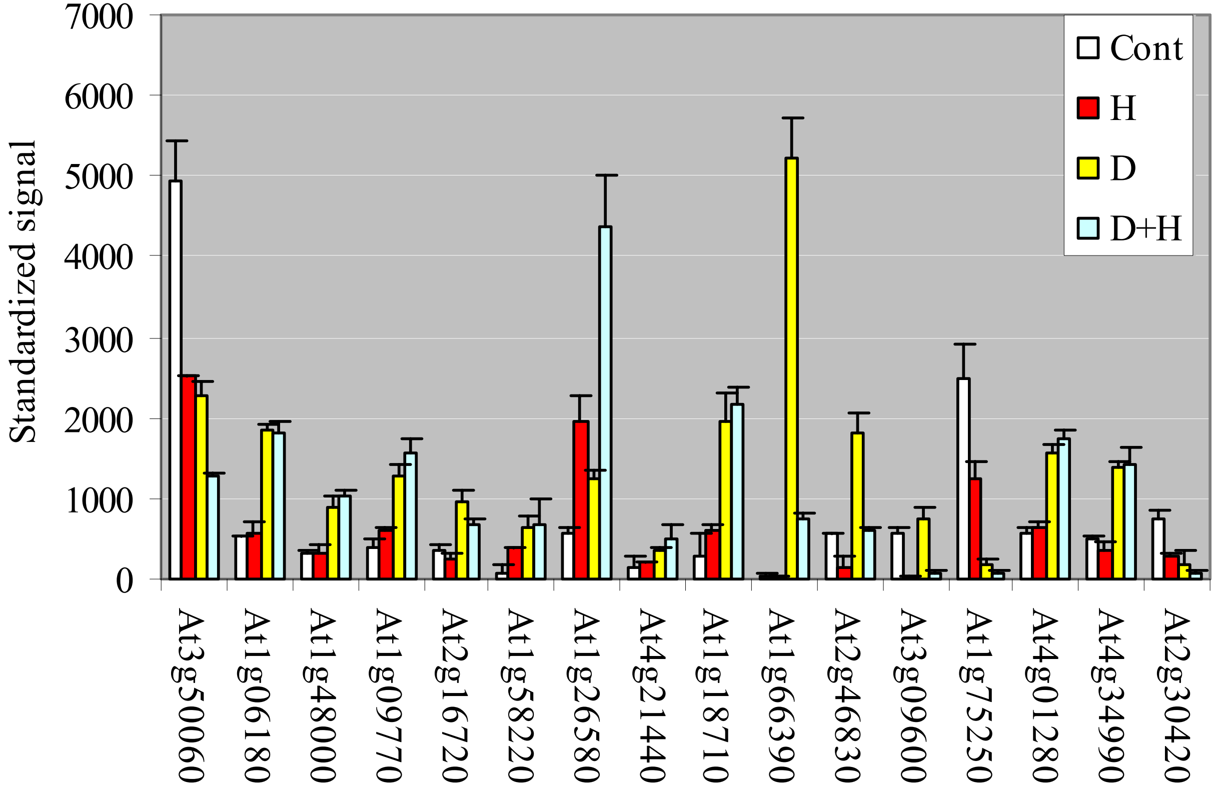

Supplementary Fig. 1. Expression level of all *Arabidopsis* MYB transcription factors altered during drought stress, heat shock or a combination of drought stress and heat shock. RNA isolation and Affymetrix chip analysis were performed as described in Experimental Procedures. Cont, control; D, drought 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	$\log_2$ 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	254059_at	9.3
heat shock protein 17.6-II ;supported by full-length cDNA: Ceres:2281.	250296_at	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	247718_at	8
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	7.7
unknown protein similar to pollen coat protein GB:CAA63531 from [Brassica oleracea]; supported by cDNA: gi_14335127_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	244931_at	7.2
chloroplast-localized small heat shock protein, putative similar to chloroplast-localized small heat shock protein GI:6601536 from [Funaria hy	262148_at	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	254234_at	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.	266294_at	6.4
putative ascorbate peroxidase strong similarity to ascorbate peroxidase GB:CAA56340	258695_at	6.4
nonspecific lipid-transfer protein precursor - like nonspecific lipid-transfer protein precursor, Brassica napus, EMBL:AF101038;supported by	247717_at	6.4
heat shock protein 70 identical to heat shock protein 70 GB:CAA05547 GI:3962377 [Arabidopsis thaliana]; supported by cDNA: gi_15809831_	256245_at	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	262482_at	6
late embryogenesis-abundant protein, putative similar to late embryogenesis-abundant protein GI:17828 from [Brassica napus];supported by	262128_at	6
dehydrin RAB18-like protein (sp P30185) ; supported by cDNA: gi_16226664_gb_AF428458.1_AF428458	247095_at	5.8
unknown protein EST gb|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	264510_at	5.7
unknown protein ; supported by cDNA: gi_13265448_gb_AF324676.2_AF324676	263881_at	5.7
peptidylprolyl isomerase	248657_at	5.7
unknown protein ; supported by cDNA: gi_15028356_gb_AY045981.1_	266462_at	5.5
hypothetical protein contains Pfam profile: PF01535 domain of unknown function (contains 3 copies)	260062_at	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]	262307_at	5.3
putative protein predicted protein	254823_at	5.3
elongation factor 1B 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_	247723_at	5.1
serine protease-like protein serine protease OMI - Homo sapiens, EMBL:AF020760	246733_at	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	265228_s_at	4.9
putative protein CDPK substrate protein 1, Mesembryanthemum crystallinum, EMBL:AF219972;supported by full-length cDNA: Ceres:13378.	246724_at	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-ric	265111_at	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:AAD46402 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	250784_at	4.7
NADH dehydrogenase subunit 7	244925_at	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	253819_at	4.6
1,4-alpha-glucan branching enzyme protein soform SBE2.2 precursor	250906_at	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.	261077_at	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	253576_at	4.5
maturase	244926_s_at	4.5
unknown protein ; supported by cDNA: gi_14532707_gb_AY039978.1_	267080_at	4.4
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:2330885 from [Trichomonas vaginal	261957_at	4.4
Arm repeat containing protein - like arm repeat containing protein homolog, Arabidopsis thaliana, EMBL:AL133314	251407_at	4.4
putative protein predicted proteins, Arabidopsis thaliana	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	257817_at	4.3
hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 144447.	246582_at	4.3
NADH dehydrogenase subunit 9	244943_at	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+	255891_at	4.2
putative protein intracellular protein Mg11, mouse, PIR:I49127; supported by cDNA: gi_14488068_gb_AF389282.1_AF389282	249403_at	4.2
70kD heat shock protein ;supported by full-length cDNA: Ceres:98979.	265675_at	4.1

phytochrome E	254680_at	4.1
low-temperature-induced 65 kD protein (sp|Q04980)	248352_at	4.1
RuBisCO subunit binding-protein beta subunit precursor; chaperonin, 60 kDa	248021_at	4.1
cytochrome c oxidase subunit 2	244950_at	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
NADH dehydrogenase subunit 5 (nad5) (trans-splicing part 1 of 2)	257338_s_at	3.9
Expressed protein ; supported by cDNA: gi_14532529_gb_AY039889.1_	266550_s_at	3.8
hypothetical protein predicted by genemark.hmm	264217_at	3.8
Myb-related transcription factor mixta, putative similar to Myb-related transcription factor mixta GI:485866 from [Antirrhinum majus]	261431_at	3.8
hypothetical protein predicted by genemark.hmm	259463_at	3.8
hypothetical protein predicted by genefinder	258827_at	3.8
unknown protein ; supported by cDNA: gi_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
hypothetical protein	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	252546_at	3.7
putative protein similar to unknown protein (gb|AAC73025.1); supported by cDNA: gi_14532515_gb_AY039882.1_	250825_at	3.7
DNA excision repair cross-complementing protein; similar to human Xeroderma pigmentosum group B DNA repair protein (gb|AAC49987.1) ;	249307_s_at	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
hypothetical protein	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	250036_at	3.6
putative protein similar to unknown protein (gb|AAD21732.1)	249850_at	3.6
unknown protein ;supported by full-length cDNA: Ceres:534.	248218_at	3.6
putative protein nonspecific 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
water stress-induced protein, putative similar to water stress-induced protein GI:454879 from [Oryza sativa]; supported by cDNA: gi_1521576	245627_at	3.6
NADH dehydrogenase subunit 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
hypothetical protein similar to Anthocyanin 5-aromatic acyltransferase GB:BAA74428	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 cD	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
hypothetical protein	257759_at	3.5
transcription factor-like protein ;supported by full-length cDNA: Ceres:114015.	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_gb	245775_at	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_	254667_at	3.4
putative protein cellulose synthase catalytic subunit, Arabidopsis thaliana, gb:AF027173;supported by full-length cDNA: Ceres:112955.	254189_at	3.4
lysine-ketoglutarate reductase/saccharopine ; supported by cDNA: gi_2052507	253373_at	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
hypothetical protein	244954_s_at	3.3
putative N2,N2-dimethylguanosine tRNA methyltransferase similar to N2,N2-dimethylguanosine tRNA methyltransferase GB:CAA20101 GI:6	259075_at	3.3
putative protein several hypothetical proteins - Arabidopsis thaliana	252151_at	3.2
aspartic protease, putative similar to aspartic protease GI:1326164 from [Brassica napus]	264741_at	3.2

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 gb|X82404 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
ubiquinol--cytochrome-c reductase-like protein ubiquinol--cytochrome-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: gi_15450646_gb_AY052691.1_	250826_at	2.9
RGA-like protein putative member of the VHIID domain transcription factor family RGAL - Arabidopsis thaliana, EMBL:AJ224957	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
hypothetical protein	257323_at	2.9
hypothetical protein predicted by genscan and genefinder	266590_at	2.8
G-box binding bZIP transcription factor identical to PIR:S20885; supported by cDNA: gi_600862_gb_U17891.1_ATU17891	266555_at	2.8
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|18135	264522_at	2.8
hypothetical protein predicted by genefinder	263975_at	2.8
FtsH protease, putative similar to zinc dependent protease GI:7650138 from [Arabidopsis thaliana]	262626_at	2.8
mutM homologue-1 identical to mutM homologue-1 GI:3550982 from [Arabidopsis thaliana]; 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:BAA37110, 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_1433	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)); suppor	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 putative DNA binding protein - Arabidopsis thaliana, TREMBL:ATAC2339_3; supported by cDNA: gi_16649060_gb_AY0599	251644_at	2.6
pectin methyl-esterase-like protein pectin methyl-esterase PER - Medicago truncatula, EMBL:AJ249611;supported by full-length cDNA: Cere	250606_s_at	2.6
kinase - like protein RING3 protein, Homo sapiens, EMBL:X96670; supported by cDNA: gi_16604680_gb_AY059785.1_	250191_at	2.6
glucose-6-phosphate dehydrogenase	249372_at	2.6
putative protein contains similarity to cyclin	248988_at	2.6
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 prot	264372_at	2.5
putative gigantea protein strong similarity to GB:CAB56039 from [Arabidopsis thaliana]; supported by cDNA: gi_6002679_gb_AF105064.1_A	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	262452_at	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
putative protein predicted protein, Arabidopsis thaliana	250050_at	2.5
acetyl-CoA synthetase-like protein	249869_at	2.5
Fdr1 Cen - like protein Fdr1, Oryza sativa, EMBL:AF159883	247511_at	2.5
unknown protein	247340_at	2.5
ribosomal protein L16	244944_s_at	2.5
hypothetical protein	257321_at	2.5
putative tropinone reductase	266278_at	2.4
unknown protein ; supported by cDNA: gi_14334955_gb_AY035151.1_	265629_at	2.4
hypothetical protein Similar to Nicotiana tumor-related protein (gb|26453)	264661_at	2.4
unknown protein	264156_at	2.4
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_11908125_gb_AF326910.1_AF326910	264102_at	2.4
unknown protein	263296_at	2.4
disulfide isomerase-related protein, putative similar to GB:AAB50217 from [Homo sapiens]	261167_at	2.4
protein phosphatase 2C (AtP2C-HA) identical to protein phosphatase 2C (AtP2C-HA) GB:AJ003119 [Arabidopsis thaliana] (Plant Mol. Biol. 3	259922_at	2.4
unknown protein	259718_at	2.4
hypothetical protein contains similarity to invertase inhibitor GB:CAA73333 GI:2765240 from [Nicotiana tabacum]; supported by full-length cD	259616_at	2.4
(1-4)-beta-mannan endohydrolase precursor, putative similar to (1-4)-beta-mannan endohydrolase precursor GI:9836826 from [Lycopersicon	259442_at	2.4
phi-1-like protein similar to phi-1 (phosphate induced protein) GB:BAA33810 [Nicotiana tabacum]	258605_at	2.4
unknown protein contains RanBP1 domain;supported by full-length cDNA: Ceres:108414.	258313_at	2.4
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:108820.	257985_at	2.4
unknown protein similar to hypothetical protein GB:CAB43880; supported by cDNA: gi_15146307_gb_AY049295.1_	257056_at	2.4
chaperonin 60 beta, putative very similar to GB:JT0901 from [Arabidopsis thaliana] (Gene 111 (2), 175-181 (1992))	256983_at	2.4
Eukaryotic translation initiation factor 5, putative Eukaryotic translation initiation factor 5 [Zea mays] GI:4160402; supported by cDNA: gi_158	256502_at	2.4
hypothetical protein	253350_at	2.4
Expressed protein ; supported by full-length cDNA: Ceres: 263956.	253047_at	2.4
Spot 3 protein and vacuolar sorting receptor homolog/AtELP1 ; supported by cDNA: gi_15081792_gb_AY048289.1_	252027_at	2.4
protein kinase-like protein Pto kinase interactor 1 - Lycopersicon esculentum, EMBL:U28007; supported by cDNA: gi_15451117_gb_AY0546	251494_at	2.4
ferritin 1 precursor ;supported by full-length cDNA: Ceres:1100.	251109_at	2.4
putative protein putative proteins - Arabidopsis thaliana; supported by cDNA: gi_15292802_gb_AY050835.1_	251084_at	2.4
putative protein crp1 protein, Zea mays, PIR:T01685	250987_at	2.4
putative protein P58 protein, Bos primigenius taurus, PIR:A56534;supported by full-length cDNA: Ceres:146009.	250930_at	2.4
fatty acid elongase - like protein KCS1 fatty acid elongase 3-ketoacyl-CoA synthase 1, Arabidopsis thaliana, EMBL:AF053345	250891_at	2.4
chaperonin 60 alpha chain - like protein chaperonin 60 alpha chain precursor, garden pea, PIR:T06518	249977_at	2.4
phytochrome C (sp|P14714)	249666_at	2.4
putative protein predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_15810554_gb_AY056316.1_	249614_at	2.4
dihydroflavonol 4-reductase	249215_at	2.4
putative protein similar to unknown protein (pir||H71431);supported by full-length cDNA: Ceres:31680.	248763_at	2.4
unknown protein	248774_at	2.4
unknown protein ;supported by full-length cDNA: Ceres:253359.	248228_at	2.4
similar to unknown protein (gb|AAF63134.1)	247803_at	2.4
protein kinase ; supported by cDNA: gi_16974578_gb_AY060555.1_	247384_at	2.4
putative retroelement pol polyprotein	266187_at	2.3
hypothetical protein predicted by genscan; supported by cDNA: gi_15028050_gb_AY045882.1_	265596_at	2.3

putative RNA-binding protein ; supported by cDNA: gi_6650522_gb_AF101056.1_AF101056	265266_at	2.3
gamma glutamyl hydrolase, putative similar to gamma glutamyl hydrolase GI:1680711 from [Glycine max];supported by full-length cDNA: Ce	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]; supporte	258815_at	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	256861_at	2.3
unknown protein ;supported by full-length cDNA: Ceres:36434.	256061_at	2.3
UDP-glucose glucosyltransferase, 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 cyclin C homolog 1, Schizosaccharomyces pombe, PATCHX:G2055413	254526_at	2.3
trehalose-6-phosphate phosphatase - like protein trehalose-6-phosphate phosphatase (AtTPPA), PID:g2944178	254321_at	2.3
abscisic acid responsive elements-binding factor(ABF3) identical to abscisic acid responsive elements-binding factor (ABF3) GI:6739280 from	253263_at	2.3
putative sugar transporter protein sugar transporter, Arabidopsis thaliana, db_xref=PID:g1495273	253188_at	2.3
putative protein glutamic acid-rich protein precursor, Plasmodium falciparum (GARP), PIR2:A54514	253111_at	2.3
putative protein various predicted proteins, Arabidopsis thaliana	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	250956_at	2.3
cysteine proteinase inhibitor-like protein ;supported by full-length cDNA: Ceres:27304.	250811_at	2.3
putative protein strong similarity to unknown protein (emb|CAB62118.1)	250786_at	2.3
putative protein strong similarity to unknown protein (gb|AAC98056.1)	250237_at	2.3
FtsH protease, putative similar to FtsH-like protein Pftf precursor GI:4325041 from [Nicotiana tabacum]	250162_at	2.3
putative protein mDj10, Mus musculus, EMBL:AB028860; supported by cDNA: gi_15450366_gb_AY052284.1_	249613_at	2.3
putative protein similar to unknown protein (pir||T05226);supported by full-length cDNA: Ceres:96.	249174_at	2.3
unknown protein ;supported by full-length cDNA: Ceres:25275.	248709_at	2.3
permease	248558_at	2.3
homogentisate 1,2-dioxygenase ;supported by full-length cDNA: Ceres:6599.	248193_at	2.3
protein phosphatase 2C ABI2 (PP2C) (sp|O04719)	247957_at	2.3
putative protein similar to unknown protein (dbj BAA96220.1); supported by full-length cDNA: Ceres: 16835.	247295_at	2.3
atfp6-like protein	247128_at	2.3
AP2 domain containing protein AP2 domain containing protein RAP2.4 - Arabidopsis thaliana, EMBL:AF003097	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	257339_s_at	2.3
NAM / CUC2 -like protein nap gene, Arabidopsis thaliana, PID:g2780192; supported by cDNA: gi_15912330_gb_AY056443.1_	253132_at	2.3
hypothetical protein predicted by genefinder; supported by cDNA: gi_16323181_gb_AY057695.1_	267248_at	2.2
putative beta-alanine-pyruvate aminotransferase ;supported by full-length cDNA: Ceres:147543.	267035_at	2.2
unknown protein ; supported by cDNA: gi_15010737_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
putative WD-40 repeat protein similar to TUP1(GB:AF079369); supported by cDNA: gi_13605894_gb_AF367346.1_AF367346	265259_at	2.2
hypothetical protein	265233_s_at	2.2
hypothetical protein	265238_s_at	2.2
ribosomal protein identical to ribosomal protein GI:806279 from [Arabidopsis thaliana]	265032_at	2.2
stress related protein, putative similar to stress related protein GI:5802955 from [Vitis riparia];supported by full-length cDNA: Ceres:14043.	264968_at	2.2
hypothetical protein similar to membrane associated salt inducible protein isolog; similar to F21B7.16 and F21B7.18	264819_at	2.2
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:25383.	264186_at	2.2
unknown protein ;supported by full-length cDNA: Ceres:151404.	264086_at	2.2
hypothetical protein predicted by genscan	263471_at	2.2
unknown protein	262677_at	2.2
beta-VPE nearly identical to beta-VPE GB:BAA09615 GI:1805364 [Arabidopsis thaliana]; supported by cDNA: gi_14194096_gb_AF367254.1_	262644_at	2.2
transcription factor, putative similar to transcription factor GB:CAA74050 GI:2398525 from [Arabidopsis thaliana]	261803_at	2.2
fatty acid elongase 3-ketoacyl-CoA synthase, putative similar to GB:AAC99312 from [Arabidopsis thaliana] (Plant J. (1999) In press); support	261420_at	2.2
hypothetical protein contains Pfam profile: PF01965 ThiJ/PfpI family;supported by full-length cDNA: Ceres:101735.	260616_at	2.2
endochitinase isolog	260568_at	2.2
feebly-like protein similar to feebly protein GB:S70648 [Lycopersicon esculentum] (tomato knockout developed into small fragile plants)	260060_at	2.2
unknown protein	259942_at	2.2
putative thioredoxin similar to protein disulfide isomerase precursor GB:P29828 [Medicago sativa]; Pfam HMM hit: Thioredoxins	259757_at	2.2
hypothetical protein contains bromodomain, predicted by genscan; supported by cDNA: gi_16323116_gb_AY057662.1_	259164_at	2.2
unknown protein	258264_at	2.2
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
CLC-b chloride channel protein identical to CLC-b chloride channel protein GB:CAA96058 from [Arabidopsis thaliana] (J. Biol. Chem. 271 (52	256751_at	2.2
pinhead-like protein similar to pinhead [Arabidopsis thaliana] GI:5107374	256293_at	2.2
unknown protein contains Pfam profile: PF00917 MATH domain; supported by cDNA: gi_12083245_gb_AF332419.1_AF332419	256021_at	2.2
putative chalcone synthase similar to plant chalcone and stilbene synthases;supported by full-length cDNA: Ceres:21877.	255703_at	2.2
putative microfibril-associated protein	255093_s_at	2.2
cytochrome P450 cytochrome P450, Arabidopsis thaliana; supported by cDNA: gi_15293092_gb_AY050980.1_	254562_at	2.2
putative protein KIAA0682 protein, Homo sapiens, AB014582	254527_at	2.2
subtilisin proteinase - like subtilisin-like proteinase ag12, Alnus glutinosa, PIR2:S52769; supported by cDNA: gi_16649028_gb_AY059884.1_	254377_at	2.2
putative protein deubiquitinating enzyme (DUB-1), Mus musculus, PIR2:JC6133	253542_at	2.2
putative protein	253407_at	2.2
thaumatin-like protein thaumatin-like protein, Arabidopsis thaliana, Pir2:S71175; supported by cDNA: gi_13430505_gb_AF360165.1_AF3601	253104_at	2.2
anthranilate phosphoribosyltransferase-like protein anthranilate phosphoribosyltransferase - Pisum sativum, PIR:T06460; supported by cDNA	251563_at	2.2
putative protein leucine zipper-EF-hand containing transmembrane protein 1 - Mus musculus, EMBL:AF061026	251432_at	2.2
unknown protein ;supported by full-length cDNA: Ceres:22350.	250554_at	2.2
expressed protein predicted protein, Synechocystis sp., PIR:S77152; supported by full-length cDNA: Ceres: 5331.	249454_at	2.2

putative protein contains similarity to unknown protein (pir||T08554); supported by full-length cDNA: Ceres: 266884.	247945_at	2.2
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 [Arabi	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
AP2 domain transcription factor	263823_s_at	2.1
FtsH protease, putative contains similarity to chloroplast FtsH protease GI: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
hypothetical protein contains similarity to MTN3 (nodule development protein) GB:Y08726 GI:1619601 from [Medicago truncatula];supported	260876_at	2.1
unknown protein	260155_at	2.1
unknown protein ;supported by full-length cDNA: Ceres:114376.	259977_at	2.1
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 [Ipomoea 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, G-box 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
myb-related protein M4 ;supported 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
acyl-CoA oxidase (gb|AAC13497.1) ; supported by cDNA: gi_3044211_gb_AF057043.1_AF057043	247176_at	2.1
putative protein myosin heavy chain, chicken, PIR:S24348;supported by full-length cDNA: Ceres:147806.	246796_at	2.1
luminal binding protein ; supported by cDNA: gi_1303694_dbj_D84414.1_ATHBIPA	245956_s_at	2.1
transcriptional adaptor like protein ; supported by cDNA: gi_15215639_gb_AY050348.1_	245288_at	2.1
putative protein disulfide-isomerase	245175_at	2.1
unknown protein Location of EST gb|N95878	264167_at	2.1
putative protein disulfide isomerase ; supported by cDNA: gi_15810003_gb_AY054270.1_	267605_at	2
hypothetical protein predicted by genscan and genefinder; supported by cDNA: gi_4837732_gb_AF085354.1_AF085354	267512_at	2
putative potassium transporter	267423_at	2
hypothetical protein predicted by genscan	267268_at	2
putative casein kinase I	266651_at	2
putative pumilio/Mpt5 family RNA-binding protein	266288_s_at	2
hypothetical protein	265147_at	2
unknown protein ;supported by full-length cDNA: Ceres:13385.	264985_at	2
putative acyl-CoA synthetase ; supported by cDNA: gi_15450592_gb_AY052664.1_	263811_at	2
putative protein RIO1 protein, Saccharomyces cerevisiae, PIR:S61006;supported by full-length cDNA: Ceres:42141.	263532_s_at	2
bZIP transcription factor (POSF21) identical to GB:Q04088; supported by cDNA: gi_15982853_gb_AY057534.1_	263253_at	2
putative zinc-binding protein similar to zinc-binding protein (gi|3249068)	263259_at	2
unknown protein	262860_at	2
putative cytochrome P450 monooxygenase strong similarity to gb|X97864 cytochrome P450 from Arabidopsis thaliana and is a member of th	262780_at	2
hypothetical protein similar to hypothetical protein GB:AAD45997 GI:5668770 from (Arabidopsis thaliana)	262322_at	2
transcription factor, putative similar to Transcription factor GB:CAA74053 GI:2398533 from [Arabidopsis thaliana];supported by full-length cD	262098_at	2
hypothetical protein contains similarity to PP2 lectin polypeptide GI:410436 from [Cucurbita maxima]; supported by cDNA: gi_15292968_gb_	262061_at	2
gibberellin 3 beta-hydroxylase, putative similar to gibberellin 3 beta-hydroxylase GI:3982753 from [Arabidopsis thaliana]; supported by cDNA	261768_at	2
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:28026.	260622_at	2
hypothetical protein predicted by genscan+	260594_at	2
ankyrin-like protein similar to ankyrin proteins: GB:CAA48803 [Mus musculus], GB:CAA40279 [Homo sapiens], GB:AAB47551 [Rattus norve	258794_at	2
rotamase FKBP (ROF1) identical to rotamase FKBP (ROF1) GB:U49453 [Arabidopsis thaliana] (Mol. Gen. Genet. 252 (5), 510-517 (1996));	257822_at	2

metalloprotease, putative similar to metalloprotease 1 GB:AAC67244 from [Homo sapiens]	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:	256880_at	2
isoamylase-like protein probable isoamylase (EC 3.2.1.68) su1 - Zea mays,PIR2:T01321	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_AY0350	253550_at	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: gi_15810430_gb_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 Lls1	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
putative 26S protease regulatory subunit 6A Similar to probable Mg-dependent ATPase (pir|S56671). ESTs gb|T46782,gb|AA04798 come fr	264657_at	1.9
hypothetical protein contains similarity to glycogenin GI:165512 from [Oryctolagus 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]	261689_at	1.9
hypothetical protein predicted by genemark.hmm	261524_at	1.9
unknown protein contains similarity to set protein GI:338038 from [Homo sapiens];supported by full-length cDNA: Ceres:27467.	261406_at	1.9
Ca2+-dependent membrane-binding protein annexin idenctical to GB:AAD34236 from [Arabidopsis thaliana];supported by full-length cDNA: C	261285_at	1.9
phosphoethanolamine N-methyltransferase, putative similar to GB:AAF61950 from [Spinacia oleracea]; supported by cDNA: gi_16226648_g	261309_at	1.9
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:19486.	260875_at	1.9
MYB-related protein identical to GB:CAA90748 GI:1263093 from [Arabidopsis thaliana]	260784_at	1.9
unknown protein ;supported by full-length cDNA: Ceres:18355.	259342_at	1.9
unknown protein similar to HYP1 GB:CAA55187 from [Arabidopsis thaliana]	259318_at	1.9
unknown protein similar to possible apospory-associated protein C GB:Q40784 [Pennisetum ciliare];supported by full-length cDNA: Ceres:41	259186_at	1.9
putative serine carboxypeptidase precursor identical to serine carboxypeptidase precursor GB:P32826 [Arabidopsis thaliana] up to residue 51	258970_at	1.9
putative ATPase (ISW2-like) similar to ISW2 (ATPase component of a two subunit chromatin remodeling complex) GB:6324879 [Saccharom	258904_at	1.9
unknown protein ; supported by cDNA: gi_15292900_gb_AY050884.1_	258838_at	1.9
unknown protein contains Pfam profiles: PF00036 EF hand (2 copies); supported by cDNA: gi_14334439_gb_AY034911.1_	257677_at	1.9
DNA-binding protein, putative similar to GB:AAF32491 from [Triticum aestivum] (Mol. Cell. Biol. 19 (12), 8113-8122 (1999))	257291_at	1.9
dem-like protein similar to dem GB:CAA73973 from [Lycopersicon esculentum] (Plant Cell (1998) 10, 1-12)	257029_at	1.9
DREB2B transcription factor identical to dehydration response element binding transcription factor DREB2B GB:BAA33795 [Arabidopsis thali	256430_at	1.9
DnaJ protein, putative contains Pfam profile: PF00226: DnaJ domain;supported by full-length cDNA: Ceres:25796.	256221_at	1.9
putative zinc finger protein	255094_at	1.9
putative protein hypothetical protein, Synechocystis sp., PIR2:S76637	254715_at	1.9
putative protein ARI protein, Drosophila melanogaster, X98309; supported by cDNA: gi_15292860_gb_AY050864.1_	253236_at	1.9
putative protein phospholipase D, Arabidopsis thaliana, gb:U84568; supported by cDNA: gi_11761141_dbj_AB031047.1_AB031047	253120_at	1.9
hypothetical protein	252400_at	1.9
putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:106702.	251896_at	1.9
RING finger - like protein DNA-binding Mel-18 protein, Homo sapiens, PIR:JN0717supported by full-length cDNA: Ceres:20931.	251897_at	1.9
Sar1-like GTP binding protein small GTP-binding protein Bsar1a - Brassica campestris, EMBL:U55035	251217_at	1.9
putative protein similar to unknown protein (pir||T01270)	250742_at	1.9
putative protein similar to unknown protein (gb|AAF23188.1)	250728_at	1.9
putative protein hypothetical bacterial proteins	250570_at	1.9
putative protein similar to unknown protein (sp|P37707);supported by full-length cDNA: Ceres:6903.	249237_at	1.9
unknown protein	249134_at	1.9
putative protein contains similarity to G-box binding factor;supported by full-length cDNA: Ceres:25211.	249074_at	1.9

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) (sp|P20431) ; 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_1	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 fro	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 n	259733_at	1.8
CONSTANS family zinc finger protein, putative contains Pfam profile: PF01760: CONSTANS family zinc finger; supported by cDNA: gi_143	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: C	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	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 [Bradyrhizobiu	257052_at	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	255590_at	1.8
polycomb group - like protein similar to A. thaliana homeotic protein curlyleaf, GenBank accession number Y10580; supported by cDNA: gi_4	255510_at	1.8
putative ribosomal protein L19 similar to L19 from several species; supported by cDNA: gi_14423511_gb_AF386993.1_AF386993	255520_at	1.8
coded for by A. thaliana cDNA T75804 similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91)	255474_at	1.8
putative pre-mRNA splicing factor similar to yeast pre-mRNA splicing factors; supported by cDNA: gi_16604550_gb_AY059720.1_	255382_at	1.8
putative ABC transporter similar to Guillardia theta ABC transporter, GenBank accession number AF041468; supported by cDNA: gi_155291	255305_at	1.8
UV-damaged DNA binding factor - like protein XPE UV-damaged DNA binding factor, Mus musculus, BAA84699	255226_at	1.8
putative protein anthocyanin rhamnosyltransferase -Petunia x hybrida, PID:g454253	255032_at	1.8
putative protein hypothetical protein F7H19.70 - Arabidopsis thaliana, PID:e1310057	254848_at	1.8
putative protein ; supported by cDNA: gi_16323185_gb_AY057697.1_	254764_at	1.8
potassium channel protein AKT3 ; supported by cDNA: gi_1100897_gb_U40154.1_ATU40154	254305_at	1.8
putative serine/threonine kinase MAP3K delta-1 protein kinase, Arabidopsis thaliana,PID:g2253010; supported by cDNA: gi_15810436_gb_A	254269_at	1.8
transcriptional activator CBF1-like protein strong similarity to transcriptional activator CBF1, Arabidopsis thaliana00	254066_at	1.8
protein phosphatase ABI1 ; supported by cDNA: gi_14334799_gb_AY035073.1_	253994_at	1.8
AIM1 protein ; supported by cDNA: gi_16648890_gb_AY059815.1_	253759_at	1.8
protein phosphatase 2C - like protein protein phosphatase 2C, Schizosaccharomyces pombe, PIR2:S54297; supported by cDNA: gi_16209	253453_at	1.8
putative protein kinase protein kinase, Spinacia oleracea, PIR2:S42867	253359_at	1.8
arginine decarboxylase SPE2 ; supported by cDNA: gi_14517491_gb_AY039581.1_	253203_at	1.8
putative protein crp1-hcf111 allele,encoding a chloroplast protein -Zea mays,PID:g3289002	253019_at	1.8
putative protein	252990_at	1.8
putative protein proline-rich protein A41R, Chlorella virus PBCV-1, PIR:T17531;supported by full-length cDNA: Ceres:27481.	251550_at	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
FtsH 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
autophagocytosis protein - like autophagocytosis protein AUT1, Saccharomyces cerevisiae, PIR:S45130;supported by full-length cDNA: Cere	247542_at	1.8
putative protein predicted protein, Arabidopsis thaliana	247487_at	1.8
putative protein embryo-specific protein 3, Arabidopsis thaliana, PIR:T48490	247459_at	1.8
non-phototropic hypocotyl 3 (gb|AAF05914.1) ; supported by cDNA: gi_6224711_gb_AF180390.1_AF180390	247288_at	1.8
unknown protein	246957_at	1.8
transcription factor-like protein light-induced protein CPRF-2 - Petroselinum crispum, PIR:S16321	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
protein phosphatase - like protein phosphatase-2C, Mesembryanthemum crystallinum, EMBL:AF075581;supported by full-length cDNA: Cere	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
NADH dehydrogenase subunit 3 Protein sequence is in conflict with the conceptual translation	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
unknown protein highly similar to T21L14.19; similar to GP|2191153|AF007269 and GP|2252859|AF013294	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
hypothetical protein	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
alanine--tRNA ligase, putative similar to alanine--tRNA 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	261433_s_at	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	258380_at	1.7
protein kinase, putative similar to serine/threonine protein kinase GB:NP_032667 from [Mus musculus]	258186_s_at	1.7
unknown protein ; supported by cDNA: gi_14423467_gb_AF386971.1_AF386971	258154_at	1.7

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
HAPp48,5 protein identical to HAPp48,5 GB:Y09562 [Arabidopsis thaliana]	256902_s_at	1.7
unknown protein ;supported by full-length cDNA: Ceres:3056.	256441_at	1.7
deoxyguanosine kinase, putative similar to deoxyguanosine kinase [Homo sapiens] GI:1480198;supported by full-length cDNA: Ceres:3878.	256341_at	1.7
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
ferredoxin--NADP+ reductase - like protein ferredoxin--NADP+ 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	253293_at	1.7
putative protein predicted protein, Arabidopsis thaliana; supported by cDNA: gi_15451175_gb_AY054668.1_	253062_at	1.7
cinnamyl alcohol dehydrogenase -like protein, LCADa	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	252606_at	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_AF370176	251964_at	1.7
fructokinase - like protein fructokinase, Lycopersicon esculentum, EMBL:LEU62329	251935_at	1.7
putative protein arm repeat containing protein, Brassica napus, AF024625	251862_at	1.7
putative protein hypothetical proteins - Arabidopsis thaliana; supported by cDNA: gi_14334587_gb_AY034967.1_	251356_at	1.7
neoxanthin cleavage enzyme nc1	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
putative protein contains similarity to zinc finger protein;supported by full-length cDNA: Ceres:3542.	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, EMBL:AK001734; supported by cDNA: gi_14532679_gb_AY039964.1_	250402_at	1.7
transporter-like protein ;supported by full-length cDNA: Ceres:27439.	250252_at	1.7
unknown protein	250104_at	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 (dbj|BAA76827.1); supported by cDNA: gi_14532601_gb_AY039925.1_	249181_at	1.7
putative protein similar to unknown protein (gb|AAD20092.1)	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: Ceres	247513_at	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_	247222_at	1.7
putative protein strong similarity to unknown protein (pir||T04718); supported by cDNA: gi_15529177_gb_AY052213.1_	247013_at	1.7
RuvB DNA helicase-like protein ; supported by cDNA: gi_16974567_gb_AY061754.1_	247014_at	1.7
RING finger-like protein RING-H2 finger protein RHG1a - 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	245659_at	1.7
putative phosphatidylinositol-4-phosphate 5-kinase ; supported by cDNA: gi_13925628_gb_AF260903.1_AF260903	267081_at	1.7
putative protein strong similarity to unknown protein (pir||T05518)	248495_at	1.7
putative protein similar to unknown protein (emb|CAB51351.1)	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
putative vacuolar sorting receptor identical to GB:U79960; contains a calcium-binding EGF-like domain signature	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	266466_at	1.6
putative elongation factor	266407_at	1.6
unknown protein ; supported by cDNA: gi_16604650_gb_AY059770.1_	266121_at	1.6
20S proteasome subunit (PAA2) identical to GB:AF043519; supported by cDNA: gi_15450622_gb_AY052679.1_	266036_s_at	1.6
hypothetical protein	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.	265339_at	1.6
hypothetical protein	265230_s_at	1.6
putative senescence-associated protein 12 ;supported by full-length cDNA: Ceres:40806.	264787_at	1.6
hypothetical protein similar to receptor-like protein kinase GI:7529754 from [Arabidopsis thaliana]	264479_at	1.6
unknown protein similar to Lambda-PRL2 Arabidopsis thaliana cDNA clone GB:R30041	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	263824_at	1.6
unknown protein similar to cell differentiation protein GB:AAC36682 from (Homo sapiens)	263685_at	1.6
DNA-directed RNA polymerase II, third largest subunit	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

hypothetical 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
unknown 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, gi|3255965 and yeast p	262800_at	1.6
unknown protein strong similarity to gb|Y09533 involved in starch metabolism from Solanum tuberosum and contains a PF|01326 Pyruvate p	262784_at	1.6
heat 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	262299_at	1.6
hypothetical protein predicted by genemark.hmm	262238_at	1.6
AP2 domain containing protein, putative similar to AP2 domain containing protein GI:2281649 from [Arabidopsis thaliana];supported by full-le	262197_at	1.6
splicing factor Prp8, putative similar to splicing factor Prp8 GI:3661610 from [Homo sapiens]	262068_at	1.6
type 2 peroxiredoxin, putative similar to type 2 peroxiredoxin GI:4928472 from [Brassica rapa subsp. pekinensis];supported by full-length cDN	261919_at	1.6
scarecrow-like 3 identical to GB:AAD24404 GI:4580515 from [Arabidopsis thaliana] (Plant J. 18 (1), 111-119 (1999)); supported by cDNA: gi_	261866_at	1.6
transcriptional regulator, putative similar to transcriptional regulator GI:4836767 from [Zea mays]	261837_s_at	1.6
ATP-dependent Clp protease proteolytic subunit (ClpR1) identical to nClpP5 GB:BAA82069 GI:5360595 from [Arabidopsis thaliana];supporte	261634_at	1.6
hypothetical protein contains similarity to zinc finger protein GI:1399465 from [Cryptosporidium parvum];supported by full-length cDNA: Ceres	261376_at	1.6
Expressed protein ; supported by cDNA: gi_13926326_gb_AF372912.1_AF372912	261272_at	1.6
hypothetical protein predicted by genemark.hmm	261176_at	1.6
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:98874.	261124_at	1.6
unknown protein ;supported by full-length cDNA: Ceres:40419.	261144_s_at	1.6
tropinone reductase-I, putative similar to GB:L20473 from [Datura stramonium] (Proc. Natl. Acad. Sci. U.S.A. 90, 9591-9595 (1993)); support	261084_at	1.6
F-box protein family contains similarity to F-box protein FBX3 GI:6103643 from [Homo sapiens]	260949_at	1.6
unknown 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
hypothetical protein identical to hypothetical protein GB:AAF81322 GI:8920600 from (Arabidopsis thaliana)	260700_at	1.6
glyoxalase I, putative similar to GB:Y13239 from [Brassica juncea] (Plant J. 17 (4), 385-395 (1999))	260619_at	1.6
unknown protein similar to putative cytoskeletal protein GI:1732517 from [Arabidopsis thaliana]; supported by cDNA: gi_1732516_gb_U6274	260638_at	1.6
hypothetical protein predicted by genscan+, contains Viral RNA helicase domain	260283_at	1.6
putative 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	260235_at	1.6
putative ATPase contains Pfam profile: PF00004 ATPases associated with various cellular activities (AAA)	260089_at	1.6
putative serine/threonine-protein kinase similar to SERINE/THREONINE-PROTEIN KINASE ASK1 GB:P43291 from [Arabidopsis thaliana];su	259724_at	1.6
hypothetical protein ; supported by cDNA: gi_13937176_gb_AF372942.1_AF372942	259545_at	1.6
hypothetical protein ; supported by cDNA: gi_15081631_gb_AY048208.1_	259516_at	1.6
Expressed protein ; supported by cDNA: gi_14532525_gb_AY039887.1_	259416_at	1.6
beta-glucosidase identical to beta-glucosidase GB:AAC31962 [Arabidopsis thaliana]; supported by cDNA: gi_3420934_gb_AF082157.1_AF0	259173_at	1.6
unknown 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
putative 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	258701_at	1.6
unknown protein	258635_at	1.6
unknown protein ;supported by full-length cDNA: Ceres:39933.	258348_at	1.6
putative casein kinase I similar to casein kinase I GB:CAA55396 from [Arabidopsis thaliana]; supported by cDNA: gi_15809823_gb_AY05417	258300_at	1.6
acid phosphatase type 5 identical to GB:CAB63938 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:113666.	258158_at	1.6
putative myc-like DNA-binding protein similar to GB:AAB72192 from [Arabidopsis thaliana]	257990_at	1.6
unknown 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
hypothetical protein predicted by genemark.hmm	256208_at	1.6
putative protein	256027_at	1.6
hypothetical protein ;supported by full-length cDNA: Ceres:37204.	255980_at	1.6
unknown protein ;supported by full-length cDNA: Ceres:23788.	255957_at	1.6
p68 RNA helicase, putative similar to p68 RNA helicase (Schizosaccharomyces pombe) GI:173419	255749_at	1.6
predicted OR23 protein of unknown function	255469_at	1.6
hypothetical protein ;supported by full-length cDNA: Ceres:40589.	254683_at	1.6
putative 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
putative protein ; supported by cDNA: gi_13991647_gb_AF359388.1_AF359388	254043_at	1.6
hypothetical protein ;supported by full-length cDNA: Ceres:113230.	253689_at	1.6
putative protein putative ATPase - Haematobia irritans,PID:g525318;supported by full-length cDNA: Ceres:4.	253630_at	1.6
putative protein ; supported by cDNA: gi_13605598_gb_AF361625.1_AF361625	253388_at	1.6
MYB-like protein myb-related protein Y49, Arabidopsis thaliana, PIR:S58292	253219_at	1.6
putative protein F56F10.1, Caenorhabditis elegans, PATX:G1688051	253079_s_at	1.6
beta-galactosidase like protein ; supported by cDNA: gi_15810492_gb_AY056285.1_	253090_at	1.6
putative protein ; supported by cDNA: gi_13605658_gb_AF361810.1_AF361810	252856_at	1.6
flavanone 3-hydroxylase (FH3) ;supported by full-length cDNA: Ceres:36653.	252123_at	1.6
putative 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
histone deacetylase -like protein histone deacetylase, HD2-p39, nucleolar, Zea mays, PIR:T04141	250912_at	1.6
glucuronosyl transferase-like protein	250750_at	1.6
sorting nexin-like protein	250714_at	1.6
ABA-responsive protein - like ABA-responsive protein, Hordeum vulgare, EMBL:AF026538	250279_at	1.6
sigma-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
prolylcarboxypeptidase-like protein ;supported by full-length cDNA: Ceres:122449.	249860_at	1.6

putative protein	249622_at	1.6
putative protein hypothetical protein - Synechocystis sp., PIR:S76678	249433_at	1.6
glutathione transferase-like ;supported by full-length cDNA: Ceres:37349.	249316_s_at	1.6
pitrilysin	249218_at	1.6
PINHEAD (gb|AAD40098.1); translation initiation factor	249115_at	1.6
putative protein similar to unknown protein (pir||T05524);supported by full-length cDNA: Ceres:767.	248952_at	1.6
putative protein similar to unknown protein (sp P74035); supported by cDNA: gi_15292692_gb_AY050780.1_	248906_at	1.6
unknown protein ;supported by full-length cDNA: Ceres:302.	248834_at	1.6
unknown protein	248067_at	1.6
putative protein similar to unknown protein (emb|CAB62440.1)	248016_at	1.6
GTP binding protein-like	247891_at	1.6
putative protein predicted proteins, Arabidopsis thaliana and Oryza sativa; supported by cDNA: gi_14532713_gb_AY039981.1_	247466_at	1.6
putative protein contains similarity to auxin-independent growth promoter	247186_at	1.6
unknown protein ;supported by full-length cDNA: Ceres:124621.	247139_at	1.6
hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 12819.	246581_at	1.6
putative protein	246533_at	1.6
putative protein AAA family protein Bor, Drosophila melanogaster, EMBL:AF227209	246461_at	1.6
sucrose-phosphate synthase-like protein sucrose-phosphate synthase (EC 2.4.1.14) isoform 1 - Citrus unshiu, EMBL:AB005023; supported	246076_at	1.6
alpha-galactosidase - like protein alpha-galactosidase, coffee, PIR:T50781	246055_at	1.6
sucrose-UDP glucosyltransferase	245998_at	1.6
unknown protein	245787_at	1.6
dormancy-associated protein, putative similar to dormancy-associated protein GI:2995990 from [Arabidopsis thaliana]; supported by cDNA:	245668_at	1.6
cysteine proteinase contains similarity to papain-like cysteine proteinase isoform I GI:7381219 from [Ipomoea batatas]	245483_at	1.6
putative protein	245427_at	1.6
putative protein various predicted proteins, Arabidopsis thaliana	254457_at	1.5
fatty acid elongase - like protein fatty acid elongase 1(Fae1), Arabidopsis thaliana, U29142	253285_at	1.5
putative myosin heavy chain	267314_at	1.5
FtsH protease (VAR2) identical to zinc dependent protease VAR2 GI:7650138 from [Arabidopsis thaliana]	267196_at	1.5
putative AMP deaminase ; supported by cDNA: gi_15810524_gb_AY056301.1_	267095_at	1.5
putative RNA helicase	266932_s_at	1.5
hexokinase (ATHXK2) ; supported by cDNA: gi_1899024_gb_U28215.1_ATU28215	266702_at	1.5
unknown protein	266362_at	1.5
putative PCI domain protein proteasome, COP9-complex and eIF3-domain protein; members of multi-protein complexes;supported by full-le	266310_at	1.5
unknown protein ; supported by cDNA: gi_14532581_gb_AY039915.1_	266315_at	1.5
unknown protein	266188_at	1.5
putative mitochondrial translation elongation factor G	266127_s_at	1.5
putative prolylcarboxypeptidase	265990_at	1.5
unknown protein	265760_at	1.5
hypothetical protein	265425_at	1.5
putative MYB family transcription factor ; supported by cDNA: gi_1020156_gb_U26937.1_ATU26937	265359_at	1.5
hypothetical protein contains similarity to zinc finger protein rts2 GB:U16133 GI:563244 from [Saccharomyces cerevisiae]; supported by cDN	265079_at	1.5
putative prohibitin 2 B-cell receptor associated protein;supported by full-length cDNA: Ceres:6208.	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%+ id	265045_s_at	1.5
putative chloroplast membrane protein, ALBINO3 similar to GB:AAB61458	265011_at	1.5
phosphatidylinositol 3-kinase, putative similar to phosphatidylinositol 3-kinase GI:736338 from [Glycine max]; supported by cDNA: gi_555699	264927_at	1.5
unknown protein Location of EST gb|AA395277 gb|T44807;supported by full-length cDNA: Ceres:36286.	264894_at	1.5
unknown protein location of EST gb|H36530, gb|AA395402, and gb|T43793	264772_at	1.5
unknown protein location of EST gb|T46445	264776_at	1.5
unknown protein similar to putative inositol polyphosphate 5 -phosphatase GI:3212848 from [Arabidopsis thaliana]	264683_at	1.5
unknown protein	264597_at	1.5
tat-binding protein, putative Highly Similar to branched-chain amino acid aminotransferase; Location of EST gb|T44177 and gb|AA395381; s	264524_at	1.5
hypothetical protein contains similarity to nuclear protein GI:1236985 from [Homo sapiens]; supported by cDNA: gi_14423425_gb_AF386950.	264486_at	1.5
unknown protein similar to ESTs gb|N96021 and gb|N96863	264458_at	1.5
HSP100/ClpB, putative similar to HSP100/ClpB GI:9651530 [Phaseolus lunatus]	264402_at	1.5
hypothetical protein predicted by genemark.hmm	264224_at	1.5
putative rubisco subunit binding-protein alpha subunit ;supported by full-length cDNA: Ceres:25773.	264069_at	1.5
putative GTP cyclohydrolase	264045_at	1.5
putative DnaJ protein ;supported by full-length cDNA: Ceres:10312.	264002_at	1.5
cyclophilin (CYP2) Same as GB: AF020434;supported by full-length cDNA: Ceres:35643.	264019_at	1.5
unknown protein	263972_at	1.5
putative citrate synthase ;supported by full-length cDNA: Ceres:17416.	263986_at	1.5
putative fructose bisphosphate aldolase ;supported by full-length cDNA: Ceres:13024.	263921_at	1.5
unknown protein	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
hypothetical protein predicted by genscan	263200_at	1.5
heat-shock protein, putative similar to heat-shock protein GI:472939 from [Helianthus annuus];supported by full-length cDNA: Ceres:97415.	263150_at	1.5
unknown protein Similar to gb|U51990 pre-mRNA-splicing factor hPrp18 from Homo sapiens. ESTs gb|T46391 and gb|AA721815 come from	263116_s_at	1.5
purple acid phosphatase precursor identical to SP:Q38924	263083_at	1.5
mak16-like protein-related similar to MAK16 PROTEIN GB:P10962 GI:127112 from [Saccharomyces cerevisiae] (Proc. Natl. Acad. Sci. U.S.	263039_at	1.5
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_13430457_gb_AF360141.1_AF360141	262964_at	1.5
putative inosine-5-monophosphate dehydrogenase strong similarity to gb|L34684 inosine monophosphate dehydrogenase (IMPDH) from Ara	262754_at	1.5
unknown protein EST gb|H77143 comes from this gene; supported by cDNA: gi_15293206_gb_AY051037.1_	262570_at	1.5
unknown protein Location of est 278F3T7 (gb|AA650690)	262521_at	1.5
ATPase, putative similar to chromaffin granule ATPase II GB:AAD03352 GI:4115341 from [Bos taurus]	262275_at	1.5
beta-glucosidase, putative similar to beta-glucosidase GI:5030906 from [Polygonum tinctorium]; supported by cDNA: gi_15146265_gb_AY04	262118_at	1.5
unknown protein ; supported by cDNA: gi_6520232_dbj_AB028233.1_AB028233	262080_at	1.5
mRNA export protein, putative similar to mRNA export protein GB:AAC28126 GI:1903456 from [Homo sapiens];supported by full-length cDN	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)	261644_s_at	1.5
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:24737.	261625_at	1.5
unknown protein ; supported by cDNA: gi_16604588_gb_AY059739.1_	261538_at	1.5
unknown protein	261250_at	1.5
hypothetical protein predicted by genemark.hmm	261219_at	1.5

subtilisin-like serine protease similar to subtilisin-type protease precursor GI:14150446 from [Glycine max];supported by full-length cDNA: Cer	261224_at	1.5
unknown protein	261168_at	1.5
homeodomain protein BELL1, putative similar to GB:AAB05099 from [Arabidopsis thaliana] (Cell 83 (5), 735-742 (1995));supported by full-ler	261120_at	1.5
unknown protein	260995_at	1.5
unknown protein similar to unknown protein GB:AAF18609 GI:6598419 from [Arabidopsis thaliana]	260884_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 by cDNA:	260780_at	1.5
Ring3-like bromodomain protein similar to Ring3 GB:BAA25416 GI:3041763 from [Mus musculus], contains Pfam profile:PF00439 Bromodon	260787_at	1.5
RING-H2 finger protein RHA3a, putative similar to RING-H2 finger protein RHA3a GI:3790573 from [Arabidopsis thaliana]; supported by cDN	260770_at	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
hypothetical 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
unknown 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
alpha 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
Mutator-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	258679_at	1.5
putative 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 [Daucus carota] (Physiol. Plantarum (1999) 107, 159-165)	258507_at	1.5
hypothetical protein predicted by genemark.hmm	257864_at	1.5
mitogen activated protein kinase kinase, putative similar to mitogen activated protein kinase kinase GB:AAC32599 from [Oryza sativa]	257801_at	1.5
unknown protein	257685_at	1.5
unknown protein contains Pfam profile:PF00439 bromodomain:Bromodomain	257146_at	1.5
unknown 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_	257022_at	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	256590_at	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
unknown protein	256229_at	1.5
putative protein contains similarity to pseudouridine synthases; supported by cDNA: gi_13430549_gb_AF360187.1_AF360187	255985_at	1.5
hypothetical protein predicted by genscan+	255994_at	1.5
hypothetical protein predicted by genscan and genefinder; similar to EGAD|50981|YBR228W	255866_at	1.5
hypothetical protein similar to putative phloem transcription factor GI:7630279 from [Apium graveolens]	255725_at	1.5
putative myb-related DNA-binding protein	255614_at	1.5
hypothetical 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; supportec	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
glycine-rich protein glycine-rich cell wall structural protein - garden petunia,Pir2:A26099	253619_at	1.5
putative protein hypothetical protein - Synechocystis sp. (strain PCC 6803),PIR2:S76076	253585_at	1.5
predicted protein ; supported by cDNA: gi_15292824_gb_AY050846.1_	253524_at	1.5
sulfolipid biosynthesis protein SQD1 ; supported by cDNA: gi_14190482_gb_AF380641.1_AF380641	253386_at	1.5
formamidase - like protein formamidase, Methylophilus methylotrophus, PIR2:S74213; supported by cDNA: gi_14334653_gb_AY035000.1_	253048_at	1.5
phosphoenolpyruvate carboxykinase (ATP) -like protein ; supported by cDNA: gi_13937136_gb_AF372922.1_AF372922	253041_at	1.5
hypothetical protein several hypothetical proteins - Arabidopsis thaliana	252473_s_at	1.5
putative protein predicted proteins, Arabidopsis thaliana	252402_s_at	1.5
serine 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_A	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
alpha-soluble NSF attachment protein ; supported by cDNA: gi_6013203_gb_AF177989.1_AF177989	251721_s_at	1.5
putative protein several hypothetical proteins - Arabidopsis thaliana;supported by full-length cDNA: Ceres:112338.	251530_at	1.5
squamosa promoter binding protein-like 12	251450_at	1.5
palmitoyl-protein thioesterase precursor - like palmitoyl-protein thioesterase precursor, Mus musculus, EMBL:AF071025; supported by full-ler	251408_at	1.5
serine/threonine-protein kinase-like protein serine/threonine kinase UNC51.2 - Mus musculus, EMBL:AF145922; supported by cDNA: gi_143	251273_at	1.5
aldose reductase-like protein aldose reductase - Hordeum vulgare, EMBL:Z48360	251100_at	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 ; supported by cDNA: gi_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
putative protein	250946_at	1.5
putative protein ; supported by cDNA: gi_1019903_gb_U37587.1_ATU37587	250899_at	1.5
F1F0-ATPase inhibitor - like protein F1F0-ATPase inhibitor protein, OsIF1-1, Oryza sativa, EMBL:AB029059; supported by full-length cDNA:	250863_at	1.5
RNA helicase-like protein	250529_at	1.5
putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:403.	250332_at	1.5
translocon Tic40-like protein ; supported by cDNA: gi_16226312_gb_AF428299.1_AF428299	250080_at	1.5
putative protein strong similarity to unknown protein (gb|AAD21756.1); supported by cDNA: gi_15146184_gb_AY049233.1_ although this cD	249703_at	1.5
receptor serine/threonine protein kinase -like receptor serine/threonine kinase PR5K, Arabidopsis thaliana, EMBL:AT48698	249552_s_at	1.5
unknown protein ;supported by full-length cDNA: Ceres:101366.	249456_at	1.5
GTPase activator protein of Rab-like small GTPases-like protein	249281_at	1.5
putative protein strong similarity to unknown protein (gb|AAF24960.1)	249133_at	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 (pir||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
putative protein contains similarity to unknown protein (pir||T05510)	248499_at	1.5
putative protein contains similarity to unknown protein (pir||T26512)	248463_at	1.5
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	246893_at	1.5
dehydration-induced protein RD22 ; supported by cDNA: gi_16974545_gb_AY060560.1_	246908_at	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 ; 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
gunknown protein contains non-consensus TG donor splice site at exon 1	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, -	FX-r2-Ec-bioB-3	1.4
unknown protein ;supported by full-length cDNA: Ceres:35441.	267483_at	1.4
putative DNA2-NAM7 helicase family protein	267489_s_at	1.4
putative UDP-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
putative beta-1,3-glucanase	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	265519_at	1.4
hypothetical protein predicted by genscan and genefinder, contains a Bem1/NCF1/PI3K domain (prosite:QDOC50195)	265535_at	1.4
Expressed protein ; supported by cDNA: gi_14335135_gb_AY037247.1_	265474_at	1.4
putative bHLH transcription factor	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
hypothetical protein	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 (sp|P17812|PYRG_HUMAN); similar to ESTs gb|AA660762, gb|AA220982, dbj|AU008137,	264529_at	1.4
hypothetical 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 GI: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.	264219_at	1.4
unknown protein contains similarity to splicing factor required for vegetative and meiotic growth GI:2959374 from [Schizosaccharomyces pom	264221_s_at	1.4
putative peroxidase ;supported by full-length cDNA: Ceres:113695.	264001_at	1.4
putative cryptochrome 2 apoprotein Match to Arabidopsis photolysase (PHH1) gene (gb|X99061) and cryptochrome 2 apoprotein (CRY2) (gb|	263669_at	1.4

transcription factor ZAP1 identical to GP:1064883:X92976	263626_at	1.4
hypothetical protein	263505_s_at	1.4
unknown protein ; supported by cDNA: gi_15810174_gb_AY056101.1_	263333_at	1.4
putative protein kinase contains a protein kinase domain profile (PDOC00100); supported by cDNA: gi_13605880_gb_AF367339.1_AF367339	263274_at	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 Hs	262814_at	1.4
hypothetical protein identical to hypothetical protein GB:AAD50051 GI:5734786 from [Arabidopsis thaliana]; supported by cDNA: gi_1508169	262419_at	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	261806_at	1.4
vacuolar assembly protein vps41, putative similar to vacuolar assembly protein vps41 GI:1835787 from [Lycopersicon esculentum]	261783_at	1.4
hypothetical protein contains similarity to Na+/H+ antiporter GI:1655701 from [Xenopus laevis]	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 (20	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]	260194_at	1.4
hypothetical protein similar to hypothetical protein GB:CAB37532 from [Arabidopsis thaliana], predicted by genscan+;supported by full-length	260127_at	1.4
F-box protein FKF1/ADO3, AtFBX2a identical to FKF1 GI:6960305 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	259705_at	1.4
unknown protein	259489_at	1.4
unknown protein ; supported by cDNA: gi_16930412_gb_AF419560.1_AF419560	259418_at	1.4
methionine aminopeptidase I (MAP1), putative similar to methionine aminopeptidase I (MAP1) GI:975722 from [Saccharomyces cerevisiae];	259363_at	1.4
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:18207.	259235_at	1.4
putative mRNA capping enzyme, RNA guanylyltransferase contains similarty 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	258775_at	1.4
hypothetical protein predicted by genscan; supported by cDNA: gi_15982780_gb_AY057497.1_	258660_at	1.4
putative cytochrome P450 similar to GB:Q05047 from [Catharanthus roseus]	258114_at	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]	257981_at	1.4
seed maturation protein, putative similar to seed maturation protein (PM36) GB:AAD51624 [Glycine max];supported by full-length cDNA: Cer	257888_at	1.4
SNF1 related protein kinase (ATSRPK1) identical to SNF1 related protein kinase (ATSRPK1) GB:AB027153 [Arabidopsis thaliana]; supporte	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	257227_at	1.4
Expressed protein ; supported by full-length cDNA: Ceres: 93242.	257193_at	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:	256300_at	1.4
transcription factor HBP-1B-like nearly identical to transcription factor HBP-1B SP:P43273 [Arabidopsis thaliana (Mouse-ear cress)]; supporte	256269_at	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:O74940 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	255664_at	1.4
hypothetical protein	255611_at	1.4
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-coumarate--CoA ligase - like protein 4-coumarate--CoA 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	254776_at	1.4
vacuolar sorting receptor-like protein BP-80 vacuolar sorting receptor, Pisum sativum, PATCHX:G1737222	254500_at	1.4
auxin response factor 9 (ARF9) ; supported by cDNA: gi_4580574_gb_AF082176.1_AF082176	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	253625_at	1.4
putative protein tetratricopeptide repeat protein - Homo sapiens,PID:g1688074;supported by full-length cDNA: Ceres:12573.	253633_at	1.4
putative protein KIAA0800 protein, Homo sapiens, EMBL:AB018343	253560_at	1.4

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_	253279_at	1.4
hypothetical protein ;supported by full-length cDNA: Ceres:115167.	253232_at	1.4
putative protein various predicted proteins, Arabidopsis thaliana	252901_at	1.4
putative protein 70K peroxisomal membrane protein, Rattus norvegicus ,PIR2:A35723; supported by cDNA: gi_15320528_gb_AF378120.1_	252830_at	1.4
disease resistance protein RPP13-like protein disease resistance protein RPP8 - Arabidopsis thaliana, EMBL:AF089710; supported by cDNA	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 predicted 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:A	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_AB046	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
putative protein similar to unknown protein (sp|P42251); supported by cDNA: gi_13430795_gb_AF360310.1_AF360310	249201_at	1.4
putative protein similar to unknown protein (pir||T02918); supported by full-length cDNA: Ceres: 26596.	249122_at	1.4
ATP dependent copper transporter ; supported by cDNA: gi_14194134_gb_AF367273.1_AF367273	249027_at	1.4
putative protein strong similarity to unknown protein (emb|CAB87688.1)	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 (gb 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	247228_at	1.4
DNA binding protein TGA1a homolog ;supported by full-length cDNA: Ceres:31032.	247199_at	1.4
2-oxoglutarate dehydrogenase, E1 component	247155_at	1.4
unknown protein	247063_at	1.4
anthranilate N-hydroxycinnamoyl/benzoyltransferase-like protein ;supported by full-length cDNA: Ceres:32856.	247038_at	1.4
putative protein predicted protein, Oryza sativa	246909_at	1.4
farnesylated protein ATFP6-like protein farnesylated protein ATFP6 - Arabidopsis thaliana, EMBL:U64909	246429_at	1.4
putative protein hnRNP A/B related protein - Felis catus, EMBL:AF153444; supported by cDNA: gi_14194148_gb_AF367280.1_AF367280	246292_at	1.4
putative protein	246283_at	1.4
putative protein ;supported by full-length cDNA: Ceres:13475.	246225_at	1.4
putative protein hypothetical protein F2A19.120 - Arabidopsis thaliana, PIR:T47944	246173_s_at	1.4
putative protein CD2 cytoplasmic domain binding protein - Homo sapiens, EMBL:AF104222;supported by full-length cDNA: Ceres:13887.	245887_at	1.4
ferredoxin-dependent glutamate synthase ; supported by cDNA: gi_3869250_gb_U39287.1_ATU39287	245701_at	1.4
RNA-binding protein-like	245714_at	1.4
pyruvate,orthophosphate dikinase	245528_at	1.4
ATP-dependent Clp protease proteolytic subunit (ClpR4), putative similar to ATP-dependent Clp protease proteolytic subunit GI:7264063 fror	245400_at	1.4
putative protein similarity to ALR - Homo sapiens~contains EST gb:Aa39558600	245237_at	1.4
small nuclear ribonucleoprotein U1A identical to GB:Z49991; supported by cDNA: gi_15450590_gb_AY052663.1_	245124_at	1.4
unknown protein ; supported by cDNA: gi_16930450_gb_AF419579.1_AF419579	245119_at	1.4
putative xylulose kinase	263773_at	1.4
metal ion transporter, putative similar to metal ion transporter GI:5853313 from [Arabidopsis thaliana]	261845_at	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	1.3
hypothetical protein predicted by genscan; similar to SP|Q09298|YQO9_CAEEL	267632_at	1.3
putative RING zinc finger protein	267581_at	1.3
hypothetical protein predicted by genscan	267508_at	1.3
unknown protein	267073_at	1.3
unknown protein ;supported by full-length cDNA: Ceres:39666.	266848_at	1.3
60S ribosomal protein L30 ;supported by full-length cDNA: Ceres:34564.	266822_at	1.3
putative amino acid acetyltransferase	266826_at	1.3
unknown protein ; supported by cDNA: gi_14030738_gb_AF375460.1_AF375460	266617_at	1.3
putative splicing factor ;supported by full-length cDNA: Ceres:16224.	266534_at	1.3
ferredoxin-dependent glutamate synthase (GLU2)	266365_at	1.3
unknown protein	266389_s_at	1.3
putative ubiquitin activating enzyme	266333_at	1.3
unknown protein	266189_at	1.3
unknown protein ;supported by full-length cDNA: Ceres:39558.	266170_at	1.3
unknown protein	265807_at	1.3
Expressed protein ; supported by full-length cDNA: Ceres: 157460.	265770_at	1.3
putative MYB family transcription factor	265700_at	1.3
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 (BCKDHB)	265070_at	1.3
Rubisco subunit binding-protein beta subunit identical to chaperonin 60 beta precursor GB:JT0901 from [Arabidopsis thaliana]; supported by	265076_at	1.3
unknown protein Contains similarity to pre-mRNA processing protein PRP39 gb L29224 from S. cerevisiae. ESTs gb|R64908 and gb|T88158	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	1.3
putative ligand-gated ion channel protein Similar to Arabidopsis putative ion-channel PID:g2262157 (gb|AC002329); supported by cDNA: gi_	264587_at	1.3
unknown protein	264563_s_at	1.3
unknown protein ; supported by cDNA: gi_13430435_gb_AF360130.1_AF360130	264548_at	1.3
unknown protein similar to salt-inducible protein (gi|375717); similar to ESTs gb|R30192 and gb|AA651017	264452_at	1.3
hypothetical protein predicted by genefinder; supported by cDNA: gi_15983441_gb_AF424595.1_AF424595	264408_at	1.3
unknown protein similarity to stromal cell-derived factor 2, Mus musculus, PIR2:JC5105; contains EST gb:T22533, AA067386, Z18160;suppo	264382_at	1.3
putative isoamylase Similar to gi|1652733 glycogen operon protein GlgX from Synechocystis sp. genome gb|D90908. ESTs gb|H36690, gb|A	264360_at	1.3
hypothetical protein predicted by genemark.hmm	264268_at	1.3
hypothetical protein predicted by genscan+	264142_at	1.3
unknown protein ;supported by full-length cDNA: Ceres:41712.	263978_at	1.3
putative homeodomain transcription factor ; supported by cDNA: gi_13877516_gb_AF353094.1_AF353094	263956_at	1.3
unknown protein ;supported by full-length cDNA: Ceres:20834.	263755_at	1.3
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:119045.	263538_at	1.3
hypothetical protein predicted by genscan	263488_at	1.3
putative RING zinc finger protein	263424_at	1.3
putative nonsense-mediated mRNA decay protein ; supported by cDNA: gi_15810402_gb_AY056240.1_	263334_at	1.3
putative glyoxalase II	263243_at	1.3
hypothetical protein predicted by genefinder; supported by cDNA: gi_14423545_gb_AF387010.1_AF387010	263075_at	1.3
lipase, putative contains Pfam profile: PF00657 Lipase/Acylhydrolase with GDSL-like motif; supported by cDNA: gi_13937188_gb_AF37294	262748_at	1.3
TPR-repeat protein contains multiple TPR domains: Pfam profile: PF00515	262691_at	1.3
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-length	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	1.3
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: Ceres:	261149_s_at	1.3
unknown protein ; supported by cDNA: gi_16974626_gb_AY060591.1_	260989_at	1.3
hypothetical protein similar to hypothetical protein GB:AAB67625 GI:2342727 from [Arabidopsis thaliana]; supported by full-length cDNA: Cer	260840_at	1.3
unknown protein ; supported by cDNA: gi_15028086_gb_AY045900.1_	260832_at	1.3
storage protein, putative similar to GB:CAA53781 from [Dioscorea cayenensis] (Plant Mol. Biol. 28 (3), 369-380 (1995)); supported by cDNA:	260626_at	1.3
poly(A)-specific ribonuclease, putative similar to GB:CAA06683 from [Homo sapiens]	260593_at	1.3
unknown protein	260436_at	1.3
unknown protein identical to most of OBP32pep protein (fragment) GB:S71212 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:2	260304_at	1.3
unknown protein ; supported by cDNA: gi_13878054_gb_AF370290.1_AF370290	260157_at	1.3
putative RNA-binding protein contains Pfam profile: PF00076 RNA recognition motif. (aka RRM, RBD, or RNP domain); similar to putative pr	260160_at	1.3
unknown protein	259993_at	1.3
putative protein kinase C-terminal region similar to MAP3K delta-1 protein kinase GB:CAA74591 [Arabidopsis thaliana]; contains Pfam profile	259957_at	1.3
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	1.3
putative UDP-glucose:glycoprotein glucosyltransferase similar to UDP-glucose:glycoprotein glucosyltransferase precursor GB:Q09332 [Droso	259936_at	1.3
transfactor, putative similar to GI:4519671 from [Nicotiana tabacum]	259832_at	1.3
unknown protein	259835_at	1.3
unknown protein	259689_x_at	1.3
unknown protein ; supported by cDNA: gi_15293080_gb_AY050974.1_	259666_at	1.3
spindly (gibberellin signal transduction protein) identical to spindly GB:AAC49446 [Arabidopsis thaliana]; supported by cDNA: gi_1589777_gb	259259_at	1.3
homeobox-leucine zipper protein HAT5 (HD-ZIP protein 5) (HD-ZIP protein ATHB-1) identical to homeobox-leucine zipper protein HAT5 (HD-	259165_at	1.3
unknown protein ;supported by full-length cDNA: Ceres:801.	259055_at	1.3

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	258844_at	1.3
unknown protein	258687_at	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: gi: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_	258094_at	1.3
FtsH protease, putative contains similarity to cell division protein FtsH GI:1652085 from [Synechocystis sp. PCC 6803]	258048_at	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:	257887_at	1.3
unknown protein contains an RNase_PH domain;supported by full-length cDNA: Ceres:104182.	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-leng	257655_at	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_	257007_at	1.3
unknown protein contains PF00612 IQ:IQ calmodulin-binding motif	256822_at	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
putative protein predicted protein, Arabidopsis thaliana and various predicted ATP dependent RNA helicases	255600_s_at	1.3
putative NAM-like protein	255585_at	1.3
hypothetical protein similar to C. elegans protein B0414.8, GenBank accession number 2088768	255560_at	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_	255441_at	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	254645_at	1.3
RNase L inhibitor-like protein RNase L inhibitor (clone 8), Homo sapiens	254615_at	1.3
hypothetical protein	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-leng	254445_at	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	253799_at	1.3
putative protein predicted protein. Arabidopsis thaliana; supported by cDNA: gi_15293152_gb_AY051010.1_	253739_at	1.3
X-Pro dipeptidase - like protein (fragment) X-Pro dipeptidase, Homo 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.	253223_at	1.3
putative ubiquitin-dependent proteolytic protein ubiquitin fusion-degradation protein - Mus musculus, PID:g1654348; supported by cDNA: gi_	252931_at	1.3
starch phosphorylase H (cytosolic form) - like protein starch phosphorylase H, cytosolic isoform, Vicia faba, PIR:T12091; supported by cDNA	252468_at	1.3
putative protein br-1 protein (NITRIC OXIDE SYNTHASE) - Helix pomatia,PID:e234055	252410_at	1.3
putative transcription factor MYB94 ; supported by cDNA: gi_3941527_gb_AF062918.1_AF062918	252408_at	1.3
hypothetical protein	252362_at	1.3
putative protein CRP1 protein, Zea mays, gb:AAC25599	252305_at	1.3
putative protein lea32, Arabidopsis thaliana, EMBL:ATH131342;supported by full-length cDNA: Ceres:35969.	252229_at	1.3
U1 snRNP 70K protein ; supported by cDNA: gi_14532499_gb_AY039874.1_	252182_at	1.3
putative protein hypothetical protein F16F14.4 - Arabidopsis thaliana: EMBL:AC007047; supported by cDNA: gi_14423521_gb_AF386998.1_	252097_at	1.3
mucin -like protein hemomucin, Drosophila melanogaster, EMBL:DM42014;supported by full-length cDNA: Ceres:34197.	252117_at	1.3
receptor-protein kinase-like protein receptor-like protein kinase, Catharanthus roseus, PIR:T10060; supported by cDNA: gi_14334759_gb_AY	252066_at	1.3
putative protein predicted protein, Arabidopsis thaliana	251937_at	1.3
putative protein predicted proteins, Arabidopsis thaliana	251951_s_at	1.3
beta-ketoacyl-ACP reductase - like protein beta-ketoacyl-ACP reductase, Cuphea lanceolata, EMBL:X64566	251780_s_at	1.3
putative protein translation releasing factor RF-2 - Synechocystis sp., PIR:S76448	251670_at	1.3

hypothetical protein	251614_at	1.3
putative protein ferritin 1 precursor - Arabidopsis thaliana, EMBL:X94248	251347_at	1.3
putative protein putative protein BcDNA.GH03694 - Drosophila melanogaster, EMBL:AF181626	251316_s_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 phytochrome-associated protein 3 (PAP3) - Arabidopsis thaliana, EMBL:AF088280	251245_at	1.3
ATP-dependent RNA helicase-like protein ATP-dependent RNA helicase (EC 3.6.-.-) - Homo sapiens, PIR:JC5785	251265_at	1.3
putative protein predicted protein, Arabidopsis thaliana; supported by cDNA: gi_14334781_gb_AY035064.1_	251153_at	1.3
putative protein hypothetical proteins - Arabidopsis thaliana	251078_at	1.3
putative protein histone H2A, garden pea, PIR:JQ1183; supported by full-length cDNA: Ceres: 1553.	251011_at	1.3
putative protein various predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:98672.	250931_at	1.3
putative protein contains similarity to unknown protein (gb AAF19567.1)	250809_at	1.3
SET-domain protein-like ; supported by cDNA: gi_13517742_gb_AF344444.1_AF344444	250817_at	1.3
arginine-tRNA-protein transferase 1 homolog ; supported by cDNA: gi_3806097_gb_AF079100.1_AF079100	250754_at	1.3
ankyrin-like protein	250761_at	1.3
cell division related protein-like	250711_at	1.3
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_150281	250483_at	1.3
putative protein NLI-interacting factor isoform T1, Gallus gallus, EMBL:AF189773;supported by full-length cDNA: Ceres:151766.	250298_at	1.3
CCAAT box binding factor/ transcription factor Hap2a	250320_at	1.3
unknown protein	250232_at	1.3
unknown protein ; supported by cDNA: gi_15215581_gb_AY050319.1_	250211_at	1.3
putative protein amino acid transport protein, Arabidopsis thaliana, EMBL:U39783	250161_at	1.3
Expressed protein ; supported by cDNA: gi_16648944_gb_AY059842.1_	250134_at	1.3
GTP-binding protein obg -like GTP-binding protein obg, Bacillus subtilis, PIR:B32804	249993_at	1.3
squamosa promoter binding protein-like 7 ; supported by cDNA: gi_13605911_gb_AF367355.1_AF367355	249960_at	1.3
alkaline/neutral invertase ; supported by cDNA: gi_15912342_gb_AY056449.1_	249898_at	1.3
putative protein 5 -AMP-ACTIVATED PROTEIN KINASE, BETA-1 SUBUNIT, pig, SWISSPROT:AAKB_PIG; supported by cDNA: gi_169743	249425_at	1.3
40S ribosomal protein S9-like 40S ribosomal protein S9 - Chlamydomonas sp.,EMBL:AU066528;supported by full-length cDNA: Ceres:4140	249427_at	1.3
protein import receptor TOM20, mitochondrial-like	249322_at	1.3
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]	248818_at	1.3
unknown protein	248771_at	1.3
unknown protein	248694_at	1.3
putative protein strong similarity to unknown protein (pir||T09376)	248630_at	1.3
putative protein contains similarity to unknown protein (pir||T01052)	248616_at	1.3
ATP-dependent Clp protease ATP-binding subunit ClpX2, putative similar to CLP protease regulatory subunit CLPX GI:2674203 from [Arabid	248575_at	1.3
putative protein contains similarity to salt-inducible protein	248547_at	1.3
Notchless protein homolog	248326_at	1.3
O-methyltransferase ;supported by full-length cDNA: Ceres:33790.	248200_at	1.3
putative protein similar to unknown protein (pir||T05472);supported by full-length cDNA: Ceres:30073.	248148_at	1.3
DNA topoisomerase I (sp P30181)	248099_at	1.3
putative protein similar to unknown protein (ref|NP_004583.1); supported by cDNA: gi_14532719_gb_AY039984.1_	248106_at	1.3
HEAT SHOCK PROTEIN 81-2 (HSP81-2) (sp|P55737)	248045_at	1.3
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	1.3
putative protein predicted proteins, Arabidopsis thaliana	247698_at	1.3
aspartyl aminopeptidase - like protein aspartyl aminopeptidase, Homo sapiens, EMBL:AF005050;supported by full-length cDNA: Ceres:1265	247624_at	1.3
putative protein supported by cDNA: Ceres: 146274.	247491_at	1.3
peroxisomal Ca-dependent solute carrier - like protein peroxisomal Ca-dependent solute carrier, Oryctolagus cuniculus, EMBL:AF004161; su	247498_at	1.3
unknown protein	247393_at	1.3
putative protein similar to unknown protein (pir||T00246)	247277_at	1.3
putative protein similar to unknown protein (gb|AAB71479.1|)	247062_at	1.3
putative protein contains similarity to MYB-like DNA-binding protein; supported by cDNA: gi_14532517_gb_AY039883.1_	247012_at	1.3
unknown protein ;supported by full-length cDNA: Ceres:8440.	246953_at	1.3
putative protein	246926_at	1.3
acid phosphatase-like protein purple acid phosphatase - Ipomoea batatas, EMBL:AJ006224; supported by cDNA: gi_15292756_gb_AY0508	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	1.3
hypothetical protein ;supported by full-length cDNA: Ceres:108940.	246196_at	1.3
G-box-binding factor 1 ; supported by cDNA: gi_15450987_gb_AY054574.1_	246211_at	1.3
IPP transferase - like protein tRNA delta(2)-isopentenylpyrophosphate transferase (IPP transferase), Pseudomonas putida, EMBL:AF016312	246152_at	1.3
putative protein VAC8 protein, Saccharomyces cerevisiae, PIR:S50446	246062_at	1.3
24 kDa vacuolar protein - like 24 kDa vacuolar protein VP24, Ipomoea batatas, EMBL:AB025531	245991_at	1.3
pinoresinol-lariciresinol reductase, putative similar to pinoresinol-lariciresinol reductase GB:AAF63508 GI:7542583 from [Thuja plicata];suppo	245792_at	1.3
hypothetical protein predicted by genemark.hmm	245724_at	1.3
Expressed protein ; supported by cDNA: gi_11762135_gb_AF324994.1_AF324994	245684_at	1.3
Expressed protein ;supported by cDNA: gi:14423393	245521_at	1.3
hypothetical protein	245481_at	1.3
Expressed protein ; supported by full-length cDNA: Ceres: 16319.	245373_s_at	1.3
casein kinase I ; supported by cDNA: gi_15450524_gb_AY052364.1_	245294_at	1.3
hypothetical protein ; supported by cDNA: gi_16323154_gb_AY057681.1_	245272_at	1.3
photolyase/blue-light receptor (PHR2) ;supported by full-length cDNA: Ceres:34800.	245150_at	1.3
cytochrome c biogenesis orf206	244945_at	1.3
unknown protein	258783_at	1.3
unknown protein	256013_at	1.3

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
unknown protein	266934_at	1.2
unknown protein	266855_at	1.2
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 (gi|2190992); 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 108M14T7, gb|T41823 and 108M14XP 3 , gb|AA395002; supported by cDNA: gi_14335101_gb_AY03723	263692_at	1.2
putative 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 GI:2582643 from [Arabidopsis thaliana] (Plant Mol. Biol. 39 (4), 761-773 (19	263035_at	1.2
conserved hypothetical protein	263037_at	1.2
Expressed protein ; supported by full-length cDNA: Ceres: 18244.	262746_at	1.2
unknown protein ESTs gb|R90323, gb|R90338. gb|Z25504 and gb|AA651448 come from this gene	262576_at	1.2
hypothetical protein predicted by genscan+	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:1389566 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	262227_s_at	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	262054_s_at	1.2
S-ribonuclease binding protein SBP1, putative similar to S-ribonuclease binding protein SBP1 GI:6760451 from [Petunia hybrida];supported b	261832_at	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 f	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 (Arabid	260323_at	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
putative ABC transporter contains Pfam profile: PF00005 ABC transporter	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_15450410	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 [Arabidopsis th	259408_at	1.2
putative lectin contains Pfam profile: PF01419 jacalin-like lectin domain; similar to jasmonate inducible protein GB:Y11483 (Brassica napus),	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_AY05037	259194_at	1.2
lysyl-tRNA synthetase identical to lysyl-tRNA synthetase; LysRS GB:AAD17333 [Arabidopsis thaliana]; supported by cDNA: gi_4325323_gb_	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 contai	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 specific D	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: Cere	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: Cere	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 [Mu	256911_at	1.2
alpha-glucan phosphorylase, putative similar to alpha-glucan phosphorylase, L isozyme 1 precursor GB:P04045 from [Solanum tuberosum] (	256746_at	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 cDNA:	254952_at	1.2
putative protein 24 kDa seed maturation protein - Glycine max,PID:g4102690;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 protein induced upon wounding - Arabidopsis thaliana, PID:e257749;supported by full-length cDNA: Ceres:34176.	254157_at	1.2
putative protein immunophilin FKBP46 - Spodoptera frugiperda (fall armyworm),PIR2:A55320; supported by cDNA: gi_15982871_gb_AY057	254076_at	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 (apric	253709_at	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 by c	253438_at	1.2
putative protein beta transducin-like protein, Podospora anserina, gb:L28125; supported by cDNA: gi_11141604_gb_AF277458.1_AF27745	253443_at	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; supported	252372_at	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_AF360274	252068_at	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; supp	251578_at	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_AY059	251289_at	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_	251191_at	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 (sp|P36540)	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
Expressed protein ; supported by full-length cDNA: Ceres: 121432.	249026_at	1.2
unknown protein ;supported by full-length cDNA: Ceres:36901.	248966_at	1.2
Expressed protein ; supported by full-length cDNA: Ceres: 13184.	248813_at	1.2
VAMP (vesicle-associated membrane protein)-associated protein-like ;supported by full-length cDNA: Ceres:14236.	248796_at	1.2
putative protein similar to unknown protein (dbj|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_AF360242.1_AF360242	247044_at	1.2
putative protein strong similarity to unknown protein (ref|NP_005638.1); supported by cDNA: gi_16323187_gb_AY057698.1_	247002_at	1.2
putative protein	246846_at	1.2
CRS2-like protein CRS2 - Zea mays, EMBL:AF225708	246492_at	1.2
putative protein Tat-SF1 - Homo sapiens, 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_150282	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)	248226_at	1.2
putative protein various predicted proteins, Arabidopsis thaliana	246899_at	1.2
hypothetical protein predicted by genemark.hmm; 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.	267212_at	1.1
unknown protein ;supported by full-length cDNA: Ceres:2337.	267078_at	1.1
hypothetical protein predicted by genscan	267020_at	1.1
hypothetical protein predicted by genscan	266903_at	1.1
unknown protein	266732_at	1.1
putative CCCH-type zinc finger protein ;supported by full-length cDNA: Ceres:101255.	266695_at	1.1
putative cinnamoyl CoA reductase ;supported by full-length cDNA: Ceres:14133.	266578_at	1.1
putative preprotein translocase SECY protein Identical to GB:U37247; targeted to the thylakoid membrane; the protein has a chloroplast targ	266018_at	1.1
putative cytochrome P450 identical to GB:D78604; supported by cDNA: gi_15450907_gb_AY054534.1_	266000_at	1.1
putative spliceosome associated protein ;supported by full-length cDNA: Ceres:38968.	265930_at	1.1
putative nucleosome assembly protein	265940_at	1.1
hypothetical protein predicted by genefinder	265885_at	1.1
putative acyl-CoA oxidase possibly a peroxisomal component	265843_at	1.1
putative membrane transporter ; supported by cDNA: gi_13605838_gb_AF367318.1_AF367318	265741_at	1.1
hypothetical protein predicted by genscan	265728_at	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	264922_s_at	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	264330_at	1.1
trehalose-6-phosphate synthase, putative similar to trehalose-6-phosphate synthase GI:297792 from [Kluyveromyces lactis]	264246_at	1.1
heme activated protein, putative similar to heme activated protein GI:6289057 from (Arabidopsis thaliana); supported by full-length cDNA: Ce	264190_at	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
ankyrin-like protein	263459_at	1.1
putative acetolactate synthase	263460_at	1.1
UDP-glucose:indole-3-acetate beta-D-glucosyltransferase, putative similar to UDP-glucose:indole-3-acetate beta-D-glucosyltransferase GI:2	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 cD	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:37444.	262496_at	1.1
hypothetical protein predicted by genscan; supported by cDNA: gi_14334811_gb_AY035079.1_	262503_at	1.1
unknown protein ;supported by full-length cDNA: Ceres:3024.	262171_at	1.1
unknown protein ;supported by full-length cDNA: Ceres:101924.	261948_at	1.1
hypothetical protein similar to hypothetical protein GB:AAF25977 GI:6714281 from [Arabidopsis thaliana]	261701_at	1.1
2-isopropylmalate synthase, putative similar to 2-isopropylmalate synthase GB:AF004165 GI:2213881 from [Lycopersicon pennellii]	261668_at	1.1
unknown protein contains similarity to actin-related protein GB:BAA74577 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 ((I	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
transcription factor TINY, putative similar to transcription factor TINY GB:CAA64359 GI:1246403 from [Arabidopsis thaliana];supported by full	261059_at	1.1
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:34178.	261026_at	1.1
glyoxalase II, putative similar to GI:1644427 from (Arabidopsis thaliana); supported by cDNA: gi_15450394_gb_AY052298.1_	260986_at	1.1
unknown protein similar to Cryptosporidium parvum elongation factor-2 GB:U21667 GI:706974 from [Cryptosporidium parvum]	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_AF1143	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]	259672_at	1.1
putative DNA-binding protein predicted by genscan, multiple est matches; Pfam HMM hit: helix-loop-helix DNA-binding domain;supported by	259645_at	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	259240_at	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
putative DNA gyrase subunit B similar to putative DNA gyrase subunit GB:O50627 [Bacillus halodurans]	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 a	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
putative RNA helicase similar to RNA helicase GB:CAA09200 from [Arabidopsis thaliana]	258449_s_at	1.1
Expressed protein ; supported by full-length cDNA: Ceres: 18951.	258397_at	1.1
putative leucine-rich repeat transmembrane protein kinase similar to leucine-rich repeat transmembrane protein kinase 1 GB:AAC27894 from	258357_at	1.1
unknown protein similar to hypothetical protein GB:CAB36798 from [Arabidopsis thaliana]	258361_at	1.1

