliana /REF=U37281 /DEF=actin-2 mRNA, complete cds /LEN=1637 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 pri		0.9
unknown protein	267642_at	0.9
unknown protein	267511_at	0.9
hypothetical protein predicted by genscan and genefinder; supported by cDNA: gi_4837732_gb_AF085354.1_AF085354	267512_at	0.9
	267446_s_at	0.9 0.9
unknown protein putative phosphoribosyl pyrophosphate synthetase	267373_at 267365_at	0.9
putative methionine aminopeptidase ; supported by cDNA: gi 11320961 gb AF250964.1 AF250964	267189 at	0.9
	267194_s_at	0.9
unknown protein	267163_at	0.9
Expressed protein ; supported by full-length cDNA: Ceres: 40603.	267114_at	0.9
unknown protein ; supported by cDNA; gj _15010737_gb_AY045670.1_	266984_at	0.9
putative katanin ;supported by full-length cDNA: Ceres:119620. putative protein kinase contains a protein kinase domain profile (PDOC00100)	266905_at 266911_at	0.9 0.9
putative protein isupported by full-length cDAs Ceres: 900.	266924 at	0.9
unknown protein ; supported by cDNA: gi_14532595_gb_AY039922.1_	266809 at	0.9
unknown protein	266818_at	0.9
hypothetical protein predicted by genefinder and genscan; supported by cDNA: gi_14532607_gb_AY039928.1_	266734_at	0.9
putative zinc transporter ;supported by full-length cDNA: Ceres:207558.	266718_at	0.9
hypothetical protein predicted by genscan and genefinder eukaryotic translation initiation factor 3 delta subunit; supported by cDNA: gi 1036802 gb U36765.1 ATU36765	266593_at 266554 s at	0.9 0.9
unknown protein ; supported by CDNA: gi_16604341_gb_AY058069.1_	266557_at	0.9
putative phospholipase ;supported by full-length cDNA: Ceres:33373.	266485 at	0.9
putative GTP-binding protein	266471_at	0.9
	266448_s_at	0.9
hypothetical protein predicted by genscan; supported by cDNA: gi_15293096_gb_AY050982.1_	266422_at	0.9
hypothetical protein predicted by genscan and genefinder;supported by full-length cDNA: Ceres:11854.	266370_at	0.9 0.9
putative dTDP-glucose 4-6-dehydratase ;supported by full-length cDNA: Ceres:28205. unknown protein ; supported by full-length cDNA: Ceres: 948.	266205_s_at 266228 at	0.9
hypothetical protein predicted by genscan	266080 at	0.9
putative alcohol dehydrogenase	266087_at	0.9
unknown protein ; supported by cDNA: gi_14596216_gb_AY042896.1_	265999_at	0.9
hypothetical protein predicted by genscan and genefinder	265892_at	0.9
unknown protein ;supported by full-length cDNA: Ceres:12261.	265911_at	0.9
putative protein phosphatase 2C ; supported by cDNA: gi_14517519_gb_AY039595.1_ unknown protein	265886_at 265807_at	0.9 0.9
putative protein kinase contains a protein kinase domain profile (PDOC00100); supported by cDNA: gi 15028152 gb AY046026.1	265661 at	0.9
hypothetical protein predicted by genscan and genefinder; supported by cDNA: gi 15450829 gb AV054495.1	265650 at	0.9
putative DnaJ protein ; supported by cDNA: gi_14194100_gb_AF367256.1_AF367256	265613_at	0.9
unknown protein predicted by genscan and genefinder	265538_at	0.9
putative bHLH transcription factor	265452_at	0.9
hypothetical protein predicted by genscan; supported by full-length cDNA: Ceres: 32660. putative tyrosine decarboxylase	265402_at 265305_at	0.9 0.9
putative vacuolar sorting receptor similar to (gi]3033390); similar to EST dbj[C72582	265161_at	0.9
putative myosin heavy chain similar to ESTs emb[Z35215 and emb[Z35018	265019 at	0.9
auxin-induced protein, putative similar to auxin-induced protein(atb2) GI:6562980 from [Arabidopsis thaliana]	264911_at	0.9
unknown protein Location of EST gb/AA395277 gb/T44807;supported by full-length cDNA: Ceres:36286.	264894_at	0.9
	264667_s_at	0.9
unknown protein similar to ubiquitin C-terminal hydrolase-like protein GI:9759113 from [Arabidopsis thaliana]; supported by cDNA: gi_15724237_gb_ unknown protein similar to ATP-citrate-lyase; Location of EST gb]Z34587. Highly similar to F8A5.32, gb]2462746 and similar to ATP-citrate-lyase, gi		0.9 0.9
uniform protein similar to the data protein Similar to hypothetical protein F09E5.8 dpl/37429 from C. elegans. ESTs dpT42019 and dpl/97002 and		0.9
	264335_s_at	0.9
hypothetical protein contains similarity to calcium-independent phospholipase GI:7670058 from [Homo sapiens]	264283_at	0.9
hypothetical protein contains similarity to toluene tolerance protein Ttg2A GI:4336798 from [Pseudomonas putida]; supported by cDNA: gi_13605494		0.9
putative vacuolar proton-ATPase subunit	264080_at	0.9
putative GTP cyclohydrolase plastid division protein (FtsZ) identical to AF089738; supported by cDNA: gi_15292820_gb_AY050844.1_	264045_at 263906_at	0.9 0.9
platitie auxin-responsive protein (182) autorities apported by cDNA: gi 15292824 gb AY05084.1	263786_at	0.9
malate oxidoreductase ((malic enzyme)	263717_at	0.9
unknown protein contains similarity to gi 1653332 extragenic suppressor (SuhB) from Synechocystis sp. gb D90912 and is a member of the Inositol r		0.9
putative cryptochrome 2 apoprotein Match to Arabidopsis photolysase (PHH1) gene (gb X99061) and cryptochrome 2 apoprotein (CRY2) (gb U4339)	_	0.9
putative ADP-ribosylation factor; supported by cDNA: gi_15450780_gb_AY054470.1_	263297_at	0.9
fructokinase, putative predicted by genefinder putative protein kinase/endoribonuclease ; supported by cDNA: gi 13194577 gb AF308596.1 AF308596	263163_at 263076_at	0.9 0.9
putative protein supported by full-length cDNA: Ceres:157730.	262982 at	0.9
water stress-induced protein, putative similar to water stress-induced protein, GI:454880 from [Oryza sativa]; supported by full-length cDNA: Ceres:	262958 at	0.9
unknown protein ; supported by cDNA: gi_13937148_gb_AF372928.1_AF372928	262919_at	0.9
hypothetical protein predicted by genemark.hmm	262874_at	0.9
unknown protein ESTs gb]R65381 and gb]T44635 come from this gene	262811_at	0.9
putative ATP-dependent RNA helicase similar to gb L13612 DEAD-box protein (dbp45A) from Drosophila melanogaster and is a member of PF 0027 heat sheet action avaitative contained from profiles DE000411 HeadQidebe contailling regularization and the stat		0.9
heat shock protein, putative contains Pfam profile: PF00011 Hsp20/alpha crystallin family;supported by full-length cDNA: Ceres:21735. NAM(no apical meristem) protein, putative similar to NAM protein GI:6066595 from (Petunia hybrida); supported by cDNA: gi 13605664 gb AF3614	262629_at 262514_at	0.9 0.9
unknown protein ; supported by full-length cDNA: Ceres:37444.	262496 at	0.9
chloroplast FtsH protease almost identical to chloroplast FtsH protease GI:1483215, SP:Q39102 from [Arabidopsis thaliana]	262473_at	0.9
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:230.	262397_at	0.9
unknown protein contains similarity to zinc finger and C2 domain protein GI:9957238 from [Arabidopsis thaliana]; supported by full-length cDNA: Cere		0.9
hypothetical protein similar to putative curved-DNA binding protein GI:6966662 from [Campylobacter jejuni];supported by full-length cDNA: Ceres:37: UDB calcutore 4 compares putative similar to GI:201367 from (Cumpylobacter jejuni];supported by full-length cDNA: Ceres:37:	262194_at 261953 at	0.9
UDP-galactose 4-epimerase, putative similar to GI:3021357 from (Cyamopsis tetragonoloba) (Plant Sci. 142, 147-154 (1999)) proteasome regulatory subunit, putative similar to 26S proteasome regulatory complex subunit p30 GB:AAF08395 GI:6434966 from [Drosophila me		0.9 0.9
type 2 per originatory subtrive similar to type 2 per oxired oxin GL4928472 from [Brassica rapa subsp. pekinensis];supported by full-tength cDNA: Cer		0.9
phosphoribosylanthranilate transferase, putative similar to phosphoribosylanthranilate transferase GI:1396053 from [Pisum sativum]	261935_at	0.9
unknown protein	261839_at	0.9
prolyl endopeptidase, putative similar to prolyl endopeptidase GI:6561876 from [Mus musculus]	261770_at	0.9
unknown protein	261774_at	0.9

DNA-binding protein PcMYB1, putative similar to DNA-binding protein PcMYB1 GB:U67133 GI:2224898 from [Petroselinum crispum]; supported by f	261637 at	0.9
DNA-binding protein, putative similar to DNA binding protein CCA1 from [Arabidopsis thaliana]	261569 at	0.9
unknown protein	261558 at	0.9
hypothetical protein	261553 at	0.9
hypothetical protein predicted by genemark.hmm	261383 at	0.9
ferredoxinNADP reductase precursor, putative similar to GB:M25528 from [Mesembryanthemum crystallinum]	261218 at	0.9
hypothetical protein contains similarity to nascent polypeptide associated complex alpha chain GI:6752882 from [Pinus taeda], supported by full-lengt		0.9
unknown protein ; supported by cDNA; gi 15215745 gb AY050402.1	261208 at	0.9
unknown protein ; supported by full-length cDNA: Ceres:12024.	261200_at 261147 at	0.9
	_	0.9
hypothetical protein predicted by genemark.hmm hypothetical protein predicted by genemark.html	261086_at	
hypothetical protein similar to hypothetical protein GB:CAB45785 GI:5262156 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:3998.	_	0.9
hypothetical protein similar to carboxypinyl-carboxyphosphonate phosphorylmutase GB:O49290 from [Arabidopsis thaliana]	260902_at	0.9
decoy identical to GB:AAB51588 GI:1931612 from [Arabidopsis thaliana]: supported by cDNA: gi_1842110_gb_U87586.1_ATU87586	260781_at	0.9
	260786_s_at	0.9
putative SF16 protein {Helianthus annuus}	260610_at	0.9
stearoyl-ACP desaturase ; supported by cDNA: gi_15081681_gb_AY048233.1_	260570_at	0.9
unknown protein ; supported by cDNA: gi_15810460_gb_AY056269.1_	260501_at	0.9
hypothetical protein; supported by cDNA: gi 15292844 gb AY050856.1	260489 at	0.9
ARG1 protein (Altered Response to Gravity) identical to GB:AAD13758; supported by cDNA: gi_4249661_gb_AF089810.1_AF089810	260445 at	0.9
putative peptide transporter similar to peptide transporter GB:AAC32034 [Hordeum vulgare]; supported by full-length cDNA: Ceres: 22243.	260410 at	0.9
putative lipase similar to lipase GB:CAA74737 from [Drosophila melanogaster]; supported by cDNA: gi_15293100_gb_AY050984.1_	260393 at	0.9
fructokinase (Frk1), putative similar to fructokinase (Frk1) GI:2102690 from (Lycopersicon esculentum)	260343 at	0.9
putative disease resistance protein similar to disease resistance protein RPP1-WsC GB:AAC72979 [Arabidopsis thaliana]	260312 at	0.9
putative RING zinc finger protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)	260330 at	0.9
	260286 at	0.9
unknown protein similar to hypothetical proteins GB:AAD39276 [Arabidopsis thaliana], GB:CAB53491 [Oryza sativa], supported by full-length CDNA:	260227 at	0.9
andown procein animat in importante process of production animating, of consoler in (or year sative), supported by functional of the putative (proxygenase similar to 13-lipoxygenase GB:CAA65269 [Solanum tuberosum]	260190 at	0.9
	_	0.9
DNA-directed RNA polymerase subunit, putative similar to Gi6723961 from [Schizosaccharomyces pombe]	260049_at	
putative DNA-binding protein contains Pfam profile: PF01388 ARID DNA binding domain	259967_at	0.9
	259969_at	0.9
unknown protein ;supported by full-length cDNA: Ceres:114376.	259977_at	0.9
putative UDP-glucose:glycoprotein glucosyltransferase similar to UDP-glucose:glycoprotein glucosyltransferase precursor GB:Q09332 [Drosophila m	259936_at	0.9
putative ABC transporter contains Pfam profile: PF00005 ABC transporter 2	259937_s_at	0.9
hypothetical protein ;supported by full-length cDNA: Ceres:110945.	259862_at	0.9
putative DnaJ protein similar to dnaJ-like protein GB:CAA72705 [Arabidopsis thaliana]; Pfam HMM hit:DnaJ, prokaryotic heat shock protein	259876_at	0.9
unknown protein	259835 at	0.9
arm repeat-containing protein, putative similar to GI:2558938 from [Brassica napus] (Proc. Natl. Acad. Sci. U.S.A. 95 (1), 382-387 (1998))	259826 at	0.9
nucellin-like protein similar to nucellin GB:AAB96882 [Hordeum vulgare] (nucellin: similar to aspartic protease and its specific expression in nucellar (		0.9
putative phorbol ester / diacylglycerol binding protein Pfam HMM hit: Phorbol esters / diacylglycerol binding domain	259673 at	0.9
DNA-directed RNA polymerase identical to DNA-directed RNA polymerase, mitochondrial precursor GB:P92969 [Arabidopsis thaliana]	259672 at	0.9
hypothetical protein predicted by genscan	259642 at	0.9
putative DNA-binding protein predicted by genscan, multiple est matches; Pfam HMM hit: helix-loop-helix DNA-binding domain;supported by full-leng		0.9
	259610 at	0.9
hypothetical protein ; supported by cDNA; gj_13430675_gb_AF360250.1_AF360250	259518_at	0.9
protein phosphatase 2A regulatory subunit, putative similar to protein phosphatase 2A regulatory subunit GI:683502 from [Arabidopsis thaliana]	259407_at	0.9
protein phosphatase 2A regulatory subunit, putative similar to protein phosphatase 2A regulatory subunit GI:683502 from [Arabidopsis thaliana] serin threonin-kinase, putative similar to serin threonin-kinase GI:2887282 from (Drosophila melanogaster); supported by cDNA: gi_15450801_gb_A2	259407_at 259362_s_at	0.9 0.9
protein phosphatase 2A regulatory subunit, putative similar to protein phosphatase 2A regulatory subunit GI:683502 from [Arabidopsis thaliana] serin threonin-kinase, putative similar to serin threonin-kinase GI:2887282 from (Drosophila melanogaster); supported by cDNA: gi_15450801_gb_A2 putative sodium proton exchanger similar to sodium proton exchanger Nhx1 GB:AAD16946 [Arabidopsis thaliana]	259407_at 259362_s_at 259081_at	0.9 0.9 0.9
protein phosphatase 2A regulatory subunit, putative similar to protein phosphatase 2A regulatory subunit GI:683502 from [Arabidopsis thaliana] serin threonin-kinase, putative similar to serin threonin-kinase GI:2887282 from (Drosophila melanogaster); supported by cDNA: gi_15450801_gb_A2 putative sodium proton exchanger similar to sodium proton exchanger Nhx1 GB:AAD16946 [Arabidopsis thaliana] unknown protein	259407_at 259362_s_at 259081_at 259047_at	0.9 0.9 0.9 0.9
protein phosphatase 2A regulatory subunit, putative similar to protein phosphatase 2A regulatory subunit GI:683502 from [Arabidopsis thaliana] serin threonin-kinase, putative similar to serin threonin-kinase GI:2887282 from (Drosophila melanogaster); supported by cDNA: gi_15450801_gb_A2 putative sodium proton exchanger similar to sodium proton exchanger Nhx1 GB:AAD16946 [Arabidopsis thaliana] unknown protein unknown protein predicted by genscan; est match;supported by full-length cDNA: Ceres:3820.	259407_at 259362_s_at 259081_at 259047_at 259038_at	0.9 0.9 0.9 0.9 0.9
protein phosphatase 2A regulatory subunit, putative similar to protein phosphatase 2A regulatory subunit GI:683502 from [Arabidopsis thaliana] serin threonin-kinase, putative similar to serin threonin-kinase GI:2887282 from (Drosophila melanogaster); supported by cDNA: gi_15450801_gb_A2 putative sodium proton exchanger similar to sodium proton exchanger Nhx1 GB:AAD16946 [Arabidopsis thaliana] unknown protein unknown protein protein similar to unknown protein by full-length cDNA: Ceres:3820.	259407_at 259362_s_at 259081_at 259047_at 259038_at 258997_at	0.9 0.9 0.9 0.9 0.9 0.9
protein phosphatase 2A regulatory subunit, putative similar to protein phosphatase 2A regulatory subunit GI:683502 from [Arabidopsis thaliana] serin threonin-kinase, putative similar to serin threonin-kinase GI:2887282 from (Drosophila melanogaster); supported by cDNA: gi_15450801_gb_A2 putative sodium proton exchanger similar to sodium proton exchanger Nhx1 GB:AAD16946 [Arabidopsis thaliana] unknown protein unknown protein proticed by genscan; est match; supported by full-length cDNA: Ceres: 3820. hypothetical protein similar to unknown protein putative aspartate kinase similar to aspartate kinase GB:CAA67376 (Arabidopsis thaliana); supported by full-length cDNA: Ceres: 6203.	259407_at 259362_s_at 259081_at 259047_at 259038_at 258997_at 258977_s_at	0.9 0.9 0.9 0.9 0.9 0.9 0.9
protein phosphatase 2A regulatory subunit, putative similar to protein phosphatase 2A regulatory subunit GI:683502 from [Arabidopsis thaliana] serin threonin-kinase, putative similar to serin threonin-kinase GI:2887282 from [Drosophila melanogaster); supported by cDNA: gi_15450801_gb_A2 putative sodium proton exchanger similar to sodium proton exchanger Nhx1 GB:AAD16946 [Arabidopsis thaliana] unknown protein unknown protein predicted by genscan; est match;supported by full-length cDNA: Ceres:3820. hypothetical protein similar to unknown protein putative aspartate kinase similar to aspartate kinase GB:CAA67376 (Arabidopsis thaliana); supported by full-length cDNA: Ceres: 6203. unknown protein similar to unknown proteins GB:AAD24625 [Arabidopsis thaliana], GB:AAC73026 [Arabidopsis thaliana]	259407_at 259362_s_at 259081_at 259047_at 259038_at 258997_at 258977_s_at 258933_at	0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9
protein phosphatase 2A regulatory subunit, putative similar to protein phosphatase 2A regulatory subunit GI:683502 from [Arabidopsis thaliana] serin threonin-kinase, putative similar to serin threonin-kinase GI:2887282 from [Drosophila melanogaster); supported by cDNA: gi_15450801_gb_A2 putative sodium proton exchanger similar to sodium proton exchanger Nhx1 GB:AAD16946 [Arabidopsis thaliana] unknown protein unknown protein predicted by genscan; est match; supported by full-length cDNA: Ceres:3820. hypothetical protein similar to unknown protein putative aspartate kinase similar to aspartate kinase GB:CAA67376 (Arabidopsis thaliana); supported by full-length cDNA: Ceres: 6203. unknown protein similar to unknown proteins GB:AAD24625 [Arabidopsis thaliana], GB:AAC73026 [Arabidopsis thaliana] putative dehydroquinase shikimate dehydrogenase similar to dehydroquinase shikimate dehydrogenase GB:S46210 [Nicotiana tabacum]	259407_at 259362_s_at 259081_at 259047_at 259038_at 258997_at 258997_s_at 258933_at 258933_at	0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9
protein phosphatase 2A regulatory subunit, putative similar to protein phosphatase 2A regulatory subunit GI:683502 from [Arabidopsis thaliana] serin threonin-kinase, putative similar to serin threonin-kinase GI:2887282 from (Drosophila melanogaster); supported by cDNA: gi_15450801_gb_A2 putative sodium proton exchanger similar to sodium proton exchanger Nhx1 GB:AAD16946 [Arabidopsis thaliana] unknown protein unknown protein predicted by genscan; est match;supported by full-length cDNA: Ceres:3820. hypothetical protein similar to unknown protein putative aspartate kinase similar to aspartate kinase GB:CAA67376 (Arabidopsis thaliana); supported by full-length cDNA: Ceres: 6203. unknown protein similar to unknown proteins GB:AAD24625 [Arabidopsis thaliana], GB:AAC73026 [Arabidopsis thaliana] putative dehydroquinase shikimate dehydrogenase similar to dehydroquinase shikimate dehydrogenase GB:S46210 [Nicotiana tabacum] Expressed protein ; supported by full-length cDNA: Ceres: 9573.	259407_at 259362_s_at 259081_at 259047_at 259038_at 258997_at 258977_s_at 258933_at 258908_at 2589848_at	0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9
protein phosphatase 2A regulatory subunit, putative similar to protein phosphatase 2A regulatory subunit GI:683502 from [Arabidopsis thaliana] serin threonin-kinase, putative similar to serin threonin-kinase GI:2887282 from [Drosophila melanogaster); supported by cDNA: gi_15450801_gb_A2 putative sodium proton exchanger similar to sodium proton exchanger Nhx1 GB:AAD16946 [Arabidopsis thaliana] unknown protein unknown protein predicted by genscan; est match; supported by full-length cDNA: Ceres:3820. hypothetical protein similar to unknown protein putative aspartate kinase similar to aspartate kinase GB:CAA67376 (Arabidopsis thaliana); supported by full-length cDNA: Ceres: 6203. unknown protein similar to unknown proteins GB:AAD24625 [Arabidopsis thaliana], GB:AAC73026 [Arabidopsis thaliana] putative dehydroquinase shikimate dehydrogenase similar to dehydroquinase shikimate dehydrogenase GB:S46210 [Nicotiana tabacum]	259407_at 259362_s_at 259081_at 259047_at 259038_at 258997_at 258977_s_at 258933_at 258908_at 2589848_at	0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9
protein phosphatase 2A regulatory subunit, putative similar to protein phosphatase 2A regulatory subunit GI:683502 from [Arabidopsis thaliana] serin threonin-kinase, putative similar to serin threonin-kinase GI:2887282 from (Drosophila melanogaster); supported by cDNA: gi_15450801_gb_A2 putative sodium proton exchanger similar to sodium proton exchanger Nhx1 GB:AAD16946 [Arabidopsis thaliana] unknown protein unknown protein predicted by genscan; est match;supported by full-length cDNA: Ceres:3820. hypothetical protein similar to unknown protein putative aspartate kinase similar to aspartate kinase GB:CAA67376 (Arabidopsis thaliana); supported by full-length cDNA: Ceres: 6203. unknown protein similar to unknown proteins GB:AAD24625 [Arabidopsis thaliana], GB:AAC73026 [Arabidopsis thaliana] putative dehydroquinase shikimate dehydrogenase similar to dehydroquinase shikimate dehydrogenase GB:S46210 [Nicotiana tabacum] Expressed protein ; supported by full-length cDNA: Ceres: 9573.	259407_at 259362_s_at 259081_at 259047_at 259038_at 258997_at 258977_s_at 258933_at 258908_at 2589848_at	0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9
protein phosphatase 2A regulatory subunit, putative similar to protein phosphatase 2A regulatory subunit GI:683502 from [Arabidopsis thaliana] serin threonin-kinase, putative similar to serin threonin-kinase GI:2887282 from [Drosophila melanogaster); supported by cDNA: gi_15450801_gb_A2 putative sodium proton exchanger similar to sodium proton exchanger Nhx1 GB:AAD16946 [Arabidopsis thaliana] unknown protein unknown protein predicted by genscan; est match;supported by full-length cDNA: Ceres:3820. hypothetical protein similar to unknown protein putative aspartate kinase similar to aspartate kinase GB:CAA67376 (Arabidopsis thaliana); supported by full-length cDNA: Ceres: 6203. unknown protein similar to unknown proteins GB:AAD24625 [Arabidopsis thaliana], GB:AAC73026 [Arabidopsis thaliana] putative dehydroquinase shikimate dehydrogenase similar to dehydroquinase shikimate dehydrogenase GB:S46210 [Nicotiana tabacum] Expressed protein ; supported by full-length cDNA: Crees: 9573. putative T-complex protein 1, theta subunit (TCP-1-Theta) similar to T-complex protein 1, theta subunit (TCP-1-Theta) GB:P42932 [Mus musculus]; :	259407_at 259362_s_at 259081_at 259047_at 25897_at 258997_at 258933_at 258908_at 258988_at 258848_at 258816_at	0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9
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unknown protein	256422_at	0.9
unknown protein ;supported by full-length cDNA: Ceres:110819.	256327_at	0.9
6-phosphogluconate dehydrogenase, putative similar to 6-phosphogluconate dehydrogenase GB:BAA22812 GI:2529229 [Glycine max]; supported bi		0.9
C2H2-type zinc finger protein, putative contains multiple zinc finger domains: PF00096: Zinc finger, C2H2 type; supported by cDNA: gi_15809914_g		0.9
disease resistance protein, putative similar to disease resistance protein RPP1-WsB [Arabidopsis thaliana] GI:9279731; supported by cDNA: gi_145		0.9
unknown protein	256173_at	0.9
unknown protein	256106_at	0.9
MAP kinase, putative similar to MAP3K delta-1 protein kinase GI:2253010 from [Arabidopsis thaliana]	256121_at	0.9
ubiquitin, putative similar to ubiquitin GI:10177083 from [Arabidopsis thaliana]; supported by cDNA: gi_16974595_gb_AY060574.1_	256071_at	0.9
unknown protein	255991_at	0.9
hypothetical protein predicted by genscan+	255994_at	0.9
basic blue protein, putative similar to basic blue protein GI:668810 from [Medicago sativa]	255896_at	0.9
lysine and histidine specific transporter, putative similar to lysine and histidine specific transporter GI:2576361 from [Arabidopsis thaliana] coded for by A. thaliana cDNA T20615 ;supported by full-length cDNA: Ceres;37305.	255726_at	0.9
	255626_at	0.9 0.9
putative GTP pyrophosphokinase similar to bacterial GTP pyrophosphokinases (ReIA) similar to B. subtilis ReIA (EC 2.7.6.5), GenBank accession n hypothetical protein	255522_at 255526 at	0.9
putative chloroplast outer envelope 86-like protein similar to P. sativum outer envelope 86 protein OEP86, GenBank accession number Z31581; sup	_	0.9
putative unortiplast outer envelope ourine proteins similar to r . saturan outer envelope ou protein outer os, centra in accession number 20101, sup putative protein other predicted proteins, Arabidopsis thaliana; supported by full-length CDNA: Ceres;34781.	254858 at	0.9
putative protein various producted proteins, hadroopsis trainaris, suppried by initiality initiality initiality and the second	254742 at	0.9
putative protein G9A protein, Mus musculus, AF109906; supported by cDNA; gj 13517758, gb_AF344452.1_AF344452	254745 at	0.9
putative disease resistance protein Cf-4. Lycopersicon hirsutum, gb:AJ002235	254735 at	0.9
glycine-rich cell wall protein-like glycine-rich protein 1.0 precursor, Phaseolus vulgaris, PIR1:S01821; supported by cDNA: gi 14030676 gb AF3754		0.9
g, and g,	254594 at	0.9
RNase Linhibitor-like protein RNase Linhibitor (clone 8), Homo sapiens	254615 at	0.9
kinase-like protein protein kinase rck, Mus musculus, PIR2:148733; supported by cDNA: gi_14532759_gb_AY040004.1_	254560 at	0.9
putative protein p47 - Homo sapiens,PID:g5531827	254348 at	0.9
hypothetical protein ;supported by cDNA: gi_15028306_gb_AY045956.1_	254304_at	0.9
phosphatase like protein phosphoprotein phosphatase (EC 3.1.3.16) PPT - rat	254211_at	0.9
hypothetical protein	254178_at	0.9
putative protein hypothetical protein, Synechocystis sp., PIR:S76577; supported by full-length cDNA: Ceres:30708.	254187_at	0.9
putative protein protein induced upon wounding - Arabidopsis thaliana, PID:e257749;supported by full-length cDNA: Ceres:34176.	254157_at	0.9
protein kinase (AFC2) ; supported by cDNA: gi_601788_gb_U16177.1_ATU16177	254131_at	0.9
putative protein met-10+ protein, Neurospora crassa, PIR2:S46697	253912_at	0.9
putative beta-glucosidase beta-glucosidase BGQ60 precursor - barley, PIR2:A57512	253835_at	0.9
putative protein hypothetical protein - Schizosaccharomyces pombe, PID:e1295810	253803_at	0.9
heat-shock protein heat-shock protein hsp40-human, PIR2:JN0912; supported by cDNA: gi_14596114_gb_AY042845.1_	253778_at	0.9
hypothetical protein	253782_at	0.9
hypothetical protein;supported by cDNA: gi_14335143_gb_AY037251.1_	253596_s_at	0.9
putative protein KIAA0800 protein, Homo sapiens, EMBL:AB018343	253560_at	0.9
DNA topoisomerase like- protein Bacillus subtilis DNA Topoisomerase I; PID:G520753	253566_at	0.9
putative protein predicted protein, Arabidopsis thaliana, gb:AC002337	253431_at	0.9
putative protein predicted protein, Synechocystis sp., PIR2:S74814; supported by cDNA: gi_14334011_gb_AF302188.1_AF302188	253394_at	0.9
putative protein RNA-binding protein LAH1, Saccharomyces cerevisiae,PIR2:B48600; supported by cDNA: gi_15810396_gb_AY056237.1_	253396_at	0.9
putative protein AT.I.24, Arabidopsis thaliana, gb:U63815;supported by full-length cDNA: Ceres:4868.	253382_at	0.9
putative protein aminotransferase (AspC family), Aquifex aeolicus, PIR2:D70479; supported by cDNA: gi_15912290_gb_AY056423.1_	253308_at	0.9
putative protein predicted protein, Arabidopsis thaliana, PATCHX:G2347201 putative protein predicted protein A TM017A05.4 Arabidopsis thalianaBAC TM017A05, PID:g2435512	253266_s_at 253109 at	0.9 0.9
thaumatin-like protein thaumatin-like protein, Arabidopsis thaliana, Priz:S71175; supported by cDNA; gi 13430505 gb AF360165.1 AF360165	253109_at 253104_at	0.9
uraunaunaunaunaunaunaunaunaunaunaunaunauna	253104_at 253097_at	0.9
putative protein predicted protein, Arabidopsis thaliana; supported by cDNA: gi_15451175_gb_AY054668.1_	253062 at	0.9
squalere epoxidase - like protein squalere epoxidase, Panax ginseng, AB003516;supported by full-length cDNA: Ceres:118648.	253039 at	0.9
guarine operations and protein disk guarine operations, in the ground of the second receiption o	253032 at	0.9
hypothetical protein	252960 at	0.9
putative protein vsf-1 protein, Lycopersicon esculentum, PIR2:S52203; supported by cDNA: gi_15100048_gb_AF401297.1_AF401297	252969 at	0.9
2-dehydro-3-deoxyphosphoheptonate aldolase ; supported by cDNA: gi 166687 gb M74819.1 ATHDHS1	252831 at	0.9
carboxypeptidase precursor-like protein carboxypeptidase Y-like protein, Arabidopsis thaliana, EMBL:M81130; supported by cDNA; gi 15215795 gl		0.9
hypothetical protein several hypothetical proteins - Arabidopsis thaliana	252473 s at	0.9
arm repeat containing protein homolog arm repeat containing protein - Brassica napus, EMBL:AF024625; supported by cDNA: gi_14596006_gb_AY	252486_at	0.9
putative protein finger protein SIG1, Saccharomyces cerevisiae, PIR2:A56015;supported by full-length cDNA: Ceres:122162.	252371_at	0.9
hypothetical protein	252362_at	0.9
GTPase activating -like protein GTPase activating protein gyp7, Yarrowia lipolytica, EMBL:YLGYP7	252310_at	0.9
putative protein ;supported by full-length cDNA: Ceres:26235.	252269_at	0.9
hypothetical protein ; supported by cDNA: gi_16604640_gb_AY059765.1_	252171_at	0.9
putative protein saposin precursor - Homo sapiens, PIR:SAHUP;supported by full-length cDNA: Ceres:93651.	252075_at	0.9
gamma response I protein ; supported by cDNA: gi_14335159_gb_AY037259.1_	252038_at	0.9
putative protein growth-regulating factor 1, Oryza sativa, EMBL:AF201895	252015_at	0.9
Gluthatione reductase, chloroplast precursor; supported by cDNA: gi_15451193_gb_AY054677.1_	251860_at	0.9
Expressed protein ; supported by full-length cDNA: Ceres: 102807.	251813_at	0.9
vacuolar protein sorting protein 33a-like protein vacuolar protein sorting protein 33a, Rattus norvegicus ,PIR2:JC5720; supported by cDNA: gi_1389i spliceosomal - like protein spliceosomal protein SAP 130, Homo sapiens, EMBL:HSAJ1443	251818_at 251837_s_at	0.9 0.9
spincessmiar - like protein bluck Specific aprices and protein SAM 100, nonino sepients, cmbic-inoxu 1440 phosphatase - like protein DUAL SPECIFICITY PROTEIN PHOSPHATASE 5, Rattus norwegicus, SWISSPROT:DUS5 RAT; supported by cDNA; g		0.9
pilospiralase interpreter bolic secon form enterpreter and an antibility of the second s	251629 at	0.9
The finegratule protein several zinc finger proteins - Arabidopsis thaliana	251586 at	0.9
under unger miger miger horden serier alter in einer procession in Machadisa and and and and and and and and and an	251526 at	0.9
protein synthesis initiation factor - like eukaryotic protein synthesis initiation factor, Homo sapiens, EMBL:AF104913	251431_at	0.9
putative protein	251415 at	0.9
actin - like protein actin 3, Drosophila melanogaster, PIR:A03000;supported by full-length cDNA: Ceres:38096.	251340 at	0.9
putative protein phosphoprotein phosphatase (EC 3.1.3.16) 1A-alpha - Homo sapiens, PIR:S22423;supported by full-length cDNA: Ceres:20050.	251259_at	0.9
putative dTDP-glucose 4-6-dehydratase contains non-consensus AT donor splice site at exon 1 and non-consensus AC acceptor splice site at exon		0.9
ribonuclease II-like protein ribonuclease II family protein, Deinococcus radiodurans, PIR:C75571	251040_at	0.9
ABC transporter -like protein NBD-like protein POP, Arabidopsis thaliana, EMBL:AF127664;supported by full-length cDNA: Ceres:21701.	251020_at	0.9
putative protein ; supported by cDNA: gi_14596134_gb_AY042855.1_	250898_at	0.9
F1F0-ATPase inhibitor - like protein F1F0-ATPase inhibitor protein, OsIF1-1, Oryza sativa, EMBL:AB029059; supported by full-length cDNA: Ceres:		0.9
unknown protein	250822_at	0.9
unknown protein ;supported by full-length cDNA: Ceres:150381.	250792_at	0.9
splicing factor 3a ; supported by cDNA: gi_14532639_gb_AY039944.1_	250715_at	0.9
putative protein similar to unknown protein (gb AAF32477.1);supported by full-length cDNA: Ceres:117588.	250737_at	0.9

transcription factor HBP-1b homolog (sp[P43273) ; supported by cDNA: gi_217826_dbj_D10042.1_ATHAHBP1B WD-repeat protein-like ; supported by cDNA: gi_15450909_gb_AY054535.1_	250671_at 250539_at	0.9 0.9
cellulose synthase catalytic subunit	250505_at	0.9
cytochrome P450 - like protein cytochrome P450, Helianthus tuberosus, EMBL:HTCYP81L putative protein TH65 protein, Arabidopsis thaliana, EMBL:AJ001729	250423_s_at 250429 at	0.9 0.9
beta-adaptin-like protein A; subiopside distance, and a subicipation and a subicipation beta-adaptin-like protein A; subicipation beta-adaptin-like protein b; subicipation	250352 at	0.9
putative esterase - like protein cinl protein - imported, Butyrivibrio fibrisolvens, PIR:T44624; supported by full-length cDNA: Ceres:7912.	250299_at	0.9
putative protein putative secreted protein SCF41.30c, Streptomyces coelicolor, EMBL:SCF41_30	250268_s_at	0.9
putative protein GCN4-complementing protein, Arabidopsis thaliana, EMBL:AJ130878	250285_at	0.9
putative protein weak homology with predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:21821.	250233_at	0.9 0.9
polynucleotide phosphorylase UDP-glucose pyrophosphorylase ; supported by cDNA: gi 13430663 gb AF360244.1 AF360244	250196_at 250074_at	0.9
putative protein nuclear FMRP interacting protein 1 NUFIP1, Home sapiens, EMBL:AF159548	250009 at	0.9
putative protein similar to unknown protein (dbj BAA92923.1)	249899_at	0.9
alpha-adaptin	249909_s_at	0.9
26S proteasome, non-ATPase regulatory subunit ;supported by full-length cDNA: Ceres:23276.	249796_at	0.9
beta-glucosidase -like protein prunasin hydrolase isoform PHA precursor, Prunus serotina, EMBL:AF221526 putative protein SIAH1 protein, Brassica napus, EMBL:BNA245479	249636_at	0.9
putative protein similar to unknown protein (sp P54493) putative protein similar to unknown protein (sp P54493)	249595_at 249510_at	0.9 0.9
raffinose synthase -like protein raffinose synthase Rfs, Cucumis sativus, EMBL:AF073744	249411 at	0.9
unknown protein	249315_at	0.9
glutathione transferase AtGST 10 (emb CAA10457.1) ; supported by cDNA: gi_15451157_gb_AY054659.1_	249291_at	0.9
folylpolyglutamate synthase-like protein	249304_at	0.9
unknown protein ; supported by cDNA; gi_15081800_gb_AY048293.1_	249308_at	0.9
FtsH protease, putative similar to FtsH protease GI:13183728 from [Medicago sativa] putative protein similar to unknown protein (pir  S76082)	249244_at 249193_at	0.9 0.9
putative protein similar to unknown protein (pp)P42251); supported by cDNA: gi 13430795 gb AF360310.1 AF360310	249201 at	0.9
unknown protein (supported by full-length cDNA: Ceres: 1558.	249204_at	0.9
berberine bridge enzyme-like protein	249047_at	0.9
unknown protein ;supported by full-length cDNA: Ceres:21404.	249007_at	0.9
putative protein similar to unknown protein (pir  T08416)	248944_at	0.9
disease resistance protein-like AP47 50p (gb AAB88283.1) ; supported by cDNA: gi_14326519_gb_AF385713.1_AF385713	248890_at 248858_at	0.9 0.9
nr +r our (gulandoucus, r), supported by Lorins, gr (= 1020118_gul_ni 000113, r_ni 000113	248805_at	0.9
putative protein contains similarity to unknown protein (up)[7:9006);supported by full-length cDNA: Ceres:15623.	248757_at	0.9
putative protein similar to unknown protein (pir  H71431);supported by full-length cDNA: Ceres:31680.	248763_at	0.9
protein kinase (EC 2.7.1.37) 5 (pir  JN0505) ; supported by cDNA: gi_15809918_gb_AY054227.1_	248720_at	0.9
unknown protein	248737_at	0.9
unknown protein	248694_at	0.9
receptor protein kinase putative protein contains similarity to alpha/beta hydrolase; supported by cDNA: gi 13877626 gb AF370514.1 AF370514	248590_at 248531_at	0.9 0.9
putative protein contains similarity to alti-inducible protein	248547_at	0.9
putative protein strong similarity to unknown protein (b)AD25781.1)	248497 at	0.9
putative protein contains similarity to poly(A)-binding protein II;supported by full-length cDNA: Ceres:10876.	248447_at	0.9
cytochrome P450	248353_at	0.9
prolyl tRNA synthetase	248339_at	0.9
Notchless protein homolog Avr9 elicitor response protein-like ; supported by cDNA: gi 14423409 gb AF386942.1 AF386942	248326_at 248262_at	0.9 0.9
putative protein similar to unknown protein (pii)[134137]	248266 at	0.9
importin beta	248268_at	0.9
26S proteasome regulatory particle chain RPT6-like protein ;supported by full-length cDNA: Ceres:38213.	248220_at	0.9
trigger factor-like protein	248094_at	0.9
myosin heavy chain-like	248032_at	0.9
SNF1 related protein kinase-like protein ; supported by cDNA: gi_14334389_gb_AY034100.1_ MAP kinase ; supported by cDNA: gi_14532571_gb_AY039910.1_	247867_at 247819 at	0.9 0.9
Ran binding protein 1 homolog - like Ran binding protein 1 homolog, Arabidopsis thaliana, EMBL:ATU62742	247819_at 247771_at	0.9
Test protease, putative contains similarity to cell division protein Test honolog 3 SP:P73437 (EC 3.4.24) [strain PCC6803] [Synechocystis sp.]	247766 at	0.9
protein kinase 6 - like protein kinase 6, Glycine max, PIR:S29851; supported by cDNA: gi_17063197_gb_AY062096.1_	247750_at	0.9
putative protein	247630_at	0.9
putative protein flavin-containing monooxygenase FMO3, Oryctolagus cuniculus, SWISSPROT:FMO3_RABIT; supported by full-length cDNA Ceres		0.9
signal recognition particle - like protein signal recognition particle 68, Homo sapiens, EMBL:AF195951; supported by CDNA; gi_15293136_gb_AY05		0.9
Mei2-like protein Mei2-like protein, Arabidopsis thaliana, EMBL:D86122; supported by cDNA: gi_2443328_dbj_D86122.1_D86122 putative protein various predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:14414.	247506_at 247461_at	0.9 0.9
plasma membrane proton ATPase-like	247439_at	0.9
putative protein	247422_at	0.9
, putative protein contains similarity to receptor-like protein kinase;supported by full-length cDNA: Ceres:31105.	247383_at	0.9
2-nitropropane dioxygenase-like protein ;supported by full-length cDNA: Ceres:207555.	247283_at	0.9
putative protein strong similarity to unknown protein (emb/CAB89363.1)	247265_at	0.9
asparagine synthetase (gb]AAC72837.1); supported by cDNA: gi_3859535_gb_AF095453.1_AF095453	247218_at	0.9
trehalose-6-phosphate phosphatase PHD finger protein - like PHD finger protein 3, Homo sapiens, EMBL:AF091622	247228_at 246893 at	0.9 0.9
putative protein isoperiallin v epimerase, Streptomyces clavuligerus, EMBL:M32324	246832 at	0.9
gutamy-IRNA synthetase; supported by cDNs gi_3435195_gb_AF067773.1_AF067773	246845_at	0.9
Lon protease homolog 2 precursor almost identical to Lon protease homolog 2 mitochondrial precursor SP:P93655, GI:1848290 from [Arabidopsis	t 246850_at	0.9
glutathione synthetase gsh2 non-consensus AT donor splice site at exon 6, AC acceptor splice site at exon 7; supported by cDNA: gi_758451_gb_L		0.9
cytochrome P450 ; supported by cDNA: gi_3164141_dbj_D78606.1_D78606	246620_at	0.9
alpha-mannosidase -like protein mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase, mouse, PIR:A41641	246567_at	0.9
putative protein hypothetical protein F14P3.15 - Arabidopsis thaliana, EMBL:AC009755 Exportin1 (XPO1) protein ; supported by cDNA: gi 15810122 gb AY056126.1	246564_at 246424 at	0.9 0.9
Lapoint (Ar Ori ) proteint , supported by full-length CDNA: Grees 10216.	246434_at	0.9
actin interacting protein ; supported by cDNA; gi_16604325_gb_AY058061.1_	246162_at	0.9
putative protein predicted proteins - Arabidopsis thaliana	246110_at	0.9
zinc finger protein ;supported by full-length cDNA: Ceres:152664.	246069_at	0.9
cinnamyl-alcohol dehydrogenase - like protein cinnamyl-alcohol dehydrogenase, apple tree, PIR:T16995;supported by full-length cDNA: Ceres:6744		0.9
alpha-galactosidase - like protein alpha-galactosidase, coffee, PIR:T50781 ukrowy protein contribute similarity to anthroniuta surface large subwirk GL:1374671 from (Rushnera antidice)al	246055_at	0.9
unknown protein contains similarity to anthranilate synthase large subunit GI:1374671 from [Buchnera aphidicola]	245745_at	0.9 0.9
dormancy-associated protein, putative similar to dormancy-associated protein GI:2995990 from [Arabidopsis thaliana]; supported by cDNA: gi 1433		

transcription factor like protein	245480_at	0.9
hypothetical protein	245442_at	0.9
indole-3-acetate beta-glucosyltransferase like protein ;supported by full-length cDNA: Ceres:35383.	245352 at	0.9
hypothetical protein ;supported by full-length cDNA: Ceres;39922.	245365 at	0.9
Expressed protein ; supported by full-length cDNA: Ceres: 95834.	245306 at	0.9
phytoene dehydrogenase precursor (phytoene desaturase); supported by cDNA: gi 14532765 gb AY040007.1	245284 at	0.9
Expressed protein ; supported by cDNA: gi_5764394_gb_AF159587.1_AF159587	245256 at	0.9
hypothetical protein predicted by genscan; similar to SPIP34568 YNV5_CAEEL;supported by full-length cDNA: Ceres:8256.	245062 at	0.9
ATPase III subunit	245026 at	0.9
RNA polymerase beta subunit-2	244997 at	0.9
putative RING3 protein	257352 at	0.9
disease resistance protein, putative similar to disease resistance protein GB:AAC78591 GI:3894383 from [Lycopersicon esculentum]	259421 at	0.9
usease resistance protein putative similar to disease resistance protein 65.Accross 16.3554565 non [Lyopersion escuentum] putative protein various predicted proteins, Arabidopsis thaliana	253170 at	0.9
unknown protein	_	
•	263680_at	0.8
nodule inception protein, putative similar to nodule inception protein GI:6448579 from (Lotus japonicus)	259540_at	0.8
unknown protein ; supported by cDNA: gi_14334819_gb_AY035083.1_	258093_at	0.8
unknown protein ; supported by full-length cDNA: Ceres: 118290.	256232_at	0.8
putative protein SP8 binding protein, Cucumis sativus, PIR2:JC6203	253603_at	0.8
copper transport protein - like protein copper transporter protein Arabidopsis thaliana,PID:g1082054	252502_at	0.8
protein phosphatase 2A 62 kDa B regulatory subunit (gb AAD45158.1) ; supported by cDNA: gi_5533378_gb_AF165429.1_AF165429	249081_at	0.8
S-locus protein, putative similar to S-locus protein 5 GI:6069485 from [Brassica rapa]	246322_at	0.8
receptor kinase, putative similar to CLV1 receptor kinase GB:AAB58929 GI:2160756 from [Arabidopsis thaliana]	264537_at	0.8
Arabidopsis thaliana /REF=U37281 /DEF=actin-2 mRNA, complete cds /LEN=1637 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 pri-		0.8
Arabidopsis thaliana /REF=U37281.1 /DEF=actin-2 mRNA, complete cds /LEN=1637 (_5, _M, _3 represent transcript regions 5 prime, Middle, and %	-Athal-Actin_	0.8
putative CCCH-type zinc finger protein also an ankyrin-repeat protein; supported by cDNA: gi_14335105_gb_AY037232.1_	267534_at	0.8
putative protein kinase contains a protein kinase domain profile (PDOC00100)	267550_at	0.8
putative beta-galactosidase ; supported by cDNA: gi_14517398_gb_AY039534.1_	267556_at	0.8
putative cytochrome P450	267500_s_at	0.8
unknown protein ;supported by full-length cDNA: Ceres:35578.	267504_at	0.8
putative receptor-like protein kinase	267490 at	0.8
putative beta-glucosidase	267392 at	0.8
hypothetical protein predicted by grail and genscan	267396 at	0.8
citrate synthase similar to GB:X17528, 10 possible frameshifts in that submission.;supported by full-length cDNA: Ceres:16528.	267368 at	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 123915.	267036 at	0.8
putative myrosinase-binding protein ;supported by full-length cDNA: Ceres:39069.	266989 at	0.8
unknown protein	266963 at	0.8
putative phospholipase	266977 at	0.8
unknown protein ;supported by full-length cDNA: Ceres:39666.	266848 at	0.8
unknown protein	266858 at	0.8
F-box protein family, AtFBX5 contains similarity to F-box protein FBL2 GI:6010699 from [Rattus norvegicus]	266815 at	0.8
Public AAA-type ATPase	266777 at	0.8
	266796 at	0.8
predicted by genscan		
unknown protein	266758_at	0.8
similar to late embryogenesis abundant proteins	266728_at	0.8
putative N-acetyl-gamma-glutamyl-phosphate reductase ; supported by cDNA: gj_16604367_gb_AY058082.1_	266704_at	0.8
putative glyoxysomal malate dehydrogenase precursor ; supported by cDNA: gi_16226836_gb_AF428346.1_AF428346	266457_at	0.8
putative clathrin binding protein (epsin)	266436_at	0.8
putative ubiquitin activating enzyme	266333_at	0.8
Mutator-like transposase similar to MURA transposase of maize Mutator transposon; supported by cDNA: gi_15982768_gb_AY057491.1_	266318_at	0.8
putative proline-rich protein	266283_at	0.8
putative leucine aminopeptidase identical to GB:X63444; supported by cDNA: gi_14334665_gb_AY035006.1_	265996_at	0.8
putative nucleosome assembly protein	265940_at	0.8
hypothetical protein predicted by genscan and genefinder	265764_at	0.8
	265727_at	0.8
hypothetical protein predicted by genscan	265697_at	0.8
70kD heat shock protein ;supported by full-length cDNA: Ceres:98979.	265675_at	0.8
unknown protein predicted by genscan	265691_at	0.8
putative C2H2-type zinc finger protein likely a nucleic acid binding protein; supported by cDNA: gi_4585204_gb_AF095588.1_AF095588	265662_at	0.8
CDC27/NUC2-like protein TPR-repeat protein	265585_at	0.8
putative cellular apoptosis susceptibility protein	265453_at	0.8
hypothetical protein predicted by genscan	265455 at	0.8
unknown protein ;supported by full-length cDNA: Ceres:108956.	265384_at	0.8
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:37455.	265192_at	0.8
		0.8
		0.8
putative chloroplast membrane protein, ALBNO3 similar to GB:AAB61458	265011_at	0.8
hypothetical protein predicted by genemark.hmm; supported by CDNA: gi 13926194 gb AF370571.1 AF370571	264959 at	0.8
clathrin adaptor medium chain protein MUIB, putative similar to clathrin adaptor medium chain protein MUIB GI:4704421 from [Mus musculus]	264914 at	0.8
pruvate dehydrogenase E1 alpha subunits torogly similar to GB:AAD39331;supported by full-length CDNA: Ceres:41337.	264871_at	0.8
hypothetical protein similar to hypothetical protein GB:014360	264818 at	0.8
putative protein kinase similar to MAP3K delta-1 protein kinase (Y14199); supported by cDNA: gi 11127924 gb AF305913.1 AF305913	264780 at	0.8
putative protein kinase similar to war-so ceta-1 protein kinase (114139), supported by conve. gr 1121324_g0_Ar-303913.1_Ar-303913 putative leucy1-RNA synthetase Strong similarity to S, pombe leucy1-RNA synthetase (dplZ73100)		0.8
nutative 2.3-hisphosphoglycerate-independent phosphoglycerate mutase Strong similarity to P communic phosphoglycerate mutase (abIX70652).	264705_at 264668_at	0.8 0.8
putative 2,3-bisphosphoglycerate-independent phosphoglycerate mutase Strong similarity to R. communis phosphoglycerate mutase (gb X70652). E	264668_at	
Expressed protein ; supported by full-length cDNA: Ceres: 6319.	264668_at 264673_at	
Expressed protein ; supported by full-length cDNA: Ceres: 6319. unknown protein EST gb R64758 comes from this gene; supported by cDNA: gi_15450400_gb_AY052301.1_	264668_at 264673_at 264676_at	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 6319. unknown protein EST gb R64758 comes from this gene; supported by cDNA: gi_15450400_gb_AY052301.1_ putative U2 small nuclear ribonucleoprotein A (U2 SNRNP-A) Identical to A. thaliana U2 SnRNP-specific A protein (gb X69137). ESTs gb ATTS070	264668_at 264673_at 264676_at 264678_at	0.8 0.8
Expressed protein ; supported by full-length cDNA: Ceres: 6319. unknown protein EST gbl/R64758 comes from this gene; supported by cDNA: gi_15450400_gb_AY052301.1_ putative U2 small nuclear ribonucleoprotein A (U2 SNRNP-A) Identical to A. thaliana U2 SnRNP-specific A protein (gb X69137). ESTs gb ATTS070 unknown protein ; supported by cDNA: gi_13430645_gb_AF360235.1_AF360235	264668_at 264673_at 264676_at 264678_at 264615_at	0.8 0.8 0.8
Expressed protein ; supported by full-length cDNA: Ceres: 6319. unknown protein EST gb]R64758 comes from this gene; supported by cDNA: gi_15450400_gb_AY052301.1_ putative U2 small nuclear ribonucleoprotein A (U2 SNRNP-A) Identical to A. thaliana U2 SnRNP-specific A protein (gb]X69137). ESTs gb]ATTS070 unknown protein ; supported by cDNA: gi_13430645_gb_AF360235.1_AF360235 hypothetical protein predicted by genemark.hmm	264668_at 264673_at 264676_at 264678_at 264615_at 264428_at	0.8 0.8 0.8 0.8
Expressed protein ; supported by full-length cDNA: Ceres: 6319. unknown protein EST gb[R64758 comes from this gene; supported by cDNA: gi_15450400_gb_AY052301.1_ putative U2 small nuclear ribonucleoprotein A (U2 SNRNP-A) Identical to A. thaliana U2 SnRNP-specific A protein (gb X69137). ESTs gb ATTS070 unknown protein ; supported by cDNA: gi_13430645_gb_AF360235.1_AF360235 hypothetical protein predicted by genemark.hmm putative pyrophosphate-fructose-6-phosphate 1-phosphotransferase similar to pyrophosphate-dependent phosphofuctokinase beta subunit gb Z328:	264668_at 264673_at 264676_at 264678_at 264615_at 264428_at 264386_at	0.8 0.8 0.8 0.8 0.8
Expressed protein ; supported by full-length cDNA: Ceres: 6319. unknown protein EST gb[R64758 comes from this gene; supported by cDNA: gi_15450400_gb_AY052301.1_ putative U2 small nuclear ribonucleoprotein A (U2 SNRNP-A) Identical to A. thaliana U2 SnRNP-specific A protein (gb]X69137). ESTs gb]ATTS070 unknown protein ; supported by cDNA: gi_13430645_gb_AF360235.1_AF360235 hypothetical protein predicted by genemark.hmm putative pyrophosphate-fructose-6-phosphate 1-phosphotransferase similar to pyrophosphate-dependent phosphofuctokinase beta subunit gb]Z328 unknown protein Contains similarity to gb]AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding domain C2 PF[00168.]	264668_at 264673_at 264676_at 264678_at 264615_at 264428_at 264386_at 264351_at	0.8 0.8 0.8 0.8 0.8 0.8
Expressed protein ; supported by full-length cDNA: Ceres: 6319. unknown protein EST gb[R64758 comes from this gene; supported by cDNA: gi_15450400_gb_AY052301.1_ putative U2 small nuclear ribonucleoprotein A (U2 SNRNP-A) Identical to A. thaliana U2 SnRNP-specific A protein (gb X69137). ESTs gb ATTS070 unknown protein ; supported by cDNA: gi_13430645_gb_AF360235.1_AF360235 hypothetical protein predicted by genemark.hmm putative pyrophosphate-fructose-6-phosphate 1-phosphotransferase similar to pyrophosphate-dependent phosphofuctokinase beta subunit gb Z328: unknown protein Cnatins similarity to gb AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding domain C2 PF 00168.1 hypothetical protein similar to hypothetical protein GI:5541664 from [Arabidopsis thaliana]	264668_at 264673_at 264676_at 264678_at 264615_at 264428_at 264386_at 2643851_at 264308_at	0.8 0.8 0.8 0.8 0.8 0.8 0.8
Expressed protein ; supported by full-length cDNA: Ceres: 6319. unknown protein EST gb]R64758 comes from this gene; supported by cDNA: gi_15450400_gb_AY052301.1_ putative U2 small nuclear ribonucleoprotein A (U2 SNRNP-A) Identical to A. thaliana U2 SnRNP-specific A protein (gb]X69137). ESTs gb]ATTS070 unknown protein ; supported by cDNA: gi_13430645_gb_AF360235.1_AF360235 hypothetical protein predicted by genemark.hmm putative pyrophosphate-fructose-6-phosphate 1-phosphotransferase similar to pyrophosphate-dependent phosphofuctokinase beta subunit gb]Z328: unknown protein Contains similarity to gb]AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding domain C2 PF]00168.1 hypothetical protein ;supported by full-length cDNA: Ceres:16387.	264668_at 264673_at 264676_at 264678_at 264615_at 264428_at 264386_at 264326_at 264351_at 264308_at 264308_at	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
Expressed protein ; supported by full-length cDNA: Ceres: 6319. unknown protein EST gb[R64758 comes from this gene; supported by cDNA: gi_15450400_gb_AY052301.1_ putative U2 small nuclear ribonucleoprotein A (U2 SNRNP-A) Identical to A. thaliana U2 SnRNP-specific A protein (gb]X69137). ESTs gb]ATTS070 unknown protein ; supported by cDNA: gi_13430645_gb_AF360235.1_AF360235 hypothetical protein predicted by genemark.hmm putative pyrophosphate-fructose-6-phosphate 1-phosphotransferase similar to pyrophosphate-dependent phosphofuctokinase beta subunit gb]Z328: unknown protein Contains similarity to gb]AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding domain C2 PF[00168.1] hypothetical protein similar to hypothetical protein GI:5541664 from [Arabidopsis thaliana] unknown protein ; supported by full-length cDNA: Ceres: 16387. unknown protein ; supported by cDNA: gi_15081790_gb_AY048288.1_	264668_at 264673_at 264676_at 264678_at 264615_at 264428_at 264386_at 2643851_at 264308_at 264286_at 264265_at	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
Expressed protein ; supported by full-length cDNA: Ceres: 6319. unknown protein EST gbl/R64758 comes from this gene; supported by cDNA: gi_15450400_gb_AY052301.1_ putative U2 small nuclear ribonucleoprotein A (U2 SNRNP-A) Identical to A. thaliana U2 SnRNP-specific A protein (gb X69137). ESTs gb ATTS070 unknown protein ; supported by cDNA: gi_13430645_gb_AF360235.1_AF360235 hypothetical protein predicted by genemark.hmm putative pyrophosphate-fructose-6-phosphate 1-phosphotransferase similar to pyrophosphate-dependent phosphofuctokinase beta subunit gb Z328: unknown protein Contains similarity to gb AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding domain C2 PF 00168.1 hypothetical protein similar to hypothetical protein GI:5541664 from [Arabidopsis thaliana] unknown protein ; supported by full-length cDNA: Ceres:16387. unknown protein ESTs gb Z34075, gb Z34835 and gb AA404888 come from this gene	264668_at 264675_at 264675_at 264675_at 264615_at 264428_at 264386_at 264386_at 264386_at 264386_at 264286_at 264286_at 264286_at 264298_at	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
Expressed protein ; supported by full-length cDNA: Ceres: 6319. unknown protein EST gb[R64758 comes from this gene; supported by cDNA: gi_15450400_gb_AY052301.1_ putative U2 small nuclear ribonucleoprotein A (U2 SNRNP-A) Identical to A. thaliana U2 SnRNP-specific A protein (gb]X69137). ESTs gb]ATTS070 unknown protein ; supported by cDNA: gi_13430645_gb_AF360235.1_AF360235 hypothetical protein predicted by genemark.hmm putative pyrophosphate-fructose-6-phosphate 1-phosphotransferase similar to pyrophosphate-dependent phosphofuctokinase beta subunit gb]Z328: unknown protein Contains similarity to gb]AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding domain C2 PF[00168.1] hypothetical protein similar to hypothetical protein GI:5541664 from [Arabidopsis thaliana] unknown protein ; supported by full-length cDNA: Ceres: 16387. unknown protein ; supported by cDNA: gi_15081790_gb_AY048288.1_	264668_at 264673_at 264676_at 264678_at 264615_at 264428_at 264386_at 2643851_at 264308_at 264286_at 264265_at	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
Expressed protein ; supported by full-length cDNA: Ceres: 6319. unknown protein EST gbl/R64758 comes from this gene; supported by cDNA: gi_15450400_gb_AY052301.1_ putative U2 small nuclear ribonucleoprotein A (U2 SNRNP-A) Identical to A. thaliana U2 SnRNP-specific A protein (gb X69137). ESTs gb ATTS070 unknown protein ; supported by cDNA: gi_13430645_gb_AF360235.1_AF360235 hypothetical protein predicted by genemark.hmm putative pyrophosphate-fructose-6-phosphate 1-phosphotransferase similar to pyrophosphate-dependent phosphofuctokinase beta subunit gb Z328: unknown protein Contains similarity to gb AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding domain C2 PF 00168.1 hypothetical protein similar to hypothetical protein GI:5541664 from [Arabidopsis thaliana] unknown protein ; supported by full-length cDNA: Ceres:16387. unknown protein ESTs gb Z34075, gb Z34835 and gb AA404888 come from this gene	264668_at 264673_at 264676_at 264676_at 264678_at 264615_at 264428_at 264386_at 264386_at 264308_at 264326_at 264265_at 264266_at 264206_at	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
Expressed protein ; supported by full-length cDNA: Ceres: 6319. unknown protein EST gb]R64758 comes from this gene; supported by cDNA: gi_15450400_gb_AY052301.1_ putative U2 small nuclear ribonucleoprotein A (U2 SNRNP-A) Identical to A. thaliana U2 SnRNP-specific A protein (gb]X69137). ESTs gb]ATTS070 unknown protein ; supported by cDNA: gi_13430645_gb_AF360235.1_AF360235 hypothetical protein predicted by genemark.hmm putative pyrophosphate-fructose-6-phosphate 1-phosphotransferase similar to pyrophosphate-dependent phosphofuctokinase beta subunit gb]Z328: unknown protein contains similarity to gb]AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding domain C2 PF[00168.1 hypothetical protein ; supported by full-length cDNA: Ceres:16387. unknown protein ; supported by full-length cDNA: Ceres:16387. unknown protein ; supported by full-length cDNA: Ceres:16387. unknown protein ; supported by full-length cDNA: Geres:16387. unknown protein ; supported by GDNA: gi_15081790_gb_AY048288.1_ unknown protein ; supported by GDNA: gi_15081790_gb_AY048288.1_ unknown protein ; supported by GB:CAA72903 from [Arabidopsis thaliana]; supported by cDNA: gi_14334597_gb_AY034972.1_	264668_at 264673_at 264676_at 264676_at 264678_at 264615_at 264428_at 264386_at 264386_at 264308_at 264326_at 264265_at 264266_at 264206_at	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8

	264172_at 264123 at	0.8 0.8
	264125_at 264118_at	0.8
•	264069_at	0.8
	264044_at	0.8
•	264011_at 263904 at	0.8 0.8
	263824_at	0.8
	263776_s_at	0.8
	263777_at	0.8 0.8
	263557_at 263457_at	0.8
	263275_at	0.8
	263250_at	0.8
	263200_at 263010_at	0.8 0.8
	263007_at	0.8
endo-beta-1,4-glucanase, putative similar to endo-beta-1,4-glucanase GB:AAC12685 GI:3025470 from [Pinus radiata];supported by full-length cDN/	262980_at	0.8
	262941_at	0.8
hypothetical protein contains similarity to transcriptional repressor SIN3B GI:2921547 from [Mus musculus] auxin response factor 1 identical to auxin response factor 1 GI:2245378 from [Arabidopsis thaliana]; supported by cDNA: gi_2245377_gb_U83245.1_	262900_at 262914_at	0.8 0.8
	262849_at	0.8
	262662_at	0.8
4-hydroxyphenylpyruvate dioxygenase (HPD) identical to 4-hydroxyphenylpyruvate dioxygenase (HPD) SP:P93836 [Arabidopsis thaliana (Mouse-ea hypothetical protein predicted by genscan+	262635_at 262532_at	0.8 0.8
unknown protein Smithar to gb/S4260 POS5 gene product from Saccharomyces cerevisiae. EST gb/W43879 comes from this gene; supported by cE		0.8
	262471_at	0.8
	262274_at	0.8
	262280_at 262248 at	0.8 0.8
	262208 at	0.8
unknown protein contains similarity to WD-40 repeat protein GI:4519417 from [Homo sapiens]	262145_at	0.8
late embryogenis abundant protein, putative similar to late embryogenis abundant protein 5 GI:2981167 from [Nicotiana tabacum];supported by full-		0.8
SAR DNA binding protein, putative similar to SAR DNA binding protein GB:BAA31260 GI:3288883 from [Oryza sativa]; supported by full-length cDN flavin-containing monooxygenase FMO3 gI:349533 from [Oryctolagus cuniculus]	262094_at 261913_at	0.8 0.8
protein serine/threonine phosphatase alpha, putative similar to protein serine/threonine phosphatase alpha GB:AAC69437 GI:3811109 from [Plasmc2		0.8
	261668_at	0.8
•	261674_at	0.8
	261681_at 261652_at	0.8 0.8
	261604_at	0.8
serine/threonine kinase, putative similar to serine/threonine kinase GB:CAA73067.1 GI:2632252 from [Sorghum bicolor]; supported by cDNA: gi_144		0.8
	261540_at 261434_at	0.8 0.8
	261413_at	0.8
unknown protein	261424_at	0.8
	261375_at	0.8
	261319_at 261339 at	0.8 0.8
	261253_at	0.8
	261231_at	0.8
	261207_at	0.8
	261139_at 261033 at	0.8 0.8
	261050_at	0.8
histidine decarboxylase, putative similar to histidine decarboxylase GB:BAA78331 GI:4996105 from [Brassica napus]; supported by cDNA: gi_15011		0.8
	260793_at 260798_at	0.8 0.8
	260665 at	0.8
very-long-chain fatty acid condensing enzyme CUT1, putative similar to GB:AAD37122 from [Arabidopsis thaliana]; supported by full-length cDNA: C	260667_at	0.8
	260677_at	0.8
unknown protein contains similarity to tub homolog GI:2072160 from [Homo sapiens]; supported by cDNA: gi_13877766_gb_AF370146.1_AF370146 unknown protein	260586_at	0.8 0.8
	260521_at	0.8
mannosyl-oligosaccharide alpha-1,2-mannosidase, putative similar to mannosyl-oligosaccharide alpha-1,2-mannosidase (Mus musculus) GI:474280		0.8
unknown protein putative RNA-binding domain contains Pfam profile: PF00806 Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain) (5 cor	260436_at	0.8 0.8
	260395_at 260321_at	0.8
putative glycerophosphodiester phosphodiesterase similar to glycerophosphoryl diester phosphodiesterase GB:AAF12f49 from [Deinococcus radiodu	260254_at	0.8
	260157_at	0.8
putative protein phosphatase 2C similar to protein phosphatase 2C GB:CAA72341 [Medicago sativa]; contains Pfam profile: PF00481 Protein phospl unknown protein	259934 at	0.8 0.8
putative exportin, tRNA (nuclear export receptor for tRNAs) similar to exportin, tRNA (nuclear export receptor for tRNAs) GB:6005954 [Homo sapien		0.8
	259848_at	0.8
	259647_at 259416 at	0.8 0.8
	259395_at	0.8
putative polynucleotide phosphorylase similar to polynucleotide phosphorylase GB:AAC50039 (Pisum sativum), identical to putative polynucleotide r	259344_at	0.8
	259319_at	0.8
putative porin similar to outer mitochondrial membrane porin (voltage-dependent anion-selective channel protein) (VDAC) (POM 34) GB:P42055 (So putative DNA gyrase subunit B similar to putative DNA gyrase subunit GB:O50627 [Bacillus halodurans] 2	259270_at 259138 s at	0.8 0.8
unknown protein similar to hypothetical proteins: GB:AAB61107 [Arabidopsis thaliana], GB:AAC00578, [Arabidopsis thaliana]	259117_at	0.8
	259048_at	0.8
	259051_at 259039_at	0.8 0.8
	258966_at	0.8
	258921_at	0.8

hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:101876.	258878 at	0.8
putative glucan synthase similar to glucan synthase GB:AAD11794 [Filobasidiella neoformans var. neoformans]	258826 at	0.8
	258771 at	0.8
putative RING zinc finger protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger); supported by full-length cDNA: Ceres: 3875		0.8
importin alpha identical to GB:AAC27644 from [Arabidopsis thaliana] (Plant Cell (1996) 8(8), 1337-1352), supported by full-length cDNA: Ceres:9351		0.8
kinesin-like protein similar to mitotic centromere-associated kinesin GB:AAC27660 from [Homo sapiens]; supported by cDNA: gi 15810128 gb AY0		0.8
DNA-binding protein contains AP2 domain, identical to AP2 domain containing protein RAP2.2 from B:AAC49768 from [Arabidopsis thaliana]; supp		0.8
	258218 at	0.8
	258173 at	0.8
	258101 at	0.8
	258051 at	0.8
		0.8
	257940_at	0.8
	257876_at	
	257893_at	0.8
	257838_at	0.8
SNF1 related protein kinase (ATSRPK1) identical to SNF1 related protein kinase (ATSRPK1) GB:AB027153 [Arabidopsis thaliana]; supported by cDI	_	0.8
	257746_at	0.8
	257709_at	0.8
	257703_at	0.8
	257657_at	0.8
unknown protein contains Pfam profile: PF00400 WD domain, G-beta repeat; supported by cDNA: gi_15081810_gb_AY048298.1_	257661_at	0.8
hypothetical protein predicted by genemark.hmm	257260_at	0.8
protein kinase, putative contains similarity to serine/threonine-protein kinase homolog GB:Q61136 from [Mus musculus], contains Pfam profile: PF0(	256995_at	0.8
subtilisin-like serine protease, putative contains similarity to cucumisin-like serine protease GI:3176874 from [Arabidopsis thaliana]	256997_at	0.8
glycolate oxidase, putative similar to GB:999542 from [Spinacia oleracea] (J. Biol. Chem. 264 (6), 3624-3628 (1989)), contains Pfam profile: PF01072	257004_s_at	0.8
lysyl-tRNA synthetase, putative similar to GB:P73443 from [Synechocystis PCC6803], contains Pfam profile: PF00152 tRNA synthetases class II (D,	256963 at	0.8
PHD-finger protein, putative contains Pfam profile: PF00628 PHD-finger; supported by full-length cDNA: Ceres:95660.	256889 at	0.8
	256848 at	0.8
DEAD box helicase protein, putative similar to DEAD box helicase protein GB:NP 006764 from [Homo sapiens], contains Pfam profile: PF00270 DI		0.8
	256624 at	0.8
	256534 at	0.8
	256491 at	0.8
	256479 at	0.8
•		
	256356_s_at	0.8
	256230_at	0.8
	256209_at	0.8
	256142_at	0.8
	256074_at	0.8
hypothetical protein contains similarity to peptidyl-prolyl cis-trans isomerase E GI:4406227 from [Homo sapiens]; supported by cDNA: gi_1498063_gl	256068_at	0.8
glutamyl-tRNA reductase, putative similar to glutamyl-tRNA reductase GI:1694925 from [Cucumis sativus]	256020_at	0.8
14-3-3 protein GF14epsilon (grf10) identical to 14-3-3 protein GF14 epsilon GI:5802798, SP:P48347 from [Arabidopsis thaliana]; supported by full-lei	255966_at	0.8
putative small nuclear ribonucleoprotein U2B ;supported by full-length cDNA: Ceres:34995.	255871_at	0.8
hypothetical protein predicted by genefinder and genscan; supported by full-length cDNA: Ceres:119054.	255818_at	0.8
unknown protein contains Pfam profile: PF02135 TAZ zinc finger	255762_at	0.8
wall-associated kinase, putative similar to wall-associated kinase 1 GI:3549626 from [Arabidopsis thaliana]; supported by cDNA: gi 15529241 gb A	255740 at	0.8
putative WD repeat membrane protein ; supported by cDNA: gi 15912316 gb AY056436.1	255711 at	0.8
putative SecA-type chloroplast protein transport factor non-consensus GA donor splice site at exon 4	255540 at	0.8
	255543 at	0.8
	255561 at	0.8
	255507 at	0.8
	255380 at	0.8
	255382 at	0.8
	255296 at	0.8
	255240 at	0.8
	255151_at	0.8
	255016_at	0.8
	255020_at	0.8
	254925_at	0.8
	254894_at	0.8
	254734_at	0.8
	254691_at	0.8
	254693_at	0.8
	254646_at	0.8
putative protein ; supported by cDNA: gi_14190356_gb_AF378856.1_AF378856	254580_at	0.8
potassium transporter-like protein putative potassium transporter AtKT2p & AtKT1p, Arabidopsis thaliana, Patchx:G2384669 & Patchx:G2384671	254520_at	0.8
putative protein probable membrane protein YFR005c, Saccharomyces cerevisiae, PIR2:S56260 2	254353_s_at	0.8
putative protein chS-Rex-b - Gallus gallus (chicken),gb:L10333;supported by full-length cDNA: Ceres:39185.	254227_at	0.8
tyrosine transaminase like protein tyrosine transaminase (EC 2.6.1.5) - rat, EMBL:X02741; supported by cDNA: gi 15076852 gb AF268090.1 AF2	254232 at	0.8
NADPH-ferrihemoprotein reductase ATR1; supported by cDNA: gi 15451215 gb AY054688.1	254127 at	0.8
abscisic acid-induced - like protein abscisic acid-induced protein HVA22, Hordeumvulgare, PIR2:A48892;supported by full-length cDNA: Ceres:2853	254085 at	0.8
putative protein various Caenorhabditis elegans predicted proteins	253977 at	0.8
	253949 at	0.8
	253900 at	0.8
	253876 at	0.8
putative NADH dehydrogenase NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain NDI - yeast, PIR2:S26704;supported by full-length cDNA: C		0.8
	253770 at	0.8
	253751 at	0.8
	-	
	253758_at	0.8
	253705_at	0.8
pyrophosphate-dependent phosphofructo-1-kinase-like protein pyrophosphate-dependent phosphofructo-1-kinase - Prunus armeniaca (apricot),PID:		0.8
nucleotide pyrophosphatase - like protein nucleotide pyrophosphatase homolog, Oryza sativa, gb:T03293; supported by cDNA: gi_13877570_gb_AF		0.8
	253549_at	0.8
	253517_at	0.8
putative protein ribosomal protein YmL14 precursor, mitochondrial - Saccharomyces cerevisiae, PIR2:S50921; supported by full-length cDNA: Ceres:		0.8
methyltransferase - like protein methyltransferase DPH5, Saccharomyces cerevisiae, PIR2:S30890; supported by cDNA: gi_13605812_gb_AF3673(		0.8
	253377_at	0.8
nucellin -like protein nucellin - Hordeum vulgare, PIR:G2290202; supported by full-length cDNA: Ceres:24738.	253331_at	0.8

putative protein Caenorhabditis elegans cosmid, gene T16G1.11,PID:e1349366; supported by cDNA: gi_14335023_gb_AY037191.1_ glucosyltransferase -like protein immediate-early salicylate-induced glucosyltransferase, Nicotiana tabacum, PIR2:T03747; supported by cDNA gi:14:		
	253336 at	0.8
		0.8
	253212_s_at	0.8
putative protein ;supported by full-length cDNA: Ceres:21838.	253171_at	0.8
putative protein bZIP protein - Arabidopsis thaliana,PID:g600855	253185_at	0.8
NAD+ dependent isocitrate dehydrogenase subunit 1 ;supported by full-length cDNA: Ceres:12228.	253196 at	0.8
putative protein SPINDLY protein, Petunia x hybrida, Y17720	253093_at	0.8
cellulose synthase catalytic subunit (Ath-A) ; supported by cDNA: gi_2827140_gb_AF027173.1_AF027173	252886_at	0.8
putative protein hypothetical protein, Schizosaccharomyces cerevisae, Z99168	252867_at	0.8
putative protein dehydrogenases of bacterial genome projects;supported by full-length cDNA: Ceres:114123.	252671 at	0.8
putative protein Na+-dependent inorganic phosphate cotransporter, Rattus norvegicus, U07609FUNC 99	252444_at	0.8
beta-D-glucan exohydrolase - like protein beta-D-glucan exohydrolase, Nicotiana tabacum, TREMBL:AB017502_1	252445_at	0.8
putative progesterone-binding protein homolog Atmp2 ; supported by cDNA: gi_4960153_gb_AF153283.1_AF153283	252338_at	0.8
putative protein transcribed gene of unknown function, Arabidopsis thaliana, EMBL:ATH132745	252226 at	0.8
putative protein UDP-glucose:(glucosyl) LPS alpha1.3-glucosyltransferase WaaO, E.coli, EMBL:AF019746	252179 at	0.8
U1 snRNP 70K protein ; supported by cDNA: gi_14532499_gb_AY039874.1_	252182_at	0.8
epoxide hydrolase-like protein epoxide hydrolase homolog - Glycine max, PIR:T07145; supported by cDNA: gi_13937212_gb_AF372961.1_AF3729	252095_at	0.8
putative protein DMR-N9 PROTEIN, Mus musculus, SWISSPROT:DMR9_MOUSE	251967 at	0.8
putative protein zinc finger protein GCS1 - Saccharomyces cerevisiae, PIR:S47006	251905 at	0.8
transporter-like protein oligopeptide transporter (LeOPT1) - Lycopersicon esculentum, EMBL:AF016713	251916_at	0.8
peptide transport - like protein peptide transport protein, Hordeum vulgare, PIR:T04378;supported by full-length cDNA: Ceres:117581.	251882_at	0.8
protein disulfide-isomerase-like protein protein disulphide isomerase, Fasciola hepatica	251840 at	0.8
putative protein unnamed sequence, Homo sapiens, EMBL:AK001088; supported by cDNA: gi 15215685 gb AY050371.1	251828 at	0.8
putative protein non-consensus TT donor splice site at exon 4; met-10+ protein - Neurospora crassa, PIR:JC4255; supported by cDNA: gi_1660463;		0.8
anthranilate phosphoribosyltransferase-like protein anthranilate phosphoribosyltransferase - Pisum sativum, PIR:T06460; supported by cDNA: gi_14		0.8
putative protein Bet1 homolog - Rattus norvegicus, EMBL:RN42755; supported by cDNA: gi_14030602_gb_AF368175.1_AF368175	251579_at	0.8
putative protein RanBP7/importin 7 - Homo sapiens, EMBL:AF098799	251495 at	0.8
putative protein polyamine oxidase (EC 1.5.3.11) precursor - Zea mays plasmid pCR2.1;supported by full-length cDNA: Ceres:16421.	251505_at	0.8
multi resistance protein homolog multi resistance protein mrp - Arabidopsis thaliana, EMBL:ATMRPPROT	251457_s_at	0.8
URIDYLATE KINASE-like protein URIDYLATE KINASE - Arabidopsis thaliana, EMBL:AF000147; supported by full-length cDNA: Ceres: 16800.	251426 at	0.8
putative protein RING finger protein AO7, Mus musculus, EMBL:AF171060	251403 at	0.8
	-	
putative protein paladin - Mus musculus, EMBL:MMPAL	251296_at	0.8
beta-glucosidase-like protein several beta-glucosidases	251230_at	0.8
putative protein putative protein F15G16.70 - Arabidopsis thaliana, EMBL:AL132959; supported by cDNA: gi 15810023 gb AY054280.1	251191 at	0.8
putative protein putative transcription factor HUA2, Arabidopsis thaliana, EMBL:AF116556	251203 at	0.8
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aldose reductase-like protein aldose reductase - Hordeum vulgare, EMBL:Z48360	251100_at	0.8
putative protein unknown protein At2g37660 - Arabidopsis thaliana, EMBL:AC004684; supported by cDNA: gi_15294289_gb_AF410336.1_AF41033	251038_at	0.8
putative protein various predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:13930.	251005 at	0.8
putative protein	250941 at	0.8
	_	0.8
myotubularin - like protein myotubularin, Homo sapiens, EMBL:U46024	250833_at	0.8
putative protein rngB protein, Dictyostelium discoideum, PIR:S68824; supported by cDNA: gi 15724205 gb AF412043.1 AF412043	250851 at	0.8
glycolate oxidase subunit D-like; D-lactate dehydrogenase-like; supported by cDNA: gi 15010679 gb AY045641.1	250691 at	0.8
	250603_at	
putative protein mature parasite-infected erythrocyte surface antigen, Plasmodium falciparum, EMBL:AF056936		0.8
RNA helicase-like protein	250529_at	0.8
sulfate transporter ; supported by cDNA: gi_2114105_dbj_AB003591.1_AB003591	250475 at	0.8
bromodomain protein - like bromodomain protein (BRDT), Homo sapiens, EMBL:AF019085	250424 at	0.8
RNA binding protein - like ma binding protein, Schizosaccharomyces pombe, PIR:T39586	250436_at	0.8
putative protein hypothetical bacterial proteins; supported by cDNA: gi_15724207_gb_AF412044.1_AF412044	250442_at	0.8
transcription factor like protein transcription factor TINY, Arabidopsis thaliana, PIR:T01076	250379 at	0.8
putative protein rjs protein, Mus musculus, PIR:T14317;supported by full-length cDNA: Ceres:266544.	250382 at	0.8
putative protein various predicted proteins, Drosophila melanogaster, Caenhorhabditis elegans, Homo sapiens; supported by full-length cDNA: Cere		0.8
putative protein predicted protein, Arabidopsis thaliana	250355_at	0.8
	250356 at	0.8
clathrin binding protein - like Af10-protein, Avena fatua, EMBL:U80041	250320_at	0.8
clathrin binding protein - like Af10-protein, Avena fatua, EMBL:U80041		
CCAAT box binding factor/ transcription factor Hap2a		0.8
CCAAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein	250243_at	
CCAAT box binding factor/ transcription factor Hap2a		0.8
CCAAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein	250243_at	0.8 0.8
CCAAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (emb CAB86638.1) alpha-mannosidase	250243_at 250202_at 250203_at	0.8
CCAAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (emb CAB86638.1) alpha-mannosidase putative protein similar to unknown protein (ref NP_057085.1);supported by full-length cDNA: Ceres:38057.	250243_at 250202_at 250203_at 250222_at	0.8 0.8
CCAAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (emb]CAB86638.1) alpha-mannosidase putative protein similar to unknown protein (ref NP_057085.1);supported by full-length cDNA: Ceres:38057. pescadillo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadillo, Homo sapiens, EMBL:U78310	250243_at 250202_at 250203_at 250222_at 250192_at	0.8 0.8 0.8
CCAAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (emb CAB86638.1) alpha-mannosidase putative protein similar to unknown protein (ref NP_057085.1);supported by full-length cDNA: Ceres:38057. pescadillo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadillo, Homo sapiens, EMBL:U78310 putative protein similar to unknown protein (pir  T09939);supported by full-length cDNA: Ceres:23754.	250243_at 250202_at 250203_at 250222_at 250192_at 250013_at	0.8 0.8 0.8 0.8
CCAAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (emb CAB86638.1) alpha-mannosidase putative protein similar to unknown protein (ref NP_057085.1);supported by full-length cDNA: Ceres:38057. pescadillo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadillo, Homo sapiens, EMBL:U78310 putative protein similar to unknown protein (pir  T09939);supported by full-length cDNA: Ceres:23754. Ruv DNA-helicase-like protein ;supported by full-length cDNA: Ceres:113109.	250243_at 250202_at 250203_at 250222_at 250192_at 250013_at 249938_at	0.8 0.8 0.8 0.8 0.8
CCAAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (emb CAB86638.1) alpha-mannosidase putative protein similar to unknown protein (ref NP_057085.1);supported by full-length cDNA: Ceres:38057. pescadillo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadillo, Homo sapiens, EMBL:U78310 putative protein similar to unknown protein (pir  T09939);supported by full-length cDNA: Ceres:23754.	250243_at 250202_at 250203_at 250222_at 250192_at 250013_at 249938_at	0.8 0.8 0.8 0.8
CCAAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (emb]CAB86638.1) alpha-mannosidase putative protein similar to unknown protein (ref NP_057085.1);supported by full-length cDNA: Ceres:38057. pescadillo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadillo, Homo sapiens, EMBL:U78310 putative protein similar to unknown protein (pir  T09939);supported by full-length cDNA: Ceres:23754. Ruv DNA-helicase-like protein ;supported by full-length cDNA: Ceres:113109. putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348	250243_at 250202_at 250203_at 250222_at 250192_at 250013_at 249938_at 249912_at	0.8 0.8 0.8 0.8 0.8 0.8
CCAAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (emb]CAB86638.1) alpha-mannosidase putative protein similar to unknown protein (ref]NP_057085.1);supported by full-length cDNA: Ceres:38057. pescadillo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadillo, Homo sapiens, EMBL:U78310 putative protein similar to unknown protein (pir  T09939);supported by full-length cDNA: Ceres:23754. Ruv DNA-helicase-like protein ;supported by full-length cDNA: Ceres:113109. putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348 putative protein similar to unknown protein (gb AAD20392.1)	250243_at 250202_at 250203_at 250222_at 250192_at 250013_at 249938_at 249912_at 249825_at	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
CCAAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (emb CAB86638.1) alpha-mannosidase putative protein similar to unknown protein (ref NP_057085.1);supported by full-length cDNA: Ceres:38057. pescadillo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadillo, Homo sapiens, EMBL:U78310 putative protein similar to unknown protein (pir  T09939);supported by full-length cDNA: Ceres:23754. Ruv DNA-helicase-like protein ;supported by full-length cDNA: Ceres:113109. putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348 putative protein similar to unknown protein (gb AAF01580.1)	250243_at 250202_at 250203_at 250222_at 2500192_at 250013_at 249938_at 249912_at 249825_at 249835_s_at	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
CCAAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (emb]CAB86638.1) alpha-mannosidase putative protein similar to unknown protein (ref]NP_057085.1);supported by full-length cDNA: Ceres:38057. pescadillo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadillo, Homo sapiens, EMBL:U78310 putative protein similar to unknown protein (pir  T09939);supported by full-length cDNA: Ceres:23754. Ruv DNA-helicase-like protein ;supported by full-length cDNA: Ceres:113109. putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348 putative protein similar to unknown protein (gb AAD20392.1)	250243_at 250202_at 250203_at 250222_at 250192_at 250013_at 249938_at 249912_at 249825_at	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
CCAAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (emb CAB86638.1) alpha-mannosidase putative protein similar to unknown protein (ref NP_057085.1);supported by full-length cDNA: Ceres:38057. pescadillo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadillo, Homo sapiens, EMBL:U78310 putative protein similar to unknown protein (pir  T09939);supported by full-length cDNA: Ceres:23754. Ruv DNA-helicase-like protein ;supported by full-length cDNA: Ceres:113109. putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348 putative protein similar to unknown protein (gb AAF01580.1)	250243_at 250202_at 250203_at 250222_at 2500192_at 250013_at 249938_at 249912_at 249825_at 249835_s_at	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
CCAAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (emb]CAB86638.1) alpha-mannosidase putative protein similar to unknown protein (ref NP_057085.1);supported by full-length cDNA: Ceres:38057. pescadillo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadillo, Homo sapiens, EMBL:U78310 putative protein similar to unknown protein (pir  T09939);supported by full-length cDNA: Ceres:23754. Ruv DNA-helicase-like protein ;supported by full-length cDNA: Ceres:113109. putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348 putative protein similar to unknown protein (gb AAF01580.1) putative protein ; supported by cDNA: gi_3747110_gb_AF095641.1_AF095641 receptor-protein kinese-like protein	250243_at 250202_at 250203_at 250222_at 250192_at 250013_at 249938_at 249912_at 249825_at 249825_at 249800_at 249800_at 249763_at	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
CCAAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (emb]CAB86638.1) alpha-mannosidase putative protein similar to unknown protein (ref NP_057085.1);supported by full-length cDNA: Ceres:38057. pescadillo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadillo, Homo sapiens, EMBL:U78310 putative protein similar to unknown protein (pir  T09339);supported by full-length cDNA: Ceres:23754. Ruv DNA-helicase-like protein ;supported by full-length cDNA: Ceres:113109. putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348 putative protein similar to unknown protein (gb AAF31706.1); putative protein similar to unknown protein (gb AAF31706.1); putative protein similar to unknown protein (gb AAF31706.1) putative protein similar to unknown protein (gb AAF31706.1) putative protein similar to unknown protein (gb AAF01580.1) MtN3-like protein ; supported by cDNA: gi_3747110_gb_AF095641.1_AF095641 receptor-protein kinase-like protein putative protein similar to unknown protein (pir  T40675); supported by cDNA: gi_14335067_gb_AY037213.1_	250243_at 250202_at 250203_at 250222_at 250192_at 250013_at 249912_at 249912_at 249825_at 249825_at 249800_at 249701_at	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
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CCAAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (emb CAB86638.1) alpha-mannosidase putative protein similar to unknown protein (ref NP_057085.1);supported by full-length cDNA: Ceres:38057. pescadillo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadillo, Homo sapiens, EMBL:U78310 putative protein similar to unknown protein (pir  T09939);supported by full-length cDNA: Ceres:23754. Ruv DNA-helicase-like protein ;supported by full-length cDNA: Ceres:113109. putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348 putative protein similar to unknown protein (gb AAF017680.1) putative protein similar to unknown protein (gb AAF017680.1) MtN3-like protein ; supported by cDNA: gi_3747110_gb_AF095641.1_AF095641 receptor-protein kinase-like protein putative protein similar to unknown protein (pir  T40675); supported by cDNA: gi_14335067_gb_AY037213.1_ putative protein similar to unknown protein (gb AAD21756.1); supported by cDNA: gi_15146184_gb_AY049233.1_although this cDNA may protein kinase-like	250243_at 250202_at 250203_at 250222_at 250192_at 250192_at 249938_at 249912_at 249835_s_at 249835_s_at 249800_at 249763_at 249701_at 249703_at 249703_at	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
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CCAAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (emb]CAB86638.1) alpha-mannosidase putative protein similar to unknown protein (ref NP_057085.1);supported by full-length cDNA: Ceres:38057. pescadillo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadillo, Homo sapiens, EMBL:U78310 putative protein similar to unknown protein (pir  T09939);supported by full-length cDNA: Ceres:23754. Ruv DNA-helicase-like protein ;supported by full-length cDNA: Ceres:113109. putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348 putative protein similar to unknown protein (gb AAF01580.1) MtN3-like protein ; supported by cDNA: gi_3747110_gb_AF095641.1_AF095641 receptor-protein kinase-like protein putative protein similar to unknown protein (pir  T40675); supported by cDNA: gi_14335067_gb_AY037213.1_ putative protein similar to unknown protein (gb AAD21756.1); supported by cDNA: gi_15146184_gb_AY049233.1_ although this cDNA may protein kinase-like	250243_at 250202_at 250203_at 250222_at 250192_at 250192_at 249938_at 249912_at 249835_s_at 249835_s_at 249800_at 249763_at 249701_at 249703_at 249703_at	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
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CCAAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (emb]CAB86638.1) alpha-mannosidase putative protein similar to unknown protein (ref NP_057085.1);supported by full-length cDNA: Ceres:38057. pescadillo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadillo, Homo sapiens, EMBL:U78310 putative protein similar to unknown protein (pir  T09939);supported by full-length cDNA: Ceres:23754. Ruv DNA-helicase-like protein ;supported by full-length cDNA: Ceres:113109. putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348 putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348 putative protein similar to unknown protein (gb AAF01580.1) MtN3-like protein ; supported by cDNA: gi_3747110_gb_AF095641.1_AF095641 receptor-protein kinase-like protein putative protein similar to unknown protein (pir  T40675); supported by cDNA: gi_14335067_gb_AY037213.1_ putative protein similar to unknown protein (pir AD2756.1); supported by cDNA: gi_15146184_gb_AY049233.1_ although this cDNA may protein kinase-like v-SNARE AtVT11a ribosomal protein L5 - like ribosomal protein L5, rice putative protein similarity to DegP2 protease GI:13172275 from [Arabidopsis thaliana] putative protein similarity to Unknown protein (gb AAF19684.1) putative protein similarity to Unknown protein (gb AF19684.1) putative protein similarity to Unknown protein (gb AF19684.1) putative protein similarity to Unknown protein (gb AF19684.1)	250243_at 250202_at 250203_at 250222_at 250192_at 250013_at 249938_at 249912_at 249835_s_at 249800_at 249763_at 249763_at 249701_at 249767_at 249678_at 249466_at 249433_at 24936_at 249238_at 249238_at 249238_at	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
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CCAAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (emb]CAB86638.1) alpha-mannosidase putative protein similar to unknown protein (ref NP_057085.1);supported by full-length cDNA: Ceres:38057. pescadillo - like protein embryonic development allele: hl2, Danio rerio, EMBL:U77627 pescadillo, Homo sapiens, EMBL:U78310 putative protein similar to unknown protein (pir  T09939);supported by full-length cDNA: Ceres:23754. Ruv DNA-helicase-like protein ;supported by full-length cDNA: Ceres:113109. putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348 putative protein similar to unknown protein (gb AAF01580.1) MtN3-like protein ; supported by cDNA: gi_3747110_gb_AF095641.1_AF095641 receptor-protein kinase-like protein (pir  T40675); supported by cDNA: gi_14335067_gb_AY037213.1_ putative protein similar to unknown protein (gb AAD21756.1); supported by cDNA: gi_15146184_gb_AY049233.1_although this cDNA may protein kinase-like v-SNARE AtVT11a ribosomal protein L5 - like ribosomal protein L5, rice putative protein strong similarity to unknown protein (gb AAD21756.768 DegP protease contains similarity to Unknown protein (gb AAF19684.1) putative protein strong similarity to unknown protein (gb AAF19684.1) putative protein strong similarity to unknown protein (gb AAF19684.1) putative protein notains similarity to unknown protein (gb AAF19684.1) putative protein notains similarity to glutathione-S-transferase/glutaredoxin;supported by full-length cDNA: Ceres: 12455. putative protein similar to unknown protein (gb AAF19684.1) putative protein similarity to unknown protein (gb AAF19684.1) putative protein similarity to glutathione-S-transferase/glutaredoxin;supported by full-length cDNA: Ceres: 12455. putative protein similarity to unknown protein (gb AAF19684.1) ; supported by full-length cDNA: Ceres: 12455.	250243_at 250202_at 250203_at 250222_at 250192_at 250192_at 249938_at 249912_at 249835_s_at 249835_s_at 249800_at 249763_at 249701_at 249701_at 249676_at 249676_at 249676_at 249453_at 249453_at 249453_at 249453_at 249456_at 249396_at 249278_at 249323_at 249278_at 249378_at 24	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
CCAAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (emb]CAB86638.1) alpha-mannosidase putative protein similar to unknown protein (ref NP_057085.1);supported by full-length cDNA: Ceres:38057. pescadillo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadillo, Homo sapiens, EMBL:U78310 putative protein similar to unknown protein (pir  T09393);supported by full-length cDNA: Ceres:23754. Ruv DNA-helicase-like protein ;supported by full-length cDNA: Ceres:113109. putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348 putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348 putative protein similar to unknown protein (gb AAF01580.1) MtN3-like protein ; supported by cDNA: gi_3747110_gb_AF095641.1_AF095641 receptor-protein kinase-like protein putative protein similar to unknown protein (pir  T40675); supported by cDNA: gi_14335067_gb_AY037213.1_ putative protein similarity to unknown protein (bj AAD21756.1); supported by cDNA: gi_15146184_gb_AY049233.1_ although this cDNA may protein kinase-like v-SNARE AtVT11a ribosomal protein L5 - like ribosomal protein L5, rice putative protein strong similarity to DegP2 protease Gi:13172275 fom [Arabidopsis thaliana] putative protein strong similarity to gutatinone-S-transferase/glutaredoxin;supported by full-length cDNA: Ceres:4645. 20S proteasome subunit PAF1 (gb AAC32062.1) ; supported by full-length cDNA: Ceres: 12455.	250243_at 250202_at 250203_at 250222_at 250192_at 250192_at 249938_at 249912_at 249835_s_at 249835_s_at 249805_at 249763_at 249763_at 249701_at 249703_at 249768_at 249466_at 249433_at 249396_at 249233_at 24923_at 24923_at 24923_at 24923_at	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
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CCAAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (emb[CAB86638.1) alpha-mannosidase putative protein similar to unknown protein (ref NP_057085.1); supported by full-length cDNA: Ceres:38057. pescadillo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadillo, Homo sapiens, EMBL:U78310 putative protein similar to unknown protein (pir  T09939); supported by full-length cDNA: Ceres:23754. Ruv DNA-helicase-like protein ; supported by full-length cDNA: Ceres:113109. putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348 putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348 putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348 putative protein similar to unknown protein (gb AAF01580.1) MtN3-like protein ; ported by CDNA: gi_3747110_gb_AF095641.1_AF095641 receptor-protein kinase-like protein putative protein similar to unknown protein (gb AAD21756.1); supported by cDNA: gi_15146184_gb_AY049233.1_ although this cDNA may protein kinase-like v-SNARE AtVTI1a ribosomal protein L5 - like ribosomal protein L5, rice putative protein similarity to unknown protein (gb AAP178678 DegP protease contains similarity to DegP2 protease GI:13172275 form [Arabidopsis thaliana] putative protein similarity to glutathione-S-transferase/glutaredoxin,supported by full-length cDNA: Ceres:4645. 20S proteaseome subunit PAF1 (gb)AAC32062.1); supported by full-length cDNA: Ceres: 12455. putative protein similar to unknown protein (gb]AF19684.1) putative protein similarity to glutathione-S-transferase/glutaredoxin,supported by full-length cDNA: Ceres: 12455. putative protein similar to unknown protein (gb]A2620; supported by full-length cDNA: Ceres: 12455. putative protein similar to unknown protein (gb]A2620; supported by full-length cDNA: Ceres: 12455. putative	250243_at 250202_at 250202_at 250192_at 250192_at 249912_at 249912_at 249825_at 249835_s_at 249800_at 249763_at 249701_at 249701_at 249703_at 249770_at 249678_at 249678_at 249453_at 249453_at 249453_at 249456_at 249278_at 249678_at 248009_at 248798_at 248809_at 248809_at	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
CCAAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (emb CAB86638.1) alpha-mannosidase putative protein similar to unknown protein (ref NP_057085.1);supported by full-length cDNA: Ceres:38057. pescadillo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadillo, Homo sapiens, EMBL:U78310 putative protein similar to unknown protein (pir  T09939);supported by full-length cDNA: Ceres:23754. Ruv DNA-helicase-like protein :supported by full-length cDNA: Ceres:113109. putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348 putative protein similar to unknown protein (gb AAF01580.1) putative protein similar to unknown protein (gb AAF01580.1) MtN3-like protein :supported by cDNA: gi_3747110.gb_AF095641 receptor-protein kinase-like protein putative protein similar to unknown protein (pir  T40675); supported by cDNA: gi_14335067_gb_AY037213.1_ putative protein similar to unknown protein (gb AAF01580.1); supported by cDNA: gi_15146184_gb_AY049233.1_ although this cDNA may protein kinase-like v-SNARE AtVT11a ribosomal protein L5 - like ribosomal protein L5, rice putative protein sing similarity to unknown protein (gb AAF19684.1) putative protein sing similarity to Unknown protein (gb AAF19684.1) putative protein sing similarity to glutathione-S-transferase/glutaredoxin;supported by full-length cDNA: Ceres:4645. 20S protease contains similarity to glutathione-S-transferase/glutaredoxin;supported by full-length cDNA: Ceres:12455. putative protein similar to unknown protein (gb AAF19684.1) putative protein simila	250243_at 250202_at 250203_at 250202_at 250192_at 250192_at 249938_at 249912_at 249835_s_at 249835_s_at 249805_at 249763_at 249763_at 249763_at 249768_at 249466_at 249453_at 249466_at 249433_at 249396_at 249233_at 249233_at 249278_at 249233_at 249263_at 249278_at 249233_at 249263_at 249278_at 249263_at 249278_at 249263_at 249278_at 249263_at 249278_at 249263_at 249278_at 249263_at 249278_at 249263_at 249264_at 249264_at 249264_at 249264_at 249264_at 249276_at 249276_at 249264_at 249264_at 249266_at 249276_at	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
CCAAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (emb[CAB86638.1) alpha-mannosidase putative protein similar to unknown protein (ref NP_057085.1); supported by full-length cDNA: Ceres:38057. pescadillo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadillo, Homo sapiens, EMBL:U78310 putative protein similar to unknown protein (pir  T09939); supported by full-length cDNA: Ceres:23754. Ruv DNA-helicase-like protein ; supported by full-length cDNA: Ceres:113109. putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348 putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348 putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348 putative protein similar to unknown protein (gb AAF01580.1) MtN3-like protein ; ported by CDNA: gi_3747110_gb_AF095641.1_AF095641 receptor-protein kinase-like protein putative protein similar to unknown protein (gb AAD21756.1); supported by cDNA: gi_15146184_gb_AY049233.1_ although this cDNA may protein kinase-like v-SNARE AtVTI1a ribosomal protein L5 - like ribosomal protein L5, rice putative protein similarity to unknown protein (gb AAP178678 DegP protease contains similarity to DegP2 protease GI:13172275 form [Arabidopsis thaliana] putative protein similarity to glutathione-S-transferase/glutaredoxin,supported by full-length cDNA: Ceres:4645. 20S proteaseome subunit PAF1 (gb)AAC32062.1); supported by full-length cDNA: Ceres: 12455. putative protein similar to unknown protein (gb]AF19684.1) putative protein similarity to glutathione-S-transferase/glutaredoxin,supported by full-length cDNA: Ceres: 12455. putative protein similar to unknown protein (gb]A2620; supported by full-length cDNA: Ceres: 12455. putative protein similar to unknown protein (gb]A2620; supported by full-length cDNA: Ceres: 12455. putative	250243_at 250202_at 250202_at 250192_at 250192_at 249912_at 249912_at 249825_at 249835_s_at 249800_at 249763_at 249701_at 249701_at 249703_at 249770_at 249678_at 249678_at 249453_at 249453_at 249453_at 249456_at 249278_at 249678_at 248009_at 248798_at 248809_at 248809_at	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
CCAAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (emb[CAB86638.1) alpha-mannosidase putative protein similar to unknown protein (ref NP_057085.1);supported by full-length cDNA: Ceres:38057. pescadilo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadillo, Homo sapiens, EMBL:U78310 putative protein similar to unknown protein (pir [T09939];supported by full-length cDNA: Ceres:23754. Ruv DNA-helicase-like protein ;supported by full-length cDNA: Ceres:13109. putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348 putative protein similar to unknown protein (gb AAF01580.1) MN3-like protein ; supported by cDNA: gi_3747110_gb_AF095641.1_AF095641 receptor-protein kinase-like protein putative protein similar to unknown protein (pir)[T40675); supported by cDNA: gi_14335067_gb_AY037213.1_ putative protein similar to unknown protein (pir)[T40675); supported by cDNA: gi_15146184_gb_AY049233.1_ although this cDNA may protein kinase-like protein - Synechocystis sp. PIR:S76678 DegP protein strong similarity to unknown protein (bj/AAF19684.1) putative protein similarity to unknown protein (bj/AAF19684.1) putative protein similarity to unknown protein (bj/AAF19684.1) putative protein similarity to Uuknown protein (bj/AAF19684.1) putative protein similarit to unknown protein (bj/AAF19684.1) putative protein similar to unknown protein (bj/AAF196863_gb_L2255.5) putative protein similar to unknown protein (bj/AAF19684.1) putative protein simil	250243_at 250202_at 250203_at 250222_at 250192_at 250192_at 249938_at 249912_at 249835_at 249835_s_at 249805_at 249763_at 249763_at 249701_at 249703_at 249763_at 249763_at 249678_at 249466_at 249433_at 249436_at 249233_at 24923_at 24923_at 24923_at 24923_at 24923_at 24923_at 24923_at 24926_at 24923_at 24926_at 248266_at 248766_at 248766_at 248766_at	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
CCAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (emb[CAB86638.1) alpha-mannosidase putative protein similar to unknown protein (ref[NP_057085.1);supported by full-length cDNA: Ceres:38057. pescadilo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadilo, Homo sapiens, EMBL:U78310 putative protein similar to unknown protein (yll[T09939);supported by full-length cDNA: Ceres:23754. Rv DNA-helicase-like protein : supported by full-length cDNA: Ceres:11309. putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348 putative protein similar to unknown protein (gb AAF20382.1) putative protein similar to unknown protein (gb AAF01580.1) treeptor-protein kinase-like protein supported by cDNA: gi_3747110_gb_AF095641.1_AF095641 receptor-protein kinase-like protein putative protein similar to unknown protein (gb/AF01580.1) v=SNARE AtVT11a putative protein similar to unknown protein (gb/AAF0156.1); supported by cDNA: gi_15146184_gb_AY049233.1_ although this cDNA may protein kinase-like v=SNARE AtVT11a ribosomal protein L5 - like ribosomal protein L5, rice putative protein similarity to unknown protein (gb/AAF19684.1) putative protein similarity to UB2P2 protease GI:13172275 from [Arabidopsis thaliana] putative protein pothetical protein - Synechocystis sp., PIR:S76678 DegP protease contains similarity to UB2P2 protease GI:13172275 from [Arabidopsis thaliana] putative protein contains similarity to UB4AF19684.1) putative protein contains similarity to UB4AF19684.1) putative protein contains similarity to UB4AF19684.1) putative protein similar to unknown protein (gb]AAF19684.1) putative protein similar to unknown protein (gb]AAF19684.1) putative protein similar to unknown protein (gb]AAF19684.1] putative protein similar to unknown protein (gb]AAF19684.1] putative protein similar to unknown protein (gb]AAF19684.1] putative protein similar to unknown protein (gb]AAF1	250243_at 250202_at 250202_at 250192_at 250192_at 250192_at 249938_at 249912_at 249835_s_at 249835_s_at 249800_at 249763_at 249701_at 249703_at 249701_at 249676_at 249453_at 249453_at 249453_at 249454_at 249454_at 249233_at 249233_at 249264_at 249122_at 248926_at 248926_at 248926_at 248796_at 248796_at 248796_at 248796_at 248796_at 248796_at 248796_at 248796_at 248796_at 248743_at 248743_at 248713_at	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
CCAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (emb]CAB86638.1) alpha-mannosidase putative protein similar to unknown protein (ref]NP_057085.1);supported by full-length cDNA: Ceres:38057. pescadilo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadilo, Homo sapiens, EMBL:U78310 putative protein similar to unknown protein (pl]T0939);supported by full-length cDNA: Ceres:23754. Ruv DNA-helicase-like protein ;supported by full-length cDNA: Ceres:13109. putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348 putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348 putative protein similar to unknown protein (gb AAF01506.1) MN3-like protein i supported by cDNA: gi_3747110_gb_AF095641.1_AF095641 receptor-protein kinase-like protein putative protein similar to unknown protein (pl]T40675); supported by cDNA: gi_14335067_gb_AY037213.1_ putative protein similar to unknown protein (gb]AAD21756.1); supported by cDNA: gi_15146184_gb_AY049233.1_ although this cDNA may protein kinase-like v-SNARE ALVT11a ribosomal protein L5 - like ribosomal protein L5, rice putative protein strong similarity to unknown protein (gb]AAF19684.1) putative protein strong similarity to unknown protein (gb]AF19684.10 putative protein strong similarity to unknown protein (gb]AF19684.10 putative protein strong similarity to unknown protein (gb]AF19684.10 putative protein similar to unknown protein (pl]T02918); supported by full-length cDNA: Ceres: 26596. putative protein similar to unknown protein (pl]T02918); supported by full-length cDNA: Ceres: 109127. Casesin kinase II beta chain ; supported by cDNA: gi_468283.gb_L22563.1_ATHCKIB VAMP (vesicle-associated membrane protein)-associated protein-like ;supported by full-length cDNA: Ceres:109127. Casesin kinase II beta chain ; supported by cDNA: gi_468283.gb_L22563.1_ATHCKIB VAMP	250243_at 25020_at 25020_at 250222_at 250192_at 250192_at 249912_at 249912_at 249825_at 249825_at 249800_at 249703_at 249703_at 249703_at 249703_at 249703_at 249676_at 249453_at 249453_at 249453_at 249456_at 249278_at 249278_at 249278_at 249278_at 249278_at 249278_at 249278_at 249278_at 249278_at 249278_at 249278_at 249276_at 249276_at 248206_at 248766_at 248743_at 248743_at 248766_at 248743_at 248766_at 248743_at 248766_at 248743_at 248766_at 248743_at 248766_at 248743_at	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8
CCAT box binding factor/ transcription factor Hap2a cobalamin biosynthesis protein putative protein similar to unknown protein (ref[NP_057085.1); supported by full-length cDNA: Ceres:38057. pescadilo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadilo, Homo sapiens, EMBL:U78310 putative protein similar to unknown protein (ref[NP_057085.1); supported by full-length cDNA: Ceres:38057. pescadilo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadilo, Homo sapiens, EMBL:U78310 putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: Ceres:23754. Rvv DNA-helicase-like protein : supported by full-length cDNA: Ceres:11309. putative protein similar to unknown protein (gb AAF20382.1) putative protein similar to unknown protein (gb AAF01580.1) MtN3-like protein : supported by cDNA: gi_3747110_gb_AF095641.1_AF095641 receptor-protein kimase-like protein putative protein similar to unknown protein (pl/I]T40675); supported by cDNA: gi_14335067_gb_AY037213.1_ putative protein similar to unknown protein (gb/AAF0156.1); supported by cDNA: gi_15146184_gb_AY049233.1_ although this cDNA may protein kimase-like v-SNARE AtVT11a ribosomal protein L5 - like ribosomal protein L5, rice putative protein similarity to unknown protein (gb/AAF19684.1) putative protein similarity to UB2P2 protease GI:13172275 from [Arabidopsis thaliana] putative protein contains similarity to UB2P2 protease GI:13172275 from [Arabidopsis thaliana] putative protein similar to unknown protein (gb/AAF19684.1) putative protein somal similarity to unknown protein (gb/AAF19684.1) putative protein similar to unknown protein (gb/	250243_at 250202_at 250202_at 250192_at 250192_at 250192_at 249938_at 249912_at 249835_s_at 249835_s_at 249800_at 249763_at 249701_at 249703_at 249701_at 249676_at 249453_at 249453_at 249453_at 249454_at 249454_at 249233_at 249233_at 249264_at 249122_at 248926_at 248926_at 248926_at 248796_at 248796_at 248796_at 248796_at 248796_at 248796_at 248796_at 248796_at 248796_at 248743_at 248743_at 248713_at	0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8

n	ucleotide-binding protein; supported by cDNA: gi 13430793 gb AF360309.1 AF360309	248462 at	0.8
	utative protein similar to unknown protein (gb AAF03497.1)	248410 at	0.8
	Inform protein ; supported by CDNA: gi 15810027 gb AY054282.1	248289 at	0.8
	utative protein similar to unknown protein (gb AAD26950.1); supported by full-length cDNA: Ceres: 33791.	248261 at	0.8
	ectinesterase ; supported by cDNA: gi 15293286 gb AY051077.1	248263 at	0.8
	rosine aministransferase	248207 at	0.8
	utative protein similar to unknown protein (pir  T05472);supported by full-length cDNA: Ceres:30073.	248148 at	0.8
	haperone GrpE-like protein ;supported by full-length cDNA: Ceres:20790.	248101_at	0.8
	utative protein similar to unknown protein (refNP 004583.1); supported by cDNA; ai 14532719 gb AY039984.1	248106 at	0.8
•	utative protein similar to unknown protein (refINP 032765.1)	248081_at	0.8
	BC transporter-like protein ; supported by cDNA; gi 99641/20 gb AF287699.1 AF287699	247806 at	0.8
	outative protein predicted proteins, Arabidopsis thaliana and Oryza sativa CTB evidebudgenea II. (2.4 dibudgenu 2.6 budgenea 4.6 bestella grafhage, like protein CTB evidebudgenea II. (2.4 dibudgenu 2.6 budgenea 4.6 bestella grafhage.	247741_at	0.8
	3TP cyclohydrolase II / 3,4-dihydroxy-2-butanone-4-phoshate synthase - like protein GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone-4-phoshate :		0.8
	outative protein predicted protein, Arabidopsis thaliana	247556_at	0.8
	I-protein promoter binding factor-like protein	247452_at	0.8
	lutaredoxin-like protein ; supported by full-length cDNA: Ceres: 96557.	247418_at	0.8
	nknown protein ;supported by full-length cDNA: Ceres:114951.	247372_at	0.8
	dc2-like protein kinase-like protein supported by full-length cDNA: Ceres: 22817.	247334_at	0.8
	utative protein contains similarity to RNA-binding protein	247276_at	0.8
	istone acetyltransferase	247238_at	0.8
	utative protein contains similarity to unknown protein (gb AAF47170.1);supported by full-length cDNA: Ceres:13188.	247209_at	0.8
	putative membrane protein hypothetical protein F19K16.31 - Arabidopsis thaliana, EMBL:AC011717	246945_s_at	0.8
	putative protein predicted protein, Oryza sativa	246909_at	0.8
	putative protein phytochrome-associated protein 1, Arabidopsis thaliana, EMBL:AF088281;supported by full-length cDNA: Ceres:2499.	246861_at	0.8
	butative amino acid aminotransferase branched-chain amino acid aminotransferase - Pseudomonas aeruginosa, SWISSPROT:ILVE_PSEAE; suppc	246786_at	0.8
;	5-enolpyruvylshikimate-3-phosphate (EPSP) synthase, putative similar to 5-enolpyruvylshikimate-3-phosphate (EPSP) synthase GI:2583124 from (#2	246627_s_at	0.8
1	E2F transcription factor -like protein E2F protein, Triticum sp., EMBL:TSP238590	246568_at	0.8
- 1	Jbiquitin-fusion degradation protein-like ubiquitin-fusion degradation protein - Homo sapiens, EMBL:AF043117; supported by cDNA: gi_15215855_g	246541_at	0.8
1	nositol 1,3,4-Trisphosphate 5/6 kinase ;supported by full-length cDNA: Ceres:30653.	246451_at	0.8
s	yntaxin homologue ;supported by full-length cDNA: Ceres:8257.	246453_at	0.8
١	ND40-repeat protein transducin homolog sazD - Homo sapiens, EMBL:U02609; supported by cDNA: gi 15810484 gb AY056281.1	246457_at	0.8
(	quinone oxidoreductase -like protein probable quinone oxidoreductase (EC 1.6.5.5) P1, Arabidopsis thaliana, PIR:S57611	246463 at	0.8
5	ugar transporter - like protein D-XYLOSE-PROTON SYMPORTER (D-XYLOSE TRANSPORTER), Lactobacillus brevis, SWISSPROT:XYLT LACE	246466 at	0.8
	ulfate transporter ATST1; supported by cDNA: gi 2285884 dbj D89631.1 D89631	246310 at	0.8
	G-protein, putative contains Pfam profile: PF00503: G-protein alpha subunit	246312 at	0.8
	nknown protein	246287 at	0.8
	nknown protein	246288 at	0.8
	mino acid permease, putative contains Pfam profile: PF00324: Amino acid permease	246260 at	0.8
	ypothetical protein	246262 at	0.8
	utative protein	246234 at	0.8
	utative protein predicted protein, Oryza sativa; supported by cDNA: gi_15081722_gb_AY048254.1_	246160 at	0.8
	utative protein BEM46 bem1/bud5 suppressor, Schizosacharomyces pombe, bem1/bud5 suppressor, EMBL:SP29892;supported by full-length cD		0.8
	ev interacting protein miss - like rev interacting order miss. Schizosaccharomyces poner modus superised, LindLor 2004, supported by full-length cDNA: Ceres: 303		0.8
		245928 s at	0.8
	Sector adverse songer protein vspr , supported of numerical context sources. Adverse sources adverse adverse adverse sources adverse sources adverse adverse adverse sources adverse adver	245929 at	0.8
	acono denyarogenase ince protein acono denyarogenase o, vita vitinera, Limbura resolos opponed by rainengui conve. Ceres, 130000. denosine nucleotide translocator ; supported by cDNA; gi 15292846 gb AY050857.1	_	0.8
		245854_at	
	protein kinase, putative similar to protein kinase GI:717180 from (Arabidopsis thaliana)	245825_at	0.8
	nknown protein contains similarity to obtusifoliol 14-alpha-demethylase (CYP51) GB:Y09292 GI:1707854 from [Triticum aestivum];supported by full-		0.8
	nknown protein ;supported by full-length cDNA: Ceres:8255.	245780_at	0.8
	nknown protein ;supported by full-length cDNA: Ceres:39155.	245730_at	0.8
	urine permease identical to purine permease GI:7620007 from [Arabidopsis thaliana]; supported by cDNA: gi_7620006_gb_AF078531.1_AF078531	_	0.8
	nknown protein similar to putative Tub family protein GI:3738302 from [Arabidopsis thaliana]	245633_at	0.8
	ypothetical protein	245601_at	0.8
	ypothetical protein	245618_at	0.8
	ET1 like protein	245496_at	0.8
h	ypothetical protein	245439_at	0.8
	utative protein	245418_at	0.8
1	ATP-dependent Clp protease proteolytic subunit (ClpR4), putative similar to ATP-dependent Clp protease proteolytic subunit GI:7264063 from [Syne		0.8
E	expressed protein ; supported by full-length cDNA: Ceres: 16319.	245373_s_at	0.8
la	actate dehydrogenase (LDH1) ;supported by full-length cDNA: Ceres:33509.	245324_at	0.8
	arnesyl-pyrophosphate synthetase FPS2 ; supported by cDNA: gi_1146162_gb_L46349.1_ATHFPS2R	245301_at	0.8
	anscription factor like protein ; supported by cDNA: gi_16226918_gb_AF428368.1_AF428368	245271_at	0.8
	viral resistance protein, putative similar to viral resistance protein GI:7110565 from [Arabidopsis thaliana]	245219_at	0.8
е	thylene response sensor (ERS) identical to GB:U21952:ATU21952; supported by cDNA: gi_15450903_gb_AY054532.1_	245098_at	0.8
р	utative cytochrome P450 ; supported by cDNA: gi_15810181_gb_AY056105.1_	245101_at	0.8
р	utative cytochrome P450	245075_at	0.8
ri	bosomal protein L16	244983_at	0.8
ri	bosomal protein S12 (trans-splice part 2 of 2)	244940 at	0.8
h	ypothetical protein similar to polyketide hydroxylases from several bacterial species	257410_at	0.8
h	ypothetical protein Similar to gi 1573829 HI0816 aminopeptidase P homolog (pepP) from Haemophilus influenzae genome gb U32764	263707_at	0.7
E	xpressed protein ; supported by full-length cDNA: Ceres: 36399.	262782 at	0.7
	nknown protein ; supported by cDNA: gi 16930706 gb AF436837.1 AF436837	261130 at	0.7
E	xpressed protein ; supported by cDNA; gi 15810240 gb AY056159.1	257010 at	0.7
	utative protein retinoblastoma binding protein 2, Homo sapiens, PIR:I78879	254464 at	0.7
	putative protein protein phosphatase 2C, Medicago sativa, PID:g2582800	253512 at	0.7
	putative protein ThiJ protein. Escherichia coli, PIR:H64771	253320 at	0.7
	sutative protein predicted proteins, Arabidopsis thaliana	251809 at	0.7
	utative protein predicted proteins, Homo sapiens, Drosophila melanogaster and Caenorhabditis elegans.	250156 at	0.7
	utative protein proteins similarity to TNA-damage-inducible protein P	249016 at	0.7
	bilgopeptide transporter -like protein oligopeptide transporter (LeOPT1), Lycopersicon esculentum, EMBL:AF016713	246566 at	0.7
	ngopeptide dansporter interprisent protein ongopeptide dansporter (LeCP + 1), Eycoperation esculardini, EvideAro tor 13 bijquitin-specific protease 8 (UBP8), putative similar to ubiquitin-specific protease 8 partial sequence Gi:1193469 [Arabidopsis thaliana]	240500_at 245683 at	0.7
	Junquim-specific protease o (Opro), putative similar to doiquim-specific protease o partial sequence 01. 1993409 (Alabidopsis unaliana) Arabidopsis thaliana (REF=U37281 / DEF=actin-2 mRNA, complete cdS /LEN=1637 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 pri-		0.7
	Adduopsis inaliaria (AEF-037261/DEF-adurt-1mirka), complete cus (AEA+03762, -M, -STepresent utanscript regions 3 prime, micule, and 3 pri- nknown protein similar to GP[522127]qni[PID]e349073[235639 and GP[2224677]qni]PID[10121664]AB002366	267609 at	0.7
	nknown protein similar to GP/522127 (gni(PID/6349075)2.35639 and GP/2224677 (gni(PID/01021664)AB002366 utative VP1/ABI3 family regulatory protein	267609_at 267519_at	0.7
	utative lipase ; supported by full-length cDNA: Ceres: 207043.	267496_at	0.7
	utative glutaredoxin ;supported by full-length cDNA: Ceres:39560.	267497_at	0.7
p	utative protein kinase contains a protein kinase domain profile (PDOC00100)	267422_at	0.7

G protein alpha subunit 1 (GPA1) identical to GB:M32887; supported by cDNA: gi_14326501_gb_AF385704.1_AF385704	267375_at	0.7
hypothetical protein	267378_at	0.7
putative isoamylase	267356_at	0.7
unknown protein ; supported by cDNA: gi_14194142_gb_AF367277.1_AF367277	267214_at	0.7
putative beta-alanine-pyruvate aminotransferase ;supported by full-length cDNA: Ceres:147543.	267035_at	0.7
hypothetical protein predicted by genefinder	266938_at	0.7
putative small GTP-binding protein contains an ATP/GTP-binding site motif A (P-loop); contains an ADP-ribosylation factors family signature for protein		0.7
putative nucleotide-binding protein ;supported by full-length cDNA: Ceres:33511.	266801_at	0.7
unknown protein predicted by genefinder and genscan; supported by cDNA: gi_16612270_gb_AF439832.1_AF439832	266738_at	0.7
	266720_s_at	0.7
unknown protein	266721_at	0.7
putative Na+-dependent inorganic phosphate cotransporter profile putation dependent in constant in contracted by cDNA: di 14522650, db AV0300541	266672_at	0.7 0.7
cyclic nucleotide and calmodulin-regulated ion channel ; supported by cDNA: gi_14532659_gb_AY039954.1_ unknown protein ; supported by cDNA: gi 16024935 gb AY050658.1	266520_at 266501_at	0.7
hypothetical protein The first 3 exons is identical to that of GB:AJ224957. This gene appears to be a truncated version of that in GB:AJ224957.; supp		0.7
putative protein the mate occurs is lacing and inter to CB-322-507. In gene appendix the protein tension of inter to CB-322-507, support protein tension of inter to CB-322-507.		0.7
plutation est-transferase identical to GB:X89216;supported by full-length cDNA: Ceres:6528.	266299 at	0.7
	266075 s at	0.7
putative glutamate/ornithine acetyltransferase ;supported by full-length cDNA: Ceres:121873.	265965 at	0.7
	265941 s at	0.7
unknown protein ;supported by full-length cDNA: Ceres:104853.	265867 at	0.7
unknown protein ; supported by cDNA: gi 15810154 gb AY056142.1	265875 at	0.7
proline iminopeptidase identical to GP:1710151:U72711; supported by cDNA: gi 15450388 gb AY052295.1	265575 at	0.7
unknown protein	265576_at	0.7
unknown protein	265583_at	0.7
unknown protein predicted by genscan	265495_at	0.7
Expressed protein ; supported by cDNA: gi_14335135_gb_AY037247.1_	265474_at	0.7
putative AAA-type ATPase similar to 26S proteosome regulatory subunit 8; supported by cDNA: gi_15450827_gb_AY054494.1_	265340_at	0.7
unknown protein predicted by genefinder	265283_at	0.7
putative ribose phosphate pyrophosphokinase ;supported by full-length cDNA: Ceres:35051.	265270_at	0.7
beta-fructosidase nearly identical to beta-fructosidase GB:CAA67560 GI:1429209 (Arabidopsis thaliana); supported by cDNA: gi_14517549_gb_AY0		0.7
putative b-keto acyl reductase similar to GB:AAB82765, protein is involved with cuticular wax biosynthesis	265012_at	0.7
hypothetical protein predicted by genemark.hmm	264936_at	0.7
unknown protein ;supported by full-length cDNA: Ceres:99231.	264848_at	0.7
unknown protein similar to F5J6.8 and C. elegans C42D8.3;supported by full-length cDNA: Ceres:2578.	264850_at	0.7
putative indole-3-acetate beta-glucosyltransferase similar to GB:AAB64022; supported by cDNA: gi_14423541_gb_AF387008.1_AF387008	264873_at 264696 at	0.7 0.7
unknown protein unknown protein	264707 at	0.7
hypothetical protein similar to hypothetical protein GI:7019676 from [Arabidopsis thaliana]	264629 at	0.7
hypothetical protein similar to anytorin like protein GI:7268141 from [rabidopsis thaliana]; supported by cDNA: gi 14194106 gb AF367259.1 AF367	_	0.7
unknown protein EST gb/N65787 comes from this gene	264437 at	0.7
putative sensory transduction histidine kinase similar to GB:AAD21777; similar to ESTs gb/AA712891 and gb/AA042438; supported by cDNA: gi_13{	_	0.7
putative myb-related transcription factor Similar to myb-related transcription factor (THM27) gb X95296 from Solanum lycopersicum. ESTs gb T420C		0.7
unknown protein	264154 at	0.7
hypothetical protein predicted by genemark.hmm	264133 at	0.7
latex-abundant protein, putative similar to latex-abundant protein GI:4235430 from [Hevea brasiliensis]	264120_at	0.7
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_15081627_gb_AY048206.1_	264098_at	0.7
unknown protein	264031_at	0.7
putative peroxidase ;supported by full-length cDNA: Ceres:113695.	264001_at	0.7
hypothetical protein predicted by genefinder	263939_at	0.7
	263878_s_at	0.7
putative glucan synthase	263891_at	0.7
unknown protein ;supported by cDNA: gi_15450510_gb_AY052357.1_	263787_at	0.7
putative ubiquitin activating enzyme	263747_at	0.7
26S proteasome regulatory subunit S2 contains an APC-complex (cyclosome) and proteasome component repeat (PS50248); supported by cDNA: (		0.7
putative ethylene receptor (ERS2) EST gb W43451 comes from this gene	263653_at	0.7
unknown protein	263654_at	0.7
hypothetical protein predicted by genscan	263526_at	0.7
putative ribonuclease E	263322_at	0.7
putative glyoxalase II Expressed particle : supported by cDNA: gi 15292050, gb, AV050950.1	263243_at	0.7
Expressed protein ; supported by cDNA: gi_15293050_gb_AY050959.1_ unknown protein similar to hypothetical protein GB:AAF27089 GI:6730668 from (Arabidopsis thaliana)	263210_at 263014_at	0.7 0.7
unknown protein similar to hypothetical protein GL-ver 27000 CL-050000 non (vitabilopsis thailana)	262969 at	0.7
transcription initiation factor, putative similar to transcription initiation factor iif, beta subunit GB:CAA22523 GI:4049502 from [Schizosaccharomyces	262950 at	0.7
gama-tocopherol methyltransferase almost identical to gamma-tocopherol methyltransferase GI:4106538 from [Arabidopsis thaliana];supported by	262875 at	0.7
ammonium transporter, pultative similar to ammonium transporter GI:5880357 from [Arabidopsis thaliana]; supported by cDNA: gi 4324713 gb AF	262883 at	0.7
putative cytochrome P450 monooxygenase identical to gb/D78605 cytochrome P450 monooxygenase from Arabidopsis thaliana and is a member of		0.7
unknown protein	262775 at	0.7
putative clathrin-coat assembly protein similar to gb L26291 clathrin-associated protein unc-101 from Caenorhabditis elegans and is a member of the	262787_at	0.7
unknown protein ESTs gb F15498, gb H37515, gb T41906, gb T22448, gb W43356 and gb T20739 come from this gene; supported by full-length cD	262709_at	0.7
vacuolor sorting protein 35, putative similar to vacuolar sorting protein 35 GB:AAF02778 GI:6049847 [Homo sapiens]	262695_at	0.7
integral membrane protein, putative contains Pfam profile: PF00892 Integral membrane protein DUF6	262623_at	0.7
unknown protein ESTs gb F20110 and gb F20109 come from this gene	262577_at	0.7
tuftelin-interacting-like protein Similar to tuftelin-interacting proteins [Mus musculus] (gi]3851164 and gi[5059423)	262524_at	0.7
threenine synthase, putative similar to threenine synthase GI:4850369 from [Arabidopsis thaliana]	262380_at	0.7
Niemann-Pick C disease protein-like protein similar to Niemann-Pick C disease protein GB:AAB63982 GI:2276463 from [Homo sapiens]	262264_at	0.7
unknown protein ; supported by cDNA: gi_13605689_gb_AF361826.1_AF361826	262272_at	0.7
hypothetical protein predicted by genemark.hmm	262237_at	0.7
AP2 domain containing protein, putative similar to AP2 domain containing protein GI:2281649 from [Arabidopsis thaliana];supported by full-length cC		0.7
unknown protein (supported by full-length cDNA: Ceres:3024.	262171_at	0.7
cytochrome c oxidase subunit, putative similar to cytochrome c oxidase subunit GI:267 from [Bos taurus];supported by full-length cDNA: Ceres:2536 unknown sertain		0.7
unknown protein BTG1 binding factor 1, putative similar to BTG1 binding factor 1 GI:6016012 from [Homo sapiens]	261880_at	0.7 0.7
metal ion transporter, putative similar to metal ion transporter GI:5853313 from [Arabidopsis thaliana]	261841_at 261845 at	0.7
hypothetical protein contains similarity to amino acid permease GI:7415521 from [Oryza sativa]		0.7
hypothetical protein similar to hypothetical protein GB:AAE25977 GI:6714281 from [Arabidopsis thaliana]	261785_at 261701_at	
hypothetical protein similar to hypothetical protein GB:AAF25977 GI:6714281 from [Arabidopsis thaliana] unknown protein similar to hypothetical protein GB:AAF26001 GI:6714305 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:94234.	261785_at 261701_at 261669_at	0.7 0.7

unknown protein similar to putative esterase GB:AAD17422 GI:4335745 from [Arabidopsis thaliana]	261607_at	0.7
unknown protein ;supported by full-length cDNA: Ceres:8976.	261566_at	0.7
protein kinase, putative contains Pfam profile: PF00069 Eukaryotic protein kinase domain	261547_at	0.7
unknown protein	261467_at	0.7
unknown protein	261469_at	0.7
protein kinase, putative (fragment) similar to GB:BAA94509 from [Populus nigra]	261436_at	0.7
unknown protein ;supported by full-length cDNA: Ceres:920.	261377_at	0.7
hypothetical protein predicted by genemark.hmm	261323_at	0.7
hypothetical protein predicted by genemark.hmm	261301_at	0.7
putative NPK1-related protein kinase 2 predicted by genemark.hmm	261312 at	0.7
unknown protein ;supported by full-length cDNA: Ceres:3807.	261154 at	0.7
hypothetical protein contains similarity to transcription factor TFIID GB:U57693 GI:1373376 from (Homo sapiens); supported by cDNA: gi 15810158		0.7
	261044 at	0.7
	261008 at	0.7
	260979 at	0.7
	260949 at	0.7
ATP-dependent Clp protease proteolytic subunit (ClpP5) identical to nClpP1 GB:BAA82065 GI:5360579 from [Arabidopsis thaliana]; supported by full		0.7
	260842 at	0.7
······································	260817 at	0.7
	260455 at	0.7
	260373 at	0.7
	260311 at	0.7
putative U3 small nucleolar ribonucleoprotein protein identical to putative U3 small nucleolar ribonucleoprotein GB:AAF07373 (Arabidopsis th	_	0.7
putative monodehydroascorbate reductase similar to monodehydroascorbate reductase GB:AAD28178 [Brassica juncea]; supported by cDNA; gi 14		0.7
	260302 at	0.7
	259993 at	0.7
hydroxypruvate reductase (HPR) identical to hydroxypyruvate reductase (HPR) GB:D85339 [Arabidopsis thaliana] (Plant Cell Physiol 1997 Apr;38(4		0.7
	259874 at	0.7
	259875 s at	0.7
	259882 at	0.7
	259794 at	0.7
	259766 at	0.7
acyl-CoA synthetase, putative similar to City 03032 from (Brassica napus) (Plant Mol. Biol. 33 (5), 911-922 (1997)); supported by cDNA: gi 145326		0.7
	259542 at	0.7
		0.7
	259519_at	
	259500_at	0.7
hypothetical protein contains similarity to ribosomal protein S15; supported by cDNA: gi_13605576_gb_AF361614.1_AF361614 type 2A protein serine/threonine phosphatase 55 kDa B regulatory subunit almost identical to type 2A protein serine/threonine phosphatase 55 kDa E	259505_at	0.7
	_	0.7 0.7
	259382_s_at	
	259241_at	0.7
	259159_at	0.7
thioglucosidase 3D precursor identical to thioglucosidase 3D precursor GB:S57621 [Arabidopsis thaliana]; supported by cDNA: gi_14423459_gb_AF but the state is a state of the		0.7
	258856_at	0.7 0.7
putative helicase similar to C-terminal half of transcription-repair coupling factor (TRCF) GB:Q55750 [Synechocystis PCC6803]; contains Pfam profile putative MVB related archite a july collected particle (PCCA07300)		0.7
	258723_at	
	258689_at	0.7
	258651_at	0.7
	258554_at	0.7
	258474_at	0.7
	258430_at	0.7
PP1/PP2A phosphatases pleiotropic regulator PRL2 identical to GB:Q39190 from [Arabidopsis thaliana]; supported by cDNA: gi_15809827_gb_AY00	_	0.7
	258324_at	0.7
putative long-chain acyL-GoA synthetase similar to malonyl CoA synthetase GB:AAF28840 from [Bradyrhizoblum] aponicum]; supported by full-length		0.7
	258158_at	0.7
	258091_at	0.7
	258071_s_at	0.7
cysteine proteinase non-consensus AT acceptor site at exon 3; contains similarity to cysteine protease CYP1 GI:2828252, TDI-65 GI:5726641 from		0.7
fertilization-independent endosperm protein identical to GB:AAD23584 from [Arabidopsis thaliana]; supported by cDNA: gi_4567094_gb_AF129516.		0.7
	257956_at	0.7
	257903_at	0.7
transcriptional regulator protein, putative similar to ATAN11 GB:AAC18912 [Arabidopsis thaliana] (Genes Dev. 11 (11), 1422-1434 (1997)); contains		0.7
	257783_at	0.7
	257730_at	0.7
	257652_at	0.7
chaperonin, putative similar to CHAPERONIN CPN60-2, MITOCHONDRIAL PRECURSOR GB:Q05046 from [Cucurbita maxima];supported by full-le		0.7
	257285_at	0.7
	257250_at	0.7
	257262 at	0.7
4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein, putative similar to ThiJ GB:AAA82704 [Escherichia coli]; likely encodes tw		0.7
Even and a set in a superior of the full learning DNA. On set 0004	257216_at	0.7
	257216_at 257169_at	~ -
unknown protein ; supported by cDNA: gi_15215846_gb_AY050453.1_	257216_at 257169_at 257095_at	0.7
unknown protein ; supported by cDNA: gi_15215846_gb_AY050453.1_ squamosa promoter binding protein-like 5 identical to GB:CAB56571 from [Arabidopsis thaliana]	257216_at 257169_at 257095_at 257051_at	0.7
unknown protein ; supported by cDNA: gi_15215846_gb_AY050453.1_ squamosa promoter binding protein-like 5 identical to GB:CAB56571 from [Arabidopsis thaliana] zinc finger protein, putative contains Pfam profiles: PF00097 Zinc finger, C3HC4 type (RING finger) (2 copies)	257216_at 257169_at 257095_at 257051_at 257062_at	0.7 0.7
unknown protein ; supported by cDNA: gi_15215846_gb_AY050453.1_ squamosa promoter binding protein-like 5 identical to GB:CAB56571 from [Arabidopsis thaliana] zinc finger protein, putative contains Pfam profiles: PF00097 Zinc finger, C3HC4 type (RING finger) (2 copies) adenosine triphosphatase, putative similar to vacuolar adenosine triphosphatase subunit D GB:AAC83085 from [Mus musculus] 2	257216_at 257169_at 257095_at 257051_at 257062_at 256988_s_at	0.7 0.7 0.7
unknown protein ; supported by cDNA: gi_15215846_gb_AY050453.1_ squamosa promoter binding protein-like 5 identical to GB:CAB56571 from [Arabidopsis thaliana] zinc finger protein, putative contains Pfam profiles: PF00097 Zinc finger, C3HC4 type (RING finger) (2 copies) adenosine triphosphatase, putative similar to vacuolar adenosine triphosphatase subunit D GB:AAC83085 from [Mus musculus] unknown protein	257216_at 257169_at 257095_at 257051_at 257062_at 256988_s_at 256915_at	0.7 0.7 0.7 0.7
unknown protein ; supported by cDNA: gi_15215846_gb_AY050453.1_ squamosa promoter binding protein-like 5 identical to GB:CAB56571 from [Arabidopsis thaliana] zinc finger protein, putative contains Pfam profiles: PF00097 Zinc finger, C3HC4 type (RING finger) (2 copies) adenosine triphosphatase, putative similar to vacuolar adenosine triphosphatase subunit D GB:AAC83085 from [Mus musculus] unknown protein cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450	257216_at 257169_at 257095_at 257051_at 257062_at 256988_s_at 256915_at 256870_at	0.7 0.7 0.7 0.7 0.7
unknown protein ; supported by cDNA: gi_15215846_gb_AY050453.1_ squamosa promoter binding protein-like 5 identical to GB:CAB56571 from [Arabidopsis thaliana] zinc finger protein, putative contains Pfam profiles: PF00097 Zinc finger, C3HC4 type (RING finger) (2 copies) adenosine triphosphatase, putative similar to vacuolar adenosine triphosphatase subunit D GB:AAC83085 from [Mus musculus] unknown protein cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450 unknown protein similar to CW14 GB:BAA87958 from [Arabidopsis thaliana]; supported by cDNA: gi_15450961_gb_AY054561.1_	257216_at 257169_at 257095_at 257051_at 257062_at 256988_s_at 256915_at 256870_at 256747_at	0.7 0.7 0.7 0.7 0.7 0.7
unknown protein ; supported by cDNA: gi_15215846_gb_AY050453.1_ squamosa promoter binding protein-like 5 identical to GB:CAB56571 from [Arabidopsis thaliana] zinc finger protein, putative contains Pfam profiles: PF00097 Zinc finger, C3HC4 type (RING finger) (2 copies) adenosine triphosphatase, putative similar to vacuolar adenosine triphosphatase subunit D GB:AAC83085 from [Mus musculus] unknown protein cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450 unknown protein simportein 5 GB:BAA87958 from [Arabidopsis thaliana]; supported by cDNA: gi_15450961_gb_AY054561.1_ unknown protein ;supported by full-length cDNA: Ceres:38478.	257216_at 257169_at 257095_at 257095_at 257062_at 256988_s_at 256915_at 256970_at 256970_at 256747_at 256663_at	0.7 0.7 0.7 0.7 0.7 0.7 0.7
unknown protein ; supported by cDNA: gi_15215846_gb_AY050453.1_ squamosa promoter binding protein-like 5 identical to GB:CAB56571 from [Arabidopsis thaliana] zinc finger protein, putative contains Pfam profiles: PF00097 Zinc finger, C3HC4 type (RING finger) (2 copies) adenosine triphosphatase, putative similar to vacuolar adenosine triphosphatase subunit D GB:AAC83085 from [Mus musculus] unknown protein cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450 unknown protein similar to CW14 GB:BAA87958 from [Arabidopsis thaliana]; supported by cDNA: gi_15450961_gb_AY054561.1_ unknown protein ;supported by full-length cDNA: Ceres:38478. hypothetical protein predicted by genemark.hmm	257216_at 257169_at 257055_at 257051_at 257062_at 256988_s_at 256915_at 256670_at 2566747_at 256663_at 256673_at	0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7
unknown protein ; supported by cDNA: gi_15215846_gb_AY050453.1_ squamosa promoter binding protein-like 5 identical to GB:CAB56571 from [Arabidopsis thaliana] zinc finger protein, putative contains Pfam profiles: PF00097 Zinc finger, C3HC4 type (RING finger) (2 copies) adenosine triphosphatase, putative similar to vacuolar adenosine triphosphatase subunit D GB:AAC83085 from [Mus musculus] unknown protein cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450 unknown protein similar to CW14 GB:BAA87958 from [Arabidopsis thaliana]; supported by cDNA: gi_15450961_gb_AY054561.1_ unknown protein ; supported by full-length cDNA: Ceres:38478. hypothetical protein predicted by genemark.hmm ABC transporter, putative contains Pfam profile: PF00005: ABC transporter 2	257216_at 257169_at 257095_at 257051_at 257062_at 256915_at 256970_at 256870_at 256663_at 256673_at 256573_at	0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7
unknown protein ; supported by cDNA: gi_15215846_gb_AY050453.1_ squamosa promoter binding protein-like 5 identical to GB:CAB56571 from [Arabidopsis thaliana] zinc finger protein, putative contains Pfam profiles: PF00097 Zinc finger, C3HC4 type (RING finger) (2 copies) adenosine triphosphatase, putative similar to vacuolar adenosine triphosphatase subunit D GB:AAC83085 from [Mus musculus] unknown protein cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450 unknown protein isupported by full-length cDNA: Ceres:38478. hypothetical protein predicted by genemark.hmm ABC transporter, putative contains Pfam profile: PF00005: ABC transporter arginine N-methyltransferase 3, putative similar to arginine N-methyltransferase 3 GB:AAC40158 [Rattus norvegicus]	257216_at 257169_at 257095_at 257051_at 257051_at 2560915_at 2560915_at 2560910_at 256670_at 256670_at 256673_at 256573_at 256308_s_at 256328_at	0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7
unknown protein ; supported by cDNA: gi_15215846_gb_AY050453.1_ squamosa promoter binding protein-like 5 identical to GB:CAB56571 from [Arabidopsis thaliana] zinc finger protein, putative contains Pfam profiles: PF00097 Zinc finger, C3HC4 type (RING finger) (2 copies) adenosine triphosphatase, putative similar to vacuolar adenosine triphosphatase subunit D GB:AAC83085 from [Mus musculus] unknown protein cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450 unknown protein is similar to CW14 GB:BAA87958 from [Arabidopsis thaliana]; supported by cDNA: gi_15450961_gb_AY054561.1_ unknown protein predicted by genemark.hmm ABC transporter, putative contains Pfam profile: PF00005: ABC transporter arginine N-methyltransferase 3, putative similar to arginine N-methyltransferase 3 GB:AAC40158 [Rattus norvegicus] sulphate transporter, putative similar to high affinity sulphate transporter GB:X96431 GI:1217966 [Hordeum vulgare]; supported by cDNA: gi_119334	257216_at 257065_at 257095_at 257051_at 257062_at 256988_s_at 256976_at 256970_at 256747_at 256663_at 256573_at 256308_s_at 256284_at	0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7
unknown protein ; supported by cDNA: gi_15215846_gb_AY050453.1_ squamosa promoter binding protein-like 5 identical to GB:CAB56571 from [Arabidopsis thaliana] zinc finger protein, putative contains Pfam profiles: PF00097 Zinc finger, C3HC4 type (RING finger) (2 copies) adenosine triphosphatase, putative similar to vacuolar adenosine triphosphatase subunit D GB:AAC83085 from [Mus musculus] unknown protein cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450 unknown protein similar to CW14 GB:BAA87958 from [Arabidopsis thaliana]; supported by cDNA: gi_15450961_gb_AY054561.1_ unknown protein ; putative contains Pfam profile: PF00067 cytochrome P450 unknown protein ; supported by full-length cDNA: Ceres:38478. hypothetical protein predicted by genemark.hmm ABC transporter, putative contains Pfam profile: PF00005: ABC transporter arginine N-methyltransferase 3, putative similar to arginine N-methyltransferase 3 GB:AAC40158 [Rattus norvegicus] sulphate transporter, putative similar to high affinity sulphate transporter GB:X96431 GI:1217966 [Hordeum vulgare]; supported by cDNA: gi_119334 beta-fructofuranosidase identical to beta-fructofuranosidase GI:6683112 from [Arabidopsis thaliana]; supported by cDNA: gi_6683111_dbj_AB02931	257216_at 257169_at 257095_at 257095_at 257051_at 256086_s_at 256087_at 2560747_at 256673_at 256573_at 256573_at 25628_at 256244_at 256244_at	0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7
unknown protein ; supported by cDNA: gi_15215846_gb_AY050453.1_ squamosa promoter binding protein-like 5 identical to GB:CAB56571 from [Arabidopsis thaliana] zinc finger protein, putative contains Pfam profiles: PF00097 Zinc finger, C3HC4 type (RING finger) (2 copies) adenosine triphosphatase, putative similar to vacuolar adenosine triphosphatase subunit D GB:AAC83085 from [Mus musculus] unknown protein cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450 unknown protein similar to CW14 GB:BAA87958 from [Arabidopsis thaliana]; supported by cDNA: gi_15450961_gb_AY054561.1_ unknown protein ;supported by full-length cDNA: Ceres:38478. hypothetical protein predicted by genemark.hmm ABC transporter, putative contains Pfam profile: PF00005: ABC transporter ABC transporter, putative contains Pfam profile: PF00005: ABC transporter arginine N-methyltransferase 3, putative similar to arginine N-methyltransferase 3 GB:AAC40158 [Rattus norvegicus] sulphate transporter, putative similar to high affinity sulphate transporter GB:X96431 GI:1217966 [Hordeum vulgare]; supported by cDNA: gi_11934 beta-fructofuranosidase identical to beta-fructofuranosidase GI:6683112 from [Arabidopsis thaliana]; supported by cDNA: gi_6683111_dbj_AB02931 unknown protein ;supported by full-length cDNA: Ceres:38751.	257216_at 257169_at 257095_at 257095_at 257051_at 2560848_s_at 256915_at 256870_at 2566770_at 2566773_at 256573_at 256573_at 256288_at 256244_at 256244_at 256017_at	0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7
unknown protein ; supported by cDNA: gi_15215846_gb_AY050453.1_ squamosa promoter binding protein-like 5 identical to GB:CAB56571 from [Arabidopsis thaliana] zinc finger protein, putative contains Pfam profiles: PF00097 Zinc finger, C3HC4 type (RING finger) (2 copies) adenosine triphosphatase, putative similar to vacuolar adenosine triphosphatase subunit D GB:AAC83085 from [Mus musculus] unknown protein cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450 unknown protein isupported by full-length cDNA: Ceres:38478. hypothetical protein predicted by genemark.hmm ABC transporter, putative contains Pfam profile: PF00005: ABC transporter arginine N-methyltransferase 3, putative similar to arginine N-methyltransferase 3 GB:AAC40158 [Rattus norvegicus] sulphate transporter, putative similar to high affinity sulphate transporter GB:X96431 GI:1217966 [Hordeum vulgare]; supported by cDNA: gi_11934 beta-fructofuranosidase identical to beta-fructofuranosidase GI:6863112 from [Arabidopsis thaliana]; supported by cDNA: gi_6683111_dbj_AB02931 <sup>1</sup> unknown protein; supported by pull-length cDNA: Ceres:38751. inositol polyphosphates 5-phosphatase II, putative similar to insoitol polyphosphate 5-phosphatase II GI:9945302 from [Mus musculus]; supported by	257216_at 257169_at 257095_at 257095_at 257051_at 257062_at 256915_at 256970_at 256870_at 256670_at 256677_at 256673_at 256038_s_at 256288_at 256284_at 256017_at 256017_at 255098_at	0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7
unknown protein ; supported by cDNA: gi_15215846_gb_AY050453.1_ squamosa promoter binding protein-like 5 identical to GB:CAB56571 from [Arabidopsis thaliana] zinc finger protein, putative contains Pfam profiles: PF00097 Zinc finger, C3HC4 type (RING finger) (2 copies) adenosine triphosphatase, putative similar to vacuolar adenosine triphosphatase subunit D GB:AAC83085 from [Mus musculus] unknown protein cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450 unknown protein similar to CW14 GB:BAA87958 from [Arabidopsis thaliana]; supported by cDNA: gi_15450961_gb_AY054561.1_ unknown protein similar to CW14 GB:BAA87958 from [Arabidopsis thaliana]; supported by cDNA: gi_15450961_gb_AY054561.1_ unknown protein predicted by genemark.hmm ABC transporter, putative contains Pfam profile: PF00005: ABC transporter arginine N-methyltransferase 3, putative similar to arginine N-methyltransferase 3 GB:AAC40158 [Rattus norvegicus] sulphate transporter, putative similar to high affinity sulphate transporter GB:X96431 GI:1217966 [Hordeum vulgare]; supported by cDNA: gi_119334 beta-fructofuranosidase identical to beta-fructofuranosidase GI:6683112 from [Arabidopsis thaliana]; supported by cDNA: gi_6683111_dbj_AB02931! unknown protein ; supported by full-length cDNA: Ceres:38751. inositol polyphosphate 5-phosphatase II, putative similar to inostol polyphosphate 5-phosphatase II GI:9945302 from [Mus musculus]; supported by glycyl tRNA synthetase, putative similar to glycyl tRNA synthetase GI:577711 from [Homo sapiens]; supported by full-length cDNA: Ceres:29666.	257216_at 257195_at 257095_at 257095_at 257095_at 256085_s_at 256085_at 256070_at 256673_at 256673_at 256273_at 256288_at 256284_at 256150_at 256244_at 256000_at	0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7
unknown protein ; supported by cDNA: gi_15215846_gb_AY050453.1_ squamosa promoter binding protein-like 5 identical to GB:CAB56571 from [Arabidopsis thaliana] zinc finger protein, putative contains Pfam profiles: PF00097 Zinc finger, C3HC4 type (RING finger) (2 copies) adenosine triphosphatase, putative similar to vacuolar adenosine triphosphatase subunit D GB:AAC83085 from [Mus musculus] unknown protein cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450 unknown protein similar to CW14 GB:BAA87958 from [Arabidopsis thaliana]; supported by cDNA: gi_15450961_gb_AY054561.1_ unknown protein similar to CW14 GB:BAA87958 from [Arabidopsis thaliana]; supported by cDNA: gi_15450961_gb_AY054561.1_ unknown protein predicted by genemark.hmm ABC transporter, putative contains Pfam profile: PF00005: ABC transporter arginine N-methyltransferase 3, putative similar to arginine N-methyltransferase 3 GB:AAC40158 [Rattus norvegicus] sulphate transporter, putative similar to high affinity sulphate transporter GB:X96431 GI:1217966 [Hordeum vulgare]; supported by cDNA: gi_119334 beta-fructofuranosidase identical to beta-fructofuranosidase GI:6683112 from [Arabidopsis thaliana]; supported by cDNA: gi_6683111_dbj_AB02931! unknown protein ; supported by full-length cDNA: Ceres:38751. inositol polyphosphate 5-phosphatase II, putative similar to inostol polyphosphate 5-phosphatase II GI:9945302 from [Mus musculus]; supported by glycyl tRNA synthetase, putative similar to glycyl tRNA synthetase GI:577711 from [Homo sapiens]; supported by full-length cDNA: Ceres:29666.	257216_at 257169_at 257095_at 257095_at 257051_at 257062_at 256915_at 256970_at 256870_at 256670_at 256677_at 256673_at 256038_s_at 256288_at 256284_at 256017_at 256017_at 255098_at	0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7 0.7

