**Supplementary Table 1.** Transcripts significantly elevated/suppressed (>3-fold) in Arabidopsis plants treated with MV in the light (50 µM, 2 h). Ratio in log base 2 were calculated by using the average expression values of MV-treated versus control samples after normalized, log-transformed RMA outputs of the two independent experiments.

| **Probe set name** | **Gene** | **TAIR description** | **Ratio $\log_2$ MV 2 h/ control** |
|---|---|---|---|
| 250351_at | At5g12030 | heat shock protein 17.6A | 5.207 |
| 262911_s_at | At1g59860 | class I heat shock protein (17.6A-CI) | 4.626 |
| 266294_at | At2g29500 | class I small heat shock protein (17.6B-CI) | 4.481 |
| 252515_at | At3g46230 | class I heat shock protein (17.4-CI) | 4.279 |
| 263150_at | At1g54050 | class III heat shock protein (17.4-CIII) | 4.078 |
| 250296_at | At5g12020 | class II heat shock protein (17.6-CII) | 4.044 |
| 264202_at | At1g22810 | member of the DREB subfamily A-5 of ERF/AP2 transcription factor family | 3.977 |
| 257670_at | At3g20340 | unknown protein | 3.893 |
| 258133_at | At3g24500 | ethylene-responsive transcriptional coactivator, putative similar to GB:AAD46402 from [Lycopersicon esculentum] (Plant J. 18 (6), 589-600 (1999));supported by full-length cDNA: Ceres:158734. | 3.791 |
| 261021_at | At1g26380 | hypothetical protein similar to reticuline oxidase-like protein GB:CAB45850 GI:5262224 from [Arabidopsis thaliana]; supported by cDNA: gi_13430839_gb_AF360332.1_AF360332 | 3.773 |
| 256576_at | At3g28210 | zinc finger protein (PMZ), putative identical to putative zinc finger protein (PMZ) GB:AAD37511 GI:5006473 [Arabidopsis thaliana] | 3.744 |
| 254408_at | At4g21390 | serine/threonine kinase - like protein serine/threonine kinase BRLK, Brassica oleracea, gb:Y12531 | 3.731 |
| 257536_at | At3g02800 | unknown protein | 3.655 |
| 256044_at | At1g07160 | protein phosphatase 2C, putative similar to protein phosphatase 2C GI:2582800 from [Medicago sativa] | 3.604 |
| 260248_at | At1g74310 | heat shock protein 101 (HSP101) identical to heat shock protein 101 GI:6715468 GB:AAF26423 from [Arabidopsis thaliana] | 3.546 |
| 266590_at | At2g46240 | hypothetical protein predicted by genscan and genefinder | 3.527 |
| 263374_at | At2g20560 | putative heat shock protein; supported by full-length cDNA: Ceres:25528. | 3.454 |
| 250781_at | At5g05410 | DREB2A (dbj\|BAA33794.1); supported by cDNA: gi_3738229_dbj_AB007790.1_AB007790 | 3.443 |
| 265499_at | At2g15480 | putative glucosyltransferase | 3.438 |
| 265501_at | At2g15490 | putative glucosyltransferase | 3.428 |
| 260399_at | At1g72520 | putative lipoxygenase similar to lipoxygenase GB:CAB56692 [Arabidopsis thaliana]; supported by cDNA: gi_15810254_gb_AY056166.1_ | 3.375 |
| 257918_at | At3g23230 | ethylene responsive element binding protein, putative similar to EREBP-4 GB:BAA07323 from [Nicotiana tabacum] | 3.371 |
| 261443_at | At1g28480 | glutaredoxin, putative similar to glutaredoxin GI:2244924 from [Arabidopsis thaliana]; supported by cDNA: gi_13358219_gb_AF325030.2_AF325030 | 3.365 |
| 262656_at | At1g14200 | zinc finger (C3HC4-type RING finger) family protein | 3.290 |
| 261838_at | At1g16030 | heat shock protein hsp70, putative similar to heat shock protein hsp70 GI:1771478 from [Pisum sativum] | 3.284 |
| 261394_at | At1g79680 | wall-associated kinase 2, putative similar to wall-associated kinase 2 GI:4826399 from [Arabidopsis thaliana] | 3.283 |
| 253046_at | At4g37370 | cytochrome P450 - like protein cytochrome P450, Glycyrrhiza echinata, AB001379;supported by full-length cDNA: Ceres:253698. | 3.279 |
| 256245_at | At3g12580 | HSP70 (heat shock protein 70) | 3.266 |
| 248657_at | At5g48570 | peptidylprolyl isomerase | 3.258 |