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_149	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
predicted protein ; supported by full-length cDNA: Ceres: 11106.	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 (RelA) similar to B. subtilis RelA (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
putative protein Homo sapiens deubiquitinating enzyme UnpEL (UNP),PID:g2656141; supported by cDNA: gi_15450766_gb_AY054463.1_	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 rhamnose--anthocyanidin-3-glucoside rhamnosyltransferase - like protein UDP rhamnose--anthocyanidin-3-glucoside rhamnosyltransfe	253879_s_at	1.1
putative protein hypothetical chloroplast protein RF19, Guillardia theta, PIR2:S73274;supported by full-length cDNA: Ceres:32397.	253857_at	1.1
putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:19314.	253789_at	1.1
early auxin-inducible protein 11 (IAA11) ; supported by cDNA: gi_972924_gb_U18413.1_ATU18413	253791_at	1.1
hypothetical protein ;supported by full-length cDNA: Ceres:249331.	253751_at	1.1
putative 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
hypothetical protein ; supported by cDNA: gi_14335143_gb_AY037251.1_	253596_s_at	1.1
hypothetical protein ;supported by full-length cDNA: Ceres:151518.	253520_at	1.1
putative protein crp1 protein, Zea mays, Z14393	253495_at	1.1
putative protein mixed-lineage protein kinase, Homo sapiens, PIR:A53800	253473_at	1.1
putative protein	253343_at	1.1
putative protein hemolysin, 38K, Synechocystis sp., Pir2:S75595	253351_at	1.1
putative protein	253143_at	1.1
DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain	253133_at	1.1
putative protein zinc finger protein, Arabidopsis thaliana, gb:L76926	253105_at	1.1
Expressed protein ; supported by full-length cDNA: Ceres: 147351.	252946_at	1.1
putative protein several hypothetical proteins - Arabidopsis thaliana	252475_s_at	1.1
putative protein proline transport helper PTH1 - Candida albicans, EMBL:Y18210	252426_at	1.1
putative peptide transporter peptide transporter (ptr1), Hordeum vulgare, AF023472; supported by cDNA: gi_13877878_gb_AF370202.1_AF	252377_at	1.1
putative protein KIAA0226 gene product - Homo sapiens,PID:d1013904; supported by cDNA: gi_14532611_gb_AY039930.1_	252353_at	1.1
putative protein	252344_s_at	1.1
RNA-directed RNA polymerase RNA-directed RNA polymerase	252261_at	1.1
putative protein hypothetical protein - Schizosaccharomyces 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_152	252100_at	1.1
hypothetical protein	252086_at	1.1
monodehydroascorbate reductase (NADH) - like protein monodehydroascorbate reductase (NADH), Lycoperison esculentum, PIR:T06407;su	252024_at	1.1
RNA helicase -like protein RNA helicase, Mus musculus, PIR:I49731; 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	251657_at	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 77A3p, 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 thaliana, EMBL:D38110supported by full-length cDNA:	250543_at	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
eukaryotic cap-binding protein (gb|AAC17220.1) ; supported by cDNA: gi_3108208_gb_AF028809.1_AF028809	250033_at	1.1
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
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
casein kinase II alpha subunit ; supported by cDNA: gi_391602_dbj_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-acid--CoA ligase-like protein long-chain-fatty-acid--CoA 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	246180_at	1.1
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, TREM	246050_s_at	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	245913_at	1.1
putative protein	245881_at	1.1
putative protein DNA-binding protein - Triticum aestivum, EMBL:AF091837;supported by full-length cDNA: Ceres:249741.	245888_at	1.1
SIR2-family protein sirtuin type 4 (SIRT4) - Homo sapiens, EMBL:AF083109; supported by cDNA: gi_15028032_gb_AY045873.1_	245895_at	1.1
GTL1 - like protein GTL1, Arabidopsis thaliana, EMBL:ATAJ3215; supported by cDNA: gi_14423451_gb_AF386963.1_AF386963	245861_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
prolin-rich protein, putative similar to prolin-rich protein GI:21045 from [Phaseolus vulgaris]	245688_at	1.1
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_16648668_gb_AY058110.1_	245629_at	1.1
SYBL1 like protein	245513_at	1.1
DEF (CLA1) protein ; supported by cDNA: gi_14334451_gb_AY034917.1_	245281_at	1.1
hypothetical protein ; supported by cDNA: gi_16226250_gb_AF428283.1_AF428283	245269_at	1.1
unknown protein	257477_at	1.1
RIBOSOMAL PROTEIN, putative similar to 30S RIBOSOMAL PROTEIN S1 GB:P46228 from [Synechococcus sp.]	261507_at	1.1
FKBP-type peptidyl-prolyl cis-trans isomerases, putative contains Pfam profile: PF00254 FKBP-type peptidyl-prolyl cis-trans isomerases	258175_at	1.1
FKBP-type peptidyl-prolyl cis-trans isomerase, putative contains Pfam profile: PF00254 FKBP-type peptidyl-prolyl cis-trans isomerases	256230_at	1.1
putative protein various predicted proteins, Arabidopsis thaliana	250194_at	1.1
putative protein predicted proteins, Arabidopsis thaliana, D.melanogaster, C.elegans and S.pombe	246714_at	1.1
unknown protein	259207_at	1

MYB - like protein cM4 myb transcription factor, Arabidopsis thaliana, gb:S58280; supported by cDNA: gi_14423389_gb_AF386932.1_AF386	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 lipase ; 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
putative WD-40 repeat protein, MSI4 almost identical to GB:2599091; contains a Trp-Asp (WD-40) repeat signature; supported by cDNA: gi_	265946_s_at	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
putative glutamyl-tRNA reductase 2 precursor similar to GB:P49294 and to A. thaliana HEMA2 (gb|U27118)	264660_at	1
putative U2 small nuclear ribonucleoprotein A (U2 SNRNP-A) Identical to A. thaliana U2 SnRNP-specific A protein (gb|X69137). ESTs gb|AT	264678_at	1
unknown protein ; supported by cDNA: gi_13430645_gb_AF360235.1_AF360235	264615_at	1
hypothetical protein predicted by genemark.hmm	264539_at	1
hypothetical protein predicted by genscan+	264491_at	1
Expressed protein ; supported by full-length cDNA: Ceres: 39286.	264443_at	1
spermidine synthase, putative similar to spermidine synthase GI:4138109 from [Lycopersicon esculentum]; supported by cDNA: gi_14030636	264317_at	1
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_15081627_gb_AY048206.1_	264098_at	1
unknown protein	264011_at	1
putative ABC transporter related to multi drug resistance proteins and P-glycoproteins	263904_at	1
hypothetical protein predicted by genscan	263899_at	1
putative RNA polymerase sigma-70 factor ; supported by cDNA: gi_7209639_dbj_AB029916.1_AB029916	263846_at	1
putative ubiquitin fusion-degradation protein ;supported by full-length cDNA: Ceres:34470.	263756_at	1
putative NADPH dependent mannose 6-phosphate reductase ; supported by full-length cDNA: Ceres: 21730.	263758_s_at	1
hypothetical protein predicted by genscan and genefinder; supported by cDNA: gi_14596224_gb_AY042900.1_	263556_at	1
F-box protein ORE9, AtFBL7 identical to F-box containing protein ORE9 GI:15420162 from [Arabidopsis thaliana]	263490_at	1
putative importin (nuclear transport factor) protein	263448_at	1
putative prohibitin ;supported by full-length cDNA: Ceres:6176.	263375_s_at	1
putative RNA-binding protein ;supported by full-length cDNA: Ceres:4595.	263355_at	1
Expressed protein ; supported by full-length cDNA: Ceres: 264189.	263209_at	1
unknown protein ;supported by full-length cDNA: Ceres:21223.	263110_at	1
unknown protein ; supported by cDNA: gi_16930680_gb_AF436824.1_AF436824	263050_at	1
similar to glucose inhibited division protein A from prokaryotes	263053_at	1
unknown protein	263023_at	1
T76725 come from this gene.	263010_at	1
unknown protein ;supported by full-length cDNA: Ceres:9435.	262947_at	1
hypothetical protein predicted by genemark.hmm	262941_at	1
hypothetical protein contains similarity to 30S ribosomal protein S5 GI:6969105 from [Campylobacter jejuni]; supported by cDNA: gi_1433489	262880_at	1
unknown protein ; supported by cDNA: gi_15028136_gb_AY046018.1_	262881_at	1
cytochrome B561, putative similar to cytochrome GB:AAD11424 GI:4206110 [Mesembryanthemum crystallinum]	262831_at	1
unknown protein EST gb|N37870 comes from this gene	262794_at	1
mercaptopyruvate sulfurtransferase (Mst2/Rdh2) identical to mercaptopyruvate sulfurtransferase GI:6009983 and thiosulfate sulfurtransferase	262712_at	1
flavin-containing amine oxidase contains Pfam profile: PF01593 Flavin containing amine oxidase	262668_at	1
hypothetical protein	262621_at	1
hypothetical protein predicted by genemark.hmm	262562_at	1
putative ubiquitin-conjugating enzyme First 212 a.a. are 41% identical to Ubiquitin-Conjugating Enzyme E2 [Saccharomyces cerevisiae] (gi|48	262537_s_at	1

putative translation initiation factor IF2 Except for first 311 amino acids, 41% identical to translation initiation factor IF2 [Bacillus subtilis] (gi|1	262483_at	1
putative protein disulfide isomerase precursor Similar to gb|Z11499 protein disulfide isomerase from Medicago sativa. ESTs gb|AI099693, gb	262504_at	1
unknown protein Similar to gb|X84260 POS5 gene product from Saccharomyces cerevisiae. EST gb|W43879 comes from this gene; support	262506_at	1
hypothetical protein similar to hypothetical protein GB:AAD49998 GI:5734733 from [Arabidopsis thaliana]	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
protein kinase, putative similar to mitogen activated protein kinase kinase GB:AAC32599 GI:3450842 from [Oryza sativa]	261974_at	1
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:206286.	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_	261720_at	1
hypothetical protein similar to hypothetical protein GB:AAF25987 GI:6714291 from [Arabidopsis thaliana]	261663_at	1
unknown protein similar to putative lipase GB:AAF36744 GI:7109480 from [Arabidopsis thaliana]	261667_at	1
DNA-binding protein PcMYB1, putative similar to DNA-binding protein PcMYB1 GB:U67133 GI:2224898 from [Petroselinum crispum];suppor	261637_at	1
hypothetical protein similar to guanine nucleotide exchange factor-like protein GB:CAB82690 GI:7329696 from [Arabidopsis thaliana]	261621_at	1
protein kinase, putative contains Pfam profile: PF00069 Eukaryotic protein kinase domain	261547_at	1
receptor protein kinase, putative contains Pfam profiles: PF00069 Eukaryotic protein kinase domain, PF00560 Leucine Rich Repeat	261552_at	1
peroxidase ATP4a identical to GB:CAA67309 GI:1429213 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 39968.	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
hypothetical protein predicted by genscan+	261277_at	1
calreticulin, putative similar to GB:AAF06346 from [Vitis vinifera]	261248_at	1
NAM protein, putative similar to NAM protein GI:6066594 from [Petunia hybrida]; supported by cDNA: gi_14334571_gb_AY034959.1_	261192_at	1
unknown protein	261112_at	1
sec14 cytosolic factor, putative similar to SP:P24859 from [Kluyveromyces lactis]	261116_at	1
oligouridylate binding protein, putative similar to GB:CAB75429 from (Nicotiana plumbaginifolia) (EMBO J. 19, 1638-1649 (2000));supported	261040_at	1
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_13430817_gb_AF360321.1_AF360321	260927_at	1
glycine-rich RNA-binding protein grp1a, putative similar to glycine-rich RNA-binding protein grp1a GB:L31374 GI:496232 from [Sinapis alba]	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
unknown protein ; supported by full-length cDNA: Ceres: 2381.	260442_at	1
putative RNA-binding domain contains Pfam profile: PF00806 Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain	260398_at	1
putative heme oxygenase similar to heme oxygenase GB:AAD22107 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:101223.	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 profil	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
unknown protein ;supported by full-length cDNA: Ceres:108165.	260099_at	1
unknown protein similar to putative protein GB:CAB38899 [Arabidopsis thaliana]	260055_at	1
endoplasmic reticulum alpha-mannosidase, putative similar to GI:5579331 from [Homo sapiens]; supported by cDNA: gi_15450803_gb_AY0	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 [Ho	259920_at	1
unknown protein	259812_at	1
RNA-binding protein MEI2, putative similar to GI:6650523 from [Arabidopsis thaliana]	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:AAF002	259717_at	1
hypothetical protein contains similarity to myosin heavy chain cardiac muscle specific isoform 1 GI:7416982 from (Argopecten irradians); sup	259659_at	1
hypothetical protein	259532_at	1
unknown protein	259470_at	1
unknown protein similar to putative dehydrogenase GI:1922246 from [Arabidopsis thaliana]; supported by cDNA: gi_15408534_dbj_AB0320	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
putative SAR DNA-binding protein-1 similar to GB:AAC16330 from [Pisum sativum]; supported by cDNA: gi_11878186_gb_AF302491.1_AF3	259311_at	1
putative glycogen synthase similar to glycogen synthase precursor (Granule-Bound Starch Synthase II) GB:Q43093 from [Pisum sativum]; su	259277_at	1
unknown protein	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	259246_s_at	1
unknown protein similar to putative phytochelatin synthetase GB:CAA07251 [Arabidopsis thaliana], Pfam HMM hit: TNFR/NGFR cysteine-ric	259122_at	1
putative zeta-carotene desaturase precursor nearly identical to zeta-carotene desaturase precursor GB:AAA91161 [Arabidopsis thaliana];sup	259092_at	1
hypothetical protein similar to hypothetical protein GB:AAB72157 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:1132.	259012_at	1
putative DnaJ protein Pfam HMM hit: DnaJ, prokaryotic heat shock protein	258909_at	1
hypothetical protein similar to hypothetical protein GB:AAC17075 [Arabidopsis thaliana]; supported by cDNA: gi_15810358_gb_AY056218.1_	258804_at	1
putative alpha-L-arabinofuranosidase contains similarity to alpha-L-arabinofuranosidase A precursor GB:P42254 [Aspergillus niger]; support	258774_at	1
hypothetical protein similar to hypothetical protein GB:AAF23212 GI:6671952 from (Arabidopsis thaliana)	258756_at	1
IAA-amino acid hydrolase (ILR1) identical to IAA-amino acid hydrolase (ILR1) GB:U23794 [Arabidopsis thaliana];supported by full-length cDN	258610_at	1
Rab escort protein, putative similar to choroideremia-like Rab escort protein GB:2NP_001812 from [Homo sapiens]	258536_at	1
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_14334461_gb_AY034922.1_	258522_at	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	258489_at	1
cell division protein FtsH-like protein similar to cell division protein FtsH GB:AAD35665 from [Thermotoga maritima];supported by full-length c	258494_at	1
alternative oxidase 1a precursor identical to GB:Q39219 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:116257.	258452_at	1
ubiquitin-specific protease 25 (UBP25) similar to GI:11993490; supported by cDNA: gi_11993489_gb_AF302673.1_AF302673	258372_at	1
hypothetical protein predicted by genemark.hmm	258255_at	1
unknown protein contains Pfam profile: PF00076 RNA recognition motif	258229_at	1
putative pectinesterase similar to pectinesterase precursor GB:Q43043 [Petunia integrifolia]; contains Pfam profile: PF01095 pectinesterase;s	258193_at	1
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_15028198_gb_AY045922.1_	258206_at	1
dehydrogenase, putative similar to dihydropyrimidine dehydrogenase GB:BAA89789 from [Homo sapiens]; supported by cDNA: gi_1433471	258162_at	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 (	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 profil	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 su	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 cD	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_	253308_at	1
putative protein protein kinase APK1, Arabidopsis thaliana, PIR2:S28615; supported by cDNA: gi_16612248_gb_AF439824.1_AF439824	253184_at	1
putative protein probable membrane protein YBL019w, yeast, PIR2:S45753	253126_at	1
heat shock protein 70 like protein dnaK-type molecular chaperone PHSP1 -Pisum sativum,PID:g20835	253013_at	1
putative protein	253022_at	1
putative protein ubiquitin fusion degradation protein - Schizosaccharomyces pombe, PID:e1132723	252947_at	1
isovaleryl-CoA-dehydrogenase precursor (IVD) ;supported by full-length cDNA: Ceres:33674.	252570_at	1
glucosyltransferase-like protein UDP-glucose glucosyltransferase - Arabidopsis thaliana, EMBL:AB016819;supported by full-length cDNA: C	252482_at	1
FtsH protease, putative contains similarity to FtsH protease GI:13183728 from [Medicago sativa]	252449_at	1
putative protein PrMC3 - Pinus radiata,PID:g4154352	252315_at	1
putative protein N7 protein - Medicago truncatula, EMBL:CAA76808;supported by full-length cDNA: Ceres:99337.	252336_at	1
putative progesterone-binding protein homolog Atmp2 ; supported by cDNA: gi_4960153_gb_AF153283.1_AF153283	252338_at	1
putative protein	252141_at	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	252031_at	1
transporter-like protein oligopeptide transporter (LeOPT1) - Lycopersicon esculentum, EMBL:AF016713	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
Ca-dependent solute carrier - like protein peroxisomal Ca-dependent solute carrier, Oryctolagus cuniculus, EMBL:AF004161;supported by fu	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	251738_at	1
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	251628_at	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_	251467_at	1
protein synthesis initiation factor - like eukaryotic protein synthesis initiation factor, Homo sapiens, EMBL:AF104913	251431_at	1
dihydrodipicolinate synthase precursor ;supported by full-length cDNA: Ceres:37907.	251392_at	1
tubulin gamma-1 chain	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 ln2, 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	250858_at	1
putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:34592.	250861_at	1
AtPH1-like protein ;supported by full-length cDNA: Ceres:109246.	250748_at	1
eukaryotic translation initiation factor 3 subunit-like protein	250758_at	1
transcription factor HBP-1b homolog (sp|P43273) ; 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
putative protein putative secreted protein SCF41.30c, Streptomyces coelicolor, EMBL:SCF41_30	250268_s_at	1
putative protein GCN4-complementing protein, Arabidopsis thaliana, EMBL:AJ130878	250285_at	1
unknown protein	250238_at	1
putative protein	250179_at	1
protein kinase MSK-3 - like protein kinase MSK-3, A.medicago, PIR:S37642	250141_at	1
unknown protein ; supported by cDNA: gi_14423559_gb_AF387017.1_AF387017	250131_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	249164_at	1
putative protein contains similarity to RNA-binding protein; supported by cDNA: gi_15215747_gb_AY050403.1_	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.	248493_at	1
arginine/serine-rich splicing factor RSP41 homolog ; supported by cDNA: gi_13877816_gb_AF370171.1_AF370171	248369_at	1
RNA-binding protein-like	248294_at	1
ATP-dependent Clp protease ATP-binding subunit ClpX1 identical to CLP protease regulatory subunit CLPX GI:2674203 from [Arabidopsis th	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.	247835_at	1
ABC transporter-like protein ; supported by cDNA: gi_9964120_gb_AF287699.1_AF287699	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)	247390_at	1
putative protein contains similarity to FtsH	247235_at	1
putative protein similar to unknown protein (dbj BAA75199.1)	247187_at	1
oligopeptidase A ; supported by cDNA: gi_15028226_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; supported 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 thaliana]	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_at	1
hypothetical protein	257319_at	1
hypothetical protein	257336_at	1
hypothetical protein similar to polyketide hydroxylases from several bacterial species	257410_at	1
unknown protein	257519_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]	262888_at	0.9
unknown protein	260620_at	0.9
putative long-chain acyl-CoA synthetase similar to malonyl CoA synthetase GB:AAF28840 from [Bradyrhizobium japonicum];supported by full	258312_at	0.9
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_AF401297	252969_at	0.9
phosphatidylinositol-4-phosphate 5-kinase-like protein phosphatidylinositol-4-phosphate 5-kinase AtPIP5K1 - Arabidopsis thaliana, EMBL:AB	251711_at	0.9
Arabidopsis thaliana /REF=U37281.1 /DEF=actin-2 mRNA, complete cds /LEN=1637 (_5, _M, _3 represent transcript regions 5 prime, Middl	X-Athal-Actin_	0.9
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 PIR|S76698|S76698; 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-tRNA synthetase	267446_s_at	0.9
putative U5 small nuclear ribonucleoprotein, an RNA helicase	267454_at	0.9
putative related to microbial divalent cation tolerance proteins ; supported by cDNA: gi_12963360_gb_AF327524.1_AF327524	267405_at	0.9
putative translation initiation factor eIF-2B epsilon subunit	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_15027912_gb_AY045813.1_	267246_at	0.9
putative serine carboxypeptidase I ;supported by full-length cDNA: Ceres:33165.	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	267214_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 katanin ;supported by full-length cDNA: Ceres:119620.	266905_at	0.9
unknown protein ;supported by full-length cDNA: Ceres:9000.	266924_at	0.9
putative poly(A) polymerase ; supported by cDNA: gi_14532699_gb_AY039974.1_	266659_at	0.9
unknown protein	266620_at	0.9
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_gb_AY035	266155_at	0.9
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_14517549_g	265118_at	0.9
carboxyphosphonoenolpyruvate mutase, putative similar to carboxyphosphonoenolpyruvate mutase GI:47149 from [Streptomyces hygroscop	264954_at	0.9
unknown protein ; supported by cDNA: gi_13926184_gb_AF370567.1_AF370567	264958_at	0.9
auxin-induced protein, putative similar to auxin-induced atb2 GI:6562980 from [Arabidopsis thaliana]; supported by cDNA: gi_6562979_gb_A	264928_at	0.9
hypothetical protein similar to hypothetical protein GB:O14360	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_AF305913	264780_at	0.9
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 cDNA: gi_	264637_at	0.9
putative sensory transduction histidine kinase similar to GB:AAD21777; similar to ESTs gb|AA712891 and gb|AA042438; supported by cDNA	264448_at	0.9
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_464136_dbj_D1	264405_at	0.9

hypothetical protein contains similarity to ubiquitin protein ligase GI:2827198 from [Mus musculus]	264335_s_at	0.9
hypothetical protein similar to hypothetical protein GI:5541664 from [Arabidopsis thaliana]	264308_at	0.9
unknown protein	264254_at	0.9
putative calcium-binding protein, calreticulin similar to GB:AAA80652;supported by full-length cDNA: Ceres:27210.	264260_at	0.9
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_13430619_gb_AF360222.1_AF360222	264192_at	0.9
unknown protein Similar to hypothetical protein C34B7.2 gb|1729503 from C. elegans cosmid gb|Z83220	264197_at	0.9
unknown protein ESTs gb|Z34075, gb|Z34835 and gb|AA404888 come from this gene	264198_at	0.9
putative tRNA adenylyltransferase Similar to tRNA adenylyltransferase gb|U15930 from Lupinus albus. EST gb|AA721797 comes from this ge	264212_at	0.9
unknown protein	264154_at	0.9
unknown protein ; supported by cDNA: gi_15450672_gb_AY052704.1_	264123_at	0.9
enolase (2-phospho-D-glycerate hydroylase) ; supported by cDNA: gi_15809969_gb_AY054253.1_	263924_at	0.9
hypothetical protein predicted by genscan; supported by cDNA: gi_16648990_gb_AY059865.1_	263883_at	0.9
unknown protein	263708_at	0.9
unknown protein	263654_at	0.9
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	0.9
14-3-3 protein GF14mu (grf9) identical to GF14 mu GI:3551052, SP:Q96299 from [Arabidopsis thaliana];supported by full-length cDNA: Cere	263494_at	0.9
putative bZIP transcription factor contains a bZIP transcription factor basic domain signature (PDOC00036); supported by cDNA: gi_1545083	263414_at	0.9
unknown protein ; supported by cDNA: gi_15810336_gb_AY056207.1_	263326_at	0.9
putative methylmalonate semi-aldehyde dehydrogenase	263275_at	0.9
putative pre-mRNA splicing factor similar to splicing factor hPRP17 (gi|3283220); similar to ESTs emb|F15435 and dbj|AUO62661	263261_at	0.9
hypothetical protein predicted by genscan+	263220_at	0.9
putative lipoamide dehydrogenase component of the pyruvate dehydrogenase complex E3, contains PF|00010 helix-loop-helix DNA-binding	263117_at	0.9
flavanone 3-hydroxylase, putative similar to flavanone 3-hydroxylase GI:727410 from [Persea americana]; supported by cDNA: gi_13507544	263135_at	0.9
hypothetical protein predicted by genscan and genefinder;supported by full-length cDNA: Ceres:95679.	263097_at	0.9
putative alanine aminotransferase similar to alanine aminotransferase GB:BAA77260 GI:4730884 from [Oryza sativa]; supported by c	262988_at	0.9
hypothetical protein contains similarity to DNA-binding protein (PcMYB1) GI:2224896 from [Petroselinum crispum]	263007_at	0.9
Dhp1-like protein similar to Dhp1 protein GB:BAA04601 GI:496393 from [Schizosaccharomyces pombe]; supported by cDNA: gi_11875627_	262923_at	0.9
hypothetical protein contains similarity to protein kinase (PK6) GI:170046 from [Glycine max]	262934_s_at	0.9
hypothetical protein predicted by genemark.hmm	262874_at	0.9
plastid RNA polymerase sigma-subunit identical to plastid RNA polymerase sigma-subunit GI:2398851 from [Arabidopsis thaliana]; supported	262879_at	0.9
putative SPL1-related protein similar to GB:CAB56770, part of the SBP-box gene family that codes for transcription factors	262798_at	0.9
anter-specific proline-rich -like protein (APG-like) similar to anter-specific proline-rich protein (APG) SP:P40602 [Arabidopsis thaliana (Mouse-	262682_at	0.9
integral membrane protein, putative contains Pfam profile: PF00892 Integral membrane protein DUF6	262623_at	0.9
unknown protein ESTs gb|N96028, gb|F14286, gb|T20680, gb|F14443, gb|AA657300 and gb|N65244 come from this gene; supported by c	262505_at	0.9
threonine synthase, putative similar to threonine synthase GI:4850369 from [Arabidopsis thaliana]	262380_at	0.9
unknown protein similar to hypothetical protein GB:AAF07360 from [Arabidopsis thaliana]; supported by cDNA: gi_15810007_gb_AY054272.	262346_at	0.9
unknown protein ;supported by full-length cDNA: Ceres:8932.	262313_at	0.9
unknown protein ; supported by cDNA: gi_13605689_gb_AF361826.1_AF361826	262272_at	0.9
root hairless 1 (RHL1) similar to root hairless 1 GI:3219355 from [Arabidopsis thaliana]; supported by cDNA: gi_3219354_gb_AF062371.1_A	262249_at	0.9
GTP-binding protein, putative similar to GTP-binding protein GB:AAF31009 GI:6899606 from [Ureaplasma urealyticum]	262086_at	0.9
unknown protein	262003_at	0.9
unknown protein	261853_at	0.9
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_14517415_gb_AY039543.1_	261861_at	0.9
DNA-binding protein, putative similar to helicase-like transcription factor GB:CAA86572 GI:1658307 from [Homo sapiens]; supported by cDN	261862_at	0.9
hypothetical protein contains similarity to 17-beta-hydroxysteroid dehydrogenase type IV GI:2315980 from [Gallus gallus]	261771_at	0.9
small nuclear ribonucleoprotein, putative similar to small nuclear ribonucleoprotein GI:600749 from [Homo sapiens]; supported by full-length	261725_at	0.9
hypothetical protein predicted by genemark.hmm	261655_at	0.9
unknown protein ; supported by cDNA: gi_15294231_gb_AF410307.1_AF410307	261582_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
homeobox transcription factor Hox7, putative similar to homeobox transcription factor Hox7 GI:19486 from [Lycopersicon peruvianum]	261494_at	0.9
hypothetical protein predicted by genemark.hmm	261500_at	0.9
hypothetical protein predicted by genscan+	261463_at	0.9
unknown protein similar to Glu-tRNAGln amidotransferase subunit B GB:AAB83965; supported by cDNA: gi_11078539_gb_AF239836.1_AF	261307_at	0.9
unknown protein	261259_at	0.9
hypothetical protein predicted by genemark.hmm	261238_at	0.9
heat shock factor protein hsf8, putative predicted by genemark.hmm; supported by cDNA: gi_15028376_gb_AY045991.1_	261206_at	0.9
uridine diphosphate glucose epimerase identical to GB:CAA90941 from [Arabidopsis thaliana] (Arch. Biochem. Biophys. 327 (1), 27-34 (199	261211_at	0.9
hypothetical protein predicted by genemark.hmm	261132_at	0.9
unknown protein	261071_at	0.9
molybdopterin biosynthesis CNX3 protein, putative similar to molybdopterin biosynthesis CNX3 protein GB:Q39056 from [Arabidopsis thalian	261044_at	0.9
ATP-dependent Clp protease proteolytic subunit (ClpP5) identical to nClpP1 GB:BAA82065 GI:5360579 from [Arabidopsis thaliana];supporte	260912_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
hypothetical protein predicted by genscan+	260785_at	0.9
serine/threonine phosphatase PP7, putative similar to GB:CAA03886 from [Arabidopsis thaliana] (Biochem. Mol. Biol. Int. 44 (4), 703-715 (1	260717_at	0.9
putative pre-mRNA splicing factor RNA helicase	260525_at	0.9
ferredoxin precusor isolog ;supported by full-length cDNA: Ceres:20637.	260481_at	0.9
Eukaryotic initiation factor 5A , putative similar to eukaryotic initiation factor 5A (2) (Nicotiana plumbaginifolia) GI:19702;supported by full-le	260350_at	0.9
unknown protein ; supported by full-length cDNA: Ceres: 96657.	260356_at	0.9
putative acetylornithine transaminase similar to ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT) GB:O04866 from (Aln	260286_at	0.9
hypothetical protein predicted by genscan+	259959_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
nodule inception protein, putative similar to nodule inception protein GI:6448579 from (Lotus japonicus)	259540_at	0.9
dioxygenase, putative similar to dioxygenase GI:1666096 from [Marah macrocarpus]	259445_at	0.9
unknown protein ; supported by full-length cDNA: Ceres: 20582.	259403_at	0.9
unknown protein	259302_at	0.9
putative nucleotide repair protein similar to nucleotide repair protein GB:CAA05781 from [Lilium longiflorum];supported by full-length cDNA: C	259304_at	0.9
unknown protein ;supported by full-length cDNA: Ceres:142966.	259305_at	0.9
putative DNA binding protein similarity to RAV2 DNA binding protein GB:BAA34251 [Arabidopsis thaliana]	259293_at	0.9
unknown protein ; supported by cDNA: gi_15028084_gb_AY045899.1_	259230_at	0.9
unknown protein ;supported by full-length cDNA: Ceres:102038.	259184_at	0.9
putative sodium proton exchanger similar to sodium proton exchanger Nhx1 GB:AAD16946 [Arabidopsis thaliana]	259081_at	0.9
DegP protease contains similarity to degP GI:2623992 from [Bradyrhizobium japonicum]	259048_at	0.9
unknown protein N-terminus similar to unknown protein GB:AAD25613 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 38529.	258921_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
putative GTP pyrophosphokinase similar to GTP PYROPHOSPHOKINASE GB:O87331 from [Corynebacterium glutamicum]; supported by cD	258207_at	0.9
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
putative protein kinase, ATN1 almost identical (1 amino acid) to GB:S61766 from [Arabidopsis thaliana]; supported by cDNA: gi_16604327_g	257972_at	0.9
gda-1, putative similar to gda-1 GB:CAA74993 from [Pisum sativum];supported by full-length cDNA: Ceres:3049.	257790_at	0.9
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
glycine hydroxymethyltransferase, putative similar to glycine hydroxymethyltransferase GI:438246 from [Solanum tuberosum]	255946_at	0.9
unknown protein	255963_at	0.9
hypothetical protein similar to RING3-like bromodomain protein GI:3033386 from [Arabidopsis thaliana]; supported by cDNA: gi_15810438_gb	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:	255066_at	0.9
putative protein	255077_at	0.9
putative protein predicted protein W02G9.1 Caenorhabditis elegans cosmid W02G9, PID:g3165571; supported by cDNA: gi_15450340_gb_A	254863_at	0.9
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	254455_at	0.9
putative protein	254417_at	0.9
Expressed protein ; supported by full-length cDNA: Ceres: 16643.	254388_at	0.9
CDP-diacylglycerol synthetase-like protein CDP-diacylglycerol synthetase, Arabidopsis thaliana, PATCHX:E218681;supported by full-length	254360_at	0.9
putative Ap2 domain protein DNA-binding protein Pti6 - Lycopersicon esculentum,PID:g2213785; supported by cDNA: gi_15982736_gb_AY0	254235_at	0.9
putative protein hypothetical protein, Synechocystis sp., PIR:S76577;supported by full-length cDNA: Ceres:30708.	254187_at	0.9
Expressed protein ; supported by full-length cDNA: Ceres: 28506.	254190_at	0.9
Rab geranylgeranyl transferase like protein (fragment) Rab geranylgeranyl transferase (EC 2.5.1.-) alpha chain, human, PIR2:JC5538	254156_at	0.9
HSP90-like protein HSP90 homolog - Catharanthus roseus, PIR2:S39558; supported by cDNA: gi_14532541_gb_AY039895.1_	254166_at	0.9
superoxide dismutase (EC 1.15.1.1) (Fe)(fragment) ;supported by full-length cDNA: Ceres:32935.	254098_at	0.9
putative protein various predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:20902.	254081_at	0.9
sucrase-like protein sucrose cleavage protein - potato, Pir2:S51376;supported by full-length cDNA: Ceres:111209.	253980_at	0.9
putative protein	253805_at	0.9
arginine methyltransferase (pam1) ; supported by full-length cDNA: Ceres: 38601.	253695_at	0.9
putative protein myosin heavy chain, neuronal, Rattus norvegicus, Pir1:S21801; supported by cDNA: gi_14334773_gb_AY035060.1_	253523_at	0.9
putative zinc finger protein hypothetical protein YLR387c, Saccharomyces cerevisiae, PIR2:S51474; supported by cDNA: gi_13878012_gb_A	253526_at	0.9
putative protein ribosomal protein YmL14 precursor, mitochondrial - Saccharomyces cerevisiae,PIR2:S50921;supported by full-length cDNA:	253538_at	0.9
P-Protein - like protein P-Protein precursor, Solanum tuberosum, gb:Z99770; supported by cDNA: gi_14596024_gb_AY042800.1_	253387_at	0.9
aminopeptidase- like protein aminopeptidase, Mus musculus, U35646	253360_at	0.9
putative protein ThiJ protein, Escherichia coli, PIR:H64771	253320_at	0.9
putative protein RING-finger protein, Lotus japonicus, PIR2:S49446	253265_at	0.9
hypothetical protein	253288_at	0.9
bZIP transcription factor ATB2	253245_at	0.9
putative protein	253208_at	0.9
protein kinase - like protein protein kinase SRPK1, Mus musculus, PID:d1026227	253137_at	0.9
putative protein transcription factor IIIB chain BRF1, Saccharomycescerevisiae, PIR2:A44072	253144_at	0.9
putative protein ribonuclease III, Bacillus subtilis, PIR2:B69693	253095_at	0.9
cytochrome P450-like protein	253097_at	0.9
glycine hydroxymethyltransferase like protein glycine hydroxymethyltransferase -Solanum tuberosum,PID:g438247;supported by full-length c	253009_at	0.9
putative protein T19C21.18 Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence, PID:g3395439	252986_at	0.9
ES43 like protein ES43 protein - barley, PIR2:S44281;supported by full-length cDNA: Ceres:8278.	252925_at	0.9

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_AY035	252883_at	0.9
myo-inositol-1-phosphate synthase ;supported by full-length cDNA: Ceres:1978.	252863_at	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	252354_at	0.9
Expressed protein ; supported by full-length cDNA: Ceres: 26537.	252366_at	0.9
peroxidase ;supported by full-length cDNA: Ceres:39678.	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
pasticcino 1 ; supported by cDNA: gi_15810452_gb_AY056265.1_	251932_at	0.9
putative protein proteophosphoglycan, Leishmania major, PIR:T46707supported by full-length cDNA: Ceres:6954.	251859_at	0.9
putative protein unnamed sequence, Homo sapiens, EMBL:AK001088; supported by cDNA: gi_15215685_gb_AY050371.1_	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	251529_at	0.9
putative protein RanBP7/importin 7 - Homo sapiens, EMBL:AF098799	251495_at	0.9
putative protein polyamine oxidase (EC 1.5.3.11) precursor - Zea mays plasmid pCR2.1;supported by full-length cDNA: Ceres:16421.	251505_at	0.9
actin - like protein actin 3, Drosophila melanogaster, PIR:A03000;supported by full-length cDNA: Ceres:38096.	251340_at	0.9
putative protein ISOPENICILLIN N EPIMERASE - Streptomyces clavuligerus, EMBL:M32324;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	250693_at	0.9
Mei2-like protein Mei2-like protein - Arabidopsis thaliana, EMBL:D86122	250617_at	0.9
myosin heavy chain-like protein ; supported by cDNA: gi_1732514_gb_U62744.1_ATU62744	250548_at	0.9
microbody NAD-dependent malate dehydrogenase ; supported by cDNA: gi_14335145_gb_AY037252.1_	250498_at	0.9
putative protein prdeicted proteins, Schizosaccharomyces pombe	250281_at	0.9
auxin reponsive - like protein Nt-gh3 deduced protein, Nicotiana tabacum, EMBL:AF123503	250293_s_at	0.9
putative protein similar to unknown protein (emb|CAB86638.1)	250202_at	0.9
putative protein similar to unknown protein (ref|NP_057085.1);supported by full-length cDNA: Ceres:38057.	250222_at	0.9
putative protein various predicted proteins, Arabidopsis thaliana	250144_at	0.9
APG5 (autophagy 5)-like protein	250088_at	0.9
chromo domain protein polycomb-like protein, Daucus carota, PIR:T14294; supported by cDNA: gi_15625406_gb_AF387639.1_AF387639	250060_at	0.9
MAP kinase -like protein ATMPK9, Arabidopsis thaliana, EMBL:AB038694	249964_at	0.9
putative protein similar to unknown protein (ref|NP_015265.1); supported by cDNA: gi_12007446_gb_AF322255.1_AF322255	249864_at	0.9
putative protein similar to unknown protein (pir||C72413)	249849_at	0.9
serine palmitoyltransferase ; supported by cDNA: gi_15292790_gb_AY050829.1_	249799_at	0.9
nucleolar protein-like	249672_at	0.9
putative protein unnamed ORF, Homo sapiens, EMBL:AK001192	249611_at	0.9
putative protein SIAH1 protein, Brassica napus, EMBL:BNA245479	249595_at	0.9
RING finger -like protein RING-H2 zinc finger protein ATL4, Arabidopsis thaliana, EMBL:AF132014	249398_at	0.9
urophorphyrin III methylase (gb|AAB92676.1) ; supported by cDNA: gi_1146164_gb_L47479.1_ATHUPM1R	249325_at	0.9
unknown protein	249313_at	0.9
MAP kinase ; supported by cDNA: gi_15983508_gb_AF424629.1_AF424629	249239_at	0.9
FtsH protease, putative similar to FtsH protease GI:13183728 from [Medicago sativa]	249244_at	0.9
brain and reproductive organ-expressed protein-like	249192_at	0.9
1-aminocyclopropane-1-carboxylate oxidase ; supported by cDNA: gi_15983808_gb_AY056810.1_	249128_at	0.9
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	249036_at	0.9
putative protein strong similarity to unknown protein (gb|AAC61825.1); supported by cDNA: gi_15081732_gb_AY048259.1_	248976_at	0.9
unknown protein	248956_at	0.9
cullin ;supported by full-length cDNA: Ceres:101723.	248882_at	0.9
receptor-like protein kinase ; supported by cDNA: gi_13605826_gb_AF367312.1_AF367312	248698_at	0.9
heat shock protein 70 (gb|AAF27639.1) ; supported by cDNA: gi_6746591_gb_AF217459.1_AF217459	248582_at	0.9
histone acetyltransferase ;supported by full-length cDNA: Ceres:123936.	248508_at	0.9
nucleotide-binding protein ; supported by cDNA: gi_13430793_gb_AF360309.1_AF360309	248462_at	0.9
unknown protein ;supported by full-length cDNA: Ceres:36309.	248378_at	0.9
DNA-directed RNA polymerase II subunit-like protein ;supported by full-length cDNA: Ceres:8268.	248386_at	0.9
beta-carotene hydroxylase	248311_at	0.9
PP2A regulatory subunit ;supported by full-length cDNA: Ceres:19116.	248300_at	0.9
DnaJ protein-like	248301_at	0.9
26S proteasome regulatory particle chain RPT6-like protein ;supported by full-length cDNA: Ceres:38213.	248220_at	0.9
unknown protein ;supported by full-length cDNA: Ceres:22860.	248235_at	0.9
GDSL-motif lipase/hydrolase-like protein	248118_at	0.9
DNA topoisomerase I	248109_at	0.9
putative protein similar to unknown protein (ref|NP_032765.1)	248081_at	0.9
unknown protein ; supported by cDNA: gi_13899122_gb_AF370556.1_AF370556	248031_at	0.9
putative protein similar to unknown protein (gb|AAF54217.1)	247993_at	0.9
Ca2+-transporting ATPase-like protein (emb|CAB79748.1)	247937_at	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 (sp|P54122)	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: g	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
valine--tRNA ligase-like protein several bacterial valine--tRNA 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	246191_at	0.9
26S proteasome AAA-ATPase subunit RPT6a - like protein 26S proteasome AAA-ATPase subunit RPT6a, Arabidopsis thaliana, EMBL:AF12	246147_s_at	0.9
putative protein predicted proteins, H. sapiens, D. melanogaster and others	246094_at	0.9
putative protein thiamin pyrophosphokinase, Schizosaccharomyces pombe, PIR:S52350	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 farnesyl cysteine carboxyl methyltransferase, Rattus norvegicus, EMBL:AF075595	246053_at	0.9
putative protein predicted proteins, Arabidopsis thaliana and Synechocystis 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	246060_at	0.9
putative protein predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_13877640_gb_AF370521.1_AF370521	246010_at	0.9
cysteine proteinase RD21A identical to thiol protease RD21A SP:P43297 from [Arabidopsis thaliana]	245803_at	0.9
unknown protein contains similarity to calmodulin GI:166304 from [Achlya klebsiana]; supported by cDNA: gi_13358218_gb_AF325029.2_AF	245732_at	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
viral resistance protein, putative, 5 partial similar to viral resistance protein GI:7110565 from [Arabidopsis thaliana]	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	245114_at	0.9
hypothetical protein predicted by genscan; similar to SP|P34568|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
putative protein similar to unknown protein (pir||T05803)	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	-r2-At-Actin-M_	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_	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
putative N-acetyl-gamma-glutamyl-phosphate reductase ; supported by cDNA: gi_16604367_gb_AY058082.1_	266704_at	0.8
unknown protein ;supported by full-length cDNA: Ceres:13821.	266635_at	0.8
putative transportin	266523_at	0.8
putative phospholipid cytidylyltransferase	266399_at	0.8
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: Ce	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 thalian	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 f	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 escul	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 [Arabi	262823_at	0.8
putative clathrin-coat assembly protein similar to gb|L26291 clathrin-associated protein unc-101 from Caenorhabditis elegans and is a memb	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_124077	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-	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|AA605	262588_at	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;supporte	262500_at	0.8
unknown protein	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: gi_6520211_dbj_AB028226.1_AB028226	262078_at	0.8
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:3454.	262095_at	0.8
unknown protein	262014_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
unknown protein	261885_at	0.8
CCR4-associated factor, putative\0CCR4-associated factor, putative similar to CCR4-ASSOCIATED FACTOR 1 GB:Q60809 from [Mus mus	261887_at	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:1	261745_at	0.8
unknown protein ;supported 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, putative similar to 30S RIBOSOMAL PROTEIN S1 GB:P46228 from [Synechococcus sp.]; supported by cDNA: gi_1	261522_at	0.8
Expressed protein ; supported by cDNA: gi_13877958_gb_AF370242.1_AF370242	261388_at	0.8
hypothetical protein contains similarity to peroxisome membrane protein PEX2 GI:2623264 from [Mus musculus]; supported by full-length cD	261348_at	0.8
proton pump interactor, putative similar to GB:CAB43882 from [Arabidopsis thaliana]	261365_at	0.8
unknown protein	261366_at	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	0.8
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	261231_at	0.8
flower pigmentation protein ATAN11 identical to GB:AAC18912 from [Arabidopsis thaliana] (Genes Dev. 11 (11), 1422-1434 (1997));support	261202_at	0.8
TATA binding protein-associated factor, putative similar to GB:CAA74021 from [Arabidopsis thaliana]; supported by cDNA: gi_15293056_gb_	261126_at	0.8
disease resistance protein, putative similar to GB:AAC15780 from [Lycopersicon pimpinellifolium] (Cell 84 (3), 451-459 (1996))	261070_at	0.8
developmentally regulated GTP-binding protein identical to GB:AAB67830 from (Arabidopsis thaliana) (Plant Mol. Biol. 39 (1), 75-82 (1999));	261036_at	0.8
glyoxalase II isozyme, putative similar to glyoxalase II isozyme GB:AAC49865 GI:2570338 from [Arabidopsis thaliana];supported by full-lengt	260954_at	0.8
scarecrow-like 1 identical to scarecrow-like 1 GB:AAF21043 GI:6644390 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:10	260878_at	0.8
19S proteosome subunit 9, putative similar to 19S proteosome subunit 9 GB:AAC34120 GI:3450889 from [Arabidopsis thaliana];supported b	260842_at	0.8
unknown protein ; supported by cDNA: gi_16604612_gb_AY059751.1_	260747_at	0.8
myb-related DNA-binding protein, putative similar to GB:U67132 from [Petroselinum crispum] (Plant J. 11 (5), 1079-1093 (1997))	260732_at	0.8
unknown protein ; supported by cDNA: gi_15810124_gb_AY056127.1_	260675_at	0.8
hypothetical protein predicted by genemark.hmm	260681_at	0.8
unknown protein ; supported by cDNA: gi_13605638_gb_AF361800.1_AF361800	260587_at	0.8
RNA-binding protein, putative similar to GB:AAF29078 from [Homo sapiens];supported by full-length cDNA: Ceres:10976.	260487_at	0.8
hypothetical protein ; supported by cDNA: gi_15292844_gb_AY050856.1_	260489_at	0.8
phosphatidylinositol-4-phosphate 5-kinase isolog	260466_at	0.8
putative alpha-amylase similar to alpha-amylase GB:AAA91884 [Solanum tuberosum]; supported by cDNA: gi_15215737_gb_AY050398.1_	260412_at	0.8
unknown protein	260373_at	0.8
unknown protein similar to hypothetical proteins GB:AAD39276 [Arabidopsis thaliana], GB:CAB53491 [Oryza sativa];supported by full-length	260227_at	0.8
putative lipoxygenase similar to 13-lipoxygenase GB:CAA65269 [Solanum tuberosum]	260190_at	0.8
putative G protein-coupled receptor similar to G protein-coupled receptor 69A GB:NP_006046 from [Homo sapiens]	260145_at	0.8
unknown protein ;supported by full-length cDNA: Ceres:269548.	260137_at	0.8
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:38940.	260096_at	0.8
DNA-directed RNA polymerase subunit, putative similar to GI:6723961 from [Schizosaccharomyces pombe]	260049_at	0.8
putative nuclear matrix constituent protein 1 (NMCP1) similar to nuclear matrix constituent protein 1 (NMCP1) GB:BAA20407 [Daucus carota]	260031_at	0.8
putative DNA-binding protein contains Pfam profile: PF01388 ARID DNA binding domain	259967_at	0.8
hypothetical protein ;supported by full-length cDNA: Ceres:147838.	259976_at	0.8
putative RNA-binding protein contains Pfam profile: PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain); supported by cDN	259984_at	0.8
putative P-type transporting ATPase similar to ATPase II GB:AAD34706 [Homo sapiens]	259910_at	0.8
putative translation initiation factor IF-2 similar to translation initiation factor IF-2 GB:P39730 [Saccharomyces cerevisiae]	259872_at	0.8
putative phorbol ester / diacylglycerol binding protein Pfam HMM hit: Phorbol esters / diacylglycerol binding domain	259673_at	0.8
protein kinase, putative similar to protein kinase GI:2852447 from (Arabidopsis thaliana)	259541_at	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 20443.	259542_at	0.8
unknown protein ; supported by cDNA: gi_14423507_gb_AF386991.1_AF386991	259500_at	0.8
protein serine/threonine kinase, putative similar to protein serine/threonine kinase GI:7248457 from [Lophopyrum elongatum]; supported by c	259437_at	0.8
GTP-binding protein(RAB11D), putative similar to RAB11D GI:1370148 from [Lotus japonicus]; supported by cDNA: gi_12083263_gb_AF332	259395_at	0.8
protein phosphatase 2A regulatory subunit, putative similar to protein phosphatase 2A regulatory subunit GI:683502 from [Arabidopsis thalia	259407_at	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_A	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	0.8
hypothetical protein similar to Ku70-binding protein GB:AAD31085 [Homo sapiens]; supported by cDNA: gi_13877934_gb_AF370230.1_AF3	259056_at	0.8
hypothetical protein	259059_at	0.8
putative GTP-binding protein similar to GTP-binding protein GB:BAA02108 [Pisum sativum], HMM hit: Ras family (contains ATP/GTP bindin	259061_at	0.8
unknown protein predicted by genscan; est match;supported by full-length cDNA: Ceres:3820.	259038_at	0.8
unknown protein similar to unknown proteins GB:AAD24625 [Arabidopsis thaliana], GB:AAC73026 [Arabidopsis thaliana]	258933_at	0.8
hypothetical protein similar to symbiosis related proteins: GB:AAB53650 [Laccaria bicolor], GB:P87068 [Laccaria bicolor];supported by full-le	258880_at	0.8
putative helicase similar to C-terminal half of transcription-repair coupling factor (TRCF) GB:Q55750 [Synechocystis PCC6803]; contains Pfa	258861_at	0.8
putative 26S proteosome regulatory subunit	258871_at	0.8
unknown protein ;supported by full-length cDNA: Ceres:320.	258771_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 full-length cDNA: Ceres: 28024.	258747_at	0.8
unknown protein similar to a region of DNAJ domain-containing protein MCJ GB:AAD38506; supported by full-length cDNA: Ceres: 5219.	258716_at	0.8
unknown protein ; supported by cDNA: gi_15983478_gb_AF424614.1_AF424614	258647_at	0.8
putative tyrosyl-tRNA synthetase similar to TYROSYL-TRNA SYNTHETASE GB:P04077 from [Bacillus caldotenax]	258475_at	0.8
putative DNA binding protein identical to putative DNA binding protein GB:AAF27433 from [Arabidopsis thaliana]; supported by cDNA: gi_150	258324_at	0.8
putative phospholipase D similar to phospholipase D1 GB:AAC78487 [Brassica oleracea], GB:Q38882 [Arabidopsis thaliana]; supported by c	258226_at	0.8
hypothetical protein contains Pfam profile: PF01535 domain of unknown function (4 copies)	258149_at	0.8
hypothetical protein predicted by genemark	257963_at	0.8
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:116381.	257855_at	0.8
light regulated protein, putative similar to light regulated protein precursor GB:Q03200 [Oryza sativa] (Plant Mol. Biol. 22 (1), 165-170 (1993))	257832_at	0.8
unknown protein	257783_at	0.8
RNA helicase, putative contains Pfam profiles: PF00636 RNase3 domain, PF00035 Double-stranded RNA binding motif; supported by cDNA	257678_at	0.8
unknown protein contains Pfam profile:PF00806 Pumilio-family RNA binding domains; supported by cDNA: gi_15010673_gb_AY045638.1_	257652_at	0.8
unknown protein	257612_at	0.8
glucose-6-phosphate 1-dehydrogenase, putative similar to glucose-6-phosphate 1-dehydrogenase GB:CAB52674 from [Arabidopsis thalian	257144_at	0.8
prohibitin, putative similar to prohibitin GB:AAC49691 from [Arabidopsis thaliana] (Plant Mol. Biol. (1997) 33 (4), 753-756);supported by full-le	257149_at	0.8
ATPase, putative similar to spastin protein GB:CAB60141 from [Homo sapiens] (Hum. Mol. Genet. (2000) 9, 637-644)	257046_at	0.8
unknown protein	256940_at	0.8
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:103959.	256851_at	0.8
multispanning membrane protein, putative similar to transmembrane 9 superfamily member 2 GB:NP_004791 from [Homo sapiens] (Gene 21	256776_at	0.8
hypothetical protein similar to putative pre-rRNA processing protein GB:AAF23213 GI:6671953 from [Arabidopsis thaliana]	256661_at	0.8
unknown protein similar to putative RING zinc finger protein GB:AAF15909 GI:6539239 from [Arabidopsis thaliana]	256611_at	0.8
myosin identical to myosin GB:CAB61875 GI:6491702 [Arabidopsis thaliana]	256623_at	0.8
hypothetical protein	256579_at	0.8
unknown protein	256530_at	0.8
55 kDa B regulatory subunit of phosphatase 2A nearly identical to 55 kDa B regulatory subunit of phosphatase 2A [Arabidopsis thaliana] GI:7	256187_at	0.8
Ser Thr protein kinase, putative similar to Ser Thr protein kinase GI:2598067 from (Zea mays)	256110_at	0.8
hypothetical protein predicted by genscan+; supported by cDNA: gi_15810574_gb_AY056326.1_	256069_at	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
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
putative NifU-like metallocluster assembly factor similar to apricot NifU homolog partial CDS, GenBank accession number U95179; supporte	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
putative LRR receptor-like protein kinase similar to Z. mays leucine-rich repeat transmembrane protein kinase LRRTPK 1, GenBank accessi	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; s	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
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
aspartate--tRNA 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
putative protein YHR077c (NMD2,IFS1) protein -Saccharomyces cerevisiae,PID:g555939; supported by cDNA: gi_14334747_gb_AY035047.	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
putative histone deacetylase similar to maize nucleolar histone deacetylase (U82815); supported by cDNA: gi_11066134_gb_AF195545.1_A	252625_at	0.8
dTDP-glucose 4-6-dehydratases-like protein dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana,PIR:S58282;supported by full-l	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
putative protein senescence-associated protein 12 - Hemerocallis hybrid cultivar, EMBL:AF082032; supported by cDNA: gi_15215687_gb_A	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
putative protein putative protein T18N14_30 on this BAC	252069_s_at	0.8
putative serine/threonine protein kinase Pto kinase interactor 1 -Lycopersicon esculentum,PID:g3668069; supported by cDNA: gi_16648894_	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
phosphatase - like protein DUAL SPECIFICITY PROTEIN PHOSPHATASE 5, Rattus norwegicus, SWISSPROT:DUS5_RAT; supported by c	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	251497_at	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
(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase -like protein beta-hydroxyacyl-ACP dehydratase precursor, Toxoplasma gondii, EMB	250470_at	0.8
putative protein predicted proteins, Homo sapiens, Drosophila melanogaster, Caenorhabditis elegans	250377_at	0.8
pre-mRNA splicing factor ATP-dependent RNA helicase -like protein PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE	250273_at	0.8
acetolactate synthase-like protein	250111_at	0.8

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
SAR DNA-binding protein - like SAR DNA-binding protein-1, garden pea, PIR:T06377	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	0.8
putative protein predicted protein, Oryza sativa; supported by cDNA: gi_15081722_gb_AY048254.1_	246160_at	0.8
subtilisin-like protein subtilisin/kexin isozyme SKI-1 precursor - Rattus norvegicus, EMBL:AF094821	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:6760451 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	245618_at	0.8
RNA polymerase II fifth largest subunit like protein	245569_at	0.8
hypothetical protein	245502_at	0.8
hypothetical protein	245430_at	0.8
auxin-responsive protein IAA1 ;supported by full-length cDNA: Ceres:33860.	245397_at	0.8
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_	245280_at	0.8
phytoene dehydrogenase precursor (phytoene desaturase) ; supported by cDNA: gi_14532765_gb_AY040007.1_	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	245278_at	0.8
F12A21.17 similar to signal recognition particle 72kD gi|5902124	245187_s_at	0.8
F12A21.19 unknown protein; similar to ESTs gb|AI996033.1, and dbj|AV563431.1	245188_at	0.8
unknown protein	245131_s_at	0.8
putative TGACG-sequence-specific bZIP DNA-binding protein	245092_at	0.8
ubiquitin-specific protease 5 (UBP5), putative similar to GI:6648604; supported by cDNA: gi_6648603_gb_AF048705.1_AF048705	245100_at	0.8
putative cytochrome P450	245075_at	0.8
putative cyclin ;supported by full-length cDNA: Ceres:22595.	245043_at	0.8

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_13430715_gb_AF	256404_at	0.8
putative protein polygalacturonase(EC 3.2.1.15) precursor - Erwinia carotovora,PID:g42330	253326_at	0.8
putative protein other predicted Arabidopsis thaliana proteins	253037_at	0.8
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|aaa16326.1||m98495 prot	260503_at	0.7
hypothetical protein predicted by genscan+	259884_at	0.7
eukaryotic translation initiation factor 4E, putative similar to SP:O23252 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 prime, Middle, a	X-r2-At-Actin-3_	0.7
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 GB:AJ010713; contains a chalcone and stilbene synthase active site (PF00195); su	267377_at	0.7
Expressed protein ; supported by full-length cDNA: Ceres: 40603.	267114_at	0.7
unknown protein	267072_at	0.7
hypothetical protein predicted by genscan; supported by cDNA: gi_15146245_gb_AY049264.1_	266889_at	0.7
putative embryo-abundant protein contains a bZIP transcription factor basic domain signature (PDOC00036)	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_ATH1PPHA	266238_at	0.7
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 signature	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 thaliana]	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	265761_at	0.7
unknown protein predicted by genscan	265691_at	0.7
putative protein kinase contains a protein kinase domain profile (PDOC00100); supported by cDNA: gi_15028152_gb_AY046026.1_	265661_at	0.7
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	265521_at	0.7
ferredoxin--nitrite 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-containing monoox	265122_at	0.7
hypothetical protein ; supported by cDNA: gi_14334789_gb_AY035068.1_	265074_at	0.7
HD-Zip protein, putative similar to HD-Zip protein GI:2145356 from [Arabidopsis thaliana]; supported by cDNA: gi_16974580_gb_AY060556.	265060_at	0.7
putative glucanase	264875_at	0.7
putative glycine-rich, zinc-finger DNA-binding protein genomic copy of EST T76328 cold-shock signature from position 22 to 41 [YGFITPDD	264789_at	0.7
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-length 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|Z48402 come f	264322_at	0.7
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 thaliana];support	264204_at	0.7
putative myb-related transcription factor Similar to myb-related transcription factor (THM27) gb|X95296 from Solanum lycopersicum. ESTs g	264210_at	0.7
hypothetical protein contains similarity to toluene tolerance protein Ttg2A GI:4336798 from [Pseudomonas putida]; supported by cDNA: gi_13	264165_at	0.7
unknown protein	264128_at	0.7
replicase, putative similar to replicase GI:166841 from [Arabidopsis thaliana]; supported by cDNA: gi_15292902_gb_AY050885.1_	264099_at	0.7
unknown protein similar to putative CREB-binding protein GI:7025854 from [Arabidopsis thaliana]; supported by cDNA: gi_12597460_gb_AF3	264101_at	0.7
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:39762.	263809_at	0.7
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_	263762_at	0.7
putative pre-mRNA splicing factor PRP19 similar to GB:AAB80652; supported by cDNA: gi_14532631_gb_AY039940.1_	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	263643_at	0.7
putative receptor-like protein kinase	263590_at	0.7
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|AI993440.1, 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_	263077_at	0.7
exonuclease, putative similar to 5 -3 exonuclease GI:1894792 from [Mus musculus]; supported by cDNA: gi_11875625_gb_AF286718.1_AF	262961_at	0.7
hypothetical protein predicted by genemark.hmm	262859_at	0.7
gamma-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:O75694 [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 me	262826_at	0.7
putative ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase highly similar to ribulose-1,5 bisphosphate car	262648_at	0.7
putative pattern formation protein EMB30 highly similar to GB:Q42510; supported by cDNA: gi_1209630_gb_U36432.1_ATU36432	262614_at	0.7
4-hydroxyphenylpyruvate dioxygenase (HPD) identical to 4-hydroxyphenylpyruvate dioxygenase (HPD) SP:P93836 [Arabidopsis thaliana (Mo	262635_at	0.7
oxidoreductase, putative contains Pfam profile: PF00671 Iron/Ascorbate oxidoreductase family; supported by cDNA: gi_13878118_gb_AF37	262638_at	0.7
ubiquitin-specific protease 15 (UBP15) almost identical to ubiquitin-specific protease 15 GI:11993475 [Arabidopsis thaliana], 7 amino acid dif	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/P	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_	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]	261935_at	0.7
chloroplast drought-induced stress protein, putative similar to chloroplast drought-induced stress protein GI:2582821 from [Solanum tuberos	261751_at	0.7
hypothetical protein predicted by genemark.hmm	261628_at	0.7
putative lipase 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_	261354_at	0.7
aminoacylase, putative similar to aminoacylase I GI:1844 from [Sus scrofa]	261326_s_at	0.7
hypothetical protein contains similarity to nascent polypeptide associated complex alpha chain GI:6752882 from [Pinus taeda];supported by f	261189_at	0.7
hypothetical protein predicted by genemark.hmm	261173_at	0.7
unknown protein ; supported by full-length cDNA: Ceres: 13391.	261038_at	0.7
hypothetical protein contains similarity to transcription factor TFIID GB:U57693 GI:1373376 from (Homo sapiens); supported by cDNA: gi_15	261041_at	0.7
hypothetical protein similar to unknown protein GB:AAF32477 GI:6957733 from [Arabidopsis thaliana]	261043_at	0.7
flavonol 3-o-glucosyltransferase, putative similar to flavonol 3-o-glucosyltransferase GB:Q40287 from [Manihot esculenta]	261048_at	0.7
hypothetical protein similar to Pto kinase interactor 1 GB:AAC61805 GI:3668069 from [Lycopersicon esculentum]	260924_at	0.7
hypothetical protein predicted by genscan+	260663_at	0.7
translation elongation factor EF-1 alpha identical to GB:AAB07881 from [Arabidopsis thaliana] (Mol. Gen. Genet. 219 (1-2), 106-112 (1989))	260677_at	0.7
putative SF16 protein {Helianthus annuus}	260610_at	0.7
putative AP2 domain transcription factor pFAM domain (PF00847); supported by full-length cDNA: Ceres: 41462.	260498_at	0.7
unknown protein	260375_at	0.7
putative N-terminal acetyltransferase similar to N-TERMINAL ACETYLTRANSFERASE GB:P12945 from (Saccharomyces cerevisiae)	260282_at	0.7
unknown protein contains zinc finger, C3HC4 type (RING finger) domain	260168_at	0.7
ethylene-response protein, ETR1 identical to GB:P49333 from [Arabidopsis thaliana] (Science 262 (5133), 539-544 (1993))	260133_at	0.7
hypothetical protein C-term similar to C-term of apoptosis inhibitor GB:AAC70265 [Lymantria dispar nucleopolyhedrovirus]; supported by cDN	260042_at	0.7
putative heat shock transcription factor contains Pfam profile: PF00447 HSF-type DNA-binding domain; N-terminal portion similar to heat sho	259992_at	0.7
putative chlorophyll A-B binding protein similar to chlorophyll A-B binding protein GB:P12470 [Nicotiana plumbaginifolia]; contains Pfam profil	259970_at	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
putative exportin, tRNA (nuclear export receptor for tRNAs) similar to exportin, tRNA (nuclear export receptor for tRNAs) GB:6005954 [Homo	259919_at	0.7
unknown protein ;supported by full-length cDNA: Ceres:9231.	259765_at	0.7
putative aminotransferase similar to kynurenine aminotransferase GB:S48737 [Rattus norvegicus], similar to aspartate aminotransferase GB:	259710_at	0.7
putative 20S proteasome beta subunit PBC2 identical to residues 14-204 of 20S proteasome beta subunit PBC2 GB:AAC32069 [Arabidopsis	259712_at	0.7
unknown protein ;supported by full-length cDNA: Ceres:37735.	259475_at	0.7
hypothetical protein contains similarity to hepatocellular carcinoma-associated antigen 59 GI:7158847 from [Homo sapiens]; supported by cD	259415_at	0.7
hypothetical protein gene model predicted by genscan and genefinder; supported by cDNA: gi_13430665_gb_AF360245.1_AF360245	259330_at	0.7
putative 3 exoribonuclease contains Pfam profile: PF01138 3 exoribonuclease family; supported by cDNA: gi_13358209_gb_AF325018.2_A	259227_at	0.7
putative glycerol-3-phosphate dehydrogenase similar to glycerol-3-phosphate dehydrogenase GB:BAA08926 [Mus musculus]	259146_at	0.7
unknown protein	259121_at	0.7
unknown protein Pfam HMM hit: Regulator of chromosome condensation (RCC1)	259125_at	0.7
putative protein kinase contains Pfam profile: Eukaryotic protein kinase domain	259074_at	0.7
hypothetical protein similar to hypothetical protein GB:P40055 [Saccharomyces cerevisiae], Pfam HMM hit: WD domain, G-beta repeats	258965_at	0.7
putative DNA gyrase subunit A similar to DNA gyrase A subunit GB:BAA10380 [Synechocystis sp]	258966_at	0.7
unknown protein C-terminal portion similar to mannosyltransferase GB:BAA28328 [Escherichia coli];supported by full-length cDNA: Ceres:17	258917_at	0.7
Expressed protein ; supported by full-length cDNA: Ceres: 9573.	258848_at	0.7
unknown protein	258833_at	0.7
putative RNA-binding protein similar putative nucleic acid binding protein GB:CAB39665 [Arabidopsis thaliana]; Pfam HMM hit: KH domain fa	258790_at	0.7
unknown protein ;supported by full-length cDNA: Ceres:269248.	258609_at	0.7
putative DEAD/DEAH box helicase contains Pfam profile: PF00270 DEAD/DEAH box helicase; supported by cDNA: gi_15081734_gb_AY048	258554_at	0.7
putative stearoyl-acyl carrier protein desaturase similar to stearoyl-acyl carrier protein desaturase GB:CAA07349 from [Linum usitatissimum];	258485_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

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 fa	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-lengt	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:	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:29	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 isoleucine--tRNA 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:G238	254520_at	0.7
putative protein retinoblastoma binding protein 2, Homo sapiens, PIR:I78879	254464_at	0.7
anthocyanidin synthase - like protein putative leucoanthocyanidin dioxygenase, Arabidopsis thaliana, PID:g1575699	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
protein kinase - like protein ADK1 protein kinase, Arabidopsis thaliana, PIR2:A55661	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 - Caenorhabditis 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_gb	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
hypothetical protein	252960_at	0.7
beta-D-glucan 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 GTP-binding protein beta chain homolog, Nicotiana tabacum, PIR:T16970;supported by full-length cDNA: Ceres:33776.	252252_at	0.7
putative protein various predicted proteins, Arabidopsis thaliana	252245_at	0.7
putative protein transcribed gene of unknown function, Arabidopsis thaliana, EMBL:ATH132745	252226_at	0.7
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, PIR: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, EMBL:U52079	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)	249144_at	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_	248591_at	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

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	247098_at	0.7
putative protein contains similarity to ATP binding protein associated with cell differentiation;supported by full-length cDNA: Ceres:2489.	247075_at	0.7
putative protein similar to unknown protein (pir||T38383); supported by cDNA: gi_15810344_gb_AY056211.1_	247045_at	0.7
cytochrome P450-like protein CYTOCHROME P450 71B1 - Thlaspi arvense, EMBL:L24438	246947_at	0.7
endopeptidase - like protein O-sialoglycoprotein endopeptidase, Methanococcus jannaschii, pir:A64441;supported by full-length cDNA: Cere	246879_at	0.7
putative protein various predicted proteins, Arabidopsis thaliana, Caenorhabditis elegans and Drosophila melanogaster; supported by cDNA:	246843_at	0.7
putative protein predicted proteins, Arabidopsis thaliana	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 cDNA: Ceres:2270.	246481_s_at	0.7
cellulose synthase catalytic subunit (IRX3) ; supported by cDNA: gi_4886755_gb_AF088917.1_AF088917	246425_at	0.7
glutaredoxin, putative similar to glutaredoxin GI:1732424 from [Ricinus communis]	246384_at	0.7
putative transmembrane protein G5p yeast Sac1 protein, PIR:A33622	246300_at	0.7
acyl-coA dehydrogenase Mus musculus glutaryl-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: gi_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
hypothetical protein	257325_at	0.7
hypothetical protein predicted by genemark.hmm	257487_at	0.7
unknown protein contains Pfam profile:PF00400 WD domain, G-beta repeat	257553_at	0.7
hypothetical protein similar to putative protein GB:CAB52443 [Arabidopsis thaliana]	259285_at	0.7
hypothetical protein contains similarity to glucosidase I GI:2344809 from [Homo sapiens]	264228_at	0.6
hypothetical protein predicted by genscan	263521_at	0.6
putative RING zinc finger protein contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger);supported by full-length cDNA: Cere	262167_at	0.6
protein serine/threonine phosphatase alpha, putative similar to protein serine/threonine phosphatase alpha GB:AAC69437 GI:3811109 from [	261743_s_at	0.6
unknown protein	261060_at	0.6
transcription factor, putative similar to SP:O88060 from [Streptomyces coelicolor]	259929_at	0.6
hypothetical protein	257189_at	0.6
putative protein predicted gene T10G3.5, Caenorhabditis elegans, PATCHX:E308128; supported by cDNA: gi_16604600_gb_AY059745.1_	253468_at	0.6
putative protein various predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:13930.	251005_at	0.6
putative protein similar to unknown protein (dbj|BAA91806.1); supported by cDNA: gi_13877730_gb_AF370128.1_AF370128	249092_at	0.6
putative protein strong similarity to unknown protein (dbj|BAA93030.1)	247142_at	0.6
putative protein predicted proteins, Drosophila melanogaster, Caenorhabditis elegans and Arabidopsis thaliana	246750_at	0.6
J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)	FFX-BioDn-5_	0.6
X03453 Bacteriophage P1 cre recombinase protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)	FFX-CreX-5_	0.6
Escherichia coli /REF=J04423 /DEF=E coli bioC protein corresponding to nucleotides 4257-4573 of J04423 /LEN=777 (-5 and -3 represent tr	X-r2-Ec-bioC-	0.6
Escherichia coli /REF=J04423 /DEF=E coli bioD gene dethiobiotin synthetase corresponding to nucleotides 5024-5244 of J04423 /LEN=676 (	X-r2-Ec-bioD-	0.6
Arabidopsis thaliana /REF=U37281 /DEF=actin-2 mRNA, complete cds /LEN=1637 (-5, -M, -3 represent transcript regions 5 prime, Middle, a	X-r2-At-Actin-5_	0.6
Arabidopsis thaliana /REF=U37281 /DEF=actin-2 mRNA, complete cds /LEN=1637 (_5, _M, _3 represent transcript regions 5 prime, Middle,	X-Athal-Actin_3	0.6
unknown protein similar to GP|522127|gnl|PID|e349073|Z35639 and GP|2224677|gnl|PID|d1021664|AB002366	267609_at	0.6
putative nitrate transporter	267612_at	0.6
putative protein kinase contains a protein kinase domain profile (PDOC00100)	267564_at	0.6
Expressed protein ; supported by cDNA: gi_15010573_gb_AY045588.1_	267371_at	0.6
GDP dissociation inhibitor identical to GB:D83531;supported by full-length cDNA: Ceres:29536.	267236_at	0.6
putative GTP-binding protein (extra large) ; supported by cDNA: gi_15451169_gb_AY054665.1_	267136_at	0.6
unknown protein	266971_at	0.6
hypothetical protein predicted by genefinder	266938_at	0.6
putative pyruvate dehydrogenase E1 beta subunit ;supported by full-length cDNA: Ceres:38439.	266904_at	0.6
SKP1/ASK1-related, putative similar to glycoprotein FP21 SP:P52285 from [Dictyostelium discoideum]	266922_s_at	0.6
putative glucosyltransferase	266869_at	0.6
unknown protein identical to GB:AAC31827	266816_at	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	266338_at	0.6
putative tropinone reductase	266280_at	0.6
putative tropinone reductase ;supported by full-length cDNA: Ceres:1637.	266291_at	0.6
glutathione S-transferase identical to GB:X89216;supported by full-length cDNA: Ceres:6528.	266299_at	0.6
putative phloem-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 genscan;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;s	265129_at	0.6
unknown protein similar to ESTs gb|R30049 and gb|T46176;supported by full-length cDNA: Ceres:102343.	265101_at	0.6
T-complex chaperonin protein , epsilon subunit identical to GB:O04450, similar to ESTs gb|R29812, emb|Z38124, gb|AA297087, gb|R29812,	265010_at	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
F-box protein family, AtFBX3 contains similarity to stamina pistilloidia GI:4101570, the pea ortholog of Fim and UFO from [Pisum sativum];su	264955_at	0.6
receptor-like kinase, putative similar to somatic embryogenesis receptor-like kinase GI:2224910 from [Daucus carota]; supported by cDNA: g	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-sialyltransferase (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	264249_at	0.6
unknown protein	264218_at	0.6
hypothetical protein predicted by genemark.hmm	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	264193_at	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	0.6
MADS-box protein (AGL3) ; supported by cDNA: gi_1737494_gb_U81369.1_ATU81369	264041_at	0.6
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|AA597906, 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|M93122	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 tuberosu	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	262869_s_at	0.6
purple acid phosphatase, putative contains Pfam profile: PF02227 Purple acid phosphatase	262830_at	0.6
unknown protein ; supported by cDNA: gi_16612297_gb_AF439842.1_AF439842	262849_at	0.6
lipase, putative contains Pfam profile: PF00657 Lipase/Acylhydrolase 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
unknown protein contains similarity to translation initiation factor eIF-2B GI:623032 from [Rattus norvegicus]	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	261864_s_at	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	261632_at	0.6
ADP-glucose pyrophosphorylase, putative similar to ADP-glucose pyrophosphorylase GB:X78900 GI:556623 from [Beta vulgaris]	261642_at	0.6
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
unknown protein ;supported by full-length cDNA: Ceres:39874.	261155_at	0.6
transcription factor MYC7E, putative similar to transcription factor MYC7E GB:AAD15818 GI:4321762 from [Zea mays]	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];suppor	261018_at	0.6
hypothetical protein contains similarity to vacuolating cytotoxin (vacA) GI:6634155 from [Helicobacter pylori]	260938_at	0.6
hypothetical protein predicted by genemark.hmm	260922_at	0.6
hypothetical protein predicted by genemark.hmm	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	260830_at	0.6
unknown protein	260718_at	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 cD	260602_at	0.6
Expressed protein ; supported by cDNA: gi_13605678_gb_AF361820.1_AF361820	260500_at	0.6
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:40765.	260479_at	0.6
Ser/Thr kinase ;supported by full-length cDNA: Ceres:100245.	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_	260310_at	0.6
putative RING zinc finger protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)	260330_at	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))	260020_at	0.6
hydroxypyruvate reductase (HPR) identical to hydroxypyruvate reductase (HPR) GB:D85339 [Arabidopsis thaliana] (Plant Cell Physiol 1997 A	260014_at	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
Expressed protein ; supported by full-length cDNA: Ceres: 30602.	259789_at	0.6
putative replication factor C similar to replication factor C GB:P40937 [Homo sapiens]	259732_at	0.6
putative DNA-binding protein similarity to short region of heat shock transcription factors: GB:CAB10177, GB:AAC31792, GB:CAA16745, GB	259711_at	0.6
unknown protein	259651_at	0.6
hypothetical protein	259633_at	0.6
hypothetical protein	259551_at	0.6
hypothetical protein	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]	259423_at	0.6
putative aminopeptidase similar to X-prolyl aminopeptidase GB:NP_006514 from [Homo sapiens]	259296_at	0.6
putative nodulin similar to nodulin GB:AAA91034 from [Medicago sativa];supported by full-length cDNA: Ceres:16718.	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	259190_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:22512.	259192_at	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	258999_at	0.6
unknown protein contains Pfam profile: PF00498 Forkhead-associated (FHA) domain (putative nuclear protein)	258822_s_at	0.6
unknown protein similar to hypothetical protein KIAA0188 GB: Q14693 from [Homo sapiens]	258721_at	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	258478_at	0.6
phospholipase D, putative similar to phospholipase D GB:BAA32278 from [Candida albicans]	258430_at	0.6
putative glycolate oxidase similar to glycolate oxidase GB:BAA03131 from [Cucurbita sp.]	258359_s_at	0.6
unknown protein ; supported by cDNA: gi_13430465_gb_AF360145.1_AF360145	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]	258221_at	0.6
unknown protein ; supported by cDNA: gi_13605520_gb_AF361586.1_AF361586	258165_at	0.6
chaperonin subunit, putative similar to cytosolic chaperonin, delta-subunit GB:CAA09989 [Glycine max]; contains Pfam profile: PF00118 TCF	258152_at	0.6
putative UDP-glucose glucosyltransferase similar to GB:Q40284 from [Manihot esculenta]	257940_at	0.6
hypothetical protein predicted by genscan+	257923_at	0.6
putative protein peroxidase - Lycopersicon esculentum, PIR:S32768	257890_s_at	0.6
unknown protein contains Pfam profile: PF01535 domain of unknown function (2 copies)	257827_at	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.	257169_at	0.6
lipid transfer protein, putative similar to GB:AAB47967 from [Hordeum vulgare], contains Pfam profile: PF00279 Plant lipid transfer protein far	257066_at	0.6
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_15146180_gb_AY049231.1_	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.	256523_at	0.6
hypothetical protein contains similarity to glucose-repressible alcohol dehydrogenase transcriptional effector GI:3859723 from (Candida albica	256491_at	0.6

hypothetical protein predicted by genemark.hmm	256493_at	0.6
hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 126401.	256413_at	0.6
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:108003.	256399_at	0.6
arginyl-tRNA synthetase nearly identical to arginyl-tRNA synthetase [Arabidopsis thaliana] GI:2632103; supported by cDNA: gi_14030684_gb	256365_at	0.6
disease resistance protein, putative similar to disease resistance protein RPP1-WsB [Arabidopsis thaliana] GI:9279731; supported by cDNA:	256303_at	0.6
sulphate transporter, putative similar to high affinity sulphate transporter GB:X96431 GI:1217966 [Hordeum vulgare]; supported by cDNA: gi_	256244_at	0.6
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:112350.	256142_at	0.6
hypothetical protein contains similarity to photoperiod sensitivity quantitative trait locus (Hd1) GI:11094203 from [Oryza sativa];supported by fu	256060_at	0.6
integral membrane protein, putative similar to integral membrane protein 1 (Itm1) GI:508542 from [Mus musculus]	256029_at	0.6
hypothetical protein contains Pfam profile: PF01344 kelch motif	255947_at	0.6
unknown protein contains similarity to protein phosphatase 2C GI:3777604 from [Rattus norvegicus]; supported by cDNA: gi_16226855_gb_A	255910_at	0.6
Deetiolated1 (DET1) light signal transduction protein	255799_at	0.6
putative calmodulin-binding heat shock protein	255677_at	0.6
putative protein transport factor ; supported by cDNA: gi_14334823_gb_AY035085.1_	255555_at	0.6
putative protein similar to A. thaliana protein F15K9.3, GenBank accession number 3850566	255466_at	0.6
predicted protein of unknown function	255418_at	0.6
putative GH3-like protein similar to soybean GH3 auxin-inducible protein, GenBank accession number X60033; supported by cDNA: gi_1664	255403_at	0.6
putative WD-repeat membrane protein ; supported by cDNA: gi_16604678_gb_AY059784.1_	255278_at	0.6
D123 -like protein protein D123, Rattus norvegicus, EMBL:AAB60521	255227_at	0.6
putative protein chromatin structural protein homolog Supt5hp - Mus musculus,PID:g2754752	255136_s_at	0.6
putative protein Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence, gene T30B22.22, PID:g2529679	255028_at	0.6
putative DNA-directed RNA polymerase DNA-directed RNA polymerase (EC 2.7.7.6) II largestchain - mouse, PIR2:A28490	255009_at	0.6
putative protein m6A methyltransferase - Homo sapiens, PID:g2460037; supported by cDNA: gi_15028132_gb_AY046016.1_	255015_at	0.6
Expressed protein ; supported by full-length cDNA: Ceres: 11425.	254953_at	0.6
putative translation elongation factor ts elongation factor ts (tsf) RP087 - Rickettsia prowazekii, PIR2:F71717	254932_at	0.6
protein phosphatase type 1 PP1BG ;supported by full-length cDNA: Ceres:20905.	254923_at	0.6
putative protein other predicted proteins from various species;supported by full-length cDNA: Ceres:12532.	254788_at	0.6
putative protein HYA22 protein, Homo sapiens, PIR2:JC5707	254681_at	0.6
Expressed protein ; supported by full-length cDNA: Ceres: 29009.	254628_at	0.6
putative protein proline-rich protein APG, Arabidopsis thaliana, PIR2:S21961	254596_at	0.6
UV-damaged DNA-binding protein- like damage-specific DNA binding protein 1, Homo sapiens, PIR2:I38908	254452_at	0.6
putative MADS Box / AGL protein MADS-box protein AGL14, Arabidopsis thaliana, gb:U20184; supported by cDNA: gi_11545542_gb_AF31	254286_at	0.6
gamma-glutamylcysteine synthetase ; supported by cDNA: gi_15912188_gb_AY056372.1_	254270_at	0.6
putative potassium transport protein (TRH1) high-affinity potassium transport protein KUP1, Arabidopsis thaliana, EMBL:AC004165	254214_at	0.6
polyprenyltransferase like protein para-hydroxybenzoate polyprenyltransferase (EC 2.5.1.-) precursor - yeast (Saccharomyces cerevisiae), E	254230_at	0.6
ubiquitin-specific protease 16 (UBP16), putative similar to ubiquitin-specific protease 16 GI:11993477 [Arabidopsis thaliana]; supported by cD	254128_at	0.6
putative protein various predicted proteins, Arabidopsis thaliana	254078_at	0.6
hypothetical protein ; supported by cDNA: gi_14517537_gb_AY039604.1_	254050_s_at	0.6
arginyl-tRNA synthetase	254004_at	0.6
putative protein	253959_at	0.6
putative protein Uvi31, Schizosaccharomyces pombe, G1381578;supported by full-length cDNA: Ceres:112720.	253972_at	0.6
phosphoprotein phosphatase (PPX-1)	253928_at	0.6
putative protein	253897_at	0.6
putative protein ;supported by full-length cDNA: Ceres:11590.	253823_at	0.6
putative protein SNF7 protein - Saccharomyces cerevisiae,PIR2:S52590;supported by full-length cDNA: Ceres:7471.	253735_at	0.6
hypothetical protein ;supported by full-length cDNA: Ceres:117732.	253642_at	0.6
SERINE CARBOXYPEPTIDASE II - like protein serine-type carboxypeptidase, Hordeum vulgare, PIR2:S44191; supported by cDNA: gi_152	253600_at	0.6
hypothetical protein ; supported by cDNA: gi_13605745_gb_AF361854.1_AF361854	253452_at	0.6
synaptobrevin-like protein synaptobrevin-like protein, Mus musculus;supported by full-length cDNA: Ceres:41543.	253462_at	0.6
putative protein ATAC98, Arabidopsis thaliana; supported by cDNA: gi_15292682_gb_AY050775.1_	253465_at	0.6
putative protein ;supported by full-length cDNA: Ceres:29964.	253422_at	0.6
putative protein CDC28/cdc2-like kinase associating arginine-serine cyclophilin, Homo sapiens, PIR2:JC5314	253429_at	0.6
Tic22 -like protein strong homology to Tic22 -Pisum sativum, PID:g3769671	253381_at	0.6
hypothetical protein	253314_at	0.6
Expressed protein ; supported by full-length cDNA: Ceres: 14385.	253324_at	0.6
putative protein Human (H326) mRNA, Homo sapiens, gb:U06631	253176_at	0.6
cinnamyl-alcohol dehydrogenase ELI3-1 ; supported by cDNA: gi_13430625_gb_AF360225.1_AF360225	252983_at	0.6
SEC14 - like protein phosphatidylinositol-phosphatidylcholine transfer protein SEC14, Yarrowia lipolytica, PIR2:S43745; supported by cDNA:	252884_at	0.6
putative transposase hypothetical protein a, maize transposable element Ac - Zea mays, PIR:T02916	252847_at	0.6
protein-tyrosine-phosphatase-like protein protein-tyrosine-phosphatase - Schizosaccharomyces pombe, PIR:A55446	252647_at	0.6
hypothetical protein ;supported by full-length cDNA: Ceres:124275.	252321_at	0.6
vacuolar sorting protein 35 homolog vacuolar sorting protein 35 - Homo sapiens, EMBL:AF191298	252150_at	0.6
putative protein hypothetical protein - Synechocystis sp., EMBL:D90903;supported by full-length cDNA: Ceres:266414.	252122_at	0.6
Cytochrom P450 -like protein CYTOCHROME P450 97B2, Glycine max., gb:O48921	251969_at	0.6
putative protein crp1 protein, Zea mays, PIR:T01685; supported by cDNA: gi_15982930_gb_AY057573.1_	251936_at	0.6
putative protein Hsp70 binding protein HspBP1 - Homo sapiens, EMBL:AF093420;supported by full-length cDNA: Ceres:37834.	251919_at	0.6
FKBP12 interacting protein (FIP37) ; supported by cDNA: gi_3859943_gb_AF084570.1_AF084570	251887_at	0.6
phosphatidylglycerophosphate synthase - like protein phosphatidylglycerophosphate synthase, Pseudomonas fluorescens, EMBL:L29642 co	251819_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
beta-1,3-glucanase - like protein probable beta-1,3-glucanase, Triticum aestivum, PIR:T06268; supported by full-length cDNA: Ceres: 8980.	251804_at	0.6
putative protein exostose-related protein 2, Homo sapiens, PIR:JC5935	251764_at	0.6
putative protein unknown protein At2g40800 - Arabidopsis thaliana, EMBL:AC007660	251685_at	0.6
putative protein strictosidine synthase (EC 4.3.3.2) - Rauvolfia mannii (fragment)	251679_at	0.6
1-acylcerol-3-phosphate acyltransferase - like protein 1-acylcerol-3-phosphate acyltransferase, Brassica napus, Z49860;supported by full-len	251596_at	0.6
serine/threonine-specific protein kinase -like protein serine/threonine-specific protein kinase NAK, Arabidopsis thaliana, PIR:S38326	251539_at	0.6
putative protein protein-tyrosine kinase, Dictyostelium discoideum, PIR:A35670	251542_at	0.6
farnesyltransferase subunit A (FTA) ; supported by cDNA: gi_3142697_gb_AF064542.1_AF064542	251464_at	0.6
putative protein hypothetical protein At2g45740 - Arabidopsis thaliana, EMBL:AC004665	251352_at	0.6
DEAD box RNA helicase RH12	251362_at	0.6
putative protein several hypothetical proteins - Arabidopsis thaliana; supported by cDNA: gi_14517361_gb_AY039515.1_	251308_at	0.6
putative protein Pm5 protein - Homo sapiens, PIR:S21977	251269_at	0.6
beta-glucosidase-like protein several beta-glucosidases	251230_at	0.6
hypothetical protein	251148_at	0.6