	255845_at	0.7 0.7
	255792_at 255766 at	0.7
	255676 at	0.7
	255678 at	0.7
	255688_at	0.7
	255552_at	0.7
	255529_at	0.7
	255488_at	0.7
	255452_at 255434_at	0.7 0.7
	255365 at	0.7
	255328 at	0.7
		0.7
	254920_at	0.7
	254890_at	0.7
	254722_at	0.7
glycine-rich RNA-binding protein AtGRP2 - like glycine-rich RNA binding protein 2, Arabidopsis thaliana, AJ002892;supported by full-length cDNA: C	_	0.7
	254645_at 254592 at	0.7 0.7
	254549 at	0.7
	254299 at	0.7
	254147 at	0.7
Rab geranylgeranyl transferase like protein (fragment) Rab geranylgeranyl transferase (EC 2.5.1) alpha chain, human, PIR2: JC5538	254156_at	0.7
putative protein ; supported by cDNA: gi_15810434_gb_AY056256.1_	254169_at	0.7
	254089_at	0.7
putative protein similarity to multidrug resistance protein, Mus musculus, PIR1:DVMS1~Contains ABC transporters family signature, (LSGGQRQRV,	-	0.7
	254073_at	0.7
	253969_at	0.7
	253946_at 253903 at	0.7 0.7
	253834 at	0.7
	253783 at	0.7
	253708 at	0.7
putative protein, fragment prolidase - Suberites domuncula,PID:e1289868	253719_at	0.7
	253649_at	0.7
	253663_at	0.7
	253558_at	0.7
	253520_at	0.7
	253524_at	0.7
	253497_at 253418_at	0.7 0.7
	253300 at	0.7
	253314 at	0.7
	253321 at	0.7
putative protein ethylene-responsive element binding protein homolog, Stylosanthes hamata, U91857	253259_at	0.7
putative protein	253189_at	0.7
	253198_at	0.7
	253126_at	0.7
	252939_at	0.7
SEC14 - like protein phosphatidylinositol-phosphatidylcholine transfer protein SEC14, Yarrowia lipolytica, PIR2:S43745; supported by cDNA: gi_143 shikimate kinase - like protein shikimate kinase precursor, Lycopersicon esculentum, qb:S21584	252884_at 252900 at	0.7 0.7
	252900_at 252904 at	0.7
	252880 at	0.7
	252828 at	0.7
	252832_at	0.7
	252743_at	0.7
	252680_at	0.7
	252644_at	0.7
	252648_at	0.7
	252572_at 252588_at	0.7 0.7
	252512 at	0.7
	252462 at	0.7
	252335 at	0.7
NAC2-like protein NAC2 - Arabidopsis thaliana, EMBL:AF201456; supported by cDNA: gi_16604578_gb_AY059734.1_	252278_at	0.7
F-box protein family, AtFBL16 contains similarity to SKP1 interacting partner 2 GI:10716949 from [Arabidopsis thaliana]	252242_at	0.7
	252208_at	0.7
crooked neck-like protein crooked neck protein (CRN) - Drosophila melanogaster, SWISSPROT:CRN_DROME; supported by cDNA: gi_15293116_f		0.7
	252031_at	0.7
	251826_at 251781_at	0.7 0.7
	251800 at	0.7
putative protein EXOENZYMES REGULATORY PROTEIN AEPA PRECURSOR, SWISSPROT: AEPA ERWCA; supported by cDNA: gi 16209665		0.7
	251636_at	0.7
40S ribosomal protein S2 homolog 40S ribosomal protein S2 - Arabidopsis thaliana, SWISSPROT:RS2_ARATH; supported by full-length cDNA: Ceru		0.7
	251559_at	0.7
	251539_at	0.7
	251487_at	0.7
	251362_at	0.7
putative protein putative protein At2g46260 - Arabidopsis thaliana, EMBL:AC005397; supported by cDNA: gi_12006854_gb_AF292397.1_AF29239 auxin propone forder to like protein auvin represent forder 0. Arabidopsis thaliana, EME/LAC005397; supported by cDNA: gi_620627, ab AV0692164		0.7
auxin response factor-like protein auxin response factor 9 - Arabidopsis thaliana, PIR:T08917; supported by cDNA: gi_16604602_gb_AY059746.1_ multifunctional aminoacyl-tRNA ligase - Homo sapiens, PIR:SYHUQT; supported by cDNA: gi_16	251289_at 251264_at	0.7 0.7
	251264_at 251265_at	0.7
	251265_at	0.7
	251217_at	0.7
	251222_at	0.7

hypothetical protein	251224 at	0.7
rac-GTP binding protein -like RACC small GTP binding protein, Zea mays, EMBL:AF126054; supported by cDNA: gi 16648802 gb AY058178.1	251158 at	0.7
F-box protein family, AtFBL3 contains similarity to leucine-rich repeats containing F-box protein FBL3 GI:5919219 from [Homo sapiens]	251104 at	0.7
putative protein peroxisomal Ca-dependent solute carrier - Oryctolagus cuniculus, EMBL:AF004161;supported by full-length cDNA: Ceres:249772.	251106 at	0.7
putative protein putative hydrolase At2g32150 - Arabidopsis thaliana, EMBL:AC006223;supported by full-length cDNA: Ceres:36724.	251028 at	0.7
DP-2 transcription factor - like transcription factor DP-2, Homo sapiens, PIR:A57381	251052_at	0.7
dnaK-type molecular chaperone hsc70.1	250995_at	0.7
putative protein various predicted proteins, Arabidopsis thaliana	250879_at	0.7
cellulose synthase catalytic subunit (gb/AAC39336.1); supported by cDNA: gi 2827142 gb AF027174.1 AF027174	250827 at	0.7
putative protein contains similarity to endo-beta-N-acetylglucosaminidase	250775_at	0.7
arginine-tRNA-protein transferase 1 homolog; supported by cDNA: gi 3806097 gb AF079100.1 AF079100	250754 at	0.7
putative protein similar to unknown protein (pir  T27191);supported by full-length cDNA: Ceres:249722.	250532_at	0.7
flavonol synthase (FLS) (sp[Q96330) ;supported by full-length cDNA: Ceres:23924.	250533_at	0.7
microbody NAD-dependent malate dehydrogenase ; supported by cDNA: gi_14335145_gb_AY037252.1_	250498_at	0.7
alpha-glucosidase 1 ; supported by cDNA: gi_15450744_gb_AY053414.1_	250336_at	0.7
putative protein strong similarity to unknown protein (emb CAB87679.1)	250326_at	0.7
dihydropyrimidinase; supported by cDNA: gi_13878036_gb_AF370281.1_AF370281	250318_at	0.7
putative protein contains similarity to unknown protein (gb AAF03441.1)	250218_at	0.7
putative protein COP9 complex subunit 3, Mus musculus, EMBL:AF071313;supported by full-length cDNA: Ceres:121028.	250188_at	0.7
putative protein various predicted proteins, Arabidopsis thaliana	250144_at	0.7
putative protein	250077_at	0.7
translocon Tic40-like protein ;supported by cDNA: gi_16226312_gb_AF428299.1_AF428299	250080_at	0.7
putative protein unnamed ORF, Mus musculus, EMBL:AB041577; supported by cDNA: gi_11494361_gb_AF280057.1_AF280057	249998_at	0.7
putative protein predicted proteins, Arabidopsis thaliana	250005_at	0.7
FAR1 - like protein far-red impaired response protein (FAR1), Arabidopsis thaliana, EMBL:AF159587	249953_at	0.7
putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:37828.	249957_at	0.7
kinase associated protein phosphatase ; supported by cDNA: gi_15027992_gb_AY045853.1_	249924_at	0.7
unknown protein	249841_at	0.7
putative protein contains similarity to unknown protein (emb CAB62012.1)	249806_at	0.7
unknown protein	249740_at	0.7
acetyl-CoA synthetase ; supported by cDNA; gi_15028046_gb_AY045880.1_	249638_at	0.7
promoter-binding protein like ascorbate oxidase promoter-binding protein, winter squash, PIR:T09661; supported by cDNA: gi_15983796_gb_AY05( total as a statistical data as a statistical barge as a statistical data as a statisticad data as a	_	0.7
putative protein KIAA0409 protein, Homo sapiens, EMBL:AB007869	249360_at	0.7
protein import receptor TOM20, mitochondrial-like	249322_at	0.7
putative protein similar to unknown protein (gb)AAD56319.1)	249298_at	0.7
homeotic protein BEL1 homolog ; supported by cDNA: gi_15146192_gb_A7V49237.1_	249309_at	0.7
putative protein similar to unknown protein (gb)AAF18661.1);supported by full-length cDNA: Ceres:7878.	249199_at	0.7
putative protein contains similarity to unknown protein (dbj BAA76827.1); supported by cDNA: gi_14532601_gb_AY039925.1_	249181_at	0.7
ATP sulfurylase precursor (50) 4AD26634.1)	249112_at	0.7
alcohol dehydrogenase (EC 1.1.1.1) class III (piri)[571244) ;supported by full-length cDNA: Ceres:33315.	249077_at	0.7
nuclear cap-binding protein; CBP20 (gb)AAD29697.1) non-consensus AT donor splice site at exon 4, AC acceptor splice site at exon 5; supported by		0.7
cyclin-dependent protein kinase-like protein ; supported by cDNA: gi_15983484_gb_AF424617.1_AF424617 putative protein contains similarity to unknown;supported by full-length cDNA: Ceres:4029.	249050_at 249025 at	0.7 0.7
putative protein strong similarity to unknown, sopported by ten-length CDIA. Ceres.4029. putative protein strong similarity to unknown protein (gb)AcC61825.1); supported by CDIA: <u>gi</u> _15081732_gb_AY048259.1_	249025_at 248976_at	0.7
potatre protein suorg animany to animony boten (ger-voor 22.1), supported by corver, gr_10001102_go_1104020.1_	248996_at	0.7
pectin activestivesterase ;supported by full-length cDNA: Ceres:39005.	248968_at	0.7
urea active transporter-like protein	248970_at	0.7
urea active transporter inte protein	248970_at 248956_at	0.7
unknown protein ;supported by full-length cDNA: Ceres:40096.	248930_at 248738_at	0.7
unknown protein ; supported by full-length CDNA: Ceres:25275.	248709 at	0.7
putative protein similar to unknown protein (gb/AF-31026.1)	248648 at	0.7
heat shock protein 70 (gb[AAF27639.1); supported by cDNA: gi_6746591_gb_AF217459.1_AF217459	248582 at	0.7
FRO1 and FRO2-like protein	248540 at	0.7
putative protein contains similarity to unknown protein (pir  T05510)	248499 at	0.7
histone acetyltransferase ;supported by full-length cDNA: Ceres:123936.	248508 at	0.7
putative protein similar to unknown protein (pir  \$76207);supported by full-length cDNA: Ceres:258748.	248459 at	0.7
unknown protein	248293 at	0.7
ATP-dependent Clp protease ATP-binding subunit ClpX1 identical to CLP protease regulatory subunit CLPX GI:2674203 from [Arabidopsis thaliana]	248255 at	0.7
putative protein similar to unknown protein (gb AAF34839.1); supported by cDNA: gi_13926341_gb_AF372918.1_AF372918	248230 at	0.7
putative protein strong similarity to unknown protein (pir  T04799)	248095_at	0.7
putative protein contains similarity to cytochrome oxidase assembly factor	248049_at	0.7
unknown protein	248006_at	0.7
26S proteasome AAA-ATPase subunit RPT3 (gb AAF22523.1)	247810_at	0.7
phosphoinositide specific phospholipase C ; supported by cDNA: gi_1526413_dbj_D38544.1_ATHATPLC1	247794_at	0.7
S-receptor kinase homolog 2 precursor S-receptor kinase homolog 2 precursor, Arabidopsis thaliana, PIR:S27754	247602_at	0.7
pseudo-response regulator 1 ; supported by cDNA: gi_7576353_dbj_AB041530.1_AB041530	247525_at	0.7
putative protein rhoGAP, Homo sapiens, EMBL:Z23024; supported by full-length cDNA: Ceres: 152557.	247545_at	0.7
peptide methionine sulfoxide reductase - like protein peptide methionine sulfoxide reductase, Arabidopsis thaliana, PIR:T49886; supported by full-ler		0.7
putative protein strong similarity to unknown protein (emb CAB86899.1)	247389_at	0.7
beta-xylosidase	247266_at	0.7
putative protein similar to unknown protein (ref[NP_014115.1);supported by full-length cDNA: Ceres:14033.	247249_at	0.7
4-alpha-glucanotransferase ; supported by cDNA: gi_14335103_gb_AY037231.1_	247216_at	0.7
oligopeptidase A ; supported by cDNA: gi_15028226_gb_AY045936.1_	247152_at	0.7
amino acid transporter protein-like anthranilate N-hydroxycinnamoyl/benzoyltransferase-like protein ;supported by full-length cDNA: Ceres:32856.	247120_at	0.7 0.7
anumannate v-nyaroxyonnamoyi/benzoyiiransierase-like protein _supported by luin-lengin CDVA. Ceres.52050. unknown protein	247038_at 246961_at	0.7
threonyl-tRNA synthetase ; supported by cDNA: gi 15081625 gb AY048205.1	246961_at	0.7
NHE1 Na+/H+ exchanger ; supported by cDNA: gi 6650176 gb AF056190.1 AF056190	_	0.7
seryl-tRNA synthetase ; supported by cDNA: gi 15293240 gb AY051054.1	246763_at 246780 at	0.7
putative protein clathrin assembly protein short form, Rattus norvegicus, EMBL:AF041373	246780_at 246653_at	0.7
putative protein clarinin assembly protein short form, Ratius horvegicus, EMBL:Ar-041373 putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:40501.	246655_at 246611_at	0.7
hypothetical protein	240011_at 246513_at	0.7
vypolicitasi protein valinerRNA ligase-like protein several bacterial valinetRNA ligases	246509 at	0.7
carbonic anhydrase, putative similar to carbonic anhydrase 1 Gl:882241 from [Flaveria linearis]	246396 at	0.7
30S ribosmal protein S11, putative contains Pfam profile: PF00411: Ribosomal protein S11; supported by full-length cDNA: Ceres: 36981.	246266 at	0.7
putative protein	246245 at	0.7
heat shock transcription factor HSF4 ; supported by cDNA: gi_1619920_gb_U68017.1_ATU68017	246214_at	0.7

Expressed protein ; supported by full-length cDNA: Ceres: 37542.	246193_at	0.7
protein kinase tousled ; supported by cDNA: gi_433051_gb_L23985.1_ATHTGPA	246134_at	0.7
receptor-like protein kinase - like protein receptor-like protein kinase, Arabidopsis thaliana, EMBL:M84659;supported by full-length cDNA: Ceres:206 cytochrome-b5 reductase - like protein cytochrome-b5 reductase, Saccharomyces cerevisiae, PIR:S37800;supported by full-length cDNA: Ceres:33!		0.7 0.7
putative protein predicted protein, Oryza sativa; supported by cDNA: gi 15146277 gb AY049280.1	246126 at	0.7
putative protein serine-arginine-rich splicing regulatory protein SRRP86, Rattus norvegicus, EMBL:AF234765	246039_at	0.7
putative protein predicted proteins, Arabidopsis thaliana and Synechocystis sp.	246057_at	0.7
glucose-6-phosphate 1-dehydrogenase	245977_at	0.7
aspartate aminotransferase Asp2; supported by cDNA: gi_693689_gb_U15033.1_ATU15033	245951_at	0.7
putative protein HERC2 - Homo sapiens, EMBL:AF071172 unknown protein contains similarity to transfactor GB:BAA75684 GI:4519671 from [Nicotiana tabacum]; supported by cDNA: gi 15723594 gb AY04	245851_at	0.7 0.7
	245764 s at	0.7
unknown protein contains similarity to calmodulin Gl:166304 from [Achlya klebsiana]; supported by cDNA: gi 13358218 gb AF325029.2 AF325029		0.7
hypothetical protein	245600_at	0.7
Expressed protein ; supported by full-length cDNA: Ceres: 307.	245321_at	0.7
putative protein ; supported by cDNA: gi_13358188_gb_AF324997.2_AF324997	245308_at	0.7
cytosolic C-acetylserine(thiol)/yase (EC 4.2.99.8); supported by cDNA: gi_15027936_gb_AY045825.1_	245286_at	0.7
glucosyltransferase like protein ; supported by cDNA: gi_2149126_gb_U81293.1_ATU81293 hypothetical protein ; supported by cDNA: gi_16226250_gb_AF428283.1_AF428283	245277_at 245269_at	0.7 0.7
putative TGACG-sequence-specific bZIP DNA-binding protein	245092 at	0.7
unknown protein ;supported by cDNA: gi_16930450_gb_AF419579.1_AF419579	245119_at	0.7
putative cyclin ;supported by full-length cDNA: Ceres:22595.	245043_at	0.7
PSII K protein	245050_at	0.7
cytochrome b/f 3-methyl-2-oxobutanoate hydroxy-methyl-transferase	244977_at 266598 at	0.7 0.7
unknown protein	267030 at	0.6
pEARLI 4 protein Same as GB: L43081; supported by cDNA: gi_871781_gb_L43081.1_ATHPEARA	265440 at	0.6
unknown protein ; supported by cDNA: gi_14334723_gb_AY035035.1_	264485_at	0.6
putative ribonucleoside-diphosphate reductase large subunit ; supported by cDNA: gi_14334813_gb_AY035080.1_	263882_at	0.6
hypothetical protein predicted by genscan+	263220_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:93312.	262607_at	0.6
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat eukaryotic translation elongation factor 2, putative similar to eukaryotic translation elongation factor 2 GB:NP 001952 [Homo sapiens]	258212_at 257758 at	0.6 0.6
phosphatidylinositol-4-phosphate 5-kinase, putative similar to phosphatidylinositol-4-phosphate 5-kinase GI:3702691 from [Arabidopsis thaliana]; suj		0.6
putative sugar transporter	255295_at	0.6
putative protein several hypothetical proteins - Arabidopsis thaliana	254803_at	0.6
hypothetical protein ; supported by cDNA: gi_15982924_gb_AY057570.1_	253374_at	0.6
putative protein dJ69E11.3, Homo sapiens, AL021397	253287_at	0.6 0.6
Expressed protein ; supported by full-length cDNA: Ceres: 114014. putative protein merozoite surface antigen 2, Plasmodium falciparum, PIR:A45637	252822_at 252112_at	0.6
putative protein PrMC3, Pinus radiata, EMBL:AF110333	251200 at	0.6
putative protein contains similarity to unknown protein (gb/AAF72944.1)	250525_at	0.6
pre-mRNA splicing factor ATP-dependent RNA helicase -like protein PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE PRP16,		0.6
putative protein contains similarity to polyA polymerase	249821_at	0.6
disease resistance protein-like	248873_at	0.6
ras-related small GTP-binding protein-like ;supported by full-length cDNA: Ceres:1492. EspB-like protein	248792_at 248276_at	0.6 0.6
putative protein	246283 at	0.6
Arabidopsis thaliana /REF=U37281 /DEF=actin-2 mRNA, complete cds /LEN=1637 (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 p-		0.6
putative RING zinc finger protein ; supported by cDNA: gi_16648813_gb_AY058184.1_	267539_at	0.6
unknown protein	267524_at	0.6
putative serine carboxypeptidase II ; supported by cDNA: gi_14517521_gb_AY039596.1_ aspartate aminotransferase (AAT1) identical to GB:U15026;supported by full-length cDNA: Ceres:34360.	267264_at 267151 at	0.6 0.6
asparate animotransierase (vATT) identicatio costo 13020,supported by Cini-region Curva, Ceres.34300. putative ADP ribosylation factor 1 GTPase activating protein ; supported by CDNA; g1 4334619 gb AY034983.1	267179 at	0.6
putative MVB family transcription factor	267141_at	0.6
hypothetical protein predicted by genefinder	267063_at	0.6
unknown protein	267068_at	0.6
putative DnaJ protein	267070_at	0.6
hypothetical protein predicted by genscan putative urease accessory protein ; supported by full-length cDNA: Ceres: 18513.	267031_at 267001_at	0.6 0.6
putative choline kinase ; supported by full-length CDNA: Ceres:37620.	266861_at	0.6
putative protein kinase contains a protein kinase domain profile (PDOC00100)	266803 at	0.6
unknown protein	266732_at	0.6
unknown protein ; supported by cDNA: gi_15810142_gb_AY056136.1_	266609_at	0.6
hypothetical protein predicted by genscan and genefinder	266574_at	0.6
cycloartenol synthase identical to SP:P38605; supported by cDNA: gi_452445_gb_U02555.1_U02555 putative cysteinyl-tRNA synthetase ; supported by cDNA: gi_15293250 gb_AY051059.1_	266495_at 266478_at	0.6 0.6
unknown protein ; supported by cDNA; gi 16612316 gb AF439849.1 AF439849	266480 at	0.6
20S proteasome subunit C8 (PAG1/PRC8_ARATH) identical to GB:Y13693,supported by full-length cDNA: Ceres:8342.	266312_at	0.6
putative proliferating cell nuclear antigen, PCNA ;supported by full-length cDNA: Ceres:342.	266297_at	0.6
putative RNA-binding protein ; supported by cDNA: gi_16226862_gb_AF428354.1_AF428354	266240_at	0.6
chloroplast membrane protein (ALBINO3) identical to GB:U89272;supported by full-length cDNA: Ceres:31457.	266224_at	0.6
putative C2H2-type zinc finger protein chloroplast single subunit DNA-dependent RNA polymerase identical to GB:Y08722	266110_at 265991_at	0.6 0.6
putative ribophorin I	265858_at	0.6
putative DnaJ protein	265850_at	0.6
unknown protein	265793_at	0.6
hypothetical protein predicted by genscan	265698_at	0.6
putative RAD50 DNA repair protein ; supported by CDNA: gi_7110147_gb_AF168748.1_AF168748	265678_at	0.6
unknown protein ; supported by cDNA: gi_15450376_gb_AY052289.1_ 12-oxophytodienoate-10,11-reductase ; supported by cDNA: gi_15294261 gb_AF410322.1 AF410322	265657_at 265530_at	0.6 0.6
isinilar to cold acclimation protein WCOR413 [Triticum aestivum] supported by full-length cDNA: Ceres:7835.	265480_at	0.6
unknown protein	265398_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:91878.	265375_at	0.6
	265228_s_at	0.6
branched-chain alpha-keto acid decarboxylase E1 beta subunit similar to Bovine branched chain alpha-keto acid dehydrogenase (BCKDHB) E1-beta putative prohibitin 2 B-cell receptor associated protein;supported by full-length cDNA: Ceres:6208.	265070_at 265037_at	0.6 0.6
paranto promotori z o con recopior accontator protoni, supportor by funciengui contra, contos.0200.	_00007_at	0.0

	264875_at	0.6
	264844_at 264793 at	0.6 0.6
	264795 at	0.6
	264778_at	0.6
hypothetical protein predicted by genscan	264689_at	0.6
putative acetyl-CoA acyltransferase Strong similarity to Cucumis acetyl-CoA acyltransferase (gb D70895);supported by full-length cDNA: Ceres:1258		0.6
putative prolyl 4-hydroxylase, alpha subunit ;supported by full-length cDNA: Ceres:36054. auxin-resistance protein AXR1 E1 ubiquitin-like activating enzyme; identical to GB:P42744; supported by cDNA: gi 15215701 gb AY050379.1	264592_at 264585 at	0.6 0.6
auxin-resistance protein Axr 1 E i ouriguin-like auxiaring enzyme, identical to GB.P42744, supported by CDIAX. g[ 13215701_gb_X1030575.1_ hypothetical protein predicted by genemark.hmm	264565_at	0.6
hypothetical protein predicted by genscan; supported by cDNA: gi_15450913_gb_AY054537.1_	264447_at	0.6
unknown protein similar to salt-inducible protein (gi 375717); similar to ESTs gb/R30192 and gb/AA651017	264452_at	0.6
	264421_at	0.6
hypothetical protein similar to membrane protein PTM1 precursor isolog GI:1931644 from [Arabidopsis thaliana]	264429_at	0.6
spermidine synthase, putative similar to spermidine synthase GI:4138109 from [Lycopersicon esculentum]; supported by cDNA: gi_14030636_gb_A hypothetical protein contains similarity to glucosidase I GI:2344809 from [Homo sapiens]	264317_at 264228_at	0.6 0.6
	264204 at	0.6
hypothetical protein contains Prim profile: PF01535 PPR repeat	264177_at	0.6
	264064_at	0.6
	264041_at	0.6
	263976_at 263989 at	0.6 0.6
	263897_at	0.6
	263835 at	0.6
	263791_at	0.6
	263796_at	0.6
	263763_at	0.6
	263662_at 263621_at	0.6 0.6
	263533 at	0.6
	263493 at	0.6
putative protein kinase contains a protein kinase domain profile (PDOC00100)	263461_at	0.6
	263478_at	0.6
unknown protein	263456_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:120231. unknown protein ; supported by cDNA: gi 15027886 gb AY045800.1	263303_at 263331_at	0.6 0.6
	263212 at	0.6
	263199_at	0.6
unknown protein	263171_at	0.6
	263156_at	0.6
cytochrome P450, putative similar to cytochrome P450 GI:4176420 from [Arabidopsis thaliana] hypothetical protein contains similarity to serine threonine kinase GI:166813 from [Arabidopsis thaliana]; supported by cDNA: gi 14334553 gb AY032	263120_at	0.6 0.6
hypothetical protein predicted by genscan and geneficier; supported by full-length cDNA: Ceres: 95679.	263097_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:21947.	262945 at	0.6
pyruvate dehydrogenase e1 alpha subunit, putative similar to pyruvate dehydrogenase e1 alpha subunit GI:473168 from [Solanum tuberosum];supp	262908_at	0.6
	262856_at	0.6
	262770_at	0.6
	262700_at 262668_at	0.6 0.6
	262609_at	0.6
DEIH-box RNA/DNA helicase identical to DEIH-box RNA/DNA helicase GB:BAA84364 GI:5881579 [Arabidopsis thaliana]; supported by cDNA: gi_58		0.6
	262565_at	0.6
Expressed protein ; supported by full-length cDNA: Ceres: 6612.	262512_at	0.6
unknown protein Contains similarity to gb U07707 epidermal growth factor receptor substrate (eps15) from Homo sapiens and contains 2 PF 00036 E leaf development protein Argonaute identical to GB:AAC18440 from (Arabidopsis thaliana); supported by cDNA: gi_2149639_gb_U91995.1_ATU919		0.6 0.6
	262253 s at	0.6
eukaryotic initiation factor 5 (eIF-5), putative similar to eukaryotic initiation factor 5 (eIF-5) GI:1008880 from [Phaseolus vulgaris]	262193_at	0.6
sulfate transporter, putative similar to sulfate transporter GI:2114106 from [Arabidopsis thaliana]; supported by cDNA: gi_1498119_dbj_D85416.1_A	262134_at	0.6
hypothetical protein predicted by genscan+; supported by cDNA: gi_6520211_dbj_AB028226.1_AB028226	262078_at	0.6
	262062_s_at	0.6
protein disulfide isomerase, putative similar to GB:AAA85099 GI:687235 from [Onchocerca volvulus]; supported by cDNA: gi_14423497_gb_AF386{ CCR4-associated factor, putative\0CCR4-associated factor, putative similar to CCR4-ASSOCIATED FACTOR 1 GB:Q60809 from [Mus musculus]\0		0.6 0.6
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi 14517415 gb AY039543.1	261861 at	0.6
S-ribonuclease binding protein SBP1, putative similar to S-ribonuclease binding protein SBP1 GI:6760451 from [Petunia hybrida]; supported by full-le	261832_at	0.6
	261709_at	0.6
	261661_at	0.6
	261676_at 261498_at	0.6 0.6
	261465_at	0.6
		0.6
	261363_at	0.6
	261316_at	0.6
	261326_s_at 261170_at	0.6 0.6
	261144_s_at	0.6
	261075_at	0.6
transformer-SR ribonucleoprotein, putative similar to GB:Y09506 from [Nicotiana tabacum] (Plant Mol. Biol. 35 (3), 261-269 (1997)); supported by c[		0.6
hypothetical protein similar to hypothetical protein GB:CAB80918 GI:7267606 from [Arabidopsis thaliana]	261052_at	0.6
	261053_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:11931. hypothetical protein predicted by genemark.hmm	261014_at 260993 at	0.6 0.6
glyoxalase II isozyme putative similar to glyoxalase II isozyme GB:AAC49865 GI:2570338 from [Arabidopsis thaliana];supported by full-length cDN/		0.6
	260876_at	0.6
unknown protein	260751_at	0.6
actin 8 almost identical to actin 8 GI:1669389 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:34479.	260765_at	0.6
Expressed protein ; supported by full-length cDNA: Ceres: 29302. unknown protein ; supported by cDNA: gi_15810124_gb_AY056127.1_	260769_at 260675_at	0.6 0.6

Unknown protein ; supported by cDNA: gi_15028352_gb_AY045979.1_	260508_at	0.6
unknown protein ; supported by full-length cDNA: Ceres: 2381.	260442 at	0.6
putative RNA-binding protein similar to RNA-binding protein GB:S46286 from [Nicotiana sylvestris]	260245 at	0.6
putative MYB family transcription factor contains Pfam profile: PF00249 Myb-like DNA-binding domain; similar to N-term of myb GB:CAA72218 [Oryz		0.6
unknown protein contains zinc finger, C3HC4 type (RING finger) domain	260168 at	0.6
unknown protein ;supported by full-length CDNA: Ceres:108165.	260099 at	0.6
ethylene-insensitive3-like3 (EIL3) identical to ethylene-insensitive3-like3 (EIL3) GB:AF004215 [Arabidopsis thaliana] (Cell 89 (7), 1133-1144 (1997))		0.6
		0.6
beta-1.3-glucanase precursor, putative similar to Gl:4097948 from [Oryza sativa] (Gene 223 (1-2), 311-320 (1998))	259823_at	
RNA and export factor binding protein, putative similar to GI:7159943 from [Mus musculus] (RNA 6(4), 638-650 (2000)); supported by cDNA; gi_15;		0.6
	259752_at	0.6
putative cleavage and polyadenylation specificity factor similar to cleavage and polyadenylation specificity factor 73 kDa subunit GB:AAF00224 from		0.6
disease resistance protein contains domains associated with disease resistance genes in plants: TIR/NB-ARC/LRR	259629_at	0.6
hypothetical protein	259560_at	0.6
hypothetical protein ; supported by cDNA: gi_1518449_gb_U43340.1_ATU43340	259517_at	0.6
hypothetical protein ; supported by cDNA: gi_9954167_gb_AF159052.1_AF159052	259513_at	0.6
unknown protein ; supported by cDNA: gi 15028126 gb AY046013.1	259501 at	0.6
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:6115.	259436 at	0.6
	259437 at	0.6
DNA binding protein GT-1, putative similar to DNA binding protein GT-1 GI:598073 from (Arabidopsis thaliana)	259412 at	0.6
methionine aminopeptidase I (MAP1), putative similar to methionine aminopeptidase I (MAP1) GI:975722 from [Saccharomyces cerevisiae]; support		0.6
putative cytoskeleton-associated protein similar to cytoskeleton-associated protein 1 GB:4502849 [Homo sapiens]	259141_at	0.6
putative oriotocar associated protein similar or oriotocarcical activated protein kinase kinase GB:AAC32599 [Oryza sativa]	259080 at	0.6
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:19154.	259037_at	0.6
unknown protein	258949_at	0.6
putative 26S proteosome regulatory subunit	258871_at	0.6
unknown protein ; supported by cDNA: gi_15294217_gb_AF410300.1_AF410300	258839_at	0.6
putative RNA-binding protein similar putative nucleic acid binding protein GB:CAB39665 [Arabidopsis thaliana]; Pfam HMM hit: KH domain family of I		0.6
putative bZIP transcription factor contains Pfam profile: PF00170 bZIP transcription factor; contains similarity to TGACG-sequence specific DNA-binc		0.6
hydroxyacylglutathione hydrolase cytoplasmic (glyoxalase II) (GLX II) identical to hydroxyacylglutathione hydrolase cytoplasmic (glyoxalase II) (GLX		0.6
shaggy related protein kinase, ASK-GAMMA identical to GB:P43289;supported by full-length cDNA: Ceres:17739.	258743_s_at	0.6
putative pectate lyase simliar to pectate lyase precursor GB:P40972 from [Nicotiana tabacum]	258719_at	0.6
unknown protein similar to hypothetical protein KIAA0188 GB: Q14693 from [Homo sapiens]	258721_at	0.6
unknown protein	258698 at	0.6
putative RHO GDP-dissociation inhibitor 1 similar to RHO GDP-dissociation inhibitor 1 GB:P19803 [Bos taurus]; supported by full-length cDNA: Ceres	258637 at	0.6
putative protein kinase similar to protein kinase (APK1A) GB:Q06548 [Arabidopsis thaliana]; contains Pfam profile: PF00069 Eukaryotic protein kinas		0.6
hypothetical protein predicted by genscan+	258505 at	0.6
neutral invertase, protative similar to neutral invertase GB:CAA76145 from [Daucus carota] (Physiol. Plantarum (1999) 107, 159-165)	258507 at	0.6
unknown protein	258502 at	0.6
unknown protein ;supported by full-length cDNA: Ceres:38468.	258435 at	0.6
hypothetical protein contains similarity to ion channel protein from [Arabidopsis thaliana]; supported by cDNA: gi 8131897 gb AF148541.1 AF1485-		0.6
unknown protein ; supported by cDNA: gi_13358213_gb_AF325024.2_AF325024	258223_at	0.6
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:20484.	258161_at	0.6
	258134_at	0.6
Expressed protein ; supported by cDNA: gi_15912240_gb_AY056398.1_	258140_at	0.6
hypothetical protein	258141_at	0.6
putative WD-repeat protein (WDR1-like) similar to WDR1 protein GB:AAD05042 [Gallus gallus] (Genomics 56 (1), 59-69 (1999))	258146_at	0.6
	258123_at	0.6
Expressed protein ; supported by full-length cDNA: Ceres: 26411.	258092_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:40534.	258040_at	0.6
unknown protein	257983_at	0.6
putative myc-like DNA-binding protein similar to GB:AAB72192 from [Arabidopsis thaliana]	257990_at	0.6
hypothetical protein predicted by genemark;supported by full-length cDNA: Ceres:108568.	257967_at	0.6
ribosomal protein, putative similar to 60S ribosomal protein L5 GB:P49625 from [Oryza sativa];supported by full-length cDNA: Ceres:32753.	257906_at	0.6
alpha-mannosidase, putative similar to lysosomal alpha-mannosidase GB:AAC34130 [Homo sapiens] (Hum. Mol. Genet. 6 (5), 717-726 (1997)); sur	257834_at	0.6
hypothetical protein predicted by genscan+	257248 at	0.6
hypothetical protein predicted by genscan+	257208 at	0.6
unknown protein ;supported by full-length cDNA: Ceres:256351.	257150_at	0.6
cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450	257112 at	0.6
hypothetical protein predicted by genemark.hmm	257000 at	0.6
hypothetical protein contains similarity to flavonol synthase (FLS) GB:Q41452 from [Solanum tuberosum], contains Pfam profile: PF00671 Iron/Asco		0.6
hypothetical protein ; supported by cDNA: gi_15293218 gb_AY051043.1_	256881_at	0.6
RNA-binding protein, putative similar to RNA-binding protein (RZ-1) GB:BA12064 [Nicotiana sylvestris]; contains Pfam profile: PF00076 RNA reco		0.6
unknown protein	256658 at	0.6
hypothetical protein		
	256585_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:20812.	256523_at	0.6
	256431_s_at	0.6
MYB-family transcription factor, putative contains Pfam profile: PF00249 Myb-like DNA-binding domain;supported by full-length cDNA: Ceres:10939		0.6
auxin conjugate hydrolase (ILL5) identical to auxin conjugate hydrolase [Arabidopsis thaliana] (ILL5) GI:5725649; contains nonconsensus AT accepto:		0.6
unknown protein	256041_at	0.6
calcium dependent protein kinase, putative similar to calcium dependent protein kinase GI:587499 from [Oryza sativa]	255936_at	0.6
Deetiolated1 (DET1) light signal transduction protein	255799_at	0.6
predicted protein	255713_s_at	0.6
putative calmodulin-binding heat shock protein	255677_at	0.6
hypothetical protein	255616_at	0.6
hypothetical protein ;supported by full-length cDNA: Ceres:25253.	255586_at	0.6
putative ABC transporter		0.6
	255594_at	0.6
contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 166.20) and to legume lectins beta domain (Pfam: lectin_legB.hmm, score		
contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 166.20) and to legume lectins beta domain (Pfam: lectin_legB.hmm, score: putative glycosyltransferase similar to A. thaliana protein T20K9.11, GenBank accession number 3445207; supported by cDNA: gi 16209668 gb A	255502_at	0.6
putative glycosyltransferase similar to A. thaliana protein T20K9.11, GenBank accession number 3445207; supported by cDNA: gi_16209668_gb_A	 255502_at 255483_at	0.6
putative glycosyltransferase similar to A. thaliana protein T20K9.11, GenBank accession number 3445207; supported by cDNA: gi_16209668_gb_A putative GH3-like protein similar to soybean GH3 auxin-inducible protein, GenBank accession number X60033; supported by cDNA: gi_16649142_g	255502_at 255483_at 255403_at	0.6 0.6
putative glycosyltransferase similar to A. thaliana protein T20K9.11, GenBank accession number 3445207; supported by cDNA: gi_16209668_gb_A putative GH3-like protein similar to soybean GH3 auxin-inducible protein, GenBank accession number X60033; supported by cDNA: gi_16649142_g putative malonyl-CoA decarboxylase	255502_at 255483_at 255403_at 255327_at	0.6 0.6 0.6
putative glycosyltransferase similar to A. thaliana protein T20K9.11, GenBank accession number 3445207; supported by cDNA: gi_16209668_gb_A putative GH3-like protein similar to soybean GH3 auxin-inducible protein, GenBank accession number X60033; supported by cDNA: gi_16649142_g putative malonyl-CoA decarboxylase Arabidopsis thaliana flavin-type blue-light photoreceptor (SW:Q43125) (Pfam: PF00875, Score=765.2, E=2.6e-226, N=1); supported by cDNA: gi_1	255502_at 255483_at 255403_at 255327_at 255068_at	0.6 0.6 0.6 0.6
putative glycosyltransferase similar to A. thaliana protein T20K9.11, GenBank accession number 3445207; supported by cDNA: gi_16209668_gb_A putative GH3-like protein similar to soybean GH3 auxin-inducible protein, GenBank accession number X60033; supported by cDNA: gi_16649142_g putative malonyl-CoA decarboxylase Arabidopsis thaliana flavin-type blue-light photoreceptor (SW:Q43125) (Pfam: PF00875, Score=765.2, E=2.6e-226, N=1); supported by cDNA: gi_1 calmodulin-domain protein kinase CDPK isoform 4 (CPK4)	255502_at 255483_at 255403_at 255327_at 255068_at 255039_at	0.6 0.6 0.6 0.6 0.6
putative glycosyltransferase similar to A. thaliana protein T20K9.11, GenBank accession number 3445207; supported by cDNA: gi_16209668_gb_A putative GH3-like protein similar to soybean GH3 auxin-inducible protein, GenBank accession number X60033; supported by cDNA: gi_16649142_g putative malonyl-CoA decarboxylase Arabidopsis thaliana flavin-type blue-light photoreceptor (SW:Q43125) (Pfam: PF00875, Score=765.2, E=2.6e-226, N=1); supported by cDNA: gi_1 calmodulin-domain protein kinase CDPK isoform 4 (CPK4) putative protein; supported by full-length cDNA: Ceres: 93362.	255502_at 255483_at 255403_at 255327_at 255068_at 255039_at 254957_at	0.6 0.6 0.6 0.6 0.6 0.6
putative glycosyltransferase similar to A. thaliana protein T20K9.11, GenBank accession number 3445207; supported by cDNA: gi_16209668_gb_A putative GH3-like protein similar to soybean GH3 auxin-inducible protein, GenBank accession number X60033; supported by cDNA: gi_16649142_g putative malonyl-CoA decarboxylase Arabidopsis thaliana flavin-type blue-light photoreceptor (SW:Q43125) (Pfam: PF00875, Score=765.2, E=2.6e-226, N=1) ; supported by cDNA: gi_1 calmodulin-domain protein kinase CDPK isoform 4 (CPK4) putative protein ; supported by full-length cDNA: Ceres: 93362. hypothetical protein ; supported by cDNA: gi_16648694_gb_AY058123.1_	255502_at 255483_at 255403_at 255327_at 255068_at 255039_at 254957_at 254814_at	0.6 0.6 0.6 0.6 0.6 0.6 0.6
putative glycosyltransferase similar to A. thaliana protein T20K9.11, GenBank accession number 3445207; supported by cDNA: gi_16209668_gb_A putative GH3-like protein similar to soybean GH3 auxin-inducible protein, GenBank accession number X60033; supported by cDNA: gi_16649142_g putative malonyl-CoA decarboxylase Arabidopsis thaliana flavin-type blue-light photoreceptor (SW:Q43125) (Pfam: PF00875, Score=765.2, E=2.6e-226, N=1) ; supported by cDNA: gi_1 calmodulin-domain protein kinase CDPK isoform 4 (CPK4) putative protein ; supported by full-length cDNA: Ceres: 93362. hypothetical protein ; supported by cDNA: gi_16648694_gb_AY058123.1_ putative trehalose-6-phosphate phosphatase (AtTPPA) trehalose-6-phosphate phosphatase - Arabidopsis thaliana, PID:g2944178; supported by cD	255502_at 255483_at 255403_at 255327_at 255038_at 255039_at 254957_at 254945_at 254814_at 254806_at	0.6 0.6 0.6 0.6 0.6 0.6 0.6
putative glycosyltransferase similar to A. thaliana protein T20K9.11, GenBank accession number 3445207; supported by cDNA: gi_16209668_gb_A putative GH3-like protein similar to soybean GH3 auxin-inducible protein, GenBank accession number X60033; supported by cDNA: gi_16649142_g putative malonyl-CoA decarboxylase Arabidopsis thaliana flavin-type blue-light photoreceptor (SW:Q43125) (Pfam: PF00875, Score=765.2, E=2.6e-226, N=1) ; supported by cDNA: gi_1 calmodulin-domain protein kinase CDPK isoform 4 (CPK4) putative protein ; supported by full-length cDNA: Ceres: 93362. hypothetical protein ; supported by cDNA: gi_16648694_gb_AY058123.1_	255502_at 255483_at 255403_at 255327_at 255038_at 255039_at 254957_at 254945_at 254814_at 254806_at	0.6 0.6 0.6 0.6 0.6 0.6

teosinte branched1 - like protein teosinte branched1 protein - Zea mays, PIR2:T04347	254670_at	0.6
aspartate kinase-homoserine dehydrogenase - like protein ak-hsdh bifunctional enzyme precursor, Arabidopsis thaliana, PIR2:S46497	254535_at	0.6
lectin like protein lectin phloem protein PP2, winter squash, PIR2:S38462;supported by full-length cDNA: Ceres:17437.	254551 at	0.6
putative protein gamma-SNAP protein, bovine, PIR2:S32369;supported by full-length cDNA: Ceres:267158.	254476 at	0.6
hypothetical protein	254455 at	0.6
Translation factor EF-1 alpha - like protein translation factor EF-1 alpha genfamily, Arabidopsis thaliana, PATCHX:G1532164	254300 at	0.6
	254259 s at	0.6
putative protein ;supported by full-length cDNA: Ceres:20769.	254164 at	0.6
putative protein histidine-rich calcium-binding protein precursor, rabbit, PIR2:A34373	254143 at	0.6
ubiquitin-specific protease 16 (UBP16), putative similar to ubiquitin-specific protease 16 GI:11993477 [Arabidopsis thaliana]; supported by cDNA: gi	_	0.6
putative protein cylicin II - human, PID:q758587; supported by cDNA; gi 14423517 gb AF386996.1 AF386996	254058 at	0.6
putative protein immunophilin FKBP46 - Spodoptera frugiperda (fall armyworm),PIR2:A55320; supprited by cDNA: gi 15982871 gb AY057543.1	254076 at	0.6
putative protein various predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 122917.	254048 at	0.6
	253941_at	0.6
putative protein		
putative protein Ran_GTP binding protein 5, Homo sapiens, Y08890	253881_at	0.6
hypothetical protein	253888_at	0.6
putative protein zinc-finger protein S12569, Oryza sativa, PIR3:JE0115;supported by full-length cDNA: Ceres:41557.	253854_at	0.6
arginine methyltransferase (pam1); supported by full-length cDNA: Ceres: 38601.	253695_at	0.6
putative protein KIAA0210 gene, Homo sapiens, gb:D86965; supported by cDNA: gi_5032257_gb_AF126057.2_AF126057	253647_at	0.6
putative protein component of aniline dioxygenase (GMP synthase like protein) - Acinetobacter sp., PID:d1013698; supported by full-length cDNA: Ce		0.6
aspartatetRNA ligase - like protein aspartyl tRNA synthetase, Drosophila melanogaster, EMBL:AF113612	253561_at	0.6
monogalactosyldiacylglycerol synthase - like protein monogalactosyldiacylglycerol synthase, Cucumis sativus, PID:g1805254; supported by cDNA: ç		0.6
putative protein myosin heavy chain-B, neuronal - Gallus gallus, PIR:B43402; supported by cDNA: gi_13430501_gb_AF360163.1_AF360163	253425_at	0.6
putative potassium transporter AtKT5p (AtKT5)	253330_at	0.6
putative protein acetylpolyamine aminohydrolase (aphA) homolog -Archaeoglobus fulgidus, PIR2:B69266; supported by cDNA: gi_15529219_gb_AY	253337_at	0.6
dynamin-like protein ADL2	253306_at	0.6
putative protein ;supported by full-length cDNA: Ceres:8161.	253322_at	0.6
caffeoyl-CoA O-methyltransferase - like protein caffeoyl-CoA 3-O-methyltransferase, Populus tremuloides, PID:G857578; supported by full-length cD	253276_at	0.6
extra-large G-protein - like extra-large G-protein, Arabidopsis thaliana, AF060942	253257_at	0.6
putative protein	253208 at	0.6
ankyrin repeat-containing protein 2 ;supported by full-length cDNA: Ceres:34698.	253139 at	0.6
plasma membrane-type calcium ATPase (ACA2); supported by cDNA: gi_3335059_gb_AF025842.1_AF025842	253063 at	0.6
putative protein	253022 at	0.6
hypothetical protein	253025 at	0.6
putative protein	252990 at	0.6
putative transcription factor (MYB4) ; supported by cDNA: gi 3941411 gb AF062860.1 AF062860	252958 at	0.6
phenyiannus runthetase - like protein phenyialanyi-trana synthetase beta chain, cytosolic, Saccharomyces cerevisiae, PIR1:YFBYAC	252941 at	0.6
priori yalan yana ayina tase - ne protein protegian yana yana tase ola onani, cytoson, odoviatori yose celevialo, riki in birko putative protein various predicted proteins, Arabidopsis thaliana	252901_at	0.6
putative protein validas protein-like nucleica acid binding protein - Oryza sativa, PIR:T02745	252764 at	0.6
nucleic acto animaly protein inter indexe and animaly protein - Organ saturation in to 2740 putative protein predicted protein, Drosophila melanogaster, EMBL:AE003789	252704_at 252738 at	0.6
putative histone deacetylase similar to maize nucleolar histone deacetylase (U28215); supported by cDNA: gi_11066134_gb_AF195545.1_AF19554		0.6
cysteine proteinase AALP, putative similar to AALP protein GI:7230640 from [Arabidopsis thaliana] and barley aleurain	252622_at	0.6
histidyl-tRNA synthetase ; supported by cDNA: gi_3659908_gb_AF020715.1_AF020715	252516_at	0.6
putative protein mitotic phosphoprotein 90 - Xenopus laevis, EMBL:U95102;supported by full-length cDNA: Ceres: 114884.	252478_at	0.6
putative protein sn-glycerol-3-phosphate permease - Haemophilus influenzae, PID:g3603157; supported by CDN2; gj_13430515_gb_AF360170.1_A		0.6
putative protein N7 protein - Medicago truncatula, EMBL:CAA76808;supported by full-length cDNA: Ceres:99337.	252336_at	0.6
RNA-directed RNA polymerase RNA-directed RNA polymerase	252261_at	0.6
putative protein mRNA of unknown function, Homo sapiens, EMBL:HS598F21A_1	252207_at	0.6
protein kinase SPK-2 ;supported by full-length cDNA: Ceres:3988.	252166_at	0.6
putative clathrin coat assembly protein clathrin coat assembly protein-like - Homo sapiens, PID:g1669533	252188_at	0.6
putative protein ATP binding protein - Homo sapiens, PID:d1022739	252127_at	0.6
putative protein hypothetical protein - Synechocystis sp., EMBL:D90903;supported by full-length cDNA: Ceres:266414.	252122_at	0.6
plastid division protein FtsZ-like FtsZ protein, Gentiana lutea, EMBL:AF205859; supported by cDNA: gi_14488049_gb_AF384167.1_AF384167	252001_at	0.6
putative protein predicted proteins, Arabidopsis thaliana	252014_at	0.6
AP3-complex beta-3A adaptin subunit-like protein AP-3 complex beta3A subunit, Homo sapiens, EMBL:HSU91931; supported by cDNA: gi_166046	251808_at	0.6
tetrahydrofolylpolyglutamate synthase precursor - like protein tetrahydrofolylpolyglutamate synthase precursor, Mus musculus, PIR:S65755; support	251759_at	0.6
putative protein exostose-related protein 2, Homo sapiens, PIR:JC5935	251764_at	0.6
putative protein conserved hypothetical protein SPCC330.09 - Schizosaccharomyces pombe, PIR:T41319	251678_at	0.6
putative protein polygalacturonase (EC 3.2.1.15) precursor, Erwinia carotovora, PIR:S11773	251645_at	0.6
putative protein contains alternative donor splice site TT at exon 2, hypothetical protein C14A4.1 - Caenorhabditis elegans, PIR:T19243; supported b	251578 at	0.6
putative protein hypothetical protein At2g44090- Arabidopsis thaliana, EMBL:AC004005	251437_at	0.6
beta-tubulin cofactor - like protein beta-tubulin folding cofactor D, Homo sapiens, EMBL:HSA6417	251383_at	0.6
putative protein rec, Homo sapiens, EMBL:AB023584	251386_at	0.6
dihydrodipicolinate synthase precursor ;supported by full-length cDNA: Ceres:37907.	251392_at	0.6
proteasome component C5 supported by full-length cDNA: Ceres:26273.	251337 at	0.6
60S RIBOSOMAL PROTEIN L7A protein 60S RIBOSOMAL PROTEIN L7A - Oryza sativa, SWISSPROT:RL7A ORYSA;supported by full-length cDI		0.6
putative protein CGI-77 protein, Homo sapiens, EMBL:AF151836;supported by full-length cDNA: Ceres:153131.	251149 at	0.6
hypothetical protein ; supported by cDNA: gi 15292666 gb AY050767.1	251083 at	0.6
putative protein RING-H2 finger protein RHA3a - Arabidopsis thaliana, EMBL:AF078824	251066_at	0.6
putative protein receptor protein kinases	251071_at	0.6
DnaJ homologue (gb[AAB91418.1]) ; supported by cDNA: gi_2689719_gb_AF037168.1_AF037168	250672 at	0.6
unknown protein ; supported by cDNA: gi 16648868 gb AY059804.1	250540 at	0.6
	250458 s at	0.6
argininosucinate lyase (AtArgH); supported by cDNA: gi 15028082, gb AY045898.1	250403 at	0.6
agrimosucentia ryace (rate in the last of the second	250405_at	0.6
parate protein induced in propried and synaptic strengthese share section in the synaptic relates in operation of the protein	250111_at	0.6
unknown protein	250104_at	0.6
phytoen synthase (gb AAB65697.1) ;supported by full-length cDNA: Ceres:15761.	250095 at	0.6
privolene syminase (gprAxbosor, r), supported by immergin cDAx, ceres, 10701. chromo domain protein polycomb-like protein, Daucus carota, PIR:T14294; supported by cDNA; gi 15625406 gb AF387639.1 AF387639	250095_at 250060_at	0.6
GTP-binding protein obg -like GTP-binding protein obg, Bacillus subtilis, PIR:B32804	250060_at 249993_at	0.6
putative protein predicted proteins, Homo sapiens, Schizosaccharomyces pombe, Caenorhabditis elegans, Saccharomyces cerevisiae, Drosophila r bistopa departures (the protein part of the protein part of the protein protein protein protein protein protein		0.6
histone deacetylase-like protein non-consensus AT donor splice site at exon 3, AC acceptor splice site at exon 4	249901_at	0.6
glucosyltransferase-like protein ; supported by cDNA: gj_16648763_gb_AY058158.1_	249911_at	0.6
putative protein similar to unknown protein (gb AAD12714.1)	249845_at	0.6
nucleolar protein-like	249672_at	0.6
putative protein unnamed ORF, Homo sapiens, EMBL:AK001192	249611_at	0.6
	_	
receptor protein kinase - like protein receptor serine/threonine kinase PR5K, Arabidopsis thaliana, EMBL:AT48698	249486_at	0.6

disease resistance - like protein resistance gene Cf-4, Lycopersicon hirsutum, EMBL:LHJ002235	249393_at 0.6
protein kinase-like	249293_at 0.6
SKP1/ASK1 (At2) identical to UIP2 GI:3719211 from [Arabidopsis thaliana]	249228_at 0.6
putative protein similar to unknown protein (emb CAB66408.1);supported by full-length cDNA: Ceres:106836.	249231_at 0.6
phytochelatin synthase (gb AAD41794.1); supported by cDNA: gi_14532653_gb_AY039951.1_	249078_at 0.6
tubulin beta-4 chain (sp P24636); supported by cDNA: gi_14334935_gb_AY035141.1_	249049_at 0.6
unknown protein ;supported by full-length CDNA: Ceres:36901.	248966_at 0.6
serine threonine protein kinase ; supported by cDNA: gi_14486383_gb_AY035225.1_	248910_at 0.6
bHLH protein-like protein serine threonine kinase-like	248864_at 0.6 248821_at 0.6
	248821_at 0.6 248800 at 0.6
40S ribosomal protein S19 ; supported by cDNA: gi_15028320_gb_AY045963.1_ putative protein strong similarity to unknown protein (emb CAB71043.1); supported by cDNA: gi 15810326 gb AY056202.1	248600_at 0.6 248721_at 0.6
SCARECROW gene regulator-like ; supported by cDNA: gi_8132288_gb_AF153443.1_AF153443	248689 at 0.6
unknown protein ;supported by full-length cDNA: Ceres:147765.	248592 at 0.6
ATP-dependent Clp protease ATP-binding subunit ClpX2, putative similar to CLP protease regulatory subunit CLPX GI:2674203 from	
arginine-aspartate-rich RNA binding protein-like; supported by cDNA: gi_1699050 gb_U78867.1_ATU78867	248403 at 0.6
putative protein contains similarity to peptidase	248426 at 0.6
photoassimilate-responsive protein PAR-like protein ;supported by full-length cDNA: Ceres:17872.	248333 at 0.6
developmental protein SINA (seven in absentia)	248256_at 0.6
NADH-dependent glutamate synthase	248267_at 0.6
putative protein similar to unknown protein (sp/P29618);supported by full-length cDNA: Ceres:95459.	248270_at 0.6
Expressed protein ; supported by full-length cDNA: Ceres: 2034.	248272_at 0.6
unknown protein	248243_at 0.6
unknown protein	248131_at 0.6
putative protein contains similarity to integral membrane protein	248134_at 0.6
putative protein contains similarity to polyadenylate-binding protein 5; supported by full-length cDNA: Ceres: 107768.	248147_at 0.6
cell division protein FtsZ chloroplast homolog precursor (sp[Q42545); supported by cDNA: gi_14334637_gb_AY034992.1_	248105_at 0.6
selenium-binding protein-like	248075_at 0.6
outward rectifying potassium channel KCO ;supported by full-length cDNA: Ceres:32253.	248027_at 0.6
unknown protein ; supported by cDNA: gi_13899122_gb_AF370556.1_AF370556	248031_at 0.6 247960 at 0.6
N-myristoyl transferase ;supported by full-length cDNA: Ceres:36525. putative protein similar to unknown protein (gb AAD55473.1);supported by full-length cDNA: Ceres:7233.	247960_at 0.6 247931_at 0.6
protein carboxyl methylase-like	247931_at 0.0
unknown protein	247907 at 0.6
SPP30 - like protein SPP30, Solanum chacoense, EMBL:AF136010;supported by full-length cDNA: Ceres:269675.	247842 at 0.6
outer membrane lipoprotein - like outer membrane lipoprotein, Citrobacter freundii, PIR:140710;supported by full-length cDNA: Ceres:1	
putative protein Not2p, Homo sapiens, EMBL:AF180473; supported by cDNA: gi 12006938 gb AF295433.1 AF295433	247695 at 0.6
replication protein A1 - like probable replication protein A1, Oryza sativa, EMBL:AF009179;supported by full-length cDNA: Ceres:4085	
histone deacetylase - like histone deacetylase HDA2, Mus musculus, PIR:T13964	247558_at 0.6
calnexin - like protein calnexin homolog, Arabidopsis thaliana, EMBL:AT08315;supported by full-length cDNA: Ceres:2869.	247494_at 0.6
AtOXA1 ;supported by full-length cDNA: Ceres:96723.	247460_at 0.6
unknown protein ;supported by cDNA: gi_15809801_gb_AY054168.1_	247446_at 0.6
histidinol dehydrogenase ;supported by full-length cDNA: Ceres:40175.	247303_at 0.6
ankyrin-like protein	247316_at 0.6
unknown protein	247241_at 0.6
unknown protein ;supported by cDNA: gi_14334503_gb_AY034943.1_	247203_at 0.6
3-dehydroquinate synthase-like protein ;supported by full-length cDNA: Ceres:117923.	247138_at 0.6
GTP-binding protein-like	247098_at 0.6
unknown protein ;supported by full-length cDNA: Ceres:8440.	246953_at 0.6
tSNARE AtTLG2a ; supported by cDNA: gi_4932458 gb_AF067789.2 AF067789	246803_at 0.6
putative protein hypothetical protein slr1702 - Synechocystis sp., PIR:S75312; supported by cDNA: gi_13877992_gb_AF370259.1_AF	_
serine/threonine protein kinase SOS2 (gb AAF62923.1); supported by cDNA: gi_14701909_gb_AF395081.1_AF395081 hypothetical protein predicted by genemark.hmm	246614_at 0.6 246576_at 0.6
pyrroline-5-carboxylate reductase ;supported by full-length cDNA: Ceres:36386.	246594 at 0.6
dolichyl-phosphate-manoseglycolipid alpha-manosyltransferase-like protein dolichyl-phosphate-manoseglycolipid alpha-mannos	
N2.N2-dimethylguanine RNA methyltransferase-like protein several N2.N2-dimethylguanine RNA methyltransferases	246521 at 0.6
amino acid permease, putative contains Pfam profile: PF00324: Amino acid permease	246259_at 0.6
MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN ; supported by cDNA: gi_1263313_gb_L47323.1_ATHCNX1R	246131 at 0.6
putative protein predicted proteins - Arabidopsis thaliana	246112 at 0.6
putative protein KED, Nicotiana tabacum, EMBL:AB009883	246059_at 0.6
putative protein ER66 - Lycopersicon esculentum, EMBL:AF096260	245910_at 0.6
putative subunit of TOC complex chloroplast gene Toc64 - Pisum sativum, EMBL:AF179282	245879_at 0.6
sulfate transporter ; supported by cDNA: gi_2626752_dbj_AB008782.1_AB008782	245855_at 0.6
G-Box binding protein, putative similar to G-Box binding protein 2 GB:AAD42938 GI:5381313 from [Catharanthus roseus]	245786_at 0.6
hypothetical protein contains similarity to glucosidase II beta-subunit GI:5452942 from [Mus musculus]	245727_at 0.6
hypothetical protein	245619_at 0.6
phytochrome D	245487_at 0.6
hypothetical protein	245374_at 0.6
casein kinase I ; supported by cDNA: gi_15450524_gb_AY052364.1	245294_at 0.6
syntaxin ; supported by cDNA: gi_2149379_gb_U85036.1_ATU85036	245278_at 0.6
scarecrow-like 13 (SCL13); supported by cDNA: gi_16930432_gb_AF419570.1_AF419570	245247_at 0.6
putative protein similarity to NCA2 protein, yeast, PIR:S54389~Contains Homeobox domain signature and profile AA305-328	245206_at 0.6
transcription factor IIB (TFIIB) identical to GB:P48512; contains a transcription factor TFIIB repeat signature (PDOC00624);supported b putative protein kinase contains a protein kinase domain profile (PDOC00100)	by full-length c 245114_at 0.6 245074_at 0.6
ATPase a subunit	245074_at 0.6 244995 at 0.6
ribosomal protein S14	245005 at 0.6
hypothetical protein predicted by genscan	257447_at 0.6
putative alpha/beta hydrolase contains Pfam profile: PF00561 alpha/beta hydrolase fold; predicted by genscan	257533 at 0.6
unknown protein contains Pfam profile:PF00400 WD domain, G-beta repeat	257553 at 0.6
unknown protein ESTs gb/AA042402,gb/ATTS1380 come from this gene	264572_at 0.6
inositol 1,3,4-trisphosphate 5/6-kinase-like protein inositol 1,3,4-trisphosphate 5/6-kinase (EC 2.7) - Arabidopsis thaliana, PIR2:JC5	
putative dolichyl-phosphate beta-glucosyltransferase ; supported by cDNA: gi_15810210_gb_AY056120.1_	266986_at 0.5
hypothetical protein predicted by genscan	265521_at 0.5
putative ARF1 family auxin responsive transcription factor	265454_at 0.5
hypothetical protein predicted by genscan and grail	265429_at 0.5
26S proteasome regulatory subunit, putative similar to GB:AAC04490 from [Arabidopsis thaliana]	261174_at 0.5
glycine-rich RNA-binding protein grp1a, putative similar to glycine-rich RNA-binding protein grp1a GB:L31374 GI:496232 from [Sinapis	alba] 260923_at 0.5

unknown protein	260719_at	0.5
putative choline kinase similar to GB:AAC49376 from [Glycine max]	260244_at	0.5
shaggy-like kinase, putative similar to Petunia Shaggy kinase 4 GI:619894 from [Petunia hybrida]; supported by cDNA: gi_14334749_gb_AY035048		0.5
putative T-complex protein 1, ETA subunit similar to T-complex protein 1, ETA subunit GB:P80313 [Mus musculus]	258776_at	0.5
unknown protein similar to hypothetical protein GB:CAB10220 from [Arabidopsis thaliana]	257916_at	0.5 0.5
Expressed protein ; supported by full-length cDNA: Ceres: 12588. putative protein	257152_at 254797 at	0.5
putative protein DNA polymerase III holoenzyme tau subunit, Thermus thermophilus, gb:AF025391	254643 at	0.5
putative protein MSP1 protein, Sancharomyces cerevisia, PIR2:A49506;supported by full-length cDNA: Ceres:142160.	253861_at	0.5
serine threenine-protein kinase-like protein Ca2+ calmodulin-dependent protein kinase - Rattus norvegicus, PIR-A57156; supported by cDNA: gi 14		0.5
	251725 at	0.5
nicotianamine synthase (dbjlBAA74589.1)	250832 at	0.5
putative protein	250421 at	0.5
putative protein strong similarity to unknown protein (pir  T04769); supported by cDNA: gi_14030630_gb_AF375406.1_AF375406	248977_at	0.5
putative protein contains similarity to unknown protein (dbj BAA13214.1)	248465_at	0.5
zinc finger protein	247054_at	0.5
putative protein ;supported by full-length cDNA: Ceres:108509.	246840_at	0.5
putative protein predicted proteins, Arabidopsis thaliana	245900_at	0.5
NADH dehydrogenase subunit 4	244929_at	0.5
	Athal-25SrRN	0.5
Arabidopsis thaliana /REF=M64116 /DEF=glyceraldehyde 3-phosphate dehydrogenase C subunit (GapC) gene, complete cds /LEN=1295 (_5,M,A		0.5
heme oxygenase 1 (HO1) identical to GB:AF132475; annotation updated per Seth J. Davis at University of Wisconsin-Madison; supported by full-len	_	0.5
putative uricase subunit similar to nodulin-35; identical to GB:Y11120;supported by full-length cDNA: Ceres:38538.	267374_at	0.5
putative translation initiation factor eIF-2B delta subunit GDP dissociation inhibitor identical to GB:D83531;supported by full-length cDNA: Ceres:29536.	267229_s_at 267236 at	0.5 0.5
Core dissociation immotion relinicanto de Dosso r, supported by numeriquir cores. 25000. hypothetical protein predicted by rail: supported by full-length CDNA: Cores: 35095.	267152 at	0.5
upbutered protein prediced by grain, supported by inimergur correct ceres. Society. Despondence of the second	267112 at	0.5
unknown protein ; supported by full-length cDNA: Ceres:2337.	267078 at	0.5
unknown protein	267040 at	0.5
hypothetical protein predicted by genefinder	267048 at	0.5
	267009 at	0.5
utative ABC transporter related to multi drug resistance proteins and P-glycoproteins	266856 at	0.5
unknown protein ;supported by full-length cDNA: Ceres:26655.	266657 at	0.5
unknown protein ;supported by full-length cDNA: Ceres:12086.	266646_at	0.5
unknown protein ; supported by cDNA: gi_14532581_gb_AY039915.1_	266315_at	0.5
unknown protein ;supported by cDNA: gi_13358176_gb_AF324984.2_AF324984	266207_at	0.5
subtilisin-like serine protease, putative contains similarity to cucumisin-like serine protease GI:3176874 from [Arabidopsis thaliana]	266022_at	0.5
putative carbonyl reductase	266015_at	0.5
putative disease resistance protein	265917_at	0.5
putative lipase	265646_at	0.5
putative ferredoxin ; supported by full-length cDNA: Ceres: 26333.	265649_at	0.5
unknown protein	265570_at	0.5
putative N-acetylglucosaminyltransferase	265366_at	0.5
unknown protein putetie lywiag histige papelia pameraag similer to CP-AAC40895, similer to EST shlT12004, supported by sDNA; si 0202850, dbi AB046240, 1	265098_at	0.5
putative lysine/histidine-specific permease similar to GB:AAC49885, similar to EST gb[T13994; supported by cDNA: gi_9293859_dbj_AB046210.1_/ auxin-induced protein, putative similar to auxin-induced atb2 GI:6562980 from [Arabidopsis thaliana]; supported by cDNA: gi_6562979 gb_AF05771		0.5 0.5
autri-induced protein, putative similar to autri-induced allo Grooodson rindi and to A, thandboys intrainana, supported by CDAX, grooodson group and the standard state for channel protein similar to ligand-gated ion channel protein similar to ligand-gated ion channels and to A, thaliana protein T21B4.3; supported by CDAX, grooodson to ligand-gated ion channel protein similar to ligand-gated ion channels and to A, thaliana protein T21B4.3; supported by CDAX, gr		0.5
updative ligance particular in the protein similar to grandrogate unit of an analysis of the statistical protein similar to putative serine/threeonine kinase G14585880 from [Arabidopsis thaliana],supported by full-length cDNA: Gres:13461.	264767_at	0.5
	264722 at	0.5
putative K+ channel, beta subunit similar to GB:AAA87294;supported by full-length cDNA: Ceres:23300.	264607 at	0.5
utative heat-shock protein similar to GB:AAD39315;supported by full-length cDNA: Ceres:37036.	264464 at	0.5
putative phragmoplastin similar to dynamin-like protein phragmoplastin (gi 3341679); similar to ESTs gb W43823, gb N37665, gn R90466, gb T8840	_	0.5
hypothetical protein predicted by genemark.hmm	264427 at	0.5
putative translation initiation factor eIF-2, gamma subunit similar to gb/U37354 from S. pombe. ESTs gb/T41979, gb/N37284 and gb/N37529 come fi	264327_at	0.5
hypothetical protein contains non-consensus donor splice site AT at exon 4 and acceptor splice site at exon5; Contains similarity to serine/threonine r	264331_at	0.5
hypothetical protein similar to hypothetical protein GI:2894569 from [Arabidopsis thaliana]; supported by cDNA: gi_15028186_gb_AY045916.1_	264289_at	0.5
replicase, putative similar to replicase GI:166841 from [Arabidopsis thaliana]; supported by cDNA: gi_15292902_gb_AY050885.1_	264099_at	0.5
unknown protein ;supported by full-length cDNA: Ceres:5167.	263900_at	0.5
putative s-adenosylmethionine synthetase ;supported by full-length cDNA: Ceres:13320.	263838_at	0.5
putative indole-3-glycerol phosphate synthase ;supported by full-length cDNA: Ceres:3006.	263807_at	0.5
putative ATP-dependent RNA helicase	263435_at	0.5
	263447_s_at	0.5
putative histone H2B ;supported by full-length cDNA: Ceres:14965.	263412_at	0.5
putative ubiquitin-like protein ; supported by cDNA: gi_14334545_gb_AY035177.1_ ; unknown protein similar to ESTs gb T43206, gb H76501, gb AA651577, and gb AA605326;supported by full-length cDNA: Ceres:7488.	263422_s_at 263206 at	0.5 0.5
transport protein, putative similar to transport protein GI7268121 from (Arabidopsis Halinan); supported by CINA: gi 15912296 gb AV956426.1	263185 at	0.5
transport protein, putative similar to transport protein 61.7200121 norm (Nationopsis transmins), supported by Converging 10512230 gp-A1000420.1	263143 at	0.5
hypothetical protein similar to hypothetical ABC transporter ATP-binding protein GI:9953395 from [Microcystis aeruginosa]	263000 at	0.5
information protein summar to information to DNA: Ceres: 13758.	262955_at	0.5
sterol glucosyltransferase, putative similar to sterol glucosyltransferase GI:4731867 from [Dictyostelium discoideum]	262722 at	0.5
putative ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase highly similar to ribulose-1,5 bisphosphate carboxylase		0.5
unknown protein ; supported by cDNA: gi 15215593 gb AY050325.1	262634 at	0.5
oxidoreductase, putative contains Pfam profile: PF00671 Iron/Ascorbate oxidoreductase family; supported by cDNA: gi 13430545 gb AF360185.1		0.5
unknown protein Similar to gb AJ005073 Alix (ALG-2-interacting protein X) from Mus musculus. ESTs gb R90133, gb Z17944 and gb AA605465 con	262588_at	0.5
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:117456.	262398_at	0.5
	262319_s_at	0.5
	262306_s_at	0.5
unknown protein	262308_at	0.5
alpha-xylosidase precursor identical to alpha-xylosidase precursor GB:AAD05539 GI:4163997 from [Arabidopsis thaliana]; supported by cDNA: gi_1{		0.5
unknown protein ; supported by cDNA: gi_6520226_dbj_AB028230.1_AB028230	262079_at	0.5
unknown protein ;supported by full-length cDNA: Ceres:37300.	261900_at	0.5
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:93534.	261787_at	0.5
non-phototropic hypocotyl, putative similar to non-phototropic hypocotyl 3 GB:AAF05914 GI:6224712 from [Arabidopsis thaliana] calcaliculus putative similar to administrational and a calcaliculus from (Arabidopsis thaliana) and a calcaliculus CB-14 A	261796_at	0.5
calreticulin, putative similar to calreticulin GB:AAC49697 GI:2052383 from [Arabidopsis thaliana]; supported by cDNA: gi_2052382_gb_U66345.1_A		0.5
unknown protein ;supported by full-length cDNA: Ceres:33310.	261677_at 261622_at	0.5
hypothetical protein predicted by genemark.hmm ribosomal protein L9, putative similar to RIBOSOMAL PROTEIN L9 GB:P49209 from [Arabidopsis thaliana]	261622_at 261620_s_at	0.5 0.5
	_0.020_0_al	0.0

phytochrome kinase substrate 1, putative similar to phytochrome kinase substrate 1 GI:5020168 from [Arabidopsis thaliana]; supported by full-length		0.5
calcium-dependent protein kinase, putative similar to calcium-dependent protein kinase GI:604880 from [Arabidopsis thaliana]; supported by cDNA:		0.5
unknown protein	261258_at	0.5
NAM protein, putative similar to NAM protein GI:6066594 from [Petunia hybrid]; supported by cDNA; gi_14334571_gb_AY034959.1_ https://doi.org/10.1016/jb.101610101010101010101010101010101010101	261192_at	0.5
transcription factor IIA large subunit similar to GB:CAA11525 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:19512. 2 transcriptional activator RF2a, putative similar to transcriptional activator RF2a GB:AF005492 GI:2253277 from [Oryza sativa];supported by full-length	261079_s_at	0.5 0.5
	260789 s at	0.5
RING-H2 finger protein RHA3a, putative similar to RING-H2 finger protein RHA3a GI:3790573 from [Arabidopsis thaliana]; supported by cDNA: gi 1		0.5
unknown protein contains similarity to nucellin GI:2290203 from [Hordeum vulgare]; supported by cDNA: gi 13430539 gb AF360182.1 AF360182	260772 at	0.5
polygalacturonase PG1, putative similar to GB:AAD46483 from [Glycine max] (Mol. Plant Microbe Interact. 12 (6), 490-498 (1999)); supported by cD	260727_at	0.5
unknown protein	260595_at	0.5
putative glucosyltransferase ;supported by full-length cDNA: Ceres:34407.	260567_at	0.5
putative salt-inducible protein	260523_at	0.5
Expressed protein ; supported by cDNA: gi_13605678_gb_AF361820.1_AF361820 Ser/Thr kinase :supported by full-length cDNA: Ceres:100245.	260500_at	0.5
unknown protein similar to hypothetical protein GB:CAA10289 [Cicer arietinum]	260480_at 260401_at	0.5 0.5
	260387 at	0.5
Expressed protein ; supported by full-length CDNA: Ceres: 16467.	260352 at	0.5
putative glycerol kinase similar to GLYCEROL KINASE GB:069664 from (Mycobacterium tuberculosis)	260274_at	0.5
unknown protein contains Pfam profile: PF00561 alpha/beta hydrolase fold;supported by full-length cDNA: Ceres:36063.	260232_at	0.5
putative protein kinase Pfam HMM hit: Eukaryotic protein kinase domain; C-term region is similar to C-term region of chicken protein kinase PITSLRE		0.5
	260172_s_at	0.5
calmodulin-4 identical to GB:Q03510 from [Arabidopsis thaliana] (Plant Mol. Biol. 22 (2), 215-225 (1993)); supported by full-length cDNA: Ceres: 698 untersected and the second s		0.5
unknown protein putative MAP kinase similar to mitogen-activated protein kinase GB:A56042 [Dictyostelium discoideum]; contains Pfam profile: PF00069 Eukaryotic r	260069_at	0.5 0.5
putative wirk initiase similar to mitogenerativate protein timase 60.20042 [bictydsteinum discoldenti], contains nam prome. Proceeds burking the approximate protein supported by full-length CDNA (Ceres: 270659.	260045_at	0.5
cell division control protein, putative similar to SP:P40986 from [Saccharomyces cerevisiae]	259960 at	0.5
putative casein kinase I similar to casein kinase I GB:CAA55395 [Arabidopsis thaliana]; supported by cDNA: gi 16648960 gb AY059850.1	259865 at	0.5
unknown protein contains similarity to cytochrome oxidase I GI:1289267 from (Xantholinus sp.); supported by full-length cDNA: Ceres:6875.	259594_at	0.5
unknown protein ;supported by full-length cDNA: Ceres:37735.	259475_at	0.5
unknown protein similar to putative dehydrogenase GI:1922246 from [Arabidopsis thaliana]; supported by cDNA: gi_15408534_dbj_AB032060.1_AB		0.5
	259335_s_at	0.5
unknown protein andriw finites 4.5 biachardath andre (awarang and a shuit N mathulkan fanna Lainille ta thulang 4.5 biachardath andre (aw	259302_at	0.5
putative ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I similar to ribulose-1,5-bisphosphate carboxylase/oxy RNA helicase, DRH1 identical to RNA helicase DRH1 GB:BAA28347 [Arabidopsis thaliana]; supported by cDNA: gi 15215693 gb AY050375.1	259258_at 259194 at	0.5 0.5
transport protein SEC13, putative similar to protein transport protein SEC13 GB:P53024 [Pichia pastoris]; supported by full-length cDNA: Ceres:3733	_	0.5
autopart production registry, paratro entrance protein autopart protein au	259060 at	0.5
unknown protein similar to unknown protein GB:BAA83351 [Oryza sativa]; supported by cDNA: gi_14334835_gb_AY035091.1_	258992_at	0.5
unknown protein similar to putative guanine nucleotide binding protein GB:CAB08769 [Schizosaccharomyces pombe]; supported by cDNA: gi_16648	258994_at	0.5
unknown protein contains Pfam profile: PF00514 armadillo/beta-catenin-like repeats (4 copies);supported by full-length cDNA: Ceres:34582.	258954_at	0.5
unknown protein similar to putative Anion exchanger family members: GB:AAD39673, GB:AAD55295 [Arabidopsis thaliana]	258913_at	0.5
Mutator-like transposase similar to MURA transposase of maize Mutator transposon	258789_at	0.5
putative Ras-like GTP-binding protein contains Pfam profile: PF00071 Ras family;supported by full-length cDNA: Ceres:10506. putative myo-inositol monophosphatase similar to myo-inositol-1(or 4)-monophosphatase 3 (IMP 3) GB:P54928 [Lycopersicon esculentum];supporter	258656_at	0.5 0.5
disease resistance gene (RPM1) identical to disease resistance gene (RPM1) GB:X87851 [Arabidopsis thalana]	258544 at	0.5
galactose kinase identical to GB:AAB94084 from [Arabidopsis thaliana] (Plant Mol. Biol. (1999) 39 (5), 1003-1012); supported by cDNA: gi 2736185		0.5
putative tyrosyl-tRNA synthetase similar to TYROSYL-TRNA SYNTHETASE GB:P04077 from [Bacillus caldotenax]	258475_at	0.5
unknown protein	258448_at	0.5
20S proteasome subunit PAE2 identical to 20S proteasome subunit PAE2 GB:AAC32061 from [Arabidopsis thaliana]; supported by cDNA: gi_34210		0.5
hypothetical protein predicted by genemark	258317_at	0.5
hypothetical protein predicted by genemark unknown protein ; supported by cDNA: gi 14334929 gb AY035138.1	258292_at 258298 at	0.5 0.5
unknown protein similar to serine/threonine kinase receptor associated protein GB:NP 035629 [Mus musculus], unr-interacting protein GB:NP 0091	_	0.5
putative acetyltransferase similar to dihydrolipoamide S-acetyltransferase GB:AAD46491 from [Zea mays]; supported by CDNA: gi_13605806_gb_AF		0.5
aldose 1-epimerase, putative similar to ALDOSE 1-EPIMERASE PRECURSOR GB:P05149 from [Acinetobacter calcoaceticus]; supported by cDNA		0.5
integral membrane protein, putative contains Pfam profile: PF01554 uncharacterized membrane protein family	258179_at	0.5
hypothetical protein contains Pfam profile: PF01535 domain of unknown function (4 copies)	258149_at	0.5
Expressed protein ; supported by full-length cDNA: Ceres: 12996.	258041_at	0.5
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:108820.	257985_at	0.5
Expressed protein ; supported by full-length cDNA: Ceres: 32454. hypothetical protein	257659_at 257641_s_at	0.5 0.5
S-adenosyl-L-homocysteinas, putative similar to S-adenosyl-L-homocysteinase GB:AAD56048 from [Lupinus luteus]; supported by cDNA: gi 15292		0.5
putative protein phosphatase type 2C similar to protein phosphatase type 2C GB:AAD17805 from [Lotus japonicus]	257050_at	0.5
fucosyltransferase, putative similar to Fuct c3 protein GB:CAB52254 from [Vigna radiata] (J. Biol. Chem. (1999) 274 (31), 21830-21839)	257031_at	0.5
unknown protein similar to auxin-independent growth promoter GB: A44226 [Nicotiana tabacum];supported by full-length cDNA: Ceres:36984.	256879_at	0.5
	256836_at	0.5
multispanning membrane protein, putative similar to transmembrane 9 superfamily membrane 2 GB:NP_004791 from [Homo sapiens] (Gene 216 (199) handbellut to the superfamily membrane in Control of the superfamily memb	256776_at	0.5
hypothetical protein contains similarity to transporter proteins; supported by cDNA: gi_15810468_gb_AY056273.1_ hypothetical protein similar to putative acyl-CoA:1-acylglycerol-3-phosphate acyltransferase GB:AAF21074 from [Arabidopsis thaliana]	256650_at 256652_at	0.5 0.5
unknown protein sumported by full-length CDNA: Ceres:42677.	256543 at	0.5
oxidoreductase, putative contains Pfam profile: PF01408: oxidoreductase, Gfo/Idh/MocA family	256514 at	0.5
unknown protein	256489_at	0.5
pheromone receptor, putative (AR401) identical to AR401 [Arabidopsis thaliana] GI:1669601;supported by full-length cDNA: Ceres:3969.	256380_at	0.5
GTPase, putative contains Pfam profile: PF01926 GTPase of unknown function	256274_at	0.5
omega-6 fatty acid desaturase, endoplasmic reticulum (FAD2) identical to omega-6 fatty acid desaturase, endoplasmic reticulum (FAD2) SP:P46315		0.5
betaine aldehyde dehydrogenase, putative similar to betaine aldehyde dehydrogenase (BADH) GI:1813537 [Spinacia oleracea]	256246_at	0.5
zinc finger protein, putative similar to zinc finger protein GI:8843731 from [Arabidopsis thaliana] aminoalcoholphosphotransferase identical to aminoalcoholphosphotransferase GI:3661593 from [Arabidopsis thaliana]; supported by cDNA: gi 3661	256149_at 256134_at	0.5 0.5
animolacionophicamiserase democante amanconophiciphicamiserase on sources in our preasing supported by converging on the predicted by genscan+; supported by CDNA; gi 15810574 gb AY056326.1	256069 at	0.5
hypothetical protein protains plana by generating approved by generating into a gene	256043_at	0.5
unknown protein contains similarity to alternative NADH-dehydrogenase GI:3718005 from [Yarrowia lipolytica];supported by full-length cDNA: Ceres:		0.5
unknown protein	255963_at	0.5
unknown protein	255928_at	0.5
putative pseudouridine synthase	255864_at	0.5
hypothetical protein similar to putative phloem transcription factor GI:7630279 from [Apium graveolens]	255725_at	0.5
hypothetical protein putative protein similar to nucleolin protein; supported by cDNA: gi 13605915 gb AF367357.1 AF367357	255640_at 255598_at	0.5 0.5
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predicted protein of unknown function similar to M. truncatula MtN21, GenBank accession number Y15293; F11O4.14 was picked up in a screen for		
	255578_at	0.5
predicted OR23 protein of unknown function	255469_at	0.5
score=37.6, E=2.9e-07, N=3	255194_at	0.5
putative alpha NAC stong similarity to Nascent polypeptide associated complex alpha chain - human, PIR2:S49326; supported by cDNA: gi_150279	254981_at	0.5
predicted protein of unknown function	254936_at	0.5
ACC synthase (AtACS-6) ; supported by cDNA: gi_16226285_gb_AF428292.1_AF428292	254926_at	0.5
putative transport protein Na(+) dependent transporter (Sbf family) - Aquifex aeolicus, PIR2:E70482; supported by cDNA: gi_15215838_gb_AY0504		0.5
hydrolase-like protein 2-hydroxy-6-oxohepta-2,4-dienoate hydrolase (EC 3.7) - Synechocystis sp., PIR2:S77427; supported by full-length cDNA: C	254783_at	0.5
putative protein several hypothetical proteins - Arabidopsis thaliana	254800_at	0.5
putative protein predicted protein, Arabidopsis thaliana; supported by cDNA: gi_14326542_gb_AF385725.1_AF385725	254704_at	0.5
DAG-like protein DAG precursor, Antirrhinum majus, MNOS:S71747	254493_at	0.5
peroxidase prxr1 ;supported by full-length cDNA: Ceres:20758.	254386_at	0.5
putative protein various predicted proteins, Arabidopsis thaliana	254320_at	0.5
calcium-dependent protein kinase (CDPK6) ;supported by full-length cDNA: Ceres:37278.	254224_at	0.5
ubiquitin activating enzyme - like protein ubiquitin activating enzyme, Lycopersicon esculentum, gb:AJ011118;supported by full-length cDNA: Ceres:		0.5
glutamine cyclotransferase precursor - like protein glutamine cyclotransferase precursor, Carica papaya, AF061240;supported by full-length cDNA: (	_	0.5
	254050_s_at	0.5
arginyl-IRNA synthetase	254004_at	0.5
putative uracil phosphoribosyl transferase uracil phosphoribosyl transferase, Saccharomyces cerevisiae, PIR2:JH0147supported by full-length cDNA putative uracil phosphoribosyl transferase uracil phosphoribosyl transferase, Saccharomyces cerevisiae, PIR2:JH0147supported by full-length cDNA patients in PDP20 error to Understand the full length and the physical sector of the physical sect		0.5
putative protein ENOD20 gene, Medicago truncatula, X99467; supported by full-length cDNA: Ceres: 33380.	253875_at	0.5
putative acyl-CoA binding protein strong similarity to acyl-CoA binding protein - Arabidopsis thaliana, PID:g4128197;supported by full-length cDNA: C reported life protein strong similarity to acyl-CoA binding protein - Arabidopsis thaliana, PID:g4128197;supported by full-length cDNA: C		0.5
receptor-like protein kinase 5 precursor (RLK5) ; supported by cDNA: gi_166849_gb_M84660.1_ATHRLPKC putative protein predicted proteins, Arabidopsis thaliana	253779_at 253686 at	0.5 0.5
putative protein produce proteins, Arabidopsis inaliana threonine synthase	253000_at	0.5
uneovine syntase putative protein	253577_at	0.5
Expressed protein ; supported by full-length cDNA: Ceres: 37878.	253548 at	0.5
putative protein Fidipidine, Drosophila melanogaster, gb:AJ011928; supported by cDNA: gi 14334641 gb AY034994.1	253441_at	0.5
protein kinase AME3; supported by cDNA: gi_64213_dbj_D45355.1_ATHPKAME3C	253395 at	0.5
Tic22 -like protein strong homology to Tic22 -Pisum sativum, PID:g3769671	253381_at	0.5
hypothetical protein ; supported by cDNA: gi_16604594_gb_AY059742.1_	253310 at	0.5
Phosphoglycerate dehydrogenase - like protein Phosphoglycerate dehydrogenase, Arabidopsis thaliana, PATCHX:D1021238;supported by full-leng		0.5
subtilisin-like serine protease similar to SBT1, a subtilase from tomato plants GI:1771160 from [Lycopersicon esculentum]	253218 at	0.5
	253220 s at	0.5
putative protein protein kinase APK1, Arabidopsis thaliana, PIR2:S28615; supported by cDNA: gi 16612248 gb AF439824.1 AF439824	253184 at	0.5
putative protein protein kinase 6, Glycine max, PIR2:S29851	253158 at	0.5
putative protein predicted protein, Synechocystis sp., PIR2:S75747;supported by full-length cDNA: Ceres:42841.	253160 at	0.5
homeodomain - like protein several homeodomain transcription factors; supported by cDNA: gi 15081750 gb AY048268.1	253131 at	0.5
putative protein CRP1, Zea mays, gb:AF073522;supported by full-length cDNA: Ceres:5482.	253116_at	0.5
aldehyde dehydrogenase like protein aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) 4, microsomal, rat, PIR2:A41028	253083_at	0.5
putative protein beta-ketoadipate enol-lactone hydrolase, Acinetobacter sp., L05770; supported by cDNA: gi_15810302_gb_AY056190.1_	253053_at	0.5
putative protein various predicted proteins	253071_at	0.5
putative protein permease 1 - Mesembryanthemum crystallinum,PID:g3202040	253021_at	0.5
ES43 like protein ES43 protein - barley, PIR2:S44281;supported by full-length cDNA: Ceres:8278.	252925_at	0.5
putative protein	252909_at	0.5
	252883_at	0.5
putative transposase hypothetical protein a, maize transposable element Ac - Zea mays, PIR:T02916	252847 at	
		0.5
	252344_s_at	0.5
putative protein APRIL protein, Homo sapiens, EMBL:HSAPRIL_1	252344_s_at 252174_at	0.5 0.5
putative protein APRIL protein, Homo sapiens, EMBL:HSAPRIL_1 GDP-D-mannose-4,6-dehydratase (MUR1) ;supported by full-length cDNA: Ceres:11217.	252344_s_at 252174_at 252121_at	0.5 0.5 0.5
putative protein APRIL protein, Homo sapiens, EMBL:HSAPRIL_1 GDP-D-mannose-4,6-dehydratase (MUR1) ;supported by full-length cDNA: Ceres:11217. mucin -like protein hemomucin, Drosophila melanogaster, EMBL:DM42014;supported by full-length cDNA: Ceres:34197.	252344_s_at 252174_at 252121_at 252117_at	0.5 0.5 0.5 0.5
putative protein APRIL protein, Homo sapiens, EMBL:HSAPRIL_1 GDP-D-mannose-4,6-dehydratase (MUR1) ;supported by full-length cDNA: Ceres:11217. mucin-like protein hemomucin, Drosophila melanogaster, EMBL:DM42014;supported by full-length cDNA: Ceres:34197. putative protein hinf protein -Nicotiana tabacum,PID:e259431;supported by full-length cDNA: Ceres:92178.	252344_s_at 252174_at 252121_at 252117_at 252058_at	0.5 0.5 0.5 0.5 0.5
putative protein APRIL protein, Homo sapiens, EMBL:HSAPRIL_1 GDP-D-mannose-4,6-dehydratase (MUR1) ;supported by full-length cDNA: Ceres:11217. mucin -like protein hemomucin, Drosophila melanogaster, EMBL:DM42014;supported by full-length cDNA: Ceres:34197. putative protein hin1 protein -Nicotiana tabacum,PID:e259431;supported by full-length cDNA: Ceres:92178. hypothetical protein KIAA0253 protein, Homo saoiens, SWISSPROT:Y253_HUMAN	252344_s_at 252174_at 252121_at 252117_at 252058_at 252062_at	0.5 0.5 0.5 0.5 0.5 0.5
putative protein APRIL protein, Homo sapiens, EMBL:HSAPRIL_1 GDP-D-mannose-4,6-dehydratase (MUR1) ;supported by full-length cDNA: Ceres:11217. mucin -like protein hemorucin, Drosophila melanogaster, EMBL:DM42014;supported by full-length cDNA: Ceres:34197. putative protein hin1 protein -Nicotiana tabacum,PID:e259431;supported by full-length cDNA: Ceres:92178. hypothetical protein KIAA0253 protein, Homo saoiens, SWISSPROT:Y253_HUMAN beta-galactosidase precursor - like protein beta-galactosidase precursor, Carica papaya, EMBL:AF064786; supported by cDNA: gi_13605856_gb_A	252344_s_at 252174_at 252121_at 252117_at 252058_at 252062_at 251996_at	0.5 0.5 0.5 0.5 0.5 0.5 0.5
putative protein APRIL protein, Homo sapiens, EMBL:HSAPRIL_1 GDP-D-mannose-4,6-dehydratase (MUR1) ;supported by full-length cDNA: Ceres:11217. mucin -like protein hemomucin, Drosophila melanogaster, EMBL:DM42014;supported by full-length cDNA: Ceres:34197. putative protein hin1 protein -Nicotiana tabacum,PID:e259431;supported by full-length cDNA: Ceres:92178. hypothetical protein KIAA0253 protein, Homo saoiens, SWISSPROT:Y253_HUMAN beta-galactosidase precursor - like protein beta-galactosidase precursor, Carica papaya, EMBL:AF064786; supported by cDNA: gi_13605856_gb_A nodulin / glutamate-ammonia ligase - like protein MtN6 - nodulin 6, Medicago truncatula, EMBL:MET133118	252344_s_at 252174_at 252121_at 252117_at 252058_at 252062_at 251996_at 251973_at	0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5
putative protein APRIL protein, Homo sapiens, EMBL:HSAPRIL_1 GDP-D-mannose-4,6-dehydratase (MUR1) ;supported by full-length cDNA: Ceres:11217. mucin -like protein hemomucin, Drosophila melanogaster, EMBL:DM42014;supported by full-length cDNA: Ceres:34197. putative protein hin1 protein -Nicotiana tabacum,PID:e259431;supported by full-length cDNA: Ceres:92178. hypothetical protein KIAA0253 protein, Homo saoiens, SWISSPROT:Y253_HUMAN beta-galactosidase precursor - like protein beta-galactosidase precursor, Carica papaya, EMBL:AF064786; supported by cDNA: gi_13605856_gb_A nodulin / glutamate-ammonia ligase - like protein MtN6 - nodulin 6, Medicago truncatula, EMBL:MET133118 putative protein KIAA0544 protein, Homo sapiens, EMBL:AB011116;supported by full-length cDNA: Ceres:110247.	252344_s_at 252174_at 252121_at 252121_at 252058_at 252062_at 251996_at 251973_at 251959_at	0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5
putative protein APRIL protein, Homo sapiens, EMBL:HSAPRIL_1 GDP-D-mannose-4,6-dehydratase (MUR1) ;supported by full-length cDNA: Ceres:11217. mucin -like protein hemomucin, Drosophila melanogaster, EMBL:DM42014;supported by full-length cDNA: Ceres:34197. putative protein hin1 protein -Nicotiana tabacum,PID:e259431;supported by full-length cDNA: Ceres:92178. hypothetical protein KIAA0253 protein, Homo saoiens, SWISSPROT:Y253_HUMAN beta-galactosidase precursor - like protein beta-galactosidase precursor, Carica papaya, EMBL:AF064786; supported by cDNA: gi_13605856_gb_A nodulin / glutamate-ammonia ligase - like protein MtN6 - nodulin 6, Medicago truncatula, EMBL:ME1133118 putative protein KIAA0544 protein, Homo sapiens, EMBL:AB011116;supported by full-length cDNA: Ceres:110247. synaptobrevin -like protein vesicle-associated membrane protein 7B (At VAMP7B), Arabidopsis thaliana, EMBL:AF025333	252344_s_at 252174_at 252121_at 252117_at 252058_at 252062_at 251996_at 251973_at 251975_at 251959_at 251877_at	0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5
putative protein APRIL protein, Homo sapiens, EMBL:HSAPRIL_1 GDP-D-mannose-4,6-dehydratase (MUR1) ;supported by full-length cDNA: Ceres:11217. mucin -like protein hemomucin, Drosophila melanogaster, EMBL:DM42014;supported by full-length cDNA: Ceres:34197. putative protein hin1 protein -Nicotiana tabacum,PID:e259431;supported by full-length cDNA: Ceres:92178. hypothetical protein KIAA0253 protein, Homo saoiens, SWISSPROT:Y253_HUMAN beta-galactosidase precursor - like protein beta-galactosidase precursor, Carica papaya, EMBL:AF064786; supported by cDNA: gi_13605856_gb_A nodulin / glutamate-ammonia ligase - like protein MtN6 - nodulin 6, Medicago truncatula, EMBL:MET133118 putative protein KIAA0544 protein, Homo sapiens, EMBL:AB011116;supported by full-length cDNA: Ceres:110247.	252344_s_at 252174_at 252121_at 252117_at 252058_at 252062_at 251996_at 251973_at 251959_at 251877_at 251705_at	0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5
putative protein APRIL protein, Homo sapiens, EMBL:HSAPRIL_1 GDP-D-mannose-4,6-dehydratase (MUR1) ;supported by full-length cDNA: Ceres:11217. mucin -like protein hemomucin, Drosophila melanogaster, EMBL:DM42014;supported by full-length cDNA: Ceres:34197. putative protein hin1 protein -Nicotiana tabacum,PID:e259431;supported by full-length cDNA: Ceres:92178. hypothetical protein KIAA0253 protein, Homo saoiens, SWISSPROT:Y252_HUMAN beta-galactosidase precursor - like protein beta-galactosidase precursor, Carica papaya, EMBL:AF064786; supported by cDNA: gi_13605856_gb_A nodulin / glutamate-ammonia ligase - like protein MtN6 - nodulin 6, Medicago truncatula, EMBL:ME1133118 putative protein KIAA0544 protein, Homo sapiens, EMBL:AB011116;supported by full-length cDNA: Ceres:110247. synaptobrevin -like protein vesicle-associated membrane protein 78 (At VAMP7B), Arabidopsis thaliana, EMBL:AF025333 DNA-binding protein-like DNA-binding protein 4 WRKY4 - Nicotiana tabacum, EMBL:AF193771;supported by full-length cDNA: Ceres:34847.	252344_s_at 252174_at 252121_at 252117_at 252058_at 252062_at 251996_at 251973_at 251959_at 251877_at 251705_at	0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5
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putative protein APRIL protein, Homo sapiens, EMBL:HSAPRIL_1 GDP-D-manose-4,6-dehydratase (MUR1) :supported by full-length cDNA: Ceres:11217. mucin -like protein hemomucin, Drosophila melanogaster, EMBL:DM42014;supported by full-length cDNA: Ceres:34197. putative protein hint protein -Nicotiana tabacum,PID:e259431;supported by full-length cDNA: Ceres:32178. hypothetical protein KIAA0544 protein, Homo sapiens, EMBL:MO113016; Supported by full-length cDNA: Ceres:10247. synaptobrevin -like protein vesicle-associated membrane protein 7B (AI VAMP7B), Arabidopsis thaliana, EMBL:AF025333 DNA-binding protein-like DNA-binding protein 4 WRKY4 - Nicotiana tabacum, EMBL:AF193771;supported by full-length cDNA: Ceres:34847. putative protein MULTICOPY SUPPRESSOR OF RAS1 - Schizosaccharomyces pombe, EMBL:D78582;supported by full-length cDNA: Ceres:4015 dnaJ-like protein DNAJ protein - Schizosaccharomyces pombe, PIR:T39697;supported by full-length cDNA: Ceres:35847. putative protein MULTICOPY SUPPRESSOR OF RAS1 - Schizosaccharomyces pombe, EMBL:D78582;supported by full-length cDNA: Ceres:4015 dnaJ-like protein DNAJ protein - Schizosaccharomyces pombe, PIR:T39697;supported by full-length cDNA: Ceres:120719. 1-acylcorol-3phosphate acyltransferase, like protein 1-acylcorol-3phosphate acyltransferase, Brassica napus, Z49680;supported by full-length cDNA: gl_16209701_gb_AY0576 Rab CDP disocitation inhilbitor ; supportein MRS2 - Saccharomyces cerevisiae, PIR:S6204; supported by cDNA: gl_16209701_gb_AY0576 Rab CDP disocitation inhilbitor ; supported by cLANG: gl_2446980_dl_2A0055601 transketolase - like protein transketolase, Solanum tuberosum, EMBL:Z60099:supported by full-length cDNA: Ceres:15659. putative protein alkB protein -R25A6740 - Arabidopsis thaliana, EMBL:AC004665 putative protein alkB protein -Scherichia coli, PIR:BVECKB disease resistance - like protein transketolase, supported by full-length cDNA: Ceres:1427. peptide methionine sulfoxide reductase (msr) ; supported by full-length cDNA: Ceres:3104. putative protein inskE	252344_s_at 252174_at 252174_at 252121_at 252121_at 252121_at 252052_at 251996_at 251996_at 251973_at 251959_at 251975_at 251657_at 251657_at 251506_at 251536_at 251536_at 251536_at 251352_at 251362_at 251362_at 250401_at 250401_at 250401_at 25047_at 25047_at 25047_at 25047_at 25047_at 25047_at 25047_at 25047_at 25047_at 25047_at 25044_at 249846_at 249347_at 249347_at	$\begin{array}{c} 0.5\\ 0.5\\ 0.5\\ 0.5\\ 0.5\\ 0.5\\ 0.5\\ 0.5\\$
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putative protein APRIL protein, Homo sapiens, EMBL:HSAPRIL_1 GDP-D-mannose-4,6-dehydratase (MUR1) isupported by full-length cDNA: Ceres:11217. mucin -like protein hemomucin, Drosophila melanogaster, EMBL:DM42014;supported by full-length cDNA: Ceres:34197. putative protein hind protein -Nicotiana tabacum,PID:e259431;supported by full-length cDNA: Ceres:32178. hypothetical protein KIAA0542 protein beta-galactosidase precursor, Carica papaya, EMBL:AF064786; supported by cDNA: gi_13605856_gb_A nodulin / glutamate-ammonia ligase - like protein MtNA - nodulin 6, Medicago funcatula, EMBL:AF064786; supported by cDNA: gi_13605856_gb_A nodulin / glutamate-ammonia ligase - like protein MtNA - nodulin 6, Medicago funcatula, EMBL:AF064786; supported by cDNA: ceres:34847. putative protein KIAA0544 protein, Homo sapiens, EMBL:AB011116;supported by full-length cDNA: Ceres:10247. synaptobrevin - like protein a VBK74 - Nicotiana tabacum, EMBL:AF193771;supported by full-length cDNA: Ceres:34847. putative protein MLVITCOPY SUPPRESSOR OF RAS1 - Schizosaccharomyces pombe, [RTSG97:supported by full-length cDNA: Ceres:34015 dnaJ-like protein FbAD protein - Schizosaccharomyces pombe, PIRT-Sg997:supported by full-length cDNA: Ceres:34015 dnaJ-like protein MtAC protein Schizosaccharomyces pombe, PIRT-SG2064; supported by full-length cDNA: Ceres:34534. putative protein intochondria RNA splicin gortein MRS2 - Saccharomyces cerevisae. PIR:S62064; supported by full-length cDNA: Gress:15659. putative protein intoskotakase, Solanum tuberosum, EMBL:A50099 supported by full-length cDNA: Ceres:15659. putative protein insketolase, Solanum tuberosum, EMBL:A50099 supported by full-length cDNA: Ceres:15659. putative protein insketolase, Solanum tuberosum, EMBL:A500995 supported by full-length cDNA: Ceres:16659. putative protein insketolase, Solanum tuberosum, EMBL:A500995 supported by full-length cDNA: Ceres:16659. putative protein inke protein rp.8, Arabidopsis thaliana, EMBL:AF089711; supported by cDNA: gi_15292720_gb_AY050794.1_ short chain alchof	252344_s_at 252174_at 252174_at 252121_at 252117_at 252058_at 252058_at 251996_at 251996_at 251975_at 251959_at 251705_at 251657_at 251657_at 251652_at 251538_at 251538_at 251538_at 251538_at 251538_at 251396_at 251326_at 251326_at 251326_at 251326_at 250360_at 250401_at 250609_at 250401_at 25047_at 250047_at 250047_at 250047_at 250047_at 250047_at 250047_at 250047_at 250047_at 250047_at 250047_at 250047_at 250047_at 250047_at 250047_at 250047_at 249946_at 249946_at 249748_at 249748_at 249748_at 249748_at 249748_at 249748_at 249748_at 249208_at	$\begin{array}{c} 0.5\\ 0.5\\ 0.5\\ 0.5\\ 0.5\\ 0.5\\ 0.5\\ 0.5\\$
putative protein APRIL protein, Homo sapiens, EMBL:HSAPRIL_1 GDP-D-manose-4.6-dehydratase (MUR1) isupported by full-length cDNA: Ceres:11217. mucin -like protein henomucin, Drosophila melanogaster, EMBL:DM42014;supported by full-length cDNA: Ceres:34197. putative protein hind protein -Nicotiana tabacum, PID:e259431 supported by full-length cDNA: Ceres:32178. hypothetical protein KIAA0544 protein, Homo sapiens, SWISSPROT:Y253_HUMAN beta-galactosidase precursor - like protein beta-galactosidase precursor, Carica papaya, EMBL:AF064786; supported by cDNA: gi_13605856_gb_A nodulin / glutamate-ammonia ligase - like protein MIN- nodulin 6, Medicago funcatula, EMBL:MET133118 putative protein KIAA0544 protein, Homo sapiens, EMBL:AB011116;supported by full-length cDNA: Ceres:110247. synaptobrevin -like protein vesicle-associated membrane protein 78 (At VAMP7B). Arabidopsis thaliana, EMBL:AF025333 DNA-binding protein -NLI protein - Schizosaccharomyces pombe, PIRT:193771;supported by full-length cDNA: Ceres:34847. putative protein FNDA: Protein FND2 - Homo sapiens, EMBL:AF1945997:supported by full-length cDNA: Ceres:35534. putative protein FNDA: protein FND2 - Homo sapiens, EMBL:AF19459997:supported by full-length cDNA: Ceres:35534. putative protein FNDA: protein FND2 - Homo sapiens, EMBL:AF1945997:supported by full-length cDNA: ceres:35534. putative protein inholtor is supported by cDNA: gj_246980. djb_A8005560 1_A8005560 transket0ase - like protein transketolase, Solanum tuberosum, EMBL:Z50099.supported by full-length cDNA: Ceres:15659. putative protein halkP protein cashidopsis thaliana, EMBL:AC004665 putative protein halkP cortein ransketolase, MBL:AF15489771; supported by cDNA: gj_15292720_gb_AY050794.1_ short chani alkB protein - Schizosaccharomyces pombe and Drosophila melanogaster; supported by full-length cDNA putative protein hypothetical protein Al2g45740 - Arabidopsis thaliana, EMBL:AF089711; supported by cDNA: gj_15292720_gb_AY050794.1_ short chani alchol dehydrogenase-like; supported by cDNA: gj_13430055_gb_A	252344_s_at 252174_at 252174_at 252121_at 252121_at 2520262_at 251976_at 251996_at 251973_at 251975_at 251627_at 251657_at 251652_at 251506_at 251506_at 251506_at 251508_at 251508_at 251508_at 251508_at 251508_at 251508_at 251302_at 250763_at 250401_at 250401_at 250401_at 250131_at 249924_at 249924_at 249924_at 249724_at 249347_at 249347_at 249209_at 249172_at	$\begin{array}{c} 0.5\\ 0.5\\ 0.5\\ 0.5\\ 0.5\\ 0.5\\ 0.5\\ 0.5\\$

putative protein contains similarity to unknown protein (dbj]BAA90946.1)	248601_at	0.5
putative protein strong similarity to unknown protein (pir  T09896); supported by cDNA: gi_14334595_gb_AY034971.1_	248530_at	0.5
protein kinase ATM1-like protein	248541_at	0.5
putative protein similar to unknown protein (pir  T31651);supported by full-length cDNA: Ceres:32353.	248492_at	0.5
potassium/proton antiporter-like protein ;supported by full-length cDNA: Ceres:118693.	248375_at	0.5
putative protein similar to unknown protein (pir (569291)	248391_at	0.5
putative protein contains similarity to acyl-CoA binding protein;supported by full-length cDNA: Ceres:35856.	248269_at	0.5
putative protein contains similarity to unknown protein (gb AAC64884.1)	248124_at	0.5
DNA topoisomerase ( (sp P30181)	248099_at	0.5
putative protein contains similarity to NRK-related kinase	248060_at	0.5
Expressed protein ; supported by full-length cDNA: Ceres: 92808.	248002_at	0.5
histone acetyltransferase HAT B	247972_at	0.5
putative PRL1 associated protein ;supported by full-length cDNA: Ceres:150336.	247790_at	0.5
putative protein similar to unknown protein (sp)Q42463)	247453_at	0.5
putative protein strong similarity to unknown protein (gb AAD55296.1)	247429_at	0.5
putative protein hypersensitive-induced response protein HIR3, Zea mays, EMBL:AF236375;supported by full-length cDNA: Ceres:2641.	247403_at	0.5 0.5
beta-galactosidase (emb CAB64742.1); supported by cDNA: gi_16649044_gb_AY059892.1_ putative protein contains similarity to unknown protein (gb AAF44992.1); supported by cDNA: gi 15028246 gb AY046038.1	247356_at	0.5
putative protein contains similarity to unknown protein (gip/AAF44992.1), supported by CDINA. gr_15026246_gb_A1046036.1_ putative protein strong similarity to unknown protein (pir/105573)	247256_at 247183 at	0.5
	247165_at	0.5
unknown protein unknown protein	247100_at 247112_at	0.5
calcium-dependent protein kinase ;supported by full-length cDNA: Ceres:18901.	247112_at 247137_at	0.5
calcum-operative protein protein minase, supported by ruin-length conve. Ceres, rosort, doite/hi-di-phosphooligosaccharide-protein divoctransferase (oligosacchari/transferase)-like _supported by full-length cDNA; Ceres:18419.	247137_at 247058 at	0.5
unitary-cu-priority industry i	247058_at	0.5
putative protein similar to diricitioni protein (gbpAD23674.1) putative protein	246956_at	0.5
putative protein many predicted proteins, Arabidopsis thaliana	246808 at	0.5
voltage-dependent anion-selective channel protein hsr2 (supported by full-length cDNA: Ceres:1417.	240000_at 246546 at	0.5
volage-dependent anion-selective drammer protein insiz, supported by idinengin conve. Ceres, 1417. putative protein hypothetical proteins - Arabidopsis thaliana	246340_at 246497 at	0.5
putative protein nypotretical proteins - Adabtopsis analaria putative protein putative N-acettytransferase F13E7.7 - Arabidopsis thaliana, EMBL:AC018363	246448 at	0.5
hypothetical protein	246449 at	0.5
hypothetical protein contains similarity to cytochrome oxidase subunit GI:440282 from [Ceratoqlyphina styracicola]	246404 at	0.5
unknown protein contains similarity to beta-1.4 manosvitransferase GI:6970470 from [Homo sapiens]	246351 at	0.5
receptor-like serine/threonine kinase, putative similar to receptor-like serine/threonine kinase GI:2465923 from [Arabidopsis thaliana]; supported by (		0.5
putative protein serine kinase SRPK2, Hone sapiens, EMBL:AC005070	246334 at	0.5
putative protein admite transmethrane protein G5p yeast Sac1 protein, PIR-A33622	246300 at	0.5
putative transmission protein copy possibility protein, increased by cDNA; gi 15810384 gb AY056231.1	245972 at	0.5
Pto kinase interactor, putative similar to Pto kinase interactor 1 G1568069 from [Lycopersicon esculentum]	245845 at	0.5
hypothetical protein contains similarity to cycl A protein Gl:6358548 from [Antirrhinum graniticum]; supported by cDNA: gi_14334669_gb_AY035008.		0.5
amino acid permease, putative almost identical to amino acid permease GI:608673 from [Arabidopsis thaliana]	245740 at	0.5
Expressed protein ; supported by cDNA; gi 15912292 gb AY056424.1	245716 at	0.5
alkaline/neutral invertase, putative similar to alkaline/neutral invertase GI:9758657 from [Arabidopsis thaliana]	245681 at	0.5
anamonication interface, parameter animan to anamonication interface of 5150007 non practicepsis transmissi transport protein	245625 at	0.5
phosphatase like protein	245557 at	0.5
pitative protein	245492 at	0.5
Expressed protein ; supported by cDNA: gi 14334421 gb AY034902.1	245280 at	0.5
Expressed protein; supported by CDNA; g] 15215826 gb AY050443.1	245289 at	0.5
hypothetical protein ; supported by cDNA; gi 15810232, gb AY056155.1	245265 at	0.5
Expressed protein non-consensus GG donor splice site at exon 1 and 6; CT acceptor splice site at exon 2; supported by cDNA: gi:13605660	245216 at	0.5
PSI P700 apported apported by CHVL gl. record apple and a chvir and b, or acceptor spine and a chvir z, supported by CHVL gl. recorded PSI P700	245006 at	0.5
putative ser/thr protein kinase similar to GB:AAD21713	264549 at	0.5

unknown problein         262832 g. ett.         -8           putative suukni-induced problein suukni-induced problein 10A, Glycine max, PIR2-JQ1099         225065, d.         -7.8           Expressed problein is supported by fulk-length cDNA: Ceres: T152.         27705, at.         -7.7           putative suchni-is to SP P023P4 (Drochychis xulfikoli), contains Plem proble: PF00139 legume lectins beta domain; supported by fulk-length cDNA: Ceres: T152.         27705, at.         -7.7           putative problem is milar to tharmatin GB: AAD55090 (Mits riparia); contains Plem profle: PF00314 Thaumatin family; supported by fulk-length cDNA: Ceres: T1496.         281684, at.         -6.2           hypothetical problem is milar to traumatin GB: AAD55090 (Mits riparia); contains Plem profle: PF00314 Thaumatin family; supported by fulk-length cDNA: Ceres: T149.         286800, at.         -6.1           hypothetical problem predicted by genefinder         286680, at.         -6.1         286880, at.         -6.2           hypothetical problem indicted by genefinder         286680, at.         -6.1         286892, at.         -6.3           hypothetical problem indicted by genefinder         286680, at.         -6.1         284822, at.         -6.1           hypothetical problem indicted by genefinder         286680, at.         -6.3         -6.3         284822, at.         -6.1           hypothetical problem problem indito thorbothy fulk-length cDNA: Ceres: 171.         284822		Table 4: Transcripts suppressed during a combination of drought stress and heat shock compared to unstressed plants	Affimetrix number	log <sub>2</sub> fold supressed
antifungi protein-like (PDF1 z)         249052 at         7.8           Expressed protein supported by full-length cDNA: Ceres: 7152.         26658 at         7.7           putative protein proteinds protein SPP02374 (Donbyrchis vicilializ): contains Plam profile: PF00139 legume lectins beta domain; supported by CDNA; gt         257206, at         7.4           putative protein basic lection: zpport transcription activator shoot-forming PKSF1 - Paulownia kawakamii, EMBL: AF046834, supported by CDNA; gt         125925, at         4.5           mthaumatin - Rise protein similar to thaumatin GB: AA0550300 (Vita riparla): contains Plam profile: PF00314 Thaumatin family, supported by CDNA; gt         125925, at         4.3           unknown protein         genemark.hmm         264800, at         6.1           unknown protein         supported by Hull-ength cDNA: Ceres: 5171.         24495, at         6.1           unknown protein: regulated protein activator shanking to gbbcrefluit-regulated protein 2 precursor (GAST1) homolog gb(U1765 from A. thaliana)         266805, at         5.5           unknown protein: regulated protein GAA10289 (Circa aretinum): supported by full-ength cDNA: Ceres: 15010         246450, at         5.5           unknown protein         ya4169, at         5.2         246800, at         5.5           unknown protein         ya41640, at         5.5         246802, at         5.5           unknown protein         ya41640, at		unknown protein	262832_s_at	-8
Expressé protein ; supported by full-length cDNA: Ceres: 1712. putative lecitia: Pro20274 [Conctryphic wildiolia]: contains Pfam profile: PF00139 legume lecitias beta domain; supported by tDNA; £ 252706, at -7.4 putative protein indire to lecitis: PF02747 [Conctryphic wildiolia]: contains Pfam profile: PF00139 legume lecitias beta domain; supported by full-length putative protein basic leucia: gapper transcription activitors insolv forming PKSF1 - Paulownia kawakamii, EMBL:AF046934; supported by full-length cDNA: Ceres: 15495. hypothetical protein smitar to tumantin GB-AA055500 [Vitis riparis]: contains Pfam profile: PF00314 Thaumatin famIky; supported by full-length cDNA: Ceres: 15495. hypothetical protein smitar to tumanow protein (cmb)(CAA71173 ) putative protein similar to tumanow protein (cmb)(CAA71173 ) putative protein similar to tumanow protein (cmb)(CAA71173 ) putative protein similar to tumanow protein (cmb)(CAA71173 ) putative protein activitation (Fagurent) contain Supported by full-length cDNA: Ceres: 5171. putative protein similar to tumanow protein (cmb)(CAA71173 ) putative protein similar to tumanow protein (cmb)(CAA71173 ) putative protein activitation (Fagurent) contain Supported by full-length cDNA: Ceres: 3080 protein (Care Supported by full-length cDNA: Ceres: 3080 contain Supported by full-length cDNA: Ceres: 3080 contain (Fagurent) contain (Fa		putative auxin-induced protein auxin-induced protein 10A, Glycine max., PIR2:JQ1099	252965_at	-7.9
putative protein prediced proteins, SP-P02374 (non-by-chis viciliolia): contains Plam profile: FP00139 legume lectins beta domain; supported by fON-1; g25720, at -5. putative protein prediced proteins, rabidopis thaliana putative protein prediced proteins, rabidopis thaliana methods in protein accord by full-length CDAX: Ceres: 15495. proteins apported by full-length CDAX: Ceres: 15495. putative protein is supported by full-length CDAX: Ceres: 15495. putative protein is supported by full-length CDAX: Ceres: 15471. putative grobes instinator to incover protein (fragment) protein accord protein (fragment) putative protein is supported by full-length CDAX: Ceres: 3081. unknown protein is supported by full-length CDAX: Ceres: 3081. unknown protein is supported by full-length CDAX: Ceres: 3081. protein accord in fragment) protein accord in fragment) protein accord in fragment fragment (fragment) protein accord in fragment) putative protein accord in fragment) putative protein accord in fragment) putative protein accord (FR-K) kie protein fragment) putative protein accord (FR-K) kie protein fragment (FR-K) kie protein procursor (GR-P43062 (Arabidopsis thaliana), similar to wound induced protein (FR-K) putative protein accord (FR-K) kie protein by full-length CDAX: Ceres: 25034. putative protein accord (FR-K) kie protein by full-length CDAX: Ceres: 25034. putative protein accord (FR-K) kie protein by full-length CDAX: Ceres: 25034. putative protein accord (FR-K) kie protein by full-length CDAX: Ceres: 25034. putative protein accord (FR-K) kie protein by full-length CDAX: Ceres: 25034. putative protein accord (FR-K) kie protein by full-length CDAX: Ceres: 25034. putativ	i	antifungal protein-like (PDF1.2)	249052_at	-7.8
putative protein predicted proteins, Arabidopsis finaliana cativator shootforming PKSF1 - Paulownia kawakamii, EMBLAF046934,supported by full-length 25175, at 5, pyothetical protein similar to thaumatin GB-AAD55090 [Vitis riparia]; contains Pfem profile. PF00314 Thaumatin figm. Supported by CDN. ij 1 259925, at 6,3 cunknown protein similar to thaumatin GB-AAD55090 [Vitis riparia]; contains Pfem profile. PF00314 Thaumatin figm. Supported by full-length CDNA: Ceres. 15495. hypothetical protein predicted by genemark.htm cunknown protein isupported by full-length cDNA: Ceres. 1571. putative protein similar to unknown protein (entp(CAA711731)). putative protein auxin-induced protein B, mung bean, PIR-T1044. putative expansin (AEXPP) (arbidito bearsandin (B-KPA1104702), apported by full-length cDNA: Ceres. 25504. 256897, at 4.5. putative expansin (AEXPP) (arbidito bearsandin (B-KPA1104702), apported by cDNA: gl_150500; db, 2600489 (ml-Hight cDNA: Ceres. 25504. 256897, at 4.5. putative expansin auxin-protein binomin (Arabidopsis thaliana) Gi-1041702; apported by cDNA: gl_1521507; at 4.5. putative expansin auxin-protein binomin (Arabidopsis thaliana) Gi-1041702; apported by cDNA: gl_1521507; at 4.5. putative expansin auxin-protein binomin (Arabidopsis thaliana) Gi-1041702; apported by cDNA: gl_1521507; at 4.5. putative expansin auxin-		Expressed protein ; supported by full-length cDNA: Ceres: 7152.	266658_at	-7.7
putative protein basic leucine zipper transcription activator shock-forming PKSF1 - Paulownia kawakami, EMBL:AFD46934;supported by full-length cDNA: dig.         251684_at.         6.4           thaumstin-like protein similar to thaumatin GB:AAD55090 (Wits riparis): contains Pfam profile: PF00314 Thaumatin famity: supported by cDNA: git.         259849_at.         6.2           unknown protein         supported by full-length cDNA: Ceres: 15495.         248889_at.         6.2           unknown protein         supported by full-length cDNA: Ceres: 5171.         264343_at.         6.1           putative protein similar to known protein (engl-CAT1173.1)         264383_at.         6.6           putative protein similar to known protein (engl-CAT1173.1)         264383_at.         6.6           putative protein asupported by full-length cDNA: Ceres: 3101.0         244380_at.         6.5           unknown protein         supporteint asupported by full-length cDNA: Ceres: 108086.         259272_at.         6.5           unknown protein         supporteint asupported by full-length cDNA: Ceres: 3100.0         24480_at.         6.5           unknown protein         supporteint asupported by full-length cDNA: Ceres: 3108.0         24880_at.         6.5           unknown protein         supporteint asupported by full-length cDNA: Ceres: 310.0         24880_at.         6.5           unknown protein         supportend by cDNA: Geres: 310.0         24880_at.		putative lectin similar to lectin SP:P02874 [Onobrychis viciifolia]; contains Pfam profile: PF00139 legume lectins beta domain; supported by cDNA: c	257206 at	-7.4
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putative protein auxin-induced protein 6B, mung bean, PIR-T10942         25197 <sup>-</sup> , at         5.2           unknown protein , supported by full-length cDNA: Ceres:4309.         248062 at         5.2           putative protein         250942 at         5.1           putative protein         250942 at         5.1           response regulator 6 (ARR6) ; supported by cDNA: gl_3953600_dbj_AB008489.1_AB008489         250942 at         5.1           expansin (AE-XP1) (dentical to expansin (AI-EXP1) (Arabidopsis thaliana) GI:1041702; supported by full-length cDNA: Ceres:255048.         25629 at         5.1           glutathione S-transferase, putative similar to glutathione S-transferase GI:860955 from [Hyoscyamus muticus]; supported by cDNA: gl_15215607 (262119 s. at         4.9           hythothetical protein         putative glucosyltransferase GB:AD15455 GI:4263795 from (Arabidopsis thaliana)         265175 at         4.9           hystorhetical protein         putative protein         251846 at         4.8           myrosinase-associated protein, putative similar to myrosinase-associated protein GI:1769967 from [Brassica napus]; supported by cDNA: gl_15800         263161 at         4.8           hystorhetical protein         S21846 at         4.7         256562 at         4.7           hystorhetical protein         putative protein         251846 at         4.8           myrosinase-associated protein, putative similar to myrosinase-associ				
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		putative tyrosine aminotransferase ;supported by full-length cDNA: Ceres:14570.	263539_at	-4.3
putative auxin-induced protein similar to SAUR GB:BAA25434 [Raphanus sativus] 259331_at -4.3				
		putative auxin-induced protein similar to SAUR GB:BAA25434 [Raphanus sativus]	259331_at	-4.3

Everyoned protein : outproted by full length oDNA: Coroci: 41224	255969 at	-4.3
Expressed protein ; supported by full-length cDNA: Ceres: 41224. unknown protein similarity to HSR201 protein, Nicotiana tabacum, gb:X95343; contains EST gb:R65039	264403 at	-4.3 -4.2
xyloglucan endo-transglycosylase-like protein ; supported by full-length cDNA: Ceres:12301.	204405_at	-4.2
putative auxin-regulated protein	264016 at	-4.2
hypothetical protein predicted by genefinder and genscan	260472 at	-4.2 -4.2
putative two-component response regulator protein; supported by cDNA: gi 11870067 gb AF305721.1 AF305721		-4.2 -4.1
putative two-component response regulator protein , supported by CDNA. gr_116/0007_gb_AF303721.1_AF303721 putative DNA-binding protein (RAV2-like) identical to residues 34-352 of RAV2 GB:BAA34251 (Arabidopsis thaliana):supported by full-length cDNA:	266078_at	
	_	-4.1
unknown protein identical to GB:AAD56318 (Arabidopsis thaliana)	259211_at	-4.1
putative protein predicted protein, Arabidopsis thaliana	249919_at	-4.1
putative protein predicted proteins from various species, Human, yeast, Oryctolagus sp.	247621_at	-4.1
	266746_s_at	-4
Expressed protein ; supported by full-length cDNA: Ceres: 10388.	264262_at	-4
histone H2A ; supported by full-length cDNA: Ceres: 8.	263264_at	-4
putative monodehydroascorbate reductase (NADH) similar to monodehydroascorbate reductase (NADH) GB: JU0182 [Cucumis sativus]; supported	258941_at	-4
serine/threonine kinase - like protein serine/threonine kinase, Brassica oleraceae	254250_at	-4
ethylene responsive element binding factor-like protein (AtERF6) ; supported by cDNA: gi_3298497_dbj_AB013301.1_AB013301	245250_at	-4
putative antifungal protein	257365_x_at	-4
hypothetical protein similar to putative MADS-box protein GI:4580382 from [Arabidopsis thaliana]	262902_x_at	-3.9
putative pectate lyase pectate lyase, Musa acuminata, PATX:E209876;supported by full-length cDNA: Ceres:36681.	254119_at	-3.9
putative protein	252661_at	-3.9
vegetative storage protein-like ;supported by full-length cDNA: Ceres:27372.	249073_at	-3.9
putative protein	247754 at	-3.9
similar to latex allergen from Hevea brasiliensis ;supported by full-length cDNA: Ceres:1999.	245038 at	-3.9
unknown protein	265327 at	-3.8
Expressed protein ; supported by full-length cDNA: Ceres: 31015.	259479 at	-3.8
unknown protein ;supported by full-length cDNA: Ceres:4861.	258480 at	-3.8
unknown protein predicted by genscan+supported by full-length cDNA: Ceres:153279.	258468 at	-3.8
peroxidase ATP19a	254914 at	-3.8
putative protein hypothetical protein - Arabidopsis thaliana,PIR2:H71441;supported by full-length cDNA: Ceres:4642.	254746 at	-3.8
putative protein similar to unknown protein (gb/AAD32884.1)	248123 at	-3.8
unknown protein ; supported by cDNA; gi 14517479 gb AY039575.1	266017 at	-3.7
Expressed protein ; supported by cDNA: gi 14335055 gb AY037207.1	256766 at	-3.7
putative protein similar to transcriptional regulator	255298 at	-3.7
putative protein DNA damage-inducible protein - Synechocystis sp.,PIR2:S77364	252921 at	-3.7
	249378 at	-3.7
putative protein microtubule-associated protein homolog, Drosophila melanogaster, EMBL:T13564	_	-3.7
putative protein similar to unknown protein (pir  T05752);supported by full-length cDNA: Ceres:109272.	248164_at	
	245866_s_at	-3.7
unknown protein location of ESTs est VBVBD05, gbJZ30807 and VBVBD05, gbJZ30808;supported by full-length cDNA: Ceres:39763.	265066_at	-3.6
unknown protein similar to hypothetical protein GB:AAF27090 GI:6730669 from (Arabidopsis thaliana);supported by full-length cDNA: Ceres:101864	_	-3.6
unknown protein ;supported by full-length cDNA: Ceres:20378.	260527_at	-3.6
unknown protein ; supported by full-length cDNA: Ceres: 38378.	259664_at	-3.6
delta tonoplast integral protein (delta-TIP) identical to delta tonoplast integral protein (delta-TIP) GB:U39485 [Arabidopsis thaliana] (Plant Cell 8 (4),		-3.6
putative pectinacetylesterase protein pectinacetylesterase precursor, Vigna radiata, PIR2:S68805;supported by full-length cDNA: Ceres:34674.	254578_at	-3.6
putative protein small auxin up-regulated RNA, Malus domestica, gb:Z93766	253207_at	-3.6
dUTP pyrophosphatase-like protein dUTP pyrophosphatase - Lycopersicon esculentum,PIR2:JQ1599; supported by cDNA: gi_13878142_gb_AF37	252442_at	-3.6
putative protein hypersensitivity-related hsr201 protein - Nicotiana tabacum,PIR2:T03274	252317_at	-3.6
beta-1,3-glucanase	251673_at	-3.6
thionin Thi2.2 ;supported by full-length cDNA: Ceres:1523.	249645_at	-3.6
calcium-binding protein - like cbp1 calcium-binding protein, Lotus japonicus, EMBL:LJA251808; supported by cDNA: gi_16648829_gb_AY058192.1	249417_at	-3.6
histone H2A - like protein histone H2A, parsley, PIR:S11498;supported by full-length cDNA: Ceres:20036.	247651_at	-3.6
F12A21.6 hypothetical protein	245193_at	-3.6
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:10798.	263535_at	-3.5
flax rust resistance protein, putative similar to flax rust resistance protein GI:4588066 from [Linum usitatissimum]; supported by full-length cDNA: C		-3.5
33 kDa secretory protein-like ; supported by cDNA: gi 15292980 gb AY050924.1	248686 at	-3.5
putative protein similar to unknown protein (pir/IT05055)	248047 at	-3.5
disease presistance protein RPP1-WSB, putative similar to disease resistance protein RPP1-WsB GI:9279731 from [Arabidopsis thaliana]	246405 at	-3.5
putative ethylene response element binding protein (EREBP) ;supported by full-length cDNA: Ceres:6397.	266821 at	-3.4
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putative endoxyloglucan glycosyltransferase identical to GB:D16454;supported by full-length cDNA: Ceres:15276.	266215_at	-3.4
unknown protein similar to gb T45484, emb Z30724, and emb Z30531	264824_at	-3.4
virus resistance protein, putative similar to virus resistance protein GI:558886 from [Nicotiana glutinosa]	262382_at	-3.4
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:4146.	256796_at	-3.4
myb-related protein similar to GI:7981380 from [Lycopersicon esculentum]	256503_at	-3.4
hypothetical protein	255978_at	-3.4
putative protein	250575 at	-3.4
glutaredoxin	245505 at	-3.4
putative protein	249505 at	-3.4
putative harpin-induced protein ;supported by full-length cDNA: Ceres:19481.	263951 at	-3.3
hypothetical protein similar to calmodulin-like protein GB:CAB42906 [Arabidopsis thaliana]; Pfam HMM hit: EF hand; supported by full-length cDNA:	_	-3.3
putative calmodulin similar to calmodulin GB:P04352 [Chlamydomonas reinhardtii]; containing], mar numming profile: PP0036 EF hand (4 copies); supported t		-3.3
unknown protein ; supported by CDNA; gi 15529233 gb AY052241.1	258225 at	-3.3
leucine rich repeat protein, putative contains multiple LRR repeats Pfam profile: PF00560; supported by full-length cDNA: Ceres: 29675.	256237 at	-3.3
putative protein ENDD16, Medicago truncatula, X99466;supported by full-length cDNx, Ceres;6308.	253480 at	-3.3
	_	
cytochrome P450 monooxygenase - like protein cytochrome P450 monooxygenase CYP91A2, Arabidopsis thaliana, D78607;supported by full-leng		-3.3
hypothetical protein	252361_at	-3.3
bZIP DNA-binding protein-like putative bZIP DNA-binding protein - Capsicum chinense, EMBL:AF127797	246522_at	-3.3
putative pectinesterase	245052_at	-3.3
unknown protein	248963_at	-3.3
putative glutaredoxin ;supported by full-length cDNA: Ceres:21006.	266516_at	-3.2
unknown protein ;supported by full-length cDNA: Ceres:32647.	265400_at	-3.2
hypothetical protein predicted by genscan; supported by cDNA: gi_15724317_gb_AF412099.1_AF412099	265342_at	-3.2
hypothetical protein predicted by genemark.hmm	261221_at	-3.2
unknown protein ; supported by full-length cDNA: Ceres: 16614.	259841_at	-3.2
putative phosphate/phosphoenolpyruvate translocator similar to phosphate/phosphoenolpyruvate translocator precursor GB:AAB40648 [Nicotiana ta	259185_at	-3.2
unknown protein ; supported by full-length cDNA: Ceres: 368.	256617_at	-3.2
Similar to receptor kinase	255654 at	-3.2
putative phi-1-like phosphate-induced protein ;supported by full-length cDNA: Ceres:3552.	255064 at	-3.2
putative protein CGI-131 protein, Homo sapiens, AF151889;supported by full-length cDNA: Ceres:24573.	254387 at	-3.2
putative polygalacturonase polygalacturonase (EC 3.2.1.15) - avocado, EMBL:X66426	254221 at	-3.2
putative protein centrin, Marsilea vestita;supported by full-length cDNA; Ceres:13072.	253915 at	-3.2
putative calcium-binding protein calcium binding domains (EF hand) of several proteins	252417 at	-3.2
putative protein predicted protein, Arabidopsis thaliana	249918 at	-3.2
unknown protein	249932 at	-3.2
unknown protein ; supported by cDNA: gi 14190416 gb AF378886.1 AF378886	249894 at	-3.2
ethylene responsive element binding factor 5 (ATERF5) (spl080341); supported by cDNA: gi 14326511 gb AF385709.1 AF385709	248799 at	-3.2
Expressed protein ; supported by full-length cDNA: Ceres: 15227.	248509 at	-3.2
putative phytochelatin synthetase - like putative phytochelatin synthetase, Arabidopsis thaliana, EMBL:ATH6787	247604_at	-3.2
putative protein similar to unknown protein (qb/AAF67766.1);supported by full-length cDNA: Ceres:512.	246997 at	-3.2
Expressed protein ; supported by full-length cDNA: Ceres: 30087.	245318 at	-3.2
cytochrome b6-f complex, subunit V	243916_at	-3.2
similar to cold acclimation protein WCOR413 [Triticum aestivum]	_	-3.2 -3.1
	267288_at	-3.1
unknown protein ; supported by cDNA: gi_15294169_gb_AF410276.1_AF410276	266552_at	
unknown protein Similar to acid phosphatase; Location of ESTs 110C2T7, gb/T42036, and 110C2XP, gb/A1100245; supported by cDNA: gi_13926		-3.1
class 1 non-symbiotic hemoglobin (AHB1) identical to GP:2581783:U94998;supported by full-length cDNA: Ceres:18195.	263096_at	-3.1
ubiquitin-fusion protein, putative similar to ubiquitin-fusion protein GI:9725 from [Manduca sexta]; supported by full-length cDNA: Ceres:34600.	262196_at	-3.1
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:157.	260804_at	-3.1
lipase/hydrolase, putative contains Pfam profile: PF00657 Lipase/Acylhydrolase with GDSL-like motif; supported by full-length cDNA: Ceres: 6680.	259786_at	-3.1
AIG2-like protein similar to AIG2 protein GB:P54121 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:28511.	258002_at	-3.1
hypothetical protein contains similarity to MtN3(nodulin) protein GB:Y08726 GI:1619601 from [Medicago truncatula]; supported by cDNA: gi_15809§		-3.1
sucrose-phosphate synthase - like protein sucrose-phosphate synthase, Zea mays, PIR2:JQ1329	255016_at	-3.1
response reactor 2 (ATRR2) ; supported by cDNA: gi_3273197_dbj_AB010916.1_AB010916	252374_at	-3.1
putative protein latex protein allergen Hev b 7 - Hevea brasiliensis, EMBL:AF113546; supported by cDNA: gi_15912226_gb_AY056391.1_	251174_at	-3.1
protein phosphatase - like protein protein phosphatase 2C homolog, Mesembryanthemum crystallinum, EMBL:AF097667	251017_at	-3.1
putative protein ;supported by full-length cDNA: Ceres:1336.	250968_at	-3.1
unknown protein ;supported by full-length cDNA: Ceres:207075.	249836_at	-3.1

	0.45755	
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:42217.	245755_at	-3.1
Expressed protein ; supported by full-length cDNA: Ceres: 37809.	245329_at	-3.1
ribosomal protein L23	244988_s_at	-3.1
unknown protein ;supported by full-length cDNA: Ceres:32244.	267034_at	-3
unknown protein	265539_at	-3
unknown protein ;supported by full-length cDNA: Ceres:102453.	263981_at	-3
unknown protein	260904_at	-3
12-oxophytodienoate reductase (OPR2) identical to 12-oxophytodienoate reductase OPR2 GB:AAC78441 [Arabidopsis thaliana]	259875_s_at	-3
hypothetical protein predicted by genscan+	259385_at	-3
DNA-binding protein RAV1 identical to RAV1 GI:3868857 from [Arabidopsis thaliana]; supported by cDNA: gi_3868856_dbj_AB013886.1_		-3
putative GDSL-motif lipase/acylhydrolase contains Pfam profile: lipase/acylhydrolase with GDSL-like motif;supported by full-length cDNA:		-3
putative disease resistance protein similar to disease resistance protein RPP1-WsC GB:AAC72979 [Arabidopsis thaliana]; supported by cl		-3
glycine-rich RNA-binding protein, putative similar to glycine-rich RNA-binding protein GI:17818 from [Brassica napus]	255962_at	-3
pEARLI 1 ; supported by cDNA: gi_871779_gb_L43080.1_ATHPEAR	254805_at	-3
histone H3 - like protein histone H3, Arabidopsis thaliana, PIR:S06250	250434_at	-3
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:6295.	264672_at	-2.9
glutaredoxin, putative similar to glutaredoxin GI:2244924 from [Arabidopsis thaliana]; supported by cDNA: gi_13358219_gb_AF325030.2_		-2.9
putative chlorophyll A-B binding protein similar to chlorophyll A-B binding protein 151 precursor (LHCP) GB:P27518 from [Gossypium hirsu		-2.9
Expressed protein ; supported by full-length cDNA: Ceres: 32396.	251142_at	-2.9
NaCl-inducible Ca2+-binding protein-like; calmodulin-like ; supported by cDNA: gi_13358217_gb_AF325028.2_AF325028	248607_at	-2.9
DC1.2 homologue - like protein DC1.2 homologue, Nicotiana tabacum, EMBL:AB009888	247478_at	-2.9
ethylene-responsive element - like protein ethylene-responsive element binding protein homolog, Stylosanthes hamata, EMBL:U91857; su		-2.9
putative protein	246270_at	-2.9
phosphate-induced (phi-1) protein, putative similar to phi-1 GB:BAA33810 GI:3759184 from [Nicotiana tabacum]; supported by full-length c		-2.9
glutaredoxin homolog	245506_at	-2.9
putative protein contains similarity to elicitor-inducible receptor-like protein	247087_at	-2.9
omega-3 fatty acid desaturase identical to GB:D26508 and GB:D17579; supported by cDNA: gi_1030693_dbj_D17579.1_ATHFADIER2	266865_at	-2.8
expansin AtEx6 identical to GB U30480; supported by full-length cDNA: Ceres: 17914.	266790_at	-2.8
putative alcohol dehydrogenase	266761_at	-2.8
putative copper/zinc superoxide dismutase identical to GP:3273753:AF061519;supported by full-length cDNA: Ceres:39796.	266165_at	-2.8
hypothetical protein predicted by genscan	265724_at	-2.8
superoxidase dismutase identical to GB:P24704;supported by full-length cDNA: Ceres:33493.	264809_at	-2.8
zinc finger protein ATZF1, putative identical to GB:BAA25989; supported by cDNA: gi_3123711_dbj_D89051.1_D89051	264624_at	-2.8
putative response regulator 3 similar to ESTs gb T43772, emb Z34204, gb AA067391, and emb Z34620, implicated in His-to-Asp phospho		-2.8
late embryogenis abundant protein, putative similar to late embryogenis abundant protein 5 GI:2981167 from [Nicotiana tabacum]; support		-2.8
GAST1-like protein similar to GAST1 protein precursor GB:P27057 [Lycopersicon esculentum] (induced by gibberellins, inhibited by ABA I	Plant J 1 260221_at	-2.8
unknown protein ; supported by full-length cDNA: Ceres: 21882.	258249_s_at	-2.8
putative zinc finger protein contains Pfam profile: PF00641 Zn-finger in Ran binding protein and others; supported by full-length cDNA: Cere	es:8265. 258222_at	-2.8
unknown protein ; supported by full-length cDNA: Ceres: 148308.	256456_at	-2.8
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:12509.	256442_at	-2.8
putative gamma-glutamyltransferase gamma-glutamyltransferase, Arabidopsis thaliana, PIR2:S58286	252906_at	-2.8
Histone H4 - like protein histone H4, Zea mays, PIR:HSZM4;supported by full-length cDNA: Ceres:22146.	252562_s_at	-2.8
glutaredoxin -like protein glutaredoxin, castor bean, PIR:S54825	251196_at	-2.8
unknown protein ; supported by cDNA: gi_15810044_gb_AY054291.1_	250828_at	-2.8
histone H3 - like protein histone H3, Arabidopsis thaliana, PIR:S06250	250433_at	-2.8
putative protein putative DNA-binding protein - Arabidopsis thaliana, EMBL:AC011765;supported by full-length cDNA: Ceres:4734.	249383_at	-2.8
Expressed protein ; supported by full-length cDNA: Ceres: 36971.	248460_at	-2.8
putative protein similar to unknown protein (pir  T04819)	248139_at	-2.8
hypothetical protein ; supported by full-length cDNA: Ceres: 933.	245304_at	-2.8
unknown protein ;supported by full-length cDNA: Ceres:125631.	267209_at	-2.7
putative metalloproteinase similar to GB:AAB61099	264866_at	-2.7
hypothetical protein predicted by genemark.hmm	261772_at	-2.7
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:3200.	261456_at	-2.7
chloroplast nucleoid DNA binding protein, putative similar to chloroplast nucleoid DNA binding protein GB:BAA22813 GI:2541876 from [Ni		-2.7
putative elicitor-responsive gene similar to elicitor-responsive gene-3 GB:AAC35866 from [Oryza sativa];supported by full-length cDNA: Ce	eres:1896 260083_at	-2.7
unknown protein ; supported by cDNA: gi_14596082_gb_AY042829.1_	259791_at	-2.7
nicotianamine synathase, putative similar to nicotianamine synathase [Arabidopsis thaliana] GI:4220614	259632_at	-2.7

delta 9 desaturase, putative similar to delta 9 desaturase GI:2970034 from [Arabidopsis thaliana]	259391_s_at	-2.7
Inknown protein contains helix-loop-helix DNA binding motif	259010_at	-2.7
putative syntaxin contains Pfam profile: PF00804 syntaxin;supported by full-length cDNA: Ceres:38899.	258786_at	-2.7
putative pectate lyase similar to pectate lyase 2 GB:AAF19196 [Musa acuminata]; supported by full-length cDNA: Ceres: 124816.	258552_at	-2.7
sutative flowering-time gene CONSTANS (COL2) identical to putative flowering-time gene CONSTANS (COL2) GB:AAB67879 GI:1507699 (Arab		-2.7
protein kinase, putative contains Pfam profile: PF00069: Eukaryotic protein kinase domain	256366_at	-2.7
Expressed protein ; supported by cDNA: gi_14190492_gb_AF380646.1_AF380646	253423_at	-2.7
utative protein similar to unknown protein (dbj BAA92898.1);supported by full-length cDNA: Ceres:97314.	249230_at	-2.7
putative protein hypothetical protein F16B3.27 - Arabidopsis thaliana, EMBL:AC021640;supported by full-length cDNA: Ceres:18222.	246505_at	-2.7
transcriptional co-activator-like protein putative transcriptional co-activator (KIWI) - Arabidopsis thaliana, EMBL:AF053302	245930_at	-2.7
putative protein similarity to predicted proteins, Arabidopsis thaliana	245155_at	-2.7
ATPase alpha subunit	245024_at	-2.7
dynein light chain, putative similar to dynein light chain 1, cytoplasmic SP:Q15701 [Homo sapiens]	257504_at	-2.7
outative protein contains similarity to ATFP3	248527_at	-2.7
athogenesis-related PR-1-like protein identical to GB:M90508; supported by cDNA: gi_166860_gb_M90508.1_ATHRPRP1A	266385_at	-2.6
putative nonspecific lipid-transfer protein precursor; supported by full-length cDNA: Ceres: 24286.	265656_at	-2.6
pypothetical protein similar to embryo-abundant protein GB:L47672 GI:1350530 from [Picea glauca]; supported by cDNA: gi_14335021_gb_AY03		-2.6
ypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:271253.	265067_at	-2.6
poyltransferase identical to GB:BAA78386; supported by cDNA: gi_4996285_dbj_AB020975.1_AB020975	264613_at	-2.6
Inknown protein ;supported by full-length cDNA: Ceres:11114.	263628_at	-2.6
Inknown protein similar to putative DNA-binding protein GI:6714399 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:92341.	261942_at	-2.6
endo-xyloglucan transferase, putative similar to endo-xyloglucan transferase GI:2244732 from [Gossypium hirsutum];supported by full-length cDI	_	-2.6
DNA-binding protein, putative similar to DNA binding protein CCA1 from [Arabidopsis thaliana]	261569_at	-2.6
Inknown protein ;supported by full-length cDNA: Ceres:142725.	259980_at	-2.6
auxin-induced protein, putative similar to SP:P33083 from [Glycine max]:supported by full-length cDNA: Ceres:9311.	259783_at	-2.6
auxin-induced protein, putative similar to SP:P33083 from [Glycine max]:supported by full-length cDNA: Ceres:4119.	259790_s_at	-2.6
inknown protein	258419_at	-2.6
putative cytochrome c oxidase subunit Vb similar to cytochrome oxidase IV GB:223590 [Bos taurus]; contains Pfam profile: PF01215 cytochrome	c 258274_at	-2.6
inknown protein ;supported by full-length cDNA: Ceres:96816.	257793_at	-2.6
inknown protein	256633_at	-2.6
putative protein other hypothetical proteins in Arabidopsis thaliana; supported by cDNA: gi_6457330_gb_AF188329.1_AF188329	252060_at	-2.6
putative protein contains similarity to DNA-binding protein	249890_at	-2.6
imino acid permease 6 (emb CAA65051.1)	248619_at	-2.6
putative protein similar to unknown protein (emb CAA71173.1);supported by full-length cDNA: Ceres:19542.	248327_at	-2.6
sp4 like protein ; supported by cDNA: gi_15451019_gb_AY054590.1_	245296_at	-2.6
iypothetical protein ; supported by cDNA: gi_15810232_gb_AY056155.1_	245265_at	-2.6
outative expansin	267158_at	-2.5
Expressed protein ; supported by full-length cDNA: Ceres: 7600.	266500_at	-2.5
nypothetical protein predicted by genscan	266070_at	-2.5
inknown protein Location of EST gb T41885 and gb AA395021	264521_at	-2.5
Inknown protein	262694_at	-2.5
chalcone isomerase, putative similar to GI:4126399 from (Citrus sinensis);supported by full-length cDNA: Ceres:116131.	260982_at	-2.5
AtHVA22c identical to AtHVA22c GB:AF141661 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:108964.	260368_at	-2.5
sucrose transport protein SUC1 identical to GB:S38197 from [Arabidopsis thaliana]; supported by cDNA: gi_15146267_gb_AY049275.1_	260143_at	-2.5
permin-like protein similar to germin precursor GB:P26759 [Triticum aestivum]; contains Pfam profile: PF01072 Germin family;supported by full-le		-2.5
xpressed protein ; supported by full-length cDNA: Ceres: 35429.	258349_at	-2.5
inknown protein identical to unknown protein GI:9755444 from (Arabidopsis thaliana); supported by full-length cDNA: Ceres: 110066.	255856 at	-2.5
utative receptor-like protein kinase	255344 s at	-2.5
putative protein probable arabinogalactan protein precursor, Lycopersicon esculentum, PIR2:S55925; supported by cDNA: gi 11935087 gb AF3		-2.5
inknown protein ;supported by full-length cDNA: Ceres:262293.	250665 at	-2.5
glutaredoxin -like protein glutaredoxin, castor bean, PIR:S54825;supported by full-length cDNA: Ceres:92720.	249996 at	-2.5
utative protein similar to unknown protein (pir  T00970); supported by cDNA: gi 15215722 gb AY050390.1	249817 at	-2.5
utative protein similar to unknown protein (ph/hrss2471.1)	249659 s at	-2.5
utative protein similar to unknown protein (gb)AF04428.1);supported by full-length cDNA: Ceres:27668.	248028 at	-2.5
	246905 at	-2.5
Duranve drotein Isuddoned dvitui-lendin CLINA: Ceres:22013.		
putative protein ;supported by full-length cDNA: Ceres:22013. jermin-like protein ; supported by cDNA: gi_14517363_gb_AY039516.1_	246004 at	-2.5