| 250182_at | At5g14470 | putative protein predicted proteins, Arabidopsis thaliana and Phalaenopsis sp. | 3.131 |
| 264746_at | At1g62300 | transcription factor WRKY6 (WRKY6) | 3.124 |
| 245005_at | rps14 | ribosomal protein S14 | 3.086 |

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|---|---|---|---|
| 260978_at | At1g53540 | 17.6 kDa heat shock protein (AA 1-156) identical to GI:4376161 from (Arabidopsis thaliana) (Nucleic Acids Res. 17 (19), 7995 (1989)) | 3.073 |
| 261899_at | At1g80820 | cinnamoyl CoA reductase, putative similar to cinnamoyl CoA reductase GB:AAF43141 GI:7239228 from [Populus tremuloides]; supported by full-length cDNA: Ceres: 32255. | 3.071 |
| 252269_at | At3g49580 | putative protein ;supported by full-length cDNA: Ceres:26235. | 3.049 |
| 261450_s_at | At1g21110 | O-methyltransferase, putative similar to GB:AAF28353 from [Fragaria x ananassa] | 3.046 |
| 249770_at | At5g24110 | member of WRKY Transcription Factor; Group III, WRKY30 | 3.003 |
| 256526_at | At1g66090 | disease resistance protein, putative similar to disease resistance protein RPP1-WsA [Arabidopsis thaliana] GI:3860163; supported by full-length cDNA: Ceres: 93530. | 2.978 |
| 244990_s_at | rpl23-01 | hypothetical protein | 2.899 |
| 250449_at | At5g10830 | embryonic abundant protein -like embryonic abundant protein EMB34, white spruce, PIR:T09281 | 2.883 |
| 252265_at | At3g49620 | putative protein SRG1 protein - Arabidopsis thaliana, PIR:S44261 | 2.875 |
| 246777_at | At5g27420 | RING-H2 zinc finger protein-like RING-H2 zinc finger protein ATL6 - Arabidopsis thaliana, EMBL:AF132016;supported by full-length cDNA: Ceres:106078. | 2.860 |
| 254241_at | At4g23190 | serine/threonine kinase - like protein serine/threonine kinase, Brassica oleracea | 2.854 |
| 266841_at | At2g26150 | member of Heat Stress Transcription Factor (Hsf) family, HsfA2 | 2.846 |
| 266010_at | At2g37430 | zinc finger (C2H2 type) family protein (ZAT11) | 2.844 |
| 250149_at | At5g14700 | cinnamoyl CoA reductase - like protein cinnamoyl CoA reductase, Populus tremuloides, EMBL:AF217958;supported by full-length cDNA: Ceres:17229. | 2.842 |
| 260005_at | At1g67920 | unknown protein ;supported by full-length cDNA: Ceres:13102. | 2.834 |
| 256306_at | At1g30370 | lipase, putative contains Pfam profile: PF01764: Lipase | 2.833 |
| 262229_at | At1g68620 | unknown protein; supported by cDNA: gi_14335125_gb_AY037242.1_ | 2.825 |
| 258336_at | At3g16050 | putative ethylene-inducible protein similar to ethylene-inducible protein GB:M88254 from [Hevea brasiliensis]; supported by cDNA: gi_4103951_gb_AF029980.1_AF029980 | 2.814 |
| 246858_at | At5g25930 | receptor-like protein kinase - like receptor-like protein kinase 5, Arabidopsis thaliana, PIR:S27756 | 2.764 |
| 260602_at | At1g55920 | serine acetyltransferase identical to GB:CAA84371 from [Arabidopsis thaliana] (Eur. J. Biochem. 227 (1-2), 500-509 (1995)); supported by cDNA: gi_926938_gb_L42212.1_ATHSAT1G | 2.748 |
| 252908_at | At4g39670 | putative protein | 2.743 |
| 259037_at | At3g09350 | hypothetical protein predicted by genscan+;supported by full-length cDNA: Ceres:19154. | 2.731 |
| 263783_at | At2g46400 | member of WRKY Transcription Factor; Group III, WRKY46 | 2.726 |
| 245250_at | At4g17490 | ethylene responsive element binding factor-like protein (AtERF6); supported by cDNA: gi_3298497_dbj_AB013301.1_AB013301 | 2.714 |
| 253044_at | At4g37290 | hypothetical protein ;supported by full-length cDNA: Ceres:41783. | 2.706 |
| 265221_s_at | At2g02010 | putative glutamate decarboxylase; supported by cDNA: gi_13605709_gb_AF361836.1_AF361836 | 2.703 |
| 266737_at | At2g47140 | putative alcohol dehydrogenase; supported by cDNA: gi_13878112_gb_AF370319.1_AF370319 | 2.699 |