putative protein CGI-77 protein, Homo sapiens, EMBL:AF151836;supported by full-length cDNA: Ceres:153131.	251149_at	0.6
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
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 yllC, 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
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
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
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
SCARECROW gene regulator-like ; supported by cDNA: gi_8132288_gb_AF153443.1_AF153443	248689_at	0.6
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
pectinesterase ; supported by cDNA: gi_15293286_gb_AY051077.1_	248263_at	0.6
membrane related protein-like ;supported by full-length cDNA: Ceres:37644.	248199_at	0.6
cyclic nucleotide and calmodulin-regulated ion channel supported by cDNA: gi_15027930_gb_AY045822.1_; supported by cDNA: gi_163231	248153_at	0.6
translation initiation factor-like protein	248146_at	0.6
putative protein contains similarity to NRK-related kinase	248060_at	0.6
selenium-binding protein-like	248075_at	0.6
beta-amylase ; supported by cDNA: gi_15027954_gb_AY045834.1_	248029_at	0.6
heat shock protein (emb|CAA72514.1)	248043_s_at	0.6
beta-1,3-glucanase-like protein	247963_at	0.6
N-myristoyl transferase ;supported by full-length cDNA: Ceres:36525.	247960_at	0.6
Expressed protein	247924_at	0.6
similar to unknown protein (pir||S75584) ;supported by full-length cDNA: Ceres:3488.	247816_at	0.6
phytochelatin synthetase - like protein putative phytochelatin synthetase, Arabidopsis thaliana, EMBL:ATH6787;supported by full-length cDN	247552_at	0.6
putative protein various predicted proteins from different species; supported by cDNA: gi_15912286_gb_AY056421.1_	247555_at	0.6
putative protein predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 38273.	247443_at	0.6
putative protein predicted protein, Arabidopsis thaliana	247398_at	0.6
putative protein contains similarity to kinase	247368_at	0.6
histidinol dehydrogenase ;supported by full-length cDNA: Ceres:40175.	247303_at	0.6
UVB-resistance protein UVR8 (gb|AAD43920.1) ; supported by cDNA: gi_5478529_gb_AF130441.1_AF130441	247307_at	0.6
putative protein strong similarity to unknown protein (gb|AAF01562.1)	247312_at	0.6
fructose-bisphosphatase-like protein ;supported by full-length cDNA: Ceres:1888.	247278_at	0.6
auxin-independent growth promoter-like protein	247237_at	0.6
4-alpha-glucanotransferase ; supported by cDNA: gi_14335103_gb_AY037231.1_	247216_at	0.6
unknown protein	247166_at	0.6
unknown protein ; supported by cDNA: gi_14334479_gb_AY034931.1_	247114_at	0.6
3-dehydroquinate synthase-like protein ;supported by full-length cDNA: Ceres:117923.	247138_at	0.6
selenium-binding protein-like	247100_at	0.6
succinate dehydrogenase flavoprotein alpha subunit (emb|CAA05025.1) ; supported by cDNA: gi_15010745_gb_AY045674.1_	247060_at	0.6
formin-like protein	246995_at	0.6
putative protein similar to unknown protein (gb|AAD25674.1)	246958_at	0.6
putative protein crp1 protein - Zea mays, PIR:T01685	246964_at	0.6
hexose transporter - like protein hexose transporter HT2, Lycopersicon esculentum, EMBL:LES132224; supported by cDNA: gi_15010579_g	246831_at	0.6
putative protein isopenicillin N epimerase, Streptomyces clavuligerus, EMBL:M32324	246832_at	0.6
cyclin H-like protein cycH (CAK associated cyclinH homolog) - Populus tremula x Populus tremuloides, EMBL:AF092743	246762_at	0.6
putative protein predicted protein, Drosophila melanogaster; supported by cDNA: gi_14334591_gb_AY034969.1_	246748_at	0.6
putative protein kinesin heavy chain-like protein, potato, PIR:T07397	246759_at	0.6
signal recognition particle 54 kDa protein 2 (SRP54), putative similar to signal recognition particle 54 kDa protein 2 (SRP54) GI:556901 from	246628_at	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:6970470 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	0.6
unknown protein	246288_at	0.6
tubulin-like protein	246278_at	0.6
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
SNF1 like protein kinase ; supported by cDNA: gi_13249502_gb_AY007221.1_	245563_at	0.6
phosphatase like protein	245557_at	0.6
hypothetical 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~C	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	257459_at	0.6
putative protein similarity to NCA2 protein, yeast, PIR:S54389~Contains Homeobox domain signature and profile AA305-328	245206_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:6967.	265284_at	0.5
unknown protein contains similarity to guanine nucleotide exchange factor GI:4220427 from [Homo sapiens]; supported by cDNA: gi_158113	264961_at	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	262501_at	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];sup	259225_at	0.5
unknown protein ; supported by cDNA: gi_15027906_gb_AY045810.1_	257989_at	0.5
hypothetical protein	256172_at	0.5
unknown protein contains similarity to apoptosis-related protein TFAR19 GI:2407068 from [Homo sapiens];supported by full-length cDNA: Ce	256001_at	0.5
putative protein hypothetical protein T29E15.27 - Arabidopsis thaliana,PID:g3738334	253586_s_at	0.5
DNA topoisomerase like- protein Bacillus subtilis DNA Topoisomerase I; PID:G520753	253566_at	0.5
ubiquitin-specific protease 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-l	246148_at	0.5
hypothetical protein contains similarity to virulence regulator GI:9106522 from [Xylella fastidiosa]	245751_s_at	0.5
X03453 Bacteriophage P1 cre recombinase protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)	AFFX-CreX-3_a	0.5
Arabidopsis thaliana /REF=U84969 /DEF=ubiquitin (UBQ11) gene, complete cds /LEN=1140 (_5, _M, _3 represent transcript regions 5 prime	X-Athal-Ubq_M	0.5
unknown protein ; supported by cDNA: gi_13605814_gb_AF367306.1_AF367306	267558_at	0.5
E2, ubiquitin-conjugating enzyme 2 (UBC2) identical to gi:2689242, SP:P42745; supported by cDNA: gi_12083309_gb_AF332451.1_AF332	267484_at	0.5
CPDK-related protein kinase CDPK:calcium dependent protein kinase; supported by cDNA: gi_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_	266421_at	0.5
unknown protein	266424_at	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_	265481_at	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
similar to glucose 1-dehydrogenase (AB000617); similar to EST gb|T88100 similar to oxidoreductase-like protein GB:CAB75763 GI:7019662	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_	264700_at	0.5
unknown protein Contains similarity to Bos beta-mannosidase (gb|U46067); supported by cDNA: gi_15028222_gb_AY045934.1_	264656_at	0.5
hypothetical protein contains similarity to Nicotiana tabacum membrane-associated salt-inducible protein (GB:U08285);supported by full-lengt	264591_at	0.5
putative 60S ribosomal protein L17 similar to GB:P51413 from [Arabidopsis thaliana]; similar to ESTs gb|L33542 and gb|AA660016;supported	264438_at	0.5
putative heat-shock protein similar to GB:AAD39315;supported by full-length cDNA: Ceres:37036.	264464_at	0.5
hypothetical protein predicted by genemark.hmm	264428_at	0.5
putative chromodomain-helicase-DNA-binding protein similarity to Mi-2, Homo sapiens, GB:X86691; supported by cDNA: gi_6318929_gb_AF	264384_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	264327_at	0.5
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-le	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.	264150_at	0.5
mercaptopyruvate sulfurtransferase (Mst1/Rdh1) identical to mercaptopyruvate sulfurtransferase GI:6009981 and thiosulfate sulfurtransferase	264095_at	0.5
translin-like protein ; supported by cDNA: gi_14596008_gb_AY042792.1_	263843_at	0.5
putative vacuolar proton-ATPase subunit ; supported by cDNA: gi_15450750_gb_AY053417.1_	263764_at	0.5
putative cap-binding protein ; supported by cDNA: gi_15192737_gb_AF272891.1_AF272891	263727_at	0.5
putative DNA-directed RNA polymerase II subunit	263621_at	0.5
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	262950_at	0.5
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_15146253_gb_AY049268.1_	262952_at	0.5
unknown protein ;supported by full-length cDNA: Ceres:21947.	262945_at	0.5
auxin response factor 1 identical to auxin response factor 1 GI:2245378 from [Arabidopsis thaliana]; supported by cDNA: gi_2245377_gb_U8	262914_at	0.5
lipase, putative contains Pfam profile: PF00657 Lipase/Acylhydrolase with GDSL-like motif; supported by cDNA: gi_15027914_gb_AY04581	262749_at	0.5
unknown protein ESTs gb|F15498, gb|H37515, gb|T41906, gb|T22448, gb|W43356 and gb|T20739 come from this gene;supported by full-le	262709_at	0.5
sterol glucosyltransferase, putative similar to sterol glucosyltransferase GI:4731867 from [Dictyostelium discoideum]	262722_at	0.5
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.	262340_at	0.5
unknown protein	262280_at	0.5
unknown protein contains similarity to 1-aminocyclopropane-1-carboxylate deaminases	262247_at	0.5
hypothetical protein predicted by genscan+	262207_at	0.5
hypothetical protein contains similarity to protien kinase C (PRKC) GI:155789 from [Aplysia californica]	262209_at	0.5
hypothetical protein contains similarity to nodule-specific protein Nlj70 GI:3329366 from [Lotus japonicus]	262216_at	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-l	261767_s_at	0.5
hypothetical protein predicted by genemark.hmm	261622_at	0.5
unknown protein similar to putative esterase GB:AAD17422 GI:4335745 from [Arabidopsis thaliana]	261607_at	0.5
ribosomal protein L9, putative similar to RIBOSOMAL PROTEIN L9 GB:P49209 from [Arabidopsis thaliana]	261620_s_at	0.5
NAC domain protein, putative similar to NAC domain protein NAM GB:AAD17313 GI:4325282 from [Arabidopsis thaliana];supported by full-le	261564_at	0.5
hypothetical protein	261553_at	0.5
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; P	261513_at	0.5
unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_	261519_at	0.5
mitochondrial ribosomal protein, putative similar to GB:CAA83057 from [Saccharomyces cerevisiae]; supported by cDNA: gi_14030694_gb_	261418_at	0.5
hypothetical protein predicted by genemark.hmm	261322_at	0.5
unknown protein	261299_at	0.5
unknown protein ;supported by full-length cDNA: Ceres:6332.	261225_at	0.5
unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_	261209_at	0.5
homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica)	261139_at	0.5
unknown protein	261075_at	0.5
hypothetical protein contains similarity to RNA helicase (HRH1) GB:D50487 GI:1742909 from [Homo sapiens]	261008_at	0.5
transmembrane protein, putative similar to TRANSMEMBRANE PROTEIN TMP21 GB:Q63584 from [Rattus norvegicus]	260852_at	0.5
protein kinase interactor, putative similar to Pto kinase interactor GB:1AAC61805 GI:3668069 from [Lycopersicon esculentum]; supported by	260835_at	0.5
glutathione transferase, putative similar to glutathione transferase GI:2853219 from [Carica papaya]; supported by full-length cDNA: Ceres: 3	260746_at	0.5
chaperonin CPN10 identical to SP:P34893 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:26943.	260714_at	0.5
unknown protein ;supported by full-length cDNA: Ceres:41461.	260665_at	0.5
unknown protein	260613_at	0.5
putative WD-40 repeat protein	260526_at	0.5
putative glyoxalase II ; supported by cDNA: gi_2570339_gb_U90928.1_ATU90928	260552_at	0.5
unknown protein	260446_at	0.5
hypothetical protein predicted by genscan+	260455_at	0.5
putative RING zinc finger protein Pfam HMM hit: zinc finger, C3HC4 type (RING finger)	260321_at	0.5
GMP synthase similar to GMP synthase GB:6323873 [Saccharomyces cerevisiae]	260294_at	0.5
putative RNA-binding protein similar to RNA-binding protein GB:S46286 from [Nicotiana sylvestris]	260245_at	0.5
hypothetical protein predicted by genscan; supported by cDNA: gi_15292714_gb_AY050791.1_	259864_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
hypothetical protein similar to nodule inception protein GB:CAB61243 [Lotus japonicus]	259888_at	0.5
cytosolic factor, putative similar to GI:807956 from [Saccharomyces cerevisiae]; supported by cDNA: gi_15081613_gb_AY048199.1_	259804_at	0.5
RNA and export factor binding protein, putative similar to GI:7159943 from [Mus musculus] (RNA 6 (4), 638-650 (2000)); supported by cDNA	259825_at	0.5
lipase/hydrolase, putative contains Pfam profile: PF00657 Lipase/Acylhydrolase with GDSL-like motif;supported by full-length cDNA: Ceres:2	259788_at	0.5
unknown protein similar to GB:AAB81674 [Arabidopsis thaliana]	259763_at	0.5
replication factor, putative similar to GI:4972952 from [Mus musculus] (Mamm. Genome (2000) In press)	259690_at	0.5
hypothetical protein	259519_at	0.5
hypothetical protein similar to unknown protein GI:3335359 from [Arabidopsis thaliana]	259430_at	0.5
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:6115.	259436_at	0.5
DNA binding protein GT-1, putative similar to DNA binding protein GT-1 GI:598073 from (Arabidopsis thaliana)	259412_at	0.5
unknown protein largely predicted by genscan; supported by cDNA: gi_11138670_gb_AF257187.1_AF257187	259215_at	0.5
hypothetical protein similar to putative glycosylation enzyme GB:AAD14462 [Arabidopsis thaliana], putative protein GB:CAB43880 [Arabidop	259174_at	0.5
hypothetical protein predicted by genefinder; supported by cDNA: gi_16604636_gb_AY059763.1_	259156_at	0.5

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.	258977_s_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
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 SA (P4	258799_at	0.5
putative T-complex protein 1, theta subunit (TCP-1-Theta) similar to T-complex protein 1, theta subunit (TCP-1-Theta) GB:P42932 [Mus mus	258816_at	0.5
putative GTP-binding protein (ATFP8) identical to ATFP8 GB:AAD00111 [Arabidopsis thaliana]; supported by cDNA: gi_4097556_gb_U64911	258730_at	0.5
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:O07051 from [Aeromonas jandaei];supported by full-lengt	258599_at	0.5
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 from [Ara	258106_at	0.5
unknown protein ; supported by cDNA: gi_15983782_gb_AY056797.1_	258061_at	0.5
hypothetical protein predicted by genemark	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_	258044_at	0.5
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_AY050828.1	257756_at	0.5
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 majus]; s	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_1387812	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_143344	256765_at	0.5
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
hypothetical protein	256483_at	0.5
unknown protein	256485_at	0.5
putative clathrin heavy chain similar to clathrin heavy chain GB:AAC49294 [Glycine max]	256437_s_at	0.5
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 [Arabidopsis 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_AF339146	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: Ceres:	255231_at	0.5
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:I48733; 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_AY0	254530_at	0.5
putative protein hypothetical protein YPL065w yeast, PIR2:S60925	254422_at	0.5
receptor like protein (fragment) ES43 protein, barley, PIR2:S44281	254342_at	0.5
putative protein putative protein F6I18_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 cDNA: gi_	254074_at	0.5
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 by 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:1195	253535_at	0.5
monogalactosyldiacylglycerol synthase - like protein monogalactosyldiacylglycerol synthase, Cucumis sativus, PID:g1805254; supported by	253489_at	0.5
aspartate aminotransferase ;supported by full-length cDNA: Ceres:33414., Ceres:103854.	253481_at	0.5
protein kinase AME3 ; supported by cDNA: gi_642133_dbj_D45355.1_ATHPKAME3C	253395_at	0.5
homeobox gene ATH1	253411_at	0.5
putative protein AT.I.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	253328_at	0.5
Putative S-phase-specific ribosomal protein	253248_at	0.5
putative protein ;supported by full-length cDNA: Ceres:21838.	253171_at	0.5
putative protein predicted protein, Arabidopsis thaliana;supported by full-length cDNA: Ceres:1368.	253183_at	0.5

putative protein CRP1, Zea mays, gb:AF073522;supported by full-length cDNA: Ceres:5482.	253116_at	0.5
putative protein permease 1 - Mesembryanthemum crystallinum,PID:g3202040	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-	252542_at	0.5
putative protein	252552_at	0.5
putative protein Na+-dependent inorganic phosphate cotransporter, 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
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	252174_at	0.5
putative protein	251869_at	0.5
putative protein various Arabidopsis thaliana predicted proteins	251853_at	0.5
serine/threonine-specific protein kinase -like serine/threonine-specific protein kinase NAK, Arabidopsis thaliana, PIR:S38326	251789_at	0.5
putative protein strictosidine synthase (EC 4.3.3.2) - Rauvolfia 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	251667_at	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	250916_at	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	0.5
unknown protein ; supported by cDNA: gi_16648868_gb_AY059804.1_	250540_at	0.5
putative protein 110K5.11, unknown protein, Sorghum bicolor, EMBL:AF124045; supported by cDNA: gi_13605727_gb_AF361845.1_AF361	250409_at	0.5
glucosyltransferase -like protein glucosyltransferase IS5a, salicylate-induced, common tobacco, PIR:T03747	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
thioredoxin ; supported by full-length cDNA: Ceres: 7791.	249385_at	0.5
glutathione transferase AtGST 10 (emb|CAA10457.1) ; supported by cDNA: gi_15451157_gb_AY054659.1_	249291_at	0.5
putative protein similar to unknown protein (gb|AAF19669.1)	249253_at	0.5
alcohol dehydrogenase (EC 1.1.1.1) class III (pir||S71244) ;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 (pir||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
unknown protein	248737_at	0.5
unknown protein	248745_at	0.5
putative protein contains similarity to unknown protein (dbj|BAA91655.1)	248612_at	0.5
adenylate kinase ;supported by full-length cDNA: Ceres:21741.	248506_at	0.5
unknown protein	248471_at	0.5
putative protein similar to unknown protein (gb|AAF03497.1)	248410_at	0.5
unknown protein	248394_at	0.5
putative protein similar to unknown protein (pir |S77462); supported by cDNA: gi_15081647_gb_AY048216.1_	248287_at	0.5
putative protein similar to unknown protein (gb|AAF34839.1); supported by cDNA: gi_13926341_gb_AF372918.1_AF372918	248230_at	0.5
ubiquitin-like protein SMT3-like ; supported by full-length cDNA: Ceres: 13697.	248103_at	0.5
cell division protein FtsZ chloroplast homolog precursor (sp|Q42545) ; supported by cDNA: gi_14334637_gb_AY034992.1_	248105_at	0.5
molybdopterin synthase sulphurylase (gb|AAD18050.1) ; supported by cDNA: gi_4337039_gb_AF124159.1_AF124159	248108_at	0.5
serine O-acetyltransferase (EC 2.3.1.30) Sat-52 (pir||S71207) ;supported by full-length cDNA: Ceres:119783.	247982_at	0.5
lipid transfer protein; glossy1 homolog	247884_at	0.5
putative protein predicted proteins, Arabidopsis thaliana and Oryza sativa	247741_at	0.5
putative protein predicted proteins, C.elegans and D.melanogastersupported by full-length cDNA: Ceres:105188.	247587_at	0.5
histone deacetylase - like histone deacetylase HDA2, Mus musculus, PIR:T13964	247558_at	0.5
glutaredoxin-like protein ; supported by full-length cDNA: Ceres: 96557.	247418_at	0.5
putative protein contains similarity to ARI-like RING zinc finger protein	247345_at	0.5
phosphatidylinositol 4-kinase (emb|CAB37928.1)	247321_s_at	0.5
immunophilin (gb|AAB57847.1) ;supported by full-length cDNA: Ceres:10243.	247281_at	0.5
putative protein contains similarity to unknown protein (emb|CAB89361.1);supported by full-length cDNA: Ceres:106187.	247248_at	0.5
ABC transporter-like	247232_at	0.5
ReMembR-H2 protein JR700 (gb|AAF32325.1) ; supported by cDNA: gi_14334831_gb_AY035089.1_	247108_at	0.5
putative protein small unique nuclear receptor co-repressor (SUN-CoR) - Mus musculus, EMBL:AF031426; supported by full-length cDNA: C	246921_at	0.5
seryl-tRNA synthetase ; supported by cDNA: gi_15293240_gb_AY051054.1_	246780_at	0.5
putative protein RING finger rngB protein, cytosolic - Dictyostelium discoideum, PIR:S68824	246731_at	0.5
putative protein hypothetical protein slr1702 - Synechocystis sp., PIR:S75312; supported by cDNA: gi_13877992_gb_AF370259.1_AF37025	246736_at	0.5
ribosomal protein S1 ;supported by full-length cDNA: Ceres:4565.	246673_at	0.5

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	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**	**log$_2$ 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	256245_at	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
ubiquinol--cytochrome-c reductase-like protein ubiquinol--cytochrome-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	4.1
putative protein predicted proteins - Arabidopsis thaliana	246178_s_at	4
hypothetical protein	244901_at	4
hypothetical protein	266014_s_at	3.9
hypothetical protein	263502_s_at	3.9
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	255430_at	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
hypothetical protein	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
unknown protein ;supported by full-length cDNA: Ceres:31665.	265670_s_at	3.2
ethylene-responsive transcriptional coactivator, putative similar to GB:AAD46402 from [Lycopersicon esculentum] (Plant J. 18 (6), 589-600 (1999));s	258133_at	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
predicted protein	266012_s_at	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
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	259329_at	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	254074_at	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	262452_at	2.8
putative short-chain type dehydrogenase/reductase similar to short-chain type dehydrogenase/reductase GB:Q08632 [Picea abies]; supported by cD	258815_at	2.8
putative jasmonic acid regulatory protein similar to jasmonic acid 2 GB:AAF04915 from [Lycopersicon esculentum];supported by full-length cDNA: Ce	258395_at	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
ribosomal protein L16	244944_s_at	2.7
hypothetical protein	244904_at	2.7
ATP synthase subunit 9	257339_s_at	2.7
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_16648713_gb_AY058133.1_	261539_at	2.6

similar to 14KD proline-rich protein DC2.15 precursor (sp|P14009); similar to ESTs emb|Z17709 and emb|Z47685 similar to hybrid proline-rich protei	265111_at	2.6
thaumatin-like protein thaumatin-like protein, Arabidopsis thaliana, Pir2:S71175; supported by cDNA: gi_13430505_gb_AF360165.1_AF360165	253104_at	2.6
low-molecular-weight heat shock protein - like cytosolic class I small heat-shock protein HSP17.5, Castanea sativa, EMBL:CSA9880	249575_at	2.6
hypothetical protein	265227_s_at	2.5
hypothetical protein	265229_s_at	2.5
hypothetical protein	265230_s_at	2.5
hypothetical protein	244921_s_at	2.5
subtilisin-like serine protease contains similarity to subtilisin-like protease AIR3 GI:4218991 from [Arabidopsis thaliana]	254979_at	2.5
hypothetical protein	265242_at	2.4
putative heat shock protein ;supported by full-length cDNA: Ceres:25528.	263374_at	2.4
transformer-SR ribonucleoprotein, putative similar to GB:Y09506 from [Nicotiana tabacum] (Plant Mol. Biol. 35 (3), 261-269 (1997)); supported by cD	261081_at	2.4
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:24933.	260744_at	2.4
putative protein similar to unknown protein (pir||T07711);supported by full-length cDNA: Ceres:23920.	247431_at	2.4
putative protein similar to unknown protein (emb|CAB89402.1)	247181_at	2.4
unknown protein ; supported by cDNA: gi_15450380_gb_AY052291.1_	266316_at	2.3
putative galactinol synthase ;supported by full-length cDNA: Ceres:124236.	263320_at	2.3
unknown protein ;supported by full-length cDNA: Ceres:9435.	262947_at	2.3
putative protein RING-H2 zinc finger protein ATL4 - Arabidopsis thaliana, EMBL:AF132014;supported by full-length cDNA: Ceres:3137.	252751_at	2.3
AP2 domain transcription factor-like protein	248389_at	2.3
NADH dehydrogenase subunit 3 Protein sequence is in conflict with the conceptual translation	244920_s_at	2.3
70kD heat shock protein ;supported by full-length cDNA: Ceres:98979.	265675_at	2.2
hypothetical protein	265238_s_at	2.2
hypothetical protein	263510_s_at	2.2
ethylene-responsive element binding factor, putative similar to ethylene-responsive element binding factor GI:8809573 from [Nicotiana sylvestris];su	261470_at	2.2
heat shock transcription factor HSF1, putative similar to GB:S52641 from [Arabidopsis thaliana] (Plant Mol. Biol. 26, 353-362 (1994)); supported by	258139_at	2.2
putative protein similar to unknown protein (pir||T05226);supported by full-length cDNA: Ceres:96.	249174_at	2.2
hypothetical protein	257318_at	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	259879_at	2.1
unknown protein very similar to unknown protein GB:AAC39468 from [Arabidopsis thaliana]; supported by cDNA: gi_14335087_gb_AY037223.1_	258402_at	2.1
hypothetical protein	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
TINY-like transcription factor Contains similarity to transcription factor (TINY) isolog T02O04.22 gb|2062174 from A. thaliana BAC gb|AC001645;sup	264202_at	2
hypothetical protein	263503_s_at	2
unknown protein ;supported by full-length cDNA: Ceres:35218.	256522_at	2

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	254667_at	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_	249923_at	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
putative protein various predicted proteins, Arabidopsis thaliana	250493_at	1.9
potassium-dependent sodium-calcium exchanger - like protein cone sodium-calcium potassium exchanger (NCKX), Homo sapiens, EMBL:AF17798	250053_at	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
cytochrome c biogenesis orf452	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	255926_at	1.8
DRE CRT-binding protein DREB1C involved in low-temperature-responsive gene expression00; supported by cDNA: gi_3738227_dbj_AB007789.1_	254075_at	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	257022_at	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
putative beta-1,3-glucanase	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
hypothetical protein	266013_s_at	1.6
hypothetical protein	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 ;supported by full-length cDNA: Ceres:41730.	254721_at	1.6
putative protein hypothetical protein YPL065w yeast, PIR2:S60925	254422_at	1.6
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_AF325	246506_at	1.6
luminal binding protein ; supported by cDNA: gi_1303694_dbj_D84414.1_ATHBIPA	245956_s_at	1.6
dormancy-associated protein, putative similar to dormancy-associated protein GI:2995990 from [Arabidopsis thaliana]; supported by cDNA: gi_1433	245668_at	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
trehalose-6-phosphate phosphatase - like protein trehalose-6-phosphate phosphatase (AtTPPA), PID:g2944178	254321_at	1.5
Expressed protein ; supported by full-length cDNA: Ceres: 28506.	254190_at	1.5
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	251563_at	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
unknown protein	267518_at	1.4
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	264653_at	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)); s	263035_at	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	257053_at	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
putaive DNA-binding protein DNA-binding protein WRKY3 - Petroselinum crispum, PIR2:S72445;supported by full-length cDNA: Ceres:11953.	253535_at	1.4
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

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 c	261564_at	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	259984_at	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	257822_at	1.3
unknown protein similar to At14a protein GB:AAD26355 GI:4589123 [Arabidopsis thaliana]; supported by cDNA: gi_16226582_gb_AF428437.1_AF4	256603_at	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
copper amine oxidase like protein (fragment2) copper amine oxidase - Cicer arietinum,PID:e1335964	254833_s_at	1.3

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 cD	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
hypothetical protein	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	258805_at	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
mitochondrial inner membrane translocase component, putative similar to mitochondrial inner membrane translocase component Tim17a GI:437852	255941_at	1.2
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 embryo-specific protein 3, Arabidopsis thaliana, PIR:T48490	247459_at	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 Mlo 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
unknown protein similar to EST gb|AA650671 and gb|T20610	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	264331_at	1.1
symbiosis-related protein, putative similar to symbiosis-related protein GI:2072022 from [Laccaria bicolor];supported by full-length cDNA: Ceres:191	264285_at	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	262948_at	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	262098_at	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	261957_at	1.1
type 2 peroxiredoxin, putative similar to type 2 peroxiredoxin GI:4928472 from [Brassica rapa subsp. pekinensis];supported by full-length cDNA: Cer	261919_at	1.1
chloroplast drought-induced stress protein, putative similar to chloroplast drought-induced stress protein GI:2582821 from [Solanum tuberosum];sup	261751_at	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 cD	261315_at	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	250858_at	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];su	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: Cer	261896_at	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_	261293_at	1
unknown protein ; supported by cDNA: gi_15450466_gb_AY052334.1_	261209_at	1
flavonol 3-o-glucosyltransferase, putative similar to flavonol 3-o-glucosyltransferase GB:Q40287 from [Manihot esculenta]	261048_at	1
unknown protein ; supported by cDNA: gi_15028364_gb_AY045985.1_	261019_at	1
F-box protein family contains similarity to F-box protein FBX3 GI:6103643 from [Homo sapiens]	260949_at	1
RNA recognition motif-containing protein SEB-4 similar to RNA recognition motif-containing protein SEB-4 GI:8895698 from [Xenopus laevis];suppor	260806_at	1
putative protein kinase similar to protein kinase APK1A GB:Q06548 [Arabidopsis thaliana]; contains Pfam profile: PF00069 Eukaryotic protein kinase	260415_at	1
hypothetical protein predicted by genscan+; supported by cDNA: gi_14335049_gb_AY037204.1_	260310_at	1
hypothetical protein similar to putative protein GB:CAA18164 [Arabidopsis thaliana]; supported by cDNA: gi_13878144_gb_AF370335.1_AF370335	260243_at	1
unknown protein	260155_at	1
60S ribosomal protein L18A, putative similar to GI:3128228 from [Arabidopsis thaliana] (Nature 402 (6763), 761-768 (1999));supported by full-length	260026_at	1
hypothetical protein ;supported by full-length cDNA: Ceres:147838.	259976_at	1
unknown protein	259934_at	1
putative thioredoxin similar to protein disulfide isomerase precursor GB:P29828 [Medicago sativa]; Pfam HMM hit: Thioredoxins	259757_at	1
hypothetical protein contains similarity to myosin heavy chain cardiac muscle specific isoform 1 GI:7416982 from (Argopecten irradians); supported b	259659_at	1
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:18207.	259235_at	1
unknown protein ;supported by full-length cDNA: Ceres:102038.	259184_at	1
putative D-ribulose-5-phosphate 3-epimerase similar to D-ribulose-5-phosphate 3-epimerase GB:AAF01048 [Oryza sativa]; contains non-consensus	258999_at	1
E2, ubiquitin-conjugating enzyme 11 (UBC11) identical to gi:12643427, SP:P35134;supported by full-length cDNA: Ceres:21455.	258678_at	1
unknown protein ;supported by full-length cDNA: Ceres:35949.	258608_at	1
hypothetical protein similar to receptor protein kinases: GB:CAB43834, GB:S71277 [Arabidopsis thaliana]	258557_at	1
unknown protein	258364_at	1
unknown protein	258282_at	1
ethylene responsive element binding factor, putative similar to GB:BAA32420 from [Arabidopsis thaliana], contains Pfam profile: PF00847 P2 domai	257675_at	1
DNA-binding protein, putative similar to GB:AAF32491 from [Triticum aestivum] (Mol. Cell. Biol. 19 (12), 8113-8122 (1999))	257291_at	1
prohibitin, putative similar to prohibitin GB:AAC49691 from [Arabidopsis thaliana] (Plant Mol. Biol. (1997) 33 (4), 753-756);supported by full-length c	257149_at	1
unknown protein contains similarity to plastid protein GB:AAB80660 from [Arabidopsis thaliana], contains Pfam profile: PF00076 RNA recognition m	256805_at	1
unknown protein ; supported by cDNA: gi_14194136_gb_AF367274.1_AF367274	256343_at	1
unknown protein ; supported by cDNA: gi_13358195_gb_AF325003.2_AF325003	256114_at	1
hypothetical protein contains similarity to photoperiod sensitivity quantitative trait locus (Hd1) GI:11094203 from [Oryza sativa];supported by full-lengt	256060_at	1
unknown protein ;supported by full-length cDNA: Ceres:38751.	256017_at	1
putative SWI/SNF complex subunit SW13	255846_at	1
predicted OR23 protein of unknown function	255469_at	1
putative protein predicted protein W02G9.1 Caenorhabditis elegans cosmid W02G9, PID:g3165571; supported by cDNA: gi_15450340_gb_AY0522	254863_at	1
putative protein	254795_at	1
hypothetical protein ; supported by full-length cDNA: Ceres: 14794.	254626_at	1
Expressed protein ; supported by full-length cDNA: Ceres: 16643.	254388_at	1
hypothetical protein ;supported by full-length cDNA: Ceres:6848.	254356_at	1
water channel - like protein plasma membrane intrinsic protein 1c, Arabidopsis thaliana, PIR2:S44083;supported by full-length cDNA: Ceres:3982.	254239_at	1
HSP90-like protein HSP90 homolog - Catharanthus roseus, PIR2:S39558; supported by cDNA: gi_14532541_gb_AY039895.1_	254166_at	1
receptor kinase-like protein receptor-like protein kinase, RLK3 - Arabidopsis thaliana,PID:e1363211	254063_at	1
Expressed protein ; supported by full-length cDNA: Ceres: 9546.	254041_at	1

hypothetical protein	253796_at	1
SOF1 protein-like protein SOF1 (involved in rRNA processing) protein-yeast; supported by cDNA: gi_13937178_gb_AF372943.1_AF372943	253777_at	1
glycine-rich protein glycine-rich cell wall structural protein - garden petunia,Pir2:A26099	253619_at	1
ribosomal protein L11 homolog several ribosomal proteins L11;supported by full-length cDNA: Ceres:95636.	253138_at	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 hin1 protein, Nicotiana tabacum, PIR:T03265;supported by full-length cDNA: Ceres:1678.	251879_at	1
putative protein GTP-binding regulatory protein beta chain, Dictyostelium discoideum, PIR:A47370; supported by cDNA: gi_13430701_gb_AF36026	251888_at	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	251507_at	1
RING-H2 zinc finger protein ATL4 ; supported by cDNA: gi_4928398_gb_AF132014.1_AF132014	251412_at	1
putative protein HIRA interacting protein 4 (dnaJ-like) - Homo sapiens, EMBL:AJ001309;supported by full-length cDNA: Ceres:37292.	251182_at	1
putative protein Myb-related transcriptional activator mybSt1, Solanum tuberosum, EMBL:S74753	251132_at	1
putative protein various predicted proteins, Arabidopsis thaliana	250965_at	1
Expressed protein ; supported by full-length cDNA: Ceres: 12197.	250921_at	1
putative protein	250572_at	1
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
ribosomal protein L33 - like ribosomal protein L33, Rickettsia prowazekii, PIR:E71650	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
hypothetical protein	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 protein contains similarity to unknown protein (emb|CAB87908.1);supported by full-length cDNA: Ceres:152842.	249793_at	1
putative uridylate kinase similar to uridylate kinase GB:CAB13524 [Bacillus subtilis], GB:P74457 [Synechocystis PCC6803]; supported by cDNA: gi_	258885_at	0.9
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 contains a 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_12963360_gb_AF327524.1_AF327524	267405_at	0.9
putative WRKY-type DNA binding protein ; supported by cDNA: gi_15027912_gb_AY045813.1_	267246_at	0.9
unknown protein	267069_at	0.9
unknown protein	267017_at	0.9
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
unknown protein ; supported by cDNA: gi_15028290_gb_AY045948.1_	265481_at	0.9
pEARLI 4 protein Same as GB: L43081; supported by cDNA: gi_871781_gb_L43081.1_ATHPEARA	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	265041_at	0.9
ribosomal protein identical to ribosomal protein GI:806279 from [Arabidopsis thaliana]	265032_at	0.9
unknown protein ESTs gb|H37208,gb|H36853 come from this gene	264665_at	0.9
allyl alcohol dehydrogenase, putative similar to allyl alcohol dehydrogenase GI:9758497 from [Arabidopsis thaliana]; supported by cDNA: gi_143351	264637_at	0.9
unknown protein Similar to Glycine SRC2 (gb|AB000130). ESTs gb|H76869,gb|T21700,gb|ATTS5089 come from this gene; supported by cDNA: gi_	264655_at	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

hypothetical protein predicted by genemark.hmm	262897_at	0.9
unknown protein ;supported by full-length cDNA: Ceres:17521.	262801_at	0.9
alpha-xylosidase precursor identical to alpha-xylosidase precursor GB:AAD05539 GI:4163997 from [Arabidopsis thaliana]; supported by cDNA: gi_1	262230_at	0.9
AP2 domain containing protein, putative similar to AP2 domain containing protein GI:2281649 from [Arabidopsis thaliana];supported by full-length c	262197_at	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	262135_at	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	262061_at	0.9
gibberellin 3 beta-hydroxylase, putative similar to gibberellin 3 beta-hydroxylase GI:3982753 from [Arabidopsis thaliana]; supported by cDNA: gi_19	261768_at	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	261122_at	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	259225_at	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_AY0267	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-l	257151_at	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

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_AF	254707_at	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
fatty acid hydroxylase - like protein fatty acid hydroxylase Fah1p, Arabidopsis thaliana, PID:g2736147; supported by cDNA: gi_14994242_gb_AY04	254448_at	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 (sp|Q96252) ; 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

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 b	247933_at	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	247717_at	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
RAN1 small Ras-like GTP-binding nuclear protein (Ran-1) ;supported by full-length cDNA: Ceres:9480.	246153_s_at	0.9
putative protein BEM46 bem1/bud5 suppressor, Schizosaccharomyces pombe, bem1/bud5 suppressor, EMBL:SP29892;supported by full-length cD	246090_at	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:I46078	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
putative plasma membrane intrinsic protein ;supported by full-length cDNA: Ceres:36296.	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	266119_at	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
aquaporin (plasma membrane intrinsic protein 2C) water channel protein in plasma membrane;supported by full-length cDNA: Ceres:11998.	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

hypothetical protein	265195_at	0.8
putative presenilin similar to presenilin GB:AAD23630;supported by full-length cDNA: Ceres:43026.	264807_at	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 22723.	264441_at	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 39286.	264443_at	0.8
postsynaptic protein CRIPT, putative similar to postsynaptic protein CRIPT GI:3098551 from [Rattus norvegicus]; supported by full-length cDNA: Ce	264399_at	0.8
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_at	0.8
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

hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:157.	260804_at	0.8
serine carboxypeptidase precursor, putative similar to GB:AAD42963 from [Matricaria chamomilla]	260739_at	0.8
expressed protein ; supported by full-length cDNA: Ceres: 256275.	260708_at	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 105765.	260409_at	0.8
unknown protein ;supported by full-length cDNA: Ceres:96702.	260357_at	0.8
unknown protein similar to hypothetical proteins GB:AAD39276 [Arabidopsis thaliana], GB:CAB53491 [Oryza sativa];supported by full-length cDNA:	260227_at	0.8
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:38940.	260096_at	0.8
unknown protein	259945_at	0.8
unknown protein similar to GB:AAB81674 [Arabidopsis thaliana]	259763_at	0.8
unknown protein similar to GB:AAD41433;supported by full-length cDNA: Ceres:146543.	259706_at	0.8
unknown protein ; supported by cDNA: gi_15293080_gb_AY050974.1_	259666_at	0.8
hypothetical protein	259583_at	0.8
cathepsin B-like cysteine protease, putative similar to cathepsin B-like cysteine proteinase GI:609175 from [Nicotiana rustica]	259441_at	0.8
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_15810522_gb_AY056300.1_	259406_at	0.8
unknown protein ;supported by full-length cDNA: Ceres:5232.	259357_at	0.8
unknown protein ;supported by full-length cDNA: Ceres:22512.	259192_at	0.8
putative disease resistance protein similar to putative disease resistance protein GB:AAF01514 from clone F9F8	258894_at	0.8
putative ATPase (ISW2-like) similar to ISW2 (ATPase component of a two subunit chromatin remodeling complex) GB:6324879 [Saccharomyces ce	258904_at	0.8
DAG protein, putative similar to DAG PROTEIN GB:Q38732 from [Antirrhinum majus]	258526_at	0.8
unknown protein ;supported by full-length cDNA: Ceres:15303.	258394_at	0.8
DNA-binding protein contains AP2 domain, identical to AP2 domain containing protein RAP2.2 from GB:AAC49768 from [Arabidopsis thaliana];supp	258366_at	0.8
putative ethylene-inducible protein similar to ethylene-inducible protein GB:M88254 from [Hevea brasiliensis]; supported by cDNA: gi_4103951_gb_	258336_at	0.8
hypothetical protein similar to hypothetical protein GB:CAB36714 from [Arabidopsis thaliana], contains Pfam profile: PF01485 IBR domain	258230_s_at	0.8
indoleacetic acid (IAA)-inducible gene (IAA7) identical to (IAA7) gene GB:U18409 [Arabidopsis thaliana] (J. Mol. Biol. 251 (4), 533-549 (1995));supp	257769_at	0.8
unknown protein	257619_at	0.8
chaperonin, putative similar to CHAPERONIN CPN60-2, MITOCHONDRIAL PRECURSOR GB:Q05046 from [Cucurbita maxima];supported by full-l	257608_at	0.8
hypothetical protein contains Pfam profile: PF01535 domain of unknown function	257188_at	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 93242.	257193_at	0.8
lipid transfer protein, putative similar to GB:AAB47967 from [Hordeum vulgare], contains Pfam profile: PF00279 Plant lipid transfer protein family; su	257066_at	0.8
mitochondrial chaperonin hsp60 identical to mitochondrial chaperonin hsp60 GB:Z11547 [Arabidopsis thaliana] (Plant Mol. Biol. 18 (5), 873-885 (19	256905_at	0.8
hypothetical protein contains similarity to RNA polymerase transcriptional regulation mediator GB:AAC26869 from [Homo sapiens]	256812_at	0.8
cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450; supported by cDNA: gi_15292830_gb_AY050849.1_	256589_at	0.8
unknown protein	256530_at	0.8
Eukaryotic translation initiation factor 5, putative Eukaryotic translation initiation factor 5 [Zea mays] GI:4160402; supported by cDNA: gi_15810338_	256502_at	0.8
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:12509.	256442_at	0.8
26S proteasome regulatory subunit S12, putative nearly identical to 26S proteasome regulatory subunit S12 (MOV34) SP:O24412 [Arabidopsis thal	256249_at	0.8
hypothetical protein contains similarity to receptor protein kinase-like protein GI:10177178 from [Arabidopsis thaliana]	256030_at	0.8
unknown protein ; supported by cDNA: gi_16648676_gb_AY058114.1_	255960_at	0.8
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_13877978_gb_AF370252.1_AF370252	255939_at	0.8
predicted protein of unknown function ; supported by cDNA: gi_15809916_gb_AY054226.1_	255710_at	0.8
Shaggy related protein kinase tetha ; supported by cDNA: gi_17063157_gb_AY062099.1_	255635_at	0.8
putative protein	255651_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	255379_at	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
disease resistance protein RPP13-like protein disease resistance protein RPP8 - Arabidopsis thaliana, EMBL:AF089710; supported by cDNA: gi_14	252485_at	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
palmitoyl-protein thioesterase precursor - like palmitoyl-protein thioesterase precursor, Mus musculus, EMBL:AF071025; supported by full-length cD	251408_at	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

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	247718_at	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 30313.	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_AY0	246831_at	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	246171_at	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
putative protein phosphatase 2C	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:	262957_s_at	0.7
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_15146253_gb_AY049268.1_	262952_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 inosine-5-monophosphate dehydrogenase strong similarity to gb|L34684 inosine monophosphate dehydrogenase (IMPDH) from Arabidopsi	262754_at	0.7
unknown protein similar to gb|AJ224359 surfeit locus protein 5 (surf5b) from Homo sapiens;supported by full-length cDNA: Ceres:143886.	262714_s_at	0.7
unknown protein ESTs gb|H37295 and gb|R64895 come from this gene;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	262601_at	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	262574_at	0.7
unknown protein EST gb|T21171 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	262495_at	0.7
ribosomal protein S9, putative similar to ribosomal protein S9 GI:5456946 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 25038	262172_at	0.7
unknown protein ; supported by cDNA: gi_15294195_gb_AF410289.1_AF410289	262175_at	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	0.7
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	261767_s_at	0.7
small nuclear ribonucleoprotein, putative similar to small nuclear ribonucleoprotein GI:600749 from [Homo sapiens]; supported by full-length cDNA:	261725_at	0.7
protein kinase, putative identical to bHLH protein GB:CAA67885 GI:1465368 from [Arabidopsis thaliana]; supported by cDNA: gi_14335047_gb_AY	261713_at	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	261581_at	0.7
endoplasmic reticulum-type calcium-transporting ATPase 4 identical to GB:AAD29957 from [Arabidopsis thaliana] (Plant Physiol. 120 (1999) In pres	261433_s_at	0.7
unknown protein ;supported by full-length cDNA: Ceres:727.	261336_at	0.7
developmentally regulated GTP-binding protein identical to GB:AAB67830 from (Arabidopsis thaliana) (Plant Mol. Biol. 39 (1), 75-82 (1999)); suppor	261036_at	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	260350_at	0.7
E2, ubiquitin-conjugating enzyme, putative similar to putative protein GB:CAB43411 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:58	260180_at	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 protea	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	259982_at	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	259983_at	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	259363_at	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_	259312_at	0.7
O-acetylserine (thiol) lyase identical to O-acetylserine (thiol) lyase GB:BAA21628 [Arabidopsis thaliana]; supported by cDNA: gi_2281779_dbj_AB00	259172_at	0.7
unknown protein similar to hin1 GB:CAA68848 [Nicotiana tabacum]; supported by cDNA: gi_9502173_gb_AF264698.1_AF264698	259071_at	0.7
putative ubiquinol-cytochrome C reductase complex ubiquinone-binding protein (QP-C) similar to ubiquinol-cytochrome C reductase complex ubiquin	258772_at	0.7
low temperature and salt responsive protein LTI6A identical to low temperature and salt responsive protein LTI6A GB:AAC97512 from [Arabidopsis t	258735_at	0.7
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	258412_at	0.7
unknown protein ;supported by full-length cDNA: Ceres:112601.	258432_at	0.7
hypothetical protein	258262_at	0.7
hypothetical protein similar to putative transposase of transposable element Ac GB:CAA25635 [Zea mays]	258246_s_at	0.7
putative GTP pyrophosphokinase similar to GTP PYROPHOSPHOKINASE GB:O87331 from [Corynebacterium glutamicum]; supported by cDNA: gi_	258207_at	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
cytochrome P450, putative similar to cytochrome P450 GB:O65784 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 262802.	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	257052_at	0.7
dem-like protein similar to dem GB:CAA73973 from [Lycopersicon esculentum] (Plant Cell (1998) 10, 1-12)	257029_at	0.7
unknown protein	256375_at	0.7
GTPase, putative contains Pfam profile: PF01926 GTPase of unknown function	256274_at	0.7
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	255176_s_at	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	253672_at	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 2.7.7.6) II largest chain	253133_at	0.7
peroxidase - like protein peroxidase, Arabidopsis thaliana, gb:X98314	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	252927_at	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	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.	251883_at	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 putative proteins - different species; supported by cDNA: gi_14517419_gb_AY039545.1_	251187_at	0.7
putative protein	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.	250935_at	0.7
putative protein ; supported by full-length cDNA: Ceres: 270908.	250923_at	0.7
putative protein ; supported by cDNA: gi_2160689_gb_U73526.1_ATU73526	250900_at	0.7
helicase-like transcription factor-like protein	250807_at	0.7
putative protein similar to unknown protein (pir||T02514);supported by full-length cDNA: Ceres:117347.	250777_at	0.7
putative protein contains similarity to RNA-binding protein;supported by full-length cDNA: Ceres:36764.	250721_at	0.7
diadenosine 5,5-P1,P4-tetraphosphate hydrolase-like protein ; supported by cDNA: gi_13937174_gb_AF372941.1_AF372941	250705_at	0.7
calnexin homolog	250625_at	0.7
putative protein 110K5.11, unknown protein, Sorghum bicolor, EMBL:AF124045; supported by cDNA: gi_13605727_gb_AF361845.1_AF361845	250409_at	0.7
putative protein predicted protein, Arabidopsis thaliana	250145_at	0.7
putative protein predicted proteins, Arabidopsis thaliana	250155_at	0.7
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	246489_at	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	245938_at	0.7
GTL1 - like protein GTL1, Arabidopsis thaliana, EMBL:ATAJ3215; supported by cDNA: gi_14423451_gb_AF386963.1_AF386963	245861_at	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	245781_at	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	259978_at	0.6

hypothetical protein predicted by genemark;supported by full-length cDNA: Ceres:123678.	257969_at	0.6
hypothetical protein	254502_at	0.6
transporter -like protein N system amino acids transporter NAT-1, Mus musculus, EMBL:AF159856	249535_at	0.6
putative protein large number of predicted zinc finger proteins, Arabidopsis thaliana, Homo sapiens and others	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 transcrip	X-r2-Ec-bioC-	0.6
Arabidopsis thaliana /REF=U84969 /DEF=ubiquitin (UBQ11) gene, complete cds /LEN=1140 (_5, _M, _3 represent transcript regions 5 prime, Middl	X-Athal-Ubq_5	0.6
putative leucine-rich repeat disease resistance protein	267596_s_at	0.6
hypothetical protein predicted by genefinder and genscan;supported by full-length cDNA: Ceres:23742.	267553_s_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:35578.	267504_at	0.6
unknown protein ; supported by full-length cDNA: Ceres: 9990.	267510_at	0.6
unknown protein	267524_at	0.6
30S ribosomal protein S5 ; supported by full-length cDNA: Ceres: 38063.	267435_at	0.6
unknown protein ; supported by cDNA: gi_13899086_gb_AF370538.1_AF370538	267379_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:9398.	267364_at	0.6
unknown protein	267323_at	0.6
Expressed protein ; supported by full-length cDNA: Ceres: 114879.	267309_at	0.6
diacylglycerol O-acyltransferase ; supported by cDNA: gi_15450799_gb_AY054480.1_	267280_at	0.6
hypothetical protein predicted by genefinder	267199_at	0.6
ERD15 protein identical to GB D30719; supported by full-length cDNA: Ceres: 31388.	267104_at	0.6
unknown protein	267116_at	0.6
unknown protein	267072_at	0.6
unknown protein	267018_at	0.6
putative pyruvate dehydrogenase E1 beta subunit ;supported by full-length cDNA: Ceres:38439.	266904_at	0.6
hypothetical protein predicted by genscan	266916_at	0.6
remorin identical to GB:M25268, a non-specific DNA binding protein; may be involved in intercellular communication; supported by cDNA: gi_15028	266897_at	0.6
40S ribosomal protein S15A	266684_at	0.6
putative CCCH-type zinc finger protein ;supported by full-length cDNA: Ceres:101255.	266695_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:26655.	266657_at	0.6
putative thiamin biosynthesis protein	266673_at	0.6
putative zinc-finger protein (B-box zinc finger domain)	266514_at	0.6
putative protein kinase contains a protein kinase domain profile (PDOC00100)	266428_at	0.6
unknown protein	266285_at	0.6
putative aquaporin (water channel protein) ; supported by cDNA: gi_15010777_gb_AY045690.1_	266172_at	0.6
putative trehalose-6-phosphate synthase	266072_at	0.6
hypothetical protein predicted by genefinder; supported by cDNA: gi_13877832_gb_AF370179.1_AF370179	266001_at	0.6
unknown protein ; supported by cDNA: gi_14334541_gb_AY035175.1_	265739_at	0.6
putative alanine acetyl transferase ;supported by full-length cDNA: Ceres:21201.	265668_at	0.6
putative S1 self-incompatibility protein	265517_at	0.6
hypothetical protein contains Pfam profile: PF01363 FYVE zinc finger; supported by full-length cDNA: Ceres: 15739.	265035_at	0.6
unknown protein Location of EST gb|AA395277 gb|T44807;supported by full-length cDNA: Ceres:36286.	264894_at	0.6
putative RING zinc finger protein ; supported by cDNA: gi_3790572_gb_AF078824.1_AF078824	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

uracil phosphoribosyltransferase, putative similar to uracil phosphoribosyltransferase 1 GB:AAD28199 GI:4704662 from [Arabidopsis thaliana]	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	264529_at	0.6
unknown protein similar to ESTs gb|T42386, gb|H36247, gb|N38423, gb|T21830, and gb|AA585725; supported by cDNA: gi_14423427_gb_AF3869	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|N963	264446_at	0.6
unknown protein similar to salt-inducible protein (gi|375717); similar to ESTs gb|R30192 and gb|AA651017	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	264405_at	0.6
hypothetical protein predicted by genscan	264171_at	0.6
hypothetical protein contains similarity to lipid transfer protein GI:498038 from (Senecio odorus)	264146_at	0.6
putative GTP cyclohydrolase	264045_at	0.6
putative protein phosphatase	263862_at	0.6
unknown protein	263829_at	0.6
putative ferritin	263831_at	0.6
cysteine proteinase similar to cysteine proteinase RD19A (thiol protease) GI:435618, SP:P43296 from [Arabidopsis thaliana];supported by full-lengt	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 ge	263116_s_at	0.6
putative bZIP transcription factor contains a bZIP transcription factor basic domain signature (PDOC00036); supported by cDNA: gi_14335073_gb_	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
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_13605620_gb_AF361636.1_AF361636	262965_at	0.6
unknown protein ESTs gb|H37032, gb|R6425, gb|Z34651, gb|N37268, gb|AA713172 and gb|Z34241 come from this gene;supported by full-length c	262600_at	0.6
unknown protein ESTs gb|N96028, gb|F14286, gb|T20680, gb|F14443, gb|AA657300 and gb|N65244 come from this gene; supported by cDNA: gi_	262505_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:33047.	262399_at	0.6
Expressed protein ; supported by full-length cDNA: Ceres: 10252.	262338_at	0.6
E2, ubiquitin-conjugating enzyme, putative similar to ubiquitin-conjugating enzyme GB:P35135 from [Lycopersicon esculentum]; supported by cDNA	262341_at	0.6
putative cyclin similar to cyclin GB:4502627 from [Homo sapiens];supported by full-length cDNA: Ceres:33877.	262296_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:3024.	262171_at	0.6
hypothetical protein predicted by genemark.hmm	262182_at	0.6
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:463.	262160_at	0.6
unknown protein contains similarity to peroxin-2 GI:6103008 from [Pichia pastoris];supported by full-length cDNA: Ceres:96370.	262114_at	0.6
splicing factor Prp8, putative similar to splicing factor Prp8 GI:3661610 from [Homo sapiens]	262068_at	0.6
unknown protein	262014_at	0.6
ribosomal protein L7, putative similar to ribosomal protein L7 GB:AAA03081 GI:307388 from [Homo sapiens]	261911_at	0.6
ethylene responsive element binding factor 3 (AtERF3) identical to GB:O80339 GI:7531109 from [Arabidopsis thaliana]; supported by cDNA: gi_343	261874_at	0.6
unknown protein ; supported by cDNA: gi_12083327_gb_AF332460.1_AF332460	261793_at	0.6
unknown protein ; supported by full-length cDNA: Ceres: 20257.	261723_at	0.6
hypothetical protein predicted by genemark.hmm	261597_at	0.6

hypothetical protein predicted by genemark.hmm	261500_at	0.6
unknown protein contains similarity to DNA dependent reverse transcriptase GI:2920563 from [Spraguea lophii]	261426_at	0.6
unknown protein contains similarity to set protein GI:338038 from [Homo sapiens];supported by full-length cDNA: Ceres:27467.	261406_at	0.6
unknown protein similar to 50S ribosomal protein L32; supported by full-length cDNA: Ceres: 10780.	261268_at	0.6
v-SNARE protein AtVTI1b, putative similar to GB:AAF24062 from [Arabidopsis thaliana]; supported by cDNA: gi_6690275_gb_AF114751.1_AF1147	261276_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:3807.	261154_at	0.6
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	261084_at	0.6
unknown protein contains similarity to transaldolase GB:P30148 from [Escherichia coli];supported by full-length cDNA: Ceres:7590.	260967_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.	260830_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:114093.	260793_at	0.6
unknown protein similar to hypothetical protein GI:7770340 from (Arabidopsis thaliana);supported by full-length cDNA: Ceres:114920.	260766_at	0.6
hypothetical protein predicted by genemark.hmm	260715_at	0.6
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:40884.	260682_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:1402.	260671_at	0.6
unknown protein similar to putative cytoskeletal protein GI:1732517 from [Arabidopsis thaliana]; supported by cDNA: gi_1732516_gb_U62745.1_ATU	260638_at	0.6
putative small nuclear ribonucleoprotein polypeptide F	260564_at	0.6
hypothetical protein predicted by genefinder	260418_s_at	0.6
unknown protein	260375_at	0.6
putative flavonol sulfotransferase similar to flavonol 4 -sulfotransferase GB:P52837 from [Flaveria chloraefolia];supported by full-length cDNA: Ceres	260387_at	0.6
unknown protein contains two Kelch motifs; supported by full-length cDNA: Ceres: 32885.	260287_at	0.6
gibberellin regulatory protein, putative similar to GB:CAA75492 from [Arabidopsis thaliana]; supported by cDNA: gi_15777856_gb_AY048749.1_	260141_at	0.6
putative DnaJ protein similar to dnaJ-like protein GB:CAA72705 [Arabidopsis thaliana]; Pfam HMM hit:DnaJ, prokaryotic heat shock protein	259876_at	0.6
auxin-induced protein, putative similar to SP:P33083 from [Glycine max];supported by full-length cDNA: Ceres:147801.	259787_at	0.6
unknown protein	259497_at	0.6
unknown protein supported by full-length cDNA: Ceres:29750.	259378_at	0.6
hypothetical protein C-term portion similar to unknown protein GB:AAC09350 [Homo sapiens]	259336_at	0.6
hypothetical protein predicted using genefinder;supported by full-length cDNA: Ceres:20442.	259340_at	0.6
unknown protein similar to hypothetical protein GB:AAC23643 [Arabidopsis thaliana]	259232_at	0.6
unknown protein ; supported by full-length cDNA: Ceres: 29837.	259236_at	0.6
Expressed protein ; supported by full-length cDNA: Ceres: 20097.	259214_at	0.6
hypothetical protein predicted by genscan	259060_at	0.6
unknown protein	259068_at	0.6
unknown protein	258892_at	0.6
hypothetical protein similar to symbiosis related proteins: GB:AAB53650 [Laccaria bicolor], GB:P87068 [Laccaria bicolor];supported by full-length cD	258880_at	0.6
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:8992.	258792_at	0.6
hydroxyacylglutathione hydrolase cytoplasmic (glyoxalase II) (GLX II) identical to hydroxyacylglutathione hydrolase cytoplasmic (glyoxalase II) (GLX	258775_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:269248.	258609_at	0.6
putative tRNA pseudouridine synthase similar to tRNA pseudouridine synthase A GB:P07649 [Escherichia coli]	258538_at	0.6
unknown protein ; supported by cDNA: gi_13878146_gb_AF370336.1_AF370336	258518_at	0.6
importin alpha identical to GB:AAC27644 from [Arabidopsis thaliana] (Plant Cell (1996) 8(8), 1337-1352);supported by full-length cDNA: Ceres:9351	258531_at	0.6
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_15450370_gb_AY052286.1_	258501_at	0.6
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	257832_at	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	257655_at	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	257218_at	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	256430_at	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	255883_at	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
putative 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 ;supported by full-length cDNA: Ceres:11590.	253823_at	0.6
Expressed protein ; supported by full-length cDNA: Ceres: 31814.	253825_at	0.6
putative protein ;supported by full-length cDNA: Ceres:10077.	253814_at	0.6
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
hypothetical 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_	253284_at	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
transcription 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

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

putative protein seven transmembrane domain orphan receptor, Mus musculus, EMBL:AF051098;supported by full-length cDNA: Ceres:96808.	246793_at	0.6
putative protein	246737_at	0.6
CRS2-like protein CRS2 - Zea mays, EMBL:AF225708	246492_at	0.6
arginine/serine-rich protein, putative similar to arginine/serine-rich protein GI:6601502 from [Arabidopsis thaliana]; supported by cDNA: gi_1502795	246324_at	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
gunknown protein contains non-consensus TG donor splice site at exon 1	245227_s_at	0.6
unknown protein	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-depend	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
J04423 E coli bioD gene dethiobiotin synthetase (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)	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	X-r2-Ec-bioD-	0.5
Arabidopsis thaliana /REF=U84969 /DEF=ubiquitin (UBQ11) gene, complete cds /LEN=1140 (_5, _M, _3 represent transcript regions 5 prime, Midd	K-Athal-Ubq_3	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

putative nonspecific lipid-transfer protein ; supported by cDNA: gi_15146309_gb_AY049296.1_	266421_at	0.5
unknown protein	266366_at	0.5
putative RGA1, giberellin repsonse modulation protein identical to GB:Y11336, member of SCARECROW family; supported by cDNA: gi_15529229_	266331_at	0.5
putative beta-ketoacyl-CoA synthase	266319_s_at	0.5
hypothetical protein predicted by genscan	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	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 RlpF (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 cD	264435_at	0.5
hypothetical protein contains similarity to F-box protein Fbx7 GI:6164624 from [Homo sapiens]	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
putative putative 60S ribosomal protein L17 identical to GB:AAB80655; supported by full-length cDNA: Ceres: 4513.	263665_at	0.5
unknown protein	263638_at	0.5
putative fatty acid elongase ;supported by full-length cDNA: Ceres:115769.	263443_at	0.5

putative glyoxalase II	263243_at	0.5
Expressed protein ; supported by full-length cDNA: Ceres: 27081.	263182_at	0.5
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	263170_at	0.5
unknown protein EST gb|F14156 comes from this gene;supported by full-length cDNA: Ceres:16491.	262821_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
hypothetical protein ;supported by full-length cDNA: Ceres:2663.	262678_at	0.5
unknown protein	262618_at	0.5
hypothetical protein Similar to gi|4377403 Polypeptide Deformylase from Chlamydia pneumoniae genome gb|AE001687; supported by cDNA: gi_11	262573_at	0.5
unknown protein EST gb|AA586241 comes from this gene	262488_at	0.5
unknown protein ; supported by full-length cDNA: Ceres:37444.	262496_at	0.5
threonine synthase, putative similar to threonine synthase GI:4850369 from [Arabidopsis thaliana]	262380_at	0.5
Expressed protein ; supported by full-length cDNA: Ceres: 97474.	262340_at	0.5
Niemann-Pick C disease protein-like protein similar to Niemann-Pick C disease protein GB:AAB63982 GI:2276463 from [Homo sapiens]	262264_at	0.5
unknown protein contains similarity to 1-aminocyclopropane-1-carboxylate deaminases	262247_at	0.5
DNA binding protein, putative similar to GB:BAA23142 GI:2580438 from [Oryza sativa]; supported by cDNA: gi_15912302_gb_AY056429.1_	262028_at	0.5
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:1981.	261938_at	0.5
J8-like protein similar to DnaJ homologue J8 GB:AAC72399 GI:3851670 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:4150.	261901_at	0.5
unknown protein ; supported by full-length cDNA: Ceres: 42087.	261902_at	0.5
unknown protein contains similarity to autocrine motility factor receptor GI:5931955 from [Homo sapiens]	261904_at	0.5
pirin-like protein similar to pirin GB:AAF22236 GI:6651245 from [Lycopersicon esculentum]	261876_at	0.5
thioredoxin h, putative similar to thioredoxin h GI:4928460 from [Hevea brasiliensis];supported by full-length cDNA: Ceres:2054.	261821_at	0.5
unknown protein ;supported by full-length cDNA: Ceres:113571.	261822_at	0.5
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 cockayne syndrome complementation group A protein GB:U28413 GI:975301 from (Homo sapiens)	261644_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	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	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)); sup	261211_at	0.5
unknown protein ;supported by full-length cDNA: Ceres:33426.	261076_at	0.5
unknown protein identical to SP:O50061 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: 19263.	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 full-length cDNA: Ceres: 6907.	260650_at	0.5
putative MYB family transcription factor similar to GB:AAD33584 from [Arabidopsis thaliana] (Plant Mol. Biol. 40 (4), 579-590 (1999)); supported by	260652_at	0.5
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	260588_at	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-leng	260388_at	0.5
receptor protein kinase, putative similar to receptor protein kinase GI:1389566 from (Arabidopsis thaliana); supported by cDNA: gi_4204848_gb_U5	260345_at	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	260258_at	0.5
GAST1-like protein similar to GAST1 protein precursor GB:P27057 [Lycopersicon esculentum] (induced by gibberellins, inhibited by ABA Plant J 199	260221_at	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	259705_at	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 GlsA (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 cD	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
hypothetical protein predicted by genemark.hmm	256493_at	0.5
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:10873.	256452_at	0.5
hypothetical protein predicted by genscan+; supported by cDNA: gi_14334761_gb_AY035054.1_	256426_at	0.5
unknown protein ; supported by full-length cDNA: Ceres: 38207.	256353_at	0.5
unknown protein ; supported by cDNA: gi_15450991_gb_AY054576.1_	256267_at	0.5
unknown protein	256041_at	0.5
unknown protein ; supported by cDNA: gi_15146333_gb_AY049308.1_	256034_at	0.5
hypothetical protein predicted by genscan+; supported by full-length cDNA: Ceres: 12511.	256016_at	0.5
putative PTR2 family peptide transporter	255877_at	0.5
40S ribosomal protein S26	255819_s_at	0.5
putative PRP19-like spliceosomal protein WD-40 repeat protein	255830_at	0.5
p68 RNA helicase, putative similar to p68 RNA helicase (Schizosaccharomyces pombe) GI:173419	255749_at	0.5
scarecrow-like 6 (SCL6)	255698_at	0.5
Expressed protein ; supported by full-length cDNA: Ceres: 11036.	255659_at	0.5
putative acetyltransferase similar to Digitalis lanata lanatoside 15 -O-acetyltransferase, GenBank accession number AJ011567	255607_at	0.5
putative ribosomal protein L19 similar to L19 from several species; supported by cDNA: gi_14423511_gb_AF386993.1_AF386993	255520_at	0.5
putative fibrillin ; supported by full-length cDNA: Ceres: 1461.	255364_s_at	0.5
coded for by A. thaliana cDNA T41604	255288_at	0.5
ferredoxin--NADP+ reductase - like protein ferredoxin--NADP+ reductase, Pisum sativum, PIR:T06773;supported by full-length cDNA: Ceres:33486.	255230_at	0.5
hypothetical protein	255185_at	0.5
putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:17600.	254372_at	0.5
putative protein NADH oxidoreductase complex I subunit- like protein, Caenorhabditis elegans, AF143152	254378_at	0.5
symbiosis-related like protein symbiosis-related protein, Laccaria bicolor,PATX:G2072023;supported by full-length cDNA: Ceres:14759.	254346_at	0.5
putative ribosomal protein S10 40S ribosomal protein S10 - Lumbricus rubellus, PID:e1329701; supported by cDNA: gi_14334535_gb_AY035172.1	254049_at	0.5
putative protein RING zinc finger protein, Gallus gallus	253958_at	0.5
ubiquitin-like protein ubiquitin-like protein - Arabidopsis thaliana (thale cress), PID:e259962; supported by full-length cDNA: Ceres: 29414.	253952_at	0.5
putative RING zinc finger protein Arabidopsis thaliana RMA1 mRNA, PID:d1029538	253865_at	0.5
putative protein heat shock protein 101 - Triticum aestivum,PID:g4558484	253614_at	0.5
small nuclear ribonucleoprotein homolog small nuclear ribonucleoprotein E - Homo sapiens,PIR2:A32127;supported by full-length cDNA: Ceres:382	253607_at	0.5
putative protein	253574_at	0.5
kinase binding protein - like Skb1 protein homolog, Homo sapiens, PIR2:T03842	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_	252975_s_at	0.5
Phospholipase like protein Arabidopsis thaliana pEARLI 4 mRNA, PID:g871782	252976_s_at	0.5
putative protein	252918_at	0.5
hypothetical protein	252612_at	0.5

B12D-like protein B12D protein - Hordeum vulgare,PIR2:S60284	252348_at	0.5
hypothetical protein	252362_at	0.5
MTN3-like protein MtN3 gene product - Medicago truncatula,PID:e1169583; supported by cDNA: gi_13605687_gb_AF361825.1_AF361825	252327_at	0.5
putative protein predicted protein, Arabidopsis thaliana	252250_at	0.5
cyclin D3-like protein Nicotiana tabacum NtcycD3-1 - Nicotiana tabacum, EMBL:AB015222;supported by full-length cDNA: Ceres:36056.	252189_at	0.5
putative protein predicted protein, Arabidopsis thaliana	252204_at	0.5
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:I38861;supported by full-length cDNA: Ce	251184_at	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:	250863_at	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_	250439_at	0.5
membrane translocase - like protein inner mitochondrial membrane translocase Tim17b, Homo sapiens, EMBL:AF034790;supported by full-length c	250333_at	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

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 number**	**log$_2$ fold increase**
late embryogenesis abundant protein LEA like ; supported by cDNA: gi_15293004_gb_AY050936.1_	250648_at	8.6
senescence-associated protein (SAG29) ;supported by full-length cDNA: Ceres:38843.	245982_at	7.8
unknown 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	262128_at	5.9
putative sucrose synthetase similar to several plant sugar synthetases similar to P. sativum second sugar synthetase, GenBank accession number	255521_at	5.9
nonspecific lipid-transfer protein precursor - like nonspecific lipid-transfer protein precursor, Brassica napus, EMBL:AF101038;supported by full-leng	247718_at	5.9
Myb-related transcription factor, putative similar to GB:AAF66727 from [Petunia x hybrida] (Plant Cell 11 (8), 1433-1444 (1999)); supported by cDN	260140_at	5.8
hypothetical protein similar to Anthocyanin 5-aromatic acyltransferase GB:BAA74428	265091_s_at	5.6
nonspecific lipid-transfer protein precursor - like nonspecific lipid-transfer protein precursor, Brassica napus, EMBL:AF101038;supported by full-leng	247717_at	5.6
homeodomain transcription factor (ATHB-7) identical to SP:P46897; supported by cDNA: gi_15027938_gb_AY045826.1_	266327_at	5.3
putative metal-binding protein highly similar to GB:AAD09511; supported by cDNA: gi_15450582_gb_AY052659.1_	264729_at	5.3
putative protein predicted protein	254823_at	5.3
1,4-alpha-glucan branching enzyme protein soform SBE2.2 precursor	250906_at	5.3
putative protein helix-loop-helix protein DEL -Antirrhinum majus,PIR2:A42220	255056_at	5.2
dihydroflavonol 4-reductase	249215_at	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	256603_at	5
putative protein putative protein - Arabidopsis thaliana, EMBL:AL078465.1;supported by full-length cDNA: Ceres:121300.	252319_at	5
putative protein similar to unknown protein (emb|CAB62340.1);supported by full-length cDNA: Ceres:103870.	248505_at	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_	266098_at	4.9
putative AVR9 elicitor response protein similar to GB:AAC69935; supported by cDNA: gi_14488077_gb_AF389287.1_AF389287	264583_at	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
putative protein predicted protein, Arabidopsis thaliana	253344_at	4.9
flavanone 3-hydroxylase (FH3) ;supported by full-length cDNA: Ceres:36653.	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]	265216_at	4.8
putative ADP-glucose pyrophosphorylase large subunit	263544_at	4.8
putative protein strictosidine synthase (EC 4.3.3.2) - Rauvolfia mannii (fragment); supported by cDNA: gi_13877836_gb_AF370181.1_AF370181	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	249351_at	4.8
unknown protein ; supported by cDNA: gi_14532707_gb_AY039978.1_	267080_at	4.7
putative indole-3-acetate beta-glucosyltransferase similar to indole-3-acetate beta-glucosyltransferase GB:AAD32293	263230_at	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	256245_at	4.6
gibberellin-regulated protein GASA3 precursor ; supported by cDNA: gi_15450402_gb_AY052302.1_	255048_at	4.6
anthocyanidin synthase - like protein putative leucoanthocyanidin dioxygenase, Arabidopsis thaliana, PID:g1575699	254283_s_at	4.6
low-temperature-induced protein 78 (sp|Q06738) ; supported by cDNA: gi_348691_gb_L22567.1_ATHCOR78A	248337_at	4.6
hypothetical protein similar to hypothetical protein GI:4539438 from [Arabidopsis thaliana]	261233_at	4.6
SRG1-like protein Strong homology to SRG1 protein, a new member of the Fe(II)/ascorbate oxidase superfamily, Similar to SRG1 protein [Arabidop	262482_at	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	262347_at	4.4
putative protein hypothetical protein At2g37870 - Arabidopsis thaliana, EMBL:AC007661;supported by full-length cDNA: Ceres:5920.	251928_at	4.4
flavonol 3-O-glucosyltransferase-like	248185_at	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]	256924_at	4.3
delta-1-pyrroline-5-carboxylate synthetase	251775_s_at	4.3
DNA excision repair cross-complementing protein; similar to human Xeroderma pigmentosum group B DNA repair protein (gb|AAC49987.1) ; suppo	249307_s_at	4.3
bHLH transcription factor	248867_at	4.3
unknown protein ; supported by cDNA: gi_15451043_gb_AY054602.1_	248223_at	4.3
unknown protein	262940_at	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	258559_at	4.2
unknown protein identical to LEA-like protein GB:CAA10352 from [Arabidopsis thaliana]	258347_at	4.2
putative protein similar to unknown protein (gb|AAC73025.1); supported by cDNA: gi_14532515_gb_AY039882.1_	250825_at	4.2
low-temperature-induced 65 kD protein (sp|Q04980)	248352_at	4.2
RuBisCO subunit binding-protein beta subunit precursor; chaperonin, 60 kDa	248021_at	4.2
receptor-like protein kinase	247197_at	4.2
putative protein CDPK substrate protein 1, Mesembryanthemum crystallinum, EMBL:AF219972;supported by full-length cDNA: Ceres:13378.	246724_at	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.	261077_at	4.1
B regulatory subunit of protein phosphatase 2A, putative similar to B regulatory subunit of protein phosphatase 2A GI:2160694 from (Arabidopsis t	259359_at	4.1
hypothetical protein	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	249403_at	4.1
hypothetical protein predicted by genefinder	257436_s_at	4.1
oxidase, putative similar to oxidase GB:AAA32870 GI:166876 from (Arabidopsis thaliana);supported by full-length cDNA: Ceres:152458.	260706_at	4
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	250083_at	4
protein phosphatase 2C - like ABA induced protein phosphatase 2C, Fagus sylvatica, EMBL:FSY277743; supported by cDNA: gi_15809791_gb_AY	247723_at	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: gi_13358195_gb_AF325003.2_AF325003	256114_at	3.9
dehydrin Xero2 ; supported by cDNA: gi_15809983_gb_AY054260.1_	252102_at	3.9
Expressed protein ; supported by cDNA: gi_14517386_gb_AY039528.1_	245283_at	3.9

nodulin-like protein	267044_at	3.8
unknown protein ;supported by full-length cDNA: Ceres:100283.	265907_at	3.8
putative RNA helicase A 3 end of this gene is located at the beginning of F10A8, GB:AAD14515	265731_at	3.8
glucose-6-phosphate/phosphate-translocator precursor, putative similar to glucose-6-phosphate/phosphate-translocator precursor GI:2997591 from	264400_at	3.8
methionine/cystathionine gamma lyase, putative similar to methionine gamma-lyase GB:CAA04124.1 GI:2330885 from [Trichomonas vaginalis]; sup	261957_at	3.8
branched-chain alpha keto-acid dehydrogenase, putative similar to branched-chain alpha keto-acid dehydrogenase GB:AAC69851 GI:3822223 from	260900_s_at	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	257817_at	3.8
unknown protein contains Pfam profile: PF00430 ATP synthase B/B CF(0); supported by cDNA: gi_15810372_gb_AY056225.1_	257732_at	3.8
putative protein predicted protein, Arabidopsis thaliana	254289_at	3.8
putative major latex protein major latex protein type 1 - Arabidopsis thaliana, EMBL:X91960; supported by cDNA: gi_13605713_gb_AF361838.1_AF	254234_at	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	265119_at	3.7
mutM homologue-1 identical to mutM homologue-1 GI:3550982 from [Arabidopsis thaliana]; supported by cDNA: gi_3820619_gb_AF099970.1_AF0	262129_at	3.7
unknown protein	259322_at	3.7
putative N2,N2-dimethylguanosine tRNA methyltransferase similar to N2,N2-dimethylguanosine tRNA methyltransferase GB:CAA20101 GI:6901242	259075_at	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
hypothetical protein predicted by genscan+	267397_at	3.6
hypothetical protein similar to membrane associated salt inducible protein isolog; similar to F21B7.18 and F21B7.21	264816_at	3.6
putative 3-methylcrotonyl-CoA carboxylase ESTs gb|H35836, gb|AA651295 and gb|AA721862 come from this gene; supported by cDNA: gi_53370	263118_at	3.6
cinnamoyl CoA reductase, putative similar to cinnamoyl CoA reductase GB:AAF43141 GI:7239228 from [Populus tremuloides]; supported by full-len	261899_at	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	248936_at	3.6
receptor-like protein kinase precursor - like receptor-like protein kinase precursor, Madagascar periwinkle, PIR:T10060	247686_at	3.6
pectinacetylesterase precursor, putative similar to pectinacetylesterase precursor GI:1431629 from [Vigna radiata]	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
aldehyde dehydrogenase homolog, putative similar to aldehyde dehydrogenase homolog GI:913941 from [Brassica napus]; supported by cDNA: gi_	263157_at	3.5
Myb-related transcription factor mixta, putative similar to Myb-related transcription factor mixta GI:485866 from [Antirrhinum majus]	261431_at	3.5
hypothetical protein	259568_at	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	250558_at	3.5
hypothetical protein contains similarity to DNA polymerase III, epsilon subunit GI:8163241 from [Chlamydia muridarum]	245743_at	3.5
anthocyanin2, putative similar to anthocyanin2 (An2) GI:7673088 from [Petunia integrifolia]; supported by cDNA: gi_3941507_gb_AF062908.1_AF0	245628_at	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.	260357_at	3.4
hypothetical protein	257759_at	3.4
serine/threonine-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) (sp|P13114) ;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	246922_at	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_	266550_s_at	3.3
putative aldehyde dehydrogenase ; supported by cDNA: gi_14334931_gb_AY035139.1_	265188_at	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 thalia	258964_at	3.3
At14a-1 protein identical to At14a protein GB:AAD26355 GI:4589123 [Arabidopsis thaliana] [Gene 230 (1), 33-40 (1999)]	256601_s_at	3.3
hypothetical protein predicted by genemark.hmm	255929_at	3.3
hypothetical protein	255687_at	3.3
RNA helicase - like protein Cdc28p, Schizosaccharomyces pombe, PID:G1439562	254675_at	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	245775_at	3.3
water stress-induced protein, putative similar to water stress-induced protein GI:454879 from [Oryza sativa]; supported by cDNA: gi_15215761_gb_	245627_at	3.3
putative protein various hypothetical proteins from Arabidopsis thaliana	254917_at	3.3
beta-VPE nearly identical to beta-VPE GB:BAA09615 GI:1805364 [Arabidopsis thaliana]; supported by cDNA: gi_14194096_gb_AF367254.1_AF367	262644_at	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	249487_at	3.2
heat shock transcription factor-like protein	249117_at	3.2
putative serine carboxypeptidase I ;supported by full-length cDNA: Ceres:33165.	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_	256789_at	3.1
putative protein predicted proteins, Arabidopsis thaliana	252782_at	3.1
putative protein various predicted proeteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:6263.	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_	263811_at	3
putative aminotransferase similar to beta-alanine-pyruvate aminotransferase GB:BAA19549 [Rattus norvegicus], alanine-glyoxylate aminotransferas	258983_at	3