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ribosomal protein L2	244987_s_at 244933 at	-2.5 -2.5
NADH dehydrogenase ND4L	244955_at 257191 at	-2.5 -2.5
Expressed protein ; supported by full-length cDNA: Ceres: 2083. putative steroid sulfotransferase ; supported by cDNA: gi 599639 emb Z46823.1 ATTS4391	264042 at	-2.5 -2.4
unknown protein ;supported by full-length cDNA; Ceres:15081.	263431 at	-2.4
Expressed protein ; supported by cDNA: gi 15293050 gb AY050959.1	263210 at	-2.4 -2.4
protein kinase, putative contains similarity to many predicted protein kinases; supported by cDNA; gi 13430527 gb AF360176.1 AF360176	261308 at	-2.4
expansi no identicate of the AF61712 from [Arabidopsis thaliana];supported by full-length cDNA: <u>Ceres:14132</u> .	261266 at	-2.4
expansion 52 precursor, putative similar to BcU30466 from [Cucumis sativus];supported by full-length cDNX; Ceres:11011.	261226 at	-2.4
hypothetical protein	259523 at	-2.4
unknown protein similar to unknown protein GB:AAC62613 [Arabidopsis thaliana]; supported by cDNA: gi 14532567 gb AY039908.1	259018_at	-2.4
ribonucleotide reductase small subunit, putative similar to RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN GB:P49730 from [Ni		-2.4
Expressed protein ; supported by full-length cDNA: Ceres: 11616.	257204 at	-2.4
putative protein	255652 at	-2.4
putative protein similar to T5J8.18	255450 at	-2.4
putative Fe(II)/ascorbate oxidase SRG1 protein - Arabidopsis thaliana, PIR2:S44261	254975 at	-2.4
serine/threonine kinase - like protein serine/threonine kinase, Brassica oleracea; supported by cDNA: gi 14423417 gb AF386946.1 AF386946	254255 at	-2.4
fructose-bisphosphate aldolase - like protein fructose-bisphosphate aldolase, Arabidopsis thaliana, PIR1:ADMU:supported by full-length cDNA: Ce	—	-2.4
predicted protein ; supported by cDNA: gi 15293232 gb AY051050.1	253525 at	-2.4
NAC-domain protein-like ;supported by full-length cDNA. Ceres:29829.	249940 at	-2.4
putative protein contains similarity to surface protein; supported by cDNA: gi 16648846 gb AY058201.1	249037 at	-2.4
DNA (cytosine-5)-methyltransferase (DNA methyltransferase) (DNA metase) (sp P34881) ; supported by cDNA: gi 304106 gb L10692.1 ATHME	248597 at	-2.4
putative protein similar to unknown protein (gb/AAC24386.1)	248191_at	-2.4
Isp4-like protein ; supported by full-length cDNA: Ceres: 3109.	247284_at	-2.4
calmodulin-binding - like protein calmodulin-binding protein TCB60, Nicotiana tabacum, EMBL:U58971	246821_at	-2.4
putative protein ;supported by full-length cDNA: Ceres:16131.	246200_at	-2.4
putative protein auxin-induced basic helix-loop-helix transcription factor, Gossypium hirsutum, EMBL:AF165924; supported by cDNA: gi_15724267	246011_at	-2.4
glutaredoxin	245504_at	-2.4
hypothetical protein predicted by genscan and genefinder	257382_at	-2.4
hypothetical protein similar to GB:AAB97719 from [Arabidopsis thaliana]	258409_at	-2.4
putative proline-rich protein ; supported by full-length cDNA: Ceres: 28853.	267260_at	-2.3
putative acetone-cyanohydrin lyase	267126_s_at	-2.3
unknown protein ;supported by full-length cDNA: Ceres:31586.	267092_at	-2.3
calmodulin (cam2)	267064_at	-2.3
nodulin-like protein	265414_at	-2.3
unknown protein ; supported by cDNA: gi_6691164_gb_AF218765.1_AF218765	263498_at	-2.3
putative glucosyltransferase ; supported by full-length cDNA: Ceres: 114997.	263473_at	-2.3
putative GDSL-motif lipase/hydrolase similar to APG proteins; pFAM domain PF00657;supported by full-length cDNA: Ceres:121397.	263482_at	-2.3
unknown protein ;supported by full-length cDNA: Ceres:641.	263421_at	-2.3
disease resistance protein, putative similar to disease resistance protein GI:9758876 from [Arabidopsis thaliana]	262383_at	-2.3
unknown protein ;supported by full-length cDNA: Ceres:12408.	262168_at	-2.3
tubulin alpha-2/alpha-4 chain, putative identical to tubulin alpha-2/alpha-4 chain GB:P29510 from [Arabidopsis thaliana]; supported by cDNA: gi_15		-2.3
hypothetical protein similar to YGL010w-like protein GB:AAC32136 [Picea mariana]	260211_at	-2.3
hypothetical protein (supported by full-length CDNA: Ceres: 265772.	259550_at	-2.3
response regulator 5, putative similar to response regulator 5 GI:3953599 from [Arabidopsis thaliana]; supported by cDNA: gi_3953602_dbj_AB008 putative pectinesterase contains similarity to pectinesterase GB:AAB57671 [Citrus sinensis]	259466_at	-2.3 -2.3
unknown protein contains Pfam profile:PF00295 Polygalacturonase;supported by full-length cDNA: Ceres:38575.	258764_at 258528 at	-2.3 -2.3
unknown protein ; supported by cDNA: gi 15451205 gb AY054683.1	258526_at	-2.3
hypothetical protein contains Pfam profile: PF01657 Domain of unknown function; supported by cDNA: gi 14334417 gb AY034900.1	257264 at	-2.3
unknown protein	257074 at	-2.3
unknown protein similar to cell wall-plasma membrane linker protein GB:CAA64425 from [Brassica napus]	256825 at	-2.3
	255662 at	-2.3
pEARLI 1-like protein Arabidopsis thaliana pEARLI 1 mRNA, PID:g871780	254818 at	-2.3
Expressed protein radiadops training pEncie 1 minutes, 1 e.g. of 100	253305 at	-2.3
endo-xyloqlucan transferase - like protein endo-xyloqlucan transferase. Gossypium hirsutum, D88413;supported by full-length CDNA: Ceres:14263	_	-2.3
putative protein hypothetical protein F4118.26 - Arabidopsis thaliana, PIR:T02471;supported by full-length cDNA: Ceres: 30454.	251336 at	-2.3
putative protein	250075 at	-2.3
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putative protein contains similarity to ornithine cyclodeaminase;supported by full-length cDNA: Ceres:114678.	248330_at	-2.3
peroxidase ;supported by full-length cDNA: Ceres:124846.	247812_at	-2.3
putative protein predicted protein, Arabidopsis thaliana;supported by full-length cDNA: Ceres:32599.	246550_at	-2.3
NADH dehydrogenase ND6	244934_at	-2.3
putative disease resistance protein	267546_at	-2.2
unknown protein ; supported by cDNA: gi_14326466_gb_AF385686.1_AF385686	266460_at	-2.2
Expressed protein ; supported by full-length cDNA: Ceres: 5586.	264164_at	-2.2
hypothetical protein predicted by genscan; supported by cDNA: gi 15810330 gb AY056204.1	263800 at	-2.2
unknown protein location of EST TAT5A03; 5 end, gb/Z26679	262656 at	-2.2
invertase, putative similar to neutral invertase GB:76145 GI:4200165 from [Daucus carota]	262038 at	-2.2
hypothetical protein predicted by genemark.hmm	260656 at	-2.2
unknown protein similar to hypothetical protein GB:AAD12705 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:40506.	260179 at	-2.2
auxin-induced protein, putative similar to SP:P33083 from [Glycine max]:supported by full-length cDNA: Ceres:29931.	259784 at	-2.2
GTP-binding protein RAB7D, putative similar to GI:1370187 from [Lotus japonicus] (Plant J. 11 (2), 237-250 (1997)); supported by cDNA: gi 15718	_	-2.2
unknown protein ; supported by CDNA: gi 15028124 gb AY046012.1	258728 at	-2.2
xyloglucan endotransglycosylase, putative similar to xyloglucan endotransglycosylase 1 GB:CAA10231 from [Fagus sylvatica] (Plant Physiol.(1999		-2.2
sprograding transmission of the second secon		-2.2
unknown protein : supported by full-length cDNA: Ceres:35273.	255817 at	-2.2
putative protein polyphosphoinositide binding protein Ssh2, Glycine max, gb:T05953	255082 at	-2.2
		-2.2
acyl carrier - like protein acyl carrier protein, Cuphea lanceolata, PIR2:542026;supported by full-length cDNA: Ceres:11559.	254102_at	-2.2
auxin-induced protein - like auxin-inducible SAUR gene, Raphanus sativus, AB000708;supported by full-length cDNA: Ceres:10140.	252972_at	
putative protein hypothetical protein - Arabidopsis thaliana, EMBL:CAB38293;supported by full-length cDNA: Ceres:17840.	252220_at	-2.2
hypothetical protein ; supported by cDNA: gi_13605735_gb_AF361849.1_AF361849	252170_at	-2.2
putative protein polygalacturonase - Lycopersicon esculentum, EMBL:AF118567; supported by cDNA: gi_13358184_gb_AF324992.2_AF324992	251261_at	-2.2
polygalacturonase inhibiting protein ;supported by full-length cDNA: Ceres:35527.	250669_at	-2.2
putative serine rich protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:36958.	250327_at	-2.2
DNA helicase-like	249677_at	-2.2
putative protein similar to unknown protein (emb CAB79759.1)	247880_at	-2.2
putative protein similar to unknown protein (emb CAB61744.1); supported by full-length cDNA: Ceres: 31648.	247214_at	-2.2
sugar transporter like protein	246238_at	-2.2
auxin-induced protein, putative similar to SP:P33083 from [Glycine max]	257506_at	-2.2
myb-like protein isolog	267495_at	-2.1
putative PREG1-like negative regulator	266873_at	-2.1
histone H4 identical to GB:M17133 and GB:M17132;supported by full-length cDNA: Ceres:32642.	266226_at	-2.1
unknown protein ; supported by full-length cDNA: Ceres: 29227.	265116_at	-2.1
glutathione transferase, putative similar to glutathione S-transferase GB: AAF22517 GI:6652870 from [Papaver somniferum]; supported by full-lengt		-2.1
unknown protein ;supported by full-length cDNA: Ceres:25136.	264635_at	-2.1
putative mutT domain protein	263852_at	-2.1
unknown protein	262092_at	-2.1
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_16648778_gb_AY058166.1_	259373_at	-2.1
unknown protein similar to putative protein GB:CAB38214 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:6052.	258811_at	-2.1
unknown protein ; supported by cDNA: gi_14532647_gb_AY039948.1_	258535_at	-2.1
unknown protein contains similarity to 3-methyladenine-DNA glycosidase I GB:P05100 from [Escherichia coli]; supported by full-length cDNA: Ceres	257701_at	-2.1
S-adenosyl-L-homocysteinas, putative similar to S-adenosyl-L-homocysteinase GB:AAD56048 from [Lupinus luteus]; supported by cDNA: gi_1529;		-2.1
beta-fructofuranosidase identical to beta-fructofuranosidase GI:6683112 from [Arabidopsis thaliana]; supported by cDNA: gi_6683111_dbj_AB0293	256150_at	-2.1
putative protein RING-H2 finger protein RHA1a, Arabidopsis thaliana,AF078683	255802_s_at	-2.1
unknown protein contains similarity to chlorophyllase GI:7415999 from [Chenopodium album]; supported by full-length cDNA: Ceres: 31589.	255786_at	-2.1
putative protein Cyclic beta-1-3-glucan synthase, Bradyrhizobium japonicum, AF047687	254773_at	-2.1
heat shock protein - like heat shock protein 17, Triticum aestivum, PIR1:HHWT17;supported by full-length cDNA: Ceres:23223.	254384_at	-2.1
putative protein embryo-abundant protein (EMB34), Picea glauca, PID:g1350531	254318_at	-2.1
putative protein annexin VII, Dictyostelium discoideum, PIR1:LUDO7	254262_at	-2.1
putative protein ;supported by full-length cDNA: Ceres:265.	253172_at	-2.1
lipid-transfer protein-like protein nonspecific lipid transfer protein, loblolly pine, PIR:S51816;supported by full-length cDNA: Ceres:8461.	252711_at	-2.1
hypothetical protein	252501_at	-2.1
SF16 -like protein SF16 protein, pollen specific, helianthus annuus, PIR:T13992;supported by full-length cDNA: Ceres:39013.	252280_at	-2.1
putative protein several hypothetical proteins - Arabidopsis thaliana; supported by cDNA: gi_15010763_gb_AY045683.1_	252098_at	-2.1
putative protein hypothetical protein At2g41240 - Arabidopsis thaliana, EMBL:AC005662	251677_at	-2.1
	_	

	ie- 251626 at	-2.1
putative protein prib5, Ribes nigrum, EMBL:RNI7578;supported by full-length cDNA: Ceres:31361.	251400 at	-2.1
nknown protein	250857 at	-2.1
nucleoid DNA-binding protein cnd41 - like protein nucleoid DNA-binding protein cnd41, chloroplast, common tobacco, PIR:T01996	250445_at	-2.1
utative protein similar to unknown protein (gb]AAB61527.1)	249727_at	-2.1
mino acid permease	249346 at	-2.1
utative protein similar to unknown protein (pir  T04427)	248943 s at	-2.1
known protein	247878 at	-2.1
istone H4 - like protein histone H4, Zea mays, PIR:HSZM4:supported by full-length cDNA: Ceres:15418.	247692 s at	-2.1
ypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:124269.	247092_5_at 245840 at	-2.1
hosphate/phosphoenolpyruvate translocator - like protein ;supported by full-length cDNA: Ceres:100777.	245698_at	-2.1
SI 9KDa protein	244932_at	-2.1
nknown protein ; supported by cDNA: gi_16612242_gb_AF439822.1_AF439822	266489_at	-2
ypothetical protein predicted by genscan and genefinder	265892_at	-2
xpressed protein ; supported by full-length cDNA: Ceres: 38093.	265025_at	-2
xpressed protein ; supported by full-length cDNA: Ceres: 17126.	264725_at	-2
xpressed protein ; supported by cDNA: gi_13926282_gb_AF372895.1_AF372895	263632_at	-2
nknown protein	262970_at	-2
alcium-dependent protein kinase, putative similar to calcium-dependent protein kinase GB:AAC25423 GI:3283996 [Nicotiana tabacum]	262671_at	-2
ypothetical protein predicted by genemark.hmm	262151_at	-2
denine phosphoribosyltransferase almost identical to adenine phosphoribosyltransferase GI:1402894 from [Arabidopsis thaliana]	262039 at	-2
equilatory protein HAL3B similar to GB:AAB53106 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres; 412.	261306 at	-2
gantal, protein predicted by genemark.hmm	260919 at	-2
lower development protein cycloidea (cyc3), putative similar to flower development protein cycloidea (cyc3) GI:6358611 from [Misopates orontiu	_	-2
Vicin, putative similar to GB:CAB77269 from [Pisum sativum]	260506 at	-2
Nonwn protein supported by CDNA: Ceres: 13335	260072 at	-2
ypothetical protein predicted by genefinder	259743 at	-2
nodanese-like family protein contains rhodanese-like domain PF:00581;supported by full-length cDNA: Ceres:30880.	258989 at	-2
	—	
nknown protein ;supported by full-length cDNA: Ceres:8544.	256785_at	-2
nknown protein ;supported by full-length cDNA: Ceres:31357.	256674_at	-2
lisease resistance protein, putative similar to disease resistance protein RPP1-WsA [Arabidopsis thaliana] GI:3860163; supported by full-length		-2
utative protein	255692_at	-2
systeine proteinase contains similarity to cysteine proteinase RD21A (thiol protease) GI:435619, SP:P43297 from [Arabidopsis thaliana]	254915_s_at	-2
acid phosphatase-like protein acid phosphatase-1 (EC 3.1.3) - Lycopersicon esculentum, PIR2: T06587; supported by cDNA: gi_15293022_gb_		-2
utative protein	253345_at	-2
putative auxin-regulated protein auxin-induced protein X15, Glycine max, PIR2:JQ1097;supported by full-length cDNA: Ceres:10510.	253255_at	-2
butative LEA protein Picea glauca late embryogenesis abundant protein (EMB8), PID:g1350545;supported by full-length cDNA: Ceres:36702.	252132_at	-2
yntaxin-like protein synt4 ;supported by full-length cDNA: Ceres:37248.	252053 at	-2
utative protein multisynthetase complex auxiliary component p43 - Cricetulus griseus, EMBL:AF021800;supported by full-length cDNA: Ceres:2	30 251442 at	-2
putative protein outer envelope membrane protein E 6.7 - chloroplast Spinacia oleracea, PIR:A35958; supported by cDNA; gi 15724349 gb AF	41 251155 at	-2
utative protein ;supported by full-length cDNA: Ceres:40252.	250936 at	-2
4-sterol C-methyltransferase ; supported by cDNA: gi_11066104_gb_AF195648.1_AF195648	250254 at	-2
- stellor C-meruny franslerase, supported by CDAX, gr_11000104_gb_At 150040.1_At 150040	250234_at 250217 at	-2
beta-amylase-like proten beta-amylase - Prunus armeniaca, EMBL:AF139501;supported by full-length cDNA: Ceres:30798.	250217_at 250007 at	-2
-phosphogluconolactonase-like protein (supported by full-length cDNA: Ceres:13806.	249732 at	-2
	_	
ectin acetylesterase (supported by full-length cDNA: Ceres:39005.	248968_at	-2
istone H3 (sp[P05203); supported by cDNA: gi_13926210_gb_AF370577.1_AF370577	247192_at	-2
pospory-associated protein C-like	247101_at	-2
ypothetical protein similar to putative disease resistance protein GB:AAC14512 GI:2739389 from [Arabidopsis thaliana]	245765_at	-2
ADH dehydrogenase 49KDa protein	244937_at	-2
utative protein similar to unknown protein (emb CAB67623.1)	250696_at	-2
ypothetical protein predicted by genscan and genefinder	266363_at	-1.9
eta-expansin ;supported by full-length cDNA: Ceres:109135.	265443_at	-1.9
nknown protein similar to hypothetical protein GI:9665091 from [Arabidopsis thaliana]	264998_at	-1.9
	264096 at	-1.9
xpressed protein ; supported by full-length cDNA: Ceres: 2681.		
xpressed protein ; supported by full-length CDNA: Ceres: 2681. utative s-adenosylmethionine synthetase ;supported by full-length cDNA: Ceres:13320.	263838 at	-1.9

putative CONSTANS-like B-box zinc finger protein ; supported by cDNA: gi_12698721_gb_AF323666.1_AF323666	263252_at	-1.9
hypothetical protein predicted by genemark.hmm	263126_at	-1.9
peptide transporter, putative predicted by genemark.hmm; supported by cDNA: gi_15810442_gb_AY056260.1_	261958_at	-1.9
acid phosphatase, putative similar to acid phosphatase GI:5360721 from [Lupinus albus]; supported by cDNA: gi_13605749_gb_AF361856.1_AF31		-1.9
hypothetical protein predicted by genemark hmm; supported by full-length cDNA: Ceres: 268411.	261351_at	-1.9
putative ABC transporter similar to ABC transporters: GB:BAA77876 [Escherichia coli], GB:P07655 [Escherichia coli]; contains Pfam profile: PF000	_	-1.9
peptide transporter, putative similar to peptide transporter PTR2-B SP:P46032 [Arabidopsis thaliana (Mouse-ear cress)]; supported by full-length cl	_	-1.9
myb-related transcription factor, putative similar to GI:1430846 from [Lycopersicon esculentum] Expressed protein ; supported by full-length cDNA: Ceres: 42300.	259822_at 259603 at	-1.9 -1.9
unknown protein ; supported by cDNA: gi 15028026 gb AY045870.1	259460 at	-1.9
	259382 s at	-1.9
receptor kinase, putative similar to receptor kinase GB:AAA33715 from [Petunia integrifolia];supported by full-length cDNA: Ceres:22221.	258159 at	-1.9
unknown protein ;supported by full-length cDNA: Ceres;7192.	258183 at	-1.9
unknown protein ; supported by cDNA; gi 15810494 gb AY056286.1	257071 at	-1.9
	256577 at	-1.9
dutamine synthetase, putative similar to glutamine synthetase [Raphanus sativus] GI:1526564;supported by full-length cDNA: Ceres:2662.	256524 at	-1.9
zinc-finger protein, putative similar to GI:S262161 from [Arabidopsis thaliana]; supported by cDNA: gi 16323142 gb AY057675.1	256469 at	-1.9
RING zinc finger protein contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger)	256446 at	-1.9
unknown protein	256262_at	-1.9
calcium-binding protein, putative similar to calcium-binding protein GI:6901652 from [Olea europaea];supported by full-length cDNA: Ceres:19462.	256129 at	-1.9
transcriptional activator CBF1, putative similar to transcriptional activator CBF1 GI:1899058 from [Arabidopsis thaliana	255937 at	-1.9
pEARLI 1-like protein Arabidopsis thaliana pEARLI 1 mRNA, PID:g871780; supported by cDNA: gi 15450470 gb AY052336.1	254832 at	-1.9
extensin-like protein extensin-like protein, Zea mays, PIR2:S49915	254770_at	-1.9
1-aminocyclopropane-1-carboxylate synthase - like protein 1-aminocyclopropane-1-carboxylate synthase. Arabidopsis thaliana, S71174; supported	253066 at	-1.9
putative thaumatin-like protein thaumatin-like protein precursor Mdtl1, pathogenesis-related - Malus domestica, PID:g3643249;supported by full-len	252954_at	-1.9
putative protein 24 kDa seed maturation protein, Glycine max., EMBL:AF004806	251903_at	-1.9
putative protein similar to unknown protein (pir  T02514);supported by full-length cDNA: Ceres:117347.	250777_at	-1.9
putative protein similar to unknown protein (pir  T09909)	250307_at	-1.9
putative protein S-receptor kinase PK3 precursor, maize, PIR:T02753;supported by full-length cDNA: Ceres:154037.	249983_at	-1.9
putative protein contains similarity to calmodulin;supported by full-length cDNA: Ceres:99348.	249197_at	-1.9
unknown protein ;supported by full-length cDNA: Ceres:31129.	248186_at	-1.9
putative protein strong similarity to unknown protein (emb CAB89350.1)	247240_at	-1.9
putative protein similar to unknown protein (emb CAB66910.1);supported by full-length cDNA: Ceres:36946.	247161_at	-1.9
RING-H2 zinc finger protein-like RING-H2 zinc finger protein ATL6 - Arabidopsis thaliana, EMBL:AF132016;supported by full-length cDNA: Ceres:1	_	-1.9
beta-1,3-glucanase class I precursor ;supported by full-length cDNA: Ceres:3176.	245393_at	-1.9
cysteine proteinase inhibitor like protein ; supported by full-length cDNA: Ceres: 31946.	245323_at	-1.9
AR781, similar to yeast pheromone receptor identical to GB:D88743, corrected a frameshift found in the original record (at 69530 bp), sequence su	_	-1.9
unknown protein	257381_at	-1.9
unknown protein	267545_at	-1.8
putative ammonium transporter	267142_at	-1.8
calcium binding protein (CaBP-22) identical to GB:Z12136;supported by full-length cDNA: Ceres:123659.	267076_at	-1.8
hypothetical protein predicted by genefinder	266774_at	-1.8
putative CCCH-type zinc finger protein identical to GB:UB1238;supported by full-length cDNA: Ceres:39893.	266656_at	-1.8
unknown protein ;supported by full-length cDNA: Ceres:10986. hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:8450.	266476_at 266311 at	-1.8 -1.8
unknown protein	266157 at	-1.0 -1.8
putative beta-1,3-glucanase	265377 at	-1.8
putative bera-r, s-grucanase putative RING zinc finger protein ; supported by cDNA: gi 3790572 gb AF078824.1 AF078824	264854 at	-1.8
sugar carrier protein, putative similar to sugar carrier protein GI:169735 from [Ricinus communis]	264482 at	-1.8
butative NPK1-related protein kinase 2 similar to intrate chlorate transporter GB:Q05085 from (Arabidopsis thaliana); supported by cDNA; gi 16666	264348 at	-1.8
protein kinase, putative Simisinilar to protein kinase Gi:7573438598 from (Populas nigra)	264240 at	-1.8
Expressed protein ; supported by full-length cDNA: Ceres: 38277.	264004 at	-1.8
putative glucosyltransferase ; supported by cDNA: gi 15809993 gb AY054265.1	263847 at	-1.8
putative glutaredoxin Strong similarity to gb/Z49699 glutaredoxin from Ricinus communis	263168 at	-1.8
glucose transporter almost identical to glucose transporter GB:P23586 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres; 33727.	262456 at	-1.8
unknown protein (supported by full-length CDNA: Ceres:21798.	262283 at	-1.8
unknown protein	261981 at	-1.8
		-

hypothetical protein predicted by genemark.hmm	261247_at	-1.8
unknown protein ; supported by full-length cDNA: Ceres: 100293.	260877_at	-1.8
putative FKBP type peptidyl-prolyl cis-trans isomerase	260542_at	-1.8
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:99920.	260427_at	-1.8
AP2-containing DNA-binding protein contains Pfam profile: PF00847 AP2 domain	259793_at	-1.8
putative serine/threonine kinase ; supported by cDNA: gi_15010571_gb_AY045587.1_	259538_at	-1.8
putative ribose 5-phosphate isomerase identical to putative ribose 5-phosphate isomerase GB:AAD57010 (Arabidopsis thaliana); similar to ribose 5	_	-1.8
unknown protein ;supported by cDNA: gi_15081621_gb_AY048203.1_	259020_at	-1.8
cinnamyl alcohol dehydrogenase identical to GB:P48523 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:4357.	258023_at	-1.8
unknown protein contains similarity to auxin-induced protein GB:P33082 from [Glycine max]	257690_at	-1.8
unknown protein ; supported by full-length cDNA: Ceres: 105122.	257300_at	-1.8
hypothetical protein predicted by genscan; supported by cDNA: gi_15292884_gb_AY050876.1_	257057_at	-1.8
calmodulin, putative similar to GB:P07463 from [Paramecium tetraurelia] (Cell 62 (1), 165-174 (1990))	256755_at	-1.8
unknown protein ; supported by cDNA: gi_15293280_gb_AY051074.1_	256266_at	-1.8
receptor protein kinase, putative contains Pfam profiles: PF00069: Eukaryotic protein kinase domain, multiple PF00560: Leucine Rich Repeat	256168_at	-1.8
leucine zipper protein, putative similar to leucine zipper protein GI:10177020 from [Arabidopsis thaliana]	256050_at	-1.8
putative protein A. thaliana hypothetical protein F1N20.70, GenBank accession number AL022140;supported by full-length cDNA: Ceres:118778.	255285_at	-1.8
Expressed protein ; supported by full-length cDNA: Ceres: 42850.	254609_at	-1.8
putative protein AR411 - Arabidopsis thaliana (thale cress), PID:g1669603; supported by cDNA: gi_13507100_gb_AF272748.1_AF272748	254231_at	-1.8
putative protein ;supported by full-length cDNA: Ceres:16463.	254103_at	-1.8
nucleotide pyrophosphatase -like protein nucleotide pyrophosphatase, Oryza sativa, gb:T03293; supported by cDNA: gi_13430713_gb_AF360269.	253697_at	-1.8
putative pollen allergen pollen allergen - Pinus radiata, PID:g2935527; supported by cDNA: gi_14190354_gb_AF378855.1_AF378855	252997_at	-1.8
putative chloroplast prephenate dehydratase similar to bacterial PheA gene products	252652_at	-1.8
histone H2B ;supported by full-length cDNA: Ceres:32930.	252561_at	-1.8
receptor protein kinase - like protein CLAVATA1 receptor kinase, Arabidopsis thaliana, EMBL:ATU96879	252272_at	-1.8
3-isopropylmalate dehydratase-like protein (small subunit) 3-isopropylmalate dehydratase, small subunit - Thermotoga maritima, PIR:A72363	251524_at	-1.8
transport protein subunit - like S61B_ARATH PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT, Arabidopsis thaliana, SWISSPROT:S61	251422_at	-1.8
unknown protein ;supported by full-length cDNA: Ceres:7709.	251395_at	-1.8
putative protein prenylated rab acceptor 1 - Homo sapiens, EMBL:AF112202;supported by full-length cDNA: Ceres:22460.	250663_at	-1.8
Expressed protein ; supported by full-length cDNA: Ceres: 252311.	250537_at	-1.8
unknown protein ;supported by cDNA: gi_14190364_gb_AF378860.1_AF378860	250099_at	-1.8
auxin-induced protein-like	250012_x_at	-1.8
serine carboxypeptidase II-like protein	249847_at	-1.8
putative protein contains similarity to photomorphogenesis repressor protein; supported by cDNA: gi_14532633_gb_AY039941.1_	249798_at	-1.8
UDP-glucose dehydrogenase-like protein UDP-glucose dehydrogenase - Glycine max, EMBL:U53418	249469_at	-1.8
putative protein contains similarity to DNA-3-methyladenine glycosylase I;supported by full-length cDNA: Ceres:29551.	249008_at	-1.8
putative protein contains similarity to FKBP-type peptidyl-prolyl cis-trans isomerase	248962_at	-1.8
GDSL-motif lipase/hydrolase-like protein ;supported by full-length cDNA: Ceres:18389.	248912_at	-1.8
putative protein similar to unknown protein (pir  T05562); supported by full-length cDNA: Ceres: 158397.	248551_at	-1.8
putative protein contains similarity to ethylene responsive element binding factor;supported by full-length cDNA: Ceres:2347.	248448_at	-1.8
putative protein contains similarity to 40S ribosomal protein S10;supported by full-length cDNA: Ceres:91769.	248331_at	-1.8
1,4-benzoquinone reductase-like; Trp repressor binding protein-like	248162_at	-1.8
putative protein various predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:28528.	246860_at	-1.8
copper amine oxidase, putative similar to copper amine oxidase GI:3819099 from [Cicer arietinum]	246603_at	-1.8
beta-D-glucan exohydrolase - like protein beta-D-glucan exohydrolase, Nicotiana tabacum, EMBL:AB017502	246184_at	-1.8
putative protein retinal glutamic acid-rich protein, bovine, PIR:A40437;supported by full-length cDNA: Ceres:24151.	246108_at	-1.8
phytochrome kinase substrate 1 - like protein	245696_at	-1.8
Expressed protein ; supported by full-length cDNA: Ceres: 21980.	245642_at	-1.8
F12A21.7 hypothetical protein;supported by full-length cDNA: Ceres:34552.	245197_at	-1.8
putative WRKY-type DNA-binding protein ; supported by cDNA: gi_13506742_gb_AF224704.1_AF224704	245051_at	-1.8
PSII K protein	245050_at	-1.8
carboxytransferase beta subunit	245016_at	-1.8
unknown protein ;supported by full-length cDNA: Ceres:8081.	256793_at	-1.8
unknown protein	267055_at	-1.7
putative phosphomannomutase ;supported by full-length cDNA: Ceres:998.	266928_at	-1.7
putative sugar transporter ;supported by full-length cDNA: Ceres:114959.	265768_at	-1.7
putative phosphatidic acid phosphatase ;supported by full-length cDNA: Ceres:19163.	265737_at	-1.7

unknown protein ;supported by full-length cDNA: Ceres:1697.	265716_at	-1.7
putative caltractin ;supported by full-length cDNA: Ceres:7802.	265460_at	-1.7
putative glycosyl transferase similar to GB:AAC78704	264857_at	-1.7
	264501_at	-1.7
hypothetical protein predicted by genscan; supported by cDNA: gi_13937239_gb_AF372975.1_AF372975	264434_at	-1.7
putative leucine-rich repeat disease resistance protein ;supported by full-length cDNA: Ceres:20900.	263330_at	-1.7
hypothetical protein similar to putative transporter GI:6598860 from [Arabidopsis thaliana]	262935_at	-1.7
unknown protein	262868_at	-1.7
delta 9 desaturase identical to delta 9 desaturase GB:BAA25180 GI:2970034 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 10(		-1.7
putative helix-loop-helix DNA-binding protein contains Pfam profile: PF00010 Helix-loop-helix DNA-binding domain	260070_at	-1.7
putative calmodulin similar to calmodulin GB:P02596 [Renilla reniformis]; contains Pfam profile: PF00036 EF hand (4 copies); supported by full-lengt	260076_at	-1.7
phosphatidylinositol synthase (PIS1) identical to phosphatidylinositol synthase (PIS1) GB:AJ000539;supported by full-length cDNA: Ceres:34210.	260006_at	-1.7
unknown protein ;supported by full-length cDNA: Ceres:29624.	259979_at	-1.7
putative transcription factor similar to myb-related transcription factor 24 GB:S71287; supported by full-length cDNA: Ceres:31592.	259751_at	-1.7
putative signal peptidase similar to MITOCHONDRIAL INNER MEMBRANE PROTEASE SUBUNIT 2 GB:P46972 [Saccharomyces cerevisiae]	259199_at	-1.7
class 2 non-symbiotic hemoglobin identical to class 2 non-symbiotic hemoglobin GB:AAB82770 [Arabidopsis thaliana]; supported by full-length cDN	258920_at	-1.7
putative MYB-related protein similar to MYB-related protein GB:CAA73305	258723_at	-1.7
putative oxidoreductase similar to phytoene desaturase GB:P28553 from [Glycine max];supported by full-length cDNA: Ceres:17350.	258708_at	-1.7
hypothetical protein similar to auxin-induced proteins GB:P33083, GB:P33082 [Glycine max]	258653_at	-1.7
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:262487.	258551_at	-1.7
unknown protein	258100_at	-1.7
dihydrolipoamide S-acetyltransferase identical to GB:AAD55139 from [Arabidopsis thaliana]; supported by cDNA: gi 14335165 gb AY037262.1	258086 at	-1.7
hypothetical protein ; supported by full-length cDNA: Ceres: 107260.	256383_at	-1.7
Expressed protein ; supported by full-length cDNA: Ceres: 11615.	256091 at	-1.7
glycine hydroxymethyltransferase - like protein glycine hydroxymethyltransferase, Homo sapiens, PIR2:A46746	254740 s at	-1.7
beta-1,3-glucanase-like protein strong simlarity to endo-beta-1,3-beta-D-glucosidase, Nicotiana tabacum, PIR2:S46495	254665 at	-1.7
	254331 s at	-1.7
serine threonine kinase - like protein KI domain interacting kinase 1 (KIK1), Zea mays; supported by cDNA: gi_13506746_gb_AF224706.1_AF2247	254265 s at	-1.7
putative protein extensin, Catharanthus roseus, D86853	254093 at	-1.7
low temperature and salt responsive protein homolog low temperature and salt responsive protein LTI6A - Arabidopsis thaliana, PID:g4039153	253627 at	-1.7
pectinesterase - like protein pectinesterase, Prunus persica, X95991; supported by cDNA gi 14190428 gb AF378892.1 AF378892	253372 at	-1.7
	253284 at	-1.7
amidophosphoribosyltransferase 2 precursor	253252 at	-1.7
vacuolar H+-transporting ATPase 16K chain ;supported by full-length cDNA: Ceres:24998.	253200 at	-1.7
putative protein AT.I.24-7, Arabidopsis thaliana, gb:U63815	253215 at	-1.7
hypothetical protein supported by full-length cDNA: Ceres:21166.	252877 at	-1.7
R2R3-MYB transcription factor; supported by cDNA: gi 15983427 gb AF424588.1 AF424588	252193 at	-1.7
uracil phosphoribosyltransferase-like protein uracil phosphoribosyltransferase - Nicotiana tabacum, PIR:T03969;supported by full-length cDNA: Cei	-	-1.7
nucleoid DNA-binding - like protein nucleoid DNA-binding protein cnd41, chloroplast, common tobacco, PIR:T01996; supported by full-length cDNA		-1.7
putative protein	251727 at	-1.7
responce reactor 4 ; supported by cDNA: gi 3273201 dbj AB010918.1 AB010918	251665 at	-1.7
beta-1,3-glucanase 2 (BG2) (PR-2) ;supported by full-length cDNA: Ceres:21719.	251625 at	-1.7
LAX1 / AUX1 -like permease	251133 at	-1.7
putative protein predicted proteins in castor bean, Arabidopsis thaliana and alfalfa.; supported by full-length cDNA: Ceres: 25522.	250366 at	-1.7
putative protein predicted protein, Arabidopsis thaliana	250168 at	-1.7
proline-richh protein predicted protein F24P17.17 - Arabidopsis thaliana, EMBL:AC011623	250002 at	-1.7
putative protein similar to unknown protein (emb/CAB89401.1)	249071 at	-1.7
zinc finger protein Zat12 ;supported by full-length cDNA: Ceres:40576.	247655 at	-1.7
structural protein - like glycine-rich cell wall structural protein 1 precursor, Oryza sativa, PIR:KNRZG1;supported by full-length cDNA: Ceres:9324.	247541 at	-1.7
putative protein similar to unknown protein (emb/CAB62301.1)	247030 at	-1.7
putative protein similar to unknown protein (piri/T08445);supported by full-length cDNA: Ceres:11651.	246952 at	-1.7
transmembrane protein FT27/PFT27-like ;supported by full-length cDNA: Ceres:12993.	246619 at	-1.7
acetyltransferase-like protein Glucosamine-6-phosphate acetyltransferase EMeg32 protein - Mus musculus, EMBL:AJ001006	246518 at	-1.7
S-adenosylmethionine decarboxylase (adoMetDC2); supported by cDNA; gi 16930682; gb AF436825.1 AF436825	246490 at	-1.7
	245987 at	-1.7
hypothetical protein predicted by generark.hmm	245771 at	-1.7
ATP-sulfurylase; supported by CDNA: gi_459143_gb_U06275.1_ATU06275	245254_at	-1.7
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ATPase I subunit	245025 at	-1.7
hypothetical protein predicted by genefinder; supported by cDNA: gi 14334633 gb AY034990.1	267279 at	-1.6
actin 3 identical to GB:U29480;supported by full-length cDNA: Ceres: 19581.	267175 s at	-1.6
expressed protein supported by cDNA: Ceres:16674; supported by cDNA: gi 13878170 gb AF370348.1 AF370348	267038 at	-1.6
putative auxin transport protein ; supported by cDNA: gi 7109714 gb AF087016.1 AF087016	266300 at	-1.6
unknown protein ; supported by full-length cDNA: Ceres: 1517.	265416_at	-1.6
putative sulphate transporter protein strongly similar to GB:BAA75015, location of EST gb/W43788 and gb/N96564; supported by cDNA: gi_457991	264901_at	-1.6
unknown protein similar to ESTs gb AA605440 and gb H37232;supported by full-length cDNA: Ceres:30716.	264834_at	-1.6
unknown protein Location of EST gb T45589;supported by full-length cDNA: Ceres:145854.	264523_at	-1.6
NAM (no apical meristem)-like protein similar to petunia NAM (X92205) and A. thaliana sequences ATAF1 (X74755) and ATAF2 (X74756); probable	263584_at	-1.6
putative cytochrome P450 monooxygenase identical to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067 C	262793_at	-1.6
AMP-binding protein, putative contains Pfam profile: PF00501 AMP-binding enzyme	262698_at	-1.6
hypothetical protein similar to hypothetical protein GB:CAB36801 GI:4455265 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 40		-1.6
Expressed protein ; supported by full-length cDNA: Ceres: 102374.	262290_at	-1.6
Expressed protein ; supported by full-length cDNA: Ceres: 102054.	262286_at	-1.6
AP2 domain containing protein, putative similar to AP2 domain containing protein RAP2.1 GI:2281627 from [Arabidopsis thaliana]	262211_at	-1.6
pectinesterase, putative similar to pectinesterase GI:1944574 from [Lycopersicon esculentum]; supported by cDNA: gi_15982770_gb_AY057492.1	261728_at	-1.6
unknown protein	261175_at	-1.6
2,4-D inducible glutathione S-transferase, putative similar to 2,4-D inducible glutathione S-transferase GI:2920666 from [Glycine max]; supported by		-1.6
integral membrane protein, putative similar to GB:U43629 from [Beta vulgaris] (Plant Physiol. 110 110 (2), 511-520 (1996)); supported by cDNA: gi		-1.6
ACC oxidase, putative similar to ACC oxidase GI:587086 from [Brassica oleracea]; supported by cDNA: gi_15028038_gb_AY045876.1_	260637_at	-1.6
Expressed protein ; supported by cDNA: gi_15294273_gb_AF410328.1_AF410328	260601_at	-1.6
hypothetical protein predicted by genefinder	260522_x_at	-1.6
calmodulin-related protein similar to GB:P25070 from [Arabidopsis thaliana], contains Pfam profile: PF00036 EF hand (4 copies);supported by full-liver protein uncertainty and the DNA is a contained of the DC 20005 (1 A DC 20005).	_	-1.6
unknown protein ; supported by cDNA: gi_13937162_gb_AF372935.1_AF372935	259665_at	-1.6
hypothetical protein predicted by genemark.hmm putative methionine synthase similar to cobalamin-independent methionine synthase GB:AAC50037 [Arabidopsis thaliana];supported by full-length (	259398_at	-1.6 -1.6
unknown protein HMM hit: 2Fe-2S iron-sulfur cluster binding domain;supported by full-length cDNA: Ceres:29120.	259016 at	-1.6
putative 40S ribosomal protein S17 similar to 40S ribosomal protein S17 GB:AAD50774 [Lycopersicon esculentum];supported by full-length cDNA: (		-1.6
hypothetical protein predicted by genefinder:supported by full-length CDNA: Ceres:8992.	258792 at	-1.6
putative RING zinc finger protein similar to RING-H2 zinc finger protein ATL6 GB:AAD33584 from [Arabidopsis thaliana]:supported by full-length cD	258436 at	-1.6
putative signal peptidase 21kDa subunit similar to signal peptidase 21kDa subunit GB:BAA76439 [Rattus norvegicus]; contains Pfam profile: PF004	_	-1.6
putative delta 9 desaturase similar to delta 9 desaturase GB BAA25180 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:25205.	258250 at	-1.6
Cdc45-like protein similar to Cdc45 GB:AAC67520 [Xenopus laevis] (EMBO J. 17, 5699-5707 (1998)) (required for the initiation of eukarvotic DNA	257813 at	-1.6
sugar transport, putative similar to D-XYLOSE-PROTON SYMPORTER GB:052733 from [Lactobacillus brevis]	257805 at	-1.6
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:35773.	257600 at	-1.6
unknown protein ;supported by full-length cDNA: Ceres:35218.	256522 at	-1.6
RNA-binding protein similar to GI:829254 from [Arabidopsis thaliana]	256419_at	-1.6
guanine nucleotide-binding protein, putative similar to guanine nucleotide-binding protein GI:9294068 from [Arabidopsis thaliana]; supported by full-	256144_at	-1.6
predicted protein ; supported by cDNA: gi_15027984_gb_AY045849.1_	256093_at	-1.6
UDP-glucose glucosyltransferase identical to UDP-glucose glucosyltransferase GI:3928543 from [Arabidopsis thaliana]; supported by cDNA: gi_12C	255942_at	-1.6
putative YABBY3 axial regulator ;supported by cDNA: gi_14335013_gb_AY037186.1_	255709_at	-1.6
growth factor like protein antisense basic fibroblast growth factor GFG - Rattus norvegicus, PID:g1518635;supported by full-length cDNA: Ceres:14		-1.6
calcium-binding protein - like calcium-binding protein, Solanum tuberosum, gb:L02830	254487_at	-1.6
putative dihydrolipoamide succinyltransferase dihydrolipoamide succinyltransferase (EC 2.3.1.61) precursor - rat, Pir2:A41015;supported by full-len		-1.6
hypothetical protein ;supported by full-length cDNA: Ceres:18040.	253817_at	-1.6
hypothetical protein	253367_at	-1.6
putative protein ;supported by full-length cDNA: Ceres:15747.	252821_at	-1.6
serine/proline-rich protein	252615_at	-1.6
putative protein pectinesterase - Arabidopsis thaliana, PIR:S51370; supported by cDNA: gi_14517535_gb_AY039603.1_	252406_at	-1.6
protein translocation complex sec61 gamma chain-like protein protein translocation complex sec61 gamma chain, endoplasmic reticulum - Canis lu		-1.6
putative protein EREBP-3 homolog, Stylosanthes hamata, EMBL:091982; supported by cDNA; gi_15010555_gb_AY045579.1	252214_at	-1.6
UTP-glucose glucosyltransferase - like protein UTP-glucose glucosyltransferase, Manihot esculenta, PIR:S41951; supported by cDNA: gi_1514627		-1.6
phenylalanine ammonia-lyase ;supported by full-length cDNA: Ceres:110886.	251984_at	-1.6
putative protein similar to unknown protein (gb AAF01528.1) asparaginase ; supported by cDNA: gi 14517439 gb AY039555.1	250796_at 250547 at	-1.6 -1.6
putative protein KIAA0255 gene, Homo sapiens, EMBL:HSD444	250547_at 250422 at	-1.0 -1.6
Padaro proton far a ozoo gono, fionto adpiono, Lindel nobert	200722_ai	-1.0

histone H2B like protein (emb CAA69025.1)	249916_at	-1.6
putative protein similar to unknown protein (gb AAD29063.1)	249777_at	-1.6
Expressed protein ; supported by full-length cDNA: Ceres: 32450.	249719_at	-1.6
putative protein predicted proteins, Arabidopsis thaliana;supported by full-length CDNA: Ceres:249321.	249422_at	-1.6
tubulin beta-4 chain (splP24636) ; supported by cDNA: gi_14334935_gb_AY035141.1_	249049_at	-1.6
putative protein similar to unknown protein (pir  T04792)	248085_at	-1.6
pectate lyase ;supported by cDNA: gi_16648839_gb_AY058197.1_	247377_at	-1.6
adenylate kinase ;supported by full-length cDNA: Ceres:13667.	247382_at	-1.6
	247388_s_at	-1.6
2-oxoglutarate/malate translocator; supported by cDNA: gi_15810580_gb_AY056329.1_	247289_at	-1.6
60S ribosomal protein L26 ;supported by full-length cDNA: Ceres:2561.	247010_at	-1.6
putative protein ;supported by full-length cDNA: Ceres:39563.	245981_at	-1.6
putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:19897.	246000_at	-1.6
Expressed protein ; supported by full-length cDNA: Ceres: 6580.	245336_at	-1.6
hypothetical protein	245018_at	-1.6
ribosomal protein L16	244983_at	-1.6
putative cytochrome b5	267544_at	-1.5
MADS-box protein (AGL20) ; supported by full-length cDNA: Ceres: 5467.	267509_at	-1.5
60S acidic ribosomal protein P0	267349_at	-1.5
expressed protein supported by full-length cDNA: Ceres:3350	266950_at	-1.5
ribonuclease, RNS1 identical to ribonuclease SP:P42813, GI:561998 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:27242.	266743_at	-1.5
putative chorismate mutase/prephenate dehydratase ;supported by full-length cDNA: Ceres:37739.	266257_at	-1.5
unknown protein ;supported by full-length cDNA: Ceres:31665.	265670_s_at	-1.5
unknown protein	265411_at	-1.5
hypothetical protein contains similarity to MHC class II antigen GI:9502037 from [Aotus nancymaae]; supported by full-length cDNA: Ceres: 1542.	265001_at	-1.5
unknown protein ; supported by full-length cDNA: Ceres: 270281.	264342_at	-1.5
unknown protein similar to PHZF, catalyzing the hydroxylation of phenazine-1-carboxylic acid to2-hydroxy-phenazine-1-carboxylic acid; ESTs gb H	264355_at	-1.5
putative auxin-regulated protein	264014_at	-1.5
unknown protein ;supported by full-length cDNA: Ceres:24255.	263901_at	-1.5
ABC transporter, putative similar to ABC transporter GI:9279716 from [Arabidopsis thaliana]	262899 at	-1.5
NADPH-dependent codeinone reductase, putative similar to NADPH-dependent codeinone reductase GI:6478210 from [Papaver somniferum]; sup	262913_at	-1.5
hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 19759.	262878_at	-1.5
unknown protein strong similarity to gi 3367522 F8K4.9 from Arabidopsis thaliana BAC gb AC004392. EST gb W43487 comes from this gene	262813 at	-1.5
receptor kinase (CLV1) identical to receptor kinase (CLV1) GB:AAB58929 GI:2160756 [Arabidopsis thaliana]	262728 at	-1.5
ribonuclease contains similarity to RNase GI:7768564 from [Nicotiana tabacum]	262657 at	-1.5
unknown protein Contains a PF 00175 Oxidoreductase FAD/NADH-binding domain. ESTs gb H76345 and gb AA651465 come from this gene; supp	262572 at	-1.5
virus resistance protein, putative similar to virus resistance protein GI:558886 from [Nicotiana glutinosa]	262381 at	-1.5
hypothetical protein similar to hypothetical protein GI:9294146 from [Arabidopsis thaliana]	262236 at	-1.5
	262259 s at	-1.5
hypothetical protein predicted by genemark.hmm	262009 at	-1.5
dirigent protein, putative similar to dirigent protein GI:6694693 from [Forsythia intermedia]	261914 at	-1.5
Expressed protein ; supported by full-length cDNA: Ceres: 19170.	261488 at	-1.5
O-methyltransferase, putative similar to GB:AAF28353 from [Fragaria x ananassa];supported by full-length cDNA: Ceres:101583.	261453 at	-1.5
14-3-3 protein GF14omega (grf2) identical to GF14omega isoform GI:487791 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:252i	260775 at	-1.5
hypothetical protein predicted by genscan+	260167 at	-1.5
unknown protein	260081 at	-1.5
unknown protein ; supported by full-length cDNA: Ceres: 14237.	259909 at	-1.5
auxin-induced protein, putative similar to SP:P33083 from [Glycine max];supported by full-length cDNA: Ceres:147801.	259787 at	-1.5
short chain alcohol dehydrogenase, putative similar to GI:2739279 from [Nicotiana tabacum] (Plant Mol. Biol. 29 (5), 1027-1038 (1995))	259669 at	-1.5
unknown protein ;supported by full-length cDNA: Ceres:17545.	259474 at	-1.5
unknown protein ;supported by full-length cDNA: Ceres:38495.	258606 at	-1.5
unknown protein very similar to unknown protein GB:AAC39468 from [Arabidopsis thaliana]; supported by cDNA: gi 14335087 gb AY037223.1	258402 at	-1.5
putative pectin methylesterase similar to pectin methylesterase GB:Q42534 from [Arabidos)is thaliana];supported by full-length cDNA: Ceres:13261		-1.5
unknown protein ; supported by CDNA; gi 16974601 gb AY060578.1	258244 at	-1.5
cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450	257623 at	-1.5
polygalacturonase, putative similar to endopolygalacturonase GB:225933 from [Lycopersicon esculentum];supported by full-length cDNA: Ceres:17		-1.5
proline oxidase, mitochondrial precursor (osmotic stress-induced proline dehydrogenase) identical to GB:P92983 from [Arabidosis thaliana] (Plant		-1.5

hypothetical protein contains similarity to flavonol synthase (FLS) GB:Q41452 from [Solanum tuberosum], contains Pfam profile: PF00671 Iron/Asc		-1.5
unknown protein	256828_at	-1.5
unknown protein 12-oxophytodienoate reductase, putative similar to 12-oxophytodienoate reductase OPR1 GI:3882355 from [Arabidopsis thaliana]	256337_at	-1.5 -1.5
putative protein ; supported by cDNA: gi 14596204 gb AY042890.1	255895_at 254705 at	-1.5
reticuline oxidase -like protein reticuline oxidase, Eschscholzia californica, PIR:A41533; supported by cDNA: gi 15983492 gb AF424621.1 AF424		-1.5
V-ATPase subunit G (vag2 gene)	254432_at 254216 at	-1.5
possible apospory-associated like protein Pennisetum ciliare possible apospory-associated mRNA clone pSUB C, PID:g549984;supported by full-le	_	-1.5
putative protein ; supported by cDNA: gi 15810482 gb AY056280.1	253925 at	-1.5
putative protein LEDI-3 protein, Lithospermum erythronizon	253909 at	-1.5
histone H2A- like protein histone H2A.4, Triticum aestivum, PIR2:S53521; supported by full-length cDNA: Ceres: 927.	253920 at	-1.5
photosystem II protein W - like photosystem II protein W, Porphyra purpurea, pappinger States, supported by full-length cDNA: Ceres: 2419.	253790 at	-1.5
Proline-rich APG - like protein proline-rich protein APG, Arabidopsis thaliana, PIR2:S21961:supported by full-length cDNA: Ceres:324.	253736 at	-1.5
putative protein (fragment) calcineurin B, Naegleria gruberi, gb;U04380	253412 at	-1.5
putative protein dihydrokaempferol 4-reductase (EC 1.1.1.219) -synechocystis, PIR2:S75325; supported by cDNA; gi 13926212 gb AF370578.1	_	-1.5
Expressed protein ; supported by full-length cDNA: Ceres: 22456.	252823 at	-1.5
putative protein pectinesterase homolog - Pinus radiata,PIR2:T08112	252437 at	-1.5
Expressed protein ; supported by cDNA; gi 16323485 gb AY059131.1	252328 at	-1.5
putative protein various predicted proteins, Brassica rapa, Arabidopsis thaliana; supported by full-length cDNA: Ceres:26538.	251013 at	-1.5
RIBOSOMAL PROTEIN S28- like ribosomal protein S28, Arabidopsis thaliana, EMBL:ATRP28A	250895 at	-1.5
ubiquinol-cytochrome C reductase complex ubiquinone-binding protein (QP-C)-like protein (gb/AAF19563.1)	250800 at	-1.5
transcription factor-like protein ethylene responsive element binding factor 5 - Arabidopsis thaliana, EMBL:AB008107; supported by cDNA: gi 1552		-1.5
myo-inositol-1-phosphate synthase -like protein myo-inositol-1-phosphate synthase, Nicotiana paniculata, EMBL:AB032073	250471_at	-1.5
AtAGP4 ; supported by cDNA: gi_13926257_gb_AF372885.1_AF372885	250437_at	-1.5
putative protein similar to unknown protein (pir  T09909)	250306_at	-1.5
2-oxoglutarate/malate translocator precursor -like protein 2-oxoglutarate/malate translocator precursor, spinach, SWISSPROT.SOT1_SPIOL; supp	250278_at	-1.5
putative protein various predicted proteins	249920_at	-1.5
putative protein similar to unknown protein (emb CAB62461.1);supported by full-length cDNA: Ceres:268701.	249752_at	-1.5
putative protein similar to unknown protein (pir  S75227);supported by full-length cDNA: Ceres:22.	249524_at	-1.5
beta-1,3-glucanase-like protein	249214_at	-1.5
carnitine/acylcarnitine translocase-like protein ;supported by full-length cDNA: Ceres:13730.	248838_at	-1.5
acetyl-CoA C-acetyltransferase;supported by cDNA: gi_16604582_gb_AY059736.1_	248690_at	-1.5
unknown protein ;supported by full-length cDNA: Ceres:116332.	248646_at	-1.5
putative protein similar to unknown protein (gb AAD25141.1);supported by full-length cDNA: Ceres:33455.	248419_at	-1.5
fructokinase1 ; supported by cDNA: gi_13878052_gb_AF370289.1_AF370289	248381_at	-1.5
putative protein contains similarity to unknown protein (dbj BAA90637.1)	248309_at	-1.5
ankyrin-repeat-containing protein-like	248169_at	-1.5
putative protein farnesylated protein GMFP5, Glycine max, EMBL:U64916	247594_at	-1.5
putative protein similar to unknown protein (emb CAB62102.1);supported by full-length cDNA: Ceres:40250.	246996_at	-1.5
hypothetical protein contains similarity to phytoene dehydrogenase (PDH1) GI:433144 from [Cercospora nicotianae]	246411_at	-1.5
putative protein ; supported by full-length cDNA: Ceres: 123997.	246275_at	-1.5
lipophosphoglycan biosynthetic protein - like lipophosphoglycan biosynthetic protein (LPG2), Leishmania donovani, TREMBL:LD26175	246143_at	-1.5
hydroxymethylbilane synthase ;supported by full-length CDNA: Ceres:3051.	246033_at	-1.5
putative protein 22kDa peroxisomal membrane protein-like - Homo sapiens, EMBL:AF250136;supported by full-length cDNA: Ceres:6789.	245937_at	-1.5
homeobox-leucine zipper protein HAT1 (hd-zip protein 1) supported by full-length cDNA: Ceres:34167.	245362_at	-1.5
Expressed protein ; supported by full-length cDNA: Ceres: 14223.	245370_at	-1.5
ribosomal protein ;supported by full-length cDNA: Ceres:15384. hypothetical protein ;supported by full-length cDNA: Ceres:17977.	245372_at 245310 at	-1.5 -1.5
NADH dehydrogenase ND1	245310_at 244936 at	-1.5
DNA polymerase alpha subunit IV (primase)-like protein	244930_at 249276 at	-1.5
putative DNA-binding protein similar to AP2 and RAV1	249276_at 255582 at	-1.5
putative protein various predicted proteins, Arabidopsis thaliana	250962_at	-1.5
unknown protein	267400 at	-1.4
unknown protein ; supported by cDNA: gi 13877742 gb AF370134.1 AF370134	267339 at	-1.4
unknown protein	266956 at	-1.4
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:9671.	266334 at	-1.4
calmodulin identical to GB:1812; supported by CDNA: gi 16650 gb M38380.1 ATHCAM2	266317 at	-1.4
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putative cytochrome b5 ;supported by full-length cDNA: Ceres:3743.	266326_at	-1.4
predicted protein ;supported by cDNA: Ceres:168	266059_at	-1.4
putative cytidine deaminase ;supported by full-length cDNA: Ceres:152285.	265943_at	-1.4
putative purine-rich single-stranded DNA-binding protein; supported by cDNA: gi_15450692_gb_AY052714.1_	265677_at	-1.4
putative thioredoxin M ; supported by cDNA: gi_6539611_gb_AF095751.1_AF095751	265476_at	-1.4
3-ketoacyl-acyl carrier protein synthase III (KAS III) identical to 3-ketoacyl-acyl carrier protein synthase III (KAS III) GB:CAA72385 GI:1888359 (Aral		-1.4 -1.4
unknown protein ;supported by full-length cDNA: Ceres:25812. Expressed protein ; supported by full-length cDNA: Ceres: 108558.	265057_at 264579_at	-1.4 -1.4
similar to early nodulins	264379_at 264377 at	-1.4 -1.4
antigen receptor, putative similar to antigen receptor GI:3982955 from [Ginglymostoma cirratum];supported by full-length cDNA: Ceres:4326.	264161 at	-1.4
hypothetical protein predicted by genscan+; supported by full-length cDNA: Ceres:36412.	264091 at	-1.4
putative cytochrome P450	264052 at	-1.4
hypothetical protein predicted by grail;supported by full-length cDNA: Ceres:2928.	263980 at	-1.4
putative auxin-induced protein, IAA17/AXR3-1 Identical to Arabidopsis gb/AF040632 and gb/U49073 IAA17/AXR3 gene. ESTs gb/H36782 and gb/F		-1.4
arginine decarboxylase identical to GP:1590814:U52851; supported by cDNA: gi 1590813 gb U52851.1 ATU52851	263241_at	-1.4
putative fructokinase; supported by full-length cDNA: Ceres: 17664.	263250 at	-1.4
myrosinase-associated protein, putative similar to myrosinase-associated protein GI:1769969 from [Brassica napus]:supported by full-length cDNA	_	-1.4
nodulin-like protein similar to MtN21 GB:CAA75575 GI:2598575 from [Medicago truncatula] (Mol. Plant Microbe Interact. 9 (4), 233-242 (1996)); su	262951 at	-1.4
hypothetical protein similar to hypothetical protein GB:AAF24593 GI:6692128 from [Arabidopsis thaliana]	262552_at	-1.4
putative amino acid transporter Very similar to amino acid transporter AAT1 [Arabidopsis thaliana] (gi 1076291)	262522_at	-1.4
unknown protein ;supported by full-length cDNA: Ceres:95546.	262396_at	-1.4
unknown protein	261944_at	-1.4
3-deoxy-D-arabino-heptulosonate 7-phosphate, putative similar to 3-deoxy-D-arabino-heptulosonate 7-phosphate GI:170224 from [Nicotiana tabac	261933_at	-1.4
choline kinase, putative similar to CHOLINE/ETHANOLAMINE KINASE GB:Q9Y259 from [Homo sapiens]	261506_at	-1.4
transcription factor, putative contains AP2 domain	261327_at	-1.4
thioredoxin identical to GB:CAA84610 from [Arabidopsis thaliana] (Proc. Natl. Acad. Sci. U.S.A. 92 (12), 5620-5624 (1995)); supported by full-length	261145_at	-1.4
lipase-like protein similar to lipase GB:AAD01804 GI:4103627 from [Dianthus caryophyllus];supported by full-length cDNA: Ceres:12912.	260791_at	-1.4
UDP-glucose glucosyltransferase, putative similar to UDP-glucose glucosyltransferase GI:3928543 from [Arabidopsis thaliana]	260799_at	-1.4
myb-related protein, putative similar to GB:CAB91874 from [Lycopersicon esculentum]	260664_at	-1.4
unknown protein	260635_at	-1.4
putative lipoxygenase similar to lipoxygenase GB:CAB56692 [Arabidopsis thaliana]; supported by cDNA: gi_15810254_gb_AY056166.1_	260399_at	-1.4
homeobox gene 13 protein identical to homeobox gene 13 protein gb/AAF20996.1[AF208044_1 [Arabidopsis thaliana];supported by full-length cDN.	_	-1.4
phosphoethanolamine N-methyltransferase, putative similar to GI:7407189 from [Spinacia oleracea]	259842_at	-1.4
putative ribose 5-phosphate isomerase similar to ribose 5-phosphate isomerase GB:6677767 from [Mus musculus]; supported by full-length cDNA: (		-1.4
putative AUX1-like permease similar to AUX1 (regulator of root gravitropism, putative permease) GB:CAA67308 [Arabidopsis thaliana]; supported t	259660_at 259661_at	-1.4 -1.4
Expressed protein ; supported by full-length cDNA: Ceres: 14943. unknown protein	259160 at	-1.4 -1.4
stress related protein, putative similar to stress related protein GB:AAD51854 from [Vitis riparia];supported by full-length cDNA: Ceres:13300.	259100_at 259105 at	-1.4 -1.4
putative glucan endo-1-3-beta-glucosidase similar to glucan endo-1-3-beta-glucosidase precursor GB:P52409 [Triticum aestivum];supported by full-	· · · · <u>-</u> · · ·	-1.4
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:6768.	258676 at	-1.4
putative 40 procent protected by generative and protect by training of the second seco	258486 at	-1.4
early auxin-induced protein, IAA19 identical to IAA19 GB:AA884356 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 94231.	258399 at	-1.4
putative ribosomal protein similar to ribosomal protein L41 GB:AAA34366 from [Candida maltosa]; supported by full-length cDNA: Ceres: 13557.	258296 at	-1.4
unknown protein ;supported by full-length cDNA: Ceres:8259.	258275 at	-1.4
protein phosphatase 2A regulatory subunit isoform B delta identical to GB:AAD02810 from [Arabidopsis thaliana]; supported by cDNA: gi 4106339	_	-1.4
hypothetical protein predicted by genscan+; supported by cDNA: gi 13937132 gb AF372920.1 AF372920	257794 at	-1.4
integral membrane protein, putative contains Pfam profile: PF01554 uncharacterized membrane protein family; supported by cDNA: gi 16323120	_	-1.4
MYB family transcription factor (hsr1), putative identical to myb-like protein GB:AJ007289 [Arabidopsis thaliana] (Plant J. 20 (1), 57-66 (1999));supp	257140 at	-1.4
MAP kinase kinase 4 (ATMKK4) identical to MAP kinase kinase 4 [Arabidopsis thaliana]; supported by cDNA: gi_13265419_gb_AF324667.2_AF32	256183_at	-1.4
pathogenesis-related group 5 protein, putative similar to pathogenesis-related group 5 protein GI:2749943 from [Brassica rapa]; supported by cDN/	256125_at	-1.4
unknown protein	256046_at	-1.4
ribosomal protein, putative similar to ribosomal protein L35a GI:57118 from [Rattus norvegicus]; supported by full-length cDNA: Ceres: 2778.	256065_at	-1.4
unknown protein ;supported by full-length cDNA: Ceres:108615.	255908_s_at	-1.4
putative chitinase similar to peanut type II chitinase, GenBank accession number X82329, E.C. 3.2.1.14	255595_at	-1.4
H+-transporting ATP synthase-like protein H+-transporting ATP synthase (EC 3.6.1.34) delta chain precursor, chloroplast - Nicotiana tabacum, PIR/		-1.4
extensin - like protein hybrid proline-rich protein, Zea mays, PIR2:JQ1663	254314_at	-1.4
cytokinin oxidase - like protein cytokinin oxidase, Zea mays, gb:Y18377; supported by cDNA: gi_15450760_gb_AY054460.1_	253696_at	-1.4

putative protein ; supported by full-length cDNA: Ceres: 2891.	253670_at	-1.4
cytochrome P450 monooxygenase ;supported by full-length cDNA: Ceres:13745.	253534_at	-1.4
putative protein mRNAs from Ricinus communis and Medicago sativa, Z81012 and L36159;supported by full-length cDNA: Ceres:37529.	253437_at	-1.4
putative protein GATA transcription factor 3, Arabidopsis thaliana, gb:Y13650	253406_at	-1.4
putative protein SPOP, Homo sapiens, AJ000644;supported by full-length cDNA: Ceres:122670.	253061_at	-1.4
hypothetical protein hypothetical protein - Arabidopsis thaliana chromosome 4 AP2 contig, PID:e353223; supported by full-length cDNA: Ceres:100-	252133_at	-1.4
putative calmodulin calmodulin - Tetrahymena pyriformis (SGC5),PIR1:MCTE; supported by cDNA: gi_14190470_gb_AF380635.1_AF380635	252037_at	-1.4
40S ribosomal protein S21 homolog ribosomal protein S21, cytosolic - Oryza sativa, PIR:S38357;supported by full-length cDNA: Ceres:26837.	251921_at	-1.4
tryptophan synthase alpha chain ; supported by full-length cDNA: Ceres: 40110.	251847_at	-1.4
F-box protein family, AtFBL17 contains similarity to F-box protein FBL2 GI:6010699 from [Rattus norvegicus]	251850_at	-1.4
putative protein hypothetical protein F22K20.16 - Arabidopsis thaliana, EMBL:AC002291	251701_at	-1.4
putative protein unknown protein 110K5.12 - Sorghum bicolor, TREMBL:AF124045_5;supported by full-length cDNA: Ceres:142358.	251704_at	-1.4
putative protein NODULIN-26 - Glycine max, EMBL:X04782; supported by full-length cDNA: Ceres: 32275.	251661 at	-1.4
glutaredoxin -like protein glutaredoxin, castor bean, PIR:S54825	251195_at	-1.4
putative protein ; supported by cDNA: gi 13358223 gb AF325034.2 AF325034	251036 at	-1.4
60S ribosomal protein - like 60S ribosomal protein L36, Arabidopsis thaliana, EMBL:AC004684;supported by full-length cDNA: Ceres:30903.	251018 at	-1.4
putative protein hypothetical proteins - Arabidopsis thaliana; supported by full-length cDNA: Ceres: 12022.	250618 at	-1.4
peptide methionine sulfoxide reductase-like protein peptide methionine sulfoxide reductase (msr) - Arabidopsis thalina, EMBL:AJ133753	250633 at	-1.4
putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:263168.	250398 at	-1.4
putative protein many predicted proteins, Arabidopsis thaliana; supported by cDNA; gi 15983504 gb AF424627.1 AF424627	250110 at	-1.4
plasma membrane associated protein -like plasma membrane associated protein, Hordeum vulgare, EMBL:AF218627;supported by full-length cDN	_	-1.4
disease resistance protein-like	249029 at	-1.4
putative protein similar to unknown protein (gb/AAF24540.1);supported by full-length cDNA: Ceres:141753.	248923 at	-1.4
putative protein similar to unknown protein (pir  T05073)	248865 at	-1.4
FRQ2-like protein; NADPH oxidase-like	248566 s at	-1.4
unknown protein ; supported by full-length cDNA: Ceres: 266744.	248377 at	-1.4
putative protein contains similarity to MYB family transcription factor	248246 at	-1.4
calcineurin B-like protein 2 (ablAAC26009.1) :supported by full-length cDNA: Ceres:37280.	248001 at	-1.4
putative protein non-consensus CG donor splice site at exon 1, GA donor splice site at exon 3, similar to unknown protein (pirt T04268);supported b	_	-1.4
	246523_at	-1.4
blue copper binding protein ;supported by full-length cDNA: Ceres:7767.	246099 at	-1.4
b2/P transferior family protein similar to seed storage protein opaque-2(bZIP family)GI:168428 from Zea mays; supported by cDNA; gi 15/		-1.4
hypothetical protein similar to hypothetical protein GI:6524175 from (Arabidopsis thaliana); supported by full-length cDNA: Ceres:3618.	245816 at	-1.4
hypothetical protein similar to putative protein of operation of the protection of 1/331195 from Glycine max	245637 at	-1.4
unknown protein predicted by genscan; supported by CDNA: gi 3822215 gb AF074948.	245138 at	-1.4
hypothetical protein	244965 at	-1.4
putative oxidoreductase similar to adventitious rooting related oxygenase GB:CAA12386 from [Malus domestica]	260149 at	-1.4
unknown protein	267383 at	-1.4
putative SET-domain transcriptional regulator	267290 at	-1.3
putative of r-domain transport protein SEC13 ;supported by full-length cDNA: Ceres:36577.	267277 at	-1.3
putative protein transport protein SEC to , supported by tennengin Contx. Ceres.door //	267135 at	-1.3
similar to SOR1 from the fungus Cercospora nicotianae	267138 s at	-1.3
copia-like retroelement pol polyprotein ; supported by full-length cDNA: Ceres: 14718.	266696 at	-1.3
putative proline-rich protein ; supported by cDNA: gi 13265425 gb AF324669.2 AF324669	266588 at	-1.3
putative prome-non protein , supported by CDNA. gr_13203425_gb_AP324009.2_AP324009	266570 at	-1.3
	_	-1.3
unknown protein ; supported by cDNA: gi_14334561_gb_AY035185.1_	266329_at	
putative C-4 sterol methyl oxidase ;supported by full-length cDNA: Ceres:23439.	266289_at 265704 at	-1.3 -1.3
hypothetical protein predicted by genscan	_	
unknown protein ; supported by full-length cDNA: Ceres: 25575.	265459_at	-1.3
putative secretory carrier-associated membrane protein	265419_at	-1.3
unknown protein	264774_at	-1.3
putative superoxide-generating NADPH oxidase flavocytochrome highly similar to GB:CAA70769, FRO1 and GB:CAA70770, FRO2 from [Arabidop		-1.3
hypothetical protein similar to carnitine racemase like protein GI:7268149 from [Arabidopsis thaliana]	264627_at	-1.3
hypothetical protein contains similarity to phosphate/phosphoenolpyruvate translocator precursor GI:1778141 from [Arabidopsis thaliana]	264419_s_at	-1.3
unknown protein predicted by genscan and grail, supported by full-length cDNA: Ceres:14105.	264380_at	-1.3
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:114613.	263930_at	-1.3
unknown protein ;supported by full-length cDNA: Ceres:33232.	263880_at	-1.3

putative WRKY-type DNA binding protein ; supported by cDNA: gi_15430276_gb_AY046275.1_	263783_at	-1.3
unknown protein ;supported by cDNA: gi_15724183_gb_AF411794.1_AF411794	263799_at	-1.3
unknown protein ;supported by full-length cDNA: Ceres:14471.	263737_at	-1.3
unknown protein ; supported by full-length cDNA: Ceres: 97914.	263541_at	-1.3
unknown protein ;supported by cDNA: gi_13605844_gb_AF367321.1_AF367321	263499_at	-1.3
putative anthranilate N-hydroxycinnamoyl/benzoyltransferase ;supported by full-length cDNA: Ceres:105546.	263382_at	-1.3
delta 9 desaturase ALMOST identical (4 aa diff t) to GP:2970036;supported by full-length cDNA: Ceres:21841.	263249_at	-1.3
unknown protein ;supported by cDNA: gi_15146251_gb_AY049267.1_	263046_at	-1.3
hypothetical protein Pfam	262533_at	-1.3
putative G protein coupled receptor identical to putative G protein coupled receptor GI:2104224 from [Arabidopsis thaliana]; supported by cDNA: gi_	262234_at	-1.3
hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 38293.	261940_at	-1.3
pectin methylesterase, putative similar to pectin methylesterase GI:1617583 from [Lycopersicon esculentum]; supported by cDNA: gi_14334991_gl	261826_at	-1.3
S-adenosyl-methionine-sterol-C-methyltransferase, putative almost identical to S-adenosyl-methionine-sterol-C-methyltransferase GI:2246456 from	261727_at	-1.3
clathrin coat assembly protein AP17, putative similar to clathrin coat assembly protein AP17 GB:CAA65533 GI:2959358 from [Zea mays]	261733_at	-1.3
hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 13874.	261057_at	-1.3
beta-galactosidase, putative similar to beta-galactosidase GI:3299896 from [Lycopersicon esculentum]; supported by cDNA: gi_16604399_gb_AYC	260944_at	-1.3
unknown protein contains similarity to UDPG glucosyltransferase GB:AAB62270 GI:2232354 from [Solanum berthaultii];supported by full-length cDI	260955_at	-1.3
DNA binding protein, putative similar to DNA binding protein WRKY3 GB:U56834 GI:1432055 from [Petroselinum crispum]	260882_at	-1.3
TINY-like protein similar to TINY GB:CAA64359 GI:1246403 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:19721.	260856_at	-1.3
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:29740.	260867_at	-1.3
mitochondrial NAD-dependent malate dehydrogenase identical to mitochondrial NAD-dependent malate dehydrogenase GI:3929649 from [Arabidor	260615_at	-1.3
putative molybdopterin synthase large subunit; supported by cDNA: gi 13605721 gb AF361842.1 AF361842	260572 at	-1.3
unknown protein ; supported by cDNA: gi_15912212_gb_AY056384.1_	260371_at	-1.3
unknown protein similar to Ca+2-binding EF hand protein GB:AAB71227 [Glycine max]; supported by full-length cDNA: Ceres:5143.	260208 s at	-1.3
hypothetical protein predicted by genscan+	260109 at	-1.3
hypothetical protein	260051 at	-1.3
hypothetical protein predicted by genefinder	259996_at	-1.3
thaumatin-like protein (PR-5) similar to thaumatin GB:AAD55090 [Vitis riparia]; contains Pfam profile: PF00314 Thaumatin family; supported by cDN		-1.3
putative thymidine kinase similar to thymidine kinase GB:AAC31168 [Oryza sativa]; supported by full-length cDNA: Ceres: 19188.	259224 at	-1.3
putative ribosomal protein S2 similar to putative ribosomal protein S2 GB:CAA74226 [Mitochondrion Triticum aestivum]; supported by full-length cDN	259196 at	-1.3
unknown protein similar to putative protein GB:CAA22987 [Arabidopsis thaliana]	259181 at	-1.3
unknown protein ;supported by full-length cDNA: Ceres:9221.	259106 at	-1.3
germin-like protein similar to germin type 2 GB:S71254 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:19265.	258938 at	-1.3
threonine dehydratase/deaminase (OMR1) identical to threonine dehydratase/deaminase (OMR1) GB:AAC97936, GB:AF096281 [Arabidopsis thali		-1.3
unknown protein similar to hypothetical proteins GB:CAB16818, GB:AAD55277	258911 at	-1.3
Expressed protein ; supported by full-length cDNA: Ceres: 32612.	258713 at	-1.3
putative adenosine kinase similar to adenosine kinase GB:CAB40376 [Zea mays]; supported by cDNA: gi 12017761 gb AF180894.1 AF180894	258658 at	-1.3
putative S-adenosylmethionine:2-demethylmenaquinone methyltransferase similar to S-adenosylmethionine:2-demethylmenaquinone methyltransfe	258614 at	-1.3
hypothetical protein predicted by genemark.hmm, contains Pfam profile:PF00320 GATA zinc finger:supported by full-length cDNA: Ceres:110655.	258529 at	-1.3
unknown protein	258462 at	-1.3
AIG2-like protein similar to AIG2 protein GB:P54121 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:5137.	258000 at	-1.3
hypothetical protein predicted genemark;supported by full-length cDNA: Ceres:255040.	258021 at	-1.3
unknown protein ;supported by full-length cDNA: Ceres:92314.	257925 at	-1.3
unknown protein	257867 at	-1.3
hypothetical protein predicted by genemark.hmm	257748 at	-1.3
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:104278.	257751 at	-1.3
non-race specific disease resistance protein, putative contains non-consensus CT donor splice site at exon 1; potential pseudogene; similar to non-	_	-1.3
hypothetical protein ;supported by full-length cDNA: Ceres:9965.	257093 at	-1.3
unknown protein	257076 at	-1.3
ADP-ribosylation factor, putative similar to ADP-ribosylation factor GB:P91924 [Dugesia japonica]; supported by full-length cDNA: Ceres: 24097.	256838 at	-1.3
hypothetical protein predicted by genscan	256427 at	-1.3
hypothetical protein contains similarity to photosystem II 22 kDa protein GI:6006279 from [Arabidopsis thaliana];supported by full-length cDNA: Cere		-1.3
coded for by A. thaliana cDNA R30513	255716 at	-1.3
putative inorganic phosphatase ; supported by cDNA: gi 15450871 gb AY054516.1	255587 at	-1.3
contains similarity to a protein kinase domain (Pfam: pkinase.htm, score: 165.48), to lequme lectins beta domain (Pfam: lectin legB.hmm, score: 1	255503 at	-1.3
putative vacuolar ATPase similar to vacuolar ATPase. GenBank accession number P50408;supported by full-length cDNA: Ceres: 10207.	255498 at	-1.3
	254835_s_at	-1.3
	· ···	

Expressed protein ; supported by full-length cDNA: Ceres: 266299.	254505_at	-1.3
putative protein storage protein - Populus deltoides, PIR2:S31580	254150_at	-1.3
hypothetical protein	254137_at	-1.3
putative Proline synthetase associated protein Proline synthetase associated - Homo sapiens, PID:d1037830; supported by full-length cDNA: Ceres		-1.3
putative protein ;supported by full-length cDNA: Ceres:113484.	253891_at	-1.3
glycine-rich protein like glycine-rich protein 5 - Arabidopsis thaliana,PIR2:JQ1064; supported by full-length cDNA: Ceres: 33435.	253754_at	-1.3
putative auxin-induced protein high similarity to auxin-induced protein 15A, soybean, PIR2:JQ1096; supported by cDNA: gi_13194817_gb_AF3495	253103_at	-1.3
CCR4-associated factor 1-like protein CAF1_MOUSE CCR4-ASSOCIATED FACTOR 1 - Mus musculus, SWISSPROT:CAF1_MOUSE; supported	252679_at	-1.3
protein kinase - like receptor-like protein kinase RLK3, Arabidopsis thaliana, EMBL:ATH011674	252549_at	-1.3
putative protein several oxidases, mainly gibberellin 20-oxidases	252529_at	-1.3
putative protein several hypothetical proteins - Arabidopsis thaliana	252474_at	-1.3
hypothetical protein various predicted proteins, Arabidopsis thaliana	252205_at	-1.3
expressed protein supported by cDNA: gi:15450891	252048_at	-1.3
putative protein photosystem II oxygen evolving complex protein 2 precursor (psbP), Fritillariaagrestis, EMBL:AF037458;supported by full-length cE	251784_at	-1.3
cysteine synthase AtcysC1 ;supported by full-length cDNA: Ceres:32851.	251322_at	-1.3
ATMRK1 ;supported by full-length cDNA: Ceres:253505.	251170_at	-1.3
serine/threonine protein kinase ATPK10 ;supported by cDNA: gi_13249133_gb_AF302111.1_AF302111	251059_at	-1.3
high affinity nitrate transporter - like protein high affinity nitrate transporter, Oryza sativa, EMBL:AB008519; supported by cDNA: gi_14334783_gb_/	250151_at	-1.3
GASA4 ; supported by cDNA: gi_950098_gb_U15683.1_ATU15683	250109_at	-1.3
putative protein similar to unknown protein (pir  T41692);supported by full-length cDNA: Ceres:31527.	250097_at	-1.3
unknown protein ;supported by full-length cDNA: Ceres:141953.	249750_at	-1.3
hypothetical protein ;supported by full-length cDNA: Ceres:40348.	249625_at	-1.3
acyltransferase -like protein Anthocyanin 5-aromatic acyltransferase, Gentiana triflora, EMBL:AB010708; supported by full-length cDNA: Ceres:378/	249493_at	-1.3
unknown protein ;supported by full-length cDNA: Ceres:42577.	249288_at	-1.3
putative protein similar to unknown protein (pir  T09377)	249211 at	-1.3
putative protein similar to unknown protein (pir  T00965);supported by full-length cDNA: Ceres:777.	249076 at	-1.3
NBD-like protein (gb AAD20643.1) ;supported by full-length cDNA: Ceres:33802.	249063 at	-1.3
putative protein similar to unknown protein (pir  T04426),supported by full-length cDNA: Ceres:27099.	248951 at	-1.3
putative protein similar to unknown protein (gb/AAC61815.1);supported by full-length cDNA: Ceres:254442.	248868 at	-1.3
integral membrane protein-like	248392 at	-1.3
unknown protein ;supported by full-length cDNA: Ceres:148254.	248282 at	-1.3
GS1-like protein supported by full-length cDNA: Ceres:110980.	247908 at	-1.3
D-xylose-H+ symporter - like protein D-xylose-H+ symporter, Lactobacillus brevis, EMBL:AF045552	247709 at	-1.3
putative Rab5-interacting protein - like putative Rab5-interacting protein, Homo sapiens, EMBL:AF112213	247725 at	-1.3
cytoplasmic ribosomal protein S15a - like cytoplasmic ribosomal protein S15a, Arabidopsis thaliana, EMBL:ATAF1412; supported by full-length cDN	247654 at	-1.3
putative protein	247628 at	-1.3
putative protein strong similarity to unknown protein (gb/AAD55298.1); supported by cDNA: gi 14423505 gb AF386990.1 AF386990	247444 at	-1.3
putative protein predicted proteins, Arabidopsis thaliana	247448 at	-1.3
permease 1 - like protein permease 1, common ice plant, PIR:T12309; supported by cDNA: gi 14334659 gb AY035003.1	247404 at	-1.3
receptor protein kinase-like protein	247153 at	-1.3
putative protein predicted protein, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 108472.	246744 at	-1.3
glucose 6 phosphate/phosphate translocator-like protein glucose 6 phosphate/phosphate translocator - Arabidopsis thaliana, EMBL:AF233658; sur	246445 at	-1.3
hypothetical protein predicted by genemark.hmm	246408 at	-1.3
hypothetical protein	245414 at	-1.3
SUPERMAN like protein	245383 at	-1.3
Expressed protein ; supported by full-length cDNA: Ceres: 5455.	245334 at	-1.3
unknown protein ;supported by full-length cDNA: Ceres:101081.	267459 at	-1.3
unknown protein ; supported by cDNA; gi_16930468_gb_AF419588.1_AF419588	267381 at	-1.2
putative LIM-domain protein	267355 at	-1.2
putative receptor-like protein kinase same as GB:X95909 (polymorphism exists at a GA repeat. We found 6 copies in our sequence whereas only 5		-1.2
30S ribosomal protein S31 supported by full-length cDNA: Ceres:4723.	267088 at	-1.2
putative myrosinase-binding protein ;supported by full-length cDNA: Ceres:39069.	266989 at	-1.2
Expressed protein ; supported by full-length CDNA: Ceres: 19349.	266906 at	-1.2
profilin 1 ; supported by cDNA: gi_1353769 gb_U43325.1_ATU43325	266701 at	-1.2
unknown protein	266566 at	-1.2
60S acidic ribosomal protein P2 ;supported by full-length cDNA: Ceres:19986.	266258 at	-1.2
unknown protein ; supported by cDNA: gi 16604321 gb AY058059.1	266101 at	-1.2

unknown protein	266071_at	-1.2
enoyl-ACP reductase (enr-A)	266035_at	-1.2
predicted by genscan and genefinder ;supported by full-length cDNA: Ceres:120459.	265732_at	-1.2
putative RNA-binding glycine rich protein (RGP-2); supported by full-length cDNA: Ceres:18569.	265641_at	-1.2
Expressed protein ; supported by full-length cDNA: Ceres: 11006.	265456_at	-1.2
unknown protein	265265_at	-1.2
50S ribosomal protein L3 ;supported by full-length cDNA: Ceres:142861.	265247_at	-1.2
unknown protein contains similarity to seed protein B32E GI:19046 from [Hordeum vulgare]	264951_at	-1.2
	264904_s_at	-1.2
unknown protein similar to putative glycosyl transferase GI:7268597 from [Arabidopsis thaliana]; supported by cDNA: gi_13878002_gb_AF370264.1		-1.2
unknown protein ;supported by full-length cDNA: Ceres:2935.	264609_at	-1.2
unknown protein ;supported by full-length cDNA: Ceres:1011.	264590_at	-1.2
carbonic anhydrase, putative similar to carbonic anhydrase GI:882241 from [Flaveria linearis]; supported by full-length cDNA: Ceres: 38715.	264313_at	-1.2
	264279_s_at	-1.2
	264189_s_at	-1.2
putative 40S ribosomal protein S18 Match to ribosomal S18 gene mRNA gb Z28701, DNA gb Z23165 from A. thaliana. ESTs gb T21121, gb Z1775		-1.2
ethylene reponse factor-like AP2 domain transcription factor	264083_at	-1.2
putative cyclin-dependent kinase regulatory subunit	264061_at	-1.2
metalloproteinase, putative similar to metalloproteinase GI:3128477 from [Arabidopsis thaliana]	263731_at	-1.2
unknown protein Similar to Nicotiana lesion-inducing ORF (gb]U66269)	263651_at	-1.2
putative xyloglucan-specific glucanase identical to GB:D63509;supported by full-length cDNA: Ceres:18876.	263598_at	-1.2
putative fatty acid elongase ;supported by full-length cDNA: Ceres:115769.	263443_at	-1.2
Expressed protein ; supported by full-length cDNA: Ceres: 19631.	263318_at	-1.2
ubiquitin extension protein (UBQ2) identical to GI:166930, GI:166931; supported by cDNA: gi_13430797_gb_AF360311.1_AF360311	263289_at	-1.2
putative auxin-induced protein similar to gb D14414 Indole-3-acetic acid induced protein from Vigna radiata. ESTs gb AA712892 and gb Z17613 cor	_	-1.2
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:109912.	262711_at	-1.2
unknown protein	262432_at	-1.2
DNA-binding factor, putative similar to GT-2 factor GB: CAA51289 GI:416490 from [Arabidopsis thaliana]	261594_at	-1.2
pyruvate dehydrogenase E1 alpha subunit identical to pyruvate dehydrogenase E1 alpha subunit GB:AAB86803 GI:2454182 from [Arabidopsis thal		-1.2
unknown protein ;supported by full-length cDNA: Ceres:108746.	261455_at	-1.2
beta tubulin 1, putative similar to GB:AAD02498 from [Arabidopsis thaliana] (Plant Mol. Biol. 39 (1), 171-176 (1999)); supported by cDNA: gi_13605 putative calcium-binding protein, calreticulin similar to SP:P12858 from [Arabidopsis thaliana]		-1.2 -1.2
unknown protein ;supported by full-length cDNA: Ceres:41505.	261197_at 261105 at	-1.2
signal recognition particle 19 kDa protein subunit, putative similar to GB:U19030 from [Oryza sativa] (Plant Mol. Biol. 34 (3), 507-515 (1997)); suppr	260726 at	-1.2
unknown protein ; supported by cDNA: gi 13358204 gb AF325013.2 AF325013	260686 at	-1.2
Expressed protein; supported by full-length cDNA: Ceres: 91704.	260549 at	-1.2
unknown protein	260281 at	-1.2
plasma membrane associated protein, putative similar to GI:6851373 from [Hordeum vulgare]	259774 at	-1.2
endo-beta 1,4-glucanase, putative similar to GI:4972236 from [Fragaria x ananassa] (Plant Mol. Biol. 40, 323-332 (1999)); supported by cDNA: gi_	259736 at	-1.2
MAP kinase, putative similar to MAP kinase 5 GI/4239889 from [Zea mays]	259428 at	-1.2
unknown protein	259434 at	-1.2
hypothetical protein similar to putative glycosyl transferase GI:6862930 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:117402.	259358 at	-1.2
putative auxin-induced protein similar to SAUR GB:BAA25434 [Raphanus sativus]	259332 at	-1.2
unknown protein similar to hypothetical protein GB:S33464 [Arabidopsis thaliana]; supported by cDNA: gi_14517447_gb_AY039559.1_	259228 at	-1.2
unknown protein similar to hypothetical protein GB:AAD27575 [Sorghum bicolor];supported by full-length cDNA: Ceres:23057.	259131 at	-1.2
unknown protein Pfam HMM hit: FKBP-type peptidyl-prolyl cis-trans isomerases	258929 at	-1.2
putative wound-induced basic protein similar to wound-induced basic protein GB:Q09020 [Phaseolus vulgaris] (Plant Physiol. 101 (4), 1409 (1993))	258821 at	-1.2
hypothetical protein supported by full-length cDNA: Ceres:4427.	258793 at	-1.2
putative serine carboxypeptidase II similar to serine carboxypeptidase II (CP-MII) GB:CAA70815 [Hordeum vulgare]	258633 at	-1.2
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:19531.	258657 at	-1.2
putative jasmonic acid regulatory protein similar to jasmonic acid 2 GB:AAF04915 from [Lycopersicon esculentum]; supported by cDNA: gi_120604;	258385_at	-1.2
MAP kinase kinase 5 identical to GB:BAA28831 from [Arabidopsis thaliana]; supported by cDNA: gi_3219272_dbj_AB015316.1_AB015316	258046_at	-1.2
cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450; supported by cDNA: gi_13430717_gb_AF360271.1_AF360271	257636_at	-1.2
unknown protein ;supported by full-length cDNA: Ceres:3457.	257644_at	-1.2
unknown protein contains Pfam profile: PF01165 ribosomal protein S21; supported by cDNA: gi_14532553_gb_AY039901.1_	256753_at	-1.2
histone H2A, putative similar to histone H2A GB:AAF64418 GI:7595337 from [Arabidopsis thaliana] (Proc. Natl. Acad. Sci. U.S.A. 97 (2), 948-953 (	256666_at	-1.2
unknown protein ;supported by cDNA: gi_14532501_gb_AY039875.1_	256627_at	-1.2

	256438_s_at	-1.2
unknown protein contains similarity to alternative NADH-dehydrogenase GI:3718005 from [Yarrowia lipolytica]; supported by full-length cDNA: Ceres		-1.2
putative uroporphyrinogen decarboxylase ; supported by cDNA: gi_14334767_gb_AY035057.1_	255826_at	-1.2
60S ribosomal protein L23 ;supported by full-length cDNA: Ceres:28563.	255789_at	-1.2
PROLIFERA similar to S. cerevisiae MCM2-3-5 genes required for the initiation of DNA replication; supported by cDNA: gi_675490_gb_139954.1_A	_	-1.2
DNA-binding protein ;supported by full-length cDNA: Ceres:28019.	255037_at	-1.2
putative ribosomal protein L9, cytosolic ribosomal protein L9, cytosolic - garden pea, PIR2:S19978;supported by full-length cDNA: Ceres:21228.	254980_at	-1.2
RING-H2 finger protein RHA1a -like protein ;supported by full-length cDNA: Ceres:21591.	254922_at	-1.2
Expressed protein ; supported by full-length cDNA: Ceres: 11649.	254761_at	-1.2
fatty acid elongase - like protein (cer2-like) cer2, Arabidopsis thaliana, X93080	254737_at	-1.2
pollen-specific protein - like 18.3K protein precursor, pollen, Zea mays, PIR2:JQ1107	254620_at	-1.2
ras-like GTP-binding protein strong homology to GTP-binding protein ric2, Oryza sativa, S38741	254641_at	-1.2
putative protein glycine/proline-rich protein GPRP, Arabidopsis thaliana, PIR2:S65780; supported by full-length cDNA: Ceres: 8188.	254559_at	-1.2
putative pectinacetylesterase pectinacetylesterase precursor, Vigna radiata, PIR2:S68805	254573_at	-1.2
hypothetical protein	254484_at	-1.2
cell-cell signaling protein csgA - like cell-cell signaling protein csgA, Synechocystis sp., PIR2:S77176	254485_at	-1.2
	254259_s_at	-1.2
	254163_s_at	-1.2
putative mitochondrial uncoupling protein mitochondrial uncoupling protein, Arabidopsis thaliana (thale cress), PATX:E1316826;supported by full-le	_	-1.2
putative protein qkl-7, Mus musculus	253964_at	-1.2
xyloglucan endo-1,4-beta-D-glucanase precursor ;supported by full-length cDNA: Ceres:19156.	253666_at	-1.2
putative protein	253414_at	-1.2
putative protein predicted protein, Arabidopsis thaliana;supported by full-length cDNA: Ceres:4354.	253165_at	-1.2
DnaJ-like protein DnaJ-like protein, Phaseolus vulgaris, PATX:G1684851	253125_at	-1.2
Inositol monophosphatase - like protein Mono-phosphatase, Streptomyces anulatus, X92429	252934_at	-1.2
hypothetical protein ; supported by cDNA: gi_15529203_gb_AY052226.1_	252853_at	-1.2
putative protein AP2 domain containing protein RAP2.4, Arabidopsis thaliana	252859_at	-1.2
cysteine proteinase contains similarity to cysteine proteinase RD21A (thiol protease) GI:435619, SP:P43297 from [Arabidopsis thaliana];supported	252692_at	-1.2
hypothetical protein ;supported by full-length cDNA: Ceres:35598.	252231_at	-1.2
hypothetical protein ;supported by full-length cDNA: Ceres:93591.	252165_at	-1.2
putative protein	251788_at	-1.2
synaptic glycoprotein SC2-like protein synaptic glycoprotein SC2 spliced variant, Homo sapiens, EMBL:AF038958;supported by full-length cDNA: (		-1.2
cyclophilin-like protein ROC7, cyclophilin, Arabidopsis thaliana, EMBL:AF192490;supported by full-length cDNA: Ceres:94608.	251772_at	-1.2
putative protein	251720_at	-1.2
DNA-binding protein-like DNA-binding protein 4 WRKY4 - Nicotiana tabacum, EMBL:AF193771;supported by full-length cDNA: Ceres:34847.	251705_at	-1.2
putative protein hypothetical protein 238 - Porphyra purpurea, PIR:S73123	251519_at	-1.2
putative protein various predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_15982839_gb_AY057527.1_	250939_at	-1.2
putative protein predicted protein, Arabidopsis thaliana	250563_at	-1.2
mitochondrial phosphate translocator	250206_at	-1.2
expressed protein contains similarity to ABC transporter, ATP-binding protein; supported by full-length cDNA: Ceres:151943.	250198_at	-1.2
CCR4-associated factor-like protein	249928_at	-1.2
flavanone 3-hydroxylase-like protein; supported by full-length cDNA: Ceres: 149654.	249754_at	-1.2
putative protein similar to unknown protein (pir][S76575)	249685_at	-1.2
Nicotiana lesion-inducing like ; supported by full-length cDNA: Ceres: 327.	249159_at	-1.2
ethylene responsive element binding factor 2 (ATERF2) (sp O80338) ;supported by full-length cDNA: Ceres:3012.	248794_at	-1.2
transport protein particle component Bet3p-like protein ;supported by full-length cDNA: Ceres:122866.	248127_at	-1.2
putative protein similar to unknown protein (pir  T06631)	248074_at 248044 at	-1.2 -1.2
putative protein similar to unknown protein (pir  T05049)	_	-1.2 -1.2
unknown protein purchting protein protein (picture protein (picture) (pictur	247959_at 247930_at	-1.2 -1.2
putative protein similar to unknown protein (pir  T04261);supported by full-length cDNA: Ceres:6181.	_	
Expressed protein ; supported by full-length cDNA: Ceres: 267411.	247882_at 247745_at	-1.2 -1.2
copper transport protein	_	-1.2 -1.2
actin depolymerizing factor 4 - like protein actin depolymerizing factor 4, Arabidopsis thaliana, EMBL:AF102822;supported by full-length cDNA: Cer	_	-1.2 -1.2
photosystem I reaction centre subunit psaN precursor (PSI-N) (sp P49107) ; supported by cDNA: gi_1237123_gb_U32176.1_ATU32176 unknown protein ; supported by full-length cDNA: Ceres: 20274.	247320_at 247211_at	-1.2 -1.2
prolyl 4-hydroxylase, alpha subunit-like protein	247211_at 247124_at	-1.2 -1.2
leucine-rich repeats containing protein grr1 - Glycine max. EMBL:AF019910	247124_at 246935 at	-1.2 -1.2
Counce from regional containing protein gir ( = Gyoine filds, Emble Al 015910	270300_at	-1.2

SigA binding protein ; supported by cDNA: gi_14596086_gb_AY042831.1_	246293_at	-1.2
ribosomal protein, chloroplast ribosomal protein PsCL18 precursor, chloroplast - Pisum sativum, PIR:R5PM18; supported by cDNA: gi_14596188_(	_	-1.2
putative protein non-consensus donor splice site GA at exon 1; predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_16209695_gb_AYI		-1.2
glutaredoxin ;supported by full-length cDNA: Ceres:115597.	246092_at	-1.2
Expressed protein ; supported by cDNA: gi_15809953_gb_AY054245.1_	245264_at	-1.2
F12A21.4 similar to iEP4 gb AAD11468.1	245215_at	-1.2
hypothetical protein predicted by genscan	245029_at	-1.2
photosystem II G protein	245011_at	-1.2
putative expansin ;supported by full-length cDNA: Ceres:17353.	267590_at	-1.1
unknown protein ;supported by full-length cDNA: Ceres:26701.	267366_at	-1.1
hypothetical protein	267293_at	-1.1
unknown protein	267239_at	-1.1
glutathione S-transferase identical to GB:D17673; supported by cDNA: gi_443698_dbj_D17673.1_ATHERD13	267154_at	-1.1
origin recognition complex protein identical to GB:U40269;supported by full-length cDNA: Ceres:42701.	267173_at	-1.1
unknown protein ;supported by full-length cDNA: Ceres:16403.	266979_at	-1.1
putative AP2 domain transcription factor pFAM domain (PF00847)supported by full-length cDNA: Ceres:31044.	266820_at	-1.1
3-isopropylmalate dehydratase, small subunit ; supported by cDNA: gi_16974632_gb_AY060594.1_	266395_at	-1.1
unknown protein ;supported by full-length cDNA: Ceres:40283.	266413_at	-1.1
unknown protein	266366_at	-1.1
putative rac GTPase activating protein	266324_at	-1.1
putative tropinone reductase	266277_at	-1.1
uknown protein	266285 at	-1.1
unknown protein supported by full-length cDNA: Ceres:8247.	265872 at	-1.1
unknown protein	265831 at	-1.1
hypothetical protein predicted by genscan	265840 at	-1.1
60S ribosomal protein L27	265730 at	-1.1
40S ribosomal protein S12 ;supported by full-length cDNA: Ceres:13453.	265671 at	-1.1
putative replication protein A1 ;supported by full-length cDNA: Ceres:7536.	265695 at	-1.1
Expressed protein ; supported by cDNA: gi 13605516 gb AF361584.1 AF361584	265597 at	-1.1
unknown protein	265317 at	-1.1
putative receptor protein kinase similar to brassinosteroid insensitive protein	265250 at	-1.1
putative ADP-ribosylation factor; supported by cDNA; gi 13926231 gb AF372875.1 AF372875	265187 at	-1.1
unknown protein similar to ESTs gb/T76678 and gb/AI165001;supported by full-length cDNA: Ceres:251549.	265130 at	-1.1
hypothetical protein predicted by genefinder	265083 at	-1.1
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:2118.	264636 at	-1.1
hypothetical protein Contains similarity to Rattus AMP-activated protein kinase (gb)X95577); supported by cDNA: gi 9965728 gb AF250335.1 AF2		-1.1
germin-like protein Identical to Arabidopsis germin-like protein, gil1755178. Location of EST 180L10T7, gil906417; supported by cDNA: gi 132654!		-1.1
hypothetical protein predicted by grail	264379 at	-1.1
unknown protein Strong similarity to gb/D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb/H37281, gb/T44 2		-1.1
aromatic rich glycoprotein, putative similar to aromatic rich glycoprotein GI:1762428 from [Arabidopsis thaliana]; supported by cDNA: gi 1762583 (		-1.1
unknown protein ESTs gb T04610, gb N38459, gb T45174, gb R30481 and gb N64971 come from this gene;supported by full-length cDNA: Ceres:		-1.1
unknown protein supported by full-length cDNA: Ceres:37537.	264201 at	-1.1
putative nitrilase-associated protein Alternative splicing exists based on EST evidence	264028 at	-1.1
Expressed protein ; supported by full-length cDNA: Ceres: 19643.	264022 at	-1.1
Expressed protein ; supported by full-length cDNA: Ceres: 97088.	263842 at	-1.1
putative sarcosine oxidase	263788 at	-1.1
unknown protein ; supported by cDNA: gi 15451039 gb AY054600.1	263715 at	-1.1
hypothetical protein predicted by genefinder	263674 at	-1.1
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:113395.	263629 at	-1.1
unknown protein similar to hypothetical protein GB:AAB81674;supported by full-length cDNA: Ceres:6280.	263582 at	-1.1
aniatowi protein supported by full-length cDNA: Ceres:28779.	263410 at	-1.1
ADP-ribosylation factor 1 ;supported by full-length cDNA: Ceres:34414.	263321 at	-1.1
putative sugar transporter protein nearly identical to Arabidopsis sugar transporter, gi 1495273	262797 at	-1.1
putative sugar transporter protein nearly identical to Arabidopsis sugar transporter, gi 149273 putative ubiquinolcytochrome-c reductase Similar to gb/X79273 cytochrome c reductase hinge protein subunit from Solanum tuberosum. ESTs gb		-1.1
unknown protein identical to unknown protein GB:AAD55493 (Arabidopsis thaliana); supported by cDNA: gi 13358235 gb AF325047.2 AF325047		-1.1
hypothetical protein denical to unknown protein GB:AAD53493 (Arabidopsis trailana); supported by cDNA: g_13358235_gb_AF325047.2_AF325047 hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:5052.	262262_at 262285_at	-1.1 -1.1
allergen, putative similar to allergen (Ole e 1) GI:2465129 from [Olea europaea];supported by full-length cDNA: Ceres:22488.	262265_at 262195 at	-1.1 -1.1
	202135_at	-1.1

hypothetical protein predicted by genemark.hmm	262085_at	-1.1
cytochrome c oxidase subunit, putative similar to cytochrome c oxidase subunit Vb GI:1841354 from [Oryza sativa]; supported by full-length cDNA;	262048_at	-1.1
50S ribosomal protein L21 chloroplast precursor (CL21) identical to GB:P51412 GI:1710424 from [Arabidopsis thaliana]; supported by cDNA: gi_16		-1.1
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:119546.	261951_at	-1.1
hypothetical protein predicted by genemark.hmm helix-loop-helix protein homolog, putative similar to helix-loop-helix protein homolog GB:BAA87957 GI:6520231 from [Arabidopsis thaliana]	261742_at 261717_at	-1.1 -1.1
Expressed protein ; supported by full-length cDNA: Ceres: 11759.	261717_at 261638 at	-1.1 -1.1
RAS-related protein , supported by rull-length cDNA. Ceres. 17759.	261036_at	-1.1
unknown protein ; supported by cDNA: gi 15450636 gb AY052686.1	261252_at 261193 at	-1.1
dihydrolipoamide S-acetyltransferase, putative similar to GI:5881963 from (Arabidopsis thaliana) (Plant Physiol. 120 (2), 443-452 (1999));supported		-1.1
untroum protein	261143 at	-1.1
putative cytochrome c oxidase Vc subunit	260579 at	-1.1
unknown protein : supported by full-length cDNA: Ceres:40573.	260429 at	-1.1
putative ADP-ribosylation factor 1 nearly identical to ADP-ribosylation factor 1 GB:P36397 [Arabidopsis thaliana];supported by full-length cDNA: Cer		-1.1
hypothetical protein predicted by genefinder	260205 at	-1.1
	259955 s at	-1.1
unknown protein ;supported by full-length cDNA: Ceres:21305.	259838 at	-1.1
putative isoprenylated protein similar to ATFP7 GB:AAD09511;supported by full-length cDNA: Ceres:39127.	259753 at	-1.1
thylakoid-bound ascorbate peroxidase identical to thylakoid-bound ascorbate peroxidase GB:CAA67426 [Arabidopsis thaliana]; supported by full-len	_	-1.1
unknown protein ; supported by full-length cDNA: Ceres: 13599.	259660 at	-1.1
protein kinase, putative similar to GI:7573596 from [Populus nigra]	259671 at	-1.1
hypothetical protein	259530 at	-1.1
plasma membrane intrinsic protein 1c, putative similar to plasma membrane intrinsic protein 1c GI:472875 from [Arabidopsis thaliana]	259431_at	-1.1
putative cystathionine gamma-synthase similar to cystathionine gamma-synthase GB:AAB41235 from [Arabidopsis thaliana]; supported by cDNA: g	259279_at	-1.1
putative 60S ribosomal protein L22 similar to 60S ribosomal protein L22 GB:AAF02883; supported by full-length cDNA: Ceres: 8244.	259112_at	-1.1
acyl carrier protein 1 precursor (ACP) identical to GB:P11829 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 14291.	259095_at	-1.1
unknown protein similar to hin1 GB:CAA68848 [Nicotiana tabacum]; supported by cDNA: gi_9502173_gb_AF264698.1_AF264698	259071_at	-1.1
unknown protein similar to unknown protein GB:AAD21471 [Arabidopsis thaliana]; supported by cDNA: gi_15810316_gb_AY056197.1_	259072_at	-1.1
adenylate translocator identical to adenylate translocator GB:X65549 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:36818.	258680_at	-1.1
S-adenosylmethionine decarboxylase identical to GB:Q96286 from [Arabidopsis thaliana]; supported by cDNA: gi_14596072_gb_AY042824.1_	258500_at	-1.1
putative s-adenosylmethionine synthetase similar to S-ADENOSYLMETHIONINE SYNTHETASE GB:Q96552 from [Catharanthus roseus];supporter	_	-1.1
unknown protein similar to unknown protein GB:AAF30339 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:22328.	258393_at	-1.1
protein kinase C-receptor/G-protein, putative similar to uanine nucleotide binding protein (G protein), beta polypeptide GB:NP_006089 [Homo sapie		-1.1
hypothetical protein similar to CGI-18 protein GB:AAD27727 [Homo sapiens]	258049_at	-1.1
hypothetical protein	257875_at	-1.1
gamma tonoplast intrinsic protein nearly identical to gamma tonoplast intrinsic protein 2 (TIP2) GB:AF057137 [Arabidopsis thaliana]; supported by (	_	-1.1
unknown protein ; supported by cDNA: gi_15146273_gb_AY049278.1_	257272_at	-1.1
	257228_at	-1.1
serine acetyltransferase (Sat-1) identical to serine acetyltransferase (Sat-1) GB:U22964 [Arabidopsis thaliana] (Plant Mol. Biol. 30 (5), 1041-1049 (		-1.1
disease resistance protein, putative similar to GB:AAD13301 from [Lycopersicon esculentum], contains Pfam profiles: PF00560 Leucine Rich Repe		-1.1
ribosomal protein L27, putative similar to 60S RIBOSOMAL PROTEIN L27 GB:P41101 from [Solanum tuberosum]; supported by full-length cDNA: (	_	-1.1 -1.1
unknown protein	256673_at	-1.1
unknown protein membrane import protein, putative similar to membrane import protein GB:AAF20172 GI:6636407 [Drosophila melanogaster]; supported by cDNA:	256622_at 256628_at	-1.1
peroxidase, putative similar to peroxidase ATP26a GB:CAA72487 GI:1890317 [Arabidopsis thaliana]; supported by cDNA: gi 14334599 gb AY03-		-1.1
Expressed protein ; supported by cDNA: gi 15450408 gb AY052305.1	256304 at	-1.1
phosphoglycerate kinase, putative similar to phosphoglycerate kinase [Nicotiana tabacum] GI:1161600; supported by cDNA; gi 15810504 gb AYC		-1.1
mitogen-activated protein kinase, putatve similar to mitogen-activated protein kinase GLS815410 from [Oryza sativa]; supported by cDNA: gi 1502		-1.1
UDP-qlucose qlucosyltransferase, putative similar to UDP-qlucose qlucosyltransferase GI/453245 from [Manihot esculenta]; supported by full-length		-1.1
hypothetical protein predicted by genscan+	255880 at	-1.1
unknown protein	255852 at	-1.1
unknown protein similar to beta-1,3-glucanase-like protein GI:9758115 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:32195.	255779 at	-1.1
unknown protein similar to unknown protein GI:6714347 from [Arabidopsis thaliana];supported by full-length CDNA: Ceres:103226.	255733 at	-1.1
acidic ribosomal protein p1 similar to acidic ribosomal protein p1 supported by full-length cDNA: Ceres:26442.	255657 at	-1.1
putative DNA-binding protein similar to wild oat DNA-binding protein ABF2. GenBank accession number Z48431	255596 at	-1.1
protoporphyrinogen oxidase ; supported by cDNA: gi 14423413 gb AF386944.1 AF386944	255537 at	-1.1
putative ribonucleoprotein similarity to ovarian RNA-binding protein and translational control factor (bruno)- Drosphila melanogaster, EMBL:DMU58§		-1.1
	—	

putative xyloglucan endotransglycosylase ;supported by full-length cDNA: Ceres:17748.	255433_at	-1.1
putative protein hypothetical protein - Arabidopsis thaliana,PIR:F71409;supported by full-length cDNA: Ceres:22715.	255243_at	-1.1
putative protein	255035_at	-1.1 -1.1
RING-H2 finger protein RHA1b ;supported by full-length cDNA: Ceres:37097. ammonium transport protein (AMT1) ; supported by cDNA: qi 14335079 qb AY037219.1	254919_at 254723 at	-1.1
extensin-like protein extensin-like protein - maize, PIR2:S49915	254725_at 254635_at	-1.1
neoxanthin cleavage enzyme-like protein neoxanthin cleavage enzyme, Lycopersicon esculentum, PATX:E325797; supported by cDNA: gi 159837	_	-1.1
putative protein FKBP-type peptidyl-prolyl cis-trans isomerase, Synechocystis sp., PIR2:S75144	254545 at	-1.1
	254239 at	-1.1
PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT, like PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT, ORYZA SATIV		-1.1
Expressed protein ; supported by cDNA: gi 15028040 gb AY045877.1	253827 at	-1.1
putative protein ; supported by full-length cDNa: Ceres:10077.	253814 at	-1.1
putative protein hypothetical protein T25K17.20 - Arabidopsis thaliana,PIR2:T06005; supported by full-length cDNA: Ceres: 7308.	253730 at	-1.1
cytidine deaminase 6 (CDA6)	253679 at	-1.1
putative protein ;supported by full-length cDNA: Ceres:2508.	253440 at	-1.1
hypothetical protein ;supported by full-length cDNA: Ceres:35221.	253389 at	-1.1
clathrin assembly protein AP19 homolog ;supported by full-length cDNA: Ceres:22906.	253199 at	-1.1
Expressed protein ; supported by full-length cDNA: Ceres: 17990.	253045 at	-1.1
adenosine-5-phosphosulfate-kinase	252870_at	-1.1
putative protein ;supported by full-length cDNA: Ceres:37341.	252876_at	-1.1
hypothetical protein	252612_at	-1.1
mitogen-activated protein kinase 3 ; supported by cDNA: gi_14423447_gb_AF386961.1_AF386961	252592_at	-1.1
Expressed protein ; supported by full-length cDNA: Ceres: 157151.	252412_at	-1.1
putative protein bundle sheath defective protein 2 - Zea mays, EMBL:AF126742; supported by cDNA: gi_13877966_gb_AF370246.1_AF370246	252409_at	-1.1
putative protein GMFP7 isoprenylated protein, Glycine max., gb:AAD09515;supported by full-length cDNA: Ceres:250092.	252296_at	-1.1
E2, ubiquitin-conjugating enzyme, putative UEV1Bs - Homo sapiens,PID:g2689608;supported by full-length cDNA: Ceres:16125.	252059_at	-1.1
dTDP-glucose 4-6-dehydratase -like protein dTDP-glucose 4-6-dehydratase, Cicer arietinum, EMBL:AJ275318 contains non-consensus AT donor 🗧		-1.1
sugar-phosphate isomerase - like protein gutq/kpsf family sugar-p isomerase, Chlamydia pneumoniae, PIR: E72068; supported by full-length cDNA:	_	-1.1
pectate lyase - like protein pectate lyase, Musa acuminata, X92943	251864_at	-1.1
beta-N-acetylhexosaminidase -like protein various beta-N-acetylhexosaminidases; supported by full-length cDNA: Ceres: 118286.	251782_at	-1.1
putative protein hypothetical protein At2g44080 - Arabidopsis thaliana, EMBL:AC004005	251436_at	-1.1
putative protein hypothetical protein At2g46330 - Arabidopsis thaliana, EMBL:AC006526; supported by full-length cDNA: Ceres: 11394.	251281_at	-1.1
putative protein nucleoid DNA-binding protein cnd41, chloroplast - Nicotiana tabacum, EMBL:D26015; supported by cDNA: gi_14532549_gb_AY03	_	-1.1
cytochrome c oxidase subunit 5c-like protein cytochrome c oxidase subunit 5c - Oryza sativa, EMBL:AB027123;supported by full-length cDNA: Cer	_	-1.1
shock protein SRC2-like shock protein SRC2 - Glycine max, PIR:107080	251232_at	-1.1
one helix protein (OHP) ;supported by full-length cDNA: Ceres:16704.	251031_at	-1.1
putative protein predicted proteins, Archaeoglobus fulgidus, Synechocystis sp.;supported by full-length cDNA: Ceres:125255.	250842_at	-1.1 -1.1
putative protein various predicted proteins, Arabidopsis thaliana	250435_at 250376 at	-1.1 -1.1
putative protein putative protein predicted proteins, Arabidopsis thaliana	250376_at 250353 at	-1.1
putative protein hydroxyproline-rich glycoprotein, kidney bean, PIR:A29356	250353_at 250323 at	-1.1
Expressed protein ; supported by cDNA: gi 16649124 gb AY059932.1	250100 at	-1.1
putative protein ;supported by full-length cDNA: Ceres:1198.	250098 at	-1.1
putative protein redicted proteins, Drosophila melanogaster, supported by full-length cDNA: Ceres:41525.	249988 at	-1.1
putative protein glycine-rich protein GRP22, rape, PIR:S31415	249969 at	-1.1
congluting gamma - like protein conglutin gamma precursor, Lupinus angustifolius, PIR:S21426; supported by cDNA: gi 15010797 gb AY045700.1	_	-1.1
	249726 at	-1.1
glutamate-ammonia ligase ; supported by cDNA: gi 16226386 gb AF428386.1 AF428386	249581 at	-1.1
14-3-3 protein GF14psi (grf3/RCI1) identical to 14-3-3 protein GF14 psi GI:1168200, SP:P42644; supported by cDNA: gi 166716 gb L09110.1 A	_	-1.1
putative protein similar to unknown protein (pir/IS75762)	249519 at	-1.1
dihydroxyacetone 3-phosphate reductase (dhaprd)	249366 at	-1.1
unknown protein ;supported by full-length cDNA: Ceres:126660.	249284_at	-1.1
beta-1,3-glucanase-like protein ;supported by full-length cDNA: Ceres:11988.	249235_at	-1.1
serine carboxypeptidase II-like ; supported by cDNA: gi_13605556_gb_AF361604.1_AF361604	249216_at	-1.1
Expressed protein ; supported by full-length cDNA: Ceres: 6893.	249162_at	-1.1
putative protein contains similarity to unknown protein (gb AAD21709.1); supported by cDNA: gi_15215714_gb_AY050386.1_	249035_at	-1.1
GDSL-motif lipase/hydrolase-like protein	248921_at	-1.1

putative protein contains similarity to bHLH DNA-binding protein;supported by full-length cDNA: Ceres:35890.	248839_at	-1.1
ATP citrate lyase ; supported by cDNA: gi_14334787_gb_AY035067.1_	248608_at	-1.1
putative protein similar to unknown protein (pir  T08406)	248614_at	-1.1
putative protein similar to unknown protein (sp P42404);supported by full-length cDNA: Ceres:15004.	248348_at	-1.1
putative protein contains similarity to GPI-anchored protein	247996_at	-1.1
nucleosome assembly protein	247955_at	-1.1
bis(5 -adenosyl)-triphosphatase-like; also similar to fragile histidine triad	247860_at	-1.1
zinc finger protein - like dof6 zinc finger protein, Arabidopsis thaliana, PIR:T47501;supported by full-length cDNA: Ceres:20852.	247625_at	-1.1
protein transport protein subunit - like protein transport protein SEC61 beta subunit, Arabidopsis thaliana, SWISSPROT:S61B_ARATH	247632_at	-1.1
S-receptor kinase homolog 2 precursor S-receptor kinase homolog 2 precursor, Arabidopsis thaliana, PIR:S27754	247602_at	-1.1
Cf-5 disease resistance protein - like Hcr2-0B, Lycopersicon esculentum, EMBL:AF053995	247569_at	-1.1
putative protein predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_13877822_gb_AF370174.1_AF370174	247407_at	-1.1
unknown protein ;supported by full-length cDNA: Ceres:16323.	247373_at	-1.1
unknown protein ;supported by full-length cDNA: Ceres:25419.	247149_at	-1.1
senescence-associated protein almost identical to ketoconazole resistant protein GI:928938 from [Arabidopsis thaliana] ;supported by full-length cD	247107_at	-1.1
putative protein hypothetical protein - Ricinus communis, EMBL:Z81012;supported by full-length cDNA: Ceres:1351.	246919_at	-1.1
E2, ubiquitin-conjugating enzyme, putative ubiquitin-conjugating enzyme, Pichia pastoris, PIR:A53848; supported by full-length cDNA: Ceres: 1028	246862_at	-1.1
nodulin - like protein early nodulin N93, Glycine max, EMBL:D13506;supported by full-length cDNA: Ceres:21669.	246863 at	-1.1
ferrochelatase-I	246870 at	-1.1
putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:38304.	246792 at	-1.1
CARBONIC ANHYDRASE 2 ; supported by cDNA: gi 13265565 gb AF324712.2 AF324712	246596 at	-1.1
putative protein predicted protein, Drosophila melanogaster	246462 at	-1.1
auxin-induced basic helix-loop-helix transcription factor, putative similar to auxin-induced basic helix-loop-helix transcription factor GI:5731257 from	_	-1.1
RP19 gene for chloroplast ribosomal protein CL9 ;supported by full-length cDNA: Ceres:13554.	246339 at	-1.1
putative protein ;supported by full-length cDNA: Ceres:14064.	245980 at	-1.1
putative franscriptional co-activator (KIWI) ; supported by cDNA: gi 2997683 gb AF053302.1 AF053302	245896 at	-1.1
putative c2h2 zinc finger transcription factor	245711 at	-1.1
unknown protein ; supported by full-length cDNA; Ceres:24560.	245665 at	-1.1
ethylene responsive element binding factor 1 (frameshift !); supported by cDNA: gi 3434966 dbj AB008103.1 AB008103	245252 at	-1.1
unknown protein ;supported by full-length cDNA: Ceres:23203.	245143 at	-1.1
hypothetical protein	2450145_at	-1.1
		-1.1
hypothetical protein	244961_at 244935 at	-1.1
NADH dehydrogenase subunit	_	-1.1
putative RNA-binding protein contains Procite RNP1 putative RNA-binding region, similar to GB:AAC33496; supported by cDNA: gi_13605870_gt		
hypothetical protein ;supported by full-length cDNA: Ceres:5.	265479_at	-1.1
OEP8 like protein	245514_at	-1.1
Expressed protein ; supported by full-length cDNA: Ceres: 27620.	267591_at	-1
TCP1-chaperonin cofactor A isolog supported by full-length cDNA: Ceres:1853.	267494_at	-1
putative squamosa-promoter binding protein supported by full-length cDNA: Ceres:10375.	267460_at	-1
unknown protein ;supported by full-length cDNA: Ceres:8402.	267370_at	-1
putative malonyl-CoA:Acyl carrier protein transacylase ;supported by full-length cDNA: Ceres:299.	267308_at	-1
unknown protein	267230_at	-1
unknown protein	267069_at	-1
putative cytochrome P450 ;supported by full-length cDNA: Ceres:158108.	266996_at	-1
putative protein kinase contains a protein kinase domain profile (PDOC00100)	266946_at	-1
acyl carrier protein identical to GB:L23574; supported by cDNA: gi_15450374_gb_AY052288.1_	266890_at	-1
unknown protein	266813_at	-1
putative expansin Experimental evidence from Dr. Daniel Cosgrove at Penn State Univ. <dcosgrove@psu.edu></dcosgrove@psu.edu>	266770_at	-1
unknown protein ;supported by full-length cDNA: Ceres:26967.	266716_at	-1
unknown protein ;supported by full-length cDNA: Ceres:10341.	266483_at	-1
hypothetical protein predicted by genefinder; supported by cDNA: gi_15215635_gb_AY050346.1_	266463_at	-1
putative cinnamoyl-CoA reductase	266202_at	-1
putative microtubule-associated protein ; supported by cDNA: gi_15724331_gb_AF412106.1_AF412106	266106_at	-1
Expressed protein ; supported by full-length cDNA: Ceres: 109069.	266094_at	-1
unknown protein	265883_at	-1
putative integral membrane protein	265713_at	-1
cysteine proteinase contains similarity to cysteine protease SPCP1 GI:13491750 from [Ipomoea batatas]	265665 at	-1

cytochrome b5, putative similar to cytochrome b5 GI:4240120 from [Arabidopsis thaliana]; supported by cDNA: gi_15146311_gb_AY049297.1_	264926_at	-1
flowering signals mediating protein FT identical to flowering signals mediating protein FT GI:4903012 from [Arabidopsis thaliana]; supported by cDN	264638_at	-1
putative auxin-induced protein, IAA12 similar to GB:S58498,supported by full-length cDNA: Ceres:40608.	264605_at	-1
adenine phosphoribosyltransferase 1, APRT identical to GB:P31166; similar to ESTs gb[N65531, gb]R90631, gb]T21275, and gb]AA713070; suppo	264439_at	-1
unknown protein	264385_at	-1
unknown protein	264172_at	-1
unknown protein	264173_at 264130 at	-1 -1
hypothetical protein predicted by genemark.hmm putative auxin-regulated protein :supported by full-length cDNA: Ceres:7141.	264021 at	-1 -1
putative auxin-regulated protein ,supported by full-length CDNA. Ceres. / 141. putative receptor-like protein kinase	263913 at	-1 -1
unknown protein ;supported by full-length cDNA: Ceres:24885.	263920 at	-1
unknown protein	263869 at	-1
putative cyclic nucleotide-regulated ion channel protein	263777 at	-1
ArRer18 ;supported by full-length cDNA: Ceres:92908.	263516_at	-1
unknown protein ;supported by full-length cDNA: Ceres:6899.	263305 at	-1
aspartate-semialdehyde dehydrogenase, putative similar to aspartate-semialdehyde dehydrogenase SP:031219 [Legionella pneumophila];support		-1
	262661 s at	-1
oxidoreductase, putative contains Pfam profile: PF00671 Iron/Ascorbate oxidoreductase family	262616 at	-1
receptor-like protein kinase, putative similar to receptor-like protein kinase GB:AAC95353 GI:4008010 from [Arabidopsis thaliana]	262507 at	-1
acyl CoA synthetase, putative similar to acyl CoA synthetase GI:1617267 from [Brassica napus]	262414 at	-1
hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 10855.	262411 at	-1
auxin transport protein REH1, putative similar to auxin transport protein REH1 GI:3377509 from [Oryza sativa]; supported by cDNA: gi_5817300_gl	262263_at	-1
isocitrate dehydrogenase, putative similar to isocitrate dehydrogenase GI:166385 from [Medicago sativa]; supported by full-length cDNA: Ceres:415	261920_at	-1
hypothetical protein contains similarity to prephenate dehydratase GI:1008717 from [Amycolatopsis methanolica]; supported by cDNA: gi_15810502	261758_at	-1
unknown protein	261782_at	-1
unknown protein contains Pfam profile: PF00255 glutathione peroxidases;supported by full-length cDNA: Ceres:30238.	261530_at	-1
Expressed protein ; supported by full-length cDNA: Ceres: 14314.	261439_at	-1
hypothetical protein predicted by genemark.hmm	261073_at	-1
ascorbate oxidase promoter-binding protein, putative similar to ascorbate oxidase promoter-binding protein GB:D45066 GI:853689 from [Cucurbita	260887_at	-1
unknown protein similar to unknown protein GB:AAB67633 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:18194.	260895_at	-1
	260898_at	-1
zinc finger protein, putative similar to zinc finger protein ID1 GB:AAC18941 GI:3170601 from [Zea mays]	260776_at	-1
Expressed protein ; supported by full-length cDNA: Ceres: 17110.	260685_at	-1
hypothetical protein predicted by genemark.hmm;supported by full-length toDNA: Ceres;95383.	260651_at	-1
putative signal recognition particle protein 14kD, ATSRP14; supported by full-length cDNA: Ceres: 97249.	260569_at	-1
putative trypsin inhibitor ;supported by full-length cDNA: Ceres:85. hypothetical protein predicted by genscan+	260547_at 260277 at	-1 -1
putative 3-isopropylmalate dehydrogenase similar to 3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR GB:P29102 from (Brassica napus		-1 -1
30S ribosomal protein S17, chloroplast precursor (CS17) identical to 30S ribosomal protein S17, chloroplast precursor GB:P16180 [Arabidopsis that		-1 -1
unknown protein	260103_at	-1
putative RING zinc finger protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)	260065 at	-1
putative cancel and angle protein similar to calmoduli-binding protein GB:AAB37246 [Nicotiana tabacum]	260068 at	-1
hypothetical protein supported by full-length cDNA: Ceres: 19640.	259863 at	-1
unknown protein ; supported by full-length cDNA: Ceres:34166.	259856 at	-1
photosystem I subunit VI precursor identical to photosystem I subunit VI precursor [Arabidopsis thaliana] GI:5734524; supported by full-length cDNA	_	-1
auxin-induced protein, putative similar to SP:P33083 from [Glycine max]	259773 at	-1
unknown protein similar to phosphate translocators: glucose-6-phosphate/phosphate-translocator precursor GB:AAC08524 [Zea mays], phosphate.	_	-1
hypothetical protein	259560 at	-1
unknown protein contains similarity to copper zinc superoxide dismutase GI:5689611 from (Arabidopsis thaliana); supported by cDNA: gi 15215657	259511 at	-1
putative APG protein similar to anter-specific proline-rich protein APG precursor SP:P40602 (Arabidopsis thaliana); contains Pfam profile: PF00657	259375_at	-1
unknown protein	259325_at	-1
hypothetical protein similar to F1N21.1 GB:AAB95230 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:28199.	259198_at	-1
putative protein kinase similar to ATMRK1, an Arabidopsis protein kinase related to mammal mixed-lineage kinases and Raf protein kinases GB:BH		-1
unknown protein similar to unknown protein GB:AAC62889 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:15153.	259154_at	-1
unknown protein similar to GB:CAB05547 [Caenorhabditis elegans]	259085_at	-1
heat-shock protein (At-hsc70-3) identical to (At-hsc70-3) (cytosolic Hsp70) GB:CAA76606 [Arabidopsis thaliana]; supported by cDNA: gi_15292924.	258979_at	-1
putative dehydrogenase contains Pfam profiles: PF00106 short chain dehydrogenase, PF00678 short chain dehydrogenase reductase C-terminus;	258976_at	-1

putative pectinacetylesterase similar to GB:CAA6728 from [Vigna radiata]; supported by cDNA: gl_15292826_gb_AY050847.1288642_at       -1         unknown protein       288642_at       -1         MNO3-like protein similar to MN3 GB:CAA69976 from [Medicago truncatula]       288418_at       -1         MNO3-like protein similar to MN3 GB:CAA69976 from [Medicago truncatula]       288642_at       -1         MNO3-like protein similar to MN3 GB:CAA69976 from [Medicago truncatula]       28601_at       -1         monosaccharide transport protein, SUPported by full-length cDNA: Ceres:32718.       28709_at       -1         unknown protein       257868_at       -1       -2         unknown protein       257710_at       -2       -2         unknown protein       257710_at       -2       -2         unknown protein       10       257717_at       -2       -2         unknown protein			
inknown protein         226842 at 1           inknown protein         227789 at 1           inknown protein         227717 at 1           inknown protein         227778 at 1           inknown protein         227778 at 1           inknown protein         226842 at 1           inknown protein         226842 at 1 <t< td=""><td></td><td></td><td>-1</td></t<>			-1
unknown protein26811gtheosenal protein L29, putative similar to 60S Arbosonal protein L29 GBP 25886 from [Ratius norvegicus]25847gunknown protein25847g25847gMN3 ke protein similar to MN3 GB: CAA6976 from [Medicago truncatula]CAR6976 from [Medicago truncatula]25847gAlG2-like protein ismilar to ALG2 protein GB: P4211 from [Xrbaidopsis thaliana]; supported by CDNA: g_1586596_gb_AF367325_1_225842gMN3 ke protein similar to ALG2 protein GB: P4211 from [Xrbaidopsis thaliana]; supported by CDNA: g_1586596_gb_AF367325_1_225758gUnknown protein25726g257766gUnknown protein25726g257766gUnknown protein25726g257776gUnknown protein1941-length cDNA: Ceres: 2048.257771_gUnknown protein257771_g257775_gUnknown protein1941-length cDNA: Ceres: 2048.257771_gUnknown protein1941-length cDNA: Ceres: 2048.257775_g25645_gUnknown protein1941-length cDNA: Ceres: 2048.25645_g25645_gUnknown protein1941-length cDNA: Ceres: 2031.25645_g25645_gUnknown protein1941-length cDNA: Ceres: 2031.25645_g25645_gUnknown protein1941-length cDNA:	putative pectinacetylesterase similar to GB:CAA67728 from [Vigna radiata]; supported by cDNA: gi_15292826_gb_AY050847.1_	258750_at	-1
inbosomal protein128 (28) Absorbed from [Ratus forwegicus]28847_at	unknown protein ;supported by full-length cDNA: Ceres:24905.	_	-1
unknown protein         258472, at -1           AURADM         257499, at -1           hypothetical protein products by genefinder:supported by full-length CDNA: Ceres.32718.         257682, at -1           unknown protein         257710, at -1           unknown protein         2577710, at -1           Unknown protein         256782, at -1           Offorom protein Supported by full-length CDNA: Ceres: 21643.         256782, at -1           Unknown protein         256822, at -1           Unknown protein         256824, at -1		_	-1
unknown protein28441 atMN3-like protein similar to MIN3 GB:CAA69976 from [Medicago truncatula]254421, atAIC2-like protein similar to AIC2 protein GB:P54121 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 32718.286001, atmonosacchardreit transport protein, STP4 detinction GG: S25000 Frunt (Arabidopsis thaliana); supported by cDNA: gj_13005905, gb_AF3673521, L257888, athypothetical protein protein supported by full-length cDNA: Ceres: 3044.257888, at257787, atcyclopropane-fatty-acycl-phospholipid synthase, putative similar to cyclopropane-fatty-acyl-phospholipid synthase, putative similar to CH2.257171, athypothetia protein, jusported by full-length cDNA: Ceres: 176.286467, at286467, athypothetia protein, jusported by full-length cDNA: Ceres: 178.286682, at28649, athypothetia protein, jusported by full-length cDNA: Ceres: 2011.286497, at286497, atArknown protein : supported by full-length cDNA: Ceres: 3201.286497, at286497, atArknown protein : supported by full-length cDNA: Ceres: 3203.286497, at286497, atArknown protein : supported by full-length cDNA: Ceres: 3204.286497, at286497, atArknown protein : supported by full-length cDNA: Ceres: 3204.286497, at286497, atArkno			
NIM3-kke protein similar to AK2 orbit of Mikel Statiana] supported by full-length CDNA: Ceres: 32718.       258001 at			
ALG2-like protein similar to ALG2 protein GBP:54121 from [Arabidopsis thaliana]; supported by cDNA: g13805905_gb_AF387322.1_# 257938_dt 257888_dt 25788_dt 25787_dt 25787_dt 25771_dt 25771_dt 25777_dt 25777_d			
monesaccharide transport protein, STP4 identical to GB:S28009 from [Arabidopsis thaliana]227838, atunknown protein227838, atunknown protein227838, atunknown protein227838, atunknown protein227838, atunknown protein227828, atunknown protein227828, atunknown protein227828, atunknown protein227727, atunknown protein227727, atunknown protein, supported by full-length cDNA: Ceres: 30464.227717, atunknown protein, supported by full-length cDNA: Ceres: 15287.256893, atunknown protein, supported by full-length cDNA: Ceres: 14287.256693, atunknown protein, supported by full-length cDNA: Ceres: 14287.256469, atunknown protein, supported by full-length cDNA: Ceres: 14287.256468, atunknown protein256458, at256458, atunknown protein256458, at256458, atunknown protein256458, at256458, atunknown protein256458, at256334, at256334, at256334, at256334, atunknown protein256342, at256334, at256458, at256334, at256334, at256458, at256334, at256334, at256458, at25633, at256334, at256458, at25633, at256334, at256458, at256548, at256548, at <td< td=""><td></td><td></td><td></td></td<>			
hypothetical protein protein         257858, at         -           unknown protein         257868, at         -           unknown protein         257868, at         -           unknown protein         257868, at         -           unknown protein         257878, at         -           unknown protein         257878, at         -           unknown protein         257779, at         -           cyclopropane-fathy-acyt-hospholipid synthase cBI-20010 [Escherichia coli         257777, at         -           unknown protein         pothetide protein, 5 approted by full-length cDNA: Ceres: 5178.         -         256626, at         -           Unknown protein supported by full-length cDNA: Ceres: 1777, at         -         256626, at         -         256626, at         -         256626, at         -         256626, at         -         256455, at         -         256455, at         -         256456, at         -         256456, at         -         256462, at         -         256364, at         -         256364, at         -         256364, at         -         256364, at         -         256362, at		_	
<ul> <li>unknown protein</li> <li>protein</li> <li>protein</li></ul>		_	
unknown protein         257828_ait	hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:924.	_	
unknown protein :supported by full-ength cDNA: Ceres: 20618.         257710_st		_	
unknown protein257279_st-1cyclopropane-fathy-acyl-phospholipid synthase GB:20010 [Escherichia coll]257775_st-1unknown protein2590711_st-2unknown proteincollar ported by full-length cDNA: Ceres: 6176.258682_st-2ORF1, putative similar to ORF1 G1457716 from (Arabidopsis thaliana): supported by cDNA: gi_16649160_gb_AY059960.1_256485_st-2ORF1, putative similar to ORF1 G1457716 from (Arabidopsis thaliana): supported by cDNA: gi_16649160_gb_AY059960.1_256485_st-2unknown proteinputative similar to Al: 1209755 from [Beta vulgaris] (Plant Physiol. 110 110 (2), 511-520 (1996)): supported by cDNA: gi_256455_at-1unknown proteinputative similar to AP2 domain transcription factor G1-4567204 from [Arabidopsis thaliana]256040_gtAP2 domain transcription factor, putative similar to AP2 domain transcription factor G1-4567204 from [Arabidopsis thaliana]256970_gt-10DPL-fucces synthetase, putative similar to AP2 domain transcription factor G1-4567204 from [Arabidopsis thaliana]256070_gt-11DPUATIVE NAM (no apical meristem)-like protein : supported by CDNA: gi_15244212 from [Homo sapiens]: supported by CDNA: ceres: 37600_gt255774_gt-12Expressed protein : supported by CDNA: Ceres: 18459.25563_gt-1-12expressed protein : supported by full-length CDNA: Ceres: 18459.25563_gt-1-13drobal are protein indulin gene MM21 - Medicago truncatula, PID: e1172471; supported by full-length CDNA: Ceres: 3706_gt-2-147 Vike protein indulin gene MM21 - Medicago truncatula, PID: e1172471; supported by CDNA: gi_10880466_gb_AF195891.256682_gt-1<		_	
cyclopropane-fatly-acyl-phospholipid synthase, putative similar to cyclopropane-fatly-acyl-phospholipid synthase GB:P30010 [Escherichia coli]257175, a.t.unknown protein : supported by full-length CDNA: Ceres: 5176.256323, at.ORF1, putative similar to ORF1 G1:457716 from (Arabidopsis thaliana); supported by cDNA: gi_16649160_gb_AY059950.1_256426, at.Integral membrane protein, putative similar to G1:209755 from [Beta vulgaris] (Plant Physiol. 110 110 (2), 511-520 (1996)); supported by full-length cDNA: Ceres: 2031.256436, at.AP2 domain transcription factor, putative similar to BCI:209755 from [Beta vulgaris] (Plant Physiol. 110 110 (2), 511-520 (1996)); supported by full-length cDNA: Ceres: 2031.256434, at.AP2 domain transcription factor, putative similar to BCP-2 domain transcription factor G1:4567204 from [Arabidopsis thaliana]256009, at.AP2 domain transcription factor, putative similar to BCP-1 ducose synthetase G1:6580725 from [Versinia pseudotuberculosis]supported by full-length cDNA: Ceres: 27800255071, at.GDP-1-fucose synthetase, putative similar to BCP-1 ducose synthetase G1:6580725 from [Versinia pseudotuberculosis]supported by full-length cDNA: Ceres: 37302.255719, at.cyntative NAM (no apical meristing) is coported by cDNA: gi_1524215_gb_AF410299255719, at.unknown protein : supported by full-length cDNA: Ceres: 1465.255524, at.coded for by A. thaliana cDNA 143463 similar to auxin-induced protein256445, at.myonteris : supported by full-length cDNA: Ceres: 2780025574, at.coded for by A. thaliana cDNA 143463 similar to auxin-induced protein256454, at.myonteris : supported by full-length cDNA: Ceres: 37		_	
unknown protein : supported by full-ength cDNA: Ceres: 5176. unknown protein: Supported by full-ength cDNA: Ceres: 5176. Unknown protein: Supported by full-ength cDNA: Ceres: 5176. ORF1, putative similar to ORF1 G1:457716 from (Arabidopsis thaliana): supported by cDNA: gi_16649160_gb_AY059950.1_ 256465_at -1 DNA: Ceres: 1443. Integral membrane protein, putative similar to G1:208755 from [Beta vulgaris] (Plant Physiol. 110 110 (2), 511-520 (1996)); supported by cDNA: gi_ 256485_at -1 unknown protein : supported by full-ength cDNA: Ceres: 2031. AP2 domain transcription factor, putative similar to AP2 domain transcription factor G1:4567204 from [Arabidopsis thaliana] 256342_at -1 Putative similar to ribosomal protein S18 G1:308725 from [Peta vulgaris] (Plant Physiol. 110 110 (2), 511-520 (1996)); supported by cDNA: gi_ 256306_at -1 256306_at -1 256306_at -1 256307_at -1 256307_at -1 256307_at -1 256307_at -1 256307_at -1 256307_at -1 255301_at -2 255719_at -2 255719_at -2 255719_at -2 255719_at -2 255719_at -2 255719_at -2 255719_at -2 25574_at -2 255719_at -2 25574_at -2 25586_at -2 25586_at -2 25586_at -2 25586_at -2 25586			
unknown protein contains Pfan profile/F00279 LTP:Plant lipid transfer protein family;supported by full-length cDNA: Ceres: 19287.         266937_at            ORF1 G1457716 from (Arabidopsis thaliana); supported by cDNA: gi_16649160_gb_AY059950.1_         256425_at            Unknown protein is supported by full-length cDNA: Ceres: 14433.         256435_at          256435_at            Unknown protein         imported by full-length cDNA: Ceres: 2031.         256342_at          256342_at            AP2 domain transcription factor, putative similar to folsomal protein S1G G13422 from [Homo sapiens]; supported by CDNA: Ceres: 27800         255077_at            GDP-L-fucose synthetase, putative similar to folsomal protein S1G G13422 from [Homo sapiens]; supported by full-length cDNA: Ceres: 3700.         255074_at            Unknown protein         signation active signatactive signation active signation active signation activ			
hypothetical protein, 5 partial26622 at 26495 at 26495 atORF1, putative similar to CFI Cl437716 from (Arabidopsis thaliana); supported by CDNA: gi_16649160_gb_AY059950.1_ 266495_at266495_at 266455_atunknown protein ; supported by full-length cDNA: Ceres:14433. integral membrane protein, putative similar to Cl:1209755 from [Beta vulgaris] (Plant Physiol. 110 110 (2), 511-520 (1996)); supported by cDNA: gi 266465_at266455_atunknown protein ; unknown protein ; supported by full-length cDNA: Ceres: 2031.266302_at 265342_at266342_at 265032_atAP2 domain transcription factor, putative similar to CDP-L-fucces synthetase (Cl680725 from [Versinia pseudotuberculosis]; supported by full-length cDNA: Ceres: 37302.2555774_at 255774_atODP-L-fucces synthetase (Cl680725 from [Versinia pseudotuberculosis]; supported by full-length cDNA: Ceres: 18459.255574_at 255784_atCoded for by A. thaliana cDNA 143845 similar to auxin-induced protein hypothetical protein subported by full-length cDNA: Ceres: 18459.255512_at 25574_atnodulin-like protein nodulin gene MHX2 1- Medicago truncatula, PID:e1172471; supported by cDNA: gi_1080496_gb_aF195891.255042_at 255042_atnotation-like protein naduus protein (glbAC79139.1)245421_at 245421_atnotation-like protein naduus protein (glbAC79139.1)254542_at 25542_atnotation-like protein in supported by full-lengt cDNA: Ceres:3293.25396_at 25391_atnotative protein in supported by full-length cDNA: Ceres:3293.25386_at 25391_atnotative protein in supported by full-length cDNA: Ceres:2142.25364_at 25524_atnotative protein sinubate of by full-length cDNA: Ceres:2143			
OFF1 putative similar to CRF1 CI457716 from (Arabidopsis thaliana); supported by cDNA: gi_16649160_gb_AY059950.1_256497_atunknown proteinStep497_att			
unknown protein26645atintegral membrane protein, putative similar to Gl:1209765 from [Beta vulgaris] (Plant Physiol. 110 110 (2), 511-520 (1996)); supported by cDNA: gi26645unknown protein26647atAP2 domain transcription factor, putative similar to AP2 domain transcription factor. putative similar to CDP1-fuccose synthetase. Putative similar to ADX: Ceres: 18459.2565794atcoded for by A. thalana cDNA T43485 similar to auxin-induced protein2555749.at-nodulin-like protein nodulin gene MIN21 - Medicago truncatula, PID=1172471;supported by full-length cDNA: Ceres: 18459.256652.atarabinogalacta-protein hondolg arabinogalacta-protein hondolg arabinogalacta-protein singlor to unknown protein isquported by full-length cDNA: Ceres: 1293.255719.atarabinogalacta-protein kninkown protein (gb]AAC79139.1)24449.at-25562.atatelnine phosphoribosyltransferase, Triticum aestivum, T06263; supported by full-length cDNA: Ceres: 1293.253869.atputative protein similar to nuknown protein (gb]AAC79139.1)245449.at-atelnine phosphoribosyltransferase, PID:2380571.253869.253869.putative prot			
Integral membrane protein, putative similar to GI:1209755 from [Beta vulgaris] (Plant Physiol. 110 110 (2), 511-520 (1996)); supported by cDNA: geta 5666 at unknown protein ; supported by full-length cDNA: Ceres: 2031.256342_at -1AP2 domain transcription factor, putative similar to AP2 domain transcription factor GI:4567204 from [Arabidopsis thaliana]25600_at -1inbosomal protein S18, putative similar to BCP1-fucces synthetase GI:65802725 from [Yersinia pseudotuberculosis], supported by full-length cDDA: Ceres: 27800255901_at -1GDP1-fucces synthetase, putative similar to GDP1-fucces synthetase GI:65802725 from [Yersinia pseudotuberculosis], supported by full-length cDNA: Ceres: 37302.255719_at -1Expressed protein : supported by full-length cDNA: Ceres: 37302.255719_at -1coded for by A. thaliana cDNA T43845 similar to auxin-induced protein255645_at -1nyobticical protein is upported by full-length cDNA: Ceres: 18459.255645_at -1putative NAM gene MIN21 - Medicago truncatula, PID:e1172471;supported by full-length cDNA: Ceres: 40485.25552_at -1arabinogalactan-protein roby protein similar to unknown protein (gbIAC7913) 1254549_at -1adenine phosphoribosyltransferase (EC 2.4.2.7) - like protein adenine phosphoribosyltransferase, Triticum aestivum, T06263; supported by full-length cDNA: Ceres: 42155.25386_at -1putative protein is supported by full-length cDNA: Ceres: 3236.25386_at -1putative protein is supported by full-length cDNA: Ceres: 3236.25386_at -1putative protein is supported by full-length cDNA: Ceres: 3336.25347_at -1		_	-1
unknown protein       256396_at       -1         unknown protein ; supported by full-length cDNA: Ceres: 2031.       256342_at       -1         AP2 domain transcription factor, putative similar to AP2 domain transcription factor GI:4567204 from [Arabidopsis thaliana]       256009_at       -1         GDPL-Liccose synthetase, putative similar to CDP-Liccose synthetase, CIS680725 from [Yersinia pseudotuberculosis]; supported by full-length cDNA: Ceres: 37302.       255719_at       -1         Expressed protein ; supported by full-length cDNA: Ceres: 37302.       255524_at       -1         Involondin-like protein modulin gene MtN21 - Medicago truncatula, PID:e1172471; supported by cDNA: gi 1528426; supported by cDNA: gi 10880496_gb_AF195891.       255080_at       -1         rabinogalactan-protein hondolg arabinogalactan-protein hondolg arabinogalactan-		_	-1
unknown protein ; supported by full-length cDNA: Ceres: 2031.256342_at-1AP2 domain transcription factor S18, putative similar to AP2 domain transcription factor G1:4567204 from [Arabidopsis thaliana]256009_at-1ribosomal protein S18, putative similar to AP2 domain transcription factor G1:4567204 from [Arabidopsis thaliana]256009_at-1GDP1_fucces synthetase, putative similar to AP2 domain transcription factor G1:4567204 from [Yersinia pseudotuberculosis];supported by full-length cDNA: Ceres: 37302.255719_at-1unknown protein ; supported by full-length cDNA: Ceres: 18459.256643_at-1coded for by A thaliana CDNA: T3845 similar to auxin-induced protein255544_at-1hypothetical protein similar to pectinesterase25552_at-1nodulin-like protein nomolog arabinogalactan-protein - Arabidopsis thaliana,PID:g3883126; supported by cDNA: Geres:40485.25552_at-1arabinogalactan-protein homolog arabinogalactan-protein - Arabidopsis thaliana,PID:g3883126; supported by cDNA: g1 0880496_gb_AF195891.254500_at-1putative protein similar to unknown protein (gb]AAC79139.1)254521_at-1-2adenine phosphoritosyltransferase (EC 24.2.7) - like protein admine phosphoritosyltransferase, Triticum aestivum, T06263; supported by full-length cDNA: Ceres: 3203253816_at-1putative protein similar to unknown protein (gb]AAC79139.1)254521_at-1adenine phosphoritosyltransferase (EC 24.2.7) - like protein admine phosphoritosyltransferase, EC 24.2.7) - like protein admine phosphoritosyltransferase, EC 34386_at-1putative protein singhore by full-length cDNA: Ceres: 42155.253816_at <td>integral membrane protein, putative similar to GI:1209755 from [Beta vulgaris] (Plant Physiol. 110 110 (2), 511-520 (1996)); supported by cDNA: gi</td> <td>256458_at</td> <td>-1</td>	integral membrane protein, putative similar to GI:1209755 from [Beta vulgaris] (Plant Physiol. 110 110 (2), 511-520 (1996)); supported by cDNA: gi	256458_at	-1
AP2 domain transcription factor, putative similar to AP2 domain transcription factor GI:467226 from [Arabidopsis thaliana]25600_{-tt}1ribosomal protein S18, putative similar to GDP-L-fucces synthetase GI:6580725 from [Yersinia pseudotuberculosis], supported by full-length DD255971_at-1putative NAM (no apical meristem)-like protein : supported by CDNA: gj_15294215_gb_AF410299.1_AF410299255794_at-1putative NAM (no apical meristem)-like protein : supported by CDNA: gj_15294215_gb_AF410299.1_AF410299255794_at-1coded for by A. thaliana cDNA T43845 similar to auxin-induced protein256645_at-1hypothetical protein nondulin gene MIN21 - Medicago truncatula, PID:e1172471;supported by full-length cDNA: Ceres:40485.255624_at-1rabiorgalactan-protein honolog arabingalactan-protein - Arabidopsis thaliana,PID:g3883126; supported by cDNA: gj_1080496_gb_AF19898.255864_at-1putative protein valous predicted protein similar to unknown protein (gb]AAC79139.1)254549_at-1putative protein valous protein by full-length cDNA: Ceres:10485.25391_at-1trutte protein similar to unknown protein (gb]AAC79139.1)25454_at-1putative protein similar to unknown protein (gb]AAC79139.1)25454_at-1putative protein brosphoribosyltransferase, Diponea tifida,PID:g383694253816_at-2putative protein similar to unknown protein (gb]AAC79139.1)25454_at-1putative protein simalse to unknown protein (gb]AAC79139.1)25454_at-1putative protein simalse to unknown protein (gb]AAC79139.1)25386_at-1putative protein sinsported by	unknown protein	256396_at	-1
ribosomal protein S18, putative similar to ribosomal protein S18 GI:38422 from [Homo sapiens]; supported by cDNA: Ceres:27800255977_et1GDP-L-fucose synthetase, putative similar to GDP-L-fucose synthetase GI:6580725 from [Yersinia pseudotuberculosis]; supported by full-length cDNA: Ceres:37302.255719_at-1Dutative NAM (no apical meristem)-like protein : supported by cDNA: GI : 15294215_gb_AFE410299 1_AFE410299255719_at-1Coded for by A. thaliana cDNA T43845 similar to auxin-induced protein255643_at-1Nypothetical protein similar to pectinesterase255719_at-2Indulin-like protein noting gene MIX21 - Medicago truncatula, PID:e1172471;supported by full-length cDNA: Ceres:40485.255129_at-1arabinogalactan-protein homolog arabinogalactan-protein - Arabidopsis thaliana,PID:g3833126; supported by cDNA: gi_10880496_gb_AF195891.255080_at-1putative protein ration gene MIX21 - Medicago truncatula, PID:e1172471;supported by cDNA: gi_15718417_dbj_AB071851AB07185125552_at-1putative protein ration geno antibiolia,PIR2:S39567; supported by cDNA: gi_15718417_dbj_AB071851AB07185125542_at-1putative protein similar to unknown protein (db/AC79139.1)254549_at-1-2adenine phosphoribosyltransferase (EC 2.4.2.7)like protein nabingalactan-protein kinase, pomoea trifida,PID:g336954253311_at-1putative protein is supported by full-length cDNA: Ceres: 1233523385_at-1putative protein hypothetical protein supported by full-length cDNA: Ceres: 1233523385_at-1putative protein hypothetical protein protein supported by full-length cDNA: Ceres: 1238572 <t< td=""><td></td><td>_</td><td>-1</td></t<>		_	-1
GDP-L-fucose synthetase, putative similar to GDP-L-fucose synthetase GI:6580725 from [Yersinia pseudotuberculosis]; supported by full-length cDNA: Ceres:37302255719_at-1putative NAM (no apical meristem)-like protein ; supported by full-length cDNA: Ceres:37302255719_at-1Expressed protein ; supported by full-length cDNA: Ceres:3730225563_at-1coded for by A. thaliana cDNA T43845 similar to auxin-induced protein25664_at-1hypothetical protein nondulin gene MIN21 - Medicago truncatula, PID:e1172471; supported by full-length cDNA: Ceres:40485.25562_at-1rabinoglactan-protein nondulin gene MIN21 - Medicago truncatula, PID:e1172471; supported by cDNA: gi_1080046_gb_AF195891.255080_at-1arabinoglactan-protein nondulin gene MIN21 - Medicago truncatula, PID:e1172471; supported by cDNA: gi_1080046_gb_AF195891.255080_at-1putative protein vainus predicted proteins254549_at-1254549_at-1putative protein vainus predicted proteins254549_at-1254549_at-1putative protein vainus predicted proteins254549_at-1254549_at-1putative protein sinuar to unknown protein (bjAAC79139.1)254521_at-1-1adenine phosphoribosyltransferase (EC 2.4.2.7) - like protein adenine phosphoribosyltransferase, Triticum aestivum, T06263; supported by full-length cDNA: Ceres: 12935.253856_at-1putative protein issupported by full-length cDNA: Ceres: 12935.253856_at-1-1putative protein hypothetical protein - Arabidopsis thaliana, PID:g383023; supported by full-length cDNA: Ceres: 3202253815_at-1 <td>AP2 domain transcription factor, putative similar to AP2 domain transcription factor GI:4567204 from [Arabidopsis thaliana]</td> <td>256009_at</td> <td>-1</td>	AP2 domain transcription factor, putative similar to AP2 domain transcription factor GI:4567204 from [Arabidopsis thaliana]	256009_at	-1
putative NAM (no apical meristem)-like protein ; supported by cDNA: gi_15294215_gb_AF410299.1_AF410299255794_at-1unknown protein ; supported by full-length cDNA: Ceres: 37302.25579_at-1Expressed protein ; supported by full-length cDNA: Ceres: 1459.25663_at-1coded for by A. thaliana cDNA T43845 similar to auxin-induced protein25664_at-1nodulin-like protein nodulin gene MtN21 - Medicago truncatula, PID:e1172471;supported by full-length cDNA: Ceres:40485.255129_at-1arabinogalactan-protein homolog arabinogalactan-protein - Arabidopsis thaliana,PID:g3863126; supported by cDNA: gi_10860496_gb_AF195891.255080_at-1putative protein various predicted proteins255624_at-1-1putative protein various predicted proteins254621_at-1adenine phosphoribosyltransferase (EC 2.4.2.7) - like protein adenine phosphoribosyltransferase, Triticum aestivum, T06263; supported by full-length cDNA: Ceres: 32911_at-1Expressed protein ; supported by full-length cDNA: Ceres: 12935.253859_at-1putative receptor protein kinase receptor protein kinase, lpomoea trifida,PID:g836954253815_at-1putative protein potter by supported by full-length cDNA: Ceres: 3202253815_at-1putative protein hypothetical protein supported by full-length cDNA: Ceres: 3215.253866_at-1putative protein hypothetical protein supported by full-length cDNA: Ceres: 3215.25386_at-1putative protein hypothetical protein Suppane on putative protein hypothetical protein supported by full-length cDNA: Ceres: 3322253815_at-1putative protein hyp		255977_at	-1
unknown protein ;supported by full-length cDNA: Ceres: 37302.255716_at-1Expressed protein ; supported by full-length cDNA: Ceres: 18459.255633_at-1coded for by A. thaliana cDNA T33845 similar to auxin-induced protein255645_at-1nodulin-like protein similar to pectinesterase255524_at-1nodulin-like protein nowolig grabinogalactan-protein - Arabidopsis thaliana, PID:g3883126; supported by cDNA: Geres: 40485.255129_at-1arabinogalactan-protein homolog arabinogalactan-protein - Arabidopsis thaliana, PID:g3883126; supported by cDNA: Geres: 40485.255052_at-1putative protein various predicted proteins254549_at-1-24522_at-1adenine phosphoribosyltransferase (EC 2.4.2.7) - like protein adenine phosphoribosyltransferase, Triticum aestivum, T06263; supported by full-length cDNA: Ceres: 12935.254328_at-1putative protein is supported by full-length cDNA: Ceres: 12935.25385_at-1-1putative protein hypothetical protein - soybean pollen allergen (cim1) protein - soybean, PIR2:S48032; supported by full-length cDNA: Ceres: 3202253746_at-1putative protein hypothetical protein - Arabidopsis thaliana, PID:g4337210253427_at-1253427_at-1putative protein hypothetical protein in TP17520.25347_at-1253427_at-1putative protein hypothetical protein in TP17520.25347_at-125342_at-1putative protein hypothetical protein in CDNA: Ceres: 39326.25342_at-125342_at-1putative protein hypothetical protein in Supported by full-length cDNA: Ceres: 39		255901_at	-1
Expressed protein ; supported by full-length cDNA: Ceres: 18459.25563_at-1coded for by A. thaliana cDNA 743645 similar to auxin-induced protein25564_at-1hypothetical protein similar to pectinesterase25524_at-1nodulin-like protein induciog arabinogalactan-protein- Arabidopsis thaliana.PID_3863126; supported by cDNA: gi_10880496_gb_AF195851255000_atrarb7-like protein various predicted proteins- Arabidopsis thaliana.PID_3863126; supported by cDNA: gi_10880496_gb_AF195851255052_atputative protein various predicted proteins254549_at-1putative protein various predicted proteins254521_at-1adenine phosphorbosyltransferase (EC 2.4.2.7) - like protein adenine phosphoribosyltransferase, Triticum aestivum, T06263; supported by full-length cDNA: Ceres: 12935.25385_atputative protein is supported by full-length cDNA: Ceres: 12935.25385_at-1putative protein hypothetical protein synopheted by full-length cDNA: Ceres: 12935.25385_at-1putative protein hypothetical protein - Arabidopsis thaliana, PID_9433721025376_at-1putative protein hypothetical protein - F/R1b/308, Saccharomyces cerevisiae, Pir2:S69718; supported by cDNA: gi_15982681_gb_AY057538.125346_at-1putative protein hypothetical protein F17H15.20 Arabidopsis thaliana chromsome II BAC F17H15, PID_93643606253401_at-1putative protein hypothetical protein F17H15.20 Arabidopsis thaliana chromsome II BAC F17H15, PID_93643606253401_at-1putative protein hypothetical protein F17H15.20 Arabidopsis thaliana chromsome II BAC F17H15, PID_93643606253401_at-1 </td <td></td> <td>_</td> <td>-1</td>		_	-1
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hypothetical protein similar to pectinesterase25524_at-1nodulin-like protein nodulin gene MIN21 - Medicago truncatula, PID:e1172471;supported by full-length cDNA: Ceres:40485.25512a_at-1arabinogalactan-protein homolog arabinogalactan-protein - Arabidopsis thaliana, PID:g388126; supported by cDNA: gi_10880496_gb_AF19581255052_at-1putative protein various predicted proteins254549_at-1putative protein various predicted proteins254521_at-1adenine phosphoribosyltransferase (EC 2.4.2.7) - like protein adenine phosphoribosyltransferase, Triticum aestivum, T06263; supported by full-lengt254321_at-1putative protein visina se receptor protein kinase receptor protein kinase receptor protein kinase receptor protein kinase, Ipomoea trifida, PID:g836954253856_at-1Expressed protein ; supported by full-length cDNA: Ceres: 12935.253856_at-1putative protein protein solphane on protein solphane on protein solphane, PID:g4337210253716_at-1putative protein hypothetical protein - Arabidopsis thaliana, PID:g433721025376_at-1putative protein hypothetical protein F17H15.20 Arabidopsis thaliana, ATU6321253467_at-1putative protein hypothetical protein F17H15.20 Arabidopsis thaliana, ATU632125344366253407_at-1putative protein hypothetical protein F17H15.20 Arabidopsis thaliana, ATU632125347_at-1-1putative protein hypothetical protein F17H15.20 Arabidopsis thaliana, ATU632125347_at-1-1putative protein hypothetical protein F17H15.20 Arabidopsis thaliana, ATU632125347_at-1-1 <td></td> <td></td> <td>-1</td>			-1
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Expressed protein ; supported by full-length cDNA: Ceres: 39326.253384_at-1putative protein Cyanophora paradoxa cyanelle, predicted protein; supported by full-length cDNA: Ceres: 2912.253197_at-1RING-H2 finger protein RHA3b ; supported by full-length cDNA: Ceres: 31493.253140_at-1ras-related small GTP-binding protein ras-related small GTP-binding protein Rho1Ps, garden pea, Pir2:A47525; supported by full-length cDNA: Ceres: 318_at-1ribosomal - like protein ribosomal protein L12, Liberobacter africanum, U09675; supported by full-length cDNA: Ceres: 41011.253058_at-1putative protein phosphatase-2c (PP2C) - Mesembryanthemum crystallinum, PID:g3608412252992_at-1glycine-rich protein 2 (GRP2) ; supported by cDNA: gi_14326486_gb_AF385696.1_AF385696252957_at-1extensin - like protein prolein-rich protein, Solanum tuberosum, AJ000997; supported by full-length cDNA: Ceres:2315.252971_at-1cinnamyl-alcohol dehydrogenase CAD1 ; supported by full-length cDNA: Ceres:34593.252943_at-1			
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RING-H2 finger prótein RHA3b253140_at-1ras-related small GTP-binding protein ras-related small GTP-binding protein Rho1Ps, garden pea, Pir2:A47525;supported by full-length cDNA: Cere253140_at-1ribosomal - like protein ribosomal protein L12, Liberobacter africanum, U09675;supported by full-length cDNA: Ceres:41011.253058_at-1putative protein phosphatase-2c protein phosphatase-2c (PP2C) - Mesembryanthemum crystallinum, PID;3608412252992_at-1glycine-rich protein 2 (GRP2) ; supported by cDNA: gi_14326486_gb_AF385696.1_AF385696252957_at-1extensin - like protein prolein-rich protein, Solanum tuberosum, AJ000997;supported by full-length cDNA: Ceres:2315.25291_at-1cinnamyl-alcohol dehydrogenase CAD1 ; supported by full-length cDNA: Ceres:34593.252943_at-1			
ras-related small GTP-binding protein ras-related small GTP-binding protein Rho1Ps, garden pea, Pir2:A47525;supported by full-length cDNA: Cer 253118_at ribosomal - like protein ribosomal protein L12, Liberobacter africanum, U09675;supported by full-length cDNA: Ceres:41011. 253058_at -1 putative protein phosphatase-2c protein phosphatase-2c (PP2C) - Mesembryanthemum crystallinum, PID:g3608412 25299_at -1 glycine-rich protein 2 (GRP2) ; supported by cDNA: gi_14326486_gb_AF385696.1_AF385696 extensin - like protein proline-rich protein, Solanum tuberosum, AJ000997;supported by full-length cDNA: Ceres:2315. 252971_at -1 cinnamyl-alcohol dehydrogenase CAD1 ; supported by full-length cDNA: Ceres:34593. 252943_at -1			
ribosomal - like protein ribosomal protein L12, Liberobacter africanum, U09675;supported by full-length cDNA: Ceres:41011. 253058_at -1 putative protein phosphatase-2c protein phosphatase-2c (PP2C) - Mesembryanthemum crystallinum, PID:g3608412 252992_at -1 glycine-rich protein 2 (GRP2) ; supported by cDNA: gi_14326486_gb_AF385696.1_AF385696 252957_at -1 extensin - like protein proline-rich protein, Solanum tuberosum, AJ000997;supported by full-length cDNA: Ceres:2315. 252971_at -1 cinnamyl-alcohol dehydrogenase CAD1 ;supported by full-length cDNA: Ceres:34593. 252943_at -1		_	
putative protein phosphatase-2c protein phosphatase-2c (PP2C) - Mesembryanthemum crystallinum, PID:g3608412252992_at-1glycine-rich protein 2 (GRP2) ; supported by cDNA: gi_14326486_gb_AF385696.1_AF385696252957_at-1extensin - like protein proline-rich protein, Solanum tuberosum, AJ000997;supported by full-length cDNA: Ceres:2315.252971_at-1cinnamyl-alcohol dehydrogenase CAD1 ; supported by full-length cDNA: Ceres:34593.252943_at-1			
glycine-rich protein 2 (GRP2) ; supported by cDNA: gi_14326486_gb_AF385696.1_AF385696252957_at-1extensin - like protein proline-rich protein, Solanum tuberosum, AJ000997;supported by full-length cDNA: Ceres:2315.252971_at-1cinnamyl-alcohol dehydrogenase CAD1 ;supported by full-length cDNA: Ceres:34593.252943_at-1		_	
extensin - like protein proline-rich protein, Solanum tuberosum, AJ000997;supported by full-length cDNA: Ceres:2315. 252971_at -1 cinnamyl-alcohol dehydrogenase CAD1 ;supported by full-length cDNA: Ceres:34593. 252943_at -1		-	
cinnamyl-alcohol dehydrogenase CAD1 ;supported by full-length cDNA: Ceres:34593. 252943_at -1		_	
cytochrome P450 - like protein cytochrome P450, Sinapis alba, AF069494; supported by cDNA: gi_15028134_gb_AY046017.1_ 252827_at -1			
	cytochrome P450 - like protein cytochrome P450, Sinapis alda, AP059494; supported by cDNA: gi_15028134_gb_AY046017.1_	252827_at	-1