| 262325_at | At1g64160 | dirigent protein, putative similar to dirigent protein GB:AAF25365 GI:6694709 from [Thuja plicata] | 2.668 |
| 249459_at | At5g39580 | peroxidase ATP24a | 2.664 |
| 255284_at | At4g04610 | 5-adenylylsulfate reductase ;supported by full-length cDNA: Ceres:40330. | 2.662 |
| 251774_at | At3g55840 | nematode resistance protein-like protein Hs1pro-1 nematode resistance gene, Beta procumbens, EMBL:BPU79733;supported by full-length cDNA: Ceres:149697. | 2.635 |
| 253268_s_at | At4g34135 | glucosyltransferase -like protein immediate-early salicylate-induced glucosyltransferase, Nicotiana tabacum, PIR2:T03747;supported by cDNA gi:14334981 | 2.634 |
| 247047_at | At5g66650 | putative protein contains similarity to unknown protein (gb AAC17084.1); supported by cDNA: gi_14596230_gb_AY042903.1_ | 2.615 |
| 260668_at | At1g19530 | unknown protein ;supported by full-length cDNA: Ceres:39579. | 2.606 |
| 247293_at | At5g64510 | putative protein similar to unknown protein (pir \|T03813) | 2.599 |
| 246532_at | At5g15870 | putative protein beta-glucan-elicitor receptor - Glycine max, EMBL:D78510 | 2.568 |
| 262518_at | At1g17170 | putative glutathione transferase One of three repeated putative glutathione transferases. 72% identical to glutathione transferase [Arabidopsis thaliana] (gi\|4006934) | 2.552 |
| 261474_at | At1g14540 | anionic peroxidase, putative similar to anionic peroxidase GI:170202 from [Nicotiana sylvestris] | 2.549 |
| 249264_s_at | At5g41740 | disease resistance protein-like | 2.548 |

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|---|---|---|---|
| 254158_at | At4g24380 | putative protein dihydrofolate reductase - Schizosaccharomyces pombe,PID:e1320950;supported by full-length cDNA: Ceres:27155. | 2.539 |
| 255543_at | At4g01870 | predicted protein of unknown function similar to bacterial tolB proteins but unclear if T7B11.13 is involved in viral transport | 2.526 |
| 254343_at | At4g21990 | PRH26 protein ;supported by full-length cDNA: Ceres:36866. | 2.520 |
| 248934_at | At5g46080 | serine/threonine protein kinase-like protein | 2.514 |
| 267451_at | At2g33710 | member of the ERF (ethylene response factor) subfamily B-4 of ERF/AP2 transcription factor family | 2.513 |
| 256756_at | At3g25610 | ATPase II, putative similar to GB:AAD34706 from [Homo sapiens] (Biochem. Biophys. Res. Commun. 257 (2), 333-339 (1999)) | 2.496 |
| 259428_at | At1g01560 | MAP kinase, putative similar to MAP kinase 5 GI:4239889 from [Zea mays] | 2.487 |
| 260804_at | At1g78410 | hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:157. | 2.478 |
| 260405_at | At1g69930 | putative glutathione transferase similar to glutathione transferase GB:CAA09188 [Alopecurus myosuroides] | 2.465 |
| 259792_at | At1g29690 | Significant homology to the MACPF (membrane attack complex and perforin) domain of complements and perforin proteins | 2.464 |
| 252487_at | At3g46660 | glucosyltransferase-like protein UDP-glucose glucosyltransferase - Arabidopsis thaliana, EMBL:AB016819; supported by cDNA: gi_15081808_gb_AY048297.1_ | 2.438 |
| 263182_at | At1g05575 | Expressed protein; supported by full-length cDNA: Ceres: 27081. | 2.420 |
| 256181_at | At1g51820 | light repressible receptor protein kinase, putative similar to light repressible receptor protein kinase GI:1321686 from (Arabidopsis thaliana) | 2.419 |
| 261459_at | At1g21100 | O-methyltransferase, putative similar to GB:AAF28353 from [Fragaria x ananassa]; supported by cDNA: gi_15982843_gb_AY057529.1_ | 2.412 |
| 266368_at | At2g41380 | putative embryo-abundant protein | 2.408 |
| 267384_at | At2g44370 | DC1 domain-containing protein; similar to DC1 domain-containing protein [Arabidopsis thaliana] (TAIR:AT2G17740.1) | 2.396 |
| 248134_at | At5g54860 | putative protein contains similarity to integral membrane protein | 2.389 |