RNA-binding protein, putative contains Pfam profile: PF00806 Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain) (8 co	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	262619_at	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	245748_at	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	259957_at	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:CAB56770, GB:CAB56773 [Arabidopsis thaliana]	259971_at	2.6
protein phosphatase 2C (AtP2C-HA) identical to protein phosphatase 2C (AtP2C-HA) GB:AJ003119 [Arabidopsis thaliana] (Plant Mol. Biol. 38 (5), 8	259922_at	2.6
early light-induced protein identical to early light-induced protein GB:AAB88391 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:14	258321_at	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.	255787_at	2.6
putative protein membrane-associated salt-inducible protein, Nicotiana tabacum; supported by cDNA: gi_15810160_gb_AY056145.1_	254581_at	2.6
fatty acid elongase - like protein KCS1 fatty acid elongase 3-ketoacyl-CoA synthase 1, Arabidopsis thaliana, EMBL:AF053345	250891_at	2.6
3-keto-acyl-CoA thiolase 2 (gb|AAC17877.1) ; supported by cDNA: gi_3192892_gb_AF062590.1_AF062590	248625_at	2.6
putative protein KIAA0066, Homo sapiens, EMBL:HSORFKG1O	247828_at	2.6
peptidylprolyl isomerase (cyclophilin)-like ; supported by cDNA: gi_17063169_gb_AY062106.1_	246980_at	2.6
hypothetical protein predicted by genemark.hmm; supported by full-length cDNA: Ceres: 144447.	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
RGA-like protein putative member of the VHIID domain transcription factor family RGAL - Arabidopsis thaliana, EMBL:AJ224957	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	246076_at	2.6
4-alpha-glucanotransferase	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
unknown protein highly similar to T21L14.19; similar to GP|2191153|AF007269 and GP|2252859|AF013294	267644_s_at	2.4
ferredoxin-dependent glutamate synthase (GLU2)	266365_at	2.4
unknown protein ; supported by cDNA: gi_14517457_gb_AY039564.1_	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
potassium transporter, putative similar to potassium transporter GI:2654088 from [Arabidopsis thaliana]	264338_at	2.4
unknown protein	264156_at	2.4
aldehyde oxidase identical to GP:3172044:gnl:PID:d1029570:AB010080; supported by cDNA: gi_5672671_dbj_AB016622.1_AB016622	263570_at	2.4
bZIP transcription factor (POSF21) identical to GB:Q04088; supported by cDNA: gi_15982853_gb_AY057534.1_	263253_at	2.4
putative zinc-binding protein similar to zinc-binding protein (gi|3249068)	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	263158_at	2.4
hypothetical protein predicted by genemark.hmm	263127_at	2.4
unknown protein strong similarity to gb|Y09533 involved in starch metabolism from Solanum tuberosum and contains a PF|01326 Pyruvate phospha	262784_at	2.4
jacalin, putative similar to jacalin GI:289164 from [Artocarpus heterophyllus]	262357_at	2.4
unknown protein ; supported by cDNA: gi_13937194_gb_AF372951.1_AF372951	262164_at	2.4
unknown protein contains similarity to eukaryotic initiation factor 4B GI:6739515 from [Triticum aestivum]; supported by cDNA: gi_14335083_gb_AY0	261827_at	2.4
unknown protein ; supported by cDNA: gi_15450710_gb_AY052723.1_	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
unknown protein ; supported by full-length cDNA: Ceres: 20582.	259403_at	2.4
putative serine/threonine protein kinase similar to serine/threonine-specific kinase GB:S68589 [Arabidopsis thaliana]; Pfam HMM hits: putative serin	258982_at	2.4
putative protein phosphatase-2C similar to protein phosphatase-2C GB:AAC36699 from [Mesembryanthemum crystallinum]; supported by cDNA: gi_	258901_at	2.4
unknown protein similar to hypothetical protein GB:CAB43880; supported by cDNA: gi_15146307_gb_AY049295.1_	257056_at	2.4
subtilisin proteinase - like subtilisin-like proteinase ag12, Alnus glutinosa, PIR2:S52769; supported by cDNA: gi_16649028_gb_AY059884.1_	254377_at	2.4
putative protein cellulose synthase catalytic subunit, Arabidopsis thaliana, gb:AF027173;supported by full-length cDNA: Ceres:112955.	254189_at	2.4
putative protein hypothetical proteins	252525_at	2.4
putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:106702.	251896_at	2.4
putative protein predicted protein, Arabidopsis thaliana	251753_at	2.4
putative protein putative protein At2g46380 - Arabidopsis thaliana, EMBL:AC006526	251332_at	2.4
putative protein ;supported by full-length cDNA: Ceres:7731.	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
unknown protein	247340_at	2.4
ABC transporter protein 1-like ; supported by cDNA: gi_15912314_gb_AY056435.1_	247222_at	2.4
putative protein	246946_at	2.4
HSP100/ClpB, putative similar to HSP100/ClpB GI:9651530 [Phaseolus lunatus]	246554_at	2.4
alpha-galactosidase - like protein alpha-galactosidase, coffee, PIR:T50781;supported by full-length cDNA: Ceres:156141.	246036_at	2.4
Dr4(protease inhibitor) identical to Dr4 GI:469114 from [Arabidopsis thaliana]; supported by cDNA: gi_13877842_gb_AF370184.1_AF370184	245736_at	2.4
ATPase I subunit	245025_at	2.4
ribosomal protein S8	244981_at	2.4
unknown protein	256329_at	2.3
hypothetical protein predicted by genscan	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	265200_s_at	2.3
lactoylglutathione lyase-like protein Similar to protein gb|Z74962 from Brassica oleracea which is similar to bacterial YRN1 and HEAHIO proteins. E	264372_at	2.3
hypothetical protein contains similarity to lipid transfer protein GI:498038 from (Senecio odorus)	264146_at	2.3
glucosyltransferase, putative similar to beta-(1-3)-glucosyl transferase GB:AAC62210 GI:3687658 from [Bradyrhizobium japonicum	263031_at	2.3
unknown protein	262860_at	2.3
ferrodoxin NADP oxidoreductase, putative similar to ferrodoxin NADP oxidoreductase GB:X99419 GI:1480346 from [Pisum sativum]supported by ful	261806_at	2.3
Ca2+-dependent membrane-binding protein annexin idenctical to GB:AAD34236 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:2	261285_at	2.3
unknown protein	260585_at	2.3
unknown protein	259718_at	2.3
hypothetical protein	259570_at	2.3
unknown protein	258264_at	2.3
leucine-rich repeat disease resistance protein, putative, 5 partial similar to NL0C GB:AAD13302 from [Lycopersicon esculentum] (Mol. Plant Microb	257592_at	2.3
isoamylase-like protein probable isoamylase (EC 3.2.1.68) su1 - Zea mays,PIR2:T01321	255070_at	2.3
UDP rhamnose--anthocyanidin-3-glucoside rhamnosyltransferase - like protein UDP rhamnose--anthocyanidin-3-glucoside rhamnosyltransferase, P	253879_s_at	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
putative protein	250956_at	2.3
diacylglycerol kinase (ATDGK1) ; supported by cDNA: gi_1374771_dbj_D63787.1_ATHATDGK1	250556_at	2.3
glucose-6-phosphate dehydrogenase	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	248487_at	2.3
auxin response factor - like protein auxin response factor 9, Arabidopsis thaliana, PIR:T08917	247508_at	2.3
putative protein myosin heavy chain, chicken, PIR:S24348;supported by full-length cDNA: Ceres:147806.	246796_at	2.3
ATPase-like protein	246282_at	2.3
hypothetical protein	246232_at	2.3
PSII 47KDa protein	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
G-box binding bZIP transcription factor identical to PIR:S20885; supported by cDNA: gi_600862_gb_U17891.1_ATU17891	266555_at	2.2
hypothetical protein predicted by genscan	265902_at	2.2
hypothetical protein predicted by genscan; supported by cDNA: gi_15028050_gb_AY045882.1_	265596_at	2.2
myrosinase-binding protein homolog, putative almost identical to myrosinase-binding protein homolog GI:2997767 from [Arabidopsis thaliana]; supp	265058_s_at	2.2
unknown protein ;supported by full-length cDNA: Ceres:13385.	264985_at	2.2
step II splicing factor, putative similar to step II splicing factor SLU7 GB:AAD13774 GI:4249705 (Homo sapiens)	264633_at	2.2
hypothetical protein predicted by genscan and genefinder; supported by cDNA: gi_15450730_gb_AY053407.1_	263384_at	2.2
dTDP-glucose 4,6-dehydratase, putative similar to dTDP-glucose 4,6-dehydratase GI:5921157 from [Streptomyces avermitilis]; supported by cDNA:	263134_at	2.2
hypthetical protein contains similarity to spliceosome associated protein SAP 145 GI:1173904 from [Homo sapiens]	261872_s_at	2.2
hypothetical protein predicted by genemark.hmm	261113_at	2.2
hypothetical protein predicted by genemark.hmm	261065_at	2.2
putative O-linked GlcNAc transferase similar to O-linked GlcNAc transferase GB:AAB63465 [Caenorhabditis elegans]	258575_at	2.2
ethylene-responsive transcriptional coactivator, putative similar to GB:AAD46402 from [Lycopersicon esculentum] (Plant J. 18 (6), 589-600 (1999));s	258133_at	2.2
putative sucrose cleavage protein similar to GB:S51376 from [Solanum tuberosum]supported by full-length cDNA: Ceres:40179.	257970_at	2.2
dynamin-like protein similar to phragmoplastin GB:CAB56619 from [Nicotiana tabacum]	257045_at	2.2
hypothetical protein	256384_at	2.2
26S proteasome regulatory subunit S12, putative nearly identical to 26S proteasome regulatory subunit S12 (MOV34) SP:O24412 [Arabidopsis thal	256249_at	2.2
putative protein	254807_at	2.2
putative protein Mei2-like protein, Arabidopsis thaliana, gb:D86122	254679_at	2.2
putative protein hypothetical protein, Synechocystis sp., PIR2:S76701	254642_at	2.2
putative protein Arabidopsis thaliana nap gene,PID:e1234813;supported by full-length cDNA: Ceres:38344.	253872_at	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	253263_at	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.	249626_at	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
putative protein contains similarity to protein kinase	247918_at	2.2
ABC transporter homolog PnATH - like PnATHABC transporter homolog, Populus nigra, EMBL:AB041505	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
gibberellin 2- oxidase identical to gibberellin 2- oxidase GI:4678366 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:156482.	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	267489_s_at	2.1
putative thiamin biosynthesis protein	266673_at	2.1
unknown protein predicted by genscan; supported by cDNA: gi_16930416_gb_AF419562.1_AF419562	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
starch branching enzyme II	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	263696_at	2.1
transcription factor ZAP1 identical to GP:1064883:X92976	263626_at	2.1
putative tetracycline transporter protein	263574_at	2.1
purple acid phosphatase precursor identical to SP:Q38924	263083_at	2.1
unknown protein ;supported by full-length cDNA: Ceres:35675.	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
scarecrow-like 1 identical to scarecrow-like 1 GB:AAF21043 GI:6644390 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:109490.	260878_at	2.1
Expressed protein ; supported by full-length cDNA: Ceres: 13270.	260670_at	2.1
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
putative cytochrome P450 similar to cytochrome P450 71B2 GB:O65788 [Arabidopsis thaliana]	258277_at	2.1
putative MAP kinase similar to GB:AAD52659 from [Oryza sativa]	258119_at	2.1
HAPp48,5 protein identical to HAPp48,5 GB:Y09562 [Arabidopsis thaliana]	256902_s_at	2.1
hypothetical protein	255621_at	2.1
putative fibrillin ; supported by full-length cDNA: Ceres: 1461.	255364_s_at	2.1
putative beta-glucosidase beta-glucosidase BGQ60 precursor - barley, PIR2:A57512; supported by cDNA: gi_15982821_gb_AY057518.1_	253841_at	2.1
putative protein	253407_at	2.1
putative protein F35D11.3, Caenorhabditis elegans, PATX:G868225	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
putative protein putative DNA binding protein - Arabidopsis thaliana, TREMBL:ATAC2339_3; supported by cDNA: gi_16649060_gb_AY059900.1_	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	250693_at	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
putative protein contains similarity to G-box binding factor;supported by full-length cDNA: Ceres:25211.	249074_at	2.1
ATP-dependent Clp protease ATP-binding subunit (ClpC1) almost identical to ClpC GI:2921158 from [Arabidopsis thaliana]	248480_at	2.1
unknown protein ;supported by full-length cDNA: Ceres:534.	248218_at	2.1
protein phosphatase 2C ABI2 (PP2C) (sp|O04719)	247957_at	2.1
Fdr1 Cen - like protein Fdr1, Oryza sativa, EMBL:AF159883	247511_at	2.1
putative protein strong similarity to unknown protein (emb|CAB62118.1)	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	246800_at	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
hypothetical protein	251522_at	2
putative salt-inducible protein	257395_at	2
unknown protein	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	267319_at	2
hypothetical protein predicted by genefinder; supported by cDNA: gi_16323181_gb_AY057695.1_	267248_at	2
hypothetical protein predicted by genscan	266405_at	2
putative mitochondrial translation elongation factor G	266127_s_at	2
putative SEC1 family transport protein similar to SLY1 proteins and vesicle transport proteins; supported by cDNA: gi_15215769_gb_AY050414.1_	265822_at	2
similar to flavin-binding monooxygenase-like protein (Z71258); similar to ESTs gb|R30018 and gb|H36886 similar to flavin-containing monooxygenas	265122_at	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	264360_at	2
putative protein phosphatase 2C ;supported by full-length cDNA: Ceres:22316.	263711_at	2
unknown protein	263545_at	2
putative myo-inositol 1-phosphate synthase ; supported by cDNA: gi_15450746_gb_AY053415.1_	263433_at	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 c	262600_at	2

26S proteasome ATPase subunit, putative similar to 26S proteasome ATPase subunit GI:1395190 from [Spinacia oleracea];supported by full-length	262227_s_at	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
putative two-component phosphorelay mediator similar to two-component phosphorelay mediators (ATHP1-3) GB:BAA37110, GB:BAA37111, GB:B	259329_at	2
putative disease resistance protein similar to putative disease resistance protein GB:AAF01514 from clone F9F8	258893_at	2
putative disease resistance protein similar to putative disease resistance protein GB:AAF01514 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	258226_at	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	258139_at	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_	255305_at	2
putative microfibril-associated protein	255093_s_at	2
putative protein anthocyanin rhamnosyltransferase -Petunia x hybrida, PID:g454253	255032_at	2
putative major latex protein major latex protein type 1 - Arabidopsis thaliana, EMBL:X91960;supported by full-length cDNA: Ceres:108949.	254225_at	2
ABC transporter - like protein ABC transporter-7, Mus musculus, gb:U43892; supported by cDNA: gi_9964118_gb_AF287698.1_AF287698	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_	250402_at	2
putative protein similar to unknown protein (gb|AAF00631.1);supported by full-length cDNA: Ceres:10299.	250028_at	2
prolylcarboxypeptidase-like protein ;supported by full-length cDNA: Ceres:122449.	249860_at	2
tryptophan synthase beta chain	249515_at	2
glutathione transferase-like ;supported by full-length cDNA: Ceres:37349.	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
unknown protein	245787_at	2
proline-rich protein, putative similar to proline-rich protein GI:3242079 from [Capsicum annuum]; supported by cDNA: gi_14334847_gb_AY035097.1	245749_at	2
pyruvate,orthophosphate dikinase	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 (R	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	267168_at	1.9
Expressed protein ; supported by full-length cDNA: Ceres: 34622.	266537_at	1.9
putative tropinone reductase	266278_at	1.9
putative peptide/amino acid transporter	266108_at	1.9
NADC homolog identical to GP|1216074|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	263751_at	1.9
unknown protein ;supported by full-length cDNA: Ceres:31655.	263517_at	1.9
cold-regulated protein cor15a precursor ; supported by cDNA: gi_14532457_gb_AY039853.1_	263497_at	1.9
ent-kaurene synthase, putative similar to ent-kaurene synthase GI:3056725 from [Arabidopsis thaliana]; supported by cDNA: gi_3056724_gb_AF03	262891_at	1.9
unknown protein Location of est 278F3T7 (gb|AA650690)	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_	261922_at	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	260590_at	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	260162_at	1.9
putative ATPase contains Pfam profile: PF00004 ATPases associated with various cellular activities (AAA)	260089_at	1.9
feebly-like protein similar to feebly protein GB:S70648 [Lycopersicon esculentum] (tomato knockout developed into small fragile plants)	260060_at	1.9
hypothetical protein predicted by genscan+	259899_at	1.9
unknown protein ; supported by cDNA: gi_16930412_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	259226_at	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	258357_at	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
protein kinase, putative similar to serine/threonine protein kinase GB:NP_032667 from [Mus musculus]	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	258167_at	1.9
putative cytochrome P450 similar to GB:Q05047 from [Catharanthus roseus]; supported by cDNA: gi_15292786_gb_AY050827.1_	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	258047_at	1.9
unknown protein	257612_at	1.9

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	256892_at	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_AF386993.1_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
copper amine oxidase like protein (fragment2) copper amine oxidase - Cicer arietinum,PID:e1335964	254833_s_at	1.9
3-hydroxyisobutyryl-coenzyme A hydrolase - like protein 3-hydroxyisobutyryl-coenzyme A hydrolase, Homo sapiens, U66669;supported by full-lengt	254776_at	1.9
putative disease resistance protein Hcr9-9A, Lycopersicon pimpinellifolium, gb:AJ002236	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
putative protein F56F10.1, Caenorhabditis elegans, PATX:G1688051	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 nexin-like protein	250714_at	1.9
putative protein similar to unknown protein (gb|AAF19552.1)	250303_at	1.9
transporter-like protein ;supported by full-length cDNA: Ceres:27439.	250252_at	1.9
kinase - like protein RING3 protein, Homo sapiens, EMBL:X96670; supported by cDNA: gi_16604680_gb_AY059785.1_	250191_at	1.9
putative protein predicted protein, Arabidopsis thaliana	250050_at	1.9
putative protein similar to unknown protein (gb|AAC80581.1)	249908_at	1.9
acetyl-CoA synthetase-like protein	249869_at	1.9
putative protein contains similarity to integral membrane protein	249759_at	1.9
putative protein	249622_at	1.9
disease resistance protein-like non-consensus TT donor splice site at exon 1	249320_at	1.9
N-carbamyl-L-amino acid amidohydrolase-like protein	249103_at	1.9
putative protein strong similarity to unknown protein (pir||E71441); supported by cDNA: gi_16974604_gb_AY060580.1_	248766_at	1.9
putative protein contains similarity to unknown protein (gb|AAF49898.1); supported by cDNA: gi_15724227_gb_AF412054.1_AF412054	248549_at	1.9
putative protein contains similarity to nuclear movement protein nudC;supported by full-length cDNA: Ceres:38105.	248258_at	1.9
O-methyltransferase ;supported by full-length cDNA: Ceres:33790.	248200_at	1.9
fimbrin	248082_at	1.9
pyrophosphate-dependent phosphofructo-1-kinase-like protein ; supported by cDNA: gi_14532861_gb_AY040055.1_	247983_at	1.9
cysteine proteinase AALP identical to AALP protein GI:7230640 from [Arabidopsis thaliana]; similar to barley aleurain;supported by full-length cDNA:	247627_at	1.9
succinate dehydrogenase flavoprotein alpha subunit (emb|CAA05025.1) ; supported by cDNA: gi_15010745_gb_AY045674.1_	247060_at	1.9
natural resistance-associated macrophage protein ; supported by cDNA: 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 ferredoxin--NADP+ 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 GP|2623296|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	265109_s_at	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	264851_at	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
putative protein RIO1 protein, Saccharomyces cerevisiae, PIR:S61006;supported by full-length cDNA: Ceres:42141.	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	263221_at	1.8
putative protein kinase Strong similarity to gb|X71057 protein kinase from Nicotiana tabacum and contains PF|00069 eukaryotic protein kinase doma	263222_at	1.8
mak16-like protein-related similar to MAK16 PROTEIN GB:P10962 GI:127112 from [Saccharomyces cerevisiae] (Proc. Natl. Acad. Sci. U.S.A. 85 (	263039_at	1.8
unknown protein EST gb|H77143 comes from this gene; supported by cDNA: gi_15293206_gb_AY051037.1_	262570_at	1.8
hypothetical protein similar to hypothetical protein GB:AAF24581 GI:6692116 from [Arabidopsis thaliana]; supported by cDNA: gi_15724299_gb_AF	262345_at	1.8
ATP-dependent Clp protease proteolytic subunit (ClpR1) identical to nClpP5 GB:BAA82069 GI:5360595 from [Arabidopsis thaliana];supported by full	261634_at	1.8
putative GTP-binding protein similar to NGP-1 GB:Q13823 from (Homo sapiens)	261314_at	1.8
transcription factor TINY, putative similar to transcription factor TINY GB:CAA64359 GI:1246403 from [Arabidopsis thaliana];supported by full-length	261059_at	1.8
hypothetical protein similar to Pto kinase interactor 1 GB:AAC61805 GI:3668069 from [Lycopersicon esculentum]	260924_at	1.8
putative heme oxygenase similar to heme oxygenase GB:AAD22107 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:101223.	260396_at	1.8
putative heat shock protein similar to GB:CAB03279 from [Caenorhabditis elegans]	260251_at	1.8
putative protein kinase Pfam HMM hit: Eukaryotic protein kinase domain	260036_at	1.8
unknown protein ;supported by full-length cDNA: Ceres:13102.	260005_at	1.8

unknown 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
hypothetical protein similar to GB:CAB55886 [Homo sapiens], GB:BAA09774 [Homo sapiens], GB:CAA87778 [Caenorhabditis elegans]	259759_at	1.8
unknown protein	259644_at	1.8
protein kinase, putative similar to GI:7573596 from [Populus nigra]	259670_at	1.8
myosin-like protein contains Pfam profile: PF00658 Poly-adenylate binding protein, unique domain.; supported by cDNA: gi_15081708_gb_AY0482	259609_at	1.8
putative lectin contains Pfam profile: PF01419 jacalin-like lectin domain; similar to jasmonate inducible protein GB:Y11483 (Brassica napus), myrosi	259381_s_at	1.8
unknown protein ;supported by full-length cDNA: Ceres:18355.	259342_at	1.8
unknown protein similar to unknown protein GB:AAC32238 (Arabidopsis thaliana)	259169_at	1.8
reversibly glycosylated polypeptide-1 identical to reversibly glycosylated polypeptide-1 (implicated in cell wall biosynthesis) GB:AAC50000 [Arabidop	259077_s_at	1.8
hypothetical protein predicted by genscan	258696_at	1.8
hypothetical protein predicted by genemark.hmm	258525_at	1.8
putative protein disulfide isomerase similar to protein disulfide isomerase GB:AAD55566 from [Volvox carteri f. nagariensis]	258329_at	1.8
hypothetical protein contains Pfam profile: PF01055 Glycosyl hydrolases family 31; supported by cDNA: gi_16648902_gb_AY059821.1_	258109_at	1.8
unknown protein contains an RNase_PH domain;supported by full-length cDNA: Ceres:104182.	257857_s_at	1.8
rotamase FKBP (ROF1) identical to rotamase FKBP (ROF1) GB:U49453 [Arabidopsis thaliana] (Mol. Gen. Genet. 252 (5), 510-517 (1996)); support	257822_at	1.8
DNA-binding protein, putative similar to GB:AAF32491 from [Triticum aestivum] (Mol. Cell. Biol. 19 (12), 8113-8122 (1999))	257291_at	1.8
monooxygenase, putatve contains Pfam profile: PF01360 Monooxygenase	257240_at	1.8
purple acid phosphatase, putative similar to purple acid phosphatase GB:CAA06921 [Ipomoea batatas]	257087_at	1.8
hypothetical protein predicted by genscan+	257073_at	1.8
hypothetical protein predicted by genscan+	257044_at	1.8
beta-amylase, putative similar to beta-amylase GB:CAB58423 [Arabidopsis thaliana]; supported by cDNA: gi_14194172_gb_AF367293.1_AF36729	256861_at	1.8
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_16930516_gb_AF419612.1_AF419612	256858_at	1.8
Myb-family transcription factor, putative contains Pfam profile: PF00249: Myb-like DNA-binding domain	256198_at	1.8
lipid transfer protein, putative similar to lipid transfer protein GI:9279661 from [Arabidopsis thaliana]; supported by cDNA: gi_15028044_gb_AY0458	256145_at	1.8
transcription factor identical to transcription factor GI:304113 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:33016.	255953_at	1.8
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:37923.	255900_at	1.8
putative protein	255527_at	1.8
putative WD-repeat protein similar to L. erythrorhizon LEC14B, GenBank accession number Q40153	255468_at	1.8
predicted protein of unknown function	255418_at	1.8
putative methyltransferase	254994_at	1.8
CLV1 receptor kinase like protein CLAVATA1 receptor kinase, Arabidopsis th., PATX:G2160756	254515_at	1.8
putative protein tripeptidyl-peptidase II, Homo sapiens, Pir:S54376	254433_at	1.8
receptor-like serine/threonine protein kinase ARK3	254416_at	1.8
PRH26 protein ;supported by full-length cDNA: Ceres:36866.	254343_at	1.8
Expressed protein ; supported by full-length cDNA: Ceres: 20948.	254278_at	1.8
pumilio-like protein abdominal segment formation protein pumilio - fruitfly, PIR2:A46221; supported by cDNA: gi_13430771_gb_AF360298.1_AF360	254045_at	1.8
protein kinase - like protein ADK1 protein kinase, Arabidopsis thaliana, PIR2:A55661	253764_s_at	1.8
AIM1 protein ; supported by cDNA: gi_16648890_gb_AY059815.1_	253759_at	1.8
signal recognition particle receptor-like protein signal recognition particle receptor - Homo sapiens,PIR2:A29440	253625_at	1.8
putative protein probable transcription regulator protein - Sorghum bicolor,PIR2:T03446;supported by full-length cDNA: Ceres:34151.	252323_at	1.8
dehydrin-like protein dehydrin Xero2 - Arabiodopsis thaliana, EMBL:U19536	252137_at	1.8
putative protein various predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:4829.	252023_at	1.8
pasticcino 1 ; supported by cDNA: gi_15810452_gb_AY056265.1_	251932_at	1.8
RING finger - like protein DNA-binding Mel-18 protein, Homo sapiens, PIR:JN0717supported by full-length cDNA: Ceres:20931.	251897_at	1.8
ABC transporter-like protein putative multi resistance protein mrp - Arabidopsis thaliana, EMBL:ATMRPPROT	251503_at	1.8
putative protein	250960_at	1.8
low density lipoprotein B-like protein	250112_at	1.8
unknown protein ; supported by cDNA: gi_15912298_gb_AY056427.1_	249886_at	1.8
ankyrin repeat protein EMB506 ; supported by cDNA: gi_5911311_gb_AF026167.1_AF026167	249404_at	1.8
disease resistance protein-like	248848_at	1.8
putative protein contains similarity to unknown protein (gb|AAF56975.1)	248458_at	1.8
heat shock protein (emb|CAA72514.1)	248043_s_at	1.8
unknown protein ;supported by full-length cDNA: Ceres:21044.	247990_at	1.8
beta-galactosidase (emb CAB64746.1)	247348_at	1.8
putative protein similar to unknown protein (sp|P55606); supported by cDNA: gi_14190422_gb_AF378889.1_AF378889	247077_at	1.8
putative protein protein At2g40060 - Arabidopsis thaliana, EMBL:AF002109;supported by full-length cDNA: Ceres:93427.	246305_at	1.8
putative protein	246247_at	1.8
aminopeptidase-like protein ; supported by cDNA: gi_13430673_gb_AF360249.1_AF360249	246219_at	1.8
TINY-like protein ; supported by cDNA: gi_16323158_gb_AY057683.1_	246222_at	1.8
polyubiquitin (UBQ4) identical to GI:17677	245989_s_at	1.8
hypothetical protein	245482_at	1.8
disease resistance RPP5 like protein	245451_at	1.8
putative protein	245427_at	1.8
ATPase alpha subunit	245024_at	1.8
ribosomal protein S11	244979_at	1.8
putative cytochrome P450	267567_at	1.7
cinnamate-4-hydroxylase molecular marker C4H (GB:U71080); supported by cDNA: gi_1773288_gb_U71081.1_ATU71081	267470_at	1.7
putative beta-1,3-glucanase	267335_s_at	1.7
similar to late embryogenesis abundant proteins ; supported by full-length cDNA: Ceres: 2450.	267212_at	1.7
putative cytochrome P450	266995_at	1.7
unknown protein	266757_at	1.7
putative arginine N-methyltransferase	266687_at	1.7
hexokinase (ATHXK2) ; supported by cDNA: gi_1899024_gb_U28215.1_ATU28215	266702_at	1.7
putative glutathione S-transferase ; supported by cDNA: gi_14423533_gb_AF387004.1_AF387004	266267_at	1.7
20S proteasome subunit (PAA2) identical to GB:AF043519; supported by cDNA: gi_15450622_gb_AY052679.1_	266036_s_at	1.7
unknown protein ;supported by full-length cDNA: Ceres:39669.	265388_s_at	1.7
putative MYB family transcription factor ; supported by cDNA: gi_1020156_gb_U26937.1_ATU26937	265359_at	1.7
putative RNA-binding protein ; supported by cDNA: gi_6650522_gb_AF101056.1_AF101056	265266_at	1.7
unknown protein	265273_at	1.7
hypothetical protein contains similarity to zinc finger protein rts2 GB:U16133 GI:563244 from [Saccharomyces cerevisiae]; supported by cDNA: gi_13	265079_at	1.7
putative protein kinase, ADK1 dual specificity kinase 1; Location of ESTs 184A2XP 3 , gb|AA651408 and est 184A2T7, gb|H37603. 99%+ identity w	265045_s_at	1.7
putative phosphoglucomutase similar to GB:AAD13031 and GB:AAC50049, location of ESTs gb|W43354, gb|N37499 and gb|N96251; supported by	264903_at	1.7
unknown protein location of EST gb|T46445	264776_at	1.7
hypothetical protein contains similarity to nuclear protein GI:1236985 from [Homo sapiens]; supported by cDNA: gi_14423425_gb_AF386950.1_AF3	264486_at	1.7
putative beta-galactosidase	264078_at	1.7
putative kinesin heavy chain ; supported by cDNA: gi_14532683_gb_AY039966.1_	263762_at	1.7
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:25127.	263589_at	1.7

ankyrin-like protein	263459_at	1.7
putative acetolactate synthase	263460_at	1.7
putative RING zinc finger protein	263424_at	1.7
unknown protein ;supported by full-length cDNA: Ceres:21223.	263110_at	1.7
NADP-isocitrate dehydrogenase, putative similar to NADP-isocitrate dehydrogenase GI:5764653 from [Citrus limon]; supported by cDNA: gi_127443	262962_at	1.7
hypothetical protein similar to hin1 GB:Y07563 GI:1619320 Nicotiana tabacum;supported by full-length cDNA: Ceres:21639.	262930_at	1.7
putative heat-shock protein strong similarity to gb|Z70314 heat-shock protein from Arabidopsis thaliana and is a member of the PF|00012 Hsp70 prot	262814_at	1.7
amine oxidase, putative similar to amine oxidase GB:AAD49420 GI:5733089 [Canavalia lineata]	262667_at	1.7
putative prenyl transferase (prephytoene pyrophosphatase dehydrogenase) Except for first 55 amino acids, 52% identical to Prenyl transferase [Cya	262526_at	1.7
transcription factor, putative similar to transcription factor GI:304113 from [Arabidopsis thaliana]; supported by cDNA: gi_16209662_gb_AY057596.1	262137_at	1.7
receptor-like kinase, putative similar to receptor-like kinase GI:1783311 from [Brassica oleracea]	261819_at	1.7
hypothetical protein similar to unknown protein GI:6539269 from [Arabidopsis thaliana]	261421_at	1.7
starch synthase, putative similar to starch synthase GI:21613 from [Solanum tuberosum];supported by full-length cDNA: Ceres:7714.	261191_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
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:19486.	260875_at	1.7
Ring3-like bromodomain protein similar to Ring3 GB:BAA25416 GI:3041763 from [Mus musculus], contains Pfam profile:PF00439 Bromodomain	260787_at	1.7
protein phosphatase 2C, putative similar to protein phosphatase 2C GI:3242077 from (Arabidopsis thaliana)	260712_at	1.7
hypothetical protein predicted by genemark.hmm	260647_at	1.7
glyoxalase I, putative similar to GB:Y13239 from [Brassica juncea] (Plant J. 17 (4), 385-395 (1999))	260619_at	1.7
storage protein, putative similar to GB:CAA53781 from [Dioscorea cayenensis] (Plant Mol. Biol. 28 (3), 369-380 (1995)); supported by cDNA: gi_158	260626_at	1.7
hypothetical protein contains Pfam profile: PF01965 ThiJ/PfpI family;supported by full-length cDNA: Ceres:101735.	260616_at	1.7
unknown protein contains a region similar to uridine kinase GB:AAF09747 from [Deinococcus radiodurans]	260372_at	1.7
putative lipase similar to monoglyceride lipase GB:NP_035974 from [Mus musculus];supported by full-length cDNA: Ceres:36954.	260153_at	1.7
ATP-dependent RNA helicase, putative similar to ATP-dependent RNA helicase [Schizosaccharomyces pombe] GI:218533; supported by cDNA: gi_	259597_at	1.7
hypothetical protein ; supported by cDNA: gi_12659317_gb_AF331066.1_AF331066	259512_at	1.7
putative ATPase (ISW2-like) similar to ISW2 (ATPase component of a two subunit chromatin remodeling complex) GB:6324879 [Saccharomyces ce	258904_at	1.7
putative 2,3-bisphosphoglycerate-independent phosphoglycerate mutase similar to 2,3-bisphosphoglycerate-independent phosphoglycerate mutase	258679_at	1.7
putative WD-repeat protein contains Pfam profile: PF00400 WD domain, G-beta repeat (7 copies)	258268_at	1.7
unknown protein similar to MRP-like ABC transporter GB:AAC49791 from [Arabidopsis thaliana]	258033_at	1.7
hypothetical protein predicted by genemark; supported by cDNA: gi_15450957_gb_AY054559.1_	258027_at	1.7
dihydrolipoamide dehydrogenase, putative similar to dihydrolipoamide dehydrogenase GB:CAA88451 [Synechocystis PCC6803] (Microbiology 143	257895_at	1.7
monodehydroascorbate reductase similar to cytosolic monodehydroascorbate reductase GB:BAA77214 [Oryza sativa]; supported by cDNA: gi_1453	257227_at	1.7
hypothetical protein	257181_at	1.7
ubiquitin-specific protease 14 (UBP14), putative similar to ubiquitin-specific protease 14 GI:11993473 [Arabidopsis thaliana]	257085_at	1.7
metalloprotease, putative similar to metalloprotease 1 GB:AAC67244 from [Homo sapiens]	257033_at	1.7
hypothetical protein predicted by genemark.hmm	256596_at	1.7
cytosolic IMP-GMP specific 5 -nucleotidase, putative similar to GI:2668557 from [Bos taurus]	256504_at	1.7
NADPH oxidoreductase, putative similar to GI:1708420 from [Arabidopsis thaliana] (J. Biol. Chem. 270 (44), 26224-26231 (1995));supported by full-	256454_at	1.7
DNA polymerase A family protein, putative contains Pfam profile: PF00476: DNA polymerase family A	256204_at	1.7
amino acid permease I identical to amino acid permease I GI:22641 from [Arabidopsis thaliana]; supported by cDNA: gi_404018_gb_L16240.1_ATH	256022_at	1.7
hypothetical protein	255723_at	1.7
putative chalcone synthase similar to plant chalcone and stilbene synthases;supported by full-length cDNA: Ceres:21877.	255703_at	1.7
polycomb group - like protein similar to A. thaliana homeotic protein curlyleaf, GenBank accession number Y10580; supported by cDNA: gi_4185506	255510_at	1.7
coded for by A. thaliana cDNA T75804 similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91)	255474_at	1.7
predicted protein of unknown function similar to P. falciparum O1 protein, GenBank accession number AF030694	255495_at	1.7
putative protein similar to plant nucleic acid-binding proteins;supported by full-length cDNA: Ceres:6568.	255496_at	1.7
putative protein several hypothetical proteins - Arabidopsis thaliana	254872_at	1.7
vacuolar sorting receptor-like protein BP-80 vacuolar sorting receptor, Pisum sativum, PATCHX:G1737222	254500_at	1.7
putative serine/threonine kinase MAP3K delta-1 protein kinase, Arabidopsis thaliana,PID:g2253010; supported by cDNA: gi_15810436_gb_AY05625	254269_at	1.7
FtsH protease, putative contains similarity to zinc dependent protease GI:7650138 from [Arabidopsis thaliana]	254181_at	1.7
serine/threonine kinase-like protein serine/threonine kinase - Sorghum bicolor,PID:e1184911; supported by cDNA: gi_14532685_gb_AY039967.1_	254167_at	1.7
putative protein pmt2 methyltransferase - Schizosaccharomyces pombe,PID:e1362538	254079_at	1.7
proton pump interactor non-consensus GA donor splice site at exon 5	253868_at	1.7
putative protein tetratricopeptide repeat protein - Homo sapiens,PID:g1688074;supported by full-length cDNA: Ceres:12573.	253633_at	1.7
cinnamyl alcohol dehydrogenase - like protein cinnamyl alcohol dehydrogenase, Populus deltoides, PATCHX:G288753; supported by cDNA: gi_143	253277_at	1.7
putative protein ; supported by cDNA: gi_13605658_gb_AF361810.1_AF361810	252856_at	1.7
glucosyltransferase-like protein UDP-glucose glucosyltransferase - Arabidopsis thaliana, EMBL:AB016819;supported by full-length cDNA: Ceres:12	252482_at	1.7
disease resistance protein RPP13-like protein disease resistance protein RPP8 - Arabidopsis thaliana, EMBL:AF089710; supported by cDNA: gi_14	252485_at	1.7
putative protein various predicted proteins, Arabidopsis thaliana	252392_s_at	1.7
MAP kinase ; supported by cDNA: gi_14194094_gb_AF367253.1_AF367253	252079_at	1.7
alpha-galactosidase-like protein alpha galactosidase - Phaseolus vulgaris, PIR:T10860	251729_at	1.7
putative protein strictosidine synthase (EC 4.3.3.2) - Rauvolfia mannii (fragment);supported by full-length cDNA: Ceres:98698.	251658_at	1.7
CaLB protein	251351_s_at	1.7
putative protein several hypothetical proteins - Arabidopsis thaliana	251211_s_at	1.7
neoxanthin cleavage enzyme nc1	251146_at	1.7
putative protein similar to unknown protein (sp|P36540)	250726_at	1.7
pyruvate kinase	250526_at	1.7
putative protein	250380_at	1.7
protein kinase MSK-3 - like protein kinase MSK-3, A.medicago, PIR:S37642	250141_at	1.7
putative protein contains similarity to unknown protein (emb|CAB89315.1); supported by cDNA: gi_15451067_gb_AY054614.1_	249863_at	1.7
putative protein DNA DAMAGE-RESPONSIVE PROTEIN 48, Saccharomyces cerevisiae, EMBL:SCDDR48A; supported by cDNA: gi_16604363_gb	249416_at	1.7
putative protein GTP-binding proteins - different species	249434_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 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_	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_	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
putative 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
PPR-repeat protein, putative contains multiple PPR domains: PF01535: PPR repeat	246313_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	245956_s_at	1.7
sucrose-phosphate synthase -like protein sucrose-phosphate synthase isoform 1, Citrus unshiu, PIR:S72648	245904_at	1.7
allergen like protein	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)	249086_at	1.6
putative protein various predicted proteins, Arabidopsis thaliana	246899_at	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	267423_at	1.6
Expressed protein ; supported by cDNA: gi_14334701_gb_AY035024.1_	266802_at	1.6
putative squamosa-promoter binding protein	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.	266170_at	1.6
putative calmodulin-binding protein ; supported by cDNA: gi_15983494_gb_AF424622.1_AF424622	266019_at	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 m	265108_s_at	1.6
unknown protein	264563_s_at	1.6
hypothetical protein predicted by genemark.hmm	264472_at	1.6
hypothetical protein Contains similarity to transcription initiation factor IIE, alpha subunit gb|X63468 from Homo sapiens; supported by cDNA: gi_158	264368_at	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 (RelA/SpoT homolog) identical to RSH3 (RelA/SpoT homolog) GI:7141308 from [Arabidopsis thaliana]; supported by cDNA: gi_7141307_gb_	263159_at	1.6
dynamin, putative similar to dynamin-1 SP:P21575 [Rattus norvegicus (Rat)];supported by full-length cDNA: Ceres:12880.	262837_at	1.6
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|0	262780_at	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); supporte	262378_at	1.6
hypothetical protein similar to putative disease resistance protein GB:CAB40943 GI:4586107 from [Arabidopsis thaliana]	262326_at	1.6
unknown protein identical to unknown protein GB:AAD55492 (Arabidopsis thaliana)	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	261309_at	1.6
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:98874.	261124_at	1.6
unknown protein	261112_at	1.6
homeodomain protein BELL1, putative similar to GB:AAB05099 from [Arabidopsis thaliana] (Cell 83 (5), 735-742 (1995));supported by full-length cD	261120_at	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]	260203_at	1.6
putative trehalose-6-phosphate synthase similar to trehalose-6-phosphate synthase GB:CAA69879 [Arabidopsis thaliana]; supported by cDNA: gi_1	260010_at	1.6
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	259705_at	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.	259186_at	1.6
digalactosyldiacylglycerol synthase identical to digalactosyldiacylglycerol synthase GB:AAD42378 [Arabidopsis thaliana]; supported by cDNA: gi_53	259070_at	1.6
putative MAP3K epsilon protein kinase similar to MAP3K epsilon protein kinase GB:CAA12272 [Arabidopsis thaliana], GB:CAB54520 [Brassica nap	258632_s_at	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	258286_at	1.6
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:116381.	257855_at	1.6
unknown protein	257084_at	1.6
Expressed protein ; supported by cDNA: gi_15215805_gb_AY050432.1_	257007_at	1.6
UDP-glucose dehydrogenase, putative UDP-glucose 6-dehydrogenase (UDPGDH) GB:Q96558 from [Glycine max];supported by full-length cDNA:	256745_at	1.6
Eukaryotic translation initiation factor 5, putative Eukaryotic translation initiation factor 5 [Zea mays] GI:4160402; supported by cDNA: gi_15810338_	256502_at	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]	256119_at	1.6
putative myb-related DNA-binding protein	255614_at	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	254305_at	1.6
nucleosome assembly protein I-like protein ; supported by cDNA: gi_15450807_gb_AY054484.1_	253996_at	1.6
pyrophosphate-dependent phosphofructo-1-kinase pyrophosphate-dependent phosphofructo-1-kinase, Prunus armeniaca, U93272; supported by c	253987_at	1.6
26S proteasome subunit 4-like protein Drosophila melanogaster 26S proteasome subunit 4 ATPase, PID:g1066065; supported by cDNA: gi_143346	253755_at	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	253237_at	1.6
MYB-like protein myb-related protein Y49, Arabidopsis thaliana, PIR:S58292	253219_at	1.6
dnaJ-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.	252424_at	1.6
putative protein KIAA0226 gene product - Homo sapiens,PID:d1013904; supported by cDNA: gi_14532611_gb_AY039930.1_	252353_at	1.6
peroxidase ;supported by full-length cDNA: Ceres:39678.	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	251780_s_at	1.6
PROBABLE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 8 ; supported by cDNA: gi_2789659_gb_AF040102.1_AF040102	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	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; supporte	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 - Metar	246976_s_at	1.6
protein phosphatase - like protein phosphatase-2C, Mesembryanthemum crystallinum, EMBL:AF075581;supported by full-length cDNA: Ceres:2334	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
putative tropinone reductase ;supported by full-length cDNA: Ceres:14555.	266292_at	1.5
putative membrane channel protein ;supported by full-length cDNA: Ceres:10159.	266225_at	1.5
putative retroelement pol polyprotein	266187_at	1.5
putative vacuolar protein sorting-associated protein ; supported by cDNA: gi_15081710_gb_AY048248.1_	266096_at	1.5
putative alpha-carboxyltransferase ; supported by cDNA: gi_6851090_gb_AF056969.1_AF056969	266099_at	1.5
unknown protein	265974_at	1.5
unknown protein	265900_at	1.5
unknown protein	265706_at	1.5
putative WRKY DNA-binding protein ; supported by cDNA: gi_13506736_gb_AF224701.1_AF224701	265718_at	1.5
putative chloroplast outer membrane protein	265412_at	1.5
putative RNA methyltransferase	265274_at	1.5
UDP-N-acetylglucosamine pyrophosphorylase-like protein similar to sperm associated antigen 2, GB:4507759 from [Homo sapiens], similar to ESTs	265103_at	1.5
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	1.5
putative 26S protease regulatory subunit 6A Similar to probable Mg-dependent ATPase (pir|S56671). ESTs gb|T46782,gb|AA04798 come from this	264657_at	1.5
putative glutathione S-transferase TSI-1 similar to glutathione S-transferase TSI-1 (gi|2190992); similar to ESTs gb|R29860, emb|Z29757, and emb|	264436_at	1.5
unknown protein ESTs gb|H36966, gb|R65511, gb|T42324 and gb|T20569 come from this gene	264362_at	1.5
unknown protein Contains similarity to gb|Z69902 from C. elegans	264321_at	1.5
hypothetical protein similar to hypothetical protein GI:7378617 from [Arabidopsis thaliana]	264310_at	1.5
unknown protein contains similarity to tryparedoxin GI:3851498 from [Crithidia fasciculata];supported by full-length cDNA: Ceres:34936.	264219_at	1.5
hypothetical protein predicted by genscan and genefinder;supported by full-length cDNA: Ceres:17483.	264111_at	1.5
putative citrate synthase ;supported by full-length cDNA: Ceres:17416.	263986_at	1.5
putative GDSL-motif lipase/hydrolase similar to APG proteins; pFAM domain PF00657;supported by full-length cDNA: Ceres:39762.	263809_at	1.5
putative photomorphogenesis repressor protein	263779_at	1.5
DNA-directed RNA polymerase II, third largest subunit	263564_s_at	1.5
putative heat shock protein ; supported by cDNA: gi_15450722_gb_AY053403.1_	263483_at	1.5
putative protein kinase contains a protein kinase domain profile (PDOC00100); supported by cDNA: gi_13605880_gb_AF367339.1_AF367339	263274_at	1.5
dynamin-like protein	263278_at	1.5
FtsH protease, putative contains similarity to chloroplast FtsH protease GI:5804782 from [Nicotiana tabacum]	262937_at	1.5
unknown protein ; supported by cDNA: gi_15028136_gb_AY046018.1_	262881_at	1.5
mercaptopyruvate sulfurtransferase (Mst2/Rdh2) identical to mercaptopyruvate sulfurtransferase GI:6009983 and thiosulfate sulfurtransferase GI:581	262712_at	1.5
hypothetical protein	262621_at	1.5
putative protein disulfide isomerase precursor Similar to gb|Z11499 protein disulfide isomerase from Medicago sativa. ESTs gb|AI099693, gb|R6522	262504_at	1.5
unknown protein ; supported by full-length cDNA: Ceres: 39741.	262204_at	1.5

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 esculentum]	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: 39968.	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 by cDNA: gi_189	260780_at	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_2352083_gb_U9661	260339_at	1.5
putative alanine aminotransferase similar to alanine aminotransferase GB:AAB01685 (Chlamydomonas reinhardtii); supported by full-length cDNA: C	260309_at	1.5
unknown protein similar to unknown protein GB:AAD21437 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:31039.	260259_at	1.5
hypothetical protein similar to hypothetical protein GB:CAB37532 from [Arabidopsis thaliana], predicted by genscan+;supported by full-length cDNA:	260127_at	1.5
putative nuclear matrix constituent protein 1 (NMCP1) similar to nuclear matrix constituent protein 1 (NMCP1) GB:BAA20407 [Daucus carota] (involv	260031_at	1.5
RNA-binding protein MEI2, putative similar to GI:6650523 from [Arabidopsis thaliana]	259769_at	1.5
sphingosine-1-phosphate lyase, putative similar to sphingosine-1-phosphate lyase [Homo sapiens] GI:4160532; supported by cDNA: gi_13430507_	259598_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
hypothetical protein contains similarity to hepatocellular carcinoma-associated antigen 59 GI:7158847 from [Homo sapiens]; supported by cDNA: gi_	259415_at	1.5
putative lectin contains Pfam profile: PF01419 jacalin-like lectin domain; similar to jasmonate inducible protein GB:Y11483 (Brassica napus), myrosi	259383_at	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 [Rattus norvegicus];	258794_at	1.5
hypothetical protein similar to hypothetical protein GB:AAC17075 [Arabidopsis thaliana]; supported by cDNA: gi_15810358_gb_AY056218.1_	258804_at	1.5
L-allo-threonine aldolase, putative similar to L-ALLO-THREONINE ALDOLASE GB:O07051 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: gi_14194122_gb_	258084_at	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 Pfam profile: PF004	257887_at	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_AY040029.1_	257252_at	1.5
mitochondrial chaperonin hsp60 identical to mitochondrial chaperonin hsp60 GB:Z11547 [Arabidopsis thaliana] (Plant Mol. Biol. 18 (5), 873-885 (19	256905_at	1.5
far-red impaired response protein, putative similar to GB:far-red impaired response protein GB:AAD51282 from [Arabidopsis thaliana] (Genes Dev. (	256820_at	1.5
alpha-glucan phosphorylase, putative similar to alpha-glucan phosphorylase, L isozyme 1 precursor GB:P04045 from [Solanum tuberosum] (J. Bioc	256746_at	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 (SSRP1) SP:Q08943 [Mus	256590_at	1.5
putative clathrin heavy chain similar to clathrin heavy chain GB: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) [Arabidopsis thaliana] GI	256305_at	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 [Arabidopsis 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 O. 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	254992_at	1.5
UDP-galactose 4-epimerase - like protein UDP-galactose 4-epimerase, Cyamopsis tetragonoloba, AJ005082;supported by full-length cDNA: Ceres:	254952_at	1.5
putative protein other hypothetical proteins - Arabidopsis thaliana	254965_at	1.5
putative translation elongation factor ts elongation factor ts (tsf) RP087 - Rickettsia prowazekii, PIR2:F71717	254932_at	1.5
putative protein beta-transducin repeats containing protein - Homo sapiens,PID:e1284220	254913_at	1.5
putative SWH1 protein SWH1 protein - yeast, PIR2:S47536	254817_at	1.5
putative protein ;supported by full-length cDNA: Ceres:100165.	254577_at	1.5
putative protein cyclin C homolog 1, Schizosaccharomyces pombe, PATCHX:G2055413	254526_at	1.5
trehalose-6-phosphate phosphatase - like protein trehalose-6-phosphate phosphatase (AtTPPA), PID:g2944178	254321_at	1.5
transcriptional activator CBF1-like protein strong similarity to transcriptional activator CBF1, Arabidopsis thaliana00	254066_at	1.5
putative protein	253805_at	1.5
cinnamoyl-CoA reductase - like protein cinnamoyl-CoA reductase, Saccharum officinarum, gb:AJ231134; supported by full-length cDNA: Ceres: 150	253638_at	1.5
putative protein hypothetical protein - Synechocystis sp. (strain PCC 6803),PIR2:S76076	253585_at	1.5
putative protein bcop gene product - Drosophila melanogaster,PID:g472343	253528_s_at	1.5
putative protein kinase protein kinase, Spinacia oleracea, PIR2:S42867	253359_at	1.5
aminopeptidase- like protein aminopeptidase, Mus musculus, U35646	253360_at	1.5
calmodulin-domain protein kinase CDPK isoform 5 (CPK5) ; supported by cDNA: gi_1399272_gb_U31834.1_ATU31834	253167_at	1.5
protein kinase - like protein protein kinase SRPK1, Mus musculus, PID:d1026227	253137_at	1.5
putative protein glutamic acid-rich protein precursor, Plasmodium falciparum (GARP), PIR2:A54514	253111_at	1.5
putative protein various predicted proteins, Arabidopsis thaliana	253092_at	1.5
DNA-binding protein - like DNA-binding protein R kappa B, Homo sapiens, PIR:S52863	252546_at	1.5
putative protein several hypothetical proteins	252496_at	1.5
putative peptide transporter peptide transporter (ptr1), Hordeum vulgare, AF023472; supported by cDNA: gi_13877878_gb_AF370202.1_AF370202	252377_at	1.5
serine palmitoyltransferase-like protein	252331_s_at	1.5
putative protein various predicted proteins, Arabidopsis thaliana	252290_at	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	250408_at	1.5
putative protein similar to unknown protein (emb|CAB51351.1)	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 prec	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 (pir||T05524);supported by full-length cDNA: Ceres:767.	248952_at	1.5
ADPG pyrophosphorylase small subunit (gb AAC39441.1) ; supported by cDNA: gi_15146247_gb_AY049265.1_	248687_at	1.5
peptidylprolyl isomerase	248657_at	1.5
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
dehydration-induced protein RD22 ; supported by cDNA: gi_16974545_gb_AY060560.1_	246908_at	1.5
chaperonin gamma chain - like protein chaperonin containing TCP-1 complex gamma chain, African clawed frog, PIR:S54210; supported by cDNA:	246830_at	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
viral resistance protein, putative, 5 partial similar to viral resistance protein GI:7110565 from [Arabidopsis thaliana]	245218_s_at	1.5
mitochondrial chaperonin (HSP60)	245164_at	1.5
ribosomal 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	267050_at	1.4
putative ABC transporter	266990_at	1.4
unknown protein	266855_at	1.4
putative casein kinase I	266651_at	1.4
TINY-like AP2 domain transcription factor ; supported by cDNA: gi_13878156_gb_AF370341.1_AF370341	266661_at	1.4
unknown protein ; supported by cDNA: gi_14030738_gb_AF375460.1_AF375460	266617_at	1.4
unknown protein	266185_at	1.4
unknown protein	266090_at	1.4
putative WD-40 repeat protein, MSI4 almost identical to GB:2599091; contains a Trp-Asp (WD-40) repeat signature; supported by cDNA: gi_259909	265946_s_at	1.4
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:21954.	265912_at	1.4
unknown protein ;supported by full-length cDNA: Ceres:121540.	265871_at	1.4
putative nitrilase ;supported by full-length cDNA: Ceres:20875.	265642_at	1.4
Expressed protein ; supported by full-length cDNA: Ceres: 16367.	265627_at	1.4
hypothetical protein predicted by genefinder	265310_at	1.4
unknown protein similar to putative tyrosine phosphatase GB:AAF81798 GI:8926334 from [Oryza sativa];supported by full-length cDNA: Ceres:8301.	265073_at	1.4
putative plastid RNA polymerase sigma-subunit similar to GB:BAA22427 and EST gb|N65838; supported by cDNA: gi_2353172_gb_AF015543.1_AF	264781_at	1.4
unknown protein location of EST gb|H36530, gb|AA395402, and gb|T43793	264772_at	1.4
5 -adenylylphosphosulfate reductase, putative similar to 5 -adenylylphosphosulfate reductase GI:1336168 from [Arabidopsis thaliana];supported by	264745_at	1.4
hypothetical protein similar to hypothetical protein GI:4455225 from [Arabidopsis thaliana]; supported by cDNA: gi_15293160_gb_AY051014.1_	264701_at	1.4
unknown protein	264597_at	1.4
putative cinnamyl alcohol dehydrogenase similar to cinnamyl alcohol dehydrogenase, gi|1143445; supported by cDNA: gi_15983385_gb_AF424567	264514_at	1.4
unknown protein similar to ESTs gb|N96021 and gb|N96863	264458_at	1.4
hypothetical protein contains similarity to glycosyltransferase GI:871530 from [Saccharomyces cerevisiae]	264291_at	1.4
beta-glucosidase, putative similar to beta-glucosidase GI:9758949 from [Arabidopsis thaliana]	264271_at	1.4
unknown protein contains similarity to splicing factor required for vegetative and meiotic growth GI:2959374 from [Schizosaccharomyces pombe]; su	264221_s_at	1.4
receptor kinase, putative similar to receptor kinase 1 GI:9294449 from [Arabidopsis thaliana]	264223_s_at	1.4
putative gigantea protein strong similarity to GB:CAB56039 from [Arabidopsis thaliana]; supported by cDNA: gi_6002679_gb_AF105064.1_AF10506	264211_at	1.4
unknown protein similar to putative CREB-binding protein GI:7025854 from [Arabidopsis thaliana]; supported by cDNA: gi_12597460_gb_AF323954.	264101_at	1.4
RNA helicase, putative similar to RNA helicase GI:3776015 from [Arabidopsis thaliana]; supported by cDNA: gi_15983391_gb_AF424570.1_AF424	263679_at	1.4
unknown protein Location of ESTs 108M14T7, gb|T41823 and 108M14XP 3 , gb|AA395002; supported by cDNA: gi_14335101_gb_AY037230.1_	263692_at	1.4
receptor kinase, putative similar to receptor kinase 1 [Brassica rapa] GB:BAA23676	262926_s_at	1.4
glyceraldehyde-3-phosphate dehydrogenase, putative similar to glyceraldehyde-3-phosphate dehydrogenase GI:1100222 from [Pinus sylvestris]	262939_s_at	1.4
unknown protein contains similarity to helicase GI:914852 from [Homo sapiens]	262906_at	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] (gi|40	262516_at	1.4
cytochrome b245 beta chain homolog RbohAp108, putative similar to cytochrome b245 beta chain homolog RbohAp108 GB:T03826 GI:7484893 fro	262344_at	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
putative DnaJ protein contains Pfam profile: PF00226 DnaJ, prokaryotic heat shock protein; similar to hypothetical protein GB:AAD55462 (Arabidops	262053_at	1.4
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]	261642_at	1.4
CAF protein identical to RNA helicase/RNAseIII CAF protein GB:AAF03534 GI:6102610 from [Arabidopsis thaliana]; supported by cDNA: gi_115596	261584_at	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	260000_at	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	259724_at	1.4
myb-related transcription factor (cpm10), putative similar to myb-related transcription factor (cpm10) GB:U33915 GI:1002795 from [Craterostigma pl	259618_at	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
alpha subunit of F-actin capping protein supported by full-length cDNA: Ceres:33531.	259111_at	1.4
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-	258649_at	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_159827	258556_at	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
hypothetical protein predicted by genemark.hmm	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_	256186_at	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:O74940 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	255487_at	1.4
hypothetical protein	255429_at	1.4
hypothetical protein	255348_at	1.4
putative protein glutamic acid-rich protein precursor - Plasmodium falciparum, PIR2:A54514	255128_at	1.4
putative zinc finger protein	255094_at	1.4
putative protein hypothetical protein sll1775 - Synechocystis sp.,PIR2:S77106	255008_at	1.4
lipase-like protein monoglyceride lipase - Mus musculus, PID:e1184892;supported by full-length cDNA: Ceres:6822.	255010_at	1.4
putative translation initiation factor IF-2 translation initiation factor IF-2 - Haemophilus influenzae, PIR2:E64114	254904_at	1.4
putative protein hypothetical protein, Synechocystis sp., PIR2:S76637	254715_at	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
protein phosphatase ABI1 ; supported by cDNA: gi_14334799_gb_AY035073.1_	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
formamidase - like protein formamidase, Methylophilus methylotrophus,PIR2:S74213;supported by full-length cDNA: Ceres:23732.	253042_at	1.4
glycine hydroxymethyltransferase like protein glycine hydroxymethyltransferase -Solanum tuberosum,PID:g438247;supported by full-length cDNA: C	253009_at	1.4
putative protein hypothetical protein At2g28360 - Arabidopsis thaliana, EMBL:AAD20690	252613_at	1.4
isovaleryl-CoA-dehydrogenase precursor (IVD) ;supported by full-length cDNA: Ceres:33674.	252570_at	1.4
protein kinase - like protein Raf protein kinase homolog CTR1 - Arabidopsis thaliana,PIR2:A45178	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	252131_at	1.4
CDC48 - like protein transitional endoplasmic reticulum ATPase, Arabidopsis thaliana, PIR:S60112	251975_at	1.4
TATA box binding protein (TBP) associated factor (TAF) -like protein TAF-172, Homo sapiens, EMBL:AF038362	251876_at	1.4
FKBP12 interacting protein (FIP37) ; supported by cDNA: gi_3859943_gb_AF084570.1_AF084570	251887_at	1.4
putative protein GTP-binding regulatory protein beta chain, Dictyostelium discoideum, PIR:A47370; supported by cDNA: gi_13430701_gb_AF36026	251888_at	1.4
putative protein MSP58 - nucleolar protein, Mus musculus, EMBL:AF015309; supported by cDNA: gi_17063177_gb_AY062111.1_	251866_at	1.4
putative protein	251646_at	1.4
putative zinc-finger protein zinc-finger protein - Schizosaccharomyces pombe, PIR:T41264	251253_at	1.4
putative protein PGP237-11, Petunia x hybrida, EMBL:AF049930	251198_at	1.4
putative protein SqdX protein, Synechococcus PCC7942, EMBL:SP45308; supported by cDNA: gi_15028316_gb_AY045961.1_	251143_at	1.4
putative protein putative proteins - Arabidopsis thaliana; supported by cDNA: gi_15292802_gb_AY050835.1_	251084_at	1.4
putative protein histone H2A, garden pea, PIR:JQ1183; supported by full-length cDNA: Ceres: 1553.	251011_at	1.4
putative protein P58 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_AF387016.1_AF387016	250897_at	1.4
cell division related protein-like	250711_at	1.4
ubiquitin activating enzyme 2 (UBA2) identical to gi:1703477	250729_at	1.4
transcription factor-like protein ; supported by cDNA: gi_14334943_gb_AY035145.1_	250598_at	1.4
putative protein heparanase precursor, Homo sapiens, EMBL:AF155510	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
putative protein contains similarity to unknown protein (pir||T05576)	250305_at	1.4
unknown protein	250238_at	1.4
isocitrate dehydrogenase - like protein isocitrate dehydrogenase, Nicotiana tabacum, pir:T04356	250197_at	1.4
2-hydroxyphytanoyl-CoA lyase-like protein	250094_at	1.4
putative protein contains similarity to transcription regulator; supported by cDNA: gi_13877644_gb_AF370523.1_AF370523	250035_at	1.4
2-isopropylmalate synthase-like; homocitrate synthase-like ; supported by cDNA: gi_12330688_gb_AF327648.1_AF327648	249866_at	1.4
putative protein contains similarity to DsPTP1 protein	249792_at	1.4
putative protein tyrosine aminotransferase-like; also similar to nicotianamine aminotransferase	249688_at	1.4
expressed protein predicted protein, Synechocystis sp., PIR:S77152; supported by full-length cDNA: Ceres: 5331.	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 GI:10716947 from [Arabidopsis thaliana];supported by full-length cDNA: C	247863_at	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
putative protein similar to unknown protein (pir||T01734)	247410_at	1.4
glucosidase II alpha subunit	247298_at	1.4
putative protein contains similarity to auxin-independent growth promoter	247186_at	1.4
2-oxoglutarate dehydrogenase, E1 component	247155_at	1.4
lysosomal Pro-X carboxypeptidase	247156_at	1.4
putative protein contains similarity to MYB-like DNA-binding protein; supported by cDNA: gi_14532517_gb_AY039883.1_	247012_at	1.4
calcium-dependent protein kinase ; supported by cDNA: gi_289189_gb_L14771.1_ATHCALLIPR	246955_at	1.4
transcription factor-like protein light-induced protein CPRF-2 - Petroselinum crispum, PIR:S16321	246962_s_at	1.4
putative protein CG6949 - Drosophila melanogaster, EMBL:AE003739	246767_at	1.4
protein kinase -like protein Ste-20 related kinase SPAK, Homo sapiens, EMBL:AF099989	246583_at	1.4
putative protein KIAA1468 - Homo sapiens, EMBL:AB040901	246496_at	1.4
putative protein KIAA1012 protein - Homo sapiens, EMBL:AB023229	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 c	246417_at	1.4
putative protein hypothetical protein F2A19.120 - Arabidopsis thaliana, PIR:T47944	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
putative protein	245881_at	1.4
chorismate synthase, putative similar to chorismate synthase GI:452796 from [Synechocystis sp.]; supported by cDNA: gi_15982823_gb_AY05751	245832_at	1.4
hypothetical protein contains similarity to virulence regulator GI:9106522 from [Xylella fastidiosa]	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
F12A21.2 hypothetical protein; supported by cDNA: gi_14326581_gb_AF385745.1_AF385745	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|Q09298|YQO9_CAEEL	267632_at	1.3
putative protein disulfide isomerase ; supported by cDNA: gi_15810003_gb_AY054270.1_	267605_at	1.3
26S proteasome regulatory subunit	267543_at	1.3
hypothetical protein predicted by genscan	267508_at	1.3
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.	266767_at	1.3
putative CCCH-type zinc finger protein ;supported by full-length cDNA: Ceres:101255.	266695_at	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	265957_at	1.3
unknown protein	265779_at	1.3
putative glucan synthase	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	264927_at	1.3
NBS/LRR disease resistance protein, putative similar to NBS/LRR disease resistance protein GI:3309619 from [Arabidopsis thaliana]; supported by	264885_s_at	1.3
putative DNA-binding protein, Myb Identical to A. thaliana Myb-like protein (gb|D58424); supported by cDNA: gi_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	264524_at	1.3
CTP synthase-like protein similar to ctp synthase (sp|P17812|PYRG_HUMAN); similar to ESTs gb|AA660762, gb|AA220982, dbj|AU008137, gb|AI0	264529_at	1.3
unknown protein similar to EST gb|N96077; supported by cDNA: gi_15810035_gb_AY054286.1_	264407_at	1.3
putative aspartic proteinase similar to GB:AAC49730;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	264322_at	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	1.3
unknown protein ; supported by cDNA: gi_15810174_gb_AY056101.1_	263333_at	1.3
putative nonsense-mediated mRNA decay protein ; supported by cDNA: gi_15810402_gb_AY056240.1_	263334_at	1.3
putative GTP-binding protein Similar to WO8E3.3 gi|3880615 putative GTP-binding protein from C. elegans cosmid gb|Z92773. EST gb|AA597331 c	263224_at	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	263116_s_at	1.3
hypothetical protein predicted by genscan and genefinder	263085_at	1.3
glutathione S-transferase, putative similar tosimilar to glutathione S-transferase GB:AAF29773 GI:6856103 from (Gossypium hirsutum); supported b	262916_at	1.3
putative membrane-associated salt-inducible protein strong similarity to gi|3367521 F8K4.8 from Arabidopsis thaliana BAC gb|AC004392;supported	262822_at	1.3
anthranilate N-hydroxycinnamoyl/benzoyltransferase, putative similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase GB:Z84384 GI:22390	262744_at	1.3
lipase, putative contains Pfam profile: PF00657 Lipase/Acylhydrolase with GDSL-like motif; supported by cDNA: gi_13937188_gb_AF372948.1_AF	262748_at	1.3
putative translation initiation factor IF2 Except for first 311 amino acids, 41% identical to translation initiation factor IF2 [Bacillus subtilis] (gi|124209)	262483_at	1.3
hypothetical protein similar to hypothetical protein GB:AAD50003 GI:5734738 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:3759	262452_at	1.3
hypothetical protein identical to hypothetical protein GB:AAD50051 GI:5734786 from [Arabidopsis thaliana]; supported by cDNA: gi_15081691_gb_A	262419_at	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	262173_at	1.3
beta-glucosidase, putative similar to beta-glucosidase GI:5030906 from [Polygonum tinctorium]; supported by cDNA: gi_15146265_gb_AY049274.1	262118_at	1.3
putative heat-shock protein contains Pfam profile: PF00012 Heat shock hsp70 proteins; similar to heat-shock proteins GB:CAA94389, GB:AAD5546	262054_s_at	1.3
calcium-dependent protein kinase identical to GB:BAA04830 GI:604881 from [Arabidopsis thaliana]; supported by cDNA: gi_15293094_gb_AY0509	262026_at	1.3
glutamate decarboxylase (gad), putative similar to glutamate decarboxylase (gad) GI:294111 from [Petunia hybrida]; supported by cDNA: gi_11849	261970_at	1.3
hypothetical protein predicted by genemark.hmm	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	261907_at	1.3
scarecrow-like protein similar to SCARECROW GB:AAB06318 GI:1497987 from [Arabidopsis thaliana]; supported by cDNA: gi_14334475_gb_AY03	261860_at	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-tRNAGln 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_	261127_at	1.3
hypothetical protein contains Pfam profile: PF00534 glycosyl transferases group 1	261138_at	1.3
sec14 cytosolic factor, putative similar to SP:P24859 from [Kluyveromyces lactis]	261116_at	1.3
unknown protein ; supported by cDNA: gi_16974626_gb_AY060591.1_	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_AT	260638_at	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:BAA21132, GB:BAA06285 [Brassica rapa]; Pfam HMM hit: Eukaryotic	260303_at	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	260155_at	1.3
hypothetical protein predicted by genscan	260087_at	1.3
putative chlorophyll A-B binding protein similar to chlorophyll A-B binding protein GB:P12470 [Nicotiana plumbaginifolia]; contains Pfam profile: PF00	259970_at	1.3
cytosolic factor, putative similar to GI:807956 from [Saccharomyces cerevisiae]; supported by cDNA: gi_15081613_gb_AY048199.1_	259804_at	1.3
unknown protein	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: Ce	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	259442_at	1.3
protein phosphatase 2A 65 kDa regulatory subunit identical to protein phosphatase 2A 65 kDa regulatory subunit GB:X82002 [Arabidopsis thaliana]	259408_at	1.3
unknown protein	259292_at	1.3
hypothetical protein predicted by genscan	259219_at	1.3
beta-glucosidase identical to beta-glucosidase GB:AAC31962 [Arabidopsis thaliana]; supported by cDNA: gi_3420934_gb_AF082157.1_AF082157	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 [Nicotiana tabacum];supported by full-length	259132_at	1.3
putative ribosomal-protein S6 kinase (ATPK19) identical to putative ribosomal-protein S6 kinase (ATPK19) GB:D42061 [Arabidopsis thaliana] (FEB	258682_at	1.3
unknown protein	258635_at	1.3
unknown protein	258316_at	1.3
unknown protein ;supported by full-length cDNA: Ceres:141813.	258078_at	1.3
unknown protein similar to CGI-18 protein GB:AAD27727 [Homo sapiens]	258053_at	1.3
unknown protein	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 kinase GB:AAC32599 from [Oryza sativa]	257801_at	1.3
CTP-synthetase, putative similar to CTP synthetase GB:U49350 GI:1515356 (Mus musculus)	257702_at	1.3
Expressed protein ; 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	256036_at	1.3
carbamoylphosphate synthetase, putative similar to carbamoylphosphate synthetase GI:6552726 from [Medicago sativa]; supported by cDNA: gi_14	256002_at	1.3
hypothetical protein predicted by genscan+	255891_at	1.3
hypothetical protein predicted by genscan and genefinder; similar to EGAD|50981|YBR228W	255866_at	1.3
putative steroid dehydrogenase ; supported by cDNA: gi_16226672_gb_AF428460.1_AF428460	255797_at	1.3
predicted protein of unknown function	255681_at	1.3
hypothetical protein	255573_at	1.3
putative sugar transporter	255294_at	1.3
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
putative protein IEF SSP 9502, Homo sapiens, PATCHX:G177765	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	1.3
putative protein receptor protein kinase, Ipomoea trifida	254247_at	1.3
argininosuccinate synthase -like protein argininosuccinate synthase, Aquifex aeolicus, PIR2:B70398	254134_at	1.3
putative protein proliferating-cell nucleolar antigen P120 -Homo sapiens,PIR2:A48168	253975_at	1.3
putative aconitase Pumpkin mRNA for aconitase, Cucurbita sp.,PID:g868003; supported by cDNA: gi_15215803_gb_AY050431.1_	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_	253387_at	1.3
putative protein ; supported by cDNA: gi_13605598_gb_AF361625.1_AF361625	253388_at	1.3
gamma-VPE (vacuolar processing enzyme) ; supported by cDNA: gi_13877794_gb_AF370160.1_AF370160	253358_at	1.3
putative protein hemolysin, 38K, Synechocystis sp., Pir2:S75595	253351_at	1.3
putative protein B subunit of propionyl-CoA carboxylase, Mycobacterium tuberculosis, PATCHX:E290075; supported by cDNA: gi_14423377_gb_AF	253279_at	1.3
Nonclathrin coat protein gamma - like protein coat protein gamma-cop, Bos primigenius	253231_at	1.3
putative squalene synthase non-consensus GC donor splice site at exon 3, squalene synthase 2 (SQS2), Arabidopsis thaliana; supported by cDNA:	253206_at	1.3
putative protein predicted proteins, Arabidopsis thaliana	253107_at	1.3
putative protein KIAA0776 protein, Homo sapiens, EMBL:AB018319; supported by cDNA: gi_14334491_gb_AY034937.1_	252513_at	1.3
FtsH protease, putative contains similarity to FtsH protease GI:13183728 from [Medicago sativa]	252449_at	1.3
putative protein	252431_at	1.3
ubiquitin-specific protease 26 (UBP26) similar to GI:11993492; RNA binding protein - Homo sapiens, EMBL:AB016089 (N-terminus), several ubiquit	252275_at	1.3
hypothetical protein ; supported by cDNA: gi_13507562_gb_AF360347.1_AF360347	252276_at	1.3
putative protein putative protein - Drosophila melanogaster, EMBL:AF132172	252239_at	1.3
putative disease resistance protein	252126_at	1.3
putative protein ; supported by cDNA: gi_14517539_gb_AY039605.1_	252134_at	1.3
putative protein senescence-associated protein 12 - Hemerocallis hybrid cultivar, EMBL:AF082032; supported by cDNA: gi_15215687_gb_AY05037	252099_at	1.3
RNA helicase -like protein RNA helicase, Mus musculus, PIR:I49731; supported by cDNA: gi_15982880_gb_AY057548.1_	251989_at	1.3

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
translation releasing factor RF-1 -like protein translation releasing factor RF-1, Synechocystis sp., PIR:S76914	251193_at	1.3
hypothetical protein RNA polymerase II CTD phosphatase (CTDP1), Homo sapiens, EMBL:AF154115	251134_at	1.3
putative protein predicted protein, Arabidopsis thaliana; supported by cDNA: gi_13430449_gb_AF360137.1_AF360137	251015_at	1.3
putative protein ; supported by cDNA: gi_14190430_gb_AF378893.1_AF378893	250970_at	1.3
putative protein ; supported by cDNA: gi_1019903_gb_U37587.1_ATU37587	250899_at	1.3
putative protein contains similarity to unknown protein (pir||D70614); supported by cDNA: gi_14334951_gb_AY035149.1_	250824_at	1.3
putative protein similar to unknown protein (pir||T01270)	250742_at	1.3
DnaJ-like protein ; supported by cDNA: gi_15810414_gb_AY056246.1_	250755_at	1.3
putative protein contains similarity to zinc finger protein;supported by full-length cDNA: Ceres:3542.	250736_s_at	1.3
putative protein SF16 protein, pollen specific - Helianthus annuus, PIR:T13992	250613_at	1.3
calnexin homolog	250625_at	1.3
putative protein p100 co-activator - Mus musculus, EMBL:AB021491	250626_at	1.3
transcription factor OBF4	250463_at	1.3
putative protein predicted protein, Arabidopsis thaliana	250274_at	1.3
sigma-like factor (gb|AAC97954.1) ; supported by cDNA: gi_3983259_gb_AF101075.1_AF101075	250255_at	1.3
putative protein CGI-67, Homo sapiens, EMBL:AF151825	250175_at	1.3
putative protein p53 inducible protein PIR121, Homo sapiens, EMBL:AF160973	250041_at	1.3
MAP kinase -like protein ATMPK9, Arabidopsis thaliana, EMBL:AB038694	249964_at	1.3
alkaline/neutral invertase ; supported by cDNA: gi_15912342_gb_AY056449.1_	249898_at	1.3
putative protein mDj10, Mus musculus, EMBL:AB028860; supported by cDNA: gi_15450366_gb_AY052284.1_	249613_at	1.3
unknown protein ;supported by full-length cDNA: Ceres:101366.	249456_at	1.3
nuclear pore protein -like nuclear pore protein gp210 precursor, rat, PIR:S04921	249354_at	1.3
disease resistance protein-like	249264_s_at	1.3
maize crp1 protein-like	249247_at	1.3
unknown protein	249134_at	1.3
electron transfer flavoprotein beta-subunit-like ;supported by full-length cDNA: Ceres:120707.	249158_at	1.3
cullin ;supported by full-length cDNA: Ceres:101723.	248882_at	1.3
putative protein contains similarity to (pir||T14814)	248901_at	1.3
eukaryotic release factor 1 homolog (gb|AAA91169.1) ; supported by cDNA: gi_15215862_gb_AY050462.1_	248749_at	1.3
putative protein contains similarity to unknown protein (pir||T01052)	248616_at	1.3
putative protein contains similarity to unknown protein (emb|CAB87278.1)	248393_at	1.3
putative protein similar to unknown protein (gb|AAD38661.1); supported by cDNA: gi_13430647_gb_AF360236.1_AF360236	248305_at	1.3
pyruvate kinase ;supported by full-length cDNA: Ceres:109919.	248283_at	1.3
FtsH protease, putative similar to ATP-dependent metalloprotease FtsH1 GI:3600100 from [Mus musculus]	248303_at	1.3
putative protein similar to unknown protein (gb|AAF54217.1)	247993_at	1.3
unknown protein	248005_at	1.3
pyruvate kinase ;supported by full-length cDNA: Ceres:31580.	247989_at	1.3
serine/threonine protein kinase ; supported by cDNA: gi_13249118_gb_AF295665.1_AF295665	247820_at	1.3
aspartyl aminopeptidase - like protein aspartyl aminopeptidase, Homo sapiens, EMBL:AF005050;supported by full-length cDNA: Ceres:126533.	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	247609_at	1.3
pyrophosphate-dependent phosphofructo-1-kinase - like protein pyrophosphate-dependent phosphofructo-1-kinase, Prunus armeniaca, EMBL:U932	247534_at	1.3
quinone oxidoreductase - like protein quinone oxidoreductase homolog, Vigna unguiculata, PIR:T11672;supported by full-length cDNA: Ceres:3719	247513_at	1.3
putative protein contains similarity to protein kinase	247309_at	1.3
phosphatidylinositol 4-kinase (emb|CAB37928.1)	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
beta-ureidopropionase	247275_at	1.3
poly(A)-binding protein II-like ; supported by cDNA: gi_14423493_gb_AF386984.1_AF386984	247173_at	1.3
acyl-CoA oxidase (gb|AAC13497.1) ; supported by cDNA: gi_3044211_gb_AF057043.1_AF057043	247176_at	1.3
putative protein contains similarity to RING3 protein	247147_at	1.3
unknown protein ; supported by cDNA: gi_14334479_gb_AY034931.1_	247114_at	1.3
unknown protein	247063_at	1.3
floral homeotic protein apetala2-like ;supported by full-length cDNA: Ceres:4623.	247041_at	1.3
nodulin - like protein nodulin, Glycine max, EMBL:AF065435	246927_s_at	1.3
eukaryotic translation initiation factor - like protein eukaryotic translation initiation factor 3, Nicotiana tabacum, EMBL:Y11996; supported by cDNA: g	246865_s_at	1.3
SAR DNA-binding protein - like SAR DNA-binding protein-1, garden pea, PIR:T06377	246809_s_at	1.3
putative protein kinesin heavy chain-like protein, potato, PIR:T07397	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 [Lycop	246628_at	1.3
putative protein HR21spA protein involved in DNA double-strand break repair - Mus musculus, EMBL:X98293	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	246412_at	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	245938_at	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 GB:AAC36170 GI:3608137 from [Arabidopsis thaliana]; supported by cDNA: gi_11044956_emb_AJ2515	245796_at	1.3
hyoscyamine 6-dioxygenase hydroxylase, putative similar to hyoscyamine 6-dioxygenase hydroxylase GB:P24397 from [Hyoscyamus niger];suppor	245756_at	1.3
lysophospholipase homolog, putative similar to lysophospholipase homolog GI:2801536 from [Oryza sativa]; supported by cDNA: gi_15028212_gb_	245734_at	1.3
unknown protein	245744_at	1.3
calcium lipid binding protein - like GC donor splice site at exon 3; supported by cDNA: gi_16604592_gb_AY059741.1_	245702_at	1.3
UFD1 like protein ; supported by full-length cDNA: Ceres: 207652.	245313_at	1.3
HSP like protein ; supported by cDNA: gi_15293148_gb_AY051008.1_	245293_at	1.3
putative protein similarity to ALR - Homo sapiens~contains EST gb:Aa39558600	245237_at	1.3
unknown protein ; supported by cDNA: gi_14334431_gb_AY034907.1_	245116_at	1.3
putative beta-1,3-glucanase ;supported by full-length cDNA: Ceres:95083.	245039_at	1.3
hypothetical protein predicted by genscan+	261463_at	1.3
transfactor, putative similar to transfactor GI:4519671 from [Nicotiana tabacum]; supported by cDNA: gi_15010721_gb_AY045662.1_	262921_at	1.2
putative protein similar to unknown protein (gb|AAB63610.1)	248213_at	1.2

unknown protein ; supported by cDNA: gi_13877620_gb_AF370511.1_AF370511	267577_at	1.2
unknown protein ; supported by cDNA: gi_13430537_gb_AF360181.1_AF360181	267513_at	1.2
putative glucosyltransferase	267300_at	1.2
ubiquitin activating enzyme 1 (UBA1) identical to GB:U80808	267301_at	1.2
FtsH protease (VAR2) identical to zinc dependent protease VAR2 GI:7650138 from [Arabidopsis thaliana]	267196_at	1.2
unknown protein	267132_at	1.2
putative ABC transporter related to multi drug resistance proteins and P-glycoproteins	266964_at	1.2
plasma membrane proton ATPase (PMA) identical to GB:M24107; supported by cDNA: gi_166745_gb_M24107.1_ATHHATPA	266939_at	1.2
remorin identical to GB:M25268, a non-specific DNA binding protein; may be involved in intercellular communication; supported by cDNA: gi_15028	266897_at	1.2
unknown protein ;supported by full-length cDNA: Ceres:40283.	266413_at	1.2
putative beta-amylase	266357_at	1.2
putative ligand-gated ion channel subunit ; supported by cDNA: gi_5759099_gb_AF170494.1_AF170494	266337_at	1.2
putative pumilio/Mpt5 family RNA-binding protein	266284_at	1.2
putative glutathione S-transferase ; supported by cDNA: gi_15450462_gb_AY052332.1_	266181_at	1.2
putative helicase ; supported by cDNA: gi_16648974_gb_AY059857.1_	266122_at	1.2
putative MYB family transcription factor	265700_at	1.2
hypothetical protein predicted by genscan	265728_at	1.2
50S ribosomal protein L4 ;supported by full-length cDNA: Ceres:156843.	265594_at	1.2
putative cyclic nucleotide and calmodulin-regulated ion channel protein	265544_at	1.2
putative WD-40 repeat protein similar to TUP1(GB:AF079369); supported by cDNA: gi_13605894_gb_AF367346.1_AF367346	265259_at	1.2
putative PHD-type zinc finger protein	265225_at	1.2
unknown protein ; supported by cDNA: gi_1669598_dbj_D88746.1_D88746	265059_at	1.2
T-complex chaperonin protein , epsilon subunit identical to GB:O04450, similar to ESTs gb|R29812, emb|Z38124, gb|AA297087, gb|R29812, gb|T1	265010_at	1.2
U2 snRNP auxiliary factor, large subunit, putative similar to GI:3850823 from (Nicotiana plumbaginifolia) (J. Biol. Chem. 273 (51), 34603-34610 (199	264922_s_at	1.2
RNA polymerase subunit identical to RNA polymerase subunit GI:514324 from [Arabidopsis thaliana]; supported by cDNA: gi_14423463_gb_AF386	264924_at	1.2
unknown protein	264878_at	1.2
putative protochlorophyllide reductase similar to protochlorophyllide reductase precusor; similar to ESTs gb|R30630, gb|T46162, emb|Z26728, gb|A	264839_at	1.2
unknown protein	264698_at	1.2
shaggy-like protien kinase, kappa Identical to A. thaliana AtK-1 (gb|X79279)	264686_at	1.2
unknown protein similar to putative inositol polyphosphate 5 -phosphatase GI:3212848 from [Arabidopsis thaliana]	264683_at	1.2
hypothetical protein contains similarity to caltractin GI:3688162 from [Arabidopsis thaliana]	264628_at	1.2
putative protein kinase contains a protein kinase domain profile (PDOC00100)	264621_at	1.2
unknown protein Similar to Caenorhabditis unknown protein T03F1.1 (gb|U88169	264570_at	1.2
putative phytochrome A similar to GB:AAA21351; supported by cDNA: gi_14517371_gb_AY039520.1_	264508_at	1.2
multi-drug resistance protein Strong similarity to MRP-like ABC transporter gb|U92650 from A. thaliana and canalicular multi-drug resistance protein	264330_at	1.2
coatomer alpha subunit, putative similar to coatomer alpha subunit GI:4567286 from [Arabidopsis thaliana]	264309_at	1.2
gamma glutamyl hydrolase, putative similar to gamma glutamyl hydrolase GI:1680711 from [Glycine max];supported by full-length cDNA: Ceres:413	264300_at	1.2
unknown protein	264218_at	1.2
hypothetical protein predicted by genemark.hmm	264224_at	1.2
CRK1 protein, putative similar to CRK1 protein GI:7671528 from [Beta vulgaris]; supported by cDNA: gi_13877618_gb_AF370510.1_AF370510	264193_at	1.2
Expressed protein ; supported by full-length cDNA: Ceres: 42267.	264163_at	1.2
unknown protein	264063_at	1.2
putative DnaJ protein ;supported by full-length cDNA: Ceres:10312.	264002_at	1.2
unknown protein ; supported by cDNA: gi_15450787_gb_AY054474.1_	263954_at	1.2
putative phosphatidylinositol/phosphatidylcholine transfer protein	263749_at	1.2
putative NADPH dependent mannose 6-phosphate reductase ; supported by full-length cDNA: Ceres: 21730.	263758_s_at	1.2
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:119045.	263538_at	1.2
molybdopterin synthase (CNX2) ;supported by full-length cDNA: Ceres:33192.	263472_at	1.2
En/Spm-like transposon protein related to En/Spm transposon family of maize	263352_at	1.2
putative RING zinc finger protein ; supported by cDNA: gi_13265496_gb_AF324691.2_AF324691	263325_at	1.2
zinc finger protein, putative similar to zinc finger protein GI:3618316 from [Oryza sativa];supported by full-length cDNA: Ceres:34830.	263128_at	1.2
hypothetical protein predicted by genscan and genefinder	263101_s_at	1.2
unknown protein	263104_at	1.2
unknown protein ; supported by cDNA: gi_16930680_gb_AF436824.1_AF436824	263050_at	1.2
putative mitotic control protein dis3 ; supported by cDNA: gi_15982744_gb_AY057479.1_	263077_at	1.2
conserved hypothetical protein	263037_at	1.2
putative ATP-dependent RNA helicase similar to GB:AAB88651, similar to human U5 snRNP-specific 200kD protein, gi|3255965 and yeast pre-mR	262800_at	1.2
putative pyrophosphate-dependent phosphofructokinase alpha subunit similar to GB:AAC67587 from [Citrus X paradisi] and GB:Q41140 from [Ricinu	262806_at	1.2
unknown protein similar to elongation factor G SP:P34811 [Glycine max (Soybean)]; supported by cDNA: gi_14532623_gb_AY039936.1_	262645_at	1.2
unknown protein EST gb|N65467 comes from this gene;supported by full-length cDNA: Ceres:30239.	262598_at	1.2
hypothetical protein predicted by genemark.hmm	262562_at	1.2
putative ubiquitin-conjugating enzyme First 212 a.a. are 41% identical to Ubiquitin-Conjugating Enzyme E2 [Saccharomyces cerevisiae] (gi|480374).	262537_s_at	1.2
alanine--tRNA ligase, putative similar to alanine--tRNA ligase GB:S32671 from [Arabidopsis thaliana]	262468_at	1.2
unknown protein	262430_s_at	1.2
hypothetical protein predicted by genemark.hmm	262221_at	1.2
xylosidase, putative similar to xylosidase GI:2102655 from [Aspergillus niger]	262181_at	1.2
dynamin-like protein similar to dynamin GB:AAA37324 GI:487857 from [Mus musculus]; supported by cDNA: gi_15146178_gb_AY049230.1_	262077_at	1.2
myrosinase precursor, putative	261884_at	1.2
transcriptional regulator, putative similar to transcriptional regulator GI:4836767 [Zea mays]	261891_at	1.2
UDP glucose:flavonoid 3-o-glucosyltransferase, putative similar to UDP glucose:flavonoid 3-o-glucosyltransferase GB:AAB81683 GI:2564114 from [	261804_at	1.2
unknown protein similar to hypothetical protein GB:CAA20583 GI:3549672 from [Arabidopsis thaliana]	261682_at	1.2
unknown protein ; supported by cDNA: gi_15028128_gb_AY046014.1_	261520_at	1.2
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_16041649_gb_AF355754.2_AF355754	261444_at	1.2
unknown protein contains similarity to set protein GI:338038 from [Homo sapiens];supported by full-length cDNA: Ceres:27467.	261406_at	1.2
unknown protein ; supported by cDNA: gi_15912328_gb_AY056442.1_	261354_at	1.2
unknown protein ; supported by full-length cDNA: Ceres: 117183.	261269_at	1.2
heat shock factor protein hsf8, putative predicted by genemark.hmm; supported by cDNA: gi_15028376_gb_AY045991.1_	261206_at	1.2
unknown protein	261064_at	1.2
unknown protein	260629_at	1.2
putative ATP-dependent RNA helicase ; supported by cDNA: gi_16323191_gb_AY057700.1_	260532_at	1.2
putative alpha-amylase similar to alpha-amylase GB:AAA91884 [Solanum tuberosum]; supported by cDNA: gi_15215737_gb_AY050398.1_	260412_at	1.2
putative protein kinase contains Pfam profile: PF00069 Eukaryotic protein kinase domain	260419_at	1.2
hypothetical protein contains Pfam profile: PF01535 Domain of unknown function	260331_at	1.2
hypothetical protein ;supported by full-length cDNA: Ceres:108322.	260301_at	1.2
hypothetical protein contains Pfam profile: PF01344 Kelch motif	260214_at	1.2
F-box protein FKF1/ADO3, AtFBX2a identical to FKF1 GI:6960305 and Adagio 3 GI:13487072 from [Arabidopsis thaliana]	259990_s_at	1.2
hypothetical protein predicted by genefinder, contains protein kinase domain	259950_at	1.2