histone H2B -like protein histone H2B1, upland cotton, PIR:T09722;supported by full-length cDNA: Ceres:10517.	252560_at	-1
putative protein mitochondrial ATP SYNTHASE 6 KD SUBUNIT - Solanum tuberosum, SWISSPROT:P80497	252524_at	-1
phosphoprotein phosphatase ;supported by full-length cDNA: Ceres:32787.	252471_at	-1
GTP-binding protein Rab11 ; supported by full-length cDNA: Ceres: 35596.	252472_at	-1
signal recognition particle subunit 9 - like signal recognition particle subunit 9, Zea mays, EMBL:Y10117;supported by full-length cDNA: Ceres:146:		-1
putative protein sugar transporter 2, Drosophila melanogaster, EMBL:AF199484	252308_at	-1
putative protein predicted protein, Arabidopsis thaliana	252250_at	-1
anthranilate N-hydroxycinnamoyl/benzoyltransferase - like protein anthranilate N-hydroxycinnamoyl/benzoyltransferase, Dianthus caryophyllus	252199_at	-1
LS1-like protein AT-LS1 product - Arabidopsis thaliana, EMBL:X58827;supported by full-length cDNA: Ceres:107294.	252076_at	-1
inorganic pyrophosphatase -like protein inorganic pyrophosphatase, Solanum tuberosum, PIR:T07399;supported by full-length cDNA: Ceres:40186		-1
putative protein several hypothetical Na(+)/H(+) antiporter	251906_at	-1
histone H4-like protein several histone H4 proteins;supported by full-length cDNA: Ceres:13571.	251924_at	-1
putative protein several hypothetical proteins; supported by cDNA: gi_13878168_gb_AF370347.1_AF370347	251930_at	-1
putative protein GATA transcription factor 3, Arabidopsis thaliana, Y13650; supported by cDNA: gi_15724333_gb_AF412107.1_AF412107	251861_at	-1
ribosomal L23a - like protein various ribosomal L23a proteins;supported by full-length cDNA: Ceres:17531.	251783_at	-1
putative protein ;supported by full-length cDNA: Ceres:12522.	251640_at	-1
putative protein various predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 104796.	251406_at	-1
Expressed protein ; supported by full-length cDNA: Ceres: 42545.	251409_at	-1
tRNA isopentenyl transferase -like protein tRNA isopentenyl transferase, Arabidopsis thaliana, EMBL:AF109376; supported by cDNA: gi_14278981		-1
putative protein	250980_at	-1
putative protein ; supported by cDNA: gi_15724319_gb_AF412100.1_AF412100	250929_at	-1
putative protein	250948_at	-1
putative protein	250881_at	-1
phosphate/phosphoenolpyruvate translocator protein-like	250743_at	-1
WD-repeat protein-like	250584_at	-1
serine-type carboxypeptidase II-like protein carboxypeptidase D - Triticum aestivum, PIR:A29639; supported by cDNA: gi_13877962_gb_AF37024-		-1
S-adenosylmethionine:2-demethylmenaquinone methyltransferase-like protein ; supported by full-length cDNA: Ceres: 13819.	250129_at	-1
synaptobrevin-like protein	249930_at	-1
DegP protease contains similarity to DegP protease precursor GI:2565436 from [Arabidopsis thaliana]	249421_at	-1
hypothetical protein	249355_at	-1
putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:16724.	249375_at	-1
putative protein similar to unknown protein (pir  C71410)	249118_at	-1
serine/threonine protein kinase-like protein	248934_at	-1
phosphate/triose-phosphate translocator precursor (gb AAC83815.1); supported by full-length cDNA: Ceres:36058.	248886_at	-1
peptidyl-prolyl cis-trans isomerase-like protein ;supported by full-length cDNA: Ceres:143222.	248664_at	-1
unknown protein ; supported by cDNA: gi_14326507_gb_AF385707.1_AF385707	248624_at	-1
	248521_s_at	-1
putative protein similar to unknown protein (emb CAA71173.1)	248321_at	-1
putative protein strong similarity to unknown protein (pir  T05748); supported by cDNA: gi_15010657_gb_AY045630.1_	248177_at	-1
glucose-6-phosphate/phosphate translocator; supported by full-length cDNA: Ceres:26107.	248144_at	-1
unknown protein ;supported by full-length cDNA: Ceres:38464.	248145_at	-1
ubiquitin-like protein	248092_at	-1
wax synthase-like protein	248080_at	-1
NOI protein, nitrate-induced	248025_at	-1
60S acidic ribosomal protein P3 ; supported by full-length cDNA: Ceres: 8695.	247900_at	-1
putative protein similar to unknown protein (pir  D64592);supported by full-length cDNA: Ceres:113904.	247881_at	-1
GTP-binding protein - like GTP-binding protein, garden pea, PIR:T06447	247597_at	-1
putative protein	247486_at	-1
putative protein predicted proteins, Arabidopsis thaliana	247394_at	-1
Arac10 ;supported by cDNA: gi_3702963_gb_AF079485.1_AF079485	247405_at	-1
unknown protein	247415_at	-1
putative protein strong similarity to unknown protein (emb[CAB76911.1)	247362_at	-1
glutamate-tRNA ligase ; supported by cDNA: gi_11078545_gb_AF241841.1_AF241841	247319_at	-1
40S ribosomal protein S28 (sp P34789) ;supported by full-length cDNA: Ceres:36501.	247267_at	-1
ZW10-like protein ; supported by cDNA: gi_14334941_gb_AY035144.1_	247261_at	-1
invertase inhibitor homolog (emb[CAA73335.1); supported by full-length cDNA: Ceres:25884.	247246_at	-1
CLE21, putative CLAVATA3/ESR-Related 21 (CLE21)	247254_at	-1

putative protein contains similarity to unknown protein (gb AAF18680.1)	247125_at	-1
SCARECROW gene regulator	247057_at	-1
cyclin D3-like protein ;supported by full-length cDNA: Ceres:36467.	247034_at	-1
ADP-ribosylation factor-like protein ;supported by full-length cDNA: Ceres:35979.	247008_at	-1
putative protein predicted proteins, Arabidopsis thaliana and Oryza sativa	246822_at	-1
60S ribosomal protein L22 - like ribosomal protein L22 (cytosolic), Rattus norvegicus, PIR:S52084; supported by full-length cDNA: Ceres: 19722.	246745_at	-1
putative protein ; supported by cDNA: gi_14532675_gb_AY039962.1_ cytochrome P450 ; supported by cDNA: gi_3164141 dbj_D78606.1_D78606	246749_at	-1 -1
copper amine oxidase, putative similar to copper amine oxidase GI:685197 from [Pisum sativum]	246620_at 246601 at	-1 -1
plant adhesion molecule 1 (PAM1) ;supported by full-length cDNA: Ceres:39585.	246482 at	-1
putative protein with poly glutamic acid stretch hypothetical protein F16B3.13 - Arabidopsis thaliana, EMBL:AC021640; supported by full-length cDI		-1 -1
minor allergen ;supported by full-length cDNA: Ceres:35084.	246201 at	-1
dynein light chain - like protein dynein light chain LC6, Anthocidaris crassispina, EMBL:AB004830	246144 at	-1
putative protein predicted protein At2g2560 - Arabidopsis thaliana, EMBL:AC007070;supported by full-length cDNA: Ceres:6674.	245853 at	-1
light-harvesting complex protein similar to light-harvesting complex protein GI:22752 from Pinus Sylvestris];supported by full-length cDNA: Ceres:41	-	-1
histone H2A, putative similar to histone H2A GI:9758956 from [Arabidopsis thaliana]; supported by CDNA: gi 13877850_gb_AF370188.1_AF37018		-1
extension like protein	245479 at	-1
Li3 protein ;supported by full-length cDNA: Ceres:29150.	245354 at	-1
hypothetical protein ; supported by cDNA: gi 15292862 gb AY050865.1	245290 at	-1
	245167 s at	-1
PSII   protein	245023 at	-1
PSI   protein	245017 at	-1
ribosomal protein L20	244970 at	-1
PSII 47KDa protein	244972 at	-1
Expressed protein ; supported by full-length cDNA: Ceres: 970.	249721 at	-1
putative carboxypeptidase; supported by cDNA: gi 15724217 gb AF412049.1 AF412049	264071 at	-1
protein kinase, putative similar to many predicted protein kinases	261339_at	-1
unknown protein predicted by genscan; similar to GP 9826 X07453; supported by full-length cDNA: Ceres: 12267.	267637_at	-0.9
Expressed protein ; supported by cDNA: gi_15724149_gb_AF411777.1_AF411777	267578_at	-0.9
hypothetical protein predicted by genfinder	267586_at	-0.9
hypothetical protein predicted by genscan	267057_at	-0.9
unknown protein ;supported by cDNA: gi_16323164_gb_AY057686.1_	267084_at	-0.9
hypothetical protein predicted by genscan	267019_at	-0.9
60S ribosomal protein L35 ;supported by full-length cDNA: Ceres:11583.	266980_at	-0.9
phytocyanin identical to GB:U90428; supported by full-length cDNA: Ceres: 19760.	266884_at	-0.9
unknown protein ;supported by cDNA: gi_14423465_gb_AF386970.1_AF386970	266887_at	-0.9
Expressed protein ; supported by full-length cDNA: Ceres: 124634.	266808_at	-0.9
unknown protein	266799_at	-0.9
predicted by genefinder and genscan	266742_at	-0.9
putative chloroplast RNA binding protein precursor ; supported by cDNA: gi_14596022_gb_AY042799.1_	266642_at	-0.9
E2, ubiquitin-conjugating enzyme 6 (UBC6) identical to gi 431267, SP:P42750, PIR:S52661; contains a ubiquitin-conjugating enzymes active site (I	266604_at	-0.9
unknown protein ;supported by cDNA: gi_15081683_gb_AY048234.1_	266521_at	-0.9
unknown protein	266512_at	-0.9
unknown protein ; supported by cDNA: gi_15912210_gb_AY056383.1_	266479_at	-0.9
unknown protein ; supported by cDNA: gi_16649150_gb_AY059945.1_	266481_at	-0.9
60S acidic ribosomal protein P2 ;supported by full-length cDNA: Ceres:36076.	266256_at	-0.9
unknown protein ;supported by full-length cDNA: Ceres:114031.	266167_at	-0.9 -0.9
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:9149.	265823_at 265798_at	-0.9 -0.9
unknown protein ; supported by cDNA: gi_14596214_gb_AY042895.1_	265742 at	-0.9 -0.9
putative ribose 5-phosphate isomerase ; supported by cDNA: gi_15809809_gb_AY054172.1_ unknown protein ;supported by full-length cDNA: Ceres:27566.	265386 at	-0.9 -0.9
auxin-regulated protein (IAA8) ;supported by full-length cDNA: Ceres:37274.	265366_at	-0.9 -0.9
unknown protein ; supported by full-length cDNA: Ceres: 39285.	265219_at	-0.9 -0.9
60S ribosomal protein L24 ;supported by full-length cDNA: Ceres:14564.	265219_at	-0.9 -0.9
putative 3-oxoacyl [acv]-carrier protein] reductase similar to proteins from several bacterial species, similar to ESTs emb[Z37189, db]H74525, db]37	_	-0.9
unknown protein contains Pfam profile:PF01762 Galactosyltransferase	264978 at	-0.9
putative calcium-dependent protein kinase (U90439) similar to ESTs gb T46119, gb H76837, and gb H36948; supported by cDNA: gi_6318612_gb_	-	-0.9
	_000_ut	0.0

putative cytochrome C strong similarity to GB:P00050 and GB:CAB39628; supported by full-length cDNA: Ceres: 31770.	264727_at	-0.9
putative 2,3-bisphosphoglycerate-independent phosphoglycerate mutase Strong similarity to R. communis phosphoglycerate mutase (gb/X70652).	264668_at	-0.9
putative RAS-related protein, RAB11C Strong similarity to A. thaliana ara-2 (gb ATHARA2). ESTs gb ATTS2483,gb ATTS2484,gb AA042159 come	_	-0.9
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:26961.	263999_at	-0.9
En/Spm-like transposon protein related to En/Spm transposon family of maize;supported by full-length cDNA: Ceres:41214. hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:2576.	263979_at 263929_at	-0.9 -0.9
Expressed protein ; supported by full-length cDNA: Ceres: 267559.	263772 at	-0.9
putative 40S ribosomal protein S15 Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb/R29788,gb/ATTS0365 come from this gene; sur	_	-0.9
putative too huboshiai protein o to strong similarity to oryza too huboshiai protein o to. Loris guirtzarioo,guirti roosoo come nom uns gene, suj unknown protein	263438 at	-0.9
GOS ribosomal protein L14 ;supported by full-length cDNA: Ceres:15198.	263372 at	-0.9
putative snRNP splicing factor ;supported by full-length cDNA: Ceres:97480.	263332 at	-0.9
unknown protein ; supported by cDNA: gi 15982806 gb AY057510.1	263298 at	-0.9
putative vacuolar proton-ATPase 16 kDa proteolipid identical to GB:L44581	263267 at	-0.9
unknown protein	263247 at	-0.9
unknown protein ;supported by full-length cDNA: Ceres:39571.	263180_at	-0.9
spore germination protein c2 similar to 2-hexaprenyl-1,4-naphthoquinone methyltransferase GB:BAA25267 GI:2982680 from [Micrococcus luteus]	263044_at	-0.9
alcohol dehydrogenase, putative similar to alcohol dehydrogenase GI:551256 from [Nicotiana tabacum]	262870_at	-0.9
putative lipase similar to gb X02844 lipase precursor from Staphylococcus hyicus. ESTs gb Al239406 and gb T76725 come from this gene	262786_at	-0.9
phosphoribosyl diphosphate synthase identical to phosphoribosyl diphosphate synthase GI:4902470 from (Arabidopsis thaliana); supported by cDN	_	-0.9
unknown protein location of ESTs 144D22XP 3 , gb AA404877 and 144D22T7, gb T75757;supported by full-length cDNA: Ceres:5665.	262612_at	-0.9
unknown protein ; supported by cDNA: gi_15215593_gb_AY050325.1_	262634_at	-0.9
unknown protein Location of est 136A23T7 (gb T45563); supported by full-length cDNA: Ceres: 28177.	262539_at	-0.9
hypothetical protein similar to hypothetical protein GB:AAF24576 GI:6692111 from [Arabidopsis thaliana]	262329_at	-0.9
unknown protein similar to hypothetical protein GB:AAF24562 GI:6692097 from [Arabidopsis thaliana]; supported by cDNA: gi_15010675_gb_4Y04		-0.9
serine threonine kinase, putative similar to GB:CAA73067 from (Sorghum bicolor) (Plant Mol. Biol. 36 (4), 529-539 (1998)); supported by cDNA: gi_ AP2 domain containing protein, putative similar to AP2 domain containing protein GI:2281633 from [Arabidopsis thaliana]; supported by cDNA: gi_	262244_at 262135 at	-0.9 -0.9
somatic embryogenesis receptor-like kinase, putative similar to somatic embryogenesis receptor-like kinase GI:2224910 from [Daucus carota]:supp	_	-0.9
plastid ribosomal protein S6, putative similar to plastid ribosomal protein S6 precursor GB:AAF64311 GI:7582401 from [Spinacia oleracea]; support	_	-0.9
product hostophic product of participation of the second product o	261873 at	-0.9
unknown protein ; supported by full-length cDNA: Ceres: 32430.	261791 at	-0.9
cinnamoyl CoA reductase, putative similar to cinnamoyl CoA reductase GI:2058310 from [Eucalyptus gunnii]; supported by full-length cDNA: Ceres	_	-0.9
calreticulin, putative similar to calreticulin GB:AAC49697 GI:2052383 from [Arabidopsis thaliana]; supported by cDNA: gi 2052382 gb U66345.1 /		-0.9
ribonucleoprotein, putative similar to 33 KDA RIBONUCLEOPROTEIN GB:P19684 from [Nicotiana sylvestris]; supported by full-length cDNA: Ceres		-0.9
histone H4 identical to GB:M36659 from [Zea mays] (Plant Physiol. Biochem. 25, 235-247 (1987)); supported by full-length cDNA: Ceres: 27686.	261408_s_at	-0.9
unknown protein ;supported by full-length cDNA: Ceres:151637.	261407_at	-0.9
Expressed protein ; supported by full-length cDNA: Ceres: 21406.	261254_at	-0.9
unknown protein ;supported by full-length cDNA: Ceres:207684.	261201_at	-0.9
vacuolar ATP synthase subunit C, putative similar to GB:AAF20146 from [Arabidopsis thaliana] (Genes Dev. (1999) In press); supported by cDNA:	261210_at	-0.9
tubulin alpha-2/alpha-4 chain identical to SP:P29510 from [Arabidopsis thaliana]; supported by cDNA: gi_16648843_gb_AY058199.1_	261129_at	-0.9
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:19718.	260871_at	-0.9
unknown protein similar to hypothetical protein GB:CAB10239 GI:2244816 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 4905.	_	-0.9
fructose 1,6-bisphosphatase, putative similar to cytosolic fructose-1,6-bisphosphatase GB:AAD28755 GI:4741918 from [Musa acuminata]	260837_at	-0.9
unknown protein serine carboxypeptidase precursor, putative similar to GB:AAD42963 from [Matricaria chamomilla]	260818_at 260739_at	-0.9 -0.9
polyphosphoinositide binding protein, putative similar to GB:AAB42905 from [Glycine max]; supported by cDNA: gi_16930446_gb_AF419577.1_AF	260604 at	-0.9
polyprosphonostice binding protect particle similar to binAs ceres:42038.	260548 at	-0.9
putative trypsin inhibitor ; supported by CDNA: gi 15292710 gb AV050789.1	260551 at	-0.9
unknown protein jsuported by full-length cDNA: Ceres:17921.	260441 at	-0.9
hypothetical protein similar to GB:AAB61488 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:34864.	260411 at	-0.9
putative aminolevulinate dehydratase similar to aminolevulinate dehydratase GB:1097877 [Lycopersicon esculentum]; supported by cDNA: gi 1193	_	-0.9
unknown protein contains two Kelch motifs; supported by full-length cDNA: Ceres: 32885.	260287 at	-0.9
nodulin-like protein similar to nodule-specific protein NIj70 GB:AAC39500 from (Lotus japonicus); supported by cDNA: gi_14334879_gb_AY035113.	260288_at	-0.9
putative histone H2A similar to histone H2A GB:CAA73155 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 10668.	260154_at	-0.9
unknown protein ;supported by full-length cDNA: Ceres:111031.	260003_at	-0.9
nodulin-like protein similar to nodulin GB:P16313 [Glycine max]	259871_at	-0.9
blue copper protein, putative similar to GI:562778 from [Pisum sativum] (Thesis (1994) BIOLOGICAL SCIENCES, DURHAM UNIVERSITY); suppo	259801_at	-0.9
unknown protein	259546_at	-0.9

hypothetical protein ; supported by cDNA: gi_14532585_gb_AY039917.1_	259561_at	-0.9
putative mitochondrial processing peptidase alpha subunit similar to mitochondrial processing peptidase GB:X66284 (Solanum tuberosum); suppo	_	-0.9
	259237_at	-0.9
unknown protein	259250_at	-0.9
putative thylakoid lumen rotamase similar to thylakoid lumen rotamase GB:CAA72792 [Spinacia oleracea]; supported by full-length cDNA: Ceres:38.		-0.9
unknown protein ;supported by full-length cDNA: Ceres:22225.	259104_at	-0.9
unknown protein similar to nodule-specific protein NIj70 GB:AAC39500 (Lotus japonicus)	259005_at	-0.9
unknown protein ;supported by full-length cDNA: Ceres:97.	258875_at	-0.9
GTP cyclohydrolase I similar to GTP cyclohydrolase I GB:P22288 [Rattus norvegicus]; contains Pfam profile: PF01227 GTP cyclohydrolase I	258834_at	-0.9
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:100676.	258787_at	-0.9
putative coatomer zeta subunit (zeta-coat protein) similar to coatomer zeta subunit (zeta-coat protein) GB:P35604 (Bos taurus)	258710_s_at	-0.9
unknown protein	258662_at	-0.9
thioredoxin f1 identical to thioredoxin f1 GB:AF144385 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:11767.	258607_at	-0.9
putative phosphatidate phosphohydrolase similar to phosphatidate phosphohydrolase GB:AAB50246 from [Rattus norvegicus]; supported by full-len	258481_at	-0.9
unknown protein ;supported by full-length cDNA: Ceres:15303.	258394_at	-0.9
putative transport protein similar to transport protein GB:AAB00858 from [Arabidopsis thaliana]	258332_at	-0.9
photosystem I subunit VI precursor identical to GB:CAB52749 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:9633.	258285_at	-0.9
beta-glucosidase, putative similar to beta-glucosidase BGQ60 precursor GB:A57512 [Hordeum vulgare]; supported by full-length cDNA: Ceres:1198	258151_at	-0.9
expansin At-EXP5 identical to expansin At-EXP5 GB:AAB38071 from [Arabidopsis thaliana]; supported by cDNA: gi_1041703_gb_U30478.1_ATU3	258003_at	-0.9
unknown protein	257983_at	-0.9
hypothetical protein similar to hypothetical protein GB:AAD50054 from [Arabidopsis thaliana]	257964_at	-0.9
actin 2 identical to GB:AAB37098 from [Arabidopsis thaliana], Plant J. 10 (1), 107-121 (1996);supported by full-length cDNA: Ceres:3819.	257749_at	-0.9
histone H3, putative similar to histone H3 GB:P05203 [Petroselinum crispum]; supported by cDNA: gi_14335141_gb_AY037250.1_	257714_at	-0.9
60S ribosomal protein, putative similar to 60S RIBOSOMAL PROTEIN L13A GB:P35427 from [Rattus norvegicus]; supported by full-length cDNA: C	257599_at	-0.9
salicylic acid carboxyl methyltransferase, putative similar to GB:AAF00108 from [Clarkia breweri]	257254_at	-0.9
zinc finger protein, putative contains Pfam profile: PF01760 CONSTANS family zinc finger; supported by full-length cDNA: Ceres:258241.	257262 at	-0.9
ras-related GTP-binding protein contains Pfam profile: PF00071 ras family	257235_at	-0.9
unknown protein ;supported by full-length cDNA: Ceres:20771.; supported by cDNA: gi 10880500 gb AF195893.1 AF195893	256964 at	-0.9
Expressed protein ; supported by full-length cDNA: Ceres: 38257.	256979_at	-0.9
hypothetical protein predicted by genemark.hmm, contains Pfam profile:PF00076 rrm:RNA recognition motif	256770 at	-0.9
galactosidase, putative similar to BETA-GALACTOSIDASE PRECURSOR (LACTASE) GB:P48980 from [Lycopersicon esculentum]	256772 at	-0.9
hypothetical protein predicted by genemark.hmm	256741 at	-0.9
unknown protein	256698 at	-0.9
omega-3 fatty acid desaturase, chloroplast precursor identical to omega-3 fatty acid desaturase, chloroplast precursor SP:P46310 (Arabidopsis tha	256417 s at	-0.9
Expressed protein ; supported by full-length cDNA: Ceres: 11938.	256092 at	-0.9
unknown protein ;supported by full-length cDNA: Ceres:28780.	256062 at	-0.9
transcription factor, putative similar to transcription factor BTF3 homolog GI:2982299 from [Picea mariana]; supported by full-length cDNA: Ceres:11	255902 at	-0.9
lemir (miraculin), putative similar to lemir (miraculin) GI:2654440 from [Lycopersicon esculentum]; supported by cDNA; gi 12083239 gb AF332416		-0.9
unknown protein ;supported by full-length cDNA: Ceres:12461.	255854 at	-0.9
sulfate adenylyltransferase identical to sulfate adenylyltransferase GI:487404 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:213;	255785 at	-0.9
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:232413.	255775 at	-0.9
myb factor, putative similar to myb factor GI:1946266 from [Oryza sativa]; supported by cDNA: gi 3941465 gb AF062887.1 AF062887	255753 at	-0.9
Expressed protein ; supported by full-length cDNA: Ceres: 28726.	255554 at	-0.9
	255504 at	-0.9
putative sugar transporter	255294 at	-0.9
coded for by A. thaliana cDNA T44741	255255 at	-0.9
Expressed protein ; supported by full-length cDNA: Ceres: 1734.	255104 at	-0.9
receptor protein kinase-like protein receptor protein kinase-like protein - Arabidopsis thaliana, PIR2:T05898	255116 at	-0.9
putative pollen-specific protein pollen-specific protein precursor - common tobacco, PIR2:S22495	254815 at	-0.9
blue copper-binding protein, 15K (lamin) supported by full-length cDNA: Ceres:41510.	254789 at	-0.9
protein ch-42 precursor, chloroplast :supported by full-length CDNA: Ceres:7501.	254623 at	-0.9
putative rotein several hypothetical proteins - Arabidopsis thatiana; supported by cDNA: gi_15320409_dbj_AB039927.1_AB039927	254563 at	-0.9
photosystem II oxygen-evolving complex protein 3 - like photosystem II oxygen-evolving complex protein 3, Spinacia oleracea, PIR2:S00008;suppc		-0.9
predicted protein	254303 at	-0.9
putative protein pectinesterase - Citrus sinensis, PID:q2098705	254110 at	-0.9
putative protein other hypothetical proteins Arabidopsis thaliana	254029 at	-0.9
putative acidic ribosomal protein acidic ribosomal protein P3a - maize, PIR2:T02037	254030 at	-0.9
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mitogen activated protein kinase kinase (nMAPKK) ;supported by full-length cDNA: Ceres:31259.	253993_at	-0.9
putative protein stem-specific protein - Nicotiana tabacum,PID:g20037;supported by full-length cDNA: Ceres:35207.	253874_at	-0.9
hypothetical protein	253818_at	-0.9
H+-transporting ATPase type 2, plasma membrane ;supported by cDNA: gi_14334803_gb_AY035075.1_	253609_at	-0.9
Expressed protein ; supported by cDNA: gi_15028200_gb_AY045923.1_	253551_at	-0.9
putative protein ;supported by full-length cDNA: Ceres:8742.	253272_at	-0.9
Expressed protein ; supported by full-length cDNA: Ceres: 279.	253234_at	-0.9
cysteine protease XCP1 identical to papain-type cysteine endopeptidase XCP1 GI:6708181 from [Arabidopsis thaliana]	253191_at	-0.9
cytochrome P450 - like protein cytochrome P450, Glycyrrhiza echinata, AB001379;supported by full-length cDNA: Ceres:253698.	253046_at	-0.9
	253059_s_at	-0.9
putative amino acid transport protein amino acid transport protein - Arabidopsis thaliana, PID:g2576363;supported by full-length cDNA: Ceres:3843		-0.9
probable H+-transporting ATPase H+-transporting ATPase (EC 3.6.1.35) 57K chain - Arabidopsis thaliana, PIR2:A31886; supported by cDNA: gi_1	252998_at	-0.9
putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:35002.	252879_at	-0.9
Expressed protein ; supported by cDNA: gi_15292972_gb_AY050920.1_	252763_at	-0.9
leucine-rich repeat protein LRP -like leucine-rich repeat protein LRP, tomato, PIR:T07079	252703_at	-0.9
calmodulin 7 ; supported by full-length cDNA: Ceres: 7008.	252713_at	-0.9
putative protein predicted proteins, Arabidopsis thaliana	252533_at	-0.9
putative protein ;supported by full-length cDNA: Ceres:25829.	252463_at	-0.9
putative protein putative hydrolyse - Arabidopsis thaliana, PID:g4191785;supported by full-length cDNA: Ceres:262295.	252433_at	-0.9
Expressed protein ; supported by cDNA: gi_14326548_gb_AF385728.1_AF385728	252390_at	-0.9
Expressed protein ; supported by full-length cDNA: Ceres: 3817.	252352_at	-0.9
ADP-RIBOSYLATION FACTOR -like protein ARF3 ADP-RIBOSYLATION FACTOR, Arabidopsis thaliana, SWISSPROT:ARF3_ARATH	252225_at	-0.9
putative protein various predicted proteins	252178_at	-0.9
putative protein polyphosphoinositide binding protein Ssh2 - Glycine max, PIR:T05953; supported by cDNA: gi_16930482_gb_AF419595.1_AF419	252080_at	-0.9
transcription factor NF-Y, CCAAT-binding - like protein transcription factor NF-Y, CCAAT-binding, Zea mays, PIR:S22820	251991_at	-0.9
putative protein In2-1 protein, Zea mays, P49248	251820_at	-0.9
putative protein protein of unknown function - Corydalis sempervirens, EMBL:X63595; supported by cDNA: gi_7684291_dbj_D84226.1_D84226	251739_at	-0.9
putative protein hypothetical protein At2g41330 - Arabidopsis thaliana, EMBL:AC005662; supported by cDNA: gi_15451041_gb_AY054601.1_	251663_at	-0.9
putative protein hypothetical protein SPCC320.08 - Schizosaccharomyces pombe, PIR:T41303	251516 s at	-0.9
60S RIBOSOMAL PROTEIN L38-like protein 60S RIBOSOMAL PROTEIN L38 - Lycopersicon esculentum, EMBL:X69979; supported by cDNA: gi	251486 at	-0.9
homeobox-leucine zipper protein HAT3; supported by cDNA: gi 527632 gb U09338.1 ATU09338	251374 at	-0.9
putative protein putative protein At2g46160 - EMBL:AC005397; supported by cDNA: gi 16226238 gb AF428280.1 AF428280	251330 at	-0.9
putative protein several hypothetical proteins;supported by full-length cDNA: Ceres:29280.	251285 at	-0.9
putative protein	251058 at	-0.9
Expressed protein ; supported by full-length cDNA: Ceres: 22246.	250922 at	-0.9
putative protein contains similarity to unknown protein (gb/AAF19573.1);supported by full-length cDNA: Ceres:118003.	250810 at	-0.9
short chain alcohol dehydrogenase-like ;supported by full-length cDNA: Ceres:111427.	250763 at	-0.9
putative protein similar to unknown protein (emb CAB88360.1);supported by full-length cDNA: Ceres:29476.	250764 at	-0.9
	250682 x at	-0.9
unknown protein ; supported by full-length CDNA: Ceres: 17482.	250668 at	-0.9
putative protein PTD008, Homo sapiens, EMBL:AF078861;supported by full-length cDNA: Ceres:226.	250553 at	-0.9
putative protein synaptobrevin-like protein SybI1, Mus musculus, EMBL:MMU133536	250412 at	-0.9
putative protein 23 kDa polypeptide of water-oxidizing complex of photosystem II, Nicotiana tabacum, EMBL:NT23WOP2B	250371 at	-0.9
putative protein SF21 protein, Helianthus annuus, EMBL: AF189148; supported by cDNA: gi 13605683 gb AF361823.1 AF361823	250337 at	-0.9
NADP dependent malic enzyme - like protein NADP dependent malic enzyme, P.vulgaris, EMBL:PVME1G, supported by CDNA: gi 16226465 gb		-0.9
transporter-like protein	250248 at	-0.9
plastid-specific ribosomal protein 6 precursor (Psrp-6) - like plastid-specific ribosomal protein 6 precursor (Psrp-6), Spinacia oleracea, EMBL:AF24{		-0.9
glutamate dehydrogenase (EC 1.4.1) 1 (pir  S71217) ; supported by cDNA: gi 15146203 gb AY049243.1	250032 at	-0.9
NADH:ubiguinone oxidoreductase - like protein NADH:ubiguinone oxidoreductase PGIV subunit, Homo sapiens, EMBL:AF044953; supported by fu	_	-0.9
ATP-dependent Clp protease proteolytic subunit (ClpP2), putative similar to SP:Q9X6W8 ATP-dependent Clp protease proteolytic subunit (EC 3.4.	_	-0.9
40S ribosomal protein S11 supported by full-length cDNA: Ceres:33187.	249795 at	-0.9
unknown protein	249736 at	-0.9
Tig1 protein (emb CAB45372.1)	249739 at	-0.9
zinc finger - like protein predicted protein, Drosophila melanogaster, EMBL:AE003589	249370 at	-0.9
putative protein strong similarity to unknown protein (gb/AAF94433.1)	249220 at	-0.9
putative protein similar to unknown protein (pir/[T05076])supported by full-length cDNA: Ceres:42747.	248870 at	-0.9
60S acidic ribosomal protein P1-like protein supported by full-length cDNA: Ceres:14401.	248768_at	-0.9
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respiratory burst oxidase protein ; supported by cDNA: gi 3242788 gb AF055357.1 AF055357	248719 at	-0.9
small zinc finger-like protein ; supported by full-length cDNA: Ceres:33833.	248473 at	-0.9
unknown protein	248387 at	-0.9
membrane associated protein ; supported by cDNA: gi 1800146 gb U83655.1 ATU83655	248195 at	-0.9
unknown protein ;supported by full-length cDNA: gr_1000140_gb_003033.1_A1003033	248195_at 248172 at	-0.9
unknown protein , supported by ruin-length CDNA. Ceres. 19914. unknown protein	248079 at	-0.9
60S ribosomal protein L31 ;supported by full-length cDNA: Ceres:14992.	247978 at	-0.9 -0.9
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putative protein similar to unknown protein (pir  T04270);supported by full-length cDNA: Ceres:110454.	247980_at	-0.9
porin-like protein ;supported by full-length cDNA: Ceres:23726.	247923_at	-0.9 -0.9
endoxyloglucan transferase (gb AAD45127.1); supported by cDNA: gi_1244751_gb_U43485.1_ATU43485	247866_at	-0.9 -0.9
putative protein protein tyrosine phosphatase-like protein, PTPLB, Mus musculus, EMBL:AF169286	247689_at	
ras-GTPase-activating protein SH3-domain binding protein - like G3BP ras-GTPase-activating protein SH3-domain binding protein, Mus musculus,		-0.9
ethylene responsive element binding factor - like ethylene responsive element binding factor 5, Arabidopsis thaliana, SWISSPROT:ERF5_ARATH;	_	-0.9
peptide transporter	247440_at	-0.9
homeobox-leucine zipper protein ATHB-5 (HD-zip protein ATHB-5) (splP46667) ; supported by cDNA: gi_13358240_gb_AF325054.2_AF325054	247191_at	-0.9
auxin-induced protein IAA9 (pir  T05902) ;supported by full-length cDNA: Ceres:31563.	247148_at	-0.9
putative protein similar to unknown protein (gb)AAF64534.1);supported by full-length cDNA: Ceres:4831.	247037_at	-0.9
putative protein similar to unknown protein (gb/AAC18972.1); supported by cDNA: gi_15293188_gb_AY051028.1_	246998_at	-0.9
porin-like protein ;supported by full-length cDNA: Ceres:12964.	247007_at	-0.9
putative protein apoptosis-related protein PNAS-4, Homo sapiens, EMBL:AF229834;supported by full-length cDNA: Ceres:263500.	246931_at	-0.9
putative protein predicted protein, Arabidopsis thaliana	246885_at	-0.9
putative cytidine deaminase - like putative cytidine deaminase, Cicer arietinum, EMBL:AJ006764;supported by full-length cDNA: Ceres:37242.	246702_at	-0.9
putative protein EXOSTOSIN-1 (PUTATIVE TUMOR SUPPRESSOR PROTEIN EXT1) - Homo sapiens, EMBL:S79639	246682_at	-0.9
glycine/proline-rich protein glycine/proline-rich protein GPRP - Arabidopsis thaliana, EMBL:X84315	246440_at	-0.9
hypothetical protein ;supported by full-length cDNA: Ceres:22757.	246443_at	-0.9
integral membrane protein, putative similar to integral membrane protein GI:3288599 from [Rattus norvegicus]; supported by full-length cDNA: Cere	_	-0.9
ribosomal protein L36-like ribosomal protein L36 - Synechocystis sp., PIR:S77481; supported by full-length cDNA: Ceres:28109.	246073_at	-0.9
phospholipase - like protein various predicted phospholipase proteins;supported by full-length cDNA: Ceres:253499.	246041_at	-0.9
AKIN beta1; supported by full-length cDNA: Ceres: 41668.	246028_at	-0.9
rec - like protein	245695_at	-0.9
ribonucleoprotein like protein	245605_at	-0.9
CCAAT-binding transcription factor subunit A(CBF-A)	245592_at	-0.9
disease resistance RPP5 like protein (fragment)	245460_at	-0.9
hypothetical protein ;supported by full-length cDNA: Ceres:16090.	245394_at	-0.9
hypothetical protein ; supported by full-length cDNA: Ceres: 12451.	245368_at	-0.9
Expressed protein ; supported by full-length cDNA: Ceres: 7101.	245337_at	-0.9
putative mitochondrial carrier protein similar to SP:P40556:YIA6_YEAST and SP:P39953:YEA6_YEAST;supported by full-length cDNA: Ceres:1203	_	-0.9
ATPase III subunit	245026_at	-0.9
auxin induced protein, putative similar to AUXIN-INDUCED PROTEIN X10A GB:P33080 from [Glycine max]	257460_at	-0.9
amylogenin; reversibly glycosylatable polypeptide ;supported by full-length cDNA: Ceres:7365.	250130_at	-0.9
photoreceptor-interacting protein-like ; supported by cDNA: gi_15146317_gb_AY049300.1_	247048_at	-0.9
putative glucanse	267595_at	-0.8
unknown protein	267517_at	-0.8
unknown protein	267348_at	-0.8
hypothetical protein predicted by genscan and genefinder; supported by full-length cDNA: Ceres:20125.	267294_at	-0.8
putative serine carboxypeptidase I ; supported by cDNA: gi_14334757_gb_AY035052.1_	267262_at	-0.8
	267233_s_at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:6950.	267238_at	-0.8
60S ribosomal protein L7 ;supported by full-length cDNA: Ceres:36813.	267213_at	-0.8
	267115_s_at	-0.8
hypothetical protein predicted by genefinder	266899_at	-0.8
unknown protein predicted by genscan and genefinder; supported by cDNA: gi_15983421_gb_AF424585.1_AF424585	266703_at	-0.8
unknown protein ; supported by cDNA: gi_15450758_gb_AY053421.1_	266553_at	-0.8
glycine decarboxylase complex H-protein ; supported by cDNA: gi_15810183_gb_AY056106.1_	266517_at	-0.8
unknown protein	266473_at	-0.8
calmodulin-like protein identical to GB:X68054;supported by full-length cDNA: Ceres:11537.	266371_at	-0.8
tubulin beta-7 chain identical to GB:M84704;supported by full-length cDNA: Ceres:17240.	266295_at	-0.8

putative glutathione S-transferase ;supported by full-length cDNA: Ceres:24361.	266296_at	-0.8
60S ribosomal protein L10A;supported by cDNA: gi_13430467_gb_AF360146.1_AF360146	266210_at	-0.8
putative SCARECROW gene regulator	266131_at	-0.8
putative transport protein SEC61 beta-subunit ; supported by cDNA: gi_13878102_gb_AF370314.1_AF370314	266105_at	-0.8
putative RING zinc finger protein ; supported by full-length cDNA: Ceres: 92525.	266016_at	-0.8
putative adenylate kinase ;supported by full-length cDNA: Ceres:15831.	265958_at	-0.8
putative histone H2B ;supported by full-length cDNA: Ceres:31973.	265960_at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:38690.	265771_at	-0.8
hypothetical protein predicted by genefinder	265776_at	-0.8
unknown protein ; supported by full-length cDNA: Ceres: 14111.	265281_at	-0.8
unknown protein	265203_at	-0.8
1-aminocyclopropane-1-carboxylate oxidase Identical to 1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase) gb[X66719 (EAT1). ESTs gb] <sup>-</sup>	265194_at	-0.8
unknown protein	265148_at	-0.8
hypothetical protein contains similarity to 2-ketocyclohexanecarboxyl-CoA hydrolase GI:3243084 from [Rhodopseudomonas palustris]	264920_at	-0.8
oligopeptide transporter, putative similar to oligopeptide transporter 1-1 GI:510238 from [Arabidopsis thaliana]	264736_at	-0.8
putative pectate lyase A11 similar to GB:CAB36835;supported by full-length cDNA: Ceres:37952.	264611_at	-0.8
unknown protein	264616_at	-0.8
putative prolyl 4-hydroxylase, alpha subunit ;supported by full-length cDNA: Ceres:36054.	264592_at	-0.8
unknown protein similar to hypothetical protein GI:4079632 from [Arabidopsis thaliana]	264424_at	-0.8
polygalacturonase isoenzyme 1 beta subunit, putative similar to polygalacturonase isoenzyme 1 beta subunit GI:1762585 from [Lycopersicon escul	264277_at	-0.8
putative signal sequence receptor, alpha subunit (SSR-alpha) Same as GP: 1174448;supported by full-length cDNA: Ceres:27787.	264020_at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:15743.	263985_at	-0.8
unknown protein	263942_at	-0.8
unknown protein	263914_at	-0.8
putative cyclic nucleotide-regulated ion channel protein	263776_s_at	-0.8
putative tyrosine aminotransferase ; supported by cDNA: gi_15293106_gb_AY050987.1_	263714_at	-0.8
putative protein kinase C inhibitor (Zinc-binding protein) Similar to gb/Z29643 protein kinase C inhibitor (PKCI) from Zea mays and a member of HIT	263701_at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:14886.	263710_at	-0.8
putative RNA-binding protein Identical to gb/Y10557 g5bf gene from Arabidopsis thaliana. ESTs gb/R30578, gb/R90475, gb/T22384, gb/T22425, gt	263676_at	-0.8
ankyrin-like protein EST gb/ATTS0956 comes from this gene;supported by full-length cDNA: Ceres:108617.	263662_at	-0.8
putative receptor-like protein kinase ; supported by cDNA: gi_16648754_gb_AY058153.1_	263478_at	-0.8
putative beta-hydroxyacyl-ACP dehydratase ; supported by full-length cDNA: Ceres: 30185.	263432_at	-0.8
unknown protein ; supported by full-length cDNA: Ceres: 11283.	263399 at	-0.8
putative photosystem I reaction center subunit II precursor Strong similarity to gb/X14017 from Spinacia oleracea. ESTs gb/R30423, gb/T42998, gb	263114 at	-0.8
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:5677.	263133_at	-0.8
putative obtusifoliol 14-alpha demethylase strong similarity to gb/U74319 obtusifoliol 14-alpha demethylase (CYP51) from Sorghum bicolor and is a	262820 at	-0.8
thioredoxin, putative similar to thioredoxin GI:142153 from [Synechococcus PCC6301]	262721 at	-0.8
calmodulin, putative similar to calmodulin-6 SP:Q03509 [Arabidopsis thaliana (Mouse-ear cress)]	262639 at	-0.8
unknown protein Strong similarity to gb/AF096285 serine-threonine kinase receptor-associated protein from Mus musculus and contains 5 PF/0040	262597 at	-0.8
hypothetical protein predicted by genscan+	262490 at	-0.8
putative 20S proteasome beta subunit PBC2 almost identical to GB:AAC32069 from [Arabidopsis thaliana], EST gb[T76747 comes from this gene;	262497 at	-0.8
thioredoxin, putative similar to thioredoxin x GB:AAF15952 GI:6539616 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:22429.	262418 at	-0.8
unknown protein ; supported by cDNA: gi 12642919 gb AF339720.1 AF339720	262402 at	-0.8
protein phosphatase type 2C, putative similar to GB:AAD17805 from (Lotus japonicus) (Proc. Natl. Acad. Sci. U.S.A. 96 (4), 1738-1743 (1999))	262408 at	-0.8
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:24864.	262170 at	-0.8
putative GDP-mannose pyrophosphorylase similar to GDP-mannose pyrophosphorylase A GB:AAD38517 (Homo sapiens); supported by cDNA: gi	262174 at	-0.8
GTP-binding protein, putative similar to GTP-binding protein NGB GB:AAD09830 GI:4191616 from [Homo sapiens]	261882 at	-0.8
transcription factor, putative similar to WRKY transcription factor GB:BAA87058 GI:6472585 from [Nicotiana tabacum];supported by full-length cDN	261892 at	-0.8
hypothetical protein contains similarity to AP2 DNA-binding domain protein GI:1732030 from [Zea mays]; supported by cDNA: gi 15028184 gb AY	261794 at	-0.8
unknown protein ; supported by cDNA: gi 15450426 gb AY052314.1	261721 at	-0.8
acyl-(acyl carrier protein) thioesterase, putative almost identical to acyl-(acyl carrier protein) thioesterase GB:CAA85387 GI:634003 from [Arabidop:	261722 at	-0.8
unknown protein similar to hypothetical protein GB:AAF22901 GI:6664319 from [Arabidopsis thaliana]; supported by cDNA: gi_16930480_gb_AF41	261696_at	-0.8
hypothetical protein similar to hypothetical protein GB:AAF25986 GI:6714290 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 126	261671 at	-0.8
hypothetical protein predicted by genemark.hmm	261597 at	-0.8
unknown protein contains similarity to extensin-like protein GB:CAA19879 GI:3297821 from [Arabidopsis thaliana]	261598 at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:3365.	261561_at	-0.8
globulin-like protein similar to GB:7595348 from [Cucumis melo];supported by full-length cDNA: Ceres:40551.	261415_at	-0.8
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hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_13878106_gb_AF370316.1_AF370316	261338_at	-0.8
1-aminocyclopropane-1-carboxylate synthase, putative similar to GB:U35779 from [Triticum aestivum] (Plant Mol. Biol. 31 (5), 1009-1020 (1996));		-0.8
unknown protein ;supported by full-length cDNA: Ceres:32887. chloroplast thylakoidal processing peptidase, putative similar to chloroplast thylakoidal processing peptidase GB:CAA71502 GI:2769566 from [Ara	261032_at	-0.8 -0.8
ethylene response factor, putative similar to ethylene response factor 1 GB:AAD03544 GI:4128208 from [Arabidopsis thaliana]	260783 at	-0.8 -0.8
enviene response racio, putative similar to enviene response racion (GB,ACD03044 GL4120206 non [Arabidopsis trialiana] putative tryssin inhibitor : supported by full-length CDNA: Ceres: 15927.	260546 at	-0.8
putative in ypain minioion, supported by runnengin converses rosers.	260172 s at	-0.8
Expressed protein ; supported by cDNA: gi 16648699 gb AY058126.1	260046 at	-0.8
putative UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide)-pyrophosphoryl-undecaprenol N-acetylglucosamine transferase similar to pu		-0.8
putative 305 ribosomal protein S13 similar to putative 305 ribosomal protein S13, chloroplast precursor GB:P42732 [Arabidopsis thaliana]	259678 at	-0.8
inorganic pyrophosphatase, putative similar to inorganic pyrophosphatase GI:790478 from [Nicotiana tabacum]; supported by cDNA: gi 166633 (	_	-0.8
allene oxide cyclase, putative similar to allene oxide cyclase GI:8977961 from [Lycopersicon esculentum]; supported by cDNA: gi 16323064 gb		-0.8
putative small nuclear ribonucleoprotein polypeptide G similar to small nuclear ribonucleoprotein polypeptide G GB:4507133 [Homo sapiens]	259288 at	-0.8
putative 40S ribosomal protein s14 similar to 40S ribosomal protein S14 GB:P19950 [Zea mays]; supported by full-length cDNA: Ceres: 7969.	259239_at	-0.8
putative actin similar to actin 1 GB:P02578 [Acanthamoeba castellanii];supported by full-length cDNA: Ceres:103956.	259242_at	-0.8
carbonic anhydrase, chloroplast precursor identical to carbonic anhydrase, chloroplast precursor GB:P27140 [Arabidopsis thaliana]; supported by	c 259161_at	-0.8
vacuolar membrane ATPase subunit G (AVMA10) identical to vacuolar membrane ATPase subunit G (AVMA10) GB:AF181688 [Arabidopsis thalia	n 258958_at	-0.8
putative ribosomal protein S28 similar to ribosomal protein S28 GB:P34789 [Arabidopsis thaliana]	258937_at	-0.8
glutathione S-transferase identical to glutathione S-transferase GB:AAB09584 from [Arabidopsis thaliana]; supported by cDNA: gi_1575751_gb_U	_	-0.8
putative aspartyl protease contains Pfam profile: PF00026 Eukaryotic aspartyl protease;supported by full-length cDNA: Ceres:40409.	258615_at	-0.8
unknown protein contains Pfam profile: PF00106 short chain dehydrogenase	258467_at	-0.8
hypothetical protein contains similarity to putative phosphate/phosphoenolpyruvate translocator protein GB:AAD20711 from [Arabidopsis thaliana]		-0.8
unknown protein	258318_at	-0.8
hypothetical protein similar to hypothetical protein GB:AAF01546 from [Arabidopsis thaliana]	257999_at	-0.8
unknown protein ; supported by cDNA: gi_15010765_gb_AY045684.1_	257894_at	-0.8
disease resistance protein, putative similar to Hcr2-5b GB:AAC78595 [Lycopersicon esculentum] (Plant Cell 10, 1915-1926 (1998)); contains Pfar		-0.8
unknown protein similar to TCP3 GB:AAC24010 [Arabidopsis thaliana]	257267_at	-0.8 -0.8
ER lumen retaining receptor (HDEL receptor), putative similar to GB:P35402 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:23 GATA transcription factor 1 (AtGATA-1) identical to GATA transcription factor 1 (AtGATA-1) GB:Y13648 [Arabidopsis thaliana];supported by full-le		-0.8 -0.8
unknown protein contains Pfam profile: PF00153 mitochondrial carrier proteins;supported by full-length cDNA: Ceres:39353.	256819 at	-0.8
dirigent protein, putative similar to dirigent protein GB:AF25366 from [Thuig plicata]	256781 at	-0.8
Expressed protein ; supported by full-length cDNA: Ceres; 22461.	256743 at	-0.8
serine/arginine-rich protein, putative similar to serine/arginine-rich protein GB:AAF17288 GI:6572475 from [Arabidopsis thaliana]; supported by cI		-0.8
actin 11 (ACT11) identical to actin 11 (ACT11) SP:P53496 (Plant J. 10:189-202(1996));supported by full-length cDNA: Ceres:38101.	256275 at	-0.8
guanine nucleotide regulatory protein, putative similar to guanine nucleotide regulatory protein GI:452360 from [Vicia faba]; supported by full-leng	_	-0.8
Expressed protein ; supported by full-length cDNA: Ceres: 250775.	256064 at	-0.8
hypothetical protein predicted by genefinder and genscan;supported by full-length cDNA: Ceres:15024.	255824_at	-0.8
unknown protein ; supported by cDNA: gi_15293076_gb_AY050972.1_	255827_at	-0.8
putative serine carboxypeptidase II	255842_at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:19302.	255816_at	-0.8
hypothetical protein similar to putative two-component response regulator protein GI:6623883 from [Arabidopsis thaliana]; supported by full-length	_	-0.8
probable cytochrome P450	255690_at	-0.8
stress-induced protein OZI1 precursor ; supported by cDNA: gi_790582_gb_U20347.1_ATU20347	255629_at	-0.8
predicted protein of unknown function; supported by full-length cDNA: Ceres: 8114.	255440_at	-0.8
putative protein ADRENODOXIN PRECURSOR (adx1), Rickettsia prowazekii, gb:CAA14664;supported by full-length cDNA: Ceres:17223.	255233_at	-0.8
hypothetical protein ; supported by full-length cDNA: Ceres: 94438.	255130_at	-0.8
putative protein various kinesin light chains;supported by full-length cDDNA: Ceres:2538.	254951_at	-0.8 -0.8
nucleoside diphosphate kinase 3 (ndpk3) ; supported by cDNA: gi_14334559_gb_AY035184.1_ putative protein hypothetical protein - Brassica napus,PIR2:S42651	254958_at 254928 at	-0.8 -0.8
oleoyl-[acyl-carrier-protein] hydrolase-like protein oleoyl-[acyl-carrier-protein] hydrolase - Brassica napus, PIR2:S40407	254798 at	-0.8
pherophorin - like protein pherophorin-S, Volvox carteri, PIR:T10798	254649 at	-0.8
putative protein ; supported by cDNA: gi_15292760_gb_4Y050814.1_	254561 at	-0.8
putative protein , supported by contracting and a supported by full-length cDNA: Ceres:18947.	254491 at	-0.8
Expressed protein ; supported by full-length cDNA: Ceres: 23587.	254429 at	-0.8
PRH26 protein ; supported by full-length cDNA: Ceres:36866.	254343 at	-0.8
magnesium-protoporphyrin IX methyltransferase - like protein magnesium-protoporphyrin IX methyltransferase, Synechocystis sp, PIR2:S71781;		-0.8
putative DNA binding protein DNA binding protein ACBF - Nicotiana tabacum, PID:g1899188; supported by cDNA: gi_15450813_gb_AY054487.1	253955_at	-0.8

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putative protein ; supported by cDNA: gi_15810138_gb_AY056134.1_ tryptophan synthase beta-subunit (TSB2) :supported by full-length cDNA: Ceres:104687.	_	).8 ).8
Expressed protein ; supported by full-length cDNA: Ceres: 42507.		).8
stress responsive protein homolog low temperature and salt responsive protein LTI6A - Arabidopsis thaliana, PID:g4039153		).8
putative protein hypothetical protein F9F13.130 - Arabidopsis thaliana, PIR2:110590;supported by full-length cDNA: Ceres:21252.		).8
platter protein type later protein S6 - like ribosomal protein S6, Arabidopsis thaliana, PID;g2662469; supported by cDNA; gi 15292738 gb AY050803.1		).8
Expressed protein : supported by full-length CDNA: Ceres: 104432.		).8
male sterility 2-like protein and sterility protein 2. Brassica napus, gb:X99922; supported by cDNA: gi 16323106 gb AY057657.1	_	).8
putative protein ; supported by CDNA: qi 14517511 qb AY039591.1	_	).8
putative protein cyclin delta-1, Arabidopsis thaliana, SWISS-PROT:P42751		).8
putative protein cylicin II - bovine, PIR2:146014		0.8
putative protein tubulin-folding cofactor C, Homo sapiens, U61234	252868 at -0	
putative protein ;supported by full-length cDNA: Ceres:20457.	_	0.8
putative protein	252676 at -0	9.8
putative protein	252659 at -0	9.8
acidic ribosomal protein P2 -like acidic ribosomal protein P2, maize, PIR:S54179	252643_at -0	8.0
cytoplasmic ribosomal protein S15a -like cytoplasmic ribosomal protein S15a, Arabidopsis thaliana, EMBL:ATAF1412	252566_at -0	8.0
putative protein DCL PROTEIN, CHLOROPLAST PRECURSOR (DEFECTIVE CHLOROPLASTS AND LEAVES PROTEIN) - Lycopersicc	on escule: 252481_at -0	8.0
Expressed protein ; supported by full-length cDNA: Ceres: 122249.	252389_at -0	8.0
cytosolic ribosomal protein S11 ;supported by full-length cDNA: Ceres:40559.	252297_at -0	8.0
6-phosphogluconolactonase - like protein 6-phosphogluconolactonase (6PGL ), Homo sapiens, EMBL:HSA243972;supported by full-lengt	th cDNA: 252282_at -0	8.0
calmodulin-like protein flagellar calmodulin - Naegleria gruberi, PID:g458232; supported by cDNA: gi_166647_gb_L12115.1_ATHCALLGA	A 252136_at -0	8.(
hypothetical protein ; supported by cDNA: gi_15450654_gb_AY052695.1_	252010_at -0	9.8
pectate lyase -like protein pectate lyase, Musa acuminata, EMBL:MAPEL;supported by full-length cDNA: Ceres:119092.	251982_at -0	9.8
hypothetical protein ER6 protein - Lycopersicon esculentum, EMBL:AF096262; supported by full-length cDNA: Ceres: 269951.	_	9.8
phosphoribosylformylglycinamidine cyclo-ligase precursor; supported by cDNA: gi_16974614_gb_AY060585.1_		).8
putative protein predicted pectate-lyase, Arabidopsis thaliana, PIR:T06728	_	9.8
ABC transporter - like protein breast cancer resistance protein 1 BCRP1, Mus musculus, EMBL:NP_036050; supported by cDNA: gi_1502		).8
putative protein ferritin 2 precursor - Vigna unguiculata, PIR:T08124;supported by full-length cDNA: Ceres:33282.	251735_at -0	
40S ribosomal protein S26 homolog several 40S ribosomal protein S26; supported by cDNA: gi_14532523_gb_AY039886.1_		).8
putative protein hypothetical protein T24P15.10 - Arabidopsis thaliana, PIR:T00928		9.8
E2 ubiquitin-conjugating-like enzyme Ahus5 ; supported by cDNA: gi_14596100_gb_AY042838.1_	251561_at -0	
ribosomal protein L11-like ribosomal protein L11, cytosolic, Arabidopsis thaliana, PIR:S49033;supported by full-length cDNA: Ceres:1404		9.8
putative protein COP1-interacting protein CIP8 - Arabidopsis thaliana, EMBL:AF162150	_	8.(
putative protein embryonic abundant protein EMB34 - Picea glauca, EMBL:L47672	_	).8
delta-8 sphingolipid desaturase ;supported by full-length cDNA: Ceres:34427. putative protein hypothetical proteins - Arabidopsis thaliana	_	).8 . o
mRNA binding protein precursor - like mRNA binding protein precursor (chloroplast protein), Lycopersicon esculentum, EMBL:AF106660;		
putative protein HSPC172, Homo sapiens, EMBL:AF161520;supported by full-length cDNA: Ceres:9788.	250993 at -0	
putative protein (supported by full-length cDNA: Ceres:13812.	_	).8
putative protein subported by interengin Correct Correct Correct Participation (Correct Correct Correct Correct) putative protein similar to unknown protein (pirl[T12959);supported by full-length cDNA: Ceres:252000.	_	).8
putative protein similar to unknown protein (sp[71392), appointed by tainengal conv. Cores.202000.	_	).8
copine-like protein copine VII protein - Homo sapiens, EMBL:AJ133798; supported by cDNA: gi 14488103 gb AF389301.1 AF389301	250581 at -0	
inorganic pyrophosphatase - like protein cytosolic inorganic pyrophosphatase, Homo sapiens, EMBL:AF108211;supported by full-length c		).8
putative protein ; supported by full-length cDNA: Ceres: 12170.		).8
isopentenyl pyrophosphate:dimethyllallyl pyrophosphate isomerase	_	).8
apyrase (gb]AAF00612.1); supported by cDNA: gi 6006800 gb AF156783.1 AF156783	_	).8
putative protein predicted proteins, Arabidopsis thaliana	_	).8
putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:32414.	249987 at -0	
60S ribosomal protein L10A; supported by cDNA: gi 14335147 gb AY037253.1	249945 at -0	
cytochrome c1 precursor; supported by cDNA; gi 15215623 gb AY050340.1		
putative protein similar to unknown protein (emb CAB62355.1);supported by full-length cDNA: Ceres:94968.	249330_at -0	
unknown protein ;supported by full-length cDNA: Ceres:16944.		8.(
putative protein similar to unknown protein (gb AAD10670.1)		8.(
putative protein strong similarity to unknown protein (pir/IT04426)	248945_at -0	8.0
indole-3-glycerol phosphate synthase ; supported by cDNA: gi_15215597_gb_AY050327.1_	248688_at -0	9.8
cytochrome b5 (dbj BAA74840.1) ; supported by full-length cDNA: Ceres: 27167.	248682_at -0	9.8

unknown protein ;supported by cDNA: gi_13605737_gb_AF361850.1_AF361850	248588_at	-0.8
receptor protein kinase-like	248568_at	-0.8
putative protein strong similarity to unknown protein (pir  T02324); supported by cDNA: gi_15028278_gb_AY046054.1_	248335_at	-0.8
putative protein similar to unknown protein (pir [S77140); supported by full-length cDNA: Ceres: 14354.	248285_at	-0.8
putative protein similar to unknown protein (pir  T02893)	248302_at	-0.8
thylakoid lumenal 17.4 kD protein, chloroplast precursor (P17.4) (sp[P81760); supported by cDNA: gi_13899114_gb_AF370552.1_AF370552	248224_at	-0.8
unknown protein ;supported by cDNA: gi_16323225_gb_AY057717.1_	248098_at	-0.8
40S ribosomal protein S30 homolog (emb[CAB79697.1)	247968_at	-0.8
unknown protein ; supported by cDNA: gi 16226274 gb AF428289.1 AF428289	247903 at	-0.8
ATGP1 ; supported by cDNA: gi_13358229_gb_AF325040.2_AF325040	247852 at	-0.8
I-box binding factor - like protein I-box binding factor, Lycopersicon esculentum, EMBL:LES243339	247768 at	-0.8
putative protein leucine zipper-containing protein, Lycopersicon esculentum, PIR:S21495; supported by cDNA: gi 14334437 gb AY034910.1	247693 at	-0.8
putative protein predicted proteins from various species	247636 at	-0.8
RNA helicase	247606_at	-0.8
tubulin beta-2/beta-3 chain (spIP29512) ;supported by full-length cDNA: Ceres:39002.	247442 s at	-0.8
amino acid transporter AAP4 (pirl[S51169) ;supported by full-length cDNA: Ceres:116681.	247304 at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:10032.	247328 at	-0.8
unknown protein ; supported by full-length CDNA: Ceres: 25655.	247213 at	-0.8
50S ribosmal protein L29 ; supported by full-length cDNA: Ceres: 16740.	247201 at	-0.8
putative protein strong similarity to unknown protein (pir/[]T10240)	247132 at	-0.8
putative protein strong similarity to unknown protein (pin) 10240) putative protein contains similarity to pathogenesis-related protein;supported by full-length cDNA: Ceres:2152.	247074 at	-0.8
unknown protein	246989 at	-0.8
putative protein hypothetical protein Sb07 - Picea mariana, EMBL:AF051204	246936 at	-0.8
40S ribosomal protein S19 - like 40S ribosomal protein S19, Cyanophora paradoxa, EMBL:CPA245654;supported by full-length cDNA: Ceres:2717	_	-0.8
adenylate kinase -like protein adenylate kinase (EC 2.7.4.3), chloroplast, maize, PIR:S45634	246651_at	-0.8
acetyl-CoA carboxylase ;supported by full-length cDNA: Ceres:20286.	246613_at	-0.8
hypothetical protein predicted by genemark.hmm	246410_at	-0.8
chlorophyll synthetase ; supported by cDNA: gi_14596066_gb_AY042821.1_	246308_at	-0.8
RUB1-conjugating enzyme RCE1, putative similar to gi:6635457; supported by cDNA: gi_6635456_gb_AF202771.1_AF202771	246218_at	-0.8
peptidyl-prolyl cis-trans isomerase - like protein peptidyl-prolyl cis-trans isomerase A.thaliana; supported by full-length cDNA: Ceres:25533.	246040_at	-0.8
IAA7 like protein	245593_at	-0.8
hypothetical protein ;supported by full-length cDNA: Ceres:30327.	245396_at	-0.8
Expressed protein ; supported by full-length cDNA: Ceres: 34967.	245326_at	-0.8
selenium-binding protein like ; supported by cDNA: gi_14532843_gb_AY040046.1_	245285_s_at	-0.8
GDP-mannose pyrophosphorylase updated per Conklin PL et al, PNAS 1999, 96(7):4198-203; supported by full-length cDNA: Ceres:37775.	245060_at	-0.8
unknown protein	257407_at	-0.8
unknown protein	267621_at	-0.8
unknown protein	256771_at	-0.8
putative protein various predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:111923.	250300_at	-0.8
NADPH:protochlorophyllide oxidoreductase A (gb AAC49043.1); supported by cDNA: gi_968974_gb_U29699.1_ATU29699	248197_at	-0.8
hypothetical protein predicted by genscan;contains protein kinase domain	264378_at	-0.8
putative phosphoserine aminotransferase	263047 at	-0.8
unknown protein ; supported by cDNA: gi 16648938 gb AY059839.1	261320 at	-0.8
unknown protein	256913 at	-0.8
phloem serpin-1, putative similar to phloem serpin-1 GI:9937311 from [Cucurbita maxima]	264733 at	-0.8
rhodanese-like family protein ;supported by full-length cDNA: Ceres:1382.	267635 at	-0.7
unknown protein ; supported by full-length cDNA: Ceres: 28982.	267638 at	-0.7
unknown protein similar to GP 2245012[gnl]PID]e327000[297341; supported by cDNA: gi 15293230 gb AY051049.1	267592 at	-0.7
putative ribosomal protein S27 ;supported by full-length cDNA: Ceres:18662.	267507 at	-0.7
putative integral membrane protein	267520 at	-0.7
histone H1 (supported by full-length cDNA: Ceres:1820.	267492 at	-0.7
fatty acid hydroxylase (FAH1) identical to GB:AF021804; supported by cDNA: gi 15215595 gb AY050326.1	267318 at	-0.7
putative transport protein ;supported by full-length cDNA: Ceres:26825.	267219 at	-0.7
unknown protein	267235 at	-0.7
putative adenosine phosphosulfate kinase identical to GB:U05238;supported by full-length cDNA: Ceres:14216.	267235_at 267112 at	-0.7
nodulin-like protein ; supported by cDNA: gi 16930478 gb AF419593.1 AF419593	266993 at	-0.7
putative small nuclear ribonucleoprotein D2 ;supported by full-length cDNA: Ceres:26123.	_	-0.7
putative small nuclear hound coprotein D2, supported by full-length CDNA. Celes.20125.	266482_at	-0.7

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unknown protein	266445_at	-0.7
mevalonate diphosphate decarboxylase identical to GB:Y14325;supported by full-length cDNA: Ceres:35493.	266414_at	-0.7
hypothetical protein predicted by genefinder	266345_at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 112146.	266264_at	-0.7
unknown protein supported by cDNA: gi:13926173	265952_at	-0.7
putative peptide methionine sulfoxide reductase	265804_at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 18284.	265819_at	-0.7
hypothetical protein predicted by genefinder	265777_at	-0.7
	265593_s_at	-0.7
putative peroxidase ATP2a ;supported by full-length cDNA: Ceres:3571.	265471_at	-0.7
E2, ubiquitin-conjugating enzyme, putative ;supported by full-length cDNA: Ceres:27679.	265357_at	-0.7
unknown protein	265143_at	-0.7
unknown protein 3 -end of protein contains similarity to thioredoxins; supported by cDNA: gi_15215811_gb_AY050435.1_	265104_at	-0.7
unknown protein similar to unknown protein GB:AAD55495	264893_at	-0.7
3-hydroxy-3-methylglutaryl-coenzyme A reductase 2 (HMG2 protein catalyzes the conversion of 3-hydroxy-3-methylgluatryl-CoA to mevalonate, th	_	-0.7
unknown protein similar to leucine-rich repeat protein GB:AAC79105; supported by cDNA: gi_12083225_gb_AF332409.1_AF332409	264840_at	-0.7
putative thioredoxin-m similar to thioredoxin m-type precursor; similar to ESTs gb T13714, gb H76398, gb N37762, gb AA042639, gb T21104, emb	264845_at	-0.7
putative transcription factor similar to transcription factor SF3 (pir IS37656); similar to ESTs gb T42207, gb N37716, and emb Z17491;supported by	_	-0.7
hypothetical protein predicted by genscan+	264337_at	-0.7
unknown protein strong similarity to hypothetical protein gb/Y09823 from A. thaliana. ESTs gb/T76118, gb/T04263 and gb/ATYU9823 come from th	_	-0.7
bZIP-like protein similar to bZIP (leucine zipper) protein, GenBank Accession Number 600855	264176_at	-0.7
proteasome alpha subunit, putative similar to proteasome alpha subunit GI:8671494 from [Oryza sativa]	264140_at	-0.7
putative DOF zinc finger protein ;supported by full-length cDNA: Ceres:16423.	264056_at	-0.7
40S ribosomal protein S16 Same as GB:Q42340;supported by full-length cDNA: Ceres:29241.	263821_s_at	-0.7
60s ribosomal protein L34 identical to GB:Q42351, location of EST 105E2T7, gb T22624; supported by full-length cDNA: Ceres:7182.	263691_at	-0.7
putative ferredoxin-thioredoxin reductase ;supported by full-length cDNA: Ceres:40781.	263624_at	-0.7
putative NAD+ dependent isocitrate dehydrogenase subunit 2, IDH2 genomic copy of ICDH2 cDNA U81994, ESTs R29962, R29955 catalyzes the	263583_at	-0.7
ADP-ribosylation factor 3	263529_at	-0.7
hypothetical protein	263442_at	-0.7
40S ribosomal protein S14 ;supported by full-length cDNA: Ceres:41471.	263286_at	-0.7
acetyl-CoA carboxylase, putative similar to acetyl-CoA carboxylase GI:1100253 from [Arabidopsis thaliana]	263193_at	-0.7
60s ribosomal protein I27a. similar to 60S RIBOSOMAL PROTEIN L27A GB:P49637 GI:1710530 from [Arabidopsis thaliana]; supported by full-lengt		-0.7
E2, ubiquitin-conjugating enzyme, putative similar to DNA-binding protein GB:AAB72016 GI:1066082 from [Homo sapiens]; supported by cDNA: gi	_	-0.7
unknown protein similar to pectinesterase GB:X85216 GI:732912 [Phaseolus vulgaris];supported by full-length cDNA: Ceres:33355.	262844_at	-0.7
endomembrane protein, putative similar to endomembrane protein emp70 precursor isolog GB:AAF67014 GI:7677068 [Homo sapiens]; supported	262846_at	-0.7
unknown protein	262693_at	-0.7
ribosomal protein L18, putative similar to ribosomal protein L18 GI:3980238 from [Thermotoga maritima]	262235_at	-0.7
ribosomal protein S9, putative similar to ribosomal protein S9 GI:5456946 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 25038		-0.7
ribosomal protein L30, putative similar to ribosomal protein L30 GI:388034 from [Homo sapiens]; supported by full-length cDNA: Ceres: 19274.	262163_at	-0.7
hypothetical protein predicted by genemark.hmm	262010_at	-0.7
J8-like protein similar to DnaJ homologue J8 GB:AAC72399 GI:3851670 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:4150.	261901_at	-0.7
ADP-ribosylation factor, putative similar to ADP-ribosylation factor GI:166586 from [Arabidopsis thaliana]	261831_at	-0.7
40S ribosomal protein S12, putative similar to 40S ribosomal protein S12 GI:4263712 from [Arabidopsis thaliana]; supported by full-length cDNA: Cr		-0.7
unknown protein ; supported by full-length cDNA: Ceres: 30167.	261790_at	-0.7
hypothetical protein similar to unknown protein GB:AAD23672 GI:4567258 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:40816.		-0.7
tubulin alpha-6 chain, putative identical to tubulin alpha-6 chain GB:P29511 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:1538		-0.7
DNA binding protein ACBF, putative similar to DNA binding protein ACBF GB:U90212 GI:1899187 from [Nicotiana tabacum]	261603_at	-0.7
fatty acid elongase 3-ketoacyl-CoA synthase 1 identical to GB:AAC99312 GI:4091810 from [Arabidopsis thaliana]	261570_at	-0.7
polyphosphoinositide binding protein, putative similar to polyphosphoinositide binding protein Ssh2p GB:AAB94599 GI:2739046 from [Glycine max]	_	-0.7
hypothetical protein predicted by genemark.hmm	261509_at	-0.7
ribosomal protein S15 identical to GB:AAA61608 from [Arabidopsis thaliana] (Plant Physiol. 106 (1), 401-402 (1994)); supported by full-length cDN,	_	-0.7
	261362_s_at	-0.7
pectinesterase, putative similar to GB:Z94058 from [Lycopersicon esculentum]; supported by cDNA: gi_16648888_gb_AY059814.1_	261363_at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 271765.	261318_at	-0.7
C-8,7 sterol isomerase identical to GB:AAD03489 from [Arabidopsis thaliana] (Plant Mol. Biol. 38 (5), 807-815 (1998)); supported by full-length cDN	_	-0.7
ribosomal protein L11, putative similar to chloroplast ribosomal protein L11 Gl:21312 from [Spinacia oleracea]; supported by full-length cDNA: Cere:	_	-0.7
putative small nuclear ribonucleoprotein polypeptide F	260564_at	-0.7

		- <b>-</b>
60S ribosomal protein L38	260538_at	-0.7
putative ribosomal protein similar to ribosomal protein L33B GB:NP_014877 from [Saccharomyces cerevisiae]; supported by full-length cDNA: Cere		-0.7
putative IAA6 protein similar to IAA6 protein GB:S5849 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:147711.	260152_at	-0.7
NAM-like protein similar to NAM (no apical meristem) GB:CAA63101 from [Petunia x hybrida];supported by full-length cDNA: Ceres:21243.	260156_at	-0.7
hypothetical protein predicted by genscan+;supported by full-length cDDA: Ceres:30065.	260056_at	-0.7
unknown protein; supported by cDNA: gi_15450975_gb_AY054568.1_	260058_at	-0.7
hypothetical protein predicted by genemark.hmm	259850_at	-0.7
unknown protein	259655_at	-0.7
beta-glucosidase, putative identical to GI:6651430 from [Arabidopsis thaliana]; supported by cDNA: gi_14532461_gb_AY039855.1_	259640_at	-0.7
hypothetical protein ; supported by cDNA: gi_14596112_gb_AY042844.1_	259515_at	-0.7
hypothetical protein	259529_at	-0.7
putative 40S fibosomal protein S3A (S phase specific) similar to 40S fibosomal protein S3A (S phase specific protein GBIS289) GB:P49396 [Brassi		-0.7
unknown protein similar to putative protein GB:CAB36768 [Arabidopsis thaliana];supported by full-length cDNA: Ceres: 8898.	259013_at	-0.7
putative 40S ribosomal protein S19 similar to 40S ribosomal protein S19 GB:P40978 [Oryza sativa]; supported by full-length cDNA: Ceres: 41619.	258858_at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 5806.	258859_at	-0.7
unknown protein ; supported by full-length cDNA: Ceres: 18019.	258845_at	-0.7
unknown protein ;supported by full-length cDNA: Ceres:250294.	258788_at	-0.7
unknown protein	258692_at	-0.7
unknown protein ;supported by full-length cDNA: Ceres:27471.	258641_at	-0.7
apyrase (Atapy1) identical to apyrase (Atapy1) GB:AF093604 [Arabidopsis thaliana]; supported by CDNA: gi_6002630_gb_AF093604.1_AF093604	258567_at	-0.7
ribosomal protein L29, putative similar to ribosomal protein L29 GI:7559366 (Panax ginseng);supported by full-length cDNA: Ceres:315.	258532_at	-0.7
thioredoxin m4 identical to GB:AAF15951 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 42151.	258398_at	-0.7
putative ribosomal protein similar to ribosomal protein L37 GB:BAA04888 from [Homo sapiens];supported by full-length CDNA: Ceres:14710.	258284_at	-0.7
unknown protein contains Pfam profile: PF01738 Dienelactone hydrolase family:supported by full-length cDNA: Ceres:11339.	258102_at	-0.7
putative 2Fe-2S iron-sulfur cluster protein contains Pfam profile: PF00111 2Fe-2S iron-sulfur cluster binding domains; supported by cDNA: gi_1459		-0.7
unknown protein; supported by cDNA: gi_7658238_gb_AF198179.1_AF198179	257913_at	-0.7
unknown protein ;supported by full-length cDNA: Ceres:32010.	257831_at	-0.7
60S ribosomal protein, putative similar to 60S RIBOSOMAL PROTEIN L30 GB:O49884 from [Lupinus luteus];supported by full-length cDNA: Ceres		-0.7
Expressed protein ; supported by cDNA: gi_15810238 gb_AY056158.1_	257706_at	-0.7
phosphate transporter, putative contains Pfam profile: PF01384 phosphate transporter family	257311_at	-0.7
glutathione reductase, cytosolic identical to GB:P48641 from [Arabidopsis thaliana] (); supported by cDNA: gi_14532809_gb_AY040029.1_	257252_at	-0.7
disease resistance protein, putative similar to GB:AAD13301 from [Lycopersicon esculentum], contains Pfam profiles: PF00560 Leucine Rich Repe		-0.7
myrosinase-associated protein, putative similar to myrosinase-associated protein GB:CAA71238 from [Brassica napus]	257072_at	-0.7
hypothetical protein predicted by genscan+	256984_at	-0.7
PREG-like protein, putative similar to PREG-like protein GB:AAC32127 from [Picea mariana]	256894_at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 8691.	256856_at	-0.7
ATP sulfurylase, putative similar to ATP sulfurylase GB:AAF19185 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:20342.	256835_at	-0.7
unknown protein	256433_at	-0.7 -0.7
protein phosphatase 2C, putative contains Pfam profile: PF00481 Protein phosphatase 2C	256279_at	
unknown protein ;supported by full-length cDNA: Ceres:19056.	256215_at	-0.7
GTP-binding protein (SAR1B) identical to GTP-binding protein (SAR1B) [Arabidopsis thaliana (Mouse-ear cress)] SP:Q01474; supported by full-len;	_	-0.7
unknown protein ; supported by full-length cDNA: Ceres: 22928.	256225_at	-0.7
pyruvate dehydrogenase E1 beta subunit, putative similar to pyruvate dehydrogenase E1 beta subunit GI:2982328 from [Picea mariana]; supported Expressed protein ; supported by full-length cDNA: Ceres: 11843.	255968 at	-0.7 -0.7
	_	
unknown protein	255764_at	-0.7 -0.7
contains weak similarity to S. cerevisiae BOB1 protein (PIR:S45444)	255714_at	-0.7
putative transcription factor ; supported by cDNA: gi_15450989_gb_AY054575.1_ putative transposon protein	255538_at 255366 x at	-0.7 -0.7
putative mitogen-activated protein kinase	255148 at	-0.7
putative protein disulfide isomerase	255061 at	-0.7
putative protein ascorbate peroxidase - Spinacia oleracea, PIR2:S66265;supported by full-length cDNA: Ceres:37435.	255078 at	-0.7
putative protein ascorbate peroxidase - Spinacia oleracea, PIR2:S66265, supported by full-length CDNA: Ceres:37435. putative protein ;supported by full-length cDNA: Ceres:7769.	255078_at 254950 at	-0.7 -0.7
MAP kinase (ATMPK5) possible internal deletion at position 161, missing one A residue; reference GI:457401; supported by cDNA: gi 457401 dbj		-0.7
HhoA protease precursor, putative identical to putative protease HhoA precursor [Arabidopsis thaliana] SP:Q9SEL7 GI:6690272 (unpublished, Len:		-0.7
hypothetical protein	254069_at 254154 at	-0.7
DRE CRT-binding protein DREB1C involved in low-temperature-responsive gene expression00; supported by cDNA: gi 3738227 dbj AB007789.1	254154_at 254075 at	-0.7 -0.7
putative protein NorM, Vibrio parahaemolyticus, gb:AB010463	254075_at 254077 at	-0.7
parate protein reality, there parallelenoighous, gold be readed	2010//_00	-0.7

putative protein probabile membrane protein YBL102w, yeast, PR2: S4593         25987 [.at           protobilorophylide reductase prevensor :supported by full-lengt nDAX: Cares: 3741.         25837 [.at           Expressed protein : supported by PA2: supported by GNA: gi_1203231 gb_AF332402.1_AF332402         25377 [.at           Phylochrome-associated protein PA2: supported by GDAX gi_1203231 gb_AF332402.1_AF332402         25378 [.at           Expressed protein : Stop and by Ull-lengt nDAX: Cares: 3741.         25386 [.at           EST GB-N377 spans last introm and 3 end of gene contains similarity to melotic sering proteins Proteinas SUP (S468325 from [Lycopersion esculetts)         25385 [.at           AG2-kike protein RING-H2 finger RING-H			
protochrophylinke reductase precursor : supported by full-length CDA: Ceres 3871. 253871, at Expressed protein : supported by CDA: ag 15009777, gb, AY035471, 253742, AF332402, 1A5332402, 1A532402, 1A53		_	-0.7
Expressed protein : supported by CDNA: g1, 15609977, gb, AV054257.1_         253377, at           Phytochrome-escolated protein PAP2 : supported by CDNA: g1, 12603213, gb, A7332402.1_A7332402         253749, at           Expressed protein S156 hornolog ribosomal protein S156 - Brassica napus, PIR2: S20945; supported by full-length CDNA: Ceres: 341.         253845, at           EST GB:N3777 spans last intrue nad 3: end of gene contains similarity to motics cere inter proteins end PG:16468325 form (Lycopersion escuelt)         25360, at           Ald2:Like protein Al22 protein nad3: end of gene contains similarity to motics cere inter proteins end PG:16468325 form (Lycopersion escuelt)         253500, at           Statisticate - Rite protein RAV1a - Arabidopsis thaliana, PIO 3790591; supported by CDNA: g1, 15209839, gb_AY054187.1_         253580, at           Statisticate - Rite protein RAV1a - Arabidopsis thaliana, PIO 3790591; supported by CDNA: g1, 1523281, at         253380, at           Statisticate - Rite protein mask = analystate - induced glucosyltransferase, Nicotiana tabacum, PIR2:T03747.supported by CDNA g1: 253282, at         253391, at           glucosyltransferase-kike protein glutafinicne transferase, papaya, PIR: T07971 supported by full-length CDNA. Ceres: 19003.         25211, at           GTP-binding protein arx3 : supported by CDNA: g1, 1433917, g4, 1433917, g4, 1433917, g4, 1433917, g4, 1433917, g4, 1433917, g4, 143917, g4, 13907687, g4, Ar3618058, supported by CDNA: g1, 12605687, g4, Ar36180, supported by full-length CDNA. Ceres: 1903, at           CTP-binding protein arx3, supported by CDNA: g1, 1433917, g4, 1433917, g4, 1433917, g4,		_	-0.7
phytochrome-associated protein PAP2; supported by cDNA; gj. 1203213, gb, AF332402, 1, AF332402 (1, AF33440 (1, A			-0.7
nbisomal protein S16 homolog ribosomal protein S16a - Brässica napus, PIR2 s20945; supported by full-length CDNA: Ceres: 18105.         253804, at           Expressed protein is supported by full-length CDNA: Ceres: 341.         253804, at           EST G8:N3777 spans last intrue protein ARX1a - Arabidopsis thaliana, PIO 3790591; supported by full-length CDNA: Ceres: 341.         253804, at           AIG2-like protein RING-142 finger salivjate-induced glucosyltransferase, Nicotiana tabacum, PIR2:T03747; supported by CDNA gi 1282521, at           Expressed protein Supported by AuN- gi 148254_gb. U384161_ATU38416         253388, at           ARRer1A : supported by CDNA: gi 148254_gb. U384161_ATU38416         253271, at           GTD-binding protein agritum RING-20, Arabidopsis thaliana, pir1:2192         252601_g_st           GTD-binding protein agritum RING-20, Arabidopsis Thaliana, pir1:2192         25261, at           GST Cohinding protein agritum RING-20, Arabidopsis Thaliana, pir1:2192         25261, at           GST Cohinding protein ASI RING-CSMAL PROTEIN S20, ARABIDOPSIS THALIANA, PID:13500966, supported by full-length CDNA: Ceres:3402.         252614, at           GST Cohinding protein Size find RING-RING-20, Arabidopsis thaliana, RING-LA70585, su			-0.7
Expressed protein : supported by full-ength cDNA: Ceres: 28443. 25369, at Utative protein G protein Reis subminike proteins. Schlatsoma mansoni. gb.U30281; supported by full-ength cDNA: Ceres: 341. 253650, at Utative protein RNG-Hz finger protein RN16, At another a Arabidopsis thaliana, PLO 3730901; supported by cDNA: gi_1509389, gb_AY054187.1. 253580, at 254545, at 253545, at 253545, at 253545, at 253245, at 253245, at 253221, at Protein Schlats protein RNG-HZ finger protein RN16, At another a submit Schlats at a submit Reise Re			-0.7
putative protein G protein beta suburit-like protein. Schistosoma mansoni, gb.U30261; supported by full-length CDNA: Ceres: 341. 25366, gt putative protein RIG-742 finger protein RHX1a - Arabidopsis thaliana, PTIC3X: 61127806 Expressed protein AIG2 protein, Arabidopsis thaliana, PTIC3X: 61127806 Expressed protein AIG2 protein, Arabidopsis thaliana, PTIC3X: 61127806 Expressed protein AIG2 protein, immediate-aesity salicytate-induced glucosytimasferase, Nicotiana tabacum, PIR2:T03747; supported by cDNA: gt:1-253268, g.at periditylprobyl isomerase (cyclophilin): supported by full-length cDNA: Ceres: 37. Protein AIG2 protein view of the protein glucosytimasferase, Nicotiana tabacum, PIR2:T03747; supported by cDNA gt:1-253268, g.at vacuolar H(-) ATPase subunit-like protein Vacuolar proton pump subunit SFD alpha isoform - Homo sapiens, EMBLAF-112204; supported by CDNA gt: 14325826, g.at glutabitione transferase, like protein glutathione transferase, papay, PIR:T09781 supported by full-length cDNA: Ceres: 12466. 252613, g.at GTP-Binding protein ara-3; supported by CDNA: gt: 14334917, gb.AY036132.1 4036 rbosomal protein 4050 robio. Main. 2007 robio.			-0.7
EST GENX37377 spans last intron and 3 end of gene contains similarity to meiotic serine protein asis TMP CiteRe325 from [Lycopersion esculent 253860, at 25386, at 25		_	-0.7
putative protein RIM-LP2 finger protein RHX1a "Arabidopsis thaliana, PICUX-SU127006 AIG2-like protein AIG2 protein, Arabidopsis thaliana, PATCHX.51127006 Expressed protein AIG2 protein, Arabidopsis thaliana, PATCHX.51127006 Expressed protein AIG2 protein, Arabidopsis thaliana, PATCHX.51127006 Expressed protein AIG2 protein, supported by full-length cDNA: Ceres: 24628 peptidydrolyl somerase (cyclophilm): supported by full-length cDNA: Geres: 37. Errelate-6-fydrolyslas (FAHT): supported by full-length cDNA: Geres: 21468. ARETA : supported by full-length cDNA: Geres: 21468. ARETA : supported by full-length cDNA: Geres: 21468. Torr-binding protein arX3: supported by full-length cDNA: Geres: 37. Errelate-6-fydrolen arX3: supported by full-length cDNA: Geres: 37. 252717, at 405 fibosomal protein AVS apported by CDNA: gj. 14334017 (g). AVX35122. 252801 s. at 717-binding protein AVS apported by CDNA: gj. 14334017 (g). AVX35122 252801 s. at 7187-binding protein AVS apported by CDNA: gj. 14334017 (g). AVX35125 252227, at 7187-binding protein AVS apported by CDNA: gj. 1433401 (g). AVX3512 25127, at 7187-binding protein AVS apported by CDNA: gj. 1433401 (g). AVX3512 25127, at 7187-binding protein AVS apported by CDNA: gj. 1433401 (g). AVX3512 25147, at 7187-binding protein AVS apported by CDNA: gj. 1433401 (g). AVX3512 25147, at 7187-binding protein AVX3512 protein MX3 Gene protein AVX3512 protein S4735122. 726177, at 7187-binding protein AVX3512, at 726172, at 726172, at 726172, at 726172, at 726172, at 7261727, at 7261727, at 7261727, at 7261727, at 7261727, at 72	putative protein G protein beta subunit-like protein, Schistosoma mansoni, gb:U30261; supported by full-length cDNA: Ceres: 341.	253645_at	-0.7
AIG2:like protein AIG2 protein, Arabidopsis thaliana, PATCHX:G1127006       25345_pt         Expressed protein : supported by full-length CDNX: Ceres: 34629.       253291_pt         Iglucosytransferase-like protein immediate-early salicylate-induced glucosytransferase, Nicotiana tabacum, PIR2:T03747,supported by cDNA g1: 253286_st       25308_pt         Iferulate-5-hydroxytase (FAH1): supported by CDNA g1: 1488254_gb_U38416.1_ATU38416       25308_pt         ARRer1A: supported by full-length CDNA: Ceres: 21486.       253013_pt         Vacuular H(+) ATPase subunitilike protein Vacuular proton pump subunit SFD alpha isoform - Homo sapiens, EMBL:AF112204; supported by cDNX       262712_pt         1glutathione transferase-like protein Stoomal proteinS20, Arabidopsis thaliana, pint 1712992       252610_st         2GTP-binding protein ars-3: supported by CDNA: g1:14334917_gb_AY030132.1       252514_at         405 ribosomonal protein SOS-MAL PROTEIN S20. ARABIDOPSIS THALIANA, PID:g1350956; supported by full-length cDNA: 25277_at       25277_at         Dranched-chain-amino-acid transminase-like protein bronched-chain-amino-acid transminase-like protein bronched-chain-amino-acid transminase-like protein bronched-chain-amino-acid transminase-like protein Aug4 Protein Protein-14:12135; supported by CINA: g1:1252829_g_p AV05080.1_2       25195_at         uncouring protein acid and protein SPEC19C2:12 - 2 Enizosaccharomyces pombe, PIR:13903:supported by CINA: g1:13926251_gb_A73782       25			-0.7
Expressed protein : supported by full-length cDNA: Ceres: 24629. 25329_1at glucosyltransfersae - like protein immediate-averty salicylate-induced glucosyltransfersae, Nicotiana tabacum, PIR2:T03747,supported by cDNA; G1: 425326 a. 2 gentidylprolyl isomerase (cyclophilm): supported by CDNA: g1: 438265 4.g. bJ.38416.1 ATU38416 AREr TA : supported by full-length cDNA: Ceres: 21466. 25391, at vacuolar H(+)-ATPases subunit-like protein vacuolar proton pump subunit SFD alpha isoform - Homo sapiens, EMBL-AF112204; supported by cDN. 252712, at vacuolar H(+)-ATPases subunit-like protein vacuolar proton pump subunit SFD alpha isoform - Homo sapiens, EMBL-AF112204; supported by CDN. 252712, at vacuolar H(+)-ATPases subunit-like protein vacuolar proton pump subunit SFD alpha isoform - Homo sapiens, EMBL-AF112204; supported by CDN. 252712, at vacuolar H(+)-ATPases public vacuolar proton pump subunit SFD alpha isoform - Homo sapiens, EMBL-AF112305 DTP- binding protein ara: 3: pupported by CDN. 252143, at vacuolar protein vacuolar protein vacuolar proton pump subunit SFD alpha isoform - Homo sapiens, EMBL-AF112350 DTP- binding protein ara: 3: pupported by CDN. 252143, at vacuolar protein vacuolar protein s20-like protein hdOS RIBCOS/DML, PROTEIN S20 - ARABIDOPSID THALIANA, PID: g1360966; supported by CDN. 252143, at vacuolar betroid delyhogenese homotoge runostual.ppported by CDNA: g1.13800380; pported by CDNA: g1.13802380; supported by CDNA: g1.13802380; supported by CDNA: g1.13802380; supported by CDNA: g1.1282822, g2, AV050880.1, 251995, at uncucler envelpe membrane protein - ike Integral nuclear envelpe immembrane protein, Homo sapiens, EMBL-KF11235; supported by CDNA: g1.13802332, pp.147632232, p4.7462261, p4.7146226 putative protein phytothetical protein SA244600 - Arabidopsis thaliana, EMBL-AA27462 putative protein phytothetical protein SA244600 - Arabidopsis thaliana, EMBL-AA27462 putative protein phytothetical protein SA244600 - Arabidopsis thaliana, LAB031739; supported by CDNA: g1.13926251 gb, 245143, at ribosomal	putative protein RING-H2 finger protein RHX1a - Arabidopsis thaliana, PID:g3790591; supported by cDNA: gi_15809839_gb_AY054187.1_ 2	253580_at	-0.7
glucosyltransferase -like protein immediate-early salicylate-induced glucosyltransferase, Nicotiana tabacum, PIR2:T03747;supported by cDN4;1: 253261_at erulate-5-hydroxylase (FAH1) : supported by LDN4: gl_1488254_gb_U38116.1_ATU38416 25308_at ARRer1A : supported by full-length cDNA : Ceres:37. 25271_at dost inbsommal protein 05 inbs 05	AIG2-like protein AIG2 protein, Arabidopsis thaliana, PATCHX:G1127806 2	253545_at	-0.7
peptidyiproly isomerase (cyclophilm): supported by full-length cDNA: Ceres: 37.253221_atrevalues-57ydroylase (FAH1): supported by cDNA: gi_1488254_gb_U38416.1_ATU38416253088_atvacuolar H(+)-ATPase subunit-like protein vacuolar proton pump subunit SFD alpha isoform - Homo sapiens, EMBL:AF112204; supported by cDN252845_atvacuolar H(+)-ATPase subunit-like protein guathione transferase, papay, PIR-T09781; supported by full-length cDNA: Ceres:19003.252712_at405 ribosomal protein 405 ribosomal protein 520.1ke protein 405 RiBOSOMAL PROTEIN 520ARABIDOPSIS THALIANA, PID;g1350956; supported by full-length cDNA:252813_at405 ribosomal protein s20.1ke protein du SRIBOSOMAL PROTEIN 520ARABIDOPSIS THALIANA, PID;g1350956; supported by full-length cDNA:252813_at405 ribosomal protein steroid dehytrogenase homologHomo sapiens, EMBL:AF1673650; supported by full-length cDNA: Ceres:3460.25217_at25271_at252327_at25237_atburative protein steroid dehytrogenase homologHomo sapiens, EMBL:AF167365; supported by full-length cDNA: Geres:3460.25217_atputative protein steroid dehytrogenase homologHomo sapiens, EMBL:AF167365; supported by full-length cDNA: Geres:3260.25199_atuncoupling protein (ucp/PUMP) ; supported by cDNA: gi_7673022_gb_AF1462261_AF146226261482_atputative protein sits inke RRP:S13 m RNA for cryotapismi inbosomal protein RRP:S13M RNA for cryotapismi inbosomal protein S13, ikz ARPS13A mRNA for cryotapismi inbosomal protein	Expressed protein ; supported by full-length cDNA: Ceres: 24629. 2	253291_at	-0.7
IncludesEvidencyCertes: 21466.253086_atAIRer1A : supported by full-length cDNA: Ceres: 21466.252813_atvacular H(+)ATPase subuni-like protein vacuolar proton pump subunit SFD alpha isoform - Homo sapiens, EMBL:AF112204; supported by cDN252845_atglutathione transferase-like protein glutathione transferase, papaya, PIR:T09781; supported by full-length cDNA: Ceres:19003.252712_atdSo fbsoommal protein S20, Arabidopsis thaliana, print 12992252801_atdSo fbsoommal protein S20, Arabidopsis thaliana, PRABIDOPSIS THALIANA, PID:g1350956; supported by full-length cDNA:252813_atdSo fbsoommal protein S20, Arabidopsis thaliana, FARABIDOPSIS THALIANA, PID:g1350956; supported by full-length cDNA:252814_atdSo fbsoommal protein S202520712_at252271_atbranched-Chain-amino-acid transminase, Steptomyces coelcolor, PIR:70905; supported by 252874_at252927_atputative protein protein protein provined chain-amino-acid transminase, Steptomyces coelcolor, PIR:70905; supported by 252874_at251993_atuncear envelope membrane protein - like LBR Integral nuclear envelope inner membrane protein, Homo sapiens, EMBL:MSICBR0, supported by 201A: g1:5292892_gb_AY008880.1_251993_atunceureling protein (DPUMP) : supported by 201A: g1:7673022_gb_AF1462261_AF1462261251902_at251902_atuntative protein instransmemer protein -Ike LBR Integral nuclear envelope inner membrane protein, Homo sapiens, EMBL:AF1732.25137_atuptative protein protein SPC Supported by 201A: g1:78903_supported by 201A: g1:7926251_gb_A7278225117_atunceureling protein supported by 201A: g1:493381_gb_A76933361_aF625225137_atuptative protein nypo	glucosyltransferase -like protein immediate-early salicylate-induced glucosyltransferase, Nicotiana tabacum, PIR2:T03747;supported by cDNA gi:1, 25	53268_s_at	-0.7
ARRer1A : supported by full-length cDNA: Ceres: 21465.       252013, at         vacuolar H/L-ATTRaes subunit like protein vacuolar proton pump subunit SFD alpha isoform - Homo sapiens, EMBL:AF112204: supported by CDNA: 21272, at       252712, at         403 ribsomonal protein 405 ribsomoral proteinS20, Arabidopsis fhaliana, pri 12992       252611, at         6Th-binding protein arts-3: supported by CDNA: c] (1439417_gb, AV035132.1_       225214, at         405 ribsomal protein S20-like protein 40S RIBOSOMAL PROTEIN S20 - ARABIDOPSIS THALIANA, PID:g1350956; supported by full-length CDNA: 22237, at       252274, at         405 ribsomal protein S20-like protein anongenes, EMBL:AF12956; supported by cDNA: g1_13605687_gb, AF361825, LAF361825       252274, at         branched-chain-amino-acid transaminase. Like protein branched-chain-amino-acid transaminase, SITE/OT8805, supported by CDNA: g1_1520802, gb, AY050800, 1       252167, at         peroxiredoxin - like protein protein - NA2, Arabidopsis thaliana, EMBL:AF121365, supported by full-length cDNA: Ceres: 32640, 2       251993, at         uncelar envelope membrane protein - SIA: SIA: SIA: SIA: SIA: SIA: SIA: SIA:	peptidylprolyl isomerase (cyclophilin) ;supported by full-length cDNA: Ceres:37. 2	253221_at	-0.7
<ul> <li>vacudar H(<sup>+</sup>) ATPase subunit-like protein Vacudar proton pump subunit SFD alpha isoform - Homo Sapiens, EMBL:AF112204; supported by CDN 25244<sup>-</sup> at 90 stosomonal protein 40s ribsomonal protein 40s ribsomonal protein 40s ribsomonal protein 520; Arabidopsis thaliana, pir.112992</li> <li>CFD-Inding protein ara-3; supported by CDN 214334917_gb_Ar035132.1_</li> <li>GTD-Inding protein ara-3; supported by CDN 214334917_gb_Ar035132.1_</li> <li>CFD-Standar A, Standar A, Sta</li></ul>	ferulate-5-hydroxylase (FAH1); supported by cDNA: gi 1488254 gb U38416.1 ATU38416 2	253088 at	-0.7
glutathione transferase, papaya, PIR-T09781 supported by full-length cDNA: Ceres:19003.       2252712_at         40S ribsomomal protein 40S ribsomomal proteinS20, Arabidopsis thaliana, pir.T12992       225201_s_at         6TP-binding protein ars3 ; supported by cDNA: gl_14334917_gb_AY035132_1_       225214_at         40S ribsomal protein S20-like protein 40S RIBOSOMAL PROTEIN S20 - ARABIDOPSIS THALIANA,PID:g1350956; supported by full-length cDNA       252274_at         40S ribsomal protein s20-like protein ars6 RIBOSOMAL PROTEIN S20 - ARABIDOPSIS THALIANA,PID:g1350956; supported by full-length cDNA: Ceres:34560.       252274_at         40S ribsomal protein steroid dehydrogenase homolog. Homo sapiens, EMBL-AF078650.supported by cDNA: gi_15292892_gb_AY050880.1_       251983_at         uncouping protein (ucp7)UMP); supported by cDNA: gi_757022_gb_AF1462261_AF146226       251902_at         putative protein (ucp7)UMP); supported by cDNA: gi_757022_gb_AF1462261_AF146226       251459_at         putative protein protein S13-like ARP513A RNA for cytoplasmic hibma. RMBL:AF121366; supported by full-length cDNA: Ceres:32264.       251483_at         putative protein nix S1: RMR ARP513A RNA for cytoplasmic hibosomal protein S13, rabidopsis thaliana, AB031739; supported by cDNA: gi_7332, gb_AF18323.       25137_at         putative protein nothor stamsmetrane recyclin, function stamsmetrane recyclin and rabidon stamsamica, clove pink, PIR:T10717; supported by cDNA: gi_151228_b_p.       25137_at         putative protein nothor stamsmetrane recyclin functin stamsmetrane recyclin, function stamsmetrane recyclin function s	AtRer1A ; supported by full-length cDNA: Ceres; 21466.	252913 at	-0.7
glutathione transferase, papaya, PIR-T09781 supported by full-length cDNA: Ceres:19003.       2252712_at         40S ribsomomal protein 40S ribsomomal proteinS20, Arabidopsis thaliana, pir.T12992       225201_s_at         6TP-binding protein ars3 ; supported by cDNA: gl_14334917_gb_AY035132_1_       225214_at         40S ribsomal protein S20-like protein 40S RIBOSOMAL PROTEIN S20 - ARABIDOPSIS THALIANA,PID:g1350956; supported by full-length cDNA       252274_at         40S ribsomal protein s20-like protein ars6 RIBOSOMAL PROTEIN S20 - ARABIDOPSIS THALIANA,PID:g1350956; supported by full-length cDNA: Ceres:34560.       252274_at         40S ribsomal protein steroid dehydrogenase homolog. Homo sapiens, EMBL-AF078650.supported by cDNA: gi_15292892_gb_AY050880.1_       251983_at         uncouping protein (ucp7)UMP); supported by cDNA: gi_757022_gb_AF1462261_AF146226       251902_at         putative protein (ucp7)UMP); supported by cDNA: gi_757022_gb_AF1462261_AF146226       251459_at         putative protein protein S13-like ARP513A RNA for cytoplasmic hibma. RMBL:AF121366; supported by full-length cDNA: Ceres:32264.       251483_at         putative protein nix S1: RMR ARP513A RNA for cytoplasmic hibosomal protein S13, rabidopsis thaliana, AB031739; supported by cDNA: gi_7332, gb_AF18323.       25137_at         putative protein nothor stamsmetrane recyclin, function stamsmetrane recyclin and rabidon stamsamica, clove pink, PIR:T10717; supported by cDNA: gi_151228_b_p.       25137_at         putative protein nothor stamsmetrane recyclin functin stamsmetrane recyclin, function stamsmetrane recyclin function s	vacuolar H(+)-ATPase subunit-like protein Vacuolar proton pump subunit SFD alpha isoform - Homo sapiens, EMBL:AF112204: supported by cDN, 2	252845 at	-0.7
405 ribsomomal protein 405 ribsomomal protein 520, Arabidopsis thaliana, pir T12992       252601 s_ at         GTP-binding protein ara-3 ; supported by cDNA: gi_14334917_gb_AY035132.1_       25251.at         405 ribsommal protein S20-like protein 405 RIBOSOMAL PROTEIN S20 - ARABIDOPSIS THALIANA,PID:g1350956;supported by full-length cDNA       25241.at         405 ribsomomal protein S20-like protein 405 RIBOSOMAL PROTEIN S20 - ARABIDOPSIS THALIANA,PID:g1350956;supported by full-length cDNA       25247.at         branched-chain-amino-acid transminase, tike protein tornched-chain-amino-acid transminase, Streptomyces coelicolor, PIR:T29053;supported by 2014; gi_15292892, gb_AY050880.1_       25199.at         peroxiredoxin like protein protein - like LBR Integral nuclear envelope inner membrane protein, Homo sapiens, EMBL-HSLBR10; supported by 2199.at       251902_at         putative protein hypothetical protein sA2044000 - Arabidopsis thaliana, EMBL:AAC27462       251483_at       251370_at         putative protein protein fush of cytoplasmic ribosomal protein S13 - like AIRPS13A mRNA for cytoplasmic ribosomal protein S13 - like AIRPS13A mRNA for cytoplasmic ribosomal protein S13 - like AIRPS13A mRNA for cytoplasmic ribosomal protein S13 - like AIRPS13A mRNA for cytoplasmic ribosomal protein S13 - like AIRPS13A mRNA for cytoplasmic ribosomal protein S1419       251372_at         putative protein hypothetical protein S1419 factor protein - Spinacia oleracea, EMBL:AJ133751; supported by cDNA: gi_1326261_gb_AF3728       251172_at         putative protein choroplast ribosome recycling factor protein - Spinacia oleracea, EMBL:AJ133751; supported by cDNA: gi_1326261_gb_AF37		_	-0.7
GTP-binding protein ar-3 : supported by CDNA: gi_14334917 gb_AV0351521_       25251_at         40S ribosomal protein S20-like protein 40S RIBOSOMAL PROTEIN S20 - ARABIDOPSIS THALIANA, PID:g1350956; supported by full-length CDNA       252327_at         40S ribosomal protein S20-like protein 40S RIBOSOMAL PROTEIN S20 - ARABIDOPSIS THALIANA, PID:g1350956; supported by full-length CDNA       252327_at         branched-chain-amino-acid transaminase - like protein branched-chain-amino-acid transaminase, Streptomyces coelicolor, PIR:T29053; supported       252274_at         peroxiredoxin - like protein peroxiredoxin TPx2, Arabidopsis thaliana, EMBL:AF121356, supported by cDNA: gi_15222822_gb_AV505080.1       251995_at         nuclear envelope membrane protein - like LBR Integral nuclear envelope inner membrane protein, Homo sapiens, EMBL:HSLBR10; supported by CJ143_at       251905_at         putative protein protein s176 KLR KHPS13A mRNA for cytoplassis thaliana, EMBL:AAC7482       251485_at         putative protein s133 like KHPS13A mRNA for cytoplassis thaliana, EMBL:AAC7482       251370_at         ribosomal protein S17 like KHPS13A mRNA for cytoplassis thaliana, AB031739; supported by cDNA: gi_1592651_gb_A75728       251377_at         putative protein ontoin stamsembrane recion and ATP binding region, Mus musculus, EMBL:AB133751; supported by cDNA: gi_1592651_gb_Z7572       251172_at         putative protein in contains transmethrane region and ATP length cDNA. Ceres:25769.       25087a_at         putative protein contains transmethrane region and ATP lending region, Mus musculus, EMBL:AB133751; supported b		_	-0.7
405 ribosomal protein S20-like protein 405 RIBOSOMAL PROTEIN S20 - ARABIDOPSIST HALLANA,PID:g1360968; supported by full-length cDNA       252412_at         MTN3-like protein MtN3 gene product - Medicago truncatula,PID:e1169583; supported by cDNA: gj_13605867_gb_AF3618251_AF361825       25227_at         putative protein steroid dehydrogenase homolog - Homo sapiens, EMBL:AF078850; supported by full-length cDNA: Geres:23829_gb_A7050880.1_       251933_at         proxinetoxin - like protein peroxinedoxin TP82, Arabidopsis thaliana, EMBL:AF078850; supported by full-length cDNA: Geres:23829_gb_A7050880.1_       251995_at         uncoupling protein (ucp/PUMP) ; supported by cDNA: gj_7273022_gb_AF1462261_AF146226       251483_at         putative protein hypothetical proteins Af2244600 - Arabidopsis thaliana, EMBL:AF027462       251483_at         putative protein hypothetical proteins Af2244600 - Arabidopsis thaliana, EMBL:AF027462       251473_at         putative protein hypothetical proteins Af244600 - Arabidopsis thaliana, EMBL:AF027462       251473_at         putative protein hypothetical proteins Af2944601 - Arabidopsis thaliana, EMBL:AF027462       251472_at         putative protein       25137_at       25137_at         putative protein S27 ; supported by cDNA: gj_419381_gb_AF083336 1_AF08336       25127_at       251172_at         putative protein       25147_at       25147_at       25127_at       25127_at       25127_at       25127_at       25127_at       25127_at       25127_at       25127_at			-0.7
NTN3-like protein MIN3 gene product - Medicago truncatula, PID:e1169583: supported by cDNA: gi_1306587_gb_AF36182525327_atbranched-chain-amino-acid transaminase. Ike protein branched-chain-amino-acid transaminase. Streptomyces coelicolor, PIR:729053; supported252274_atputative protein steroid dehydrogenase homolog - Homo sapiens, EMBL-AF078850; supported by cDNA: gi_15292892_gb_AY050880.1_251967_atnuclear envelope membrane protein i. Ike IRe Integrat nuclear envelope inner membrane protein, Homo sapiens, EMBL-HSLBR10; supported by CDNA: gi_7673022_gb_AF146226.1_AF146226251483_atputative protein hypothetical protein SPBC19C2.12 - Schizosaccharomyces pombe, PIR:739803; supported by full-length cDNA: Ceres:3266.251459_atputative protein phypothetical protein SPBC19C2.12 - Schizosaccharomyces pombe, PIR:739803; supported by cDNA: gi_13926261_gb_at25137_atputative protein phypothetical protein SPBC19C2.12 - Schizosaccharomyces pombe, PIR:739803; supported by cDNA: gi_141925137_atputative protein phypothetical protein SPBC19C2.12 - Schizosaccharomyces pombe, PIR:739803; supported by cDNA: gi_141925137_atputative protein protein S13 , ike AtRPS13A mRNA for cytoplasmic ribosomal protein S13, vrabidopsis thaliana, AB031739; supported by cDNA: gi_13926251_gb_AF378225137_atputative protein chicroptast ribosome recycling factor protein - Spinacia oleracea, EMBL:AJ133751; supported by cDNA: gi_13926251_gb_AF3782251144_atputative protein chicroptast nibosome recycling factor protein - Spinacia oleracea, EMBL:AJ133751; supported by full-length cDNA: Ceres:25769250843_atGTP-binding protein (blp/AD020231); supported by full-length cDNA: Ceres:3634.250978_at2cytoshome P450 90A1 (spi/A2569); supp		_	-0.7
branched-chain-æmino-æid transæminase -like protein branched-chain-æmino-æid transæminase, Streptomyces coelicolor, PIR:T29053; supported by putative protein steroid dehydrogenase homolog - Homo sapiens, EMBL:AF078850;supported by full-length cDNA: Ceres:34560. 252167. at peroxitedoxin - like protein peroxitedoxin TP×2, Arabidopsis thaliana, EMBL:AF121356; supported by full-length cDNA: Ceres:34560. 251995. at uncoupling protein (ucjp/PUMP) ; supported by (2, 7673022, gp.AF1462261, AF146226 putative protein hypothetical proteins AF244800 - Arabidopsis thaliana, EMBL:AF121356; supported by full-length cDNA: Ceres:29264. 251902, at putative protein hypothetical proteins AF244800 - Arabidopsis thaliana, EMBL:AFC27462 putative protein protos, Ribes nigrum, EMBL:RNT7578; supported by full-length cDNA: Ceres:15792. 251370, at ribosomal protein S27 ; supported by cDNA: gi_1493861_gb_AF0833361_AF083336 putative protein hypothetical proteins Af244800 - Arabidopsis thaliana, AF083336 putative protein S27 ; supported by cDNA: gi_4193881_gb_AF0833361_AF083336 putative protein S27 ; supported by cDNA: gi_4193881_gb_AF0833361_AF083336 putative protein fubs, Ribes nerecycling factor protein - Spinacia oleracea, EMBL:AJ133751; supported by cDNA: gi_1591228_gb 251144_at putative protein cortains transmembrane region and ATP binding region, Mus musculus, EMBL:AB030189.1 putative protein doroplast ribosome recycling factor protein - Spinacia oleracea, EMBL:AB030189.1 putative protein fastrocyclic NOVA-like RNA-binding protein, Hom sapiens, U70477; supported by full-length cDNA: Geres:25769. 250843_at CFT-binding protein starsymembrane region and ATP binding region, Mus musculus, EMBL:AB030189.1 putative protein similar to unknown protein (db]AA60971_1, Supported by full-length cDNA: Ceres:15324. 250978_at putative protein similar to unknown protein (db]AA602129_1, Supported by full-length cDNA: Ceres:104017. 250733_at putative protein similar to unknown protein (db]BAA6874_1, Supported by full-length cDNA: Ceres:2052. 250687_at			-0.7
putative protein stroid dehydrogenase homolog - Homo sapiens, EMBL:AF078650.supported by CDNA: Genes:34560.252167_etperoxiredoxin - like protein peroxin- like LBR integral nuclear envolepe inner membrane protein i, Homo sapiens, EMBL:HSLBR10; supported by CDNA: gi_7573022_gb_AF146226 1_AF146226 1_AF146226251995_atunclear envolepe membrane protein - like LBR integral nuclear envolepe inner membrane protein, Homo sapiens, EMBL:HSLBR10; supported by CDNA: gi_7673022_gb_AF146226 1_AF146226 1_AF146226251483_atputative protein hypothetical proteins SPBC19C2.12 - Schizosaccharomyces pombe, PIR:T39803; supported by full-length cDNA: Ceres:3264.251459_atputative protein hypothetical proteins AL2g44600 - Arabidopsis thaliana, EMBL:AAC27462251470_atputative protein S75, Ribes nigrum, EMBL:RN17578; supported by full-length cDNA: Ceres:15792.251370_atribosomal protein S27 ; supported by cDNA: gi_1493381_gb_AF083336			-0.7
peroxiredoxin - like protein peroxiredoxin TPx2, Arabidopsis thaliana, EMBL:AF121356; supported by cDNA: gi_15292892_gb_AY050880.1_ 251993_at nuclear envelope membrane protein - like LBR integral nuclear envelope inner membrane protein, Homo sapiens, EMBL:HSLBR10, supported by cDNA: 251993_at putative protein (usp/PUMP); supported by cDNA: gi_0767022_gb_AF1462261, AF146226 putative protein hypothetical proteins AF2944600 - Arabidopsis thaliana, EMBL:AAC27462 putative protein protein (spPUMP); supported by cDNA: Sig_0767022_gb_AF146226 putative protein protein StB2 HSC1902_12 - Schizosaccharomyces pombe, PIR-T39803; supported by full-length cDNA: Ceres:92264. 251459_at putative protein protein StB3 - like AtRPS13A mRNA for cytoplasmic ribosomal protein S13, Arabidopsis thaliana, AB031739; supported by cDNA: gi_1419_251341_at ribosomal protein S13 - like AtRPS13A mRNA for cytoplasmic ribosomal protein S13, Arabidopsis thaliana, AB031739; supported by cDNA: gi_15912268_gb_ 251367_at putative protein contains transmembrane region and ATP binding region, Mus musculus, EMBL:AAD33751; supported by cDNA: gi_15912268_gb_ 25048_at putative RNA-binding protein astrocytic NOVA-like RNA-binding protein, Homo sapiens, U70477; supported by cDNA: gi_15912268_gb_ 25048_at putative protein contains transmembrane region and ATP binding region, Mus musculus, EMBL:AB030189.1 250978_at putative protein (supported by cDNA: gi_9909197_gb_AF175769.1_AF175769 250843_at Expressed protein ; supported by CDNA: gi_9909197_gb_AF175769.1_AF175769 250843_at 250752_at 2-cys peroxitedoxin-like protein ; supported by full-length cDNA: Ceres:36334. 2-cys peroxitedoxin-like protein ; supported by full-length cDNA: Ceres:16400. 250733_at putative protein similar to unknown protein (db)BAA86974.1); supported by full-length cDNA: Ceres:104017. 250667_at putative protein similar to unknown protein (db)BA486974.1); supported by full-length cDNA: Ceres:20752. 250687_at ABC transporter-like protein ; supported by full-length cDNA: Ceres:15560. 250649_at p		_	-0.7
nuclear envelope membrane protein - like LBR integral nuclear envelope inner membrane protein, Homo sapiens, EMBL:HSLBR10; supported by c uncoupling protein (ucp/PUMP) ; supported by cDNA: gi_7673022 gb_AF146226.1_AF146226 putative protein hypothetical protein SPBC19C2.12 - Schizosaccharomyces pombe, PIR:T39803; supported by full-length cDNA: Ceres:9264. 251483_at putative protein hypothetical protein SAPBC19C2.12 - Schizosaccharomyces pombe, PIR:T39803; supported by full-length cDNA: Ceres:9264. 251483_at putative protein protein ST3. like AtRPS13A mRNA for cytoplasmic ribosomal protein S13, Arabidopsis thaliana, AB031739; supported by cDNA: gi_1419 25137_at ribosomal protein S27 ; supported by cDNA: gi_4193381_gb_AF083336.1_AF083336 putative protein chloroplast ribosome recycling factor protein - Spinacia oleracea, EMBL:AJ133751; supported by cDNA: gi_15912266_ub_ putative protein chloroplast ribosome recycling factor protein - Spinacia oleracea, EMBL:AL20747; supported by cDNA: gi_15912266_ub_ putative protein contains transmembrane region and ATP binding pretion, Homo sapiens, UT0477; supported by cDNA: gi_15912266_ub_ putative protein (gb AZD0203.1) ; supported by full-length cDNA: Ceres: 6734. 2:cys peroxinedoxin-like protein simular to unknown protein (gb AAF02129.1); supported by full-length cDNA: Ceres: 16740. 2:cys peroxinedoxin-like protein ; supported by full-length cDNA: Ceres: 15640. putative protein ; supported by cDNA: gi_9502175_gb_AF137569. ABC transporter-like protein ; supported by full-length cDNA: Ceres: 15640. 2:cos peroxinedoxin-like protein ; supported by full-length cDNA: Ceres: 15640. 2:cos peroxinedoxin-like protein ; supported by full-length cDNA: Ceres: 15640. 2:cos perotein similar to unknown protein (db]BAAF02129.1); supported by full-length cDNA: Ceres: 20752. ABC transporter-like protein ; supported by cDNA: gi_9502175_gb_AF339289. 1:AF346898. 1:AE24699. 2:cos perioritheronine protein kindes supported by full-length cDNA: Ceres: 15600. 2:cos periorithero		_	-0.7
uncoupling protein (ucp/PUMP) ; supported by cDNA: gi_7673022_gb_AF146226251902_at			-0.7
putative protein hypothetical protein SPBC19C2.12 - Schizosaccharomyces pombe, PIR:T39803;supported by full-length cDNA: Ceres:2264.251483_atputative protein hypothetical proteins At2g44600 - Arabidopsis thaliana, EMBL:AAC27462251459_atputative protein prib5, Ribes nigrum, EMBL:RNT278;supported by full-length cDNA: Ceres:15792.251370_atribosomal protein S13 -like AtRPS13A mRNA for cytoplasmic ribosomal protein S13, Arabidopsis thaliana,AB031739; supported by cDNA: gi_1493381_gb_AF083336.1_AF083336251357_atputative protein251270_at251177_atputative protein251270_at251177_atputative protein250078_at251172_atputative protein250078_at251172_atputative protein cholroplast ribosome recycling factor protein - Spinacia oleracea, EMBL:AJ133751; supported by cDNA: gi_15912268_gb_251144_atputative protein contains transmembrane region and ATP binding region, Mus musculus, EMBL:AB030189.1250978_atputative protein (gb/AAD09203.1) ; supported by full-length cDNA: Ceres:6734.250813_atExpressed protein ; supported by full-length cDNA: Ceres:15640.250752_at2-cy seroxiredoxin-like protein ; supported by full-length cDNA: Ceres:15640.25073_atputative protein ismilar to unknown protein (db)AAF02129.1); supported by full-length cDNA: Ceres:20752.250867_atABC transporter-like protein ; supported by full-length cDNA: Ceres:15640.25076_atputative protein ismilar to unknown protein (db)BAA66974.1); supported by full-length cDNA: Ceres:20752.250687_atABC transporter-like protein ; supported by full-length cDNA: Ceres:15640.250676_atput			-0.7
putative protein hypothetical proteins At2g44600 - Arabidopsis thaliana, EMBL:AAC27462 251459_at putative protein prib5, Ribes nigrum, EMBL:RNI7578;supported by full-length cDNA: Ceres:15792. 251370_at ribosomal protein S27 ; supported by cDNA: gi_4193381_gb_AF083336.1_AF083336 putative protein chloroplast ribosome recycling factor protein - Spinacia oleracea, EMBL:AJ133751; supported by cDNA: gi_13926251_gb_AF3728 putative protein chloroplast ribosome recycling factor protein - Spinacia oleracea, EMBL:AJ133751; supported by cDNA: gi_13926251_gb_AF3728 putative protein chloroplast ribosome recycling factor protein - Spinacia oleracea, EMBL:AJ133751; supported by cDNA: gi_13926251_gb_AF3728 putative protein chloroplast ribosome recycling factor protein - Spinacia oleracea, EMBL:AJ133751; supported by cDNA: gi_13926251_gb_AF3728 putative protein contains transmembrane region and ATP binding region, Mus musculus, EMBL:AB030189.1 250978_at putative protein as transmembrane region and ATP binding protein, Homo sapiens, U70477; supported by full-length cDNA: Ceres:25769. 250843_at GTP-binding protein (gb AAD09203.1); supported by full-length cDNA: Ceres:6734. 250818_at expressed protein ; supported by cDNA: gi_9909197_gb_AF175769.1_AF175769 cytchcrome P459 09A1 (spi)Q42569); supported by full-length cDNA: Ceres:36334. 250752_at -2cys peroxiredoxin-like protein ; supported by full-length cDNA: Ceres:15640. 250734_at harpin-induced protein ismilar to unknown protein (gb AAF02129.1); supported by full-length cDNA: Ceres:20552. 250687_at -ABC transporter like protein ; supported by cDNA: gi_9502175_gb_AF264699 nucleoid DNA-binding-like protein ; supported by full-length cDNA: Ceres:1560. 2506867_at -abpin-induced protein-like protein ; supported by full-length cDNA: Ceres:20752. 250687_at -abc transporter-like protein ; supported by full-length cDNA: Ceres:5233. 250545_at -petin methylesterase - like protein pectin methylesterase, Melandrium album, EMBL:MAPME beta-xylosidase - like protein pectin wethylesterase, Melandri		_	-0.7
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putative protein contains transmembrane region and ATP binding region, Mus musculus, EMBL:AB030189.1250978_atputative RNA-binding protein astrocytic NOVA-like RNA-binding protein, Homo sapiens, U70477;supported by full-length cDNA: Ceres:25769.250843_atGTP-binding protein (gb AAD09203.1) ;supported by full-length cDNA: Ceres:6734.250813_atExpressed protein ; supported by cDNA: gi_9909197_gb_AF175769.250818_atcytochrome P450 90A1 (sp[Q42569) ; supported by full-length cDNA: Ceres:16640.250732_atputative protein similar to unknown protein (gb AAF02129.1);supported by full-length cDNA: Ceres:104017.250734_atharpin-induced protein-like ; supported by cDNA: gi_9502175_gb_AF264699.1_AF264699250676_atputative protein similar to unknown protein (db)[BAA60974.1);supported by full-length cDNA: Ceres:20752.250687_atABC transporter-like protein ; supported by full-length cDNA: Ceres:5520.250661_atserine/threonine protein kinase ; supported by full-length cDNA: Ceres:5520.250661_atserine/threonine protein kinase ; supported by full-length cDNA: Ceres:5323.250545_atpectin methylesterase - like protein pectin methylesterase, Melandrium album, EMBL:MAPME250490_atbeta-xylosidase - like protein beta-xylosidase, Aspergllus nidulans, EMBL:ANXLND; supported by cDNA: gi_15982752_gb_AY057483.1_250444_atputative protein ; supported by cDNA: gi_15028030_gb_AY045872.1_25038_atputative protein contains similarity to transmembrane transport protein; supported by full-length cDNA: Ceres:249596.25033_at			-0.7
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ABC transporter-like protein ; supported by cDNA: gi_14488081_gb_AF389289.1_AF389289       250690_at         nucleoid DNA-binding-like protein ; supported by full-length cDNA: Ceres:15560.       250661_at         serine/threonine protein kinase ; supported by full-length cDNA: Ceres:5323.       250545_at         pectin methylesterase - like protein pectin methylesterase, Melandrium album, EMBL:MAPME       250440_at         beta-xylosidase - like protein beta-xylosidase, Aspergllus nidulans, EMBL:ANXLND; supported by cDNA: gi_15982752_gb_AY057483.1_       250444_at         putative protein predicted proteins, Arabidopsis thaliana       250417_at         putative protein       250330_gb_AY045872.1_       250330_at         putative protein contains similarity to transmembrane transport protein; supported by full-length cDNA: Ceres:249596.       250315_at	harpin-induced protein-like ; supported by cDNA: gi_9502175_gb_AF264699.1_AF264699 2	250676_at	-0.7
nucleoid DNA-binding-like protein ;supported by full-length cDNA: Ceres:15560.       250661_at         serine/threonine protein kinase ;supported by full-length cDNA: Ceres:5323.       250545_at         pectin methylesterase - like protein pectin methylesterase, Melandrium album, EMBL:MAPME       250440_at         beta-xylosidase - like protein beta-xylosidase, Aspergllus nidulans, EMBL:ANXLND; supported by cDNA: gi_15982752_gb_AY057483.1       250444_at         putative protein predicted proteins, Arabidopsis thaliana       250437_at         putative protein       ; supported by cDNA: gi_15028030_gb_AY045872.1_       250386_at         putative protein contains similarity to transmembrane transport protein; supported by full-length cDNA: Ceres:249596.       250315_at	putative protein similar to unknown protein (dbj BAA86974.1); supported by full-length cDNA: Ceres:20752. 2	250687 <sup>–</sup> at	-0.7
serine/threonine protein kinase ;supported by full-length cDNA: Ceres:5323.       250545_at         pectin methylesterase - like protein pectin methylesterase, Melandrium album, EMBL:MAPME       250440_at         beta-xylosidase - like protein beta-xylosidase, Aspergllus nidulans, EMBL:ANXLND; supported by cDNA: gi_15982752_gb_AY057483.1_       250444_at         putative protein predicted proteins, Arabidopsis thaliana       250417_at         putative protein ; supported by cDNA: gi_15028030_gb_AY045872.1_       250336_at         putative protein contains similarity to transmembrane transport protein; supported by full-length cDNA: Ceres:249596.       250315_at	ABC transporter-like protein ; supported by cDNA; qi 14488081 qb AF389289.1 AF389289 2	250690 at	-0.7
pectin methylesterase - like protein pectin methylesterase, Melandrium album, EMBL:MAPME       250490_at         beta-xylosidase - like protein beta-xylosidase, Aspergllus nidulans, EMBL:ANXLND; supported by cDNA: gi_15982752_gb_AY057483.1_       250444_at         putative protein predicted proteins, Arabidopsis thaliana       250417_at         putative protein ; supported by cDNA: gi_15028030_gb_AY045872.1_       250386_at         putative protein contains similarity to transmembrane transport protein; supported by full-length cDNA: Ceres:249596.       250315_at	nucleoid DNA-binding-like protein :supported by full-length cDNA: Ceres:15560. 2	250661 at	-0.7
pectin methylesterase - like protein pectin methylesterase, Melandrium album, EMBL:MAPME       250490_at         beta-xylosidase - like protein beta-xylosidase, Aspergllus nidulans, EMBL:ANXLND; supported by cDNA: gi_15982752_gb_AY057483.1_       250444_at         putative protein predicted proteins, Arabidopsis thaliana       250417_at         putative protein ; supported by cDNA: gi_15028030_gb_AY045872.1_       250336_at         putative protein       250330_at         putative protein contains similarity to transmembrane transport protein; supported by full-length cDNA: Ceres:249596.       250315_at	serine/threonine protein kinase :supported by full-length cDNA; Ceres:5323. 2	250545 at	-0.7
beta-xylosidase - like protein beta-xylosidase, Aspergllus nidulans, EMBL:ANXLND; supported by cDNA: gi_15982752_gb_AY057483.1250444_atputative protein predicted proteins, Arabidopsis thaliana250417_atputative protein ; supported by cDNA: gi_15028030_gb_AY045872.1_250368_atputative protein25030_atputative protein contains similarity to transmembrane transport protein; supported by full-length cDNA: Ceres:249596.250315_at			-0.7
putative protein predicted proteins, Arabidopsis thaliana250417_atputative protein ; supported by cDNA: gi_15028030_gb_AY045872.1_250368_atputative protein250330_atputative protein contains similarity to transmembrane transport protein; supported by full-length cDNA: Ceres:249596.250315_at		_	-0.7
putative protein ; supported by cDNA: gi_15028030_gb_AY045872.1_       250368_at         putative protein       250330_at         putative protein contains similarity to transmembrane transport protein;supported by full-length cDNA: Ceres:249596.       250315_at		_	-0.7
putative protein 250330_at putative protein contains similarity to transmembrane transport protein;supported by full-length cDNA: Ceres:249596. 250315_at		_	-0.7
putative protein contains similarity to transmembrane transport protein; supported by full-length cDNA: Ceres:249596. 250315_at			-0.7
			-0.7
nutative protein isupported by full-length cDNA: Ceres: 5392		_	-0.7
		_	-0.7
			-0.7
			-0.7

substitue exerts in similar to unlurging exerts in (dbilD & A00242 d) supremented by full log sthe sDNA. Consert 040	250027 -+	07
putative protein similar to unknown protein (dbjlbAA90342.1);supported by full-length cDNA: Ceres:1816.	250027_at	-0.7
putative protein similar to unknown protein (emb[CAB88996.1); supported by full-length cDNA: Ceres: 7688.	249943_at	-0.7
PGPD14 protein ;supported by full-length cDNA: Ceres:41666.	249862_at	-0.7
2-isopropylmalate synthase-like protein	249867_at	-0.7
unknown protein ;supported by full-length cDNA: Ceres:25723.	249811_at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 19092.	249778_at	-0.7
cationic amino acid transporter -like protein cationic amino acid transporter-1, rat, PIR:T46813	249640_at	-0.7
His-Asp Phosphotransfer Signal Transducer AHP3 ; supported by cDNA: gi_15293020_gb_AY050944.1_	249473_at	-0.7
glutaredoxin -like protein glutaredoxin, castor bean, PIR:S54825; supported by full-length cDNA: Ceres: 23800.	249380_at	-0.7
succinate dehydrogenase iron-protein subunit -like succinate dehydrogenase iron-protein subunit (SDHB), Oryza sativa, EMBL:AB017428; support	249343_at	-0.7
Expressed protein ; supported by cDNA: gi_13605534_gb_AF361593.1_AF361593	249268 at	-0.7
Cys2/His2-type zinc finger protein 3 (dbj BAA85109.1) ;supported by full-length cDNA: Ceres:9878.	249139 at	-0.7
aluminum-induced protein-like ; supported by full-length cDNA: Ceres: 12484.	249121 at	-0.7
phytochelatin synthase (gb[AAD41794.1); supported by cDNA: gi 14532653 gb AY039951.1	249078 at	-0.7
putative protein similar to unknown protein (pirl T04881)	249021 at	-0.7
serine threonine protein kinase ; supported by cDNA; qi 14486383 qb AY035225.1	248910 at	-0.7
Rab-type small GTP-binding protein-like; supported by full-length cDNA: Ceres: 102017.	248914 at	-0.7
MutT domain protein-like ; supported by cDNA: gi 14596036 gb AY042806.1	248765 at	-0.7
ribosomal protein S27 ;supported by full-length cDNA: gr_14390030_gb_A1042000.1_	248705_at 248747 at	-0.7
drought-induced protein Di19-like protein ; supported by cDNA: gi 13937215 gb AF372963.1 AF372963	248747_at 248595 at	-0.7
	_	
Expressed protein ; supported by cDNA: gi_7715088_gb_AF2167561_AF216756	248511_at	-0.7
trehalose-6-phosphate phosphatase ; supported by cDNA: gi_2944177_gb_AF007778.1_AF007778	248404_at	-0.7
histone H2A (gb AAF64418.1) ; supported by full-length cDNA: Ceres: 4875.	248175_at	-0.7
unknown protein	248068_at	-0.7
CONSTANS-like B-box zinc finger protein-like ;supported by full-length cDNA: Ceres:6639.	247921_at	-0.7
ribosomal protein S4 - like ribosomal protein S4, Arabidopsis thaliana, PIR:T48480;supported by full-length cDNA: Ceres:22434.	247815_at	-0.7
dTDP-glucose 4-6-dehydratase - like protein dTDP-glucose 4-6-dehydratase, Cicer arietinum, EMBL:CAR275318;supported by full-length cDNA: C	247720_at	-0.7
putative protein COP1-interacting protein CIP8, Arabidopsis thaliana, EMBL:AF162150; supported by cDNA: gi_15450686_gb_AY052711.1_	247708_at	-0.7
putative protein various predicted proteins from prokaryotic and eukaryotic species; supported by cDNA: gi_14190378_gb_AF378867.1_AF378867	247642_at	-0.7
60S ribosomal protein L12 - like 60S RIBOSOMAL PROTEIN L12 (like), Arabidopsis thaliana, PIR:T45883;supported by full-length cDNA: Ceres:42	247584_at	-0.7
DNA binding protein - like DNA binding protein EREBP-4, Nicotiana tabacum, PIR:T02434;supported by full-length cDNA: Ceres:92102.	247543_at	-0.7
putative protein various predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 6441.	247464 at	-0.7
dihydroneopterin aldolase-like protein	247409 at	-0.7
putative protein contains similarity to acetyltransferase; supported by full-length cDNA: Ceres: 31971.	247330 at	-0.7
unknown protein	247169 at	-0.7
GATA-binding transcription factor-like protein	247086 at	-0.7
receptor-like protein kinase supported by full-length cDNA: Ceres:110712.	246986 at	-0.7
unknown protein ;supported by full-length cDNA: Ceres:2518.	247006 at	-0.7
unknown protein ;supported by full-length cDNA: Ceres:9946.	247009 at	-0.7
putative multispanning membrane protein GC donor splice site at exon 6; KIAA0255 - Homo sapiens, EMBL:D87444; supported by cDNA; gi 1343	_	-0.7
Attgamma - like protein B regulatory subunit of PP2A, Arabidopsis thaliana, EMBL:ATU73528; supported by cDNA: gi 16604606 gb AY059748.	246907 at	-0.7
protein phosphatase-2C PP2C-like ; supported by CDNA; gi 16974563 gb AY061752.1	246622 at	-0.7
40S RIBOSOMAL PROTEIN S19 - like 40S RIBOSOMAL PROTEIN S19 - Oryza sativa, SWISSPROT:RS19 ORYSA:supported by full-length cDN		-0.7
too REDGOMAL FROME TO TEIN 319 - INE 403 REDGOMAL FROMEIN 319 - 01228 sativa, SWISSFROM RSTS, SUPPORT SA, Supported by Interength CDM	246519 at	-0.7
	_	
phosphoribosyl-ATP pyrophosphohydrolase (At-IE) identical to phosphoribosyl-ATP pyrophosphohydrolase (At-IE) [Arabidopsis thaliana] GI:34618i		-0.7
cytochrome-b5 reductase - like protein cytochrome-b5 reductase, Saccharomyces cerevisiae, PIR:S37800;supported by full-length cDNA: Ceres:3		-0.7
putative protein predicted proteins, Homo sapiens and Caenorhabditis elegans; supported by full-length cDNA: Ceres: 31390.	246008_at	-0.7
putative protein predicted proteins, Drosophila melanogaster and Caenorhabditis elegans	246015_at	-0.7
ribosomal protein L10-like ribosomal protein L10- Nicotiana tabacum, EMBL:AB010879;supported by full-length cDNA: Ceres:29083.	245852_at	-0.7
defender against cell death protein, putative similar to defender against cell death protein GB:AAC36169 GI:3608136 from [Arabidopsis thaliana]	245791_at	-0.7
RNA-binding glycine-rich protein, putative similar to RNA-binding glycine-rich protein (RGP-1a) GI:436789 from [Nicotiana sylvestris]	245778_at	-0.7
MAP kinase, putative similar to MAP kinase kinase 5 GI:3219273 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:112118.	245731_at	-0.7
cytochrome c oxidoreductase like protein	245524_at	-0.7
cyanohydrin lyase like protein ;supported by full-length cDNA: Ceres:5546.	245349_at	-0.7
hypothetical protein ;supported by full-length cDNA: Ceres:22637.	245364_at	-0.7
ribosomal protein ; supported by full-length cDNA: Ceres: 18153.	245311_at	-0.7
hypothetical protein ;supported by full-length cDNA: Ceres:40736.	245331_at	-0.7

hypothetical protein ; supported by cDNA: gi_15912320_gb_AY056438.1_	245266_at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 19973.	245198_at	-0.7
unknown protein ;supported by cDNA: gi_15215824_gb_AY050442.1_	245123_at	-0.7
NADH dehydrogenase subunit	245010_at	-0.7
PSI J protein	244967 at	-0.7
PSILT protein	244973_at	-0.7
NADH dehydrogenase ND4	244962 at	-0.7
hypothetical protein predicted by genemark.hmm	257556 at	-0.7
	_	
putative growth regulator protein similar to Nicotiana tabacum auxin-independent growth promoter, axi 1 gi 559921	262647_at	-0.7
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:10873.	256452_at	-0.7
hypothetical protein	252535_at	-0.7
receptor protein kinase (IRK1), putative similar to receptor protein kinase (IRK1) GI:836953 from [Ipomoea trifida]	264757_at	-0.7
putative aspartyl protease contains Pfam profile: PF00026 Eukaryotic aspartyl proteases; similar to (CND41) chloroplast nucleoid DNA binding prote	261346_at	-0.7
unknown protein	267623 at	-0.6
putative C2H2-type zinc finger protein likely a nucleic acid binding protein; supported by cDNA: gi_14517523_gb_AY039597.1_	267535 at	-0.6
unknown protein	267516 at	-0.6
putative UDP-N-acetylglucosamine pyrophosphorylase ;supported by full-length cDNA: Ceres:5509.	267432 at	-0.6
	_	
putative thromboxane-A synthase ; supported by cDNA: gi_15810029_gb_AY054283.1_	267380_at	-0.6
hypothetical protein predicted by genefinder	267161_at	-0.6
high affinity Ca2+ antiporter identical to GB:U57411, except a possible frameshift at base 58008. Sequence has been confirmed with 5 sequencing	_	-0.6
60S ribosomal protein L23A identical to GB:AF034694;supported by full-length cDNA: Ceres:22479.	266981_at	-0.6
unknown protein ; supported by full-length cDNA: Ceres: 10164.	266789_at	-0.6
60S ribosomal protein L31 ;supported by cDNA: gi_15450424_gb_AY052313.1_	266700_at	-0.6
putative trytophanyl-tRNA synthetase	266648 at	-0.6
putative Na+-dependent inorganic phosphate cotransporter	266672 at	-0.6
glutathione S-transferase (GST6) identical to GB:X95295. Based on identical cDNA hits, the translation is now 40 AAs longer at the N-terminal, and	_	-0.6
hypothetical protein predicted by grail	266474 at	-0.6
putative strictosidine synthase identical to GB:AF076979; involved in alkaloid biosynthesis	266391 at	-0.6
unknown protein identical to GB:AAB82643supported by full-length cDNA: Ceres:17187.	266123 at	-0.6
	_	-0.6
unknown protein ;supported by full-length cDNA: Ceres:34688.	266137_at	
putative multispanning membrane protein similar to MURA transposase of maize Mutator transposon	265994_at	-0.6
unknown protein predicted by genscan and genefinder	266004_at	-0.6
unknown protein ; supported by cDNA: gi_15027852_gb_AY045783.1_	265773_at	-0.6
unknown protein	265720_at	-0.6
putative chlorophyll a/b binding protein ; supported by full-length cDNA: Ceres: 6454.	265722_at	-0.6
putative hydrolase ;supported by cDNA: gi_15982855_gb_AY057535.1_	265680_at	-0.6
unknown protein predicted by genscan; supported by cDNA: gi 13877800 gb AF370163.1 AF370163	265663 at	-0.6
F-box protein family, AtFBL6 contains similarity to grr1 GI:2407790 from [Glycine max]	265633 at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:10730.	265611 at	-0.6
putative dioxygenase ; supported by cDNA: gi_15292706_gb_AY050787.1_	265615 at	-0.6
putative phosphate/phosphoenolpyruvate translocator protein ; supported by cDNA: gi 15809997 gb AY054267.1	265617 at	-0.6
	_	
unknown protein	265620_at	-0.6
60S ribosomal protein L12 ;supported by full-length cDNA: Ceres:23523.	265445_at	-0.6
putative ribosomal protein L6 ; supported by full-length cDNA: Ceres: 692.	265338_at	-0.6
unknown protein	265245_at	-0.6
unknown protein ;supported by cDNA: gi_14335017_gb_AY037188.1_	265189_at	-0.6
hypothetical protein similar to hypothetical protein GB:AAB61516 from F21J9;supported by full-length cDNA: Ceres:27548.	264869_at	-0.6
unknown protein similar to ESTs emb Z27038, gb AA451546, emb Z29876, gb T45359 and gb R90316;supported by full-length cDNA: Ceres:1114-	264837 at	-0.6
serine threonine protein phosphatase (type 2A) identical to type 2A serine threonine protein phosphatase GB:AAC49668 (Arabidopsis thaliana); sur	264703 at	-0.6
putative chloroplast nucleoid DNA-binding protein contains similarity to peptidase family A1	264619 at	-0.6
unknown protein ; supported by cDNA: gi 14039801 gb AF366368.1 AF366368	264547 at	-0.6
putative glutathione S-transferase TSI-1 similar to glutathione S-transferase (sp[Q03666]GTX4_TOBAC); similar to EST gb[H36275; supported by c		-0.6
unknown protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 31830.	264306 at	-0.6
	_	
unknown protein contains similarity to ycf37 gene product gb/1001425 from Synechocystis sp. genome gb/D63999. ESTs gb/T43026, gb/R64902, c		-0.6
putative cyclin-dependent kinase regulatory subunit ;supported by full-length cDNA: Ceres:5750.	264070_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:36719.	263796_at	-0.6
unknown protein	263750_at	-0.6

	000000 at	0.0
putative 60s ribosomal protein L10 Nearly identical to ribosomal protein L10.e, Wilm s tumor suppressor homologue, gi[17682 (Z15157), however d unknown protein similar to unknown protein GB:AAC79135, ESTs gb[T20423, gb]AA712864, gb]H76323 and gb[Z25560 come from this gene;supp	_	-0.6 -0.6
unknown protein SITs gb/N65789,gb/T04628 come from this gene;supported by full-length cDNA: Ceres:28606.	263660 at	-0.6
unknown protein EST gb/T45093 comes from this gene;supported by full-length CDNA: Ceres:8374.	263661 at	-0.6
60S ribosmal protein L39	263585 at	-0.6
	263400 s at	-0.6
putative CCCH-type zinc finger protein also an ankryin-repeat protein	263379 at	-0.6
alanine-glyoxylate aminotransferase :supported by full-length cDNA: Ceres:8306.	263350 at	-0.6
	263048 s at	-0.6
pollen allergen-like protein similar to major allergen Bet v 1 GB:CAA96544 GI:1321726 from [Betula pendula]; supported by full-length cDNA: Ceres		-0.6
tubulin beta-1 chain identical to GB:P12411 GI:135442 from [Arabidopsis thaliana](Gene 63 (1), 87-102 (1988))	262978_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:15169.	262876_at	-0.6
signal response protein (GAI) identical to GAI GB:CAA75492 GI:2569938 [Arabidopsis thaliana] (Genes Dev. In press); supported by cDNA: gi_166	262850_at	-0.6
putative pyrophosphate-dependent phosphofructokinase alpha subunit similar to GB:AAC67587 from [Citrus X paradisi] and GB:Q41140 from [Ricir		-0.6
putative DNA binding protein similar to gb U90212 DNA binding protein ACBF from Nicotiana tabacum and contains 3 PF 00076 RNA recognition n	262824_at	-0.6
puative calcium-transporting ATPase similar to gb AF038007 FIC1 gene from Homo sapiens and is a member of the PF 00122 E1-E2 ATPase famil	262772_at	-0.6
unknown protein	262700_at	-0.6
putative RING-H2 zinc finger protein ESTs gb N37587, gb T04684, gb AA394318, gb Z35014 and gb AA713343 come from this gene; supported by		-0.6
auxin response factor 1, putative similar to auxin response factor 1 GI:2245378 from [Arabidopsis thaliana]	262566_at	-0.6
hypothetical protein similar to hypothetical protein GB:AAD50047 GI:5734782 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:967	262417_at	-0.6
unknown protein identical to hypothetical protein GB:AAD46040 GI:5668814 from (Arabidopsis thaliana); supported by full-length cDNA: Ceres:1061	_	-0.6
hypothetical protein contains similarity to disulphide isomerase GI:4581959 from [Caenorhabditis briggsae]; supported by cDNA: gi_16649012_gb_/		-0.6
phosphoglucomutase, putative similar to phosphoglucomutase GI:534981 from [Spinacia oleracea]	262309_at	-0.6
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:40196.	262284_at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres; 7260.	262058_at	-0.6
sterol delta7 reductase identical to GB:AAF63498 GI:7542561 from [Arabidopsis thaliana]; supported by cDNA: gi_1245181_gb_U49398.1_ATU493 this device between this device both the device both	_	-0.6
thioredoxin h, putative similar to thioredoxin h GI:4928460 from [Hevea brasiliensis];supported by full-length cDNA: Ceres:2054.	261821_at	-0.6
	261804_at 261785 at	-0.6 -0.6
hypothetical protein contains similarity to amino acid permease GI:7415521 from [Oryza sativa] hypoxanthine ribosyl transferase, putative similar to hypoxanthine ribosyl transferase GB:AAC46403 GI:2689037 from [Vibrio parahaemolyticus];su	_	-0.6 -0.6
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:36233.	261483 at	-0.6
E2, ubiquitin-conjugating enzyme 1 (UBC1) identical og ida1269, SP:P25865;supported by full-length cDNA: Ceres:18146.	261484 at	-0.6
hypothetical protein contains similarity to cytochrome c oxidase subunit I GI:5678701 from [Loligo pealei]; supported by full-length cDNA: Ceres: 314		-0.6
Expressed protein : supported by cDNA: gi 15293296 gb AY051082.1	261417 at	-0.6
DNA repair protein RAD23, putative similar to RAD23 protein, isoform II GI:1914684 from [Daucus carota];supported by full-length cDNA: Ceres:40	261352 at	-0.6
unknown protein ; supported by cDNA: gi 14334567 gb AY034957.1	261273 at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 13526.	261203 at	-0.6
unknown protein contains Pfam profile: PF02190 ATP-dependent protease La (LON) domain	261141 at	-0.6
unknown protein	261029_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:143451.	260724_at	-0.6
putative WRKY-type DNA binding protein ;supported by full-length cDNA: Ceres:114256.	260528_at	-0.6
endomembrane protein EMP70 precusor isolog; supported by cDNA: gi_15451171_gb_AY054666.1_	260482_at	-0.6
putative 40S ribosomal protein SA (laminin receptor-like protein) identical to laminin receptor-like protein GB:U01955 [Arabidopsis thaliana]; support		-0.6
unknown protein ;supported by full-length cDNA: Ceres:18367.	260367_at	-0.6
unknown protein contains Pfam profile: PF00561 alpha/beta hydrolase fold	260297_at	-0.6
putative dolichyl-phosphate mannosyltransferase polypeptide 2 similar to dolichyl-phosphate mannosyltransferase polypeptide 2 GB:4503365 (Hom	_	-0.6
unknown protein ;supported by full-length cDNA: Ceres:151718.	260106_at	-0.6
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:28316.	260078_at	-0.6
Expressed protein ; supported by cDNA: gi_15529158_gb_AY052203.1_	260012_at	-0.6
unknown protein	259847_at	-0.6
putative phosphatidylinositol-4-phosphate-5-kinase similar to phosphatidylinositol-4-phosphate-5-kinase GB:CAB63377 [Arabidopsis thaliana]	259677_at	-0.6
nitrate reductase 1 (NR1) identical to nitrate reductase 1 (NR1) GB:P11832 [Arabidopsis thaliana]; supported by cDNA: gi_15983498_gb_AF424624 by use that is a product of the product of t		-0.6
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:21940. nuclear transport factor 2, putative similar to nuclear transport factor 2 (NTF2) [Oryza sativa] GI:5360221; supported by full-length cDNA: Ceres: 27	259663_at	-0.6 -0.6
serine carboxypeptidase II, putative similar to H.vulgare gene encoding serine carboxypeptidase II, CP-MII GI:1731989; supported by cDNA: gi 16		-0.6 -0.6
hypothetical protein similar to ripening-induced protein [Fragaria vesca] GI:2465015;supported by full-length cDNA: Ceres:16091.	259548 at	-0.6 -0.6
chlorophyll binding protein, putative similar to chlorophyll binding protein GI:169213 from [Petunia hybrida]	259491 at	-0.6
	u	0.0

unknown protein ;supported by full-length cDNA: Ceres:13659.	259477_at	-0.6
unknown protein ; supported by cDNA: gi_16604552_gb_AY059721.1_	259349_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:7246.	259257_at	-0.6
reversibly glycosylated polypeptide-1 identical to reversibly glycosylated polypeptide-1 (implicated in cell wall biosynthesis) GB:AAC50000 [Arabido]		-0.6
unknown protein similar to hin1 GB:CAA68848 [Nicotiana tabacum] supported by full-length cDNA: Ceres:8166.	259102_at	-0.6
unknown protein ; supported by cDNA: gi_13877548_gb_AF370475.1_AF370475	259023_at	-0.6
hypothetical protein predicted by genscan+	258972_at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 2153.	258919_at	-0.6
unknown protein ; supported by cDNA: gi_15294217_gb_AF410300.1_AF410300	258839_at	-0.6
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:21672.	258742_at	-0.6
unknown protein ; supported by full-length cDNA: Ceres: 9458.	258681_at	-0.6
putative isocitrate dehydrogenase (NAD+) similar to isocitrate dehydrogenase (NAD+) GB:CAA65502 [Nicotiana tabacum]; supported by full-length (		-0.6
putative protein kinase contains Pfam profiles: PF00069 Eukaryotic protein kinase domain, PF00560 Leucine Rich Repeat (5 copies); supported by	258616_at	-0.6
unknown protein ;supported by cDNA: gi_13605546_gb_AF361599.1_AF361599	258623_at	-0.6
ATP citrate lyase, putative similar to ATP citrate lyase GI:5304837 (Cyanophora paradoxa); supported by cDNA: gi_15292848_gb_AY050858.1_	258515_at	-0.6
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_15450370_gb_AY052286.1_	258501_at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 6490.	258470_at	-0.6
AP2 domain containing protein RAP2.3 identical to GB:AAC49769 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:35981.	258434_at	-0.6
putative RAS-related GTP-binding protein similar to RAS-related GTP-binding protein GB:AAD22451.1 from [Gossypium hirsutum]; supported by full	258314_at	-0.6
putative transcription factor similar to transcription factor GB:CAA74050 from [Arabidopsis thaliana]	258198_at	-0.6
Eukaryotic initiation factor 4A, putative supported by cDNA: Ceres:29310, gi:15293046, gi:15450485	258210_at	-0.6
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:98961.	258089_at	-0.6
ubiquitin-specific protease 7 (UBP7), putative similar to GI:11993467; supported by cDNA: gi_11993466_gb_AF302661.1_AF302661	258045_at	-0.6
unknown protein ;supported by cDNA: gi_15809843_gb_AY054189.1_	257988_at	-0.6
hypothetical protein predicted by genscan+	257962_at	-0.6
HAL3A protein identical to GB:AAD51616 from [Arabidopsis thaliana]	257897_at	-0.6
immunophilin (FKBP15-1) identical to immunophilin (FKBP15-1) GB:U52046 [Arabidopsis thaliana] (Proc. Natl. Acad. Sci. U.S.A. 93 (14), 6964-696	257820_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:121435.	257745_at	-0.6
20S proteasome beta subunit (PBB1) identical to 20S proteasome beta subunit PBB1 (PBB1) GB:AAC32066 [Arabidopsis thaliana] (Genetics 149	257711_at	-0.6
hypothetical protein predicted by genemark.hmm	257687 at	-0.6
hydrolase, putative similar to Metal Dependent Hydrolase GB:AAD18619 from [Chlamydophila pneumoniae]	257602_at	-0.6
unknown protein	257088 at	-0.6
unknown protein	256982 at	-0.6
prefoldin-like protein similar to prefoldin subunit 2 GB:AAF17218 from [Homo sapiens]; supported by full-length cDNA: Ceres: 264413.	256936 at	-0.6
unknown protein	256948 at	-0.6
glycine-rich RNA binding protein, putative similar to glycine-rich RNA binding protein 2 (AtGRP2) GB:CAA05727 [Arabidopsis thaliana]; contains Pf	256890 at	-0.6
30S ribosomal protein S20 contains Pfam profile: PF01649 ribosomal protein S20;supported by full-length cDNA: Ceres:24271.	256855 at	-0.6
unknown protein similar to aluminum-induced protein GB:BAA25999 [Brassica napus]	256829 at	-0.6
putative disease resistance protein similar to disease resistance protein GB:AAC78591 [Lycopersicon esculentum]	256431 s at	-0.6
putative nucleic acid binding protein similar to nucleic acid binding protein Alfin-1 GB:AAA20093 [Medicago sativa]; supported by full-length cDNA: (	256414 at	-0.6
DnaJ protein, putative contains Pfam profile: PF00226 DnaJ domain	256320 at	-0.6
epsilon subunit of mitochondrial F1-ATPase identical to epsilon subunit of mitochondrial F1-ATPase [Arabidopsis thaliana] GI:1655486; supported b	256184 at	-0.6
unknown protein ; supported by cDNA: gi 14423501 gb AF386988.1 AF386988	256115 at	-0.6
unknown protein contains similarity to ubiquitin/ribosomal protein GI:1763015 from [Gallus gallus]	255951 at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:11578.	255857 at	-0.6
unknown protein	255869 at	-0.6
putative protein predicted protein, Arabidopsis thaliana:supported by full-length cDNA: Ceres:10189.	255808 at	-0.6
60S ribosomal protein L6, putative similar to 60S ribosomal protein L6 GI:7208784 from [Cicer arietinum]; supported by full-length cDNA: Ceres:573	255776 at	-0.6
3-phosphoserine phosphatase identical to 3-phosphoserine phosphatase GI:3759177 from [Arabidopsis thaliana];supported by full-length cDNA: Ce		-0.6
hypothetical protein	255643 at	-0.6
putative DNA-binding protein ; supported by cDNA: gi 15028172 gb AY045909.1	255568 at	-0.6
SAR1/GTP-binding secretory factor supported by full-length cDNA: Ceres:94610.	255505 at	-0.6
predicted glycosyl transferase similar to lgtC of Neisseria sp., GenBank accession number U14554, similar to lgtC, GenBank accession number U6		-0.6
		-0.6
putative phosphatidylylocerotransferase similar to CDP-diacylolycerol-glycerol-3-phosphate 3-phosphatidyltransferase of Synechocystis sp. GenBar	255300 at	-0.6
3(2),5-BISPHOSPHATE NUCLEOTIDASE like protein 3 (2),5-BISPHOSPHATE NUCLEOTIDASE, Arabidopsis thaliana, gb:Q42546;supported b		-0.6
nucleoside-diphosphate kinase ;supported by full-length cDNA: Ceres:30158.	255089_at	-0.6
		0.0