| 254839_at | At4g12400 | stress-induced protein sti1 -like protein stress-induced protein sti1 - Glycine max,PID:g872116 | 2.386 |
| 252345_at | At3g48640 | hypothetical protein | 2.383 |
| 248332_at | At5g52640 | cytosolic heat shock protein AtHSP81-1 | 2.380 |
| 261037_at | At1g17420 | lipoxygenase identical to GB:CAB56692 from (Arabidopsis thaliana) | 2.380 |
| 251884_at | At3g54150 | embryonic abundant protein -like embryonic abundant protein EMB34, Picea glauca, PIR:T09281; supported by full-length cDNA: Ceres: 6529. | 2.363 |
| 248164_at | At5g54490 | putative protein similar to unknown protein (pir\|\|T05752);supported by full-length cDNA: Ceres:109272. | 2.356 |
| 265670_s_at | At2g32210 | unknown protein ;supported by full-length cDNA: Ceres:31665. | 2.355 |
| 249197_at | At5g42380 | putative protein contains similarity to calmodulin;supported by full-length cDNA: Ceres:99348. | 2.350 |
| 246293_at | At3g56710 | SigA binding protein; supported by cDNA: gi_14596086_gb_AY042831.1_ | 2.349 |
| 250944_at | At5g03380 | putative protein | 2.348 |
| 245209_at | At5g12340 | putative protein similarity to predicted protein, Arabidopsis thaliana | 2.344 |
| 254759_at | At4g13180 | short-chain alcohol dehydrogenase like protein short-chain alcohol dehydrogenase -Picea abies, PIR2:S34678;supported by full-length cDNA: Ceres:748. | 2.337 |
| 263475_at | At2g31945 | Expressed protein; supported by full-length cDNA: Ceres: 258917. | 2.334 |
| 252346_at | At3g48650 | At14a-related protein, similar to At14a (GI:11994571 and GI:11994573) (Arabidopsis thaliana) | 2.328 |
| 248607_at | At5g49480 | NaCl-inducible Ca2+-binding protein-like; calmodulin-like ; supported by cDNA: gi_13358217_gb_AF325028.2_AF325028 | 2.324 |
| 248814_at | At5g46910 | transcription factor jumonji (jmj) family protein; similar to REF6 (RELATIVE OF EARLY FLOWERING 6), transcription factor [Arabidopsis thaliana] (TAIR:AT3G48430.1) | 2.318 |
| 265674_at | At2g32190 | unknown protein; supported by full-length cDNA: Ceres: 40344. | 2.303 |
| 250796_at | At5g05300 | putative protein similar to unknown protein (gb\|AAF01528.1) | 2.298 |
| 254204_at | At4g24160 | putative protein CGI-58 protein - Homo sapiens,PID:g4929585 | 2.296 |
| 263570_at | At2g27150 | aldehyde oxidase identical to GP:3172044:gnl:PID:d1029570:AB010080; supported by cDNA: gi_5672671_dbj_AB016622.1_AB016622 | 2.285 |
| 261449_at | At1g21120 | putative ATPase similar to GB:AAF28353 from [Fragaria x ananassa] | 2.282 |
| 265725_at | At2g32030 | putative alanine acetyl transferase | 2.280 |
| 264758_at | At1g61340 | late embryogenesis abundant protein, putative similar to late embryogenesis abundant protein GI:1350540 from [Picea glauca] | 2.263 |
| 247215_at | At5g64905 | PROPEP3 (Elicitor peptide 3 precursor); Identical to Elicitor peptide 3 precursor (PEP3) [Arabidopsis Thaliana]; supported by full-length cDNA: Ceres: 3657. | 2.256 |

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|---|---|---|---|
| 262085_at | At1g56060 | hypothetical protein predicted by genemark.hmm | 2.253 |
| 258606_at | At3g02840 | unknown protein ;supported by full-length cDNA: Ceres:38495. | 2.247 |
| 265841_at | At2g35710 | putative glycogenin | 2.242 |
| 252671_at | At3g44190 | putative protein dehydrogenases of bacterial genome projects;supported by full-length cDNA: Ceres:114123. | 2.233 |
| 256518_at | At1g66080 | hypothetical protein | 2.230 |
| 258282_at | At3g26910 | unknown protein | 2.230 |
| 259298_at | At3g05370 | putative disease resistance protein similar to Cf-2 disease resistance protein GB:AAC15780 from [Lycopersicon pimpinellifolium] | 2.228 |
| 262731_at | At1g16420 | hypothetical protein similar to gb\|AF098458 latex-abundant protein (LAR) from Hevea brasiliensis | 2.218 |