putative phenylalanyl-tRNA synthetase beta-subunit; PheHB similar to phenylalanyl-tRNA synthetase beta-subunit (PheHB) GB:5032011 [Homo sap	259920_at	1.2
putative ribophorin I (dolichyl-diphosphooligosaccharide-protein glycosyltransferase) similar to ribophorin I (dolichyl-diphosphooligosaccharide-protei	259883_at	1.2
beta-glucosidase, putative identical to GI:6651430 from [Arabidopsis thaliana]; supported by cDNA: gi_14532461_gb_AY039855.1_	259640_at	1.2
CONSTANS family zinc finger protein, putative contains Pfam profile: PF01760: CONSTANS family zinc finger; supported by cDNA: gi_14335053_g	259595_at	1.2
cathepsin B-like cysteine protease, putative similar to cathepsin B-like cysteine proteinase GI:609175 from [Nicotiana rustica]	259441_at	1.2
trehalose-6-phosphate synthase, putative similar to trehalose-6-phosphate synthase GI:4468259 from [Pichia angusta]	259393_at	1.2
hypothetical protein predicted by genscan+	259385_at	1.2
putative adenylylsulfate kinase similar to GB:S47640 [Arabidopsis thaliana]	259339_at	1.2
putative mRNA capping enzyme, RNA guanylyltransferase contains similarty to mRNA capping enzyme GB:BAA25198 from [Homo sapiens]	259202_at	1.2
putative phosphoribosylanthranilate transferase similar to phosphoribosylanthranilate transferase GB:CAA16616 [Arabidopsis thaliana], phosphorib	259222_at	1.2
unknown protein est hit, predicted by genscan	259190_at	1.2
lysyl-tRNA synthetase identical to lysyl-tRNA synthetase; LysRS GB:AAD17333 [Arabidopsis thaliana]; supported by cDNA: gi_4325323_gb_AF125	259069_at	1.2
heat-shock protein (At-hsc70-3) identical to (At-hsc70-3) (cytosolic Hsp70) GB:CAA76606 [Arabidopsis thaliana]; supported by cDNA: gi_15292924_	258979_at	1.2
putative ribosome recycling factor similar to ribosome recycling factor gene (RRF) GB:BAA76865 [Thermus thermophilus]	258996_at	1.2
hypothetical protein similar to hypothetical protein GB:P40055 [Saccharomyces cerevisiae], Pfam HMM hit: WD domain, G-beta repeats	258965_at	1.2
unknown protein similar to hypothetical proteins: GB:P51281 [Chloroplast Porphyra purpurea], GB:BAA16982 [Synechocystis sp], GB:P49540 [Odor	258925_at	1.2
unknown protein N-terminus similar to unknown protein GB:AAD25613 [Arabidopsis thaliana]; supported by cDNA: gi_16604638_gb_AY059764.1_	258926_s_at	1.2
unknown protein predicted by genscan, multiple est matches; supported by full-length cDNA: Ceres: 97694.	258883_at	1.2
unknown protein similar to RNA helicase GB:AAF03534	258863_at	1.2
putative RNA helicase similar to RNA helicase involved in rRNA processing GB:6321267 from [Saccharomyces cerevisiae]c, ontains DEAD and DE	258701_at	1.2
putative GTPase contains Pfam profile: PF01926 GTPase of unknown function	258545_at	1.2
fatty acid multifunctional protein (AtMFP2) identical to fatty acid multifunctional protein (AtMFP2) GB:AF123254 [Arabidopsis thaliana] (fatty acid beta	258555_at	1.2
ubiquitin-specific protease 25 (UBP25) similar to GI:11993490; supported by cDNA: gi_11993489_gb_AF302673.1_AF302673	258372_at	1.2
unknown protein contains RanBP1 domain;supported by full-length cDNA: Ceres:108414.	258313_at	1.2
unknown protein ; supported by cDNA: gi_13430465_gb_AF360145.1_AF360145	258259_s_at	1.2
unknown protein similar to unknown protein GB:AAD14522 from [Arabidopsis thaliana]	258228_at	1.2
FKBP-type peptidyl-prolyl cis-trans isomerases, putative contains Pfam profile: PF00254 FKBP-type peptidyl-prolyl cis-trans isomerases	258175_at	1.2
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:25758.	258104_at	1.2
unknown protein	257973_at	1.2
formin-like protein AHF1 identical to formin-like protein AHF1 GB:AAF14548 from [Arabidopsis thaliana]; supported by cDNA: gi_6503009_gb_AF17	257912_at	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	1.2
unknown protein	257803_at	1.2
cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450	257625_at	1.2
9-cis-epoxycarotenoid dioxygenase, putative similar to 9-cis-epoxycarotenoid dioxygenase GB:AAF26356 [Phaseolus vulgaris]; supported by cDNA:	257280_at	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	1.2
major latex protein, putative similar to major latex protein type1 GB:CAA63026 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 8841.	256880_at	1.2
unknown protein	256485_at	1.2
adenylosuccinate lyase - like protein adenylosuccinate lyase - Haemophilus influenzae	256461_s_at	1.2
lipoxygenase, putative similar to lipoxygenase GI:1407704 from [Solanum tuberosum]; supported by cDNA: gi_289202_gb_L04637.1_ATHLIPOXY	256321_at	1.2
unknown protein ; supported by cDNA: gi_14334837_gb_AY035092.1_	256310_at	1.2
unknown protein	256271_at	1.2
unknown protein	256258_at	1.2
unknown protein	256220_at	1.2
NADP-specific glutatamate dehydrogenase, putative similar to NADP-specific glutatamate dehydrogenase (NADP-GDH) SP:P28724 [Giardia lambli	256174_at	1.2
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	1.2
unknown protein ;supported by full-length cDNA: Ceres:23788.	255957_at	1.2
predicted protein ; supported by full-length cDNA: Ceres: 11106.	255668_s_at	1.2
hypothetical protein	255611_at	1.2
cathepsin B-like cysteine protease, putative similar to cathepsin B-like cysteine proteinase GI:609175 from [Nicotiana rustica]; contains an unusually	255590_at	1.2
putative CHP-rich zinc finger protein similar to several A. thaliana CHP-rich proteins	255546_at	1.2
hypothetical protein identical to T10M13.21 ; supported by cDNA: gi_15293058_gb_AY050963.1_	255509_at	1.2
hypothetical protein ;supported by full-length cDNA: Ceres:6957.	255456_at	1.2
putative protein phosphatase regulatory subunit	255421_at	1.2
predicted protein of unknown function ; supported by cDNA: gi_15810532_gb_AY056305.1_	255332_at	1.2
putative calcium dependent protein kinase	255292_s_at	1.2
putative component of vesicle-mediated transport similar to N. tabacum N-ethylmaleimide sensitive fusion protein, GenBank accession number D86	255308_at	1.2
putative thioredoxin ; supported by cDNA: gi_16648848_gb_AY058202.1_	255279_at	1.2
putative protein Homo sapiens deubiquitinating enzyme UnpEL (UNP),PID:g2656141; supported by cDNA: gi_15450766_gb_AY054463.1_	254984_s_at	1.2
putative protein a 162 kDa component of a multi-protein complex phosphorylated by Src - Mus musculus,PID:g1205976; supported by cDNA: gi_12	254873_at	1.2
putative protein	254778_at	1.2
N-acetylornithine deacetylase-like protein, fragment N-acetylornithine deacetylase (AOdD) - Dictyostelium discoideum, PID:G763048	254690_at	1.2
putative protein transcription initiation factor IID beta chain, fruit fly, Pir2:B49453; supported by cDNA: gi_15293300_gb_AY051084.1_	254463_at	1.2
3-hydroxyisobutyrate dehydrogenase -like protein 3-hydroxyisobutyrate dehydrogenase, Rattus norvegicus, Pir:A32867;supported by full-length cDN	254445_at	1.2
tubulin beta-9 chain ;supported by full-length cDNA: Ceres:36891.	254446_at	1.2
putative protein	254417_at	1.2
putative NADPH quinone oxidoreductase Pig3 Homo sapiens, PID:G2754812;supported by full-length cDNA: Ceres:4621.	254393_at	1.2
DNA-directed RNA polymerase (EC 2.7.7.6) II second largest chain	254368_at	1.2
predicted protein PVPR3 protein, Phaesolis vulgaris, PATCHX:G169363;supported by full-length cDNA: Ceres:13832.	254276_at	1.2
putative protein various predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:20902.	254081_at	1.2
protein phosphatase 2C-like protein protein phosphatase 2C-fission yeast, PIR2:S54297; supported by cDNA: gi_16604584_gb_AY059737.1_	253780_at	1.2
putative protein WREBP-1, Nicotiana tabacum, EMBL:AB017693	253784_at	1.2
putative protein predicted protein. Arabidopsis thaliana; supported by cDNA: gi_15293152_gb_AY051010.1_	253739_at	1.2
putative protein SNF7 protein - Saccharomyces cerevisiae,PIR2:S52590;supported by full-length cDNA: Ceres:7471.	253735_at	1.2
putative protein heat shock protein 101 - Triticum aestivum,PID:g4558484	253614_at	1.2
predicted protein cation transport protein ChaC, Escherichia coli, PIR2:G64868;supported by full-length cDNA: Ceres:39740.	253522_at	1.2
putative protein cellulose synthase, Agrobacterium tumefaciens, PIR2:I39714	253533_at	1.2
putative protein RING-finger protein - Lotus japonicus,PIR2:S49446; supported by cDNA: gi_15983461_gb_AF424605.1_AF424605	253539_at	1.2
predicted protein RegA gene, Dictyostelium discoideum, PATCHX:G1405368	253500_at	1.2
aspartate aminotransferase ;supported by full-length cDNA: Ceres:33414., Ceres:103854.	253481_at	1.2
putative protein ATAC98, Arabidopsis thaliana; supported by cDNA: gi_15292682_gb_AY050775.1_	253465_at	1.2
glycine hydroxymethyltransferase (EC 2.1.2.1) - like protein glycine hydroxymethyltransferase, Pisum sativum, PIR2:A42906; supported by cDNA: g	253438_at	1.2
putative protein beta transducin-like protein, Podospora anserina, gb:L28125; supported by cDNA: gi_11141604_gb_AF277458.1_AF277458	253443_at	1.2
putative poly(A) polymerase polynucleotide adenylyltransferase (EC 2.7.7.19) class I - bovine, PIR2:S17875	253399_at	1.2
putative protein hypothetical protein F17H15.20 Arabidopsis thaliana chromosome II BAC F17H15, PID:g3643606	253401_at	1.2
putative protein hypothetical protein, Synechocystis sp., PIR2:S76307; supported by cDNA: gi_14596178_gb_AY042877.1_	253235_at	1.2
putative serine/threonine protein kinase Daucus carota somatic embryogenesis receptor-like kinase, gb:U93048	253239_at	1.2

Homeodomain - like protein similaritry to homeotic protein BEL1, Arabidopsis thaliana, PIR2:A57632	253247_at	1.2
arginine decarboxylase SPE2 ; supported by cDNA: gi_14517491_gb_AY039581.1_	253203_at	1.2
putative protein membrane-associated salt-inducible protein, Nicotiana tabacum, PIR:T02047	253209_at	1.2
cyclophilin - like protein cyclophilin, Arabidopsis thaliana, PID:g2443755	253216_at	1.2
protein kinase - like protein serine/threonine-specific protein kinase APK1, Arabidopsis thaliana, PIR2:S28615	253147_at	1.2
heat shock protein 70 like protein dnaK-type molecular chaperone PHSP1 -Pisum sativum,PID:g20835	253013_at	1.2
glycosyltransferase like protein alpha-1,3-mannosyl-glycoprotein beta-1,2-N-acetylglucosaminyltransferase (EC 2.4.1.101) I - rat,PIR2:JC2076	253035_at	1.2
putative protein ubiquitin fusion degradation protein - Schizosaccharomyces pombe, PID:e1132723	252947_at	1.2
putative protein NLS receptor - Oryza sativa, PID:d1032113	252948_at	1.2
putative protein unknown mRNA, Homo sapiens, AF091072	252968_at	1.2
putative ubiquitin-dependent proteolytic protein ubiquitin fusion-degradation protein - Mus musculus, PID:g1654348; supported by cDNA: gi_169304	252931_at	1.2
myo-inositol-1-phosphate synthase ;supported by full-length cDNA: Ceres:1978.	252863_at	1.2
putative protein br-1 protein (NITRIC OXIDE SYNTHASE) - Helix pomatia,PID:e234055	252410_at	1.2
H-protein promoter binding factor-2a ;supported by full-length cDNA: Ceres:113639.	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
hypothetical protein ;supported by full-length cDNA: Ceres:124275.	252321_at	1.2
putative protein predicted proteins, Arabidopsis thaliana	251946_at	1.2
fructokinase - like protein fructokinase, Lycopersicon esculentum, EMBL:LEU62329	251935_at	1.2
putative protein TATA-binding protein-binding protein, ABT1 - Mus musculus, EMBL:AB021860	251690_at	1.2
protein kinase-like protein Pto kinase interactor 1 - Lycopersicon esculentum, EMBL:U28007; supported by cDNA: gi_15451117_gb_AY054639.1_	251494_at	1.2
hypothetical protein	251460_at	1.2
putative protein carbonyl reductase (NADPH) - Rattus norvegicus, PIR:JC5285; supported by cDNA: gi_15028054_gb_AY045884.1_	251309_at	1.2
serine/threonine-protein kinase-like protein serine/threonine kinase UNC51.2 - Mus musculus, EMBL:AF145922; supported by cDNA: gi_14334751_	251273_at	1.2
putative protein hypothetical protein At2g38190 - Arabidopsis thaliana, EMBL:AC003028	251086_at	1.2
signal recognition particle 54CP protein precursor ; supported by cDNA: gi_15293130_gb_AY050999.1_	250884_at	1.2
putative protein NAC2, Arabidopsis thaliana, EMBL:AF201456; supported by cDNA: gi_6456750_gb_AF201456.1_AF201456	250849_at	1.2
cytochrom P450 - like protein cytochrome P450 77A3p, Glycine max., PIR:T05948;supported by full-length cDNA: Ceres:7867.	250859_at	1.2
putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:34592.	250861_at	1.2
putative protein contains similarity to unknown protein (gb AAF19567.1)	250809_at	1.2
SET-domain protein-like ; supported by cDNA: gi_13517742_gb_AF344444.1_AF344444	250817_at	1.2
meiotic check point regulator-like protein	250787_at	1.2
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
cleft lip and palate associated transmembrane protein-like	250522_at	1.2
putative protein NLI-interacting factor isoform T1, Gallus gallus, EMBL:AF189773;supported by full-length cDNA: Ceres:151766.	250298_at	1.2
auxin reponsive - like protein Nt-gh3 deduced protein, Nicotiana tabacum, EMBL:AF123503	250293_s_at	1.2
transaldolase - like protein transaldolase, Solanum tuberosum, EMBL:U95923;supported by full-length cDNA: Ceres:32114.	250234_at	1.2
putative protein apospory-associated protein C, Chlamydomonas reinhardtii, EMBL:AF195243;supported by full-length cDNA: Ceres:93845.	250186_at	1.2
cinnamoyl CoA reductase - like protein cinnamoyl CoA reductase, Populus tremuloides, EMBL:AF217958;supported by full-length cDNA: Ceres:172	250149_at	1.2
unknown protein	249808_at	1.2
putative protein contains similarity to general transcription factor IIIC, polypeptide 5	249735_at	1.2
unknown protein	249100_at	1.2
protein kinase-like protein	248853_at	1.2
Expressed protein ; supported by full-length cDNA: Ceres: 13184.	248813_at	1.2
putative protein strong similarity to unknown protein (gb|AAF56406.1)	248583_at	1.2
ubiquitin activating enzyme ;supported by full-length cDNA: Ceres:26820.	248523_s_at	1.2
MtN3-like protein ;supported by full-length cDNA: Ceres:36264.	248467_at	1.2
fumarate hydratase ; supported by cDNA: gi_15529146_gb_AY052197.1_	248461_s_at	1.2
phosphoglucomutase (emb|CAB64725.1) ; supported by cDNA: gi_12004569_gb_AF216580.1_AF216580	248380_at	1.2
arginine/serine-rich splicing factor RSP41 homolog ; supported by cDNA: gi_13877816_gb_AF370171.1_AF370171	248369_at	1.2
putative protein contains similarity to unknown protein (gb|AAF64546.1); supported by cDNA: gi_14596026_gb_AY042801.1_	248176_at	1.2
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
nucleolar protein-like	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
peroxisomal targeting signal type 1 receptor	248010_at	1.2
putative protein similar to unknown protein (ref|NP_004732.1);supported by full-length cDNA: Ceres:11265.	247942_at	1.2
putative protein predicted proteins, Drosophila melanogaster and Arabidopsis thaliana	247841_at	1.2
unknown protein	247859_at	1.2
putative protein predicted proteins, Arabidopsis thaliana	247770_at	1.2
putative protein predicted proteins, Arabidopsis thaliana	247698_at	1.2
putative protein contains similarity to DNA-binding protein;supported by full-length cDNA: Ceres:112281.	247430_at	1.2
putative protein similar to unknown protein (sp|P54122)	247385_at	1.2
unknown protein	247273_at	1.2
DNA binding protein TGA1a homolog ;supported by full-length cDNA: Ceres:31032.	247199_at	1.2
putative protein contains similarity to ATP binding protein associated with cell differentiation;supported by full-length cDNA: Ceres:2489.	247075_at	1.2
putative protein similar to unknown protein (gb|AAB71479.1|)	247062_at	1.2
SKP1 interacting partner 2 (SKIP2) identical to SKP1 interacting partner 2 GI:10716949 from [Arabidopsis thaliana]	247033_at	1.2
formin-like protein	246995_at	1.2
unknown protein	246957_at	1.2
putative protein predicted protein, Oryza sativa	246892_at	1.2
protein phosphatase - like protein phosphatase-2C, Mesembryanthemum crystallinum, AF075579	246868_at	1.2
long-chain-fatty-acid--CoA ligase-like protein long-chain-fatty-acid--CoA ligase - Brassica napus, EMBL:Z72152	246789_at	1.2
replication factor C - like replication factor C 38K chain, Homo sapiens, PIR:T09573	246738_at	1.2
formate dehydrogenase (FDH) ;supported by full-length cDNA: Ceres:7530.	246595_at	1.2
putative protein ;supported by full-length cDNA: Ceres:22994.	246486_at	1.2
putative protein SART-1 protein - Homo sapiens, PIR:T00034	246447_at	1.2
putative protein predicted protein, Drosophila melanogaster, EMBL:AE003450	246469_at	1.2
putative protein cisplatin resistance-associated overexpressed protein - Homo sapiens, EMBL:AB034205; supported by cDNA: gi_15450598_gb_AY	246436_at	1.2
putative protein sequence in GenBank Accession Number AC002330	246298_at	1.2
hypothetical protein	246281_at	1.2
step II splicing factor - like protein ; supported by cDNA: gi_15912280_gb_AY056418.1_	246221_at	1.2
T-complex protein 1, beta subunit T-COMPLEX PROTEIN 1, BETA SUBUNIT, Homo sapiens, EMBL:AF026293;supported by full-length cDNA: Cer	246191_at	1.2

putative protein predicted proteins, Homo sapiens	246066_at	1.2
Pspzf zinc finger protein - like DNA binding zinc finger protein (Pspzf), Pisum sativum, EMBL:AB018422	246012_at	1.2
homoserine dehydrogenase-like protein thrA bifunctional enzyme - Escherichia coli, PIR:B64720;supported by full-length cDNA: Ceres:123335.	246027_at	1.2
chaperonin precursor, putative similar to chaperonin precursor GI:806807 from [Pisum sativum]	245876_at	1.2
receptor serine/threonine kinase PR5K, putative similar to receptor serine/threonine kinase PR5K GI:1235680 from [Arabidopsis thaliana]	245760_s_at	1.2
Expressed protein ; supported by cDNA: gi_535587_gb_L36113.1_ATHATJ	245686_at	1.2
putative phosphocholine cytidylyltransferase	245533_at	1.2
hypothetical protein	245501_at	1.2
cysteine proteinase contains similarity to papain-like cysteine proteinase isoform I GI:7381219 from [Ipomoea batatas]	245483_at	1.2
apetala2 domain TINY like protein	245445_at	1.2
F-box protein family, AtFBL4 contains similarity to grr1 GI:2407790 from [Glycine max];supported by full-length cDNA: Ceres:100411.	245344_at	1.2
putative Na+/Ca2+ antiporter ; supported by cDNA: gi_6492236_gb_AF109178.1_AF109178	245127_at	1.2
ubiquitin-specific protease 5 (UBP5), putative similar to GI:6648604; supported by cDNA: gi_6648603_gb_AF048705.1_AF048705	245100_at	1.2
PSII low MW protein	244974_at	1.2
ribosomal protein S15	244938_at	1.2
unknown protein	257377_at	1.2
hypothetical protein predicted by genscan	257534_at	1.2
putative exonuclease contains zinc-finger C2H2-type domain; similar to X.laevis XPMC2 protein (XPMC2 prevents mitotic catastrophe in fission yeas	265767_at	1.2
putative squamosa-promoter binding protein 2 similar to GB:CAB56577;supported by full-length cDNA: Ceres:42666.	264444_at	1.1
unknown protein ESTs gb|R90323, gb|R90338. gb|Z25504 and gb|AA651448 come from this gene	262576_at	1.1
receptor protein kinase, putative contains Pfam profiles: PF00069 Eukaryotic protein kinase domain, PF00560 Leucine Rich Repeat	261552_at	1.1
unknown protein	261168_at	1.1
flavonol 3-o-glucosyltransferase, putative similar to flavonol 3-o-glucosyltransferase GB:Q40287 from [Manihot esculenta]	261048_at	1.1
unknown protein	258356_at	1.1
putative protein predicted protein, Arabidopsis thaliana;supported by full-length cDNA: Ceres:114412.	251554_at	1.1
disease resistance protein	249724_at	1.1
unknown protein ; supported by cDNA: gi_15450620_gb_AY052678.1_	267468_at	1.1
Expressed protein ; supported by full-length cDNA: Ceres: 114879.	267309_at	1.1
putative casein kinase II catalytic (alpha) subunit ;supported by full-length cDNA: Ceres:38084.	267257_at	1.1
DNA-(apurinic or apyrimidinic site) lyase (ARP) identical to GB:X76912	267099_at	1.1
putative glycine dehydrogenase	266892_at	1.1
putative ligand-gated ion channel protein	266782_at	1.1
putative helicase ; supported by cDNA: gi_15027926_gb_AY045820.1_	266679_at	1.1
copia-like retroelement pol polyprotein ; supported by cDNA: gi_15028176_gb_AY045911.1_	266698_at	1.1
putative poly(A) polymerase ; supported by cDNA: gi_14532699_gb_AY039974.1_	266659_at	1.1
putative flavonol 3-O-glucosyltransferase ;supported by full-length cDNA: Ceres:29796.	266643_s_at	1.1
putative transportin	266523_at	1.1
putative zinc-finger protein (B-box zinc finger domain)	266514_at	1.1
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:20820.	266450_s_at	1.1
putative elongation factor	266407_at	1.1
hypothetical protein	266304_at	1.1
putative methionyl-tRNA synthetase ; supported by cDNA: gi_14334467_gb_AY034925.1_	266057_at	1.1
putative cytochrome P450 identical to GB:D78604; supported by cDNA: gi_15450907_gb_AY054534.1_	266000_at	1.1
unknown protein ;supported by full-length cDNA: Ceres:9001.	265961_at	1.1
unknown protein	265810_at	1.1
unknown protein	265760_at	1.1
26S proteasome subunit 4 ;supported by full-length cDNA: Ceres:36815.	265595_at	1.1
unknown protein	265201_at	1.1
unknown protein ESTs gb|H76594 and gb|H76252 come from this gene	265217_s_at	1.1
hypothetical protein contains similarity to high-glucose-regulated protein 8 GB:AAF08813 GI:6449083 from [Homo sapiens]; supported by cDNA: gi_	265078_at	1.1
unknown protein Contains similarity to pre-mRNA processing protein PRP39 gb L29224 from S. cerevisiae. ESTs gb|R64908 and gb|T88158, gb|N3	265036_at	1.1
hypothetical protein predicted by genscan	264828_at	1.1
putative violaxanthin de-epoxidase precursor (U44133) similar to EST gb|N37612; supported by cDNA: gi_1465734_gb_U44133.1_ATU44133	264799_at	1.1
putative ligand-gated ion channel protein Similar to Arabidopsis putative ion-channel PID:g2262157 (gb|AC002329); supported by cDNA: gi_571318	264587_at	1.1
unknown protein ; supported by cDNA: gi_13430435_gb_AF360130.1_AF360130	264548_at	1.1
hypothetical protein similar to hypothetical protein GB:S51583	264515_at	1.1
unknown protein similar to T cell receptor beta chain CDR3 (gi|3064031); similar to nucleoporin NUP145 (sp|P49687|N145_YEAST); similar to EST	264456_at	1.1
putative chromodomain-helicase-DNA-binding protein similarity to Mi-2, Homo sapiens, GB:X86691; supported by cDNA: gi_6318929_gb_AF18557	264384_at	1.1
trehalose-6-phosphate synthase, putative similar to trehalose-6-phosphate synthase GI:297792 from [Kluyveromyces lactis]	264246_at	1.1
putative RNA polymerase sigma-70 factor ; supported by cDNA: gi_7209639_dbj_AB029916.1_AB029916	263846_at	1.1
unknown protein ;supported by full-length cDNA: Ceres:35274.	263802_at	1.1
unknown protein ; supported by cDNA: gi_16649002_gb_AY059871.1_	263774_at	1.1
unknown protein ESTs gb|T20589, gb|T04648, gb|AA597906, gb|T04111, gb|R84180, gb|R65428, gb|T44439, gb|T76570, gb|R90004, gb|T45020,	263709_at	1.1
putative purple acid phosphatase precursor	263553_at	1.1
hypothetical protein predicted by genscan and genefinder; supported by cDNA: gi_14596224_gb_AY042900.1_	263556_at	1.1
hypothetical protein predicted by genscan	263471_at	1.1
putative glucosyltransferase ; supported by cDNA: gi_15810476_gb_AY056277.1_	263477_at	1.1
putative importin (nuclear transport factor) protein	263448_at	1.1
subtilisin-like serine protease AIR3 almost identical to subtilisin-like protease AIR3 GI:4218991 from [Arabidopsis thaliana], missing 18 aa at C-termi	263406_at	1.1
unknown protein ; supported by cDNA: gi_15810336_gb_AY056207.1_	263326_at	1.1
hypothetical protein putative acetyl-CoA carboxylase (partial) dbj|BAA07012; similar to ESTs gb|AW144916.1, gb|AI993440.1, gb|T14234, gb|H7602	263192_at	1.1
hypothetical protein predicted by genefinder; supported by cDNA: gi_14423545_gb_AF387010.1_AF387010	263075_at	1.1
putative alanine aminotransferase similar to alanine aminotransferase GB:BAA77260 GI:4730884 from [Oryza sativa]; supported by cDNA: gi	262988_at	1.1
Dhp1-like protein similar to Dhp1 protein GB:BAA04601 GI:496393 from [Schizosaccharomyces pombe]; supported by cDNA: gi_11875627_gb_AF2	262923_at	1.1
hypothetical protein contains similarity to 30S ribosomal protein S5 GI:6969105 from [Campylobacter jejuni]; supported by cDNA: gi_14334893_gb_	262880_at	1.1
unknown protein ; supported by cDNA: gi_14596044_gb_AY042810.1_	262845_at	1.1
putative inosine-5-monophosphate dehydrogenase strong similarity to gb|L34684 inosine monophosphate dehydrogenase (IMPDH) from Arabidopsi	262754_at	1.1
TPR-repeat protein contains multiple TPR domains: Pfam profile: PF00515	262691_at	1.1
hypothetical protein Is a member of the PF|01177 Aspartate-glutamate racemase family. EST gb|T43554 comes from this gene	262582_at	1.1
auxilin-like protein similar to GB:CAB40994 from [Arabidopsis thaliana], EST gb|AA042488 comes from this gene	262493_at	1.1
DNA binding protein, putative similar to DNA binding protein GI:1899187 from [Nicotiana tabacum]	262433_s_at	1.1
hypothetical protein predicted by genemark.hmm	262130_at	1.1
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:116121.	262111_at	1.1
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) GB:4758032 (Homo	262051_at	1.1
ubiquitin, putative similar to poly-ubiquitin GB:AAC13691 GI:3047318 from [Pyricularia grisea]	261947_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
unknown protein ;supported by full-length cDNA: Ceres:111522.	261686_at	1.1
unknown protein similar to unknown protein GB:AAF24950 GI:6693024 from [Arabidopsis thaliana]; supported by cDNA: gi_13605566_gb_AF36160	261651_at	1.1
hypothetical protein similar to guanine nucleotide exchange factor-like protein GB:CAB82690 GI:7329696 from [Arabidopsis thaliana]	261621_at	1.1
unknown protein	261615_at	1.1
acyl CoA thioesterase, putative similar to HIV-Nef associated acyl CoA thioesterase GB:AAB71665 GI:2318125 from [Homo sapiens]	261560_at	1.1
K Efflux antiporter KEA1 identical to GB:AAD01191 GI:4101473 from [Arabidopsis thaliana]; supported by cDNA: gi_4101472_gb_AF003382.1_AF0	261536_at	1.1
unknown protein ; supported by cDNA: gi_14532543_gb_AY039896.1_	261519_at	1.1
unknown protein contains DNA-J domain; supported by cDNA: gi_15028270_gb_AY046050.1_	261458_at	1.1
hypothetical protein predicted by genemark.hmm	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	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.	261149_s_at	1.1
unknown protein ; supported by cDNA: gi_14334841_gb_AY035094.1_	261107_at	1.1
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:34178.	261026_at	1.1
unknown protein similar to unknown protein GB:AAF34848 GI:6997186 from [Arabidopsis thaliana]	261023_at	1.1
s-adenosylmethionine synthetase identical to s-adenosylmethionine synthetase GB:P23686 from [Arabidopsis thaliana]; supported by full-length cDN	260913_at	1.1
hypothetical protein similar to hypothetical protein GB:AAB67625 GI:2342727 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 300	260840_at	1.1
chloroplast inner envelope protein, putative similar to chloroplast inner envelope protein GB:CAA92823 GI:1495768 from [Pisum sativum]	260815_at	1.1
hypothetical protein predicted by genemark.hmm	260627_at	1.1
putative protein kinase contains a protein kinase domain profile (PDOC00100)	260562_at	1.1
phosphatidylinositol-4-phosphate 5-kinase isolog	260466_at	1.1
unknown protein ;supported by full-length cDNA: Ceres:27109.	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 ki	260362_at	1.1
putative ABC transporter contains Pfam profile: PF00005 ABC transporters; similar to TAP1 protein (transporter of processed antigen) GB:AAD5303	260308_at	1.1
unknown protein	260273_at	1.1
putative N-terminal acetyltransferase similar to N-TERMINAL ACETYLTRANSFERASE GB:P12945 from (Saccharomyces cerevisiae)	260282_at	1.1
unknown protein ;supported by full-length cDNA: Ceres:269548.	260137_at	1.1
putative protein kinase contains Pfam profile: PF00069 eukaryotic protein kinase domain	260073_at	1.1
endoplasmic reticulum alpha-mannosidase, putative similar to GI:5579331 from [Homo sapiens]; supported by cDNA: gi_15450803_gb_AY054482.	260029_at	1.1
ARE1-like protein similar to ARE1 GB:CAA11566 [Rattus norvegicus], Sacm21 GB:AAC69899 [Mus musculus]; unknown function	259939_s_at	1.1
putative translation initiation factor IF-2 similar to translation initiation factor IF-2 GB:P39730 [Saccharomyces cerevisiae]	259872_at	1.1
unknown protein ;supported by full-length cDNA: Ceres:9231.	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
hypothetical protein contains similarity to 1-phosphatidylinositol-4-phosphate 5-kinase(AtPIP5K1) GI:3702691 from [Arabidopsis thaliana]	259426_at	1.1
hypothetical protein gene model predicted by genscan and genefinder; supported by cDNA: gi_13430665_gb_AF360245.1_AF360245	259330_at	1.1
unknown protein similar to hect domain and RLD 2 GB:NP_004658 [Homo sapiens]	259334_at	1.1
hypothetical protein predicted by genscan	259295_at	1.1
putative aminopeptidase similar to X-prolyl aminopeptidase GB:NP_006514 from [Homo sapiens]	259296_at	1.1
putative cell division related protein similar to GlsA (required for asymmetric cell division) GB:AAD26632 [Volvox carteri f. nagariensis]	259284_at	1.1
protein phosphatase 2C (PP2C) identical to protein phosphatase 2C (PP2C) GB:P49598 [Arabidopsis thaliana]	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 pro	259165_at	1.1
unknown protein similar to unknown protein GB:BAA24863 [Homo sapiens], unknown protein GB:BAA20831 [Homo sapiens], unknown protein GB:	259118_at	1.1
putative cysteine synthase similar to cysteine synthase GB:BAA78562 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:37566.	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
hypothetical protein predicted by genscan	258844_at	1.1
unknown protein predicted by genscan, multiple est matches; supported by cDNA: gi_15027888_gb_AY045801.1_	258801_at	1.1
hypothetical protein similar to plant IF-like protein, GB:AAD09217;supported by full-length cDNA: Ceres:110680.	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	258675_at	1.1
unknown protein	258593_at	1.1
beta-glucosidase, putative similar to beta-glucosidase GB:AAF23823 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:37856.	258512_at	1.1
putative stearoyl-acyl carrier protein desaturase similar to stearoyl-acyl carrier protein desaturase GB:CAA07349 from [Linum usitatissimum];support	258485_at	1.1
14-3-3 protein GF14nu (grf7) identical to 14-3-3 protein GF14 nu GI:1531631 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:3794	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
lipoamide dehydrogenase precursor identical to GB:AAF34796 from [Arabidopsis thaliana]	258439_at	1.1
putative selenocysteine methyltransferase similar to selenocysteine methyltransferase GB:P56707 from [Astragalus bisulcatus];supported by full-len	258322_at	1.1
unknown protein contains GMC oxidoreductase domain; supported by cDNA: gi_13605691_gb_AF361827.1_AF361827	258299_at	1.1
unknown protein	258263_at	1.1
unknown protein	258202_at	1.1
putative GTP pyrophosphokinase similar to GTP PYROPHOSPHOKINASE GB:O87331 from [Corynebacterium glutamicum]; supported by cDNA: gi_	258207_at	1.1
unknown protein ;supported by full-length cDNA: Ceres:15577.	258188_at	1.1
unknown protein contains Pfam profile: PF01738 dienelactone hydrolase family; supported by cDNA: gi_13899072_gb_AF370531.1_AF370531	258108_at	1.1
putative tyrosine phosphatase similar to GB:AAF08382 from [Drosophila melanogaster]	258007_at	1.1
hypothetical protein contains Pfam profile:PF00534 Glycosyl transferases group 1	257797_at	1.1
unknown protein ;supported by full-length cDNA: Ceres:124193.	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	257621_at	1.1
methionine aminopeptidase, putative similar to methionine aminopeptidase I GB:AAA75193 [Saccharomyces cerevisiae]; supported by cDNA: gi_11	257646_at	1.1
zinc-binding dehydrogenase, putative contains Pfam profile: PF00107 zinc-binding dehydrogenases;supported by full-length cDNA: Ceres:34261.	257212_at	1.1
unknown protein ; supported by cDNA: gi_15146182_gb_AY049232.1_	257154_at	1.1
unknown protein	257018_at	1.1
unknown protein	256986_at	1.1
unknown protein	256928_at	1.1
unknown protein similar to alpha galactosidase GB:AAA73963 [Glycine max}	256866_at	1.1
casein kinase, putative similar to casein kinase 1 GB:NP_001883 from [Homo sapiens]	256783_at	1.1
unknown protein	256754_at	1.1
unknown protein ;supported by full-length cDNA: Ceres:13928.	256724_at	1.1
dTDP-glucose 4,6-dehydratase, putative similar to dTDP-glucose 4,6-dehydratase GB:AE000666 GI:6626257 from [Methanobacterium thermoautot	256575_at	1.1
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:108003.	256399_at	1.1
ATP-dependent Clp protease proteolytic subunit (ClpP3) identical to ATP-dependent Clp protease (nClpP3) GI:5360591 (Arabidopsis thaliana)	256411_at	1.1
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	1.1
ankyrin-like protein contains Pfam profile: PF00023 Ank repeat; supported by full-length cDNA: Ceres: 153785.	256233_at	1.1
unknown protein	256229_at	1.1
hypothetical protein	255876_at	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
putative protein predicted protein, Arabidopsis thaliana and various predicted ATP dependent RNA helicases	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	255473_at	1.1
contains a short region of similarity to another Arabidopsis hypothetical protein F19K23.8 (GB:AC000375)	255475_at	1.1
putative protein similar to A. thaliana protein F15K9.3, GenBank accession number 3850566	255466_at	1.1
putative oxidoreductase 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.	255230_at	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
putative protein W15DMY32F, W25DMY32F	254657_s_at	1.1
hypothetical protein	254602_at	1.1
hypothetical protein	254501_at	1.1
putative protein various predicted proteins;supported by full-length cDNA: Ceres:17340.	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_AF082176.1_AF082176	254194_at	1.1
hsp 70-like protein heat shock 70 protein - Spinacia oleracea,PID:g2654208	254148_at	1.1
putative proteasome regulatory subunit KIAA0107 gene, Homo sapiens, D14663;supported by full-length cDNA: Ceres:38927.	254086_at	1.1
SRG1-like protein strong homology to SRG1 protein, a new member of the Fe(II)/ascorbate oxidase superfamily, PID:g479047	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,PID	253615_at	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
putative protein cyclopropane-fatty-acyl-phospholipid synthase, Escherichia coli, PIR2:A44292; supported by full-length cDNA: Ceres: 4369.	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.	252945_at	1.1
putative protein alpha-amino-epsilon-caprolactam racemase, Achromobacter obae, PIR2:JC1497; supported by cDNA: gi_5731258_gb_AF166351.1	252855_at	1.1
putative protein 70K peroxisomal membrane protein, Rattus norvegicus ,PIR2:A35723; supported by cDNA: gi_15320528_gb_AF378120.1_AF3781	252830_at	1.1
putative protein ; supported by cDNA: gi_14334983_gb_AY035165.1_	252391_at	1.1
putative protein predicted proteins, Arabidopsis thaliana	252402_s_at	1.1
betaine aldehyde dehydrogenase-like protein betaine aldehyde dehydrogenase - Amaranthus hypochondriacus,PID:g2388710; supported by cDNA:	252354_at	1.1
putative protein pir7a 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-lengt	251757_at	1.1
alpha-soluble NSF attachment protein ; supported by cDNA: gi_6013203_gb_AF177989.1_AF177989	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	251628_at	1.1
ATP-dependent RNA helicase-like protein ATP-dependent RNA helicase - Xenopus laevis, PIR:S13654;supported by full-length cDNA: Ceres:4158.	251529_at	1.1
putative protein PBK1 protein, Homo sapiens, EMBL:HSA7398	251538_at	1.1
putative protein crp1 protein, involved in post-transcriptional control of chloroplast gene expression - Zea mays, PIR:T01685	251496_at	1.1
putative protein hypothetical proteins - Arabidopsis thaliana; supported by cDNA: gi_14334587_gb_AY034967.1_	251356_at	1.1
putative protein several hypothetical proteins - Arabidopsis thaliana; supported by cDNA: gi_14517361_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, EMBL:AB025342	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_	250014_at	1.1
casein kinase-like protein	250021_at	1.1
soluble starch synthase	249785_at	1.1
acyl-peptide hydrolase-like	249690_at	1.1
putative protein tropomyosin gene 1, isoform 9D, D.melanogaster, EMBL:DMTRO13	249628_at	1.1
cysteine-tRNA ligase -like protein cysteine-tRNA ligase, Arabidopsis thaliana, PIR:T47747	249537_at	1.1
kanadaptin - like protein unnamed ORF, Homo sapiens, EMBL:AK001486	249538_at	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:O64948 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
F12A21.17 similar to signal recognition particle 72kD gi|5902124	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	259704_at	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
putative reverse-transcriptase -like protein putative reverse-transcriptase T6B13.11 -Arabidopsis thaliana,PID:g3810595	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	1
unknown protein	266839_at	1
FtsH protease, putative contains similarity to YME1 GI:295582, a member of the ftsH-SEC18-PAS1-CDC48 family of putative ATPase-encoding gen	266842_at	1
putative peptide chain release factor	266751_at	1
phytochrome B Identical to GB:X17342	266065_at	1
putative potassium/proton antiporter	265936_at	1
unknown protein ; supported by cDNA: gi_15450955_gb_AY054558.1_	265799_at	1
unknown protein similar to ovarian tumor protein; supported by cDNA: gi_16604333_gb_AY058065.1_	265630_at	1
unknown protein similarity to ubiquitin family of proteins; supported by cDNA: gi_16930424_gb_AF419566.1_AF419566	265461_at	1
hypothetical protein	265425_at	1
similar to mammalian MHC III region protein G9a	265347_at	1
histidine transport protein (PTR2-B) ; supported by cDNA: gi_13937184_gb_AF372946.1_AF372946	265220_at	1
putative auxin-induced protein ;supported by full-length cDNA: Ceres:155143.	265182_at	1
similar to glucose 1-dehydrogenase (AB000617); similar to EST gb|T88100 similar to oxidoreductase-like protein GB:CAB75763 GI:7019662 from [A	265107_s_at	1

similar to 14KD proline-rich protein DC2.15 precursor (sp|P14009); similar to ESTs emb|Z17709 and emb|Z47685 similar to hybrid proline-rich protei	265111_at	1
hypothetical protein predicted by genscan	265092_at	1
hypothetical protein contains similarity to light-induced DNA-binding protein(CG-1) GI:587503 from [Petroselinum crispum]	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.	264957_at	1
hypothetical protein predicted by genemark.hmm	264935_at	1
hypothetical protein similar to hypothetical protein GB:CAB45806	264792_at	1
unknown protein similar to L-allo-threonine aldolase (D87890); similar to ESTs gb|R30517, gb|T42772, gb|R90493, and gb|R90493;supported by ful	264777_at	1
unknown protein	264516_at	1
fumarylacetoacetate hydrolase-like protein similar to fumarylacetoacetate hydrolase, gb|L41670 from Emericella nidulans	264396_at	1
unknown protein similar to Lambda-PRL2 Arabidopsis thaliana cDNA clone GB:R30041	264354_s_at	1
unknown protein ESTs gb|T21276, gb|T45403, and gb|AA586113 come from this gene; supported by cDNA: gi_15293190_gb_AY051029.1_	264367_at	1
hypothetical protein predicted by genemark.hmm	264299_s_at	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
putative SF2/ASF splicing modulator, Srp30 similar to GB:CAB42558	264255_at	1
hypothetical protein predicted by genemark.hmm	264268_at	1
hypothetical protein predicted by genemark.hmm; supported by cDNA: Ceres: 11408 (cDNA not full-length)	264141_at	1
mercaptopyruvate sulfurtransferase (Mst1/Rdh1) identical to mercaptopyruvate sulfurtransferase GI:6009981 and thiosulfate sulfurtransferase GI:58	264095_at	1
unknown protein	264048_at	1
putative salt-inducible protein	263958_at	1
putative fructose bisphosphate aldolase ;supported by full-length cDNA: Ceres:13024.	263921_at	1
putative pyruvate kinase ;supported by full-length cDNA: Ceres:120685.	263922_s_at	1
putative ATP synthase ;supported by full-length cDNA: Ceres:31766.	263874_at	1
hypothetical protein predicted by genscan	263864_at	1
putative protein kinase contains a protein kinase domain profile (PDOC00100);supported by full-length cDNA: Ceres:123911.	263804_at	1
coatomer alpha subunit	263743_at	1
unknown protein ;supported by full-length cDNA: Ceres:20834.	263755_at	1
putative vacuolar proton-ATPase subunit ; supported by cDNA: gi_15450750_gb_AY053417.1_	263764_at	1
gamma-adaptin, putative similar to gamma-adaptin GI:2765190 from [Homo sapiens]	263728_at	1
3-methyladenine DNA glycosylase, putative Strong similarity to GB:P29102, 3-isopropylmalate dehydrogenase (IMDH) from Brassica napus. EST g	263706_s_at	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
unknown protein	263639_at	1
putative trehalose-6-phosphate phosphatase	263452_at	1
putative bZIP transcription factor contains a bZIP transcription factor basic domain signature (PDOC00036); supported by cDNA: gi_15450833_gb_A	263414_at	1
putative protein kinase contains a protein kinase domain profile (PDOC00100);supported by full-length cDNA: Ceres:13257.	263419_at	1
putative pre-mRNA splicing factor similar to splicing factor hPRP17 (gi|3283220); similar to ESTs emb|F15435 and dbj|AUO62661	263261_at	1
UDP-glucose:indole-3-acetate beta-D-glucosyltransferase, putative similar to UDP-glucose:indole-3-acetate beta-D-glucosyltransferase GI:2149127	263184_at	1
hypothetical protein predicted by genemark.hmm	263145_at	1
prenyltransferase, putative similar to prenyltransferase GI:1651651 from [Synechocystis sp.]	263122_at	1
trehalose-6-phosphate synthase, putative similar to trehalose-6-phosphate synthase GI:4468259 from [Pichia angusta]; supported by cDNA: gi_138	263136_at	1
dihydrolipoamide S-acetyltransferase, putative similar to dihydrolipoamide S-acetyltransferase GI:5669871 from [Zea mays]; supported by cDNA: gi_	262963_at	1
hypothetical protein contains similarity to protein kinase (PK6) GI:170046 from [Glycine max]	262934_s_at	1
RNA-directed RNA polymerase, putative similar to RNA-directed RNA polymerase GB:CAA09697 GI:4138282 [Nicotiana tabacum]	262888_at	1
putative glycogen synthase strong similarity to gb|X95759 soluble-starch-synthase precursor (SSIII) from Solanum tuberosum	262809_at	1
aspartate aminotransferase nearly identical to aspartate aminotransferase, cytoplasmic isozyme 2 SP:P46646 [Arabidopsis thaliana (Mouse-ear cre	262646_at	1
oxidoreductase, putative contains Pfam profile: PF00671 Iron/Ascorbate oxidoreductase family; supported by cDNA: gi_13878118_gb_AF370322.1_	262638_at	1
putative glutathione transferase One of three repeated putative glutathione transferases. 72% identical to glutathione transferase [Arabidopsis thalia	262518_at	1
Mlo protein, putative similar to Mlo protein GB:Z83834 GI:1877220 from [Hordeum vulgare];supported by full-length cDNA: Ceres:259664.	262455_at	1
serine/threonine kinase, putative similar to serine/threonine kinase GB:Y12530 GI:2181187 from [Brassica oleracea]; supported by cDNA: gi_15810	262458_at	1
unknown protein	262331_at	1
pale cress protein identical to GB:CAA65334;supported by full-length cDNA: Ceres:28047.	262316_at	1
putative cyclin similar to cyclin GB:4502627 from [Homo sapiens];supported by full-length cDNA: Ceres:33877.	262296_at	1
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	1
peptide transporter, putative similar to PEPTIDE TRANSPORTER PTR2-B GB:P46032 GI:1172704 from [Arabidopsis thaliana]	262281_at	1
hypothetical protein predicted by genscan+	262207_at	1
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_16209708_gb_AY057616.1_	262223_at	1
Avr9 elicitor response protein, putative similar to Avr9 elicitor response protein GI:4138265 from [Nicotiana tabacum]	262188_at	1
glutathione S-transferase, putative similar to glutathione S-transferase GI:860955 from [Hyoscyamus muticus]; supported by cDNA: gi_15215607_g	262119_s_at	1
hypothetical protein contains similarity to helicase-like protein NHL GI:6969265 from [Homo sapiens]	262066_at	1
hypothetical protein contains similarity to PP2 lectin polypeptide GI:410436 from [Cucurbita maxima]; supported by cDNA: gi_15292968_gb_AY0509	262061_at	1
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:206286.	261921_at	1
unknown protein	261885_at	1
unknown protein	261853_at	1
DNA-binding protein, putative similar to helicase-like transcription factor GB:CAA86572 GI:1658307 from [Homo sapiens]; supported by cDNA: gi_1	261862_at	1
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:108306.	261823_at	1
unknown protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pfam pro	261513_at	1
RIBOSOMAL PROTEIN, putative similar to 30S RIBOSOMAL PROTEIN S1 GB:P46228 from [Synechococcus sp.]; supported by cDNA: gi_150818	261522_at	1
hypothetical protein predicted by genemark.hmm	261524_at	1
hypothetical protein contains similarity to zinc finger protein GI:1399465 from [Cryptosporidium parvum];supported by full-length cDNA: Ceres:20571	261376_at	1
proton pump interactor, putative similar to GB:CAB43882 from [Arabidopsis thaliana]	261365_at	1
unknown protein	261250_at	1
hypothetical protein predicted by genemark.hmm	261183_at	1
disulfide isomerase-related protein, putative similar to GB:AAB50217 from [Homo sapiens]	261167_at	1
hypothetical protein predicted by genemark.hmm	261173_at	1
unknown protein	261179_at	1
ribokinase, putative similar to GB:AAD00536 from [Pyrobaculum aerophilum]	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	261084_at	1
hypothetical protein similar to unknown protein GB:AAF32477 GI:6957733 from [Arabidopsis thaliana]	261043_at	1
glyoxalase II, putative similar to GI:1644427 from (Arabidopsis thaliana); supported by cDNA: gi_15450394_gb_AY052298.1_	260986_at	1
26S proteasome regulatory particle triple-A ATPase subunit4, putative similar to 26S proteasome regulatory particle triple-A ATPase subunit4 GI:11	260940_at	1
peptide transporter PTR2-B, putative similar to SP:P46032 from [Arabidopsis thaliana]	260693_at	1
hypothetical protein predicted by genscan+	260663_at	1
unknown protein ; supported by full-length cDNA: Ceres: 4026.	260673_at	1
unknown protein	260679_at	1
endochitinase isolog	260568_at	1
putative electron transfer flavoprotein ubiquinone oxidoreductase	260536_at	1
putative protein kinase similar to protein kinase APK1A GB:Q06548 [Arabidopsis thaliana]; contains Pfam profile: PF00069 Eukaryotic protein kinase	260415_at	1
receptor protein kinase, putative similar to receptor protein kinase GI:1389566 from (Arabidopsis thaliana); supported by cDNA: gi_4204848_gb_U5	260345_at	1

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
unknown protein	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	259259_at	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_16604636_gb_AY059763.1_	259156_at	1
hypothetical protein predicted by genemark.hmm, contains Pfam profile:PF01553 Acyltransferase; supported by cDNA: gi_14423461_gb_AF386968	259113_at	1
26S proteasome AAA-ATPase subunit RPT5a identical to GB:AAF22525 from [Arabidopsis thaliana]; supported by cDNA: gi_5669046_gb_AF08157	259114_at	1
unknown protein	259121_at	1
putative zeta-carotene desaturase precursor nearly identical to zeta-carotene desaturase precursor GB:AAA91161 [Arabidopsis thaliana];supported	259092_at	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	258860_at	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
putative RNA helicase similar to RNA helicase GB:CAA09200 from [Arabidopsis thaliana]	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	258456_at	1
unknown protein similar to leucine-rich repeat protein GB:CAA76000 and GB:CAA76001 from [Arabidopsis thaliana]	258390_at	1
unknown protein contains Pfam profile: PF00076 RNA recognition motif	258229_at	1
Snf1-related protein kinase KIN11 (AKIN11) identical to protein kinase AKin11 GI:1729444 [Arabidopsis thaliana]	258221_at	1
phosphoprotein phosphatase, putative similar to phosphoprotein phosphatase GB:AAB18613 from [Mus musculus]	258215_at	1
glutamine synthetase, putative similar to Gln synthetase GB:228456 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:5507.	258160_at	1
chaperonin subunit, putative similar to cytosolic chaperonin, delta-subunit GB:CAA09989 [Glycine max]; contains Pfam profile: PF00118 TCP-1/cpn	258152_at	1
putative protein peroxidase - Lycopersicon esculentum, PIR:S32768	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
unknown protein contains Pfam profile: PF00400 2 WD domains, G-beta repeats	257684_s_at	1
cytochrome P450, putative similar to cytochrome P450 GB:O65784 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 262802.	257634_s_at	1
cytochrome P450 monooxygenase (CYP71B4) identical to cytochrome P450 monooxygenase (CYP71B4) GB:D78603 [Arabidopsis thaliana] (Plant	257635_at	1
cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450;supported by full-length cDNA: Ceres:149380.	257129_at	1
unknown protein similar to unknown protein GB:AAD43153 from [Arabidopsis thaliana]	256944_at	1
glutamine:fructose-6-phosphate amidotransferase, putative similar to glutamine:fructose-6-phosphate amidotransferase 2 GB:BAA74729 [Mus musc	256911_at	1
aminotransferase, putative similar to aminotransferase GB:CAA19897 from [Streptomyces coelicolor A3(2)]; supported by cDNA: gi_14334463_gb_	256765_at	1
unknown protein ; supported by cDNA: gi_13899104_gb_AF370547.1_AF370547	256683_at	1
hypothetical protein predicted by genemark.hmm	256613_at	1
protein kinase, putative contains Pfam profile: PF00069: Eukaryotic protein kinase domain	256529_at	1
deoxyguanosine kinase, putative similar to deoxyguanosine kinase [Homo sapiens] GI:1480198;supported by full-length cDNA: Ceres:3878.	256341_at	1
unknown protein	256294_at	1
protein kinase, putative contains Pfam profile: PF00069 Eukaryotic protein kinase domain	256291_at	1
transcription factor HBP-1B-like nearly identical to transcription factor HBP-1B SP:P43273 [Arabidopsis thaliana (Mouse-ear cress)]; supported by cD	256269_at	1
nascent polypeptide associated complex alpha chain, putative similar to nascent polypeptide associated complex alpha chain GB:AAF27917 GI:675	256241_at	1
unknown protein	256100_at	1
hypothetical protein similar to polygalacturonase-like protein GI:10177371 from [Arabidopsis thaliana]	256038_at	1
integral membrane protein, putative similar to integral membrane protein 1 (Itm1) GI:508542 from [Mus musculus]	256029_at	1
unknown protein contains similarity to apoptosis-related protein TFAR19 GI:2407068 from [Homo sapiens];supported by full-length cDNA: Ceres:331	256001_at	1
hypothetical protein contains Pfam profile: PF01416 tRNA pseudouridine synthase; supported by cDNA: gi_14334543_gb_AY035176.1_	255887_at	1
hypothetical protein contains similarity to PF01535 PPR repeat; supported by cDNA: gi_15450346_gb_AY052274.1_	255888_at	1
ABC transporter, putative similar to ABC transporter GI:10280532 from [Homo sapiens]	255889_at	1
kinase, putative similar to leaf rust resistance kinase Lr10 GI:1680685 from [Triticum aestivum]	255913_at	1
putative PTR2 family peptide transporter	255877_at	1
putative serine carboxypeptidase II	255842_at	1
Shaggy related protein kinase tetha ; supported by cDNA: gi_17063157_gb_AY062099.1_	255635_at	1
hypothetical protein ; supported by cDNA: gi_14517493_gb_AY039582.1_	255557_at	1
hypothetical protein similar to A. thaliana hypothetical protein from chromosome III, GenBank accession number 3068704	255492_at	1
hypothetical protein similar to A. thaliana hypothetical protein F6E13.15, GenBank accession number 3212859	255465_at	1
4-coumarate--CoA ligase - like protein 4-coumarate--CoA ligase 4CL, Arabidopsis thaliana, PIR:S57784	255263_at	1
putative protein chromatin structural protein homolog Supt5hp - Mus musculus,PID:g2754752	255136_s_at	1
neutral invertase like protein Daucus carota mRNA, PID:e1372926;supported by full-length cDNA: Ceres:156092.	255038_at	1
putative protein RNA helicase -Mus musculus,PIR2:I84741	255053_at	1
hypothetical protein	255026_at	1

choline kinase GmCK2p -like protein choline kinase GmCK2p -Glycine max,PID:g1438881;supported by full-length cDNA: Ceres:126037., Ceres:73	254998_at	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	254759_at	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:I38908	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: gi_14423555_gb_AF387015.1_AF387015	254174_at	1
HSP90-like protein HSP90 homolog - Catharanthus roseus, PIR2:S39558; supported by cDNA: gi_14532541_gb_AY039895.1_	254166_at	1
brefeldin A-sensitive Golgi protein - like brefeldin A-sensitive Golgi protein LDLC, Homo sapiens, PIR2:A53542; supported by cDNA: gi_13605802_	254087_at	1
P-glycoprotein-2 (pgp2)	254034_at	1
fimbrin-like protein (ATFIM1) ; supported by cDNA: gi_2905892_gb_U66424.1_ATU66424	253956_at	1
SERINE CARBOXYPEPTIDASE II - like protein serine-type carboxypeptidase, Hordeum vulgare, PIR2:S44191; supported by cDNA: gi_15293048_	253600_at	1
ubiquitin-specific protease 24 (UBP24), putative similar to GI:11993488; ubiquitin carboxyl-terminal hydrolase, Mus musculus, PID:D101289; suppo	253552_at	1
putative protein crp1 protein, Zea mays, Z14393	253495_at	1
sulfolipid biosynthesis protein SQD1 ; supported by cDNA: gi_14190482_gb_AF380641.1_AF380641	253386_at	1
F-box protein family, AtFBL15 contains similarity to F-box protein FBL2 GI:6063090 from [Homo sapiens]	253369_at	1
putative protein FAB1 protein, Saccharomyces cerevisiae, PIR2:S56274	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 longiflorum, 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	252527_at	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, Dictyostelium 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	250950_at	1
monodehydroascorbate reductase (NADH) - like protein monodehydroascorbate reductase (NADH), cucumber, PIR:JU0182;supported by full-length	250916_at	1
putative protein ;supported by full-length cDNA: Ceres:257390.	250882_at	1
putative protein contains similarity to unknown protein	250656_at	1
putative protein	250624_at	1
DR1-like protein TATA-binding protein-associated phosphoprotein Dr1 - Arabidopsis thaliana, EMBL:D38110supported by full-length cDNA: Ceres:3	250543_at	1
splicing factor-like protein ; supported by cDNA: gi_15451045_gb_AY054603.1_	250457_at	1
unknown protein ; supported by cDNA: gi_15983383_gb_AF424566.1_AF424566	250459_at	1
protein serine/threonine kinase-like protein putative protein serine/threonine kinase - Sorghum bicolor, EMBL:Y14600	250480_at	1
putative protein predicted proteins, Homo sapiens, Drosophila melanogaster, Caenorhabditis elegans	250377_at	1
putative protein various predicted proteins, Arabidopsis thaliana	250381_at	1
putative protein predicted proteins, Arabidopsis thaliana	250350_at	1
alpha-N-acetylglucosaminidase	250245_at	1
unknown protein	250232_at	1
early nodule-specific protein - like early nodule-specific protein, Medicago truncatula, EMBL:AF064775	250180_at	1
Expressed protein ; supported by cDNA: gi_16648944_gb_AY059842.1_	250134_at	1
potassium-dependent sodium-calcium exchanger - like protein potassium-dependent sodium-calcium exchanger (NCKX2), Rattus norvegicus, EMB	250054_at	1
putative protein non-consensus GC donor splice site at exon 1, unknown (C40) protein, Homo sapiens, EMBL:AF103798	250042_at	1
putative protein FACTOR ASSOCIATED WITH N-SMASE ACTIVATION, Homo sapiens, SWISSPROT:FAN_HUMAN	249989_at	1
putative protein 2 -hydroxyisoflavone reductase (EC 1.3.1.45) - Nicotiana tabacum, PIR:T02202;supported by full-length cDNA: Ceres:17121.	250006_at	1
putative protein contains similarity to two-component response regulator protein; supported by cDNA: gi_10281005_dbj_AB046955.1_AB046955	249741_at	1
fimbrin ; supported by cDNA: gi_15027846_gb_AY045780.1_	249720_at	1
DNA helicase-like	249677_at	1
unknown protein	249679_at	1
5-oxoprolinase -like protein 5-oxoprolinase (ATP-hydrolyzing) (EC 3.5.2.9) - rat, PIR:T42756	249585_at	1
receptor serine/threonine protein kinase -like receptor serine/threonine kinase PR5K, Arabidopsis thaliana, EMBL:AT48698	249552_s_at	1
putative protein crp1, Zea mays, PIR:T01685	249464_at	1
putative protein strong similarity to unknown protein (pir||T13026)	249303_at	1

cell cycle control crn (crooked neck) protein-like	249269_at	1
glucose-6-phosphate isomerase, cytosolic (GPI) (phosphoglucose isomerase) (PGI) (phosphohexose isomerase) (PHI) (sp|P34795) ; supported by	249163_at	1
26S proteasome AAA-ATPase subunit RPT4a (gb|AAF22524.1) ; supported by cDNA: gi_13937182_gb_AF372945.1_AF372945	249180_at	1
putative protein strong similarity to unknown protein (gb|AAF24960.1)	249133_at	1
1-aminocyclopropane-1-carboxylate oxidase ; supported by cDNA: gi_15983808_gb_AY056810.1_	249128_at	1
protein transport protein SEC23 ; supported by cDNA: gi_15810472_gb_AY056275.1_	249106_at	1
PINHEAD (gb|AAD40098.1); translation initiation factor	249115_at	1
putative protein similar to unknown protein (dbj|BAA91806.1); supported by cDNA: gi_13877730_gb_AF370128.1_AF370128	249092_at	1
WD-repeat protein-like	249066_at	1
Expressed protein ; supported by full-length cDNA: Ceres: 121432.	249026_at	1
disease resistance protein-like	248994_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
unknown protein ;supported by full-length cDNA: Ceres:114691.	248881_at	1
putative protein contains similarity to RNA-binding protein;supported by full-length cDNA: Ceres:265530.	248869_at	1
putative protein contains similarity to maturase-related protein	248815_at	1
putative protein strong similarity to unknown protein (gb|AAF07790.1)	248755_at	1
putative protein contains similarity to acyl-CoA thioesterase	248697_at	1
receptor-like protein kinase ; supported by cDNA: gi_13605826_gb_AF367312.1_AF367312	248698_at	1
isoleucyl-tRNA synthetase	248634_at	1
putative protein strong similarity to unknown protein (gb|AAD32890.1)	248574_at	1
putative protein strong similarity to unknown protein (pir||T04010)	248581_at	1
adenylate kinase ;supported by full-length cDNA: Ceres:21741.	248506_at	1
unknown protein	248471_at	1
receptor protein kinase-like	248454_at	1
unknown protein ;supported by full-length cDNA: Ceres:36309.	248378_at	1
AP2 domain transcription factor-like protein	248389_at	1
RNA-binding protein-like	248294_at	1
putative protein 3 (2), 5 -bisphosphate nucleotidase protein-like; also similar to yeast halotolerance protein HAL2;supported by full-length cDNA: Ce	248155_at	1
putative protein similar to unknown protein (pir||T40314)	247977_at	1
putative protein contains similarity to protein kinase; supported by cDNA: gi_15810440_gb_AY056259.1_	247985_at	1
apospory-associated protein C	247929_at	1
contains similarity to phosphoesterase	247854_at	1
dTDP-glucose 4-6-dehydratase - like protein dTDP-glucose 4-6-dehydratase, Cicer arietinum, EMBL:CAR275318;supported by full-length cDNA: Ce	247720_at	1
GTP-binding protein rab11 - like GTP-binding protein rab11, Arabidopsis thaliana, PIR:T12965; supported by cDNA: gi_13877728_gb_AF370127.1_	247722_at	1
protein disulfide isomerase precursor - like protein disulfide isomerase precursor, Volvox carteri, EMBL:AF110784;supported by full-length cDNA: C	247588_at	1
putative protein kinase-like transmembrane protein TMKL1 precursor, Arabidopsis thaliana, EMBL:ATTMKL1	247533_at	1
putative protein predicted protein, Arabidopsis thaliana	247487_at	1
KED - like protein KED, Nicotiana tabacum, EMBL:AB009883	247480_at	1
1-deoxy-D-xylulose 5-phosphate reductoisomerase (DXR) ;supported by full-length cDNA: Ceres:117626.	247401_at	1
diacylglycerol kinase	247346_at	1
pectin methylesterase-like protein supported by full-length cDNA: Ceres: 21903.	247239_at	1
putative protein similar to unknown protein (gb AAD20127.1); supported by full-length cDNA: Ceres: 11225.	247140_at	1
putative protein strong similarity to unknown protein (ref|NP_005638.1); supported by cDNA: gi_16323187_gb_AY057698.1_	247002_at	1
putative protein hypothetical proteins - Arabidopsis thaliana	246979_s_at	1
CLC-d chloride channel protein	246886_at	1
putative protein predicted proteins, Arabidopsis thaliana	246820_at	1
UDP-glucose dehydrogenase-like protein UDP-glucose 6-dehydrogenase - Glycine max, EMBL:U53418; supported by cDNA: gi_15810322_gb_AY	246511_at	1
Carboxylesterase-like protein sterol esterase - Rattus norvegicus, EMBL:Z22803	246524_at	1
putative protein several hypothetical proteins - Arabidopsis thaliana	246478_at	1
14-3-3 protein GF14upsilon (grf5) identical to 14-3-3 protein GF14 upsilon GI:2232148 from [Arabidopsis thaliana] ; supported by cDNA: gi_1433453	246489_at	1
putative protein predicted proteins - Arabidopsis thaliana;supported by full-length cDNA: Ceres:34944.	246452_at	1
lethal leaf-spot 1 homolog Lls1	246335_at	1
high mobility group protein 2-like ; supported by cDNA: gi_15912190_gb_AY056373.1_	246311_at	1
cytochrome P450, putative contains Pfam profile: PF00067: Cytochrome P450; supported by cDNA: gi_15912336_gb_AY056446.1_	246268_at	1
tubulin-like protein	246278_at	1
G-box-binding factor 1 ; supported by cDNA: gi_15450987_gb_AY054574.1_	246211_at	1
26S proteasome AAA-ATPase subunit RPT6a - like protein 26S proteasome AAA-ATPase subunit RPT6a, Arabidopsis thaliana, EMBL:AF123395;s	246147_s_at	1
putative protein VAC8 protein, Saccharomyces cerevisiae, PIR:S50446	246062_at	1
protein phosphatase 2A regulatory subunit B-like protein protein phosphatase 2A 62 kDa B regulatory subunit, Arabidopsis thaliana, TREMBL:AF1	246050_s_at	1
lipoic acid synthase - like protein lipoic acid synthase, Arabidopsis thaliana, PIR:T44259;supported by full-length cDNA: Ceres:152427.	246005_at	1
SIR2-family protein sirtuin type 4 (SIRT4) - Homo sapiens, EMBL:AF083109; supported by cDNA: gi_15028032_gb_AY045873.1_	245895_at	1
potassium transport protein-like several potassium transport proteins	245897_at	1
GTL1 - like protein GTL1, Arabidopsis thaliana, EMBL:ATAJ3215; supported by cDNA: gi_14423451_gb_AF386963.1_AF386963	245861_at	1
pinoresinol-lariciresinol reductase, putative similar to pinoresinol-lariciresinol reductase GB:AAF63508 GI:7542583 from [Thuja plicata];supported by	245792_at	1
putative protein ;supported by full-length cDNA: Ceres:29990.	245699_at	1
RNA-binding protein-like	245714_at	1
hypothetical protein predicted by genemark.hmm	245659_at	1
unknown protein ;supported by full-length cDNA: Ceres:21415.	245626_at	1
acylaminoacyl-peptidase like protein	245594_at	1
SNF1 like protein kinase ; supported by cDNA: gi_13249502_gb_AY007221.1_	245563_at	1
hypothetical protein	245502_at	1
hypothetical protein	245517_at	1
Expressed protein ;supported by cDNA: gi:14423393	245521_at	1
disease resistance RPP5 like protein	245456_at	1
hypothetical protein	245430_at	1
putative serine protease-like protein	245432_at	1
G2484-1 protein	245415_at	1
hypothetical protein ; supported by cDNA: gi_16323154_gb_AY057681.1_	245272_at	1
putative dihydrodipicolinate synthase ;supported by full-length cDNA: Ceres:26817.	245145_at	1
subtilisin-like serine protease contains similarity to subtilisin-like protease C1 GI:13325079 from [Glycine max]	245088_at	1
hypothetical protein predicted by genscan	264806_at	1
unknown protein	256505_at	1
unknown protein	267071_at	0.9
hypothetical protein predicted by genemark.hmm; supported by cDNA: gi_13430457_gb_AF360141.1_AF360141	262964_at	0.9
hypothetical protein	262669_at	0.9
putative ethylene receptor (EIN4) similar to ethylene receptor GB:AAC31123 [Malus domestica], identical to putative ethylene receptor GB:AAD024	258818_at	0.9
unknown protein	248771_at	0.9

peroxidase	248382_at	0.9
Expressed protein ; supported by cDNA: gi_16209721_gb_AY057621.1_	245682_at	0.9
transfactor, putative similar to GI:4519671 from [Nicotiana tabacum]	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	-r2-At-Actin-5	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
putative tyrosyl-tRNA synthetase	267446_s_at	0.9
unknown protein	267373_at	0.9
putative phosphoribosyl pyrophosphate synthetase	267365_at	0.9
putative methionine aminopeptidase ; supported by cDNA: gi_11320961_gb_AF250964.1_AF250964	267189_at	0.9
putative ARP2/3 protein complex subunit p41	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: gi_15010737_gb_AY045670.1_	266984_at	0.9
putative katanin ;supported by full-length cDNA: Ceres:119620.	266905_at	0.9
putative protein kinase contains a protein kinase domain profile (PDOC00100)	266911_at	0.9
unknown protein ;supported by full-length cDNA: Ceres:9000.	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	266593_at	0.9
eukaryotic translation initiation factor 3 delta subunit ; supported by cDNA: gi_1036802_gb_U36765.1_ATU36765	266554_s_at	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
unknown protein ;supported by full-length cDNA: Ceres:12017.	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
putative dTDP-glucose 4-6-dehydratase ;supported by full-length cDNA: Ceres:28205.	266205_s_at	0.9
unknown protein ; supported by full-length cDNA: Ceres: 948.	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_	265886_at	0.9
unknown protein	265807_at	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_AY054495.1_	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.	265402_at	0.9
putative tyrosine decarboxylase	265305_at	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
hypothetical protein identical to hypothetical protein GB:AAB60753	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_	264639_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, gi	264504_at	0.9
putative Proline synthetase associated protein Similar to hypothetical protein F09E5.8 gb|U37429 from C. elegans. ESTs gb|T42019 and gb|N97000	264349_at	0.9
hypothetical protein contains similarity to ubiquitin protein ligase GI:2827198 from [Mus musculus]	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	264165_at	0.9
putative vacuolar proton-ATPase subunit	264080_at	0.9
putative GTP cyclohydrolase	264045_at	0.9
plastid division protein (FtsZ) identical to AF089738; supported by cDNA: gi_15292820_gb_AY050844.1_	263906_at	0.9
putative auxin-responsive protein ; supported by cDNA: gi_15292854_gb_AY050861.1_	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	263705_at	0.9
putative cryptochrome 2 apoprotein Match to Arabidopsis photolysase (PHH1) gene (gb|X99061) and cryptochrome 2 apoprotein (CRY2) (gb|U4339	263669_at	0.9
putative ADP-ribosylation factor ; supported by cDNA: gi_15450780_gb_AY054470.1_	263297_at	0.9
fructokinase, putative predicted by genefinder	263163_at	0.9
putative protein kinase/endoribonuclease ; supported by cDNA: gi_13194577_gb_AF308596.1_AF308596	263076_at	0.9
unknown 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	262706_at	0.9
heat shock protein, putative contains Pfam profile: PF00011 Hsp20/alpha crystallin family;supported by full-length cDNA: Ceres:21735.	262629_at	0.9
NAM(no apical meristem) protein, putative similar to NAM protein GI:6066595 from (Petunia hybrida); supported by cDNA: gi_13605664_gb_AF361	262514_at	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	262314_at	0.9
hypothetical protein similar to putative curved-DNA binding protein GI:6968662 from [Campylobacter jejuni];supported by full-length cDNA: Ceres:37	262194_at	0.9
UDP-galactose 4-epimerase, putative similar to GI:3021357 from (Cyamopsis tetragonoloba) (Plant Sci. 142, 147-154 (1999))	261953_at	0.9
proteasome regulatory subunit, putative similar to 26S proteasome regulatory complex subunit p30 GB:AAF08395 GI:6434966 from [Drosophila me	261955_at	0.9
type 2 peroxiredoxin, putative similar to type 2 peroxiredoxin GI:4928472 from [Brassica rapa subsp. pekinensis];supported by full-length cDNA: Cer	261919_at	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
ferredoxin--NADP 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	261189_at	0.9
unknown protein ; supported by cDNA: gi_15215745_gb_AY050402.1_	261208_at	0.9
unknown protein ;supported by full-length cDNA: Ceres:112024.	261147_at	0.9
hypothetical protein predicted by genemark.hmm	261086_at	0.9
hypothetical protein similar to hypothetical protein GB:CAB45785 GI:5262156 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:3998.	261056_at	0.9
hypothetical protein similar to carboxyvinyl-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
unknown protein similar to Cryptosporidium parvum elongation factor-2 GB:U21667 GI:706974 from [Cryptosporidium parvum]	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
putative acetylornithine transaminase similar to ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT) GB:O04866 from (Alnus gluti	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
putative lipoxygenase similar to 13-lipoxygenase GB:CAA65269 [Solanum tuberosum]	260190_at	0.9
DNA-directed RNA polymerase subunit, putative similar to GI:6723961 from [Schizosaccharomyces pombe]	260049_at	0.9
putative DNA-binding protein contains Pfam profile: PF01388 ARID DNA binding domain	259967_at	0.9
putative pyrophosphate-dependent phosphofructokinase alpha subunit similar to pyrophosphate-dependent phosphofructokinase alpha subunit GB:A	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	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	259733_at	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	259645_at	0.9
bZIP protein, putative similar to GI:600855 from [Arabidopsis thaliana] (Plant Physiol. 109 (2), 723 (1995)); supported by cDNA: gi_15450410_gb_A	259610_at	0.9
hypothetical protein ; supported by cDNA: gi_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
serin threonin-kinase, putative similar to serin threonin-kinase GI:2887282 from (Drosophila melanogaster); supported by cDNA: gi_15450801_gb_A	259362_s_at	0.9
putative sodium proton exchanger similar to sodium proton exchanger Nhx1 GB:AAD16946 [Arabidopsis thaliana]	259081_at	0.9
unknown protein	259047_at	0.9
unknown protein predicted by genscan; est match;supported by full-length cDNA: Ceres:3820.	259038_at	0.9
hypothetical protein similar to unknown protein	258997_at	0.9
putative aspartate kinase similar to aspartate kinase GB:CAA67376 (Arabidopsis thaliana); supported by full-length cDNA: Ceres: 6203.	258977_s_at	0.9
unknown protein similar to unknown proteins GB:AAD24625 [Arabidopsis thaliana], GB:AAC73026 [Arabidopsis thaliana]	258933_at	0.9
putative dehydroquinase shikimate dehydrogenase similar to dehydroquinase shikimate dehydrogenase GB:S46210 [Nicotiana tabacum]	258908_at	0.9
Expressed protein ; supported by full-length cDNA: Ceres: 9573.	258848_at	0.9
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];	258816_at	0.9
unknown protein ; supported by cDNA: gi_16226859_gb_AF428353.1_AF428353	258731_at	0.9
hypothetical protein contains Pfam profile: PF01535 domain of unknown function	258573_at	0.9
putative mudrA protein similar to mudrA protein GB:S59141 [Zea mays]	258550_at	0.9
putative chaperonin similar to chaperonin subunit 6a (zeta) GB:NP_033968 from [Mus musculus];supported by full-length cDNA: Ceres:116386.	258482_at	0.9
unknown protein similar to hypothetical protein GB:CAB36798 from [Arabidopsis thaliana]	258361_at	0.9
putative pectinesterase similar to pectinesterase precursor GB:Q43043 [Petunia integrifolia]; contains Pfam profile: PF01095 pectinesterase;supporte	258193_at	0.9
dehydrogenase, putative similar to dihydropyrimidine dehydrogenase GB:BAA89789 from [Homo sapiens]; supported by cDNA: gi_14334711_gb_A	258162_at	0.9
unknown protein ; supported by cDNA: gi_14423467_gb_AF386971.1_AF386971	258154_at	0.9
putative cytochrome P450 similar to GB:Q05047 from [Catharanthus roseus]	258113_at	0.9
putative cytochrome P450 similar to GB:Q05047 from [Catharanthus roseus]; supported by cDNA: gi_15529168_gb_AY052208.1_	258063_at	0.9
unknown protein ; supported by cDNA: gi_14334715_gb_AY035031.1_	258085_at	0.9
ubiquitin-specific protease 7 (UBP7), putative similar to GI:11993467; supported by cDNA: gi_11993466_gb_AF302661.1_AF302661	258045_at	0.9
unknown protein ; supported by cDNA: gi_15027906_gb_AY045810.1_	257989_at	0.9
hypothetical protein contains Pfam profile: PF01535 domain of unknown function (2 copies)	257744_at	0.9
unknown protein ; supported by cDNA: gi_15010791_gb_AY045697.1_	257660_at	0.9
cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450	257623_at	0.9
unknown protein	257594_at	0.9
unknown protein	257268_at	0.9
syntaxin-like protein similar to syntaxin 5A GB:NP_003155 from [Homo sapiens] (J. Mol. Neurosci. (1997) 8 (2), 159-161)	257157_at	0.9
t-complex polypeptide 1 homologue identical to t-complex polypeptide 1 homologue GB:D11351 [Arabidopsis thaliana]; supported by cDNA: gi_2178	257125_at	0.9
putative 3-hydroxybutyryl-CoA dehydrogenase similar to 3-HYDROXYBUTYRYL-COA DEHYDROGENASE GB:Q45223 from [Bradyrhizobium japon	257052_at	0.9
unknown protein contains Pfam profile: PF01188 Mandelate racemase/muconate lactonizing enzyme family; supported by cDNA: gi_13878120_gb_	257067_at	0.9
unknown protein	257019_at	0.9
RNA helicase, putative similar to RNA helicase GB:CAA09195 from [Arabidopsis thaliana]; supported by cDNA: gi_15215677_gb_AY050367.1_	257023_at	0.9
unknown protein	256927_at	0.9
unknown protein	256932_at	0.9
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:41717.	256804_at	0.9
unknown protein contains PF00612 IQ:IQ calmodulin-binding motif	256822_at	0.9
20S proteasome subunit PAC1 identical to GB:AAC32057 from [Arabidopsis thaliana] (Genetics (1998) 149 (2), 677-692);supported by full-length c	256795_at	0.9
putative protein dihydrolipoamide S-acetyltransferase precursor GB:CAB41340 GI:4678949 [Arabidopsis thaliana]; supported by cDNA: gi_5881964_	256682_at	0.9
hypothetical protein predicted by genscan+	256605_at	0.9
unknown protein	256480_at	0.9

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 b	256328_at	0.9
C2H2-type zinc finger protein, putative contains multiple zinc finger domains: PF00096: Zinc finger, C2H2 type; supported by cDNA: gi_15809914_g	256344_at	0.9
disease resistance protein, putative similar to disease resistance protein RPP1-WsB [Arabidopsis thaliana] GI:9279731; supported by cDNA: gi_145	256303_at	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:6688810 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]	255726_at	0.9
coded for by A. thaliana cDNA T20615 ;supported by full-length cDNA: Ceres:37305.	255626_at	0.9
putative GTP pyrophosphokinase similar to bacterial GTP pyrophosphokinases (RelA) similar to B. subtilis RelA (EC 2.7.6.5), GenBank accession n	255522_at	0.9
hypothetical protein	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	255482_at	0.9
putative protein other predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:34781.	254858_at	0.9
putative protein various predicted 3-isopropylmalate dehydratases/aconitate hydratases; supported by cDNA: gi_15027970_gb_AY045842.1_	254742_at	0.9
putative protein G9A protein, Mus musculus, AF109906; supported by cDNA: gi_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_AF375	254667_at	0.9
putative protein	254594_at	0.9
RNase L inhibitor-like protein RNase L inhibitor (clone 8), Homo sapiens	254615_at	0.9
kinase-like protein protein kinase rck, Mus musculus, PIR2:I48733; 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	253266_s_at	0.9
putative protein predicted protein A_TM017A05.4 Arabidopsis thalianaBAC TM017A05, PID:g2435512	253109_at	0.9
thaumatin-like protein thaumatin-like protein, Arabidopsis thaliana, Pir2:S71175; supported by cDNA: gi_13430505_gb_AF360165.1_AF360165	253104_at	0.9
cytochrome P450-like protein	253097_at	0.9
putative protein predicted protein, Arabidopsis thaliana; supported by cDNA: gi_15451175_gb_AY054668.1_	253062_at	0.9
squalene epoxidase - like protein squalene epoxidase, Panax ginseng, AB003516;supported by full-length cDNA: Ceres:118648.	253039_at	0.9
guanine nucleotide-exchange protein -like guanine nucleotide-exchange protein -Bos taurus,PID:g2674107	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_g	252606_at	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_1389	251818_at	0.9
spliceosomal - like protein spliceosomal protein SAP 130, Homo sapiens, EMBL:HSAJ1443	251837_s_at	0.9
phosphatase - like protein DUAL SPECIFICITY PROTEIN PHOSPHATASE 5, Rattus norwegicus, SWISSPROT:DUS5_RAT; supported by cDNA: g	251786_at	0.9
villin 3 fragment ; supported by cDNA: gi_3415116_gb_AF081203.1_AF081203	251629_at	0.9
zinc finger-like protein several zinc finger proteins - Arabidopsis thaliana	251586_at	0.9
putative protein several serine/threonine-specific protein kinases	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	251234_s_at	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:	250863_at	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	250671_at	0.9
WD-repeat protein-like ; supported by cDNA: gi_15450909_gb_AY054535.1_	250539_at	0.9
cellulose synthase catalytic subunit	250505_at	0.9
cytochrome P450 - like protein cytochrome P450, Helianthus tuberosus, EMBL:HTCYP81L	250423_s_at	0.9
putative protein TH65 protein, Arabidopsis thaliana, EMBL:AJ001729	250429_at	0.9
beta-adaptin-like protein A ; supported by cDNA: gi_7385050_gb_AF216385.1_AF216385	250352_at	0.9
putative esterase - like protein cinI 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
polynucleotide phosphorylase	250196_at	0.9
UDP-glucose pyrophosphorylase ; supported by cDNA: gi_13430663_gb_AF360244.1_AF360244	250074_at	0.9
putative protein nuclear FMRP interacting protein 1 NUFIP1, Homo 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	249636_at	0.9
putative protein SIAH1 protein, Brassica napus, EMBL:BNA245479	249595_at	0.9
putative protein similar to unknown protein (sp P54493)	249510_at	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]	249244_at	0.9
putative protein similar to unknown protein (pir||S76082)	249193_at	0.9
putative protein similar to unknown protein (sp|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	248890_at	0.9
AP47 50p (gb|AAB88283.1) ; supported by cDNA: gi_14326519_gb_AF385713.1_AF385713	248858_at	0.9
putative protein similar to unknown protein (dbj|BAA90625.1)	248805_at	0.9
putative protein contains similarity to unknown protein (pir||T39016);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	248590_at	0.9
putative protein contains similarity to alpha/beta hydrolase; supported by cDNA: gi_13877626_gb_AF370514.1_AF370514	248531_at	0.9
putative protein contains similarity to salt-inducible protein	248547_at	0.9
putative protein strong similarity to unknown protein (gb|AAD25781.1)	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	248326_at	0.9
Avr9 elicitor response protein-like ; supported by cDNA: gi_14423409_gb_AF386942.1_AF386942	248262_at	0.9
putative protein similar to unknown protein (pir||T34137)	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_	247867_at	0.9
MAP kinase ; supported by cDNA: gi_14532571_gb_AY039910.1_	247819_at	0.9
Ran binding protein 1 homolog - like Ran binding protein 1 homolog, Arabidopsis thaliana, EMBL:ATU62742	247771_at	0.9
FtsH protease, putative contains similarity to cell division protein FtsH homolog 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	247577_at	0.9
signal recognition particle - like protein signal recognition particle 68, Homo sapiens, EMBL:AF195951; supported by cDNA: gi_15293136_gb_AY05	247505_at	0.9
Mei2-like protein Mei2-like protein, Arabidopsis thaliana, EMBL:D86122; supported by cDNA: gi_2443328_dbj_D86122.1_D86122	247506_at	0.9
putative protein various predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:14414.	247461_at	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	247228_at	0.9
PHD finger protein - like PHD finger protein 3, Homo sapiens, EMBL:AF091622	246893_at	0.9
putative protein isopenicillin N epimerase, Streptomyces clavuligerus, EMBL:M32324	246832_at	0.9
glutamyl-tRNA synthetase ; supported by cDNA: 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_U	246785_at	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	246564_at	0.9
Exportin1 (XPO1) protein ; supported by cDNA: gi_15810122_gb_AY056126.1_	246424_at	0.9
root cap 1 (RCP1) ;supported by full-length cDNA: Ceres: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:6748	246042_at	0.9
alpha-galactosidase - like protein alpha-galactosidase, coffee, PIR:T50781	246055_at	0.9
unknown protein contains similarity to anthranilate synthase large subunit GI:1374671 from [Buchnera aphidicola]	245745_at	0.9
dormancy-associated protein, putative similar to dormancy-associated protein GI:2995990 from [Arabidopsis thaliana]; supported by cDNA: gi_1433	245668_at	0.9