S18.A ribosomal protein ;supported by full-length cDNA: Ceres:24071.	255000_at	-0.6
translation initiation factor IF-1, putative similar to translation initiation factor IF-1 GI:124198 from [Spinacia oleracea]	254910_at	-0.6
putative protein	254694_at	-0.6
heat shock transcription factor - like protein heat shock transcription factor, Zea mays, PIR2:S61448	254592_at	-0.6
ATP binding protein - like nucleotide-binding protein, Homo sapiens, PIR2:JC4010;supported by full-length cDNA: Ceres:13295. putative protein RNPL, Homo sapiens, PIR2:G01859;supported by full-length cDNA: Ceres:251841.	254529_at 254504 at	-0.6 -0.6
endomembrane-associated protein ; supported by full-length cDNA: Ceres: 20592.	254504_at 254492 at	-0.0 -0.6
putative protein light induced protein homolog, Arabidopsis thaliana, PATCHX:E326816;supported by full-length cDNA: Ceres:35323.	254358 at	-0.6
predicted protein induced protein ERG25, Saccharomyces cerevisiae, PIR2:S64354	254333 at	-0.6
predicted protein hypothetical protein - Caenorhabditis elegans,PID:e1350884;supported by full-length cDNA: Ceres:8254.	254165 at	-0.6
RNA-binding protein RNP-T precursor; supported by cDNA; p: 15294253 gb AF410318.1 AF410318	254126 at	-0.6
geranylgeranylated protein ATGP4; supported by CDNA: gi 2097566 gb U64921.1 ATU64921	254106 at	-0.6
putative protein ClpC protease - Spinacia oleracea, PID:e4105131; supported by full-length cDNA; Ceres; 28122.	254072 at	-0.6
putative protein	253927 at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 8827.	253832 at	-0.6
putative protein ; supported by full-length cDNA: Ceres:8077.	253562 at	-0.6
putative protein various predicted proteins	253361 at	-0.6
putative protein ;supported by full-length cDNA: Ceres:31672.	253304 at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 6401.	253275 at	-0.6
hypothetical protein ; supported by cDNA; gi 13899098 gb AF370544.1 AF370544	253283 at	-0.6
putative protein similarity predicted protein, Synechocystis sp., PIR2:S76285	253251 at	-0.6
putative protein ; supported by full-length cDNA: Ceres: 18715.	253230 at	-0.6
putative cyclase associated protein CAP adenylyl cyclase-associated protein CAP2, Rattus norvegicus, PIR2:JC4386; supported by cDNA: gi_316{		-0.6
Rho1Ps homolog Rac-like protein ; supported by cDNA: gi_1732518_gb_U62746.1_ATU62746	253225_at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 1095.	253117_at	-0.6
H+-transporting ATPase 16K chain P2, vacuolar ;supported by full-length cDNA: Ceres:31833.	252926_at	-0.6
putative protein ;supported by full-length cDNA: Ceres:4740.	252942_at	-0.6
ribosomal protein S29 - like ribosomal protein S29, rat, PIR:S30298;supported by full-length cDNA: Ceres:2749.	252693_s_at	-0.6
putative protein predicted proteins, Arabidopsis thaliana	252683_at	-0.6
lipoxygenase AtLOX2;supported by cDNA: gi_431257_gb_L23968.1_ATHATLO	252618_at	-0.6
actin depolymerizing factor 1 (ADF1) ;supported by full-length cDNA: Ceres:1907.	252564_at	-0.6
rac GTP binding protein Arac8 ; supported by cDNA: gi_3702965_gb_AF079486.1_AF079486	252375_at	-0.6
putative protein MEL-26, Caenorhabditis elegans, U67737; supported by cDNA: gi_14532781_gb_AY040015.1_	252367_at	-0.6
putative protein ; supported by full-length cDNA: Ceres: 40302.	252234_at	-0.6
60S RIBOSOMAL PROTEIN - like 60S RIBOSOMAL PROTEIN L26, Brassica rapa, EMBL:BRD495; supported by cDNA: gi_13877790_gb_AF370		-0.6
non-specific lipid transfer protein ;supported by full-length cDNA: Ceres:8400.	252115_at	-0.6
putative heat shock transcription factor heat shock transcription factor HSF30 - Peruvian tomato, PIR2:S25480	252081_at	-0.6
ubiquitin extension protein (UBQ1) identical to GI:166929, GI:166930;supported by full-length cDNA: Ceres:18586.	252056_at	-0.6
zinc finger - like protein zinc finger protein 216, Homo sapiens, EMBL:AF062072; supported by cDNA: gi_14596166_gb_AY042871.1_	252009_at	-0.6
ubiquinolcytochrome-c reductase-like protein ubiquinolcytochrome-c reductase, 8K chain, potato, PIR:T07369; supported by cDNA: gi_1545102	_	-0.6
GTPase AtRAB8 ;supported by full-length cDNA: Ceres:27384.	251960_at	-0.6
elicitor responsive/phloem -like protein FIERG2 protein, Oryza sativa, PIR:T04363	251790_at	-0.6
putative protein prenylated Rab acceptor 1 - Homo sapiens, EMBL:AJ133534;supported by full-length cDNA: Ceres:11163.	251732_at	-0.6
hypothetical protein ;supported by full-length CDNA: Ceres: 14487.	251624_at	-0.6
acetylglutamate kinase-like protein acetylglutamate kinase - Synechocystis sp., PIR:S77509;supported by full-length cDNA: Ceres:40830.	251639_at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 19033.	251601_at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 22956. U6 snRNA-associated Sm-like protein U6 snRNA-associated Sm-like protein LSm6 - Homo sapiens, EMBL:AF182292; supported by full-length cDI	251602_at 251447 at	-0.6 -0.6
putative protein prib5, Ribes nigrum, EMBL:RNI7578	251447_at 251418 at	-0.6 -0.6
putative protein unknown protein At2q47690 - Arabidopsis thaliana, EMBL:AC005309; supported by full-length cDNA: Ceres: 6853.	251418_at	-0.6
putative protein unknown protein Al2g47 090 - Arabidopsis inaliana, EndELAC000009, supported by full-length CDNA. Ceres. 0000. putative chloroplast inner envelope protein membrane protein, 37K, precursor, chloroplast inner envelope, common tobacco, PIR:T03230;supporte	_	-0.0 -0.6
putative chloroplast inner envelope protein memorane protein, 37K, precursor, chloroplast inner envelope, common tobacco, PiR. 103230, supportei putative protein serine/threonine protein kinase ATPK10 - Arabidopsis thaliana, EMBL:D30622; supported by cDNA: gi_13249126_gb_AF295669.1		-0.6 -0.6
putative protein semientreonne protein kinase ATERTO - Alabidopsis manana, EMBE. D30022, supported by CDNA. gr_13249120_gb_AE293009. T	250969 at	-0.0 -0.6
putative protein	250909_at 250944 at	-0.0 -0.6
putative protein proline-rich protein APG, Arabidopsis thaliana, PIR:S21961; supported by full-length cDNA: Ceres: 13022.	250944_at 250918 at	-0.6
sulphite reductase ; supported by cDNA: gi_13358216_gb_AF325027.2_AF325027	250846 at	-0.6
putative protein phosphatase protein tyrosine phosphatase-like protein PTPLB, Mus musculus, EMBL:AF169286	250428_at	-0.6
	u	0.0

putative protein predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 13625.	250301_at	-0.6
cystatin (emb CAA03929.1) ; supported by full-length cDNA: Ceres: 5698.	250316_at	-0.6
putative protein various predicted proteins, Arabidopsis thaliana	250160_at	-0.6
zinc finger -like protein zinc finger protein 1, Arabidopsis thaliana, PIR:T48874	249991_at	-0.6
pectinacetylesterase	249807 at	-0.6
hypothetical protein ;supported by full-length cDNA: Ceres:17485.	249472 at	-0.6
putative protein vanilloid receptor gene, CTNS, Homo sapiens, EMBL:AF168787;supported by full-length cDNA: Ceres:18435.	249373 at	-0.6
F-box protein family, AtFBX6 contains similarity to unusual floral organs (UFO) GI:4376159 from [Arabidopsis thaliana]	249140 at	-0.6
auxin-induced protein AUX2-11 (sp P33077)	249109 at	-0.6
putative protein similar to unknown protein (gb AAD10689.1); supported by cDNA: gi 14334449 gb AY034916.1	249065 at	-0.6
unknown protein ; supported by cDNA; ai 13926304 ab AF372903.1 AF372903	248975 at	-0.6
cytochrome P450	248964 at	-0.6
3-oxoacyl-[acyl-carrier-protein] synthase I precursor (beta-ketoacyl-acp synthase I) (KAS I) (sp[P52410) ;supported by full-length cDNA: Ceres:389	_	-0.6
	248828 at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:12344.	248760 at	-0.6
NADH dehvdrogenase 10.5K chain-like protein ; supported by full-length cDNA: Ceres: 39633.	248746 at	-0.6
	248740_at 248676 at	-0.6
putative protein similar to unknown protein (gb AAC72543.1)	_	
U6 snRNA-associated Sm-like protein-like	248678_at	-0.6
putative protein similar to unknown protein (sp P43335);supported by full-length cDNA: Ceres:8788.	248449_at	-0.6
2-oxoglutarate dehydrogenase E2 subunit ; supported by cDNA; gi_14596218_gb_AY042897.1_	248088_at	-0.6
light-inducible protein ATLS1-like ;supported by full-length cDNA: Ceres:1152.	247943_at	-0.6
putative protein predicted protein, Arabidopsis thaliana	247715_at	-0.6
imidazoleglycerol-phosphate synthase subunit H - like imidazoleglycerol-phosphate synthase subunit H homolog, Archaeoglobus fulgidus, PIR:E69		-0.6
ring finger protein - like ring finger protein, Cicer arietinum, EMBL:AB026262	247595_at	-0.6
putative protein ; supported by full-length cDNA: Ceres: 7022.	247572_at	-0.6
glutamate-1-semialdehyde 2,1-aminomutase 1 precursor (GSA 1) (glutamate-1-semialdehyde aminotransferase 1) (GSA-AT 1) (sp P42799)	247392_at	-0.6
unknown protein	247322_at	-0.6
GTP-binding protein ; supported by full-length cDNA: Ceres: 30437.	247202_at	-0.6
14-3-3 protein GF14kappa (grf8) identical to 14-3-3 protein GF14 kappa GI:5802794, SP:P48348 from [Arabidopsis thaliana]; supported by full-leng	247188_at	-0.6
putative protein similar to unknown protein (emb CAB66916.1);supported by full-length cDNA: Ceres:9323.	247109_at	-0.6
putative protein similar to unknown protein (pir  T05276); supported by cDNA: gi_15292834_gb_AY050851.1_	247049_at	-0.6
putative protein	246974_at	-0.6
ribosomal protein S21 - like ribosomal protein S21, Zea mays, PIR:T03945;supported by full-length cDNA: Ceres:93174.	246747_at	-0.6
putative protein predicted protein, Arabidopsis thaliana;supported by full-length cDNA: Ceres:98046.	246593_at	-0.6
seed maturation -like protein seed maturation protein PM23, Glycine max., EMBL:AF116752;supported by full-length cDNA: Ceres:106301.	246547_at	-0.6
putative protein ;supported by full-length cDNA: Ceres:21085.	246548_at	-0.6
hypothetical protein	246346_at	-0.6
E2, ubiquitin-conjugating enzyme 17 (UBC17) identical to gi:2801446; supported by full-length cDNA: Ceres:40968.	246195_at	-0.6
hypothetical protein ; supported by full-length cDNA: Ceres: 38847.	246074_at	-0.6
succinyl-CoA-ligase alpha subunit ;supported by full-length cDNA: Ceres:10292.	246035_at	-0.6
Expressed protein genomic sequence interrupted by a stop codon in exon 4, resequencing necessary to remove ambiguity; otherwise supported by		-0.6
putative protein predicted proteins - Arabidopsis thaliana;supported by full-length cDNA: Ceres:2537.	245984_at	-0.6
putative protein ;supported by full-length cDNA: Ceres:42742.	245906_at	-0.6
unknown protein	245877_at	-0.6
amino acid permease, putative almost identical to amino acid permease GI:608673 from [Arabidopsis thaliana]	245740_at	-0.6
unknown protein	245660_at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 12256.	245367_at	-0.6
elicitor like protein ; supported by full-length cDNA: Ceres: 1718.	245340_at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 7632.	245338_at	-0.6
ankyrin like protein ; supported by cDNA: gi_16604604_gb_AY059747.1_	245274_at	-0.6
F12A21.13 putative photosystem II Core Complex sp[049347]PSBY_ARATH; similar to ESTs gb BE523181, dbj AV531372.1, dbj AV527826.1, db_	245195_at	-0.6
RING finger-like protein similarity to predicted protein, Arabidopsis thaliana, AF361602~Contains Zinc finger, C3HC4 type (RING finger), signature	245207_at	-0.6
putative Ca2+-ATPase ; supported by cDNA: gi_11493642_gb_AF200739.1_AF200739	245117_at	-0.6
putative integral membrane protein ;supported by full-length cDNA: Ceres:25204.	245083_at	-0.6
ribosomal protein S16	245049_at	-0.6
large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase	245015_at	-0.6
cytochrome f	245020_at	-0.6

buschedian and in	244002 a at	0.6
hypothetical protein putative RSZp22 splicing factor	244993_s_at 257435 at	-0.6 -0.6
DNA-3-methyladenine glycosidase, putative similar to DNA-3-methyladenine glycosidase GB:CAB60736 GI:6434028 from [Staphylococcus aureus		-0.6
hypothetical protein predicted by generark.hmm, contains Pfam profile:PF00320 GATA:GATA zinc finger	257571 at	-0.6
hypothetical protein	257583 at	-0.6
hypothetical protein ; supported by full-length cDNA: Ceres: 26019.	245317 at	-0.6
unknown protein ; supported by cDNA: gi 15810460 gb AY056269.1	260501 at	-0.6
Expressed protein ; supported by cDNA: gi_16612239_gb_AF439821.1_AF439821	253973_at	-0.6
putative protein unknown protein T12H1.25 - Arabidopsis thaliana, EMBL:AC009177	246772_at	-0.6
ras-related small GTP-binding protein RAB1c ; supported by cDNA: gi_15529160_gb_AY052204.1_	245299_at	-0.6
mitochondrial F1-ATPase, gamma subunit (ATP3_ARATH) ;supported by full-length cDNA: Ceres:26812.	267600_at	-0.5
putative receptor-like protein kinase ; supported by cDNA: gi_15292872_gb_AY050870.1_	267619_at	-0.5
30S ribosomal protein S5 ; supported by full-length cDNA: Ceres: 38063.	267435_at	-0.5
putative heme A:farnesyltransferase ; supported by cDNA: gi_15028298_gb_AY045952.1_	267342_at	-0.5
unknown protein	267310_at	-0.5
putative mitochondrial carrier protein ;supported by full-length cDNA: Ceres: 150522.	267274_at	-0.5
6,7-dimethyl-8-ribityllumazine synthase precursor; supported by cDNA: gi_15292958_gb_AY050913.1_	267188_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:150205.	266949_s_at	-0.5
putative ABC transporter related to multi drug resistance proteins and P-glycoproteins	266856_at	-0.5
putative RAV-like B3 domain DNA binding protein glycine decarboxylase complex H-protein identical to GB:U27144;supported by full-length cDNA: Ceres:24194.	266760_at	-0.5 -0.5
similar to gibberellin-regulated proteins	266636_at 266613 at	-0.5 -0.5
50S ribosomal protein L27 ;supported by full-length cDNA: Ceres:17067.	266535 s at	-0.5
unknown protein ; supported by cDNA; qi 13605586 qb AF361519.1 AF361619	266551 at	-0.5
unknown protein	266352 at	-0.5
putative RGA1, giberellin repsonse modulation protein identical to GB:Y11336, member of SCARECROW family; supported by cDNA: gi 15529225	_	-0.5
putative tropinone reductase ; supported by CDNA: gi 14334839 gb AY035093.1	266265 at	-0.5
putative protease inhibitor ;supported by full-length cDNA: Ceres:11662.	266168 at	-0.5
putative CCAAT-binding transcription factor subunit identical to GB:Y13723; contains a CBF/NF-Y subunit signature (PDOC00578) present in mem	266171 at	-0.5
unknown protein	266075_s_at	-0.5
hypothetical protein predicted by genefinder; supported by cDNA: gi_13877832_gb_AF370179.1_AF370179	266001_at	-0.5
putative cleavage and polyadenylation specifity factor	265888_at	-0.5
putative aldolase ;supported by full-length cDNA: Ceres:22418.	265735_at	-0.5
hypothetical protein predicted by genscan	265698_at	-0.5
putative myosin heavy chain ; supported by cDNA: gi_15982766_gb_AY057490.1_	265679_at	-0.5
hypothetical protein similar to hypothetical protein GB:AAD18138; supported by full-length cDNA: Ceres: 23166.	265547_at	-0.5
putative RING-H2 zinc finger protein ;supported by full-length cDNA: Ceres:7201.	265472_at	-0.5
unknown protein	265427_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:34875.	265415_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:108956. cytosolic cyclophilin (ROC3) ;supported by full-length cDNA: Ceres:23995.	265384_at 265352 at	-0.5 -0.5
unknown protein weak similarity to C3HC4 zinc finger;supported by full-length cDNA: Ceres:156298.	265023 at	-0.5
zinc finger protein 7, ZFP7; supported by cDNA: gi 790684 gb L39650.1 ATHZFPG	265029 at	-0.5
putative auxin transport protein strongly similar to auxin transport protein GB:AAD52697; supported by cDNA: gi 15450508 gb AY052356.1	264900 at	-0.5
putative coproporphyrinogen III oxidase similar to GB:S39523 and ESTs gb/A4586260 and dbj/D46620; supported by CDNA: gi 14624991 dbj AB(		-0.5
unknown protein similar to EST ablH37293:supported by full-length cDNA: Ceres:7188.	264808 at	-0.5
unknown protein similar to ESTs gb/T42386, gb/H36247, gb/N38423, gb/T21830, and gb/AA585725; supported by cDNA: gi 14423427 gb AF386	_	-0.5
aminomethyltransferase-like precursor protein very strong similarity to aminomethyltransferase precursor gb/U79769 from Mesembryanthemum cry		-0.5
putative vesicle transport protein Contains similarity to vesicle trafficking protein gb/U91538 from Mus musculus. ESTs gb/F15494 and gb/F14097 c		-0.5
pantothenate kinase, putative similar to pantothenate kinase GI:4191500 from [Aspergillus nidulans]	264244_at	-0.5
latex-abundant protein, putative similar to latex-abundant protein GI:4235430 from (Hevea brasiliensis)	264178_at	-0.5
Expressed protein ; supported by full-length cDNA: Ceres: 20090.	264023_at	-0.5
putative phosphoprotein phosphatase ; supported by cDNA: gi_16930440_gb_AF419574.1_AF419574	263990_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:39503.	263952_s_at	-0.5
putative WRKY-type DNA binding protein ;supported by cDNA: gi_15991743_gb_AF425836.1_AF425836	263797_at	-0.5
putative vanadate resistance protein theorem PNC identical to the operation of the protein of th	263722_at	-0.5
ribonuclease, RNS3 identical to ribonuclease SP:P42815, GI:562000 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:9623.	263689_at	-0.5

putative protein transport protein SEC23 similar to human SEC23	263542_at	-0.5
putative histone H2B ;supported by full-length cDNA: Ceres:14965.	263412_at	-0.5
putative beta-1,4-N-acetylglucosaminyltransferase contains similarity to gi 4417304 F15O11.7 putative beta-1,4-mannosyl-glycoprotein beta-1,4-N-		-0.5
multicatalytic endopeptidase identical to GB:CAA73619, ESTs gb H36972, gb T22551 and gb T13800 come from this gene;supported by full-length		-0.5
unknown protein ESTs gb T22508, gb H36196 and gb Al100134 come from this gene	262581_at	-0.5
unknown protein similar to hypothetical protein GB:AAF24587 GI:6692122 from [Arabidopsis thaliana]; supported by cDNA: gi_16604307_gb_AY05		-0.5
unknown protein EST gb AA586241 comes from this gene	262488_at	-0.5
hypothetical protein contains similarity to hedgehog-interacting protein GI:4868122 from [Mus musculus]	262215_at	-0.5
glutamate decarboxylase (gad), putative similar to glutamate decarboxylase (gad) GI:294111 from [Petunia hybrida]; supported by cDNA: gi_11849		-0.5
salt-tolerance zinc finger protein identical to salt-tolerance zinc finger protein GB:CAA64820 GI:1565227 from [Arabidopsis thaliana]; supported by c	_	-0.5
unknown protein	261572_at	-0.5
acidic ribosomal protein, putative similar to 60S ACIDIC RIBOSOMAL PROTEIN P1 GB:023095 from [Arabidopsis thaliana]; supported by full-lengt	261578_at	-0.5
hypothetical protein predicted by genemark.hmm	261525_at	-0.5
tumor suppressor, putative similar to tumor suppressor GI:575354 from [Oryza sativa]; supported by cDNA: gi_14190448_gb_AF378902.1_AF3785	261490_at	-0.5
unknown protein ; supported by cDNA: gi_16604598_gb_AY059744.1_	261445_at	-0.5
RAC-like GTP-binding protein ARAC4 identical to SP:Q38919 from [Arabidopsis thaliana]; supported by cDNA: gi_1304416_gb_U45236.1_ATU452	261229_at	-0.5
hypothetical protein contains similarity to mitochondrial inner membrane protease subunit 1 GB:P28627 from [Saccharomyces cerevisiae]	260972_at	-0.5
	260767_s_at	-0.5
glycine cleavage system H protein precursor, putative similar to GB:Z37524 from [Flaveria anomala]; supported by full-length cDNA: Ceres:23118.	260704_at	-0.5
cellulose synthase catalytic subunit, putative similar to GB:AAD39534 from [Gossypium hirsutum]	260592_at	-0.5
unknown protein ; supported by full-length cDNA: Ceres: 10531.	260200_at	-0.5
fructokinase, putative similar to fructokinase (Lycopersicon esculentum) GI:2102691; supported by cDNA: gi_13878132_gb_AF370329.1_AF37032	260107_at	-0.5
putative transcription factor BTF3 (RNA polymerase B transcription factor 3) similar to transcription factor BTF3 (RNA polymerase B transcription fa	260095_at	-0.5
putative RING zinc finger protein contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger); supported by full-length cDNA: Ceres: 274	259982_at	-0.5
inner mitochondrial membrane protein identical to inner mitochondrial membrane protein GB:U18126 [Arabidopsis thaliana]; supported by full-length	259890_at	-0.5
expressed protein supported by cDNA: Ceres:42692	259768_at	-0.5
glyceraldehyde-3-phosphate dehydrogenase identical to glyceraldehyde-3-phosphate dehydrogenase GI:166708 [Arabidopsis thaliana] (Gene 104,	259625_at	-0.5
bZIP transcription factor, putative contains Pfam profile: PF00170: bZIP transcription factor; supported by cDNA: gi_15028322_gb_AY045964.1_	259626_at	-0.5
hypothetical protein predicted using genefinder; supported by full-length cDNA: Ceres: 20442.	259340_at	-0.5
unknown protein similar to MICROSOMAL SIGNAL PEPTIDASE GB:P28687 from [Gallus gallus];supported by full-length cDNA: Ceres:15144.	259307_at	-0.5
calmodulin-like protein similar to calmodulin GB:AAA34015 [Glycine max], Pfam HMM hit: EF hand	259143_at	-0.5
putative ribosomal protein s19 or s24 similar to ribosomal protein S19 GB:445612 [Solanum tuberosum] and similar to ribosomal protein S24 GB:45	259090_at	-0.5
unknown protein similar to GB:AAD49104 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:38917.	259097_at	-0.5
putative 60S acidic ribosomal protein P0 similar to putative 60S acidic ribosomal protein P0 GB:P50346 [Glycine max]; supported by full-length cDN/	259006_at	-0.5
unknown protein ; supported by full-length cDNA: Ceres: 35785.	258846_at	-0.5
putative short-chain type dehydrogenase/reductase similar to short-chain type dehydrogenase/reductase GB:Q08632 [Picea abies]; supported by cl	258814_at	-0.5
unknown protein similar to putative protein GB:BAA84809 from [Oryza sativa]	258706_at	-0.5
unknown protein	258691_at	-0.5
unknown protein similar to pop3 peptide GB:AAC26526 from [Populus balsamifera subsp. trichocarpa X Populus deltoides];supported by full-length	258412_at	-0.5
subtilisin-like serine protease contains similarity to SBT1 GI:1771160 from [Lycopersicon esculentum];supported by full-length cDNA: Ceres:106539	258368 at	-0.5
unknown protein ; supported by full-length cDNA: Ceres: 11852.	258194_at	-0.5
unknown protein;supported by cDNA: gi_13384113_gb_AF337954.1_AF337954	258107_at	-0.5
unknown protein similar to NA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR GB:Q00874 from [Arabidopsis thaliana]	257974 at	-0.5
unknown protein	257996_at	-0.5
hypothetical protein contains similarity to 3-hydroxyisobutyrate dehydrogenase GB:AAC06408 from [Aquifex aeolicus]; supported by cDNA: gi 1514	257911 at	-0.5
translational inhibitor protein, putative similar to GB:NP 005827 from [Homo sapiens], contains Pfam profile: PF01042 Domain of unknown functior	257674 at	-0.5
ethylene responsive element binding factor, putative similar to GB:BAA32420 from [Arabidopsis thaliana], contains Pfam profile: PF00847 P2 doma	257675 at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:17362.	257676 at	-0.5
unknown protein	257615 at	-0.5
cytochrome c, putative similar to cytochrome c1 GB:S66866 from [Solanum tuberosum]:supported by full-length cDNA: Ceres:41320.	257148 at	-0.5
unknown protein contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger)	256917 at	-0.5
	256865_at	-0.5
putative protein similar to ATP synthase D chain (mitochondrial) SP:075947 [Homo sapiens (Human)]; supported by full-length cDNA: Ceres: 2768	256679 at	-0.5
disease resistance protein, putative similar to disease resistance protein GBAAC78591 GI:3894383 [Lycopersicon esculentum]	256620 at	-0.5
amino acid permease, putative contains Pfam profile: PF00324 amino acid permease	256567 at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:99625.	256525 at	-0.5
60S ribosomal protein L10, putative contains Pfam profile: PF00826: Ribosomal L10;supported by full-length cDNA: Ceres:35307.	256385 at	-0.5
	-	

hypothetical protein	256373_at	-0.5
unknown protein	256286_at	-0.5
unknown protein ; supported by full-length cDNA: Ceres: 9180.	256256_at	-0.5
dof zinc finger protein identical to dof zinc finger protein [Arabidopsis thaliana] GI:3608261; supported by cDNA: gi_3608260_dbj_AB017564.1_AB0	_	-0.5
unknown protein contains Pfam profile: PF00254 FKBP-type peptidyl-prolyl cis-trans isomerases;supported by full-length cDNA: Ceres:42062.	256130_at	-0.5
hypothetical protein predicted by genemark.hmm	256086_at	-0.5
PSI type II chlorophyll a/b-binding protein, putative similar to PSI type II chlorophyll a/b-binding protein GI:541565 from [Arabidopsis thaliana];suppo		-0.5
protein phosphatase type 2C, putative similar to protein phosphatase type 2C GI:4336436 from [Lotus japonicus]; supported by full-length cDNA: Ce	255967_at	-0.5
putative chloroplast 50S ribosomal protein L28 ;supported by full-length cDNA: Ceres:31633.	255850_at	-0.5
transmembrane protein, putative similar to transmembrane protein GI:535681 from [Mus musculus];supported by full-length cDNA: Ceres:40780.	255735_at	-0.5
putative nucleotide sugar epimerase	255696_at	-0.5
putative ribosomal protein S13 similar to ribosomal protein S13 (Pfam;supported by full-length cDNA: Ceres:4058.	255706_at	-0.5
hypothetical protein	255691_at	-0.5
P II nitrogen sensing protein GLB I ; supported by cDNA: gi_3885942_gb_AF095455.1_AF095455	255558_at	-0.5
putative glucan synthase component similar to 1,3-beta glucan synthase	255378_at	-0.5
putative arginase similar to arginases (Pfam: PF00491, Score=353.2, E=1.4e-119, N=1);supported by full-length cDNA: Ceres:33985.	255065_s_at	-0.5
putative protein hypothetical protein F6E13.15 - Arabidopsis thaliana,PIR2:T00682	255041_at	-0.5
hydroxymethylglutaryl-CoA synthase ;supported by full-length cDNA: Ceres:22413.	254845 at	-0.5
putative protein	254794 at	-0.5
putative protein predicted protein, Arabidopsis thaliana, PATCHX:E327449	254701 at	-0.5
putative protein ;supported by full-length cDNA: Ceres:29133.	254462 at	-0.5
putative protein gamma-SNAP protein, bovine, PIR2:S32369;supported by full-length cDNA: Ceres:267158.	254476 at	-0.5
fatty acid hydroxylase - like protein fatty acid hydroxylase Fah1p, Arabidopsis thaliana, PID:g2736147; supported by cDNA: gi 14994242 gb AY04		-0.5
putative protein Human mRNA for KIAA0050 gene, PATCHX:D1006988;supported by full-length cDNA: Ceres:6665.	254428 at	-0.5
G10 - like protein Maternal G10 like protein, Oryza sativa, PATCHX:D1002643; supported by cDNA: gi 15294271 gb AF410327.1 AF410327	254399 at	-0.5
Ribosomal protein L7Ae - like NHP2/RS6 FAMILY PROTEIN, Homo sapiens, PID:q4826860	254355 at	-0.5
dibydroorotase ; supported by cDNA; gi 2121272 gb AF000146.1 ATAF000146	254267_at	-0.5
putative protein	254117 at	-0.5
putative protein ; supported by full-length cDNA: Ceres: 10313.	253918 at	-0.5
putative protein , supported by indirengin control. Ceres 10010. putative zinc finger protein zinc finger protein SINATIO - Vitis vinifera.PID:e1423803	253838 at	-0.5
putative protein range protein range protein and provide vina vina vina vina vina vina vina vina	253766 at	-0.5
rac GTP binding protein Arac7; supported by cDNA: gi 3702961 gb AF079484.1 AF079484	_	-0.5
	253757_at	-0.5
profilin 2 ; supported by full-length cDNA: Ceres: 25886.	253727_at	-0.5 -0.5
putative protein predicted protein, Arabidopsis thaliana, PIR2:T01282;supported by full-length cDNA: Ceres:32381.	253644_at	
putative protein ; supported by full-length cDNA: Ceres: 37881.	253464_at	-0.5
	253276_at	-0.5
putative protein hypothetical protein, Arabidopsis thaliana, PATCHX:E353194; supported by cDNA: gi_13430837_gb_AF360331.1_AF360331	253282_at	-0.5
putative protein various predicted proteins; supported by full-length cDNA: Ceres: 17912.	253233_at	-0.5
Expressed protein ; supported by full-length cDNA: Ceres: 8360.	253119_at	-0.5
putative protein aminoacylase I - Sus scrofa,PID:g1845	253033_at	-0.5
Histone deacetylase ; supported by cDNA: gi_11066138_gb_AF195547.1_AF195547	252982_at	-0.5
hypothetical protein ;supported by full-length cDNA: Ceres:249631.	252995_at	-0.5
	252976_s_at	-0.5
multiubiquitin chain binding protein (MBP1) ;supported by full-length cDNA: Ceres:6757.	252955_at	-0.5
Histon H3 ;supported by full-length cDNA: Ceres:2670.	252849_at	-0.5
hypothetical protein ;supported by full-length cDNA: Ceres:123060.	252852_at	-0.5
histone H3.3 ; supported by cDNA: gi_14326561_gb_AF385735.1_AF385735	252824_at	-0.5
	252789_s_at	-0.5
putative protein several hypothetical proteins - Arabidopsis thaliana; supported by cDNA: gi_15724293_gb_AF412087.1_AF412087	252619_at	-0.5
putative protein senescence-associated protein 5 (SA5) - Hemerocallis hybrid cultivar, EMBL:AF082030; supported by full-length cDNA: Ceres: 11	252591_at	-0.5
putative protein ferripyochelin binding protein - Methanobacterium thermoautotrophicum, EMBL:AE000918.1; supported by cDNA: gi_15293166_gt		-0.5
4-coumarate-CoA ligase -like protein 4-coumarate-CoA ligase enzyme, Pinus taeda, gb:AAA92669;supported by full-length cDNA: Ceres:41541.	252293_at	-0.5
RNA-binding - like protein RNA-binding protein RBP37, Arabidopsis thaliana, PIR:T04196	252313_at	-0.5
Expressed protein ; supported by full-length cDNA: Ceres: 26994.	252181_at	-0.5
steroid 22-alpha-hydroxylase (DWF4) ; supported by cDNA: gi_15724347_gb_AF412114.1_AF412114	252184_at	-0.5
putative protein hypothetical protein T19L18.12 - Arabidopsis thaliana, PIR:T02616;supported by full-length cDNA: Ceres:32231.	252125_at	-0.5
hypothetical protein YIP1 protein, Saccharomyces cerevisiae, PIR:S64486	252002_at	-0.5
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putative protein CHLOROPLAST 30S RIBOSOMAL PROTEIN S20, SWISSPROT:R20_GUITH; supported by cDNA: gi_15810456_gb_AY056		-0.5
protein kinase C inhibitor-like protein protein kinase C inhibitor - Zea mays, PIR:S45368; supported by full-length cDNA: Ceres: 28847.	251707_at	-0.5
Expressed protein ; supported by full-length cDNA: Ceres: 255818.	251660_at	-0.5
pectinesterase precursor-like protein pectinesterase (EC 3.1.1.11) precursor - Pisum sativum, PIR:T06468; supported by cDNA: gi_16974624_g		-0.5
putative protein unknown protein At2g44130 - Arabidopsis thaliana, EMBL:AC004005;supported by full-length cDNA: Ceres:8014.	251443_at	-0.5
URIDYLATE KINASE-like protein URIDYLATE KINASE - Arabidopsis thaliana, EMBL:AF000147; supported by full-length cDNA: Ceres: 16800.	251426_at	-0.5
scarecrow - like protein scarecrow-like 6, Arabidopsis thaliana, EMBL:AF036303	251376_at	-0.5
peptidylprolyl isomerase ROC4 ;supported by full-length cDNA: Ceres:29220.	251305_at	-0.5
putative protein ER6 protein - Lycopersicon esculentum, EMBL:AF096262; supported by cDNA: gi_14334945_gb_AY035146.1_	251221_at	-0.5
hypothetical protein ;supported by full-length cDNA: Ceres:20232.	251210_at	-0.5
lectin - like protein lectin precursor LECSJAbmII, Sophora japonica, EMBL:SJU63012;supported by full-length cDNA: Ceres:41306.	251140_at	-0.5
40S ribosomal protein S17 -like 40S ribosomal protein S17, Lycopersicon esculentum, EMBL:AF161704; supported by full-length cDNA: Ceres:3		-0.5
lysine decarboxylase-like protein	250723_at	-0.5
putative protein similar to unknown protein (gb AAD38624.1)	250586_at	-0.5
putative protein similar to unknown protein (emb CAB61744.1); supported by full-length cDNA: Ceres: 12613.	250511_at	-0.5
histon H3 protein HISTONE H3.2, MINOR, Medicago sativa, SWISSPROT:H32_MEDSA	250397_at	-0.5
enhancer of rudimentary ; supported by cDNA: gi_1595811_gb_U67398.1_ATU67398	250406_at	-0.5
HY5(bZIP transcription factor family) identical to HY5 protein GI:2251084 from [Arabidopsis thaliana]	250420_at	-0.5
putative potassium transport protein glutathione-regulated potassium-efflux system protein KEFB, Escherichia coli, SWISSPROT:P45522	250329_at	-0.5
unknown protein	250247_at	-0.5
ribosomal protein precursor - like ribosomal protein S13 precursor, chloroplast Arabidopsis thaliana, PIR:S59594; supported by cDNA: gi 14517	39 250190 at	-0.5
biotin carboxyl carrier protein of acetyl-CoA carboxylase precursor (BCCP) (splQ42533) :supported by full-length cDNA: Ceres:38996.	250125 at	-0.5
thioredoxin f2 (gb]AAD35004.1); supported by cDNA; gi 4973253 gb AF144386.1 AF144386	250133 at	-0.5
putative protein PGPD14 - Petunia x hybrida, EMBL:AF049930	250000 at	-0.5
putative protein predicted proteins, Arabidopsis thaliana	249968 at	-0.5
chorismate mutase/prephenate dehydratase-like protein; supported by cDNA; gi 16604397 gb AY058097.1	249910 at	-0.5
c-myc binding protein MM-1-like protein ; supported by full-length cDNA: Ceres: 28832.	249829 at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:29189.	249838 at	-0.5
unknown protein	249776 at	-0.5
putative protein contains similarity to translation initiation factor; supported by full-length cDNA: Ceres: 11304.	249711 at	-0.5
elF4Eiso protein (emb[CAA71579.1) ;supported by full-length cDNA: Ceres:23770.	249712 at	-0.5
pyridoxal kinase like protein pyridoxal kinase, Sus scofra, EMBL:AF041255;supported by full-length cDNA: Ceres:107973.	249589 at	-0.5
putative protein MtN24 gene, Medicago truncatula, EMBL:MTY15290	249400 at	-0.5
6-phosphogluconate dehydrogenase ;supported by full-length CDDA: Ceres:109329.	249266 at	-0.5
allene oxide synthase (emb CAA73184.1); supported by cDNA; gi 6002956 gb AF172727.1 AF172727	249208 at	-0.5
N-hydroxycinnamoyl benzoyltransferase-like protein	249188 at	-0.5
putative protein similar to unknown protein (gb/AAD38250.1)	248972 at	-0.5
urea active transporter-like protein	248970 at	-0.5
50S ribosomal protein L14	248970_at 248878 at	-0.5
putative protein strong similarity to unknown protein (gb/AAF02142.1);supported by full-length cDNA; Ceres:7891.	248663 at	-0.5
		-0.5
cyclin C-like protein ;supported by full-length cDNA: Ceres:2036.	248666_at	
unknown protein ;supported by full-length cDNA: Ceres:205928.	248679_at	-0.5 -0.5
ribitol dehydrogenase-like ; supported by cDNA: gi_15146201_gb_AY049242.1_	248539_at	
putative protein strong similarity to unknown protein (gb)AAB68038.1);supported by full-length cDNA: Ceres:17208.	248433_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:20287.	248421_at	-0.5
unknown protein; supported by cDNA: gi_15809965_gb_AY054251.1_	248288_at	-0.5
proline-rich cell wall protein-like ;supported by full-length cDNA: Ceres:110653.	248259_at	-0.5
putative protein similar to unknown protein (gb AAF34833.1)	248238_at	-0.5
Expressed protein ; supported by full-length cDNA: Ceres: 39314.	247899_at	-0.5
similar to unknown protein (sp P72777)	247862_at	-0.5
putative protein predicted protein, Arabidopsis thaliana;supported by full-length cDNA: Ceres:148815.	247716_at	-0.5
GTP-binding protein ara-3 GTP-binding protein ara-3, Arabidopsis thaliana, PIR:JS0640	247699_at	-0.5
actin depolymerizing factor 3 - like protein actin depolymerizing factor 3, Arabidopsis thaliana, EMBL:AF102821;supported by full-length cDNA: (		-0.5
putative protein predicted protein, Synechocystis sp.;supported by full-length cDNA: Ceres:25855.	247583_at	-0.5
putative protein various predicted proteins, Arabidopsis thaliana	247563_at	-0.5
expressed protein similar to unknown protein (gb AAF03448.1); supported by full-length cDNA: Ceres: 97900.	247258_at	-0.5
unknown protein ; supported by cDNA: gi_13877834_gb_AF370180.1_AF370180	247177_at	-0.5

nutative protein action transport protein above. Eacharishia acli. DID:064969	246994 of	0.5
putative protein cation transport protein chaC, Escherichia coli, PIR:G64868 sugar transporter-like protein putative sugar transporter - Prunus armeniaca, EMBL:AF000952; supported by cDNA: gi 16648752 gb AY058152.1	246884_at 246508 at	-0.5 -0.5
calmodulin-3 ;supported by full-length cDNA: Ceres:16715.	246290 at	-0.5
putative protein karyopherin beta 3 - Homo sapiens, EMBL:U72761; supported by cDNA: gi 14334741 gb AY035044.1	245941 at	-0.5
putative protein NAC1 - Medicago truncatula, EMBL:ME251214	245934 at	-0.5
ribosomal protein S15-like ribosomal protein S15 - Arabidopsis thaliana, EMBL:Z23161;supported by full-length cDNA: Ceres:164.	245954_at	-0.5
cytochrome b561, putative similar to cytochrome b561 GI:291 from (Bos taurus)	245818 at	-0.5
hypothetical protein predicted by genscan+; supported by cDNA: gi 16323183 gb AY057696.1	245776 at	-0.5
unknown protein contains similarity to anthranilate synthase large subunit GI:1374671 from [Buchnera aphidicola]	245745 at	-0.5
		-0.5
hypothetical protein predicted by genemark.htm;supported by full-length cDNA: Ceres:2091.	245666 at	-0.5
nybertada protein proteina kunningsported by dimensionebra. Ones 2007.	245484 at	-0.5
disease resistance RP5 like protein	245448 at	-0.5
ubulin alpha-6 chain (TUA6); supported by cDNA; gi 16226461 gb AF428406.1 AF428406	245270 at	-0.5
unknown protein predicted by genscan	245165 at	-0.5
putative poly(A) binding protein ; supported by cDNA; gi 15292850 gb AY050859.1	245085 at	-0.5
RNA polymerase alpha subunit	244978 at	-0.5
hypothetical protein predicted by genscan+	257061 at	-0.5
hypothetical protein predicted by genscan	267549 at	-0.5
putative 1-aminocyclopropane-1-carboxylate oxidase similar to ESTs emblZ34690, gb T04168, gb H37738, gb T76913, gb T43801, amd gb T2196-	264843 at	-0.5
unknown protein ; supported by full-length cDNA: Ceres:15062.	260004 at	-0.5
unknown protein similar to GB-AAC28186	259701 at	-0.5
putative UDP-glucose glucosyltransferase similar to GB:Q40284 from [Manihot esculenta]	257949 at	-0.5
cytochrome P450 homoloa, putative similar to cytochrome P450 homolog GB:U54770 GI:1421740 from [Lycopersicon esculentum]:supported by fu	_	-0.5
homeodomain containing protein 1 ; supported by cDNA: gi 2506030 dbi D43962.1 D43962	253466 at	-0.5
putative protein hypothetical proteins - Arabidopsis thaliana	252765 at	-0.5
putative protein predicted protein, Arabidopsis thaliana	252204 at	-0.5
ethylene-regulated nuclear protein ERT2-like protein	249042 at	-0.5
putative protein similar to unknown protein (gb)AAD28645.1);supported by full-length cDNA: Ceres:14816.	248685 at	-0.5
amino acid transport protein AAP2 supported by full-length cDNA: Ceres: 114602.	245891 at	-0.5
		2.0

Table 5: Transcripts suppressed during heat shock compared to unstressed plants         Descriptions	Affimetrix number	log₂ fold supressed
Descriptions putative protein predicted proteins, Arabidopsis thaliana	247474_at	-5.8
late embryogenis abundant protein, putative similar to late embryogenis abundant protein 5 GI:2981167 from [Nicotiana tabacum];supported by fi		-5.5
unknown protein ;supported by full-length cDNA: Ceres:4309.	202113_at 248062 at	-5.2
	262832_s_at	-4.9
DNA-binding protein, putative similar to DNA binding protein CCA1 from [Arabidopsis thaliana]	261569 at	-4.8
protein kinase, putative contains Pfam profile: PF00069: Eukaryotic protein kinase domain	256366_at	-4.8
putative phytochelatin synthetase - like putative phytochelatin synthetase, Arabidopsis thaliana, EMBL:ATH6787	247604_at	-4.8
hypothetical protein similar to hypothetical protein GI:6524175 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:3618.	245816 at	-4.6
putative protein prib5, Ribes nigrum, EMBL:RNI7578;supported by full-length cDNA: Ceres:31361.	251400_at	-4.2
hypothetical protein predicted by genscan+	259385_at	-4.1
putative protein other hypothetical proteins in Arabidopsis thaliana; supported by cDNA: gi_6457330_gb_AF188329.1_AF188329	252060 at	-4.1
putative protein	251003 at	-4
putative mutT domain protein	263852 at	-3.8
putative monodehydroascorbate reductase (NADH) similar to monodehydroascorbate reductase (NADH) GB:JU0182 [Cucumis sativus]; supporte		-3.8
unknown protein	258362 at	-3.8
peroxidase ATP19a	254914_at	-3.8
unknown protein ;supported by full-length cDNA: Ceres:207075.	249836_at	-3.8
myrosinase-associated protein, putative similar to myrosinase-associated protein GI:1769967 from [Brassica napus]; supported by cDNA: gi_158		-3.7
unknown protein	249740 at	-3.7
putative protein hypothetical protein At2g41240 - Arabidopsis thaliana, EMBL:AC005662	251677_at	-3.6
hypothetical protein predicted by genscan and genefinder	265892 at	-3.5
putative chitinase similar to peanut type II chitinase, GenBank accession number X82329, E.C. 3.2.1.14	255595_at	-3.5
beta-1,3-glucanase	251673_at	-3.5
putative MYB-related protein similar to MYB-related protein GB:CAA73305	258723 at	-3.3
glutathione S-transferase-like protein; supported by cDNA: gi_11096011_gb_AF288189.1_AF288189	250083 at	-3.3
unknown protein	248963_at	-3.3
MYB-related transcription factor (CCA1)	266719_at	-3.2
hypothetical protein Similar to human BC-2 protein; Similar to human BC-2 protein, gi 2828147; supported by cDNA: gi_15529227_gb_AY05223{		-3.2
histone H3 - like protein histone H3, Arabidopsis thaliana, PIR:S06250	250433_at	-3.2
		-3.2
unknown protein	266157_at	-3.1
glutathione S-transferase, putative similar to glutathione S-transferase GI:860955 from [Hyoscyamus muticus]; supported by cDNA: gi_15215607	262119_s_at	-3.1
thaumatin-like protein similar to thaumatin GB:AAD55090 [Vitis riparia]; contains Pfam profile: PF00314 Thaumatin family; supported by cDNA: gi	259925 at	-3.1
serine/threonine-specific protein kinase - like putative protein serine /threonine kinase, Sorghum bicolor, EMBL:SBRLK1	247684_at	-3.1
putative luminal binding protein Similar to Arabidopsis luminal binding protein (gb D89342)	264648_at	-3.1
zinc finger protein, putative similar to finger protein pcp1 GB:S48856 from [Solanum tuberosum]; supported by cDNA: gi_13605632_gb_AF3617§	257610_at	-3
histone H2A - like protein histone H2A, parsley, PIR:S11498;supported by full-length cDNA: Ceres:20036.	247651_at	-3
disease resistance protein RPP1-WsB, putative similar to disease resistance protein RPP1-WsB GI:9279731 from [Arabidopsis thaliana]	246405_at	-3
putative protein hypothetical protein F17H15.20 Arabidopsis thaliana chromosome II BAC F17H15, PID:g3643606	253401_at	-2.9
DNA (cytosine-5)-methyltransferase (DNA methyltransferase) (DNA metase) (sp P34881) ; supported by cDNA: gi_304106_gb_L10692.1_ATHM	248597_at	-2.9
putative protein similar to unknown protein (emb CAA71173.1)	248322_at	-2.9

spliceosomal protein (U2B), putative similar to spliceosomal protein (U2B) GI:169588 from [Solanum tuberosum]	256052 at	-2.9
Expressed protein ; supported by full-length cDNA: Ceres: 10388.	264262_at	-2.8
AIG2-like protein similar to AIG2 protein GB:P54121 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:28511.	258002_at	-2.8
unknown protein	256577_at	-2.8
pEARLI 1 ; supported by cDNA: gi_871779_gb_L43080.1_ATHPEAR	254805_at	-2.8
beta-1,3-glucanase class I precursor ;supported by full-length cDNA: Ceres:3176.	245393_at	-2.8
putative protein other Arabidopsis hypothetical proteins	253940_at	-2.8
uknown protein	265837_at	-2.7
putative tyrosine aminotransferase ;supported by full-length cDNA: Ceres:14570.	263539_at	-2.7
starch synthase, putative similar to starch synthase GI:21613 from [Solanum tuberosum]; supported by full-length cDNA: Ceres:7714.	261191_at	-2.7
glutaredoxin, putative similar to glutaredoxin GB:CAA89699 GI:1732424 from [Ricinus communis]; supported by full-length cDNA: Ceres:125679.	260831_at	-2.7
phosphoethanolamine N-methyltransferase, putative similar to GI:7407189 from [Spinacia oleracea]	259842_at	-2.7
unknown protein ; supported by cDNA: gi_14596082_gb_AY042829.1_	259791_at	-2.7
putative flowering-time gene CONSTANS (COL2) identical to putative flowering-time gene CONSTANS (COL2) GB:AAB67879 GI:1507699 (Arab	258497_at	-2.7
putative lectin similar to lectin SP:P02874 [Onobrychis viciifolia]; contains Pfam profile: PF00139 legume lectins beta domain; supported by cDNA	257206_at	-2.7
glucosyltransferase like protein	245624_at	-2.7
ATPase alpha subunit	245024_at	-2.7
amylogenin; reversibly glycosylatable polypeptide ;supported by full-length cDNA: Ceres:7365.	250130_at	-2.7
Expressed protein ; supported by full-length cDNA: Ceres: 17422.	266767_at	-2.6
glutathione reductase, cytosolic identical to GB:P48641 from [Arabidopsis thaliana] (); supported by cDNA: gi_14532809_gb_AY040029.1_	257252_at	-2.6
NADH dehydrogenase 49KDa protein	244937_at	-2.6
putative elicitor-responsive gene similar to elicitor-responsive gene-3 GB:AAC35866 from [Oryza sativa]; supported by full-length cDNA: Ceres:18!	260083_at	-2.5
unknown protein similar to hypothetical protein GB:CAA10289 [Cicer arietinum]; supported by full-length cDNA: Ceres: 108086.	259272_at	-2.5
ribonucleotide reductase small subunit, putative similar to RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN GB:P49730 from [I	257809_at	-2.5
beta-fructofuranosidase identical to beta-fructofuranosidase GI:6683112 from [Arabidopsis thaliana]; supported by cDNA: gi_6683111_dbj_AB02{	256150_at	-2.5
sucrose-phosphate synthase - like protein sucrose-phosphate synthase, Zea mays, PIR2:JQ1329	255016_at	-2.5
dUTP pyrophosphatase-like protein dUTP pyrophosphatase - Lycopersicon esculentum, PIR2: JQ1599; supported by cDNA: gi_13878142_gb_AF		-2.5
unknown protein	247878_at	-2.5
hypothetical protein predicted by genscan	266070_at	-2.4
hypothetical protein predicted by genscan	265724_at	-2.4
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:10798.	263535_at	-2.4
pale cress protein identical to GB:CAA65334;supported by full-length cDNA: Ceres:28047.	262316_at	-2.4
	254283_s_at	-2.4
histone H2A.F/Z ;supported by full-length cDNA: Ceres:33085.	251846_at	-2.4
putative two-component response regulator protein ; supported by cDNA: gi_11870067_gb_AF305721.1_AF305721	266078_at	-2.3
beta-glucosidase, putative identical to GI:6651430 from [Arabidopsis thaliana]; supported by cDNA: gi_14532461_gb_AY039855.1_	259640_at	-2.3
S-adenosyl-L-homocysteinas, putative similar to S-adenosyl-L-homocysteinase GB:AAD56048 from [Lupinus luteus]; supported by cDNA: gi_152	_	-2.3
thionin, putative similar to thionin [Arabidopsis thaliana] GI:1181533; supported by cDNA: gi_14190504_gb_AF380652.1_AF380652	256527_at	-2.3
unknown protein contains Pfam profile: PF00917 MATH domain; supported by cDNA: gi_12083245_gb_AF332419.1_AF332419	256021_at	-2.3
cell-cell signaling protein csgA - like cell-cell signaling protein csgA, Synechocystis sp., PIR2:S77176	254485_at	-2.3
unknown protein ;supported by full-length cDNA: Ceres:262293.	250665_at	-2.3
UDP-glucose dehydrogenase-like protein UDP-glucose dehydrogenase - Glycine max, EMBL:U53418	249469_at	-2.3
putative protein similar to unknown protein (pir  T05755)	248160_at	-2.3
hypothetical protein ; supported by cDNA: gi_15810232_gb_AY056155.1_	245265_at	-2.3

putative disease resistance protein         267546_at         -22           putative caltractin ; supported by full-length CDNA: Ceres:7802.         266410_at         -22           polygalactornase PC1, putative similar to GB:AAD46483 from [Gkycine max] (Mol. Plant Microbe Interact. 12 (6), 490.498 (1999); supported by 20072, att         -22           putative phosphate/phospheenolpyruvate translocator similar to phosphate/phosphoenolpyruvate translocator precursor GB:AAB40648 [Nocialler 256185, att         -22           cinnamy alcohol dehydrogenase identical to GB:P48523 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:4357.         256023_att           putative protein precised by genscan; supported by cDNA: gi_1522884_gb_AV505076.1_         253189_att         -22           putative protein precised by genscan; supported by cDNA: gi_1522884_gb_AV505076.1_         250344_att         -22           putative protein hypersensitivity-related har201 protein - Nicotiana tabacum, PIR2:T03274         253189_att         -22           unknown protein         250434_att         -22           putative protein inhypothelical protein - Arabidopsis thaliana, PIR2:T03274         253476_att         -22           unknown protein         25044_att         -22           putative protein inhypothelical protein - Nicotiana tabacum, PIR2:T03274         264476_att         -21           putative protein inhypothelical protein - Nicotiana tabacum, PIR2:T03246_att         -21      <		007540 -1	<u> </u>
putative caltractin _supported by full-length cDNA: Ceres:7802.         265400_att         22           polygialacturonase PG1, putative similar to GB:AAD46483 from [Gycine max] (Mol. Plant Microbe Interact. 12 (.6), 490-498 (1999)]; supported by 26907Z, at         22           unknown protein         26907Z, at         22           unknown protein         26907Z, at         22           cinnamyl alcohol dehydrogenase identical to GB:P48523 from [Arabidopsis thaliana]supported by full-length cDNA: Ceres:4357.         258022_at         -22           hypothetical protein predicted by genscan, supported by cDNA: g_i r5282684_gb_AY050876.1_         220717_at         -22           putative protein         283189_at         -22           putative protein         284169_at         -22           putative protein         284169_at         -22           putative protein         284169_at         -22           unknown protein         284169_at         -22           unknown protein         284560_at         -21           putative protein similar to T5J8.18         284476_at         -21           putative protein gamma-SNAP protein, bovine, PIR2:532369; supported by full-length cDNA: Ceres:267158.         284476_at         -21           putative protein gamma-SNAP protein cnd41 - like protein nucleoid DNA-binding protein cnd41, chloroplast, common tobacco, PIR:T01996         260442_at		_	
polyaglachuronase PG1, putative similar to GB:AAD46483 from [Glycine max] (Mol. Plant Microbe Interact. 12 (6), 490-498 (1999)]; supported by 200727_at         2.22           putative phosphate/phosphoenolpyruvate translocator similar to phosphate/phosphoenolpyruvate translocator precursor GB:AAB40648 [Nicotian:         259185_at         2.22           cinnamy lacohol dehydrogenase identical to GB:PA8523 from [Arabidopsis thaliana]:supported by full-length cDNA: Ceres:4357.         258023_at         2.22           putative protein interacted by genscan: supported by CDNA: gl_15252684_gb_A'V050676.1_         2253189_at         2.22           putative protein hypersensitivity-related hsr201 protein - Nicotiana tabacum.PIR2:T03274         225217_at         2.22           ankyrin-repeat-containing protein-like         286449_gat         2.21           unknown protein         248169_at         2.22           putative protein insing protein-like         2864476_at         2.21           putative protein animize to T53.18         264476_at         2.1           putative protein approtein calcium binding domains (EF hand) of several proteins         22671_at         2.1           putative protein insilter in calcium binding domains (EF hand) of several proteins         286476_at         2.1           putative acionol dehydrogenase         22681_at         2.1         2.1           putative protein insilter to f15.21 (rams-splice part 2 of 2)         244480_at			
<ul> <li>unknöwn protein</li> <li>25907 at</li> <li>222</li> <li>cinnamy alcohol dehydrogenase identical to GB:P48233 from [Arabidopsis thaliana]supported by full-length cDNA: Ceres:4357.</li> <li>250052 at</li> <li>222</li> <li>hypothetical protein predicted by genscan; supported by cDNA; gi_15292884_gb_AY050876.1_</li> <li>2501439 at</li> <li>222</li> <li>putative protein hypersensitivity-related har/201 protein - Nicotiana tabacum, PIR2:T03274</li> <li>2501439 at</li> <li>222</li> <li>unknown protein</li> <li>mismic H5</li> <li>Arabidopsis thaliana, PIR:S06250</li> <li>261439 at</li> <li>223</li> <li>unknown protein</li> <li>putative protein hypersensitivity-related har/201 protein - Nicotiana tabacum, PIR2:T03274</li> <li>250434 at</li> <li>224</li> <li>unknown protein</li> <li>putative protein ismillar to FJS.8.18</li> <li>putative protein ismillar to FJS.8.18</li> <li>putative protein ismillar to FJS.8.18</li> <li>putative protein protein calcium-binding protein - Arabidopsis thaliana, PIR2:H71441;supported by full-length cDNA: Ceres:4642.</li> <li>254476 at</li> <li>254476 at</li> <li>254477 at</li> <li>252417 at</li> <li>2144149 protein</li> <li>putative protein</li> <li>putative protein myortein apmets-NAP protein, bovine, PIR2:S32369:supported by full-length cDNA: Ceres:4642.</li> <li>254476 at</li> <li>254476 at</li> <li>214476 at</li> <li>21</li> <li>putative protein</li> <li>putative protein</li> <li>putative protein</li> <li>putative protein hybrietical protein - Arabidopsis thaliana, PIR2:H71441;supportei cpress 267158.</li> <li>254476 at</li> <li>21</li> <li>putative protein in gamma-SNAP protein, bovine, PIR2:S32369:supported by full-length cDNA: Ceres:4642.</li> <li>244976 at</li> <li>21</li> <li>putative protein</li> <li>putative protein</li> <li>S12 (trans-splice part1 2 of 2)</li> <li>putative</li></ul>			
putative phosphate/phosphoenolog/vuvate translocator similar to phosphate/phosphoenolog/vuvate translocator precursor CBrAR40648 [Nicotian 259165_at 22         chinamy alcohol dehydrogenese identicat to GBr48523 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:4357.         258023_at 22           hypothetical protein predicted by genscan: supported by cDNA: gi_15292884_gb_AY050876.1_         25707_at 22           putative protein         253169_at 22           putative protein in presensitivity-related hsr201 protein - Nicotiana tabacum.PIR2:T03274         253477_at 22           niktorne H3 - like protein histone H3. Arabidopsis thaliana, PIR2:50250         250434_at 22           ankyrin-repeat-containing protein-like         248169_at 22           unknown protein         263549_at 2.1           putative protein insing protein-lowine, PIR2:532369:supported by full-length cDNA: Ceres:4642.         254746_at 2.1           putative protein protein calcium binding domains (EF hand) of several proteins         25417_at 2.1           putative protein finsition eradic mobiling protein nucleoid DNA-binding protein cnd41, chloroplast, common tobacco, PIR:T01996         250444_at 2.1           putative protein insiting rotein similar to face repetitis insitiana.PIR2:W174441; supportein (ALARDOR SIG) (ALARDOR SIG)         244940_at 2.1           putative protein         25417_at 2.1         2.1           putative protein insitiant to face protein nucleoid DNA-binding protein cnd41, chloroplast, common tobacco, PIR:T01996         254445_at 2.1 <td></td> <td></td> <td></td>			
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histone H3 - like protein histone H3, Arabidopsis thaliana, PIR:S06250         250434_at         -2.2           unknown protein         248199_at         -2.2           unknown protein         263549_at         -2.2           unknown protein         263549_at         -2.2           unknown protein         263549_at         -2.1           putative protein similar to T5J8.18         255450_at         -2.1           putative protein ing amma-SNAP protein, bovine, PIR2:S32369;supported by full-length cDNA: Ceres:4642.         254746_at         -2.1           putative protein         252477_at         -2.1           putative protein         252417_at         -2.1           nucleoid DNA-binding protein calcium binding domains (EF hand) of several protein scommon tobacco, PIR:T01996         250445_at         -2.1           nucleoid DNA-binding protein calcium binding to protein nucleoid DNA-binding protein cnd41, chloroplast, common tobacco, PIR:T01996         244988_s_at         -2.1           putative achoh delydrogenase         266761_at         -2.1         -2.1			
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ankyrin-répeat-containing protein-like         248165_at         -2.2           unknown protein         263549_at         -2.1           putative protein similar to T5J.8.18         255450_at         -2.1           putative protein similar to T5J.8.17         255476_at         -2.1           putative protein gamma-SNAP protein, bovine, PIR2:S3269:supported by full-length cDNA: Ceres:267158.         254476_at         -2.1           putative protein         252661_at         -2.1           putative calcum-binding protein calcum binding domains (EF hand) of several proteins         25042_at         -2.1           nucleoid DNA-binding protein calcum binding domains (EF hand) of several proteins         250445_at         -2.1           nucleoid DNA-binding protein calcum binding domains (EF hand) of several proteins         244980_at         -2.1           nucleoid DNA-binding protein calcum binding domains (EF hand) of several proteins         244980_at         -2.1           nucleoid DNA-binding protein calcum binding spotein calcum binding protein calcum binding protein calcum binding spotein calcum binding protein calcum binding protein calcum binding spotein calcum binding			
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12-oxophytodienoate reductase (OPR2) identical to 12-oxophytodienoate reductase OPR2 GB:AAC78441 [Arabidopsis thaliana]259875 s_at-2hypothetical protein ; supported by cDNA: gi_14532585_gb_AY039917.1_259561_at-2unknown protein ; supported by full-length cDNA: Ceres:96816.257793_at-2unknown protein256096_at-2putative serine carboxypeptidase II255842_at-2putative protein centrin, Marsilea vestita; supported by full-length cDNA: Ceres:13072.253915_at-2dehydrin Xero2 ; supported by cDNA: gi_15809983_gb_AY054260.1_252102_at-2beta-1,3-glucanase 2 (BG2) (PR-2) ; supported by full-length cDNA: Ceres: 21719.251625_at-2Expressed protein ; supported by full-length cDNA: Ceres: 32396.251142_at-2unknown protein ; supported by cDNA: gi_15810044_gb_AY054291.1_250826_at-2amino acid permease 6 (emb CAA65051.1)248666_s_at-2FRO2-like protein; NADPH oxidase-like248666_s_at-2putative protein contains similarity to ornithine cyclodeaminase; supported by full-length cDNA: Ceres:114678.24830_at-2isp4 like protein ; supported by cDNA: gi_15451019_gb_AY054590.1_248296_at-2			
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putative protein contains similarity to ornithine cyclodeaminase;supported by full-length cDNA: Ceres:114678. 248330_at -2 isp4 like protein ; supported by cDNA: gi_15451019_gb_AY054590.1_ 245296_at -2			
isp4 like protein ; supported by cDNA: gi_15451019_gb_AY054590.1_ 245296_at -2			
putative glutaredoxin ;supported by full-length CDINA: Ceres:21006. 266516_at -1.9			
		200510_at	-1.9

unknown protein ;supported by full-length cDNA: Ceres:22382.	266227_at	-1.9
unknown protein ;supported by cDNA: gi_15451161_gb_AY054661.1_	266142_at	-1.9
myrosinase-binding protein homolog, putative almost identical to myrosinase-binding protein homolog GI:2997767 from [Arabidopsis thaliana]; su	265058_s_at	-1.9
putative carboxypeptidase ; supported by cDNA: gi_15724217_gb_AF412049.1_AF412049	264071_at	-1.9
putative harpin-induced protein ;supported by full-length cDNA: Ceres:19481.	263951_at	-1.9
unknown protein location of EST TAT5A03; 5 end, gb Z26679	262656_at	-1.9
zinc finger protein, putative similar to zinc finger protein ID1 GB:AAC18941 GI:3170601 from [Zea mays]	260776_at	-1.9
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_14423519_gb_AF386997.1_AF386997	259617_at	-1.9
unknown protein ; supported by full-length cDNA: Ceres: 20582.	259403_at	-1.9
putative disease resistance protein similar to disease resistance protein RPP1-WsC GB:AAC72979 [Arabidopsis thaliana]; supported by cDNA: gi		-1.9
	252562_s_at	-1.9
putative protein serine/threonine protein kinase ATPK10 - Arabidopsis thaliana, EMBL:D30622; supported by cDNA: gi_13249126_gb_AF29566§	251060_at	-1.9
putative protein contains similarity to photomorphogenesis repressor protein; supported by cDNA: gi_14532633_gb_AY039941.1_	249798_at	-1.9
	249463_s_at	-1.9
amino acid permease	249346_at	-1.9
3-keto-acyl-CoA thiolase 2 (gb AAC17877.1); supported by cDNA: gi_3192892_gb_AF062590.1_AF062590	248625_at	-1.9
flavonol 3-O-glucosyltransferase-like	248185_at	-1.9
putative protein similar to unknown protein (pir  T05752);supported by full-length cDNA: Ceres:109272.	248164_at	-1.9
putative protein similar to unknown protein (gb AAF67766.1);supported by full-length cDNA: Ceres:512.	246997_at	-1.9
putative pectinesterase	245052_at	-1.9
putative myrosinase-binding protein ;supported by full-length cDNA: Ceres:39069.	266989_at	-1.8
pathogenesis-related PR-1-like protein identical to GB:M90508; supported by cDNA: gi_166860_gb_M90508.1_ATHRPRP1A	266385_at	-1.8
putative 2,3-bisphosphoglycerate-independent phosphoglycerate mutase Strong similarity to R. communis phosphoglycerate mutase (gb X70652	264668_at	-1.8
putative GDSL-motif lipase/hydrolase similar to APG proteins; pFAM domain PF00657;supported by full-length cDNA: Ceres:121397.	263482_at	-1.8
hypothetical protein	262661_s_at	-1.8
jasmonate inducible protein isolog ;supported by full-length cDNA: Ceres:119153.	259382_s_at	-1.8
Expressed protein ; supported by full-length cDNA: Ceres: 35429.	258349_at	-1.8
hypothetical protein similar to CGI-18 protein GB:AAD27727 [Homo sapiens]	258049_at	-1.8
zinc finger protein, putative contains Pfam profile: PF01760 CONSTANS family zinc finger; supported by full-length cDNA: Ceres: 258241.	257262_at	-1.8
PHD-finger protein, putative contains Pfam profile: PF00628 PHD-finger;supported by full-length cDNA: Ceres:95660.	256889_at	-1.8
serine/threonine kinase - like protein serine/threonine kinase, Brassica oleraceae	254250_at	-1.8
putative potassium transporter AtKT5p (AtKT5)	253330_at	-1.8
hypothetical protein	252345_at	-1.8
glutaredoxin -like protein glutaredoxin, castor bean, PIR:S54825	251196_at	-1.8
putative protein contains similarity to DNA-binding protein	249890_at	-1.8
putative protein similar to unknown protein (emb CAB62461.1);supported by full-length cDNA: Ceres:268701.	249752_at	-1.8
putative protein similar to unknown protein (pir  T05562); supported by full-length cDNA: Ceres: 158397.	248551_at	-1.8
tyrosine aminotransferase	248207_at	-1.8
putative protein similar to unknown protein (pir  T04819)	248139_at	-1.8
unknown protein contains similarity to anthranilate synthase large subunit GI:1374671 from [Buchnera aphidicola]	245745_at	-1.8
putative protein similarity to predicted proteins, Arabidopsis thaliana	245155_at	-1.8
NADH dehydrogenase ND1	244936_at	-1.8
calcium binding protein (CaBP-22) identical to GB:Z12136;supported by full-length cDNA: Ceres:123659.	267076_at	-1.7
unknown protein ;supported by cDNA: gi_14517479_gb_AY039575.1_	266017_at	-1.7

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5 -adenylylphosphosulfate reductase, putative similar to 5 -adenylylphosphosulfate reductase GI:1336168 from [Arabidopsis thaliana];supported	264745_at	-1.7
putative RAS-related protein, RAB11C Strong similarity to A. thaliana ara-2 (gb ATHARA2). ESTs gb ATTS2483,gb ATTS2484,gb AA042159 cor		-1.7
unknown protein similar to PHZF, catalyzing the hydroxylation of phenazine-1-carboxylic acid to2-hydroxy-phenazine-1-carboxylic acid; ESTs gb		-1.7 -1.7
putative beta-ketoacyl-CoA synthase	263606_at	
unknown protein	263565_at	-1.7
peptide transporter, putative predicted by genemark.hmm; supported by cDNA: gi_15810442_gb_AY056260.1_	261958_at	-1.7
pectin methylesterase, putative similar to pectin methylesterase GI:1617583 from [Lycopersicon esculentum]; supported by cDNA: gi_14334991_		-1.7
hypothetical protein predicted by genemark.hmm	261684_at	-1.7
unknown protein	260904_at	-1.7
flower development protein cycloidea (cyc3), putative similar to flower development protein cycloidea (cyc3) GI:6358611 from [Misopates orontiu		-1.7
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_16648778_gb_AY058166.1_	259373_at	-1.7
unknown protein	258100_at	-1.7
unknown protein ;supported by full-length cDNA: Ceres:40534.	258040_at	-1.7
disease resistance protein, putative similar to GB:AAD13301 from [Lycopersicon esculentum], contains Pfam profiles: PF00560 Leucine Rich Re		-1.7
putative inorganic phosphatase ;supported by cDNA: gi_15450871_gb_AY054516.1_	255587_at	-1.7
	254740_s_at	-1.7
serine threonine kinase - like protein KI domain interacting kinase 1 (KIK1), Zea mays; supported by cDNA: gi_13506746_gb_AF224706.1_AF22	254265_s_at	-1.7
Expressed protein ; supported by cDNA: gi_14190492_gb_AF380646.1_AF380646	253423_at	-1.7
putative auxin-induced protein auxin-induced protein 10A, Glycine max., PIR2:JQ1099	252965_at	-1.7
putative protein carbonyl reductase (NADPH) - Rattus norvegicus, PIR:JC5285; supported by cDNA: gi_15028054_gb_AY045884.1_	251309_at	-1.7
putative protein predicted protein, Arabidopsis thaliana	249919_at	-1.7
sigma-like factor (emb CAA77213.1)	249769_at	-1.7
calcium-binding protein - like cbp1 calcium-binding protein, Lotus japonicus, EMBL:LJA251808; supported by cDNA: gi_16648829_gb_AY058192	249417_at	-1.7
histone H3 (sp P05203);supported by cDNA: gi_13926210_gb_AF370577.1_AF370577	247192_at	-1.7
putative protein similar to unknown protein (emb CAB62301.1)	247030_at	-1.7
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:42217.	245755_at	-1.7
disease resistance RPP5 like protein (fragment)	245450 at	-1.7
DNA-3-methyladenine glycosidase, putative similar to DNA-3-methyladenine glycosidase GB:CAB60736 GI:6434028 from [Staphylococcus aurei	257474 at	-1.7
DNA polymerase alpha subunit IV (primase)-like protein	249276 at	-1.7
putative phosphomannomutase ;supported by full-length cDNA: Ceres:998.	266928 at	-1.6
putative glycine dehydrogenase	266892 at	-1.6
putative glutathione S-transferase ; supported by cDNA: gi_14423533_gb_AF387004.1_AF387004	266267 at	-1.6
putative membrane channel protein ;supported by full-length cDNA: Ceres: 10159.	266225 at	-1.6
unknown protein ;supported by full-length cDNA: Ceres:108956.	265384_at	-1.6
similar to flavin-containing monooxygenase (sp P36366); similar to ESTs gb R30018, gb H36886, gb N37822, and gb T88100 similar to flavin-cor		-1.6
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:36412.	264091_at	-1.6
putative RNA-binding protein Identical to gb/Y10557 g5bf gene from Arabidopsis thaliana. ESTs gb/R30578, gb/R90475, gb/T22384, gb/T22425,		-1.6
putative CONSTANS-like B-box zinc finger protein ; supported by cDNA: gi_12698721_gb_AF323666.1_AF323666	263252 at	-1.6
calreticulin, putative similar to calreticulin GB:AAC49697 GI:2052383 from [Arabidopsis thaliana]; supported by cDNA: gi_2052382_gb_U66345.1	_	-1.6
Ca2+-dependent membrane-binding protein annexin idenctical to GB:AAD34236 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres		-1.6
Cyclin, putative similar to GB:CAB77269 from [Pisum sativum]	260506 at	-1.6
unknown protein ;supported by full-length cDNA: Ceres:142725.	259980_at	-1.6
unknown protin ;supported by full-length cDNA: Ceres:37425.	259275_at	-1.6
heat-shock protein (At-hsc70-3) identical to (At-hsc70-3) (cytosolic Hsp70) GB:CAA76606 [Arabidopsis thaliana]; supported by cDNA: gi_1529292		-1.6
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disease resistance protein, putative similar to Hcr2-5b GB:AAC78595 [Lycopersicon esculentum] (Plant Cell 10, 1915-1926 (1998)); contains Pfa	257763_s_at	-1.6
unknown protein ; supported by full-length cDNA: Ceres: 148308.	256456_at	-1.6
unknown protein contains similarity to alternative NADH-dehydrogenase GI:3718005 from [Yarrowia lipolytica]; supported by full-length cDNA: Cer	256057_at	-1.6
putative cinnamoyl-CoA reductase highly similar to F4P9.36	255845_at	-1.6
PRH26 protein ;supported by full-length cDNA: Ceres:36866.	254343_at	-1.6
acid phosphatase-like protein acid phosphatase-1 (EC 3.1.3) - Lycopersicon esculentum, PIR2:T06587; supported by cDNA: gi_15293022_gb_	253731_at	-1.6
hypothetical protein	252501_at	-1.6
putative protein several hypothetical Na(+)/H(+) antiporter	251906_at	-1.6
putative protein hypothetical protein F22K20.16 - Arabidopsis thaliana, EMBL:AC002291	251701_at	-1.6
putative protein beta-(1-3)-glucosyl transferase, Bradyrhizobium japonicum, EMBL:AF047687; supported by cDNA: gi_16974551_gb_AY060563.	250892_at	-1.6
asparaginase ;supported by cDNA: gi_14517439_gb_AY039555.1_	250547_at	-1.6
putative protein similar to unknown protein (dbj BAA92898.1);supported by full-length cDNA: Ceres:97314.	249230_at	-1.6
putative protein contains similarity to calmodulin; supported by full-length cDNA: Ceres: 99348.	249197_at	-1.6
putative protein contains similarity to unknown protein (dbj BAA90637.1)	248309_at	-1.6
putative protein similar to unknown protein (gb AAD26950.1); supported by full-length cDNA: Ceres: 33791.	248261_at	-1.6
putative protein similar to unknown protein (gb AAF21150.1)	247958_at	-1.6
unknown protein	247415_at	-1.6
AtPP -like protein AtPP protein, Brassica napus, EMBL:BNA245479; supported by cDNA: gi_15293070_gb_AY050969.1_	246340_s_at	-1.6
phytochrome kinase substrate 1 - like protein	245696_at	-1.6
hypothetical protein ; supported by full-length cDNA: Ceres: 933.	245304_at	-1.6
carboxytransferase beta subunit	245016_at	-1.6
ribosomal protein L2	244987_s_at	-1.6
	244992_s_at	-1.6
protein kinase - like protein serine threonine kinase - Brassica oleracea; supported by cDNA: gi_13506748_gb_AF224707.1_AF224707	254266_at	-1.6
putative acetone-cyanohydrin lyase	267126_s_at	-1.5
putative glutathione S-transferase ;supported by full-length cDNA: Ceres:27915.; supported by cDNA: gi_11095995_gb_AF288181.1_AF288181	266746_s_at	-1.5
histone H4 identical to GB:M17133 and GB:M17132;supported by full-length cDNA: Ceres:32642.	266226_at	-1.5
putative replication protein A1 ;supported by full-length cDNA: Ceres:7536.	265695_at	-1.5
beta-expansin ;supported by full-length cDNA: Ceres:109135.	265443_at	-1.5
unknown protein contains Pfam profile:PF01762 Galactosyltransferase	264978_at	-1.5
unknown protein similar to hypothetical protein GI:9665091 from [Arabidopsis thaliana]	264998_at	-1.5
putative fructokinase ; supported by full-length cDNA: Ceres: 17664.	263250_at	-1.5
water stress-induced protein, putative similar to water stress-induced protein, GI:454880 from [Oryza sativa]; supported by full-length cDNA: Cere	262958_at	-1.5
unknown protein	262693_at	-1.5
putative prenyl transferase (prephytoene pyrophosphatase dehydrogenase) Except for first 55 amino acids, 52% identical to Prenyl transferase [(	262526_at	-1.5
lysophospholipase homolog, putative similar to lysophospholipase homolog GB:AAB97366 GI:2801536 from [Oryza sativa]	261661_at	-1.5
2,4-D inducible glutathione S-transferase, putative similar to 2,4-D inducible glutathione S-transferase GI:2920666 from [Glycine max]; supported	260745_at	-1.5
integral membrane protein, putative similar to GB:U43629 from [Beta vulgaris] (Plant Physiol. 110 110 (2), 511-520 (1996)); supported by cDNA:	260676_at	-1.5
putative peptidyl-prolyl cis-trans isomerase ; supported by cDNA: gi_15215840_gb_AY050450.1_	260530_at	-1.5
unknown protein similar to hypothetical protein GB:S33464 [Arabidopsis thaliana]; supported by cDNA: gi_14517447_gb_AY039559.1_	259228_at	-1.5
reversibly glycosylated polypeptide-1 identical to reversibly glycosylated polypeptide-1 (implicated in cell wall biosynthesis) GB:AAC50000 [Arabic		-1.5
putative pectinacetylesterase similar to GB:CAA67728 from [Vigna radiata]; supported by cDNA: gi_15292826_gb_AY050847.1_	258750_at	-1.5
Expressed protein ; supported by full-length cDNA: Ceres: 6490.	258470_at	-1.5
unknown protein ;supported by full-length cDNA: Ceres:20618.	257710_at	-1.5

cyclopropane-fatty-acyl-phospholipid synthase, putative similar to cyclopropane-fatty-acyl-phospholipid synthase GB:P30010 [Escherichia coli]	257175 s at	-1.5
disease resistance protein, putative similar to GB:AAD13301 from [Lycopersicon esculentum], contains Pfam profiles: PF00560 Leucine Rich Re		-1.5
receptor protein kinase, putative contains Pfam profiles: PF00069: Eukaryotic protein kinase domain, multiple PF00560: Leucine Rich Repeat	256168_at	-1.5
putative protein	255652 at	-1.5
growth factor like protein antisense basic fibroblast growth factor GFG - Rattus norvegicus, PID:g1518635;supported by full-length cDNA: Ceres:	_	-1.5
putative protein CGI-131 protein, Homo sapiens, AF151889;supported by full-length cDNA: Ceres:24573.	254387 at	-1.5
putative protein rape mRNA, Brassica napus, PIR2:S42651	254259 s at	-1.5
low temperature and salt responsive protein homolog low temperature and salt responsive protein LTI6A - Arabidopsis thaliana, PID:g4039153	253627_at	-1.5
putative protein AT.I.24-7, Arabidopsis thaliana, gb:U63815	253215 at	-1.5
putative protein strictosidine synthase (EC 4.3.3.2) - Rauvolfia mannii (fragment);supported by full-length cDNA: Ceres:98698.	251658 at	-1.5
UDP-GlcNAc:dolichol phosphate N-acetylglucosamine-1-phosphate transferase-like protein UDP-GlcNAc:dolichol phosphate N-acetylglucosamir		-1.5
protein phosphatase - like protein protein phosphatase 2C homolog, Mesembryanthemum crystallinum, EMBL:AF097667	251017_at	-1.5
short chain alcohol dehydrogenase-like ;supported by full-length cDNA: Ceres:111427.	250763 at	-1.5
putative protein contains similarity to ribose 5-phosphate isomerase;supported by full-length cDNA: Ceres:32092.	249002 at	-1.5
putative protein similar to unknown protein (pir  T06700)	248986_at	-1.5
urea active transporter-like protein	248970 at	-1.5
putative protein similar to unknown protein (pir  T04427)	248943 s at	-1.5
unknown protein ;supported by full-length cDNA: Ceres:15495.	248889 at	-1.5
putative protein similar to unknown protein (pir  S72530);supported by full-length cDNA: Ceres:32925.	248683 at	-1.5
putative protein similar to unknown protein (sp P29618);supported by full-length cDNA: Ceres:95459.	248270 at	-1.5
apospory-associated protein C-like	247101 at	-1.5
hypothetical protein	246281 at	-1.5
unknown protein	245744 at	-1.5
disease resistance RPP5 like protein	245448 at	-1.5
PSII 32 KDa protein	245047 at	-1.5
ATPase I subunit	245025_at	-1.5
unknown protein ;supported by cDNA: gi_14532501_gb_AY039875.1_	256627_at	-1.5
putative alliin lyase alliin lyase (EC 4.4.1.4) precursor (CYSTEINE SULPHOXIDE LYASE), onion, PIR2:S29301; supported by cDNA: gi_1529269		-1.5
S-adenosylmethionine decarboxylase (adoMetDC2); supported by cDNA: gi_16930682_gb_AF436825.1_AF436825	246490_at	-1.5
putative proline-rich protein ; supported by full-length cDNA: Ceres: 28853.	267260_at	-1.4
hypothetical protein predicted by genscan and genefinder	266363_at	-1.4
putative phosphoglucomutase similar to GB:AAD13031 and GB:AAC50049, location of ESTs gb/W43354, gb/N37499 and gb/N96251; supported	264903_at	-1.4
lipoyltransferase identical to GB:BAA78386; supported by cDNA: gi_4996285_dbj_AB020975.1_AB020975	264613_at	-1.4
unknown protein	264172_at	-1.4
unknown protein contains similarity to gi 1653332 extragenic suppressor (SuhB) from Synechocystis sp. gb D90912 and is a member of the Inosit	263705_at	-1.4
unknown protein ;supported by full-length cDNA: Ceres:11114.	263628_at	-1.4
putative NAD+ dependent isocitrate dehydrogenase subunit 2, IDH2 genomic copy of ICDH2 cDNA U81994, ESTs R29962, R29955 catalyzes th	263583_at	-1.4
putative pyrophosphate-dependent phosphofructokinase alpha subunit similar to GB:AAC67587 from [Citrus X paradisi] and GB:Q41140 from [Riv	262806_at	-1.4
unknown protein ; supported by cDNA: gi_15215593_gb_AY050325.1_	262634_at	-1.4
glutamate decarboxylase (gad), putative similar to glutamate decarboxylase (gad) GI:294111 from [Petunia hybrida]; supported by cDNA: gi_118	261970_at	-1.4
dirigent protein, putative similar to dirigent protein GI:6694693 from [Forsythia intermedia]	261914_at	-1.4
hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 268411.	261351_at	-1.4
pectinesterase, putative similar to GB:Z94058 from [Lycopersicon esculentum]; supported by cDNA: gi_16648888_gb_AY059814.1_	261363_at	-1.4
hypothetical protein predicted by genemark.hmm	261221_at	-1.4

unknown protein ;supported by full-length cDNA: Ceres:32887.	261032_at	-1.4
beta-galactosidase, putative similar to beta-galactosidase GI:3299896 from [Lycopersicon esculentum]; supported by cDNA: gi_16604399_gb_A`	260944_at	-1.4 -1.4
fructose 1,6-bisphosphatase, putative similar to cytosolic fructose-1,6-bisphosphatase GB:AAD28755 GI:4741918 from [Musa acuminata]	260837 at	-1. <del>4</del> -1.4
unknown protein ; supported by cDNA: gi_15810460_gb_AY056269.1_	260501_at	-1.4
hypothetical protein similar to YGL010w-like protein GB:AAC32136 [Picea mariana]	260211 at	-1. <del>4</del> -1.4
unknown protein	260081_at	-1. <del>4</del> -1.4
unknown protein supported by cDNA: Ceres:13335	260072 at	-1.4 -1.4
endo-beta-1,4-glucanase, putative similar to GI:4972236 from [Fragaria x ananassa] (Plant Mol. Biol. 40, 323-332 (1999)); supported by cDNA: g	_	-1.4 -1.4
putative signal peptidase similar to MITOCHONDRIAL INNER MEMBRANE PROTEASE SUBUNIT 2 GB:P46972 [Saccharomyces cerevisiae]	259730_at 259199_at	-1.4 -1.4
putative signal peptidase similar to infroethold Riak infreet memorane PROTEASE Soboliting Ob. P40972 [Sacchalomyces cerevisiae] putative 40S ribosomal protein similar to ribosomal protein S7 GB:AAD26256 from [Secale cereale];supported by full-length cDNA: Ceres:30349.	258486_at	-1.4 -1.4
hypothetical protein contains similar to hosonial protein 37 GB.AAD20250 non [Secale Cereale], supported by full-length CDNA. Ceres. 30349.		-1.4 -1.4
xyloglucan endotransglycosylase, putative similar to xyloglucan endotransglycosylase 1 GB:CAA10231 from [Fagus sylvatica] (Plant Physiol.(19)	_	-1.4
unknown protein contains Pfam profile:PF00279 LTP:Plant lipid transfer protein family;supported by full-length cDNA: Ceres:19287.	256933_at	-1.4
zinc-finger protein, putative similar to GI:5262161 from [Arabidopsis thaliana]; supported by cDNA: gi_16323142_gb_AY057675.1_	256469_at	-1.4
	256431_s_at	-1.4
nascent polypeptide associated complex alpha chain, putative similar to nascent polypeptide associated complex alpha chain GB:AAF27917 GI:		-1.4
	255065_s_at	-1.4
putative alpha NAC stong similarity to Nascent polypeptide associated complex alpha chain - human, PIR2:S49326; supported by cDNA: gi_1502		-1.4
putative pollen surface protein endosperm specific protein - Zea mays, PID:g2104712;supported by full-length cDNA: Ceres:4620.	254785_at	-1.4
SERINE CARBOXYPEPTIDASE I PRECURSOR-like protein SERINE CARBOXYPEPTIDASE I PRECURSOR - Hordeum vulgare, SWall:CBP1_		-1.4
putative dihydrolipoamide succinyltransferase dihydrolipoamide succinyltransferase (EC 2.3.1.61) precursor - rat, Pir2:A41015;supported by full-l		-1.4
putative protein predicted protein, Arabidopsis thaliana; supported by full-length cDNA: Ceres:4354.	253165_at	-1.4
guanine nucleotide-exchange protein -like guanine nucleotide-exchange protein -Bos taurus,PID:g2674107	253032_at	-1.4
Expressed protein ; supported by full-length cDNA: Ceres: 22456.	252823_at	-1.4
putative LEA protein Picea glauca late embryogenesis abundant protein (EMB8), PID:g1350545;supported by full-length cDNA: Ceres:36702.	252132_at	-1.4
putative protein several hypothetical proteins - Arabidopsis thaliana; supported by cDNA: gi_15010763_gb_AY045683.1_	252098_at	-1.4
F-box protein family, AtFBL17 contains similarity to F-box protein FBL2 GI:6010699 from [Rattus norvegicus]	251850_at	-1.4
putative protein NODULIN-26 - Glycine max, EMBL:X04782; supported by full-length cDNA: Ceres: 32275.	251661_at	-1.4
putative protein prib5, Ribes nigrum, EMBL:RNI7578	251418_at	-1.4
putative protein hypothetical protein F4I18.26 - Arabidopsis thaliana, PIR:T02471;supported by full-length cDNA: Ceres:30454.	251336_at	-1.4
cysteine synthase AtcysC1 ;supported by full-length cDNA: Ceres:32851.	251322_at	-1.4
putative protein similar to unknown protein (gb AAD38624.1)	250586_at	-1.4
serine-type carboxypeptidase II-like protein carboxypeptidase D - Triticum aestivum, PIR:A29639; supported by cDNA: gi_13877962_gb_AF3702		-1.4
beta-xylosidase - like protein beta-xylosidase, Aspergllus nidulans, EMBL:ANXLND; supported by cDNA: gi_15982752_gb_AY057483.1_	250444_at	-1.4
Glucose-1-phosphate adenylyltransferase (ApL1/adg2); supported by cDNA: gi_2149020_gb_U72290.1_ATU72290	249927_at	-1.4
histone H2B like protein (emb CAA69025.1)	249916_at	-1.4
putative protein similar to unknown protein (gb AAD29063.1)	249777_at	-1.4
putative protein DNA DAMAGE-RESPONSIVE PROTEIN 48, Saccharomyces cerevisiae, EMBL:SCDDR48A; supported by cDNA: gi_16604363_	249416_at	-1.4
33 kDa secretory protein-like ;supported by cDNA: gi_15292980_gb_AY050924.1_	248686_at	-1.4
putative protein similar to unknown protein (gb AAC24386.1)	248191_at	-1.4
xyloglucan endo-transglycosylase-like protein ;supported by full-length cDNA: Ceres:12301.	247162_at	-1.4
prolyl 4-hydroxylase, alpha subunit-like protein	247124_at	-1.4
adenylate kinase -like protein adenylate kinase (EC 2.7.4.3), chloroplast, maize, PIR:S45634	246651_at	-1.4
transcriptional co-activator-like protein putative transcriptional co-activator (KIWI) - Arabidopsis thaliana, EMBL:AF053302	245930_at	-1.4

phosphate/phosphoenolpyruvate translocator - like protein ;supported by full-length cDNA: Ceres:100777.	245698_at	-1.4
ras-related small GTP-binding protein RAB1c ; supported by cDNA: gi_15529160_gb_AY052204.1_	245299_at	-1.4
ankyrin like protein ; supported by cDNA: gi_16604604_gb_AY059747.1_	245274 at	-1.4
PSI P700 apoprotein A2	245006 at	-1.4
auxin induced protein, putative similar to AUXIN-INDUCED PROTEIN X10A GB:P33080 from [Glycine max]	257460_at	-1.4
putative auxin-regulated protein	264016_at	-1.4
L-aspartate oxidase -like protein L-aspartate oxidase, Pseudomonas aeruginosa, PIR:T46863; supported by cDNA: gi_15010649_gb_AY045626		-1.4
putative glutaredoxin ;supported by full-length cDNA: Ceres:39560.	267497_at	-1.3
glutathione S-transferase identical to GB:D17673; supported by cDNA: gi_443698_dbj_D17673.1_ATHERD13	267154_at	-1.3
putative receptor-like protein kinase same as GB:X95909 (polymorphism exists at a GA repeat. We found 6 copies in our sequence whereas only	267165_at	-1.3
hypothetical protein predicted by genscan and genefinder	266852_at	-1.3
putative ethylene response element binding protein (EREBP) ;supported by full-length cDNA: Ceres:6397.	266821_at	-1.3
putative cytidine deaminase ;supported by full-length cDNA: Ceres:152285.	265943_at	-1.3
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:9149.	265823_at	-1.3
NADC homolog identical to GP[1216074 gnl PID]e225599]F20096;supported by full-length cDNA: Ceres:2877.	265738_at	-1.3
protein kinase, putative Simisimilar to protein kinase 2 GI:7573598 from [Populus nigra]	264240_at	-1.3
unknown protein ;supported by full-length cDNA: Ceres:15743.	263985_at	-1.3
unknown protein ;supported by full-length cDNA: Ceres:36719.	263796_at	-1.3
dTDP-glucose 4,6-dehydratase, putative similar to dTDP-glucose 4,6-dehydratase GI:5921157 from [Streptomyces avermitilis]; supported by cDN	263134_at	-1.3
receptor kinase (CLV1) identical to receptor kinase (CLV1) GB:AAB58929 GI:2160756 [Arabidopsis thaliana]	262728_at	-1.3
unknown protein	261944_at	-1.3
transcription factor, putative contains AP2 domain	261327_at	-1.3
hypothetical protein predicted by genemark.hmm	261177_at	-1.3
unknown protein ;supported by full-length cDNA: Ceres:41505.	261105_at	-1.3
unknown protein contains similarity to UDPG glucosyltransferase GB:AAB62270 GI:2232354 from [Solanum berthaultii];supported by full-length c		-1.3
histidine decarboxylase, putative similar to histidine decarboxylase GB:BAA78331 GI:4996105 from [Brassica napus]; supported by cDNA: gi_15	260814_at	-1.3
Expressed protein ; supported by cDNA: gi_15294273_gb_AF410328.1_AF410328	260601_at	-1.3
polyphosphoinositide binding protein, putative similar to GB:AAB94598 from [Glycine max]; supported by cDNA: gi_16930446_gb_AF419577.1_/	260604_at	-1.3
AtHVA22c identical to AtHVA22c GB:AF141661 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:108964.	260368_at	-1.3
putative lectin contains Pfam profile: PF01419 jacalin-like lectin domain; similar to jasmonate inducible protein GB:Y11483 (Brassica napus), myr		-1.3
putative 40S ribosomal protein S17 similar to 40S ribosomal protein S17 GB:AAD50774 [Lycopersicon esculentum]; supported by full-length cDNA		-1.3
putative UDP-glucose pyrophosphorylase similar to UDP-glucose pyrophosphorylase GB:AAB71613 from [Solanum tuberosum]; supported by cD		-1.3
	258249_s_at	-1.3
protein kinase C-receptor/G-protein, putative similar to uanine nucleotide binding protein (G protein), beta polypeptide GB:NP_006089 [Homo saj		-1.3
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:924.	257858_at	-1.3
unknown protein	257076_at	-1.3
Expressed protein ; supported by cDNA: gi_14335055_gb_AY037207.1_	256766_at	-1.3
hypothetical protein contains similarity to MtN3(nodulin) protein GB:Y08726 GI:1619601 from [Medicago truncatula]; supported by cDNA: gi_1580		-1.3
unknown protein ; supported by cDNA: gi_15293280_gb_AY051074.1_	256266_at	-1.3
kinase, putative similar to leaf rust resistance kinase Lr10 GI:1680685 from [Triticum aestivum]	255913_at	-1.3
	255802_s_at	-1.3
60S ribosomal protein L6, putative similar to 60S ribosomal protein L6 GI:7208784 from [Cicer arietinum]; supported by full-length cDNA: Ceres:5		-1.3
putative oxidoreductase	255438_at	-1.3
putative membrane trafficking factor ;supported by full-length cDNA: Ceres:1463.	255325_at	-1.3

putative protein heat shock protein dnaJ - Bacillus stearothermophilus,PIR:JC4739	255088_at	-1.3
putative protein various predicted proteins; supported by full-length cDNA: Ceres: 17340.	254389_s_at	-1.3
putative protein annexin VII, Dictyostelium discoideum, PIR1:LUDO7	254262_at	-1.3
putative protein extensin, Catharanthus roseus, D86853	254093_at	-1.3
possible apospory-associated like protein Pennisetum ciliare possible apospory-associated mRNA clone pSUB C, PID:g549984;supported by full	254040_at	-1.3
uncharacterized protein ;supported by full-length cDNA: Ceres:7421.	253989 at	-1.3
putative Proline synthetase associated protein Proline synthetase associated - Homo sapiens, PID:d1037830; supported by full-length cDNA: Cer	253951_at	-1.3
putative beta-glucosidase beta-glucosidase BGQ60 precursor - barley, PIR2:A57512	253835_at	-1.3
putative beta-expansin/allergen protein soybean pollen allergen (cim1) protein - soybean, PIR2:S48032;supported by full-length cDNA: Ceres:33	253815_at	-1.3
glucosyltransferase -like protein immediate-early salicylate-induced glucosyltransferase, Nicotiana tabacum, PIR2:T03747;supported by cDNA gi	253268_s_at	-1.3
caffeoyl-CoA O-methyltransferase - like protein caffeoyl-CoA 3-O-methyltransferase, Populus tremuloides, PID:G857578; supported by full-length	253276_at	-1.3
protein kinase - like receptor-like protein kinase RLK3, Arabidopsis thaliana, EMBL:ATH011674	252549_at	-1.3
SF16 -like protein SF16 protein, pollen specific, helianthus annuus, PIR:T13992;supported by full-length cDNA: Ceres:39013.	252280_at	-1.3
calmodulin-like protein flagellar calmodulin - Naegleria gruberi, PID:g458232; supported by cDNA: gi_166647_gb_L12115.1_ATHCALLGA	252136_at	-1.3
leucoanthocyanidin dioxygenase -like protein leucoanthocyanidin dioxygenase, apple tree, PIR:S33144	251770_at	-1.3
cyclophilin-like protein ROC7, cyclophilin, Arabidopsis thaliana, EMBL:AF192490;supported by full-length cDNA: Ceres:94608.	251772_at	-1.3
putative protein	251725_at	-1.3
putative protein several hypothetical proteins - Arabidopsis thaliana;supported by full-length cDNA: Ceres:21740.	251107_at	-1.3
lysine decarboxylase-like protein	250723_at	-1.3
putative protein prenylated rab acceptor 1 - Homo sapiens, EMBL:AF112202;supported by full-length cDNA: Ceres:22460.	250663_at	-1.3
putative protein various predicted proteins, Arabidopsis thaliana	250435_at	-1.3
putative protein	250330_at	-1.3
putative protein S-receptor kinase PK3 precursor, maize, PIR:T02753;supported by full-length cDNA: Ceres:154037.	249983_at	-1.3
Ser/Thr specific protein kinase - like protein various protein kinase, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 15535.	249985_at	-1.3
putative protein contains similarity to unknown protein (emb CAB89315.1); supported by cDNA: gi_15451067_gb_AY054614.1_	249863_at	-1.3
6-phosphogluconolactonase-like protein ;supported by full-length cDNA: Ceres:13806.	249732_at	-1.3
DNA helicase-like	249677_at	-1.3
pyridoxal kinase -like protein pyridoxal kinase, Sus scofra, EMBL:AF041255;supported by full-length cDNA: Ceres:107973.	249589_at	-1.3
beta-1,3-glucanase-like protein	249214_at	-1.3
pectin acetylesterase ;supported by full-length cDNA: Ceres:39005.	248968_at	-1.3
unknown protein ;supported by cDNA: gi_14326507_gb_AF385707.1_AF385707	248624_at	-1.3
receptor protein kinase-like	248568_at	-1.3
MtN3-like protein ;supported by full-length cDNA: Ceres:36264.	248467_at	-1.3
putative protein similar to unknown protein (pir  T05049)	248044_at	-1.3
calcineurin B-like protein 2 (gb AAC26009.1) ;supported by full-length cDNA: Ceres:37280.	248001_at	-1.3
ubiquinone/menaquinone biosynthesis methyltransferase-like ; supported by cDNA: gi_15293010_gb_AY050939.1_	247901_at	-1.3
subtilisin-like serine protease contains similarity to prepro-cucumisin GI:807698 from [Cucumis melo]	247760_at	-1.3
GTP-binding protein - like GTP-binding protein, garden pea, PIR:T06447	247597_at	-1.3
putative protein similar to unknown protein (emb CAB66910.1);supported by full-length cDNA: Ceres:36946.	247161_at	-1.3
putative protein similar to unknown protein (gb AAC18972.1); supported by cDNA: gi_15293188_gb_AY051028.1_	246998_at	-1.3
calmodulin-binding - like protein calmodulin-binding protein TCB60, Nicotiana tabacum, EMBL:U58971	246821_at	-1.3
cytochrome-b5 reductase - like protein cytochrome-b5 reductase, Saccharomyces cerevisiae, PIR:S37800;supported by full-length cDNA: Ceres:		-1.3
amino acid permease, putative almost identical to amino acid permease GI:608673 from [Arabidopsis thaliana]	245740_at	-1.3
PSI P700 apoprotein A1	245007_at	-1.3

	045045	4.0
large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase	245015_at	-1.3
Expressed protein ; supported by full-length cDNA: Ceres: 970.	249721_at	-1.3
putative protein	245428_at	-1.3
unknown protein identical to unknown protein GB:AAF30301 from [Arabidopsis thaliana]; supported by cDNA: gi_16648934_gb_AY059837.1_	258472_at	-1.3
Expressed protein ; supported by cDNA: gi_15724149_gb_AF411777.1_AF411777	267578_at	-1.2
putative malonyl-CoA:Acyl carrier protein transacylase ;supported by full-length cDNA: Ceres:299.	267308_at	-1.2
putative serine carboxypeptidase II; supported by cDNA: gi_14517521_gb_AY039596.1_	267264_at	-1.2
unknown protein ;supported by full-length cDNA: Ceres:125631.	267209_at	-1.2
unknown protein ; supported by cDNA: gi_14334607_gb_AY034977.1_	267005_at	-1.2
unknown protein	266963_at	-1.2
putative Na+-dependent inorganic phosphate cotransporter	266672_at	-1.2
unknown protein	266566_at	-1.2
tubulin beta-7 chain identical to GB:M84704;supported by full-length cDNA: Ceres:17240.	266295_at	-1.2
unknown protein ;supported by full-length cDNA: Ceres:151697.	266136_at	-1.2
60S ribosomal protein L24 ;supported by full-length cDNA: Ceres:14564.	265210_at	-1.2
unknown protein ; supported by full-length cDNA: Ceres: 5171.	264343_at	-1.2
unknown protein	263878_s_at	-1.2
putative cyclic nucleotide-regulated ion channel protein	263776_s_at	-1.2
unknown protein Location of EST 228A16T7A, gb N65686;supported by full-length cDNA: Ceres:24946.	263688_at	-1.2
ankyrin-like protein EST gb/ATTS0956 comes from this gene;supported by full-length cDNA: Ceres:108617.	263662_at	-1.2
unknown protein ;supported by full-length cDNA: Ceres:15081.	263431_at	-1.2
unknown protein ; supported by cDNA: gi_13877598_gb_AF370500.1_AF370500	263386_at	-1.2
unknown protein Strong similarity to gb AF096285 serine-threonine kinase receptor-associated protein from Mus musculus and contains 5 PF 00	_	-1.2
virus resistance protein, putative similar to virus resistance protein GI:558886 from [Nicotiana glutinosa]	262382_at	-1.2
hypothetical protein similar to putative curved-DNA binding protein GI:6968662 from [Campylobacter jejuni]; supported by full-length cDNA: Ceres:		-1.2
hypothetical protein predicted by genemark.hmm	262151_at	-1.2
invertase, putative similar to neutral invertase GB:76145 GI:4200165 from [Daucus carota]	262038_at	-1.2
3-deoxy-D-arabino-heptulosonate 7-phosphate, putative similar to 3-deoxy-D-arabino-heptulosonate 7-phosphate GI:170224 from [Nicotiana taba	_	-1.2
unknown protein	261175_at	-1.2
delta 9 desaturase identical to delta 9 desaturase GB:BAA25180 GI:2970034 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 1		-1.2
phosphoenolpyruvate carboxylase 1, putative similar to phosphoenolpyruvate carboxylase 1 GI:2266947 from [Gossypium hirsutum]; supported t	_	-1.2
putative villin 2	260521_at	-1.2
hypothetical protein predicted by genscan+	260109_at	-1.2
putative ABC transporter similar to ABC transporters: GB:BAA77876 [Escherichia coli], GB:P07655 [Escherichia coli]; contains Pfam profile: PF0		-1.2
lipase/hydrolase, putative contains Pfam profile: PF00657 Lipase/Acylhydrolase with GDSL-like motif; supported by full-length cDNA: Ceres: 6680	_	-1.2
unknown protein contains similarity to cytochrome oxidase I GI:1289267 from (Xantholinus sp.);supported by full-length cDNA: Ceres:6875.	259594_at	-1.2
putative myo-inositol monophosphatase similar to myo-inositol-1(or 4)-monophosphatase 3 (IMP 3) GB:P54928 [Lycopersicon esculentum]; suppo		-1.2
putative s-adenosylmethionine synthetase similar to S-ADENOSYLMETHIONINE SYNTHETASE GB:Q96552 from [Catharanthus roseus];suppor	258415_at	-1.2
ribosomal protein, putative similar to 60S ribosomal protein L5 GB:P49625 from [Oryza sativa];supported by full-length cDNA: Ceres:32753.	257906_at	-1.2
cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450	257623_at	-1.2
cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450	257628_at	-1.2
unknown protein ;supported by cDNA: gi_15810494_gb_AY056286.1_	257071_at	-1.2
putative protein ;supported by full-length cDNA: Ceres:114734.	256676_at	-1.2
4-coumarate:CoA ligase 1 identical to 4-coumarate:CoA ligase 1 [Arabidopsis thaliana] GI:5702184; supported by cDNA: gi_609339_gb_U18675.	256186_at	-1.2

Expressed protein ; supported by full-length cDNA: Ceres: 11615.	256091 at	-1.2
putative serine/threonine protein kinase	255488 at	-1.2
putative sugar transporter	255294_at	-1.2
putative protein various kinesin light chains; supported by full-length cDNA: Ceres: 2538.	254951 at	-1.2
		-1.2
oleoyl-[acyl-carrier-protein] hydrolase-like protein oleoyl-[acyl-carrier-protein] hydrolase - Brassica napus, PIR2:S40407	254798_at	-1.2
protein ch-42 precursor, chloroplast ;supported by full-length cDNA: Ceres:7501.	254623 at	-1.2
putative protein several hypothetical proteins - Arabidopsis thaliana; supported by cDNA: gi_15320409_dbj_AB039927.1_AB039927	254563_at	-1.2
tyrosine transaminase like protein tyrosine transaminase (EC 2.6.1.5) - rat, EMBL:X02741; supported by cDNA: gi_15076852_gb_AF268090.1_A	254232_at	-1.2
putative protein other hypothetical proteins Arabidopsis thaliana	254029_at	-1.2
UDP rhamnoseanthocyanidin-3-glucoside rhamnosyltransferase - like protein UDP rhamnoseanthocyanidin-3-glucoside rhamnosyltransferase	253879_s_at	-1.2
putative protein hypothetical protein T25K17.20 - Arabidopsis thaliana, PIR2:T06005; supported by full-length cDNA: Ceres: 7308.	253730_at	-1.2
choline monooxygenase - like protein choline monooxygenase precursor, Spinacia oleracea,gb:U85780	253701_at	-1.2
putative protein (fragment) calcineurin B, Naegleria gruberi, gb;U04380	253412_at	-1.2
putative protein various predicted proteins; supported by full-length cDNA: Ceres: 206573.	253198_at	-1.2
cinnamyl-alcohol dehydrogenase CAD1 ;supported by full-length cDNA: Ceres:34593.	252943_at	-1.2
GTP-binding protein Rab11 ; supported by full-length cDNA: Ceres: 35596.	252472_at	-1.2
putative protein sn-glycerol-3-phosphate permease - Haemophilus influenzae, PID:g3603157; supported by cDNA: gi_13430515_gb_AF360170.1	252414_at	-1.2
hypothetical protein	252403_at	-1.2
branched-chain-amino-acid transaminase -like protein branched-chain-amino-acid transaminase, Streptomyces coelicolor, PIR:T29053; supporte		-1.2
hypothetical protein ;supported by full-length cDNA: Ceres:93591.	252165_at	-1.2
sedoheptulose-bisphosphatase precursor ; supported by cDNA: gi_15451177_gb_AY054669.1_	251762_at	-1.2
putative protein protein of unknown function - Corydalis sempervirens, EMBL:X63595; supported by cDNA: gi_7684291_dbj_D84226.1_D84226	251739_at	-1.2
URIDYLATE KINASE-like protein URIDYLATE KINASE - Arabidopsis thaliana, EMBL:AF000147; supported by full-length cDNA: Ceres:16800.	251426_at	-1.2
SRG1 - like protein SRG1 protein, Arabidopsis thaliana, PIR:S44261	251402_at	-1.2
putative protein latex protein allergen Hev b 7 - Hevea brasiliensis, EMBL:AF113546; supported by cDNA: gi_15912226_gb_AY056391.1_	251174_at	-1.2
putative protein HSPC172, Homo sapiens, EMBL:AF161520;supported by full-length cDNA: Ceres:9788.	250993_at	-1.2
transcription factor-like protein ethylene responsive element binding factor 5 - Arabidopsis thaliana, EMBL:AB008107; supported by cDNA: gi_15	_	-1.2
putative protein SF21 protein, Helianthus annuus, EMBL: AF189148; supported by cDNA: gi_13605683_gb_AF361823.1_AF361823	250337_at	-1.2
putative protein contains similarity to unknown protein (pir  T05576)	250305_at	-1.2
GTP-binding protein typA (tyrosine phosphorylated protein A) ; supported by cDNA: gi_16649146_gb_AY059943.1_	250256_at	-1.2
unknown protein ;supported by cDNA: gi_14190364_gb_AF378860.1_AF378860	250099_at	-1.2
putative protein contains similarity to unknown protein (emb CAB62012.1)	249806_at	-1.2
flavanone 3-hydroxylase-like protein ; supported by full-length cDNA: Ceres: 149654.	249754_at	-1.2
putative protein predicted proteins, Arabidopsis thaliana	249551_at	-1.2
acyltransferase -like protein anthocyanin acyltransferase, Perilla frutescens, EMBL:AB029340	249489_at	-1.2
electron transfer flavoprotein beta-subunit-like ;supported by full-length cDNA: Ceres:120707.	249158_at	-1.2
tubulin beta-4 chain (sp P24636) ; supported by cDNA: gi_14334935_gb_AY035141.1_	249049_at	-1.2
GDSL-motif lipase/hydrolase-like protein	248921_at	-1.2
mutT domain protein-like ;supported by full-length cDNA: Ceres:38400.	248793_at	-1.2
acetyl-CoA C-acetyltransferase ; supported by cDNA: gi_16604582_gb_AY059736.1_	248690_at	-1.2
putative protein contains similarity to ethylene responsive element binding factor; supported by full-length cDNA: Ceres:2347.	248448_at	-1.2
putative protein contains similarity to unknown protein (emb CAB87278.1)	248393_at	-1.2
putative protein similar to unknown protein (pir  T04792)	248085_at	-1.2

histone H4 - like protein histone H4, Zea mays, PIR:HSZM4;supported by full-length cDNA: Ceres:15418.	247692_s_at	-1.2
protein disulfide isomerase precursor - like protein disulfide isomerase precursor, Volvox carteri, EMBL:AF110784; supported by full-length cDNA	247588_at	-1.2
ethylene responsive element binding factor - like ethylene responsive element binding factor 5, Arabidopsis thaliana, SWISSPROT:ERF5_ARAT	l 247540_at	-1.2
2-oxoglutarate/malate translocator ; supported by cDNA: gi_15810580_gb_AY056329.1_	247289_at	-1.2
zeaxanthin epoxidase precursor ; supported by cDNA: gi_10444087_gb_AF281655.1_AF281655	247025_at	-1.2
putative protein EXOSTOSIN-1 (PUTATIVE TUMOR SUPPRESSOR PROTEIN EXT1) - Homo sapiens, EMBL:S79639	246682_at	-1.2
UDP-glucose dehydrogenase-like protein UDP-glucose 6-dehydrogenase - Glycine max, EMBL:U53418; supported by cDNA: gi_15810322_gb_	246511_at	-1.2
hypothetical protein contains similarity to phytoene dehydrogenase (PDH1) GI:433144 from [Cercospora nicotianae]	246411_at	-1.2
putative protein 22kDa peroxisomal membrane protein-like - Homo sapiens, EMBL:AF250136;supported by full-length cDNA: Ceres:6789.	245937_at	-1.2
ribonucleoprotein like protein	245605_at	-1.2
hypothetical protein ;supported by full-length cDNA: Ceres:39922.	245365_at	-1.2
unknown protein	257381_at	-1.2
putative glucanse	267595_at	-1.1
putative integral membrane protein	267520_at	-1.1
unknown protein ;supported by full-length cDNA: Ceres:8402.	267370_at	-1.1
unknown protein ;supported by cDNA: gi_16323164_gb_AY057686.1_	267084_at	-1.1
copia-like retroelement pol polyprotein ; supported by full-length cDNA: Ceres: 14718.	266696_at	-1.1
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:8450.	266311_at	-1.1
hypothetical protein predicted by genscan	266089_at	-1.1
unknown protein	265845_at	-1.1
unknown protein	265203_at	-1.1
oligopeptide transporter, putative similar to oligopeptide transporter 1-1 GI:510238 from [Arabidopsis thaliana]	264736_at	-1.1
unknown protein contains similarity to peroxidase isozyme GI:217933 from [Armoracia rusticana]	264738_at	-1.1
putative prolyl 4-hydroxylase, alpha subunit ;supported by full-length cDNA: Ceres:36054.	264592_at	-1.1
unknown protein ;supported by cDNA: gi_15450787_gb_AY054474.1_	263954_at	-1.1
putative glucosyltransferase ; supported by cDNA: gi_15809993_gb_AY054265.1_	263847_at	-1.1
malate oxidoreductase (malic enzyme)	263717_at	-1.1
putative auxin-induced protein AUX2-11 Match to Arabidopsis IAA3 (gb U18406). EST gb T04296 comes from this gene; supported by cDNA: gi_	_	-1.1
putative purple acid phosphatase precursor	263553_at	-1.1
unknown protein similar to hypothetical protein GB:AAB81674;supported by full-length cDNA: Ceres:6280.	263582_at	-1.1
putative glucosyltransferase ; supported by full-length cDNA: Ceres: 114997.	263473_at	-1.1
putative leucine-rich repeat disease resistance protein ;supported by full-length cDNA: Ceres:20900.	263330_at	-1.1
coatomer-like protein, epsilon subunit similar to GB:CAB55628 from [Homo sapiens], ESTs gb Z17908, gb AA728673, gb N96555, gb H76335, gb		-1.1
hypothetical protein similar to putative MADS-box protein GI:4580382 from [Arabidopsis thaliana]	262902_x_at	-1.1
glutathione S-transferase, putative similar to similar to glutathione S-transferase GB:AAF29773 GI:6856103 from (Gossypium hirsutum); supported		-1.1
unknown protein ;supported by full-length cDNA: Ceres:95546.	262396_at	-1.1
disease resistance protein, putative similar to disease resistance protein GI:9758876 from [Arabidopsis thaliana]	262383_at	-1.1
unknown protein similar to hypothetical protein GB:AAF24562 GI:6692097 from [Arabidopsis thaliana]; supported by cDNA: gi_15010675_gb_AY		-1.1
unknown protein contains similarity to zinc finger and C2 domain protein GI:9957238 from [Arabidopsis thaliana]; supported by full-length cDNA: C		-1.1
unknown protein identical to unknown protein GB:AAD55492 (Arabidopsis thaliana)	262289_at	-1.1
somatic embryogenesis receptor-like kinase, putative similar to somatic embryogenesis receptor-like kinase GI:2224910 from [Daucus carota];su		-1.1
wall-associated kinase 2, putative similar to receptor-like serine/threonine kinase GB:AAC50043 GI:2465923 from [Arabidopsis thaliana]	262082_s_at	-1.1
ARP protein, putative similar to ARP protein GB:CAA89858 GI:886434 from [Arabidopsis thaliana]	261601_at	-1.1
choline kinase, putative similar to CHOLINE/ETHANOLAMINE KINASE GB:Q9Y259 from [Homo sapiens]	261506_at	-1.1

hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 3200.	261456 at	-1.1
ferredoxinNADP reductase precursor, putative similar to GB:M25528 from [Mesembryanthemum crystallinum]	261218_at	-1.1
proliferating cellular nuclear antigen identical to GB:AAF40018 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:28554.	261080 at	-1.1
hypothetical protein similar to hypothetical protein GB:CAB45785 GI:5262156 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:39	—	-1.1
putative glutathione peroxidase ;supported by full-length cDNA: Ceres:30737.	260545 at	-1.1
Expressed protein ; supported by full-length cDNA: Ceres: 14943.	259661_at	-1.1
	259550 at	-1.1 -1.1
hypothetical protein ;supported by full-length cDNA: Ceres:265772.	—	-1.1 -1.1
putative lectin contains Pfam profile: PF01419 jacalin-like lectin domain; similar to jasmonate inducible protein GB:Y11483 (Brassica napus), myr		
putative methionine synthase similar to cobalamin-independent methionine synthase GB:AAC50037 [Arabidopsis thaliana]; supported by full-lengt		-1.1
acyl carrier protein 1 precursor (ACP) identical to GB:P11829 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 14291.	259095_at	-1.1
putative syntaxin contains Pfam profile: PF00804 syntaxin;supported by full-length cDNA: Ceres:38899.	258786_at	-1.1
unknown protein ; supported by cDNA: gi_15028124_gb_AY046012.1_	258728_at	-1.1
putative serine carboxypeptidase II similar to serine carboxypeptidase II (CP-MII) GB:CAA70815 [Hordeum vulgare]	258633_at	-1.1
lipoamide dehydrogenase precursor identical to GB:AAF34796 from [Arabidopsis thaliana]	258439_at	-1.1
	258419_at	-1.1
20S proteasome subunit PAE2 identical to 20S proteasome subunit PAE2 GB:AAC32061 from [Arabidopsis thaliana]; supported by cDNA: gi_342		-1.1
unknown protein contains GMC oxidoreductase domain; supported by cDNA: gi_13605691_gb_AF361827.1_AF361827	258299_at	-1.1
putative zinc finger protein contains Pfam profile: PF00641 Zn-finger in Ran binding protein and others; supported by full-length cDNA: Ceres:826{		-1.1
beta-glucosidase, putative similar to beta-glucosidase BGQ60 precursor GB:A57512 [Hordeum vulgare]; supported by full-length cDNA: Ceres:11	_	-1.1
unknown protein	257983_at	-1.1
hypothetical protein similar to hypothetical protein GB:AAD50054 from [Arabidopsis thaliana]	257964_at	-1.1
putative UDP-glucose glucosyltransferase similar to GB:Q40284 from [Manihot esculenta]	257949_at	-1.1
unknown protein	257828_at	-1.1
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:4146.	256796_at	-1.1
unknown protein ;supported by full-length cDNA: Ceres:8544.	256785_at	-1.1
UDP-glucose dehydrogenase, putative UDP-glucose 6-dehydrogenase (UDPGDH) GB:Q96558 from [Glycine max]; supported by full-length cDN/	256745_at	-1.1
hypothetical protein ; supported by full-length cDNA: Ceres: 14577.	256569_at	-1.1
protein kinase, putative contains Pfam profile: PF00069: Eukaryotic protein kinase domain	256529_at	-1.1
protein kinase, putative contains Pfam profile: PF00069: Eukaryotic protein kinase domain	256482_at	-1.1
unknown protein	255852_at	-1.1
unknown protein ;supported by cDNA: gi_15293076_gb_AY050972.1_	255827_at	-1.1
sulfate adenylyltransferase identical to sulfate adenylyltransferase GI:487404 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:21	255785_at	-1.1
unknown protein	255764_at	-1.1
unknown protein ;supported by full-length cDNA: Ceres:37302.	255719_at	-1.1
contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin_legB.hmm, score	255503_at	-1.1
nodulin-like protein nodulin gene MtN21 - Medicago truncatula, PID:e1172471;supported by full-length cDNA: Ceres:40485.	255129_at	-1.1
putative mitogen-activated protein kinase	255148_at	-1.1
putative protein ascorbate peroxidase - Spinacia oleracea,PIR2:S66265;supported by full-length cDNA: Ceres:37435.	255078_at	-1.1
flavonoid 3,5-hydroxylase -like protein flavonoid 3 ,5 -hydroxylase - Campanula medium, PID:d1003951	254835_s_at	-1.1
pEARLI 1-like protein Arabidopsis thaliana pEARLI 1 mRNA, PID:g871780; supported by cDNA: gi_15450470_gb_AY052336.1	254832 at	-1.1
hypothetical protein	254484_at	-1.1
adenine phosphoribosyltransferase (EC 2.4.2.7) - like protein adenine phosphoribosyltransferase, Triticum aestivum, T06263; supported by full-le	254328_at	-1.1
glucose-6-phosphate isomerase glucose-6-phosphate isomerase Spinacia oleracea (spinach), PATX:E1315197	254141_at	-1.1
fructose-bisphosphate aldolase - like protein fructose-bisphosphate aldolase, Arabidopsis thaliana, PIR1:ADMU; supported by full-length cDNA: C	_	-1.1
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hypothetical protein ;supported by full-length cDNA: Ceres:36080.	253765 at	-1.1
MAP kinase kinase 2 ; supported by cDNA: gi_14326470 gb_AF385688.1_AF385688	253646_at	-1.1
putative cyclase associated protein CAP adenylyl cyclase-associated protein CAP2, Rattus norvegicus, PIR2: JC4386; supported by cDNA: gi_31		-1.1
putative protein ;supported by full-length cDNA: Ceres:265.	253172_at	-1.1
calmodulin-domain protein kinase CDPK isoform 5 (CPK5) ; supported by cDNA: gi_1399272_gb_U31834.1_ATU31834	253167_at	-1.1
nuclear envelope membrane protein - like LBR integral nuclear envelope inner membrane protein, Homo sapiens, EMBL:HSLBR10; supported by	251995_at	-1.1
phenylalanine ammonia-lyase ;supported by full-length cDNA: Ceres:110886.	251984_at	-1.1
putative protein 24 kDa seed maturation protein, Glycine max., EMBL:AF004806	251903_at	-1.1
Expressed protein ; supported by cDNA: gi_11494366_gb_AF280059.1_AF280059	251816_at	-1.1
putative protein hypothetical protein At2g41330 - Arabidopsis thaliana, EMBL:AC005662; supported by cDNA: gi_15451041_gb_AY054601.1_	251663_at	-1.1
CP12 protein precursor-like protein CP12 protein precursor, chloroplast - Pisum sativum, PIR: T06562; supported by full-length cDNA: Ceres: 2721	251218_at	-1.1
tRNA isopentenyl transferase -like protein tRNA isopentenyl transferase, Arabidopsis thaliana, EMBL:AF109376; supported by cDNA: gi_142789	251154_at	-1.1
serine/threonine protein kinase ATPK10 ;supported by cDNA: gi_13249133_gb_AF302111.1_AF302111	251059_at	-1.1
putative protein ; supported by cDNA: gi_2723476_dbj_D89824.1_D89824	250901_at	-1.1
Expressed protein ; supported by cDNA: gi_9909197_gb_AF175769.1_AF175769	250818_at	-1.1
polygalacturonase inhibiting protein ;supported by full-length cDNA: Ceres:35527.	250669_at	-1.1
GTP-binding protein LepA homolog	250531_at	-1.1
sulfate transporter ;supported by cDNA: gi_2114105_dbj_AB003591.1_AB003591	250475_at	-1.1
putative protein KIAA0255 gene, Homo sapiens, EMBL:HSD444	250422_at	-1.1
24-sterol C-methyltransferase ; supported by cDNA: gi_11066104_gb_AF195648.1_AF195648	250254_at	-1.1
unknown protein	249932_at	-1.1
60S ribosomal protein L10A ;supported by cDNA: gi_14335147_gb_AY037253.1_	249945_at	-1.1
putative protein similar to unknown protein (pir  T40675); supported by cDNA: gi_14335067_gb_AY037213.1_	249701_at	-1.1
putative protein vanilloid receptor gene, CTNS, Homo sapiens, EMBL:AF168787;supported by full-length cDNA: Ceres:18435.	249373_at	-1.1
serine carboxypeptidase II-like ; supported by cDNA: gi_13605556_gb_AF361604.1_AF361604	249216_at	-1.1
antifungal protein-like (PDF1.2)	249052_at	-1.1
putative protein similar to unknown protein (gb AAF24540.1);supported by full-length cDNA: Ceres:141753.	248923_at	-1.1
bHLH protein-like	248864_at	-1.1
FRO1 and FRO2-like protein	248540_at	-1.1
putative protein similar to unknown protein (pir  T02891);supported by full-length cDNA: Ceres:112574.	248271_at	-1.1
glucose-6-phosphate/phosphate translocator ;supported by full-length cDNA: Ceres:26107.	248144_at	-1.1
MYB27 protein - like MYB27 protein, Arabidopsis thaliana, PIR:T46166; supported by cDNA: gi_3941479_gb_AF062894.1_AF062894	247696_at	-1.1
S-receptor kinase homolog 2 precursor S-receptor kinase homolog 2 precursor, Arabidopsis thaliana, PIR:S27754	247602_at	-1.1
100 kDa coactivator - like protein 100 kDa coactivator, Homp sapiens, PIR:I38968	247517_at	-1.1
putative protein	247486_at	-1.1
peptide transporter	247440_at	-1.1
putative protein similar to unknown protein (pir  T04031); supported by full-length cDNA: Ceres: 144066.	247255_at	-1.1
annexin ;supported by full-length cDNA: Ceres:1728.	247210_at	-1.1
leucine-rich repeats containing protein grr1 - Glycine max. EMBL:AF019910	246935_at	-1.1
putative protein various predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:28528.	246860_at	-1.1
putative protein predicted protein, Arabidopsis thaliana; supported by cDNA: gi_16930704_gb_AF436836.1_AF436836	246660_at	-1.1
cytochrome P450 ; supported by cDNA: gi_3164141_dbj_D78606.1_D78606	246620_at	-1.1
beta-D-glucan exohydrolase - like protein beta-D-glucan exohydrolase, Nicotiana tabacum, EMBL:AB017502	246184_at	-1.1
succinyl-CoA-ligase alpha subunit ;supported by full-length cDNA: Ceres:10292.	246035_at	-1.1

disease resistance RPP5 like protein (fragment)	245460_at	-1.1
F12A21.7 hypothetical protein;supported by full-length cDNA: Ceres:34552.	245197_at	-1.1
putative mitochondrial carrier protein similar to SP:P40556:YIA6_YEAST and SP:P39953:YEA6_YEAST; supported by full-length cDNA: Ceres:12	245152_at	-1.1
S-like ribonuclease RNS2 identical to ribonuclease 2 precursor SP:P42814, GI:289210; contains a ribonuclease T2 family histidine active site sig	245067_at	-1.1
ATP-dependent protease subunit	244971_at	-1.1
putative calcium ATPase very similar to fruit fly Ca2+-transporting ATPase, gi 114306 and fast skeletal muscle Ca-ATPase [Rana esculenta], gi 2	264526_at	-1.1
Expressed protein ; supported by cDNA: gi_13605516_gb_AF361584.1_AF361584	265597_at	-1.1
putative protein putative protein - Arabidopsis thaliana, EMBL:CAB36749.1	252335_at	-1.1
flavanone 3-hydroxylase (FH3) ;supported by full-length cDNA: Ceres:36653.	252123_at	-1.1
unknown protein similar to GP 2245012 gnl PID e327000 Z97341; supported by cDNA: gi_15293230_gb_AY051049.1_	267592_at	-1
hypothetical protein predicted by genfinder	267586_at	-1
putative beta-galactosidase ; supported by cDNA: gi_14517398_gb_AY039534.1_	267556_at	-1
unknown protein	267517_at	-1
unknown protein	267230_at	-1
high affinity Ca2+ antiporter identical to GB:U57411, except a possible frameshift at base 58008. Sequence has been confirmed with 5 sequenci	267093_at	-1
calmodulin-like protein identical to GB:D45848; supported by cDNA: gi_15983405_gb_AF424577.1_AF424577	267083_at	-1
hypothetical protein ;supported by full-length cDNA: Ceres:38891.	266805_at	-1
unknown protein	266572_at	-1
putative dioxygenase ; supported by cDNA: gi_15292706_gb_AY050787.1_	265615_at	-1
nodulin-like protein	265414_at	-1
unknown protein	265327_at	-1
putative 3-oxoacyl [acyl-carrier protein] reductase similar to proteins from several bacterial species, similar to ESTs emb Z37189, gb H74525, gb	265026_at	-1
unknown protein similar to F5J6.8 and C. elegans C42D8.3; supported by full-length cDNA: Ceres: 2578.	264850_at	-1
pyruvate dehydrogenase E1 alpha subunit strongly similar to GB:AAD39331;supported by full-length cDNA: Ceres:41337.	264871_at	-1
hypothetical protein similar to hypothetical protein GI:4455225 from [Arabidopsis thaliana]; supported by cDNA: gi_15293160_gb_AY051014.1_	264701_at	-1
unknown protein ;supported by full-length cDNA: Ceres:2935.	264609_at	-1
Expressed protein ; supported by full-length cDNA: Ceres: 108558.	264579_at	-1
putative lipase Similar to nodulins and lipase; location of EST E6C2T7, gb AA042309. similar to nodulins gi 3328240, gi 2129854 and others and	264501_at	-1
ATPase 70 kDa subunit, putative similar to ATPase 70 kDa subunit GI:558478 from [Brassica napus]; supported by full-length cDNA: Ceres:1781	264302_at	-1
putative steroid sulfotransferase ;supported by full-length cDNA: Ceres:3964.	264037_at	-1
unknown protein ;supported by full-length cDNA: Ceres:109103.	263919_at	-1
putative ribonucleoside-diphosphate reductase large subunit ; supported by cDNA: gi_14334813_gb_AY035080.1_	263882_at	-1
phenylalanine ammonia lyase (PAL1) ; supported by cDNA: gi_15028192_gb_AY045919.1_	263845_at	-1
3-methyladenine DNA glycosylase, putative Strong similarity to GB:P29102, 3-isopropylmalate dehydrogenase (IMDH) from Brassica napus. ES1	263706_s_at	-1
putative 1-aminocyclopropane-1-carboxylate oxidase Similar to Arabidopsis 2A6 (gb X83096). EST gb T76913 comes from this gene; supported t	263668_at	-1
putative myo-inositol 1-phosphate synthase ; supported by cDNA: gi_15450746_gb_AY053415.1_	263433_at	-1
fructokinase, putative predicted by genefinder	263163_at	-1
putative N-acetylglucosaminyltransferase	263105_at	-1
unknown protein ESTs gb R65381 and gb T44635 come from this gene	262811_at	-1
anter-specific proline-rich -like protein (APG-like) similar to anter-specific proline-rich protein (APG) SP:P40602 [Arabidopsis thaliana (Mouse-ear	262682_at	-1
unknown protein	262694_at	-1
hypothetical protein similar to hypothetical protein GB:CAB36801 GI:4455265 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 4	262457_at	-1
unknown protein	262432_at	-1
hypothetical protein predicted by genemark.hmm	262089_s_at	-1

isocitrate dehydrogenase, putative similar to isocitrate dehydrogenase GI:166385 from [Medicago sativa]; supported by full-length cDNA: Ceres:4		-1
GTP-binding protein, putative similar to GTP-binding protein NGB GB:AAD09830 GI:4191616 from [Homo sapiens]	261882_at	-1
unknown protein similar to hypothetical protein GB:AAF22901 GI:6664319 from [Arabidopsis thaliana]; supported by cDNA: gi_16930480_gb_AF4		-1
metallothionein-like protein identical to SP:P43392 from (Arabidopsis thaliana);supported by full-length cDNA: Ceres:12642.	261410_at	-1
hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 13874.	261057_at	-1
hypothetical protein similar to Pto kinase interactor 1 GB:AAC61805 GI:3668069 from [Lycopersicon esculentum]	260924_at	-1
putative FKBP type peptidyl-prolyl cis-trans isomerase	260542_at	-1
unknown protein ;supported by full-length cDNA: Ceres:17921.	260441_at	-1
sucrose transport protein SUC1 identical to GB:S38197 from [Arabidopsis thaliana]; supported by cDNA: gi_15146267_gb_AY049275.1_	260143_at	-1
hypothetical protein similar to Yml014wp GB:NP_013698 from [Saccharomyces cerevisiae];supported by full-length cDNA: Ceres:34418.	260128_at	-1
unknown protein ; supported by full-length cDNA: Ceres: 123862.	259981_at	-1
short chain alcohol dehydrogenase, putative similar to GI:2739279 from [Nicotiana tabacum] (Plant Mol. Biol. 29 (5), 1027-1038 (1995))	259669_at	-1
GTP-binding protein RAB7D, putative similar to GI:1370187 from [Lotus japonicus] (Plant J. 11 (2), 237-250 (1997)); supported by cDNA: gi_157	259611_at	-1
type 2A protein serine/threonine phosphatase 55 kDa B regulatory subunit almost identical to type 2A protein serine/threonine phosphatase 55 kE	259404_at	-1
unknown protein ;supported by cDNA: gi_16648950_gb_AY059845.1_	259166_at	-1
threonine dehydratase/deaminase (OMR1) identical to threonine dehydratase/deaminase (OMR1) GB:AAC97936, GB:AF096281 [Arabidopsis th	258884_at	-1
unknown protein	258897_at	-1
unknown protein ;supported by cDNA: gi_15294217_gb_AF410300.1_AF410300	258839_at	-1
unknown protein similar to putative protein GB:CAB38214 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:6052.	258811 at	-1
putative pectate lyase similar to pectate lyase precursor GB:P40972 from [Nicotiana tabacum]	258719_at	-1
putative ribosomal-protein S6 kinase (ATPK6) identical to putative ribosomal-protein S6 kinase (ATPK6) GB:D42056 [Arabidopsis thaliana] (FEB	258677 at	-1
putative adenosine kinase similar to adenosine kinase GB:CAB40376 [Zea mays]; supported by cDNA: gi_12017761_gb_AF180894.1_AF180894	258658 at	-1
putative S-adenosylmethionine:2-demethylmenaquinone methyltransferase similar to S	258614 at	-1
putative aspartyl protease contains Pfam profile: PF00026 Eukaryotic aspartyl protease; supported by full-length cDNA: Ceres: 40409.	258615 at	-1
hypothetical protein contains similarity to 50S ribosomal protein L12-C, chloroplast precursor GB:P36212 from [Arabidopsis thaliana]	258466 at	-1
	258239 at	-1
hypothetical protein	258245 at	-1
receptor kinase, putative similar to receptor kinase GB:AAA33715 from [Petunia integrifolia]; supported by full-length cDNA: Ceres: 22221.	258159_at	-1
ubiquitin-specific protease 7 (UBP7), putative similar to GI:11993467; supported by cDNA: gi_11993466_gb_AF302661.1_AF302661	258045 at	-1
AIG2-like protein similar to AIG2 protein GB:P54121 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:5137.	258000_at	-1
unknown protein ; supported by full-length cDNA: Ceres: 92670.	257755 at	-1
histone H3, putative similar to histone H3 GB:P05203 [Petroselinum crispum]; supported by cDNA: gi_14335141_gb_AY037250.1_	257714 at	-1
unknown protein contains similarity to auxin-induced protein GB:P33082 from [Glycine max]	257690_at	-1
unknown protein ;supported by full-length cDNA: Ceres:17362.	257676_at	-1
Expressed protein ; supported by full-length cDNA: Ceres: 11616.	257204 at	-1
hypothetical protein predicted by genemark.hmm	256741 at	-1
unknown protein ; supported by cDNA: gi_14423501_gb_AF386988.1_AF386988	256115_at	-1
unknown protein	256100 at	-1
	255901_at	-1
unknown protein contains similarity to chlorophyllase GI:7415999 from [Chenopodium album]; supported by full-length cDNA: Ceres: 31589.	255786_at	-1
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:232413.	255775 at	-1
hypothetical protein	255604_at	-1 -1
protoporphyrinogen oxidase ; supported by cDNA: gi_14423413_gb_AF386944.1_AF386944	255537_at	-1 -1
PROLIFERA similar to S. cerevisiae MCM2-3-5 genes required for the initiation of DNA replication; supported by cDNA: gi_675490_gb_L39954.1	_	-1 -1
FINELINE INVESTIGATION STREAM AND ST	255513_at	- 1

ļ	5-adenylylsulfate reductase ;supported by full-length cDNA: Ceres:40330.	255284_at	-1
(	xoded for by A. thaliana cDNA Z18000 ;supported by full-length cDNA: Ceres:38543.	255240_at	-1
	putative trehalose-6-phosphate phosphatase (AtTPPA) trehalose-6-phosphate phosphatase - Arabidopsis thaliana, PID:g2944178; supported by	254806_at	-1
	putative protein predicted protein, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 112156.	254722_at	-1
	bHLH protein - like bHLH protein, Arabidopsis thaliana, PATCHX:E255557	254693_at	-1
	putative protein predicted protein, Arabidopsis thaliana, PATCHX:E327449	254701 at	-1
	putative protein similar to unknown protein (gb AAC79139.1)	254521_at	-1
	putative protein storage protein - Populus deltoides, PIR2:S31580	254150 at	-1
	putative protein ; supported by cDNA: gi_15810138_gb_AY056134.1_	253922_at	-1
	putative receptor protein kinase receptor protein kinase, Ipomoea trifida,PID:g836954	253911_at	-1
	hypothetical protein ;supported by full-length cDNA: Ceres:18040.	253817_at	-1
	nucleotide pyrophosphatase -like protein nucleotide pyrophosphatase, Oryza sativa, gb:T03293; supported by cDNA: gi_13430713_gb_AF36026		-1
	EST GB:N37377 spans last intron and 3 end of gene contains similarity to meiotic serine proteinase TMP GI:6468325 from [Lycopersicon escule		-1
	putative protein diacylglycerol kinase iota - Homo sapiens, PID:g3676530; supported by cDNA: gi_13430523_gb_AF360174.1_AF360174	253578 at	-1
	putative protein ENOD16, Medicago truncatula, X99466;supported by full-length cDNA: Ceres:6308.	253480_at	-1
	putative protein predicted protein, Synechocystis sp., PIR2:S74814; supported by cDNA: gi_14334011_gb_AF302188.1_AF302188	253394_at	-1
	P-Protein - like protein P-Protein precursor, Solanum tuberosum, gb:Z99770; supported by cDNA: gi_14596024_gb_AY042800.1_	253387_at	-1
	putative protein dihydrokaempferol 4-reductase (EC 1.1.1.219) -Synechocystis, PIR2:S75325; supported by cDNA: gi_13926212_gb_AF370578.	253334 at	-1
	ankyrin repeat-containing protein 2 ;supported by full-length cDNA: Ceres:34698.	253139 at	-1
	phosphoserine aminotransferase ;supported by full-length cDNA: Ceres:34272.	253162 at	-1
	cytoplasmatic aconitate hydratase (citrate hydro-lyase)(aconitase)(EC 4.2.1.3)	253135_at	-1
	putative protein F35D11.3, Caenorhabditis elegans, PATX:G868225	253081_at	-1
		253059_s_at	-1
	vacuolar H(+)-ATPase subunit-like protein Vacuolar proton pump subunit SFD alpha isoform - Homo sapiens, EMBL:AF112204; supported by cD		-1
	disease resistance protein homolog disease resistance protein RPP1-WsB - Arabidopsis thaliana, EMBL:AF098963	252648 at	-1
	ipoxygenase AtLOX2 ; supported by cDNA: gi_431257_gb_L23968.1_ATHATLO	252618_at	-1
	chloroplast NAD-dependent malate dehydrogenase; supported by cDNA: gi_3256065_emb_Y13987.1_ATMDH	252407_at	-1
	hypothetical protein	252361_at	-1
	receptor protein kinase - like protein CLAVATA1 receptor kinase, Arabidopsis thaliana, EMBL:ATU96879	252272 at	-1
	putative calmodulin calmodulin - Tetrahymena pyriformis (SGC5),PIR1:MCTE; supported by cDNA: gi_14190470_gb_AF380635.1_AF380635	252037_at	-1
	inorganic pyrophosphatase -like protein inorganic pyrophosphatase, Solanum tuberosum, PIR:T07399;supported by full-length cDNA: Ceres:401	251961 at	-1
	synaptobrevin -like protein vesicle-associated membrane protein 7B (At VAMP7B), Arabidopsis thaliana, EMBL:AF025333	251877_at	-1
	nucleoid DNA-binding - like protein nucleoid DNA-binding protein cnd41, chloroplast, common tobacco, PIR:T01996; supported by full-length cDN	_	-1
	ryptophan synthase alpha chain ; supported by full-length cDNA: Ceres: 40110.	251847 at	-1
	putative protein	251727_at	-1
	DNA-binding protein-like DNA-binding protein 4 WRKY4 - Nicotiana tabacum, EMBL:AF193771;supported by full-length cDNA: Ceres:34847.	251705_at	-1
	glutathione peroxidase -like protein phospholipid-hydroperoxide glutathione peroxidase, spinach, PIR:JC5619;supported by full-length cDNA: Cer		-1
	putative protein outer envelope membrane protein E 6.7 - chloroplast Spinacia oleracea, PIR:A35958; supported by cDNA: gi_15724349_gb_AF		-1
	putative protein rugB protein, Dictyostelium discoideum, PIR:S68824; supported by cDNA: gi_15724205_gb_AF412043.1_AF412043	250851 at	-1
	putative protein hypothetical proteins - Arabidopsis thaliana;supported by full-length cDNA: Ceres:12022.	250618_at	-1
	byruvate kinase	250526_at	-1
	putative protein similar to unknown protein (pir  S75227);supported by full-length cDNA: Ceres:22.	249524_at	-1
	DegP protease contains similarity to DegP protease precursor GI:2565436 from [Arabidopsis thaliana]	249421 at	-1
		2.042ut	1
	putative protein similar to unknown protein (emb CAB53482.1)	249167_at	-1

serine/threonine-protein kinase Mak (male germ cell-associated kinase)-like protein ; supported by cDNA: gi_15450859 gb_AY054510.1_	248953 at	-1
magnesium chelatase subunit of protochlorophyllide reductase non-consensus AA donor splice site at exon 1, TG acceptor splice site at exon 2	248920_at	-1
carnitine/acylcarnitine translocase-like protein ;supported by full-length cDNA: Ceres:13730.	248838_at	-1
ras-related small GTP-binding protein-like ;supported by full-length cDNA: Ceres:1492.	248792_at	-1
ethylene responsive element binding factor 2 (ATERF2) (sp O80338) ;supported by full-length cDNA: Ceres:3012.	248794_at	-1
cyclin C-like protein ;supported by full-length cDNA: Ceres:2036.	248666 at	-1
putative protein similar to unknown protein (gb/AAF63814.1);supported by full-length cDNA: Ceres:40718.	248623 at	-1
fumarate hydratase ; supported by cDNA: gi_15529146_gb_AY052197.1_	248461_s_at	-1
unknown protein	248068 at	-1
bis(5 -adenosyl)-triphosphatase-like; also similar to fragile histidine triad	247860_at	-1
putative protein strong similarity to unknown protein (gb/AAD55298.1); supported by cDNA: gi_14423505_gb_AF386990.1_AF386990	247444_at	-1
GTP cyclohydrolase II; 3,4-dihydroxy-2-butanone-4-phoshate synthase (emb CAA03884.1) supported by cDNA: gi_940382_dbj_D45165.1_ATH		-1
unknown protein	246989 at	-1
putative protein hypothetical protein Sb07 - Picea mariana, EMBL:AF051204	246936 at	-1
copper amine oxidase, putative similar to copper amine oxidase GI:3819099 from [Cicer arietinum]	246603 at	-1
putative protein predicted proteins - Arabidopsis thaliana; supported by full-length cDNA: Ceres: 34944.	246452_at	-1
4-alpha-glucanotransferase	245094 at	-1
PSI 9KDa protein	244932_at	-1
NADH dehydrogenase subunit	244935 at	-1
unknown protein	267401 at	-1
putative tropinone reductase ;supported by full-length cDNA: Ceres:14555.	266292 at	-1
arginine methyltransferase-like protein	248633_at	-1
Expressed protein ; supported by full-length cDNA: Ceres: 9573.	258848 at	-1
glucose-6-phosphate dehydrogenase	249372_at	-1
putative receptor-like protein kinase ; supported by cDNA: gi_15292872_gb_AY050870.1_	267619_at	-0.9
putative C2H2-type zinc finger protein likely a nucleic acid binding protein; supported by cDNA: gi_14517523_gb_AY039597.1_	267535_at	-0.9
unknown protein ; supported by full-length cDNA: Ceres:36855.	267503_at	-0.9
putative phosphoribosylaminoimidazolecarboxamide formyltransferase	267421_at	-0.9
putative uricase subunit similar to nodulin-35; identical to GB:Y11120;supported by full-length cDNA: Ceres:38538.	267374_at	-0.9
putative thromboxane-A synthase ; supported by cDNA: gi_15810029_gb_AY054283.1_	267380_at	-0.9
unknown protein	267235_at	-0.9
putative methylenetetrahydrofolate reductase ; supported by cDNA: gi_15215809_gb_AY050434.1_	267187_s_at	-0.9
hypothetical protein predicted by genscan	267057_at	-0.9
unknown protein ; supported by cDNA: gi_15292712_gb_AY050790.1_	266898_at	-0.9
unknown protein ;supported by cDNA: gi_15450758_gb_AY053421.1_	266553_at	-0.9
putative tropinone reductase ;supported by full-length cDNA: Ceres:2618.	266293_at	-0.9
putative glutathione S-transferase ;supported by full-length cDNA: Ceres:24361.	266296_at	-0.9
putative dTDP-glucose 4-6-dehydratase ;supported by full-length cDNA: Ceres:28205.	266205_s_at	-0.9
putative ribosomal protein L7 ;supported by full-length cDNA: Ceres:13298.	265736_at	-0.9
putative alanine acetyl transferase	265725_at	-0.9
hypothetical protein predicted by genscan	265698_at	-0.9
60S ribosomal protein L12 ;supported by full-length cDNA: Ceres:23523.	265445_at	-0.9
putative riboflavin synthase alpha chain ; supported by full-length cDNA: Ceres: 528.	265389_at	-0.9
hypothetical protein predicted by genscan; supported by cDNA: gi_15724317_gb_AF412099.1_AF412099	265342_at	-0.9

unknown protein similar to unknown protein GB:AAD55495	264893 at	-0.9
zinc finger protein ATZF1, putative identical to GB:BAA25989; supported by cDNA: gi_3123711_dbj_D89051.1_D89051	264624_at	-0.9
unknown protein similar to ATP-citrate-lyase; Location of EST gb Z34587. Highly similar to F8A5.32, gb 2462746 and similar to ATP-citrate-lyase		-0.9
unknown protein similar to ESTs gb T20511, gb T45308, gb H36493, and gb AA651176;supported by full-length cDNA: Ceres:2558.	264463_at	-0.9
putative protein phosphatase 2C ;supported by full-length cDNA: Ceres:11428.	264376_at	-0.9
unknown protein predicted by genscan and grail;supported by full-length cDNA: Ceres:14105.	264380_at	-0.9
aminomethyltransferase-like precursor protein very strong similarity to aminomethyltransferase precursor gb/U79769 from Mesembryanthemum (	264394_at	-0.9
putative NPK1-related protein kinase 2 similar to nitrate chlorate transporter GB:Q05085 from (Arabidopsis thaliana); supported by cDNA: gi_166(	264348_at	-0.9
hypothetical protein predicted by grail; supported by full-length cDNA: Ceres: 2928.	263980_at	-0.9
putative MAP kinase ; supported by cDNA: gi_15724283_gb_AF412082.1_AF412082	263989_at	-0.9
putative receptor-like protein kinase	263913_at	-0.9
putative indole-3-glycerol phosphate synthase ;supported by full-length cDNA: Ceres:3006.	263807_at	-0.9
putative protein phosphatase 2C ;supported by full-length cDNA: Ceres:22316.	263711_at	-0.9
unknown protein ESTs gb T20589, gb T04648, gb AA597906, gb T04111, gb R84180, gb R65428, gb T44439, gb T76570, gb R90004, gb T4502	263709_at	-0.9
putative GDP-mannose pyrophosphorylase	263619_at	-0.9
Expressed protein ; supported by full-length cDNA: Ceres: 21909.	263630_at	-0.9
Expressed protein ; supported by cDNA: gi_13926282_gb_AF372895.1_AF372895	263632_at	-0.9
unknown protein ; supported by full-length cDNA: Ceres: 97914.	263541_at	-0.9
phosphoenolpyruvate carboxylase	263491_at	-0.9
cold-regulated protein cor15a precursor ; supported by cDNA: gi_14532457_gb_AY039853.1_	263497_at	-0.9
unknown protein similar to hypothetical protein GB:AAF27090 GI:6730669 from (Arabidopsis thaliana);supported by full-length cDNA: Ceres:1018	262986_at	-0.9
hypothetical protein similar to putative transporter GI:6598860 from [Arabidopsis thaliana]	262935_at	-0.9
endomembrane protein, putative similar to endomembrane protein emp70 precursor isolog GB:AAF67014 GI:7677068 [Homo sapiens]; supporte		-0.9
putative DNA binding protein similar to gb U90212 DNA binding protein ACBF from Nicotiana tabacum and contains 3 PF 00076 RNA recognition	262824_at	-0.9
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:109912.	262711_at	-0.9
unknown protein EST gb N65467 comes from this gene;supported by full-length cDNA: Ceres:30239.	262598_at	-0.9
20S proteasome subunit PAE1 identical to 20S proteasome subunit PAE1 GI:3421087 from [Arabidopsis thaliana]; supported by full-length cDNA:	262258_at	-0.9
unknown protein	262092_at	-0.9
protein disulfide isomerase, putative similar to GB:AAA85099 GI:687235 from [Onchocerca volvulus]; supported by cDNA: gi_14423497_gb_AF3		-0.9
unknown protein similar to putative DNA-binding protein GI:6714399 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:92341.	261942_at	-0.9
sterol delta7 reductase identical to GB:AAF63498 GI:7542561 from [Arabidopsis thaliana]; supported by cDNA: gi_1245181_gb_U49398.1_ATU4		-0.9
unknown protein ;supported by full-length cDNA: Ceres:122986.	261788_at	-0.9
ribonucleoprotein, putative similar to 33 KDA RIBONUCLEOPROTEIN GB:P19684 from [Nicotiana sylvestris]; supported by full-length cDNA: Cer		-0.9
pyruvate dehydrogenase E1 alpha subunit identical to pyruvate dehydrogenase E1 alpha subunit GB:AAB86803 GI:2454182 from [Arabidopsis th		-0.9
polyphosphoinositide binding protein, putative similar to polyphosphoinositide binding protein Ssh2p GB:AAB94599 GI:2739046 from [Glycine mathematical states and sta		-0.9
nodulin protein, putative similar to GB:2598575 from [Medicago truncatula];supported by full-length cDNA: Ceres:149985.	261335_at	-0.9
protein kinase, putative contains similarity to many predicted protein kinases; supported by cDNA: gi_13430527_gb_AF360176.1_AF360176	261308_at	-0.9
unknown protein ; supported by cDNA: gi_14334567_gb_AY034957.1_	261273_at	-0.9
thioredoxin identical to GB:CAA84610 from [Arabidopsis thaliana] (Proc. Natl. Acad. Sci. U.S.A. 92 (12), 5620-5624 (1995)); supported by full-len	_	-0.9
hypothetical protein predicted by genemark.hmm	260919_at	-0.9
hypothetical protein similar to carboxyvinyl-carboxyphosphonate phosphorylmutase GB:O49290 from [Arabidopsis thaliana]	260902_at	-0.9
biotin synthase (Bio B) ;supported by full-length cDNA: Ceres:42038.	260548_at	-0.9
Unknown protein ; supported by cDNA: gi_15028352_gb_AY045979.1_	260508_at	-0.9
hypothetical protein predicted by genefinder; supported by full-length cDNA: Ceres: 99920.	260427_at	-0.9

acid phosphatase, putative similar to GI:5360721 from (Lupinus albus)	260421_at	-0.9
putative 3-isopropylmalate dehydrogenase similar to 3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR GB:P29102 from (Brassica nap	260285_at	-0.9
unknown protein contains Pfam profile: PF00561 alpha/beta hydrolase fold;supported by full-length cDNA: Ceres:36063.	260232_at	-0.9
putative histidinol-phosphate aminotransferase similar to histidinol-phosphate aminotransferase GB:CAA70403 from [Nicotiana tabacum]	260172_s_at	-0.9
fructokinase, putative similar to fructokinase (Lycopersicon esculentum) GI:2102691; supported by cDNA: gi_13878132_gb_AF370329.1_AF370	260107_at	-0.9
Expressed protein ; supported by full-length cDNA: Ceres: 42300.	259603 at	-0.9
unknown protein ; supported by cDNA: gi_15028026_gb_AY045870.1_	259460_at	-0.9
putative mitochondrial processing peptidase alpha subunit similar to mitochondrial processing peptidase GB:X66284 (Solanum tuberosum); supp	259326_at	-0.9
putative cytoskeleton-associated protein similar to cytoskeleton-associated protein 1 GB:4502849 [Homo sapiens]	259141_at	-0.9
unknown protein similar to unknown protein GB:AAC62889 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:15153.	259154_at	-0.9
	258710_s_at	-0.9
putative GDSL-motif lipase/acylhydrolase contains Pfam profile: lipase/acylhydrolase with GDSL-like motif; supported by full-length cDNA: Ceres:1	258589 at	-0.9
putative mannose-6-phosphate isomerase similar to mannose-6-phosphate isomerase GB:NP_002426 from [Homo sapiens]; supported by full-len		-0.9
hypothetical protein contains similarity to putative phosphate/phosphoenolpyruvate translocator protein GB:AAD20711 from [Arabidopsis thaliana]		-0.9
putative coatomer complex subunit similar to subunit of coatomer complex GB:X70476 from [Homo sapiens]	258331_at	-0.9
dihydrolipoamide S-acetyltransferase identical to GB:AAD55139 from [Arabidopsis thaliana]; supported by cDNA: gi_14335165_gb_AY037262.1_		-0.9
hypothetical protein similar to hypothetical protein GB:AAF01546 from [Arabidopsis thaliana]	257999 at	-0.9
actin 2 identical to GB:AAB37098 from [Arabidopsis thaliana], Plant J. 10 (1), 107-121 (1996); supported by full-length cDNA: Ceres: 3819.	257749_at	-0.9
succinate dehydrogenase iron-protein subunit, putative similar to succinate dehydrogenase iron-protein subunit (SDHB) GB:BAA82749 [Oryza sa		-0.9
integral membrane protein, putative contains Pfam profile: PF01554 uncharacterized membrane protein family; supported by cDNA: gi_1632312(		-0.9
non-phototropic hypocotyl protein, putative similar to GB:AAF05914 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:118259.	257294 at	-0.9
Expressed protein ; supported by full-length cDNA: Ceres: 12588.	257152 at	-0.9
putative protein phosphatase type 2C similar to protein phosphatase type 2C GB:AAD17805 from [Lotus japonicus]	257050 at	-0.9
unknown protein	257074_at	-0.9
longevity factor-like protein similar to LAG1Ce-1 GB:AAD16893 from [Caenorhabditis elegans] (Genome Res.(1998) 8 (12), 1259-1272); supporte		-0.9
expressed protein supported by cDNA: gi:14334707	256956 at	-0.9
hypothetical protein	256914 at	-0.9
hypothetical protein predicted by genefinder; supported by full-length cDNA: Ceres: 23892.	256722_at	-0.9
unknown protein ;supported by full-length cDNA: Ceres:31357.	256674 at	-0.9
unknown protein ; supported by full-length cDNA: Ceres: 368.	256617_at	-0.9
hypothetical protein predicted by genscan	256427 at	-0.9
phosphoinositide specific phospholipase (AtPLC2) identical to phosphoinositide specific phospholipase (AtPLC2) GI:857374 [Arabidopsis thaliana		-0.9
mitogen-activated protein kinase, putative similar to mitogen-activated protein kinase GI:5815410 from [Oryza sativa]; supported by cDNA: gi_15		-0.9
hypothetical protein predicted by genemark.hmm	256086 at	-0.9
hypothetical protein	255978 at	-0.9
glycine-rich RNA-binding protein, putative similar to glycine-rich RNA-binding protein GI:17818 from [Brassica napus]	255962_at	-0.9
14-3-3 protein GF14epsilon (grf10) identical to 14-3-3 protein GF14 epsilon GI:5802798, SP:P48347 from [Arabidopsis thaliana];supported by ful		-0.9
ABC transporter, putative similar to ABC transporter GI:10280532 from [Homo sapiens]	255889 at	-0.9
12-oxophytodienoate reductase, putative similar to 12-oxophytodienoate reductase OPR1 GI:3882355 from [Arabidopsis thaliana]	255895_at	-0.9
coded for by A. thaliana cDNA T20615 ;supported by full-length cDNA: Ceres:37305.	255626_at	-0.9
hypothetical protein ; supported by cDNA: gi_15982914_gb_AY057565.1_	255572 at	-0.9
receptor protein kinase-like protein receptor protein kinase-like protein - Arabidopsis thaliana, PIR2:T05898	255116 at	-0.9
putative protein hypothetical protein F6E13.15 - Arabidopsis thaliana,PIR2:T00682	255041_at	-0.9
hydroxymethylglutaryl-CoA synthase ;supported by full-length cDNA: Ceres:22413.	254845_at	-0.9

putative protein KIAA0255 gene. Homo sapiens, gb:D87444	254827 at	-0.9
translation initiation factor eIF3 - like protein translation initiation factor eIF3 p66 subunit, Homo sapiens, PID:g2351378	254438_at	-0.9
putative protein riboflavin biosynthesis protein ribG, Synechocystissp., PIR2:S74377;supported by full-length cDNA: Ceres:99319.	254444 at	-0.9
tubulin beta-9 chain ;supported by full-length cDNA: Ceres:36891.	254446 at	-0.9
putative protein ribophorin II precursor, Homo sapiens, PIR2:B26168	254456 at	-0.9
putative protein alternative oxidase, Mangifera indica, PIR2:S45035; supported by cDNA: gi_15010795_gb_AY045699.1_	254335_at	-0.9
predicted protein predicted protein ERG25, Saccharomyces cerevisiae, PIR2:S64354	254333_at	-0.9
gamma-glutamylcysteine synthetase ; supported by cDNA: gi_15912188_gb_AY056372.1_	254270_at	-0.9
		-0.9
putative pectate lyase pectate lyase, Musa acuminata, PATX:E209876;supported by full-length cDNA: Ceres:36681.	254119 at	-0.9
mitogen activated protein kinase kinase (nMAPKK) ;supported by full-length cDNA: Ceres:31259.	253993_at	-0.9
photosystem II protein W - like photosystem II protein W, Porphyra purpurea, PIR2:S73268; supported by full-length cDNA: Ceres: 2419.	253790_at	-0.9
aspartate aminotransferase ;supported by full-length cDNA: Ceres:33414., Ceres:103854.	253481 at	-0.9
putative protein acetylpolyamine aminohydrolase (aphA) homolog -Archaeoglobus fulgidus,PIR2:B69266; supported by cDNA: gi_15529219_gb_	253337 at	-0.9
Nonclathrin coat protein gamma - like protein coat protein gamma-cop, Bos primigenius	253231_at	-0.9
amidophosphoribosyltransferase 2 precursor	253252_at	-0.9
putative protein Cyanophora paradoxa cyanelle, predicted protein; supported by full-length cDNA: Ceres: 2912.	253197_at	-0.9
putative protein cylicin II - bovine, PIR2:I46014	252952_at	-0.9
Inositol monophosphatase - like protein Mono-phosphatase, Streptomyces anulatus, X92429	252934_at	-0.9
shikimate kinase - like protein shikimate kinase precursor, Lycopersicon esculentum, gb:S21584	252900_at	-0.9
cytochrome P450 -like protein cytochrome P450 CYP86A1, Arabidopsis thaliana, EMBL:X90458; supported by full-length cDNA: Ceres: 120342.	252911_at	-0.9
histone H3.3 ; supported by cDNA: gi_14326561_gb_AF385735.1_AF385735	252824_at	-0.9
Expressed protein ; supported by full-length cDNA: Ceres: 157151.	252412_at	-0.9
H-protein promoter binding factor-2a ;supported by full-length cDNA: Ceres:113639.	252429_at	-0.9
putative protein saposin precursor - Homo sapiens, PIR:SAHUP;supported by full-length cDNA: Ceres:93651.	252075_at	-0.9
nodulin / glutamate-ammonia ligase - like protein MtN6 - nodulin 6, Medicago truncatula, EMBL:MET133118	251973_at	-0.9
dTDP-glucose 4-6-dehydratase -like protein dTDP-glucose 4-6-dehydratase, Cicer arietinum, EMBL:AJ275318 contains non-consensus AT dono	251945_at	-0.9
GTPase AtRAB8 ;supported by full-length cDNA: Ceres:27384.	251960_at	-0.9
putative protein GATA transcription factor 3, Arabidopsis thaliana, Y13650; supported by cDNA: gi_15724333_gb_AF412107.1_AF412107	251861_at	-0.9
ribosomal L23a - like protein various ribosomal L23a proteins;supported by full-length cDNA: Ceres:17531.	251783_at	-0.9
ABC transporter - like protein breast cancer resistance protein 1 BCRP1, Mus musculus, EMBL:NP_036050; supported by cDNA: gi_15028218_(	251785_at	-0.9
putative protein hypothetical protein SPCC320.08 - Schizosaccharomyces pombe, PIR:T41303	251516_s_at	-0.9
ribosomal protein S13 -like AtRPS13A mRNA for cytoplasmic ribosomal protein S13, Arabidopsis thaliana, AB031739; supported by cDNA: gi_14		-0.9
RING finger protein ;supported by full-length cDNA: Ceres:25801.	251321_at	-0.9
homeobox-leucine zipper protein ATHB-12 ;supported by full-length cDNA: Ceres:32615.	251272_at	-0.9
ABC transporter -like protein NBD-like protein POP, Arabidopsis thaliana, EMBL:AF127664;supported by full-length cDNA: Ceres:21701.	251020_at	-0.9
putative protein ;supported by cDNA: gi_15724319_gb_AF412100.1_AF412100	250929_at	-0.9
putative protein ;supported by full-length cDNA: Ceres:3115.	250954_at	-0.9
ABC transporter-like protein ;supported by cDNA: gi_14488081_gb_AF389289.1_AF389289	250690_at	-0.9
peptide methionine sulfoxide reductase-like protein peptide methionine sulfoxide reductase (msr) - Arabidopsis thalina, EMBL:AJ133753	250633_at	-0.9
putative protein densin-180, Rattus norvegicus, PIR:T31434	250577_at	-0.9
serine/threonine protein kinase ;supported by full-length cDNA: Ceres:5323.	250545_at	-0.9
putative protein phosphatase protein tyrosine phosphatase-like protein PTPLB, Mus musculus, EMBL:AF169286	250428_at	-0.9
clathrin binding protein - like Af10-protein, Avena fatua, EMBL:U80041	250356_at	-0.9