| 247145_at | At5g65600 | receptor protein kinase-like protein | 2.217 |
| 261564_at | At1g01720 | NAC domain protein, putative similar to NAC domain protein NAM GB:AAD17313 GI:4325282 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:20909. | 2.216 |
| 262935_at | At1g79410 | hypothetical protein similar to putative transporter GI:6598860 from [Arabidopsis thaliana] | 2.212 |
| 249752_at | At5g24660 | putative protein similar to unknown protein (emb CAB62461.1);supported by full-length cDNA: Ceres:268701. | 2.211 |
| 259705_at | At1g77450 | ANAC032 (Arabidopsis NAC domain containing protein 32) | 2.209 |
| 246405_at | At1g57630 | disease resistance protein RPP1-WsB, putative similar to disease resistance protein RPP1-WsB GI:9279731 from [Arabidopsis thaliana] | 2.208 |
| 247279_at | At5g64310 | arabinogalactan-protein (gb\|AAC77823.1) ;supported by full-length cDNA: Ceres:25423. | 2.187 |
| 248719_at | At5g47910 | respiratory burst oxidase protein; supported by cDNA: gi_3242788_gb_AF055357.1_AF055357 | 2.181 |
| 247949_at | At5g57220 | cytochrome P450 | 2.168 |
| 262571_at | At1g15430 | hypothetical protein predicted by genscan+; supported by cDNA: gi_15293248_gb_AY051058.1_ | 2.163 |
| 259979_at | At1g76600 | unknown protein ;supported by full-length cDNA: Ceres:29624. | 2.162 |
| 251054_at | At5g01540 | receptor like protein kinase receptor like protein kinase - Arabidopsis thaliana, EMBL:ATLECGENE; supported by cDNA: gi_13605542_gb_AF361597.1_AF361597 | 2.162 |
| 265008_at | At1g61560 | Mlo protein, putative similar to Mlo protein GI:1877220 from [Hordeum vulgare]; supported by cDNA: gi_14091581_gb_AF369567.1_AF369567 | 2.160 |
| 262307_at | At1g71000 | heat shock protein DnaJ, putative similar to heat shock protein DnaJ GI:5020005 from [Rhodothermus marinus] | 2.156 |
| 263228_at | At1g30700 | putative reticuline oxidase-like protein similar to GB:P30986 from [Eschscholzia californica] ( berberine bridge-forming enzyme ), ESTs gb\|F19886, gb\|Z30784 and gb\|Z30785 come from this gene; supported by cDNA: gi_16930506_gb_AF419607.1_AF419607 | 2.156 |
| 260362_at | At1g70530 | putative protein kinase similar to C-terminal region of s-receptor kinase precursor GB:JQ1677 [Brassica napus]; Pfam HMM hit: Eukaryotic protein kinase domain | 2.149 |
| 258787_at | At3g11840 | U-box domain-containing protein | 2.149 |
| 265199_s_at | At2g36770 | putative glucosyl transferase | 2.143 |
| 246464_at | At5g16980 | quinone oxidoreductase -like protein probable quinone oxidoreductase (EC 1.6.5.5) P1, Arabidopsis thaliana, PIR:S57611 | 2.140 |
| 267623_at | At2g39650 | unknown protein | 2.139 |
| 253819_at | At4g28350 | receptor protein kinase like protein lectin receptor-like serine/threonine kinase lecRK1, Arabidopsis thaliana, PIR2:S68589 | 2.136 |
| 247848_at | At5g58120 | resistance protein - like disease resistance protein RPP1-WsA, Arabidopsis thaliana, EMBL:AF098962 | 2.135 |
| 246612_at | At5g35320 | putative protein ;supported by full-length cDNA: Ceres:38281. | 2.132 |
| 254592_at | At4g18880 | member of Heat Stress Transcription Factor (Hsf) family, HsfA4A | 2.128 |
| 262360_at | At1g73080 | receptor protein kinase, putative similar to receptor protein kinase GI:1389566 from [Arabidopsis thaliana] | 2.122 |
| 246584_at | At5g14730 | putative protein predicted protein, Arabidopsis thaliana | 2.119 |
| 265093_at | At1g03905 | ABC transporter family protein; Identical to Non-intrinsic ABC protein 4 (GCN-related protein 2) (NAP4) [Arabidopsis Thaliana] (GB:Q3EDJ0;GB:Q9ZWB0); similar to POP1 [Arabidopsis thaliana] (TAIR:AT5G44110.1) | 2.113 |
| 259445_at | At1g02400 | dioxygenase, putative similar to dioxygenase GI:1666096 from [Marah macrocarpus] | 2.109 |