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 SP|P34568|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
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	-r2-At-Actin-M	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 3	K-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
putative AAA-type ATPase	266777_at	0.8
predicted by genscan	266796_at	0.8
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: gi_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
putative DNA topoisomerase III beta	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
Rubisco subunit binding-protein beta subunit identical to chaperonin 60 beta precursor GB:JT0901 from [Arabidopsis thaliana]; supported by cDNA:	265076_at	0.8
hypothetical protein Similar to human BC-2 protein; Similar to human BC-2 protein, gi|2828147; supported by cDNA: gi_15529227_gb_AY052238.1_	265044_at	0.8
putative chloroplast membrane protein, ALBINO3 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 MU1B, putative similar to clathrin adaptor medium chain protein MU1B GI:4704421 from [Mus musculus]	264914_at	0.8
pyruvate dehydrogenase E1 alpha subunit strongly similar to GB:AAD39331;supported by full-length cDNA: Ceres:41337.	264871_at	0.8
hypothetical protein similar to hypothetical protein GB:O14360	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 leucyl-tRNA synthetase Strong similarity to S. pombe leucyl-tRNA synthetase (gb|Z73100)	264705_at	0.8
putative 2,3-bisphosphoglycerate-independent phosphoglycerate mutase Strong similarity to R. communis phosphoglycerate mutase (gb|X70652). E	264668_at	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 6319.	264673_at	0.8
unknown protein EST gb|R64758 comes from this gene; supported by cDNA: gi_15450400_gb_AY052301.1_	264676_at	0.8
putative U2 small nuclear ribonucleoprotein A (U2 SNRNP-A) Identical to A. thaliana U2 SnRNP-specific A protein (gb|X69137). ESTs gb|ATTS070	264678_at	0.8
unknown protein ; supported by cDNA: gi_13430645_gb_AF360235.1_AF360235	264615_at	0.8
hypothetical protein predicted by genemark.hmm	264428_at	0.8
putative pyrophosphate-fructose-6-phosphate 1-phosphotransferase similar to pyrophosphate-dependent phosphofuctokinase beta subunit gb|Z328	264386_at	0.8
unknown protein Contains similarity to gb|AB011110 KIAA0538 protein from Homo sapiens brain and to phospholipid-binding domain C2 PF|00168.	264351_at	0.8
hypothetical protein similar to hypothetical protein GI:5541664 from [Arabidopsis thaliana]	264308_at	0.8
unknown protein ;supported by full-length cDNA: Ceres:16387.	264286_at	0.8
unknown protein ; supported by cDNA: gi_15081790_gb_AY048288.1_	264265_at	0.8
unknown protein ESTs gb|Z34075, gb|Z34835 and gb|AA404888 come from this gene	264198_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
hypothetical protein contains similarity to chloroplast membrane-associated protein IM30 GI:169106 from [Pisum sativum];supported by full-length cD	264158_at	0.8
unknown protein Similar to yeast general negative regulator of transcription subunit 1; Location of ESTs gb|T44328 and gb|AA395265	264168_at	0.8

unknown protein	264172_at	0.8
unknown protein ; supported by cDNA: gi_15450672_gb_AY052704.1_	264123_at	0.8
unknown protein	264118_at	0.8
putative rubisco subunit binding-protein alpha subunit ;supported by full-length cDNA: Ceres:25773.	264069_at	0.8
putative pyrophosphate--fructose-6-phosphate 1-phosphotransferase	264044_at	0.8
unknown protein	264011_at	0.8
putative ABC transporter related to multi drug resistance proteins and P-glycoproteins	263904_at	0.8
putative WD-40 repeat protein	263824_at	0.8
putative cyclic nucleotide-regulated ion channel protein	263776_s_at	0.8
putative cyclic nucleotide-regulated ion channel protein	263777_at	0.8
putative homeodomain transcription factor ; supported by cDNA: gi_15983780_gb_AY056796.1_	263557_at	0.8
unknown protein	263457_at	0.8
putative methylmalonate semi-aldehyde dehydrogenase	263275_at	0.8
putative fructokinase ; supported by full-length cDNA: Ceres: 17664.	263250_at	0.8
hypothetical protein predicted by genscan	263200_at	0.8
T76725 come from this gene.	263010_at	0.8
hypothetical protein contains similarity to DNA-binding protein (PcMYB1) GI:2224896 from [Petroselinum crispum]	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
hypothetical protein predicted by genemark.hmm	262941_at	0.8
hypothetical protein contains similarity to transcriptional repressor SIN3B GI:2921547 from [Mus musculus]	262900_at	0.8
auxin response factor 1 identical to auxin response factor 1 GI:2245378 from [Arabidopsis thaliana]; supported by cDNA: gi_2245377_gb_U83245.1_	262914_at	0.8
unknown protein ; supported by cDNA: gi_16612297_gb_AF439842.1_AF439842	262849_at	0.8
hypothetical protein similar to hypothetical protein GB:AAD39278 GI:5080768 from (Arabidopsis thaliana)	262662_at	0.8
4-hydroxyphenylpyruvate dioxygenase (HPD) identical to 4-hydroxyphenylpyruvate dioxygenase (HPD) SP:P93836 [Arabidopsis thaliana (Mouse-ea	262635_at	0.8
hypothetical protein predicted by genscan+	262532_at	0.8
unknown protein Similar to gb|X84260 POS5 gene product from Saccharomyces cerevisiae. EST gb|W43879 comes from this gene; supported by cD	262506_at	0.8
hypothetical protein similar to hypothetical protein GB:AAD50048 GI:5734783 from [Arabidopsis thaliana]	262471_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	262280_at	0.8
hypothetical protein predicted by genscan+; supported by cDNA: gi_14517529_gb_AY039600.1_	262248_at	0.8
hypothetical protein predicted by genscan+	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-l	262113_at	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	262094_at	0.8
flavin-containing monooxygenase FMO3, putative similar to flavin-containing monooxygenase FMO3 GI:349533 from [Oryctolagus cuniculus]	261913_at	0.8
protein serine/threonine phosphatase alpha, putative similar to protein serine/threonine phosphatase alpha GB:AAC69437 GI:3811109 from [Plasm	261743_s_at	0.8
2-isopropylmalate synthase, putative similar to 2-isopropylmalate synthase GB:AF004165 GI:2213881 from [Lycopersicon pennellii]	261668_at	0.8
unknown protein	261674_at	0.8
hypothetical protein similar to hypothetical protein GB:AAD22292 GI:6598654 from [Arabidopsis thaliana]	261681_at	0.8
dimethyladenosine transferase, putative similar to dimethyladenosine transferase GB:AAC09322 GI:3005590 from [Arabidopsis thaliana]	261652_at	0.8
unknown protein contains similarity to formin binding protein GB:AAC34811 GI:3550080 from [Homo sapiens]	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_14	261581_at	0.8
unknown protein	261540_at	0.8
receptor-like serine/threonine kinase, putative similar to GB:AAC50043 from [Arabidopsis thaliana] (Plant Mol. Biol. 37 (4), 587-596 (1998))	261434_at	0.8
unknown protein ;supported by full-length cDNA: Ceres:120232.	261413_at	0.8
unknown protein	261424_at	0.8
transcription factor, putative similar to GB:X92369 from [Antirrhinum majus];supported by full-length cDNA: Ceres:12071.	261375_at	0.8
phytochrome A supressor spa1, putative similar to GB:4809171 from [Arabidopsis thaliana]; supported by cDNA: gi_14532797_gb_AY040023.1_	261319_at	0.8
protein kinase, putative similar to many predicted protein kinases	261339_at	0.8
unknown protein ;supported by full-length cDNA: Ceres:158528.	261253_at	0.8
unknown protein ; supported by cDNA: gi_13605832_gb_AF367315.1_AF367315	261231_at	0.8
peroxisomal targeting signal type 2 receptor ; supported by cDNA: gi_15215675_gb_AY050366.1_	261207_at	0.8
homeodomain protein, putative similar to homeodomain protein GI:7239157 from (Malus domestica)	261139_at	0.8
unknown protein ;supported by full-length cDNA: Ceres:37370.	261033_at	0.8
transcription factor MYC7E, putative similar to transcription factor MYC7E GB:AAD15818 GI:4321762 from [Zea mays]	261050_at	0.8
histidine decarboxylase, putative similar to histidine decarboxylase GB:BAA78331 GI:4996105 from [Brassica napus]; supported by cDNA: gi_15011	260814_at	0.8
unknown protein ;supported by full-length cDNA: Ceres:114093.	260793_at	0.8
unknown protein contains similarity to apoptotic cell clearance receptor PtdSerR GI:11037740 from [Mus musculus]	260798_at	0.8
unknown protein ;supported by full-length cDNA: Ceres:41461.	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
translation elongation factor EF-1 alpha identical to GB:AAB07881 from [Arabidopsis thaliana] (Mol. Gen. Genet. 219 (1-2), 106-112 (1989))	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	260588_at	0.8
unknown protein	260596_at	0.8
putative villin 2	260521_at	0.8
mannosyl-oligosaccharide alpha-1,2-mannosidase, putative similar to mannosyl-oligosaccharide alpha-1,2-mannosidase (Mus musculus) GI:474280	260520_at	0.8
unknown protein	260436_at	0.8
putative RNA-binding domain contains Pfam profile: PF00806 Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain) (5 co	260398_at	0.8
putative RING zinc finger protein Pfam HMM hit: zinc finger, C3HC4 type (RING finger)	260321_at	0.8
putative glycerophosphodiester phosphodiesterase similar to glycerophosphoryl diester phosphodiesterase GB:AAF12f49 from [Deinococcus radiodu	260254_at	0.8
unknown protein ; supported by cDNA: gi_13878054_gb_AF370290.1_AF370290	260157_at	0.8
putative protein phosphatase 2C similar to protein phosphatase 2C GB:CAA72341 [Medicago sativa]; contains Pfam profile: PF00481 Protein phosp	260057_at	0.8
unknown protein	259934_at	0.8
putative exportin, tRNA (nuclear export receptor for tRNAs) similar to exportin, tRNA (nuclear export receptor for tRNAs) GB:6005954 [Homo sapien	259919_at	0.8
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	0.8
acetyl-CoA synthetase, putative similar to protein contained within GB:AE000782 from [Archaeoglobus fulgidus]	259647_at	0.8
Expressed protein ; supported by cDNA: gi_14532525_gb_AY039887.1_	259416_at	0.8
GTP-binding protein(RAB11D), putative similar to RAB11D GI:1370148 from [Lotus japonicus]; supported by cDNA: gi_12083263_gb_AF332428.1_	259395_at	0.8
putative polynucleotide phosphorylase similar to polynucleotide phosphorylase GB:AAC50039 (Pisum sativum), identical to putative polynucleotide	259344_at	0.8
Snf1-related protein kinase KIN10 (AKIN10) identical to Snf1-related protein kinase, KIN10 SP:Q38997 from [Arabidopsis thaliana]	259319_at	0.8
putative porin similar to outer mitochondrial membrane porin (voltage-dependent anion-selective channel protein) (VDAC) (POM 34) GB:P42055 (So	259270_at	0.8
putative DNA gyrase subunit B similar to putative DNA gyrase subunit GB:O50627 [Bacillus halodurans]	259138_s_at	0.8
unknown protein similar to hypothetical proteins: GB:AAB61107 [Arabidopsis thaliana], GB:AAC00578, [Arabidopsis thaliana]	259117_at	0.8
DegP protease contains similarity to degP GI:2623992 from [Bradyrhizobium japonicum]	259048_at	0.8
unknown protein similar to CGI-86 protein GB:AAD34081 [Homo sapiens], HMM hit: Alcohol/other dehydrogenases, short chain type	259051_at	0.8
unknown protein ;supported by full-length cDNA: Ceres:32811.	259039_at	0.8
putative DNA gyrase subunit A similar to DNA gyrase A subunit GB:BAA10380 [Synechocystis sp]	258966_at	0.8
unknown protein N-terminus similar to unknown protein GB:AAD25613 [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 38529.	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
unknown protein ;supported by full-length cDNA: Ceres:320.	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: 387	258714_at	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	258531_at	0.8
kinesin-like protein similar to mitotic centromere-associated kinesin GB:AAC27660 from [Homo sapiens]; supported by cDNA: gi_15810128_gb_AY0	258381_at	0.8
DNA-binding protein contains AP2 domain, identical to AP2 domain containing protein RAP2.2 from GB:AAC49768 from [Arabidopsis thaliana];supp	258366_at	0.8
methyltransferase, putative similar to methyltransferase GB:AAC01738 from [Amycolatopsis mediterranei]	258218_at	0.8
putative protein kinase similar to serine/threonine protein kinase Pto GB:AAB47421 [Lycopersicon esculentum] (Plant Cell 9 (1), 61-73 (1997))	258173_at	0.8
unknown protein	258101_at	0.8
hypothetical protein predicted by genemark.hmm	258051_at	0.8
putative UDP-glucose glucosyltransferase similar to GB:Q40284 from [Manihot esculenta]	257940_at	0.8
hypothetical protein predicted by genemark.hmm	257876_at	0.8
E2, ubiquitin-conjugating enzyme, putative similar to ubiquitin conjugating enzyme GB:CAA51706 [Saccharomyces cerevisiae] (Nature 365 (6442),	257893_at	0.8
hypothetical protein contains Pfam profile: PF01535 domain of unknown function	257838_at	0.8
SNF1 related protein kinase (ATSRPK1) identical to SNF1 related protein kinase (ATSRPK1) GB:AB027153 [Arabidopsis thaliana]; supported by cD	257771_at	0.8
chorismate mutase identical to chorismate mutase GB:Z26519 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:39613.	257746_at	0.8
unknown protein similar to negative regulator of COPII vesicle formation GB:NP_011162 from [Saccharomyces cerevisiae]	257709_at	0.8
unknown protein ; supported by full-length cDNA: Ceres: 33530.	257703_at	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 12734.	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: PF0107	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
hypothetical protein similar to hypothetical protein GB:AAC80630 from [Arabidopsis thaliana]	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 D	256797_at	0.8
hypothetical protein predicted by genemark.hmm	256624_at	0.8
unknown protein	256534_at	0.8
hypothetical protein contains similarity to glucose-repressible alcohol dehydrogenase transcriptional effector GI:3859723 from (Candida albicans)	256491_at	0.8
unknown protein	256479_at	0.8
hypothetical protein	256356_s_at	0.8
FKBP-type peptidyl-prolyl cis-trans isomerase, putative contains Pfam profile: PF00254 FKBP-type peptidyl-prolyl cis-trans isomerases	256230_at	0.8
electron transport flavoprotein, putative similar to electron transport flavoprotein [Homo sapiens] GI:182251	256209_at	0.8
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:112350.	256142_at	0.8
unknown protein ; supported by cDNA: gi_14532715_gb_AY039982.1_	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_g	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-le	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_	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
predicted protein of unknown function similar to bacterial tolB proteins but unclear if T7B11.13 is involved in viral transport	255543_at	0.8
putative hexose transporter similar to plant and fission yeast hexose (glucose) transporter proteins	255561_at	0.8
AtKAP alpha similar to AtKAP, GenBank accession number U69533; supported by cDNA: gi_14326480_gb_AF385693.1_AF385693	255507_at	0.8
putative calcium channel ; supported by cDNA: gi_13786068_gb_AF360372.1_AF360372	255380_at	0.8
putative pre-mRNA splicing factor similar to yeast pre-mRNA splicing factors; supported by cDNA: gi_16604550_gb_AY059720.1_	255382_at	0.8
hypothetical protein	255296_at	0.8
coded for by A. thaliana cDNA Z18000 ;supported by full-length cDNA: Ceres:38543.	255240_at	0.8
putative protein oxysterol-binding protein - Oryctolagus cuniculus (domestic rabbit),PIR2:A34404	255151_at	0.8
sucrose-phosphate synthase - like protein sucrose-phosphate synthase, Zea mays, PIR2:JQ1329	255016_at	0.8
isoleucine-tRNA ligase - like protein isoleucine--tRNA ligase, Homo sapiens, PIR2:I59314	255020_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
putative phospholipase D-gamma phospholipase D-gamma - Arabidopsis thaliana,PID:g2653885	254894_at	0.8
methionyl-tRNA synthetase - like protein methionyl-tRNA synthetase, Oryza sativa, AF040700	254734_at	0.8
hypothetical protein ; supported by full-length cDNA: Ceres: 38412.	254691_at	0.8
bHLH protein - like bHLH protein, Arabidopsis thaliana, PATCHX:E255557	254693_at	0.8
putative protein	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	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:285	254085_at	0.8
putative protein various Caenorhabditis elegans predicted proteins	253977_at	0.8
grpE like protein ;supported by full-length cDNA: Ceres:35284.	253949_at	0.8
translation initiation factor ; supported by full-length cDNA: Ceres: 5206.	253900_at	0.8
COP1-interacting protein 7 (CIP7) ; supported by cDNA: gi_3327867_dbj_AB012912.1_AB012912	253876_at	0.8
putative NADH dehydrogenase NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain NDI1 - yeast, PIR2:S26704;supported by full-length cDNA: C	253810_at	0.8
protein kinase ADK1-like protein protein kinase ADK1-Arabidopsis thaliana;supported by full-length cDNA: Ceres:113439.	253770_at	0.8
hypothetical protein ;supported by full-length cDNA: Ceres:249331.	253751_at	0.8
Expressed protein ;supported by cDNA: gi_15983772_gb_AY056792.1_	253758_at	0.8
hexokinase ; supported by cDNA: gi_8567421_gb_U18754.2_ATU18754	253705_at	0.8
pyrophosphate-dependent phosphofructo-1-kinase-like protein pyrophosphate-dependent phosphofructo-1-kinase - Prunus armeniaca (apricot),PID:	253709_at	0.8
nucleotide pyrophosphatase - like protein nucleotide pyrophosphatase homolog, Oryza sativa, gb:T03293; supported by cDNA: gi_13877570_gb_A	253698_at	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 7876.	253549_at	0.8
predicted protein hypothetical protein slr1919, Synechocystis sp., PIR2:S75233	253517_at	0.8
putative protein ribosomal protein YmL14 precursor, mitochondrial - Saccharomyces cerevisiae,PIR2:S50921;supported by full-length cDNA: Ceres:	253538_at	0.8
methyltransferase - like protein methyltransferase DPH5, Saccharomyces cerevisiae, PIR2:S30890; supported by cDNA: gi_13605812_gb_AF3673	253490_at	0.8
putative protein NBS/LRR disease resistance protein (RFL1) - Arabidopsis thaliana,PID:g3309619	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_	253336_at	0.8
glucosyltransferase -like protein immediate-early salicylate-induced glucosyltransferase, Nicotiana tabacum, PIR2:T03747;supported by cDNA gi:14	253268_s_at	0.8
xanthine dehydrogenase - like protein xanthine dehydrogenase, Gallus gallus, PIR:XOCHDH	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	251712_at	0.8
anthranilate phosphoribosyltransferase-like protein anthranilate phosphoribosyltransferase - Pisum sativum, PIR:T06460; supported by cDNA: gi_14	251563_at	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
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_AF4103	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
putative protein beta-(1-3)-glucosyl transferase, Bradyrhizobium japonicum, EMBL:AF047687; supported by cDNA: gi_16974551_gb_AY060563.1_	250892_at	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
putative protein mature parasite-infected erythrocyte surface antigen, Plasmodium falciparum, EMBL:AF056936	250603_at	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 rna 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	250384_at	0.8
putative protein predicted protein, Arabidopsis thaliana	250355_at	0.8
clathrin binding protein - like Af10-protein, Avena fatua, EMBL:U80041	250356_at	0.8
CCAAT box binding factor/ transcription factor Hap2a	250320_at	0.8
cobalamin biosynthesis protein	250243_at	0.8
putative protein similar to unknown protein (emb|CAB86638.1)	250202_at	0.8
alpha-mannosidase	250203_at	0.8
putative protein similar to unknown protein (ref|NP_057085.1);supported by full-length cDNA: Ceres:38057.	250222_at	0.8
pescadillo - like protein embryonic development allele: hi2, Danio rerio, EMBL:U77627 pescadillo, Homo sapiens, EMBL:U78310	250192_at	0.8
putative protein similar to unknown protein (pir||T09939);supported by full-length cDNA: Ceres:23754.	250013_at	0.8
Ruv DNA-helicase-like protein ;supported by full-length cDNA: Ceres:113109.	249938_at	0.8
putative protein similar to unknown protein (gb AAF31706.1); supported by cDNA: gi_13605898_gb_AF367348.1_AF367348	249912_at	0.8
putative protein similar to unknown protein (gb AAD20392.1)	249825_at	0.8
putative protein similar to unknown protein (gb AAF01580.1)	249835_s_at	0.8
MtN3-like protein ; supported by cDNA: gi_3747110_gb_AF095641.1_AF095641	249800_at	0.8
receptor-protein kinase-like protein	249763_at	0.8
putative protein similar to unknown protein (pir||T40675); supported by cDNA: gi_14335067_gb_AY037213.1_	249701_at	0.8
putative protein strong similarity to unknown protein (gb|AAD21756.1); supported by cDNA: gi_15146184_gb_AY049233.1_ although this cDNA may	249703_at	0.8
protein kinase-like	249678_at	0.8
v-SNARE AtVTI1a	249453_at	0.8
ribosomal protein L5 - like ribosomal protein L5, rice	249466_at	0.8
putative protein hypothetical protein - Synechocystis sp., PIR:S76678	249433_at	0.8
DegP protease contains similarity to DegP2 protease GI:13172275 from [Arabidopsis thaliana]	249396_at	0.8
putative protein strong similarity to unknown protein (gb|AAF19684.1)	249278_at	0.8
putative protein contains similarity to glutathione-S-transferase/glutaredoxin;supported by full-length cDNA: Ceres:4645.	249233_at	0.8
20S proteasome subunit PAF1 (gb|AAC32062.1) ; supported by full-length cDNA: Ceres: 12455.	249161_at	0.8
putative protein similar to unknown protein (pir||T02918); supported by full-length cDNA: Ceres: 26596.	249122_at	0.8
putative protein similar to unknown protein (sp|P42620);supported by full-length cDNA: Ceres:109127.	249075_at	0.8
casein kinase II beta chain ; supported by cDNA: gi_468263_gb_L22563.1_ATHCKIB	248826_at	0.8
VAMP (vesicle-associated membrane protein)-associated protein-like ;supported by full-length cDNA: Ceres:14236.	248796_at	0.8
GTP-binding protein-like	248809_at	0.8
sodium-dicarboxylate cotransporter-like ;supported by full-length cDNA: Ceres:107593.	248756_at	0.8
unknown protein	248743_at	0.8
putative protein contains similarity to jasmonate inducible protein;supported by full-length cDNA: Ceres:19110.	248713_at	0.8
putative protein contains similarity to salt-inducible protein	248669_at	0.8
xylulose kinase ; supported by cDNA: gi_15292818_gb_AY050843.1_	248591_at	0.8

nucleotide-binding protein ; supported by cDNA: gi_13430793_gb_AF360309.1_AF360309	248462_at	0.8
putative protein similar to unknown protein (gb|AAF03497.1)	248410_at	0.8
unknown protein ; supported by cDNA: gi_15810027_gb_AY054282.1_	248289_at	0.8
putative protein similar to unknown protein (gb|AAD26950.1); supported by full-length cDNA: Ceres: 33791.	248261_at	0.8
pectinesterase ; supported by cDNA: gi_15293286_gb_AY051077.1_	248263_at	0.8
tyrosine aminotransferase	248207_at	0.8
putative protein similar to unknown protein (pir||T05472);supported by full-length cDNA: Ceres:30073.	248148_at	0.8
chaperone GrpE-like protein ;supported by full-length cDNA: Ceres:20790.	248101_at	0.8
putative protein similar to unknown protein (ref|NP_004583.1); supported by cDNA: gi_14532719_gb_AY039984.1_	248106_at	0.8
putative protein similar to unknown protein (ref|NP_032765.1)	248081_at	0.8
ABC transporter-like protein ; supported by cDNA: gi_9964120_gb_AF287699.1_AF287699	247806_at	0.8
putative protein predicted proteins, Arabidopsis thaliana and Oryza sativa	247741_at	0.8
GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone-4-phoshate synthase - like protein GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone-4-phoshate s	247694_at	0.8
putative protein predicted protein, Arabidopsis thaliana	247556_at	0.8
H-protein promoter binding factor-like protein	247452_at	0.8
glutaredoxin-like protein ; supported by full-length cDNA: Ceres: 96557.	247418_at	0.8
unknown protein ;supported by full-length cDNA: Ceres:114951.	247372_at	0.8
cdc2-like protein kinase-like protein supported by full-length cDNA: Ceres: 22817.	247334_at	0.8
putative protein contains similarity to RNA-binding protein	247276_at	0.8
histone acetyltransferase	247238_at	0.8
putative 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
putative 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 (A	246627_s_at	0.8
E2F transcription factor -like protein E2F protein, Triticum sp., EMBL:TSP238590	246568_at	0.8
ubiquitin-fusion degradation protein-like ubiquitin-fusion degradation protein - Homo sapiens, EMBL:AF043117; supported by cDNA: gi_15215855_g	246541_at	0.8
Inositol 1,3,4-Trisphosphate 5/6 kinase ;supported by full-length cDNA: Ceres:30653.	246451_at	0.8
syntaxin homologue ;supported by full-length cDNA: Ceres:8257.	246453_at	0.8
WD40-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
sugar transporter - like protein D-XYLOSE-PROTON SYMPORTER (D-XYLOSE TRANSPORTER), Lactobacillus brevis, SWISSPROT:XYLT_LACE	246466_at	0.8
sulfate 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
unknown protein	246287_at	0.8
unknown protein	246288_at	0.8
amino acid permease, putative contains Pfam profile: PF00324: Amino acid permease	246260_at	0.8
hypothetical protein	246262_at	0.8
putative protein	246234_at	0.8
putative protein predicted protein, Oryza sativa; supported by cDNA: gi_15081722_gb_AY048254.1_	246160_at	0.8
putative protein BEM46 bem1/bud5 suppressor, Schizosaccharomyces pombe, bem1/bud5 suppressor, EMBL:SP29892;supported by full-length cD	246090_at	0.8
rev interacting protein mis3 - like rev interacting protein mis3, Schizosaccharomyces pombe, PIR:T39981;supported by full-length cDNA: Ceres:303	246060_at	0.8
vegetative storage protein Vsp1 ;supported by full-length cDNA: Ceres:32606.	245928_s_at	0.8
alcohol dehydrogenase - like protein alcohol dehydrogenase 6, Vitis vinifera, EMBL:AF195866;supported by full-length cDNA: Ceres:155666.	245929_at	0.8
adenosine nucleotide translocator ; supported by cDNA: gi_15292846_gb_AY050857.1_	245854_at	0.8
protein kinase, putative similar to protein kinase GI:717180 from (Arabidopsis thaliana)	245825_at	0.8
unknown protein contains similarity to obtusifoliol 14-alpha-demethylase (CYP51) GB:Y09292 GI:1707854 from [Triticum aestivum];supported by full-	245795_at	0.8
unknown protein ;supported by full-length cDNA: Ceres:8255.	245780_at	0.8
unknown protein ;supported by full-length cDNA: Ceres:39155.	245730_at	0.8
purine permease identical to purine permease GI:7620007 from [Arabidopsis thaliana]; supported by cDNA: gi_7620006_gb_AF078531.1_AF078531	245671_at	0.8
unknown protein similar to putative Tub family protein GI:3738302 from [Arabidopsis thaliana]	245633_at	0.8
hypothetical protein	245601_at	0.8
hypothetical protein	245618_at	0.8
LET1 like protein	245496_at	0.8
hypothetical protein	245439_at	0.8
putative protein	245418_at	0.8
ATP-dependent Clp protease proteolytic subunit (ClpR4), putative similar to ATP-dependent Clp protease proteolytic subunit GI:7264063 from [Syne	245400_at	0.8
Expressed protein ; supported by full-length cDNA: Ceres: 16319.	245373_s_at	0.8
lactate dehydrogenase (LDH1) ;supported by full-length cDNA: Ceres:33509.	245324_at	0.8
farnesyl-pyrophosphate synthetase FPS2 ; supported by cDNA: gi_1146162_gb_L46349.1_ATHFPS2R	245301_at	0.8
transcription 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
ethylene response sensor (ERS) identical to GB:U21952:ATU21952; supported by cDNA: gi_15450903_gb_AY054532.1_	245098_at	0.8
putative cytochrome P450 ; supported by cDNA: gi_15810181_gb_AY056105.1_	245101_at	0.8
putative cytochrome P450	245075_at	0.8
ribosomal protein L16	244983_at	0.8
ribosomal protein S12 (trans-splice part 2 of 2)	244940_at	0.8
hypothetical protein similar to polyketide hydroxylases from several bacterial species	257410_at	0.8
hypothetical protein Similar to gi|1573829 HI0816 aminopeptidase P homolog (pepP) from Haemophilus influenzae genome gb|U32764	263707_at	0.7
Expressed protein ; supported by full-length cDNA: Ceres: 36399.	262782_at	0.7
unknown protein ; supported by cDNA: gi_16930706_gb_AF436837.1_AF436837	261130_at	0.7
Expressed protein ; supported by cDNA: gi_15810240_gb_AY056159.1_	257010_at	0.7
putative 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
putative protein predicted proteins, Arabidopsis thaliana	251809_at	0.7
putative protein predicted proteins, Homo sapiens, Drosophila melanogaster and Caenorhabditis elegans.	250156_at	0.7
putative protein contains similarity to DNA-damage-inducible protein P	249016_at	0.7
oligopeptide transporter -like protein oligopeptide transporter (LeOPT1), Lycopersicon esculentum, EMBL:AF016713	246566_at	0.7
ubiquitin-specific protease 8 (UBP8), putative similar to ubiquitin-specific protease 8 partial sequence GI:11993469 [Arabidopsis thaliana]	245683_at	0.7
Arabidopsis thaliana /REF=U37281 /DEF=actin-2 mRNA, complete cds /LEN=1637 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 pri	-r2-At-Actin-3	0.7
unknown protein similar to GP|522127|gnl|PID|e349073|Z35639 and GP|2224677|gnl|PID|d1021664|AB002366	267609_at	0.7
putative VP1/ABI3 family regulatory protein	267519_at	0.7
putative lipase ; supported by full-length cDNA: Ceres: 207043.	267496_at	0.7
putative glutaredoxin ;supported by full-length cDNA: Ceres:39560.	267497_at	0.7
putative 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 prote	266885_at	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
hypothetical protein predicted by genefinder; supported by cDNA: gi_10280999_dbj_AB046953.1_AB046953	266720_s_at	0.7
unknown protein	266721_at	0.7
putative Na+-dependent inorganic phosphate cotransporter	266672_at	0.7
cyclic nucleotide and calmodulin-regulated ion channel ; supported by cDNA: gi_14532659_gb_AY039954.1_	266520_at	0.7
unknown protein ; supported by cDNA: gi_16024935_gb_AY050658.1_	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	266466_at	0.7
putative protein transport protein SEC12p identical to GB:M95796, contains a WD-40 repeat domain; supported by cDNA: gi_166877_gb_M95796.1	266350_at	0.7
glutathione S-transferase identical to GB:X89216;supported by full-length cDNA: Ceres:6528.	266299_at	0.7
unknown protein	266075_s_at	0.7
putative glutamate/ornithine acetyltransferase ;supported by full-length cDNA: Ceres:121873.	265965_at	0.7
recA, putative similar to GB:CAA39098 GI:48781 recA from [Legionella pneumophila]	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	265118_at	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	0.7
unknown protein	264696_at	0.7
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 ankyrin like protein GI:7268141 from [Arabidopsis thaliana]; supported by cDNA: gi_14194106_gb_AF367259.1_AF367	264484_at	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_135	264448_at	0.7
putative myb-related transcription factor Similar to myb-related transcription factor (THM27) gb|X95296 from Solanum lycopersicum. ESTs gb|T4200	264210_at	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
unknown protein	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:	263716_at	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	263243_at	0.7
Expressed protein ; supported by cDNA: gi_15293050_gb_AY050959.1_	263210_at	0.7
unknown protein similar to hypothetical protein GB:AAF27089 GI:6730668 from (Arabidopsis thaliana)	263014_at	0.7
unknown protein	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
gamma-tocopherol methyltransferase almost identical to gamma-tocopherol methyltransferase GI:4106538 from [Arabidopsis thaliana];supported by	262875_at	0.7
ammonium transporter, putative 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	262826_at	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
threonine synthase, putative similar to threonine 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 c	262197_at	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	261939_at	0.7
unknown protein	261880_at	0.7
BTG1 binding factor 1, putative similar to BTG1 binding factor 1 GI:6016012 from [Homo sapiens]	261841_at	0.7
metal ion transporter, putative similar to metal ion transporter GI:5853313 from [Arabidopsis thaliana]	261845_at	0.7
hypothetical protein contains similarity to amino acid permease GI:7415521 from [Oryza sativa]	261785_at	0.7
hypothetical protein similar to hypothetical protein GB:AAF25977 GI:6714281 from [Arabidopsis thaliana]	261701_at	0.7
unknown protein similar to hypothetical protein GB:AAF26001 GI:6714305 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:94234.	261669_at	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_	261041_at	0.7
molybdopterin biosynthesis CNX3 protein, putative similar to molybdopterin biosynthesis CNX3 protein GB:Q39056 from [Arabidopsis thaliana]	261044_at	0.7
hypothetical protein contains similarity to RNA helicase (HRH1) GB:D50487 GI:1742909 from [Homo sapiens]	261008_at	0.7
MAP kinase ATMPK9, putative similar to GI:7106544 from (Arabidopsis thaliana)	260979_at	0.7
F-box protein family contains similarity to F-box protein FBX3 GI:6103643 from [Homo sapiens]	260949_at	0.7
ATP-dependent Clp protease proteolytic subunit (ClpP5) identical to nClpP1 GB:BAA82065 GI:5360579 from [Arabidopsis thaliana];supported by full	260912_at	0.7
19S proteosome subunit 9, putative similar to 19S proteosome subunit 9 GB:AAC34120 GI:3450889 from [Arabidopsis thaliana];supported by full-le	260842_at	0.7
unknown protein	260817_at	0.7
hypothetical protein predicted by genscan+	260455_at	0.7
unknown protein	260373_at	0.7
hypothetical protein predicted by genscan+; supported by cDNA: gi_15293216_gb_AY051042.1_	260311_at	0.7
putative U3 small nucleolar ribonucleoprotein protein identical to putative U3 small nucleolar ribonucleoprotein protein GB:AAF07373 (Arabidopsis th	260323_at	0.7
putative monodehydroascorbate reductase similar to monodehydroascorbate reductase GB:AAD28178 [Brassica juncea]; supported by cDNA: gi_14	260325_at	0.7
putative sulfate transporter contains Pfam profile: PF00916 sulfate transporter family;supported by full-length cDNA: Ceres:120095.	260302_at	0.7
unknown protein	259993_at	0.7
hydroxypyruvate reductase (HPR) identical to hydroxypyruvate reductase (HPR) GB:D85339 [Arabidopsis thaliana] (Plant Cell Physiol 1997 Apr;38(4	260014_at	0.7
unknown protein	259874_at	0.7
12-oxophytodienoate reductase (OPR2) identical to 12-oxophytodienoate reductase OPR2 GB:AAC78441 [Arabidopsis thaliana]	259875_s_at	0.7
unknown protein similar to hypothetical protein GB:CAB39648 [Arabidopsis thaliana]; supported by cDNA: gi_14532697_gb_AY039973.1_	259882_at	0.7
unknown protein	259794_at	0.7
unknown protein ;supported by full-length cDNA: Ceres:10323.	259766_at	0.7
acyl-CoA synthetase, putative similar to GI:1903032 from [Brassica napus] (Plant Mol. Biol. 33 (5), 911-922 (1997)); supported by cDNA: gi_145326	259737_at	0.7
Expressed protein ; supported by full-length cDNA: Ceres: 20443.	259542_at	0.7
hypothetical protein	259519_at	0.7
unknown protein ; supported by cDNA: gi_14423507_gb_AF386991.1_AF386991	259500_at	0.7
hypothetical protein contains similarity to ribosomal protein S15; supported by cDNA: gi_13605576_gb_AF361614.1_AF361614	259505_at	0.7
type 2A protein serine/threonine phosphatase 55 kDa B regulatory subunit almost identical to type 2A protein serine/threonine phosphatase 55 kDa	259404_at	0.7
jasmonate inducible protein isolog ;supported by full-length cDNA: Ceres:119153.	259382_s_at	0.7
unknown protein similar to unknown protein GB:AAC14509 [Arabidopsis thaliana]	259241_at	0.7
unknown protein contains Pfam profile:PF00887 Acyl CoA binding protein	259159_at	0.7
thioglucosidase 3D precursor identical to thioglucosidase 3D precursor GB:S57621 [Arabidopsis thaliana]; supported by cDNA: gi_14423459_gb_AF	259009_at	0.7
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:40090.	258856_at	0.7
putative helicase similar to C-terminal half of transcription-repair coupling factor (TRCF) GB:Q55750 [Synechocystis PCC6803]; contains Pfam profile	258861_at	0.7
putative MYB-related protein similar to MYB-related protein GB:CAA73305	258723_at	0.7
putative GTPase activating protein contains Pfam profile: PF01412 Putative GTP-ase activating protein for Arf	258689_at	0.7
putative phosphatidylinositol-4-phosphate 5-kinase similar to phosphatidylinositol-4-phosphate 5-kinase GB:CAB53377 [Arabidopsis thaliana]	258651_at	0.7
putative DEAD/DEAH box helicase contains Pfam profile: PF00270 DEAD/DEAH box helicase; supported by cDNA: gi_15081734_gb_AY048260.1_	258554_at	0.7
hypothetical protein predicted by genscan	258474_at	0.7
phospholipase D, putative similar to phospholipase D GB:BAA32278 from [Candida albicans]	258430_at	0.7
PP1/PP2A phosphatases pleiotropic regulator PRL2 identical to GB:Q39190 from [Arabidopsis thaliana]; supported by cDNA: gi_15809827_gb_AY0	258380_at	0.7
putative DNA binding protein identical to putative DNA binding protein GB:AAF27433 from [Arabidopsis thaliana]; supported by cDNA: gi_15028138_	258324_at	0.7
putative long-chain acyl-CoA synthetase similar to malonyl CoA synthetase GB:AAF28840 from [Bradyrhizobium japonicum];supported by full-length	258312_at	0.7
acid phosphatase type 5 identical to GB:CAB63938 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:113666.	258158_at	0.7
hypothetical protein predicted by genmark;supported by full-length cDNA: Ceres:19279.	258091_at	0.7
unknown protein	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	258006_at	0.7
fertilization-independent endosperm protein identical to GB:AAD23584 from [Arabidopsis thaliana]; supported by cDNA: gi_4567094_gb_AF129516.	257987_at	0.7
unknown protein	257956_at	0.7
unknown protein	257903_at	0.7
transcriptional regulator protein, putative similar to ATAN11 GB:AAC18912 [Arabidopsis thaliana] (Genes Dev. 11 (11), 1422-1434 (1997)); contains	257833_at	0.7
unknown protein	257783_at	0.7
unknown protein contains Pfam profile: PF00515 tetratricopeptide repeat domain (TPR domain);supported by full-length cDNA: Ceres:23733.	257730_at	0.7
unknown protein contains Pfam profile:PF00806 Pumilio-family RNA binding domains; supported by cDNA: gi_15010673_gb_AY045638.1_	257652_at	0.7
chaperonin, putative similar to CHAPERONIN CPN60-2, MITOCHONDRIAL PRECURSOR GB:Q05046 from [Cucurbita maxima];supported by full-le	257608_at	0.7
unknown protein	257285_at	0.7
transfactor, putative similar to GB:BAA75684 from [Nicotiana tabacum];supported by full-length cDNA: Ceres:6626.	257250_at	0.7
zinc finger protein, putative contains Pfam profile: PF01760 CONSTANS family zinc finger;supported by full-length cDNA: Ceres:258241.	257262_at	0.7
4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein, putative similar to ThiJ GB:AAA82704 [Escherichia coli]; likely encodes tw	257216_at	0.7
Expressed protein ; supported by full-length cDNA: Ceres: 6801.	257169_at	0.7
unknown protein ; supported by cDNA: gi_15215846_gb_AY050453.1_	257095_at	0.7
squamosa promoter binding protein-like 5 identical to GB:CAB56571 from [Arabidopsis thaliana]	257051_at	0.7
zinc finger protein, putative contains Pfam profiles: PF00097 Zinc finger, C3HC4 type (RING finger) (2 copies)	257062_at	0.7
adenosine triphosphatase, putative similar to vacuolar adenosine triphosphatase subunit D GB:AAC83085 from [Mus musculus]	256988_s_at	0.7
unknown protein	256915_at	0.7
cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450	256870_at	0.7
unknown protein similar to CW14 GB:BAA87958 from [Arabidopsis thaliana]; supported by cDNA: gi_15450961_gb_AY054561.1_	256747_at	0.7
unknown protein ;supported by full-length cDNA: Ceres:38478.	256663_at	0.7
hypothetical protein predicted by genemark.hmm	256573_at	0.7
ABC transporter, putative contains Pfam profile: PF00005: ABC transporter	256308_s_at	0.7
arginine N-methyltransferase 3, putative similar to arginine N-methyltransferase 3 GB:AAC40158 [Rattus norvegicus]	256288_at	0.7
sulphate transporter, putative similar to high affinity sulphate transporter GB:X96431 GI:1217966 [Hordeum vulgare]; supported by cDNA: gi_11933	256244_at	0.7
beta-fructofuranosidase identical to beta-fructofuranosidase GI:6683112 from [Arabidopsis thaliana]; supported by cDNA: gi_6683111_dbj_AB02931	256150_at	0.7
unknown protein ;supported by full-length cDNA: Ceres:38751.	256017_at	0.7
inositol polyphosphate 5-phosphatase II, putative similar to inositol polyphosphate 5-phosphatase II GI:9945302 from [Mus musculus]; supported by	255984_at	0.7
glycyl tRNA synthetase, putative similar to glycyl tRNA synthetase GI:577711 from [Homo sapiens];supported by full-length cDNA: Ceres:29666.	256000_at	0.7
putative protein kinase contains a protein kinase domain profile (PDOC00100); supported by cDNA: gi_13448034_gb_AF339146.1_AF339146	255872_at	0.7

putative cinnamoyl-CoA reductase highly similar to F4P9.36	255845_at	0.7
AT-hook DNA-binding protein (AHP1) almost identical to GB:CAA10857; supported by cDNA: gi_14326503_gb_AF385705.1_AF385705	255792_at	0.7
unknown protein ;supported by full-length cDNA: Ceres:121070.	255766_at	0.7
putative beta-amylase similar to the family of glycosyl hydrolases	255676_at	0.7
predicted protein with unknown function	255678_at	0.7
putative RNA helicase similar to ATP-dependent RNA helicases	255688_at	0.7
S-adenosylmethionine synthase 2 ;supported by full-length cDNA: Ceres:36518.	255552_at	0.7
CTP synthase - like protein	255529_at	0.7
putative serine/threonine protein kinase	255488_at	0.7
hypothetical protein similar to A. thaliana hypothetical protein F15K9.11, GenBank accession number AC005278	255452_at	0.7
predicted protein of unknown function ; supported by full-length cDNA: Ceres: 711.	255434_at	0.7
putative phosphofructokinase beta subunit	255365_at	0.7
putative leucyl tRNA synthetase	255328_at	0.7
F-box protein family, AtFBW2 contains similarity to N7 protein GI:3273101 from [Medicago truncatula];supported by full-length cDNA: Ceres:11257.	255066_at	0.7
putative protein 24 kDa seed maturation protein - Glycine max,PID:g4102690;supported by full-length cDNA: Ceres:23536.	254920_at	0.7
phospholipid hydroperoxide glutathione peroxidase ;supported by full-length cDNA: Ceres:8846.	254890_at	0.7
putative protein predicted protein, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 112156.	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	254684_at	0.7
putative protein	254645_at	0.7
heat shock transcription factor - like protein heat shock transcription factor, Zea mays, PIR2:S61448	254592_at	0.7
putative protein various predicted proteins	254549_at	0.7
hypothetical protein ;supported by full-length cDNA: Ceres:29391.	254299_at	0.7
putative protein similarity Human mRNA for KIAA0156 gen - Homo sapiens, PID:d1010577	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
putative protein apoptosis gene MA3, Suberites domuncula, Y15421; supported by cDNA: gi_17063162_gb_AY062102.1_	254089_at	0.7
putative protein similarity to multidrug resistance protein, Mus musculus, PIR1:DVMS1~Contains ABC transporters family signature, (LSGGQRQRV	254068_at	0.7
splicing factor At-SRp40 contains EST gb:T45156, H3766800; supported by cDNA: gi_1667581_gb_U76607.1_ATU76607	254073_at	0.7
putative protein hypothetical protein YOR261c, yeast, PIR2:S67158;supported by full-length cDNA: Ceres:36616.	253969_at	0.7
putative APG protein proline-rich protein APG - Arabidopsis thaliana, EMBL:X60377;supported by full-length cDNA: Ceres:2574.	253946_at	0.7
kinesin-related protein katB ; supported by cDNA: gi_1438841_dbj_D21137.1_ATHKATB	253903_at	0.7
protein phosphatase homolog (PPH1)	253834_at	0.7
putative protein predicted protein, Arabidopsis thaliana	253783_at	0.7
gamma-glutamyltransferase-like protein gamma-glutamyltransferase - Arabidopsis thaliana,PIR2:S58286	253708_at	0.7
putative protein, fragment prolidase - Suberites domuncula,PID:e1289868	253719_at	0.7
putative protein predicted protein, Arabidopsis thaliana, PIR2:T01287; supported by cDNA: gi_15810172_gb_AY056100.1_	253649_at	0.7
putative villin	253663_at	0.7
kinase binding protein - like Skb1 protein homolog, Homo sapiens, PIR2:T03842	253558_at	0.7
hypothetical protein ;supported by full-length cDNA: Ceres:151518.	253520_at	0.7
predicted protein ; supported by cDNA: gi_15292824_gb_AY050846.1_	253524_at	0.7
putative protein microtubule-associated protein 1B (MAP1B), Homo sapiens, L06237	253497_at	0.7
putative protein tom-1B protein, Gallus gallus	253418_at	0.7
carbonate dehydratase - like protein carbonate dehydratase precursor, Spinacia oleracea,Pir2:S28797;supported by full-length cDNA: Ceres:6589.	253300_at	0.7
hypothetical protein	253314_at	0.7
putative protein prolyl 4-hydroxylase alpha(II)-subunit, Mus musculus, PIR2:I49135;supported by full-length cDNA: Ceres:2306.	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
putative protein various predicted proteins;supported by full-length cDNA: Ceres:206573.	253198_at	0.7
putative protein probable membrane protein YBL019w, yeast, PIR2:S45753	253126_at	0.7
NAD(P)H oxidoreductase, isoflavone reductase - like protein Pyrc2, Pyrus communis, AF071477	252939_at	0.7
SEC14 - like protein phosphatidylinositol-phosphatidylcholine transfer protein SEC14, Yarrowia lipolytica, PIR2:S43745; supported by cDNA: gi_143	252884_at	0.7
shikimate kinase - like protein shikimate kinase precursor, Lycopersicon esculentum, gb:S21584	252900_at	0.7
putative protein crp1 protein, Zea mays, EMBL:AF073522	252904_at	0.7
putative protein ;supported by full-length cDNA: Ceres:5968.	252880_at	0.7
DnaJ - like protein DnaJ-like protein, Pisum sativum, Z71640; supported by cDNA: gi_15450580_gb_AY052658.1_	252828_at	0.7
ubiquitin-specific protease 3 (UBP3) identical to GI:2347098; supported by cDNA: gi_2347097_gb_U76845.1_ATU76845	252832_at	0.7
guanine nucleotide-exchange - like protein brefeldin A-inhibited guanine nucleotide-exchange protein 2, Homo sapiens, EMBL:AF084521	252743_at	0.7
putative protein predicted protein, C.elegans, PIR:T24538	252680_at	0.7
putative protein KIAA0073, Homo sapiens, EMBL:HSORF006	252644_at	0.7
disease resistance protein homolog disease resistance protein RPP1-WsB - Arabidopsis thaliana, EMBL:AF098963	252648_at	0.7
putative protein Mlo-h1 protein - Hordeum vulgare, PIR:T05952; supported by cDNA: gi_14091575_gb_AF369564.1_AF369564	252572_at	0.7
putative protein potential transcriptional repressor Not4hp - Mus musculus, EMBL:U71269	252588_at	0.7
receptor protein kinase -like receptor-like protein kinase precursor, Madagascar periwinkle, PIR:T10060	252512_at	0.7
putative protein various predicted genes, Arabidopsis thalina and Oryza sativa	252462_at	0.7
putative protein putative protein - Arabidopsis thaliana, EMBL:CAB36749.1	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
putative protein hypothetical protein KIAA0453 (fragment), Homo sapiens, PIR:T00067	252208_at	0.7
crooked neck-like protein crooked neck protein (CRN) - Drosophila melanogaster, SWISSPROT:CRN_DROME; supported by cDNA: gi_15293116_	252100_at	0.7
putative protein 150-kD protein cluA - Dictyostelium discoideum,PID:g2281117	252031_at	0.7
ABC transporter - like protein ATP-binding cassette-sub-family G-member 2, Mus musculus, EMBL:AF140218	251826_at	0.7
P-glycoprotein - like P-glycoprotein (pmdr1), Solanum tuberosum, EMBL:U52079	251781_at	0.7
putative protein various predicted proteins;supported by full-length cDNA: Ceres:205700.	251800_at	0.7
putative protein EXOENZYMES REGULATORY PROTEIN AEPA PRECURSOR, SWISSPROT:AEPA_ERWCA; supported by cDNA: gi_16209665_	251717_at	0.7
calcium-dependent protein kinase calcium-dependent protein kinase - Fragaria x ananassa, EMBL:AF035944	251636_at	0.7
40S ribosomal protein S2 homolog 40S ribosomal protein S2 - Arabidopsis thaliana, SWISSPROT:RS2_ARATH;supported by full-length cDNA: Cer	251638_at	0.7
putative protein hypothetical protein T24P15.4 - Arabidopsis thaliana, PIR:T00923;supported by full-length cDNA: Ceres:1979.	251559_at	0.7
serine/threonine-specific protein kinase -like protein serine/threonine-specific protein kinase NAK, Arabidopsis thaliana, PIR:S38326	251539_at	0.7
cysteine synthase	251487_at	0.7
DEAD box RNA helicase RH12	251362_at	0.7
putative protein putative protein At2g46260 - Arabidopsis thaliana, EMBL:AC005397; supported by cDNA: gi_12006854_gb_AF292397.1_AF29239	251328_at	0.7
auxin response factor-like protein auxin response factor 9 - Arabidopsis thaliana, PIR:T08917; supported by cDNA: gi_16604602_gb_AY059746.1_	251289_at	0.7
multifunctional aminoacyl-tRNA ligase-like protein multifunctional aminoacyl-tRNA ligase - Homo sapiens, PIR:SYHUQT; supported by cDNA: gi_16	251264_at	0.7
ATP-dependent RNA helicase-like protein ATP-dependent RNA helicase (EC 3.6.-.-) - Homo sapiens, PIR:JC5785	251265_at	0.7
putative protein hypothetical protein BAA87851.1 - Oryza sativa, EMBL:AP000816	251267_at	0.7
Sar1-like GTP binding protein small GTP-binding protein Bsar1a - Brassica campestris, EMBL:U55035	251217_at	0.7
putative membrane protein clone:2-72. - Mus musculus, EMBL:AB030201; supported by cDNA: gi_15724186_gb_AF411796.1_AF411796	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	249415_at	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_AY049237.1_	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 (gb|AAD26634.1)	249112_at	0.7
alcohol dehydrogenase (EC 1.1.1.1) class III (pir||S71244) ;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 b	249036_at	0.7
cyclin-dependent protein kinase-like protein ; supported by cDNA: gi_15983484_gb_AF424617.1_AF424617	249050_at	0.7
putative protein contains similarity to unknown;supported by full-length cDNA: Ceres:4029.	249025_at	0.7
putative protein strong similarity to unknown protein (gb|AAC61825.1); supported by cDNA: gi_15081732_gb_AY048259.1_	248976_at	0.7
unknown protein	248996_at	0.7
pectin acetylesterase ;supported by full-length cDNA: Ceres:39005.	248968_at	0.7
urea active transporter-like protein	248970_at	0.7
unknown protein	248956_at	0.7
unknown protein ;supported by full-length cDNA: Ceres:40096.	248738_at	0.7
unknown protein ;supported by full-length cDNA: Ceres:25275.	248709_at	0.7
putative protein similar to unknown protein (gb|AAF31026.1)	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||S76207);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-le	247514_at	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	247120_at	0.7
anthranilate N-hydroxycinnamoyl/benzoyltransferase-like protein ;supported by full-length cDNA: Ceres:32856.	247038_at	0.7
unknown protein	246961_at	0.7
threonyl-tRNA synthetase ; supported by cDNA: gi_15081625_gb_AY048205.1_	246801_at	0.7
NHE1 Na+/H+ exchanger ; supported by cDNA: gi_6650176_gb_AF056190.1_AF056190	246763_at	0.7
seryl-tRNA synthetase ; supported by cDNA: gi_15293240_gb_AY051054.1_	246780_at	0.7
putative protein clathrin assembly protein short form, Rattus norvegicus, EMBL:AF041373	246653_at	0.7
putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:40501.	246611_at	0.7
hypothetical protein	246513_at	0.7
valine--tRNA ligase-like protein several bacterial valine--tRNA ligases	246509_at	0.7
carbonic anhydrase, putative similar to carbonic anhydrase 1 GI:882241 from [Flaveria linearis]	246396_at	0.7
30S ribosomal 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	246146_at	0.7
cytochrome-b5 reductase - like protein cytochrome-b5 reductase, Saccharomyces cerevisiae, PIR:S37800;supported by full-length cDNA: Ceres:33	246157_at	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	245851_at	0.7
unknown protein contains similarity to transfactor GB:BAA75684 GI:4519671 from [Nicotiana tabacum]; supported by cDNA: gi_15723594_gb_AY04	245758_at	0.7
hypothetical protein contains similarity to cockayne syndrome complementation group A protein GB:U28413 GI:975301 from [Homo sapiens]	245764_s_at	0.7
unknown protein contains similarity to calmodulin GI:166304 from [Achlya klebsiana]; supported by cDNA: gi_13358218_gb_AF325029.2_AF325029	245732_at	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 O-acetylserine(thiol)lyase (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	245277_at	0.7
hypothetical protein ; supported by cDNA: gi_16226250_gb_AF428283.1_AF428283	245269_at	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	244977_at	0.7
3-methyl-2-oxobutanoate hydroxy-methyl-transferase	266598_at	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	258212_at	0.6
eukaryotic translation elongation factor 2, putative similar to eukaryotic translation elongation factor 2 GB:NP_001952 [Homo sapiens]	257758_at	0.6
phosphatidylinositol-4-phosphate 5-kinase, putative similar to phosphatidylinositol-4-phosphate 5-kinase GI:3702691 from [Arabidopsis thaliana]; su	255959_at	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
Expressed protein ; supported by full-length cDNA: Ceres: 114014.	252822_at	0.6
putative protein merozoite surface antigen 2, Plasmodium falciparum, PIR:A45637	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,	250273_at	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.	248792_at	0.6
EspB-like protein	248276_at	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	-Athal-Actin_	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_	267264_at	0.6
aspartate aminotransferase (AAT1) identical to GB:U15026;supported by full-length cDNA: Ceres:34360.	267151_at	0.6
putative ADP ribosylation factor 1 GTPase activating protein ; supported by cDNA: gi_14334619_gb_AY034983.1_	267179_at	0.6
putative MYB 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	267031_at	0.6
putative urease accessory protein ; supported by full-length cDNA: Ceres: 18513.	267001_at	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	266495_at	0.6
putative cysteinyl-tRNA synthetase ; supported by cDNA: gi_15293250_gb_AY051059.1_	266478_at	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	266110_at	0.6
chloroplast single subunit DNA-dependent RNA polymerase identical to GB:Y08722	265991_at	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_	265657_at	0.6
12-oxophytodienoate-10,11-reductase ; supported by cDNA: gi_15294261_gb_AF410322.1_AF410322	265530_at	0.6
similar 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
hypothetical protein	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	265070_at	0.6
putative prohibitin 2 B-cell receptor associated protein;supported by full-length cDNA: Ceres:6208.	265037_at	0.6

putative glucanase	264875_at	0.6
putative glycosylation enzyme ; supported by cDNA: gi_15292806_gb_AY050837.1_	264844_at	0.6
unknown protein similar to beta-galactoside alpha-2,3-sialyltransferase (pir|IJC5251)	264793_at	0.6
unknown protein similar to ESTs emb|Z46294, gb|W43468, and gb|W43475	264795_at	0.6
unknown protein similar to C-1 (Homo sapiens) (U41816); supported by full-length cDNA: Ceres: 20276.	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	264608_at	0.6
putative prolyl 4-hydroxylase, alpha subunit ;supported by full-length cDNA: Ceres:36054.	264592_at	0.6
auxin-resistance protein AXR1 E1 ubiquitin-like activating enzyme; identical to GB:P42744; supported by cDNA: gi_15215701_gb_AY050379.1_	264585_at	0.6
hypothetical protein predicted by genemark.hmm	264542_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
ribosomal protein identical to ribosomal protein GI:166858 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:14534.	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	264317_at	0.6
hypothetical protein contains similarity to glucosidase I GI:2344809 from [Homo sapiens]	264228_at	0.6
putative sucrose transport protein, SUC2 strong similarity to GB:S38196 sucrose transport protein SUC2 from [Arabidopsis thaliana];supported by fu	264204_at	0.6
hypothetical protein contains Pfam profile: PF01535 PPR repeat	264177_at	0.6
hypothetical protein predicted by genscan	264064_at	0.6
MADS-box protein (AGL3) ; supported by cDNA: gi_1737494_gb_U81369.1_ATU81369	264041_at	0.6
unknown protein	263976_at	0.6
putative MAP kinase ; supported by cDNA: gi_15724283_gb_AF412082.1_AF412082	263989_at	0.6
putative shikimate kinase precursor	263897_at	0.6
putative eukaryotic translation initiation factor 2 alpha subunit, eIF2 ;supported by full-length cDNA: Ceres:13800.	263835_at	0.6
putative plasma membrane proton ATPase	263791_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:36719.	263796_at	0.6
Expressed protein ; supported by cDNA: gi_15027870_gb_AY045792.1_	263763_at	0.6
ankyrin-like protein EST gb|ATTS0956 comes from this gene;supported by full-length cDNA: Ceres:108617.	263662_at	0.6
putative DNA-directed RNA polymerase II subunit	263621_at	0.6
putative Rieske iron-sulfur protein ;supported by full-length cDNA: Ceres:29774.	263533_at	0.6
putative ATP-dependent RNA helicase	263493_at	0.6
putative protein kinase contains a protein kinase domain profile (PDOC00100)	263461_at	0.6
putative receptor-like protein kinase ; supported by cDNA: gi_16648754_gb_AY058153.1_	263478_at	0.6
unknown protein	263456_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:120231.	263303_at	0.6
unknown protein ; supported by cDNA: gi_15027886_gb_AY045800.1_	263331_at	0.6
unknown protein similar to ribonuclease inhibitors; supported by cDNA: gi_15810394_gb_AY056236.1_	263212_at	0.6
hypothetical protein Similar to hexosaminidase, gi|1170249, gi|1076942 and others	263199_at	0.6
unknown protein	263171_at	0.6
myrosinase-associated protein, putative similar to myrosinase-associated protein GI:1769967 from [Brassica napus];supported by full-length cDNA:	263156_at	0.6
cytochrome P450, putative similar to cytochrome P450 GI:4176420 from [Arabidopsis thaliana]	263120_at	0.6
hypothetical protein contains similarity to serine threonine kinase GI:166813 from [Arabidopsis thaliana]; supported by cDNA: gi_14334553_gb_AY03	263111_s_at	0.6
hypothetical protein predicted by genscan and genefinder;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
unknown protein contains Pfam profile: PF01417 ENTH domain	262856_at	0.6
hypothetical protein predicted by genscan	262770_at	0.6
unknown protein	262700_at	0.6
flavin-containing amine oxidase contains Pfam profile: PF01593 Flavin containing amine oxidase	262668_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:1505.	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	262636_at	0.6
hypothetical protein predicted by genscan+	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	262492_at	0.6
leaf development protein Argonaute identical to GB:AAC18440 from (Arabidopsis thaliana); supported by cDNA: gi_2149639_gb_U91995.1_ATU919	262246_at	0.6
unknown protein contains similarity to translation initiation factor eIF-2B GI:623032 from [Rattus norvegicus]	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
hypothetical protein	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	262024_at	0.6
CCR4-associated factor, putative\0CCR4-associated factor, putative similar to CCR4-ASSOCIATED FACTOR 1 GB:Q60809 from [Mus musculus]\0	261887_at	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
RNA-binding protein, putative similar to RNA-binding protein GB:CAB40027 GI:4539439 from [Arabidopsis thaliana];supported by full-length cDNA:	261709_at	0.6
lysophospholipase homolog, putative similar to lysophospholipase homolog GB:AAB97366 GI:2801536 from [Oryza sativa]	261661_at	0.6
Expressed protein ; supported by full-length cDNA: Ceres: 107675.	261676_at	0.6
receptor kinase, putative similar to receptor kinase GI:4105699 from [Arabidopsis thaliana]	261498_at	0.6
unknown protein	261465_at	0.6
protein kinase, putative similar to CRK1 protein GI:7671528 from [Beta vulgaris]	261427_at	0.6
pectinesterase, putative similar to GB:Z94058 from [Lycopersicon esculentum]; supported by cDNA: gi_16648888_gb_AY059814.1_	261363_at	0.6
MAP kinase BnMAP4K alpha1, putative similar to BnMAP4K alpha1 GI:3819697 from (Brassica napus)	261316_at	0.6
aminoacylase, putative similar to aminoacylase I GI:1844 from [Sus scrofa]	261326_s_at	0.6
growth regulator protein similar to GB:X80301 from [Nicotiana tabacum]	261170_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:40419.	261144_s_at	0.6
unknown protein	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 cD	261081_at	0.6
hypothetical protein similar to hypothetical protein GB:CAB80918 GI:7267606 from [Arabidopsis thaliana]	261052_at	0.6
hypothetical protein predicted by genemark.hmm	261053_at	0.6
unknown protein ;supported by full-length cDNA: Ceres:11931.	261014_at	0.6
hypothetical protein predicted by genemark.hmm	260993_at	0.6
glyoxalase II isozyme, putative similar to glyoxalase II isozyme GB:AAC49865 GI:2570338 from [Arabidopsis thaliana];supported by full-length cDNA	260954_at	0.6
hypothetical protein contains similarity to MTN3 (nodule development protein) GB:Y08726 GI:1619601 from [Medicago truncatula];supported by full-l	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.	260769_at	0.6
unknown protein ; supported by cDNA: gi_15810124_gb_AY056127.1_	260675_at	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	260237_at	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))	260064_at	0.6
beta-1,3-glucanase precursor, putative similar to GI:4097948 from [Oryza sativa] (Gene 223 (1-2), 311-320 (1998))	259823_at	0.6
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	259825_at	0.6
spore coat protein-like protein similar to SPORE COAT PROTEIN A GB:P07788 from [Bacillus subtilis] and BILIRUBIN OXIDASE GB:Q12737 [Myro	259752_at	0.6
putative cleavage and polyadenylation specificity factor similar to cleavage and polyadenylation specificity factor 73 kDa subunit GB:AAF00224 from	259717_at	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
protein serine/threonine kinase, putative similar to protein serine/threonine kinase GI:7248457 from [Lophopyrum elongatum]; supported by cDNA: g	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	259363_at	0.6
putative cytoskeleton-associated protein similar to cytoskeleton-associated protein 1 GB:4502849 [Homo sapiens]	259141_at	0.6
putative mitogen activated protein kinase kinase similar to mitogen 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	258790_at	0.6
putative bZIP transcription factor contains Pfam profile: PF00170 bZIP transcription factor; contains similarity to TGACG-sequence specific DNA-binc	258759_at	0.6
hydroxyacylglutathione hydrolase cytoplasmic (glyoxalase II) (GLX II) identical to hydroxyacylglutathione hydrolase cytoplasmic (glyoxalase II) (GLX	258775_at	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	258650_at	0.6
hypothetical protein predicted by genscan+	258505_at	0.6
neutral invertase, putative 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	258351_at	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
rubisco expression protein, putative similar to GB:O22034 from [Cyanidium caldarium] (J. Plant Res. 110, 235-245 (1997));supported by full-length c	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
putative MAP kinase similar to blast and wounding induced mitogen-activated protein kinase (BWMK1) GB:AAD52659 [Oryza sativa]; contains Pfam	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)); sup	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	256922_at	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:BAA12064 [Nicotiana sylvestris]; contains Pfam profile: PF00076 RNA reco	256882_at	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
putative disease resistance protein similar to disease resistance protein GB:AAC78591 [Lycopersicon esculentum]	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	256255_at	0.6
auxin conjugate hydrolase (ILL5) identical to auxin conjugate hydrolase [Arabidopsis thaliana] (ILL5) GI:5725649;contains nonconsensus AT accept	256178_s_at	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	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, scor	255502_at	0.6
putative glycosyltransferase similar to A. thaliana protein T20K9.11, GenBank accession number 3445207; supported by cDNA: gi_16209668_gb_A	255483_at	0.6
putative GH3-like protein similar to soybean GH3 auxin-inducible protein, GenBank accession number X60033; supported by cDNA: gi_16649142_	255403_at	0.6
putative malonyl-CoA decarboxylase	255327_at	0.6
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	255068_at	0.6
calmodulin-domain protein kinase CDPK isoform 4 (CPK4)	255039_at	0.6
putative protein ; supported by full-length cDNA: Ceres: 93362.	254957_at	0.6
hypothetical protein ; supported by cDNA: gi_16648694_gb_AY058123.1_	254814_at	0.6
putative trehalose-6-phosphate phosphatase (AtTPPA) trehalose-6-phosphate phosphatase - Arabidopsis thaliana, PID:g2944178; supported by cD	254806_at	0.6
SERINE CARBOXYPEPTIDASE I PRECURSOR-like protein SERINE CARBOXYPEPTIDASE I PRECURSOR - Hordeum vulgare, SWall:CBP1_HC	254791_at	0.6
putative protein HYA22 protein, Homo sapiens, PIR2:JC5707	254681_at	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
putative protein rape mRNA, Brassica napus, PIR2:S42651	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_	254128_at	0.6
putative protein cylicin II - human, PID:g758587; supported by cDNA: gi_14423517_gb_AF386996.1_AF386996	254058_at	0.6
putative protein immunophilin FKBP46 - Spodoptera frugiperda (fall armyworm),PIR2:A55320; supported 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
putative protein	253941_at	0.6
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	253639_at	0.6
aspartate--tRNA 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: g	253489_at	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
phenylalanyl-trna synthetase - like protein phenylalanyl-trna synthetase beta chain, cytosolic,Saccharomyces cerevisiae, PIR1:YFBYAC	252941_at	0.6
putative protein various predicted proteins, Arabidopsis thaliana	252901_at	0.6
nucleic acid binding protein-like nucleic acid binding protein - Oryza sativa, PIR:T02745	252764_at	0.6
putative protein predicted protein, Drosophila melanogaster, EMBL:AE003789	252738_at	0.6
putative histone deacetylase similar to maize nucleolar histone deacetylase (U82815); supported by cDNA: gi_11066134_gb_AF195545.1_AF19554	252625_at	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 cDNA: gi_13430515_gb_AF360170.1_A	252414_at	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 cD	251185_at	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
ACTIN 2/7 (sp|P53492) ; supported by cDNA: gi_1049306_gb_U37281.1_ATU37281	250458_s_at	0.6
argininosuccinate lyase (AtArgH) ; supported by cDNA: gi_15028082_gb_AY045898.1_	250403_at	0.6
putative protein ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I, Spinacia oleracea chloroplast, pir:T08996	250170_at	0.6
acetolactate synthase-like protein	250111_at	0.6
unknown protein	250104_at	0.6
phytoene synthase (gb|AAB65697.1) ;supported by full-length cDNA: Ceres:15761.	250095_at	0.6
chromo domain protein polycomb-like protein, Daucus carota, PIR:T14294; supported by cDNA: gi_15625406_gb_AF387639.1_AF387639	250060_at	0.6
GTP-binding protein obg -like GTP-binding protein obg, Bacillus subtilis, PIR:B32804	249993_at	0.6
putative protein predicted proteins, Homo sapiens, Schizosaccharomyces pombe, Caenorhabditis elegans, Saccharomyces cerevisiae, Drosophila r	249925_at	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: gi_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	248864_at	0.6
protein serine threonine kinase-like	248821_at	0.6
40S ribosomal protein S19 ; supported by cDNA: gi_15028320_gb_AY045963.1_	248800_at	0.6
putative protein strong similarity to unknown protein (emb|CAB71043.1); supported by cDNA: gi_15810326_gb_AY056202.1_	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 [Arabidopsis t	248575_at	0.6
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
N-myristoyl transferase ;supported by full-length cDNA: Ceres:36525.	247960_at	0.6
putative protein similar to unknown protein (gb|AAD55473.1);supported by full-length cDNA: Ceres:7233.	247931_at	0.6
protein carboxyl methylase-like	247926_at	0.6
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:I40710;supported by full-length cDNA: Ceres:17098.	247851_at	0.6
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:40850.	247608_at	0.6
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_AF370259	246736_at	0.6
serine/threonine protein kinase SOS2 (gb|AAF62923.1) ; supported by cDNA: gi_14701909_gb_AF395081.1_AF395081	246614_at	0.6
hypothetical protein predicted by genemark.hmm	246576_at	0.6
pyrroline-5-carboxylate reductase ;supported by full-length cDNA: Ceres:36386.	246594_at	0.6
dolichyl-phosphate-mannose--glycolipid alpha-mannosyltransferase -like protein dolichyl-phosphate-mannose--glycolipid alpha-mannosyltransferase	246598_at	0.6
N2,N2-dimethylguanine tRNA methyltransferase-like protein several N2,N2-dimethylguanine tRNA 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 by full-length c	245114_at	0.6
putative protein kinase contains a protein kinase domain profile (PDOC00100)	245074_at	0.6
ATPase a subunit	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:JC5401; supporte	255132_at	0.6
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	259396_at	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
Expressed protein ; supported by full-length cDNA: Ceres: 12588.	257152_at	0.5
putative protein	254797_at	0.5
putative protein DNA polymerase III holoenzyme tau subunit, Thermus thermophilus, gb:AF025391	254643_at	0.5
putative protein MSP1 protein, Saccharomyces cerevisia, PIR2:A49506;supported by full-length cDNA: Ceres:142160.	253861_at	0.5
serine threonine-protein kinase-like protein Ca2+ calmodulin-dependent protein kinase - Rattus norvegicus, PIR:A57156; supported by cDNA: gi_14	252616_at	0.5
putative protein	251725_at	0.5
nicotianamine synthase (dbj|BAA74589.1)	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
Arabidopsis thaliana /REF=X52320 /DEF=25S rRNA /LEN=4310	Athal-25SrRN	0.5
Arabidopsis thaliana /REF=M64116 /DEF=glyceraldehyde 3-phosphate dehydrogenase C subunit (GapC) gene, complete cds /LEN=1295 (_5, _M,	thal-GAPDH_	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	267617_at	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	267229_s_at	0.5
GDP dissociation inhibitor identical to GB:D83531;supported by full-length cDNA: Ceres:29536.	267236_at	0.5
hypothetical protein predicted by grail; supported by full-length cDNA: Ceres: 35095.	267152_at	0.5
putative adenosine phosphosulfate kinase identical to GB:U05238;supported by full-length cDNA: Ceres:14216.	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
unknown protein	267009_at	0.5
putative 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	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_	265002_at	0.5
auxin-induced protein, putative similar to auxin-induced atb2 GI:6562980 from [Arabidopsis thaliana]; supported by cDNA: gi_6562979_gb_AF05771	264928_at	0.5
putative ligand-gated ion channel protein similar to ligand-gated ion channels and to A. thaliana protein T21B4.3; supported by cDNA: gi_2708330_g	264853_at	0.5
hypothetical protein similar to putative serine/threonine kinase GI:4585880 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:13461.	264767_at	0.5
unknown protein location of EST emb|F15151	264722_at	0.5
putative K+ channel, beta subunit similar to GB:AAA87294;supported by full-length cDNA: Ceres:23300.	264607_at	0.5
putative 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	264406_at	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 f	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 p	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
putative PHD-type zinc finger protein	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_	263422_s_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
transport protein, putative similar to transport protein GI:7268121 from (Arabidopsis thaliana); supported by cDNA: gi_15912296_gb_AY056426.1_	263185_at	0.5
hypothetical protein Contains PF|00637 Clathrin 7-fold repeat. EST gb|AA721862 comes from this gene	263143_at	0.5
hypothetical protein similar to hypothetical ABC transporter ATP-binding protein GI:9955395 from [Microcystis aeruginosa]	263000_at	0.5
unknown protein ;supported by full-length cDNA: 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 carboxylas	262648_at	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_	262637_at	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
unknown protein similar to unknown protein GB:AAC63676	262319_s_at	0.5
asparaginyl-tRNA synthetase(SYNC1) protein,putative similar to SYNC1 protein GI:5670315 from [Arabidopsis thaliana]	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_15	262230_at	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]	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	261692_at	0.5
unknown protein ;supported by full-length cDNA: Ceres:33310.	261677_at	0.5
hypothetical protein predicted by genemark.hmm	261622_at	0.5
ribosomal protein L9, putative similar to RIBOSOMAL PROTEIN L9 GB:P49209 from [Arabidopsis thaliana]	261620_s_at	0.5

phytochrome kinase substrate 1, putative similar to phytochrome kinase substrate 1 GI:5020168 from [Arabidopsis thaliana];supported by full-length	261480_at	0.5
calcium-dependent protein kinase, putative similar to calcium-dependent protein kinase GI:604880 from [Arabidopsis thaliana]; supported by cDNA:	261378_at	0.5
unknown protein	261258_at	0.5
NAM protein, putative similar to NAM protein GI:6066594 from [Petunia hybrida]; supported by cDNA: gi_14334571_gb_AY034959.1_	261192_at	0.5
transcription factor IIA large subunit similar to GB:CAA11525 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:19512.	261079_s_at	0.5
transcriptional activator RF2a, putative similar to transcriptional activator RF2a GB:AF005492 GI:2253277 from [Oryza sativa];supported by full-leng	260953_at	0.5
acyl-CoA oxidase ACX3 identical to acyl-CoA oxidase ACX3 GI:8163758 from [Arabidopsis thaliana]	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	260770_at	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	260500_at	0.5
Ser/Thr kinase ;supported by full-length cDNA: Ceres:100245.	260480_at	0.5
unknown protein similar to hypothetical protein GB:CAA10289 [Cicer arietinum]	260401_at	0.5
putative flavonol sulfotransferase similar to flavonol 4 -sulfotransferase GB:P52837 from [Flaveria chloraefolia];supported by full-length cDNA: Ceres:	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:O69664 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	260191_at	0.5
putative histidinol-phosphate aminotransferase similar to histidinol-phosphate aminotransferase GB:CAA70403 from [Nicotiana tabacum]	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: 69	260138_at	0.5
unknown protein	260069_at	0.5
putative MAP kinase similar to mitogen-activated protein kinase GB:A56042 [Dictyostelium discoideum]; contains Pfam profile: PF00069 Eukaryotic	260045_at	0.5
unknown protein ;supported by full-length cDNA: Ceres:270659.	260025_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	259438_at	0.5
unknown protein similar to unknown protein GB:AAC42254 [Arabidopsis thaliana]	259335_s_at	0.5
unknown protein	259302_at	0.5
putative ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I similar to ribulose-1,5-bisphosphate carboxylase/oxy	259258_at	0.5
RNA helicase, DRH1 identical to RNA helicase DRH1 GB:BAA28347 [Arabidopsis thaliana]; supported by cDNA: gi_15215693_gb_AY050375.1_	259194_at	0.5
transport protein SEC13, putative similar to protein transport protein SEC13 GB:P53024 [Pichia pastoris];supported by full-length cDNA: Ceres:373	259119_at	0.5
hypothetical protein predicted by genscan	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_1664	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.	258656_at	0.5
putative myo-inositol monophosphatase similar to myo-inositol-1(or 4)-monophosphatase 3 (IMP 3) GB:P54928 [Lycopersicon esculentum];supporte	258613_at	0.5
disease resistance gene (RPM1) identical to disease resistance gene (RPM1) GB:X87851 [Arabidopsis thaliana]	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	258517_at	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	258373_at	0.5
hypothetical protein predicted by genemark	258317_at	0.5
hypothetical protein predicted by genemark	258292_at	0.5
unknown protein ; supported by cDNA: gi_14334929_gb_AY035138.1_	258298_at	0.5
unknown protein similar to serine/threonine kinase receptor associated protein GB:NP_035629 [Mus musculus], unr-interacting protein GB:NP_0091	258272_at	0.5
putative acetyltransferase similar to dihydrolipoamide S-acetyltransferase GB:AAD46491 from [Zea mays]; supported by cDNA: gi_13605806_gb_A	258208_at	0.5
aldose 1-epimerase, putative similar to ALDOSE 1-EPIMERASE PRECURSOR GB:P05149 from [Acinetobacter calcoaceticus]; supported by cDNA	258163_at	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.	257659_at	0.5
hypothetical protein	257641_s_at	0.5
S-adenosyl-L-homocysteinas, putative similar to S-adenosyl-L-homocysteinase GB:AAD56048 from [Lupinus luteus]; supported by cDNA: gi_15292	257173_at	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
pyruvate kinase, putative similar to pyruvate kinase isozyme A, chloroplast precursor GB:Q43117 [Ricinus communis];supported by full-length cDNA	256836_at	0.5
multispanning membrane protein, putative similar to transmembrane 9 superfamily member 2 GB:NP_004791 from [Homo sapiens] (Gene 216 (199	256776_at	0.5
hypothetical protein contains similarity to transporter proteins; supported by cDNA: gi_15810468_gb_AY056273.1_	256650_at	0.5
hypothetical protein similar to putative acyl-CoA:1-acylglycerol-3-phosphate acyltransferase GB:AAF21074 from [Arabidopsis thaliana]	256652_at	0.5
unknown protein supported 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:P4631	256277_at	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]	256149_at	0.5
aminoalcoholphosphotransferase identical to aminoalcoholphosphotransferase GI:3661593 from [Arabidopsis thaliana]; supported by cDNA: gi_3661	256134_at	0.5
hypothetical protein predicted by genscan+; supported by cDNA: gi_15810574_gb_AY056326.1_	256069_at	0.5
hypothetical protein contains Pfam profile: PF01084 ribosomal protein S18	256043_at	0.5
unknown protein contains similarity to alternative NADH-dehydrogenase GI:3718005 from [Yarrowia lipolytica];supported by full-length cDNA: Ceres:	256057_at	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	255640_at	0.5
putative protein similar to nucleolin protein; supported by cDNA: gi_13605915_gb_AF367357.1_AF367357	255598_at	0.5

predicted protein of unknown function similar to M. truncatula MtN21, GenBank accession number Y15293; F11O4.14 was picked up in a screen fo	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	254862_at	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:AJ011418;supported by full-length cDNA: Ceres:	254084_at	0.5
glutamine cyclotransferase precursor - like protein glutamine cyclotransferase precursor, Carica papaya, AF061240;supported by full-length cDNA:	254082_at	0.5
hypothetical protein ; supported by cDNA: gi_14517537_gb_AY039604.1_	254050_s_at	0.5
arginyl-tRNA synthetase	254004_at	0.5
putative uracil phosphoribosyl transferase uracil phosphoribosyl transferase,Saccharomyces cerevisiae, PIR2:JH0147supported by full-length cDNA	253970_at	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 simiarity to acyl-CoA binding protein - Arabidopsis thaliana, PID:g4128197;supported by full-length cDNA:	253840_at	0.5
receptor-like protein kinase 5 precursor (RLK5) ; supported by cDNA: gi_166849_gb_M84660.1_ATHRLPKC	253779_at	0.5
putative protein predicted proteins, Arabidopsis thaliana	253686_at	0.5
threonine synthase	253700_at	0.5
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_642133_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	253274_at	0.5
subtilisin-like serine protease similar to SBT1, a subtilase from tomato plants GI:1771160 from [Lycopersicon esculentum]	253218_at	0.5
putative protein phospholipase C, Listeria monocytogenes, PIR:A37204;supported by full-length cDNA: Ceres:4284.	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
GTP-binding - like protein GTP-binding protein DRG, Xenopus laevis, SWISS-PROT:P43690; supported by cDNA: gi_14334721_gb_AY035034.1_	252883_at	0.5
putative transposase hypothetical protein a, maize transposable element Ac - Zea mays, PIR:T02916	252847_at	0.5
putative protein	252344_s_at	0.5
putative protein APRIL protein, Homo sapiens, EMBL:HSAPRIL_1	252174_at	0.5
GDP-D-mannose-4,6-dehydratase (MUR1) ;supported by full-length cDNA: Ceres:11217.	252121_at	0.5
mucin -like protein hemomucin, Drosophila melanogaster, EMBL:DM42014;supported by full-length cDNA: Ceres:34197.	252117_at	0.5
putative protein hin1 protein -Nicotiana tabacum,PID:e259431;supported by full-length cDNA: Ceres:92178.	252058_at	0.5
hypothetical protein KIAA0253 protein, Homo saoiens, SWISSPROT:Y253_HUMAN	252062_at	0.5
beta-galactosidase precursor - like protein beta-galactosidase precursor, Carica papaya, EMBL:AF064786; supported by cDNA: gi_13605856_gb_A	251996_at	0.5
nodulin / glutamate-ammonia ligase - like protein MtN6 - nodulin 6, Medicago truncatula, EMBL:MET133118	251973_at	0.5
putative protein KIAA0544 protein, Homo sapiens, EMBL:AB011116;supported by full-length cDNA: Ceres:110247.	251959_at	0.5
synaptobrevin -like protein vesicle-associated membrane protein 7B (At VAMP7B), Arabidopsis thaliana, EMBL:AF025333	251877_at	0.5
DNA-binding protein-like DNA-binding protein 4 WRKY4 - Nicotiana tabacum, EMBL:AF193771;supported by full-length cDNA: Ceres:34847.	251705_at	0.5
putative protein MULTICOPY SUPPRESSOR OF RAS1 - Schizosaccharomyces pombe, EMBL:D78582;supported by full-length cDNA: Ceres:4015	251657_at	0.5
dnaJ-like protein DNAJ protein - Schizosaccharomyces pombe, PIR:T39697;supported by full-length cDNA: Ceres:120719.	251622_at	0.5
1-acylcerol-3-phosphate acyltransferase - like protein 1-acylcerol-3-phosphate acyltransferase, Brassica napus, Z49860;supported by full-length cDN	251596_at	0.5
putative protein F-box protein Fbl2 - Homo sapiens, EMBL:AF174589;supported by full-length cDNA: Ceres:35534.	251532_at	0.5
putative protein mitochondrial RNA splicing protein MRS2 - Saccharomyces cerevisiae, PIR:S62064; supported by cDNA: gi_16209701_gb_AY057	251508_at	0.5
Rab GDP dissociation inhibitor ; supported by cDNA: gi_2446980_dbj_AB005560.1_AB005560	251449_at	0.5
transketolase - like protein transketolase, Solanum tuberosum, EMBL:Z50099;supported by full-length cDNA: Ceres:15659.	251396_at	0.5
putative protein hypothetical protein At2g45740 - Arabidopsis thaliana, EMBL:AC004665	251352_at	0.5
putative protein alkB protein - Escherichia coli, PIR:BVECKB	251057_at	0.5
disease resistance - like protein rpp8, Arabidopsis thaliana, EMBL:AF089711; supported by cDNA: gi_15292720_gb_AY050794.1_	250829_at	0.5
short chain alcohol dehydrogenase-like ;supported by full-length cDNA: Ceres:111427.	250763_at	0.5
peptide methionine sulfoxide reductase (msr) ; supported by full-length cDNA: Ceres: 31014.	250609_at	0.5
putative protein predicted proteins, Arabidopsis thaliana, Schizosaccharomyces pombe and Drosophila melanogaster; supported by full-length cDN	250497_at	0.5
putative protein HSPC184, Homo sapiens, EMBL:AF151018; supported by cDNA: gi_14335059_gb_AY037209.1_	250401_at	0.5
tubulin beta-6 chain (sp|P29514) ; supported by cDNA: gi_13430695_gb_AF360260.1_AF360260	250317_at	0.5
callose synthase catalytic subunit -like protein putative callose synthase catalytic subunit (CFL1), Gossypium hirsutum, EMBL:AF085717	250272_at	0.5
myb-related protein - like myb-related protein 1, garden petunia, PIR:S26605	250167_at	0.5
unknown protein ; supported by cDNA: gi_14423559_gb_AF387017.1_AF387017	250131_at	0.5
galactose-1-phosphate uridyl transferase-like protein ;supported by full-length cDNA: Ceres:34699.	250029_at	0.5
Glucose-1-phosphate adenylyltransferase (ApL1/adg2) ; supported by cDNA: gi_2149020_gb_U72290.1_ATU72290	249927_at	0.5
putative protein similar to unknown protein (ref|NP_015265.1); supported by cDNA: gi_12007446_gb_AF322255.1_AF322255	249864_at	0.5
cation-transporting ATPase	249846_at	0.5
thaumatin-like protein	249748_at	0.5
putative protein similar to unknown protein (gb|AAD55417.1)	249723_at	0.5
putative protein similar to unknown protein (emb|CAB80933.1)	249347_at	0.5
brain and reproductive organ-expressed protein-like	249192_at	0.5
major surface glycoprotein-like ; supported by cDNA: gi_13430719_gb_AF360272.1_AF360272	249209_at	0.5
putative protein similar to unknown protein (gb|AAC80623.1)	249172_at	0.5
actin-like protein ; supported by cDNA: gi_15982920_gb_AY057568.1_	249127_at	0.5
putative protein contains similarity to kinase	248850_at	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 ATN1-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||C69291)	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 I (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
beta-galactosidase (emb|CAB64742.1) ; supported by cDNA: gi_16649044_gb_AY059892.1_	247356_at	0.5
putative protein contains similarity to unknown protein (gb|AAF44992.1); supported by cDNA: gi_15028246_gb_AY046038.1_	247256_at	0.5
putative protein strong similarity to unknown protein (pir||T05573)	247183_at	0.5
unknown protein	247166_at	0.5
unknown protein	247112_at	0.5
calcium-dependent protein kinase ;supported by full-length cDNA: Ceres:18901.	247137_at	0.5
dolichyl-di-phosphooligosaccharide-protein glycotransferase (oligosaccharyltransferase)-like ;supported by full-length cDNA: Ceres:18419.	247058_at	0.5
putative protein similar to unknown protein (gb|AAD25674.1)	246958_at	0.5
putative protein	246846_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.	246546_at	0.5
putative protein hypothetical proteins - Arabidopsis thaliana	246497_at	0.5
putative protein putative N-acetlytransferase 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 [Ceratoglyphina styracicola]	246404_at	0.5
unknown protein contains similarity to beta-1,4 mannosyltransferase 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	246327_at	0.5
putative protein serine kinase SRPK2, Homo sapiens, EMBL:AC005070	246334_at	0.5
putative transmembrane protein G5p yeast Sac1 protein, PIR:A33622	246300_at	0.5
putative protein predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_15810384_gb_AY056231.1_	245972_at	0.5
Pto kinase interactor, putative similar to Pto kinase interactor 1 GI:3668069 from [Lycopersicon esculentum]	245845_at	0.5
hypothetical protein contains similarity to cyc1A protein GI:6358548 from [Antirrhinum graniticum]; supported by cDNA: gi_14334669_gb_AY035008.	245774_at	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
transport protein	245625_at	0.5
phosphatase like protein	245557_at	0.5
putative protein	245492_at	0.5
Expressed protein ; supported by cDNA: gi_14334421_gb_AY034902.1_	245280_at	0.5
Expressed protein ; supported by cDNA: gi_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 apoprotein A2	245006_at	0.5
putative ser/thr protein kinase similar to GB:AAD21713	264549_at	0.5