NADP dependent malic enzyme - like protein NADP dependent malic enzyme, P.vulgaris, EMBL:PVME1G; supported by cDNA: gi_16226465_gt	250220 of	-0.9
putative protein similar to unknown protein (pir  T09909)	250339_at 250307 at	-0.9
putative protein similar to unknown protein (pirin 19909) putative protein predicted protein, Arabidopsis thaliana	250307_at 250282_at	-0.9 -0.9
phytoene synthase (gb AAB65697.1) ;supported by full-length cDNA: Ceres:15761.	250282_at 250095_at	-0.9
anthranilate phosphoribosyltransferase, chloroplast precursor (sp[Q02166); supported by cDNA: gi_15450851_gb_AY054506.1_	250095_at 250014 at	-0.9
apyrase (gb/AAF00612.1); supported by cDNA: gi_6006800_gb_AF156783.1_AF156783	250014_at	-0.9
	_	
glutaredoxin -like protein glutaredoxin, castor bean, PIR:S54825;supported by full-length cDNA: Ceres:92720. putative protein 2 -hydroxyisoflavone reductase (EC 1.3.1.45) - Nicotiana tabacum, PIR:T02202;supported by full-length cDNA: Ceres:17121.	249996_at	-0.9 -0.9
beta-amylase-like proten beta-amylase - Prunus armeniaca, EMBL:AF139501;supported by full-length cDNA: Ceres:30798.	250006_at	
NAC-domain protein-like ;supported by full-length cDNA: Ceres:29829.	250007_at 249940_at	-0.9 -0.9
	_	
soluble starch synthase	249785_at	-0.9
putative protein tyrosine aminotransferase-like; also similar to nicotianamine aminotransferase	249688_at	-0.9
glutamateammonia ligase ; supported by cDNA: gi_16226386_gb_AF428386.1_AF428386	249581_at	-0.9
putative protein similar to unknown protein (pir  T04523)	249093_at	-0.9
zinc finger protein Glo3-like	248863_at	-0.9
putative protein similar to unknown protein (gb AAB97010.1)	248705_at	-0.9
unknown protein	248312_at	-0.9
putative protein similar to unknown protein (emb CAA71173.1);supported by full-length cDNA: Ceres:19542.	248327_at	-0.9
unknown protein ;supported by full-length cDNA: Ceres:148254.	248282_at	-0.9
putative protein contains similarity to MYB family transcription factor	248246_at	-0.9
NADH-dependent glutamate synthase	248267_at	-0.9
putative protein strong similarity to unknown protein (pir  T05748); supported by cDNA: gi_15010657_gb_AY045630.1_	248177_at	-0.9
transport protein particle component Bet3p-like protein ;supported by full-length cDNA: Ceres:122866.	248127_at	-0.9
TCH4 protein (gb AAA92363.1) ; supported by cDNA: gi_14194112_gb_AF367262.1_AF367262	247925_at	-0.9
Cf-5 disease resistance protein - like Hcr2-0B, Lycopersicon esculentum, EMBL:AF053995	247569_at	-0.9
putative protein various predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 6441.	247464_at	-0.9
putative protein hypersensitive-induced response protein HIR3, Zea mays, EMBL:AF236375; supported by full-length cDNA: Ceres:2641.	247403_at	-0.9
beta-galactosidase (emb CAB64742.1); supported by cDNA: gi_16649044_gb_AY059892.1_	247356_at	-0.9
GTP-binding protein ; supported by full-length cDNA: Ceres: 30437.	247202_at	-0.9
ADP-ribosylation factor-like protein ;supported by full-length cDNA: Ceres:35979.	247008_at	-0.9
AtBgamma - like protein B regulatory subunit of PP2A, Arabidopsis thaliana, EMBL:ATU73528; supported by cDNA: gi_16604606_gb_AY05974	246907_at	-0.9
TCP-1 chaperonin-like protein t-complex-type molecular chaperone Cctz - Mus musculus, EMBL:Z31557	246480_at	-0.9
putative protein ;supported by full-length cDNA: Ceres:22994.	246486_at	-0.9
putative protein hypothetical protein F16B3.27 - Arabidopsis thaliana, EMBL:AC021640;supported by full-length cDNA: Ceres:18222.	246505_at	-0.9
SigA binding protein ;supported by cDNA: gi_14596086_gb_AY042831.1_	246293_at	-0.9
sulfate transporter ATST1 ;supported by cDNA: gi_2285884_dbj_D89631.1_D89631	246310_at	-0.9
putative protein ;supported by full-length cDNA: Ceres:36845.	246199_at	-0.9
hydroxymethylbilane synthase ;supported by full-length cDNA: Ceres:3051.	246033_at	-0.9
protein kinase, putative similar to protein kinase GI:717180 from (Arabidopsis thaliana)	245825_at	-0.9
chorismate synthase, putative similar to chorismate synthase GI:452796 from [Synechocystis sp.]; supported by cDNA: gi_15982823_gb_AY057		-0.9
light-harvesting complex protein similar to light-harvesting complex protein GI:22752 from [Pinus sylvestris]; supported by full-length cDNA: Ceres:	245806_at	-0.9
unknown protein ;supported by full-length cDNA: Ceres:39155.	245730_at	-0.9
salt-inducible protein homolog	245494_at	-0.9
similar to latex allergen from Hevea brasiliensis ;supported by full-length cDNA: Ceres:1999.	245038_at	-0.9

photosystem II G protein	245011_at	-0.9
ribosomal protein S19	244986_at	-0.9 -0.9
NADH dehydrogenase ND6	244934 at	-0.9
putative protein similar to unknown protein (emb CAB67623.1)	250696 at	-0.9
origin recognition complex protein identical to GB:U40269;supported by full-length cDNA: Ceres:42701.	267173 at	-0.9
hypothetical protein predicted by genscan+	264864_at	-0.9
hypothetical protein predicted by gensean	259642_at	-0.9
unknown protein similar to leucine-rich repeat protein GB:CAA76000 and GB:CAA76001 from [Arabidopsis thaliana]	258390_at	-0.9
putative protein	255527_at	-0.9
putative protein p47 - Homo sapiens,PID:g5531827	254348 at	-0.9
cyclophilin - like protein cyclophilin, Arabidopsis thaliana, PID:g2443755	253216_at	-0.9
putative pectinesterase pectinesterase - Lycopersicon esculentum, PID:e312172	252989_at	-0.9
CONSTANS-like 1	246523 at	-0.9
unknown protein predicted by genscan; similar to GP/9826/X07453; supported by full-length cDNA: Ceres: 12267.	267637_at	-0.9
unknown protein	267511 at	-0.8
unknown protein	267310 at	-0.8
putative CCAAT-binding transcription factor subunit	267315_at	-0.8
similar to late embryogenesis abundant proteins ; supported by full-length cDNA: Ceres: 2450.	267212_at	-0.8
aspartate aminotransferase (AAT1) identical to GB:U15026;supported by full-length cDNA: Ceres:34360.	267151 at	-0.8
	267175_s_at	-0.8
putative choline kinase ;supported by full-length cDNA: Ceres:37620.	266861_at	-0.8
1-aminocyclopropane-1-carboxylate synthase (ACS4) identical to GB:U23481; supported by cDNA: gi_12083215_gb_AF332404.1_AF332404	266830_at	-0.8
Expressed protein ; supported by cDNA: gi_14334701_gb_AY035024.1_	266802_at	-0.8
hypothetical protein predicted by grail	266668 at	-0.8
Expressed protein ; supported by full-length cDNA: Ceres: 7600.	266500 at	-0.8
mevalonate diphosphate decarboxylase identical to GB:Y14325;supported by full-length cDNA: Ceres:35493.	266414_at	-0.8
calmodulin-like protein identical to GB:X68054;supported by full-length cDNA: Ceres:11537.	266371_at	-0.8
putative tropinone reductase	266279_at	-0.8
unknown protein ; supported by cDNA: gi_16604321_gb_AY058059.1_	266101 at	-0.8
	266075_s_at	-0.8
hypothetical protein predicted by genscan	265704 at	-0.8
unknown protein	265539_at	-0.8
similar to cold acclimation protein WCOR413 [Triticum aestivum]; supported by full-length cDNA: Ceres:7835.	265480 at	-0.8
succinyl-CoA ligase beta subunit ;supported by full-length cDNA: Ceres:36904.	265257_at	-0.8
histidine transport protein (PTR2-B) ; supported by cDNA: gi_13937184_gb_AF372946.1_AF372946	265220_at	-0.8
3-ketoacyl-acyl carrier protein synthase III (KAS III) identical to 3-ketoacyl-acyl carrier protein synthase III (KAS III) GB:CAA72385 GI:1888359 (A		-0.8
T-complex chaperonin protein , epsilon subunit identical to GB:O04450, similar to ESTs gb R29812, emb Z38124, gb AA297087, gb R29812, gb		-0.8
DNAJ-like heatshock protein similar to GB:AAD39493	264865 at	-0.8
unknown protein similar to C-1 (Homo sapiens) (U41816); supported by full-length cDNA: Ceres: 20276.	264778_at	-0.8
hypothetical protein predicted by genscan; supported by full-length cDNA: Ceres:6295.	264672 at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:25136.	264635 at	-0.8
putative vesicle transport protein Contains similarity to vesicle trafficking protein gb/U91538 from Mus musculus. ESTs gb/F15494 and gb/F14097	_	-0.8
putative seryl-tRNA synthetase similar to GB:CAA73496; supported by cDNA: gi_16226852_gb_AF428351.1_AF428351	264350_at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:16387.	264286_at	-0.8

nutative sikhesellin segulated protein contains similarity to sikhesellin segulated protein 2 programs (CACTA) homeles shull 147765 from A thelians	264405 of	0.0
putative gibberellin-regulated protein contains similarity to gibberellin-regulated protein 2 precursor (GAST1) homolog gb[U11765 from A. thaliana putative sucrose transport protein, SUC2 strong similarity to GB:S38196 sucrose transport protein SUC2 from [Arabidopsis thaliana]; supported b		-0.8 -0.8
RAS-related protein, RAB7 identical GB:004157 RAS-RELATED PROTEIN RAB7 from [Arabidopsis thaliana]; supported by cDNA: gi_15718415		-0.8
Expressed protein; supported by full-length cDNA: Ceres: 2681.	264096_at	-0.8
NADH dehydrogenase, putative similar to NADH dehydrogenase GI:668984 from [Solanum tuberosum];supported by full-length cDNA: Ceres:54		-0.8
		-0.8 -0.8
putative signal sequence receptor, alpha subunit (SSR-alpha) Same as GP: 1174448;supported by full-length cDNA: Ceres:27787. putative lipase ; supported by cDNA: gi_15293128_gb_AY050998.1_	264020_at 263987 at	-0.8 -0.8
	—	
putative mitochondrial carrier protein	263943_at	-0.8
putative pyruvate kinase ;supported by full-length cDNA: Ceres:120685.	263922_s_at	-0.8
unknown protein ; supported by cDNA: gi_15294187_gb_AF410285.1_AF410285	263805_at	-0.8
coatomer alpha subunit	263743_at	-0.8
putative ferredoxin-thioredoxin reductase ;supported by full-length cDNA: Ceres:40781.	263624_at	-0.8
unknown protein	263513_at	-0.8
unknown protein	263456_at	-0.8
predicted protein ;supported by full-length cDNA: Ceres:28779.	263410_at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:641.	263421_at	-0.8
ADP-ribosylation factor 1 ;supported by full-length cDNA: Ceres:34414.	263321_at	-0.8
histone H2A; supported by full-length cDNA: Ceres: 8.	263264_at	-0.8
putative GTP-binding protein Similar to WO8E3.3 gi 3880615 putative GTP-binding protein from C. elegans cosmid gb Z92773. EST gb AA59733	263224_at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:3173.	263129_at	-0.8
class 1 non-symbiotic hemoglobin (AHB1) identical to GP:2581783:U94998;supported by full-length cDNA: Ceres:18195.	263096_at	-0.8
hypothetical protein similar to hypothetical protein GB:AAF27077 GI:6730656 from (Arabidopsis thaliana)	263015_at	-0.8
hypothetical protein contains similarity to Na+/H+ antiporter GI:1655701 from [Xenopus laevis]	263009_at	-0.8
hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 19759.	262878_at	-0.8
cytochrome B561, putative similar to cytochrome GB:AAD11424 GI:4206110 [Mesembryanthemum crystallinum]	262831_at	-0.8
dynamin, putative similar to dynamin-1 SP:P21575 [Rattus norvegicus (Rat)];supported by full-length cDNA: Ceres:12880.	262837_at	-0.8
putative sugar transporter protein nearly identical to Arabidopsis sugar transporter, gi 1495273	262797_at	-0.8
putative cytochrome P450 monooxygenase identical to gb X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF 00067	_	-0.8
unknown protein EST gb T22808 comes from this gene	262776_at	-0.8
unknown protein	262700_at	-0.8
ribonuclease contains similarity to RNase GI:7768564 from [Nicotiana tabacum]	262657_at	-0.8
peptide transporter, putative similar to PEPTIDE TRANSPORTER PTR2-B GB:P46032 GI:1172704 from [Arabidopsis thaliana]	262281_at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:12408.	262168_at	-0.8
cinnamoyl CoA reductase, puitative similar to cinnamoyl CoA reductase GI:2058310 from [Eucalyptus gunnii]; supported by full-length cDNA: Cei	_	-0.8
tubulin alpha-6 chain, putative identical to tubulin alpha-6 chain GB:P29511 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:153	261635_at	-0.8
unknown protein contains Pfam profile: PF00560 Leucine Rich Repeat (4 copies); Pfam profile: PF00069 Eukaryotic protein kinase domain; Pfam	261513_at	-0.8
Expressed protein ; supported by cDNA: gi_15293296_gb_AY051082.1_	261417_at	-0.8
protein kinase, putative similar to many predicted protein kinases	261339_at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:207684.	261201_at	-0.8
transcription factor TINY, putative similar to transcription factor TINY GB:CAA64359 GI:1246403 from [Arabidopsis thaliana]; supported by full-len	261059_at	-0.8
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:19718.	260871_at	-0.8
endochitinase isolog	260568_at	-0.8
unknown protein similar to hypothetical protein GB:CAA10289 [Cicer arietinum]	260401_at	-0.8
homeobox gene 13 protein identical to homeobox gene 13 protein gb AAF20996.1 AF208044_1 [Arabidopsis thaliana]; supported by full-length cD	260395_at	-0.8

unknown protein	260281 at	-0.8
putative glycerophosphodiester phosphodiesterase similar to glycerophosphoryl diester phosphodiesterase GB:AAF12f49 from [Deinococcus radi		-0.8
hypothetical protein predicted by genscan+	260167_at	-0.8
putative cinnamyl-alcohol dehydrogenase similar to cinnamyl-alcohol dehydrogenase GB:AAC35846 [Medicago sativa]	259911 at	-0.8
unknown protein similar to hypothetical protein GB:CAB39648 [Arabidopsis thaliana]; supported by cDNA: gi_14532697_gb_AY039973.1_	259882_at	-0.8
putative ribophorin I (dolichyl-diphosphooligosaccharide-protein glycosyltransferase) similar to ribophorin I		-0.8
putative transcription factor similar to myb-related transcription factor 24 GB:S71287;supported by full-length cDNA: Ceres:31592.	259751 at	-0.8
putative 30S ribosomal protein S13 similar to putative 30S ribosomal protein S13, chloroplast precursor GB:P42732 [Arabidopsis thaliana]	259678_at	-0.8
protein kinase, putative similar to GI:7573596 from [Populus nigra]	259671 at	-0.8
hypothetical protein	259560_at	-0.8
putative serine/threonine kinase ; supported by cDNA: gi_15010571_gb_AY045587.1_	259538_at	-0.8
developmental protein, putative similar to developmental protein DG1118 GI:3789911 from [Dictyostelium discoideum]; supported by full-length cI		-0.8
putative ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I similar to ribulose-1,5-bisphosphate carboxylase/		-0.8
putative thymidine kinase similar to thymidine kinase GB:AAC31168 [Oryza sativa]; supported by full-length cDNA: Ceres: 19188.	259224_at	-0.8
putative ribosomal protein S2 similar to putative ribosomal protein S2 GB:CAA74226 [Mitochondrion Triticum aestivum];supported by full-length cl		-0.8
putative thylakoid lumen rotamase similar to thylakoid lumen rotamase GB:CAA72792 [Spinacia oleracea];supported by full-length cDNA: Ceres:3		-0.8
stress related protein, putative similar to stress related protein GB:AAD51854 from [Vitis riparia]; supported by full-length cDNA: Ceres:13300.	259105 at	-0.8
unknown protein	259123_at	-0.8
putative ubiquitin carboxyl-terminal hydrolase similar to ubiquitin carboxyl-terminal hydrolase GB:AAF01440 [Schizosaccharomyces pombe]	258780_at	-0.8
unknown protein ; supported by cDNA: gi_13811647_gb_AF355757.1_AF355757	258717 at	-0.8
hypothetical protein predicted by genscan; supported by full-length cDNA: Ceres: 19531.	258657 at	-0.8
unknown protein ; supported by cDNA: gi_14334929_gb_AY035138.1_	258298 at	-0.8
putative signal peptidase 21kDa subunit similar to signal peptidase 21kDa subunit GB:BAA76439 [Rattus norvegicus]; contains Pfam profile: PF0	_	-0.8
putative acetyltransferase similar to dihydrolipoamide S-acetyltransferase GB:AAD46491 from [Zea mays]; supported by cDNA: gi_13605806_gb_		-0.8
nitrate transporter identical to nitrate transporter GB:CAB38706 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:111089.	258181_at	-0.8
AIG2-like protein similar to AIG2 protein GB:P54121 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:32718.	258001_at	-0.8
monosaccharide transport protein, STP4 identical to GB:S25009 from [Arabidopsis thaliana]; supported by cDNA: gi_13605905_gb_AF367352.1		-0.8
prolyl 4-hydroxylase, putative similar to PROLYL 4-HYDROXYLASE ALPHA SUBUNIT PRECURSOR GB:Q10576 from [Caenorhabditis elegans		-0.8
unknown protein	257867 at	-0.8
DnaJ protein, putative contains Pfam profile: PF00226 DnaJ domain;supported by full-length cDNA: Ceres:31309.	257654_at	-0.8
hypothetical protein	257641_s_at	-0.8
Expressed protein ; supported by full-length cDNA: Ceres: 22745.	257271_at	-0.8
myrosinase-associated protein, putative similar to myrosinase-associated protein GB:CAA71238 from [Brassica napus]	257072_at	-0.8
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:34377.	256920_at	-0.8
hypothetical protein contains similarity to flavonol synthase (FLS) GB:Q41452 from [Solanum tuberosum], contains Pfam profile: PF00671 Iron/A	256922_at	-0.8
cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450	256870_at	-0.8
hypothetical protein predicted by genemark.hmm, contains Pfam profile:PF00076 rrm:RNA recognition motif	256770_at	-0.8
membrane import protein, putative similar to membrane import protein GB:AAF20172 GI:6636407 [Drosophila melanogaster]; supported by cDN/	256628_at	-0.8
At14a-1 protein identical to At14a protein GB:AAD26355 GI:4589123 [Arabidopsis thaliana] [Gene 230 (1), 33-40 (1999)]	256601_s_at	-0.8
6-phosphogluconate dehydrogenase, putative similar to 6-phosphogluconate dehydrogenase GB:BAA22812 GI:2529229 [Glycine max]; supporte	256328_at	-0.8
integral membrane protein, putative contains Pfam profile: PF00892 Integral membrane protein DUF6	256250_at	-0.8
guanine nucleotide-binding protein, putative similar to guanine nucleotide-binding protein GI:9294068 from [Arabidopsis thaliana]; supported by fi	256144_at	-0.8
amino acid permease I identical to amino acid permease I GI:22641 from [Arabidopsis thaliana]; supported by cDNA: gi_404018_gb_L16240.1_A	256022_at	-0.8
hypothetical protein contains Pfam profile: PF00650 CRAL/TRIO domain	255923_at	-0.8

sterol-C-methyltransferase identical to sterol-C-methyltransferase GI:1061040 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:2	255885 at	-0.8
transcription factor, putative similar to transcription factor BTF3 homolog GI:2982299 from [Picea mariana]; supported by full-length cDNA: Ceres:		-0.8
MAP kinase 4 (MPK4) ;supported by full-length cDNA: Ceres:7653.	255624_at	-0.8
predicted protein of unknown function similar to M. truncatula MtN21, GenBank accession number Y15293; F11O4.14 was picked up in a screer		-0.8
drought-induced-19-like 1 similar to drought-induced-19, GenBank accession number X78584 similar to F2P16.10, GenBank accession number 2		-0.8
Expressed protein ; supported by cDNA: gi 16226696 gb AF428466.1 AF428466	255436 at	-0.8
putative glucan synthase component similar to 1,3-beta glucan synthase	255378_at	-0.8
	255344 s at	-0.8
putative phosphatidylglycerotransferase similar to CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase of Synechocystis sp. GenB		-0.8
putative procential RNA helicase -Mus musculus,PIR2:184741	255053 at	-0.8
H+-transporting ATPase chain E, vacuolar	254903 at	-0.8
beta-adaptin - like protein beta-adaptin -Homo sapiens,PID:g179333; supported by cDNA: gi_7385052_gb_AF216386.1_AF216386	254925_at	-0.8
fatty acid elongase - like protein (cer2-like) cer2, Arabidopsis thaliana, X93080	254737_at	-0.8
Expressed protein ; supported by full-length cDNA: Ceres: 266299.	254505 at	-0.8
putative protein oxysterol-binding protein, Homo sapiens, PIR2:A34581; supported by cDNA: gi_15450518_gb_AY052361.1_	254329_at	-0.8
putative protein hypothetical protein - Caenorhabditis elegans,PID:e1350884;supported by full-length cDNA: Ceres:8254.	254165_at	-0.8
putative protein ClpC protease - Spinacia oleracea, PID:g4105131; supported by full-length cDNA: Ceres: 28122.	254072 at	-0.8
putative protein qkI-7, Mus musculus	253964_at	-0.8
putative protein 150-kD protein, Dictyostelium discoideum, gb:U49332	253849 at	-0.8
hexokinase ; supported by cDNA: gi_8567421_gb_U18754.2_ATU18754	253705 at	-0.8
cellulose synthase catalytic subunit (RSW1)	253428_at	-0.8
putative protein mRNA for KIAA0079 gene, Homo sapiens	253448_at	-0.8
carbonate dehydratase - like protein carbonate dehydratase precursor, Spinacia oleracea, Pir2:S28797; supported by full-length cDNA: Ceres:658		-0.8
probable H+-transporting ATPase H+-transporting ATPase (EC 3.6.1.35) 57K chain - Arabidopsis thaliana, PIR2:A31886; supported by cDNA: gi	252998_at	-0.8
small auxin up RNA (SAUR-AC1) ;supported by full-length cDNA: Ceres:14973.	252970_at	-0.8
glucose-1-phosphate adenylyltransferase (APL3); supported by cDNA; gi_16648984_gb_AY059862.1_	252888_at	-0.8
histone H2B -like protein histone H2B1, upland cotton, PIR:T09722;supported by full-length cDNA: Ceres:10517.	252560_at	-0.8
actin depolymerizing factor 1 (ADF1) ;supported by full-length cDNA: Ceres:1907.	252564_at	-0.8
starch phosphorylase H (cytosolic form) - like protein starch phosphorylase H, cytosolic isoform, Vicia faba, PIR:T12091; supported by cDNA: gi_	252468_at	-0.8
protein translocation complex sec61 gamma chain-like protein protein translocation complex sec61 gamma chain, endoplasmic reticulum - Canis	252324_at	-0.8
30S ribosomal protein S9 -like similar to 30S ribosomal proteins	252287_at	-0.8
R2R3-MYB transcription factor ;supported by cDNA: gi_15983427_gb_AF424588.1_AF424588	252193_at	-0.8
hypothetical protein	252073_at	-0.8
fructose-bisphosphatase precursor ; supported by cDNA: gi_14532619_gb_AY039934.1_	251885_at	-0.8
putative protein	251869_at	-0.8
putative protein In2-1 protein, Zea mays, P49248	251820_at	-0.8
methionyl-tRNA synthetase (AtcpMetRS) ; supported by cDNA: gi_13605909_gb_AF367354.1_AF367354	251807_at	-0.8
bZIP protein ;supported by cDNA: gi_600854_gb_U17887.1_ATU17887	251413_at	-0.8
putative protein prib5, Ribes nigrum, EMBL:RNI7578;supported by full-length cDNA: Ceres:15792.	251370_at	-0.8
putative protein polygalacturonase - Lycopersicon esculentum, EMBL:AF118567; supported by cDNA: gi_13358184_gb_AF324992.2_AF324992	251261_at	-0.8
ABC transporter-like protein glutathione-conjugate transporter AtMRP4 - Arabidopsis thaliana, EMBL:AJ002584	251227_at	-0.8
lectin - like protein lectin precursor LECSJAbmII, Sophora japonica, EMBL:SJU63012;supported by full-length cDNA: Ceres:41306.	251140_at	-0.8
putative protein contains transmembrane region and ATP binding region, Mus musculus, EMBL:AB030189.1	250978_at	-0.8
putative protein various predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_15982839_gb_AY057527.1_	250939_at	-0.8

putative protein ; supported by cDNA: gi_14596134_gb_AY042855.1_	250898_at	-0.8
coatomer delta subunit (delta-coat protein) (delta-COP); supported by cDNA: gi 15450768 gb AY054464.1	250816 at	-0.8
cellulose synthase catalytic subunit (gb/AAC39336.1); supported by cDNA: gi_2827142_gb_AF027174.1_AF027174	250827_at	-0.8
cellulose synthase catalytic subunit	250505_at	-0.8
argininosuccinate lyase (AtArgH) ; supported by cDNA: gi_15028082_gb_AY045898.1_	250403_at	-0.8
putative protein synaptobrevin-like protein Sybl1, Mus musculus, EMBL:MMU133536	250412_at	-0.8
2-oxoglutarate/malate translocator precursor -like protein 2-oxoglutarate/malate translocator precursor, spinach, SWISSPROT:SOT1_SPIOL; sur	250278_at	-0.8
putative protein similar to unknown protein (gb AAF01580.1)	249835_s_at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:25723.	249811_at	-0.8
glucose-6-phosphate dehydrogenase ;supported by full-length cDNA: Ceres:22483.	249694_at	-0.8
14-3-3 protein GF14psi (grf3/RCI1) identical to 14-3-3 protein GF14 psi GI:1168200, SP:P42644; supported by cDNA: gi_166716_gb_L09110.1_	249514_at	-0.8
ribosomal protein L5 - like ribosomal protein L5, rice	249466_at	-0.8
putative protein ; supported by cDNA: gi_15010731_gb_AY045667.1_	249442_at	-0.8
dihydroxyacetone 3-phosphate reductase (dhaprd)	249366_at	-0.8
putative protein similar to unknown protein (emb CAB89401.1)	249071_at	-0.8
NBD-like protein (gb AAD20643.1) ;supported by full-length cDNA: Ceres:33802.	249063_at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:21404.	249007_at	-0.8
putative protein strong similarity to unknown protein (pir  T05325); supported by cDNA: gi_13605502_gb_AF361577.1_AF361577	249011_at	-0.8
putative protein similar to unknown protein (pir  T04881)	249021_at	-0.8
putative protein contains similarity to unknown; supported by full-length cDNA: Ceres: 4029.	249025_at	-0.8
putative protein strong similarity to unknown protein (pir  T04426)	248945_at	-0.8
putative protein similar to unknown protein (pir  G71444);supported by full-length cDNA: Ceres:19104.	248797_at	-0.8
ATP citrate lyase ; supported by cDNA: gi_14334787_gb_AY035067.1_	248608_at	-0.8
putative protein similar to unknown protein (pir  S75732);supported by full-length cDNA: Ceres:35710.	248537_at	-0.8
protein phosphatase 2C-like ;supported by cDNA: gi_15027924_gb_AY045819.1_	248249_at	-0.8
thylakoid lumenal 17.4 kD protein, chloroplast precursor (P17.4) (sp P81760); supported by cDNA: gi_13899114_gb_AF370552.1_AF370552	248224_at	-0.8
putative protein similar to unknown protein (pir  T04261);supported by full-length cDNA: Ceres:6181.	247930_at	-0.8
unknown protein	247907_at	-0.8
putative protein similar to unknown protein (pir  D64592);supported by full-length cDNA: Ceres:113904.	247881_at	-0.8
SPP30 - like protein SPP30, Solanum chacoense, EMBL:AF136010;supported by full-length cDNA: Ceres:269675.	247842_at	-0.8
putative protein predicted proteins, Arabidopsis thaliana	247770_at	-0.8
putative protein protein tyrosine phosphatase-like protein, PTPLB, Mus musculus, EMBL:AF169286	247689_at	-0.8
putative protein various predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 251668.	247607_at	-0.8
putative protein various predicted proteins from different species; supported by cDNA: gi_15912286_gb_AY056421.1_	247555_at	-0.8
glutamate-tRNA ligase ; supported by cDNA: gi_11078545_gb_AF241841.1_AF241841	247319_at	-0.8
ZW10-like protein ;supported by cDNA: gi_14334941_gb_AY035144.1_	247261_at	-0.8
receptor protein kinase-like protein	247153_at	-0.8
natural resistance-associated macrophage protein ; supported by cDNA: gi_6468013_gb_AF202540.1_AF202540	247001_at	-0.8
putative multispanning membrane protein GC donor splice site at exon 6; KIAA0255 - Homo sapiens, EMBL:D87444; supported by cDNA: gi_134		-0.8
ferrochelatase-I	246870_at	-0.8
glutathione synthetase gsh2 non-consensus AT donor splice site at exon 6, AC acceptor splice site at exon 7; supported by cDNA: gi_758451_gt		-0.8
acetyl-CoA carboxylase ;supported by full-length cDNA: Ceres:20286.	246613_at	-0.8
putative protein geranylgeranylated protein NTGP5 - Nicotiana tabacum, EMBL:U64926; supported by full-length cDNA: Ceres: 250561.	246539_at	-0.8
cyclic nucleotide-gated cation channel ; supported by cDNA: gi_3894398_gb_AF067798.1_AF067798	246510_at	-0.8

acetyltransferase-like protein Glucosamine-6-phosphate acetyltransferase EMeg32 protein - Mus musculus, EMBL:AJ001006	246518 at	-0.8
quinone oxidoreductase - like protein probable quinone oxidoreductase (EC 1.6.5.5) P1, Arabidopsis thaliana, PIR:S57612;supported by full-leng		-0.8
glucose 6 phosphate/phosphate translocator-like protein glucose 6 phosphate/phosphate translocator - Arabidopsis thaliana, EMBL:AF233658; s		-0.8
integral membrane protein, putative similar to integral membrane protein GI:3288599 from [Rattus norvegicus]; supported by full-length cDNA: Ce		-0.8
chlorophyll synthetase ; supported by cDNA: gi_14596066_gb_AY042821.1_	246308_at	-0.8
lipophosphoglycan biosynthetic protein - like lipophosphoglycan biosynthetic protein (LPG2), Leishmania donovani, TREMBL:LD26175	246143 at	-0.8
dynein light chain - like protein dynein light chain LC6, Anthocidaris crassispina, EMBL:AB004830	246144_at	-0.8
putative protein predicted protein, Oryza sativa; supported by cDNA: gi_15146277_gb_AY049280.1_	246126 at	-0.8
putative protein karyopherin beta 3 - Homo sapiens, EMBL:U72761; supported by cDNA: gi_14334741 gb_AY035044.1_	245941_at	-0.8
putative transcriptional co-activator (KIWI); supported by cDNA: gi_2997683_gb_AF053302.1_AF053302	245896 at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:21415.	245626_at	-0.8
transport protein	245625_at	-0.8
disease resistance RPP5 like protein	245456 at	-0.8
Expressed protein ; supported by full-length cDNA: Ceres: 12256.	245367_at	-0.8
selenium-binding protein like ; supported by cDNA: gi_14532843_gb_AY040046.1_	245285 s at	-0.8
ATP-sulfurylase ; supported by cDNA: gi_459143_gb_U06275.1_ATU06275	245254 at	-0.8
putative protein similarity to sec10, Drosophila melanogaster, AE003746~Contains Putative AMP-binding domain signature AA505-516	245211 at	-0.8
putative Ca2+-ATPase ; supported by cDNA: gi_11493642_gb_AF200739.1_AF200739	245117_at	-0.8
GDP-mannose pyrophosphorylase updated per Conklin PL et al, PNAS 1999, 96(7):4198-203; supported by full-length cDNA: Ceres:37775.	245060 at	-0.8
heme oxygenase 2 (HO2)	245027 at	-0.8
PSI I protein	245017_at	-0.8
PSII 47KDa protein	244972_at	-0.8
ribosomal protein S8	244981_at	-0.8
NADH dehydrogenase ND4L	244933 at	-0.8
unknown protein ; supported by cDNA: gi_14334723_gb_AY035035.1_	264485 at	-0.8
putative WRKY-type DNA binding protein; supported by cDNA: gi_15430276_gb_AY046275.1_	263783_at	-0.8
hypothetical protein	262062 s at	-0.8
putative isocitrate dehydrogenase (NAD+) similar to isocitrate dehydrogenase (NAD+) GB:CAA65502 [Nicotiana tabacum]; supported by full-lengtl	258655_at	-0.8
GTP-binding protein rab11 - like GTP-binding protein rab11, Arabidopsis thaliana, PIR:T12965; supported by cDNA: gi_13877728_gb_AF370127	247722_at	-0.8
Expressed protein ; supported by full-length cDNA: Ceres: 7632.	245338_at	-0.8
unknown protein	267516_at	-0.7
putative UDP-N-acetylglucosamine pyrophosphorylase ;supported by full-length cDNA: Ceres:5509.	267432_at	-0.7
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:33701.	267361_at	-0.7
similar to cold acclimation protein WCOR413 [Triticum aestivum]	267288_at	-0.7
Ran binding protein (AtRanBP1b) identical to GB:X97378	267306_at	-0.7
glutathione S-transferase identical to GB:Y12295; supported by cDNA: gi_13926309_gb_AF372905.1_AF372905	267153_at	-0.7
putative MYB family transcription factor ; supported by cDNA: gi_5823324_gb_AF175996.1_AF175996	267157_at	-0.7
putative cytochrome P450 ;supported by full-length cDNA: Ceres:158108.	266996_at	-0.7
hypothetical protein predicted by genscan	267019_at	-0.7
putative trans-prenyltransferase	266958_at	-0.7
putative ATP-dependent RNA helicase ; supported by cDNA: gi_14532475_gb_AY039862.1_	266896_at	-0.7
unknown protein	266858_at	-0.7
putative AP2 domain transcription factor pFAM domain (PF00847)supported by full-length cDNA: Ceres:31044.	266820_at	-0.7
hypothetical protein predicted by grail	266439_s_at	-0.7

hypothetical protein predicted by genscan and genefinder	266320 at	-0.7
putative rac GTPase activating protein	266324_at	-0.7
putative chorismate mutase/prephenate dehydratase ;supported by full-length cDNA: Ceres:37739.	266257_at	-0.7
putative carbonyl reductase	266015 at	-0.7
unknown protein ;supported by full-length cDNA: Ceres:98881.	265959_at	-0.7
putative peptidyl-prolyl cis-trans isomerase similar to ESS1 (S.cerevisiae) and dodo (D.melanogaster.); supported by full-length cDNA: Ceres: 126	265818 at	-0.7
unknown protein ;supported by full-length cDNA: Ceres:1697.	265716_at	-0.7
unknown protein ;supported by full-length cDNA: Ceres:15582.	265669_at	-0.7
putative purine-rich single-stranded DNA-binding protein ; supported by cDNA: gi_15450692_gb_AY052714.1_	265677_at	-0.7
F-box protein family, AtFBL6 contains similarity to grr1 GI:2407790 from [Glycine max]	265633_at	-0.7
unknown protein predicted by genefinder	265283_at	-0.7
unknown protein ; supported by full-length cDNA: Ceres: 29227.	265116_at	-0.7
myrosinase binding protein, putative similar to myrosinase binding protein GI:1711295 from [Brassica napus]	265053_at	-0.7
unknown protein similar to putative uridylyl transferase GI:4406764 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:40049.	264956_at	-0.7
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_13926194_gb_AF370571.1_AF370571	264959_at	-0.7
unknown protein Location of EST gb/Z26015 and gb/Z26014~CO2H end of protein is similar to procaryote ribosomal protein L19; supported by c[		-0.7
putative superoxide-generating NADPH oxidase flavocytochrome highly similar to GB:CAA70769, FRO1 and GB:CAA70770, FRO2 from [Arabido		-0.7
flowering signals mediating protein FT identical to flowering signals mediating protein FT GI:4903012 from [Arabidopsis thaliana]; supported by cE	264638_at	-0.7
unknown protein Location of EST gb T41885 and gb AA395021	264521_at	-0.7
hypothetical protein predicted by genscan	264114_at	-0.7
putative peroxidase ;supported by full-length cDNA: Ceres:113695.	264001_at	-0.7
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:2576.	263929_at	-0.7
putative ATP synthase ;supported by full-length cDNA: Ceres:31766.	263874_at	-0.7
unknown protein ;supported by cDNA: gi_15027948_gb_AY045831.1_	263844_at	-0.7
putative tyrosine aminotransferase ; supported by cDNA: gi_15293106_gb_AY050987.1_	263714_at	-0.7
putative aspartate kinase-homoserine dehydrogenase almost identical to gb X71364 gene for aspartate kinase homoserine dehydrogenase from	263696_at	-0.7
NAM (no apical meristem)-like protein similar to petunia NAM (X92205) and A. thaliana sequences ATAF1 (X74755) and ATAF2 (X74756); proba	263584_at	-0.7
unknown protein ;supported by cDNA: gi_13605844_gb_AF367321.1_AF367321	263499_at	-0.7
putative beta-hydroxyacyl-ACP dehydratase ; supported by full-length cDNA: Ceres: 30185.	263432_at	-0.7
	263405_s_at	-0.7
putative histone H2B ;supported by full-length cDNA: Ceres:14965.	263412_at	-0.7
unknown protein ;supported by full-length cDNA: Ceres:120231.	263303_at	-0.7
putative inositol 1,4,5-trisphosphate 5-phosphatase Highly similar to arabidopsis inositol 1,4,5-trisphosphate 5-phosphatase, gi 4688596	263202_at	-0.7
acetyl-CoA carboxylase, putative similar to acetyl-CoA carboxylase GI:1100253 from [Arabidopsis thaliana]	263193_at	-0.7
RSH3 (RelA/SpoT homolog) identical to RSH3 (RelA/SpoT homolog) GI:7141308 from [Arabidopsis thaliana]; supported by cDNA: gi_7141307_g		-0.7
hypothetical protein similar to hypothetical ABC transporter ATP-binding protein GI:9955395 from [Microcystis aeruginosa]	263000_at	-0.7
unknown protein strong similarity to gi 3367522 F8K4.9 from Arabidopsis thaliana BAC gb AC004392. EST gb W43487 comes from this gene	262813_at	-0.7
putative protein kinase	262660_at	-0.7
unknown protein Contains a PF 00175 Oxidoreductase FAD/NADH-binding domain. ESTs gb H76345 and gb AA651465 come from this gene; su		-0.7
SOUL-like protein Similar to SOUL Protein [Mus musculus] (gi 4886906) and [Homo sapiens] (gi 4886910). Location of ests PAP043 5 (gb Z270	262536_at	-0.7
chloroplast FtsH protease almost identical to chloroplast FtsH protease GI:1483215, SP:Q39102 from [Arabidopsis thaliana]	262473_at	-0.7
acyl CoA synthetase, putative similar to acyl CoA synthetase GI:1617267 from [Brassica napus]	262414_at	-0.7
hypothetical protein similar to hypothetical protein GB:AAF24576 GI:6692111 from [Arabidopsis thaliana]	262329_at	-0.7
phosphoglucomutase, putative similar to phosphoglucomutase GI:534981 from [Spinacia oleracea]	262309_at	-0.7

unknown protein ; supported by cDNA: gi_16648825_gb_AY058190.1_	262232 at	-0.7
hypothetical protein similar to hypothetical protein GI:9294146 from [Arabidopsis thaliana]	262236_at	-0.7
elongation factor, putative similar to ELONGATION FACTOR 2 GB:014460 from [Schizosaccharomyces pombe]; supported by cDNA: gi_14334(	262064_at	-0.7
unknown protein ;supported by full-length cDNA: Ceres:126074.	261852_at	-0.7
endo-xyloglucan transferase, putative similar to endo-xyloglucan transferase GI:2244732 from [Gossypium hirsutum];supported by full-length cDI	261825_at	-0.7
UDP glucose: flavonoid 3-o-glucosyltransferase, putative similar to UDP glucose: flavonoid 3-o-glucosyltransferase GB: AAB81683 GI: 2564114 fro	261804_at	-0.7
clathrin coat assembly protein AP17, putative similar to clathrin coat assembly protein AP17 GB:CAA65533 GI:2959358 from [Zea mays]	261733_at	-0.7
Mg-chelatase, putative similar to Mg-chelatase GB:AF014399 GI:2318116 from [Pisum sativum]; supported by cDNA: gi_16649072 gb_AY0599(	261695_at	-0.7
DNA binding protein ACBF, putative similar to DNA binding protein ACBF GB:U90212 GI:1899187 from [Nicotiana tabacum]	261603_at	-0.7
poly(A)-binding protein, putative similar to poly(A)-binding protein GB:AAF66825 GI:7673359 from [Nicotiana tabacum]; supported by cDNA: gi_1	261614_at	-0.7
tumor suppressor, putative similar to tumor suppressor GI:575354 from [Oryza sativa]; supported by cDNA: gi_14190448_gb_AF378902.1_AF37	261490_at	-0.7
unknown protein	261469_at	-0.7
hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 17148.	261440_at	-0.7
hypothetical protein contains similarity to ABC transporter GI:10175329 from [Bacillus halodurans]; supported by cDNA: gi_14532489_gb_AY039	261353_at	-0.7
vacuolar ATP synthase subunit C, putative similar to GB:AAF20146 from [Arabidopsis thaliana] (Genes Dev. (1999) In press); supported by cDN	261210_at	-0.7
unknown protein ; supported by full-length cDNA: Ceres: 12477.	261148_at	-0.7
chloroplast nucleoid DNA binding protein, putative similar to chloroplast nucleoid DNA binding protein GB:BAA22813 GI:2541876 from [Nicotiana	261055_at	-0.7
alanine aminotransferase, putative similar to alanine aminotransferase GB:AAC62456 GI:3694807 from [Zea mays]	260847_s_at	-0.7
14-3-3 protein GF14omega (grf2) identical to GF14omega isoform GI:487791 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:28	260775_at	-0.7
protein phosphatase 2C, putative similar to protein phosphatase 2C GI:3242077 from (Arabidopsis thaliana)	260712_at	-0.7
hypothetical protein predicted by genemark.hmm	260645_at	-0.7
putative monodehydroascorbate reductase similar to monodehydroascorbate reductase GB:AAD28178 [Brassica juncea]; supported by cDNA: gi		-0.7
unknown protein ; supported by full-length cDNA: Ceres: 10531.	260200_at	-0.7
putative UDP-N-acetylglucosamineN-acetylmuramyl-(pentapeptide)-pyrophosphoryl-undecaprenol N-acetylglucosamine transferase similar to pu	260047_at	-0.7
unknown protein ;supported by full-length cDNA: Ceres:111031.	260003_at	-0.7
unknown protein ;supported by full-length cDNA: Ceres:36337.	260009_at	-0.7
	259790_s_at	-0.7
hypothetical protein predicted by genefinder	259743_at	-0.7
spore coat protein-like protein similar to SPORE COAT PROTEIN A GB:P07788 from [Bacillus subtilis] and BILIRUBIN OXIDASE GB:Q12737 [M		-0.7
putative AUX1-like permease similar to AUX1 (regulator of root gravitropism, putative permease) GB:CAA67308 [Arabidopsis thaliana]; supported		-0.7
myosin-like protein contains Pfam profile: PF00658 Poly-adenylate binding protein, unique domain.; supported by cDNA: gi_15081708_gb_AY04	_	-0.7
unknown protein	259577_at	-0.7
hypothetical protein similar to ripening-induced protein [Fragaria vesca] GI:2465015;supported by full-length cDNA: Ceres:16091.	259548_at	-0.7
inorganic pyrophosphatase, putative similar to inorganic pyrophosphatase GI:790478 from [Nicotiana tabacum]; supported by cDNA: gi_166633_	_	-0.7
hypothetical protein predicted by genemark.hmm	259450_at	-0.7
putative cationic amino acid transporter similar to HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 GB:Q09143 [Mus musculus]	259337_at	-0.7
hypothetical protein predicted by genscan	259295_at	-0.7
putative cystathionine gamma-synthase similar to cystathionine gamma-synthase GB:AAB41235 from [Arabidopsis thaliana]; supported by cDNA:		-0.7
unknown protein est hit, predicted by genscan	259190_at	-0.7
putative 60S ribosomal protein L22 similar to 60S ribosomal protein L22 GB:AAF02883; supported by full-length cDNA: Ceres: 8244.	259112_at	-0.7
unknown protein similar to unknown protein GB:AAC62613 [Arabidopsis thaliana]; supported by cDNA: gi_14532567_gb_AY039908.1_	259018_at	-0.7
hevein-like protein precursor (PR-4) identical to hevein-like protein precursor GB:P43082 [Arabidopsis thaliana], similar to wound-induced protein		-0.7
putative T-complex protein 1, theta subunit (TCP-1-Theta) similar to T-complex protein 1, theta subunit (TCP-1-Theta) GB:P42932 [Mus musculu		-0.7
unknown protein	258761_at	-0.7

putative oxidoreductase similar to phytoene desaturase GB:P28553 from [Glycine max]; supported by full-length cDNA: Ceres: 17350.	258708 at	-0.7
putative calmodulin similar to calmodulin GB:P04352 [Chlamydomonas reinhardtii]; contains Pfam profile: PF00036 EF hand (4 copies); supported	_	-0.7
beta-glucosidase, putative similar to beta-glucosidase GB:AAF23823 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:37856.	258512 at	-0.7
hypothetical protein ;supported by full-length cDNA: Ceres:2064.	258150 at	-0.7
putative tyrosine phosphatase similar to GB:AAF08382 from [Drosophila melanogaster]	258007_at	-0.7
unknown protein	257903_at	-0.7
hypothetical protein predicted by genemark.hmm	257723 at	-0.7
unknown protein contains Pfam profile: PF00168 C2 domain; supported by cDNA: gi_15983786_gb_AY056799.1_	257734_at	-0.7
60S ribosomal protein, putative similar to 60S RIBOSOMAL PROTEIN L13A GB:P35427 from [Rattus norvegicus]; supported by full-length cDNA	257599_at	-0.7
phosphate transporter, putative contains Pfam profile: PF01384 phosphate transporter family	257311 at	-0.7
unknown protein ; supported by full-length cDNA: Ceres: 105122.	257300_at	-0.7
hypothetical protein ;supported by full-length cDNA: Ceres:9965.	257093_at	-0.7
unknown protein contains Pfam profile: PF00153 mitochondrial carrier proteins; supported by full-length cDNA: Ceres: 39353.	256819 at	-0.7
dirigent protein, putative similar to dirigent protein GB:AAF25365 from [Thuja plicata]	256781 at	-0.7
unknown protein ;supported by full-length cDNA: Ceres:108144.	256786_at	-0.7
unknown protein	256673 at	-0.7
histone H2A, putative similar to histone H2A GB:AAF64418 GI:7595337 from [Arabidopsis thaliana] (Proc. Natl. Acad. Sci. U.S.A. 97 (2), 948-953	256666_at	-0.7
unknown protein	256633_at	-0.7
unknown protein	256489 at	-0.7
myb-related protein similar to GI:7981380 from [Lycopersicon esculentum]	256503_at	-0.7
adenylosuccinate lyase - like protein adenylosuccinate lyase - Haemophilus influenzae	256461_s_at	-0.7
expansin (At-EXP1) identical to expansin (At-EXP1) [Arabidopsis thaliana] GI:1041702; supported by full-length cDNA: Ceres:255048.	256299_at	-0.7
MAP kinase kinase 4 (ATMKK4) identical to MAP kinase kinase 4 [Arabidopsis thaliana]; supported by cDNA: gi_13265419_gb_AF324667.2_AF3	256183_at	-0.7
pyruvate dehydrogenase E1 beta subunit, putative similar to pyruvate dehydrogenase E1 beta subunit GI:2982328 from [Picea mariana];support	256160_at	-0.7
unknown protein	256049_at	-0.7
hypothetical protein ;supported by full-length cDNA: Ceres:7642.	255981_at	-0.7
UDP-glucose glucosyltransferase identical to UDP-glucose glucosyltransferase GI:3928543 from [Arabidopsis thaliana]; supported by cDNA: gi_1	255942_at	-0.7
ribosomal protein L20, putative similar to ribosomal protein L20 GI:3603025 from [Guillardia theta];supported by full-length cDNA: Ceres:255.	255767_at	-0.7
3-phosphoserine phosphatase identical to 3-phosphoserine phosphatase GI:3759177 from [Arabidopsis thaliana]; supported by full-length cDNA: (	255778_at	-0.7
hypothetical protein	255631_at	-0.7
putative glycosyltransferase similar to A. thaliana protein T20K9.11, GenBank accession number 3445207; supported by cDNA: gi_16209668_gt	255483_at	-0.7
putative protein similar to T5J8.17	255451_at	-0.7
putative WD-repeat protein similar to L. erythrorhizon LEC14B, GenBank accession number Q40153	255468_at	-0.7
putative malonyl-CoA decarboxylase	255327_at	-0.7
rab7 -like protein rab7 protein -Vigna aconitifolia,PIR2:S39567; supported by cDNA: gi_15718417_dbj_AB071851.1_AB071851	255052_at	-0.7
RNA-binding protein ;supported by full-length cDNA: Ceres:2343.	254990_at	-0.7
putative protein hypothetical protein - Brassica napus,PIR2:S42651	254928_at	-0.7
phospholipid hydroperoxide glutathione peroxidase ;supported by full-length cDNA: Ceres:8846.	254890_at	-0.7
hypothetical protein	254755_at	-0.7
putative protein various predicted 3-isopropylmalate dehydratases/aconitate hydratases; supported by cDNA: gi_15027970_gb_AY045842.1_	254742_at	-0.7
translation initiation factor eIF4E ;supported by full-length cDNA: Ceres:25447.	254654_at	-0.7
ras-like GTP-binding protein strong homology to GTP-binding protein ric2, Oryza sativa, S38741	254641_at	-0.7
heat shock transcription factor - like protein heat shock transcription factor, Zea mays, PIR2:S61448	254592_at	-0.7
hyuC-like protein 5-substituted hydantoins to the corresponding L-amino acids, Pseudomonas sp.,PIR2:D42594	254496_at	-0.7

putative protein sigma70 operon, Staphylococcus aureus, PATCHX:D1020251	254460_at	-0.7
peroxidase prxr1 ;supported by full-length cDNA: Ceres:20758.	254386_at	-0.7
putative protein UDP-galactose transporter related isozyme 3, Homo sapiens, PIR2:JC5026	254291_at	-0.7
serine/threonine kinase - like protein serine/threonine kinase, Brassica oleracea; supported by cDNA: gi_14423417_gb_AF386946.1_AF386946	254255_at	-0.7
V-ATPase subunit G (vag2 gene)	254216_at	-0.7
calcium-dependent protein kinase (CDPK6) ;supported by full-length cDNA: Ceres:37278.	254224_at	-0.7
brefeldin A-sensitive Golgi protein - like brefeldin A-sensitive Golgi protein LDLC, Homo sapiens, PIR2:A53542; supported by cDNA: gi_1360580	254087_at	-0.7
putative protein cylicin II - human, PID:g758587; supported by cDNA: gi_14423517_gb_AF386996.1_AF386996	254058_at	-0.7
putative protein similarity to multidrug resistance protein, Mus musculus, PIR1:DVMS1~Contains ABC transporters family signature, (LSGGQRQ	254068_at	-0.7
putative protein various predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 122917.	254048_at	-0.7
putative protein LEDI-3 protein, Lithospermum erythrorhizon	253909_at	-0.7
putative protein hypothetical protein, Synechocystis sp., PIR2:S77328; supported by cDNA: gi_14335171_gb_AY037265.1_	253893_at	-0.7
putative protein ;supported by full-length cDNA: Ceres:113484.	253891_at	-0.7
putative protein unknown protein chromosome II BAC F6F22 - Arabidopsis thaliana, PID:g3687251; supported by full-length cDNA: Ceres: 5426.	253728_at	-0.7
putative protein D-ribulokinase - Klebsiella pneumoniae,Pir2:S78598	253612_at	-0.7
putative protein component of aniline dioxygenase (GMP synthase like protein) - Acinetobacter sp., PID:d1013698; supported by full-length cDNA:	253639_at	-0.7
putative protein component of aniline dioxygenase (GMP synthase like protein - Acinetobacter sp., PID:d1013698; supported by full-length cDNA:	253606_at	-0.7
putative protein RING-H2 finger protein RHX1a - Arabidopsis thaliana,PID:g3790591; supported by cDNA: gi_15809839_gb_AY054187.1_	253580_at	-0.7
SERINE CARBOXYPEPTIDASE II - like protein serine-type carboxypeptidase, Hordeum vulgare, PIR2:S44191; supported by cDNA: gi_1529304	253600_at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 37878.	253548_at	-0.7
putative protein ;supported by full-length cDNA: Ceres:2508.	253440_at	-0.7
pectinesterase - like protein pectinesterase, Prunus persica, X95991; supported by cDNA: gi_14190428_gb_AF378892.1_AF378892	253372_at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 38416.	253305_at	-0.7
putative protein auxin-regulated gene, Vigna radiata	253253_at	-0.7
NAD+ dependent isocitrate dehydrogenase subunit 1 ;supported by full-length cDNA: Ceres:12228.	253196_at	-0.7
clathrin assembly protein AP19 homolog ;supported by full-length cDNA: Ceres:22906.	253199_at	-0.7
ferulate-5-hydroxylase (FAH1) ; supported by cDNA: gi_1488254_gb_U38416.1_ATU38416	253088_at	-0.7
formamidase - like protein formamidase, Methylophilus methylotrophus, PIR2:S74213; supported by full-length cDNA: Ceres:23732.	253042_at	-0.7
putative protein beta-ketoadipate enol-lactone hydrolase, Acinetobacter sp., L05770; supported by cDNA: gi_15810302_gb_AY056190.1_	253053_at	-0.7
hypothetical protein ;supported by full-length cDNA: Ceres:21.	253005_at	-0.7
dnaJ-like protein CAJ1 protein, Saccharomyces cerevisiae, PIR2:S48085	252935_at	-0.7
myo-inositol-1-phosphate synthase ;supported by full-length cDNA: Ceres:1978.	252863_at	-0.7
putative protein ;supported by full-length cDNA: Ceres:15747.	252821_at	-0.7
DnaJ - like protein DnaJ-like protein, Pisum sativum, Z71640; supported by cDNA: gi_15450580_gb_AY052658.1_	252828_at	-0.7
nucleic acid binding protein-like nucleic acid binding protein - Oryza sativa, PIR:T02745	252764_at	-0.7
glutathione transferase-like protein glutathione transferase, papaya, PIR:T09781;supported by full-length cDNA: Ceres:19003.	252712_at	-0.7
dTDP-glucose 4-6-dehydratases-like protein dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana, PIR:S58282; supported by full-lengt	252527_at	-0.7
putative protein ;supported by full-length cDNA: Ceres:7104.	252033_at	-0.7
carbonic anhydrase (CAH1) ;supported by cDNA: gi_15450772_gb_AY054466.1_	252011_at	-0.7
putative protein crp1 protein, Zea mays, PIR:T01685; supported by cDNA: gi_15982930_gb_AY057573.1_	251936_at	-0.7
putative protein leucine-rich receptor-like protein kinase - Malus domestica, EMBL:AF053127	251714_at	-0.7
serine/threonine-specific protein kinase NAK ;supported by full-length cDNA: Ceres:27477.	250990_at	-0.7
putative protein myosin heavy chain, Girardia tigrina, EMBL:U91585; supported by full-length cDNA: Ceres: 9220.	250919_at	-0.7
syntaxin-like protein syntaxin-related protein Nt-syr1 - Nicotiana tabacum, EMBL:AF112863;supported by full-length cDNA: Ceres:14098.	250544_at	-0.7

NADH dehydrogenase ;supported by full-length cDNA: Ceres:38092.	250534 at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 17241.	250536_at	-0.7
26S proteasome p55 protein-like ; supported by cDNA: gi_14334433_gb_AY034908.1_	250456_at	-0.7
aspartate kinase ;supported by full-length cDNA: Ceres:94688.	250291_at	-0.7
delta subunit of mitochondrial F1-ATPase; supported by cDNA: gi_14190494_gb_AF380647.1_AF380647	250236_at	-0.7
S-adenosylmethionine:2-demethylmenaquinone methyltransferase-like protein; supported by full-length cDNA: Ceres: 13819.	250129_at	-0.7
BCS1 - like protein h-bcs1, Homo sapiens, EMBL:AF026849; supported by cDNA: gi_15810570_gb_AY056324.1_	250062 at	-0.7
putative protein similar to unknown protein (dbj BAA92923.1)	249899_at	-0.7
elF4Eiso protein (emblCAA71579.1) ;supported by full-length cDNA: Ceres:23770.	249712_at	-0.7
acetyl-CoA synthetase ; supported by cDNA: gi_15028046_gb_AY045880.1_	249638 at	-0.7
glutathione transferase AtGST 10 (emb CAA10457.1); supported by cDNA: gi_15451157_gb_AY054659.1_	249291_at	-0.7
putative protein contains similarity to surface protein; supported by cDNA: gi_16648846_gb_AY058201.1_	249037_at	-0.7
subtilisin-like serine protease contains similarity to meiotic serine proteinase TMP GI:6468325 from [Lycopersicon esculentum]	249059 at	-0.7
unknown protein ;supported by full-length cDNA: Ceres:114691.	248881 at	-0.7
putative protein contains similarity to unknown protein (gb AAF63638.1); supported by cDNA: gi_15983463_gb_AF424606.1_AF424606	248907_at	-0.7
casein kinase II beta chain ; supported by cDNA: gi_468263_gb_L22563.1_ATHCKIB	248826 at	-0.7
ethylene responsive element binding factor 5 (ATERF5) (sp[O80341); supported by cDNA: gi_14326511_gb_AF385709.1_AF385709	248799_at	-0.7
putative protein strong similarity to unknown protein (emb/CAB87804.1)	248724_at	-0.7
putative protein strong similarity to unknown protein (gb/AAD50008.1);supported by full-length cDNA: Ceres:7861.	248507 at	-0.7
	248521 s at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 36971.	248460 at	-0.7
putative protein strong similarity to unknown protein (gb AAB68038.1);supported by full-length cDNA: Ceres:17208.	248433_at	-0.7
cytochrome P450	248353_at	-0.7
putative protein strong similarity to unknown protein (pir  T02324); supported by cDNA: gi_15028278_gb_AY046054.1_	248335_at	-0.7
putative protein contains similarity to 40S ribosomal protein S10;supported by full-length cDNA: Ceres:91769.	248331 at	-0.7
Avr9 elicitor response protein-like; supported by cDNA: gi_14423409_gb_AF386942.1_AF386942	248262 at	-0.7
2-oxoglutarate dehydrogenase E2 subunit ; supported by cDNA: gi_14596218_gb_AY042897.1_	248088_at	-0.7
putative protein similar to unknown protein (gb AAF04428.1);supported by full-length cDNA: Ceres:27668.	248028 at	-0.7
putative protein similar to unknown protein (pir  T23656); supported by cDNA: gi_16648986_gb_AY059863.1_	248042 at	-0.7
S-adenosylmethionine:2-demethylmenaquinone methyltransferase-like	248007_at	-0.7
60S ribosomal protein L31 ;supported by full-length cDNA: Ceres:14992.	247978_at	-0.7
nucleosome assembly protein	247955_at	-0.7
putative protein	247754_at	-0.7
putative protein heat shock protein 40 DnaJ, Methanosarcina thermophila, EMBL:AJ010152	247733_at	-0.7
putative ripening-related protein - like putative ripening-related protein Vitis vinifera EMBL:VVI237988;supported by full-length cDNA: Ceres:9907	247706_at	-0.7
actin depolymerizing factor 3 - like protein actin depolymerizing factor 3, Arabidopsis thaliana, EMBL:AF102821; supported by full-length cDNA: C	247658_at	-0.7
40S ribsomal protein S19 - like 40S ribsomal protein S19, Oryza sativa, SWISSPROT:RS19_ORYSA	247566_at	-0.7
DNA binding protein - like DNA binding protein EREBP-4, Nicotiana tabacum, PIR:T02434;supported by full-length cDNA: Ceres:92102.	247543_at	-0.7
putative protein predicted proteins, D.melanogaster and S.pombe; supported by cDNA: gi 15294203 gb AF410293.1 AF410293	247467_at	-0.7
DC1.2 homologue - like protein DC1.2 homologue, Nicotiana tabacum, EMBL:AB009888	247478_at	-0.7
H-protein promoter binding factor-like protein	247452_at	-0.7
1-deoxy-D-xylulose 5-phosphate reductoisomerase (DXR) ;supported by full-length cDNA: Ceres:117626.	247401_at	-0.7
glutamate-1-semialdehyde 2,1-aminomutase 1 precursor (GSA 1) (glutamate-1-semialdehyde aminotransferase 1) (GSA-AT 1) (sp P42799)	247392_at	-0.7
Isp4-like protein ; supported by full-length cDNA: Ceres: 3109.	247284_at	-0.7

cellulose synthase catalytic subunit	247251 at	-0.7
putative protein similar to unknown protein (emb CAB61744.1); supported by full-length cDNA: Ceres: 31648.	247214_at	-0.7
asparagine synthetase (gb AAC72837.1); supported by cDNA: gi_3859535_gb_AF095453.1_AF095453	247218_at	-0.7
auxin-induced protein IAA9 (pir  T05902) ;supported by full-length cDNA: Ceres:31563.	247148_at	-0.7
succinate dehydrogenase flavoprotein alpha subunit (emb CAA05025.1);supported by cDNA: gi_15010745_gb_AY045674.1_	247060_at	-0.7
putative protein apoptosis-related protein PNAS-4, Homo sapiens, EMBL:AF229834; supported by full-length cDNA: Ceres:263500.	246931_at	-0.7
glutamyl-tRNA synthetase ;supported by cDNA: gi_3435195_gb_AF067773.1_AF067773	246845_at	-0.7
glycine rich protein - like glycine rich protein, Nicotiana tabacum, PIR:S54169;supported by full-length cDNA: Ceres:39561.	246741_at	-0.7
putative protein p76, Homo sapiens, EMBL:HSU81006	246650_at	-0.7
transmembrane protein FT27/PFT27-like ;supported by full-length cDNA: Ceres:12993.	246619_at	-0.7
putative protein strong similarity to unknown protein (gb AAD26879.1); supported by cDNA: gi_16323076_gb_AY057642.1_	246621_at	-0.7
nuM1 protein, putative similar to nuM1 protein GI:1279562 from [Medicago sativa]	246623_at	-0.7
formate dehydrogenase (FDH) ;supported by full-length cDNA: Ceres:7530.	246595_at	-0.7
putative protein predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 25053.	246549_at	-0.7
		-0.7
40S ribosomal protein S7-like 40S ribosomal protein S7 homolog - Brassica oleracea, EMBL:AF144752;supported by full-length cDNA: Ceres:23	246503_at	-0.7
putative protein predicted protein, Drosophila melanogaster	246462_at	-0.7
unknown protein	246320_at	-0.7
geranylgeranyl pyrophosphate synthase ;supported by full-length cDNA: Ceres:36701.	246198_at	-0.7
putative protein ;supported by full-length cDNA: Ceres:16131.	246200_at	-0.7
methionyl aminopeptidase-like protein ;supported by full-length cDNA: Ceres:18909.	246202_at	-0.7
ankyrin-repeat protein patsas protein - Drosophila melanogaster, EMBL:AF163011	246119_at	-0.7
zinc finger protein ;supported by full-length cDNA: Ceres:152664.	246069_at	-0.7
glutaredoxin ;supported by full-length cDNA: Ceres:115597.	246092_at	-0.7
NAM-like protein hypothetical protein SENU5, senescence up-regulated - Lycopersicon esculentum, EMBL:Z75524; supported by cDNA: gi_1432		-0.7
aspartate aminotransferase Asp2 ;supported by cDNA: gi_693689_gb_U15033.1_ATU15033	245951_at	-0.7
amino acid transport protein AAP2 ;supported by full-length cDNA: Ceres:114602.	245891_at	-0.7
unknown protein	245877_at	-0.7
	_	-0.7
unknown protein contains similarity to 60S acidic ribosomal protein GI:5815233 from [Homo sapiens]; supported by full-length cDNA: Ceres:6288.	245639_at	-0.7
hypothetical protein	245601_at	-0.7
hypothetical protein	245474_at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 37809.	245329_at	-0.7
isomerase like protein ;supported by full-length cDNA: Ceres:40913.	245332_at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 7101.	245337_at	-0.7
cytosolic O-acetylserine(thiol)lyase (EC 4.2.99.8); supported by cDNA: gi_15027936_gb_AY045825.1_	245286_at	-0.7
hypothetical protein ; supported by cDNA: gi_15292862_gb_AY050865.1_	245290_at	-0.7
putative thioredoxin reductase The last 2 exons encode thioredoxin. There is an EST match to exons 5-7, and the distance between exon 7 and (		-0.7
ATPase III subunit	245026_at	-0.7
NADH dehydrogenase subunit	245010_at	-0.7
hypothetical protein	245018_at	-0.7
ribosomal protein L20	244970_at	-0.7
ribosomal protein L16	244983_at	-0.7
hypothetical protein predicted by genscan and genefinder	257382_at	-0.7

unknown protein	267132 at	-0.7
DnaJ protein, putative contains Pfam profile: PF00226 DnaJ domain	256320_at	-0.7
putative protein TH65 protein, Arabidopsis thaliana, EMBL:AJ001729	250429_at	-0.7
putative protein strong similarity to unknown protein (emb CAB87904.1); supported by cDNA: gi_15028350_gb_AY045978.1_	249290_at	-0.7
putative pyrophosphatefructose-6-phosphate 1-phosphotransferase	264044_at	-0.7
single-strand nucleic acid-binding protein, putative similar to FUSE binding protein 2 GB:AAC50892 GI:1575607 from [Homo sapiens]	261988 at	-0.7
	Athal-25SrRN	-0.6
unknown protein predicted by genefinder	267630_at	-0.6
unknown protein ; supported by cDNA: gi_13877620_gb_AF370511.1_AF370511	267577 at	-0.6
putative cytochrome b5	267544_at	-0.6
, cinnamate-4-hydroxylase molecular marker C4H (GB:U71080); supported by cDNA: gi_1773288_gb_U71081.1_ATU71081	267470 at	-0.6
putative ferrochelatase precusor; supported by cDNA: gi_16226930_gb_AF428371.1_AF428371	267471_at	-0.6
unknown protein	267383 at	-0.6
coronatine-insensitive 1 (COI1), AtFBL2 identical to LRR-containing F-box protein GI:3158394 from [Arabidopsis thaliana]	267346_at	-0.6
putative protein transport protein SEC13 ;supported by full-length cDNA: Ceres:36577.	267277 <sup>-</sup> at	-0.6
putative transport protein ;supported by full-length cDNA: Ceres:26825.	267219_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:10293.	267237_s_at	-0.6
60S ribosomal protein L7 ;supported by full-length cDNA: Ceres:36813.	267213_at	-0.6
calmodulin (cam2)	267064_at	-0.6
unknown protein	267055_at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 16411.	267000_at	-0.6
putative phospholipase	266977_at	-0.6
putative protein kinase contains a protein kinase domain profile (PDOC00100)	266946_at	-0.6
ribonuclease, RNS1 identical to ribonuclease SP:P42813, GI:561998 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:27242.	266743_at	-0.6
hypothetical protein predicted by genscan; supported by cDNA: gi_15810382_gb_AY056230.1_	266662_at	-0.6
unknown protein	266599_at	-0.6
hypothetical protein predicted by genscan and genefinder;supported by full-length cDNA: Ceres:13580.	266576_at	-0.6
putative transportin	266523_at	-0.6
unknown protein ;supported by cDNA: gi_16649150_gb_AY059945.1_	266481_at	-0.6
putative glyoxysomal malate dehydrogenase precursor ; supported by cDNA: gi_16226836_gb_AF428346.1_AF428346	266457_at	-0.6
putative phospholipid cytidylyltransferase	266399_at	-0.6
20S proteasome subunit C8 (PAG1/PRC8_ARATH) identical to GB:Y13693;supported by full-length cDNA: Ceres:8342.	266312_at	-0.6
putative proliferating cell nuclear antigen, PCNA ;supported by full-length cDNA: Ceres:342.	266297_at	-0.6
putative cinnamoyl-CoA reductase	266202_at	-0.6
putative CCAAT-binding transcription factor subunit identical to GB:Y13723; contains a CBF/NF-Y subunit signature (PDOC00578) presernt in me	266171_at	-0.6
subtilisin-like serine protease, putative contains similarity to cucumisin-like serine protease GI:3176874 from [Arabidopsis thaliana]	266022_at	-0.6
putative leucine aminopeptidase identical to GB:X63444; supported by cDNA: gi_14334665_gb_AY035006.1_	265996_at	-0.6
putative Ta11-like non-LTR retroelement protein similar to GB:AAA75253; some members of this protein family have a weak CCHC zinc fingers the	265939_at	-0.6
putative sugar transporter ;supported by full-length cDNA: Ceres:114959.	265768_at	-0.6
hypothetical protein predicted by genefinder	265777_at	-0.6
putative integral membrane protein	265713_at	-0.6
similar to avrRpt2-induced protein 2	265682_at	-0.6
cysteine proteinase contains similarity to cysteine protease SPCP1 GI:13491750 from [Ipomoea batatas]	265665_at	-0.6
putative glutaredoxin ;supported by full-length cDNA: Ceres:30611.	265288_at	-0.6

putative ribose phosphate pyrophosphokinase ;supported by full-length cDNA: Ceres:35051.	265270_at	-0.6
hypothetical protein similar to putative glucosyltransferase GB:AAD15455 GI:4263795 from (Arabidopsis thaliana)	265175 at	-0.6
unknown protein similar to putative tyrosine phosphatase GB:AAF81798 GI:8926334 from [Oryza sativa];supported by full-length cDNA: Ceres:83		-0.6
hypothetical protein contains similarity to high-glucose-regulated protein 8 GB:AAF08813 GI:6449083 from [Homo sapiens]; supported by cDNA:		-0.6
unknown protein location of ESTs est VBVBD05, gb/Z30807 and VBVBD05, gb/Z30808;supported by full-length cDNA: Ceres:39763.	265066_at	-0.6
hypothetical protein predicted by genefinder; supported by full-length cDNA: Ceres:271253.	265067_at	-0.6
mitochondrial processing peptidase alpha subunit, putative similar to mitochondrial processing peptidase alpha subunit GI:9279647 from [Arabido		-0.6
NBS/LRR disease resistance protein, putative similar to NBS/LRR disease resistance protein GI:3309619 from [Arabidopsis thaliana]; supported		-0.6
putative metalloproteinase similar to GB:AAB61099	264866 at	-0.6
putative violaxanthin de-epoxidase precursor (U44133) similar to EST gb/N37612; supported by cDNA: gi_1465734_gb_U44133.1_ATU44133	264799 at	-0.6
putative GPI-anchor transamidase (U32517) similar to GB:P49018;supported by full-length cDNA: Ceres:120167.	264810 at	-0.6
phosphomethylpyrimidine kinase probable thiamin biosynthetic enzyme, location of EST gb/AA395737, gb/T21651	264771 at	-0.6
unknown protein	264696 at	-0.6
unknown protein ; supported by full-length cDNA: Ceres: 4324.	264671 at	-0.6
hypothetical protein Contains similarity to Rattus AMP-activated protein kinase (gb X95577); supported by cDNA: gi_9965728_gb_AF250335.1_A		-0.6
hypothetical protein similar to ankyrin like protein GI:7268141 from [Arabidopsis thaliana]; supported by cDNA: gi_14194106_gb_AF367259.1_AF		-0.6
putative protein import receptor similar to TOM20 (GB:CAA63223) from [Solanum tuberosum]; similar to ESTs gb[T444475, emb]Z26777, and en		-0.6
	264419 s at	-0.6
unknown protein EST gb/N96383 comes from this gene;supported by full-length cDNA: Ceres:40461.	264366 at	-0.6
putative importin alpha similar to GB:AAC27644 and GB:CAA74966	264256 at	-0.6
ribosomal protein, putative similar to ribosomal protein GI:19101 from [Hordeum vulgare]; supported by cDNA: gi_14596148_gb_AY042862.1_	264233 at	-0.6
putative cyclin-dependent kinase regulatory subunit	264061 at	-0.6
Expressed protein; supported by full-length cDNA: Ceres: 38277.	264004 at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:33232.	263880 at	-0.6
putative pre-mRNA splicing factor PRP19 similar to GB:AAB80652; supported by cDNA: gi 14532631 gb AY039940.1	263666 at	-0.6
unknown protein ; supported by cDNA: gi_6691164_gb_AF218765.1_AF218765	263498_at	-0.6
arginine decarboxylase identical to GP:1590814:U52851; supported by cDNA: gi_1590813_gb_U52851.1_ATU52851	263241_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:39571.	263180_at	-0.6
spore germination protein c2 similar to 2-hexaprenyl-1,4-naphthoquinone methyltransferase GB:BAA25267 GI:2982680 from [Micrococcus luteus	263044_at	-0.6
NADPH-dependent codeinone reductase, putative similar to NADPH-dependent codeinone reductase GI:6478210 from [Papaver somniferum]; si	262913_at	-0.6
unknown protein	262868_at	-0.6
putative beta-1,4-N-acetylglucosaminyltransferase contains similarity to gi 4417304 F15O11.7 putative beta-1,4-mannosyl-glycoprotein beta-1,4-	262768_at	-0.6
aspartate aminotransferase nearly identical to aspartate aminotransferase, cytoplasmic isozyme 2 SP:P46646 [Arabidopsis thaliana (Mouse-ear	262646_at	-0.6
putative ribokinase Except for first 69 amino acids, 33% identical to ribokinase (EC 2.7.1.15) [Bacillus subtilis] (gi 397495)	262519_at	-0.6
hypothetical protein contains similarity to developmental protein DG1118 GI:3789911 from [Dictyostelium discoideum]; supported by full-length cD		-0.6
unknown protein ;supported by full-length cDNA: Ceres:21798.	262283_at	-0.6
isochorismate synthase (icsl) identical to isochorismate synthase (icsl) GB:AF078080 (catalyzes chorismic acid to isochorismic acid Plant Physio	262177_at	-0.6
unknown protein contains similarity to WD-40 repeat protein GI:4519417 from [Homo sapiens]	262145_at	-0.6
hypothetical protein predicted by genemark.hmm	262104_at	-0.6
GTP-binding protein, putative similar to GTP-binding protein GB:AAF31009 GI:6899606 from [Ureaplasma urealyticum]	262086_at	-0.6
ADP-ribosylation factor, putative similar to ADP-ribosylation factor GI:166586 from [Arabidopsis thaliana]	261831_at	-0.6
ATP citrate-lyase, putative similar to ATP citrate-lyase GI:9229902 from [Ciona intestinalis]; supported by full-length cDNA: Ceres:36439.	261833_at	-0.6
60S ribosomal protein L10A, putative similar to 60S ribosomal protein L10A GB:AAC73045 GI:3860277 from [Arabidopsis thaliana]; supported by		-0.6
unknown protein similar to unknown protein GB:AAF24950 GI:6693024 from [Arabidopsis thaliana]; supported by cDNA: gi_13605566_gb_AF361	261651_at	-0.6

fatty acid elongase 3-ketoacyl-CoA synthase 1 identical to GB:AAC99312 GI:4091810 from [Arabidopsis thaliana]	261570 at	-0.6
carbonyl reductase, putative similar to carbonyl reductase (NADPH) GB:CAA59088 GI:666087 from [Rattus norvegicus]; supported by cDNA: gi	—	-0.6
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:36233.	261483 at	-0.6
receptor kinase, putative similar to receptor kinase GI:4105699 from [Arabidopsis thaliana]	261498 at	-0.6
glutaredoxin, putative similar to glutaredoxin GI:2244924 from [Arabidopsis thaliana]; supported by cDNA: gi_13358219_gb_AF325030.2_AF325	261443 at	-0.6
O-methyltransferase, putative similar to GB:AAF28353 from [Fragaria x ananassa];supported by full-length cDNA: Ceres:101583.	261453 at	-0.6
CMP-KDO synthetase, putative similar to GB:CAB89846 from [Zea mays]	261373_at	-0.6
unknown protein	261328_at	-0.6
unknown protein ; supported by full-length cDNA: Ceres: 117183.	261269_at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 41453.	260984 at	-0.6
26S proteasome regulatory particle triple-A ATPase subunit4, putative similar to 26S proteasome regulatory particle triple-A ATPase subunit4 GI:		-0.6
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:29740.	260867_at	-0.6
		-0.6
RING-H2 finger protein RHA3a, putative similar to RING-H2 finger protein RHA3a GI:3790573 from [Arabidopsis thaliana]; supported by cDNA: g		-0.6
mitochondrial NAD-dependent malate dehydrogenase identical to mitochondrial NAD-dependent malate dehydrogenase GI:3929649 from [Arabid		-0.6
putative molybdopterin synthase large subunit; supported by cDNA: gi_13605721_gb_AF361842.1_AF361842	260572_at	-0.6
mannosyl-oligosaccharide alpha-1,2-mannosidase, putative similar to mannosyl-oligosaccharide alpha-1,2-mannosidase (Mus musculus) GI:474.	_	-0.6
putative alpha-amylase similar to alpha-amylase GB:AAA91884 [Solanum tuberosum]; supported by cDNA: gi_15215737_gb_AY050398.1_	260412_at	-0.6
putative disease resistance protein similar to disease resistance protein RPP1-WsC GB:AAC72979 [Arabidopsis thaliana]	260312 at	-0.6
putative AP2 domain transcription factor contains Pfam profile: PF00847 AP2 domain; supported by cDNA: gi_16604674_gb_AY059782.1_	260209_at	-0.6
putative alpha galactosyltransferase similar to alpha galactosyltransferase GB:CAB52246 [Trigonella foenum-graecum] (plant cell wall matrix poly		-0.6
calmodulin-related protein similar to GB:P25070 from [Arabidopsis thaliana], contains Pfam profile: PF00036 EF hand (4 copies);supported by ful	260135_at	-0.6
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:30065.	260056_at	-0.6
putative calmodulin similar to calmodulin GB:P02596 [Renilla reniformis]; contains Pfam profile: PF00036 EF hand (4 copies); supported by full-ler	260076_at	-0.6
phosphatidylinositol synthase (PIS1) identical to phosphatidylinositol synthase (PIS1) GB:AJ000539; supported by full-length cDNA: Ceres: 34210.	260006_at	-0.6
thaumatin-like protein (PR-5) similar to thaumatin GB:AAD55090 [Vitis riparia]; contains Pfam profile: PF00314 Thaumatin family; supported by c[	259987_at	-0.6
germin-like protein similar to germin precursor GB:P26759 [Triticum aestivum]; contains Pfam profile: PF01072 Germin family; supported by full-le	259892_at	-0.6
putative catechol O-methyltransferase similar to catechol O-methyltransferase GB:CAA55358 [Vanilla planifolia]; supported by full-length cDNA: C	259878_at	-0.6
auxin-induced protein, putative similar to SP:P33083 from [Glycine max];supported by full-length cDNA: Ceres:29931.	259784_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:106626.	259587_at	-0.6
protein kinase, putative similar to protein kinase GI:2852447 from (Arabidopsis thaliana)	259541_at	-0.6
hypothetical protein	259523_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:17545.	259474_at	-0.6
Myb-related transcription activator, putative similar to MybSt1 GI:7705206 from [Solanum tuberosum]; supported by full-length cDNA: Ceres:4138	259476_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:13659.	259477_at	-0.6
DNA-binding protein RAV1 identical to RAV1 GI:3868857 from [Arabidopsis thaliana]; supported by cDNA: gi_3868856_dbj_AB013886.1_AB0138	259364_at	-0.6
unknown protein identical to GB:AAD56318 (Arabidopsis thaliana)	259211_at	-0.6
unknown protein similar to putative protein GB:CAA22987 [Arabidopsis thaliana]	259181_at	-0.6
unknown protein	259160_at	-0.6
putative auxin-independent growth promoter similar to auxin-independent growth promoter GB:A44226 [Nicotiana tabacum];supported by full-leng		-0.6
putative 40S ribosomal protein S3A (S phase specific) similar to 40S ribosomal protein S3A (S phase specific protein GBIS289) GB:P49396 [Bras		-0.6
putative ribose 5-phosphate isomerase identical to putative ribose 5-phosphate isomerase GB:AAD57010 (Arabidopsis thaliana); similar to ribose		-0.6
unknown protein similar to hypothetical protein GB:BAA29429 [Pyrococcus horikoshii];supported by full-length cDNA: Ceres:100279.	259053_at	-0.6
unknown protein contains helix-loop-helix DNA binding motif	259010_at	-0.6

hypothetical protein predicted by genscan+	258972 at	-0.6
hypothetical protein similar to calmodulin-like protein GB:CAB42906 [Arabidopsis thaliana]; Pfam HMM hit: EF hand; supported by full-length cDN	_	-0.6
putative folylpolyglutamate synthetase similar to folylpolyglutamate synthetase GB:AAA87568 [Homo sapiens]	258927 at	-0.6
putative pyruvate dehydrogenase kinase similar to pyruvate dehydrogenase kinase GB:AAC97601, [Arabidopsis thaliana]	258902 at	-0.6
putative dehydroquinase shikimate dehydrogenase similar to dehydroquinase shikimate dehydrogenase GB:S46210 [Nicotiana tabacum]	258908_at	-0.6
hypothetical protein identical to hypothetical protein GB:AAF23211 GI:6671951 from (Arabidopsis thaliana)	258755 at	-0.6
	258743_s_at	-0.6
unknown protein	258662_at	-0.6
putative long-chain-fatty-acidCoA ligase similar to putative long-chain-fatty-acidCoA ligase (brain isozyme) GB:P33124 [Rattus norvegicus]; su		-0.6
unknown protein contains Pfam profile:PF00295 Polygalacturonase;supported by full-length cDNA: Ceres:38575.	258528_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:4861.	258480 at	-0.6
unknown protein ; supported by cDNA: gi_14334415_gb_AY034899.1_	258401_at	-0.6
putative selenocysteine methyltransferase similar to selenocysteine methyltransferase GB:P56707 from [Astragalus bisulcatus]; supported by full-l		-0.6
putative phospholipase D similar to phospholipase D1 GB:AAC78487 [Brassica oleracea], GB:Q38882 [Arabidopsis thaliana]; supported by cDN/		-0.6
UDP-glucose:indole-3-acetate beta-D-glucosyltransferase, putative similar to UDP-glucose:indole-3-acetate beta-D-glucosyltransferase GB:AAB		-0.6
Expressed protein ; supported by cDNA: gi_15912240_gb_AY056398.1_	258140 at	-0.6
putative WD-repeat protein (WDR1-like) similar to WDR1 protein GB:AAD05042 [Gallus gallus] (Genomics 56 (1), 59-69 (1999))	258146 at	-0.6
putative 60S ribosomal protein L18A similar to GB:CAA08791 from [Podocoryne carnea];supported by full-length cDNA: Ceres:5961.	258090 at	-0.6
protein phosphatase 2A regulatory subunit isoform B delta identical to GB:AAD02810 from [Arabidopsis thaliana]; supported by cDNA: gi_410633	_	-0.6
expansin At-EXP5 identical to expansin At-EXP5 GB:AAB38071 from [Arabidopsis thaliana]; supported by cDNA: gi_1041703_gb_U30478.1_ATL		-0.6
unknown protein	258015 at	-0.6
hypothetical protein predicted by genemark;supported by full-length cDNA: Ceres:108568.	257967_at	-0.6
predicted protein supported by full-length cDNA: Ceres:250935.	257953 at	-0.6
AMP-binding protein, putative contains Pfam profile: PF00501 AMP-binding enzyme; similar to acyl-CoA synthetase GB:CAB54055 [Pseudomon	_	-0.6
GTP binding protein, putative similar to RAS-RELATED PROTEIN RAB7 GB:P31022 from [Pisum sativum], Plant Mol. Biol. 21 (6), 1195-1199 (1)		-0.6
root hair defective 3 (RHD3) identical to GB:AAB58375 from [Arabidopsis thaliana] (Genes Dev (1997) 11(6), 799-811)	257606 at	-0.6
mitochondrial NAD-dependent malate dehydrogenase, putative similar to mitochondrial NAD-dependent malate dehydrogenase GB:CAA10320 [/	_	-0.6
t-complex polypeptide 1 homologue identical to t-complex polypeptide 1 homologue GB:D11351 [Arabidopsis thaliana]; supported by cDNA: gi_2'		-0.6
ER lumen retaining receptor (HDEL receptor), putative similar to GB:P35402 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:23		-0.6
zinc finger protein, putative contains Pfam profiles: PF00097 Zinc finger, C3HC4 type (RING finger) (2 copies)	257062 at	-0.6
hypothetical protein predicted by genscan+	257044 at	-0.6
NAD dependent epimerase, putative contains Pfam profile: PF01370 NAD dependent epimerase/dehydratase family; supported by cDNA: gi_138		-0.6
ADP-ribosylation factor, putative similar to ADP-ribosylation factor GB:P91924 [Dugesia japonica]; supported by full-length cDNA: Ceres: 24097.		-0.6
serine/threonine protein phosphatase, putative similar to serine/threonine protein phosphatase GB:Z47076 GI:1143510 [Malus domestica]; support		-0.6
glutamine synthetase, putative similar to glutamine synthetase [Raphanus sativus] GI:1526564;supported by full-length cDNA: Ceres:2662.	256524_at	-0.6
ferredoxin, putative similar to GB:D90912 from [Synechocystis sp. PCC6803]	256468 at	-0.6
omega-3 fatty acid desaturase, chloroplast precursor identical to omega-3 fatty acid desaturase, chloroplast precursor SP:P46310 (Arabidopsis t	_	-0.6
60S ribosomal protein L10, putative contains Pfam profile: PF00826: Ribosomal L10;supported by full-length cDNA: Ceres:35307.	256385 at	-0.6
5,10-methylenetetrahydrofolate dehydrogenase:5,10-methenyltetrahydrofolate cyclohydrolase, putative similar to 5,10-methylenetetrahydrofolate		-0.6
hypothetical protein contains similarity to photosystem II 22 kDa protein GI:6006279 from [Arabidopsis thaliana];supported by full-length cDNA: Ce		-0.6
unknown protein identical to unknown protein GI:9755444 from (Arabidopsis thaliana); supported by full-length cDNA: Ceres: 110066.	255856 at	-0.6
putative uroporphyrinogen decarboxylase ; supported by cDNA: gi_14334767_gb_AY035057.1_	255826_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:19302.	255816_at	-0.6
transmembrane protein, putative similar to transmembrane protein GI:535681 from [Mus musculus];supported by full-length cDNA: Ceres:40780.		-0.6
	200700_00	0.0

DNA-binding protein RAV2, putative similar to DNA-binding protein RAV2 GI:3868859 from [Arabidopsis thaliana]; supported by cDNA: gi_15810	255742 at	-0.6
probable cytochrome P450	255690 at	-0.6
putative carrier protein similar to mitochondrial carrier family; supported by cDNA: gi_13430511_gb_AF360168.1_AF360168	255570_at	-0.6
hypothetical protein similar to A. thaliana hypothetical protein T13L16.2, GenBank accession number 2708738	255462 at	-0.6
putative calcium channel ; supported by cDNA: gi_13786068_gb_AF360372.1_AF360372	255380 at	-0.6
putative phosphofructokinase beta subunit	255365 at	-0.6
	_	-0.6
putative pollen-specific protein pollen-specific protein precursor - common tobacco, PIR2:S22495	254815 at	-0.6
putative protein putative oxidoreductase - Streptomyces lividans, PID:g3293547; supported by full-length cDNA: Ceres:6276.	254804 at	-0.6
putative protein ; supported by cDNA: gi_14596204_gb_AY042890.1_	254705_at	-0.6
Expressed protein ; supported by cDNA: gi_13430529_gb_AF360177.1_AF360177	254709 at	-0.6
neoxanthin cleavage enzyme-like protein neoxanthin cleavage enzyme, Lycopersicon esculentum, PATX:E325797; supported by cDNA: gi_1598	254564 at	-0.6
	254331 s at	-0.6
beta adaptin - like protein beta-adaptin 1, Drosophila melanogaster, PIR2:S39295	254261 at	-0.6
putative protein Pennisetum ciliare possible apospory-associated mRNA clone pSUB C, PID:g549984;supported by full-length cDNA: Ceres:2194	254223 at	-0.6
hypothetical protein	254154 at	-0.6
CER2 ;supported by full-length cDNA: Ceres:33382.	254122_at	-0.6
argininosuccinate synthase -like protein argininosuccinate synthase, Aquifex aeolicus, PIR2:B70398	254134_at	-0.6
putative protein pectinesterase - Citrus sinensis, PID:g2098705	254110 at	-0.6
putative uracil phosphoribosyl transferase uracil phosphoribosyl transferase, Saccharomyces cerevisiae, PIR2: JH0147 supported by full-length cD	253970_at	-0.6
putative protein ;supported by full-length cDNA: Ceres:112916.	253688_at	-0.6
Ca2+-transporting ATPase - like protein calmodulin-stimulated calcium-ATPase, Brassica oleracea, gb:X99972	253702_at	-0.6
putative protein hypothetical protein - Arabidopsis thaliana, PID:g3738329; supported by full-length cDNA: Ceres: 17578.	253635_at	-0.6
protein kinase - like protein protein kinase 6, Glycine max., PIR2:S29851;supported by full-length cDNA: Ceres:156374.	253564_at	-0.6
predicted protein hypothetical protein slr1919, Synechocystis sp., PIR2:S75233	253517_at	-0.6
putative protein myosin heavy chain, neuronal, Rattus norvegicus, Pir1:S21801; supported by cDNA: gi_14334773_gb_AY035060.1_	253523_at	-0.6
ribosomal protein S6 - like ribosomal protein S6, Arabidopsis thaliana, PID:g2662469; supported by cDNA: gi_15292738_gb_AY050803.1_	253487_at	-0.6
putative protein phosphate/phosphoenolpyruvate translocator, Arabidopsis thaliana, ATU66321	253427_at	-0.6
putative protein mRNAs from Ricinus communis and Medicago sativa, Z81012 and L36159;supported by full-length cDNA: Ceres:37529.	253437_at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 109432.	253302_at	-0.6
putative protein hypothetical protein, Synechocystis sp., PIR2:S76307; supported by cDNA: gi_14596178_gb_AY042877.1_	253235_at	-0.6
putative protein ; supported by cDNA: gi_14517511_gb_AY039591.1_	253049_at	-0.6
putative protein probable arabinogalactan protein precursor, Lycopersicon esculentum, PIR2:S55925; supported by cDNA: gi_11935087_gb_AF(	253050_at	-0.6
geranylgeranyl pyrophosphate synthase-related protein ;supported by full-length cDNA: Ceres:28204.; supported by cDNA: gi_13265402_gb_AFC	252996_s_at	-0.6
putative protein DNA damage-inducible protein - Synechocystis sp.,PIR2:S77364	252921_at	-0.6
putative proton pump vacuolar proton ATPase 100-kDa subunit - Dictyostelium discoideum, PID:g1384136; supported by cDNA: gi_16974582_gl	252932_at	-0.6
putative gamma-glutamyltransferase gamma-glutamyltransferase, Arabidopsis thaliana, PIR2:S58286	252906_at	-0.6
GTP-binding protein GB3 ;supported by full-length cDNA: Ceres:8545.	252875_at	-0.6
putative protein hypothetical protein slr1699 - Synechocystis sp. (strain PCC 6803), PIR:S75306; supported by cDNA: gi_14532795_gb_AY0400:	252724_at	-0.6
putative protein pectinesterase homolog - Pinus radiata,PIR2:T08112	252437_at	-0.6
40S ribosomal protein S20-like protein 40S RIBOSOMAL PROTEIN S20 - ARABIDOPSIS THALIANA, PID: g1350956; supported by full-length cDI	252413_at	-0.6
putative protein several hypothetical proteins	252329_at	-0.6
	252291_s_at	-0.6
signal recognition particle subunit 9 - like signal recognition particle subunit 9, Zea mays, EMBL:Y10117; supported by full-length cDNA: Ceres:14	252295_at	-0.6

cytosolic ribosomal protein S11 ;supported by full-length cDNA: Ceres:40559.	252297_at	-0.6
RNA-binding - like protein RNA-binding protein RBP37, Arabidopsis thaliana, PIR:T04196	252313 at	-0.6
putative protein ;supported by full-length cDNA: Ceres:15698.	252270_at	-0.6
centrin	252206_at	-0.6
putative protein RNA-binding protein 30 - Nicotiana plumbaginifolia,PIR2:S26203	252032_at	-0.6
hypothetical protein ; supported by cDNA: gi_15450654_gb_AY052695.1_	252010_at	-0.6
putative protein predicted proteins, Arabidopsis thaliana	252014_at	-0.6
fructose bisphosphate aldolase - like protein fructose bisphosphate aldolase, garden pea, PIR:S58167; supported by full-length cDNA: Ceres:344	252022_at	-0.6
sigma factor SigC ; supported by cDNA: gi_2353174_gb_AF015544.1_AF015544	251929_at	-0.6
peptide transport - like protein peptide transport protein, Hordeum vulgare, PIR:T04378; supported by full-length cDNA: Ceres:117581.	251882_at	-0.6
beta-N-acetylhexosaminidase -like protein various beta-N-acetylhexosaminidases; supported by full-length cDNA: Ceres: 118286.	251782_at	-0.6
2-oxoglutarate dehydrogenase, E1 subunit - like protein 2-oxoglutarate dehydrogenase, E1 subunit, Arabidopsis thaliana, EMBL:ART223802	251787_at	-0.6
delta-1-pyrroline-5-carboxylate synthetase	251775_s_at	-0.6
putative protein	251720_at	-0.6
responce reactor 4 ; supported by cDNA: gi_3273201_dbj_AB010918.1_AB010918	251665_at	-0.6
putative protein multisynthetase complex auxiliary component p43 - Cricetulus griseus, EMBL:AF021800;supported by full-length cDNA: Ceres:2	251442_at	-0.6
putative protein pectinesterase homolog - Pinus radiata, PIR:T08112;supported by full-length cDNA: Ceres:23716.	251181_at	-0.6
putative protein putative protein At2g15760 - Arabidopsis thaliana, EMBL:AC006438;supported by full-length cDNA: Ceres:2947.	251183_at	-0.6
ATMRK1 ;supported by full-length cDNA: Ceres:253505.	251170_at	-0.6
putative protein	250948_at	-0.6
ABC transporter -like protein ABC-type transport protein sll1276, Synechocystis sp., PIR:S77239; supported by cDNA: gi_16604564_gb_AY0597	250885_at	-0.6
fatty acid elongase - like protein KCS1 fatty acid elongase 3-ketoacyl-CoA synthase 1, Arabidopsis thaliana, EMBL:AF053345	250891_at	-0.6
putative RNA-binding protein astrocytic NOVA-like RNA-binding protein, Homo sapiens, U70477; supported by full-length cDNA: Ceres: 25769.	250843_at	-0.6
sulphite reductase ;supported by cDNA: gi_13358216_gb_AF325027.2_AF325027	250846_at	-0.6
unknown protein	250857_at	-0.6
putative protein similar to unknown protein (emb CAB88360.1);supported by full-length cDNA: Ceres:29476.	250764_at	-0.6
putative protein contains similarity to transmembrane transport protein; supported by full-length cDNA: Ceres:249596.	250315_at	-0.6
putative protein mRNA, Moritella marina, EMBL:AB025342	250275_at	-0.6
transaldolase - like protein transaldolase, Solanum tuberosum, EMBL:U95923;supported by full-length cDNA: Ceres:32114.	250234_at	-0.6
putative protein	250075_at	-0.6
glutamate dehydrogenase (EC 1.4.1) 1 (pir  S71217) ; supported by cDNA: gi_15146203_gb_AY049243.1_	250032_at	-0.6
synaptobrevin-like protein	249930_at	-0.6
chorismate mutase/prephenate dehydratase-like protein ; supported by cDNA: gi_16604397_gb_AY058097.1_	249910_at	-0.6
2-isopropyImalate synthase-like; homocitrate synthase-like ; supported by cDNA: gi_12330688_gb_AF327648.1_AF327648	249866_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:20919.	249717_at	-0.6
putative protein similar to unknown protein (pir  S75762)	249519_at	-0.6
cysteine-tRNA ligase -like protein cysteine-tRNA ligase, Arabidopsis thaliana, PIR:T47747	249537_at	-0.6
putative protein predicted proteins - Arabidopsis thaliana	249437_at	-0.6
putative protein contains similarity to 22 kDa peroxisomal membrane protein; supported by full-length cDNA: Ceres: 15499.	249137_at	-0.6
aluminum-induced protein-like ; supported by full-length cDNA: Ceres: 12484.	249121_at	-0.6
putative protein similar to unknown protein (pir  T08416)	248944_at	-0.6
3-oxoacyl-[acyl-carrier-protein] synthase I precursor (beta-ketoacyl-acp synthase I) (KAS I) (sp P52410) ;supported by full-length cDNA: Ceres:38		-0.6
AP47 50p (gb AAB88283.1) ; supported by cDNA: gi_14326519_gb_AF385713.1_AF385713	248858_at	-0.6
putative protein contains similarity to bHLH DNA-binding protein; supported by full-length cDNA: Ceres: 35890.	248839_at	-0.6

pantoate-beta-alanine ligase ;supported by full-length cDNA: Ceres:156371.	248680 at	-0.6
protein kinase ;supported by full-length cDNA: Ceres:142106.	248529_at	-0.6
unknown protein ; supported by full-length cDNA: Ceres: 266744.	248377_at	-0.6
fructokinase 1 ; supported by cDNA: gi_13878052_gb_AF370289.1_AF370289	248381 at	-0.6
putative protein similar to unknown protein (dbj BAA83359.1)	248340_at	-0.6
putative protein contains similarity to GTPase activating protein	248313_at	-0.6
pyruvate kinase ;supported by full-length cDNA: Ceres:109919.	248283_at	-0.6
membrane associated protein ; supported by cDNA: gi_1800146_gb_U83655.1_ATU83655	248195_at	-0.6
1,4-benzoquinone reductase-like; Trp repressor binding protein-like	248162_at	-0.6
protein translation factor Sui1 homolog (sp P41568)	248126_at	-0.6
putative protein contains similarity to polyadenylate-binding protein 5; supported by full-length cDNA: Ceres: 107768.	248147_at	-0.6
outward rectifying potassium channel KCO ;supported by full-length cDNA: Ceres:32253.	248027_at	-0.6
RNA-binding protein-like	247994_at	-0.6
phosphoinositide specific phospholipase C ;supported by cDNA: gi_1526413_dbj_D38544.1_ATHATPLC1	247794_at	-0.6
D-xylose-H+ symporter - like protein D-xylose-H+ symporter, Lactobacillus brevis, EMBL:AF045552	247709_at	-0.6
putative protein various predicted proteins, Arabidopsis thaliana	247470_at	-0.6
KED - like protein KED, Nicotiana tabacum, EMBL:AB009883	247480_at	-0.6
permease 1 - like protein permease 1, common ice plant, PIR:T12309; supported by cDNA: gi_14334659_gb_AY035003.1_	247404_at	-0.6
3(2),5-bisphosphate nucleotidase ; supported by cDNA: gi_15281147_gb_AY034894.1_	247313_at	-0.6
putative protein contains similarity to glutamyl-tRNA amidotransferase subunit A; supported by cDNA: gi_8163874_gb_AF223949.1_AF223949	247262_at	-0.6
ABC transporter-like	247232_at	-0.6
NifS-like aminotranfserase ; supported by cDNA: gi_15292880_gb_AY050874.1_	247164_at	-0.6
putative protein similar to unknown protein (sp P55606); supported by cDNA: gi_14190422_gb_AF378889.1_AF378889	247077_at	-0.6
cyclin D3-like protein ;supported by full-length cDNA: Ceres:36467.	247034_at	-0.6
putative protein similar to unknown protein (pir  T08445);supported by full-length cDNA: Ceres:11651.	246952_at	-0.6
unknown protein ;supported by cDNA: gi_15293272_gb_AY051070.1_	246954_at	-0.6
putative protein ;supported by full-length cDNA: Ceres:39714.	246797_at	-0.6
putative protein predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 38304.	246792_at	-0.6
putative protein predicted protein, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 98046.	246593_at	-0.6
ribosomal protein-like 40S RIBOSOMAL PROTEINs - different species; supported by full-length cDNA: Ceres: 25543.	246527_at	-0.6
stearoyl-acyl carrier protein desaturase stearoyl-acyl carrier protein desaturase sad1 - Linum usitatissimum, EMBL:AJ006957;supported by full-le	_	-0.6
hypothetical protein ;supported by full-length cDNA: Ceres:22757.	246443_at	-0.6
Ca2+/H+-exchanging protein-like Arabidopsis thaliana high affinity calcium antiporter CAX1 encoded by GenBank Accession Number U57411	246302_at	-0.6
putative nuclear DNA-binding protein G2p Mus musculus p38-2G4 protein: SwissProt Accession Number P50580; supported by cDNA: gi_145328		-0.6
unknown protein	246286_at	-0.6
hypothetical protein	246280_at	-0.6
putative protein various predicted proteins, Arabidopsis thaliana and others; supported by full-length cDNA: Ceres: 5850.	246170_at	-0.6
T-complex protein 1, beta subunit T-COMPLEX PROTEIN 1, BETA SUBUNIT, Homo sapiens, EMBL:AF026293;supported by full-length cDNA: (		-0.6
cinnamyl-alcohol dehydrogenase - like protein cinnamyl-alcohol dehydrogenase, apple tree, PIR:T16995;supported by full-length cDNA: Ceres:6	_	-0.6
glycerol-3-phosphate acyltransferase identical to glycerol-3-phosphate acyltransferase GB:Q43307 from [Arabidopsis thaliana]	245790_at	-0.6
phosphate-induced (phi-1) protein, putative similar to phi-1 GB:BAA33810 GI:3759184 from [Nicotiana tabacum]; supported by full-length cDNA: (		-0.6
rec - like protein	245695_at	-0.6
pullulanase-like protein (starch debranching enzyme)	245712_at	-0.6
hypothetical protein	245600_at	-0.6

cyanohydrin lyase like protein ;supported by full-length cDNA: Ceres:5546.	245349_at	-0.6
ribosomal protein ;supported by full-length cDNA: Ceres:15384.	245372_at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 30471.	245320 at	-0.6
putative protein ; supported by cDNA: gi_14190518_gb_AF380659.1_AF380659	245279_at	-0.6
phytoene dehydrogenase precursor (phytoene desaturase) ; supported by cDNA: gi_14532765_gb_AY040007.1_	245284 at	-0.6
putative synaptobrevin ;supported by full-length cDNA: Ceres:2443.		-0.6
60S ribosomal protein L7A ;supported by full-length cDNA: Ceres:6394.	245121 at	-0.6
putative alpha/beta hydrolase contains Pfam profile: PF00561 alpha/beta hydrolase fold; predicted by genscan	257533 at	-0.6
putative electron transfer flavoprotein ubiquinone oxidoreductase	260536_at	-0.6
glucose-6-phosphate isomerase, cytosolic (GPI) (phosphoglucose isomerase) (PGI) (phosphohexose isomerase) (PHI) (sp P34795) ; supported		-0.6
putative chlorophyll a/b binding protein ; supported by full-length cDNA: Ceres: 6454.	265722_at	-0.6
putative WD-40 repeat protein, MSI2 ;supported by full-length cDNA: Ceres:40637.	265383_at	-0.6
protein phosphatase type 2C, putative similar to GB:AAD17805 from (Lotus japonicus) (Proc. Natl. Acad. Sci. U.S.A. 96 (4), 1738-1743 (1999))	262408_at	-0.6
unknown protein ; supported by cDNA: gi_16649026_gb_AY059883.1_	261867_at	-0.6
unknown protein ; supported by cDNA: gi_15215745_gb_AY050402.1_	261208_at	-0.6
unknown protein	256173_at	-0.6
hypothetical protein predicted by genscan	255874_at	-0.6
putative potassium/H+ antiporter	255686_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:8255.	245780_at	-0.6
Arabidopsis thaliana /REF=M64116 /DEF=glyceraldehyde 3-phosphate dehydrogenase C subunit (GapC) gene, complete cds /LEN=1295 (-5, -3)	r2-At-GAPDH-	-0.5
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:38147.	267601_at	-0.5
unknown protein	267587_at	-0.5
MADS-box protein (AGL20) ; supported by full-length cDNA: Ceres: 5467.	267509_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:26701.	267366_at	-0.5
citrate synthase similar to GB:X17528, 10 possible frameshifts in that submission.;supported by full-length cDNA: Ceres:16528.	267368_at	-0.5
60S acidic ribosomal protein P0	267349_at	-0.5
putative serine carboxypeptidase I ;supported by full-length cDNA: Ceres:33165.	267256_s_at	-0.5
putative adenosine phosphosulfate kinase identical to GB:U05238;supported by full-length cDNA: Ceres:14216.	267112_at	-0.5
60S ribosomal protein L35 ;supported by full-length cDNA: Ceres:11583.	266980_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:150205.	266949_s_at	-0.5
Expressed protein ; supported by full-length cDNA: Ceres: 19349.	266906_at	-0.5
putative nucleotide-binding protein ;supported by full-length cDNA: Ceres:33511.	266801_at	-0.5
putative expansin Experimental evidence from Dr. Daniel Cosgrove at Penn State Univ. <dcosgrove@psu.edu></dcosgrove@psu.edu>	266770_at	-0.5
putative RAV-like B3 domain DNA binding protein	266760_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:12086.	266646_at	-0.5
glycine decarboxylase complex H-protein ; supported by cDNA: gi_15810183_gb_AY056106.1_	266517_at	-0.5
putative small nuclear ribonucleoprotein D2 ;supported by full-length cDNA: Ceres:26123.	266482_at	-0.5
3-isopropylmalate dehydratase, small subunit ; supported by cDNA: gi_16974632_gb_AY060594.1_	266395_at	-0.5
putative protein transport protein SEC12p identical to GB:M95796, contains a WD-40 repeat domain; supported by cDNA: gi_166877_gb_M9579		-0.5
putative auxin transport protein ;supported by cDNA: gi_7109714_gb_AF087016.1_AF087016	266300_at	-0.5
ethylene-insensitive3-like1 (EIL1) identical to GB:AF004213; related to ethylene-insensitive3 (ethylene signaling pathway)	266302_at	-0.5
putative endoxyloglucan glycosyltransferase identical to GB:D16454;supported by full-length cDNA: Ceres:15276.	266215_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:114031.	266167_at	-0.5
enoyl-ACP reductase (enr-A)	266035_at	-0.5

putative peptide methionine sulfoxide reductase	265804_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:41585.	265717 at	-0.5
putative Tub family protein	265321_at	-0.5
hypothetical protein predicted by genscan; supported by full-length cDNA: Ceres: 32047.	265336_at	-0.5
auxin-regulated protein (IAA8) ;supported by full-length cDNA: Ceres:37274.	265319_at	-0.5
unknown protein ; supported by cDNA: gi_16604403_gb_AY058100.1_	265132_at	-0.5
hypothetical protein predicted by genscan+	265162 at	-0.5
unknown protein 3 -end of protein contains similarity to thioredoxins; supported by cDNA: gi_15215811 gb_AY050435.1_	265104 at	-0.5
beta-fructosidase nearly identical to beta-fructosidase GB:CAA67560 GI:1429209 (Arabidopsis thaliana); supported by cDNA: gi_14517549 gb_A		-0.5
zinc finger protein 7, ZFP7 ; supported by cDNA: gi_790684_gb_L39650.1_ATHZFPG	265029 at	-0.5
putative thioredoxin similar to ESTs gb T46281, gb R83933, gb N65879, emb F14466, gb N96726, gb AA042340, and emb Z18150; supported by	_	-0.5
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_16209657_gb_AY057594.1_	264769_at	-0.5
germin-like protein Identical to Arabidopsis germin-like protein, gi 1755178. Location of EST 180L10T7, gi 906417; supported by cDNA: gi_13265		-0.5
adenine phosphoribosyltransferase 1, APRT identical to GB:P31166; similar to ESTs gb N65531, gb R90631, gb T21275, and gb AA713070;supj		-0.5
potassium transporter, putative similar to potassium transporter GI:2654088 from [Arabidopsis thaliana]	264247 at	-0.5
putative 40S ribosomal protein S18 Match to ribosomal S18 gene mRNA gb/Z28701, DNA gb/Z23165 from A. thaliana. ESTs gb/T21121, gb/Z17		-0.5
putative steroid sulfotransferase ; supported by cDNA: gi_599639_emb_Z46823.1_ATTS4391	264042 at	-0.5
putative auxin-regulated protein	264014_at	-0.5
unknown protein	263942_at	-0.5
putative vacuolar proton-ATPase subunit ;supported by cDNA: gi_15450750_gb_AY053417.1_	263764_at	-0.5
putative CONSTANS-like B-box zinc finger protein ; supported by cDNA: gi_16974588_gb_AY060570.1_	263739 at	-0.5
Expressed protein ; supported by cDNA: gi_13877876_gb_AF370201.1_AF370201	263550_at	-0.5
putative Rieske iron-sulfur protein ;supported by full-length cDNA: Ceres:29774.	263533_at	-0.5
putative root iron transporter protein	263480_at	-0.5
unknown protein ; supported by full-length cDNA: Ceres: 11283.	263399_at	-0.5
putative snRNP splicing factor ;supported by full-length cDNA: Ceres:97480.	263332_at	-0.5
unknown protein	263242_at	-0.5
unknown protein	263247_at	-0.5
delta 9 desaturase ALMOST identical (4 aa diff t) to GP:2970036;supported by full-length cDNA: Ceres:21841.	263249_at	-0.5
unknown protein similar to ESTs gb T43206, gb H76501, gb AA651577, and gb AA605326;supported by full-length cDNA: Ceres:7488.	263206_at	-0.5
putative glutaredoxin Strong similarity to gb Z49699 glutaredoxin from Ricinus communis	263168_at	-0.5
putative HMG protein ;supported by full-length cDNA: Ceres:24090.	263074_at	-0.5
endo-beta-1,4-glucanase, putative similar to endo-beta-1,4-glucanase GB:AAC12685 GI:3025470 from [Pinus radiata]; supported by full-length c[	262980_at	-0.5
ABC transporter, putative similar to ABC transporter GI:9279716 from [Arabidopsis thaliana]	262899_at	-0.5
xyloglucan endo-transglycosylase, putative similar to xyloglucan endo-transglycosylase GB:CAA63553 GI:1769907 [Arabidopsis thaliana], identic	262842_at	-0.5
signal response protein (GAI) identical to GAI GB:CAA75492 GI:2569938 [Arabidopsis thaliana] (Genes Dev. In press); supported by cDNA: gi_1(	262850_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:1505.	262609_at	-0.5
unknown protein Location of ests 147K6T7 (gb T75883), 91C11T7 (gb AA067428), 162K21T7 (gb R29908), 91C11XP 3 (gb AI100498), 162K21	262481_at	-0.5
Mlo protein, putative similar to Mlo protein GB:Z83834 GI:1877220 from [Hordeum vulgare];supported by full-length cDNA: Ceres:259664.	262455_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:35675.	262050_at	-0.5
unknown protein	261854_at	-0.5
acyl-(acyl carrier protein) thioesterase, putative almost identical to acyl-(acyl carrier protein) thioesterase GB:CAA85387 GI:634003 from [Arabidc	261722_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:8976.	261566_at	-0.5
acid phosphatase, putative similar to acid phosphatase GI:5360721 from [Lupinus albus]; supported by cDNA: gi_13605749_gb_AF361856.1_AF	261492_at	-0.5

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globulin-like protein similar to GB:7595348 from [Cucumis melo];supported by full-length cDNA: Ceres:40551.	261415_at	-0.5
expansin S2 precursor, putative similar to GB:U30460 from [Cucumis sativus]; supported by full-length cDNA: Ceres:11011.	261226_at	-0.5
beta tubulin 1, putative similar to GB:AAD02498 from [Arabidopsis thaliana] (Plant Mol. Biol. 39 (1), 171-176 (1999)); supported by cDNA: gi_136	_	-0.5
putative calcium-binding protein, calreticulin similar to SP:P12858 from [Arabidopsis thaliana]	261197_at	-0.5
heat shock factor protein hsf8, putative predicted by genemark.hmm; supported by cDNA: gi_15028376_gb_AY045991.1_	261206_at	-0.5
MAP3K alpha protein kinase, putative similar to MAP3K alpha protein kinase GB:CAA08994 GI:3688191 from [Arabidopsis thaliana]; supported t		-0.5
ethylene response factor, putative similar to ethylene response factor 1 GB:AAD03544 GI:4128208 from [Arabidopsis thaliana]	260783_at	-0.5
signal recognition particle 19 kDa protein subunit, putative similar to GB:U19030 from [Oryza sativa] (Plant Mol. Biol. 34 (3), 507-515 (1997)); sur		-0.5
pyruvate kinase, plastid isozyme, putative similar to GB:Z28374 from [Nicotiana tabacum] (Plant Mol. Biol. 27 (1), 79-89 (1995)); supported by cE	_	-0.5
hypothetical protein contains similarity to CDP-diacylglycerol synthase 2 GI:3892191 from [Homo sapiens]	260636_at	-0.5
ACC oxidase, putative similar to ACC oxidase GI:587086 from [Brassica oleracea]; supported by cDNA: gi_15028038_gb_AY045876.1_	260637_at	-0.5
membrane related protein CP5, putative similar to GB:AAD28760 from [Arabidopsis thaliana]; supported by cDNA: gi_16604620_gb_AY059755.	260603_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:40573.	260429_at	-0.5
putative peptide transporter similar to peptide transporter GB:AAC32034 [Hordeum vulgare]; supported by full-length cDNA: Ceres: 22243.	260410_at	-0.5
60S ribosomal protein L34, putative similar to SP:Q42351 from (Arabidopsis thaliana); supported by full-length cDNA: Ceres: 1568.	260369_at	-0.5
hypothetical protein predicted by genscan+	260277_at	-0.5
putative reductase similar to cinnamoyl CoA reductase GB:CAA12276 [Populus balsamifera subsp. trichocarpa], aldehyde reductase GB:AAD53	260260_at	-0.5
putative phosphoglucomutase similar to phosphoglucomutase GB:AAC00601 [Arabidopsis thaliana]	260207_at	-0.5
calmodulin-4 identical to GB:Q03510 from [Arabidopsis thaliana] (Plant Mol. Biol. 22 (2), 215-225 (1993)); supported by full-length cDNA: Ceres:	260138_at	-0.5
unknown protein ;supported by cDNA: gi_15450975_gb_AY054568.1_	260058_at	-0.5
putative helix-loop-helix DNA-binding protein contains Pfam profile: PF00010 Helix-loop-helix DNA-binding domain	260070_at	-0.5
unknown protein contains non-consensus GG donor splice site at exon2; modeled to est match.; supported by full-length cDNA: Ceres: 124169.	260007_at	-0.5
hypothetical protein predicted by genemark.hmm	259850 at	-0.5
Expressed protein ; supported by full-length cDNA: Ceres: 30602.	259789 at	-0.5
putative phosphatidylinositol-4-phosphate-5-kinase similar to phosphatidylinositol-4-phosphate-5-kinase GB:CAB53377 [Arabidopsis thaliana]	259677 at	-0.5
nitrate reductase 1 (NR1) identical to nitrate reductase 1 (NR1) GB:P11832 [Arabidopsis thaliana]; supported by cDNA: gi_15983498_gb_AF4246	259681 at	-0.5
20S proteasome beta subunit (PBG1) identical to 20S proteasome beta subunit (PBG1) GI:3421123 [Arabidopsis thaliana]; supported by cDNA: c		-0.5
embryo abundance protein (EMB20), putative similar to embryo abundance protein (EMB20) GI:1350503 from [Picea glauca]	259486 at	-0.5
unknown protein	259434_at	-0.5
hypothetical protein similar to putative glycosyl transferase GI:6862930 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:117402.		-0.5
glyceraldehyde-3-phosphate dehydrogenase, putative similar to glyceraldehyde-3-phosphate dehydrogenase GI:21143 from (Sinapis alba); supp		-0.5
allene oxide cyclase, putative similar to allene oxide cyclase GI:8977961 from [Lycopersicon esculentum]; supported by cDNA: gi_16323064_gb_		-0.5
	259335_s_at	-0.5
lycopene beta cyclase identical to lycopene beta cyclase GB:AAB53337 [Arabidopsis thaliana]; supported by cDNA: gi_1399182_gb_U50739.1_A		-0.5
transport protein SEC13, putative similar to protein transport protein SEC13 GB:P53024 [Pichia pastoris]; supported by full-length cDNA: Ceres:3		-0.5
putative ribosomal protein L13 similar to putative ribosomal protein L13 GB:AAC07691 [Aquifex aeolicus]	258995 at	-0.5
unknown protein similar to unknown proteins GB:AAD24625 [Arabidopsis thaliana], GB:AAC73026 [Arabidopsis thaliana]	258933_at	-0.5
glutathione S-transferase identical to glutathione S-transferase GB:AAB09584 from [Arabidopsis thaliana]; supported by cDNA: gi_1575751_gb_L	258851 at	-0.5
S-adenosylmethionine decarboxylase identical to GB:Q96286 from [Arabidopsis thaliana]; supported by cDNA: gi_14596072_gb_AY042824.1_	258500_at	-0.5
unknown protein	258418 at	-0.5
putative ribosomal protein similar to ribosomal protein L41 GB:AAA34366 from [Candida maltosa]; supported by full-length cDNA: Ceres: 13557.	258296_at	-0.5
putative Indosofial protein similar to hosofial protein L41 GB.AAA34300 from [Candida mailosa], supported by full-length CDNA. Ceres. 13557. putative WD-repeat protein contains Pfam profile: PF00400 WD domain, G-beta repeat (7 copies)	258290_at 258268 at	-0.5 -0.5
transport protein, putative similar to transport protein GB:CAB10195 from [Arabidopsis thaliana]	258265_at 258097_at	-0.5 -0.5
MAP kinase kinase 5 identical to GB:BAA28831 from [Arabidopsis thaliana]; supported by cDNA: gi_3219272_dbj_AB015316.1_AB015316		-0.5 -0.5
IVIAE KITASE KITASE STUEHIIVAI IO OD.DAAZOOST ITUIT [ATADIUOPSIS ITAITATIA], SUPPOILEU DY ODIA. YESZTZEUDEADU 15310. LEABU 15310	258046_at	-0.5

unknown protein ;supported by full-length cDNA: Ceres:121587.	258020 at	-0.5
putative UDP-glucose glucosyltransferase similar to GB:Q40284 from [Manihot esculenta]; supported by cDNA: gi_13937235_gb_AF372973.1_A	_	-0.5
hypothetical protein	257875 at	-0.5
hypothetical protein predicted by genefinder; supported by full-length cDNA: Ceres: 116381.	257855_at	-0.5
hypothetical protein predicted by genscan, similar to iojap protein GB:S28019 from [Zea mays];supported by full-length cDNA: Ceres:39638.	257856_at	-0.5
TOM20, putative similar to TOM20 GB:CAA63223 from [Solanum tuberosum];supported by full-length cDNA: Ceres:30812.	257792_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:17962.	257800 at	-0.5
hypothetical protein predicted by genemark.hmm	257687_at	-0.5
glucan endo-1,3-beta-glucosidase precursor, putative similar to GB:P52409 from [Triticum aestivum]; supported by cDNA: gi_14334497_gb_AY(		-0.5
20S proteasome subunit PAC1 identical to GB:AAC32057 from [Arabidopsis thaliana] (Genetics (1998) 149 (2), 677-692);supported by full-length		-0.5
dTDP-glucose 4,6-dehydratase, putative similar to dTDP-glucose 4,6-dehydratase GB:AE000666 GI:6626257 from [Methanobacterium thermoal		-0.5
amino acid permease, putative contains Pfam profile: PF00324 amino acid permease	256567_at	-0.5
	256437 s at	-0.5
ATP-dependent Clp protease proteolytic subunit (ClpP3) identical to ATP-dependent Clp protease (nClpP3) GI:5360591 (Arabidopsis thaliana)	256411_at	-0.5
protein phosphatase 2C, putative contains Pfam profile: PF00481 Protein phosphatase 2C	256279_at	-0.5
60S acidic ribosomal protein, putative similar to 60S acidic ribosomal protein P0 GI:2088654 [Arabidopsis thaliana]; supported by full-length cDNA		-0.5
unknown protein ; supported by cDNA: gi_15081663_gb_AY048224.1_	256076 at	-0.5
ribosomal protein, putative similar to ribosomal protein L35a GI:57118 from [Rattus norvegicus]; supported by full-length cDNA: Ceres: 2778.	256065_at	-0.5
UDP-glucose glucosyltransferase, putative similar to UDP-glucose glucosyltransferase GI:453245 from [Manihot esculenta]; supported by cDNA:		-0.5
unknown protein ;supported by full-length cDNA: Ceres:16380.	255925 at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:35273.	255817 <sup>_</sup> at	-0.5
phosphoprotein phosphatase 2A, regulatory subunit A identical to phosphoprotein phosphatase 2A, regulatory subunit A GI:1262171 from [Arabic	255731_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:25047.	255721_at	-0.5
hypothetical protein	255589_s_at	-0.5
putative ribonucleoprotein similarity to ovarian RNA-binding protein and translational control factor (bruno)- Drosphila melanogaster, EMBL:DMU5	255411_at	-0.5
hypothetical protein	255429_at	-0.5
putative xyloglucan endotransglycosylase ;supported by full-length cDNA: Ceres:17748.	255433_at	-0.5
putative GH3-like protein similar to soybean GH3 auxin-inducible protein, GenBank accession number X60033; supported by cDNA: gi_1664914	255403_at	-0.5
predicted protein of unknown function; supported by cDNA: gi_15810532_gb_AY056305.1_	255332_at	-0.5
coded for by A. thaliana cDNA AA041141 ;supported by full-length cDNA: Ceres:6687.	255290_at	-0.5
contains similarity to S. cerevisiae vacuolar protein sorting-associtaed protein VPS28 (GB:U39205)	255253 at	-0.5
putative protein ADRENODOXIN PRECURSOR (adx1), Rickettsia prowazekii, gb:CAA14664;supported by full-length cDNA: Ceres:17223.	255233_at	-0.5
putative protein hypothetical protein - Arabidopsis thaliana,PIR:F71409;supported by full-length cDNA: Ceres:22715.	255243_at	-0.5
putative protein hypothetical protein sll1775 - Synechocystis sp.,PIR2:S77106	255008_at	-0.5
putative protein beta-phosphoglucomutase - Lactobacillus sanfrancisco,PID:e1331347; supported by cDNA: gi_16648788_gb_AY058171.1_	254874_at	-0.5
putative protein ; supported by cDNA: gi_15292760_gb_AY050814.1_	254561_at	-0.5
aspartate kinase-homoserine dehydrogenase - like protein ak-hsdh bifunctional enzyme precursor, Arabidopsis thaliana, PIR2:S46497	254535_at	-0.5
lectin like protein lectin phloem protein PP2, winter squash, PIR2:S38462;supported by full-length cDNA: Ceres:17437.	254551_at	-0.5
putative protein ; supported by cDNA: gi_14488265_dbj_AB063253.1_AB063253	254306_at	-0.5
putative polygalacturonase polygalacturonase (EC 3.2.1.15) - avocado, EMBL:X66426	254221_at	-0.5
hypothetical protein	254178_at	-0.5
acyl-CoA synthetase - like protein acyl-CoA synthetase, Brassica napus, X94624; supported by cDNA: gi_15146195_gb_AY049239.1_	254192_at	-0.5
clathrin coat assembly like protein clathrin-associated protein AP50 homolog CEAP, Caenorhabditis elegans, PIR2:B49837	254172_at	-0.5
putative protein ;supported by full-length cDNA: Ceres:16463.	254103_at	-0.5

hnRNP-like protein ;supported by cDNA: gi_16930502_gb_AF419605.1_AF419605	253926 at	-0.5
fimbrin-like protein (ATFIM1); supported by cDNA: gi_2905892_gb_U66424.1_ATU66424	253956 at	-0.5
putative protein protein disulfide-isomerase (EC 5.3.4.1) -Aspergillus niger, PID: g899149; supported by cDNA: Ceres: 113279.	253899_at	-0.5
putative protein hypothetical protein F28M11.90 - Arabidopsis thaliana, Pir2:T04067	253836_at	-0.5
putative NADH dehydrogenase NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain NDI1 - yeast, PIR2:S26704;supported by full-length cDNA		-0.5
hypothetical protein	253818 at	-0.5
receptor-like protein kinase 5 precursor (RLK5); supported by cDNA: gi_166849_gb_M84660.1_ATHRLPKC	253779 at	-0.5
protein phosphatase 2C-like protein protein phosphatase 2C-fission yeast, PIR2:S54297; supported by cDNA: gi_16604584_gb_AY059737.1_	253780_at	-0.5
Expressed protein ; supported by cDNA: gi_16226360_gb_AF428378.1_AF428378	253740 at	-0.5
putative protein KIAA0260 gene, human, PID:g1665787; supported by cDNA: gi_14596060_gb_AY042818.1_	253486_at	-0.5
hypothetical protein ;supported by full-length cDNA: Ceres:35221.	253389_at	-0.5
putative protein	253414_at	-0.5
catalase ; supported by cDNA: gi_15451165_gb_AY054663.1_	253174_at	-0.5
beta-galactosidase like protein ; supported by cDNA: gi_15810492_gb_AY056285.1	253090_at	-0.5
squalene epoxidase - like protein squalene epoxidase, Panax ginseng, AB003516;supported by full-length cDNA: Ceres:118648.	253039_at	-0.5
putative protein other Arabidopsis hypothetical proteins; supported by cDNA: gi_15010783_gb_AY045693.1_	252999_at	-0.5
putative transcription factor (MYB4); supported by cDNA: gi_3941411_gb_AF062860.1_AF062860	252958_at	-0.5
auxin-induced protein - like auxin-inducible SAUR gene, Raphanus sativus, AB000708; supported by full-length cDNA: Ceres: 10140.	252972_at	-0.5
calmodulin 7 ; supported by full-length cDNA: Ceres: 7008.	252713 at	-0.5
putative chloroplast prephenate dehydratase similar to bacterial PheA gene products	252652_at	-0.5
Expressed protein ; supported by full-length cDNA: Ceres: 41162.	252624_at	-0.5
phosphoprotein phosphatase ;supported by full-length cDNA: Ceres:32787.	252471_at	-0.5
60S ribosomal protein L13, BBC1 protein ;supported by full-length cDNA: Ceres:12182.	252294_at	-0.5
hypothetical protein ;supported by full-length cDNA: Ceres:35598.	252231_at	-0.5
CDPK-related protein kinase	252158_at	-0.5
protein kinase SPK-2 ;supported by full-length cDNA: Ceres:3988.	252166_at	-0.5
hypothetical protein ;supported by cDNA: gi_13605735_gb_AF361849.1_AF361849	252170_at	-0.5
monodehydroascorbate reductase (NADH) - like protein monodehydroascorbate reductase (NADH), Lycoperison esculentum, PIR:T06407;suppc	252024_at	-0.5
60S ribosomal protein - like 60S ribosomal protein L24, Arabidopsis thaliana, EMBL:AC006282; supported by cDNA: gi_16648705_gb_AY05812	251997_at	-0.5
Gluthatione reductase, chloroplast precursor ; supported by cDNA: gi_15451193_gb_AY054677.1_	251860_at	-0.5
synaptic glycoprotein SC2-like protein synaptic glycoprotein SC2 spliced variant, Homo sapiens, EMBL:AF038958; supported by full-length cDNA	251796_at	-0.5
cytosolic triosephosphatisomerase ;supported by full-length cDNA: Ceres:28516.	251801_at	-0.5
putative protein CHLOROPLAST 30S RIBOSOMAL PROTEIN S20, SWISSPROT:RR20_GUITH; supported by cDNA: gi_15810456_gb_AY0562		-0.5
mandelonitrile lyase-like protein ADHESION OF CALYX EDGES (ACE) - Arabidopsis thaliana; supported by cDNA: gi_15982754_gb_AY057484.	251746_at	-0.5
3-isopropylmalate dehydratase-like protein (small subunit) 3-isopropylmalate dehydratase, small subunit - Thermotoga maritima, PIR:A72363	251524_at	-0.5
putative protein hypothetical protein F6G17.90 - Arabidopsis thaliana, PIR:T04738	251476_at	-0.5
cysteine synthase	251487_at	-0.5
Expressed protein ; supported by full-length cDNA: Ceres: 42545.	251409_at	-0.5
transketolase - like protein transketolase, Solanum tuberosum, EMBL:Z50099;supported by full-length cDNA: Ceres:15659.	251396_at	-0.5
putative protein embryonic abundant protein EMB34 - Picea glauca, EMBL:L47672	251360_at	-0.5
putative protein	251058_at	-0.5
60S ribosomal protein - like 60S ribosomal protein L36, Arabidopsis thaliana, EMBL:AC004684; supported by full-length cDNA: Ceres: 30903.	251018_at	-0.5
putative protein various predicted proteins, Brassica rapa, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 26538.	251013_at	-0.5
putative protein ;supported by full-length cDNA: Ceres:17471.	250969_at	-0.5

putative protein	250944_at	-0.5
monodehydroascorbate reductase (NADH) - like protein monodehydroascorbate reductase (NADH), cucumber, PIR:JU0182;supported by full-ler		-0.5
GTP-binding protein (gb AAD09203.1) ;supported by full-length cDNA: Ceres:6734.	250813 at	-0.5
phosphate/phosphoenolpyruvate translocator protein-like	250743 at	-0.5
26S proteasome regulatory subunit S12 (MOV34 protein) (sp O24412) ;supported by full-length cDNA: Ceres:34868.	250749_at	-0.5
putative protein similar to unknown protein (gb AAF02129.1);supported by full-length cDNA: Ceres:104017.	250734_at	-0.5
putative protein mammalian inositol hexakisphosphate kinase 2 - Homo sapiens, EMBL:AF177145;supported by full-length cDNA: Ceres:32892.	250607 at	-0.5
putative protein similar to unknown protein (sp P23438)supported by full-length cDNA: Ceres:16313.	250209_at	-0.5
receptor-like protein kinase	250102 at	-0.5
putative protein predicted proteins, Arabidopsis thaliana	249982_at	-0.5
unknown protein	249900 at	-0.5
26S proteasome, non-ATPase regulatory subunit ;supported by full-length cDNA: Ceres:23276.	249796_at	-0.5
putative protein similar to unknown protein (pir  T00970); supported by cDNA: gi_15215722_gb_AY050390.1_	249817_at	-0.5
putative protein	249610 at	-0.5
cytochrome b-561 (gb AAD45585.1) ;supported by full-length cDNA: Ceres:124838.	249523_at	-0.5
acyltransferase -like protein Anthocyanin 5-aromatic acyltransferase, Gentiana triflora, EMBL:AB010708; supported by full-length cDNA: Ceres:37		-0.5
raffinose synthase -like protein raffinose synthase Rfs, Cucumis sativus, EMBL:AF073744	249411 at	-0.5
succinate dehydrogenase iron-protein subunit -like succinate dehydrogenase iron-protein subunit (SDHB), Oryza sativa, EMBL:AB017428; suppo		-0.5
dynamin-like protein (pir  S59558) ;supported by full-length cDNA: Ceres:42932.	249232 at	-0.5
AtCLH2 (gb AAF27046.1) ; supported by cDNA: gi_6729676_gb_AF134302.1_AF134302	249091 at	-0.5
putative protein contains similarity to DNA-3-methyladenine glycosylase I;supported by full-length cDNA: Ceres:29551.	249008_at	-0.5
26S proteasome subunit-like protein	248957_at	-0.5
sodium-dicarboxylate cotransporter-like ;supported by full-length cDNA: Ceres:107593.	248756_at	-0.5
putative protein strong similarity to unknown protein (pir/ T05949)	248769_at	-0.5
putative protein contains similarity to adenylate kinase; supported by cDNA: gi_15146327_gb_AY049305.1_	248748 at	-0.5
putative protein contains similarity to salt-inducible protein	248669_at	-0.5
putative protein similar to unknown protein (gb/AAC72543.1)	248676_at	-0.5
pyruvate dehydrogenase E1 component beta subunit, mitochondrial precursor (PDHE1-B) (sp Q38799); supported by cDNA: gi_565064_gb_UC	248474_at	-0.5
phosphoglucomutase (emb CAB64725.1); supported by cDNA: gi_12004569_gb_AF216580.1_AF216580	248380_at	-0.5
putative protein 3 (2), 5 -bisphosphate nucleotidase protein-like; also similar to yeast halotolerance protein HAL2; supported by full-length cDNA:	248155_at	-0.5
serine threonine-specific protein kinase ATPK64 (pir  S20918)	248034_at	-0.5
heat shock protein (emb CAA72514.1)	248043_s_at	-0.5
lycopene epsilon cyclase ; supported by cDNA: gi_14532799_gb_AY040024.1_	247936_at	-0.5
porin-like protein ;supported by full-length cDNA: Ceres:23726.	247923_at	-0.5
eukaryotic initiation factor 4, eIF4-like protein ; supported by cDNA: gi_15810454_gb_AY056266.1_	247839_at	-0.5
putative protein ;supported by full-length cDNA: Ceres:38797.	247702_at	-0.5
histone H2B - like protein histone H2B, Arabidopsis thaliana, PIR:T47538;supported by full-length cDNA: Ceres:20822.	247652_at	-0.5
zinc finger protein - like dof6 zinc finger protein, Arabidopsis thaliana, PIR:T47501;supported by full-length cDNA: Ceres:20852.	247625_at	-0.5
putative protein predicted proteins from various species	247636_at	-0.5
ABC transporter homolog PnATH - like PnATHABC transporter homolog, Populus nigra, EMBL:AB041505	247593_at	-0.5
putative transcription factor MYB28 ; supported by cDNA: gi_5823328_gb_AF175998.1_AF175998	247549_at	-0.5
dehydrogenase ; supported by cDNA: gi_15383743_gb_AY039787.1_	247436_at	-0.5
putative protein strong similarity to unknown protein (emb CAB76911.1)	247362_at	-0.5
G protein-coupled receptor-like protein ; supported by cDNA: gi_15451139_gb_AY054650.1_	247175_at	-0.5

dolichyl-di-phosphooligosaccharide-protein glycotransferase (oligosaccharyltransferase)-like ;supported by full-length cDNA: Ceres:18419.	247058_at	-0.5
porin-like protein ;supported by full-length cDNA: Ceres:12964.	247007_at	-0.5
putative protein predicted protein, Arabidopsis thaliana	246895_at	-0.5
putative protein ; supported by cDNA: gi_14532675_gb_AY039962.1_	246749_at	-0.5
cysteine synthase ;supported by full-length cDNA: Ceres:154690.	246701_at	-0.5
5-enolpyruvylshikimate-3-phosphate (EPSP) synthase, putative similar to 5-enolpyruvylshikimate-3-phosphate (EPSP) synthase GI:2583124 fron	246627_s_at	-0.5
seed maturation -like protein seed maturation protein PM23, Glycine max., EMBL:AF116752;supported by full-length cDNA: Ceres:106301.	246547_at	-0.5
plant adhesion molecule 1 (PAM1) ;supported by full-length cDNA: Ceres:39585.	246482_at	-0.5
putative protein putative N-acetlytransferase F13E7.7 - Arabidopsis thaliana, EMBL:AC018363	246448_at	-0.5
thiol-disulfide interchange like protein	246226_at	-0.5
putative protein	246237_at	-0.5
putative protein predicted protein - Oryza sativa - TREMBL:AP001072_3;supported by full-length cDNA: Ceres:3689.	246026_at	-0.5
putative protein ;supported by full-length cDNA: Ceres:120101.	245948_at	-0.5
tubulin alpha-5 chain-like protein tubulin alpha-5 chain - Arabidopsis thaliana, EMBL:M84698; supported by cDNA: gi_13605804_gb_AF367301.	245915_s_at	-0.5
unknown protein contains similarity to obtusifoliol 14-alpha-demethylase (CYP51) GB:Y09292 GI:1707854 from [Triticum aestivum]; supported by	245795_at	-0.5
phenylalanine ammonia-lyase PAL3	245690_at	-0.5
hypothetical protein	245414_at	-0.5
hypothetical protein ; supported by full-length cDNA: Ceres: 12451.	245368_at	-0.5
glucosyltransferase like protein ; supported by cDNA: gi_2149126_gb_U81293.1_ATU81293	245277_at	-0.5
hydroperoxide lyase (HPOL) like protein ; supported by cDNA: gi_3822402_gb_AF087932.1_AF087932	245253_at	-0.5
kinase like protein ; supported by cDNA: gi_13430671_gb_AF360248.1_AF360248	245260_at	-0.5
Expressed protein ; supported by cDNA: gi_15809953_gb_AY054245.1_	245264_at	-0.5
Expressed protein non-consensus GG donor splice site at exon 1 and 6; CT acceptor splice site at exon 2; supported by cDNA: gi:13605660	245216_at	-0.5
chlorophyll a oxygenase identical to chlorophyll a oxygenase GI:5853117 from [Arabidopsis thaliana]; supported by cDNA: gi_5478806_dbj_AB02	245242_at	-0.5
RNA polymerase beta subunit-1	244998_at	-0.5
PSII D2 protein	245002_at	-0.5
ribosomal protein S11	244979_at	-0.5
	257365_x_at	-0.5
putative hydroxymethyltransferase similar to serine hydroxymethyltransferage GB:P50433 from [Solanum tuberosum]; supported by full-length cDI		-0.5
putative small GTP-binding protein contains an ATP/GTP-binding site motif A (P-loop); contains an ADP-ribosylation factors family signature for p	_	-0.5
unknown protein	265720_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:123128.	265446_at	-0.5
auxilin-like protein similar to GB:CAB40994 from [Arabidopsis thaliana], EST gb AA042488 comes from this gene	262493_at	-0.5
unknown protein ;supported by cDNA: gi_15982794_gb_AY057504.1_	259927_at	-0.5
3-hydroxyisobutyryl-coenzyme A hydrolase - like protein 3-hydroxyisobutyryl-coenzyme A hydrolase, Homo sapiens, U66669;supported by full-le		-0.5
putative protein cellulose synthase, Agrobacterium tumefaciens, PIR2:I39714	253533_at	-0.5
avirulence induced gene (AIG) - like protein AIG2 PROTEIN, Arabidopsis thaliana, SWISSPROT: AIG2_ARATH; supported by cDNA: gi_1433493	_	-0.5
homeotic protein BEL1 homolog ;supported by cDNA: gi_15146192_gb_AY049237.1_	249309_at	-0.5
serine threonine protein kinase ; supported by cDNA: gi_14486383_gb_AY035225.1_	248910_at	-0.5