| 266992_at | At2g39200 | similar to Mlo proteins from H. vulgare; supported by cDNA: gi_14091593_gb_AF369573.1_AF369573 | 2.107 |
| 267381_at | At2g26190 | calmodulin-binding family protein; similar to EDA39 (embryo sac development arrest 39), calmodulin binding [Arabidopsis thaliana] (TAIR:AT4G33050.3); supported by cDNA: gi_16930468_gb_AF419588.1_AF419588 | 2.100 |

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|---|---|---|---|
| 251259_at | At3g62260 | putative protein phosphoprotein phosphatase (EC 3.1.3.16) 1A-alpha - Homo sapiens, PIR:S22423;supported by full-length cDNA: Ceres:20050. | 2.096 |
| 253535_at | At4g31550 | member of WRKY Transcription Factor; Group II-d;WRKY11 | 2.090 |
| 253181_at | At4g35180 | amino acid permease - like protein Lily mRNA, Lilium longiflorum, gb:D21814;supported by full-length cDNA: Ceres:36461. | 2.090 |
| 258947_at | At3g01830 | hypothetical protein similar to calmodulin-like protein GB:CAB42906 [Arabidopsis thaliana]; Pfam HMM hit: EF hand; supported by full-length cDNA: Ceres: 7252. | 2.085 |
| 252470_at | At3g46930 | protein kinase 6-like protein protein kinase 6 - Glycine max,PIR2:S29851 | 2.082 |
| 256356_s_at | At1g66500 | hypothetical protein | 2.075 |
| 255904_at | At1g17860 | lemir (miraculin), putative similar to lemir (miraculin) GI:2654440 from [Lycopersicon esculentum]; supported by cDNA: gi_12083239_gb_AF332416.1_AF332416 | 2.048 |
| 261748_at | At1g76070 | hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:39494. | 2.043 |
| 265737_at | At2g01180 | putative phosphatidic acid phosphatase ;supported by full-length cDNA: Ceres:19163. | 2.041 |
| 260126_at | At1g36370 | putative hydroxymethyltransferase similar to serine hydroxymethyltransferage GB:P50433 from [Solanum tuberosum];supported by full-length cDNA: Ceres:122515. | 2.037 |
| 264660_at | At1g09940 | putative glutamyl-tRNA reductase 2 precursor similar to GB:P49294 and to A. thaliana HEMA2 (gb\|U27118) | 2.029 |
| 262930_at | At1g65690 | hypothetical protein similar to hin1 GB:Y07563 GI:1619320 Nicotiana tabacum;supported by full-length cDNA: Ceres:21639. | 2.029 |
| 249339_at | At5g41100 | DNA binding; similar to hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] (TAIR:AT3G26910.2) | 2.021 |
| 267028_at | At2g38470 | Member of the plant WRKY transcription factor family, WRKY33 | 2.018 |
| 248434_at | At5g51440 | mitochondrial heat shock 22 kd protein-like; supported by full-length cDNA: Ceres: 268536. | 2.016 |
| 253737_at | At4g28703 | Expressed protein; supported by full-length cDNA: Ceres: 38545. | 2.015 |
| 266615_s_at | At2g29720 | putative monooxygenase ;supported by full-length cDNA: Ceres:34214. | 2.014 |
| 245369_at | At4g15970 | Expressed protein; supported by full-length cDNA: Ceres: 124835. | 2.013 |
| 254318_at | At4g22530 | putative protein embryo-abundant protein (EMB34), Picea glauca, PID:g1350531 | 2.012 |
| 252533_at | At3g46110 | putative protein predicted proteins, Arabidopsis thaliana | 1.995 |
| 257919_at | At3g23250 | myb-related transcription factor, putative similar to myb-related transcription factor GB:CAA66952 from [Lycopersicon esculentum] | 1.986 |
| 247351_at | At5g63790 | ANAC102 (Arabidopsis NAC domain containing protein 102) | 1.980 |
| 261650_at | At1g27770 | envelope Ca2+-ATPase identical to envelope Ca2+-ATPase GB:AAD10212 GI:516118 from (Arabidopsis thaliana); supported by cDNA: gi_493621_dbj_D13983.1_ATHRCECAA | 1.976 |
| 266296_at | At2g29420 | putative glutathione S-transferase ;supported by full-length cDNA: Ceres:24361. | 1.969 |
| 261344_at | At1g79710 | hypothetical protein similar to hypothetical protein GB:AAC12874 (Synechococcus PCC7942) | 1.968 |