Table 4: Transcripts suppressed during a combination of drought stress and heat shock compared to unstressed plants	**Affimetrix number**	**$\log_2$ fold supressed**
unknown protein	262832_s_at	-8
putative auxin-induced protein auxin-induced protein 10A, Glycine max., PIR2:JQ1099	252965_at	-7.9
antifungal protein-like (PDF1.2)	249052_at	-7.8
Expressed protein ; supported by full-length cDNA: Ceres: 7152.	266658_at	-7.7
putative lectin similar to lectin SP:P02874 [Onobrychis viciifolia]; contains Pfam profile: PF00139 legume lectins beta domain; supported by cDNA:	257206_at	-7.4
putative protein predicted proteins, Arabidopsis thaliana	247474_at	-6.7
putative protein basic leucine zipper transcription activator shoot-forming PKSF1 - Paulownia kawakamii, EMBL:AF046934;supported by full-lengt	251575_at	-6.5
hypothetical protein predicted by genemark.hmm	261684_at	-6.4
thaumatin-like protein similar to thaumatin GB:AAD55090 [Vitis riparia]; contains Pfam profile: PF00314 Thaumatin family; supported by cDNA: gi_1	259925_at	-6.3
unknown protein	263549_at	-6.2
unknown protein ;supported by full-length cDNA: Ceres:15495.	248889_at	-6.2
hypothetical protein predicted by genefinder	266800_at	-6.1
unknown protein ; supported by full-length cDNA: Ceres: 5171.	264343_at	-6.1
putative protein similar to unknown protein (emb|CAA71173.1)	248322_at	-6.1
putative gibberellin-regulated protein contains similarity to gibberellin-regulated protein 2 precursor (GAST1) homolog gb|U11765 from A. thaliana	264195_at	-5.9
hypothetical protein ;supported by full-length cDNA: Ceres:38891.	266805_at	-5.6
unknown protein similar to hypothetical protein GB:CAA10289 [Cicer arietinum]; supported by full-length cDNA: Ceres: 108086.	259272_at	-5.5
disease resistance RPP5 like protein (fragment)	245450_at	-5.5
unknown protein	248190_at	-5.4
unknown protein	265837_at	-5.2
putative protein auxin-induced protein 6B, mung bean, PIR:T10942	251977_at	-5.2
unknown protein ;supported by full-length cDNA: Ceres:4309.	248062_at	-5.2
hevein-like protein precursor (PR-4) identical to hevein-like protein precursor GB:P43082 [Arabidopsis thaliana], similar to wound-induced protein (	258791_at	-5.1
putative protein	250942_at	-5.1
response regulator 6 (ARR6) ; supported by cDNA: gi_3953600_dbj_AB008489.1_AB008489	247406_at	-5.1
expansin (At-EXP1) identical to expansin (At-EXP1) [Arabidopsis thaliana] GI:1041702;supported by full-length cDNA: Ceres:255048.	256299_at	-5
putative expansin ;supported by full-length cDNA: Ceres:27553.	255822_at	-5
glutathione S-transferase, putative similar to glutathione S-transferase GI:860955 from [Hyoscyamus muticus]; supported by cDNA: gi_15215607_	262119_s_at	-4.9
thionin, putative similar to thionin [Arabidopsis thaliana] GI:1181533; supported by cDNA: gi_14190504_gb_AF380652.1_AF380652	256527_at	-4.9
putative protein	251003_at	-4.9
hypothetical protein similar to putative glucosyltransferase GB:AAD15455 GI:4263795 from (Arabidopsis thaliana)	265175_at	-4.8
unknown protein	263565_at	-4.8
myrosinase-associated protein, putative similar to myrosinase-associated protein GI:1769967 from [Brassica napus]; supported by cDNA: gi_1580	263161_at	-4.8
histone H2A.F/Z ;supported by full-length cDNA: Ceres:33085.	251846_at	-4.8
hypothetical protein ; supported by full-length cDNA: Ceres: 14577.	256569_at	-4.7
hypothetical protein	252345_at	-4.7
serine/threonine-specific protein kinase - like putative protein serine /threonine kinase, Sorghum bicolor, EMBL:SBRLK1	247684_at	-4.7
putative alanine acetyl transferase	265725_at	-4.6
putative protein similar to unknown protein (pir||S72530);supported by full-length cDNA: Ceres:32925.	248683_at	-4.6
glutaredoxin, putative similar to glutaredoxin GB:CAA89699 GI:1732424 from [Ricinus communis];supported by full-length cDNA: Ceres:125679.	260831_at	-4.5
unknown protein	258897_at	-4.5
putative pectinesterase pectinesterase - Lycopersicon esculentum, PID:e312172	252989_at	-4.5
hypothetical protein	252346_at	-4.5
putative protein similar to unknown protein (emb|CAB53482.1)	249167_at	-4.5
putative pollen surface protein endosperm specific protein - Zea mays, PID:g2104712;supported by full-length cDNA: Ceres:4620.	254785_at	-4.4
putative protein auxin-regulated gene, Vigna radiata	253253_at	-4.4
small auxin up RNA (SAUR-AC1) ;supported by full-length cDNA: Ceres:14973.	252970_at	-4.4
putative protein DRT100 protein precursor, Arabidopsis thaliana, PIR:A46260;supported by full-length cDNA: Ceres:41409.	250277_at	-4.4
putative protein proline-rich protein APG, Arabidopsis thaliana, PIR:S21961	250043_at	-4.4
putative protein predicted proteins, Arabidopsis thaliana	249609_at	-4.4
putative protein similar to unknown protein (gb|AAF63814.1);supported by full-length cDNA: Ceres:40718.	248623_at	-4.4
calmodulin-like protein identical to GB:D45848; supported by cDNA: gi_15983405_gb_AF424577.1_AF424577	267083_at	-4.3
putative tyrosine aminotransferase ;supported by full-length cDNA: Ceres:14570.	263539_at	-4.3
Expressed protein ; supported by full-length cDNA: Ceres: 27081.	263182_at	-4.3
putative auxin-induced protein similar to SAUR GB:BAA25434 [Raphanus sativus]	259331_at	-4.3

Expressed protein ; supported by full-length cDNA: Ceres: 41224.	255969_at	-4.3
unknown protein similarity to HSR201 protein, Nicotiana tabacum, gb:X95343; contains EST gb:R65039	264403_at	-4.2
xyloglucan endo-transglycosylase-like protein ;supported by full-length cDNA: Ceres:12301.	247162_at	-4.2
putative auxin-regulated protein	264016_at	-4.2
hypothetical protein predicted by genefinder and genscan	260472_at	-4.2
putative two-component response regulator protein ; supported by cDNA: gi_11870067_gb_AF305721.1_AF305721	266078_at	-4.1
putative DNA-binding protein (RAV2-like) identical to residues 34-352 of RAV2 GB:BAA34251 (Arabidopsis thaliana);supported by full-length cDNA	260037_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
putative glutathione S-transferase ;supported by full-length cDNA: Ceres:27915.; supported by cDNA: gi_11095995_gb_AF288181.1_AF288181	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
putative protein microtubule-associated protein homolog, Drosophila melanogaster, EMBL:T13564	249378_at	-3.7
putative protein similar to unknown protein (pir||T05752);supported by full-length cDNA: Ceres:109272.	248164_at	-3.7
unknown protein	245866_s_at	-3.7
unknown protein location of ESTs est VBVBD05, gb|Z30807 and VBVBD05 , gb|Z30808;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:10186	262986_at	-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)	258054_at	-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.	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	262374_s_at	-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||T05055)	248047_at	-3.5
disease resistance 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

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:	258947_at	-3.3
putative calmodulin similar to calmodulin GB:P04352 [Chlamydomonas reinhardtii]; contains Pfam profile: PF00036 EF hand (4 copies); supported	258617_at	-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 ENOD16, Medicago truncatula, X99466;supported by full-length cDNA: Ceres:6308.	253480_at	-3.3
cytochrome P450 monooxygenase - like protein cytochrome P450 monooxygenase CYP91A2, Arabidopsis thaliana, D78607;supported by full-leng	253073_at	-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	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) (sp|O80341) ; supported by cDNA: gi_14326511_gb_AF385709.1_AF385709	248799_at	-3.2
Expressed protein ; supported by full-length cDNA: Ceres: 15527.	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 (gb|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	244966_at	-3.2
similar to cold acclimation protein WCOR413 [Triticum aestivum]	267288_at	-3.1
unknown protein ; supported by cDNA: gi_15294169_gb_AF410276.1_AF410276	266552_at	-3.1
unknown protein Similar to acid phosphatase; Location of ESTs 110C2T7 , gb|T42036, and 110C2XP, gb|AI100245; supported by cDNA: gi_1392	265042_at	-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	256548_at	-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

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_AB01388	259364_at	-3
putative GDSL-motif lipase/acylhydrolase contains Pfam profile: lipase/acylhydrolase with GDSL-like motif;supported by full-length cDNA: Ceres:13	258589_at	-3
putative disease resistance protein similar to disease resistance protein RPP1-WsC GB:AAC72979 [Arabidopsis thaliana]; supported by cDNA: gi_	258537_at	-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_AF3250	261443_at	-2.9
putative chlorophyll A-B binding protein similar to chlorophyll A-B binding protein 151 precursor (LHCP) GB:P27518 from [Gossypium hirsutum];sup	258239_at	-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; supported	246932_at	-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 cDNA: Ce	245757_at	-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 phosphotransfer	263236_at	-2.8
late embryogenis abundant protein, putative similar to late embryogenis abundant protein 5 GI:2981167 from [Nicotiana tabacum];supported by full	262113_at	-2.8
GAST1-like protein similar to GAST1 protein precursor GB:P27057 [Lycopersicon esculentum] (induced by gibberellins, inhibited by ABA 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: Ceres: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 [Nicotiana t	261055_at	-2.7
putative elicitor-responsive gene similar to elicitor-responsive gene-3 GB:AAC35866 from [Oryza sativa];supported by full-length cDNA: Ceres:1896	260083_at	-2.7
unknown protein ; supported by cDNA: gi_14596082_gb_AY042829.1_	259791_at	-2.7
nicotianamine synthase, putative similar to nicotianamine synthase [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
unknown 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
putative flowering-time gene CONSTANS (COL2) identical to putative flowering-time gene CONSTANS (COL2) GB:AAB67879 GI:1507699 (Arabid	258497_at	-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
putative 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
putative protein contains similarity to ATFP3	248527_at	-2.7
pathogenesis-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
hypothetical protein similar to embryo-abundant protein GB:L47672 GI:1350530 from [Picea glauca]; supported by cDNA: gi_14335021_gb_AY037	265075_at	-2.6
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:271253.	265067_at	-2.6
lipoyltransferase identical to GB:BAA78386; supported by cDNA: gi_4996285_dbj_AB020975.1_AB020975	264613_at	-2.6
unknown protein ;supported by full-length cDNA: Ceres:11114.	263628_at	-2.6
unknown 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 cDNA	261825_at	-2.6
DNA-binding protein, putative similar to DNA binding protein CCA1 from [Arabidopsis thaliana]	261569_at	-2.6
unknown 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
unknown 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
unknown protein ;supported by full-length cDNA: Ceres:96816.	257793_at	-2.6
unknown 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
amino 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
isp4 like protein ; supported by cDNA: gi_15451019_gb_AY054590.1_	245296_at	-2.6
hypothetical protein ; supported by cDNA: gi_15810232_gb_AY056155.1_	245265_at	-2.6
putative expansin	267158_at	-2.5
Expressed protein ; supported by full-length cDNA: Ceres: 7600.	266500_at	-2.5
hypothetical protein predicted by genscan	266070_at	-2.5
unknown protein Location of EST gb|T41885 and gb|AA395021	264521_at	-2.5
unknown 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
germin-like protein similar to germin precursor GB:P26759 [Triticum aestivum]; contains Pfam profile: PF01072 Germin family;supported by full-leng	259892_at	-2.5
Expressed protein ; supported by full-length cDNA: Ceres: 35429.	258349_at	-2.5
unknown protein identical to unknown protein GI:9755444 from (Arabidopsis thaliana); supported by full-length cDNA: Ceres: 110066.	255856_at	-2.5
putative 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_AF30	253050_at	-2.5
unknown 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
putative protein similar to unknown protein (pir||T00970); supported by cDNA: gi_15215722_gb_AY050390.1_	249817_at	-2.5
putative protein similar to unknown protein (gb|AAF32471.1)	249659_s_at	-2.5
putative protein similar to unknown protein (gb|AAF04428.1);supported by full-length cDNA: Ceres:27668.	248028_at	-2.5
putative protein ;supported by full-length cDNA: Ceres:22013.	246905_at	-2.5
germin-like protein ; supported by cDNA: gi_14517363_gb_AY039516.1_	246004_at	-2.5
hypothetical protein similar to putative disease resistance protein GB:AAC14512 GI:2739389 from [Arabidopsis thaliana];supported by full-length cD	245768_at	-2.5

ribosomal protein L2	244987_s_at	-2.5
NADH dehydrogenase ND4L	244933_at	-2.5
Expressed protein ; supported by full-length cDNA: Ceres: 2083.	257191_at	-2.5
putative steroid sulfotransferase ; supported by cDNA: gi_599639_emb_Z46823.1_ATTS4391	264042_at	-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
protein kinase, putative contains similarity to many predicted protein kinases; supported by cDNA: gi_13430527_gb_AF360176.1_AF360176	261308_at	-2.4
expansin 10 identical to GB:AAF61712 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:14132.	261266_at	-2.4
expansin S2 precursor, putative similar to GB:U30460 from [Cucumis sativus];supported by full-length cDNA: 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	257809_at	-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	253971_at	-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	261639_at	-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_AB00	259466_at	-2.3
putative pectinesterase contains similarity to pectinesterase GB:AAB57671 [Citrus sinensis]	258764_at	-2.3
unknown protein contains Pfam profile:PF00295 Polygalacturonase;supported by full-length cDNA: Ceres:38575.	258528_at	-2.3
unknown protein ; supported by cDNA: gi_15451205_gb_AY054683.1_	258156_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
putative protein	255662_at	-2.3
pEARLI 1-like protein Arabidopsis thaliana pEARLI 1 mRNA, PID:g871780	254818_at	-2.3
Expressed protein ; supported by full-length cDNA: Ceres: 38416.	253305_at	-2.3
endo-xyloglucan transferase - like protein endo-xyloglucan transferase, Gossypium hirsutum, D88413;supported by full-length cDNA: Ceres:14263	253040_at	-2.3
putative protein hypothetical protein F4I18.26 - Arabidopsis thaliana, PIR:T02471;supported by full-length cDNA: Ceres:30454.	251336_at	-2.3
putative protein	250075_at	-2.3

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	259611_at	-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	257203_at	-2.2
sterol-C-methyltransferase identical to sterol-C-methyltransferase GI:1061040 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:26	255885_at	-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
acyl carrier - like protein acyl carrier protein, Cuphea lanceolata, PIR2:S42026;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	-2.2
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-leng	264986_at	-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	257173_at	-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

UDP-GlcNAc:dolichol phosphate N-acetylglucosamine-1-phosphate transferase-like protein UDP-GlcNAc:dolichol phosphate N-acetylglucosamine-	251626_at	-2.1
putative protein prib5, Ribes nigrum, EMBL:RNI7578;supported by full-length cDNA: Ceres:31361.	251400_at	-2.1
unknown 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
putative protein similar to unknown protein (gb|AAB61527.1)	249727_at	-2.1
amino acid permease	249346_at	-2.1
putative protein similar to unknown protein (pir||T04427)	248943_s_at	-2.1
unknown protein	247878_at	-2.1
histone H4 - like protein histone H4, Zea mays, PIR:HSZM4;supported by full-length cDNA: Ceres:15418.	247692_s_at	-2.1
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:124269.	245840_at	-2.1
phosphate/phosphoenolpyruvate translocator - like protein ;supported by full-length cDNA: Ceres:100777.	245698_at	-2.1
PSI 9KDa protein	244932_at	-2.1
unknown protein ; supported by cDNA: gi_16612242_gb_AF439822.1_AF439822	266489_at	-2
hypothetical protein predicted by genscan and genefinder	265892_at	-2
Expressed protein ; supported by full-length cDNA: Ceres: 38093.	265025_at	-2
Expressed protein ; supported by full-length cDNA: Ceres: 17126.	264725_at	-2
Expressed protein ; supported by cDNA: gi_13926282_gb_AF372895.1_AF372895	263632_at	-2
unknown protein	262970_at	-2
calcium-dependent protein kinase, putative similar to calcium-dependent protein kinase GB:AAC25423 GI:3283996 [Nicotiana tabacum]	262671_at	-2
hypothetical protein predicted by genemark.hmm	262151_at	-2
adenine phosphoribosyltransferase almost identical to adenine phosphoribosyltransferase GI:1402894 from [Arabidopsis thaliana]	262039_at	-2
regulatory protein HAL3B similar to GB:AAB53106 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 412.	261306_at	-2
hypothetical protein predicted by genemark.hmm	260919_at	-2
flower development protein cycloidea (cyc3), putative similar to flower development protein cycloidea (cyc3) GI:6358611 from [Misopates orontium]	260618_at	-2
Cyclin, putative similar to GB:CAB77269 from [Pisum sativum]	260506_at	-2
unknown protein supported by cDNA: Ceres:13335	260072_at	-2
hypothetical protein predicted by genefinder	259743_at	-2
rhodanese-like family protein contains rhodanese-like domain PF:00581;supported by full-length cDNA: Ceres:30880.	258989_at	-2
unknown protein ;supported by full-length cDNA: Ceres:8544.	256785_at	-2
unknown protein ;supported by full-length cDNA: Ceres:31357.	256674_at	-2
disease resistance protein, putative similar to disease resistance protein RPP1-WsA [Arabidopsis thaliana] GI:3860163; supported by full-length cD	256526_at	-2
putative protein	255692_at	-2
cysteine 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_A	253731_at	-2
putative 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
putative LEA protein Picea glauca late embryogenesis abundant protein (EMB8), PID:g1350545;supported by full-length cDNA: Ceres:36702.	252132_at	-2
syntaxin-like protein synt4 ;supported by full-length cDNA: Ceres:37248.	252053_at	-2
putative protein multisynthetase complex auxiliary component p43 - Cricetulus griseus, EMBL:AF021800;supported by full-length cDNA: Ceres:280	251442_at	-2
putative protein outer envelope membrane protein E 6.7 - chloroplast Spinacia oleracea, PIR:A35958; supported by cDNA: gi_15724349_gb_AF4	251155_at	-2
putative protein ;supported by full-length cDNA: Ceres:40252.	250936_at	-2
24-sterol C-methyltransferase ; supported by cDNA: gi_11066104_gb_AF195648.1_AF195648	250254_at	-2
nodulin-like protein	250217_at	-2
beta-amylase-like proten beta-amylase - Prunus armeniaca, EMBL:AF139501;supported by full-length cDNA: Ceres:30798.	250007_at	-2
6-phosphogluconolactonase-like protein ;supported by full-length cDNA: Ceres:13806.	249732_at	-2
pectin acetylesterase ;supported by full-length cDNA: Ceres:39005.	248968_at	-2
histone H3 (sp|P05203) ; supported by cDNA: gi_13926210_gb_AF370577.1_AF370577	247192_at	-2
apospory-associated protein C-like	247101_at	-2
hypothetical protein similar to putative disease resistance protein GB:AAC14512 GI:2739389 from [Arabidopsis thaliana]	245765_at	-2
NADH dehydrogenase 49KDa protein	244937_at	-2
putative protein similar to unknown protein (emb|CAB67623.1)	250696_at	-2
hypothetical protein predicted by genscan and genefinder	266363_at	-1.9
beta-expansin ;supported by full-length cDNA: Ceres:109135.	265443_at	-1.9
unknown protein similar to hypothetical protein GI:9665091 from [Arabidopsis thaliana]	264998_at	-1.9
Expressed protein ; supported by full-length cDNA: Ceres: 2681.	264096_at	-1.9
putative s-adenosylmethionine synthetase ;supported by full-length cDNA: Ceres:13320.	263838_at	-1.9
putative beta-ketoacyl-CoA synthase	263606_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_AF3	261492_at	-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	260002_at	-1.9
peptide transporter, putative similar to peptide transporter PTR2-B SP:P46032 [Arabidopsis thaliana (Mouse-ear cress)]; supported by full-length c	259839_at	-1.9
myb-related transcription factor, putative similar to GI:1430846 from [Lycopersicon esculentum]	259822_at	-1.9
Expressed protein ; supported by full-length cDNA: Ceres: 42300.	259603_at	-1.9
unknown protein ; supported by cDNA: gi_15028026_gb_AY045870.1_	259460_at	-1.9
jasmonate inducible protein isolog ;supported by full-length cDNA: Ceres:119153.	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
unknown protein	256577_at	-1.9
glutamine 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:5262161 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; supporte	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	246777_at	-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	245041_at	-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:U81238;supported by full-length cDNA: Ceres:39893.	266656_at	-1.8
unknown protein ;supported by full-length cDNA: Ceres:10986.	266476_at	-1.8
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:8450.	266311_at	-1.8
unknown protein	266157_at	-1.8
putative beta-1,3-glucanase	265377_at	-1.8
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
putative NPK1-related protein kinase 2 similar to nitrate chlorate transporter GB:Q05085 from (Arabidopsis thaliana); supported by cDNA: gi_16666	264348_at	-1.8
protein kinase, putative Simisimilar to protein kinase 2 GI:7573598 from [Populus 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	259098_at	-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
putative lipase Similar to nodulins and lipase; location of EST E6C2T7 , gb|AA042309. similar to nodulins gi|3328240, gi|2129854 and others and li	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	260957_at	-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-leng	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
cytochrome P450 - like protein flavonoid 3 ,5 -hydroxylase Hf1, Petunia x hybrida, PIR2:S38985	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_AF224	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
putative protein hydroxyproline-rich glycoprotein precursor, Nicotiana tabacum, PIR2:S06733; supported by cDNA: gi_15724315_gb_AF412098.1_	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: Ce	251920_at	-1.7
nucleoid DNA-binding - like protein nucleoid DNA-binding protein cnd41, chloroplast, common tobacco, PIR:T01996; supported by full-length cDNA	251899_at	-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 (pir||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
NAM-like protein hypothetical protein SENU5, senescence up-regulated - Lycopersicon esculentum, EMBL:Z75524; supported by cDNA: gi_14326	245987_at	-1.7
hypothetical protein predicted by genemark.hmm	245771_at	-1.7
ATP-sulfurylase ; supported by cDNA: gi_459143_gb_U06275.1_ATU06275	245254_at	-1.7

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_45799	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); probabl	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	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	262457_at	-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 b	260745_at	-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	260676_at	-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-	260135_at	-1.6
unknown protein ; supported by cDNA: gi_13937162_gb_AF372935.1_AF372935	259665_at	-1.6
hypothetical protein predicted by genemark.hmm	259398_at	-1.6
putative methionine synthase similar to cobalamin-independent methionine synthase GB:AAC50037 [Arabidopsis thaliana];supported by full-length	259343_s_at	-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:	258922_at	-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	258276_at	-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 eukaryotic DNA	257813_at	-1.6
sugar transport, putative similar to D-XYLOSE-PROTON SYMPORTER GB:O52733 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_12	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	254784_at	-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-le	253950_at	-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	252324_at	-1.6
putative protein EREBP-3 homolog, Stylosanthes hamata, EMBL:U91982; 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	252183_at	-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)	250796_at	-1.6
asparaginase ; supported by cDNA: gi_14517439_gb_AY039555.1_	250547_at	-1.6
putative protein KIAA0255 gene, Homo sapiens, EMBL:HSD444	250422_at	-1.6

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 (sp|P24636) ; 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
transcription factor Hap5a-like protein	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
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:1094.	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:252	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 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:13261	258369_at	-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	257651_at	-1.5
proline oxidase, mitochondrial precursor (osmotic stress-induced proline dehydrogenase) identical to GB:P92983 from [Arabidopsis thaliana] (Plant	257315_at	-1.5

hypothetical protein contains similarity to flavonol synthase (FLS) GB:Q41452 from [Solanum tuberosum], contains Pfam profile: PF00671 Iron/Asc	256922_at	-1.5
unknown protein	256828_at	-1.5
unknown protein	256337_at	-1.5
12-oxophytodienoate reductase, putative similar to 12-oxophytodienoate reductase OPR1 GI:3882355 from [Arabidopsis thaliana]	255895_at	-1.5
putative protein ; supported by cDNA: gi_14596204_gb_AY042890.1_	254705_at	-1.5
reticuline oxidase -like protein reticuline oxidase, Eschscholzia californica, PIR:A41533; supported by cDNA: gi_15983492_gb_AF424621.1_AF424	254432_at	-1.5
V-ATPase subunit G (vag2 gene)	254216_at	-1.5
possible apospory-associated like protein Pennisetum ciliare possible apospory-associated mRNA clone pSUB C, PID:g549984;supported by full-le	254040_at	-1.5
putative protein ; supported by cDNA: gi_15810482_gb_AY056280.1_	253925_at	-1.5
putative protein LEDI-3 protein, Lithospermum erythrorhizon	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, PIR2:S73268; 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_	253334_at	-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	250582_at	-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
fructokinase 1 ; 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.	245372_at	-1.5
hypothetical protein ;supported by full-length cDNA: Ceres:17977.	245310_at	-1.5
NADH dehydrogenase ND1	244936_at	-1.5
DNA polymerase alpha subunit IV (primase)-like protein	249276_at	-1.5
putative DNA-binding protein similar to AP2 and RAV1	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:L18912; supported by cDNA: gi_166650_gb_M38380.1_ATHCAM2	266317_at	-1.4

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 (Ara	265120_at	-1.4
unknown protein ;supported by full-length cDNA: Ceres:25812.	265057_at	-1.4
Expressed protein ; supported by full-length cDNA: Ceres: 108558.	264579_at	-1.4
similar to early nodulins	264377_at	-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|	263664_at	-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	263153_s_at	-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-lengt	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	260395_at	-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:	259749_at	-1.4
putative AUX1-like permease similar to AUX1 (regulator of root gravitropism, putative permease) GB:CAA67308 [Arabidopsis thaliana]; supported	259680_at	-1.4
Expressed protein ; supported by full-length cDNA: Ceres: 14943.	259661_at	-1.4
unknown protein	259160_at	-1.4
stress related protein, putative similar to stress related protein GB:AAD51854 from [Vitis riparia];supported by full-length cDNA: Ceres:13300.	259105_at	-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-	259014_at	-1.4
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:6768.	258676_at	-1.4
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
early auxin-induced protein, IAA19 identical to IAA19 GB:AAB84356 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_	258060_at	-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_	257314_at	-1.4
MYB family transcription factor (hsr1), putative identical to myb-like protein GB:AJ007289 [Arabidopsis thaliana] (Plant J. 20 (1), 57-66 (1999));sup	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	255046_at	-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 cD	249958_at	-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
FRO2-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 (gb|AAC26009.1) ;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 (pir||T04268);supported	247933_at	-1.4
CONSTANS-like 1	246523_at	-1.4
blue copper binding protein ;supported by full-length cDNA: Ceres:7767.	246099_at	-1.4
bZIP transcription factor family protein similar to seed storage protein opaque-2(bZIP family)GI:168428 from Zea mays; supported by cDNA: gi_15	245925_at	-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 purple acid phosphatase precursor GI:7331195 from [Glycine max]	245637_at	-1.4
unknown protein predicted by genscan; supported by cDNA: gi_3822215_gb_AF074948.1_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	-1.3
putative SET-domain transcriptional regulator	267290_at	-1.3
putative protein transport protein SEC13 ;supported by full-length cDNA: Ceres:36577.	267277_at	-1.3
cyclin-dependent kinase inhibitor protein identical to GB:U94772;supported by full-length cDNA: Ceres:17682.	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 chloroplast ribosomal protein L35	266570_at	-1.3
unknown protein ; supported by cDNA: gi_14334561_gb_AY035185.1_	266329_at	-1.3
putative C-4 sterol methyl oxidase ;supported by full-length cDNA: Ceres:23439.	266289_at	-1.3
hypothetical protein predicted by genscan	265704_at	-1.3
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	264751_at	-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_g	261826_at	-1.3
S-adenosyl-methionine-sterol-C-methyltransferase, putative almost identical to S-adenosyl-methionine-sterol-C-methyltransferase GI:2246456 fro	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_AY	260944_at	-1.3
unknown protein contains similarity to UDPG glucosyltransferase GB:AAB62270 GI:2232354 from [Solanum berthaultii];supported by full-length cD	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 [Arabido	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 cD	259987_at	-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 cD	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	258884_at	-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	257083_s_at	-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: Cer	255982_at	-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.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin_legB.hmm, score:	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
flavonoid 3,5-hydroxylase -like protein flavonoid 3 ,5 -hydroxylase - Campanula medium, PID:d1003951	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	253951_at	-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 cD	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; sup	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	267165_at	-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
putative thioredoxin reductase	264904_s_at	-1.2
unknown protein similar to putative glycosyl transferase GI:7268597 from [Arabidopsis thaliana]; supported by cDNA: gi_13878002_gb_AF370264.	264704_at	-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
glycoprotein(EP1), putative similar to glycoprotein(EP1) GI:349436 from [Daucus carota]; supported by cDNA: gi_14334885_gb_AY035116.1_	264279_s_at	-1.2
hypothetical protein similar to acyl-carrier protein (ACP) GI:17768 from [Brassica napus]; supported by full-length cDNA: Ceres: 1822.	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	264203_at	-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 co	262703_at	-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	261583_at	-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_1360	261230_at	-1.2
putative calcium-binding protein, calreticulin similar to SP:P12858 from [Arabidopsis thaliana]	261197_at	-1.2
unknown protein ;supported by full-length cDNA: Ceres:41505.	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)); supp	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

ribosomal protein L41 identical to ribosomal protein L41 GB:AAA79268 [Pisum sativum]	256438_s_at	-1.2
unknown protein contains similarity to alternative NADH-dehydrogenase GI:3718005 from [Yarrowia lipolytica];supported by full-length cDNA: Ceres	256057_at	-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_L39954.1_	255513_at	-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
putative protein rape mRNA, Brassica napus, PIR2:S42651	254259_s_at	-1.2
putative protein storage protein - Populus deltoides, PIR2:S31580;supported by full-length cDNA: Ceres:8772.	254163_s_at	-1.2
putative mitochondrial uncoupling protein mitochondrial uncoupling protein, Arabidopsis thaliana (thale cress), PATX:E1316826;supported by full-l	254120_at	-1.2
putative protein qkI-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:	251796_at	-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	-1.2
putative protein similar to unknown protein (pir||T05049)	248044_at	-1.2
unknown protein	247959_at	-1.2
putative protein similar to unknown protein (pir||T04261);supported by full-length cDNA: Ceres:6181.	247930_at	-1.2
Expressed protein ; supported by full-length cDNA: Ceres: 267411.	247882_at	-1.2
copper transport protein	247745_at	-1.2
actin depolymerizing factor 4 - like protein actin depolymerizing factor 4, Arabidopsis thaliana, EMBL:AF102822;supported by full-length cDNA: Cer	247656_at	-1.2
photosystem I reaction centre subunit psaN precursor (PSI-N) (sp P49107) ; supported by cDNA: gi_1237123_gb_U32176.1_ATU32176	247320_at	-1.2
unknown protein ; supported by full-length cDNA: Ceres: 20274.	247211_at	-1.2
prolyl 4-hydroxylase, alpha subunit-like protein	247124_at	-1.2
leucine-rich repeats containing protein grr1 - Glycine max. EMBL:AF019910	246935_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_	246294_at	-1.2
putative protein non-consensus donor splice site GA at exon 1; predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_16209695_gb_AY	246135_at	-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
unknown 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_AF	264625_at	-1.1
germin-like protein Identical to Arabidopsis germin-like protein, gi|1755178. Location of EST 180L10T7, gi|906417; supported by cDNA: gi_132654	264506_at	-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	264365_s_at	-1.1
aromatic rich glycoprotein, putative similar to aromatic rich glycoprotein GI:1762428 from [Arabidopsis thaliana]; supported by cDNA: gi_1762583_	264315_at	-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:	264264_at	-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
predicted 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 ubiquinol--cytochrome-c reductase Similar to gb|X79273 cytochrome c reductase hinge protein subunit from Solanum tuberosum. ESTs gb	262593_at	-1.1
unknown protein identical to unknown protein GB:AAD55493 (Arabidopsis thaliana); supported by cDNA: gi_13358235_gb_AF325047.2_AF325047	262262_at	-1.1
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:5052.	262285_at	-1.1
allergen, putative similar to allergen (Ole e 1) GI:2465129 from [Olea europaea];supported by full-length cDNA: Ceres:22488.	262195_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_1	262029_at	-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	261742_at	-1.1
helix-loop-helix protein homolog, putative similar to helix-loop-helix protein homolog GB:BAA87957 GI:6520231 from [Arabidopsis thaliana]	261717_at	-1.1
Expressed protein ; supported by full-length cDNA: Ceres: 11759.	261638_at	-1.1
RAS-related protein ARA-1 identical to SP:P19892 from [Arabidopsis thaliana] (Gene 76:313-319(1989))	261252_at	-1.1
unknown protein ; supported by cDNA: gi_15450636_gb_AY052686.1_	261193_at	-1.1
dihydrolipoamide S-acetyltransferase, putative similar to GI:5881963 from (Arabidopsis thaliana) (Plant Physiol. 120 (2), 443-452 (1999));supporte	261165_at	-1.1
unknown 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: Ce	260305_at	-1.1
hypothetical protein predicted by genefinder	260205_at	-1.1
unknown protein ;supported by full-length cDNA: Ceres:33367.	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	259707_at	-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];supporte	258415_at	-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 sapi	258155_at	-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	257313_at	-1.1
unknown protein ; supported by cDNA: gi_15146273_gb_AY049278.1_	257272_at	-1.1
NADPH:quinone oxidoreductase (NQR) nearly identical to NADPH:quinone oxidoreductase (NQR) GB:AF145234 [Arabidopsis thaliana]; supported	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 (	257194_at	-1.1
disease resistance protein, putative similar to GB:AAD13301 from [Lycopersicon esculentum], contains Pfam profiles: PF00560 Leucine Rich Repe	257100_at	-1.1
ribosomal protein L27, putative similar to 60S RIBOSOMAL PROTEIN L27 GB:P41101 from [Solanum tuberosum];supported by full-length cDNA:	256794_at	-1.1
unknown protein	256673_at	-1.1
unknown protein	256622_at	-1.1
membrane import protein, putative similar to membrane import protein GB:AAF20172 GI:6636407 [Drosophila melanogaster]; supported by cDNA:	256628_at	-1.1
peroxidase, putative similar to peroxidase ATP26a GB:CAA72487 GI:1890317 [Arabidopsis thaliana]; supported by cDNA: gi_14334599_gb_AY03	256578_at	-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_AY	256228_at	-1.1
mitogen-activated protein kinase, putative similar to mitogen-activated protein kinase GI:5815410 from [Oryza sativa]; supported by cDNA: gi_1502	256075_at	-1.1
UDP-glucose glucosyltransferase, putative similar to UDP-glucose glucosyltransferase GI:453245 from [Manihot esculenta];supported by full-lengt	256058_at	-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	255411_at	-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
RING-H2 finger protein RHA1b ;supported by full-length cDNA: Ceres:37097.	254919_at	-1.1
ammonium transport protein (AMT1) ; supported by cDNA: gi_14335079_gb_AY037219.1_	254723_at	-1.1
extensin-like protein extensin-like protein - maize, PIR2:S49915	254635_at	-1.1
neoxanthin cleavage enzyme-like protein neoxanthin cleavage enzyme, Lycopersicon esculentum, PATX:E325797; supported by cDNA: gi_159837	254564_at	-1.1
putative protein FKBP-type peptidyl-prolyl cis-trans isomerase,Synechocystis sp., PIR2:S75144	254545_at	-1.1
water channel - like protein plasma membrane intrinsic protein 1c, Arabidopsis thaliana, PIR2:S44083;supported by full-length cDNA: Ceres:3982.	254239_at	-1.1
PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT -like PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT, ORYZA SATI	254083_at	-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	251945_at	-1.1
sugar-phosphate isomerase - like protein gutq/kpsf family sugar-p isomerase, Chlamydia pneumoniae, PIR:E72068;supported by full-length cDNA:	251855_at	-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	251287_at	-1.1
cytochrome c oxidase subunit 5c-like protein cytochrome c oxidase subunit 5c - Oryza sativa, EMBL:AB027123;supported by full-length cDNA: Cer	251220_at	-1.1
shock protein SRC2-like shock protein SRC2 - Glycine max, PIR:T07080	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
putative protein various predicted proteins, Arabidopsis thaliana	250435_at	-1.1
putative protein	250376_at	-1.1
putative protein predicted proteins, Arabidopsis thaliana	250353_at	-1.1
putative protein hydroxyproline-rich glycoprotein, kidney bean, PIR:A29356	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 predicted 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
conglutin gamma - like protein conglutin gamma precursor, Lupinus angustifolius, PIR:S21426; supported by cDNA: gi_15010797_gb_AY045700.1	249923_at	-1.1
unknown protein	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	249514_at	-1.1
putative protein similar to unknown protein (pir||S75762)	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	246398_at	-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 transcriptional 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	245019_at	-1.1
hypothetical protein	244961_at	-1.1
NADH dehydrogenase subunit	244935_at	-1.1
putative RNA-binding protein contains Procite RNP1 putative RNA-binding region, similar to GB:AAC33496; supported by cDNA: gi_13605870_gb	257413_at	-1.1
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>	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	-1
hypothetical protein predicted by genemark.hmm	264130_at	-1
putative auxin-regulated protein ;supported by full-length cDNA: Ceres:7141.	264021_at	-1
putative receptor-like protein kinase	263913_at	-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
AtRer1B ;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:O31219 [Legionella pneumophila];support	262841_at	-1
hypothetical protein	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_g	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
plastid ribosomal protein L34 precursor, putative similar to plastid ribosomal protein L34 precursor GB:AAF64157 GI:7578860 from [Spinacia olerac	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 cDNA: 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.	260547_at	-1
hypothetical protein predicted by genscan+	260277_at	-1
putative 3-isopropylmalate dehydrogenase similar to 3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR GB:P29102 from (Brassica napus	260285_at	-1
30S ribosomal protein S17, chloroplast precursor (CS17) identical to 30S ribosomal protein S17, chloroplast precursor GB:P16180 [Arabidopsis tha	260165_at	-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 calmodulin-binding protein similar to calmodulin-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	259840_at	-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	259713_at	-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:B	259163_at	-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 amino acid transporter protein similar to amino acid transport protein GB:AAB82307 [Arabidopsis thaliana]; contains Pfam profile: PF01490	258729_at	-1
putative pectinacetylesterase similar to GB:CAA67728 from [Vigna radiata]; supported by cDNA: gi_15292826_gb_AY050847.1_	258750_at	-1
unknown protein ;supported by full-length cDNA: Ceres:24905.	258642_at	-1
unknown protein	258519_at	-1
ribosomal protein L29, putative similar to 60S ribosomal protein L29 GB:P25886 from [Rattus norvegicus]	258521_at	-1
unknown protein identical to unknown protein GB:AAF30301 from [Arabidopsis thaliana]; supported by cDNA: gi_16648934_gb_AY059837.1_	258472_at	-1
unknown protein	258418_at	-1
MtN3-like protein similar to MtN3 GB:CAA69976 from [Medicago truncatula]	258421_at	-1
AIG2-like protein similar to AIG2 protein GB:P54121 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:32718.	258001_at	-1
monosaccharide transport protein, STP4 identical to GB:S25009 from [Arabidopsis thaliana]; supported by cDNA: gi_13605905_gb_AF367352.1_A	257939_at	-1
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:924.	257858_at	-1
unknown protein	257868_at	-1
unknown protein	257828_at	-1
unknown protein ;supported by full-length cDNA: Ceres:20618.	257710_at	-1
unknown protein ;supported by full-length cDNA: Ceres:30464.	257279_at	-1
cyclopropane-fatty-acyl-phospholipid synthase, putative similar to cyclopropane-fatty-acyl-phospholipid synthase GB:P30010 [Escherichia coli]	257175_s_at	-1
unknown protein ; supported by full-length cDNA: Ceres: 5176.	257171_at	-1
unknown protein contains Pfam profile:PF00279 LTP:Plant lipid transfer protein family;supported by full-length cDNA: Ceres:19287.	256933_at	-1
hypothetical protein, 5 partial	256626_at	-1
ORF1, putative similar to ORF1 GI:457716 from (Arabidopsis thaliana); supported by cDNA: gi_16649160_gb_AY059950.1_	256497_at	-1
unknown protein ;supported by full-length cDNA: Ceres:14433.	256455_at	-1
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
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
ribosomal protein S18, putative similar to ribosomal protein S18 GI:38422 from [Homo sapiens]; supported by cDNA: Ceres:27800	255977_at	-1
GDP-L-fucose synthetase, putative similar to GDP-L-fucose synthetase GI:6580725 from [Yersinia pseudotuberculosis];supported by full-length cD	255901_at	-1
putative NAM (no apical meristem)-like protein ; supported by cDNA: gi_15294215_gb_AF410299.1_AF410299	255794_at	-1
unknown protein ;supported by full-length cDNA: Ceres:37302.	255719_at	-1
Expressed protein ; supported by full-length cDNA: Ceres: 18459.	255633_at	-1
coded for by A. thaliana cDNA T43845 similar to auxin-induced protein	255645_at	-1
hypothetical protein similar to pectinesterase	255524_at	-1
nodulin-like protein nodulin gene MtN21 - Medicago truncatula, PID:e1172471;supported by full-length cDNA: Ceres:40485.	255129_at	-1
arabinogalactan-protein homolog arabinogalactan-protein - Arabidopsis thaliana,PID:g3883126; supported by cDNA: gi_10880496_gb_AF195891.	255080_at	-1
rab7 -like protein rab7 protein -Vigna aconitifolia,PIR2:S39567; supported by cDNA: gi_15718417_dbj_AB071851.1_AB071851	255052_at	-1
putative protein various predicted proteins	254549_at	-1
putative protein similar to unknown protein (gb|AAC79139.1)	254521_at	-1
adenine phosphoribosyltransferase (EC 2.4.2.7) - like protein adenine phosphoribosyltransferase, Triticum aestivum, T06263; supported by full-len	254328_at	-1
putative receptor protein kinase receptor protein kinase, Ipomoea trifida,PID:g836954	253911_at	-1
Expressed protein ; supported by full-length cDNA: Ceres: 12935.	253859_at	-1
hypothetical protein ;supported by full-length cDNA: Ceres:42155.	253856_at	-1
putative beta-expansin/allergen protein soybean pollen allergen (cim1) protein - soybean, PIR2:S48032;supported by full-length cDNA: Ceres:3302	253815_at	-1
putative protein hypothetical protein - Arabidopsis thaliana, PID:g4337210	253746_at	-1
putative protein D-threonine dehydrogenase - Pseudomonas cruciviae,PID:d1035162 and to several 3-hydroxyisobutyrate dehydrogenases; suppo	253706_at	-1
putative protein hypothetical protein YDR438w, Saccharomyces cerevisiae, Pir2:S69718; supported by cDNA: gi_15982861_gb_AY057538.1_	253467_at	-1
putative protein phosphate/phosphoenolpyruvate translocator, Arabidopsis thaliana, ATU66321	253427_at	-1
putative protein hypothetical protein F17H15.20 Arabidopsis thaliana chromosome II BAC F17H15, PID:g3643606	253401_at	-1
Expressed protein ; supported by full-length cDNA: Ceres: 39326.	253384_at	-1
putative protein Cyanophora paradoxa cyanelle, predicted protein;supported by full-length cDNA: Ceres:2912.	253197_at	-1
RING-H2 finger protein RHA3b ;supported by full-length cDNA: Ceres:31493.	253140_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	-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
cytochrome P450 - like protein cytochrome P450, Sinapis alba, AF069494; 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	252295_at	-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:4018	251961_at	-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	251154_at	-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	250517_at	-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
nodulin-like protein ; supported by cDNA: gi_14532599_gb_AY039924.1_	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_	246749_at	-1
cytochrome P450 ; supported by cDNA: gi_3164141_dbj_D78606.1_D78606	246620_at	-1
copper amine oxidase, putative similar to copper amine oxidase GI:685197 from [Pisum sativum]	246601_at	-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 cD	246487_at	-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 At2g25260 - 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:4	245806_at	-1
histone H2A, putative similar to histone H2A GI:9758956 from [Arabidopsis thaliana]; supported by cDNA: gi_13877850_gb_AF370188.1_AF3701	245750_at	-1
extensin like protein	245479_at	-1
Lil3 protein ;supported by full-length cDNA: Ceres:29150.	245354_at	-1
hypothetical protein ; supported by cDNA: gi_15292862_gb_AY050865.1_	245290_at	-1
putative synaptobrevin ;supported by full-length cDNA: Ceres:2443.	245167_s_at	-1
PSII I protein	245023_at	-1
PSI I 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 (	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
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:9149.	265823_at	-0.9
unknown protein ; supported by cDNA: gi_14596214_gb_AY042895.1_	265798_at	-0.9
putative ribose 5-phosphate isomerase ; supported by cDNA: gi_15809809_gb_AY054172.1_	265742_at	-0.9
unknown protein ;supported by full-length cDNA: Ceres:27566.	265386_at	-0.9
auxin-regulated protein (IAA8) ;supported by full-length cDNA: Ceres:37274.	265319_at	-0.9
unknown protein ; supported by full-length cDNA: Ceres: 39285.	265219_at	-0.9
60S ribosomal protein L24 ;supported by full-length cDNA: Ceres:14564.	265210_at	-0.9
putative 3-oxoacyl [acyl-carrier protein] reductase similar to proteins from several bacterial species, similar to ESTs emb|Z37189, gb|H74525, gb|3	265026_at	-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	264783_at	-0.9

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 com	264669_at	-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.	263979_at	-0.9
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:2576.	263929_at	-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; su	263667_at	-0.9
unknown protein	263438_at	-0.9
60S 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|AI239406 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	262762_at	-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_AY04	262342_at	-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_	262244_at	-0.9
AP2 domain containing protein, putative similar to AP2 domain containing protein GI:2281633 from [Arabidopsis thaliana]; supported by cDNA: gi_	262135_at	-0.9
somatic embryogenesis receptor-like kinase, putative similar to somatic embryogenesis receptor-like kinase GI:2224910 from [Daucus carota];sup	262158_at	-0.9
plastid ribosomal protein S6, putative similar to plastid ribosomal protein S6 precursor GB:AAF64311 GI:7582401 from [Spinacia oleracea]; suppor	261954_at	-0.9
serine/threonine kinase, putative similar to serine/threonine kinase GI:2181189 from [Brassica oleracea]	261873_at	-0.9
unknown protein ; supported by full-length cDNA: Ceres: 32430.	261791_at	-0.9
cinnamoyl CoA reductase, puitative similar to cinnamoyl CoA reductase GI:2058310 from [Eucalyptus gunnii]; supported by full-length cDNA: Cere	261792_at	-0.9
calreticulin, putative similar to calreticulin GB:AAC49697 GI:2052383 from [Arabidopsis thaliana]; supported by cDNA: gi_2052382_gb_U66345.1_	261692_at	-0.9
ribonucleoprotein, putative similar to 33 KDA RIBONUCLEOPROTEIN GB:P19684 from [Nicotiana sylvestris];supported by full-length cDNA: Ceres	261577_at	-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.	260843_at	-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	260818_at	-0.9
serine carboxypeptidase precursor, putative similar to GB:AAD42963 from [Matricaria chamomilla]	260739_at	-0.9
polyphosphoinositide binding protein, putative similar to GB:AAB94598 from [Glycine max]; supported by cDNA: gi_16930446_gb_AF419577.1_AF	260604_at	-0.9
biotin synthase (Bio B) ;supported by full-length cDNA: Ceres:42038.	260548_at	-0.9
putative trypsin inhibitor ; supported by cDNA: gi_15292710_gb_AY050789.1_	260551_at	-0.9
unknown protein ;supported 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	260370_at	-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 Nlj70 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	259326_at	-0.9
putative 2-cys peroxiredoxin BAS1 precursor (thiol-specific antioxidant protein) similar to 2-cys peroxiredoxin BAS1 precursor (thiol-specific antioxid	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	259193_at	-0.9
unknown protein ;supported by full-length cDNA: Ceres:22225.	259104_at	-0.9
unknown protein similar to nodule-specific protein Nlj70 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:119	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:	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:1	255902_at	-0.9
lemir (miraculin), putative similar to lemir (miraculin) GI:2654440 from [Lycopersicon esculentum]; supported by cDNA: gi_12083239_gb_AF33241	255904_at	-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
drought-induced-19-like 1 similar to drought-induced-19, GenBank accession number X78584 similar to F2P16.10, GenBank accession number 21	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 protein several hypothetical proteins - Arabidopsis thaliana; 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;suppo	254398_at	-0.9
predicted protein	254303_at	-0.9
putative protein pectinesterase - Citrus sinensis, PID:g2098705	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

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
putative protein other predicted proteins Arabidopsis thaliana	253059_s_at	-0.9
putative amino acid transport protein amino acid transport protein - Arabidopsis thaliana, PID:g2576363;supported by full-length cDNA: Ceres:384	253006_at	-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
putative protein similar to unknown protein (gb|AAD23015.1)	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 Sybl1, 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_	250339_at	-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	250058_at	-0.9
glutamate dehydrogenase (EC 1.4.1.-) 1 (pir||S71217) ; supported by cDNA: gi_15146203_gb_AY049243.1_	250032_at	-0.9
NADH:ubiquinone oxidoreductase - like protein NADH:ubiquinone oxidoreductase PGIV subunit, Homo sapiens, EMBL:AF044953; supported by fu	249959_at	-0.9
ATP-dependent Clp protease proteolytic subunit (ClpP2), putative similar to SP:Q9X6W8 ATP-dependent Clp protease proteolytic subunit (EC 3.4.	249873_at	-0.9
40S ribosomal protein S11 ;supported by full-length cDNA: Ceres:33187.	249795_at	-0.9
unknown protein	249736_at	-0.9
Ttg1 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|AAF04433.1)	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

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: Ceres:19914.	248172_at	-0.9
unknown protein	248079_at	-0.9
60S ribosomal protein L31 ;supported by full-length cDNA: Ceres:14992.	247978_at	-0.9
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
endoxyloglucan transferase (gb|AAD45127.1) ; supported by cDNA: gi_1244751_gb_U43485.1_ATU43485	247866_at	-0.9
putative protein protein tyrosine phosphatase-like protein, PTPLB, Mus musculus, EMBL:AF169286	247689_at	-0.9
ras-GTPase-activating protein SH3-domain binding protein - like G3BP ras-GTPase-activating protein SH3-domain binding protein, Mus musculus,	247551_at	-0.9
ethylene responsive element binding factor - like ethylene responsive element binding factor 5, Arabidopsis thaliana, SWISSPROT:ERF5_ARATH;	247540_at	-0.9
peptide transporter	247440_at	-0.9
homeobox-leucine zipper protein ATHB-5 (HD-zip protein ATHB-5) (sp|P46667) ; 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	246378_at	-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	245152_at	-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
unknown protein	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
putative cellulose synthase	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|	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, gb	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|004	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

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));	261108_at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:32887.	261032_at	-0.8
chloroplast thylakoidal processing peptidase, putative similar to chloroplast thylakoidal processing peptidase GB:CAA71502 GI:2769566 from [Ara	260829_s_at	-0.8
ethylene response factor, putative similar to ethylene response factor 1 GB:AAD03544 GI:4128208 from [Arabidopsis thaliana]	260783_at	-0.8
putative trypsin inhibitor ;supported by full-length cDNA: Ceres:15927.	260546_at	-0.8
putative histidinol-phosphate aminotransferase similar to histidinol-phosphate aminotransferase GB:CAA70403 from [Nicotiana tabacum]	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 put	260047_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
inorganic pyrophosphatase, putative similar to inorganic pyrophosphatase GI:790478 from [Nicotiana tabacum]; supported by cDNA: gi_166633_g	259504_at	-0.8
allene oxide cyclase, putative similar to allene oxide cyclase GI:8977961 from [Lycopersicon esculentum]; supported by cDNA: gi_16323064_gb_A	259366_at	-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	259161_at	-0.8
vacuolar membrane ATPase subunit G (AVMA10) identical to vacuolar membrane ATPase subunit G (AVMA10) GB:AF181688 [Arabidopsis thalian	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_U7	258851_at	-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];	258371_at	-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 Pfam	257763_s_at	-0.8
unknown protein similar to TCP3 GB:AAC24010 [Arabidopsis thaliana]	257267_at	-0.8
ER lumen retaining receptor (HDEL receptor), putative similar to GB:P35402 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:233	257104_at	-0.8
GATA transcription factor 1 (AtGATA-1) identical to GATA transcription factor 1 (AtGATA-1) GB:Y13648 [Arabidopsis thaliana];supported by full-len	256916_at	-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:AAF25365 from [Thuja 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 cD	256649_at	-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-length	256112_at	-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 c	255734_at	-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 cDNA: Ceres:2538.	254951_at	-0.8
nucleoside diphosphate kinase 3 (ndpk3) ; supported by cDNA: gi_14334559_gb_AY035184.1_	254958_at	-0.8
putative protein hypothetical protein - Brassica napus,PIR2:S42651	254928_at	-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_AY050814.1_	254561_at	-0.8
putative protein hypothetical protein Arabidopsis thaliana;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; s	254105_at	-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

putative protein ; supported by cDNA: gi_15810138_gb_AY056134.1_	253922_at	-0.8
tryptophan synthase beta-subunit (TSB2) ;supported by full-length cDNA: Ceres:104687.	253898_s_at	-0.8
Expressed protein ; supported by full-length cDNA: Ceres: 42507.	253830_at	-0.8
stress responsive protein homolog low temperature and salt responsive protein LTI6A - Arabidopsis thaliana,PID:g4039153	253581_at	-0.8
putative protein hypothetical protein F9F13.130 - Arabidopsis thaliana,PIR2:T10590;supported by full-length cDNA: Ceres:21252.	253593_at	-0.8
ribosomal protein S6 - like ribosomal protein S6, Arabidopsis thaliana, PID:g2662469; supported by cDNA: gi_15292738_gb_AY050803.1_	253487_at	-0.8
Expressed protein ; supported by full-length cDNA: Ceres: 109432.	253302_at	-0.8
male sterility 2-like protein male sterility protein 2, Brassica napus, gb:X99922; supported by cDNA: gi_16323106_gb_AY057657.1_	253309_at	-0.8
putative protein ; supported by cDNA: gi_14517511_gb_AY039591.1_	253049_at	-0.8
putative protein cyclin delta-1, Arabidopsis thaliana, SWISS-PROT:P42751	253055_at	-0.8
putative protein cylicin II - bovine, PIR2:I46014	252952_at	-0.8
putative protein tubulin-folding cofactor C, Homo sapiens, U61234	252868_at	-0.8
putative protein ;supported by full-length cDNA: Ceres:20457.	252850_at	-0.8
putative protein	252676_at	-0.8
putative protein	252659_at	-0.8
acidic ribosomal protein P2 -like acidic ribosomal protein P2, maize, PIR:S54179	252643_at	-0.8
cytoplasmic ribosomal protein S15a -like cytoplasmic ribosomal protein S15a, Arabidopsis thaliana, EMBL:ATAF1412	252566_at	-0.8
putative protein DCL PROTEIN, CHLOROPLAST PRECURSOR (DEFECTIVE CHLOROPLASTS AND LEAVES PROTEIN) - Lycopersicon escule	252481_at	-0.8
Expressed protein ; supported by full-length cDNA: Ceres: 122249.	252389_at	-0.8
cytosolic ribosomal protein S11 ;supported by full-length cDNA: Ceres:40559.	252297_at	-0.8
6-phosphogluconolactonase - like protein 6-phosphogluconolactonase (6PGL), Homo sapiens, EMBL:HSA243972;supported by full-length cDNA:	252282_at	-0.8
calmodulin-like protein flagellar calmodulin - Naegleria gruberi, PID:g458232; supported by cDNA: gi_166647_gb_L12115.1_ATHCALLGA	252136_at	-0.8
hypothetical protein ; supported by cDNA: gi_15450654_gb_AY052695.1_	252010_at	-0.8
pectate lyase -like protein pectate lyase, Musa acuminata, EMBL:MAPEL;supported by full-length cDNA: Ceres:119092.	251982_at	-0.8
hypothetical protein ER6 protein - Lycopersicon esculentum, EMBL:AF096262; supported by full-length cDNA: Ceres: 269951.	251927_at	-0.8
phosphoribosylformylglycinamidine cyclo-ligase precursor ; supported by cDNA: gi_16974614_gb_AY060585.1_	251830_at	-0.8
putative protein predicted pectate-lyase, Arabidopsis thaliana, PIR:T06728	251810_at	-0.8
ABC transporter - like protein breast cancer resistance protein 1 BCRP1, Mus musculus, EMBL:NP_036050; supported by cDNA: gi_15028218_gb	251785_at	-0.8
putative protein ferritin 2 precursor - Vigna unguiculata, PIR:T08124;supported by full-length cDNA: Ceres:33282.	251735_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 hypothetical protein T24P15.10 - Arabidopsis thaliana, PIR:T00928	251610_at	-0.8
E2 ubiquitin-conjugating-like enzyme Ahus5 ; supported by cDNA: gi_14596100_gb_AY042838.1_	251561_at	-0.8
ribosomal protein L11 -like ribosomal protein L11, cytosolic, Arabidopsis thaliana, PIR:S49033;supported by full-length cDNA: Ceres:14042.	251552_at	-0.8
putative protein COP1-interacting protein CIP8 - Arabidopsis thaliana, EMBL:AF162150	251454_at	-0.8
putative protein embryonic abundant protein EMB34 - Picea glauca, EMBL:L47672	251360_at	-0.8
delta-8 sphingolipid desaturase ;supported by full-length cDNA: Ceres:34427.	251323_at	-0.8
putative protein hypothetical proteins - Arabidopsis thaliana	251241_s_at	-0.8
mRNA binding protein precursor - like mRNA binding protein precursor (chloroplast protein), Lycopersicon esculentum, EMBL:AF106660; supporte	251157_at	-0.8
putative protein HSPC172, Homo sapiens, EMBL:AF161520;supported by full-length cDNA: Ceres:9788.	250993_at	-0.8
putative protein ;supported by full-length cDNA: Ceres:13812.	250844_at	-0.8
putative protein similar to unknown protein (pir||T12959);supported by full-length cDNA: Ceres:252000.	250707_at	-0.8
putative protein similar to unknown protein (sp|P73920)	250727_at	-0.8
copine-like protein copine VII protein - Homo sapiens, EMBL:AJ133798; supported by cDNA: gi_14488103_gb_AF389301.1_AF389301	250581_at	-0.8
inorganic pyrophosphatase - like protein cytosolic inorganic pyrophosphatase, Homo sapiens, EMBL:AF108211;supported by full-length cDNA: Ce	250496_at	-0.8
putative protein ;supported by full-length cDNA: Ceres:12170.	250189_at	-0.8
isopentenyl pyrophosphate:dimethyllallyl pyrophosphate isomerase	250117_at	-0.8
apyrase (gb|AAF00612.1) ; supported by cDNA: gi_6006800_gb_AF156783.1_AF156783	250034_at	-0.8
putative protein predicted proteins, Arabidopsis thaliana	249982_at	-0.8
putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:32414.	249987_at	-0.8
60S ribosomal protein L10A ; supported by cDNA: gi_14335147_gb_AY037253.1_	249945_at	-0.8
cytochrome c1 precursor ; supported by cDNA: gi_15215623_gb_AY050340.1_	249324_at	-0.8
putative protein similar to unknown protein (emb CAB62355.1);supported by full-length cDNA: Ceres:94968.	249330_at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:16944.	249120_at	-0.8
putative protein similar to unknown protein (gb|AAD10670.1)	249072_at	-0.8
putative protein strong similarity to unknown protein (pir||T04426)	248945_at	-0.8
indole-3-glycerol phosphate synthase ; supported by cDNA: gi_15215597_gb_AY050327.1_	248688_at	-0.8
cytochrome b5 (dbj|BAA74840.1) ; supported by full-length cDNA: Ceres: 27167.	248682_at	-0.8

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 (sp|P29512) ;supported by full-length cDNA: Ceres:39002.	247442_s_at	-0.8
amino acid transporter AAP4 (pir||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 ribosomal 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 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	246730_at	-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|Z97341; 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.	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.	266482_at	-0.7

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
unknown protein ;supported by full-length cDNA: Ceres:12246.	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	264855_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|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	264462_at	-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	264207_at	-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 l27a. similar to 60S RIBOSOMAL PROTEIN L27A GB:P49637 GI:1710530 from [Arabidopsis thaliana];supported by full-lengt	262985_s_at	-0.7
E2, ubiquitin-conjugating enzyme, putative similar to DNA-binding protein GB:AAB72016 GI:1066082 from [Homo sapiens]; supported by cDNA: gi	262990_at	-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: 2503	262172_at	-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: C	261789_at	-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.	261740_at	-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	261635_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
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	261563_at	-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	261416_at	-0.7
ribosomal protein identical to GB:CAB81600 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:1097.	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	261228_at	-0.7
ribosomal protein L11, putative similar to chloroplast ribosomal protein L11 GI:21312 from [Spinacia oleracea];supported by full-length cDNA: Cere	261190_at	-0.7
putative small nuclear ribonucleoprotein polypeptide F	260564_at	-0.7

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	260258_at	-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 cDNA: 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 ribosomal protein S3A (S phase specific) similar to 40S ribosomal protein S3A (S phase specific protein GBIS289) GB:P49396 [Brassi	259096_at	-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:7959366 (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	258055_at	-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	257753_at	-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	257101_at	-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
protein phosphatase 2C, putative contains Pfam profile: PF00481 Protein phosphatase 2C	256279_at	-0.7
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	256224_at	-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	256160_at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 11843.	255968_at	-0.7
unknown protein	255764_at	-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_	255538_at	-0.7
putative transposon protein	255366_x_at	-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 ;supported by full-length cDNA: Ceres:7769.	254950_at	-0.7
MAP kinase (ATMPK5) possible internal deletion at position 161, missing one A residue; reference GI:457401; supported by cDNA: gi_457401_dbj	254924_at	-0.7
HhoA protease precursor, putative identical to putative protease HhoA precursor [Arabidopsis thaliana] SP:Q9SEL7 GI:6690272 (unpublished, Len	254669_at	-0.7
hypothetical protein	254154_at	-0.7
DRE CRT-binding protein DREB1C involved in low-temperature-responsive gene expression00; supported by cDNA: gi_3738227_dbj_AB007789.1	254075_at	-0.7
putative protein NorM, Vibrio parahaemolyticus, gb:AB010463	254077_at	-0.7

putative protein Human GS1 (protein of unknown function) mRNA, PID:g183653;supported by full-length cDNA: Ceres:98650.	254039_at	-0.7
putative protein probable membrane protein YBL102w, yeast, PIR2:S45393	253967_at	-0.7
protochlorophyllide reductase precursor ;supported by full-length cDNA: Ceres:36741.	253871_at	-0.7
Expressed protein ; supported by cDNA: gi_15809977_gb_AY054257.1_	253877_at	-0.7
phytochrome-associated protein PAP2 ; supported by cDNA: gi_12083213_gb_AF332402.1_AF332402	253749_at	-0.7
ribosomal protein S15a homolog ribosomal protein S15a - Brassica napus,PIR2:S20945; supported by full-length cDNA: Ceres: 18105.	253726_at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 26443.	253694_at	-0.7
putative protein G protein beta subunit-like protein, Schistosoma mansoni, gb:U30261; supported by full-length cDNA: Ceres: 341.	253645_at	-0.7
EST GB:N37377 spans last intron and 3 end of gene contains similarity to meiotic serine proteinase TMP GI:6468325 from [Lycopersicon esculent	253650_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
AIG2-like protein AIG2 protein, Arabidopsis thaliana, PATCHX:G1127806	253545_at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 24629.	253291_at	-0.7
glucosyltransferase -like protein immediate-early salicylate-induced glucosyltransferase, Nicotiana tabacum, PIR2:T03747;supported by cDNA gi:1	253268_s_at	-0.7
peptidylprolyl isomerase (cyclophilin) ;supported by full-length cDNA: Ceres:37.	253221_at	-0.7
ferulate-5-hydroxylase (FAH1) ; supported by cDNA: gi_1488254_gb_U38416.1_ATU38416	253088_at	-0.7
AtRer1A ; supported by full-length cDNA: Ceres: 21466.	252913_at	-0.7
vacuolar H(+)-ATPase subunit-like protein Vacuolar proton pump subunit SFD alpha isoform - Homo sapiens, EMBL:AF112204; supported by cDN	252845_at	-0.7
glutathione transferase-like protein glutathione transferase, papaya, PIR:T09781;supported by full-length cDNA: Ceres:19003.	252712_at	-0.7
40S ribsomomal protein 40S ribsomomal proteinS20, Arabidopsis thaliana, pir:T12992	252601_s_at	-0.7
GTP-binding protein ara-3 ; supported by cDNA: gi_14334917_gb_AY035132.1_	252514_at	-0.7
40S ribosomal protein S20-like protein 40S RIBOSOMAL PROTEIN S20 - ARABIDOPSIS THALIANA,PID:g1350956;supported by full-length cDN	252413_at	-0.7
MTN3-like protein MtN3 gene product - Medicago truncatula,PID:e1169583; supported by cDNA: gi_13605687_gb_AF361825.1_AF361825	252327_at	-0.7
branched-chain-amino-acid transaminase -like protein branched-chain-amino-acid transaminase, Streptomyces coelicolor, PIR:T29053; supported	252274_at	-0.7
putative protein steroid dehydrogenase homolog - Homo sapiens, EMBL:AF078850;supported by full-length cDNA: Ceres:34560.	252167_at	-0.7
peroxiredoxin - like protein peroxiredoxin TPx2, Arabidopsis thaliana, EMBL:AF121356; supported by cDNA: gi_15292892_gb_AY050880.1_	251993_at	-0.7
nuclear envelope membrane protein - like LBR integral nuclear envelope inner membrane protein, Homo sapiens, EMBL:HSLBR10; supported by	251995_at	-0.7
uncoupling protein (ucp/PUMP) ; supported by cDNA: gi_7673022_gb_AF146226.1_AF146226	251902_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 proteins At2g44600 - Arabidopsis thaliana, EMBL:AAC27462	251459_at	-0.7
putative protein prib5, Ribes nigrum, EMBL:RNI7578;supported by full-length cDNA: Ceres:15792.	251370_at	-0.7
ribosomal protein S13 -like AtRPS13A mRNA for cytoplasmic ribosomal protein S13, Arabidopsis thaliana,AB031739; supported by cDNA: gi_1419	251341_at	-0.7
ribosomal protein S27 ; supported by cDNA: gi_4193381_gb_AF083336.1_AF083336	251357_at	-0.7
putative protein	251270_at	-0.7
putative protein chloroplast ribosome recycling factor protein - Spinacia oleracea, EMBL:AJ133751; supported by cDNA: gi_13926251_gb_AF3728	251172_at	-0.7
anthranilate N-benzoyltransferase - like protein anthranilate N-benzoyltransferase, clove pink, PIR:T10717; supported by cDNA: gi_15912268_gb_	251144_at	-0.7
putative protein contains transmembrane region and ATP binding region, Mus musculus, EMBL:AB030189.1	250978_at	-0.7
putative RNA-binding protein astrocytic NOVA-like RNA-binding protein, Homo sapiens, U70477;supported by full-length cDNA: Ceres:25769.	250843_at	-0.7
GTP-binding protein (gb|AAD09203.1) ;supported by full-length cDNA: Ceres:6734.	250813_at	-0.7
Expressed protein ; supported by cDNA: gi_9909197_gb_AF175769.1_AF175769	250818_at	-0.7
cytochrome P450 90A1 (sp|Q42569) ; supported by full-length cDNA: Ceres: 36334.	250752_at	-0.7
2-cys peroxiredoxin-like protein ;supported by full-length cDNA: Ceres:15640.	250733_at	-0.7
putative protein similar to unknown protein (gb|AAF02129.1);supported by full-length cDNA: Ceres:104017.	250734_at	-0.7
harpin-induced protein-like ; supported by cDNA: gi_9502175_gb_AF264699.1_AF264699	250676_at	-0.7
putative protein similar to unknown protein (dbj|BAA86974.1);supported by full-length cDNA: Ceres:20752.	250687_at	-0.7
ABC transporter-like protein ; supported by cDNA: gi_14488081_gb_AF389289.1_AF389289	250690_at	-0.7
nucleoid DNA-binding-like protein ;supported by full-length cDNA: Ceres:15560.	250661_at	-0.7
serine/threonine protein kinase ;supported by full-length cDNA: Ceres:5323.	250545_at	-0.7
pectin methylesterase - like protein pectin methylesterase, Melandrium album, EMBL:MAPME	250490_at	-0.7
beta-xylosidase - like protein beta-xylosidase, Aspergllus nidulans, EMBL:ANXLND; supported by cDNA: gi_15982752_gb_AY057483.1_	250444_at	-0.7
putative protein predicted proteins, Arabidopsis thaliana	250417_at	-0.7
putative protein ; supported by cDNA: gi_15028030_gb_AY045872.1_	250368_at	-0.7
putative protein	250330_at	-0.7
putative protein contains similarity to transmembrane transport protein;supported by full-length cDNA: Ceres:249596.	250315_at	-0.7
putative protein ;supported by full-length cDNA: Ceres:5392.	250289_at	-0.7
ubiquinol--cytochrome-c reductase - like protein non-consensus AT acceptor splice site at exon 2, ubiquinol--cytochrome-c reductase, Solanum tub	250235_s_at	-0.7
receptor-like protein kinase	250102_at	-0.7
putative protein similar to unknown protein (sp|P50027);supported by full-length cDNA: Ceres:17002.	250079_at	-0.7

putative protein similar to unknown protein (dbj|BAA90342.1);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 (pir||T04881)	249021_at	-0.7
serine threonine protein kinase ; supported by cDNA: gi_14486383_gb_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: Ceres:8698.	248747_at	-0.7
drought-induced protein Di19-like protein ; supported by cDNA: gi_13937215_gb_AF372963.1_AF372963	248595_at	-0.7
Expressed protein ; supported by cDNA: gi_7715088_gb_AF216756.1_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	246923_at	-0.7
AtBgamma - 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	246538_at	-0.7
proline-rich protein other proline-rich proteins	246519_at	-0.7
phosphoribosyl-ATP pyrophosphohydrolase (At-IE) identical to phosphoribosyl-ATP pyrophosphohydrolase (At-IE) [Arabidopsis thaliana] GI:34618	246265_at	-0.7
cytochrome-b5 reductase - like protein cytochrome-b5 reductase, Saccharomyces cerevisiae, PIR:S37800;supported by full-length cDNA: Ceres:33	246157_at	-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
PSII T 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 sequencin	267093_at	-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, an	266461_at	-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
unknown protein ;supported by full-length cDNA: Ceres:34688.	266137_at	-0.6
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); su	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	264435_at	-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,	264199_at	-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

putative 60s ribosomal protein L10 Nearly identical to ribosomal protein L10.e, Wilm s tumor suppressor homologue, gi|17682 (Z15157), however	263686_at	-0.6
unknown protein similar to unknown protein GB:AAC79135, ESTs gb|T20423, gb|AA712864, gb|H76323 and gb|Z25560 come from this gene;supp	263704_at	-0.6
unknown protein ESTs 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 ribosomal protein L39	263585_at	-0.6
40S ribosomal protein; contains C-terminal domain ; supported by cDNA: gi_14190418_gb_AF378887.1_AF378887	263400_s_at	-0.6
putative CCCH-type zinc finger protein also an ankyrin-repeat protein	263379_at	-0.6
alanine-glyoxylate aminotransferase ;supported by full-length cDNA: Ceres:8306.	263350_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:5198.	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	263034_at	-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	262806_at	-0.6
putative DNA binding protein similar to gb|U90212 DNA binding protein ACBF from Nicotiana tabacum and contains 3 PF|00076 RNA recognition	262824_at	-0.6
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	262590_at	-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	262442_at	-0.6
hypothetical protein contains similarity to disulphide isomerase GI:4581959 from [Caenorhabditis briggsae]; supported by cDNA: gi_16649012_gb_	262413_at	-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_ATU49	261865_at	-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
UDP glucose:flavonoid 3-o-glucosyltransferase, putative similar to UDP glucose:flavonoid 3-o-glucosyltransferase GB:AAB81683 GI:2564114 from	261804_at	-0.6
hypothetical protein contains similarity to amino acid permease GI:7415521 from [Oryza sativa]	261785_at	-0.6
hypoxanthine ribosyl transferase, putative similar to hypoxanthine ribosyl transferase GB:AAC46403 GI:2689037 from [Vibrio parahaemolyticus];su	261516_at	-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 to gi:431259, 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: 31	261489_at	-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	260426_at	-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	260257_at	-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:CAB53377 [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_AF42462	259681_at	-0.6
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:21940.	259663_at	-0.6
nuclear transport factor 2, putative similar to nuclear transport factor 2 (NTF2) [Oryza sativa] GI:5360221; supported by full-length cDNA: Ceres: 27	259593_at	-0.6
serine carboxypeptidase II, putative similar to H.vulgare gene encoding serine carboxypeptidase II, CP-MII GI:1731989; supported by cDNA: gi_16	259599_at	-0.6
hypothetical protein similar to ripening-induced protein [Fragaria vesca] GI:2465015;supported by full-length cDNA: Ceres:16091.	259548_at	-0.6
chlorophyll binding protein, putative similar to chlorophyll binding protein GI:169213 from [Petunia hybrida]	259491_at	-0.6

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	259077_s_at	-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	258655_at	-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	255778_at	-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	255506_at	-0.6
predicted NADH dehydrogenase 24 kD subunit similar to N. crassa NADH-ubiquinone dehydrogenase 24 kD subunit precursor, GenBank accessio	255442_at	-0.6
putative phosphatidylglycerotransferase similar to CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase of Synechocystis sp. GenBa	255300_at	-0.6
3(2),5-BISPHOSPHATE NUCLEOTIDASE -like protein 3 (2),5 -BISPHOSPHATE NUCLEOTIDASE, Arabidopsis thaliana, gb:Q42546;supported b	255249_at	-0.6
nucleoside-diphosphate kinase ;supported by full-length cDNA: Ceres:30158.	255089_at	-0.6

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.	254529_at	-0.6
putative protein RNPL, Homo sapiens, PIR2:G01859;supported by full-length cDNA: Ceres:251841.	254504_at	-0.6
endomembrane-associated protein ; supported by full-length cDNA: Ceres: 20592.	254492_at	-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 predicted protein ERG25, Saccharomyces cerevisiae, PIR2:S64354	254333_at	-0.6
putative 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: gi_15294253_gb_AF410318.1_AF410318	254126_at	-0.6
geranylgeranylated protein ATGP4 ; supported by cDNA: gi_4097566_gb_U64921.1_ATU64921	254106_at	-0.6
putative protein ClpC protease - Spinacia oleracea,PID:g4105131; 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	253205_at	-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	252235_at	-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
ubiquinol--cytochrome-c reductase-like protein ubiquinol--cytochrome-c reductase, 8K chain, potato, PIR:T07369; supported by cDNA: gi_1545102	252012_at	-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.	251602_at	-0.6
U6 snRNA-associated Sm-like protein U6 snRNA-associated Sm-like protein LSm6 - Homo sapiens, EMBL:AF182292; supported by full-length cD	251447_at	-0.6
putative protein prib5, Ribes nigrum, EMBL:RNI7578	251418_at	-0.6
putative protein unknown protein At2g47690 - Arabidopsis thaliana, EMBL:AC005309; supported by full-length cDNA: Ceres: 6853.	251186_at	-0.6
putative chloroplast inner envelope protein membrane protein, 37K, precursor, chloroplast inner envelope, common tobacco, PIR:T03230;support	251118_at	-0.6
putative protein serine/threonine protein kinase ATPK10 - Arabidopsis thaliana, EMBL:D30622; supported by cDNA: gi_13249126_gb_AF295669.1	251060_at	-0.6
putative protein ;supported by full-length cDNA: Ceres:17471.	250969_at	-0.6
putative protein	250944_at	-0.6
putative protein proline-rich protein APG, Arabidopsis thaliana, PIR:S21961; supported by full-length cDNA: Ceres: 13022.	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

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: gi_13926304_gb_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	248903_at	-0.6
Lil3 protein	248828_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:12344.	248760_at	-0.6
NADH dehydrogenase 10.5K chain-like protein ; supported by full-length cDNA: Ceres: 39633.	248746_at	-0.6
putative protein similar to unknown protein (gb|AAC72543.1)	248676_at	-0.6
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	247641_at	-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	246030_at	-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

hypothetical protein	244993_s_at	-0.6
putative RSZp22 splicing factor	257435_at	-0.6
DNA-3-methyladenine glycosidase, putative similar to DNA-3-methyladenine glycosidase GB:CAB60736 GI:6434028 from [Staphylococcus aureus	257474_at	-0.6
hypothetical protein predicted by genemark.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	266760_at	-0.5
glycine decarboxylase complex H-protein identical to GB:U27144;supported by full-length cDNA: Ceres:24194.	266636_at	-0.5
similar to gibberellin-regulated proteins	266613_at	-0.5
50S ribosomal protein L27 ;supported by full-length cDNA: Ceres:17067.	266535_s_at	-0.5
unknown protein ; supported by cDNA: gi_13605586_gb_AF361619.1_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_1552922	266331_at	-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) presernt 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.	265384_at	-0.5
cytosolic cyclophilin (ROC3) ;supported by full-length cDNA: Ceres:23995.	265352_at	-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|AA586260 and dbj|D48620; supported by cDNA: gi_14624991_dbj_AB	264820_at	-0.5
unknown protein similar to EST gb|H37293;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	264445_at	-0.5
aminomethyltransferase-like precursor protein very strong similarity to aminomethyltransferase precursor gb|U79769 from Mesembryanthemum cry	264394_at	-0.5
putative vesicle transport protein Contains similarity to vesicle trafficking protein gb|U91538 from Mus musculus. ESTs gb|F15494 and gb|F14097 c	264373_at	-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	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-	262768_at	-0.5
multicatalytic endopeptidase identical to GB:CAA73619, ESTs gb|H36972, gb|T22551 and gb|T13800 come from this gene;supported by full-length	262716_at	-0.5
unknown protein ESTs gb|T22508, gb|H36196 and gb|AI100134 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	262559_at	-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_1184	261970_at	-0.5
salt-tolerance zinc finger protein identical to salt-tolerance zinc finger protein GB:CAA64820 GI:1565227 from [Arabidopsis thaliana]; supported by	261648_at	-0.5
unknown protein	261572_at	-0.5
acidic ribosomal protein, putative similar to 60S ACIDIC RIBOSOMAL PROTEIN P1 GB:O23095 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_AF378	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
unknown protein ; supported by full-length cDNA: Ceres: 11793.	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: 27	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 c	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:10653	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 functio	257674_at	-0.5
ethylene responsive element binding factor, putative similar to GB:BAA32420 from [Arabidopsis thaliana], contains Pfam profile: PF00847 P2 dom	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
NAD dependent epimerase, putative contains Pfam profile: PF01370 NAD dependent epimerase/dehydratase family; supported by cDNA: gi_138	256865_at	-0.5
putative protein similar to ATP synthase D chain (mitochondrial) SP:O75947 [Homo sapiens (Human)]; supported by full-length cDNA: Ceres: 2768	256679_at	-0.5
disease resistance protein, putative similar to disease resistance protein GB:AAC78591 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	256185_at	-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	256015_at	-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	254448_at	-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:g4826860	254355_at	-0.5
dihydroorotase ; 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 zinc finger protein zinc finger protein SINA1p - Vitis vinifera,PID:e1423803	253838_at	-0.5
putative protein ;supported by full-length cDNA: Ceres:1968.	253766_at	-0.5
rac GTP binding protein Arac7 ; supported by cDNA: gi_3702961_gb_AF079484.1_AF079484	253757_at	-0.5
profilin 2 ; supported by full-length cDNA: Ceres: 25886.	253727_at	-0.5
putative protein predicted protein, Arabidopsis thaliana, PIR2:T01282;supported by full-length cDNA: Ceres:32381.	253644_at	-0.5
putative protein ; supported by full-length cDNA: Ceres: 37881.	253464_at	-0.5
caffeoyl-CoA O-methyltransferase - like protein caffeoyl-CoA 3-O-methyltransferase, Populus tremuloides, PID:G857578;supported by full-length c	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
Phospholipase like protein Arabidopsis thaliana pEARLI 4 mRNA, PID:g871782	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
hypothetical protein ; supported by full-length cDNA: Ceres: 207539.	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_g	252326_at	-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

putative protein CHLOROPLAST 30S RIBOSOMAL PROTEIN S20, SWISSPROT:RR20_GUITH; supported by cDNA: gi_15810456_gb_AY05626	251744_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
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_gb_	251509_at	-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:390	250862_s_at	-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_1451739	250190_at	-0.5
biotin carboxyl carrier protein of acetyl-CoA carboxylase precursor (BCCP) (sp|Q42533) ;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
eIF4Eiso 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 cDNA: 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	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
cyclin C-like protein ;supported by full-length cDNA: Ceres:2036.	248666_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:205928.	248679_at	-0.5
ribitol dehydrogenase-like ; supported by cDNA: gi_15146201_gb_AY049242.1_	248539_at	-0.5
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: Cer	247658_at	-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

putative protein cation transport protein chaC, Escherichia coli, PIR:G64868	246884_at	-0.5
sugar transporter-like protein putative sugar transporter - Prunus armeniaca, EMBL:AF000952; supported by cDNA: gi_16648752_gb_AY058152.1	246508_at	-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:AF254124	245934_at	-0.5
ribosomal protein S15-like ribosomal protein S15 - Arabidopsis thaliana, EMBL:Z23161;supported by full-length cDNA: Ceres:164.	245886_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
bHLH transcription factor, putative similar to bHLH transcription factor GI:3757520 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres	245746_at	-0.5
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:20991.	245666_at	-0.5
enoyl-CoA hydratase like protein	245484_at	-0.5
disease resistance RPP5 like protein	245448_at	-0.5
tubulin 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 emb|Z34690, 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 homolog, putative similar to cytochrome P450 homolog GB:U54770 GI:1421740 from [Lycopersicon esculentum];supported by fu	256598_at	-0.5
homeodomain containing protein 1 ; supported by cDNA: gi_2506030_dbj_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