Table 6: Transcripts suppressed during drought stress compared to unstressed plants	Affimetrix number	log₂ fold supressed
putative protein basic leucine zipper transcription activator shoot-forming PKSF1 - Paulownia kawakamii, EMBL:AF046934;supported by fu		-7.3
glycine-rich RNA-binding protein, putative similar to glycine-rich RNA-binding protein GI:17818 from [Brassica napus]	251575_at 255962 at	-7
putative antifungal protein	257365 x at	-6.8
Unknown protein ; supported by full-length cDNA: Ceres: 28033.	264898 at	-5.9
unknown protein ; supported by full-length cDNA: Ceres:102453.	_	-5.7
	263981_at	
GAST1-like protein similar to GAST1 protein precursor GB:P27057 [Lycopersicon esculentum] (induced by gibberellins, inhibited by ABA PI	_	-5.7 -5.7
pEARLI 1 ; supported by cDNA: gi_871779_gb_L43080.1_ATHPEAR	254805_at	
putative expansin ;supported by full-length cDNA: Ceres:27553.	255822_at	-5.6
ethylene response factor, putative similar to ethylene response factor 1 GB:AAD03544 GI:4128208 from [Arabidopsis thaliana]	260783_at	-5.3
ethylene-responsive element - like protein ethylene-responsive element binding protein homolog, Stylosanthes hamata, EMBL:U91857; sur	_	-5.3
unknown protein	258100_at	-5.2
vegetative storage protein-like ;supported by full-length cDNA: Ceres:27372.	249073_at	-4.9
hypothetical protein predicted by genefinder	266800_at	-4.6
unknown protein ;supported by full-length cDNA: Ceres:9435.	262947_at	-4.6
putative auxin-induced protein similar to SAUR GB:BAA25434 [Raphanus sativus]	259331_at	-4.6
unknown protein	258897_at	-4.6
putative auxin-regulated protein	264016_at	-4.6
Expressed protein ; supported by full-length cDNA: Ceres: 41224.	255969_at	-4.4
thionin Thi2.2 ;supported by full-length cDNA: Ceres:1523.	249645_at	-4.4
unknown protein ;supported by full-length cDNA: Ceres:32647.	265400_at	-4.3
hevein-like protein precursor (PR-4) identical to hevein-like protein precursor GB:P43082 [Arabidopsis thaliana], similar to wound-induced p	258791_at	-4.3
putative auxin-induced protein auxin-induced protein 10A, Glycine max., PIR2:JQ1099	252965_at	-4.3
putative protein auxin-induced protein 6B, mung bean, PIR:T10942	251977_at	-4.3
proline-rich protein other proline-rich proteins	246519_at	-4.3
germin-like protein ; supported by cDNA: gi_14517363_gb_AY039516.1_	246004_at	-4.3
xyloglucan endo-transglycosylase-like protein ;supported by full-length cDNA: Ceres:12301.	247162_at	-4.2
unknown protein	248963 at	-4.2
unknown protein predicted by genscan+;supported by full-length cDNA: Ceres:153279.	258468 <sup>_</sup> at	-4.1
putative protein farnesylated protein GMFP5, Glycine max, EMBL:U64916	247594 at	-4.1
response regulator 6 (ARR6); supported by cDNA; gi 3953600 dbj AB008489.1 AB008489	247406 at	-4.1
myrosinase-associated protein, putative similar to myrosinase-associated protein GI:1769969 from [Brassica napus];supported by full-lengtl		-4
putative protein similar to transcriptional regulator	255298 at	-4
peroxidase ATP19a	254914 at	-4
antifungal protein-like (PDF1.2)	249052 at	-4
unknown protein ; supported by cDNA: gi 15529233 gb AY052241.1	258225 at	-3.9
thionin, putative similar to thionin [Arabidopsis thaliana] GI:1181533; supported by cDNA: gi 14190504 gb AF380652.1 AF380652	256527 at	-3.9
expansin (At-EXP1) identical to expansin (At-EXP1) [Arabidopsis thaliana] GI:1041702;supported by full-length CDNA: Ceres:255048.	256299 at	-3.9
putative protein similar to unknown protein (pir/IS72530);supported by full-length cDNA: Ceres:32925.	248683 at	-3.9
polyneuridine aldehyde esterase-like; also similar to alpha-hydroxynitrile lyase ;supported by full-length cDNA: Ceres:123228.	247814 at	-3.9
conglutin gamma - like protein conglutin gamma precursor, Lupinus angustifolius, PIR:S21426; supported by CDNA: gi 15010797 gb AY0-		-3.8
putative protein similar to unknown protein (pir  T05055)	248047 at	-3.8
Expressed protein ; supported by full-length cDNA: Ceres: 7152.	266658 at	-3.7
delta tonoplast integral protein (delta-TIP) identical to delta tonoplast integral protein (delta-TIP) GB:U39485 [Arabidopsis thaliana] (Plant C	_	-3.7
myb-related protein similar to GI:7981380 from [Lycopersicon esculentum]	256503 at	-3.7
putative polygalacturonase polygalacturonase (EC 3.2.1.15) - avocado, EMBL:X66426	254221 at	-3.7
	254221_at 247474 at	-3.7 -3.7
putative protein predicted proteins, Arabidopsis thaliana	_	
DC1.2 homologue - like protein DC1.2 homologue, Nicotiana tabacum, EMBL:AB009888	247478_at	-3.7 -3.6
hypothetical protein ;supported by full-length cDNA: Ceres:38891.	266805_at	
putative copper/zinc superoxide dismutase identical to GP:3273753:AF061519;supported by full-length cDNA: Ceres:39796.	266165_at	-3.6
hypothetical protein predicted by genefinder; supported by full-length cDNA: Ceres:271253.	265067_at	-3.6
putative gibberellin-regulated protein contains similarity to gibberellin-regulated protein 2 precursor (GAST1) homolog gb U11765 from A. the	204195_at	-3.6

putative protein ;supported by full-length cDNA: Ceres:1336.	250968_at	-3.6
unknown protein	263549_at	-3.5
unknown protein ; supported by full-length cDNA: Ceres: 38378.	259664_at	-3.5
putative pectinesterase contains similarity to pectinesterase GB:AAB57671 [Citrus sinensis]	258764_at	-3.5
putative heat shock transcription factor heat shock transcription factor HSF30 - Peruvian tomato, PIR2:S25480	252081_at	-3.5
putative protein putative DNA-binding protein - Arabidopsis thaliana, EMBL:AC011765;supported by full-length cDNA: Ceres:4734.	249383_at	-3.5
putative protein predicted proteins from various species, Human, yeast, Oryctolagus sp.	247621_at	-3.5
auxin-induced protein, putative similar to SP:P33083 from [Glycine max];supported by full-length cDNA: Ceres:29931.	259784_at	-3.4
putative protein MEL-26, Caenorhabditis elegans, U67737; supported by cDNA: gi_14532781_gb_AY040015.1_	252367_at	-3.4
putative protein ;supported by full-length cDNA: Ceres:16131.	246200_at	-3.4
putative expansin	267158_at	-3.3
putative endoxyloglucan glycosyltransferase identical to GB:D16454;supported by full-length cDNA: Ceres:15276.	266215 at	-3.3
unknown protein location of ESTs est VBVBD05, gb/Z30807 and VBVBD05, gb/Z30808;supported by full-length cDNA: Ceres:39763.	265066_at	-3.3
hypothetical protein predicted by genscan; supported by full-length cDNA: Ceres:6295.	264672 at	-3.3
glutaredoxin, putative similar to glutaredoxin GB:CAA89699 GI:1732424 from [Ricinus communis]; supported by full-length cDNA: Ceres:12!		-3.3
putative helix-loop-helix DNA-binding protein contains Pfam profile: PF00010 Helix-loop-helix DNA-binding domain	260070 at	-3.3
putative lectin similar to lectin SP:P02874 [Onobrychis viciifolia]; contains Pfam profile: PF00139 legume lectins beta domain; supported by	—	-3.3
Expressed protein ; supported by cDNA: gi_14190492 gb_AF380646.1_AF380646	253423 at	-3.3
unknown protein ; supported by full-length cDNA: Ceres:32244.	267034 at	-3.2
expansin AtEx6 identical to GB U30480; supported by full-length cDNA: Ceres: 17914.	266790 at	-3.2
putative pectate lyase similar to pectate lyase 2 GB:AAF19196 [Musa acuminata]; supported by full-length cDNA: Ceres: 124816.	258552 at	-3.2
Expressed protein ; supported by full-length cDNA: Ceres: 42850.	254609 at	-3.2
putative protein hypersensitivity-related hsr201 protein - Nicotiana tabacum.PIR2:T03274	252317 at	-3.2
cotton fiber expressed protein 1-like protein	248205 at	-3.2
glutaredoxin homolog	245506 at	-3.2
<b>o</b>	245506_at 259783 at	-3.2 -3.1
auxin-induced protein, putative similar to SP:P33083 from [Glycine max]; supported by full-length cDNA: Ceres:9311.		-3.1
unknown protein very similar to unknown protein GB:AAC39468 from [Arabidopsis thaliana]; supported by cDNA: gi_14335087_gb_AY0372	_	
receptor-like protein kinase receptor like protein kinase LRK1 - Arabidopsis thaliana, EMBL:ATLECGENE	252596_at	-3.1
response reactor 2 (ATRR2); supported by cDNA: gi_3273197_dbj_AB010916.1_AB010916	252374_at	-3.1
putative serine rich protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:36958.	250327_at	-3.1
	250012_x_at	-3.1
unknown protein ; supported by cDNA: gi_14190416_gb_AF378886.1_AF378886	249894_at	-3.1
Expressed protein ; supported by full-length cDNA: Ceres: 15527.	248509_at	-3.1
putative protein	247754_at	-3.1
unknown protein similar to cell wall-plasma membrane linker protein GB:CAA64425 from [Brassica napus]	256825_at	-3
putative auxin-regulated protein auxin-induced protein X15, Glycine max, PIR2:JQ1097;supported by full-length cDNA: Ceres:10510.	253255_at	-3
1-aminocyclopropane-1-carboxylate synthase - like protein 1-aminocyclopropane-1-carboxylate synthase, Arabidopsis thaliana, S71174; st	253066_at	-3
endo-xyloglucan transferase - like protein endo-xyloglucan transferase, Gossypium hirsutum, D88413;supported by full-length cDNA: Ceres	_	-3
superoxidase dismutase identical to GB:P24704;supported by full-length cDNA: Ceres:33493.	264809_at	-2.9
unknown protein contains helix-loop-helix DNA binding motif	259010_at	-2.9
unknown protein	258419_at	-2.9
putative protein similar to unknown protein (gb AAF63814.1);supported by full-length cDNA: Ceres:40718.	248623_at	-2.9
Isp4-like protein ; supported by full-length cDNA: Ceres: 3109.	247284_at	-2.9
	245866_s_at	-2.9
Expressed protein ; supported by full-length cDNA: Ceres: 102374.	262290_at	-2.8
peptide transporter, putative similar to peptide transporter PTR2-B SP:P46032 [Arabidopsis thaliana (Mouse-ear cress)]; supported by full-le	259839_at	-2.8
auxin-induced protein, putative similar to SP:P33083 from [Glycine max];supported by full-length cDNA: Ceres:147801.	259787_at	-2.8
small auxin up RNA (SAUR-AC1) ;supported by full-length cDNA: Ceres:14973.	252970_at	-2.8
prolin-rich protein, putative similar to prolin-rich protein GI:21045 from [Phaseolus vulgaris]	245688_at	-2.8
hypothetical protein similar to putative purple acid phosphatase precursor GI:7331195 from [Glycine max]	245637_at	-2.8
unknown protein ; supported by cDNA: gi_15294169_gb_AF410276.1_AF410276	266552_at	-2.7
unknown protein	265327_at	-2.7
hypothetical protein similar to putative MADS-box protein GI:4580382 from [Arabidopsis thaliana]	262902_x_at	-2.7

lipase/hydrolase, putative contains Pfam profile: PF00657 Lipase/Acylhydrolase with GDSL-like motif; supported by full-length cDNA: Ceres		-2.7
putative protein CGI-131 protein, Homo sapiens, AF151889;supported by full-length cDNA: Ceres:24573.	254387_at	-2.7
putative protein small auxin up-regulated RNA, Malus domestica, gb:Z93766	253207_at	-2.7
putative protein similar to unknown protein (gb AAF04428.1);supported by full-length cDNA: Ceres:27668.	248028_at	-2.7
putative protein similar to unknown protein (emb CAB62102.1);supported by full-length cDNA: Ceres:40250.	246996_at	-2.7
Expressed protein ; supported by full-length cDNA: Ceres: 30087.	245318_at	-2.7
dynein light chain, putative similar to dynein light chain 1, cytoplasmic SP:Q15701 [Homo sapiens]	257504_at	-2.7
putative PREG1-like negative regulator	266873_at	-2.6
unknown protein ; supported by cDNA: gi_14326466_gb_AF385686.1_AF385686	266460_at	-2.6
unknown protein ; supported by full-length cDNA: Ceres: 29227.	265116_at	-2.6
putative DNA-binding protein (RAV2-like) identical to residues 34-352 of RAV2 GB:BAA34251 (Arabidopsis thaliana); supported by full-lengtl	-	-2.6
plasma membrane intrinsic protein 1c, putative similar to plasma membrane intrinsic protein 1c GI:472875 from [Arabidopsis thaliana]	259431_at	-2.6
acyl carrier - like protein acyl carrier protein, Cuphea lanceolata, PIR2:S42026;supported by full-length cDNA: Ceres:11559.	254102_at	-2.6
putative protein auxin-regulated gene, Vigna radiata	253253_at	-2.6
putative protein many predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_15983504_gb_AF424627.1_AF424627	250110_at	-2.6
putative protein similar to unknown protein (pir  T00970); supported by cDNA: gi_15215722_gb_AY050390.1_	249817_at	-2.6
Expressed protein ; supported by full-length cDNA: Ceres: 36971.	248460_at	-2.6
putative protein auxin-induced basic helix-loop-helix transcription factor, Gossypium hirsutum, EMBL:AF165924; supported by cDNA: gi_15		-2.6
hypothetical protein predicted by genscan	266070_at	-2.5
putative aquaporin (tonoplast intrinsic protein gamma) ;supported by full-length cDNA: Ceres:36633.	263867_at	-2.5
histone H2A ; supported by full-length cDNA: Ceres: 8.	263264_at	-2.5
unknown protein similar to hypothetical protein GB:AAF27090 GI:6730669 from (Arabidopsis thaliana);supported by full-length cDNA: Ceres	262986_at	-2.5
hypothetical protein predicted by genemark.hmm	261684_at	-2.5
chalcone isomerase, putative similar to GI:4126399 from (Citrus sinensis);supported by full-length cDNA: Ceres:116131.	260982_at	-2.5
auxin-induced protein, putative similar to SP:P33083 from [Glycine max]; supported by full-length cDNA: Ceres:4119.	259790_s_at	-2.5
leucine rich repeat protein, putative contains multiple LRR repeats Pfam profile: PF00560; supported by full-length cDNA: Ceres: 29675.	256237_at	-2.5
Expressed protein ; supported by full-length cDNA: Ceres: 38416.	253305_at	-2.5
cytochrome P450 monooxygenase - like protein cytochrome P450 monooxygenase CYP91A2, Arabidopsis thaliana, D78607;supported by	253073_at	-2.5
putative protein hypothetical protein - Arabidopsis thaliana, EMBL:CAB38293;supported by full-length cDNA: Ceres:17840.	252220_at	-2.5
Expressed protein ; supported by full-length cDNA: Ceres: 32396.	251142_at	-2.5
hypothetical protein predicted by grail	266676_s_at	-2.4
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:24933.	260744_at	-2.4
unknown protein contains two Kelch motifs; supported by full-length cDNA: Ceres: 32885.	260287_at	-2.4
putative GDSL-motif lipase/acylhydrolase contains Pfam profile: lipase/acylhydrolase with GDSL-like motif; supported by full-length cDNA: C	258589_at	-2.4
unknown protein ; supported by cDNA: gi_14532647_gb_AY039948.1_	258535_at	-2.4
early auxin-induced protein, IAA19 identical to IAA19 GB:AAB84356 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 942	258399_at	-2.4
putative cytochrome c oxidase subunit Vb similar to cytochrome oxidase IV GB:223590 [Bos taurus]; contains Pfam profile: PF01215 cytoch	258274_at	-2.4
unknown protein ; supported by cDNA: gi_15451205_gb_AY054683.1_	258156_at	-2.4
unknown protein contains similarity to 3-methyladenine-DNA glycosidase I GB:P05100 from [Escherichia coli]; supported by full-length cDNA	257701_at	-2.4
hypothetical protein contains similarity to MtN3(nodulin) protein GB:Y08726 GI:1619601 from [Medicago truncatula]; supported by cDNA: gi_	256548_at	-2.4
unknown protein identical to unknown protein GI:9755444 from (Arabidopsis thaliana); supported by full-length cDNA: Ceres: 110066.	255856_at	-2.4
pEARLI 1-like protein Arabidopsis thaliana pEARLI 1 mRNA, PID:g871780; supported by cDNA: gi_15450470_gb_AY052336.1_	254832_at	-2.4
putative protein hypothetical protein - Arabidopsis thaliana, PIR2:H71441; supported by full-length cDNA: Ceres:4642.	254746_at	-2.4
protein phosphatase - like protein protein phosphatase 2C homolog, Mesembryanthemum crystallinum, EMBL:AF097667	251017_at	-2.4
putative protein microtubule-associated protein homolog, Drosophila melanogaster, EMBL:T13564	249378_at	-2.4
glutaredoxin	245505_at	-2.4
homeobox-leucine zipper protein HAT1 (hd-zip protein 1) ;supported by full-length cDNA: Ceres:34167.	245362_at	-2.4
auxin-induced protein, putative similar to SP:P33083 from [Glycine max]	257506_at	-2.4
unknown protein ;supported by full-length cDNA: Ceres:125631.	267209_at	-2.3
unknown protein Similar to acid phosphatase; Location of ESTs 110C2T7 , gb T42036, and 110C2XP, gb Al100245; supported by cDNA: g	265042_at	-2.3
hypothetical protein predicted by genemark.hmm	263126_at	-2.3
helix-loop-helix protein homolog, putative similar to helix-loop-helix protein homolog GB:BAA87957 GI:6520231 from [Arabidopsis thaliana]	261717_at	-2.3
protein kinase, putative contains similarity to many predicted protein kinases; supported by cDNA: gi_13430527_gb_AF360176.1_AF36017	261308_at	-2.3

hypothetical protein predicted by genemark.hmm	261247_at	-2.3
unknown protein ; supported by full-length cDNA: Ceres: 100293.	260877_at	-2.3
unknown protein contains Pfam profile: PF00561 alpha/beta hydrolase fold	260297_at	-2.3
auxin-induced protein, putative similar to SP:P33083 from [Glycine max]	259773_at	-2.3
hypothetical protein similar to GB:AAB97719 from [Arabidopsis thaliana]	258409_at	-2.3
unknown protein ;supported by full-length cDNA: Ceres:35273.	255817_at	-2.3
putative protein	255652_at	-2.3
heat shock protein - like heat shock protein 17, Triticum aestivum, PIR1:HHWT17;supported by full-length cDNA: Ceres:23223.	254384_at	-2.3
cytochrome P450 monooxygenase-like protein cytochrome P450 monooxygenase - Arabidopsis thaliana, EMBL:D78600	251350 at	-2.3
PGPD14 protein ;supported by full-length cDNA: Ceres:41666.	249862 at	-2.3
unknown protein ;supported by full-length cDNA: Ceres:141953.	249750 at	-2.3
xylosidase	248622 at	-2.3
thioredoxin-like 3 ; supported by cDNA: gi_4973259_gb_AF144389.1_AF144389	247524 at	-2.3
putative protein similar to unknown protein (emb/CAB61744.1); supported by full-length cDNA: Ceres: 31648.	247214 at	-2.3
	245504 at	-2.3
3-hydroxyisobutyryl-coenzyme A hydrolase	267572 at	-2.2
putative auxin transport protein ; supported by cDNA; gi 7109714 gb AF087016.1 AF087016	266300 at	-2.2
predicted by genscan and genefinder ;supported by full-length cDNA: Ceres:120459.	265732 at	-2.2
putative nonspecific lipid-transfer protein precursor ; supported by full-length cDNA: Ceres: 24286.	265656 at	-2.2
unknown protein (supported by full-length cDNA: Ceres:34827.	265387 at	-2.2
nodulin-like protein	265414 at	-2.2
unknown protein ; supported by full-length cDNA: Ceres: 5171.	264343_at	-2.2
	263182 at	-2.2
Expressed protein ; supported by full-length cDNA: Ceres: 27081.	-	-2.2
unknown protein similar to pectinesterase GB:X85216 GI:732912 [Phaseolus vulgaris];supported by full-length cDNA: Ceres:33355.	262844_at	-2.2
acid phosphatase, putative similar to acid phosphatase GI:5360721 from [Lupinus albus]; supported by cDNA: gi_13605749_gb_AF361856	261492_at	
putative elicitor-responsive gene similar to elicitor-responsive gene-3 GB:AAC35866 from [Oryza sativa];supported by full-length cDNA: Ceru	260083_at	-2.2
thaumatin-like protein (PR-5) similar to thaumatin GB:AAD55090 [Vitis riparia]; contains Pfam profile: PF00314 Thaumatin family; supported	_	-2.2
Expressed protein ; supported by full-length cDNA: Ceres: 31015.	259479_at	-2.2
cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450; supported by cDNA: gi_13430717_gb_AF360271.1_AF3602	257636_at	-2.2
gamma tonoplast intrinsic protein nearly identical to gamma tonoplast intrinsic protein 2 (TIP2) GB:AF057137 [Arabidopsis thaliana]; support	257313_at	-2.2
putative protein	255662_at	-2.2
water channel - like protein plasma membrane intrinsic protein 1c, Arabidopsis thaliana, PIR2:S44083;supported by full-length cDNA: Ceres	-	-2.2
putative pectate lyase pectate lyase, Musa acuminata, PATX:E209876;supported by full-length cDNA: Ceres:36681.	254119_at	-2.2
putative protein SPOP, Homo sapiens, AJ000644;supported by full-length cDNA: Ceres:122670.	253061_at	-2.2
putative protein contains similarity to DNA-3-methyladenine glycosylase I;supported by full-length cDNA: Ceres:29551.	249008_at	-2.2
GDSL-motif lipase/hydrolase-like protein ;supported by full-length cDNA: Ceres:18389.	248912_at	-2.2
blue copper binding protein ;supported by full-length cDNA: Ceres:7767.	246099_at	-2.2
Expressed protein ; supported by full-length cDNA: Ceres: 7600.	266500_at	-2.1
unknown protein ;supported by cDNA: gi_15450380_gb_AY052291.1_	266316_at	-2.1
putative microtubule-associated protein ; supported by cDNA: gi_15724331_gb_AF412106.1_AF412106	266106_at	-2.1
unknown protein Location of EST gb T41885 and gb AA395021	264521_at	-2.1
hypothetical protein predicted by grail	264379_at	-2.1
unknown protein	262832_s_at	-2.1
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:157.	260804_at	-2.1
sucrose transport protein SUC1 identical to GB:S38197 from [Arabidopsis thaliana]; supported by cDNA: gi_15146267_gb_AY049275.1_	260143_at	-2.1
AP2-containing DNA-binding protein contains Pfam profile: PF00847 AP2 domain	259793_at	-2.1
putative auxin-induced protein similar to SAUR GB:BAA25434 [Raphanus sativus]	259332_at	-2.1
putative protein kinase similar to ATMRK1, an Arabidopsis protein kinase related to mammal mixed-lineage kinases and Raf protein kinase:	259163_at	-2.1
rhodanese-like family protein contains rhodanese-like domain PF:00581;supported by full-length cDNA: Ceres:30880.	258989_at	-2.1
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:4146.	256796_at	-2.1
Proline-rich APG - like protein proline-rich protein APG, Arabidopsis thaliana, PIR2:S21961;supported by full-length cDNA: Ceres:324.	253736_at	-2.1
putative protein similar to unknown protein (pir  T02514);supported by full-length cDNA: Ceres:117347.	250777_at	-2.1
putative protein similar to unknown protein (gb AAD10689.1); supported by cDNA: gi_14334449_gb_AY034916.1_	249065_at	-2.1
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unknown protein ;supported by full-length cDNA: Ceres:116332.	248646_at	-2.1
integral membrane protein-like	248392_at	-2.1
unknown protein ;supported by full-length cDNA: Ceres:148254.	248282_at	-2.1
putative protein predicted protein, Arabidopsis thaliana	247715_at	-2.1
putative protein similar to unknown protein (gb AAF67766.1);supported by full-length cDNA: Ceres:512.	246997_at	-2.1
hypothetical protein similar to hypothetical protein GB:AAC26673	263293_x_at	-2.1
putative proline-rich protein ; supported by full-length cDNA: Ceres: 28853.	267260_at	-2
unknown protein ; supported by cDNA: gi_15724183_gb_AF411794.1_AF411794	263799_at	-2
class 1 non-symbiotic hemoglobin (AHB1) identical to GP:2581783:U94998;supported by full-length cDNA: Ceres:18195.	263096_at	-2
hypothetical protein predicted be genemark.hmm	262336_at	-2
invertase, putative similar to neutral invertase GB:76145 GI:4200165 from [Daucus carota]	262038_at	-2
auxin-induced protein IAA5, putative similar to auxin-induced protein IAA5 GI:972913 from [Arabidopsis thaliana]	261766_at	-2
expansin S2 precursor, putative similar to GB:U30460 from [Cucumis sativus];supported by full-length cDNA: Ceres:11011.	261226_at	-2
germin-like protein similar to germin precursor GB:P26759 [Triticum aestivum]; contains Pfam profile: PF01072 Germin family; supported by	259892_at	-2
putative calmodulin similar to calmodulin GB:P04352 [Chlamydomonas reinhardtii]; contains Pfam profile: PF00036 EF hand (4 copies); sup	258617_at	-2
unknown protein contains Pfam profile:PF00295 Polygalacturonase;supported by full-length cDNA: Ceres:38575.	258528 at	-2
hypothetical protein	258262 at	-2
putative zinc finger protein contains Pfam profile: PF00641 Zn-finger in Ran binding protein and others; supported by full-length cDNA: Ceres		-2
uknown protein	256633 at	-2
putative protein similar to T5J8.18	255450 at	-2
pEARLI 1-like protein Arabidopsis thaliana pEARLI 1 mRNA, PID:g871780	254818 at	-2
putative pollen surface protein endosperm specific protein - Zea mays, PID:g2104712;supported by full-length cDNA: Ceres:4620.	254785 at	-2
calcium-binding protein - like calcium-binding protein, Solanum tuberosum, gb:L02830	254487 at	-2
putative protein stem-specific protein - Nicotiana tabacum,PID:g20037;supported by full-length cDNA: Ceres:35207.	253874 at	-2
hypothetical protein supported by full-length cDNA: Ceres:18040.	253817 at	-2
putative auxin-induced protein high similarity to auxin-induced protein 15A, soybean, PIR2:JQ1096; supported by cDNA: gi 13194817 gb	_	-2
hypothetical protein	252361 at	-2
putative protein various predicted proteins, Brassica rapa, Arabidopsis thaliana;supported by full-length cDNA: Ceres:26538.	251013 at	-2
polygalacturonase inhibiting protein ;supported by full-length cDNA: Ceres:35527.	250669 at	-2
GASA4 ; supported by cDNA: gi 950098 gb U15683.1 ATU15683	250109 at	-2
putative protein contains similarity to FKBP-type peptidyl-prolyl cis-trans isomerase	248962 at	-2
33 kDa secretory protein-like ; supported by cDNA: gi 15292980 gb AY050924.1	248686 at	-2
putative protein similar to unknown protein (pir  T04819)	248139 at	-2
putative protein similar to unknown protein (pm) (94013) putative protein similar to unknown protein (emb CAB79759.1)	247880 at	-2
putative protein similar to direction protein - Ricinus communis, EMBL:Z81012;supported by full-length cDNA: Ceres:1351.	246919 at	-2
putative protein retinal glutamic acid-rich protein, bovine, PIR:A40437;supported by full-length cDNA: Ceres:24151.	246108 at	-2
AKIN beta1 ; supported by full-length cDNA: Ceres: 41668.	246028 at	-2
glutaredoxin ;supported by full-length cDNA: Ceres: 32219.	245392 at	-2
Expressed protein ; supported by full-length cDNA: Ceres: 6580.	245336 at	-2
putative CCCH-type zinc finger protein identical to GB:U81238;supported by full-length cDNA: Ceres:39893.	266656 at	-1.9
pathogenesis-related PR-1-like protein identical to GB:M90508; supported by cDNA: gi 166860 gb M90508.1 ATHRPRP1A	266385 at	-1.9
unknown protein ;supported by full-length cDNA: Ceres:31665.	265670_s_at	-1.9
Expressed protein ; supported by full-length cDNA: Ceres: 19631.	263318 at	-1.9
putative response regulator 3 similar to ESTs gb[T43772, emb[Z34204, gb]AA067391, and emb[Z34620, implicated in His-to-Asp phosphoti	_	-1.9
	_	
glucose transporter almost identical to glucose transporter GB:P23586 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 3:	_	-1.9
plastid ribosomal protein S6, putative similar to plastid ribosomal protein S6 precursor GB:AAF64311 GI:7582401 from [Spinacia oleracea];	261954_at	-1.9
endo-xyloglucan transferase, putative similar to endo-xyloglucan transferase GI:2244732 from [Gossypium hirsutum]; supported by full-lengt	_	-1.9
transcription factor, putative contains AP2 domain	261327_at	-1.9
TINY-like protein similar to TINY GB:CAA64359 GI:1246403 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:19721.	260856_at	-1.9
serine carboxypeptidase precursor, putative similar to GB:AAD42963 from [Matricaria chamomilla]	260739_at	-1.9
hypothetical protein predicted by genefinder; supported by full-length cDNA: Ceres:99920.	260427_at	-1.9
unknown protein ; supported by full-length cDNA: Ceres: 16614.	259841_at	-1.9
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:6768.	258676_at	-1.9

hypothetical protein predicted by genefinder; supported by full-length cDNA: Ceres: 12509.	256442_at	-1.9
transcriptional activator CBF1, putative similar to transcriptional activator CBF1 GI:1899058 from [Arabidopsis thaliana	255937_at	-1.9
putative protein	255692_at	-1.9
putative xyloglucan endotransglycosylase ;supported by full-length cDNA: Ceres:17748.	255433_at	-1.9
putative protein	254794_at	-1.9
putative protein GATA transcription factor 3, Arabidopsis thaliana, gb:Y13650	253406_at	-1.9
putative protein probable arabinogalactan protein precursor, Lycopersicon esculentum, PIR2:S55925; supported by cDNA: gi_11935087_gl		-1.9
auxin-induced protein - like auxin-inducible SAUR gene, Raphanus sativus, AB000708; supported by full-length cDNA: Ceres: 10140.	252972_at	-1.9
putative gamma-glutamyltransferase gamma-glutamyltransferase, Arabidopsis thaliana, PIR2:S58286	252906_at	-1.9
lipid-transfer protein-like protein nonspecific lipid transfer protein, loblolly pine, PIR:S51816;supported by full-length cDNA: Ceres:8461.	252711_at	-1.9
hypothetical protein	252501_at	-1.9
dUTP pyrophosphatase-like protein dUTP pyrophosphatase - Lycopersicon esculentum,PIR2:JQ1599; supported by cDNA: gi_13878142_c	252442_at	-1.9
receptor protein kinase - like protein CLAVATA1 receptor kinase, Arabidopsis thaliana, EMBL:ATU96879	252272_at	-1.9
putative protein ;supported by full-length cDNA: Ceres:40252.	250936_at	-1.9
putative protein DRT100 protein precursor, Arabidopsis thaliana, PIR:A46260;supported by full-length cDNA: Ceres:41409.	250277_at	-1.9
nodulin-like protein	250217_at	-1.9
putative protein ;supported by full-length cDNA: Ceres:1198.	250098 at	-1.9
glutaredoxin -like protein glutaredoxin, castor bean, PIR:S54825;supported by full-length cDNA: Ceres:92720.	249996 at	-1.9
calcium-binding protein - like cbp1 calcium-binding protein, Lotus japonicus, EMBL:LJA251808; supported by cDNA: gi 16648829 gb AY0	249417 at	-1.9
putative protein similar to unknown protein (pirl/T05073)	248865 at	-1.9
Expressed protein ; supported by cDNA: gi 15809953 gb AY054245.1	245264 at	-1.9
unknown protein ;supported by full-length cDNA: Ceres:23203.	245143 at	-1.9
putative WRKY-type DNA-binding protein ; supported by cDNA: gi 13506742 gb AF224704.1 AF224704	245051 at	-1.9
unknown protein	257381 at	-1.9
putative protein similar to unknown protein (emb CAB67623.1)	250696 at	-1.9
30S ribosomal protein S31 ;supported by full-length cDNA: Ceres:4723.	267088 at	-1.8
unknown protein ;supported by full-length cDNA: Ceres:31586.	267092 at	-1.8
hypothetical protein predicted by genefinder; supported by full-length cDNA: Ceres: 9671.	266334 at	-1.8
	-	-1.8
putative two-component response regulator protein ; supported by cDNA: gi_11870067_gb_AF305721.1_AF305721	266078_at 265471 at	-1.8
putative peroxidase ATP2a ;supported by full-length cDNA: Ceres:3571.	-	
aquaporin (plasma membrane intrinsic protein 2C) water channel protein in plasma membrane; supported by full-length cDNA: Ceres: 11998.		-1.8
hypothetical protein predicted by genscan; supported by cDNA: gi_15724317_gb_AF412099.1_AF412099	265342_at	-1.8
unknown protein	264385_at	-1.8
unknown protein ; supported by full-length cDNA: Ceres: 270281.	264342_at	-1.8
Expressed protein ; supported by full-length cDNA: Ceres: 10388.	264262_at	-1.8
Expressed protein ; supported by full-length cDNA: Ceres: 5586.	264164_at	-1.8
unknown protein ;supported by full-length cDNA: Ceres:641.	263421_at	-1.8
AMP-binding protein, putative contains Pfam profile: PF00501 AMP-binding enzyme	262698_at	-1.8
unknown protein EST gb AA586241 comes from this gene	262488_at	-1.8
S-adenosyl-methionine-sterol-C-methyltransferase, putative almost identical to S-adenosyl-methionine-sterol-C-methyltransferase GI:22464	_	-1.8
delta 9 desaturase identical to delta 9 desaturase GB:BAA25180 GI:2970034 from [Arabidopsis thaliana]; supported by full-length cDNA: Ce	_	-1.8
hypothetical protein predicted by genemark.hmm	260919_at	-1.8
response regulator 5, putative similar to response regulator 5 GI:3953599 from [Arabidopsis thaliana]; supported by cDNA: gi_3953602_dbj	259466_at	-1.8
MtN3-like protein similar to MtN3 GB:CAA69976 from [Medicago truncatula]	258421_at	-1.8
putative delta 9 desaturase similar to delta 9 desaturase GB:BAA25180 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 25205.	258250_at	-1.8
unknown protein ; supported by cDNA: gi_16974601_gb_AY060578.1_	258244_at	-1.8
unknown protein	256828_at	-1.8
unknown protein contains Pfam profile: PF01165 ribosomal protein S21; supported by cDNA: gi_14532553 _gb_AY039901.1_	256753_at	-1.8
unknown protein ;supported by full-length cDNA: Ceres:31357.	256674_at	-1.8
histone H2A, putative similar to histone H2A GB:AAF64418 GI:7595337 from [Arabidopsis thaliana] (Proc. Natl. Acad. Sci. U.S.A. 97 (2), 94	_	-1.8
hypothetical protein, 5 partial	256626 at	-1.8
unknown protein ; supported by full-length cDNA: Ceres:35218.	256522 at	-1.8
zinc-finger protein, putative similar to GI:5262161 from [Arabidopsis thaliana]; supported by cDNA; gi 16323142 gb AY057675.1	256469 at	-1.8
	· · · _ · ·	-

unknown protein ;supported by full-length cDNA: Ceres:28780.	256062 at	-1.8
extensin-like protein extensin-like protein, Zea mays, PIR2:S49915	254770 at	-1.8
extensin-like protein extensin-like protein - maize, PIR2:S49915	254635 at	-1.8
putative protein ; supported by full-length cDNA: Ceres: 37881.	253464 at	-1.8
putative protein predicted protein, Arabidopsis thaliana; supported by full-length cDNA: Ceres:33704.	253043 at	-1.8
histone H2A.F/Z :supported by full-length cDNA: Ceres:33085.	251846 at	-1.8
beta-1,3-glucanase	251673 at	-1.8
anthranilate N-benzoyltransferase - like protein anthranilate N-benzoyltransferase, clove pink, PIR:T10717; supported by cDNA: gi 159122	251144 at	-1.8
putative protein ; supported by cDNA: gi 13358223 gb AF325034.2 AF325034	251036 at	-1.8
6-phosphogluconolactonase-like protein supported by full-length cDNA: Ceres:13806.	249732 at	-1.8
putative protein similar to unknown protein (sp P42404);supported by full-length cDNA: Ceres:15004.	248348_at	-1.8
putative protein similar to unknown protein (pir/ T02893)	248302 at	-1.8
transcription factor Hap5a-like protein	247388_s_at	-1.8
unknown protein ;supported by full-length cDNA: Ceres:108595.	247189_at	-1.8
putative protein contains similarity to pathogenesis-related protein;supported by full-length cDNA: Ceres:2152.	247074_at	-1.8
putative protein predicted protein, Arabidopsis thaliana; supported by full-length cDNA: Ceres:32599.	246550_at	-1.8
bZIP DNA-binding protein-like putative bZIP DNA-binding protein - Capsicum chinense, EMBL:AF127797	246522_at	-1.8
putative protein hypothetical protein F16B3.27 - Arabidopsis thaliana, EMBL:AC021640;supported by full-length cDNA: Ceres:18222.	246505_at	-1.8
hypothetical protein predicted by genemark.hmm	245771_at	-1.8
SUPERMAN like protein	245383_at	-1.8
ethylene responsive element binding factor-like protein (AtERF6) ; supported by cDNA: gi_3298497_dbj_AB013301.1_AB013301	245250_at	-1.8
hypothetical protein predicted by genemark.hmm	264693_at	-1.8
TINY-like transcription factor Contains similarity to transcription factor (TINY) isolog T02O04.22 gb 2062174 from A. thaliana BAC gb AC001	264202_at	-1.8
putative serine carboxypeptidase I ; supported by cDNA: gi_14334757_gb_AY035052.1_	267262_at	-1.7
unknown protein	267116_at	-1.7
E2, ubiquitin-conjugating enzyme 6 (UBC6) identical to gi 431267, SP:P42750, PIR:S52661; contains a ubiquitin-conjugating enzymes activ	266604_at	-1.7
hypothetical protein predicted by genscan	265724_at	-1.7
putative RING zinc finger protein ; supported by cDNA: gi_3790572_gb_AF078824.1_AF078824	264854_at	-1.7
unknown protein	264774_at	-1.7
putative xyloglucan-specific glucanase identical to GB:D63509;supported by full-length cDNA: Ceres:18876.	263598_at	-1.7
unknown protein	262694_at	-1.7
ribosomal protein S9, putative similar to ribosomal protein S9 GI:5456946 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres	262172_at	-1.7
hypothetical protein ;supported by full-length cDNA: Ceres:265772.	259550_at	-1.7
class 2 non-symbiotic hemoglobin identical to class 2 non-symbiotic hemoglobin GB:AAB82770 [Arabidopsis thaliana]; supported by full-len	_	-1.7
unknown protein similar to hypothetical proteins GB:CAB16818, GB:AAD55277	258911_at	-1.7
unknown protein	258462_at	-1.7
indoleacetic acid (IAA)-inducible gene (IAA7) identical to (IAA7) gene GB:U18409 [Arabidopsis thaliana] (J. Mol. Biol. 251 (4), 533-549 (199)		-1.7
unknown protein	257615_at	-1.7
unknown protein	256262_at	-1.7
mitochondrial inner membrane translocase component, putative similar to mitochondrial inner membrane translocase component Tim17a G	_	-1.7
putative protein A. thaliana hypothetical protein F1N20.70, GenBank accession number AL022140;supported by full-length cDNA: Ceres:11	_	-1.7
pollen-specific protein - like 18.3K protein precursor, pollen, Zea mays, PIR2:JQ1107	254620_at	-1.7
cytokinin oxidase - like protein cytokinin oxidase, Zea mays, gb:Y18377; supported by cDNA: gi_15450760_gb_AY054460.1_	253696_at	-1.7
putative protein ENOD16, Medicago truncatula, X99466;supported by full-length cDNA: Ceres:6308.	253480_at	-1.7
SF16 -like protein SF16 protein, pollen specific, helianthus annuus, PIR:T13992;supported by full-length cDNA: Ceres:39013.	252280_at	-1.7
putative protein predicted protein, Arabidopsis thaliana	252250_at	-1.7
expressed protein supported by cDNA: gi:15450891	252048_at	-1.7
SRG1 - like protein SRG1 protein, Arabidopsis thaliana, PIR:S44261	251402_at	-1.7
putative protein putative protein At2g46160 - EMBL:AC005397; supported by cDNA: gi_16226238_gb_AF428280.1_AF428280	251330_at	-1.7
putative protein similar to unknown protein (gb AAF01528.1)	250796_at	-1.7
ubiquinol-cytochrome C reductase complex ubiquinone-binding protein (QP-C)-like protein (gb AAF19563.1)	250800_at	-1.7
histone H3 - like protein histone H3, Arabidopsis thaliana, PIR:S06250	250434_at	-1.7
serine carboxypeptidase II-like protein	249847_at	-1.7

putative protein contains similarity to surface protein; supported by cDNA: gi_16648846_gb_AY058201.1_	249037_at	-1.7
putative protein contains similarity to bZIP transcription factor;supported by full-length cDNA: Ceres:43004.	248606_at	-1.7
unknown protein ;supported by full-length cDNA: Ceres:31129.	248186_at	-1.7
CONSTANS-like B-box zinc finger protein-like ;supported by full-length cDNA: Ceres:6639.	247921_at	-1.7
histone H2A - like protein histone H2A, parsley, PIR:S11498;supported by full-length cDNA: Ceres:20036.	247651_at	-1.7
60S ribosomal protein L26 ;supported by full-length cDNA: Ceres:2561.	247010_at	-1.7
putative protein ;supported by full-length cDNA: Ceres:14064.	245980_at	-1.7
phosphate-induced (phi-1) protein, putative similar to phi-1 GB:BAA33810 GI:3759184 from [Nicotiana tabacum];supported by full-length cE	_	-1.7
hypothetical protein similar to putative disease resistance protein GB:AAC14512 GI:2739389 from [Arabidopsis thaliana]; supported by full-le		-1.7
hypothetical protein ; supported by cDNA: gi_15912320_gb_AY056438.1_	245266_at	-1.7
hypothetical protein similar to hypothetical protein GB:AAF24588 GI:6692123 from [Arabidopsis thaliana]	257467_at	-1.7
putative protein contains similarity to elicitor-inducible receptor-like protein	247087_at	-1.7
omega-3 fatty acid desaturase identical to GB:D26508 and GB:D17579; supported by cDNA: gi_1030693_dbj_D17579.1_ATHFADIER2	266865_at	-1.6
putative RNA-binding protein	266715_at	-1.6
putative plasma membrane intrinsic protein ;supported by full-length cDNA: Ceres:36296.	266533_s_at	-1.6
	266150_s_at	-1.6
hypothetical protein predicted by genefinder; supported by cDNA; gi_13877832_gb_AF370179.1_AF370179	266001_at	-1.6
putative histone H2B ;supported by full-length cDNA: Ceres:31973.	265960_at	-1.6
putative beta-1,3-glucanase	265377_at	-1.6
unknown protein	265265_at	-1.6
unknown protein ;supported by full-length cDNA: Ceres:25136.	264635_at	-1.6
similar to early nodulins	264377_at	-1.6
putative NPK1-related protein kinase 2 similar to nitrate chlorate transporter GB:Q05085 from (Arabidopsis thaliana); supported by cDNA: gi		-1.6
unknown protein Strong similarity to gb D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb H37281,		-1.6
hypothetical protein predicted by genefinder	263674_at	-1.6
unknown protein ; supported by full-length cDNA: Ceres: 17752.	263496_at	-1.6
hypothetical protein	263442_at	-1.6
putative fatty acid elongase ;supported by full-length cDNA: Ceres:115769.	263443_at	-1.6
auxin transport protein REH1, putative similar to auxin transport protein REH1 GI:3377509 from [Oryza sativa]; supported by cDNA: gi_581	-	-1.6
unknown protein ;supported by full-length cDNA: Ceres:21798.	262283_at	-1.6
expansin 10 identical to GB:AAF61712 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:14132.	261266_at	-1.6
plastid ribosomal protein L34 precursor, putative similar to plastid ribosomal protein L34 precursor GB:AAF64157 GI:7578860 from [Spinaci		-1.6
putative trypsin inhibitor ;supported by full-length cDNA: Ceres:15927.	260546_at	-1.6
hypothetical protein predicted by genscan+	260167_at	-1.6
hypothetical protein	259523_at	-1.6
putative phosphate/phosphoenolpyruvate translocator similar to phosphate/phosphoenolpyruvate translocator precursor GB:AAB40648 [Nic	_	-1.6
carbonic anhydrase, chloroplast precursor identical to carbonic anhydrase, chloroplast precursor GB:P27140 [Arabidopsis thaliana]; suppor	_	-1.6
unknown protein ;supported by full-length cDNA: Ceres:22225.	259104_at	-1.6
hypothetical protein similar to calmodulin-like protein GB:CAB42906 [Arabidopsis thaliana]; Pfam HMM hit: EF hand; supported by full-length	_	-1.6
putative oxidoreductase similar to phytoene desaturase GB:P28553 from [Glycine max];supported by full-length cDNA: Ceres:17350.	258708_at	-1.6
proline oxidase, mitochondrial precursor (osmotic stress-induced proline dehydrogenase) identical to GB:P92983 from [Arabidopsis thaliana	_	-1.6
Expressed protein ; supported by full-length cDNA: Ceres: 11616.	257204_at	-1.6
unknown protein ;supported by full-length cDNA: Ceres:20771.; supported by cDNA: gi_10880500_gb_AF195893.1_AF195893	256964_at	-1.6
galactosidase, putative similar to BETA-GALACTOSIDASE PRECURSOR (LACTASE) GB:P48980 from [Lycopersicon esculentum]	256772_at	-1.6
disease resistance protein, putative similar to disease resistance protein RPP1-WsA [Arabidopsis thaliana] GI:3860163; supported by full-le		-1.6
putative ribonucleoprotein similarity to ovarian RNA-binding protein and translational control factor (bruno)- Drosphila melanogaster, EMBL: I putative phi 1 like photophoto induced protein supported by full longth aDNA: Corpor 2552	_	-1.6
putative phi-1-like phosphate-induced protein ;supported by full-length cDNA: Ceres:3552.	255064_at	-1.6
magnesium-protoporphyrin IX methyltransferase - like protein magnesium-protoporphyrin IX methyltransferase, Synechocystis sp, PIR2:S7	_	-1.6
putative calcium-binding protein calcium binding domains (EF hand) of several proteins	252417_at	-1.6
putative protein various predicted proteins	252178_at	-1.6
pectate lyase -like protein pectate lyase, Musa acuminata, EMBL:MAPEL;supported by full-length cDNA: Ceres:119092.	251982_at	-1.6
transport protein subunit - like S61B_ARATH PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT, Arabidopsis thaliana, SWISSPR	_	-1.6
putative protein	250980_at	-1.6

putative protein similar to unknown protein (gb AAB61527.1)	249727_at	-1.6
putative protein predicted protein, Arabidopsis thaliana;supported by full-length cDNA: Ceres:26524.	249379_at	-1.6
unknown protein ;supported by full-length cDNA: Ceres:42577.	249288_at	-1.6
putative protein similar to unknown protein (pir IC71410)	249118_at	-1.6
putative protein similar to unknown protein (gb AAC61815.1);supported by full-length cDNA: Ceres:254442.	248868_at	-1.6
ribosomal protein, chloroplast ribosomal protein PsCL18 precursor, chloroplast - Pisum sativum, PIR:R5PM18; supported by cDNA: gi_145		-1.6
putative protein ;supported by full-length cDNA: Ceres:39563.	245981_at	-1.6
bZIP transcription factor family protein similar to seed storage protein opaque-2(bZIP family)GI:168428 from Zea mays; supported by cDNA	_	-1.6
hypothetical protein ; supported by full-length cDNA: Ceres: 933.	245304_at	-1.6
unknown protein predicted by genscan; supported by cDNA: gi_3822215_gb_AF074948.1_AF074948	245138_at	-1.6
hypothetical protein	252535_at	-1.6
hypothetical protein similar to hypothetical protein GB:AAF19755 GI:6634775 from [Arabidopsis thaliana]	261801_at	-1.6
putative protein lateral root primordia (LRP1) - Arabidopsis thaliana, EMBL:AT24702; supported by cDNA: gi_15450614_gb_AY052675.1_	251900_at	-1.6
myb-like protein isolog	267495_at	-1.5
unknown protein ; supported by cDNA: gi_13877742_gb_AF370134.1_AF370134	267339_at	-1.5
unknown protein ;supported by full-length cDNA: Ceres:6950.	267238_at	-1.5
Expressed protein ; supported by full-length cDNA: Ceres: 124634.	266808_at	-1.5
unknown protein	266813_at	-1.5
putative ethylene response element binding protein (EREBP) ;supported by full-length cDNA: Ceres:6397.	266821_at	-1.5
putative glutathione S-transferase ;supported by full-length cDNA: Ceres:27915.; supported by cDNA: gi_11095995_gb_AF288181.1_AF28.		-1.5
putative chloroplast ribosomal protein L35	266570_at	-1.5
unknown protein	266285_at	-1.5
unknown protein ; supported by cDNA: gi_15027852_gb_AY045783.1_	265773_at	-1.5
beta-expansin ;supported by full-length cDNA: Ceres:109135.	265443_at	-1.5
Expressed protein ; supported by full-length cDNA: Ceres: 38093.	265025_at	-1.5
putative sulphate transporter protein strongly similar to GB:BAA75015, location of EST gb W43788 and gb N96564; supported by cDNA: gi_	_	-1.5
putative metalloproteinase similar to GB:AAB61099	264866_at	-1.5
unknown protein Contains similarity to Rhodococcus amidase (gb D16207). ESTs gb T20504,gb H36650,gb N97423,gb H36595 come from	_	-1.5
putative mutT domain protein putative auxin-induced protein, IAA17/AXR3-1 Identical to Arabidopsis gb/AF040632 and gb/U49073 IAA17/AXR3 gene. ESTs gb/H36782 (	263852_at	-1.5 -1.5
	263498 at	-1.5
unknown protein ; supported by cDNA: gi_6691164_gb_AF218765.1_AF218765 arginine decarboxylase identical to GP:1590814:U52851; supported by cDNA: gi_1590813_gb_U52851.1_ATU52851	263241 at	-1.5 -1.5
hypothetical protein similar to hypothetical protein GB:AAF24593 GI:6692128 from [Arabidopsis thaliana]	262552 at	-1.5
unknown protein ;supported by full-length cDNA: Ceres:12408.	262168 at	-1.5
AP2 domain containing protein, putative similar to AP2 domain containing protein GI:2281633 from [Arabidopsis thaliana]; supported by cD		-1.5
unknown protein	261981 at	-1.5
Expressed protein ; supported by full-length cDNA: Ceres: 19170.	261488 at	-1.5
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:3200.	261456 at	-1.5
unknown protein	261175 at	-1.5
hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 19263.	260983 at	-1.5
hypothetical protein predicted by genemark.hmm	260656 at	-1.5
myb-related protein, putative similar to GB:CAB91874 from [Lycopersicon esculentum]	260664 at	-1.5
homeobox gene 13 protein identical to homeobox gene 13 protein gb/AAF20996.1/AF208044_1 [Arabidopsis thaliana];supported by full-leng		-1.5
hypothetical protein predicted by genefinder	259996 at	-1.5
unknown protein ;supported by full-length cDNA: Ceres:29624.	259979 at	-1.5
thaumatin-like protein similar to thaumatin GB:AAD55090 [Vitis riparia]; contains Pfam profile: PF00314 Thaumatin family; supported by cDt		-1.5
unknown protein ;supported by full-length cDNA: Ceres:21305.	259838 at	-1.5
myb-related transcription factor, putative similar to GI:1430846 from [Lycopersicon esculentum]	259822 at	-1.5
hypothetical protein predicted by genemark.hmm	259398 at	-1.5
DNA-binding protein RAV1 identical to RAV1 GI:3868857 from [Arabidopsis thaliana]; supported by cDNA: gi 3868856 dbj AB013886.1 A	_	-1.5
putative APG protein similar to anter-specific proline-rich protein APG precursor SP:P40602 (Arabidopsis thaliana); contains Pfam profile: P		-1.5
unknown protein identical to GB:AAD56318 (Arabidopsis thaliana)	259211 at	-1.5
unknown protein similar to hypothetical protein GB:AAC17612 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:251012.	259015 at	-1.5
	u	1.0

unknown protein ;supported by cDNA: gi_15081621_gb_AY048203.1_	259020_at -1.5
putative monodehydroascorbate reductase (NADH) similar to monodehydroascorbate reductase (NADH) GB:JU0182 [Cucumis s	sativus]; sur 258941_at -1.5
putative pectin methylesterase similar to pectin methylesterase GB:Q42534 from [Arabidopsis thaliana];supported by full-length of	DNA: Cere 258369_at -1.5
unknown protein	257868_at -1.5
unknown protein ;supported by full-length cDNA: Ceres:96816.	257793_at -1.5
hypothetical protein predicted by genemark.hmm	257697 at -1.5
xyloglucan endotransglycosylase, putative similar to xyloglucan endotransglycosylase 1 GB:CAA10231 from [Fagus sylvatica] (f	Plant Physic 257203 at -1.5
unknown protein	257076 at -1.5
cysteine proteinase contains similarity to cysteine proteinase RD21A (thiol protease) GI:435619, SP:P43297 from [Arabidopsis t	=
beta-1,3-glucanase-like protein strong simlarity to endo-beta-1,3-beta-D-glucosidase. Nicotiana tabacum. PIR2:S46495	254665 at -1.5
putative protein hypothetical protein T8K22.16, Arabidopsis thalianachromosome II BAC T8K22, PATX:G3184285; supported by	_
histone H2A- like protein histone H2A.4, Triticum aestivum, PIR2:S53521; supported by full-length cDNA: Ceres: 927.	253920 at -1.5
putative protein mRNAs from Ricinus communis and Medicago sativa, Z81012 and L36159;supported by full-length cDNA: Cere	_
putative potent minutes non riting communication intercept safety, 201012 and 150139, supported by numering in 5014. Cere putative thaumatin-like protein thaumatin-like protein precursor Mdt1, pathogenesis-related - Malus domestica, PID:q3643249;s	
hypothetical protein ; supported by cDNA: gi_15529203_gb_AY052226.1_	252853 at -1.5
putative protein putative zinc-finger protein - Arabidopsis thaliana,PID:g4406777;supported by full-length cDNA: Ceres:261699.	252352_at -1.5
	_
hypothetical protein	252251_at -1.5 s:36056. 252189 at -1.5
cyclin D3-like protein Nicotiana tabacum NtcycD3-1 - Nicotiana tabacum, EMBL:AB015222;supported by full-length cDNA: Cere	· · · · · · · · · · · · · · · · ·
nucleoid DNA-binding - like protein nucleoid DNA-binding protein cnd41, chloroplast, common tobacco, PIR:T01996; supported	
putative protein unknown protein At2g44130 - Arabidopsis thaliana, EMBL:AC004005;supported by full-length cDNA: Ceres:801	_
unknown protein ;supported by full-length cDNA: Ceres:7709.	251395_at -1.5
LAX1 / AUX1 -like permease	251133_at -1.5
cytochrome P450 90A1 (sp Q42569); supported by full-length cDNA: Ceres: 36334.	250752_at -1.5
putative protein	250376_at -1.5
proline-richh protein predicted protein F24P17.17 - Arabidopsis thaliana, EMBL:AC011623	250002_at -1.5
putative protein similar to unknown protein (gb AAB68039.1);supported by full-length cDNA: Ceres:1076.	248432_at -1.5
putative protein similar to unknown protein (pir  S77140); supported by full-length cDNA: Ceres: 14354.	248285_at -1.5
50S ribosomal protein L24, chloroplast precursor ;supported by full-length cDNA: Ceres:27973.	248174_at -1.5
unknown protein; supported by cDNA: gi 16226274 gb AF428289.1 AF428289	247903 at -1.5
peroxidase ;supported by full-length cDNA: Ceres:124846.	247812 at -1.5
histone H4 - like protein histone H4, Zea mays, PIR:HSZM4;supported by full-length cDNA: Ceres:15418.	247692 s at -1.5
invertase inhibitor homolog (emb[CAA73335.1) ;supported by full-length cDNA: Ceres:25884.	247246 at -1.5
putative protein ;supported by full-length cDNA: Ceres:21085.	246548 at -1.5
sugar transporter like protein	246238 at -1.5
seed imbitition protein-like seed imbitition protein Sip1 - Hordeum vulgare, EMBL:M77475	246114 at -1.5
putative protein predicted proteins - Arabidopsis thaliana; supported by full-length cDNA: Ceres:2537.	245984_at -1.5
putative protein (supported by full-length cDNA: Ceres:42742.	245906 at -1.5
histone H2A, putative similar to histone H2A GI:9758956 from [Arabidopsis thaliana]; supported by cDNA: gi 13877850 gb AF3	_
phytochrome kinase substrate 1 - like protein	245696 at -1.5
pectate lyase like protein pectate lyase -Fragaria x ananassa.PID:g2435395	254754 at -1.5
	_
Expressed protein ; supported by full-length cDNA: Ceres: 30472.	_
calmodulin (cam2)	267064_at -1.4
expressed protein supported by full-length cDNA: Ceres:3350	266950_at -1.4
predicted by genefinder and genscan	266742_at -1.4
unknown protein	266366_at -1.4
putative chlorophyll a/b binding protein ; supported by full-length cDNA: Ceres: 6454.	265722_at -1.4
hypothetical protein similar to putative glucosyltransferase GB:AAD15455 GI:4263795 from (Arabidopsis thaliana)	265175_at -1.4
unknown protein ;supported by full-length cDNA: Ceres:1011.	264590_at -1.4
putative auxin-regulated protein	264014_at -1.4
putative harpin-induced protein ;supported by full-length cDNA: Ceres:19481.	263951_at -1.4
unknown protein	263869_at -1.4
unknown protein ;supported by full-length cDNA: Ceres:11114.	263628_at -1.4
unknown protein	262970_at -1.4
	—

50S ribosomal protein L21 chloroplast precursor (CL21) identical to GB:P51412 GI:1710424 from [Arabidopsis thaliana]; supported by cDN,	262029_at	-1.4
hypothetical protein predicted by genemark.hmm	261772_at	-1.4
Expressed protein ; supported by full-length cDNA: Ceres: 11759.	261638_at	-1.4
regulatory protein HAL3B similar to GB:AAB53106 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 412.	261306_at	-1.4
RAS-related protein ARA-1 identical to SP:P19892 from [Arabidopsis thaliana] (Gene 76:313-319(1989))	261252_at	-1.4
ribosomal protein L11, putative similar to chloroplast ribosomal protein L11 GI:21312 from [Spinacia oleracea]; supported by full-length cDN.	261190_at	-1.4
chloroplast nucleoid DNA binding protein, putative similar to chloroplast nucleoid DNA binding protein GB:BAA22813 GI:2541876 from [Nic	261055_at	-1.4
putative trypsin inhibitor ; supported by cDNA: gi_15292710_gb_AY050789.1_	260551_at	-1.4
unknown protein similar to Ca+2-binding EF hand protein GB:AAB71227 [Glycine max]; supported by full-length cDNA: Ceres:5143.	260208_s_at	-1.4
30S ribosomal protein S17, chloroplast precursor (CS17) identical to 30S ribosomal protein S17, chloroplast precursor GB:P16180 [Arabidc	260165_at	-1.4
unknown protein similar to hypothetical protein GB:CAA10289 [Cicer arietinum]; supported by full-length cDNA: Ceres: 108086.	259272_at	-1.4
unknown protein similar to pop3 peptide GB:AAC26526 from [Populus balsamifera subsp. trichocarpa X Populus deltoides]; supported by ful	258412 at	-1.4
unknown protein ;supported by full-length cDNA: Ceres:8259.	258275 at	-1.4
unknown protein ;supported by full-length cDNA: Ceres:7192.	258183 at	-1.4
protein phosphatase 2A regulatory subunit isoform B delta identical to GB:AAD02810 from [Arabidopsis thaliana]; supported by cDNA: gi 41	258060 at	-1.4
MYB family transcription factor (hsr1), putative identical to myb-like protein GB:AJ007289 [Arabidopsis thaliana] (Plant J. 20 (1), 57-66 (199	257140 at	-1.4
PREG-like protein, putative similar to PREG-like protein GB:AAC32127 from [Picea mariana]	256894 at	-1.4
30S ribosomal protein S20 contains Pfam profile: PF01649 ribosomal protein S20;supported by full-length cDNA: Ceres:24271.	256855 at	-1.4
unknown protein supported by full-length cDNA: Ceres:14433.	256455 at	-1.4
pathogenesis-related group 5 protein, putative similar to pathogenesis-related group 5 protein GI:2749943 from [Brassica rapa]; supported	_	-1.4
putative uroporphyrinogen decarboxylase ; supported by cDNA: gi 14334767 gb AY035057.1	255826 at	-1.4
RING-H2 finger protein RHA1b ;supported by full-length cDNA: Ceres:37097.	254919 at	-1.4
putative pectinacetylesterase protein pectinacetylesterase precursor, Vigna radiata, PIR2:S68805;supported by full-length cDNA: Ceres:34	_	-1.4
photosystem II oxygen-evolving complex protein 3 - like photosystem II oxygen-evolving complex protein 3, Spinacia oleracea, PIR2:S0000		-1.4
hypothetical protein	254137 at	-1.4
Expressed protein ; supported by cDNA: gi 15028040 gb AY045877.1	253827 at	-1.4
pectinesterase - like protein pectinesterase, Prunus persica, X95991; supported by cDNA: gi_14190428_gb_AF378892.1_AF378892	253372 at	-1.4
serine/proline-rich protein	252615 at	-1.4
	252562 s at	-1.4
hypothetical protein	252302_s_at 252345 at	-1.4
putative protein GMFP7 isoprenylated protein, Glycine max., gb:AAD09515;supported by full-length cDNA: Ceres:250092.	2522945_at	-1.4
putative protein giver 7 isoprenylated protein, Glycine max., gb.AAD99515, supported by ruli-length CDIVA. Ceres.250092. putative protein polyphosphoinositide binding protein Ssh2 - Glycine max, PIR:T05953; supported by cDIVA. Ceres.250092.		-1.4
putative protein polyphospholiositide binding protein Ssi2 - Giycline max, Pict. 10995, supported by CDVA. gi_10950462_gb_Ar4 19595. putative protein photosystem II oxygen evolving complex protein 2 precursor (psbP), Fritillariaagrestis, EMBL:AF037458;supported by full-le		-1.4
glutaredoxin -like protein glutaredoxin, castor bean, PIR:S54825	251764_at	-1.4
2-cys peroxiredoxin-like protein (supported by full-length cDNA: Ceres:15640.	250733 at	-1.4
	_	-1.4
putative protein predicted protein, Arabidopsis thaliana	250563_at	-1.4 -1.4
putative protein similar to unknown protein (pir  T41692);supported by full-length cDNA: Ceres:31527.	250097_at	-1.4 -1.4
plastid-specific ribosomal protein 6 precursor (Psrp-6) - like plastid-specific ribosomal protein 6 precursor (Psrp-6), Spinacia oleracea, EMB	250058_at	
Expressed protein ; supported by full-length cDNA: Ceres: 19092.	249778_at	-1.4
unknown protein ;supported by full-length cDNA: Ceres:6393.	249755_at	-1.4
putative protein contains similarity to bHLH DNA-binding protein;supported by full-length cDNA: Ceres:35890.	248839_at	-1.4
small zinc finger-like protein ;supported by full-length cDNA: Ceres:33833.	248473_at	-1.4
putative protein similar to unknown protein (pirl T05752);supported by full-length cDNA: Ceres:109272.	248164_at	-1.4
Expressed protein ; supported by full-length cDNA: Ceres: 17636.	247800_at	-1.4
putative protein various predicted proteins, Arabidopsis thaliana	247563_at	-1.4
50S ribosomal protein L29; supported by full-length cDNA: Ceres: 16740.	247201_at	-1.4
putative protein predicted protein, Arabidopsis thaliana	246584_at	-1.4
hypothetical protein predicted by genemark.hmm	246408_at	-1.4
RP19 gene for chloroplast ribosomal protein CL9 ;supported by full-length cDNA: Ceres:13554.	246339_at	-1.4
putative protein	246270_at	-1.4
hydroxymethylbilane synthase ;supported by full-length cDNA: Ceres:3051.	246033_at	-1.4
Expressed protein ; supported by full-length cDNA: Ceres: 5455.	245334_at	-1.4
AR781, similar to yeast pheromone receptor identical to GB:D88743, corrected a frameshift found in the original record (at 69530 bp), sequ	245041_at	-1.4

	057400	
auxin induced protein, putative similar to AUXIN-INDUCED PROTEIN X10A GB:P33080 from [Glycine max]	257460_at	-1.4
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:117804.	263738_at	-1.4
unknown protein putative ammonium transporter	267400_at 267142_at	-1.3 -1.3
expressed protein supported by cDNA: Ceres:16674; supported by cDNA: gi 13878170 gb AF370348.1 AF370348	267038 at	-1.3
unknown protein	266799 at	-1.3
similar to gibberellin-regulated proteins	266613 at	-1.3
unknown protein identical to GB:AAB82643supported by full-length cDNA: Ceres:17187.	266123 at	-1.3
unknown protein isupported by full-length cDNA: Ceres:1697.	265716 at	-1.3
putative alanine acetyl transferase	265725 at	-1.3
putative autime acctyl transferase putative purine-rich single-stranded DNA-binding protein ; supported by cDNA: gi 15450692 gb AY052714.1	265677 at	-1.3
unknown protein ;supported by full-length cDNA: Ceres:12246.	265593 s at	-1.3
unknown protein	265317 at	-1.3
unknown protein ; supported by full-length cDNA: Ceres: 14111.	265281 at	-1.3
hypothetical protein	265230 s at	-1.3
cytochrome b5, putative similar to cytochrome b5 GI:4240120 from [Arabidopsis thaliana]; supported by cDNA: gi 15146311 gb AY04929		-1.3
putative lipase Similar to nodulins and lipase; location of EST E6C2T7, gb/AA042309. similar to nodulins gi/3328240, gi/2129854 and other	_	-1.3
unknown protein Location of EST gb/T45589;supported by full-length cDNA: Ceres:145854.	264523 at	-1.3
unknown protein similar to ESTs gb[T42386, gb]H36247, gb[N38423, gb]T21830, and gb]AA585725; supported by cDNA: gi_14423427_gb		-1.3
putative glutathione S-transferase TSI-1 similar to glutathione S-transferase (splQ03666/GTX4_TOBAC); similar to EST gb/H36275; support		-1.3
unknown protein ESTs gb T04610, gb N38459, gb T45174, gb R30481 and gb N64971 come from this gene;supported by full-length cDNA	_	-1.3
En/Spm-like transposon protein related to En/Spm transposon family of maize;supported by full-length cDNA: Ceres:41214.	263979 at	-1.3
unknown protein similar to unknown protein GB:AAD24850;supported by full-length cDNA: Ceres:3900.	263179 at	-1.3
putative lipase similar to gb/X02844 lipase precursor from Staphylococcus hylicus. ESTs gb/Al239406 and gb/T76725 come from this gene	262786 at	-1.3
unknown protein location of EST TAT5A03; 5 end, gb/Z26679	262656 at	-1.3
Expressed protein ; supported by full-length cDNA: Ceres: 109156.	262558 at	-1.3
hypothetical protein Pfam	262533 at	-1.3
virus resistance protein, putative similar to virus resistance protein GI:558886 from [Nicotiana glutinosa]	262382 at	-1.3
Expressed protein ; supported by full-length CDNA: Ceres: 102054.	262286 at	-1.3
ribosomal protein L18, putative similar to ribosomal protein L18 GI:3980238 from [Thermotoga maritima]	262235 at	-1.3
dirigent protein, putative similar to dirigent protein GI:6694693 from [Forsythia Intermedia]	261914 at	-1.3
unknown protein	261782 at	-1.3
tubulin alpha-2/alpha-4 chain, putative identical to tubulin alpha-2/alpha-4 chain GB:P29510 from [Arabidopsis thaliana]; supported by cDN/	_	-1.3
defensin AMP1, putative similar to PIR:S66219 from [Clitoria ternatea]	261135 at	-1.3
unknown protein	260635 at	-1.3
putative FKBP type peptidyl-prolyl cis-trans isomerase	260542 at	-1.3
hypothetical protein similar to GB:AAB61488 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:34864.	260411 at	-1.3
unknown protein ; supported by cDNA: gi_15912212_gb_AY056384.1_	260371 at	-1.3
calmodulin-related protein similar to GB:P25070 from [Arabidopsis thaliana], contains Pfam profile: PF00036 EF hand (4 copies);supported	_	-1.3
aquaporin, putative similar to delta tonoplast integral protein GI:1145697 [Arabidopsis thaliana]	259837 at	-1.3
blue copper protein, putative similar to GI:562778 from [Pisum sativum] (Thesis (1994) BIOLOGICAL SCIENCES, DURHAM UNIVERSITY)	_	-1.3
unknown protein ; supported by full-length cDNA: Ceres: 13599.	259660 at	-1.3
unknown protein	259325 at	-1.3
unknown protein similar to putative protein GB:CAB38214 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:6052.	258811 at	-1.3
putative RING zinc finger protein similar to RING-H2 zinc finger protein ATL6 GB:AAD33584 from [Arabidopsis thaliana];supported by full-le	258436 at	-1.3
subtilisin-like serine protease contains similarity to SBT1 GI:1771160 from [Lycopersicon esculentum];supported by full-length cDNA: Ceres		-1.3
unknown protein ; supported by full-length cDNA: Ceres: 21882.	258249 s at	-1.3
putative chlorophyll A-B binding protein similar to chlorophyll A-B binding protein 151 precursor (LHCP) GB:P27518 from [Gossypium hirsut	258239 at	-1.3
50S ribosomal protein L15, chloroplast precursor identical to GB:P25873 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:		-1.3
hypothetical protein similar to hypothetical protein GB:AAF01546 from [Arabidopsis thaliana]	257999 at	-1.3
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:104278.	257751_at	-1.3
blue copper protein, putative similar to uclacyanin I GB:AAC32038 from [Arabidopsis thaliana] (Protein Sci (1996) 5(11):2175-83);supported	_	-1.3
Sm protein, putative similar to GB:AAB62189 from [Homo sapiens], contains Pfam profile: PF01423 Sm protein; supported by full-length cDI	_	-1.3
	-	

Expressed protein ; supported by full-length cDNA: Ceres: 38257.	256979_at	-1.3
unknown protein	256698_at	-1.3
unknown protein	256622_at	-1.3
unknown protein	256433_at	-1.3
RING zinc finger protein contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger)	256446_at	-1.3
unknown protein	256337_at	-1.3
high mobility group protein (HMG1), putative similar to high mobility group protein (HMG1) GI:436423 from [Pisum sativum]	256080_at	-1.3
PSI type II chlorophyll a/b-binding protein, putative similar to PSI type II chlorophyll a/b-binding protein GI:541565 from [Arabidopsis thalian:	256015_at	-1.3
unknown protein ;supported by full-length cDNA: Ceres:12461.	255854_at	-1.3
putative NAM (no apical meristem)-like protein ;supported by cDNA: gi_15294215_gb_AF410299.1_AF410299	255794_at	-1.3
putative hypoersensitive response protein similar to N. tabacum hin1, GenBank accession number Y07563; supported by full-length cDNA: (	_	-1.3
Expressed protein ; supported by full-length cDNA: Ceres: 11649.	254761_at	-1.3
putative protein ;supported by cDNA: gi_14596204_gb_AY042890.1_	254705_at	-1.3
putative protein glycine/proline-rich protein GPRP, Arabidopsis thaliana, PIR2:S65780; supported by full-length cDNA: Ceres: 8188.	254559_at	-1.3
RNA-binding protein RNP-T precursor ; supported by cDNA: gi_15294253_gb_AF410318.1_AF410318	254126_at	-1.3
putative protein pectinesterase - Citrus sinensis, PID:g2098705	254110_at	-1.3
putative protein LEDI-3 protein, Lithospermum erythrorhizon	253909_at	-1.3
amidophosphoribosyltransferase 2 precursor	253252_at	-1.3
Expressed protein ; supported by full-length cDNA: Ceres: 17990.	253045_at	-1.3
putative protein	252603_at	-1.3
putative protein putative hydrolyse - Arabidopsis thaliana, PID:g4191785;supported by full-length cDNA: Ceres:262295.	252433_at	-1.3
syntaxin-like protein synt4 ;supported by full-length cDNA: Ceres:37248.	252053_at	-1.3
uracil phosphoribosyltransferase-like protein uracil phosphoribosyltransferase - Nicotiana tabacum, PIR:T03969;supported by full-length cD	251920 at	-1.3
putative protein 24 kDa seed maturation protein, Glycine max., EMBL:AF004806	251903 <sup>-</sup> at	-1.3
ribosomal protein L17 -like protein ribosomal protein L17, chloroplast, Nicotiana tabacum, PIR:T01744;supported by full-length cDNA: Cere	251883 at	-1.3
responce reactor 4 ; supported by cDNA: gi 3273201 dbj AB010918.1 AB010918	251665 at	-1.3
putative protein hypothetical protein 238 - Porphyra purpurea, PIR:S73123	251519 at	-1.3
putative protein multisynthetase complex auxiliary component p43 - Cricetulus griseus, EMBL:AF021800;supported by full-length cDNA: Ce	251442 at	-1.3
Expressed protein ; supported by full-length cDNA: Ceres: 17055.	251446 at	-1.3
mRNA binding protein precursor - like mRNA binding protein precursor (chloroplast protein), Lycopersicon esculentum, EMBL:AF106660; s		-1.3
putative protein predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres:263168.	250398 at	-1.3
putative protein	250075 at	-1.3
putative protein similar to unknown protein (gb/AAD25141.1);supported by full-length cDNA: Ceres:33455.	248419 at	-1.3
putative protein similar to unknown protein (emb)CAA71173.1)	248322 at	-1.3
putative protein similar to unknown protein (pir [S77462); supported by cDNA: gi 15081647 gb AY048216.1	248287 at	-1.3
putative protein contains similarity to MYB family transcription factor	248246 at	-1.3
unknown protein ;supported by full-length cDNA: Ceres:4309.	248062 at	-1.3
unknown protein	248050 at	-1.3
putative protein non-consensus CG donor splice site at exon 1, GA donor splice site at exon 3, similar to unknown protein (pirl T04268);sup	247933 at	-1.3
putative protein similar to unknown protein (pir  T04254); supported by cDNA: gi_13937150_gb_AF372929.1_AF372929	247946 at	-1.3
TCH4 protein (gb)AAA92363.1); supported by CDNA: gi 14194112 gb AF367262.1 AF367262	247925 at	-1.3
copper transport protein	247745 at	-1.3
ethylene responsive element binding factor - like ethylene responsive element binding factor 5, Arabidopsis thaliana, SWISSPROT:ERF5 /		-1.3
putative protein predicted proteins, Arabidopsis thaliana	247394 at	-1.3
putative protein predicted proteins, Arabidopsis thaliana; supported by cDNA: gi 13877822 gb AF370174.1 AF370174	247407 at	-1.3
putative protein strong similarity to unknown protein (emb/CAB76911.1)	247362 at	-1.3
unknown protein ; supported by full-length cDNA: Ceres: 25655.	247213 at	-1.3
	247192 at	-1.3
histone H3 (sp P05203) ; supported by cDNA: gi_13926210_gb_AF370577.1_AF370577	247 192_at 246644_at	-1.3
putative protein auxin-induced basic helix-loop-helix transcription factor, putative similar to auxin-induced basic helix-loop-helix transcription factor GI:57312		-1.3 -1.3
putative protein ; supported by full-length cDNA: Ceres: 123997.	246396_at 246275 at	-1.3 -1.3
phospholipase - like protein various predicted phospholipase proteins;supported by full-length cDNA: Ceres:253499.	246275_at 246041 at	-1.3
	—	-1.3 -1.3
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:124269.	245840_at	-1.5

endoxyloglucan transferase, putative similar to endoxyloglucan transferase GB:AAD45125 GI:5533313 from [Arabidopsis thaliana]; support	_	-1.3
hypothetical protein ;supported by full-length cDNA: Ceres:2505.	245388_at	-1.3
membrane channel like protein ;supported by full-length cDNA: Ceres:99796.	245399_at	-1.3
putative RNA-binding protein contains Procite RNP1 putative RNA-binding region, similar to GB:AAC33496; supported by cDNA: gi_1360!	_	-1.3
hypothetical protein predicted by genefinder and genscan	260472_at	-1.3
putative protein AtPP - Brassica napus, EMBL:AJ245479	249539_at	-1.3
hypothetical protein ; supported by full-length cDNA: Ceres: 26019.	245317_at	-1.3
30S ribosomal protein S5 ; supported by full-length cDNA: Ceres: 38063.	267435_at	-1.2
60S acidic ribosomal protein P0	267349_at	-1.2
hypothetical protein predicted by genefinder	267161_at	-1.2
unknown protein	267069_at	-1.2
unknown protein	266956_at	-1.2
phytocyanin identical to GB:U90428; supported by full-length cDNA: Ceres: 19760.	266884_at	-1.2
unknown protein ; supported by cDNA: gi_14517479_gb_AY039575.1_	266017_at	-1.2
unknown protein ;supported by full-length cDNA: Ceres:19338.	265895_at	-1.2
unknown protein	265831_at	-1.2
cysteine proteinase contains similarity to cysteine protease SPCP1 GI:13491750 from [Ipomoea batatas]	265665_at	-1.2
unknown protein ;supported by full-length cDNA: Ceres:25812.	265057_at	-1.2
putative glycosyl transferase similar to GB:AAC78704	264857_at	-1.2
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:2118.	264636_at	-1.2
zinc finger protein ATZF1, putative identical to GB:BAA25989; supported by cDNA: gi_3123711_dbj_D89051.1_D89051	264624_at	-1.2
unknown protein predicted by genscan and grail;supported by full-length cDNA: Ceres:14105.	264380_at	-1.2
antigen receptor, putative similar to antigen receptor GI:3982955 from [Ginglymostoma cirratum];supported by full-length cDNA: Ceres:432(	264161 at	-1.2
ethylene reponse factor-like AP2 domain transcription factor	264083_at	-1.2
hypothetical protein predicted by genscan; supported by full-length cDNA: Ceres: 10798.	263535 at	-1.2
nodulin-like protein similar to MtN21 GB:CAA75575 GI:2598575 from [Medicago truncatula] (Mol. Plant Microbe Interact. 9 (4), 233-242 (19		-1.2
unknown protein Location of est 136A23T7 (gb]T45563); supported by full-length cDNA: Ceres: 28177.	262539 at	-1.2
unknown protein EST gb/T21171 comes from this gene	262489 at	-1.2
unknown protein	262092 at	-1.2
hypothetical protein predicted by genemark.hmm	262010 at	-1.2
thioredoxin h, putative similar to thioredoxin h GI:4928460 from [Hevea brasiliensis]:supported by full-length cDNA: Ceres:2054.	261821 at	-1.2
fatty acid elongase 3-ketoacyl-CoA synthase 1 identical to GB:AAC99312 GI:4091810 from [Arabidopsis thaliana]	261570 at	-1.2
Expressed protein ; supported by full-length cDNA: Ceres: 271765.	261318 at	-1.2
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:250127.	261265 at	-1.2
unknown protein similar to unknown protein GB:AAB67633 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:18194.	260895 at	-1.2
integral membrane protein, putative similar to GB:U43629 from [Beta vulgaris] (Plant Physiol. 110 110 (2), 511-520 (1996)); supported by cl	260676 at	-1.2
Cyclin, putative similar to GB:CAB77269 from [Pisum sativum]	260506 at	-1.2
ferredoxin precusor isolog ;supported by full-length cDNA: Ceres:20637.	260481 at	-1.2
unknown protein similar to unknown protein GB:AAC64296 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:2571.	260271 at	-1.2
unknown protein	260103 at	-1.2
phosphatidylinositol synthase (PIS1) identical to phosphatidylinositol synthase (PIS1) GB:AJ000539;supported by full-length cDNA: Ceres:3	· · · · <b>_</b> · ·	-1.2
unknown protein ;supported by full-length cDNA: Ceres:34166.	259856 at	-1.2
unknown protein similar to GB:AADA1433;supported by full-length cDNA: Ceres:146543.	259706 at	-1.2
unknown protein ; supported by cDNA: gi 15028026 gb AY045870.1	259460 at	-1.2
hypothetical protected by generark.hmm; supported by CDNA: gi 16648778 gb AY058166.1	259373 at	-1.2
unknown protein supported by full-length cDNA: Ceres:9221.	259106 at	-1.2
unknown protein similar to hin1 GB:CAA68848 [Nicotiana tabacum]; supported by cDNA: gi 9502173 gb AF264698.1 AF264698	259071_at	-1.2
unknown protein Similar to min OB.OrAdoodo [Nicotana tabacuni], supported by CDNA. gr_socz 173_gb_Ar 2040s0. r_Ar 2040s0	258929 at	-1.2
unknown protein ;supported by full-length cDNA: Ceres:27471.	258641 at	-1.2
unknown protein ;supported by full-length cDNA: Ceres:35949.	258608 at	-1.2
unknown protein ; supported by cDNA: gi 15010765 gb AY045684.1	257894 at	-1.2
polygalacturonase, putative similar to endopolygalacturonase GB:225933 from [Lycopersicon esculentum];supported by full-length cDNA: C		-1.2
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:35773.	257600 at	-1.2
nyponicioal protein protein protein supported by denseant, supported by full-religin contra. Ceres.30773.	237000_at	-1.2

hypothetical protein contains Pfam profile: PF01657 Domain of unknown function; supported by cDNA: gi_14334417_gb_AY034900.1_	257264_at	-1.2
peroxidase, putative similar to peroxidase ATP26a GB:CAA72487 GI:1890317 [Arabidopsis thaliana]; supported by cDNA: gi_14334599_gt	-	-1.2
Expressed protein ; supported by full-length cDNA: Ceres: 31945.	256159_at	-1.2
UDP-glucose glucosyltransferase, putative similar to UDP-glucose glucosyltransferase GI:453245 from [Manihot esculenta];supported by fu		-1.2
ribosomal protein, putative similar to ribosomal protein L35a GI:57118 from [Rattus norvegicus]; supported by full-length cDNA: Ceres: 2774	_	-1.2
hypothetical protein	255978_at	-1.2
hypothetical protein predicted by genscan+	255880_at	-1.2
unknown protein contains similarity to chlorophyllase GI:7415999 from [Chenopodium album]; supported by full-length cDNA: Ceres: 31589.	_	-1.2
acidic ribosomal protein p1 similar to acidic ribosomal protein p1;supported by full-length cDNA: Ceres:26442.	255657_at	-1.2
Expressed protein ; supported by full-length cDNA: Ceres: 11036.	255659_at	-1.2
putative DNA-binding protein ; supported by cDNA: gi_15028172_gb_AY045909.1_	255568_at	-1.2
hypothetical protein similar to pectinesterase	255524_at	-1.2
F-box protein GRR1-like protein 1, AtFBL18 almost identical to GRR1-like protein 1 GI:12658970 from [Arabidopsis thaliana]	255417_at	-1.2
putative protein	255035_at	-1.2
H+-transporting ATP synthase-like protein H+-transporting ATP synthase (EC 3.6.1.34) delta chain precursor, chloroplast - Nicotiana tabaci		-1.2
pectinesterase like protein pectinesterase, Lycopersicon esculentum, PATX:E312172	254363_at	-1.2
xyloglucan endo-1,4-beta-D-glucanase precursor ;supported by full-length cDNA: Ceres:19156.	253666_at	-1.2
hypothetical protein Expressed protein ; supported by full-length cDNA: Ceres: 39326.	253510_at 253384 at	-1.2 -1.2
putative protein hydroxyproline-rich glycoprotein precursor, Nicotiana tabacum, PIR2:S06733; supported by cDNA: gi 15724315 gb AF412		-1.2 -1.2
ras-related small GTP-binding protein ras-related small GTP-binding protein Rho1Ps, garden pea, Pir2:A47525; supported by full-length cD1	_	-1.2 -1.2
putative protein ;supported by full-length cDNA: Ceres:37341.	252876 at	-1.2 -1.2
hypothetical protein ;supported by full-length cDNA: Ceres:123060.	252870_at 252852 at	-1.2
hypothetical protein ,supported by full-length cDNA. Ceres. 123000.	252652_at 252612 at	-1.2
	_	-1.2
histone H2B ;supported by full-length cDNA: Ceres:32930. putative protein several oxidases, mainly gibberellin 20-oxidases	252561_at 252529 at	-1.2
putative protein Several oxidases, mainly globerenin 20-0xidases putative protein DCL PROTEIN, CHLOROPLAST PRECURSOR (DEFECTIVE CHLOROPLASTS AND LEAVES PROTEIN) - Lycopersicon		-1.2
putative protein pectinesterase homolog - Pinus radiata, PIR2:T08112	252437 at	-1.2
putative protein bundle sheath defective protein 2 - Zea mays, EMBL:AF126742; supported by cDNA: gi 13877966 gb AF370246.1 AF37		-1.2
R2R3-MYB transcription factor; supported by cDNA: gi 15983427 gb AF424588.1 AF424588	252193 at	-1.2
putative protein predicted protein, Arabidopsis thaliana	252204 at	-1.2
putative protein protein protein, Arabidopsis manana putative protein hypothetical protein At2q46330 - Arabidopsis thaliana, EMBL:AC006526;supported by full-length cDNA: Ceres:11394.	251281 at	-1.2
putative protein hypothetical protein Al2940500 - Alabidopsis trialiana, Empl. Acoustics, supported by rule-engline CDVA. Ceres, 11354. putative protein polygalacturonase - Lycopersicon esculentum, EMBL:AF118567; supported by cDNA: gi 13358184 gb AF324992.2 AF32	_	-1.2
cytochrome c oxidase subunit 5c-like protein cytochrome c oxidase subunit 5c - Oryza sativa, EMBL:AB027123;supported by full-length cD	_	-1.2
one helix protein (OHP) ;supported by full-length cDNA: Ceres:16704.	251031 at	-1.2
putative protein (supported by full-length cDNA: Ceres:3248.	250924 at	-1.2
putative protein prenylated rab acceptor 1 - Homo sapiens, EMBL:AF112202;supported by full-length cDNA: Ceres:22460.	250663 at	-1.2
putative protein contains similarity to I-box binding factor	250524 at	-1.2
histore H3 - like protein histore H3, Arabidopsis thaliana, PIR:S06250	250433 at	-1.2
putative protein predicted proteins in castor bean, Arabidopsis thaliana and alfalfa.; supported by full-length cDNA: Ceres: 25522.	250366 at	-1.2
24-sterol C-methyltransferase ; supported by cDNA: gi_11066104_gb_AF195648.1_AF195648	250254 at	-1.2
putative protein various predicted proteins, Arabidopsis thaliana	250160 at	-1.2
putative protein similar to unknown protein (spIP50027);supported by full-length cDNA: Ceres:17002.	250079 at	-1.2
putative protein PGPD14 - Petunia x hybrida, EMBL:AF049930	250000 at	-1.2
putative protein glycine-rich protein GRP22, rape, PIR:S31415	249969 at	-1.2
Expressed protein ; supported by full-length cDNA: Ceres: 32450.	249719 at	-1.2
putative protein predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres:249321.	249422 at	-1.2
putative protein predicted proteins, Arabidopsis thaliana	249382 at	-1.2
putative protein similar to unknown protein (dbj/BAA92898.1);supported by full-length cDNA: Ceres:97314.	249230 at	-1.2
	248943 s at	-1.2
putative protein similar to unknown protein (pir  T04426);supported by full-length cDNA: Ceres:27099.	248951 at	-1.2
60S acidic ribosomal protein P1-like protein supported by full-length cDNA: Ceres:14401.	248768 at	-1.2
unknown protein	248387_at	-1.2

histone H2A (gb AAF64418.1); supported by full-length cDNA: Ceres: 4875.	248175 at	-1.2
unknown protein	247878 at	-1.2
structural protein - like glycine-rich cell wall structural protein 1 precursor, Oryza sativa, PIR:KNRZG1;supported by full-length cDNA: Ceres	_	-1.2
expressed protein similar to unknown protein (gb/AAF03448.1); supported by full-length CDNA: Ceres: 97900.	247258 at	-1.2
unknown protein ; supported by full-length cDNA: Ceres: 20274.	247211 at	-1.2
unknown protein supported by full-length cDNA: Ceres:25419.	247149 at	-1.2
unknown protein	246989 at	-1.2
putative protein hypothetical protein T20O10.160 - Arabidopsis thaliana, EMBL:AL163816	246553 at	-1.2
putative protein unknown protein F14P3.18 - Arabidopsis thaliana. EMBL:AC009755	246562 at	-1.2
unknown protein	246321 at	-1.2
transcriptional co-activator-like protein putative transcriptional co-activator (KIWI) - Arabidopsis thaliana, EMBL:AF053302	245930 at	-1.2
RNA-binding glycine-rich protein, putative similar to RNA-binding glycine-rich protein (RGP-1a) GI:436789 from [Nicotiana sylvestris]	245778 at	-1.2
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:20991.	245666 at	-1.2
Expressed protein ; supported by full-length cDNA: Ceres; 21980.	245642 at	-1.2
CCAAT-binding transcription factor subunit A(CBF-A)	245592 at	-1.2
cysteine proteinase inhibitor like protein ; supported by full-length cDNA: Ceres: 31946.	245323 at	-1.2
putative protein contains EST gb:T4504800	245229 at	-1.2
unknown protein predicted by genscan	245165 at	-1.2
hypothetical protein	244965 at	-1.2
hypothetical protein predicted by genemark	257543 at	-1.2
disease resistance protein, putative similar to disease resistance protein GB:AAC78591 GI:3894383 [Lycopersicon esculentum]	256620_at	-1.2
putative LIM-domain protein	267355 at	-1.1
similar to cold acclimation protein WCOR413 [Triticum aestivum]	267288 at	-1.1
hypothetical protein predicted by genefinder	266899 at	-1.1
unknown protein ; supported by cDNA: gi 14423465 gb AF386970.1 AF386970	266887 at	-1.1
hypothetical protein predicted by genscan	266893 at	-1.1
putative chloroplast RNA binding protein precursor; supported by cDNA: gi 14596022 gb AY042799.1	266642 at	-1.1
unknown protein ; supported by cDNA: gi_15912210_gb_AY056383.1_	266479 at	-1.1
unknown protein ;supported by cDNA: gi_14334561_gb_AY035185.1_	266329 at	-1.1
putative rac GTPase activating protein	266324_at	-1.1
putative tropinone reductase; supported by cDNA: gi 14334839 gb AY035093.1	266265 at	-1.1
histone H4 identical to GB:M17133 and GB:M17132;supported by full-length cDNA: Ceres:32642.	266226_at	-1.1
putative adenylate kinase ;supported by full-length cDNA: Ceres:15831.	265958_at	-1.1
putative cytidine deaminase ;supported by full-length cDNA: Ceres:152285.	265943_at	-1.1
putative fatty acid elongase	265918_at	-1.1
putative RNA-binding glycine rich protein (RGP-2) ;supported by full-length cDNA: Ceres:18569.	265641_at	-1.1
unknown protein ; supported by full-length cDNA: Ceres: 25575.	265459_at	-1.1
auxin-regulated protein (IAA8) ;supported by full-length cDNA: Ceres:37274.	265319_at	-1.1
50S ribosomal protein L3 ;supported by full-length cDNA: Ceres:142861.	265247_at	-1.1
unknown protein ; supported by full-length cDNA: Ceres: 12055.	265149_at	-1.1
hypothetical protein predicted by genefinder	265083_at	-1.1
unknown protein weak similarity to C3HC4 zinc finger;supported by full-length cDNA: Ceres:156298.	265023_at	-1.1
hypothetical protein contains similarity to MHC class II antigen GI:9502037 from [Aotus nancymaae]; supported by full-length cDNA: Ceres:1	265001_at	-1.1
unknown protein similar to gb T45484, emb Z30724, and emb Z30531	264824_at	-1.1
unknown protein similar to ESTs gb AA605440 and gb H37232;supported by full-length cDNA: Ceres:30716.	264834_at	-1.1
Expressed protein ; supported by full-length cDNA: Ceres: 17126.	264725_at	-1.1
putative chloroplast 50S ribosomal protein, L6 Similar to Mycobacterium RlpF (gb Z84395). ESTs gb T75785,gb R30580,gb T04698 come f	264575_at	-1.1
Expressed protein ; supported by full-length cDNA: Ceres: 2681.	264096_at	-1.1
putative DOF zinc finger protein ;supported by full-length cDNA: Ceres:16423.	264056_at	-1.1
Expressed protein ; supported by full-length cDNA: Ceres: 38277.	264004_at	-1.1
Expressed protein ; supported by full-length cDNA: Ceres: 15689.	263712_at	-1.1
putative protein kinase C inhibitor (Zinc-binding protein) Similar to gb/Z29643 protein kinase C inhibitor (PKCI) from Zea mays and a member	263701_at	-1.1
unknown protein	263515_at	-1.1

putative glutathione peroxidase ;supported by full-length cDNA: Ceres:25550.	263426_at	-1.1
60S ribosomal protein L14 ;supported by full-length cDNA: Ceres:15198.	263372_at	-1.1
putative anthranilate N-hydroxycinnamoyl/benzoyltransferase ;supported by full-length cDNA: Ceres:105546.	263382_at	-1.1
unknown protein Belongs to PF 00583 Acetyltransfersase (GNAT) family; supported by full-length cDNA: Ceres: 10117.	263113_at	-1.1
unknown protein EST gb F13926 comes from this gene;supported by full-length cDNA: Ceres:21943.	262791_at	-1.1
unknown protein location of ESTs 144D22XP 3, gb AA404877 and 144D22T7, gb T75757;supported by full-length cDNA: Ceres:5665.	262612_at	-1.1
unknown protein similar to hypothetical protein GB:AAF24587 GI:6692122 from [Arabidopsis thaliana]; supported by cDNA: gi_16604307_gi	262559_at	-1.1
lysine and histidine specific transporter, putative similar to lysine and histidine specific transporter GI:2576361 from [Arabidopsis thaliana]	262434_at	-1.1
unknown protein ;supported by full-length cDNA: Ceres:95546.	262396_at	-1.1
hypothetical protein similar to hypothetical protein GI:9294146 from [Arabidopsis thaliana]	262236_at	-1.1
unknown protein	262245_at	-1.1
AP2 domain containing protein, putative similar to AP2 domain containing protein RAP2.1 GI:2281627 from [Arabidopsis thaliana]	262211_at	-1.1
ubiquitin-fusion protein, putative similar to ubiquitin-fusion protein GI:9725 from [Manduca sexta]; supported by full-length cDNA: Ceres:346(	_	-1.1
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:2030.	262159_at	-1.1
adenine phosphoribosyltransferase almost identical to adenine phosphoribosyltransferase GI:1402894 from [Arabidopsis thaliana]	262039_at	-1.1
unknown protein similar to putative DNA-binding protein GI:6714399 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:9234	261942_at	-1.1
unknown protein ; supported by full-length cDNA: Ceres: 32430.	261791_at	-1.1
	261728_at	-1.1
unknown protein contains Pfam profile: PF00255 glutathione peroxidases;supported by full-length cDNA: Ceres:30238.	261530_at	-1.1
histone H2B identical to GB:CAA73156 from [Arabidopsis thaliana] (Plant Physiol. 115 (4), 1385-1395 (1997)); supported by full-length cDN.	261411_at	-1.1
Expressed protein ; supported by full-length cDNA: Ceres: 21406.	261254_at	-1.1
unknown protein ; supported by cDNA: gi_15028364_gb_AY045985.1_	261019_at	-1.1
mitochondrial NAD-dependent malate dehydrogenase identical to mitochondrial NAD-dependent malate dehydrogenase GI:3929649 from [/	260615_at	-1.1
60S ribosomal protein L38	260538_at	-1.1
unknown protein similar to hypothetical protein GB:AAD12705 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:40506.	260179_at	-1.1
hypothetical protein	260051_at	-1.1
unknown protein ; supported by full-length cDNA: Ceres: 14237.	259909_at	-1.1
hypothetical protein ;supported by full-length cDNA: Ceres:19640.	259863_at	-1.1
thylakoid-bound ascorbate peroxidase identical to thylakoid-bound ascorbate peroxidase GB:CAA67426 [Arabidopsis thaliana]; supported by		-1.1
putative serine/threonine kinase ; supported by cDNA: gi_15010571_gb_AY045587.1_	259538_at	-1.1
unknown protein contains similarity to copper zinc superoxide dismutase GI:5689611 from (Arabidopsis thaliana); supported by cDNA: gi_1{	—	-1.1
unknown protein unknown protein similar to unknown protein GB:AAC62613 [Arabidopsis thaliana]; supported by cDNA: gi 14532567 gb AY039908.1	259434_at	-1.1 -1.1
putative dehydrogenase contains Pfam profiles: PF00106 short chain dehydrogenase, PF00678 short chain dehydrogenase reductase C-te	259018_at	-1.1
	258938 at	-1.1
germin-like protein similar to germin type 2 GB:S71254 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:19265. putative disease resistance protein similar to disease resistance protein RPP1-WsC GB:AAC72979 [Arabidopsis thaliana]; supported by cDI	258537 at	-1.1 -1.1
unknown protein ;supported by full-length cDNA: Ceres:4861.	258480 at	-1.1
photosystem I subunit VI precursor identical to GB:CAB52749 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:9633.	258285_at	-1.1
putative 2Fe-2S iron-sulfur cluster protein contains Pfam profile: PF00111 2Fe-2S iron-sulfur cluster binding domains; supported by cDNA: (	258055 at	-1.1
hypothetical protein predicted genemark; supported by full-length cDNA: Ceres:255040.	258025_at 258021 at	-1.1
unknown protein ; supported by full-length cDNA: Ceres: 105122.	257300 at	-1.1
NADPH:quinone oxidoreductase (NQR) nearly identical to NADPH:quinone oxidoreductase (NQR) GB:AF145234 [Arabidopsis thaliana]; su	257228 at	-1.1
unknown protein ; supported by full-length cDNA: Ceres: 5176.	257171 at	-1.1
hypothetical protein predicted by genscan	256427 at	-1.1
unknown protein	256396 at	-1.1
hypothetical protein ; supported by full-length cDNA: Ceres: 107260.	256383 at	-1.1
unknown protein ;supported by full-length cDNA: Ceres:19056.	256215 at	-1.1
phosphoglycerate kinase, putative similar to phosphoglycerate kinase [Nicotiana tabacum] GI:1161600; supported by cDNA: gi 15810504	-	-1.1
sterol-C-methyltransferase identical to sterol-C-methyltransferase GI:1061040 from [Arabidopsis thaliana]; supported by cDNA: gi_10010004_		-1.1
	255908 s at	-1.1
hypothetical protein redicted by genefinder and genscan; supported by full-length cDNA: Ceres: 15024.	255824 at	-1.1
60S ribosomal protein L23 ;supported by full-length cDNA: Ceres:28563.	255789 at	-1.1
plastid protein identical to GB:Z86094; supported by full-length cDNA: Ceres: 8717.	255791_at	-1.1
	u	

putative protein RING-H2 finger protein RHA1a, Arabidopsis thaliana,AF078683	255802_s_at	-1.1
unknown protein similar to beta-1,3-glucanase-like protein GI:9758115 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:32	_	-1.1
putative transcription factor ; supported by cDNA: gi_15450989_gb_AY054575.1_	255538_at	-1.1
putative protein	255134_at	-1.1
ribosomal protein L13a like protein ribosomal protein L13a -Lupinus luteus,PID:e1237871; supported by cDNA: gi_15529277_gb_AY05226	_	-1.1
putative protein Cyclic beta-1-3-glucan synthase, Bradyrhizobium japonicum, AF047687	254773_at	-1.1
HhoA protease precursor, putative identical to putative protease HhoA precursor [Arabidopsis thaliana] SP:Q9SEL7 GI:6690272 (unpublish		-1.1
fatty acid hydroxylase - like protein fatty acid hydroxylase Fah1p, Arabidopsis thaliana, PID:g2736147; supported by cDNA: gi_14994242_g	_	-1.1
Expressed protein ; supported by full-length cDNA: Ceres: 23587.	254429_at	-1.1
Ribosomal protein L7Ae - like NHP2/RS6 FAMILY PROTEIN, Homo sapiens, PID:g4826860	254355_at	-1.1
extensin - like protein hybrid proline-rich protein, Zea mays, PIR2:JQ1663	254314_at	-1.1
predicted protein predicted protein ERG25, Saccharomyces cerevisiae, PIR2:S64354	254333_at	-1.1
putative protein extensin, Catharanthus roseus, D86853	254093_at	-1.1
putative acidic ribosomal protein acidic ribosomal protein P3a - maize, PIR2:T02037	254030_at	-1.1
Expressed protein ; supported by cDNA: gi_16612239_gb_AF439821.1_AF439821	253973_at	-1.1
putative protein ; supported by cDNA: gi_15810482_gb_AY056280.1_	253925_at	-1.1
putative protein ;supported by full-length cDNA: Ceres:10077.	253814_at	-1.1
putative protein ; supported by full-length cDNA: Ceres: 2891.	253670_at	-1.1
putative protein ;supported by full-length cDNA: Ceres:2508.	253440_at	-1.1
putative protein various predicted proteins; supported by full-length cDNA: Ceres: 17912.	253233 at	-1.1
vacuolar H+-transporting ATPase 16K chain ;supported by full-length cDNA: Ceres:24998.	253200 <sup>-</sup> at	-1.1
putative protein AP2 domain containing protein RAP2.4, Arabidopsis thaliana	252859 at	-1.1
putative protein CLATHRIN COAT ASSEMBLY PROTEIN AP180 - Mus musculus, SWISSPROT:Q61548;supported by full-length cDNA: C	_	-1.1
putative protein	252661 at	-1.1
putative chloroplast prephenate dehydratase similar to bacterial PheA gene products	252652 at	-1.1
putative protein CDP-alcohol phosphatidyltransferase - Schizosaccharomyces pombe, EMBL:CAB16578	252540 at	-1.1
hypothetical protein ; supported by CDNA: gi 13605735 gb AF361849.1 AF361849	252170_at	-1.1
putative LEA protein Picea glauca late embryogenesis abundant protein (EMB8), PID:g1350545;supported by full-length cDNA: Ceres:367(		-1.1
hypothetical protein hypothetical protein - Arabidopsis thaliana chromosome 4 AP2 contig, PID:e35223;supported by full-length cDNA: Cen		-1.1
40S ribosomal protein S21 homolog ribosomal protein S21, cytosolic - Oryza sativa, PIR:S38357;supported by full-length cDNA: Ceres:268		-1.1
pectate lyase - like protein pectate lyase, Musa acuminata, X92943	251864 at	-1.1
putative protein predicted pectate-lyase, Arabidopsis thaliana, PIR:T06728	251810 at	-1.1
synaptic glycoprotein SC2-like protein synaptic glycoprotein SC2 spliced variant, Homo sapiens, EMBL:AF038958;supported by full-length	-	-1.1
protein kinase C inhibitor-like protein protein kinase C inhibitor - Zea mays, PIR:S45368; supported by full-length cDNA: Ceres: 28847.	251707 at	-1.1
E2 ubiquitin-conjugating-like enzyme Ahus5 ; supported by cDNA: gi 14596100 gb AY042838.1	251561 at	-1.1
beta-glucosidase-like protein several beta-glucosidases - different species; supported by cDNA: gi 15028300 gb AY045953.1	251427 at	-1.1
	_	-1.1
putative protein hypothetical proteins - Arabidopsis thaliana putative protein chloroplast ribosome recycling factor protein - Spinacia oleracea, EMBL:AJ133751; supported by cDNA: gi 13926251 gb	251241_s_at	-1.1
	_	
putative protein several protein kinases - different species	251068_at	-1.1
RIBOSOMAL PROTEIN S28- like ribosomal protein S28, Arabidopsis thaliana, EMBL:ATRP28A	250895_at	-1.1
unknown protein	250857_at	-1.1
serine-type carboxypeptidase II-like protein carboxypeptidase D - Triticum aestivum, PIR:A29639; supported by cDNA: gi_13877962_gb_Al		-1.1
14-3-3 protein GF14lambda (grf6/AFT1) identical to 14-3-3 GF14lambda GI:1345595 from [Arabidopsis thaliana]; supported by cDNA: gi_14	_	-1.1
putative protein predicted proteins, Arabidopsis thaliana	250353_at	-1.1
2-oxoglutarate/malate translocator precursor -like protein 2-oxoglutarate/malate translocator precursor, spinach, SWISSPROT:SOT1_SPIO	_	-1.1
expressed protein contains similarity to ABC transporter, ATP-binding protein;supported by full-length cDNA: Ceres:151943.	250198_at	-1.1
putative protein predicted protein, Arabidopsis thaliana	250168_at	-1.1
putative protein proline-rich protein APG, Arabidopsis thaliana, PIR:S21961	250043_at	-1.1
putative protein similar to unknown protein (gb AAF32471.1)	249659_s_at	-1.1
putative protein similar to unknown protein (gb AAF03445.1)	249332_at	-1.1
RING zinc finger protein-like ;supported by full-length cDNA: Ceres:207148.	249306_at	-1.1
auxin-induced protein AUX2-11 (sp P33077)	249109_at	-1.1
unknown protein ;supported by full-length cDNA: Ceres:16944.	249120_at	-1.1

ethylene responsive element binding factor 5 (ATERF5) (sp O80341); supported by cDNA: gi_14326511_gb_AF385709.1_AF385709	248799_at	-1.1
putative protein similar to unknown protein (pir  T04431);supported by full-length cDNA: Ceres:26264.	248329_at	-1.1
putative protein strong similarity to unknown protein (pir  T05748); supported by cDNA: gi_15010657_gb_AY045630.1_	248177_at	-1.1
putative protein similar to unknown protein (gb AAC83072.1)	248004_at	-1.1
Expressed protein ; supported by full-length cDNA: Ceres: 39314.	247899_at	-1.1
porin-like protein ;supported by full-length cDNA: Ceres:23726.	247923_at	-1.1
Expressed protein ; supported by full-length cDNA: Ceres: 267411.	247882_at	-1.1
similar to unknown protein (sp P72777)	247862_at	-1.1
arabinogalactan protein - like arabinogalactan protein Pop14A9, Populus alba x Populus tremula, EMBL:AF183809; supported by full-length	247638_at	-1.1
40S ribosomal protein S28 (sp P34789) ;supported by full-length cDNA: Ceres:36501.	247267_at	-1.1
putative protein strong similarity to unknown protein (emb CAB89350.1)	247240_at	-1.1
unknown protein ; supported by cDNA: gi_13877834_gb_AF370180.1_AF370180	247177_at	-1.1
putative protein similar to unknown protein (pir  T08445);supported by full-length cDNA: Ceres:11651.	246952_at	-1.1
acetyltransferase-like protein Glucosamine-6-phosphate acetyltransferase EMeg32 protein - Mus musculus, EMBL:AJ001006	246518 at	-1.1
dirigent protein, putative similar to dirigent protein GI:6694699 from [Thuja plicata]	246395_at	-1.1
ribosomal protein L10-like ribosomal protein L10- Nicotiana tabacum, EMBL:AB010879;supported by full-length cDNA: Ceres:29083.	245852 <sup>_</sup> at	-1.1
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:42217.	245755 at	-1.1
unknown protein ;supported by full-length cDNA: Ceres:24560.	245665 at	-1.1
hypothetical protein	245574 at	-1.1
hypothetical protein :supported by full-length cDNA: Ceres:30327.	245396 at	-1.1
Lil3 protein :supported by full-length cDNA: Ceres:29150.	245354 at	-1.1
Expressed protein ; supported by full-length cDNA: Ceres: 14223.	245370 at	-1.1
putative protein ; supported by cDNA: gi 13926241 gb AF372879.1 AF372879	245309 at	-1.1
isp4 like protein ; supported by cDNA: gi 15451019 gb AY054590.1	245296 at	-1.1
F12A21.4 similar to iEP4 gb[AAD11468.1	245215 at	-1.1
F12A21.6 hypothetical protein	245193 at	-1.1
F12A21.13 putative photosystem II Core Complex sp[049347]PSBY_ARATH; similar to ESTs gb[BE523181, db][AV531372.1, db][AV52782		-1.1
ribosomal protein S16	245049 at	-1.1
hypothetical protein	245019 at	-1.1
	244922 s at	-1.1
unknown protein	257536 at	-1.1
rhodanese-like family protein ;supported by full-length cDNA: Ceres:1382.	267635 at	-1
Expressed protein ; supported by full-length cDNA: Ceres: 27620.	267591_at	-1
putative ribosomal protein S27 ;supported by full-length cDNA: Ceres:18662.	267507 at	-1
unknown protein	267239 at	-1
putative transport protein ;supported by full-length cDNA: Ceres:26825.	267219 at	-1
putative transport protein (supported by full-length block. Celes.2002). putative protein kinase contains a protein kinase domain profile (PDOC00100)	266946 at	-1
hypothetical protein predicted by genscan; supported by cDNA: gi_15146245_gb_AY049264.1_	266889 at	-1 -1
	266890 at	-1 -1
acyl carrier protein identical to GB:L23574; supported by cDNA: gi_15450374_gb_AY052288.1_	266684 at	-1 -1
40S ribosomal protein S15A	_	-1 -1
profilin 1 ; supported by cDNA: gi_1353769_gb_U43325.1_ATU43325	266701_at	
unknown protein ; supported by full-length cDNA: Ceres: 41621.	266587_at	-1
putative proline-rich protein ; supported by cDNA: gi_13265425_gb_AF324669.2_AF324669	266588_at	-1
unknown protein	266352_at	-1
calmodulin identical to GB:L18912; supported by cDNA: gi_166650_gb_M38380.1_ATHCAM2	266317_at	-1
Expressed protein ; supported by full-length cDNA: Ceres: 112146.	266264_at	-1
putative PREG1-like negative regulator	266124_at	-1
putative lipid transfer protein	265894_at	-1
unknown protein	265883_at	-1
putative sugar transporter ;supported by full-length cDNA: Ceres:114959.	265768_at	-1
putative phosphatidic acid phosphatase ;supported by full-length cDNA: Ceres:19163.	265737_at	-1
hypothetical protein predicted by genscan	265704_at	-1
60S ribosomal protein L27	265730_at	-1

putative glycine-rich protein ;supported by cDNA: gi_15215617_gb_AY050337.1_	265511_at	-1
putative RING-H2 zinc finger protein ;supported by full-length cDNA: Ceres:7201.	265472_at	-1
putative thioredoxin M ;supported by cDNA: gi_6539611_gb_AF095751.1_AF095751	265476_at	-1
unknown protein ;supported by full-length cDNA: Ceres:34875.	265415_at	-1
unknown protein ;supported by cDNA: gi_16648715_gb_AY058134.1_	265226_at	-1
unknown protein ; supported by full-length cDNA: Ceres: 39285.	265219_at	-1
unknown protein similar to hypothetical protein GI:9665091 from [Arabidopsis thaliana]	264998_at	-1
hypothetical protein ;supported by full-length cDNA: Ceres:250028.	264870_at	-1
unknown protein similar to ESTs emb Z27038, gb AA451546, emb Z29876, gb T45359 and gb R90316;supported by full-length cDNA: Cere	264837_at	-1
unknown protein similar to EST gb H37293;supported by full-length cDNA: Ceres:7188.	264808_at	-1
unknown protein similar to putative glycosyl transferase GI:7268597 from [Arabidopsis thaliana]; supported by cDNA: gi_13878002_gb_AF3	264704_at	-1
Expressed protein ; supported by full-length cDNA: Ceres: 108558.	264579_at	-1
unknown protein ;supported by full-length cDNA: Ceres:24255.	263901_at	-1
unknown protein ;supported by full-length cDNA: Ceres:24885.	263920_at	-1
Expressed protein ; supported by full-length cDNA: Ceres: 97088.	263842_at	-1
unknown protein ; supported by full-length cDNA: Ceres: 34035.	263631_at	-1
Expressed protein ; supported by cDNA: gi_13926282_gb_AF372895.1_AF372895	263632 at	-1
60S ribosomal protein L39	263585 at	-1
CONSTANS-like B-box zinc finger protein ;supported by full-length cDNA: Ceres:17434.	263537 at	-1
unknown protein	263438 at	-1
putative glutaredoxin Strong similarity to gb/Z49699 glutaredoxin from Ricinus communis	263168 at	-1
putative photosystem I reaction center subunit II precursor Strong similarity to gb/X14017 from Spinacia oleracea. ESTs gb/R30423, gb/T42	263114 at	-1
putative bZIP transcription factor contains a bZIP transcription factor basic domain signature (PDOC00036); supported by cDNA: gi_143350	263064 at	-1
unknown protein	262868 at	-1
hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 19759.	262878 at	-1
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:109912.	262711 at	-1
putative ubiquinolcytochrome-c reductase Similar to gb X79273 cytochrome c reductase hinge protein subunit from Solanum tuberosum. E	-	-1
unknown protein Contains a PF/00175 Oxidoreductase FAD/NADH-binding domain. ESTs gb/H76345 and gb/AA651465 come from this ger		-1
putative amino acid transporter Very similar to amino acid transporter AAT1 [Arabidopsis thaliana] (gi/1076291)	262522 at	-1
Expressed protein ; supported by full-length cDNA: Ceres: 103581.	262443 at	-1
flax rust resistance protein, putative similar to flax rust resistance protein GI:4588066 from [Linum usitatissimum]; supported by full-length c	_	-1
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:5052.	262285 at	-1
Expressed protein ; supported by full-length cDNA: Ceres: 5864.	262000 at	-1
hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 38293.	261940 at	-1
unknown protein ; supported by full-length cDNA: Ceres: 30167.	261790 at	-1
plastocyanin identical to plastocyanin Gl:1865683 from [Arabidopsis thaliana]	261769 at	-1
hypothetical protein predicted by genemark.hmm	261742 at	-1
unknown protein	261572_at	-1
ribonucleoprotein, putative similar to 33 KDA RIBONUCLEOPROTEIN GB:P19684 from [Nicotiana sylvestris]; supported by full-length cDN/	261577 at	-1
glutaredoxin, putative similar to glutaredoxin GI:2244924 from [Arabidopsis thaliana]; supported by cDNA; gi 13358219 gb. AF325030.2 A	-	-1
putative calcium-binding protein, calreticulin similar to SP:P12858 from [Arabidopsis thaliana]	261197 at	-1
unknown protein ; supported by cDNA: gi 17063164 gb AY062103.1	261213 at	-1
dihydrolipoamide S-acetyltransferase, putative similar to GI:5881963 from (Arabidopsis thaliana) (Plant Physiol. 120 (2), 443-452 (1999));st		-1
unknown protein identical to SP:OS0061 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:12704.	261078 at	-1
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi 14334897 gb AY035122.1	260968 at	-1
Expressed protein ; supported by full-length CDNA: Ceres: 17110.	260685 at	-1
hypothetical protection predicted by genemark.hmm;supported by full-length cDNA: Ceres:95383.	260651 at	-1
ACC oxidase, putative similar to ACC oxidase GI:587086 from [Brassica oleracea]; supported by cDNA: gi_15028038_gb_AY045876.1_	260637 at	-1
	260522 x at	-1
AtHVA22c identical to AtHVA22c GB:AF141661 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:108964.	260368 at	-1
putative aminolevulinate dehydratase similar to aminolevulinate dehydratase GB:1097877 [Lycopersicon esculentum]; supported by cDNA:		-1
putative dolichyl-phosphate mannosyltransferase polypeptide 2 similar to dolichyl-phosphate mannosyltransferase polypeptide 2 GB:450336		-1
putative denergy prospriate mannes/radioendee polypeptade 2 similar to denergy prospriate mannes/radioendee polypeptade 2 cb.+ocode putative histone H2A similar to histone H2A GB:CAA73155 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 10668.	260154 at	-1
	20010al	1

inner mitochondrial membrane protein identical to inner mitochondrial membrane protein GB:U18126 [Arabidopsis thaliana]; supported by ful	_	-1
photosystem I subunit VI precursor identical to photosystem I subunit VI precursor [Arabidopsis thaliana] GI:5734524; supported by full-lengt		-1
unknown protein similar to GB:AAB81674 [Arabidopsis thaliana]	259763_at	-1
putative AUX1-like permease similar to AUX1 (regulator of root gravitropism, putative permease) GB:CAA67308 [Arabidopsis thaliana]; sup	259680_at	-1
unknown protein ; supported by cDNA: gi_13937162_gb_AF372935.1_AF372935	259665_at	-1
Expressed protein ; supported by full-length cDNA: Ceres: 42300.	259603_at	-1
putative GAR1 protein similar to GB:P28007 from [Saccharomyces cerevisiae]; supported by full-length cDNA: Ceres: 10984.	259347_at	-1
putative 2-cys peroxiredoxin BAS1 precursor (thiol-specific antioxidant protein) similar to 2-cys peroxiredoxin BAS1 precursor (thiol-specific	_	-1
unknown protein predicted by genefinder, single est match	259247_at	-1
putative ribose 5-phosphate isomerase identical to putative ribose 5-phosphate isomerase GB:AAD57010 (Arabidopsis thaliana); similar to	259098_at	-1
unknown protein similar to hin1 GB:CAA68848 [Nicotiana tabacum];supported by full-length cDNA: Ceres:8166.	259102_at	-1
putative ribosomal protein S28 similar to ribosomal protein S28 GB:P34789 [Arabidopsis thaliana]	258937_at	-1
putative serine carboxypeptidase II similar to serine carboxypeptidase II (CP-MII) GB:CAA70815 [Hordeum vulgare]; supported by full-length	_	-1
putative wound-induced basic protein similar to wound-induced basic protein GB:Q09020 [Phaseolus vulgaris] (Plant Physiol. 101 (4), 1409	_	-1
unknown protein ; supported by cDNA: gi_15028124_gb_AY046012.1_	258728_at	-1
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:21672.	258742_at	-1
unknown protein ;supported by full-length cDNA: Ceres:15303.	258394_at	-1
AIG2-like protein similar to AIG2 protein GB:P54121 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:28511.	258002_at	-1
hypothetical protein similar to hypothetical protein GB:AAD50054 from [Arabidopsis thaliana]	257964_at	-1
unknown protein ;supported by full-length cDNA: Ceres:32010.	257831_at	-1
translational inhibitor protein, putative similar to GB:NP_005827 from [Homo sapiens], contains Pfam profile: PF01042 Domain of unknown	257674_at	-1
unknown protein ;supported by full-length cDNA: Ceres:36370.	257003_at	-1
calmodulin, putative similar to GB:P07463 from [Paramecium tetraurelia] (Cell 62 (1), 165-174 (1990))	256755_at	-1
glutamine synthetase, putative similar to glutamine synthetase [Raphanus sativus] GI:1526564; supported by full-length cDNA: Ceres:2662.	256524_at	-1
unknown protein ; supported by full-length cDNA: Ceres: 148308.	256456_at	-1
integral membrane protein, putative similar to GI:1209755 from [Beta vulgaris] (Plant Physiol. 110 110 (2), 511-520 (1996)); supported by cl	256458_at	-1
guanine nucleotide-binding protein, putative similar to guanine nucleotide-binding protein GI:9294068 from [Arabidopsis thaliana]; supporter		-1
Expressed protein ; supported by full-length cDNA: Ceres: 11843.	255968_at	-1
putative chloroplast 50S ribosomal protein L28 ;supported by full-length cDNA: Ceres:31633. unknown protein similar to unknown protein GI:6714347 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:103226.	255850_at 255733_at	-1 -1
	_	-1 -1
Expressed protein ; supported by cDNA: gi_4741922_gb_AF130849.1_AF130849 putative protein disulfide isomerase	255511_at 255061_at	-1 -1
DNA-binding protein (supported by full-length cDNA: Ceres:28019.	255037 at	-1
Expressed protein ; supported by full-length cDNA: Ceres: 266299.	254505 at	-1 -1
hypothetical protein ; supported by full-length cDNA: Ceres:6848.	254356 at	-1
predicted protein	254303 at	-1
PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT -like PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT, ORYZ	_	-1
putative ribosomal protein S10 40S ribosomal protein S10 - Lumbricus rubellus, PID:e1329701; supported by cDNA: gi 14334535 gb AY0	_	-1
putative ribosomal protein ribosomal protein L31, Nicotiana glutinosa, U23784;supported by full-length cDNA: Geres:14013.	254012 at	-1
fructose-bisphosphate aldolase - like protein fructose-bisphosphate aldolase, Arabidopsis thaliana, PIR1:ADMU;supported by full-length cD	_	-1
Expressed protein ; supported by cDNA: gi_15809977_gb_AY054257.1_	253877 at	-1
carbohydrate kinase - like protein phosphofructokinase, Babesia canis, AJ223322;supported by full-length cDNA: Ceres:799.	253858 at	-1
hypothetical protein ;supported by full-length cDNA: Ceres:42155.	253856 at	-1
putational protein population protein	253802 at	-1
photosystem II protein W - like photosystem II protein W, Porphyra purpurea, PIR2:S73268; supported by full-length cDNA: Ceres: 2419.	253790 at	-1
glycine-rich protein like glycine-rich protein 5 - Arabidopsis thaliana,PIR2:JQ1064; supported by full-length cDNA: Ceres: 33435.	253754 at	-1
putative protein "supported by full-length cDNA" Ceres:8077.	253562 at	-1
putative protein predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres:34819.	253421 at	-1
putative protein (fragment) calcineurin B, Naegleria gruberi, gb;U04380	253412 at	-1
putative protein dihydrokaempferol 4-reductase (EC 1.1.1.219) -Synechocystis, PIR2:S75325; supported by cDNA: gi 13926212 gb AF37	253334 at	-1
putative protein endothelin converting enzyme, Bos primigenius taurus, PIR2:146078	253256 at	-1
Expressed protein is supported by full-length CDNA: Ceres: 279.	253234 at	-1
RING-H2 finger protein RHA3b ;supported by full-length cDNA: Ceres:31493.	253140_at	-1
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DnaJ-like protein DnaJ-like protein, Phaseolus vulgaris, PATX:G1684851	253125_at	-1
acidic ribosomal protein P2 -like acidic ribosomal protein P2, maize, PIR:S54179	252643_at	-1
RNA binding protein -like COLD-INDUCIBLE RNA-BINDING PROTEIN, Homo sapiens, SWISSPROT:CIRP_HUMAN	252559_at	-1
hypothetical protein	252418_at	-1
putative protein pectinesterase - Arabidopsis thaliana, PIR:S51370; supported by cDNA: gi_14517535_gb_AY039603.1_	252406_at	-1
Expressed protein ; supported by cDNA: gi_16323485_gb_AY059131.1_	252328_at	-1
hypothetical protein various predicted proteins, Arabidopsis thaliana	252205_at	-1
UTP-glucose glucosyltransferase - like protein UTP-glucose glucosyltransferase, Manihot esculenta, PIR:S41951; supported by cDNA: gi_1	252183_at	-1
LS1-like protein AT-LS1 product - Arabidopsis thaliana, EMBL:X58827;supported by full-length cDNA: Ceres:107294.	252076_at	-1
transcription factor NF-Y, CCAAT-binding - like protein transcription factor NF-Y, CCAAT-binding, Zea mays, PIR:S22820	251991_at	-1
plasma membrane intrinsic protein 2a ;supported by full-length cDNA: Ceres:38965.	251962_at	-1
histone H4-like protein several histone H4 proteins;supported by full-length cDNA: Ceres:13571.	251924_at	-1
putative protein	251788_at	-1
putative protein MtN24, Medicago truncatula, EMBL:MTY15290;supported by full-length cDNA: Ceres:6434.	251795 at	-1
proline transporter 2	251752 at	-1
putative protein	251720 <sup>-</sup> at	-1
putative protein unknown protein 110K5.12 - Sorghum bicolor, TREMBL:AF124045 5;supported by full-length cDNA: Ceres:142358.	251704 at	-1
putative protein hypothetical proteins At2q44600 - Arabidopsis thaliana, EMBL:AAC27462	251459 at	-1
hypothetical protein	251414 at	-1
putative protein several hypothetical proteins; supported by full-length cDNA: Ceres:29280.	251285 at	-1
putative protein hypothetical protein AT4q29780 (F27B13.20) - Arabidopsis thaliana, EMBL:AL050352; supported by cDNA: gi 13878074 (		-1
	250942 at	-1
leucoanthocyanidin dioxygenase-like protein ;supported by full-length cDNA: Ceres:13012.	250793 at	-1
putative protein similar to unknown protein (gb/AD23015.1)	250682 x at	-1
putative protein similar to unknown protein (gr)/(122010.1)	250683_x_at	-1
thioredoxin-like; supported by cDNA: gi 4973263 gb AF144391.1 AF144391	250649 at	-1
unknown protein	250595 at	-1
putative protein 23 kDa polypeptide of water-oxidizing complex of photosystem II, Nicotiana tabacum, EMBL:NT23WOP2B	250335_at 250371 at	-1
putative protein zo noa polypeptide of water-oxidizing complex of photosystem it, Nicotiana tabacum, EMBE.N125WO12D	250265 at	-1
putative protein predeted proteins, Anabidopsis manana putative protein ;supported by full-length cDNA: Ceres:12170.	250189 at	-1
ribosomal protein precursor - like ribosomal protein S13 precursor, chloroplast Arabidopsis thaliana, PIR:S59594; supported by cDNA: gi 1-	—	-1
high affinity nitrate transporter - like protein high affinity nitrate transporter, Oryza sativa, EMBL:AB008519; supported by cDNA: gi 143347{		-1
putative protein predicted protein, Arabidopsis thaliana	249919 at	-1
	249919_at 249929 at	-1
unknown protein unknown protein	249929_at 249932 at	-1
		-1 -1
ATP-dependent Clp protease proteolytic subunit (ClpP2), putative similar to SP:Q9X6W8 ATP-dependent Clp protease proteolytic subunit (		-1 -1
squalene monooxygenase 1,2 (squalene epoxidase 1,2) (se 1,2) (sp O65402)	249775_at	-1 -1
unknown protein	249776_at	
acyltransferase -like protein Anthocyanin 5-aromatic acyltransferase, Gentiana triflora, EMBL:AB010708; supported by full-length cDNA: Ce		-1
hypothetical protein	249355_at	-1
zinc finger - like protein predicted protein, Drosophila melanogaster, EMBL:AE003589	249370_at	-1
putative protein similar to unknown protein (pir  T00965);supported by full-length cDNA: Ceres:777.	249076_at	-1
unknown protein	249004_at	-1
unknown protein ; supported by cDNA: gi_13926304_gb_AF372903.1_AF372903	248975_at	-1
putative protein contains similarity to plastid ribosomal protein L19;supported by full-length cDNA: Ceres:30034.	248798_at	-1
Expressed protein ; supported by full-length cDNA: Ceres: 28462.	248762_at	-1
putative protein similar to unknown protein (pir  T08406)	248614_at	-1
putative protein contains similarity to DNA binding protein PCF1;supported by full-length cDNA: Ceres:247645.	248385_at	-1
putative protein contains similarity to 40S ribosomal protein S10;supported by full-length cDNA: Ceres:91769.	248331_at	-1
putative protein similar to unknown protein (pir  T04792)	248085_at	-1
putative protein contains similarity to GPI-anchored protein	247996_at	-1
unknown protein	247959_at	-1
60S ribosomal protein L12 - like 60S RIBOSOMAL PROTEIN L12 (like), Arabidopsis thaliana, PIR:T45883;supported by full-length cDNA: (	247584_at	-1

putative protein predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 16638.	247585_at	-1
dihydroneopterin aldolase-like protein	247409_at	-1
photosystem I reaction centre subunit psaN precursor (PSI-N) (sp P49107); supported by cDNA: gi_1237123_gb_U32176.1_ATU32176	247320_at	-1
unknown protein ;supported by full-length cDNA: Ceres:10032.	247328_at	-1
arabinogalactan-protein (gb AAC77823.1); supported by full-length cDNA: Ceres:25423.	247279_at	-1
14-3-3 protein GF14kappa (grf8) identical to 14-3-3 protein GF14 kappa GI:5802794, SP:P48348 from [Arabidopsis thaliana], supported by		-1
homeobox-leucine zipper protein ATHB-5 (HD-zip protein ATHB-5) (sp]P46667) ; supported by cDNA: gi_13358240_gb_AF325054.2_AF32	_	-1
putative protein similar to unknown protein (emb CAB66916.1);supported by full-length cDNA: Ceres:9323.	247109_at	-1
apospory-associated protein C-like	247101_at	-1
putative protein similar to unknown protein (gb AAD20709.1)	247102_at	-1
putative protein similar to unknown protein (pir  T05276); supported by cDNA: gi_15292834_gb_AY050851.1_	247049_at	-1
unknown protein ;supported by full-length cDNA: Ceres:9946.	247009_at	-1
putative protein ferroportin1, Mus musculus, EMBL:AF226613	246847_at	-1
transmembrane protein FT27/PFT27-like ;supported by full-length cDNA: Ceres:12993.	246619_at	-1
putative protein hypothetical protein T26J14.6 - Arabidopsis thaliana, EMBL:AC011915; supported by cDNA: gi_13358202_gb_AF325010.2		-1 -1
minor allergen ;supported by full-length cDNA: Ceres:35084.	246201_at	
lipophosphoglycan biosynthetic protein - like lipophosphoglycan biosynthetic protein (LPG2), Leishmania donovani, TREMBL:LD26175	246143_at	-1 -1
putative protein predicted proteins from various species; supported by full-length cDNA: Ceres: 17786.	246156_at 246034 at	-1 -1
putative protein FH protein interacting protein FIP1, Arabidopsis thaliana, EMBL:AF174428;supported by full-length cDNA: Ceres:19508.	—	-1 -1
putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:19897. putative protein 22kDa peroxisomal membrane protein-like - Homo sapiens, EMBL:AF250136;supported by full-length cDNA: Ceres:6789.	246000_at 245937_at	-1 -1
	245957_at 245853 at	-1 -1
putative protein predicted protein At2g25260 - Arabidopsis thaliana, EMBL:AC007070; supported by full-length cDNA: Ceres:6674. hypothetical protein predicted by genscan+; supported by cDNA: gi 16323183 gb AY057696.1	245776 at	-1 -1
disease resistance RPP5 like protein (fragment)	245450 at	-1 -1
hypothetical protein	245414 at	-1 -1
Expressed protein ; supported by full-length cDNA: Ceres: 7101.	245337 at	-1 -1
cytochrome f	245020 at	-1
hypothetical protein predicted by genfinder	267586 at	-0.9
	267553 s at	-0.9
TCP1-chaperonin cofactor A isolog ;supported by full-length cDNA: Ceres:1853.	267494_at	-0.9
unknown protein	267383 at	-0.9
unknown protein ;supported by full-length cDNA: Ceres:39057.	267367 at	-0.9
fatty acid hydroxylase (FAH1) identical to GB:AF021804; supported by cDNA: gi_15215595_gb_AY050326.1_	267318 at	-0.9
putative serine carboxypeptidase I; supported by cDNA: gi 15294269 gb AF410326.1 AF410326	267265 at	-0.9
unknown protein	267041 at	-0.9
unknown protein ;supported by full-length cDNA: Ceres:16403.	266979 at	-0.9
unknown protein	266473 at	-0.9
hypothetical protein predicted by grail	266474 at	-0.9
unknown protein ;supported by full-length cDNA: Ceres:10986.	266476 at	-0.9
putative protease inhibitor ;supported by full-length cDNA: Ceres:11662.	266168 at	-0.9
predicted protein ;supported by cDNA: Ceres:168	266059 at	-0.9
unknown protein supported by cDNA: gi:13926173	265952 at	-0.9
unknown protein ;supported by full-length cDNA: Ceres:8247.	265872 at	-0.9
unknown protein	265837_at	-0.9
hypothetical protein predicted by genscan	265840 <sup>_</sup> at	-0.9
Expressed protein ; supported by full-length cDNA: Ceres: 18284.	265819_at	-0.9
40S ribosomal protein S12 ;supported by full-length cDNA: Ceres:13453.	265671_at	-0.9
unknown protein ;supported by full-length cDNA: Ceres:123225.	265626_at	-0.9
putative calmodulin-like protein	265494_at	-0.9
unknown protein		-0.9
putative ADP-ribosylation factor ;supported by cDNA: gi_13926231_gb_AF372875.1_AF372875	265187_at	-0.9
unknown protein	265148_at	-0.9
unknown protein similar to ESTs gb T76678 and gb AI165001;supported by full-length cDNA: Ceres:251549.	265130_at	-0.9

3-ketoacyl-acyl carrier protein synthase III (KAS III) identical to 3-ketoacyl-acyl carrier protein synthase III (KAS III) GB:CAA72385 GI:18883	265120_at	-0.9
unknown protein similar to small zinc finger-like protein GI:5107149 from [Oryza sativa]; supported by full-length cDNA: Ceres: 21075.	265006_at	-0.9
putative coproporphyrinogen III oxidase similar to GB:S39523 and ESTs gb AA586260 and dbj D48620; supported by cDNA: gi_14624991_	-	-0.9
putative elongation factor similar to GB:AAC67357	264664_at	-0.9
unknown protein ESTs gb H37208,gb H36853 come from this gene	264665_at	-0.9
lipoyltransferase identical to GB:BAA78386; supported by cDNA: gi_4996285_dbj_AB020975.1_AB020975	264613_at	-0.9
	264488_s_at	-0.9
postsynaptic protein CRIPT, putative similar to postsynaptic protein CRIPT GI:3098551 from [Rattus norvegicus]; supported by full-length cl	-	-0.9
carbonic anhydrase, putative similar to carbonic anhydrase GI:882241 from [Flaveria linearis]; supported by full-length cDNA: Ceres: 38715	264313_at	-0.9
aromatic rich glycoprotein, putative similar to aromatic rich glycoprotein GI:1762428 from [Arabidopsis thaliana]; supported by cDNA: gi_17(		-0.9
acyl carrier protein, putative similar to acyl carrier protein GI:1296948 from [Neurospora crassa]; supported by full-length cDNA: Ceres: 140	264162_at	-0.9
putative cyclin-dependent kinase regulatory subunit	264061_at	-0.9
Expressed protein ; supported by full-length cDNA: Ceres: 19643.	264022_at	-0.9
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:114613.	263930_at	-0.9
60s ribosomal protein L34 identical to GB:Q42351, location of EST 105E2T7, gb T22624; supported by full-length cDNA: Ceres:7182.	263691_at	-0.9
putative putative 60S ribosomal protein L17 identical to GB:AAB80655; supported by full-length cDNA: Ceres: 4513.	263665_at	-0.9
putative 40S ribosomal protein S15 Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb/R29788,gb/ATTS0365 come from this g	263667 at	-0.9
putative beta-ketoacyl-CoA synthase	263606 at	-0.9
40S ribosomal protein S14 ;supported by full-length cDNA: Ceres:41471.	263286 at	-0.9
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:5677.	263133 at	-0.9
	263048 s at	-0.9
rac-like GTP binding protein (ARAC5) identical to rac-like GTP-binding protein (ARAC5) SP:Q38937 [Arabidopsis thaliana (Mouse-ear cress		-0.9
hypothetical protein Strong similarity to gil4734005 F3L12.7 hypothetical protein from Arabidopsis thaliana BAC gb/AC007178; supported by	262569 at	-0.9
auxin response factor 1, putative similar to auxin response factor 1 GI:2245378 from [Arabidopsis thaliana]	262566 at	-0.9
hypothetical protein predicted by genscan+	262490 at	-0.9
unknown protein	262394 at	-0.9
unknown protein ; supported by cDNA: gi 12642919 gb AF339720.1 AF339720	262402 at	-0.9
H+-transporting ATPase protein, putative similar to H+-transporting ATPase chain E GB:CAB43050 GI:4850294 from [Arabidopsis thaliana]	262354 at	-0.9
serine threeonine kinase, putative similar to GB:CAA73067 from (Sorghum bicolor) (Plant Mol. Biol. 36 (4), 529-539 (1998)); supported by cE	262244 at	-0.9
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:24864.	262170 at	-0.9
DNA binding protein, putative similar to GB:BAA23142 GI:2580438 from [Oryza sativa]; supported by cDNA: gi 15912302 gb AY056429.1	-	-0.9
J8-like protein similar to Dna J homologue J8 GB:AAC72399 GI:3851670 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:4	261901 at	-0.9
40S ribosomal protein S12, putative similar to 40S ribosomal protein S12 GI:4263712 from [Arabidopsis thaliana];supported by full-length cl	261789 at	-0.9
hypothetical protein predicted by genemark.hmm	261817 at	-0.9
hypothetical protein similar to putative auxin-induced protein GI:4337198 from [Arabidopsis thaliana]	261776 at	-0.9
hypothetical protein predicted by genemark.hmm	261597 at	-0.9
unknown protein contains similarity to extensin-like protein GB:CAA19879 GI:3297821 from [Arabidopsis thaliana]	261598 at	-0.9
DNA-binding factor, putative similar to GT-2 factor GB: CAA51289 GI:416490 from [Arabidopsis thaliana]	261594 at	-0.9
E2, ubiquitin-conjugating enzyme 1 (UBC1) identical to gi:431259, SP:P25865;supported by full-length cDNA: Ceres:18146.	261484 at	-0.9
Expressed protein ; supported by full-length cDNA: Ceres: 14314.	261439 at	-0.9
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_13878106_gb_AF370316.1_AF370316	261338_at	-0.9
unknown protein	261143 at	-0.9
1-aminocyclopropane-1-carboxylate synthase, putative similar to GB:U35779 from [Triticum aestivum] (Plant Mol. Biol. 31 (5), 1009-1020 (1		-0.9
phosphatidylinositol-4-phosphate 5-kinase, putative similar to ghosphatidylinositol-4-phosphate 5-kinase GB:CAB53377 GI:5777366 from [/	260855 at	-0.9 -0.9
	—	
b-Zip DNA binding protein, putative similar to b-Zip DNA binding protein GB:CAB06697 GI:2246376 from [Arabidopsis thaliana]	260819_at	-0.9
unknown protein ; supported by cDNA: gi_13358204_gb_AF325013.2_AF325013	260686_at 260618 at	-0.9 -0.9
flower development protein cycloidea (cyc3), putative similar to flower development protein cycloidea (cyc3) GI:6358611 from [Misopates or	—	
Expressed protein ; supported by cDNA: gi_15294273_gb_AF410328.1_AF410328	260601_at	-0.9
putative small nuclear ribonucleoprotein polypeptide F	260564_at	-0.9
putative signal recognition particle protein 14kD, ATSRP14 ; supported by full-length cDNA: Ceres: 97249.	260569_at	-0.9
putative cytochrome c oxidase Vc subunit	260579_at	-0.9
putative trypsin inhibitor ;supported by full-length cDNA: Ceres:85.	260547_at	-0.9
Expressed protein ; supported by full-length cDNA: Ceres: 91704.	260549_at	-0.9

	000400	
unknown protein hypothetical protein predicted by genscan+, similar to adenosine kinase (EC 2.7.1.20) GB:S52758 from [Leishmania donovani];supported b	260460_at 260388_at	-0.9 -0.9
unknown protein similar to putative protein GB:CAA20468 [Arabidopsis thaliana]	260388_at 260314 at	-0.9
putative ribosomal protein similar to ribosomal protein L33B GB:NP 014877 from [Saccharomyces cerevisiae]; supported by full-length cDN	260258 at	-0.9
hypothetical protein predicted by genscan+	260109 at	-0.9
60S ribosomal protein L18A, putative similar to GI:3128228 from [Arabidopsis thaliana] (Nature 402 (6763), 761-768 (1999));supported by f	260026 at	-0.9
unknown protein ;supported by full-length cDNA: Ceres:142725.	259980 at	-0.9
predicted protein ; supported by cDNA: gi 13358245 gb AF325060.2 AF325060	259889 at	-0.9
hypothetical protein predicted by genefinder	259729 at	-0.9
thaumatin-like protein similar to thaumatin-like protein GB:AAB71214 [Arabidopsis thaliana]; Pfam HMM hit: Thaumatin family	259674 at	-0.9
nuclear transport factor 2, putative similar to nuclear transport factor 2 (NTF2) [Oryza sativa] GI:5380221; supported by full-length cDNA: C	_	-0.9
chlorophyll binding protein, putative similar to chlorophyll binding protein GI:169213 from [Petunia hybrida]	259491 at	-0.9
putative 40S ribosomal protein s14 similar to 40S ribosomal protein S14 GB:P19950 [Zea mays]; supported by full-length cDNA: Ceres: 796	_	-0.9
unknown protein	259250 at	-0.9
putative thylakoid lumen rotamase similar to thylakoid lumen rotamase GB:CAA72792 [Spinacia oleracea]:supported by full-length cDNA: Co	259193 at	-0.9
unknown protein similar to hypothetical protein GB:AD27575 [Sorghum bicolor];supported by full-length cDNA: Ceres:23057.	259131 at	-0.9
unknown protein similar to GB:CAB05547 [Caenorhabditis elegans]	259085 at	-0.9
unknown protein HMM hit; ZFe-2S iron-sulfur cluster binding domain;supported by full-length cDNA: Ceres:29120.	259016 at	-0.9
hypothetical protein predicted by genscan	259000_at	-0.9
putative 40S ribosomal protein S19 similar to 40S ribosomal protein S19 GB:P40978 [Oryza sativa]; supported by full-length cDNA: Ceres: 4		-0.9
putative ubiquinol-cytochrome C reductase complex ubiquinone-binding protein (QP-C) similar to ubiquinol-cytochrome C reductase complex	_	-0.9
unknown protein ;supported by full-length cDNA: Ceres:250294.	258788 at	-0.9
putative amino acid transporter protein similar to amino acid transport protein GB:AAB82307 [Arabidopsis thaliana]; contains Pfam profile: P	258729 at	-0.9
unknown protein ;supported by full-length cDNA: Ceres:24905.	258642 at	-0.9
unknown protein ; supported by cDNA: qi 13605546 qb AF361599.1 AF361599	258623 at	-0.9
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:262487.	258551 at	-0.9
unknown protein	258318 at	-0.9
putative ribosomal protein similar to ribosomal protein L37 GB:BAA04888 from [Homo sapiens]:supported by full-length cDNA: Ceres:14710	_	-0.9
putative ribosomal protein similar to ribosomal protein L41 GB:AAA34366 from [Candida maltosa]; supported by full-length cDNA: Ceres: 13	258296 at	-0.9
Expressed protein ; supported by full-length cDNA: Ceres: 29124.	258297 at	-0.9
putative shikimate kinase similar to shikimate kinase precursor GB:CAA45121 [Lycopersicon esculentum]	258281 at	-0.9
protein kinase, putative similar to GB:BAA24694 from [Arabidopsis thaliana] (Plant Cell Physiol. 38 (3), 248-258 (1997)), supported by full-le	258132 at	-0.9
dihydrolipoamide S-acetyltransferase identical to GB:AAD55139 from [Arabidopsis thaliana]; supported by cDNA: gi_14335165_gb_4Y0372	258086_at	-0.9
putative peroxiredoxin similar to peroxiredoxin Q GB:BAA90524 from [Sedum lineare]; supported by cDNA: gi_15081742_gb_AY048264.1_	258087_at	-0.9
hypothetical protein predicted by genscan+	257962_at	-0.9
cell elongation protein, Dwarf1 identical to GB:S71189 from [Arabidopsis thaliana]; supported by cDNA: gi_516042_gb_U12400.1_ATU124	257938_at	-0.9
unknown protein ;supported by full-length cDNA: Ceres:92314.	257925_at	-0.9
ribonucleotide reductase small subunit, putative similar to RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN GB:P49730 f	257809_at	-0.9
ethylene responsive element binding factor, putative similar to GB:BAA32420 from [Arabidopsis thaliana], contains Pfam profile: PF00847 F	257675_at	-0.9
Expressed protein ; supported by cDNA: gi_13877954_gb_AF370240.1_AF370240	257647_at	-0.9
unknown protein ; supported by full-length cDNA: Ceres: 2194.	257270_at	-0.9
GATA transcription factor 1 (AtGATA-1) identical to GATA transcription factor 1 (AtGATA-1) GB:Y13648 [Arabidopsis thaliana]; supported by	256916_at	-0.9
RNA-binding protein (cp33) identical to RNA-binding protein (cp33) GB:BAA06523 [Arabidopsis thaliana] (Plant Mol. Biol. 27 (3), 529-539 (*	256678_at	-0.9
unknown protein ; supported by full-length cDNA: Ceres: 33058.	256680_at	-0.9
hypothetical protein ; supported by full-length cDNA: Ceres: 14577.	256569_at	-0.9
unknown protein ;supported by full-length cDNA: Ceres:99625.	256525_at	-0.9
putative nucleic acid binding protein similar to nucleic acid binding protein Alfin-1 GB:AAA20093 [Medicago sativa]; supported by full-length	256414_at	-0.9
actin 11 (ACT11) identical to actin 11 (ACT11) SP:P53496 (Plant J. 10:189-202(1996)); supported by full-length cDNA: Ceres:38101.	256275_at	-0.9
GTP-binding protein (SAR1B) identical to GTP-binding protein (SAR1B) [Arabidopsis thaliana (Mouse-ear cress)] SP:Q01474; supported by	256224_at	-0.9
unknown protein ; supported by full-length cDNA: Ceres: 22928.	256225_at	-0.9
calcium-binding protein, putative similar to calcium-binding protein GI:6901652 from [Olea europaea];supported by full-length cDNA: Ceres:		-0.9
unknown protein contains Pfam profile: PF00254 FKBP-type peptidyl-prolyl cis-trans isomerases;supported by full-length cDNA: Ceres:4206	256130_at	-0.9
unknown protein ; supported by cDNA: gi_16648676_gb_AY058114.1_	255960_at	-0.9

	055000 -+	0.0
scarecrow-like 6 (SCL6) putative DNA-binding protein similar to wild oat DNA-binding protein ABF2, GenBank accession number Z48431	255698_at 255596_at	-0.9 -0.9
Expressed protein ; supported by full-length cDNA: Ceres: 28726.	255554 at	-0.9
putative vacuolar ATPase similar to vacuolar ATPase, GenBank accession number P50408;supported by full-length cDNA: Ceres:10207.	255498 at	-0.9
RMA1 RING zinc finger protein identical to RMA1 gi:3164222; supported by cDNA: gi 3164221 dbj AB008518.1 AB008518	255381 at	-0.9
coded for by A. thaliana cDNA T44741	255255 at	-0.9
translation initiation factor IF-1, putative similar to translation initiation factor IF-1 GI:124198 from [Spinacia oleracea]	254910 at	-0.9
Ribosomal protein L7Ae -like various L7Ae ribosomal proteins; supported by full-length cDNA: Ceres: 33381.	254831 at	-0.9
ammonium transport protein (AMT1); supported by cDNA: gi 14335079 gb AY037219.1	254723 at	-0.9
putative pectinacetylesterase pectinacetylesterase precursor, Vigna radiata, PIR2:S68805	254573 at	-0.9
putative protein FKBP-type peptidyl-prolyl cis-trans isomerase, Synechocystis sp., PIR2:S75144	254545 at	-0.9
endomembrane-associated protein; supported by full-length cDNA: Ceres: 20592.	254492 at	-0.9
V-ATPase subunit G (va2 gene)	254216 at	-0.9
hypothetical protein	254116 at	-0.9
putative protein	254117 at	-0.9
transcriptional activator CBF1 CRT CRE binding factor 1 involved in low-temperature-responsive gene expression00; supported by cDNA; c	-	-0.9
beta-carotene hydroxylase ; supported by cDNA; gi 9230269 gb AF125576.1 AF125576	254020 at	-0.9
putative protein ;supported by full-length cDNA: Ceres:5367.	253981 at	-0.9
putative protein	253927 at	-0.9
hypothetical protein ;supported by full-length cDNA: Ceres:31287.	253546 at	-0.9
Expressed protein ; supported by cDNA: gi 15028200 gb AY045923.1	253551 at	-0.9
putative protein predicted protein, Arabidopsis thaliana, PATCHX:G2252634	253475 at	-0.9
ubiquinol-cytochrome c reductase - like protein ubiquinol-cytochrome c reductase - Solanum tuberosum, X79276; supported by full-length c	_	-0.9
hypothetical protein	253367 at	-0.9
Expressed protein ; supported by cDNA: gi 16648998 gb AY059869.1	253342 at	-0.9
male sterility 2-like protein male sterility protein 2, Brassica napus, gb:X99922; supported by cDNA: gi 16323106 gb AY057657.1	253309 at	-0.9
putative ribosomal protein S16 ribosomal protein S16, Neurospora crassa, PIR2:A29927; supported by full-length cDNA: Ceres: 29919.	253201 at	-0.9
ribosomal - like protein ribosomal protein L12, Liberobacter africanum, U09675;supported by full-length cDNA: Ceres:41011.	253058 at	-0.9
homeobox protein HAT22 ;supported by full-length cDNA: Ceres:36691.	253038 at	-0.9
putative protein	252688 at	-0.9
putative protein predicted proteins, Arabidopsis thaliana	252683 at	-0.9
putative protein	252659_at	-0.9
protein kinase - like receptor-like protein kinase RLK3, Arabidopsis thaliana, EMBL:ATH011674	252549_at	-0.9
putative protein several hypothetical proteins - Arabidopsis thaliana	252475_s_at	-0.9
small zinc finger-like protein TIM9 ;supported by full-length cDNA: Ceres:9070.	252479_at	-0.9
putative protein ;supported by full-length cDNA: Ceres:25829.	252463_at	-0.9
Expressed protein ; supported by cDNA: gi_14326548_gb_AF385728.1_AF385728	252390_at	-0.9
B12D-like protein B12D protein - Hordeum vulgare,PIR2:S60284	252348_at	-0.9
Expressed protein ; supported by full-length cDNA: Ceres: 3817.	252352_at	-0.9
anthranilate N-hydroxycinnamoyl/benzoyltransferase - like protein anthranilate N-hydroxycinnamoyl/benzoyltransferase, Dianthus caryophy	252199_at	-0.9
putative protein EREBP-3 homolog, Stylosanthes hamata, EMBL:U91982; supported by cDNA: gi_15010555_gb_AY045579.1_	252214_at	-0.9
zinc finger protein zinc finger protein ID1, Zea mays, EMBL:AF058757	252175_at	-0.9
calmodulin-like protein flagellar calmodulin - Naegleria gruberi, PID:g458232; supported by cDNA: gi_166647_gb_L12115.1_ATHCALLGA	252136_at	-0.9
peroxiredoxin - like protein peroxiredoxin TPx2, Arabidopsis thaliana, EMBL:AF121356; supported by cDNA: gi_15292892_gb_AY050880.1	_	-0.9
putative protein thioredoxin-like protein, Homo sapiens, AJ010841; supported by cDNA: gi_14326509_gb_AF385708.1_AF385708	251815_at	-0.9
putative protein ferritin 2 precursor - Vigna unguiculata, PIR:T08124;supported by full-length cDNA: Ceres:33282.	251735_at	-0.9
putative protein hypothetical protein At2g41240 - Arabidopsis thaliana, EMBL:AC005662	251677_at	-0.9
putative protein hypothetical protein SPBC19C2.12 - Schizosaccharomyces pombe, PIR:T39803;supported by full-length cDNA: Ceres:922	-	-0.9
putative protein hypothetical protein At2g44080 - Arabidopsis thaliana, EMBL:AC004005	251436_at	-0.9
putative protein COP1-interacting protein CIP8 - Arabidopsis thaliana, EMBL:AF162150	251454_at	-0.9
putative protein chloroplast Cpn21 protein - Arabidopsis thaliana, EMBL:ATH010818;supported by full-length cDNA: Ceres:35721.	251425_at	-0.9
shaggy-like kinase beta	251358_at	-0.9
MADS-box protein AGL13 ; supported by cDNA: gi_862641_gb_U20183.1_ATU20183	251312_at	-0.9

RAV-like protein DNA-binding protein RAV1 - Arabidopsis thaliana, EMBL:AB013886;supported by full-length cDNA: Ceres:13757.	251302_at	-0.9
Expressed protein ; supported by full-length cDNA: Ceres: 22246.	250922_at	-0.9
putative protein predicted proteins, Archaeoglobus fulgidus, Synechocystis sp.;supported by full-length cDNA: Ceres:125255.	250842_at	-0.9
putative protein similar to unknown protein (pir  T12959);supported by full-length cDNA: Ceres:252000.	250707_at	-0.9
putative protein	250575_at	-0.9
separation anxiety protein - like separation anxiety protein, Drosophila melanogaster, EMBL:AF225902	250390_at	-0.9
putative protein	250263_at	-0.9
transporter-like protein	250248_at	-0.9
AMP-binding protein	250114_s_at	-0.9
thioredoxin f2 (gb AAD35004.1) ; supported by cDNA: gi_4973253_gb_AF144386.1_AF144386	250133_at	-0.9
unknown protein ;supported by cDNA: gi_14190364_gb_AF378860.1_AF378860	250099_at	-0.9
putative protein predicted proteins, Drosophila melanogaster; supported by full-length cDNA: Ceres: 41525.	249988_at	-0.9
tub family-like protein tubby-like protein - Lemna paucicostata, EMBL:AB023895	250001_at	-0.9
putative protein various predicted proteins	249920 at	-0.9
CCR4-associated factor-like protein	249928 at	-0.9
pectinacetylesterase	249807 <sup>_</sup> at	-0.9
putative protein similar to unknown protein (pirl/S76575)	249685 at	-0.9
hypothetical protein	249499 at	-0.9
hypothetical protein ;supported by full-length cDNA: Ceres:17485.	249472 at	-0.9
hypothetical protein ; supported by full-length cDNA: Ceres; 2842.	249424 s at	-0.9
putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:16724.	249375 at	-0.9
cytochrome c1 precursor; supported by cDNA: gi 15215623 gb AY050340.1	249324 at	-0.9
putative protein similar to unknown protein (emb CAB62355.1);supported by full-length cDNA: Ceres:94968.	249330 at	-0.9
beta-1,3-qlucanase-like protein	249214 at	-0.9
Cys2/His2-type zinc finger protein 3 (dbijBAA85109.1) ;supported by full-length cDNA: Ceres:9878.	249139 at	-0.9
putative protein contains similarity to unknown protein (dbl/AAD21709.1); supported by cDNA: gi 15215714 gb AY050386.1	249035 at	-0.9
unknown protein ;supported by full-length cDNA: Ceres:15495.	248889 at	-0.9
DNA (cytosine-5)-methyltransferase (DNA methyltransferase) (DNA metase) (spIP34881) ; supported by cDNA: gi 304106 gb L10692.1 /		-0.9
putative protein strong similarity to unknown protein (gb AAB95234.1)	248502 at	-0.9
putative protein similar to unknown protein (sp/P43335);supported by full-length cDNA: Ceres:8788.	248449 at	-0.9
unknown protein	248079 at	-0.9
putative protein similar to unknown protein (pir  T04270);supported by full-length cDNA: Ceres:110454.	247980_at	-0.9
putative protein similar to unknown protein (gb AAF21150.1)	247958 at	-0.9
light-inducible protein ATLS1-like :supported by full-length cDNA: Ceres:1152.	247943 at	-0.9
60S acidic ribosomal protein P3 ; supported by full-length cDNA: Ceres: 8695.	247900 at	-0.9
D-xylose-H+ symporter - like protein D-xylose-H+ symporter, Lactobacillus brevis, EMBL:AF045552	247709 at	-0.9
cytoplasmic ribosomal protein S15a - like cytoplasmic ribosomal protein S15a, Arabidopsis thaliana, EMBL:ATAF1412;supported by full-len	-	-0.9
zinc finger protein Zat12 ;supported by full-length cDNA: Ceres:40576.	247655 at	-0.9
zinc finger protein 2 like dof6 zinc finger protein, Arabidopsis thaliana, PIR:T47501;supported by full-length cDNA: Ceres:20852.	247625 at	-0.9
putative phytochelatin synthetase - like putative phytochelatin synthetase, Arabidopsis thaliana, EMBL:ATH6787	247604 at	-0.9
adenylate kinase ;supported by full-length cDNA: Ceres:13667.	247382 at	-0.9
unknown protein	247252_at	-0.9
receptor protein kinase-like protein	247252_at 247153 at	-0.9
SCARECROW gene regulator	247057 at	-0.9
E2, ubiquitin-conjugating enzyme, putative ubiquitin-conjugating enzyme, Pichia pastoris, PIR:A53848; supported by full-length cDNA: Cere	_	-0.9
putative protein predicted protein, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 108472.	_	-0.9
	246744_at	-0.9
ribosomal protein S21 - like ribosomal protein S21, Zea mays, PIR:T03945;supported by full-length cDNA: Ceres:93174.	246747_at	-0.9
copper amine oxidase, putative similar to copper amine oxidase GI:685197 from [Pisum sativum]	246601_at	
copper amine oxidase, putative similar to copper amine oxidase GI:3819099 from [Cicer arietinum]	246603_at	-0.9
CARBONIC ANHYDRASE 2 ; supported by cDNA: gi_13265565_gb_AF324712.2_AF324712	246596_at	-0.9
glycine/proline-rich protein glycine/proline-rich protein GPRP - Arabidopsis thaliana, EMBL:X84315	246440_at	-0.9
hypothetical protein	246346_at	-0.9
beta-D-glucan exohydrolase - like protein beta-D-glucan exohydrolase, Nicotiana tabacum, EMBL:AB017502	246184_at	-0.9

ribosomal protein L7Ae-like NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG - Homo sapiens, EMBL:D50420;supported by	<b>o –</b>	
NAM-like protein hypothetical protein SENU5, senescence up-regulated - Lycopersicon esculentum, EMBL:Z75524; supported b		
defender against cell death protein, putative similar to defender against cell death protein GB:AAC36169 GI:3608136 from [Arab		
unknown protein similar to GP 2104534 AF001308 (T10M13.11)	245176_at -0.9	
hypothetical protein predicted by genscan	245029_at -0.9	
hypothetical protein	244961_at -0.9	
orf153b orf153b	244923_s_at -0.9	
putative protein contains similarity to unknown protein (pir  T05568)	247182_at -0.9	
putative expansin ;supported by full-length cDNA: Ceres:17353.	267590_at -0.8	
putative heme A:farnesyltransferase ; supported by cDNA: gi_15028298_gb_AY045952.1_	267342_at -0.8	
hypothetical protein predicted by genefinder; supported by cDNA: gi_14334633_gb_AY034990.1_	267279_at -0.8	
hypothetical protein	267293_at -0.8	
calmodulin-like protein identical to GB:D45848; supported by cDNA: gi_15983405_gb_AF424577.1_AF424577	267083_at -0.8	
unknown protein	267018_at -0.8	
unknown protein ; supported by cDNA: gi_14335015_gb_AY037187.1_	266982_at -0.8	
hypothetical protein predicted by genscan	266916_at -0.8	
unknown protein	266825_at -0.8	
putative alcohol dehydrogenase	266761_at -0.8	
unknown protein ;supported by full-length cDNA: Ceres:26967.	266716_at -0.8	
putative ribosomal protein L28 ; supported by cDNA: gi_15292670_gb_AY050769.1_	266699_at -0.8	
putative trytophanyl-tRNA synthetase	266648_at -0.8 266521 at -0.8	
unknown protein ; supported by cDNA: gi_15081683_gb_AY048234.1_		
hypothetical protein predicted by genefinder	266545_at -0.8	
unknown protein ; supported by cDNA: gi_13605586_gb_AF361619.1_AF361619	266551_at -0.8 266512 at -0.8	
unknown protein		
glutathione S-transferase (GST6) identical to GB:X95295. Based on identical cDNA hits, the translation is now 40 AAs longer at unknown protein ; supported by cDNA: gi 16649150 gb AY059945.1	the N-termi 266461_at -0.8 266481 at -0.8	
hypothetical protein predicted by genscan	266358 at -0.8	
hypothetical protein predicted by genefinder	266345 at -0.8	
hypothetical protein predicted by generalider hypothetical protein predicted by generalisepported by full-length cDNA: Ceres:8450.	266311 at -0.8	
60S acidic ribosomal protein P2 ;supported by full-length cDNA: Ceres:36076.	266256 at -0.8	
60S acidic ribosomal protein P2 ;supported by full-length cDNA: Ceres:19986.	266258 at -0.8	
60S ribosomal protein L10A; supported by cDNA: gi 13430467 gb AF360146.1 AF360146	266210 at -0.8	
unknown protein	265953 at -0.8	
unknown protein	265620 at -0.8	
unknown protein	265539 at -0.8	
unknown protein ;supported by full-length cDNA; Ceres:27566.	265386 at -0.8	
putative photosystem I reaction center subunit IV ;supported by full-length cDNA: Ceres:27629.	265287 at -0.8	
hypothetical protein predicted by genscan and genefinder;supported by full-length cDNA: Ceres:3673.	265278 at -0.8	
glutathione transferase, putative similar to glutathione S-transferase GB: AAF22517 GI:6652870 from [Papaver somniferum];sup	_	
hypothetical protein similar to carnitine racemase like protein GI:7268149 from [Arabidopsis thaliana]	264627 at -0.8	
putative histone H2A Strong similarity to Picea histone H2A (gb X67819). ESTs gb ATTS3874,gb T46627,gb T14194 come from	-	
unknown protein Similar to Glycine SRC2 (gb/AB000130). ESTs gb/H76869,gb/T21700,gb/ATTS5089 come from this gene; sup		
hypothetical protein Contains similarity to Rattus AMP-activated protein kinase (gb/X95577); supported by cDNA: gi 9965728 gt		
sugar carrier protein, putative similar to sugar carrier protein GI:169735 from [Ricinus communis]	264482 at -0.8	
Expressed protein ; supported by full-length cDNA: Ceres: 22723.	264441 at -0.8	
putative transcription factor similar to transcription factor SF3 (pir/IS37656); similar to ESTs gb/T42207, gb/N37716, and emb/Z1		
hypothetical protein predicted by genscan+	264337 at -0.8	
histone H2A, putative similar to histone H2A GI:3204129 from [Cicer arietinum];supported by full-length cDNA: Ceres:16879.	264188 at -0.8	
unknown protein ;supported by full-length cDNA: Ceres:37537.	264201 at -0.8	
hypothetical protein predicted by genemark.hmm	264179 at -0.8	
putative cyclin-dependent kinase regulatory subunit ;supported by full-length cDNA: Ceres:5750.	264070_at -0.8	
putative steroid sulfotransferase ; supported by cDNA: gi_599639_emb_Z46823.1_ATTS4391		
	=	