| 246465_at | At5g17000 | quinone oxidoreductase - like protein probable quinone oxidoreductase (EC 1.6.5.5) P1, Arabidopsis thaliana, PIR:S57611 | 1.967 |
| 261476_at | At1g14480 | hypothetical protein contains similarity to alpha-latroinsectotoxin precursor GI:9537 from [Latrodectus tredecimguttatus] | 1.954 |
| 257840_at | At3g25250 | protein kinase, putative contains Pfam profile: PF00069 Eukaryotic protein kinase domain | 1.952 |
| 261892_at | At1g80840 | Pathogen-induced transcription factor, WRKY40 | 1.944 |
| 249903_at | At5g22690 | disease resistance protein-like | 1.938 |
| 267289_at | At2g23770 | putative protein kinase contains a protein kinase domain profile (PDOC00100) | 1.937 |
| 254926_at | At4g11280 | ACC synthase (AtACS-6); supported by cDNA: gi_16226285_gb_AF428292.1_AF428292 | 1.937 |
| 251109_at | At5g01600 | ferritin 1 precursor ;supported by full-length cDNA: Ceres:1100. | 1.937 |
| 254605_at | At4g18950 | protein kinase - like protein protein kinase 6, Glycine max., PIR2:S29851;supported by full-length cDNA: Ceres:38712. | 1.933 |
| 258277_at | At3g26830 | putative cytochrome P450 similar to cytochrome P450 71B2 GB:O65788 [Arabidopsis thaliana] | 1.933 |
| 257074_at | At3g19660 | unknown protein | 1.932 |
| 260239_at | At1g74360 | putative receptor protein kinase similar to brassinosteroid insensitive 1 GB:AAC49810 (putative receptor protein kinase); contains Pfam profiles: PF00560 Leucine Rich Repeat (17 repeats), PF00069 Eukaryotic protein kinase domain; supported by cDNA: gi_15810516_gb_AY056297.1_ | 1.930 |
| 256453_at | At1g75270 | GSH-dependent dehydroascorbate reductase 1, putative similar to GI:6939839 from [Oryza sativa];supported by full-length cDNA: Ceres:35711. | 1.924 |
| 247693_at | At5g59730 | putative protein leucine zipper-containing protein, Lycopersicon | 1.919 |

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|---|---|---|---|
|  |  | esculentum, PIR:S21495; supported by cDNA: gi_14334437_gb_AY034910.1_ |  |
| 266775_at | At2g29060 | putative SCARECROW gene regulator | 1.916 |
| 264365_s_at | At1g03220 | unknown protein Strong similarity to gb\|D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb\|H37281, gb\|T44167, gb\|T21813, gb\|N38437, gb\|Z26470, gb\|R65072, gb\|N76373, gb\|F15470, gb\|Z35182, gb\|H76373, gb\|Z34678 and gb\|Z35387 come from this | 1.908 |
| 246327_at | At1g16670 | receptor-like serine/threonine kinase, putative similar to receptor-like serine/threonine kinase GI:2465923 from [Arabidopsis thaliana]; supported by cDNA: gi_16649102_gb_AY059921.1_ | 1.907 |
| 246018_at | At5g10695 | Expressed protein; supported by full-length cDNA: Ceres: 103171. | 1.901 |
| 254922_at | At4g11370 | RING-H2 finger protein RHA1a -like protein ;supported by full-length cDNA: Ceres:21591. | 1.895 |
| 249417_at | At5g39670 | calcium-binding protein - like cbp1 calcium-binding protein, Lotus japonicus, EMBL:LJA251808; supported by cDNA: gi_16648829_gb_AY058192.1_ | 1.875 |
| 260243_at | At1g63720 | hypothetical protein similar to putative protein GB:CAA18164 [Arabidopsis thaliana]; supported by cDNA: gi_13878144_gb_AF370335.1_AF370335 | 1.868 |
| 247327_at | At5g64120 | peroxidase (emb\|CAA67551.1) ;supported by full-length cDNA: Ceres:23349. | 1.866 |
| 260869_at | At1g43800 | stearoyl acyl carrier protein desaturase, putative similar to stearoyl acyl carrier protein desaturase Lldd3A20 GB: AAD28287 GI:4704824 from [Lupinus luteus];supported by full-length cDNA: Ceres:12758. | 1.861 |
| 251428_at | At3g60140 | beta-glucosidase-like protein several beta-glucosidases - different species; supported by cDNA: gi_10834547_gb_AF159376.1_AF159376 | 1.861 |
| 250550_at | At5g07870 | N-hydroxycinnamoyl benzoyltransferase - like protein anthranilate N-benzoyltransferase, Dianthus caryophyllus, PIR:T10717 | 1.855 |