Table 5: Transcripts suppressed during heat shock compared to unstressed plants

Descriptions	**Affimetrix number**	**$\log_2$ fold supressed**
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	262113_at	-5.5
unknown protein ;supported by full-length cDNA: Ceres:4309.	248062_at	-5.2
unknown protein	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	258941_at	-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	263161_at	-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	265044_at	-3.2
histone H3 - like protein histone H3, Arabidopsis thaliana, PIR:S06250	250433_at	-3.2
O-methyltransferase - like protein caffeic acid O-methyltransferase, Pinus taeda, gb:U39301	253177_s_at	-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
unknown 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:189	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 [	257809_at	-2.5
beta-fructofuranosidase identical to beta-fructofuranosidase GI:6683112 from [Arabidopsis thaliana]; supported by cDNA: gi_6683111_dbj_AB029	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	252442_at	-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
anthocyanidin synthase - like protein putative leucoanthocyanidin dioxygenase, Arabidopsis thaliana, PID:g1575699	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	257173_at	-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	-2.2
unknown protein ;supported by full-length cDNA: Ceres:40283.	266413_at	-2.2
putative caltractin ;supported by full-length cDNA: Ceres:7802.	265460_at	-2.2
polygalacturonase PG1, putative similar to GB:AAD46483 from [Glycine max] (Mol. Plant Microbe Interact. 12 (6), 490-498 (1999)); supported by	260727_at	-2.2
unknown protein	259507_at	-2.2
putative phosphate/phosphoenolpyruvate translocator similar to phosphate/phosphoenolpyruvate translocator precursor GB:AAB40648 [Nicotiana	259185_at	-2.2
cinnamyl alcohol dehydrogenase identical to GB:P48523 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:4357.	258023_at	-2.2
hypothetical protein predicted by genscan; supported by cDNA: gi_15292884_gb_AY050876.1_	257057_at	-2.2
putative protein	253189_at	-2.2
putative protein hypersensitivity-related hsr201 protein - Nicotiana tabacum,PIR2:T03274	252317_at	-2.2
histone H3 - like protein histone H3, Arabidopsis thaliana, PIR:S06250	250434_at	-2.2
unknown protein	248190_at	-2.2
ankyrin-repeat-containing protein-like	248169_at	-2.2
unknown protein	263549_at	-2.1
putative protein similar to T5J8.18	255450_at	-2.1
putative protein hypothetical protein - Arabidopsis thaliana,PIR2:H71441;supported by full-length cDNA: Ceres:4642.	254746_at	-2.1
putative protein gamma-SNAP protein, bovine, PIR2:S32369;supported by full-length cDNA: Ceres:267158.	254476_at	-2.1
putative protein	252661_at	-2.1
putative calcium-binding protein calcium binding domains (EF hand) of several proteins	252417_at	-2.1
putative protein	250942_at	-2.1
nucleoid DNA-binding protein cnd41 - like protein nucleoid DNA-binding protein cnd41, chloroplast, common tobacco, PIR:T01996	250445_at	-2.1
ribosomal protein L23	244988_s_at	-2.1
ribosomal protein S12 (trans-splice part 2 of 2)	244940_at	-2.1
putative alcohol dehydrogenase	266761_at	-2
unknown protein similar to gb|T45484, emb|Z30724, and emb|Z30531	264824_at	-2
putative s-adenosylmethionine synthetase ;supported by full-length cDNA: Ceres:13320.	263838_at	-2
receptor-like protein kinase, putative similar to receptor-like protein kinase GB:AAC95353 GI:4008010 from [Arabidopsis thaliana]	262507_at	-2
flax rust resistance protein, putative similar to flax rust resistance protein GI:4588066 from [Linum usitatissimum]; supported by full-length cDNA:	262374_s_at	-2
12-oxophytodienoate reductase (OPR2) identical to 12-oxophytodienoate reductase OPR2 GB:AAC78441 [Arabidopsis thaliana]	259875_s_at	-2
hypothetical protein ; supported by cDNA: gi_14532585_gb_AY039917.1_	259561_at	-2
unknown protein ;supported by full-length cDNA: Ceres:96816.	257793_at	-2
unknown protein	256096_at	-2
putative serine carboxypeptidase II	255842_at	-2
putative pectinacetylesterase protein pectinacetylesterase precursor, Vigna radiata, PIR2:S68805;supported by full-length cDNA: Ceres:34674.	254578_at	-2
putative protein centrin, Marsilea vestita;supported by full-length cDNA: Ceres:13072.	253915_at	-2
dehydrin Xero2 ; supported by cDNA: gi_15809983_gb_AY054260.1_	252102_at	-2
beta-1,3-glucanase 2 (BG2) (PR-2) ;supported by full-length cDNA: Ceres:21719.	251625_at	-2
Expressed protein ; supported by full-length cDNA: Ceres: 32396.	251142_at	-2
unknown protein ; supported by cDNA: gi_15810044_gb_AY054291.1_	250828_at	-2
amino acid permease 6 (emb CAA65051.1)	248619_at	-2
FRO2-like protein; NADPH oxidase-like	248566_s_at	-2
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
putative glutaredoxin ;supported by full-length cDNA: Ceres:21006.	266516_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]; s	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	258537_at	-1.9
Histone H4 - like protein histone H4, Zea mays, PIR:HSZM4;supported by full-length cDNA: Ceres:22146.	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
putative protein predicted proteins, Arabidopsis thaliana	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

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 co	264669_at	-1.7
unknown protein similar to PHZF, catalyzing the hydroxylation of phenazine-1-carboxylic acid to2-hydroxy-phenazine-1-carboxylic acid; ESTs gb|	264355_at	-1.7
putative beta-ketoacyl-CoA synthase	263606_at	-1.7
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_	261826_at	-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	260618_at	-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	257100_at	-1.7
putative inorganic phosphatase ; supported by cDNA: gi_15450871_gb_AY054516.1_	255587_at	-1.7
glycine hydroxymethyltransferase - like protein glycine hydroxymethyltransferase, Homo sapiens, PIR2:A46746	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_AY05819	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 aure	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-co	265121_at	-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,	263676_at	-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	261692_at	-1.6
Ca2+-dependent membrane-binding protein annexin idenctical to GB:AAD34236 from [Arabidopsis thaliana];supported by full-length cDNA: Cere	261285_at	-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_152929	258979_at	-1.6

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
ribosomal protein S7	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	259077_s_at	-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	257101_at	-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:	254784_at	-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	251626_at	-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_152926	254125_at	-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 [Ri	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
fructose 1,6-bisphosphatase, putative similar to cytosolic fructose-1,6-bisphosphatase GB:AAD28755 GI:4741918 from [Musa acuminata]	260837_at	-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	-1.4
unknown protein	260081_at	-1.4
unknown protein supported by cDNA: Ceres:13335	260072_at	-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	259736_at	-1.4
putative signal peptidase similar to MITOCHONDRIAL INNER MEMBRANE PROTEASE SUBUNIT 2 GB:P46972 [Saccharomyces cerevisiae]	259199_at	-1.4
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
hypothetical protein contains similarity to 3-hydroxyisobutyrate dehydrogenase GB:AAC06408 from [Aquifex aeolicus]; supported by cDNA: gi_15	257911_at	-1.4
xyloglucan endotransglycosylase, putative similar to xyloglucan endotransglycosylase 1 GB:CAA10231 from [Fagus sylvatica] (Plant Physiol.(19	257203_at	-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
putative disease resistance protein similar to disease resistance protein GB:AAC78591 [Lycopersicon esculentum]	256431_s_at	-1.4
nascent polypeptide associated complex alpha chain, putative similar to nascent polypeptide associated complex alpha chain GB:AAF27917 GI:	256241_at	-1.4
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	-1.4
putative alpha NAC stong similarity to Nascent polypeptide associated complex alpha chain - human, PIR2:S49326; supported by cDNA: gi_150	254981_at	-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_	254791_at	-1.4
putative dihydrolipoamide succinyltransferase dihydrolipoamide succinyltransferase (EC 2.3.1.61) precursor - rat, Pir2:A41015;supported by full-l	253950_at	-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_AF370	250517_at	-1.4
beta-xylosidase - like protein beta-xylosidase, Asperglllus 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	246597_at	-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 onl	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 cD	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	260955_at	-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	259383_at	-1.3
putative 40S ribosomal protein S17 similar to 40S ribosomal protein S17 GB:AAD50774 [Lycopersicon esculentum];supported by full-length cDN	258922_at	-1.3
putative UDP-glucose pyrophosphorylase similar to UDP-glucose pyrophosphorylase GB:AAB71613 from [Solanum tuberosum]; supported by cD	258849_at	-1.3
unknown protein ; supported by full-length cDNA: Ceres: 21882.	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 sa	258155_at	-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	256548_at	-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
putative protein RING-H2 finger protein RHA1a, Arabidopsis thaliana,AF078683	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:	255776_at	-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:	246157_at	-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

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	262597_at	-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	262194_at	-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 tab	261933_at	-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	260957_at	-1.2
phosphoenolpyruvate carboxylase 1, putative similar to phosphoenolpyruvate carboxylase 1 GI:2266947 from [Gossypium hirsutum]; supported	260590_at	-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	260002_at	-1.2
lipase/hydrolase, putative contains Pfam profile: PF00657 Lipase/Acylhydrolase with GDSL-like motif;supported by full-length cDNA: Ceres:6680	259786_at	-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];supp	258613_at	-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
cysteine proteinase contains similarity to cysteine proteinase RD21A (thiol protease) GI:435619, SP:P43297 from [Arabidopsis thaliana]	254915_s_at	-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 rhamnose--anthocyanidin-3-glucoside rhamnosyltransferase - like protein UDP rhamnose--anthocyanidin-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	252274_at	-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	250582_at	-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	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_	263656_at	-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,	263223_at	-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 tosimilar to glutathione S-transferase GB:AAF29773 GI:6856103 from (Gossypium hirsutum); supporte	262916_at	-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	262342_at	-1.1
unknown protein contains similarity to zinc finger and C2 domain protein GI:9957238 from [Arabidopsis thaliana];supported by full-length cDNA: C	262314_at	-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	262158_at	-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
ferredoxin--NADP 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	261056_at	-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
hypothetical protein ;supported by full-length cDNA: Ceres:265772.	259550_at	-1.1
putative lectin contains Pfam profile: PF01419 jacalin-like lectin domain; similar to jasmonate inducible protein GB:Y11483 (Brassica napus), myr	259381_s_at	-1.1
putative methionine synthase similar to cobalamin-independent methionine synthase GB:AAC50037 [Arabidopsis thaliana];supported by full-lengt	259343_s_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
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
unknown protein	258419_at	-1.1
20S proteasome subunit PAE2 identical to 20S proteasome subunit PAE2 GB:AAC32061 from [Arabidopsis thaliana]; supported by cDNA: gi_342	258373_at	-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:8265	258222_at	-1.1
beta-glucosidase, putative similar to beta-glucosidase BGQ60 precursor GB:A57512 [Hordeum vulgare];supported by full-length cDNA: Ceres:11	258151_at	-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 cDNA	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	253971_at	-1.1

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	253205_at	-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 b	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 an	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. ES	263706_s_at	-1
putative 1-aminocyclopropane-1-carboxylate oxidase Similar to Arabidopsis 2A6 (gb|X83096). EST gb|T76913 comes from this gene; supported b	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:	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	261920_at	-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_AF	261696_at	-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 kD	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 simliar 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-adenosylmethionine:2-demethylmenaquinone methyltrans	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
putative chlorophyll A-B binding protein similar to chlorophyll A-B binding protein 151 precursor (LHCP) GB:P27518 from [Gossypium hirsutum];s	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
GDP-L-fucose synthetase, putative similar to GDP-L-fucose synthetase GI:6580725 from [Yersinia pseudotuberculosis];supported by full-length	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
protoporphyrinogen oxidase ; supported by cDNA: gi_14423413_gb_AF386944.1_AF386944	255537_at	-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	255513_at	-1

5-adenylylsulfate reductase ;supported by full-length cDNA: Ceres:40330.	255284_at	-1
coded 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_AF3602	253697_at	-1
EST GB:N37377 spans last intron and 3 end of gene contains similarity to meiotic serine proteinase TMP GI:6468325 from [Lycopersicon escule	253650_at	-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
putative protein other predicted proteins Arabidopsis thaliana	253059_s_at	-1
vacuolar H(+)-ATPase subunit-like protein Vacuolar proton pump subunit SFD alpha isoform - Homo sapiens, EMBL:AF112204; supported by cD	252845_at	-1
disease resistance protein homolog disease resistance protein RPP1-WsB - Arabidopsis thaliana, EMBL:AF098963	252648_at	-1
lipoxygenase 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 cD	251899_at	-1
tryptophan 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: Ce	251205_at	-1
putative protein outer envelope membrane protein E 6.7 - chloroplast Spinacia oleracea, PIR:A35958; supported by cDNA: gi_15724349_gb_AF	251155_at	-1
putative protein rngB 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
pyruvate 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
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	247272_at	-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	264504_at	-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:101	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	262846_at	-0.9
putative DNA binding protein similar to gb|U90212 DNA binding protein ACBF from Nicotiana tabacum and contains 3 PF|00076 RNA recognitio	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	262024_at	-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	261865_at	-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	261577_at	-0.9
pyruvate dehydrogenase E1 alpha subunit identical to pyruvate dehydrogenase E1 alpha subunit GB:AAB86803 GI:2454182 from [Arabidopsis th	261583_at	-0.9
polyphosphoinositide binding protein, putative similar to polyphosphoinositide binding protein Ssh2p GB:AAB94599 GI:2739046 from [Glycine m	261563_at	-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	261145_at	-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); sup	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
putative coatomer zeta subunit (zeta-coat protein) similar to coatomer zeta subunit (zeta-coat protein) GB:P35604 (Bos taurus)	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:	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	258483_at	-0.9
hypothetical protein contains similarity to putative phosphate/phosphoenolpyruvate translocator protein GB:AAD20711 from [Arabidopsis thaliana	258371_at	-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_	258086_at	-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 s	257713_at	-0.9
integral membrane protein, putative contains Pfam profile: PF01554 uncharacterized membrane protein family; supported by cDNA: gi_1632312	257314_at	-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	257038_at	-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 thalian	256156_at	-0.9
mitogen-activated protein kinase, putative similar to mitogen-activated protein kinase GI:5815410 from [Oryza sativa]; supported by cDNA: gi_15	256075_at	-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	255966_at	-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
putative protein storage protein - Populus deltoides, PIR2:S31580;supported by full-length cDNA: Ceres:8772.	254163_s_at	-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	251341_at	-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_g	250339_at	-0.9
putative protein similar to unknown protein (pir||T09909)	250307_at	-0.9
putative protein predicted protein, Arabidopsis thaliana	250282_at	-0.9
phytoene synthase (gb|AAB65697.1) ;supported by full-length cDNA: Ceres:15761.	250095_at	-0.9
anthranilate phosphoribosyltransferase, chloroplast precursor (sp|Q02166) ; supported by cDNA: gi_15450851_gb_AY054506.1_	250014_at	-0.9
apyrase (gb|AAF00612.1) ; supported by cDNA: gi_6006800_gb_AF156783.1_AF156783	250034_at	-0.9
glutaredoxin -like protein glutaredoxin, castor bean, PIR:S54825;supported by full-length cDNA: Ceres:92720.	249996_at	-0.9
putative protein 2 -hydroxyisoflavone reductase (EC 1.3.1.45) - Nicotiana tabacum, PIR:T02202;supported by full-length cDNA: Ceres:17121.	250006_at	-0.9
beta-amylase-like proten beta-amylase - Prunus armeniaca, EMBL:AF139501;supported by full-length cDNA: Ceres:30798.	250007_at	-0.9
NAC-domain protein-like ;supported by full-length cDNA: Ceres:29829.	249940_at	-0.9
soluble starch synthase	249785_at	-0.9
putative protein tyrosine aminotransferase-like; also similar to nicotianamine aminotransferase	249688_at	-0.9
glutamate--ammonia 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	245832_at	-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
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 genscan	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	-0.8
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
actin 3 identical to GB:U29480;supported by full-length cDNA: Ceres:19581.	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
unknown protein	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	265120_at	-0.8
T-complex chaperonin protein , epsilon subunit identical to GB:O04450, similar to ESTs gb|R29812, emb|Z38124, gb|AA297087, gb|R29812, gb|	265010_at	-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	264373_at	-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

putative gibberellin-regulated protein contains similarity to gibberellin-regulated protein 2 precursor (GAST1) homolog gb|U11765 from A. thaliana	264195_at	-0.8
putative sucrose transport protein, SUC2 strong similarity to GB:S38196 sucrose transport protein SUC2 from [Arabidopsis thaliana];supported b	264204_at	-0.8
RAS-related protein, RAB7 identical GB:O04157 RAS-RELATED PROTEIN RAB7 from [Arabidopsis thaliana]; supported by cDNA: gi_15718415	264209_at	-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	264097_s_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
putative lipase ; supported by cDNA: gi_15293128_gb_AY050998.1_	263987_at	-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	262793_at	-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: Ce	261792_at	-0.8
tubulin alpha-6 chain, putative identical to tubulin alpha-6 chain GB:P29511 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:15	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	260254_at	-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 (dolichyl-diphosphooligosaccharide-pr	259883_at	-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 c	259402_at	-0.8
putative ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I similar to ribulose-1,5-bisphosphate carboxylase/	259258_at	-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 c	259196_at	-0.8
putative thylakoid lumen rotamase similar to thylakoid lumen rotamase GB:CAA72792 [Spinacia oleracea];supported by full-length cDNA: Ceres:	259193_at	-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	258276_at	-0.8
putative acetyltransferase similar to dihydrolipoamide S-acetyltransferase GB:AAD46491 from [Zea mays]; supported by cDNA: gi_13605806_gb	258208_at	-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	257939_at	-0.8
prolyl 4-hydroxylase, putative similar to PROLYL 4-HYDROXYLASE ALPHA SUBUNIT PRECURSOR GB:Q10576 from [Caenorhabditis elegans	257844_at	-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 f	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:	255902_at	-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	255578_at	-0.8
drought-induced-19-like 1 similar to drought-induced-19, GenBank accession number X78584 similar to F2P16.10, GenBank accession number	255504_at	-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
putative receptor-like protein kinase	255344_s_at	-0.8
putative phosphatidylglycerotransferase similar to CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase of Synechocystis sp. GenB	255300_at	-0.8
putative protein RNA helicase -Mus musculus,PIR2:I84741	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	253300_at	-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; sup	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	246923_at	-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_gb	246785_at	-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	246417_at	-0.8
glucose 6 phosphate/phosphate translocator-like protein glucose 6 phosphate/phosphate translocator - Arabidopsis thaliana, EMBL:AF233658; s	246445_at	-0.8
integral membrane protein, putative similar to integral membrane protein GI:3288599 from [Rattus norvegicus]; supported by full-length cDNA: Ce	246378_at	-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-lengt	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: 12	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	264874_at	-0.7
putative superoxide-generating NADPH oxidase flavocytochrome highly similar to GB:CAA70769, FRO1 and GB:CAA70770, FRO2 from [Arabid	264751_at	-0.7
flowering signals mediating protein FT identical to flowering signals mediating protein FT GI:4903012 from [Arabidopsis thaliana]; supported by c	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
hypothetical protein similar to hypothetical protein GB:AAC27412	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	263159_at	-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	262572_at	-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:O14460 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 cD	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:2	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_	260325_at	-0.7
unknown protein ; supported by full-length cDNA: Ceres: 10531.	260200_at	-0.7
putative UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide)-pyrophosphoryl-undecaprenol N-acetylglucosamine transferase similar to p	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
auxin-induced protein, putative similar to SP:P33083 from [Glycine max];supported by full-length cDNA: Ceres:4119.	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	259752_at	-0.7
putative AUX1-like permease similar to AUX1 (regulator of root gravitropism, putative permease) GB:CAA67308 [Arabidopsis thaliana]; supporte	259680_at	-0.7
myosin-like protein contains Pfam profile: PF00658 Poly-adenylate binding protein, unique domain.; supported by cDNA: gi_15081708_gb_AY04	259609_at	-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_	259504_at	-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	259279_at	-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 protei	258791_at	-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	258816_at	-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); supporte	258617_at	-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), 948-95	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_AF	256183_at	-0.7
pyruvate dehydrogenase E1 beta subunit, putative similar to pyruvate dehydrogenase E1 beta subunit GI:2982328 from [Picea mariana];supporte	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_g	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
eIF4Eiso protein (emb|CAA71579.1) ;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
nodulin-like protein ; supported by cDNA: gi_14532599_gb_AY039924.1_	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
receptor protein kinase-like protein probable somatic embryogenesis receptor-like kinase - Daucus carota, EMBL:U93048;supported by full-lengt	246483_at	-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_143	245987_at	-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
anthocyanin2, putative similar to anthocyanin2 (An2) GI:7673088 from [Petunia integrifolia]; supported by cDNA: gi_3941507_gb_AF062908.1_A	245628_at	-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	245118_at	-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 pyrophosphate--fructose-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
Arabidopsis thaliana /REF=X52320 /DEF=25S rRNA /LEN=4310	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_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 th	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	265073_at	-0.6
hypothetical protein contains similarity to high-glucose-regulated protein 8 GB:AAF08813 GI:6449083 from [Homo sapiens]; supported by cDNA: g	265078_at	-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	265056_at	-0.6
NBS/LRR disease resistance protein, putative similar to NBS/LRR disease resistance protein GI:3309619 from [Arabidopsis thaliana]; supported	264885_s_at	-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	264625_at	-0.6
hypothetical protein similar to ankyrin like protein GI:7268141 from [Arabidopsis thaliana]; supported by cDNA: gi_14194106_gb_AF367259.1_AF	264484_at	-0.6
putative protein import receptor similar to TOM20 (GB:CAA63223) from [Solanum tuberosum]; similar to ESTs gb|T444475, emb|Z26777, and em	264490_at	-0.6
hypothetical protein contains similarity to phosphate/phosphoenolpyruvate translocator precursor GI:1778141 from [Arabidopsis thaliana]	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]; su	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	262367_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:21798.	262283_at	-0.6
isochorismate synthase (icsI) identical to isochorismate synthase (icsI) 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	261694_at	-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_	261537_at	-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	260940_at	-0.6
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:29740.	260867_at	-0.6
acyl-CoA oxidase ACX3 identical to acyl-CoA oxidase ACX3 GI:8163758 from [Arabidopsis thaliana]	260789_s_at	-0.6
RING-H2 finger protein RHA3a, putative similar to RING-H2 finger protein RHA3a GI:3790573 from [Arabidopsis thaliana]; supported by cDNA:	260770_at	-0.6
mitochondrial NAD-dependent malate dehydrogenase identical to mitochondrial NAD-dependent malate dehydrogenase GI:3929649 from [Arabid	260615_at	-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	260520_at	-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	260222_at	-0.6
calmodulin-related protein similar to GB:P25070 from [Arabidopsis thaliana], contains Pfam profile: PF00036 EF hand (4 copies);supported by fu	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-le	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_AB013	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-len	259132_at	-0.6
putative 40S ribosomal protein S3A (S phase specific) similar to 40S ribosomal protein S3A (S phase specific protein GBIS289) GB:P49396 [Bras	259096_at	-0.6
putative ribose 5-phosphate isomerase identical to putative ribose 5-phosphate isomerase GB:AAD57010 (Arabidopsis thaliana); similar to ribos	259098_at	-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	258947_at	-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
shaggy related protein kinase, ASK-GAMMA identical to GB:P43289;supported by full-length cDNA: Ceres:17739.	258743_s_at	-0.6
unknown protein	258662_at	-0.6
putative long-chain-fatty-acid--CoA ligase similar to putative long-chain-fatty-acid--CoA ligase (brain isozyme) GB:P33124 [Rattus norvegicus]; su	258563_at	-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	258322_at	-0.6
putative phospholipase D similar to phospholipase D1 GB:AAC78487 [Brassica oleracea], GB:Q38882 [Arabidopsis thaliana]; supported by cDN	258226_at	-0.6
UDP-glucose:indole-3-acetate beta-D-glucosyltransferase, putative similar to UDP-glucose:indole-3-acetate beta-D-glucosyltransferase GB:AAB	258167_at	-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	258060_at	-0.6
expansin At-EXP5 identical to expansin At-EXP5 GB:AAB38071 from [Arabidopsis thaliana]; supported by cDNA: gi_1041703_gb_U30478.1_AT	258003_at	-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	257880_at	-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	257754_at	-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 [	257213_at	-0.6
t-complex polypeptide 1 homologue identical to t-complex polypeptide 1 homologue GB:D11351 [Arabidopsis thaliana]; supported by cDNA: gi_2	257125_at	-0.6
ER lumen retaining receptor (HDEL receptor), putative similar to GB:P35402 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:2	257104_at	-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_13	256865_at	-0.6
ADP-ribosylation factor, putative similar to ADP-ribosylation factor GB:P91924 [Dugesia japonica]; supported by full-length cDNA: Ceres: 24097.	256838_at	-0.6
serine/threonine protein phosphatase, putative similar to serine/threonine protein phosphatase GB:Z47076 GI:1143510 [Malus domestica]; suppo	256629_at	-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	256417_s_at	-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	256263_at	-0.6
hypothetical protein contains similarity to photosystem II 22 kDa protein GI:6006279 from [Arabidopsis thaliana];supported by full-length cDNA: C	255982_at	-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.	255735_at	-0.6

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
MAP kinase (ATMPK5) possible internal deletion at position 161, missing one A residue; reference GI:457401; supported by cDNA: gi_457401_	254924_at	-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
cytochrome P450 - like protein flavonoid 3 ,5 -hydroxylase Hf1, Petunia x hybrida, PIR2:S38985	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:219	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:JH0147supported 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_AF	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_g	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 cD	252413_at	-0.6
putative protein several hypothetical proteins	252329_at	-0.6
peroxidase ;supported by full-length cDNA: Ceres:39678.	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-isopropylmalate 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:3	248903_at	-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	246502_at	-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_14532	246307_at	-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:	246191_at	-0.6
cinnamyl-alcohol dehydrogenase - like protein cinnamyl-alcohol dehydrogenase, apple tree, PIR:T16995;supported by full-length cDNA: Ceres:6	246042_at	-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:	245757_at	-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.	245167_s_at	-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	249163_at	-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, -3r2-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>	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	266350_at	-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	265118_at	-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	264779_at	-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_1326	264506_at	-0.5
adenine phosphoribosyltransferase 1, APRT identical to GB:P31166; similar to ESTs gb|N65531, gb|R90631, gb|T21275, and gb|AA713070;sup	264439_at	-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	264203_at	-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 [Arabid	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_A	261492_at	-0.5

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	261230_at	-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 b	260988_at	-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)); sup	260726_at	-0.5
pyruvate kinase, plastid isozyme, putative similar to GB:Z28374 from [Nicotiana tabacum] (Plant Mol. Biol. 27 (1), 79-89 (1995)); supported by cD	260653_at	-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_AY059755.1	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:AAD539	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: g	259604_at	-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.	259358_at	-0.5
glyceraldehyde-3-phosphate dehydrogenase, putative similar to glyceraldehyde-3-phosphate dehydrogenase GI:21143 from (Sinapis alba); supp	259361_at	-0.5
allene oxide cyclase, putative similar to allene oxide cyclase GI:8977961 from [Lycopersicon esculentum]; supported by cDNA: gi_16323064_gb_	259366_at	-0.5
unknown protein similar to unknown protein GB:AAC42254 [Arabidopsis thaliana]	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	259140_at	-0.5
transport protein SEC13, putative similar to protein transport protein SEC13 GB:P53024 [Pichia pastoris];supported by full-length cDNA: Ceres:3	259119_at	-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_U	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 WD-repeat protein contains Pfam profile: PF00400 WD domain, G-beta repeat (7 copies)	258268_at	-0.5
transport protein, putative similar to transport protein GB:CAB10195 from [Arabidopsis thaliana]	258097_at	-0.5
MAP kinase kinase 5 identical to GB:BAA28831 from [Arabidopsis thaliana]; supported by cDNA: gi_3219272_dbj_AB015316.1_AB015316	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	257954_at	-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	256962_at	-0.5
20S proteasome subunit PAC1 identical to GB:AAC32057 from [Arabidopsis thaliana] (Genetics (1998) 149 (2), 677-692);supported by full-lengt	256795_at	-0.5
dTDP-glucose 4,6-dehydratase, putative similar to dTDP-glucose 4,6-dehydratase GB:AE000666 GI:6626257 from [Methanobacterium thermoa	256575_at	-0.5
amino acid permease, putative contains Pfam profile: PF00324 amino acid permease	256567_at	-0.5
putative clathrin heavy chain similar to clathrin heavy chain GB:AAC49294 [Glycine max]	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 cDN	256253_at	-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:	256033_at	-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_at	-0.5
phosphoprotein phosphatase 2A, regulatory subunit A identical to phosphoprotein phosphatase 2A, regulatory subunit A GI:1262171 from [Arabi	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:DMU	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 cDN	253810_at	-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;suppo	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	251744_at	-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-len	250916_at	-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	249493_at	-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	249343_at	-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_U	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
putative antifungal protein	257365_x_at	-0.5
putative hydroxymethyltransferase similar to serine hydroxymethyltransferage GB:P50433 from [Solanum tuberosum];supported by full-length cD	260126_at	-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	266885_at	-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	254776_at	-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_143349	249441_at	-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	log$_2$ fold supressed
putative protein basic leucine zipper transcription activator shoot-forming PKSF1 - Paulownia kawakamii, EMBL:AF046934;supported by fu	251575_at	-7.3
glycine-rich RNA-binding protein, putative similar to glycine-rich RNA-binding protein GI:17818 from [Brassica napus]	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.	263981_at	-5.7
GAST1-like protein similar to GAST1 protein precursor GB:P27057 [Lycopersicon esculentum] (induced by gibberellins, inhibited by ABA Pl	260221_at	-5.7
pEARLI 1 ; supported by cDNA: gi_871779_gb_L43080.1_ATHPEAR	254805_at	-5.7
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; sup	246932_at	-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_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-lengt	263153_s_at	-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||S72530);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	249923_at	-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	258054_at	-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
putative protein predicted proteins, Arabidopsis thaliana	247474_at	-3.7
DC1.2 homologue - like protein DC1.2 homologue, Nicotiana tabacum, EMBL:AB009888	247478_at	-3.7
hypothetical protein ;supported by full-length cDNA: Ceres:38891.	266805_at	-3.6
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. th	264195_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:125	260831_at	-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	257206_at	-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
auxin-induced protein, putative similar to SP:P33083 from [Glycine max];supported by full-length cDNA: Ceres:9311.	259783_at	-3.1
unknown protein very similar to unknown protein GB:AAC39468 from [Arabidopsis thaliana]; supported by cDNA: gi_14335087_gb_AY0372	258402_at	-3.1
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
auxin-induced protein-like	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; su	253066_at	-3
endo-xyloglucan transferase - like protein endo-xyloglucan transferase, Gossypium hirsutum, D88413;supported by full-length cDNA: Ceres	253040_at	-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
unknown protein	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	259786_at	-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	260037_at	-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	246011_at	-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|AI100245; 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
glutaredoxin	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
Expressed protein ; supported by full-length cDNA: Ceres: 27081.	263182_at	-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	-2.2
putative elicitor-responsive gene similar to elicitor-responsive gene-3 GB:AAC35866 from [Oryza sativa];supported by full-length cDNA: Cer	260083_at	-2.2
thaumatin-like protein (PR-5) similar to thaumatin GB:AAD55090 [Vitis riparia]; contains Pfam profile: PF00314 Thaumatin family; supported	259987_at	-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]; suppo	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	254239_at	-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

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	258222_at	-2
unknown 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_	253103_at	-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 (emb CAB79759.1)	247880_at	-2
putative protein hypothetical 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 phosphot	263236_at	-1.9
glucose transporter almost identical to glucose transporter GB:P23586 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 33	262456_at	-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	261825_at	-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_g	253050_at	-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_	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 (pir||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
putative two-component response regulator protein ; supported by cDNA: gi_11870067_gb_AF305721.1_AF305721	266078_at	-1.8
putative peroxidase ATP2a ;supported by full-length cDNA: Ceres:3571.	265471_at	-1.8
aquaporin (plasma membrane intrinsic protein 2C) water channel protein in plasma membrane;supported by full-length cDNA: Ceres:11998.	265444_s_at	-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:2246	261727_at	-1.8
delta 9 desaturase identical to delta 9 desaturase GB:BAA25180 GI:2970034 from [Arabidopsis thaliana]; supported by full-length cDNA: C	260957_at	-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), 9	256666_at	-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	258920_at	-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 (19	257769_at	-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	255941_at	-1.7
putative protein A. thaliana hypothetical protein F1N20.70, GenBank accession number AL022140;supported by full-length cDNA: Ceres:11	255285_at	-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 cD	245757_at	-1.7
hypothetical protein similar to putative disease resistance protein GB:AAC14512 GI:2739389 from [Arabidopsis thaliana];supported by full-le	245768_at	-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
hypothetical protein	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	264348_at	-1.6
unknown protein Strong similarity to gb|D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb|H37281,	264365_s_at	-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	262263_at	-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	260898_at	-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	259185_at	-1.6
carbonic anhydrase, chloroplast precursor identical to carbonic anhydrase, chloroplast precursor GB:P27140 [Arabidopsis thaliana]; suppor	259161_at	-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-lengtl	258947_at	-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	257315_at	-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	256526_at	-1.6
putative ribonucleoprotein similarity to ovarian RNA-binding protein and translational control factor (bruno)- Drosphila melanogaster,EMBL:	255411_at	-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	254105_at	-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	251422_at	-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 |C71410)	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	246294_at	-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	245925_at	-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	266746_s_at	-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_	264901_at	-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	264653_at	-1.5
putative mutT domain protein	263852_at	-1.5
putative auxin-induced protein, IAA17/AXR3-1 Identical to Arabidopsis gb|AF040632 and gb|U49073 IAA17/AXR3 gene. ESTs gb|H36782	263664_at	-1.5
unknown protein ; supported by cDNA: gi_6691164_gb_AF218765.1_AF218765	263498_at	-1.5
arginine decarboxylase identical to GP:1590814:U52851; supported by cDNA: gi_1590813_gb_U52851.1_ATU52851	263241_at	-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	262135_at	-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	260395_at	-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 cD	259925_at	-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	259364_at	-1.5
putative APG protein similar to anter-specific proline-rich protein APG precursor SP:P40602 (Arabidopsis thaliana); contains Pfam profile: P	259375_at	-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

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 sativus]; sup	258941_at	-1.5
putative pectin methylesterase similar to pectin methylesterase GB:Q42534 from [Arabidopsis thaliana];supported by full-length cDNA: 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] (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 thaliana]	254915_s_at	-1.5
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 cDNA: gi_	254132_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
putative protein mRNAs from Ricinus communis and Medicago sativa, Z81012 and L36159;supported by full-length cDNA: Ceres:37529.	253437_at	-1.5
putative thaumatin-like protein thaumatin-like protein precursor Mdtl1, pathogenesis-related - Malus domestica, PID:g3643249;supported by	252954_at	-1.5
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.	252322_at	-1.5
hypothetical protein	252251_at	-1.5
cyclin D3-like protein Nicotiana tabacum NtcycD3-1 - Nicotiana tabacum, EMBL:AB015222;supported by full-length cDNA: Ceres:36056.	252189_at	-1.5
nucleoid DNA-binding - like protein nucleoid DNA-binding protein cnd41, chloroplast, common tobacco, PIR:T01996; supported by full-lengt	251899_at	-1.5
putative protein unknown protein At2g44130 - Arabidopsis thaliana, EMBL:AC004005;supported by full-length cDNA: Ceres:8014.	251443_at	-1.5
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_AF370188.1_A	245750_at	-1.5
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.	267555_at	-1.4
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_4	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	256125_at	-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	254578_at	-1.4
photosystem II oxygen-evolving complex protein 3 - like photosystem II oxygen-evolving complex protein 3, Spinacia oleracea, PIR2:S0000	254398_at	-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
Histone H4 - like protein histone H4, Zea mays, PIR:HSZM4;supported by full-length cDNA: Ceres:22146.	252562_s_at	-1.4
hypothetical protein	252345_at	-1.4
putative protein GMFP7 isoprenylated protein, Glycine max., gb:AAD09515;supported by full-length cDNA: Ceres:250092.	252296_at	-1.4
putative protein polyphosphoinositide binding protein Ssh2 - Glycine max, PIR:T05953; supported by cDNA: gi_16930482_gb_AF419595.1	252080_at	-1.4
putative protein photosystem II oxygen evolving complex protein 2 precursor (psbP), Fritillariaagrestis, EMBL:AF037458;supported by full-l	251784_at	-1.4
glutaredoxin -like protein glutaredoxin, castor bean, PIR:S54825	251196_at	-1.4
2-cys peroxiredoxin-like protein ;supported by full-length cDNA: Ceres:15640.	250733_at	-1.4
putative protein predicted protein, Arabidopsis thaliana	250563_at	-1.4
putative protein similar to unknown protein (pir||T41692);supported by full-length cDNA: Ceres:31527.	250097_at	-1.4
plastid-specific ribosomal protein 6 precursor (Psrp-6) - like plastid-specific ribosomal protein 6 precursor (Psrp-6), Spinacia oleracea, EMB	250058_at	-1.4
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 (pir||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

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	267400_at	-1.3
putative ammonium transporter	267142_at	-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 ;supported by full-length cDNA: Ceres:1697.	265716_at	-1.3
putative alanine acetyl transferase	265725_at	-1.3
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	264926_at	-1.3
putative lipase Similar to nodulins and lipase; location of EST E6C2T7 , gb|AA042309. similar to nodulins gi|3328240, gi|2129854 and othe	264501_at	-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	264445_at	-1.3
putative glutathione S-transferase TSI-1 similar to glutathione S-transferase (sp|Q03666|GTX4_TOBAC); similar to EST gb|H36275; suppor	264435_at	-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	264264_at	-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 hyicus. ESTs gb|AI239406 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	261639_at	-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	260135_at	-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)	259801_at	-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	258368_at	-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:	258076_at	-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);supporte	257151_at	-1.3
Sm protein, putative similar to GB:AAB62189 from [Homo sapiens], contains Pfam profile: PF01423 Sm protein;supported by full-length cD	257001_at	-1.3

<table>
<tr><td>Expressed protein ; supported by full-length cDNA: Ceres: 38257.</td><td>256979_at</td><td>-1.3</td></tr>
<tr><td>unknown protein</td><td>256698_at</td><td>-1.3</td></tr>
<tr><td>unknown protein</td><td>256622_at</td><td>-1.3</td></tr>
<tr><td>unknown protein</td><td>256433_at</td><td>-1.3</td></tr>
<tr><td>RING zinc finger protein contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger)</td><td>256446_at</td><td>-1.3</td></tr>
<tr><td>unknown protein</td><td>256337_at</td><td>-1.3</td></tr>
<tr><td>high mobility group protein (HMG1), putative similar to high mobility group protein (HMG1) GI:436423 from [Pisum sativum]</td><td>256080_at</td><td>-1.3</td></tr>
<tr><td>PSI type II chlorophyll a/b-binding protein, putative similar to PSI type II chlorophyll a/b-binding protein GI:541565 from [Arabidopsis thalian</td><td>256015_at</td><td>-1.3</td></tr>
<tr><td>unknown protein ;supported by full-length cDNA: Ceres:12461.</td><td>255854_at</td><td>-1.3</td></tr>
<tr><td>putative NAM (no apical meristem)-like protein ; supported by cDNA: gi_15294215_gb_AF410299.1_AF410299</td><td>255794_at</td><td>-1.3</td></tr>
<tr><td>putative hypoersensitive response protein similar to N. tabacum hin1, GenBank accession number Y07563;supported by full-length cDNA:</td><td>255577_at</td><td>-1.3</td></tr>
<tr><td>Expressed protein ; supported by full-length cDNA: Ceres: 11649.</td><td>254761_at</td><td>-1.3</td></tr>
<tr><td>putative protein ; supported by cDNA: gi_14596204_gb_AY042890.1_</td><td>254705_at</td><td>-1.3</td></tr>
<tr><td>putative protein glycine/proline-rich protein GPRP, Arabidopsis thaliana, PIR2:S65780; supported by full-length cDNA: Ceres: 8188.</td><td>254559_at</td><td>-1.3</td></tr>
<tr><td>RNA-binding protein RNP-T precursor ; supported by cDNA: gi_15294253_gb_AF410318.1_AF410318</td><td>254126_at</td><td>-1.3</td></tr>
<tr><td>putative protein pectinesterase - Citrus sinensis, PID:g2098705</td><td>254110_at</td><td>-1.3</td></tr>
<tr><td>putative protein LEDI-3 protein, Lithospermum erythrorhizon</td><td>253909_at</td><td>-1.3</td></tr>
<tr><td>amidophosphoribosyltransferase 2 precursor</td><td>253252_at</td><td>-1.3</td></tr>
<tr><td>Expressed protein ; supported by full-length cDNA: Ceres: 17990.</td><td>253045_at</td><td>-1.3</td></tr>
<tr><td>putative protein</td><td>252603_at</td><td>-1.3</td></tr>
<tr><td>putative protein putative hydrolyse - Arabidopsis thaliana, PID:g4191785;supported by full-length cDNA: Ceres:262295.</td><td>252433_at</td><td>-1.3</td></tr>
<tr><td>syntaxin-like protein synt4 ;supported by full-length cDNA: Ceres:37248.</td><td>252053_at</td><td>-1.3</td></tr>
<tr><td>uracil phosphoribosyltransferase-like protein uracil phosphoribosyltransferase - Nicotiana tabacum, PIR:T03969;supported by full-length cD</td><td>251920_at</td><td>-1.3</td></tr>
<tr><td>putative protein 24 kDa seed maturation protein, Glycine max., EMBL:AF004806</td><td>251903_at</td><td>-1.3</td></tr>
<tr><td>ribosomal protein L17 -like protein ribosomal protein L17, chloroplast, Nicotiana tabacum, PIR:T01744;supported by full-length cDNA: Cere</td><td>251883_at</td><td>-1.3</td></tr>
<tr><td>responce reactor 4 ; supported by cDNA: gi_3273201_dbj_AB010918.1_AB010918</td><td>251665_at</td><td>-1.3</td></tr>
<tr><td>putative protein hypothetical protein 238 - Porphyra purpurea, PIR:S73123</td><td>251519_at</td><td>-1.3</td></tr>
<tr><td>putative protein multisynthetase complex auxiliary component p43 - Cricetulus griseus, EMBL:AF021800;supported by full-length cDNA: Ce</td><td>251442_at</td><td>-1.3</td></tr>
<tr><td>Expressed protein ; supported by full-length cDNA: Ceres: 17055.</td><td>251446_at</td><td>-1.3</td></tr>
<tr><td>mRNA binding protein precursor - like mRNA binding protein precursor (chloroplast protein), Lycopersicon esculentum, EMBL:AF106660; s</td><td>251157_at</td><td>-1.3</td></tr>
<tr><td>putative protein predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:263168.</td><td>250398_at</td><td>-1.3</td></tr>
<tr><td>putative protein</td><td>250075_at</td><td>-1.3</td></tr>
<tr><td>putative protein similar to unknown protein (gb|AAD25141.1);supported by full-length cDNA: Ceres:33455.</td><td>248419_at</td><td>-1.3</td></tr>
<tr><td>putative protein similar to unknown protein (emb|CAA71173.1)</td><td>248322_at</td><td>-1.3</td></tr>
<tr><td>putative protein similar to unknown protein (pir |S77462); supported by cDNA: gi_15081647_gb_AY048216.1_</td><td>248287_at</td><td>-1.3</td></tr>
<tr><td>putative protein contains similarity to MYB family transcription factor</td><td>248246_at</td><td>-1.3</td></tr>
<tr><td>unknown protein ;supported by full-length cDNA: Ceres:4309.</td><td>248062_at</td><td>-1.3</td></tr>
<tr><td>unknown protein</td><td>248050_at</td><td>-1.3</td></tr>
<tr><td>putative protein non-consensus CG donor splice site at exon 1, GA donor splice site at exon 3, similar to unknown protein (pir||T04268);sup</td><td>247933_at</td><td>-1.3</td></tr>
<tr><td>putative protein similar to unknown protein (pir||T04254); supported by cDNA: gi_13937150_gb_AF372929.1_AF372929</td><td>247946_at</td><td>-1.3</td></tr>
<tr><td>TCH4 protein (gb|AAA92363.1) ; supported by cDNA: gi_14194112_gb_AF367262.1_AF367262</td><td>247925_at</td><td>-1.3</td></tr>
<tr><td>copper transport protein</td><td>247745_at</td><td>-1.3</td></tr>
<tr><td>ethylene responsive element binding factor - like ethylene responsive element binding factor 5, Arabidopsis thaliana, SWISSPROT:ERF5_</td><td>247540_at</td><td>-1.3</td></tr>
<tr><td>putative protein predicted proteins, Arabidopsis thaliana</td><td>247394_at</td><td>-1.3</td></tr>
<tr><td>putative protein predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_13877822_gb_AF370174.1_AF370174</td><td>247407_at</td><td>-1.3</td></tr>
<tr><td>putative protein strong similarity to unknown protein (emb|CAB76911.1)</td><td>247362_at</td><td>-1.3</td></tr>
<tr><td>unknown protein ; supported by full-length cDNA: Ceres: 25655.</td><td>247213_at</td><td>-1.3</td></tr>
<tr><td>histone H3 (sp|P05203) ; supported by cDNA: gi_13926210_gb_AF370577.1_AF370577</td><td>247192_at</td><td>-1.3</td></tr>
<tr><td>putative protein</td><td>246644_at</td><td>-1.3</td></tr>
<tr><td>auxin-induced basic helix-loop-helix transcription factor, putative similar to auxin-induced basic helix-loop-helix transcription factor GI:5731</td><td>246398_at</td><td>-1.3</td></tr>
<tr><td>putative protein ; supported by full-length cDNA: Ceres: 123997.</td><td>246275_at</td><td>-1.3</td></tr>
<tr><td>phospholipase - like protein various predicted phospholipase proteins;supported by full-length cDNA: Ceres:253499.</td><td>246041_at</td><td>-1.3</td></tr>
<tr><td>hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:124269.</td><td>245840_at</td><td>-1.3</td></tr>
</table>

endoxyloglucan transferase, putative similar to endoxyloglucan transferase GB:AAD45125 GI:5533313 from [Arabidopsis thaliana]; support	245794_at	-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	257413_at	-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	262951_at	-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 c	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	260006_at	-1.2
unknown protein ;supported by full-length cDNA: Ceres:34166.	259856_at	-1.2
unknown protein similar to GB:AAD41433;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 protein predicted by genemark.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 Pfam HMM hit: FKBP-type peptidyl-prolyl cis-trans isomerases	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	257651_at	-1.2
hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:35773.	257600_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_g	256578_at	-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	256058_at	-1.2
ribosomal protein, putative similar to ribosomal protein L35a GI:57118 from [Rattus norvegicus]; supported by full-length cDNA: Ceres: 277	256065_at	-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.	255786_at	-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 tabac	255046_at	-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	253510_at	-1.2
Expressed protein ; supported by full-length cDNA: Ceres: 39326.	253384_at	-1.2
putative protein hydroxyproline-rich glycoprotein precursor, Nicotiana tabacum, PIR2:S06733; supported by cDNA: gi_15724315_gb_AF41	253284_at	-1.2
ras-related small GTP-binding protein ras-related small GTP-binding protein Rho1Ps, garden pea, Pir2:A47525;supported by full-length cD	253118_at	-1.2
putative protein ;supported by full-length cDNA: Ceres:37341.	252876_at	-1.2
hypothetical protein ;supported by full-length cDNA: Ceres:123060.	252852_at	-1.2
hypothetical protein	252612_at	-1.2
histone H2B ;supported by full-length cDNA: Ceres:32930.	252561_at	-1.2
putative protein several oxidases, mainly gibberellin 20-oxidases	252529_at	-1.2
putative protein DCL PROTEIN, CHLOROPLAST PRECURSOR (DEFECTIVE CHLOROPLASTS AND LEAVES PROTEIN) - Lycopersicon	252481_at	-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	252409_at	-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 hypothetical protein At2g46330 - Arabidopsis thaliana, EMBL:AC006526;supported by full-length cDNA: Ceres:11394.	251281_at	-1.2
putative protein polygalacturonase - Lycopersicon esculentum, EMBL:AF118567; supported by cDNA: gi_13358184_gb_AF324992.2_AF3	251261_at	-1.2
cytochrome c oxidase subunit 5c-like protein cytochrome c oxidase subunit 5c - Oryza sativa, EMBL:AB027123;supported by full-length cD	251220_at	-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
histone H3 - like protein histone 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 (sp|P50027);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
putative protein similar to unknown protein (pir||T04427)	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	247541_at	-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 membe	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_g	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	262196_at	-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
pectinesterase, putative similar to pectinesterase GI:1944574 from [Lycopersicon esculentum]; supported by cDNA: gi_15982770_gb_AY0	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 b	259707_at	-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	259511_at	-1.1
unknown protein	259434_at	-1.1
unknown protein similar to unknown protein GB:AAC62613 [Arabidopsis thaliana]; supported by cDNA: gi_14532567_gb_AY039908.1_	259018_at	-1.1
putative dehydrogenase contains Pfam profiles: PF00106 short chain dehydrogenase, PF00678 short chain dehydrogenase reductase C-t	258976_at	-1.1
germin-like protein similar to germin type 2 GB:S71254 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:19265.	258938_at	-1.1
putative disease resistance protein similar to disease resistance protein RPP1-WsC GB:AAC72979 [Arabidopsis thaliana]; supported by cD	258537_at	-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.	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_	256228_at	-1.1
sterol-C-methyltransferase identical to sterol-C-methyltransferase GI:1061040 from [Arabidopsis thaliana];supported by full-length cDNA: C	255885_at	-1.1
unknown protein ;supported by full-length cDNA: Ceres:108615.	255908_s_at	-1.1
hypothetical protein predicted 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

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	255779_at	-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	254763_at	-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	254669_at	-1.1
fatty acid hydroxylase - like protein fatty acid hydroxylase Fah1p, Arabidopsis thaliana, PID:g2736147; supported by cDNA: gi_14994242_g	254448_at	-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_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	252851_at	-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	252132_at	-1.1
hypothetical protein hypothetical protein - Arabidopsis thaliana chromosome 4 AP2 contig, PID:e353223;supported by full-length cDNA: Ce	252133_at	-1.1
40S ribosomal protein S21 homolog ribosomal protein S21, cytosolic - Oryza sativa, PIR:S38357;supported by full-length cDNA: Ceres:268	251921_at	-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	251796_at	-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
putative protein hypothetical proteins - Arabidopsis thaliana	251241_s_at	-1.1
putative protein chloroplast ribosome recycling factor protein - Spinacia oleracea, EMBL:AJ133751; supported by cDNA: gi_13926251_gb_	251172_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_A	250517_at	-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	250439_at	-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	250278_at	-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_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, dbj|AV531372.1, dbj|AV5278	245195_at	-1.1
ribosomal protein S16	245049_at	-1.1
hypothetical protein	245019_at	-1.1
hypothetical protein	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 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
acyl carrier protein identical to GB:L23574; supported by cDNA: gi_15450374_gb_AY052288.1_	266890_at	-1
40S ribosomal protein S15A	266684_at	-1
profilin 1 ; supported by cDNA: gi_1353769_gb_U43325.1_ATU43325	266701_at	-1
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 ubiquinol--cytochrome-c reductase Similar to gb|X79273 cytochrome c reductase hinge protein subunit from Solanum tuberosum. E	262593_at	-1
unknown protein Contains a PF|00175 Oxidoreductase FAD/NADH-binding domain. ESTs gb|H76345 and gb|AA651465 come from this ger	262572_at	-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	262374_s_at	-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 GI: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_	261443_at	-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));s	261165_at	-1
unknown protein identical to SP:O50061 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 protein 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
hypothetical protein predicted by genefinder	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:	260370_at	-1
putative dolichyl-phosphate mannosyltransferase polypeptide 2 similar to dolichyl-phosphate mannosyltransferase polypeptide 2 GB:45033	260257_at	-1
putative histone H2A similar to histone H2A GB:CAA73155 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres: 10668.	260154_at	-1

inner mitochondrial membrane protein identical to inner mitochondrial membrane protein GB:U18126 [Arabidopsis thaliana];supported by ful	259890_at	-1
photosystem I subunit VI precursor identical to photosystem I subunit VI precursor [Arabidopsis thaliana] GI:5734524;supported by full-lengt	259840_at	-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	259237_at	-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	258857_at	-1
putative wound-induced basic protein similar to wound-induced basic protein GB:Q09020 [Phaseolus vulgaris] (Plant Physiol. 101 (4), 1409	258821_at	-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 c	256458_at	-1
guanine nucleotide-binding protein, putative similar to guanine nucleotide-binding protein GI:9294068 from [Arabidopsis thaliana]; supporte	256144_at	-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.	255850_at	-1
unknown protein similar to unknown protein GI:6714347 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:103226.	255733_at	-1
Expressed protein ; supported by cDNA: gi_4741922_gb_AF130849.1_AF130849	255511_at	-1
putative protein disulfide isomerase	255061_at	-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
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	254083_at	-1
putative ribosomal protein S10 40S ribosomal protein S10 - Lumbricus rubellus, PID:e1329701; supported by cDNA: gi_14334535_gb_AY0	254049_at	-1
putative ribosomal protein ribosomal protein L31, Nicotiana glutinosa, U23784;supported by full-length cDNA: Ceres:14013.	254012_at	-1
fructose-bisphosphate aldolase - like protein fructose-bisphosphate aldolase, Arabidopsis thaliana, PIR1:ADMU;supported by full-length cD	253971_at	-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
putative 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:I46078	253256_at	-1
Expressed protein ; 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

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_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 At2g44600 - 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 AT4g29780 (F27B13.20) - Arabidopsis thaliana, EMBL:AL050352; supported by cDNA: gi_13878074_	251173_at	-1
putative protein	250942_at	-1
leucoanthocyanidin dioxygenase-like protein ;supported by full-length cDNA: Ceres:13012.	250793_at	-1
putative protein similar to unknown protein (gb|AAD23015.1)	250682_x_at	-1
putative protein similar to unknown protein (pir||T14195)	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	250371_at	-1
putative protein predicted proteins, Arabidopsis thaliana	250265_at	-1
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	250190_at	-1
high affinity nitrate transporter - like protein high affinity nitrate transporter, Oryza sativa, EMBL:AB008519; supported by cDNA: gi_143347	250151_at	-1
putative protein predicted protein, Arabidopsis thaliana	249919_at	-1
unknown protein	249929_at	-1
unknown protein	249932_at	-1
ATP-dependent Clp protease proteolytic subunit (ClpP2), putative similar to SP:Q9X6W8 ATP-dependent Clp protease proteolytic subunit (	249873_at	-1
squalene monooxygenase 1,2 (squalene epoxidase 1,2) (se 1,2) (sp|O65402)	249775_at	-1
unknown protein	249776_at	-1
acyltransferase -like protein Anthocyanin 5-aromatic acyltransferase, Gentiana triflora, EMBL:AB010708;supported by full-length cDNA: Ce	249493_at	-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	247188_at	-1
homeobox-leucine zipper protein ATHB-5 (HD-zip protein ATHB-5) (sp|P46667) ; supported by cDNA: gi_13358240_gb_AF325054.2_AF32	247191_at	-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.	246506_at	-1
minor allergen ;supported by full-length cDNA: Ceres:35084.	246201_at	-1
lipophosphoglycan biosynthetic protein - like lipophosphoglycan biosynthetic protein (LPG2), Leishmania donovani, TREMBL:LD26175	246143_at	-1
putative protein predicted proteins from various species; supported by full-length cDNA: Ceres: 17786.	246156_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 predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:19897.	246000_at	-1
putative protein 22kDa peroxisomal membrane protein-like - Homo sapiens, EMBL:AF250136;supported by full-length cDNA: Ceres:6789.	245937_at	-1
putative protein predicted protein At2g25260 - Arabidopsis thaliana, EMBL:AC007070;supported by full-length cDNA: Ceres:6674.	245853_at	-1
hypothetical protein predicted by genscan+; supported by cDNA: gi_16323183_gb_AY057696.1_	245776_at	-1
disease resistance RPP5 like protein (fragment)	245450_at	-1
hypothetical protein	245414_at	-1
Expressed protein ; supported by full-length cDNA: Ceres: 7101.	245337_at	-1
cytochrome f	245020_at	-1
hypothetical protein predicted by genfinder	267586_at	-0.9
hypothetical protein predicted by genefinder and genscan;supported by full-length cDNA: Ceres:23742.	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_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	265451_at	-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_	264820_at	-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
unknown protein similar to EST gb|AA650671 and gb|T20610	264488_s_at	-0.9
postsynaptic protein CRIPT, putative similar to postsynaptic protein CRIPT GI:3098551 from [Rattus norvegicus]; supported by full-length c	264399_at	-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	264315_at	-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
unknown protein ;supported by full-length cDNA: Ceres:5198.	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	262729_at	-0.9
hypothetical protein Strong similarity to gi|4734005 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 threonine kinase, putative similar to GB:CAA73067 from (Sorghum bicolor) (Plant Mol. Biol. 36 (4), 529-539 (1998)); supported by c	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	262028_at	-0.9
J8-like protein similar to DnaJ 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 c	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	261108_at	-0.9
phosphatidylinositol-4-phosphate 5-kinase, putative similar to phosphatidylinositol-4-phosphate 5-kinase GB:CAB53377 GI:5777366 from [	260855_at	-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	-0.9
flower development protein cycloidea (cyc3), putative similar to flower development protein cycloidea (cyc3) GI:6358611 from [Misopates o	260618_at	-0.9
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

unknown protein	260460_at	-0.9
hypothetical protein predicted by genscan+, similar to adenosine kinase (EC 2.7.1.20) GB:S52758 from [Leishmania donovani];supported b	260388_at	-0.9
unknown protein similar to putative protein GB:CAA20468 [Arabidopsis thaliana]	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:5360221; supported by full-length cDNA: C	259593_at	-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	259239_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: C	259193_at	-0.9
unknown protein similar to hypothetical protein GB:AAD27575 [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: 2Fe-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	258858_at	-0.9
putative ubiquinol-cytochrome C reductase complex ubiquinone-binding protein (QP-C) similar to ubiquinol-cytochrome C reductase comple	258772_at	-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: gi_13605546_gb_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	258284_at	-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_AY0372	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:	256129_at	-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

scarecrow-like 6 (SCL6)	255698_at	-0.9
putative DNA-binding protein similar to wild oat DNA-binding protein ABF2, GenBank accession number Z48431	255596_at	-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 (vag2 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:	254074_at	-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	253436_at	-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.	251993_at	-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	251483_at	-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_at	-0.9
putative protein similar to unknown protein (pir||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-glucanase-like protein	249214_at	-0.9
Cys2/His2-type zinc finger protein 3 (dbj|BAA85109.1) ;supported by full-length cDNA: Ceres:9878.	249139_at	-0.9
putative protein contains similarity to unknown protein (gb|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) (sp|P34881) ; supported by cDNA: gi_304106_gb_L10692.1_	248597_at	-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	247654_at	-0.9
zinc finger protein Zat12 ;supported by full-length cDNA: Ceres:40576.	247655_at	-0.9
zinc finger protein - 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	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	246862_at	-0.9
putative protein predicted protein, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 108472.	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	-0.9
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 full-length	246070_at	-0.9
NAM-like protein hypothetical protein SENU5, senescence up-regulated - Lycopersicon esculentum, EMBL:Z75524; supported by cDNA: gi	245987_at	-0.9
defender against cell death protein, putative similar to defender against cell death protein GB:AAC36169 GI:3608136 from [Arabidopsis tha	245791_at	-0.9
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
unknown protein ; supported by cDNA: gi_15081683_gb_AY048234.1_	266521_at	-0.8
hypothetical protein predicted by genefinder	266545_at	-0.8
unknown protein ; supported by cDNA: gi_13605586_gb_AF361619.1_AF361619	266551_at	-0.8
unknown protein	266512_at	-0.8
glutathione S-transferase (GST6) identical to GB:X95295. Based on identical cDNA hits, the translation is now 40 AAs longer at the N-termi	266461_at	-0.8
unknown protein ; supported by cDNA: gi_16649150_gb_AY059945.1_	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 genscan;supported 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];supported by f	264986_at	-0.8
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 this gene;s	264651_at	-0.8
unknown protein Similar to Glycine SRC2 (gb|AB000130). ESTs gb|H76869,gb|T21700,gb|ATTS5089 come from this gene; supported by c	264655_at	-0.8
hypothetical protein Contains similarity to Rattus AMP-activated protein kinase (gb|X95577); supported by cDNA: gi_9965728_gb_AF25033	264625_at	-0.8
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|Z17491;suppo	264462_at	-0.8
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	264042_at	-0.8

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 f	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_at	-0.8
unknown protein identical to residues 1 to 141 of unknown protein GB:AAD55491 (Arabidopsis thaliana)	262288_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	261751_at	-0.8
acidic ribosomal protein, putative similar to 60S ACIDIC RIBOSOMAL PROTEIN P1 GB:O23095 from [Arabidopsis thaliana];supported by fu	261578_at	-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	261408_s_at	-0.8
ribosomal protein S15 identical to GB:AAA61608 from [Arabidopsis thaliana] (Plant Physiol. 106 (1), 401-402 (1994)); supported by full-leng	261416_at	-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_	261193_at	-0.8
ornithine carbamoyltransferase precursor identical to SP:O50039 from [Arabidopsis thaliana]; supported by cDNA: gi_2764517_emb_AJ000	261122_at	-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
unknown protein contains similarity to calcium-binding protein GB:CAB63264 GI:6580549 from [Lotus japonicus]; supported by cDNA: gi_13	260881_at	-0.8
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	260726_at	-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_at	-0.8
unknown protein contains Pfam profile: PF00106 short chain dehydrogenase	258467_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	258151_at	-0.8
expansin At-EXP5 identical to expansin At-EXP5 GB:AAB38071 from [Arabidopsis thaliana]; supported by cDNA: gi_1041703_gb_U30478.	258003_at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:41112.	257966_at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:270508.	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.	257214_at	-0.8
cytochrome c, putative similar to cytochrome c1 GB:S66866 from [Solanum tuberosum];supported by full-length cDNA: Ceres:41320.	257148_at	-0.8
non-race specific disease resistance protein, putative contains non-consensus CT donor splice site at exon 1; potential pseudogene; simila	257083_s_at	-0.8
ribosomal protein L27, putative similar to 60S RIBOSOMAL PROTEIN L27 GB:P41101 from [Solanum tuberosum];supported by full-length	256794_at	-0.8
unknown protein ;supported by full-length cDNA: Ceres:8544.	256785_at	-0.8
glutamyl-tRNA amidotransferase subunit A, putative similar to GB:P73558 from [Synechocystis PCC6803] (DNA Res. 3 (3), 109-136 (1996	256728_at	-0.8
ribosomal protein L41 identical to ribosomal protein L41 GB:AAA79268 [Pisum sativum]	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	255942_at	-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	255899_at	-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

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
acid phosphatase-like protein acid phosphatase-1 (EC 3.1.3.-) - Lycopersicon esculentum,PIR2:T06587; supported by cDNA: gi_1529302	253731_at	-0.8
Expressed protein ; supported by full-length cDNA: Ceres: 26443.	253694_at	-0.8
putative protein ; supported by full-length cDNA: Ceres: 23017.	253537_at	-0.8
Expressed protein ; supported by cDNA: gi_13926316_gb_AF372908.1_AF372908	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.	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.	253272_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	253006_at	-0.8
putative protein phosphatase-2c protein phosphatase-2c (PP2C) - Mesembryanthemum crystallinum, PID:g3608412	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;supp	252130_at	-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
mandelonitrile lyase-like protein ADHESION OF CALYX EDGES (ACE) - Arabidopsis thaliana; supported by cDNA: gi_15982754_gb_AY05	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_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 c	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_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.	248747_at	-0.8
60S ribosomal protein L13a ;supported by full-length cDNA: Ceres:4275.	248655_at	-0.8
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
unknown protein ; supported by full-length cDNA: Ceres: 106913.	248219_at	-0.8
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_15294	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	246538_at	-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	246427_at	-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 Caenorhabditis elegans	246015_at	-0.8
putative protein predicted protein, Arabidopsis thaliana;supported by full-length cDNA: Ceres:29453.	245999_at	-0.8
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:31356.	245747_at	-0.8
phosphate/phosphoenolpyruvate translocator - like protein ;supported by full-length cDNA: Ceres:100777.	245698_at	-0.8
ribosomal protein ;supported by full-length cDNA: Ceres:15384.	245372_at	-0.8
elicitor like protein ; supported by full-length cDNA: Ceres: 1718.	245340_at	-0.8
hypothetical protein ;supported by full-length cDNA: Ceres:17977.	245310_at	-0.8
hypothetical protein ;supported by full-length cDNA: Ceres:25991.	245316_at	-0.8
hypothetical protein ;supported by full-length cDNA: Ceres:40736.	245331_at	-0.8
hypothetical protein ; supported by cDNA: gi_15451033_gb_AY054597.1_	245297_at	-0.8
tubulin alpha-6 chain (TUA6) ; supported by cDNA: gi_16226461_gb_AF428406.1_AF428406	245270_at	-0.8
putative protein similarity to predicted proteins, Arabidopsis thaliana	245155_at	-0.8
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:33364.	245042_at	-0.8
ribosomal protein S18	244969_at	-0.8
NADH dehydrogenase subunit 3 Protein sequence is in conflict with the conceptual translation	244920_s_at	-0.8
hypothetical protein predicted by genemark.hmm, contains Pfam profile:PF00320 GATA:GATA zinc finger	257571_at	-0.8
putative cellulose synthase	267115_s_at	-0.8
putative non-LTR retrolelement reverse transcriptase	263086_at	-0.8
phosphoribosyl diphosphate synthase identical to phosphoribosyl diphosphate synthase GI:4902470 from (Arabidopsis thaliana); supported	262762_at	-0.8
hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:107869.	256222_at	-0.8
hypothetical protein	251676_at	-0.8
hypothetical protein	245495_at	-0.8
unknown protein ; supported by full-length cDNA: Ceres: 28982.	267638_at	-0.7
unknown protein ; supported by full-length cDNA: Ceres: 9990.	267510_at	-0.7
putative glycerate dehydrogenase ; supported by cDNA: gi_15724345_gb_AF412113.1_AF412113	267514_at	-0.7
auxin response transcription factor 3 (ETTIN/ARF3) identical to GB:AF007788; supported by cDNA: gi_12484198_gb_AF336917.1_AF3369	267452_at	-0.7
unknown protein ; supported by cDNA: gi_13899086_gb_AF370538.1_AF370538	267379_at	-0.7
unknown protein	267348_at	-0.7
unknown protein	267323_at	-0.7
hypothetical protein predicted by genscan and genefinder;supported by full-length cDNA: Ceres:20125.	267294_at	-0.7
putative acetone-cyanohydrin lyase	267126_s_at	-0.7
putative acetyltransferase	267145_at	-0.7
unknown protein	267055_at	-0.7
60S ribosomal protein L35 ;supported by full-length cDNA: Ceres:11583.	266980_at	-0.7
60S ribosomal protein L23A identical to GB:AF034694;supported by full-length cDNA: Ceres:22479.	266981_at	-0.7
unknown protein ; supported by full-length cDNA: Ceres: 10164.	266789_at	-0.7
ribonuclease, RNS1 identical to ribonuclease SP:P42813, GI:561998 from [Arabidopsis thaliana]; supported by full-length cDNA: Ceres:272	266743_at	-0.7
hypothetical protein predicted by grail	266678_at	-0.7
glycine decarboxylase complex H-protein identical to GB:U27144;supported by full-length cDNA: Ceres:24194.	266636_at	-0.7
putative glutaredoxin ;supported by full-length cDNA: Ceres:21006.	266516_at	-0.7
unknown protein	266445_at	-0.7
protease inhibitor II ; supported by cDNA: gi_15293090_gb_AY050979.1_	266118_at	-0.7
putative small nuclear ribonucleoprotein E ;supported by full-length cDNA: Ceres:24619.	266074_at	-0.7
predicted protein	266012_s_at	-0.7
putative ribose 5-phosphate isomerase ; supported by cDNA: gi_15809809_gb_AY054172.1_	265742_at	-0.7
putative replication protein A1 ;supported by full-length cDNA: Ceres:7536.	265695_at	-0.7
hypothetical protein predicted by genefinder	265426_at	-0.7
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:15103.	265442_at	-0.7
E2, ubiquitin-conjugating enzyme, putative ;supported by full-length cDNA: Ceres:27679.	265357_at	-0.7
hypothetical protein predicted by genscan;supported by full-length cDNA: Ceres:4845.	265333_at	-0.7
putative ribosomal protein L6 ; supported by full-length cDNA: Ceres: 692.	265338_at	-0.7
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 Z98597 from S. pombe. ESTs gb|T45575 and	265041_at	-0.7

hypothetical protein predicted by genefinder; supported by cDNA: gi_15028340_gb_AY045973.1_	265028_at	-0.7
putative protein hypothetical proteins - Arabidopsis thaliana	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	264845_at	-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, gi|17682 (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	263131_at	-0.7
60s ribosomal protein l27a. similar to 60S RIBOSOMAL PROTEIN L27A GB:P49637 GI:1710530 from [Arabidopsis thaliana];supported by f	262985_s_at	-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 obtusifoliol 14-alpha demethylase strong similarity to gb|U74319 obtusifoliol 14-alpha demethylase (CYP51) from Sorghum bicolor	262820_at	-0.7
thioredoxin, putative similar to thioredoxin GI:142153 from [Synechococcus PCC6301]	262721_at	-0.7
calmodulin, putative similar to calmodulin-6 SP:Q03509 [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
hypothetical protein contains similarity to disulphide isomerase GI:4581959 from [Caenorhabditis briggsae]; supported by cDNA: gi_166490	262413_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 cD	262234_at	-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
unknown protein	261843_at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 40238.	261756_at	-0.7
unknown protein ; supported by full-length cDNA: Ceres: 20257.	261723_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
hypothetical protein identical to hypothetical protein GB:AAF19740 GI:6634732 from [Arabidopsis thaliana];supported by full-length cDNA: C	261738_s_at	-0.7
unknown protein similar to putative esterase GB:AAD17422 GI:4335745 from [Arabidopsis thaliana;supported by full-length cDNA: Ceres:12	261608_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	261489_at	-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
unknown protein ; supported by full-length cDNA: Ceres: 11793.	260767_s_at	-0.7
hypothetical protein predicted by genemark.hmm	260715_at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 252174.	260707_s_at	-0.7
unknown protein	260281_at	-0.7
putative heat shock protein similar to GrpE protein from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:40701.	260125_at	-0.7
unknown protein ;supported by full-length cDNA: Ceres:151718.	260106_at	-0.7
unknown protein ;supported by full-length cDNA: Ceres:33367.	259955_s_at	-0.7
Expressed protein ; supported by full-length cDNA: Ceres: 253509.	259933_at	-0.7
predicted protein	259738_at	-0.7
putative ribose 5-phosphate isomerase similar to ribose 5-phosphate isomerase GB:6677767 from [Mus musculus];supported by full-length	259749_at	-0.7
putative isoprenylated protein similar to ATFP7 GB:AAD09511;supported by full-length cDNA: Ceres:39127.	259753_at	-0.7
unknown protein similar to phosphate translocators: glucose-6-phosphate/phosphate-translocator precursor GB:AAC08524 [Zea mays], ph	259713_at	-0.7
unknown protein ;supported by full-length cDNA: Ceres:17287.	259267_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
putative ribosomal protein s19 or s24 similar to ribosomal protein S19 GB:445612 [Solanum tuberosum] and similar to ribosomal protein S2	259090_at	-0.7
putative glucan endo-1-3-beta-glucosidase similar to glucan endo-1-3-beta-glucosidase precursor GB:P52409 [Triticum aestivum];supporte	259014_at	-0.7
putative chlorophyll a/b-binding protein similar to chlorophyll a/b-binding protein (CP29) GB:S33443 [Arabidopsis thaliana], identical to Lhcb	258993_at	-0.7
putative syntaxin contains Pfam profile: PF00804 syntaxin;supported by full-length cDNA: Ceres:38899.	258786_at	-0.7
ethylene-responsive protein, putative similar to ER6 protein GB:AAD46412 GI:5669654 from (Lycopersicon esculentum); supported by full-	258727_at	-0.7
unknown protein similar to putative protein GB:BAA84809 from [Oryza sativa]	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); supp	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	257225_s_at	-0.7
putative glucosyltransferase similar to UDP-glucose glucosyltransferase GB:X77459 [Manihot esculenta], UDP-glycose:flavonoid glycosyltr	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	256890_at	-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: 2	256838_at	-0.7
omega-3 fatty acid desaturase, chloroplast precursor identical to omega-3 fatty acid desaturase, chloroplast precursor SP:P46310 (Arabido	256417_s_at	-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

unknown protein	256286_at	-0.7
unknown protein ; supported by cDNA: gi_15450991_gb_AY054576.1_	256267_at	-0.7
unknown protein ;supported by full-length cDNA: Ceres:13451.	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]; s	255926_at	-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-	255734_at	-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
cytochrome P450 - like protein flavonoid 3 ,5 -hydroxylase Hf1, Petunia x hybrida, PIR2:S38985	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
putative protein storage protein - Populus deltoides, PIR2:S31580;supported by full-length cDNA: Ceres:8772.	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
ribosomal protein S29 - like ribosomal protein S29, rat, PIR:S30298;supported by full-length cDNA: Ceres:2749.	252693_s_at	-0.7
CCR4-associated factor 1-like protein CAF1_MOUSE CCR4-ASSOCIATED FACTOR 1 - Mus musculus, SWISSPROT:CAF1_MOUSE; su	252679_at	-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	251320_at	-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_	251155_at	-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	251018_at	-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	250862_s_at	-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	247708_at	-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 Ia (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 predicted 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
putative protein ;supported by full-length cDNA: Ceres:9667.	246441_at	-0.7
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
similar to SOR1 from the fungus Cercospora nicotianae	267138_s_at	-0.6

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>	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 GP|AF078823; 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	264371_at	-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, g	264203_at	-0.6
putative nitrilase-associated 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
unknown protein	263750_at	-0.6
unknown protein ; supported by cDNA: gi_13265530_gb_AF324701.2_AF324701	263760_at	-0.6
nucleic acid-binding protein, putative similar to nucleic acid-binding protein GI:168525 from [Zea mays];supported by full-length cDNA: Cere	263736_at	-0.6
ribonuclease, RNS3 identical to ribonuclease SP:P42815, GI:562000 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:962	263689_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:14886.	263710_at	-0.6
unknown protein ; supported by full-length cDNA: Ceres: 97914.	263541_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:74.	263396_at	-0.6
putative C2H2-type zinc finger protein likely a nucleic acid binding protein	263411_at	-0.6
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	262966_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	262703_at	-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	262632_at	-0.6
putative 20S proteasome beta subunit PBC2 almost identical to GB:AAC32069 from [Arabidopsis thaliana], EST gb|T76747 comes from thi	262497_at	-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 c	262174_at	-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
ribosomal protein identical to GB:CAB81600 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:1097.	261362_s_at	-0.6
AP2 domain containing protein, putative similar to AP2 domain containing protein RAP2.5 GI:2281635 from (Arabidopsis thaliana); support	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 fro	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 c	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_AY0487	260141_at	-0.6
putative transcription factor BTF3 (RNA polymerase B transcription factor 3) similar to transcription factor BTF3 (RNA polymerase B transcr	260095_at	-0.6
putative calmodulin similar to calmodulin GB:P02596 [Renilla reniformis]; contains Pfam profile: PF00036 EF hand (4 copies);supported by	260076_at	-0.6
hypothetical protein predicted by genefinder;supported by full-length cDNA: Ceres:28316.	260078_at	-0.6
plasma membrane associated protein, putative similar to GI:6851373 from [Hordeum vulgare]	259774_at	-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	259196_at	-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]; sup	259100_at	-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 [Arabidopsi	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. Bi	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

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	257753_at	-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	257141_at	-0.6
ER lumen retaining receptor (HDEL receptor), putative similar to GB:P35402 from [Arabidopsis thaliana];supported by full-length cDNA: Cer	257104_at	-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-ubiquinone dehydrogenase 24 kD subunit precursor, GenBank a	255442_at	-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	255131_at	-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
shaggy-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	254159_at	-0.6
tryptophan synthase beta-subunit (TSB2) ;supported by full-length cDNA: Ceres:104687.	253898_s_at	-0.6
putative RING zinc finger protein Arabidopsis thaliana RMA1 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.I.24-7, Arabidopsis thaliana, gb: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	252975_s_at	-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
40S ribsomomal protein 40S ribsomomal proteinS20, Arabidopsis thaliana, pir:T12992	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
E2, ubiquitin-conjugating enzyme 13 (UBC13) identical to gi:992706; supported by cDNA: gi_15215679_gb_AY050368.1_	252528_at	-0.6
RNA-binding protein-like protein various RNA-binding proteins;supported by full-length cDNA: Ceres:9763.	252464_at	-0.6
MTN3-like protein MtN3 gene product - Medicago truncatula,PID:e1169583; supported by cDNA: gi_13605687_gb_AF361825.1_AF36182	252327_at	-0.6
signal recognition particle subunit 9 - like signal recognition particle subunit 9, Zea mays, EMBL:Y10117;supported by full-length cDNA: Cer	252295_at	-0.6
putative protein hypothetical protein T19L18.12 - Arabidopsis thaliana, PIR:T02616;supported by full-length cDNA: Ceres:32231.	252125_at	-0.6
ubiquitin extension protein (UBQ1) identical to GI:166929, GI:166930;supported by full-length cDNA: Ceres:18586.	252056_at	-0.6

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	251552_at	-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_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 prdeicted proteins, Schizosaccharomyces pombe	250281_at	-0.6
putative protein ;supported by full-length cDNA: Ceres:5392.	250289_at	-0.6
putative protein polypeptide deformylase, Aquifex aeolicus, PIR:C70352;supported by full-length cDNA: Ceres:150612.	250146_at	-0.6
putative protein similar to unknown protein (dbj|BAA90342.1);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.	250007_at	-0.6
putative protein similar to unknown protein (gb|AAF02129.1);supported by full-length cDNA: Ceres:35419.	249941_at	-0.6
putative protein contains similarity to thymidine kinase;supported by full-length cDNA: Ceres:118777.	249874_at	-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 predicted proteins, Arabidopsis thaliana; 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	249514_at	-0.6
putative protein MtN24 gene, Medicago truncatula, EMBL:MTY15290	249400_at	-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	-0.6
putative protein similar to unknown protein (gb|AAF24581.1)	249258_at	-0.6
N-hydroxycinnamoyl benzoyltransferase-like protein	249188_at	-0.6
unknown protein ;supported by full-length cDNA: Ceres:32890.	249190_at	-0.6
putative protein similar to unknown protein (gb|AAF69166.1); supported by cDNA: gi_15451133_gb_AY054647.1_	249182_at	-0.6
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 protein-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
FRO2-like protein; NADPH oxidase-like	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	248557_at	-0.6
nodulin-like protein ; supported by cDNA: gi_14532599_gb_AY039924.1_	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.	247073_at	-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	246824_at	-0.6
putative protein seven transmembrane domain orphan receptor, Mus musculus, EMBL:AF051098;supported by full-length cDNA: Ceres:96	246793_at	-0.6
ADP-ribosylation factor -like protein ADP-ribosylation factor, Dugesia japonica, EMBL:DJAB1051;supported by full-length cDNA: Ceres:268	246422_at	-0.6
glucose 6 phosphate/phosphate translocator-like protein glucose 6 phosphate/phosphate translocator - Arabidopsis thaliana, EMBL:AF233	246445_at	-0.6
Ca2+/H+-exchanging protein-like Arabidopsis thaliana high affinity calcium antiporter CAX1 encoded by GenBank Accession Number U574	246302_at	-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 - Synechocystis sp., PIR:S77481;supported by full-length cDNA: Ceres:28109.	246073_at	-0.6
glutaredoxin ;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
carnitine 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
hypothetical protein	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	258314_at	-0.6

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	266927_at	-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: 2623638;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
enoyl-ACP reductase (enr-A)	266035_at	-0.5
40S ribosomal protein S5 identical to GP:3043428;supported by full-length cDNA: Ceres:8397.	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	265637_at	-0.5
hypothetical protein similar to hypothetical protein GB:AAD18138; supported by full-length cDNA: Ceres: 23166.	265547_at	-0.5
hypothetical protein ;supported by full-length cDNA: Ceres:5.	265479_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:250015.	265458_at	-0.5
putative caltractin ;supported by full-length cDNA: Ceres:7802.	265460_at	-0.5
unknown protein	265417_at	-0.5
unknown protein ; supported by full-length cDNA: Ceres: 91872.	265390_at	-0.5
lipoic acid synthase (LIP1) ; supported by cDNA: gi_14334939_gb_AY035143.1_	265392_at	-0.5
hypothetical protein predicted by genscan; supported by full-length cDNA: Ceres: 32047.	265336_at	-0.5
hypothetical protein	265227_s_at	-0.5
unknown protein	265203_at	-0.5
unknown protein Location of ESTs 203I24T7, gb|H76794 and 203I24XP, gb|AA605510;supported by full-length cDNA: Ceres:9756.	265039_at	-0.5
Expressed protein ; supported by cDNA: gi_14596174_gb_AY042875.1_	265043_at	-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	264703_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:2935.	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	264545_at	-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_	264506_at	-0.5
hypothetical protein contains similarity to phosphate/phosphoenolpyruvate translocator precursor GI:1778141 from [Arabidopsis thaliana]	264419_s_at	-0.5
unknown protein similar to hypothetical protein GI:4079632 from [Arabidopsis thaliana]	264424_at	-0.5
symbiosis-related protein, putative similar to symbiosis-related protein GI:2072022 from [Laccaria bicolor];supported by full-length cDNA: C	264285_at	-0.5
unknown protein	264054_at	-0.5
unknown protein ;supported by full-length cDNA: Ceres:33232.	263880_at	-0.5

putative ferritin	263831_at	-0.5
putative fructose bisphosphate aldolase ; supported by cDNA: gi_14334739_gb_AY035043.1_	263761_at	-0.5
unknown protein similar to unknown protein GB:AAC79135, ESTs gb|T20423, gb|AA712864, gb|H76323 and gb|Z25560 come from this ge	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|AA651244	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	262959_at	-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	262913_at	-0.5
membrane related protein CP5, putative similar to membrane related protein CP5 GI:4741929 from [Arabidopsis thaliana]; supported by cD	262884_at	-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 fami	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:	260704_at	-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	260454_at	-0.5
putative 40S ribosomal protein SA (laminin receptor-like protein) identical to laminin receptor-like protein GB:U01955 [Arabidopsis thaliana];	260426_at	-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	260176_at	-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.	259983_at	-0.5
60S ribosomal protein L37, putative similar to SP:Q43292 from [Arabidopsis thaliana]; supported by cDNA: gi_13877906_gb_AF370216.1_	259612_at	-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	259279_at	-0.5
hypothetical protein predicted by genefinder; supported by full-length cDNA: Ceres: 40813.	259171_at	-0.5
unknown protein	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-le	258712_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	258614_at	-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	257813_at	-0.5
glyceraldehyde 3-phosphate dehydrogenase A subunit (GapA) identical to glyceraldehyde 3-phosphate dehydrogenase A subunit (GapA)	257807_at	-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];supporte	257699_at	-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	257172_at	-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]; supporte	256649_at	-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_A	255904_at	-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:	255379_at	-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.A 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	254399_at	-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	253815_at	-0.5
photosystem I subunit PSI-E - like protein photosystem I chain IV precursor, Hordeum vulgare, PIR1:F1BH4; supported by cDNA: gi_11692	253738_at	-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_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
putative protein predicted proteins, Arabidopsis thaliana	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
putative protein CHLOROPLAST 30S RIBOSOMAL PROTEIN S20, SWISSPROT:RR20_GUITH; supported by cDNA: gi_15810456_gb_A	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	251524_at	-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 lgtC - 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
putative protein mammalian inositol hexakisphosphate kinase 2 - Homo sapiens, EMBL:AF177145;supported by full-length cDNA: Ceres:32	250607_at	-0.5
unknown protein ; supported by full-length cDNA: Ceres: 37422.	250454_at	-0.5
putative protein various predicted proteins, Arabidopsis thaliana	250435_at	-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-le	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