Expressed protein ; supported by full-length cDNA: Ceres: 20090.	264023_at	-0.8
Expressed protein ; supported by full-length cDNA: Ceres: 29157.	263840_at	-0.8
cysteine proteinase similar to cysteine proteinase RD19A (thiol protease) GI:435618, SP:P43296 from [Arabidopsis thaliana]; supported by 1	263757_at	-0.8
metalloproteinase, putative similar to metalloproteinase GI:3128477 from [Arabidopsis thaliana]	263731_at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:14471.	263737_at	-0.8
unknown protein ESTs gb N65789,gb T04628 come from this gene;supported by full-length cDNA: Ceres:28606.	263660_at	-0.8
unknown protein	263467_at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:6899.	263305_at	-0.8
ubiquitin extension protein (UBQ2) identical to GI:166930, GI:166931; supported by cDNA: gi_13430797_gb_AF360311.1_AF360311	263289_at	-0.8
putative vacuolar proton-ATPase 16 kDa proteolipid identical to GB:L44581	263267_at	-0.8
acetyl-CoA carboxylase, putative similar to acetyl-CoA carboxylase GI:1100253 from [Arabidopsis thaliana]	263193_at	-0.8
SKP1/ASK1 (At1) identical to Skp1a GI:3068807, Skp1p GI:1432083 and UIP1 GI:3719209 from [Arabidopsis thaliana]	262676_at	-0.8
ribonuclease contains similarity to RNase GI:7768564 from [Nicotiana tabacum]	262657_at	-0.8
putative 60s ribosomal protein L37 almost identical to GB:Q43292;supported by full-length cDNA: Ceres:11912.	262594_at	-0.8
hypothetical protein similar to hypothetical protein GB:CAB36801 GI:4455265 from [Arabidopsis thaliana]; supported by full-length cDNA: Ce	262457_at	-0.8
cytochrome P450, putative similar to cytochrome P450 GI:4688670 from [Catharanthus roseus]	262426_s_at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:33047.	262399 at	-0.8
hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 10855.	262411 <sup>_</sup> at	-0.8
unknown protein identical to residues 1 to 141 of unknown protein GB:AAD55491 (Arabidopsis thaliana)	262288 <sup>_</sup> at	-0.8
hypothetical protein predicted by genemark.hmm	262251 at	-0.8
hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 19044.	262127 at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:35811.	262049 at	-0.8
Expressed protein ; supported by full-length cDNA: Ceres: 7260.	262058 at	-0.8
unknown protein	261926 at	-0.8
unknown protein ; supported by full-length cDNA: Ceres: 42087.	261902 at	-0.8
DAG protein, putative similar to DAG protein GI:1200204 from [Antirrhinum majus]; supported by full-length cDNA: Ceres: 35647.	261824 at	-0.8
chloroplast drought-induced stress protein, putative similar to chloroplast drought-induced stress protein GI:2582821 from [Solanum tuberos		-0.8
acidic ribosomal protein, putative similar to 60S ACIDIC RIBOSOMAL PROTEIN P1 GB:023095 from [Arabidopsis thaliana]:supported by fi	_	-0.8
histone H4 identical to GB:M36659 from [Zea mays] (Plant Physiol. Biochem. 25, 235-247 (1987));supported by full-length cDNA: Ceres:27		-0.8
ribosomal protein S15 identical to GB:AAA61608 from [Arabidopsis thaliana] (Plant Physiol. 106 (1), 401-402 (1994)); supported by full-leng		-0.8
catechol O-methyltransferase, putative similar to catechol O-methyltransferase GI:4808524 from [Thalictrum tuberosum]	261216 at	-0.8
unknown protein ; supported by cDNA: gi 15450636 gb AY052686.1	261210_at 261193 at	-0.8
ornithine carbamoyltransferase precursor identical to SP:050039 from [Arabidopsis thaliana]; supported by cDNA: gi 2764517 emb AJ000	_	-0.8
hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 13874.	261057 at	-0.8
hypothetical protein contains similarity to mitochondrial inner membrane protease subunit 1 GB:P28627 from [Saccharomyces cerevisiae]	260972 at	-0.8 -0.8
	260881 at	-0.8 -0.8
unknown protein contains similarity to calcium-binding protein GB:CAB63264 GI:6580549 from [Lotus japonicus]; supported by cDNA: gi_13	—	
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:29740.	260867_at	-0.8
signal recognition particle 19 kDa protein subunit, putative similar to GB:U19030 from [Oryza sativa] (Plant Mol. Biol. 34 (3), 507-515 (1997)		-0.8
expressed protein ; supported by full-length cDNA: Ceres: 256275.	260708_at	-0.8
membrane related protein CP5, putative similar to GB:AAD28760 from [Arabidopsis thaliana]; supported by cDNA: gi_16604620_gb_AY05!	260603_at	-0.8
putative molybdopterin synthase large subunit; supported by cDNA: gi_13605721_gb_AF361842.1_AF361842	260572_at	-0.8
Expressed protein ; supported by full-length cDNA: Ceres: 105765.	260409_at	-0.8
putative B-box zinc finger protein contains Pfam profile: PF00643 B-box zinc finger; supported by full-length cDNA: Ceres: 108109.	260266_at	-0.8
E2, ubiquitin-conjugating enzyme, putative similar to putative protein GB:CAB43411 [Arabidopsis thaliana]; supported by full-length cDNA: C	260180_at	-0.8
unknown protein	260081_at	-0.8
unknown protein supported by cDNA: Ceres:13335	260072_at	-0.8
unknown protein	259847_at	-0.8
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:21940.	259663_at	-0.8
short chain alcohol dehydrogenase, putative similar to GI:2739279 from [Nicotiana tabacum] (Plant Mol. Biol. 29 (5), 1027-1038 (1995))	259669_at	-0.8
hypothetical protein ; supported by cDNA: gi_14596112_gb_AY042844.1_	259515_at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:17545.	259474_at	-0.8
hypothetical protein predicted using genefinder;supported by full-length cDNA: Ceres:20442.	259340_at	-0.8
unknown protein ;supported by cDNA: gi_16604552_gb_AY059721.1_	259349_at	-0.8

unknown protein similar to MICROSOMAL SIGNAL PEPTIDASE GB:P28687 from [Gallus gallus]; supported by full-length cDNA: Ceres:151-	259307_at	-0.8
putative small nuclear ribonucleoprotein polypeptide G similar to small nuclear ribonucleoprotein polypeptide G GB:4507133 [Homo sapiens	259288_at	-0.8
unknown protein ; supported by full-length cDNA: Ceres: 29837.	259236_at	-0.8
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:9503.	259253_at	-0.8
unknown protein similar to putative protein GB:CAB36768 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:8898.	259013_at	-0.8
GTP cyclohydrolase I similar to GTP cyclohydrolase I GB:P22288 [Rattus norvegicus]; contains Pfam profile: PF01227 GTP cyclohydrolase	258834_at	-0.8
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:8992.	258792_at	-0.8
hypothetical protein supported by full-length cDNA: Ceres:4427.	258793_at	-0.8
unknown protein	258699_at	-0.8
unknown protein ; supported by full-length cDNA: Ceres: 9458.	258681_at	-0.8
ribosomal protein L29, putative similar to 60S ribosomal protein L29 GB:P25886 from [Rattus norvegicus]	258521_at	-0.8
sterol-C5-desaturase identical to GB:AAD12944 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:7564.	258484 at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:6694.	258491 <sup>_</sup> at	-0.8
unknown protein contains Pfam profile: PF00106 short chain dehydrogenase	258467 <sup>_</sup> at	-0.8
unknown protein	258418 at	-0.8
beta-glucosidase, putative similar to beta-glucosidase BGQ60 precursor GB:A57512 [Hordeum vulgare]; supported by full-length cDNA: Cer	_	-0.8
expansin At-EXP5 identical to expansin At-EXP5 GB:AAB38071 from [Arabidopsis thaliana]; supported by cDNA: gi 1041703 gb U30478.	_	-0.8
unknown protein supported by full-length cDNA: Ceres:41112.	257966 at	-0.8
unknown protein ; supported by full-length CDNA: Ceres:27058.	257750 at	-0.8
hypothetical protein predicted by genemark.hmm	257728 at	-0.8
histone H3, putative similar to histone H3 GB:P05203 [Petroselinum crispum]; supported by cDNA: gi 14335141 gb AY037250.1	257714 at	-0.8
Expressed protein ; supported by cDNA: gi_15810238_gb_AY056158.1_	257706_at	-0.8
unknown protein ; supported by cDNA: gi 15146273 gb AY049278.1	257272_at	-0.8
hypothetical protein ;supported by full-length cDNA: Ceres:7140.	257212_at 257214_at	-0.8
		-0.8
cytochrome c, putative similar to cytochrome c1 GB:S66866 from [Solanum tuberosum];supported by full-length cDNA: Ceres:41320. non-race specific disease resistance protein, putative contains non-consensus CT donor splice site at exon 1; potential pseudogene; simila	257148_at	-0.8
ribosomal protein L27, putative similar to 60S RIBOSOMAL PROTEIN L27 GB:P41101 from [Solanum tuberosum]; supported by full-length	_	-0.8
unknown protein ;supported by full-length cDNA: Ceres:8544.	256785_at	-0.8
	256728_at	-0.8
	256438_s_at	-0.8
hypothetical protein	256373_at	-0.8
unknown protein similar to hypothetical protein GI:1469227 from [Brassica oleracea];supported by full-length cDNA: Ceres:94809.	256191_at	-0.8
putative FKBP-type peptidyl-prolyl cis-trans isomerase predicted by genscan+	256088_at	-0.8
predicted protein ; supported by cDNA: gi_15027984_gb_AY045849.1_	256093_at	-0.8
AP2 domain transcription factor, putative similar to AP2 domain transcription factor GI:4567204 from [Arabidopsis thaliana]	256009_at	-0.8
UDP-glucose glucosyltransferase identical to UDP-glucose glucosyltransferase GI:3928543 from [Arabidopsis thaliana]; supported by cDNA	_	-0.8
zinc-finger protein (C-terminal), putative similar to zinc-finger protein (C-terminal) GI:558542 from [Glycine max]; supported by full-length cD	_	-0.8
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:232413.	255775_at	-0.8
putative YABBY3 axial regulator ;supported by cDNA: gi_14335013_gb_AY037186.1_	255709_at	-0.8
Expressed protein ; supported by full-length cDNA: Ceres: 18459.	255633_at	-0.8
P II nitrogen sensing protein GLB I ; supported by cDNA: gi_3885942_gb_AF095455.1_AF095455	255558_at	-0.8
Expressed protein ; supported by full-length cDNA: Ceres: 1734.	255104_at	-0.8
arabinogalactan-protein homolog arabinogalactan-protein - Arabidopsis thaliana,PID:g3883126; supported by cDNA: gi_10880496_gb_AF	255080_at	-0.8
putative ribosomal protein L9, cytosolic ribosomal protein L9, cytosolic - garden pea, PIR2:S19978;supported by full-length cDNA: Ceres:21	254980_at	-0.8
ras-like GTP-binding protein strong homology to GTP-binding protein ric2, Oryza sativa, S38741	254641_at	-0.8
putative protein ; supported by cDNA: gi_15292760_gb_AY050814.1_	254561_at	-0.8
putative protein RNPL, Homo sapiens, PIR2:G01859;supported by full-length cDNA: Ceres:251841.	254504_at	-0.8
translation elongation factor EF-Tu precursor, chloroplast ; supported by cDNA: gi_14334791_gb_AY035069.1_	254480_at	-0.8
reticuline oxidase -like protein reticuline oxidase, Eschscholzia californica, PIR:A41533; supported by cDNA: gi_15983492_gb_AF424621.1	254432_at	-0.8
putative protein light induced protein homolog, Arabidopsis thaliana, PATCHX:E326816;supported by full-length cDNA: Ceres:35323.	254358_at	-0.8
adenine phosphoribosyltransferase (EC 2.4.2.7) - like protein adenine phosphoribosyltransferase, Triticum aestivum, T06263; supported by	254328_at	-0.8
putative mitochondrial uncoupling protein mitochondrial uncoupling protein, Arabidopsis thaliana (thale cress), PATX:E1316826;supported	254120_at	-0.8
DRE CRT-binding protein DREB1C involved in low-temperature-responsive gene expression00; supported by cDNA: gi_3738227_dbj_AB0(	254075_at	-0.8
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Expressed protein ; supported by full-length cDNA: Ceres: 31814.	253825_at	-0.8
putative protein ;supported by full-length cDNA: Ceres:1968.	253766_at	-0.8
ribosomal protein S15a homolog ribosomal protein S15a - Brassica napus,PIR2:S20945; supported by full-length cDNA: Ceres: 18105.	253726_at	-0.8 -0.8
acid phosphatase-like protein acid phosphatase-1 (EC 3.1.3) - Lycopersicon esculentum,PIR2:T06587; supported by cDNA: gi_1529302 Expressed protein ; supported by full-length cDNA: Ceres: 26443.	253731_at 253694 at	-0.8 -0.8
putative protein ; supported by full-length cDNA: Ceres: 20443.	253594_at 253537 at	-0.8
Expressed protein ; supported by cDNA: gi 13926316 gb AF372908.1 AF372908	253537_at 253482 at	-0.8
putative protein predicted protein, Caenorhabditis elegans, gb:Z70780;supported by full-length cDNA: Ceres:8739.	253385_at	-0.8
Expressed protein ; supported by full-length cDNA: Ceres: 109432.	253305_at 253302 at	-0.8
Expressed protein ; supported by full-length cDNA: Ceres: 24629.	253291 at	-0.8
putative protein ; supported by full-length cDNA: Ceres: 8742.	253291_at	-0.8
ribosomal protein L11 homolog several ribosomal proteins L11;supported by full-length cDNA: Ceres:95636.	253138 at	-0.8
putative amino acid transport protein amino acid transport protein - Arabidopsis thaliana, PID:g2576363;supported by full-length cDNA: Cer		-0.8
putative animo acid transport protein animo acid transport protein - Arabidopsis tranana, 112.92570000, supported by full-length conver. Cer putative protein phosphatase-2c protein phosphatase-2c (PP2C) - Mesembryanthemum crystallinum, PID:q3608412	252992 at	-0.8
Expressed protein ; supported by cDNA: gi 15451093 gb AY054627.1	253001 at	-0.8
putative zinc finger protein salt-tolerance protein - Arabidopsis thaliana, PID:e224078	252924 at	-0.8
putative protein ;supported by full-length cDNA: Ceres:4740.	252942 at	-0.8
putative protein ;supported by full-length cDNA: Ceres:20457.	252850 at	-0.8
Expressed protein ; supported by full-length cDNA: Ceres: 22456.	252823 at	-0.8
leucine-rich repeat protein LRP -like leucine-rich repeat protein LRP, tomato, PIR:T07079	252703 at	-0.8
cysteine proteinase contains similarity to cysteine proteinase RD21A (thiol protease) GI:435619, SP:P43297 from [Arabidopsis thaliana];su	252692 at	-0.8
putative protein cim1 induced allergen, Glycine max, EMBL:U03860;supported by full-length cDNA: Ceres:27534.	252563 at	-0.8
putative protein mitochondrial ATP SYNTHASE 6 KD SUBUNIT - Solanum tuberosum, SWISSPROT:P80497	252524 at	-0.8
Expressed protein ; supported by full-length cDNA: Ceres: 157151.	252412 at	-0.8
protein translocation complex sec61 gamma chain-like protein protein translocation complex sec61 gamma chain, endoplasmic reticulum - (	252324 at	-0.8
putative protein sugar transporter 2. Drosophila melanogaster. EMBL:AF199484	252308 at	-0.8
putative protein ; supported by full-length cDNA: Ceres: 40302.	252234 at	-0.8
putative protein steroid dehydrogenase homolog - Homo sapiens, EMBL:AF078850;supported by full-length cDNA: Ceres:34560.	252167 at	-0.8
Expressed protein ; supported by full-length cDNA: Ceres: 26994.	252181 at	-0.8
putative protein 1 photosystem II oxygen-evolving complex photosystem II oxygen-evolving complex protein 1 - potato, PIR2:S16586;suppc		-0.8
putative protein hypothetical protein F10M6.70 - Arabidopsis thaliana.PIR3:T05399; supported by cDNA: gi 15293266 gb AY051067.1	252040 at	-0.8
E2, ubiquitin-conjugating enzyme, putative UEV1Bs - Homo sapiens,PID:g2689608;supported by full-length cDNA: Ceres:16125.	252059 at	-0.8
RNA-binding protein cp29 protein ;supported by full-length cDNA: Ceres:38888.	251956 at	-0.8
leucoanthocyanidin dioxygenase -like protein leucoanthocyanidin dioxygenase, apple tree, PIR:S33144	251770 at	-0.8
	251746 at	-0.8
40S ribosomal protein S26 homolog several 40S ribosomal protein S26; supported by cDNA: gi_14532523_gb_AY039886.1_	251737 at	-0.8
putative protein ;supported by full-length cDNA: Ceres:12522.	251640 <sup>_</sup> at	-0.8
Expressed protein ; supported by full-length cDNA: Ceres: 22956.	251602_at	-0.8
putative protein CND41, chloroplast nucleoid DNA binding protein - Nicotiana tabacum, EMBL:D26015; supported by cDNA: gi_15983375_	251507_at	-0.8
60S RIBOSOMAL PROTEIN L38-like protein 60S RIBOSOMAL PROTEIN L38 - Lycopersicon esculentum, EMBL:X69979; supported by cL	251486_at	-0.8
putative protein transcription factor Pti6 - Lycopersicon esculentum, PIR:T07728;supported by full-length cDNA: Ceres:100688.	251282_at	-0.8
putative protein nucleoid DNA-binding protein cnd41, chloroplast - Nicotiana tabacum, EMBL:D26015; supported by cDNA: gi_14532549_g	251287_at	-0.8
ribosomal protein L35 - like ribosomal protein L35- cytosolic, Arabidopsis thaliana, PIR:T00549; supported by full-length cDNA: Ceres:1452€	251007_at	-0.8
putative protein contains similarity to unknown protein (gb AAF19573.1);supported by full-length cDNA: Ceres:118003.	250810_at	-0.8
putative protein similar to unknown protein (emb CAB88044.1)	250821_at	-0.8
putative protein strong similarity to unknown protein (pir  T12704)	250745_at	-0.8
unknown protein ;supported by full-length cDNA: Ceres: 17482.	250668_at	-0.8
transcription factor-like protein ethylene responsive element binding factor 5 - Arabidopsis thaliana, EMBL:AB008107; supported by cDNA:	250582_at	-0.8
putative protein	250562_at	-0.8
inorganic pyrophosphatase - like protein cytosolic inorganic pyrophosphatase, Homo sapiens, EMBL:AF108211; supported by full-length cD	250496_at	-0.8
putative protein ; supported by cDNA: gi_15028030_gb_AY045872.1_	250368_at	-0.8
putative GTP-binding protein GTP-binding protein CGPA, Caulobacter crescentus, EMBL:AF084242; supported by full-length cDNA: Ceres	250383_at	-0.8
mitochondrial phosphate translocator	250206_at	-0.8

Expressed protein ; supported by full-length cDNA: Ceres: 13951.	250225_at	-0.8
isopentenyl pyrophosphate:dimethyllallyl pyrophosphate isomerase	250117_at	-0.8
putative protein; similar to unknown protein (gb AAF26969.1)	250076_at	-0.8
chloroplast GrpE protein ; supported by cDNA: gi_13878046_gb_AF370286.1_AF370286	250061_at	-0.8
putative protein rsc43, Dictyostelium discoideum, EMBL:AF011338;supported by full-length cDNA: Ceres:6084.	249984_at	-0.8
putative protein predicted proteins. Arabidopsis thaliana:supported by full-length cDNA: Ceres:32414.	249987 at	-0.8
putative protein similar to unknown protein (emb[CAB88996.1); supported by full-length cDNA: Ceres: 7688.	249943 at	-0.8
40S ribosomal protein S11 ;supported by full-length cDNA: Ceres:33187.	249795 <sup>_</sup> at	-0.8
60S ribosomal protein L13 ; supported by cDNA: gi 14190434 gb AF378895.1 AF378895	249815 at	-0.8
putative protein similar to unknown protein (gb AAD29063.1)	249777 at	-0.8
unknown protein	249726_at	-0.8
CRS2 -like protein CRS2, Zea mays, EMBL:AF225708	249554 at	-0.8
dihydroxyacetone 3-phosphate reductase (dhaprd)	249366 at	-0.8
putative protein contains similarity to metallothionein-I gene transcription activator	249335 at	-0.8
putative protein contains similarity to 40S ribosomal protein S10; supported by cDNA: gi 14335121 gb AY037240.1	249310 at	-0.8
Expressed protein ; supported by cDNA: gi_13605534_gb_AF361593.1_AF361593	249268 at	-0.8
putative protein strong similarity to unknown protein (gb/AAF04433.1)	249220 at	-0.8
Nicotiana lesion-inducing like ; supported by full-length cDNA: Ceres: 327.	249159 at	-0.8
aluminum-induced protein-like ; supported by full-length cDNA: Ceres: 12484.	249121_at	-0.8
putative protein similar to unknown protein (pir  T38261)	249085 at	-0.8
putative protein similar to unknown protein (pir  T04247)	248877 at	-0.8
phosphate/triose-phosphate translocator precursor (gb/AAC83815.1); supported by full-length cDNA: Ceres:36058.	248886 at	-0.8
ribosomal protein S27 ;supported by full-length cDNA: Ceres:8698.	248000_at 248747 at	-0.8
	248655 at	-0.8
60S ribosomal protein L13a ;supported by full-length cDNA: Ceres:4275. amino acid permease 6 (emb CAA65051.1)	_	
	248619_at	-0.8
protein translocation complex Sec61 gamma chain (pir  T05513) ; supported by cDNA: gi_13877812_gb_AF370169.1_AF370169	248512_at	-0.8 -0.8
unknown protein ; supported by full-length cDNA: Ceres: 106913.	248219_at	
unknown protein	248190_at	-0.8
putative protein similar to unknown protein (gb AAC24386.1)	248191_at	-0.8
unknown protein ; supported by cDNA: gi_16323225_gb_AY057717.1_	248098_at	-0.8
40S ribosomal protein S30 homolog (emb CAB79697.1)	247968_at	-0.8
I-box binding factor - like protein I-box binding factor, Lycopersicon esculentum, EMBL:LES243339	247768_at	-0.8
putative Rab5-interacting protein - like putative Rab5-interacting protein, Homo sapiens, EMBL:AF112213	247725_at	-0.8
putative protein	247628_at	-0.8
putative protein predicted proteins	247611_at	-0.8
putative protein predicted proteins, Arabidopsis thaliana	247448_at	-0.8
putative protein similar to unknown protein (gb AAF17656.1)	247399_at	-0.8
Arac10 ; supported by cDNA: gi_3702963_gb_AF079485.1_AF079485	247405_at	-0.8
CLE21, putative CLAVATA3/ESR-Related 21 (CLE21)	247254_at	-0.8
GATA-binding transcription factor-like protein	247086_at	-0.8
putative protein similar to unknown protein (gb AAF64534.1);supported by full-length cDNA: Ceres:4831.	247037_at	-0.8
putative protein predicted protein, Arabidopsis thaliana	246885_at	-0.8
mevalonate kinase supported by full-length cDNA: Ceres:1045.	246778_at	-0.8
sugar transporter-like protein putative sugar transporter (SUGTL2) - Arabidopsis thaliana, EMBL:AJ249968; supported by cDNA: gi_152941	246781_at	-0.8
putative protein predicted proteins, Oryza sativa and Arabidopsis thaliana;supported by full-length cDNA: Ceres:20143.	246746_at	-0.8
40S RIBOSOMAL PROTEIN S19 - like 40S RIBOSOMAL PROTEIN S19 - Oryza sativa, SWISSPROT:RS19_ORYSA; supported by full-len	_	-0.8
putative protein predicted protein, Drosophila melanogaster	246462_at	-0.8
ADP/ATP translocase-like protein adp/atp translocase - Schizosaccharomyces pombe, PIR:T40526;supported by full-length cDNA: Ceres:3	_	-0.8
disease resistance protein RPP1-WsB, putative similar to disease resistance protein RPP1-WsB GI:9279731 from [Arabidopsis thaliana]	246405_at	-0.8
calmodulin-3 ;supported by full-length cDNA: Ceres:16715.	246290_at	-0.8
putative carrier protein peroxisomal Ca-dependent solute carrier - Oryctolagus cuniculus, EMBL:AF004161	246303_at	-0.8
peptidyl-prolyl cis-trans isomerase - like protein peptidyl-prolyl cis-trans isomerase A.thaliana; supported by full-length cDNA: Ceres:25533.	246040_at	-0.8
putative protein predicted protein, Arabidopsis thaliana, EMBL:ATZ86095;supported by full-length cDNA: Ceres:158575.	246043_at	-0.8

putative protein predicted proteins, Drosophila melanogaster and Caenorhabdilis elegans         246015, at         0.8           hypothetical protein predicted by genemark.hmm.supported by full-length cDNA: Ceres.31365.         245747, at         0.8           phophate/phoenolgnyuset translocator: like proteins supported by full-length cDNA: Ceres.31365.         245372, at         0.8           phophate/phoenolgnyuset translocator: like proteins supported by full-length cDNA: Ceres.17381.         245310, at         0.8           hypothetical protein supported by full-length cDNA: Ceres.17977.         245310, at         0.8           hypothetical protein supported by full-length cDNA: Ceres.27970.         245310, at         0.8           hypothetical protein supported by full-length cDNA: Ceres.33964.         245327, at         0.8           putative protein similarity to predicted proteins. Anabidopsis thaliana         24505, at         0.8           proteine predicted proteins. Anabidopsis thaliana         244069, at         0.8           hypothetical protein predicted proteins. Anabidopsis thaliana         244069, at         0.8           hypothetical protein predicted proteins. Anabidopsis thaliana         244069, at         0.8           hypothetical protein predicted proteins. Anabidopsis thaliana         244069, at         0.8           hypothetical protein predicted proteins. Anabidopsis thaliana         244969, at         0.8			
hypothelical protein predicted by genemark.hmm.supported by full-ength cDNA: Ceres:10377.         245674_at         -0.8           nbosomal protein supported by full-ength cDNA: Ceres:10377.         245686_at         -0.8           nbosomal protein supported by full-ength cDNA: Ceres:1718.         245372_at         -0.8           hypothetical protein supported by full-ength cDNA: Ceres:1717.         245316_at         -0.8           hypothetical protein supported by full-ength cDNA: Ceres:27991.         245316_at         -0.8           hypothetical protein supported by full-ength cDNA: Ceres:23991.         245316_at         -0.8           hypothetical protein supported by full-ength cDNA: Ceres:23991.         24527_at         -0.8           hypothetical protein supported by full-ength cDNA: Ceres:33364.         24567_at         -0.8           hypothetical protein supported by full-ength cDNA: Ceres:33364.         24566_at         -0.8           hypothetical protein supported by full-ength cDNA: Ceres:3364.         24566_at         -0.8           hypothetical protein supported by full-ength cDNA: Ceres:3067.         24566_at         -0.8           hypothetical protein supported by full-ength cDNA: Ceres:3067.         24576_at         -0.8           hypothetical protein supported by full-ength cDNA: Ceres:3076.         25776_at         -0.8           hypothetical protein supoported by full-ength cDNA: Ceres:2082.		246015_at	-0.8
phosphate/phosphoen/pyruvate/translocator - like protein supported by full-length CDNA: Ceres: 100777.         246608_att         -0.8           elictor like protein supported by full-length CDNA: Ceres: 1718.         245310_att         -0.8           hypothetical protein supported by full-length CDNA: Ceres: 1797.         245310_att         -0.8           hypothetical protein supported by full-length CDNA: Ceres: 2797.         245311_att         -0.8           hypothetical protein supported by full-length CDNA: Ceres: 20736.         245270_att         -0.8           hypothetical protein supported by cDNA: [15284507.1	putative protein predicted protein, Arabidopsis thaliana; supported by full-length cDNA: Ceres:29453.	245999_at	-0.8
ibosomal protein         243372         41           icitor like protein         244372         42           icitor like protein         244372         44           hypothelical protein         2443712         44           hypothelical protein         2445702         at           hypothelical protein         2445702         at         0.8           hypothelical protein         244572         at         0.8           hypothelical protein predicted proteins, archidopsis halana         244502         at         0.8           hypothelical protein predicted proteins, archidopsis halana         244502         at         0.8           hypothelical protein protei	hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:31356.	245747_at	-0.8
elicitor like protein ; supported by full-length cDNA: Ceres: 1718.         245310, at hypothetical protein , supported by full-length cDNA: Ceres: 27977.         245310, at construction ; supported by full-length cDNA: Ceres: 27977.         245311, at construction ; supported by full-length cDNA: Ceres: 27977.         24531, at construction ; supported by full-length cDNA: Ceres: 27977.         245321, at construction ; supported by full-length cDNA: Ceres: 2797.         245321, at construction ; supported by full-length cDNA: Ceres: 2797, at construction ; construction ; construct	phosphate/phosphoenolpyruvate translocator - like protein ;supported by full-length cDNA: Ceres:100777.	245698_at	-0.8
hypothetical protein supported by full-length cDNA: Ceres: 17977.         245316_at         -0.8           hypothetical protein supported by full-length cDNA: Ceres: 2691.         245316_at         -0.8           hypothetical protein supported by full-length cDNA: Ceres: 2691.         245297_at         -0.8           hypothetical protein supported by cDNA: g1_1262461_g0_AF242406.1_AF42406         245297_at         -0.8           hubulin alpha-6 chain (TUA6): supported by full-length cDNA: Ceres:33364.         245165_at         -0.8           hypothetical protein predicted by genemark.hum, contains Pfam profile.PF00320 GATA:GATA zinc finger         27577_1 at         -0.8           hypothetical protein predicted by genemark.hum, contains Pfam profile.PF00320 GATA:GATA zinc finger         226126_at         -0.8           hypothetical protein predicted pto genemark.hum, contains Pfam profile.PF00320 GATA:GATA zinc finger         226126_at         -0.8           hypothetical protein predicted pto genemark.hum, contains Pfam profile.PF00320 GATA:GATA zinc finger         226126_at         -0.8           hypothetical protein predicted pto genemark.hum, supported by full-length cDNA: Ceres: 107869.         256127_at         -0.8           hypothetical protein predicted pto full-length cDNA: Ceres: 28862.         26761_at         -0.7           unknown protein : supported by full-length cDNA: Ceres: 28862.         -0.7         27614_at         -0.7           unknown prot	ribosomal protein ;supported by full-length cDNA: Ceres:15384.	245372_at	-0.8
hypothetical protein supported by full-length CDNA: Ceres 25991.         245316_at         -0.8           hypothetical protein supported by full-length CDNA: Ceres 2736.         245331_at         -0.8           hypothetical protein simplarity to predicted py cDNA: gi_15226461_gb_AF4284061_4F428406         245270_at         -0.8           hypothetical protein similarity to predicted py conversion similarity to predicted py conversion similarity to predicted py senemark.hmm, contains Pfam profile.PF00320 GATA:GATA zinc finger         245042_at         -0.8           hypothetical protein predicted by genemark.hmm, contains Pfam profile.PF00320 GATA:GATA zinc finger         25771_at         -0.8           hypothetical protein predicted by genemark.hmm, contains Pfam profile.PF00320 GATA:GATA zinc finger         25771_at         -0.8           hypothetical protein sequence is in confile.with the conceptual translation         2489420_at         -0.8           hypothetical protein         257767_at         -0.8         -0.8           hypothetical protein         25767_at         -0.8         -0.8           hypothetical protein         25767_at         -0.8         -0.8         -0.8           hypothetical protein         250767_at         -0.8         -0.7         -0.8         -0.7         -0.8         -0.7         -0.8         -0.7         -0.8         -0.7         -0.8         -0.7         -0.7	elicitor like protein ; supported by full-length cDNA: Ceres: 1718.	245340_at	-0.8
nypothetical protein supported by full-length cDNA: Ceres:40736.24533 <sup>-</sup> at-0.8hypothetical protein supported by cDNA: gl_12626461_gb_AF284061_AF428406246270_at-0.8hubulin apha-6 chain (TUAB) ; supported by full-length cDNA: Gl_12626461_gb_AF2840661_AF428406246270_at-0.8hypothetical protein predicted proteins, Arabidopsis thaliana245165_gt-0.8hypothetical protein predicted by genefinder:supported by full-length cDNA: Ceres:33364.245042_gt-0.8hypothetical protein predicted by genefinder:supported by full-length cDNA: Ceres:33364.244069_gt-0.8hypothetical protein predicted by genemak:hmm, contains Plam profile-PF00320 GATA:GATA zinc finger25767_st-0.8hypothetical protein predicted by genemak:hmm, contains Plam profile-PF00320 GATA:GATA zinc finger25762_st-0.8hypothetical protein protein246490_gt-0.8-0.8-0.8hypothetical protein protein25767_st-0.8-0.8-0.8hypothetical protein25767_st-0.8-0.8-0.8-0.8hypothetical protein25767_st-0.8-0.7-0.7-0.7hypothetical protein25767_st-0.8-0.7-0.7-0.7hypothetical protein25767_st-0.8-0.7-0.7-0.7hypothetical protein25767_st-0.7-0.7-0.7-0.7-0.7-0.7-0.7hypothetical protein250767_st-0.7-0.7-0.7-0.7-0.7-0.7-0.7-0.7-0.7-0.7-0.7-0.7 </td <td>hypothetical protein ;supported by full-length cDNA: Ceres:17977.</td> <td>245310_at</td> <td>-0.8</td>	hypothetical protein ;supported by full-length cDNA: Ceres:17977.	245310_at	-0.8
injoonterical protein : supported by CDNA: gl_15246103.gb, AV064897.1_         245297_at         0.8           bublin siphe.6 chain (TLAB): supported by CDNA: gl_15224616.1_gb,AF242406.1_gF424440.1_gF4244406.1_gF4244406.1_gF4244406.1_gF4244406.1_gF4244406.1_gF424446.1_gF424446.1_gF424446.1_gF424446.1_gF424440.1_gF424440.1_gF42444.1_gF42440.1_gF424444.1_gF42440.1_gF42444.1_gF42440.1_gF42444.1_gF42440.1_gF42444.1_gF42440.1_gF42444.1_gF42440.1_gF424444.1_gF42440.1_gF424444.1_gF42440.1_gF424444.1_gF424444.1_gF4244444.1_gF424444444444.1_gF424444444444.1_gF42444444444444444.1_gF42444444444444444.1_gF4244444444444444444444444444444444444	hypothetical protein ;supported by full-length cDNA: Ceres:25991.	245316_at	-0.8
Libbin apha-e chain (TUAe); supported by CDNA: cj. 1222641 gb, AF228406 1, AF428406         245702 at         0.8           Putative protein similarity to predicted proteins, Arabidopsis thaliana         245102 at         0.8           Pubothecal protein predicted by genefinder:supported by full-length cDNA: Ceres:33364.         244090 at         0.8           NADH dehydrogenase subunit 3 Protein sequence is in conflict with the conceptual translation         244920 at         0.8           hypothetical protein predicted by genemark.hmm, contains Pfam profile:PF00320 GATA:GATA zinc finger         257115 at         0.8           putative cellulose synthase         267115 at         0.8         20306 at         0.8           putative cellulose synthase (enclust) diphosphate synthase (gl-4902470 from (Arabidopsis thaliana); supported         226722 at         0.8           hypothetical protein         280767 at         0.8         280762 at         0.8           hypothetical protein         281676 at         0.8         281676 at         0.8           hypothetical protein         281676 at         0.8         281676 at         0.8           unknown protein ; supported by full-length cDNA: Ceres: 28982.         287632 at         0.7           unknown protein ; supported by full-length cDNA: Ceres: 2990.         287452 at         0.7           unknown protein ; supported by full-length cDNA: Ceres: 1583.<	hypothetical protein ;supported by full-length cDNA: Ceres:40736.	245331_at	-0.8
putative protein similarity to predicted proteins, Arabiãopsis thaliana246155 at246hypothetical protein predicted by genefinder; supported by full-length cDNA: Ceres: 3364.246490, s. atNADH dehydrogenase subunit 3 Protein sequence is in conflict with the conceptual translation244490, s. athypothetical protein predicted by genemark.hmm, contains Pfam profile:PF00320 GATA:GATA zinc finger257571, atputative cellulose synthase267015, atputative cellulose synthase267016, atprotein predicted by genemark.hmm, contains Pfam profile:PF00320 GATA:GATA zinc finger25622, atphosphoribosyl diphosphate synthase lidentical to phosphoribosyl diphosphate synthase GI-4902470 from (Arabidopsis thaliana); supported 262762, at0.8hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 107869.2561676, athypothetical protein is supported by full-length cDNA: Ceres: 2892.267633, atunknown protein ; supported by full-length cDNA: Ceres: 2990.267614, atputative endro: is supported by full-length cDNA: Ceres: 2992.267514, atunknown protein ; supported by cDNA: gi_15724345, gb_AF412113, 1_AF412113267514, atunknown protein ; supported by full-length cDNA: Ceres: 1990.267720, atunknown protein ; supported by cDNA: gi_1589906, gb_AF370538, 1_AF370538267379, atunknown protein ; supported by cDNA: gi_1589906, gb_AF370538, 1_AF370538267374, atunknown protein ; supported by full-length cDNA: Ceres:11583.267746, st005 nibosomal protein 125, supported by full-length cDNA: Ceres:11683.267746, st01605 nibosomal protein [	hypothetical protein ; supported by cDNA: gi_15451033_gb_AY054597.1_	245297_at	-0.8
hypothetical problem predicted by genefinder;supported by full-length cDNA: Ceres:33364.         244904_2         449494.         -0.8           NADH dehydrogenase subunt 3 Protein sequence is in conflict with the conceptual translation         244920_s_s1         -0.8           hypothetical protein predicted by genemark.hmm, contains Pfam profile.PF00320 GATA:GATA zinc finger         257571_st         -0.8           putative cellulose synthase         267715_s_at         -0.8           phosphorbocyd diphosphate synthase identical to phosphorbocyd diphosphate synthase GI-4902470 from (Arabidopsis thaliana); supported         256722_at         -0.8           hypothetical protein         251676_at         -0.8           hypothetical protein         251676_at         -0.8           hypothetical protein         251676_at         -0.8           hypothetical protein         251676_at         -0.7           unknown protein ; supported by full-length cDNA: Ceres: 2982.         267510_at         -0.7           unknown protein ; supported by full-length cDNA: Ceres: 2982.         267510_at         -0.7           unknown protein ; supported by full-length cDNA: Ceres: 2982.         267714_at         -0.7           unknown protein ; supported by full-length cDNA: Ceres: 2982.         267714_at         -0.7           unknown protein ; supported by cDNA: gi_15724345_gi_0.AF370538         267742_at         -0.7	tubulin alpha-6 chain (TUA6) ; supported by cDNA: gi_16226461_gb_AF428406.1_AF428406	245270_at	-0.8
inbosomal protein S18244969 at 244969 at 244969 at 244969 at 244969 at 244969 at 244969 at 244969 at 2457571 at 0.8 0.8 0.8 0.8 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 			
NADH dehydrogenase subunit 3 Protein sequence is in conflict with the conceptual translation244202, s_at-0.8hypothetical protein predicted by genemark.hmm, contains Pfam profile;PF03200 GATA:GATA zinc finger267115, s_at-0.8putative cellulose synthase267101, s_at-0.8putative non-LTR retrolelement reverse transcriptase267102, s_at-0.8hypothetical protein267762, at-0.8hypothetical protein267622, at-0.8hypothetical protein256222, at-0.8hypothetical protein245495, at-0.8hypothetical protein245495, at-0.7unknown protein:supported by full-length cDNA: Ceres: 2892.267514, at-0.7unknown protein:supported by coll-length obc. Ceres: 990.267510, at-0.7unknown protein:supported by coll-length obc. Ceres: 990.267514, at-0.7unknown protein:supported by coll-length obc. Ceres: 990.267514, at-0.7unknown protein:supported by coll-length obc. Ceres: 990.267514, at-0.7unknown protein:supported by coll-length coll to GB:AF007788; supported by coll-length coll to GB:AF007788; supported by coll-length coll to GB:AF034814-0.7unknown protein:supported by full-length cDNA: Ceres:2153.267145, at-0.7unknown protein267145, at-0.7unknown protein267145, at-0.7unknown protein267145, at-0.7Unknown protein267145, at-0.7Unknown protein267145, at-0.7 <td>hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:33364.</td> <td>245042_at</td> <td>-0.8</td>	hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:33364.	245042_at	-0.8
hypothetical protein predicted by genemark.hmm, contains Pfam profile:PF00320 GATA:GATA zinc finger         25757_at         0.8           putative colludese synthase         267115_s_at         0.8           phosphoritosyl diphosphate synthase identical to phosphoribosyl diphosphate synthase GI:4902470 from (Arabidopsis thaliana); supported         262762_at         0.8           hypothetical protein         265762_at         0.8           hypothetical protein         267676_at         0.8           hypothetical protein         267676_at         0.8           unknown protein         supported by full-ength cDNA: Ceres: 28982.         267638_at         0.7           putative glycerate dehydrogenase : supported by cDNA: gi_15724345_gb_AF412113_AF412113         267510_at         0.7           nuknown protein         supportein         267763_at         0.7           nuknown protein         supporteid by cDNA: gi_1589086_gb_AF370538_AF37053         267323_at         0.7           unknown protein         267745_st_at         0.7         20         267452_at         0.7           unknown protein         1.35         267323_at         0.7         267332_at         0.7           unknown protein         supported by full-length cDNA: Ceres:20125.         267328_at         0.7           putative acothreac-cyanohydmin lyase         267445_a	ribosomal protein S18	_	
putative cellulose synthase267115 st.putative non-LTR retrolelement reverse transcriptase263086 st.hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:107869.256725 st.hypothetical protein245495 st.hypothetical protein245495 st.hypothetical protein245495 st.unknown protein267761 st.putative glycerate dehydrogenase : supported by full-length cDNA: Ceres: 28982.267610 st.unknown protein267761 st.putative glycerate dehydrogenase : supported by cDNA: gi_15724345 gb_AF412113.1_AF412113267610 st.auxin response transcription factor 3 (ETTINARF3) identical to GB:AF007788; supported by cDNA: gi_12899086 gb_AF370538.1_AF370538267323 st.unknown protein267323 st.0.7unknown protein26745 st.0.7unknown protein26746 st.0.7Obsomal protein 125 isupported by full-length cDNA: Ceres:20125.26724 st.0.7Unknown protein260746 st.0.7Obsomal protein 125 isupported by full-length cDNA: Ceres:2479.266890 st.0.7Obsomal protein 125 isupported by full-length cDNA: Ceres:2479.266784 st.0.7Unknown protein1.5 </td <td>NADH dehydrogenase subunit 3 Protein sequence is in conflict with the conceptual translation</td> <td>244920_s_at</td> <td></td>	NADH dehydrogenase subunit 3 Protein sequence is in conflict with the conceptual translation	244920_s_at	
putative non-LTR refrolement reverse transcriptase         263086_art         0.8           phosphoribosyl diphosphate synthase identical to phosphorbosyl diphosphate synthase GI:4902470 from (Arabidopsis thaliana); supported         262762_at         -0.8           hypothetical protein         251676_at         -0.8           hypothetical protein         251676_at         -0.8           unknown protein         supported by full-length cDNA: Ceres: 28982.         267638_at         -0.7           unknown protein         supported by cDNA: gi_15724345_gb_AF412113_1_AF412113         267514_at         -0.7           auxin response transcription factor 3 (ETTINARF3) identical to GBA: F007788; supported by cDNA: gi_13899086_gb_AF370538.1_AF370538         267378_at         -0.7           unknown protein         supported by full-length cDNA: Ceres: 10880         267145_at         -0.7           unknown protein         supported by full-length cDNA: gi_13899086_gb_AF370538.1_AF370538         267378_at         -0.7           unknown protein         supported by full-length cDNA: Ceres:20125.         267145_at         -0.7           putative acetyltransferase         267145_at         -0.7         2605 ribosomal protein 1.23 A identical to GBA: F034694; supported by full-length cDNA: Ceres:2479.         266841_at         -0.7           605 ribosomal protein         125 supported by full-length cDNA: Ceres:11583.         266743_at	hypothetical protein predicted by genemark.hmm, contains Pfam profile:PF00320 GATA:GATA zinc finger	257571_at	
phosphoribosyl diphosphate synthase identical io phosphoribosyl diphosphate synthase GI 4902470 from (Arabidopsis thaliana); supported282782_at-0.8hypothetical protein256222_at-0.8hypothetical protein251876_at-0.8hypothetical protein245495_at-0.8unknown protein25672_at-0.8putative givported by full-length cDNA: Ceres: 29892.267538_at-0.7unknown protein267510_at-0.7auxin response transcription factor 3 (ETTIN/ARF3) identical to GB:AF007788; supported by cDNA: gi_15724345_gb_AF412113.1_AF412113267514_at-0.7auxin response transcription factor 3 (ETTIN/ARF3) identical to GB:AF007788; supported by cDNA: gi_12484198_gb_AF336917.1_AF3369267452_at-0.7unknown protein267348_at-0.7267126_s.at-0.7unknown protein267323_at-0.7-0.7putative givported by cDNA: gi_13299086_gb_AF370538.1_AF370538267126_s.at-0.7putative acetone-cyanohydrin lyase267126_s.at-0.7putative acetone-cyanohydrin lyase267126_s.at-0.7putative acetone-cyanohydrin lyase267126_s.at-0.7putative acetone-cyanohydrin lyase267126_s.at-0.7conknown protein1.55_supported by full-length cDNA: Ceres:1583.267055_at-0.7conknown protein256746_at-0.7conknown protein256748_att-0.7conknown protein266789_at-0.7conknown protein266789_at-0.7conknown protein256742_at-0.			
hypothetical protein266222 at 21676 at0.8hypothetical protein251676 at-0.8hypothetical protein251676 at-0.8unknown protein : supported by full-length cDNA: Ceres: 28982.287638 at-0.7unknown protein : supported by full-length cDNA: gi_15724345 gb_AF412113.1_AF412113287614 at-0.7putative glycerate dehydrogenase : supported by cDNA: gi_15724345 gb_AF412113.1_AF412113287614 at-0.7auknown protein : supported by cDNA: gi_13899086 gb_AF370538.1_AF370538287379 at-0.7unknown protein : supported by genscan and genefinder:supported by full-length cDNA: Ceres:20125.287294 at-0.7putative acetone-cyanohydrin lyase267145 at-0.7putative acetone-cyanohydrin lyase26745 at-0.7gos ribosomal protein L33 identical to GB-XF034604; supported by full-length cDNA: Ceres:2479.26678 at-0.7unknown protein26678-361 at-0.7hypothetical protein identical to GB-XF034604; supported by full-length cDNA: Ceres:24194.26678 at-0.7unknown protein266678 at-0.7putative		_	
hypothetical protein         251676_at         -0.8           hypothetical protein         245495_at         -0.8           unknown protein         supported by full-length cDNA: Ceres: 28962.         267510_at         -0.7           putative giverate dehydrogenase : supported by cDNA: gi_15724345_gb_AF412113.1_AF412113         267511_at         -0.7           auxin response transcription factor 3 (ETTIN/ARF3) identical to GB:AF007788; supported by cDNA: gi_1379341         -0.7           unknown protein         supported by gb/sended by cDNA: gi_15724345_gb_AF310538         -0.7           unknown protein         267312_at         -0.7           unknown protein         267348_at         -0.7           putative acctone-cyanohydrin lyase         267145_at         -0.7           putative acctone-cyanohydrin lyase         267145_at         -0.7           unknown protein         2507145_at         -0.7           unknown protein         266745_at         -0.7           f00S ribosomal protein L35 (supported by full-length cDNA: Ceres:11583.         267145_at         -0.7           60S ribosomal protein L23A identical to GB:AF034694;supported by full-length cDNA: Ceres:2479.         266789_at         -0.7           f00S ribosomal protein predicted by grail         -0.7         26678_at         -0.7           f0S ribosomal protein L23A identi		_	
hybothetical protein         245496_at         -0.8           unknown protein ; supported by full-length cDNA: Ceres: 28982.         267638_at         -0.7           putative glycerate dehydrogenase ; supported by cDNA: gi_15724345_gb_AF412113.1_AF412113         267511_at         -0.7           putative glycerate dehydrogenase ; supported by cDNA: gi_15724345_gb_AF412113.1_AF412113         267514_at         -0.7           unknown protein ; supported by cDNA: gi_13899086_gb_AF370538.1_AF370538         267349_at         -0.7           unknown protein         267323_at         -0.7           unknown protein predicted by genscan and genefinder; supported by full-length cDNA: Ceres:20125.         267145_at         -0.7           putative accetyltransferase         267145_at         -0.7           unknown protein         266789_at         -0.7           unknown protein         2567452_at         -0.7           putative accetyltransferase         267145_at         -0.7           unknown protein         256980_at         -0.7           roknown protein         2367464_supported by full-length cDNA: Ceres:2479.         266980_at         -0.7           unknown protein         230 of rokasomal protein L323 kientical to GB.47034694;supported by full-length cDNA: Ceres:2479.         266678_at         -0.7           unknown protein         supported by full-length cDNA: Ce	hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:107869.	256222_at	
unknown protein ; supported by full-length cDNA: Ceres: 2882.267638_att-0.7unknown protein ; supported by full-length cDNA: Geres: 9990.267510_att-0.7auxin response transcription factor 3 (ETTIN/ARF3) identical to GB:AF007788; supported by cDNA: gi_12484198_gb_AF336917.1_AF3369267514_att-0.7auxin response transcription factor 3 (ETTIN/ARF3) identical to GB:AF007788; supported by cDNA: gi_13899086_gb_AF370538.1_AF370538267348_att-0.7unknown protein26734.2_att-0.7unknown protein267323_att-0.7putative gityce predicted by genscan and genefinder; supported by full-length cDNA: Ceres:20125.267126_s_att-0.7putative acetone-cyanohydrin lyase267145_att-0.7putative acetyltransferase267145_att-0.7unknown protein267345_att-0.7fols ribosomal protein L35supported by full-length cDNA: Ceres:11583.266980_att-0.760S ribosomal protein L35 isupported by full-length cDNA: Ceres:22479.266743_att-0.7unknown protein ; supported by full-length cDNA: Ceres:10164.266743_att-0.7ribonuclease, RNS1 identical to GB:U27144; supported by full-length cDNA: Ceres:24194.266636_att-0.7glycine decarboxylase complex H-protein identical to GB:U27144; supported by full-length cDNA: Ceres:24194.266636_att-0.7putative giutaredoxin ; supported by full-length cDNA: Ceres:24619.26614_att-0.7putative giutaredoxin ; supported by full-length cDNA: Ceres:7536.26674_att-0.7putative somal nuclear ribonucleoprotein E ; supported by full-			
unknown protein         supported by full-length cDNA: Ceres: 9990.         267510_at         -0.7           putative glycerate dehydrogenase ; supported by cDNA: gj_1572435_gb_AF412113_1_AF412113         267514_at         -0.7           auxin response transcription factor 3 (CETTIN/ARF3) identical to GB:AF007788; supported by cDNA: gj_12484198_gb_AF336917.1_AF3369         267379_at         -0.7           unknown protein         267348_at         -0.7           unknown protein         267348_at         -0.7           nunknown protein         267348_at         -0.7           nunknown protein         267329_at         -0.7           putative acetyltransferase         267145_at         -0.7           putative acetyltransferase         267145_at         -0.7           unknown protein         267326_at         -0.7           GOS ribosomal protein 123 identical to GB:AF034694;supported by full-length cDNA: Ceres:20125.         267848_at         -0.7           foos ribosomal protein 123A identical to GB:AF034694;supported by full-length cDNA: Ceres:2479.         266980_at         -0.7           foos ribosomal protein 123A identical to GB:U27144;supported by full-length cDNA: Ceres:2479.         266782_at         -0.7           nypothetical protein predicted by grail         -0.66636_at         -0.7         -0.7           nypothetical protein i supported by full-length cDNA:	nypothetical protein	245495_at	
putative glycerate dehydrogenase : supported by cDNA: gi_15724345_gb_AF412113.1_AF412113267514_at-0.7auxin response transcription factor 3 (ETTIN/ARF3) identical to GB:AF007788; supported by cDNA: gi_12484198_gb_AF336917.1_AF3369267379_at-0.7unknown protein267348_at-0.7unknown protein267348_at-0.7unknown protein267348_at-0.7unknown protein267348_at-0.7unknown protein267348_at-0.7unknown protein267345_at-0.7putative acetone-cyanohydrin lyase267145_at-0.7putative acetone-cyanohydrin lyase267145_at-0.7putative acetyltransferase267145_at-0.7unknown protein2267055_at-0.760S ribosomal protein L35 ;supported by full-length cDNA: Ceres:11583.266980_at-0.70SO ribosomal protein i: supported by full-length cDNA: Ceres:10164.266789_at-0.7unknown proteinsupported by full-length cDNA: Ceres:20106.26678_at-0.7putative glutaredoxin ;supported by full-length cDNA: Ceres:21066.266678_at-0.7putative glutaredoxin ;supported by full-length cDNA: Ceres:2106.266645_at-0.7putative glutaredoxin ;supported by cDNA: gi_15293090_gb_AY050979.1_266645_at-0.7putative glutaredoxin ;supported by cDNA: gi_15809809_gb_AY050979.1_266645_at-0.7putative nibose 5-phosphate isomerase ; supported by cDNA: Ceres:24619.266674_at-0.7putative nibose 5-phosphate isomerase ; supported by cDNA: Ceres:736.26542_at<			
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unknown protein ; supported by cDNA: gi_13899086_gb_AF370538.1_AF370538			
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unknown protein267323_at-0.7hypothetical protein predicted by genscan and genefinder; supported by full-length cDNA: Ceres:20125.2671294_at-0.7putative acetone-cyanohydrin lyase267145_at-0.7putative acetone-cyanohydrin lyase267145_at-0.7putative acetyltransferase267145_at-0.760S ribosomal protein L35 ; supported by full-length cDNA: Ceres:11583.266980_at-0.760S ribosomal protein L23A identical to GB:AF034694; supported by full-length cDNA: Ceres:22479.266981_at-0.7ribonuclease, RNS1 identical to ribonuclease SP:P42813, GI:561998 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:2678_at-0.7glycine decarboxylase complex H-protein identical to GB:U27144; supported by full-length cDNA: Ceres:24194.266678_at-0.7glycine decarboxylase complex H-protein identical to GB:U27144; supported by full-length cDNA: Ceres:24194.266678_at-0.7putative supported by full-length cDNA: Geres:21006.266118_at-0.7protease inhibitor II ; supported by cDNA: gi_15293090_gb_AY050979.1_266118_at-0.7putative ribose 5-phosphate isomerase ; supported by cDNA: gi_15809809_gb_AY054172.1_26674_at-0.7putative ribose 5-phosphate isomerase ; supported by full-length cDNA: Ceres:15103.266426_at-0.7putative replication protein AT ; supported by full-length cDNA: Ceres:27679.265426_at-0.7hypothetical protein predicted by gensen; supported by full-length cDNA: Ceres:27679.26533_at-0.7hypothetical protein predicted by gensorn, supported by full-length cDNA: Ceres:2767		_	
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unknown protein ; supported by full-length cDNA: Ceres: 10164.266789_at-0.7ribonuclease, RNS1 identical to ribonuclease SP:P42813, Gl:561998 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:272266743_at-0.7hypothetical protein predicted by grail266678_at-0.7glycine decarboxylase complex H-protein identical to GB:U27144; supported by full-length cDNA: Ceres:24194.266636_at-0.7putative glutaredoxin ; supported by full-length cDNA: Ceres:21006.266616_at-0.7unknown protein266445_at-0.7protease inhibitor II ; supported by cDNA: gi_15293090_gb_AY050979.1_266118_at-0.7putative small nuclear ribonucleoprotein E ; supported by full-length cDNA: Ceres:24619.266074_at-0.7putative ribose 5-phosphate isomerase ; supported by cDNA: gi_15809809_gb_AY054172.1_265742_at-0.7putative replication protein A1 ; supported by full-length cDNA: Ceres:7536.265426_at-0.7hypothetical protein predicted by genefinder265426_at-0.7hypothetical protein predicted by genefinder; supported by full-length cDNA: Ceres:15103.265442_at-0.7hypothetical protein predicted by genefinder ; supported by full-length cDNA: Ceres:27679.265375_at-0.7hypothetical protein predicted by genscan; supported by full-length cDNA: Ceres:2692.265333_at-0.7hypothetical protein similar to embryo-abundant protein GB:L47672 GI:1350530 from [Picea glauca]; supported by cDNA: gi_14335021_gb_265075_at-0.7		—	
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hypothetical protein similar to embryo-abundant protein GB:L47672 GI:1350530 from [Picea glauca]; supported by cDNA: gi_14335021_gb_ 265075_at -0.7			
unknown protein Contains similarity to hypothetical mitochondrial import receptor subunit gb 298597 from S. pombe. ES Is gb[145575 and c 265041_at -0.7		_	
	unknown protein Contains similarity to hypothetical mitochondrial import receptor subunit gb 298597 from S. pombe. ESTs gb[145575 and g	∠65041_at	-0.7

hypothetical protein predicted by genefinder; supported by cDNA: gi_15028340_gb_AY045973.1_	265028_at	-0.7
	264991_s_at	-0.7
unknown protein similar to leucine-rich repeat protein GB:AAC79105; supported by cDNA: gi_12083225_gb_AF332409.1_AF332409	264840_at	-0.7
putative thioredoxin-m similar to thioredoxin m-type precursor; similar to ESTs gb T13714, gb H76398, gb N37762, gb AA042639, gb T211(	-	-0.7
hypothetical protein predicted by genscan	264803_at	-0.7
putative calcium-dependent protein kinase (U90439) similar to ESTs gb T46119, gb H76837, and gb H36948; supported by cDNA: gi_6318	264783_at	-0.7
putative cytochrome C strong similarity to GB:P00050 and GB:CAB39628; supported by full-length cDNA: Ceres: 31770.	264727_at	-0.7
putative auxin-induced protein, IAA12 similar to GB:S58498;supported by full-length cDNA: Ceres:40608.	264605_at	-0.7
putative GTP-binding protein; supported by cDNA: gi_1292907_gb_U41295.1_ATU41295	264593_at	-0.7
SKP1/ASK1 (At18), putative similar to Skp1 homolog Skp1a GI:3068807 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:2720:	264465_at	-0.7
unknown protein Similar to gb U85207 snRNP core Sm protein homolog Sm-X5 from Mus musculus. EST gb AA612141 comes from this ge	264364_at	-0.7
unknown protein strong similarity to hypothetical protein gb Y09823 from A. thaliana. ESTs gb T76118, gb T04263 and gb ATYU9823 come	264207_at	-0.7
latex-abundant protein, putative similar to latex-abundant protein GI:4235430 from (Hevea brasiliensis)	264178_at	-0.7
hypothetical protein predicted by genemark.hmm	264130_at	-0.7
unknown protein contains similarity to alpha-A-globin GI:212911 from [Cairina moschata]	264134_at	-0.7
putative MADS-box protein	263995_at	-0.7
putative triosephosphate isomerase ;supported by full-length cDNA: Ceres:39351.	264018_at	-0.7
putative auxin-regulated protein ;supported by full-length cDNA: Ceres:7141.	264021_at	-0.7
hypothetical protein predicted by grail;supported by full-length cDNA: Ceres:2928.	263980_at	-0.7
putative phosphoprotein phosphatase ; supported by cDNA: gi 16930440 gb AF419574.1 AF419574	263990 at	-0.7
putative cis-Golgi SNARE protein ;supported by full-length cDNA: Ceres:2416.	263839 at	-0.7
putative 60s ribosomal protein L10 Nearly identical to ribosomal protein L10.e, Wilm s tumor suppressor homologue, gil17682 (Z15157), ho	263686 at	-0.7
unknown protein Similar to Nicotiana lesion-inducing ORF (gb/U66269)	263651 at	-0.7
hypothetical protein predicted by genscan and genefinder; supported by full-length cDNA: Ceres:7520.	263637 at	-0.7
hypothetical protein predicted by genscan and genefinder supported by full-length cDNA: Ceres:8550.	263597 at	-0.7
NAM (no apical meristem)-like protein similar to petunia NAM (X92205) and A. thaliana sequences ATAF1 (X74755) and ATAF2 (X74756);	263584 at	-0.7
AtRer1B ;supported by full-length cDNA: Ceres:92908.	263516 at	-0.7
hypothetical protein predicted by genscan	263370 at	-0.7
unknown protein ; supported by cDNA: gi 15982806 gb AY057510.1	263298 at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 264189.	263209 at	-0.7
ribosomal protein L13, putative similar to ribosomal protein L13 GI:170132 from [Spinacia oleracea];supported by full-length cDNA: Ceres:3	-	-0.7
60s ribosomal protein I27a. similar to 60S RIBOSOMAL PROTEIN L27A GB:P49637 GI:1710530 from [Arabidopsis thaliana]; supported by fi		-0.7
rubredoxin, putative similar to rubredoxin GI:4583668 from [Guillardia theta];supported by full-length cDNA: Ceres:19234.	262954 at	-0.7
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_15292930 gb_AY050899.1_	262953 at	-0.7
purple acid phosphatase, putative contains Pfam profile: PF02227 Purple acid phosphatase	262830 at	-0.7
putative obtusificiloi 14-alpha demethylase strong similarity to gb/U74319 obtusificiloi 14-alpha demethylase (CYP51) from Sorghum bicolor	262820 at	-0.7
thioredoxin, putative similar to thioredoxin G:142153 from [Synechococcus PCC6301]	262721 at	-0.7
calmodulin, putative similar to calmodulin-6 SP-203509 [Arabidopsis thaliana (Mouse-ear cress)]	262639 at	-0.7
phosphoprotein phosphatase identical to phosphoprotein phosphatase GB:AAD50050 GI:5734785 from [Arabidopsis thaliana];supported by	262476 at	-0.7
hypothetical protein similar to hypothetical protein GB:AAD50047 GI:5734782 from [Arabidopsis thaliana];supported by full-length cDNA: Ce	262417 at	-0.7
	262417_at	-0.7
hypothetical protein similar to hypothetical protein GB:AAF24576 GI:6692111 from [Arabidopsis thaliana]	262329_at	-0.7
unknown protein identical to unknown protein GB:AAD55493 (Arabidopsis thaliana); supported by cDNA: gi 13358235 gb AF325047.2 AF	262262 at	-0.7
putative G protein coupled receptor identical to putative G protein coupled receptor GI:2104224 from [Arabidopsis thaliana]; supported by c[		-0.7
unknown protein ;supported by full-length cDNA: Ceres:6082.	262162 at	-0.7
hypothetical protein predicted by genemark.hmm	262085 at	-0.7
hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 22656.	261898 at	-0.7
	261843 at	-0.7
unknown protein Expressed protein : supported by full length aDNA: Coroc: 40229		
Expressed protein ; supported by full-length cDNA: Ceres: 40238.	261756_at	-0.7
unknown protein ; supported by full-length cDNA: Ceres: 20257.	261723_at 261733 at	-0.7 -0.7
clathrin coat assembly protein AP17, putative similar to clathrin coat assembly protein AP17 GB:CAA65533 GI:2959358 from [Zea mays] hypothetical protein identical to hypothetical protein GB:AAF19740 GI:6634732 from [Arabidopsis thaliana];supported by full-length cDNA: C		-0.7
		-0.7 -0.7
unknown protein similar to putative esterase GB:AAD17422 GI:4335745 from [Arabidopsis thaliana;supported by full-length cDNA: Ceres:12	201000_at	-0.7

unknown protein	261477_at	-0.7
hypothetical protein contains similarity to cytochrome c oxidase subunit I GI:5678701 from [Loligo pealei]; supported by full-length cDNA: Ce	_	-0.7
unknown protein	261422_at	-0.7
NAM (no apical meristem)-like protein OsNAC4, putative similar to NAM (no apical meristem)-like protein OsNAC4 GI:6730938 from [Oryza	261393_at	-0.7
RAC-like GTP-binding protein ARAC4 identical to SP:Q38919 from [Arabidopsis thaliana]; supported by cDNA: gi_1304416_gb_U45236.1_/	261229_at	-0.7
tubulin alpha-2/alpha-4 chain identical to SP:P29510 from [Arabidopsis thaliana]; supported by cDNA: gi_16648843_gb_AY058199.1_	261129_at	-0.7
CLE9, putative CLAVATA3/ESR-Related 9 (CLE9); similar to hypothetical protein GB:AAF67770 GI:7705091 from [Arabidopsis thaliana];su	261012_at	-0.7
unknown protein	260904_at	-0.7 -0.7
	260767_s_at	
hypothetical protein predicted by genemark.hmm	260715_at 260707 s at	-0.7 -0.7
	260281 at	-0.7
unknown protein putative heat shock protein similar to GrpE protein from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:40701.	260261_at	-0.7 -0.7
	_	-0.7
unknown protein ;supported by full-length cDNA: Ceres:151718.	260106_at	-0.7 -0.7
unknown protein ;supported by full-length cDNA: Ceres:33367. Expressed protein ; supported by full-length cDNA: Ceres: 253509.	259955_s_at 259933 at	-0.7 -0.7
	259935_at 259738 at	-0.7
predicted protein putative ribose 5-phosphate isomerase similar to ribose 5-phosphate isomerase GB:6677767 from [Mus musculus];supported by full-length (	259736_at	-0.7 -0.7
putative house 5-phosphate isomerase similar to house 5-phosphate isomerase GB.0077707 hom [Mus husculus], supported by full-length r putative isoprenylated protein similar to ATFP7 GB:AAD09511; supported by full-length cDNA: Ceres:39127.	259749_at 259753 at	-0.7
unknown protein similar to phosphate translocators: glucose-6-phosphate/phosphate-translocator precursor GB:AAC08524 [Zea mays], ph	_	-0.7
unknown protein similar to prosphate transiocators. glucose-o-prosphate/prosphate/transiocator precursor GB.AAC00524 [zea mays], pric unknown protein ;supported by full-length cDNA: Ceres:17287.	259715_at 259267 at	-0.7
putative 60S ribosomal protein L22 similar to 60S ribosomal protein L22 GB:AAF02883; supported by full-length cDNA: Ceres: 8244.	259207_at 259112 at	-0.7
putative ribosomal protein s19 or s24 similar to ribosomal protein S19 GB:445612 [Solanum tuberosum] and similar to ribosomal protein S24	_	-0.7
putative ribusoniai protein s is of s24 similar to ribusoniai protein 3 is GD.4430 iz [Solandin tuberosuni] and similar to ribusoniai protein 32 putative glucan endo-1-3-beta-glucosidase similar to glucan endo-1-3-beta-glucosidase precursor GB:P52409 [Triticum aestivum];supported	259090_at 259014 at	-0.7
putative glucal endorro-beta-glucosidase similar to glucal endorro-beta-glucosidase preclasor GD.r 52409 [Influent aestivutii], supported	258993 at	-0.7
putative chlorophyli a/o-binding protein siniliar to chlorophyli a/o-binding protein (CP29) GB.333443 [Arabidopsis manana], identical to chicu	258786 at	-0.7
ethylene-responsive protein, putative similar to ER6 protein GB:AAD46412 GI:5669654 from (Lycopersicon esculentum); supported by full-l	_	-0.7
unknown protein similar to putative similar to ERO protein GB:AAD404 12 G: 000004 from (Eycopersicon esculentum), supported by tun-	258706 at	-0.7
unknown protein	258654 at	-0.7
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:19531.	258657_at	-0.7
putative protein kinase contains Pfam profiles: PF00069 Eukaryotic protein kinase domain, PF00560 Leucine Rich Repeat (5 copies); suppl	258616 at	-0.7
unknown protein	258519 at	-0.7
putative 40S ribosomal protein similar to ribosomal protein S7 GB:AAD26256 from [Secale cereale]; supported by full-length cDNA: Ceres:3(	258486 at	-0.7
putative flowering-time gene CONSTANS (COL2) identical to putative flowering-time gene CONSTANS (COL2) GB:AAB67879 GI:1507699	258497 at	-0.7
unknown protein similar to unknown protein GB:AAF30339 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:22328.	258393 at	-0.7
transport inhibitor response 1 (TIR1), putative similar to transport inhibitor response 1 GI:2352492 from [Arabidopsis thaliana]	258311 at	-0.7
unknown protein	258232 at	-0.7
unknown protein	258171 at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 15880.	258135 at	-0.7
unknown protein ; supported by cDNA: gi_7658238_gb_AF198179.1_AF198179	257913 at	-0.7
unknown protein contains similarity to auxin-induced protein GB:P33082 from [Glycine max]	257690 at	-0.7
50S ribosomal protein L12-C identical to ribosomal protein L12 GB:X68046 [Arabidopsis thaliana] (J. Biol. Chem. 269 (10), 7330-7336 (199	_	-0.7
putative glucosyltransferase similar to UDP-glucose glucosyltransferase GB:X77459 [Manihot esculenta], UDP-glycose:flavonoid glycosyltra	257205 at	-0.7
30S ribosomal protein S10, putative similar to 30S ribosomal protein S10 GB:P02364 [Escherichia coli] (est matches suggest the N-termina	257190 at	-0.7
E2, ubiquitin-conjugating enzyme, putative similar to ubiquitin-conjugating enzyme GB:Q95044 [Spisula solidissima]	257126 at	-0.7
unknown protein	257088 at	-0.7
prefoldin-like protein similar to prefoldin subunit 2 GB:AAF17218 from [Homo sapiens]; supported by full-length cDNA: Ceres: 264413.	256936_at	-0.7
glycine-rich RNA binding protein, putative similar to glycine-rich RNA binding protein 2 (AtGRP2) GB:CAA05727 [Arabidopsis thaliana]; con		-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 8691.	256856 at	-0.7
ADP-ribosylation factor, putative similar to ADP-ribosylation factor GB:P91924 [Dugesia japonica]; supported by full-length cDNA: Ceres: 24	256838 at	-0.7
omega-3 fatty acid desaturase, chloroplast precursor identical to omega-3 fatty acid desaturase, chloroplast precursor SP:P46310 (Arabido	_	-0.7
unknown protein ; supported by full-length CDNA; Ceres; 2031.	256342 at	-0.7
DnaJ protein, putative contains Pfam profile: PF00226 DnaJ domain	256320 at	-0.7
	u	0.7

unknown protein	256286 at	-0.7
unknown protein ; supported by cDNA: gi 15450991 gb AY054576.1	256267 at	-0.7
unknown protein ;supported by cEIVA: gr_15400831_gb_41004670.1_	256223 at	-0.7
epsilon subunit of mitochondrial F1-ATPase identical to epsilon subunit of mitochondrial F1-ATPase [Arabidopsis thaliana] GI:1655486; sup	256184 at	-0.7
guanine nucleotide regulatory protein, putative similar to guanine nucleotide regulatory protein GI:452360 from [Vicia faba]; supported by fu	256112 at	-0.7
unknown protein	256046 at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 250775.	256064 at	-0.7
ribosomal protein S18, putative similar to ribosomal protein S18 GI:38422 from [Homo sapiens]; supported by cDNA: Ceres:27800	255977 at	-0.7
	_	
unknown protein contains similarity to ubiquitin/ribosomal protein GI:1763015 from [Gallus gallus]	255951_at	-0.7
AP2 domain containing protein RAP2, putative similar to AP2 domain containing protein RAP2.4 GI:2281633 from [Arabidopsis thaliana]; su	_	-0.7
unknown protein ;supported by full-length cDNA: Ceres:11578.	255857_at	-0.7
putative protein predicted protein, Arabidopsis thaliana; supported by full-length cDNA: Ceres:10189.	255808_at	-0.7
hypothetical protein similar to putative two-component response regulator protein GI:6623883 from [Arabidopsis thaliana]; supported by full-le	_	-0.7
unknown protein ;supported by full-length cDNA: Ceres:22071.	255718_at	-0.7
stress-induced protein OZI1 precursor; supported by cDNA: gi_790582_gb_U20347.1_ATU20347	255629_at	-0.7
coded for by A. thaliana cDNA R64991 ;supported by full-length cDNA: Ceres:19543.	255477_at	-0.7
predicted protein of unknown function; supported by full-length cDNA: Ceres: 8114.	255440_at	-0.7
putative C-type U1 snRNP similar to U1 small nuclear ribonucleoprotein C;supported by full-length cDNA: Ceres:20753.	255431_at	-0.7
hypothetical protein ; supported by full-length cDNA: Ceres: 94438.	255130_at	-0.7
hypothetical protein ;supported by full-length cDNA: Ceres:1354.	254969_at	-0.7
protein phosphatase type 1 PP1BG ;supported by full-length cDNA: Ceres:20905.	254923_at	-0.7
hypothetical protein ;supported by full-length cDNA: Ceres:41730.	254721_at	-0.7
putative protein putative oncogene protein, Homo sapiens, gb:AF026816; supported by full-length cDNA: Ceres: 8361.	254686_at	-0.7
putative protein	254694_at	-0.7
putative protein predicted gene M02B7.4, Caenorhabditis elegans, PID:G1572781	254658_at	-0.7
putative protein NADH oxidoreductase complex I subunit- like protein, Caenorhabditis elegans, AF143152	254378_at	-0.7
	254331_s_at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 38360.	254279_at	-0.7
putative protein annexin VII, Dictyostelium discoideum, PIR1:LUDO7	254262_at	-0.7
putative protein AR411 - Arabidopsis thaliana (thale cress), PID:g1669603; supported by cDNA: gi_13507100_gb_AF272748.1_AF272748	254231_at	-0.7
hypothetical protein ;supported by full-length cDNA: Ceres:29155.	254161_at	-0.7
	254163_s_at	-0.7
putative alliin lyase alliin lyase (EC 4.4.1.4) precursor (CYSTEINE SULPHOXIDE LYASE), onion, PIR2:S29301; supported by cDNA: gi_15.	254125_at	-0.7
putative protein ;supported by full-length cDNA: Ceres:16463.	254103_at	-0.7
putative pathogenesis-related protein gene PR-1 protein - Medicago truncatula, PIR2:S47171	254024_at	-0.7
putative protein centrin, Marsilea vestita;supported by full-length cDNA: Ceres:13072.	253915_at	-0.7
putative protein Cs protein, Drosophila melanogaster, AF091328;supported by full-length cDNA: Ceres:158028.	253692_at	-0.7
putative protein predicted protein, Arabidopsis thaliana, PIR2:T01282;supported by full-length cDNA: Ceres:32381.	253644_at	-0.7
putative protein predicted protein, Arabidopsis thaliana;supported by full-length cDNA: Ceres:154912.	253636_at	-0.7
putative protein RING-H2 finger protein RHX1a - Arabidopsis thaliana,PID:g3790591; supported by cDNA: gi_15809839_gb_AY054187.1_	253580_at	-0.7
putative protein hypothetical protein F9F13.130 - Arabidopsis thaliana, PIR2:T10590; supported by full-length cDNA: Ceres: 21252.	253593_at	-0.7
putative protein hypothetical protein YDR438w, Saccharomyces cerevisiae, Pir2:S69718; supported by cDNA: gi_15982861_gb_AY057538	253467_at	-0.7
H+-transporting ATP synthase chain 9 - like protein H+-transporting ATP synthase, Spinacia oleracea, PIR2:S34473; supported by full-lengt	253420_at	-0.7
putative protein ; supported by full-length cDNA: Ceres: 18715.	253230_at	-0.7
clathrin assembly protein AP19 homolog ;supported by full-length cDNA: Ceres:22906.	253199_at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 8360.	253119_at	-0.7
cysteine proteinase RD19A identical to thiol protease SP:P43296, GI:435618 from [Arabidopsis thaliana]; supported by full-length cDNA: Ce	252927_at	-0.7
mitochondrial carrier - like protein AgPET8, Ashbya gossypii, EMBL:AJ006406;supported by full-length cDNA: Ceres:32654.	252878_at	-0.7
Histon H3 ;supported by full-length cDNA: Ceres:2670.	252849_at	-0.7
homeodomain - like protein ; supported by cDNA: gi_15450981_gb_AY054571.1_	252829_at	-0.7
	252693_s_at	-0.7
CCR4-associated factor 1-like protein CAF1_MOUSE CCR4-ASSOCIATED FACTOR 1 - Mus musculus, SWISSPROT:CAF1_MOUSE; sur		-0.7
protein kinase-like protein protein kinase - Solanum berthaultii, EMBL:X97980	252646_at	-0.7

putative protein	252539 at	-0.7
phosphoprotein phosphatase ;supported by full-length cDNA: Ceres:32787.	252471 at	-0.7
putative protein	252419 at	-0.7
6-phosphogluconolactonase - like protein 6-phosphogluconolactonase (6PGL), Homo sapiens, EMBL:HSA243972;supported by full-length	252282 at	-0.7
putative protein supported by full-length cDNA: Ceres:118329.	252036 at	-0.7
Expressed protein ; supported by cDNA: gi 14517465 gb AY039568.1	252039 at	-0.7
ubiquinol-cytochrome-c reductase-like protein ubiquinol-cytochrome-c reductase, 8K chain, potato, PIR:T07369; supported by cDNA: gi 1	252012 at	-0.7
putative protein HSPC058, Homo sapiens, EMBL:AF161543;supported by full-length cDNA: Ceres: 12627.	251773 at	-0.7
putative protein	251727 at	-0.7
acetylglutamate kinase-like protein acetylglutamate kinase - Synechocystis sp., PIR:S77509;supported by full-length cDNA: Ceres:40830.	251639 at	-0.7
ribosomal protein S27 ; supported by cDNA: gi_4193381_gb_AF083336.1_AF083336	251357 at	-0.7
3-methyl-2-oxobutanoate hydroxy-methyl-transferase-like protein ketopantoate hydroxymethyltransferase - Emericella nidulans, EMBL:AF1	_	-0.7
plasma membrane intrinsic protein 1a ;supported by full-length cDNA: Ceres:6690.	251324 at	-0.7
peptidylprolyl isomerase ROC4 ;supported by full-length cDNA: Ceres:29220.	251305_at	-0.7
putative protein outer envelope membrane protein E 6.7 - chloroplast Spinacia oleracea, PIR:A35958; supported by cDNA: gi 15724349 c		-0.7
putative protein ;supported by full-length cDNA: Ceres:18955.	251034_at	-0.7
60S ribosomal protein - like 60S ribosomal protein L36, Arabidopsis thaliana, EMBL:AC004684;supported by full-length cDNA: Ceres:3090(		-0.7
putative protein ; supported by full-length cDNA: Ceres: 270908.	250923 at	-0.7
putative protein proline-rich protein APG, Arabidopsis thaliana, PIR:S21961; supported by full-length cDNA: Ceres: 13022.	250918 at	-0.7
putative protein ;supported by full-length cDNA: Ceres:13812.	250844 at	-0.7
40S ribosomal protein S17 -like 40S ribosomal protein S17, Lycopersicon esculentum, EMBL:AF161704;supported by full-length cDNA: Ce	_	-0.7
harpin-induced protein-like ; supported by cDNA: gi_9502175_gb_AF264699.1_AF264699	250676 at	-0.7
nucleoid DNA-binding-like protein supported by full-length cDNA: Ceres:15560.	250661 at	-0.7
putative protein PTD008, Homo sapiens, EMBL:AF078861;supported by full-length cDNA: Ceres:226.	250553 at	-0.7
putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:2344.	250399 at	-0.7
putative protein gibberellin-responsive protein CRG16, Cucumis sativus, EMBL:D49413	250358 at	-0.7
putative protein predicted proteins, Arabidopsis thaliana; supported by cDNA: gi 15912332 gb AY056444.1	250292 at	-0.7
putative protein similar to unknown protein (gb AAF63775.1)	250249 at	-0.7
ribosomal protein L33 - like ribosomal protein L33, Rickettsia prowazekii, PIR:E71650	249975 s at	-0.7
NADH:ubiquinone oxidoreductase - like protein NADH:ubiquinone oxidoreductase PGIV subunit, Homo sapiens, EMBL:AF044953; support	249959 at	-0.7
c-myc binding protein MM-1-like protein; supported by full-length cDNA: Ceres: 28832.	249829 at	-0.7
hypothetical protein supported by full-length cDNA: Ceres:40348.	249625 at	-0.7
CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED (TCH2) ;supported by full-length cDNA: Ceres:25475.	249583_at	-0.7
putative protein similar to unknown protein (pir  S75762)	249519 at	-0.7
50S ribosomal protein L27 ;supported by full-length cDNA: Ceres:152076.	249331_at	-0.7
beta-1,3-glucanase-like protein ;supported by full-length cDNA: Ceres:11988.	249235_at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 6893.	249162_at	-0.7
putative protein similar to unknown protein (emb CAB89401.1)	249071_at	-0.7
putative protein similar to unknown protein (gb AAD10670.1)	249072_at	-0.7
unknown protein ; supported by cDNA: gi_15027902_gb_AY045808.1_	249010_at	-0.7
subtilisin-like protease	248961_at	-0.7
putative protein similar to unknown protein (pir  T05076);supported by full-length cDNA: Ceres:42747.	248870_at	-0.7
ATP synthase delta chain, mitochondrial precursor (sp Q96252); supported by cDNA: gi_1655483_dbj_D88376.1_D88376	248825_at	-0.7
Bax inhibitor-1 like ;supported by full-length cDNA: Ceres:36400.	248833_at	-0.7
acetyl-CoA C-acetyltransferase ; supported by cDNA: gi_16604582_gb_AY059736.1_	248690_at	-0.7
unknown protein ; supported by cDNA: gi_13605737_gb_AF361850.1_AF361850	248588_at	-0.7
unknown protein ;supported by full-length cDNA: Ceres:27885.	248491_at	-0.7
unknown protein ; supported by full-length cDNA: Ceres: 266744.	248377_at	-0.7
putative protein similar to unknown protein (gb AAF34833.1)	248238_at	-0.7
zinc-binding protein-like ; supported by full-length cDNA: Ceres: 21629.	248187_at	-0.7
1,4-benzoquinone reductase-like; Trp repressor binding protein-like	248162_at	-0.7
putative protein similar to unknown protein (pir  B71406);supported by full-length cDNA: Ceres:22343.	248171_at	-0.7
putative protein similar to unknown protein (gb AAD32884.1)	248123_at	-0.7

putative protein similar to unknown protein (pir  T06631)	248074_at	-0.7
endoxyloglucan transferase (gb AAD45127.1); supported by cDNA: gi_1244751_gb_U43485.1_ATU43485	247866_at	-0.7
putative protein COP1-interacting protein CIP8, Arabidopsis thaliana, EMBL:AF162150; supported by cDNA: gi_15450686_gb_AY052711.1		-0.7
ring finger protein - like ring finger protein, Cicer arietinum, EMBL:AB026262	247595_at	-0.7
zinc finger protein OBP4 - like zinc finger protein OBP4, Arabidopsis thaliana, EMBL:AF155817;supported by full-length cDNA: Ceres:1908	247601_at	-0.7
putative protein ; supported by cDNA: gi_14596034_gb_AY042805.1_	247522_at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 30313.	247434_at	-0.7
putative protein predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 38273.	247443_at	-0.7
permease 1 - like protein permease 1, common ice plant, PIR:T12309; supported by cDNA: gi_14334659_gb_AY035003.1_	247404_at	-0.7
unknown protein ;supported by full-length cDNA: Ceres:16323.	247373_at	-0.7
nucleotide diphosphate kinase la (emb CAB58230.1); supported by cDNA: gi_3063660_gb_AF058391.1_AF058391	247376_at	-0.7
pectate lyase ; supported by cDNA: gi_16648839_gb_AY058197.1_	247377_at	-0.7
2-oxoglutarate/malate translocator ; supported by cDNA: gi_15810580_gb_AY056329.1_	247289_at	-0.7
unknown protein	247169 at	-0.7
auxin-induced protein IAA9 (pir  T05902) ;supported by full-length cDNA: Ceres:31563.	247148 at	-0.7
putative protein strong similarity to unknown protein (pir  T10240)	247132 at	-0.7
unknown protein :supported by full-length cDNA: Ceres:2518.	247006 at	-0.7
nucleic acid binding protein - like nucleic acid binding protein, Oryza sativa, PIR:T02745;supported by full-length cDNA: Ceres:32443.	246856 at	-0.7
putative protein various predicted bacterial rRNA methylases	246852 at	-0.7
putative protein bredicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:38304.	246792 at	-0.7
60S ribosomal protein L22 - like ribosomal protein L22 (cytosolic), Rattus norvegicus, PIR:S52084; supported by full-length cDNA: Ceres: 1	246745 at	-0.7
putative cytidine deaminase - like putative cytidine deaminase, Cicer arietinum, EMBL:AJ006764;supported by full-length cDNA: Ceres:372	246702 at	-0.7
unknown protein ; supported by full-length cDNA: Ceres: 34587.	246631 at	-0.7
	246641 at	-0.7
putative protein ;supported by full-length cDNA: Ceres:9667.	-	
unknown protein ; supported by cDNA: gi_16648790_gb_AY058172.1_	246391_at	-0.7
hypothetical protein predicted by genemark.hmm	246410_at	-0.7
putative protein non-consensus donor splice site GA at exon 1; predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_16209695_	246135_at	-0.7
hypothetical protein (fragment?)	246109_at	-0.7
putative protein CGI-45 protein - Homo sapiens, EMBL:AF151803;supported by full-length cDNA: Ceres:24749.	246097_at	-0.7
hypothetical protein ; supported by full-length cDNA: Ceres: 38847.	246074_at	-0.7
putative protein predicted proteins, Homo sapiens and Caenorhabditis elegans; supported by full-length cDNA: Ceres: 31390.	246008_at	-0.7
hypothetical protein ;supported by full-length cDNA: Ceres:38657.	245893_at	-0.7
extensin like protein	245479_at	-0.7
hypothetical protein ;supported by full-length cDNA: Ceres:16090.	245394_at	-0.7
ferredoxin ;supported by full-length cDNA: Ceres:22861.	245347_at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 19973.	245198_at	-0.7
ribosomal protein S4	245009_at	-0.7
hypothetical protein	245018_at	-0.7
hypothetical protein	244903_at	-0.7
hypothetical protein	244921_s_at	-0.7
DNA-3-methyladenine glycosidase, putative similar to DNA-3-methyladenine glycosidase GB:CAB60736 GI:6434028 from [Staphylococcus	257474_at	-0.7
hypothetical protein predicted by genemark.hmm	257556 at	-0.7
unknown protein similar to hypothetical protein GB:CAB55689 GI:5881771 from [Arabidopsis thaliana]	257578 x at	-0.7
hypothetical protein Similar to Caenorhabditis hypothetical protein CO7A9.11 (gb/Z29094)	264644 at	-0.7
hypothetical protein predicted by genscan+	260434 at	-0.7
hypothetical protein predicted by genemark.hmm, contains Pfam profile:PF00320 GATA zinc finger;supported by full-length cDNA: Ceres:1	258529 at	-0.7
unknown protein ; supported by full-length cDNA: Ceres: 9180.	256256 at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 94923.	245305 at	-0.7
putative tropinone reductase	267573 at	-0.6
putative C2H2-type zinc finger protein likely a nucleic acid binding protein; supported by cDNA: gi 14517523 gb AY039597.1	267535 at	-0.6
putative RING zinc finger protein ;supported by full-length cDNA: Ceres:17402.	267297 at	-0.6
60S ribosomal protein L36 ;supported by full-length cDNA: Ceres:23114.	267174 at	-0.6
	267138 s at	-0.6
	_01.100_0_ut	0.0

60S ribosomal protein L18A ; supported by cDNA: gi_14596030_gb_AY042803.1_	267007_at	-0.6
hypothetical protein predicted by genscan	266901_at	-0.6
putative expansin Experimental evidence from Dr. Daniel Cosgrove at Penn State Univ. <dcosgrove@psu.edu></dcosgrove@psu.edu>	266770_at	-0.6
40S ribosomal protein S30 ;supported by cDNA: gi_16974466_gb_AY061910.1_	266705_at	-0.6
hypothetical protein predicted by grail	266647_at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 9670.	266641_at	-0.6
DegP2 protease identical to DegP2 protease GI:13172275 from [Arabidopsis thaliana]	266509_at	-0.6
hypothetical protein predicted by genefinder; supported by cDNA: gi_15215635_gb_AY050346.1_	266463_at	-0.6
putative calcium binding protein ;supported by full-length cDNA: Ceres:31535.	266447_at	-0.6
putative tropinone reductase	266277_at	-0.6
putative zinc finger protein ;supported by full-length cDNA: Ceres:14203.	266261_at	-0.6
unknown protein ; supported by full-length cDNA: Ceres: 17020.	266138_at	-0.6
putative transport protein SEC61 beta-subunit ; supported by cDNA: gi_13878102_gb_AF370314.1_AF370314	266105_at	-0.6
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:10987.	266091_at	-0.6
glycerol-3-phosphate dehydrogenase ; supported by cDNA: gi_15293068_gb_AY050968.1_	266058_at	-0.6
unknown protein predicted by genscan and genefinder	266004 at	-0.6
hypothetical protein predicted by genefinder	265777 at	-0.6
RING-H2 finger protein RHA2b identical to GPIAF078823; supported by cDNA: gi 3790570 gb AF078823.1 AF078823	265740 at	-0.6
putative integral membrane protein	265713 at	-0.6
putative myosin heavy chain ; supported by cDNA: gi 15982766 gb AY057490.1	265679 at	-0.6
hypothetical protein predicted by genefinder; supported by full-length cDNA: Ceres: 32664.	265628 at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:29905.	265478 at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 11006.	265456 at	-0.6
unknown protein ; supported by full-length cDNA: Ceres: 1517.	265416 at	-0.6
unknown protein ; supported by cDNA: gi_13430617_gb_AF360221.1_AF360221	265248 at	-0.6
zinc finger protein 7, ZFP7; supported by cDNA; gi 790684 gb L39650.1 ATHZFPG	265029 at	-0.6
hypothetical protein similar to hypothetical protein GB:AAB61516 from F21J9;supported by full-length cDNA: Ceres:27548.	264869 at	-0.6
putative nuclear transport factor similar to nuclear transport factor 2 (NTF2) from [Oryza sativa]. GB:BAA81910; similar to ESTs gb[T21347,	264446 at	-0.6
nuclear ribonucleoprotein, putative similar to nuclear ribonucleoprotein GI:32353 from [Homo sapiens]	264418 at	-0.6
pEARLI 1-like protein may be induced when levels of Aluminum become toxic or other stresses become present in the plant:supported by fu	_	-0.6
hypothetical protein contains similarity to glutamic acid/alanine-rich protein GI:6707830 from [Trypanosoma congolense]	264307 at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 13607.	264304 at	-0.6
hypothetical protein predicted by genemark.hmm	264239 at	-0.6
protein kinase, putative Simisimilar to protein kinase 2 GI:7573598 from [Populus nigra]	264240 at	-0.6
putative 40S ribosomal protein S18 Match to ribosomal S18 gene mRNA gb/Z28701, DNA gb/Z23165 from A. thaliana. ESTs gb/T21121, gl	264203 at	-0.6
putative visit biosonial protein of the Match to hoosonial of the gene minuted gb/220101, bitted gb/220100 minuted to hoosonial protein Alternative splicing exists based on EST evidence	264028 at	-0.6
hypothetical protein predicted by genefinder; supported by full-length cDNA: Ceres:26961.	263999 at	-0.6
60S ribosomal protein L11B	263973_at	-0.6
hypothetical protein predicted by genscan; supported by full-length cDNA: Ceres: 113423.	263984 at	-0.6
	263964_at	-0.6
unknown protein	263760_at	-0.6
unknown protein ; supported by cDNA: gi_13265530_gb_AF324701.2_AF324701	_	-0.6
nucleic acid-binding protein, putative similar to nucleic acid-binding protein GI:168525 from [Zea mays];supported by full-length cDNA: Cere ribonuclease, RNS3 identical to ribonuclease SP:P42815, GI:562000 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:962:	263736_at 263689 at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:14886.	263710 at	-0.6
	_	-0.6
unknown protein ; supported by full-length cDNA: Ceres: 97914.	263541_at	
unknown protein ;supported by full-length cDNA: Ceres:74.	263396_at	-0.6 -0.6
putative C2H2-type zinc finger protein likely a nucleic acid binding protein	263411_at	
unknown protein ; supported by full-length cDNA: Ceres: 552.	263420_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:39169.	263371_at	-0.6
delta 9 desaturase ALMOST identical (4 aa diff t) to GP:2970036;supported by full-length cDNA: Ceres:21841.	263249_at	-0.6
myrosinase-associated protein, putative similar to myrosinase-associated protein GI:1769967 from [Brassica napus]; supported by cDNA: g	263161_at	-0.6
hypothetical protein predicted by genemark.hmm	263024_at	-0.6
ER lumen protein retaining receptor, putative similar to ER LUMEN PROTEIN RETAINING RECEPTOR GB:O44017 GI:6685402 from [Enta	∠o∠900_at	-0.6

unknown protein ;supported by full-length cDNA: Ceres: 15169.	262876_at	-0.6
putative auxin-induced protein similar to gb D14414 Indole-3-acetic acid induced protein from Vigna radiata. ESTs gb AA712892 and gb Z17	_	-0.6
oxidoreductase, putative contains Pfam profile: PF00671 Iron/Ascorbate oxidoreductase family	262616_at	-0.6
23 kDa polypeptide of oxygen-evolving comlex (OEC) identical to 23 kDa polypeptide of oxygen-evolving comlex (OEC) GB:CAA66785 GI:1		-0.6
putative 20S proteasome beta subunit PBC2 almost identical to GB:AAC32069 from [Arabidopsis thaliana], EST gb T76747 comes from thi	_	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 10252.	262338_at	-0.6
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:40196.	262284_at	-0.6
putative GDP-mannose pyrophosphorylase similar to GDP-mannose pyrophosphorylase A GB:AAD38517 (Homo sapiens); supported by cE	_	-0.6
allergen, putative similar to allergen (Ole e 1) GI:2465129 from [Olea europaea];supported by full-length cDNA: Ceres:22488.	262195_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:35603.	262057_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:113571.	261822_at	-0.6
	261362_s_at	-0.6
AP2 domain containing protein, putative similar to AP2 domain containing protein RAP2.5 GI:2281635 from (Arabidopsis thaliana); supporte	261315_at	-0.6
unknown protein ; supported by cDNA: gi_15292702_gb_AY050785.1_	261293_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:207684.	261201_at	-0.6
unknown protein contains Pfam profile: PF02190 ATP-dependent protease La (LON) domain	261141_at	-0.6
peroxisomal targeting signal type 2 receptor almost identical to peroxisomal targeting signal type 2 receptor GB:AAD27848 GI:4689316 from	260844 at	-0.6
UDP-glucose glucosyltransferase, putative similar to UDP-glucose glucosyltransferase GI:3928543 from [Arabidopsis thaliana]	260799 at	-0.6
14-3-3 protein GF14omega (grf2) identical to GF14omega isoform GI:487791 from [Arabidopsis thaliana]; supported by full-length cDNA: Ce	260775 at	-0.6
chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:26943.	260714 at	-0.6
unknown protein :supported by full-length cDNA: Ceres:143451.	260724 at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:123140.	260666 at	-0.6
putative ADP-ribosylation factor 1 nearly identical to ADP-ribosylation factor 1 GB:P36397 [Arabidopsis thaliana];supported by full-length cD	260305 at	-0.6
hypothetical protein similar to YGL010w-like protein GB:AAC32136 [Picea mariana]	260211 at	-0.6
hypothetical protein predicted by genefinder	260205 at	-0.6
gibberellin regulatory protein, putative similar to GB:CAA75492 from [Arabidopsis thaliana]; supported by cDNA: gi 15777856 gb AY04874		-0.6
putative transcription factor BTF3 (RNA polymerase B transcription factor 3) similar to transcription factor BTF3 (RNA polymerase B transcription factor 3) similar to transcription factor BTF3 (RNA polymerase B transcription factor 3) similar to transcription factor BTF3 (RNA polymerase B transcription factor 3) similar to transcription factor BTF3 (RNA polymerase B transcription factor 3) similar to transcription factor BTF3 (RNA polymerase B transcription factor 3) similar to transcription factor BTF3 (RNA polymerase B transcription factor 3) similar to transcription factor BTF3 (RNA polymerase B transcription factor 3) similar to transcription factor BTF3 (RNA polymerase B transcription factor 3) similar to transcription factor BTF3 (RNA polymerase B transcription factor 3) similar to transcription factor BTF3 (RNA polymerase B transcription factor 3) similar to transcription factor BTF3 (RNA polymerase B transcription factor 3) similar to transcription factor BTF3 (RNA polymerase B transcription factor 3) similar to transcription factor BTF3 (RNA polymerase B transcription factor 3) similar to transcription factor BTF3 (RNA polymerase B transcription factor 3) similar to transcription factor BTF3 (RNA polymerase B transcription factor 3) similar to transcription factor BTF3 (RNA polymerase B transcription factor 3) similar to transcription factor BTF3 (RNA polymerase B transcription factor 3) similar to transcription 4) similar to transcriptin 4) similar to	260095 at	-0.6
putative ranscription ractor BTF 5 (rttva polymerase B transcription ractor 5) similar to transcription ractor BTF 5 (rttva polymerase B transcription ractor 5) similar to transcription ractor BTF 5 (rttva polymerase B transcription ractor 5) similar to transcription ractor BTF 5 (rttva polymerase B transcription ractor 5) similar to transcription ractor BTF 5 (rttva polymerase B transcription ractor 5) similar to transcription ractor BTF 5 (rttva polymerase B transcription ractor 5) similar to transcription ractor BTF 5 (rttva polymerase B transcription ractor 5) similar to transcription ractor BTF 5 (rttva polymerase B transcription ractor 5) similar to transcription ractor BTF 5 (rttva polymerase B transcription ractor 5) similar to transcription ractor BTF 5 (rttva polymerase B transcription ractor 5) similar to transcription ractor 5) simi	-	-0.6
	_	-0.0 -0.6
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:28316. plasma membrane associated protein, putative similar to GI:6851373 from [Hordeum vulgare]	260078_at 259774 at	-0.0 -0.6
	_	
Expressed protein ; supported by full-length cDNA: Ceres: 14943.	259661_at	-0.6
bZIP transcription factor, putative contains Pfam profile: PF00170: bZIP transcription factor; supported by cDNA: gi_15028322_gb_AY0459	259626_at	-0.6
hypothetical protein	259583_at	-0.6
hypothetical protein	259530_at	-0.6
unknown protein	259497_at	-0.6
protein phosphatase type 2C, putative similar to protein phosphatase type 2C GI:4336436 from [Lotus japonicus]	259506_at	-0.6
putative thymidine kinase similar to thymidine kinase GB:AAC31168 [Oryza sativa]; supported by full-length cDNA: Ceres: 19188.	259224_at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 20097.	259214_at	-0.6
putative ribosomal protein S2 similar to putative ribosomal protein S2 GB:CAA74226 [Mitochondrion Triticum aestivum]; supported by full-len	-	-0.6
calmodulin-like protein similar to calmodulin GB:AAA34015 [Glycine max], Pfam HMM hit: EF hand	259143_at	-0.6
unknown protein similar to putative protein GB:CAB40986 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:5170.	259093_at	-0.6
DNA-damage-repair/toleration protein DRT102 identical to DNA-damage-toleration protein DRT102 GB:Q05212 [Arabidopsis thaliana]; supr		-0.6
unknown protein similar to unknown protein GB:AAD21471 [Arabidopsis thaliana]; supported by cDNA: gi_15810316_gb_AY056197.1_	259072_at	-0.6
unknown protein ;supported by cDNA: gi_13877548_gb_AF370475.1_AF370475	259023_at	-0.6
vacuolar membrane ATPase subunit G (AVMA10) identical to vacuolar membrane ATPase subunit G (AVMA10) GB:AF181688 [Arabidopsis	258958_at	-0.6
hypothetical protein predicted by genefinder, Pfam HMM hit: RNA recognition motif. (aka RRM, RBD, or RNP domain), zinc finger: CCHC c	258943_at	-0.6
putative 40S ribosomal protein S17 similar to 40S ribosomal protein S17 GB:AAD50774 [Lycopersicon esculentum]; supported by full-length	258922_at	-0.6
unknown protein ; supported by full-length cDNA: Ceres: 35785.	258846_at	-0.6
putative 60S ribosomal protein L35 similar to 60S ribosomal protein L35 GB:AAC27830;supported by full-length cDNA: Ceres:23470.	258709_at	-0.6
B regulatory subunit of PP2A (AtB beta) identical to B regulatory subunit of PP2A (AtB beta) GB:U73527 [Arabidopsis thaliana] (Eur. J. Bic	258659_at	-0.6
ribosomal protein L17, putative similar to ribosomal protein L17 GB:AAA34113.1 from [Nicotiana tabacum]; supported by full-length cDNA: (	258569_at	-0.6
hypothetical protein predicted by genemark.hmm	258247_at	-0.6
unknown protein ; supported by full-length cDNA: Ceres: 11852.	258194_at	-0.6
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Expressed protein ; supported by cDNA: gi_14334997_gb_AY037178.1_	257860_at	-0.6
60S ribosomal protein, putative similar to 60S RIBOSOMAL PROTEIN L30 GB:O49884 from [Lupinus luteus]; supported by full-length cDNA	_	-0.6
hypothetical protein predicted by genemark.hmm	257724_at	-0.6
unknown protein contains Pfam profiles: PF00560 leucine rich repeat, PF00069 eukaryotic protein kinase domain	257297_at	-0.6
60S ribosomal protein L34, putative similar to 60S ribosomal protein L34 GB:P41098 [Nicotiana tabacum]; supported by cDNA: gi_1502792	_	-0.6
ER lumen retaining receptor (HDEL receptor), putative similar to GB:P35402 from [Arabidopsis thaliana]; supported by full-length cDNA: Cel	_	-0.6
hypothetical protein similar to unknown protein GB:AAC63835 from [Arabidopsis thaliana]	256942_at	-0.6
unknown protein contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger)	256917_at	-0.6
photosystem I subunit X precursor identical to photosystem I subunit X precursor [Arabidopsis thaliana] GI:5738540; supported by full-length	256309_at	-0.6
unknown protein ; supported by cDNA: gi_15982827_gb_AY057521.1_	256270_at	-0.6
predicted protein	256090_at	-0.6
leucine zipper protein, putative similar to leucine zipper protein GI:10177020 from [Arabidopsis thaliana]	256050_at	-0.6
hypothetical protein contains similarity to photoperiod sensitivity quantitative trait locus (Hd1) GI:11094203 from [Oryza sativa]; supported by	256060_at	-0.6
hypothetical protein contains similarity to photosystem II 22 kDa protein GI:6006279 from [Arabidopsis thaliana];supported by full-length cDN	255982_at	-0.6
Expressed protein ; supported by cDNA: gi_15010591_gb_AY045597.1_	255793_at	-0.6
putative protein predicted protein, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 1489.	255809_at	-0.6
hypothetical protein ; supported by full-length cDNA: Ceres: 28203.	255810 at	-0.6
putative ribosomal protein S13 similar to ribosomal protein S13 (Pfam;supported by full-length cDNA: Ceres:4058.	255706 at	-0.6
SAR1/GTP-binding secretory factor ;supported by full-length cDNA: Ceres:94610.	255505 at	-0.6
predicted NADH dehydrogenase 24 kD subunit similar to N. crassa NADH-ubiguinone dehydrogenase 24 kD subunit precursor, GenBank a	_	-0.6
putative photosystem I reaction center subunit II precursor similar to spinach PSI-D, GenBank accession number P12353;supported by full-	255457 at	-0.6
putative protein hypothetical protein ssr1391 - Synechocystis sp. (strain PCC 6803), PIR2:S75571; supported by cDNA: gi 14190426 gb A	_	-0.6
RING-H2 finger protein RHA1a -like protein ;supported by full-length cDNA: Ceres:21591.	254922 at	-0.6
hypothetical protein	254755 at	-0.6
shaqqy-like protein kinase etha (EC 2.7.1) ;supported by full-length cDNA: Ceres:256076.	254616 at	-0.6
putative snRNP protein small nuclear ribonucleoprotein B, human, PIR2:S09377;supported by full-length cDNA: Ceres:36005.	254475 at	-0.6
putative DNA-binding protein DNA-binding protein WRKY3 - Petroselinum crispum, PIR2:S72445;supported by full-length cDNA: Ceres:112		-0.6
	253898 s at	-0.6
putative RING zinc finger protein Arabidopsis thaliana RMA/ MRNA, PID:d1029538	253865 at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 42507.	253830 at	-0.6
putative zinc finger protein zinc finger protein SINA1p - Vitis vinifera,PID:e1423803	253838 at	-0.6
putative protein Arabidopsis thaliana RMA1 mRNA, PID:d1029538	253806 at	-0.6
phytochrome-associated protein PAP2; supported by cDNA; gi 12083213 gb AF332402.1 AF332402	253749 at	-0.6
putative protein hypothetical protein - Arabidopsis thaliana. PIR2:T04873	253530 at	-0.6
ribosomal protein S6 - like ribosomal protein S6. Arabidopsis thaliana, PID:g2662469; supported by cDNA: gi 15292738 gb AY050803.1	253487 at	-0.6
putative protein auxin-induced protein, Helianthus annuus, gb:AF030301; supported by cDNA: gi 15215697 gb AY050377.1	253307 at	-0.6
putative protein AT.1.24-7, Arabidopsis thaliana, db:U63815	253215 at	-0.6
putative protein predicted protein, Arabidopsis thaliana; supported by full-length cDNA: Ceres:1368.	253183 at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 1095.	253117 at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 39781.	252979 at	-0.6
putative pectinesterase pectinesterase - Lycopersicon esculentum, PID:e312172	252989 at	-0.6
putative protein other predicted proteins Arabidopsis thaliana;supported by full-length cDNA: Ceres:123929.; supported by cDNA: gi 15810.	_	-0.6
AtRer1A; supported by full-length cDNA: Ceres: 21466.	252913 at	-0.6
putative protein	252866 at	-0.6
putative protein	252676 at	-0.6
	252601 s at	-0.6
histone H2B -like protein histone H2B1, upland cotton, PIR:T09722;supported by full-length cDNA: Ceres:10517.	252560 at	-0.6
	_	-0.6
E2, ubiquitin-conjugating enzyme 13 (UBC13) identical to gi:992706; supported by cDNA: gi_15215679_gb_AY050368.1_ RNA-binding protein-like protein various RNA-binding proteins;supported by full-length cDNA: Ceres:9763.	252528_at 252464 at	-0.6 -0.6
MTN3-like protein MtN3 gene product - Medicago truncatula,PID:e1169583; supported by cDNA: gi 13605687 gb AF361825.1 AF361825.	_	-0.6
signal recognition particle subunit 9 - like signal recognition particle subunit 9, Zea mays, EMBL:Y10117;supported by full-length cDNA: Cer		-0.6 -0.6
putative protein hypothetical protein T19L18.12 - Arabidopsis thaliana, PIR:T02616;supported by full-length cDNA: Ceres:32231.	_	-0.6 -0.6
ubiquitin extension protein (UBQ1) identical to GI:166929, GI:166930;supported by full-length cDNA: Ceres:18586.	252125_at 252056 at	-0.6 -0.6
abiquitin extension protein (obsch) lucifica to Gr. 100323, Gr. 100330, supported by full-feligiti conv. Getes. 10300.	202000_at	-0.0

hypothetical protein YIP1 protein, Saccharomyces cerevisiae, PIR:S64486	252002_at	-0.6
chlorophyll a/b-binding protein ;supported by cDNA: gi_13265500_gb_AF324692.2_AF324692	251814_at	-0.6
ribosomal protein L35 -like various ribosomal L35 proteins	251834_at	-0.6
putative protein hypothetical protein F22K20.16 - Arabidopsis thaliana, EMBL:AC002291	251701_at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 255818.	251660_at	-0.6
ribosomal protein L11 -like ribosomal protein L11, cytosolic, Arabidopsis thaliana, PIR:S49033;supported by full-length cDNA: Ceres:14042		-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 42545.	251409_at	-0.6
homeobox-leucine zipper protein HAT3 ; supported by cDNA: gi_527632_gb_U09338.1_ATU09338	251374_at	-0.6
putative protein hypothetical protein T17J13.170 - Arabidopsis thaliana, PIR:T48013	251355_at	-0.6
putative protein hypothetical protein F4I18.26 - Arabidopsis thaliana, PIR:T02471;supported by full-length cDNA: Ceres:30454.	251336_at	-0.6
CP12 protein precursor-like protein CP12 protein precursor, chloroplast - Pisum sativum,PIR:T06562;supported by full-length cDNA: Ceres:	251218_at	-0.6
putative protein S1R protein - Homo sapiens, EMBL:AF113127	251163_at	-0.6
ATMRK1 ;supported by full-length cDNA: Ceres:253505.	251170_at	-0.6
putative protein latex protein allergen Hev b 7 - Hevea brasiliensis, EMBL:AF113546; supported by cDNA: gi_15912226_gb_AY056391.1_	251174_at	-0.6
putative chloroplast inner envelope protein membrane protein, 37K, precursor, chloroplast inner envelope, common tobacco, PIR:T03230;s	251118_at	-0.6
chloroplast ribosomal L1 - like protein ribosomal protein L1, S.oleracea, EMBL:SORPL1; supported by cDNA: gi 15450736 gb AY053410.	251120 at	-0.6
putative protein MED7, Homo sapiens, EMBL:AF031383;supported by full-length cDNA: Ceres:95433.	250932 s at	-0.6
putative protein similar to unknown protein (emb CAB81585.1);supported by full-length cDNA: Ceres:18108.	250762 at	-0.6
putative protein similar to unknown protein (emb CAB88360.1);supported by full-length cDNA: Ceres:29476.	250764_at	-0.6
putative protein similar to unknown protein (sp P73920)	250727 <sup>_</sup> at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:262293.	250665 at	-0.6
copine-like protein copine VII protein - Homo sapiens, EMBL:AJ133798; supported by cDNA: gi 14488103 gb AF389301.1 AF389301	250581 at	-0.6
putative protein similar to unknown protein (emb[CAB61744.1); supported by full-length cDNA: Ceres: 12613.	250511 at	-0.6
enhancer of rudimentary ; supported by cDNA: gi 1595811 gb U67398.1 ATU67398	250406 at	-0.6
putative potassium transport protein glutathione-regulated potassium-efflux system protein KEFB, Escherichia coli, SWISSPROT:P45522	250329 at	-0.6
putative protein proteins, Schizosaccharomyces pombe	250281 at	-0.6
putative protein (supported by full-length cDNA: Ceres:5392.	250289 at	-0.6
putative protein polyceptide deformylase. Aquifex aeolicus. PIR:C70352:supported by full-length cDNA: Ceres:150612.	250146 at	-0.6
putative protein similar to unknown protein (dbi/BA490342.1):supported by full-length CDNA: Ceres:1816.	250027 at	-0.6
beta-amylase-like proten beta-amylase - Prunus armeniaca, EMBL:AF139501;supported by full-length cDNA: Ceres:30798.	2500027_dt	-0.6
putative protein similar to unknown protein (gb/AAF02129.1);supported by full-length cDNA: Ceres:35419.	249941 at	-0.6
putative protein similar to unknown protein (gb/x4) of 12.5.1, supported by full-length cDNA. Ceres:118777.	249874 at	-0.0 -0.6
6-phosphogluconolactonase-like protein ;supported by full-length cDNA: Ceres:21890.	249733 at	-0.6
putative protein similar to unknown protein (emb CAB62461.1);supported by full-length cDNA: Ceres:268701.	249752 at	-0.6
putative protein similar to dikinown protein (end onboze of 1, supported by cDNA; gi 15810334 gb AY056206.1	249580 at	-0.6
14-3-3 protein GF14psi (grf3/RCI1) identical to 14-3-3 protein GF14 psi GI:1168200, SP:P42644; supported by cDNA: gi_166716_gb_L091	249500_at 249514 at	-0.0 -0.6
putative protein MtN24 gene, Medicago truncatula, EMBL:MTY15290	249400 at	-0.0 -0.6
protein kinase - like protein protein kinase ATN1, Arabidopsis thaliana, PIR:S61766	249361 at	-0.6
prohibitin (gb AAC49691.1) :supported by full-length cDNA: Ceres:37298.	249344_at	-0.0 -0.6
	249258 at	-0.6
putative protein similar to unknown protein (gb AAF24581.1)	249256_at 249188_at	-0.6
N-hydroxycinnamoyl benzoyltransferase-like protein		-0.6
unknown protein ;supported by full-length cDNA: Ceres:32890.	249190_at	-0.6 -0.6
putative protein similar to unknown protein (gb/AAF69166.1); supported by cDNA: gi_15451133_gb_AY054647.1_	249182_at	
DNA binding protein EREBP-3-like protein	249087_at	-0.6
cytochrome P450	248964_at	-0.6
NADH dehydrogenase 10.5K chain-like protein ; supported by full-length cDNA: Ceres: 39633.	248746_at	-0.6
indole-3-glycerol phosphate synthase ; supported by cDNA: gi_15215597_gb_AY050327.1_	248688_at	-0.6
U6 snRNA-associated Sm-like	248678_at	-0.6
NaCl-inducible Ca2+-binding protein-like; calmodulin-like ; supported by cDNA: gi_13358217_gb_AF325028.2_AF325028	248607_at	-0.6
	248566_s_at	-0.6
transport inhibitor response 1 (TIR1), putative similar to F-box containing protein TIR1 GI:13249030 from [Populus tremula x Populus tremu		-0.6
	248521_s_at	-0.6
unknown protein ; supported by full-length cDNA: Ceres: 21548.	248376_at	-0.6

fructokinase 1 ; supported by cDNA: gi_13878052_gb_AF370289.1_AF370289	248381_at	-0.6
unknown protein	248341_at	-0.6
GTP-binding protein-like ;supported by full-length cDNA: Ceres:16621.	248346_at	-0.6
putative protein contains similarity to RNA-binding protein; supported by full-length cDNA: Ceres: 14044.	248173_at	-0.6
putative protein similar to unknown protein (gb AAD50013.1)	248140_at	-0.6
small Ras-like GTP-binding protein (gb AAB58478.1);supported by cDNA: gi_14596016_gb_AY042796.1_	248107_at	-0.6
putative protein similar to unknown protein (pir  T07080)	248058_at	-0.6
putative protein contains similarity to unknown protein (pir  T08924);supported by full-length cDNA: Ceres:141890.	248040_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:33108.	248041 at	-0.6
calcineurin B-like protein 2 (gb AAC26009.1) ;supported by full-length cDNA: Ceres:37280.	248001_at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 17375.	247817_at	-0.6
cytochrome c oxidase subunit - like cytochrome c oxidase subunit 5c, Oryza sativa, EMBL:AB027123;supported by full-length cDNA: Ceres	247520 at	-0.6
E2, ubiquitin-conjugating enzyme 3 (UBC3) identical to gi:431261, SP:P42746;supported by full-length cDNA: Ceres:148141.	247433_at	-0.6
putative protein predicted proteins, Oryza sativa, Arabidopsis thaliana and yeast	247396 at	-0.6
putative protein contains similarity to acetyltransferase; supported by full-length cDNA: Ceres: 31971.	247330 at	-0.6
putative protein similar to unknown protein (emb CAB89373.1); supported by cDNA: gi 14334413 gb AY034898.1	247285 at	-0.6
putative protein similar to unknown protein (emb CAB16809.1); supported by full-length cDNA: Ceres: 118150.	247150 at	-0.6
WD repeat protein-like ;supported by full-length cDNA: Ceres:11277.	247106 at	-0.6
33 kDa polypeptide of oxygen-evolving complex (OEC) in photosystem II (emb[CAA75629.1) ;supported by full-length cDNA: Ceres:37218.		-0.6
leucine-rich repeats containing protein grr1 - Glycine max. EMBL:AF019910	246935 at	-0.6
putative protein various predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:28528.	246860 at	-0.6
drought-induced protein - like non-consensus AT donor splice site at exon 3, AC acceptor splice site at exon 4, drought-induced protein Di1		-0.6
putative protein seven transmembrane domain orphan receptor, Mus musculus, EMBL:AF051098;supported by full-length cDNA: Ceres:964	_	-0.6
ADP-ribosylation factor -like protein ADP-ribosylation factor, Dugesia japonica, EMBL:DJAB1051;supported by full-length cDNA: Ceres:268		-0.6
glucose 6 phosphate/phosphate translocator-like protein glucose 6 phosphate/phosphate translocator - Arabidopsis thaliana, EMBL:AF233(	_	-0.6
Ca2+/H+-exchanging protein-like Arabidopsis thaliana high affinity calcium antiporter CAX1 encoded by GenBank Accession Number U574	_	-0.6
E2, ubiquitin-conjugating enzyme 17 (UBC17) identical to gi:2801446; supported by full-length cDNA: Ceres:40968.	246195 at	-0.6
ribosomal protein L36-like ribosomal protein L36 - Synectocystis sp., PIR:S77481;supported by full-length cDNA: Ceres:28109.	246073 at	-0.6
dutared xin supported by full-length cDNA: Ceres:115597.	246092 at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 31366.	246007 at	-0.6
elongation factor 1B alpha-subunit ;supported by full-length cDNA: Ceres:26936.	245949 at	-0.6
predicted protein	245913 at	-0.6
putative protein ; supported by full-length cDNA: Ceres: 8242.	245894 at	-0.6
hypothetical protein similar to hypothetical protein GB:AAD18105 GI:4337191 from [Arabidopsis thaliana]	245784 at	-0.6
rec - like protein	245695 at	-0.6
carniting racemase like protein	245612 at	-0.6
cytochrome c oxidoreductase like protein	245524 at	-0.6
cyanohydrin lyase like protein ;supported by full-length cDNA: Ceres:5546.	245349 at	-0.6
60S ribosomal protein L15 homolog ;supported by full-length cDNA: Ceres:31538.	245355 at	-0.6
putative protein supported by full-length CDNA: Ceres:2161.	245357 at	-0.6
hypothetical protein ;supported by full-length cDNA: Ceres:42815.	245361 at	-0.6
ribosomal protein ; supported by full-length cDNA: Ceres: 18153.	245311 at	-0.6
DNA-binding homeotic protein Athb-2 ; supported by cDNA: gi 166751 gb M90394.1 ATHHOMEOA	245276 at	-0.6
ATP-sulfurylase; supported by cDNA: gi 459143 gb U06275.1 ATU06275	245254 at	-0.6
putative poly(A) binding protein ; supported by cDNA: gi 15292850 gb AY050859.1	245085 at	-0.6
unknown protein Alternative splice forms exist.;supported by full-length cDNA: Ceres:9368.	245044 at	-0.6
	244993 s at	-0.6
hypothetical protein predicted by genefinder	257398 at	-0.6
unknown protein	257495_at	-0.6
hypothetical protein	257583 at	-0.6
hypothetical protein predicted by genemark.hmm	261509 at	-0.6
unknown protein ; supported by cDNA: gi 16648938 gb AY059839.1	261320 at	-0.6
putative RAS-related GTP-binding protein similar to RAS-related GTP-binding protein GB:AAD22451.1 from [Gossypium hirsutum];supporte		-0.6
parate reaction related on - undering protein annual to recorrelated on - undering protein GD. Add22401.1 non [Gossypluin Institutin], supporte	2000 1+_al	-0.0

Expressed protein ; supported by full-length cDNA: Ceres: 7103.	258105_at	-0.6
Histone deacetylase ; supported by cDNA: gi_11066138_gb_AF195547.1_AF195547	252982_at	-0.6
Expressed protein ; supported by full-length cDNA: Ceres: 34967.	245326_at	-0.6
mitochondrial F1-ATPase, gamma subunit (ATP3_ARATH) ;supported by full-length cDNA: Ceres:26812.	267600_at	-0.5
photosystem II reaction center 6.1KD protein ;supported by full-length cDNA: Ceres:34999.	267526_at	-0.5
putative UDP-N-acetylglucosamine pyrophosphorylase ;supported by full-length cDNA: Ceres:5509.	267432_at	-0.5
putative protein transport protein SEC13 ;supported by full-length cDNA: Ceres:36577.	267277_at	-0.5
putative sugar nucleotide phosphorylase ; supported by cDNA: gi_12697582_dbj_AB037876.1_AB037876	267220_at	-0.5
unknown protein	267230_at	-0.5
60S ribosomal protein L7 ;supported by full-length cDNA: Ceres:36813.	267213_at	-0.5
putative DOF zinc finger protein	267171_at	-0.5
aquaporin (plasma membrane intrinsic protein 1B) identical to GB:Z17399, GB:Z17424, and GB:68293; supported by full-length cDNA: Cere	_	-0.5
putative phosphomannomutase ;supported by full-length cDNA: Ceres:998.	266928_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:37655.	266709_at	-0.5
defender against cell death protein identical to (but predicted longer than) GB: 2623633;supported by full-length cDNA: Ceres:3992.	266639_at	-0.5
hypothetical protein predicted by genefinder and genscan; supported by cDNA: gi_15724241_gb_AF412061.1_AF412061	266608_at	-0.5
Expressed protein ; supported by cDNA: gi_15215834_gb_AY050447.1_	266583_at	-0.5
unknown protein	266510_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:10341.	266483_at	-0.5
calmodulin-like protein identical to GB:X68054;supported by full-length cDNA: Ceres:11537.	266371_at	-0.5
putative RGA1, giberellin repsonse modulation protein identical to GB:Y11336, member of SCARECROW family; supported by cDNA: gi_1!	266331_at	-0.5
unknown protein contains non-consensus donor splice site AT at exon2 and acceptor splice site AC at exon3.	266253_at	-0.5
putative aquaporin (water channel protein); supported by cDNA: gi_15010777_gb_AY045690.1_	266172_at	-0.5
putative SCARECROW gene regulator	266131_at	-0.5
encyl-ACP reductase (enr-A)	266035_at	-0.5
	265963_s_at	-0.5
unknown protein	265847_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:38690.	265771_at	-0.5
unknown protein hypothetical protein cimiles to hypothetical protein CB(AAD19129) cymported hy fyll length cDNA: Corece 23166	265637_at	-0.5 -0.5
hypothetical protein similar to hypothetical protein GB:AAD18138; supported by full-length cDNA: Ceres: 23166.	265547_at	
hypothetical protein ;supported by full-length cDNA: Ceres:5.	265479_at	-0.5 -0.5
unknown protein ;supported by full-length cDNA: Ceres:250015. putative caltractin ;supported by full-length cDNA: Ceres:7802.	265458_at 265460 at	-0.5
	_	-0.5
unknown protein unknown protein ; supported by full-length cDNA: Ceres: 91872.	265417_at 265390 at	-0.5
lipoic acid synthase (LIP1); supported by cDNA: gi 14334939 gb AY035143.1	265390_at	-0.5
	265336 at	-0.5
hypothetical protein predicted by genscan; supported by full-length cDNA: Ceres: 32047. hypothetical protein	265227 s at	-0.5
	265203 at	-0.5
unknown protein unknown protein Location of ESTs 203/24T7, gb/H76794 and 203/24XP, gb/AA605510;supported by full-length cDNA: Ceres:9756.	_	-0.5
Expressed protein ; supported by cDNA: gi 14596174 gb AY042875.1	265039_at 265043 at	-0.5
	_	-0.5
putative JUN kinase activator protein similar to JUN activation domain binding proteins GB:AAC36344, GB:AAC36343, and GB:AAC26484;	264724_at	-0.5
serine threonine protein phosphatase (type 2A) identical to type 2A serine threonine protein phosphatase GB:AAC49668 (Arabidopsis thalia unknown protein ;supported by full-length cDNA: Ceres:2935.	264703_at 264609_at	-0.5
putative pectate lyase A11 similar to GB:CAB36835:supported by full-length cDNA: Ceres:37952.	264611 at	-0.5
photosystem I subunit V precursor, putative similar to photosystem I subunit V precursor GB:CAB52748 GI:5734520 from [Arabidopsis thali	_	-0.5
Expressed protein ; supported by cDNA: gi 14488091 gb AF389294.1 AF389294	264546 at	-0.5
germin-like protein Identical to Arabidopsis germin-like protein, gi 1755178. Location of EST 180L10T7, gi 906417; supported by cDNA: gi	_	-0.5
	264506_at 264419 s at	-0.5 -0.5
		-0.5
unknown protein similar to hypothetical protein GI:4079632 from [Arabidopsis thaliana]	264424_at	-0.5 -0.5
symbiosis-related protein, putative similar to symbiosis-related protein GI:2072022 from [Laccaria bicolor]; supported by full-length cDNA: Cu	264285_at 264054 at	-0.5 -0.5
unknown protein unknown protein ;supported by full-length cDNA: Ceres:33232.	263880 at	-0.5
uninown proton , supported by full-length obtain. Geres. Jozoz.	200000_at	-0.5

	262821 of	0.5
putative ferritin putative fructose bisphosphate aldolase ; supported by cDNA: gi 14334739 gb AY035043.1	263831_at 263761 at	-0.5 -0.5
unknown protein similar to unknown protein GB:AAC79135, ESTs gb/T20423, gb/AA712864, gb/H76323 and gb/Z25560 come from this ge	263701_at 263704 at	-0.5
putative tyrosine aminotransferase ;supported by full-length cDNA: Ceres:14570.	263539 at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:15081.	263431 at	-0.5
unknown protein ; supported by full-length cDNA: Ceres: 11283.	263399 at	-0.5
predicted protein ; supported by full-length cDNA: Ceres:28779.	263410 at	-0.5
putative snRNP splicing factor ;supported by full-length cDNA: Ceres:97480.	263332 at	-0.5
alanine-glyoxylate aminotransferase ;supported by full-length cDNA: Ceres:8306.	263350 at	-0.5
unknown protein similar to ESTs gb/H36734 and gb/A4651244	263256 at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:3173.	263129 at	-0.5
unknown protein	263142 at	-0.5
protein translation factor Sui1 homolog, putative similar to protein translation factor Sui1 homolog GI:9758256 from [Arabidopsis thaliana]; s	_	-0.5
glutathione-s-transferase, putative similar to GST3 HUMAN SP:O14880; supported by full-length cDNA: Ceres: 8446.	262932 at	-0.5
NADPH-dependent codeinone reductase, putative similar to NADPH-dependent codeinone reductase GI:6478210 from [Papaver somnifer.	_	-0.5
membrane related protein CP5, putative similar to membrane related protein CP5 GI:4741929 from [Arabidopsis thaliana]; supported by cD		-0.5
unknown protein ;supported by full-length cDNA: Ceres:17521.	262801 at	-0.5
putative translation initiation factor similar to gb/U54559 eIF3-p40 subunit from Homo sapiens and is a member of the PF/01398 Mov34 familiar	262790 at	-0.5
photosystem I subunit III precursor, putative similar to photosystem I subunit III precursor GB:U08135 GI:854707 from[Hordeum vulgare];su	262557 at	-0.5
unknown protein EST gb/T41993 comes from this gene; supported by full-length cDNA: Ceres:97320.	262499 at	-0.5
disease resistance protein, putative similar to disease resistance protein GI:9758876 from [Arabidopsis thaliana]	262383_at	-0.5
putative ubiquinol-cytochrome c reductase similar to ubiquinol-cytochrome c reductase GB:P48504 from [Solanum tuberosum]; supported b	262206_at	-0.5
Expressed protein ; supported by full-length cDNA: Ceres: 28445.	262116_at	-0.5
acyl-(acyl carrier protein) thioesterase, putative almost identical to acyl-(acyl carrier protein) thioesterase GB:CAA85387 GI:634003 from [A	261722_at	-0.5
hypothetical protein similar to hypothetical protein GB:AAC61817 GI:3668085 from [Arabidopsis thaliana]	261700_at	-0.5
unknown protein ; supported by cDNA: gi_12083293_gb_AF332443.1_AF332443	261626_at	-0.5
hypoxanthine ribosyl transferase, putative similar to hypoxanthine ribosyl transferase GB:AAC46403 GI:2689037 from [Vibrio parahaemolyt	261516_at	-0.5
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:36233.	261483_at	-0.5
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:116544.	261454_at	-0.5
C-8,7 sterol isomerase identical to GB:AAD03489 from [Arabidopsis thaliana] (Plant Mol. Biol. 38 (5), 807-815 (1998)); supported by full-len	261228_at	-0.5
unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_	261209_at	-0.5
protease, putative similar to SP:P36774 from [Myxococcus xanthus];supported by full-length cDNA: Ceres:94409.	261118_at	-0.5
chloroplast 50S ribosomal protein L31, putative similar to SP:O46917 from [Guillardia theta]; supported by full-length cDNA: Ceres:37854.	261119_at	-0.5
Expressed protein ; supported by full-length cDNA: Ceres: 1349.	261039_at	-0.5
glycine cleavage system H protein precursor, putative similar to GB:Z37524 from [Flaveria anomala];supported by full-length cDNA: Ceres::	_	-0.5
hypothetical protein contains similarity to CDP-diacylglycerol synthase 2 GI:3892191 from [Homo sapiens]	260636_at	-0.5
RING-H2 zinc finger protein (ATL3) identical to RING-H2 zinc finger protein (ATL3) GB:AF132013 (Arabidopsis thaliana); supported by cDN	_	-0.5
putative 40S ribosomal protein SA (laminin receptor-like protein) identical to laminin receptor-like protein GB:U01955 [Arabidopsis thaliana];	_	-0.5
hypothetical protein predicted by genscan+	260277_at	-0.5
unknown protein similar to Pi starvation-induced protein GB:BAA06151 from [Nicotiana tabacum]; supported by full-length cDNA: Ceres: 37;	_	-0.5
Expressed protein ; supported by full-length cDNA: Ceres: 8189.	260100_at	-0.5
3-hydroxy-3-methylglutaryl CoA reductase (AA 1-592) identical to hydroxy methylglutaryl CoA reductase (AA 1-592) GB:X15032 (Plant Mol.	_	-0.5
60S ribosomal protein L37, putative similar to SP:Q43292 from [Arabidopsis thaliana]; supported by cDNA: gi_13877906_gb_AF370216.1_		-0.5
hypothetical protein	259529_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:5232.	259357_at	-0.5
hypothetical protein similar to putative glycosyl transferase GI:6862930 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:11	259358_at	-0.5
unknown protein	259354_at	-0.5
putative cystathionine gamma-synthase similar to cystathionine gamma-synthase GB:AAB41235 from [Arabidopsis thaliana]; supported by c	_	-0.5
hypothetical protein predicted by genefinder; supported by full-length cDNA: Ceres: 40813.	259171_at	-0.5
unknown protein putative adaputate kinage similar to AdK adaputate kinage CD:SE0007 [Streptomyges seelingler]	259068_at	-0.5
putative adenylate kinase similar to AdK adenylate kinase GB:S50007 [Streptomyces coelicolor]	258998_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:97.	258875_at	-0.5
putative 40S ribosomal protein S23 similar to 40S ribosomal protein S23 (S12) GB:P46297 from [Fragaria x ananassa]; supported by full-ler	200712_S_at	-0.5

putative elongation factor P (EF-P) similar to elongation factor P (EF-P) GB:Q54760 [Synechococcus PCC7942];supported by full-length cD	258674_at	-0.5
adenylate translocator identical to adenylate translocator GB:X65549 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:36818.	258680_at	-0.5
thioredoxin f1 identical to thioredoxin f1 GB:AF144385 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:11767.	258607_at	-0.5
putative S-adenosylmethionine:2-demethylmenaquinone methyltransferase similar to S-adenosylmethionine:2-demethylmenaquinone methy	-	-0.5
hypothetical protein similar to receptor protein kinases: GB:CAB43834, GB:S71277 [Arabidopsis thaliana]	258557_at	-0.5
unknown protein identical to unknown protein GB:AAF30301 from [Arabidopsis thaliana]; supported by cDNA: gi_16648934_gb_AY059837.	258472_at	-0.5
hypothetical protein predicted by genemark.hmm	258442_at	-0.5
AP2 domain containing protein RAP2.3 identical to GB:AAC49769 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:35981.	258434_at	-0.5
receptor kinase, putative similar to receptor kinase GB:AAA33715 from [Petunia integrifolia], supported by full-length cDNA: Ceres:22221.	258159_at	-0.5
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:102455.	258079_at	-0.5
unknown protein ; supported by cDNA: gi_15809843_gb_AY054189.1_	257988_at	-0.5
unknown protein contains Pfam profile: PF01758 sodium bile acid symporter family;supported by full-length cDNA: Ceres:26683.	257908_at	-0.5
Expressed protein ; supported by full-length cDNA: Ceres: 40038.	257909_at	-0.5
Cdc45-like protein similar to Cdc45 GB:AAC67520 [Xenopus laevis] (EMBO J. 17, 5699-5707 (1998)) (required for the initiation of eukaryot		-0.5
glyceraldehyde 3-phosphate dehydrogenase A subunit (GapA) identical to glyceraldehyde 3-phosphate dehydrogenase A subunit (GapA) (	_	-0.5
unknown protein ;supported by full-length cDNA: Ceres:121435.	257745_at	-0.5
phosphoglycerate kinase, putative similar to phosphoglycerate kinase, chloroplast precursor GB:P29409 from [Spinacia oleracea];supporter		-0.5
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_16323108_gb_AY057658.1_	257707_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:6530.	257299_at	-0.5
hypothetical protein predicted by genemark.hmm, contains Pfam profile:F00575 S1:S1 RNA binding domain; supported by cDNA: gi_15146	_	-0.5
unknown protein	257074_at	-0.5
unknown protein contains Pfam profile: PF00279 LTP: Plant lipid transfer protein family; supported by full-length cDNA: Ceres: 19287.	256933_at	-0.5
unknown protein contains Pfam profile:PF00011 HSP20:Hsp20/alpha crystallin family;supported by full-length cDNA: Ceres:14572.	256934_at	-0.5
hypothetical protein contains similarity to RNA polymerase transcriptional regulation mediator GB:AAC26869 from [Homo sapiens]	256812_at	-0.5
ATHP2, putative similar to ATHP2 GB:BAA37111 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:24559.	256744_at	-0.5
serine/arginine-rich protein, putative similar to serine/arginine-rich protein GB:AAF17288 GI:6572475 from [Arabidopsis thaliana]; supported	_	-0.5
hypothetical protein	256583_at	-0.5
hypothetical protein predicted by genemark.hmm	256219_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:94739.	256067_at	-0.5
hypothetical protein ;supported by full-length cDNA: Ceres:7642.	255981_at	-0.5
plastocyanin, putative similar to plastocyanin GI:1865683 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:23406.	255886_at	-0.5
lemir (miraculin), putative similar to lemir (miraculin) GI:2654440 from [Lycopersicon esculentum]; supported by cDNA: gi_12083239_gb_AI	-	-0.5
40S ribosomal protein S26	255819_s_at	-0.5
auxin regulated protein (IAA13) GB:S58499;supported by full-length cDNA: Ceres:13741.	255788_at	-0.5
myb factor, putative similar to myb factor GI:1946266 from [Oryza sativa]; supported by cDNA: gi_3941465_gb_AF062887.1_AF062887	255753_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:37302.	255719_at	-0.5
coded for by A. thaliana cDNA R30513	255716_at	-0.5
hypothetical protein	255643_at	-0.5
putative protein kinase	255617_at	-0.5
putative L5 ribosomal protein ;supported by full-length cDNA: Ceres:22919.	255623_at	-0.5
putative protein ;supported by full-length cDNA: Ceres:156170.	255478_at	-0.5
putative M-type thioredoxin similar to A. thaliana protein F21B7.7, GenBank accession number AC002560; supported by full-length cDNA: C		-0.5
putative protein various predicted proteins; supported by cDNA: gi_15809939_gb_AY054238.1_	255221_at	-0.5
putative protein hypothetical protein - Arabidopsis thaliana,PIR:F71409,supported by full-length cDNA: Ceres:22715.	255243_at	-0.5
nucleoside-diphosphate kinase ;supported by full-length cDNA: Ceres:30158.	255089_at	-0.5
rab7 -like protein rab7 protein -Vigna aconitifolia,PIR2:S39567; supported by cDNA: gi_15718417_dbj_AB071851.1_AB071851	255052_at	-0.5
hypothetical protein	255055_at	-0.5
S18.4 ribosomal protein ;supported by full-length cDNA: Ceres:24071.	255000_at	-0.5
putative protein ;supported by full-length cDNA: Ceres:7769.	254950_at	-0.5
DnaJ-like protein DnaJ-like protein, Phaseolus vulgaris, U77935; supported by cDNA: gi_6691126_gb_AF214107.1_AF214107	254688_at	-0.5
pherophorin - like protein pherophorin-S, Volvox carteri, PIR:T10798	254649_at	-0.5
protein ch-42 precursor, chloroplast ;supported by full-length cDNA: Ceres:7501.	254623_at	-0.5
ribosomal protein L11, cytosolic ;supported by full-length cDNA: Ceres:2359.	254617_s_at	-0.5

putative protein ;supported by full-length cDNA: Ceres:29133.	254462_at	-0.5
hypothetical protein ; supported by cDNA: gi_15028392_gb_AY045999.1_	254481_at	-0.5
G10 - like protein Maternal G10 like protein, Oryza sativa, PATCHX:D1002643; supported by cDNA: gi_15294271_gb_AF410327.1_AF410		-0.5
RCc3- like protein RCc3 protein, Oryza sativa, PIR2:S53012;supported by full-length cDNA: Ceres:270276.	254327_at	-0.5
putative protein ; supported by full-length cDNA: Ceres: 6527.	254228_at	-0.5
putative protein NorM, Vibrio parahaemolyticus, gb:AB010463	254077_at	-0.5
putative protein Human GS1 (protein of unknown function) mRNA, PID:g183653;supported by full-length cDNA: Ceres:98650.	254039_at	-0.5
putative thioredoxin thioredoxin - Lilium longiflorum, PID:g308906;supported by full-length cDNA: Ceres:148597.	253990_at	-0.5
putative protein ;supported by full-length cDNA: Ceres:113484.	253891_at	-0.5
putative wound induced protein wound-induced protein - tomato (fragment), PIR2:S19773;supported by full-length cDNA: Ceres:20161.	253812_at	-0.5
putative beta-expansin/allergen protein soybean pollen allergen (cim1) protein - soybean, PIR2:S48032;supported by full-length cDNA: Cer	_	-0.5
photosystem I subunit PSI-E - like protein photosystem I chain IV precursor, Hordeum vulgare, PIR1:F1BH4; supported by cDNA: gi_11692		-0.5
putative protein D-threonine dehydrogenase - Pseudomonas cruciviae, PID:d1035162 and to several 3-hydroxyisobutyrate dehydrogenases	253706_at	-0.5
RIBOSOMAL PROTEIN S30 homolog RIBOSOMAL PROTEIN S30 - Arabidopsis thaliana, PID:e1358183	253715_at	-0.5
profilin 2 ; supported by full-length cDNA: Ceres: 25886.	253727_at	-0.5
snRNP Sm protein F - like Sm protein F, Homo sapiens, PIR:S55053; supported by full-length cDNA: Ceres: 37087.	253668_at	-0.5
Expressed protein ; supported by full-length cDNA: Ceres: 6401.	253275_at	-0.5
putative protein ;supported by full-length cDNA: Ceres:8286.	253072_at	-0.5
putative phosphatidylinositol synthase phosphatidylinositol synthase (PIS1) - Arabidopsis thaliana, PID:e1313354;supported by full-length c	252953_at	-0.5
H+-transporting ATPase 16K chain P2, vacuolar ;supported by full-length cDNA: Ceres:31833.	252926_at	-0.5
nitrilase 2 ;supported by full-length cDNA: Ceres:40532.	252678_s_at	-0.5
Expressed protein ; supported by full-length cDNA: Ceres: 122249.	252389_at	-0.5
60S RIBOSOMAL PROTEIN - like 60S RIBOSOMAL PROTEIN L26, Brassica rapa, EMBL:BRD495; supported by cDNA: gi 13877790 gb	252235 at	-0.5
putative protein	252155 <sup>_</sup> at	-0.5
non-specific lipid transfer protein ;supported by full-length cDNA: Ceres:8400.	252115 at	-0.5
putative protein ;supported by full-length cDNA: Ceres:10009.	252116 at	-0.5
putative protein ;supported by full-length cDNA: Ceres:97866.	252034_at	-0.5
	251951 s at	-0.5
putative protein Hsp70 binding protein HspBP1 - Homo sapiens, EMBL:AF093420;supported by full-length cDNA: Ceres:37834.	251919 at	-0.5
tryptophan synthase alpha chain ; supported by full-length cDNA: Ceres: 40110.	251847 at	-0.5
ribosomal L23a - like protein various ribosomal L23a proteins;supported by full-length cDNA: Ceres:17531.	251783 at	-0.5
eukaryotic translation initiation factor 6 (EIF-6) - like protein eukaryotic translation initiation factor 6 (EIF-6), Mus musculus, EMBL:AF04704	251776 at	-0.5
	251744 at	-0.5
hypothetical protein :supported by full-length cDNA: Ceres:14487.	251624 at	-0.5
beta-1,3-glucanase 2 (BG2) (PR-2) ;supported by full-length cDNA: Ceres:21719.	251625 at	-0.5
3-isopropylmalate dehydratase-like protein (small subunit) 3-isopropylmalate dehydratase, small subunit - Thermotoga maritima, PIR:A723(	_	-0.5
scarecrow - like protein scarecrow-like 6, Arabidopsis thaliana, EMBL:AF036303	251376 at	-0.5
germin-like protein (GLP10)	251297 at	-0.5
putative protein	251240 at	-0.5
putative protein ER6 protein - Lycopersicon esculentum, EMBL:AF096262; supported by cDNA: gi_14334945_gb_AY035146.1_	251221 at	-0.5
putative protein glycosyl transferase IgtC - Neisseria gonorrhoeae, EMBL:AF208062	251225 at	-0.5
putative protein putative protein At2g15760 - Arabidopsis thaliana, EMBL:AC006438;supported by full-length cDNA: Ceres:2947.	251183 at	-0.5
putative protein unknown protein At2g47690 - Arabidopsis thaliana, EMBL:AC005309; supported by full-length cDNA: Ceres: 6853.	251186 at	-0.5
lectin - like protein lectin precursor LECSJAbmII, Sophora japonica, EMBL:SJU63012;supported by full-length cDNA: Ceres:41306.	251140_at	-0.5
light-inducible protein ATLS1	251098 at	-0.5
chlorophyll a/b-binding protein CP29; supported by cDNA: gi 15081738 gb AY048262.1	251082 at	-0.5
putative protein (supported by full-length cDNA: Ceres:17471.	250969 at	-0.5
unknown protein ; supported by cDNA: gi 15810044 gb AY054291.1	250828 at	-0.5
putative protein contains similarity to unknown protein (gb AAF23194.1);supported by full-length cDNA: Ceres:5127.	250732 at	-0.5
	_	-0.5
putative protein mammalian inositol hexakisphosphate kinase 2 - Homo sapiens, EMBL:AF177145;supported by full-length cDNA: Ceres:32	_	-0.5 -0.5
unknown protein ; supported by full-length cDNA: Ceres: 37422.	250454_at 250435_at	-0.5 -0.5
putative protein various predicted proteins, Arabidopsis thaliana	_	-0.5 -0.5
AtAGP4 ; supported by cDNA: gi_13926257_gb_AF372885.1_AF372885	250437_at	-0.5

nucleoid DNA-binding protein cnd41 - like protein nucleoid DNA-binding protein cnd41, chloroplast, common tobacco, PIR:T01996	250445_at	-0.5
putative protein similar to unknown protein (pir  T09909)	250306_at	-0.5
putative protein similar to unknown protein (pir  T09909)	250307_at	-0.5
putative protein similar to unknown protein (emb CAB87627.1)	250018_at	-0.5
putative protein predicted protein, Arabidopsis thaliana	249918_at	-0.5
60S ribosomal protein L10A;supported by cDNA: gi_14335147_gb_AY037253.1_	249945_at	-0.5
putative protein similar to unknown protein (emb CAB62459.1);supported by full-length cDNA: Ceres:12030.	249753_at	-0.5
peroxidase ATP26a	249392_at	-0.5
putative protein	249395_at	-0.5
putative protein similar to unknown protein (pir  T28068); supported by full-length cDNA: Ceres: 39514.	249178_at	-0.5
Rab-type small GTP-binding protein-like ; supported by full-length cDNA: Ceres: 102017.	248914_at	-0.5
carnitine/acylcarnitine translocase-like protein ;supported by full-length cDNA: Ceres:13730.	248838_at	-0.5
acyl carrier protein-like	248753_at	-0.5
putative protein strong similarity to unknown protein (gb AAF02142.1);supported by full-length cDNA: Ceres:7891.	248663_at	-0.5
peptidyl-prolyl cis-trans isomerase-like protein ;supported by full-length cDNA: Ceres:143222.	248664_at	-0.5
drought-induced protein Di19-like protein ; supported by cDNA: gi_13937215_gb_AF372963.1_AF372963	248595_at	-0.5
von Hippel-Lindau binding protein (VHL binding protein; VBP) like ; supported by cDNA: gi_13878182_gb_AF370354.1_AF370354	248589_at	-0.5
acid phosphatase	248440_at	-0.5
trehalose-6-phosphate phosphatase ; supported by cDNA: gi_2944177_gb_AF007778.1_AF007778	248404_at	-0.5
putative protein similar to unknown protein (emb CAA71173.1)	248321_at	-0.5
cytochrome b5 (dbj BAA74839.1) ;supported by full-length cDNA: Ceres:31303.	248217_at	-0.5
vacuolar sorting protein-like; embryogenesis protein H beta 58-like protein ;supported by full-length cDNA: Ceres:41458.	248221_at	-0.5
translation initiation factor-like protein	248146_at	-0.5
NOI protein, nitrate-induced	248025_at	-0.5
ADP/ATP translocase-like protein ;supported by full-length cDNA: Ceres:111544.	248023_at	-0.5
elongin - like protein elongin C, Drosophila melanogaster, PIR:JC5794; supported by cDNA: gi_15028384_gb_AY045995.1_	247721_at	-0.5
putative protein ;supported by full-length cDNA: Ceres:38797.	247702_at	-0.5
actin depolymerizing factor 4 - like protein actin depolymerizing factor 4, Arabidopsis thaliana, EMBL:AF102822;supported by full-length cD	247656_at	-0.5
putative protein ; supported by full-length cDNA: Ceres: 7022.	247572_at	-0.5
COP1-interacting protein CIP8 ; supported by cDNA: gi_5929905_gb_AF162150.1_AF162150	247219_at	-0.5
putative protein contains similarity to protein arginine methyltransferase	247168_at	-0.5
ferredoxin-NADP+ reductase	247131_at	-0.5
putative protein hypothetical proteins - Arabidopsis thaliana;supported by full-length cDNA: Ceres:42528.	246975_at	-0.5
putative protein apoptosis-related protein PNAS-4, Homo sapiens, EMBL:AF229834;supported by full-length cDNA: Ceres:263500.	246931_at	-0.5
nodulin - like protein early nodulin N93, Glycine max, EMBL:D13506;supported by full-length cDNA: Ceres:21669.	246863_at	-0.5
putative protein ; supported by cDNA: gi_14532675_gb_AY039962.1_	246749_at	-0.5
60S ribosomal protein - like 60S ribosomal protein L18, Arabidopsis thaliana, SWISSPROT:RL18_ARATH; supported by cDNA: gi_158101!	246758_at	-0.5
40S ribosomal protein S19 - like 40S ribosomal protein S19, Cyanophora paradoxa, EMBL:CPA245654;supported by full-length cDNA: Cer	246730_at	-0.5
sugar transporter-like protein putative sugar transporter - Prunus armeniaca, EMBL:AF000952; supported by cDNA: gi_16648752_gb_AY0:	246508_at	-0.5
RING-H2 zinc finger protein-like RING-H2 zinc finger protein ATL4 - Arabidopsis thaliana, EMBL:AF132014	246439_at	-0.5
hypothetical protein ;supported by full-length cDNA: Ceres:96001.	246442_at	-0.5
auxin regulated protein IAA18, putative similar to auxin regulated protein IAA18 GI:2618725 from [Arabidopsis thaliana]; supported by full-lei	246376_at	-0.5
putative protein predicted protein At2g41010 - Arabidopsis thaliana, EMBL:AC004261;supported by full-length cDNA: Ceres:39584.	246289_at	-0.5
methionyl aminopeptidase-like protein ;supported by full-length cDNA: Ceres:18909.	246202_at	-0.5
hypothetical protein ; supported by cDNA: gi_15028060_gb_AY045887.1_	246205_at	-0.5
Expressed protein ; supported by full-length cDNA: Ceres: 99394.	246159_at	-0.5
putative protein ribosomal protein S8 - Zea mays, PIR:T04088;supported by full-length cDNA: Ceres:29997.	246068_at	-0.5
Expressed protein ; supported by full-length cDNA: Ceres: 103171.	246018_at	-0.5
putative protein NAC1 - Medicago truncatula, EMBL:AF254124	245934_at	-0.5
symbiosis-related like protein ;supported by full-length cDNA: Ceres:17851.	245391_at	-0.5
hypothetical protein ;supported by full-length cDNA: Ceres:22637.	245364_at	-0.5
Expressed protein ; supported by full-length cDNA: Ceres: 37809.	245329_at	-0.5
Expressed protein ; supported by full-length cDNA: Ceres: 1297.	245097_at	-0.5

putative integral membrane protein ;supported by full-length cDNA: Ceres:25204.	245083_at	-0.5	
PSI I protein	245017_at	-0.5	
hypothetical protein	244906_at	-0.5	
hypothetical protein	257318_at	-0.5	
hypothetical protein	257325_at	-0.5	
hypothetical protein	257334_at	-0.5	
unknown protein	257407_at	-0.5	
putative RSZp22 splicing factor	257435_at	-0.5	
hypothetical protein	257513 s at	-0.5	
hypothetical protein predicted by genscan+	257061 at	-0.5	
unknown protein ; supported by cDNA: gi_15028228_gb_AY045937.1_	267185_at	-0.5	
putative AHP2 similar to GB:BAA36336;supported by full-length cDNA: Ceres:452.	264838 at	-0.5	
hypothetical protein predicted by genscan; supported by cDNA: gi 15292714 gb AY050791.1	259864 at	-0.5	
aminoalcoholphosphotransferase, putative similar to aminoalcoholphosphotransferase GB:AAA67719 from [Glycine max]	257933 at	-0.5	
Expressed protein ; supported by full-length cDNA: Ceres: 99521.	254362 at	-0.5	
putative protein ; supported by cDNA: gi_15724319_gb_AF412100.1_AF412100	250929 at	-0.5	
F-box protein family, AtFBX6 contains similarity to unusual floral organs (UFO) GI:4376159 from [Arabidopsis thaliana]	249140 at	-0.5	
signal peptidase ; supported by cDNA: gi 3044217 gb AF057144.1 AF057144	246784 at	-0.5	
proteasome chain protein ; supported by full-length cDNA: Ceres: 24266.	245315 at	-0.5	
putative nucleotide sugar epimerase	245133 at	-0.5	