| 249575_at | At5g37670 | low-molecular-weight heat shock protein - like cytosolic class I small heat-shock protein HSP17.5, Castanea sativa, EMBL:CSA9880 | 1.850 |
| 259297_at | At3g05360 | putative disease resistance protein similar to Cf-2 disease resistance protein GB:AAC15780 from [Lycopersicon pimpinellifolium] | 1.843 |
| 246870_at | At5g26030 | ferrochelatase-I | 1.837 |
| 264083_at | At2g31230 | ethylene reponse factor-like AP2 domain transcription factor | 1.833 |
| 248686_at | At5g48540 | 33 kDa secretory protein-like; supported by cDNA: gi_15292980_gb_AY050924.1_ | 1.831 |
| 263230_at | At1g05665 | putative indole-3-acetate beta-glucosyltransferase similar to indole-3-acetate beta-glucosyltransferase GB:AAD32293 | 1.827 |
| 248611_at | At5g49520 | member of WRKY Transcription Factor; Group II-c, WRKY48 | 1.823 |
| 245711_at | At5g04340 | putative c2h2 zinc finger transcription factor | 1.813 |
| 250916_at | At5g03630 | monodehydroascorbate reductase (NADH) - like protein monodehydroascorbate reductase (NADH), cucumber, PIR:JU0182;supported by full-length cDNA: Ceres:34156. | 1.812 |
| 249719_at | At5g35735 | Expressed protein; supported by full-length cDNA: Ceres: 32450. | 1.800 |
| 265327_at | At2g18210 | unknown protein | 1.795 |
| 246001_at | At5g20790 | putative protein predicted protein, Arabidopsis thaliana;supported by full-length cDNA: Ceres:267031. | 1.793 |
| 254652_at | At4g18170 | member of WRKY Transcription Factor; Group II-c, WRKY28 | 1.792 |
| 252825_at | At4g39890 | small GTP-binding protein - like SR1 Nt-rab6, Nicotiana tabacum, L29273; supported by cDNA: gi_14423429_gb_AF386952.1_AF386952 | 1.786 |
| 256968_at | At3g21070 | Encodes a protein with NAD(H) kinase activity. | 1.784 |
| 246108_at | At5g28630 | putative protein retinal glutamic acid-rich protein, bovine, PIR:A40437;supported by full-length cDNA: Ceres:24151. | 1.780 |
| 264953_at | At1g77120 | alcohol dehydrogenase identical to alcohol dehydrogenase GI:469467 from (Arabidopsis thaliana); supported by full-length cDNA: Ceres: 4033. | 1.779 |
| 254215_at | At4g23700 | putative Na+/H+-exchanging protein Na+/H+-exchanging protein slr1595 - Synechocystis sp., EMBL:D90902 | 1.778 |
| 266155_at | At1g64950 | cytochrome p450, putative similar to cytochrome p450 GI:438242 from [Solanum melongena]; supported by cDNA: gi_14334809_gb_AY035078.1_ | 1.775 |
| 247655_at | At5g59820 | zinc finger protein Zat12 ;supported by full-length cDNA: Ceres:40576. | 1.774 |
| 258682_at | At3g08720 | putative ribosomal-protein S6 kinase (ATPK19) identical to putative ribosomal-protein S6 kinase (ATPK19) GB:D42061 [Arabidopsis thaliana] (FEBS Lett. 358 (2), 199-204 (1995)); supported by cDNA: gi_15292784_gb_AY050826.1_ | 1.774 |
| 252214_at | At3g50260 | putative protein EREBP-3 homolog, Stylosanthes hamata, EMBL:U91982; supported by cDNA: gi_15010555_gb_AY045579.1_ | 1.769 |
| 265797_at | At2g35710 | glycogenin glucosyltransferase (glycogenin)-related; similar to glycogenin glucosyltransferase (glycogenin)-related [Arabidopsis thaliana] (TAIR:AT4G16600.1); supported by full-length cDNA: Ceres: 9996. | 1.768 |
| 261005_at | At1g26420 | hypothetical protein similar to reticuline oxidase-like protein GB:CAB45850 GI:5262224 from [Arabidopsis thaliana] | 1.765 |

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| 256583_at | At3g28850 | glutaredoxin family protein; similar to glutaredoxin family protein [Arabidopsis thaliana] (TAIR:AT5G39865.1) | 1.757 |
| 257644_at | At3g25780 | Encodes allene oxide cyclase (AOC3), one of the enzymes involved in jasmonic acid biosynthesis;supported by full-length cDNA: Ceres:3457. | 1.756 |
| 263866_at | At2g36950 | putative farnesylated protein ;supported by full-length cDNA: Ceres:19570. | 1.756 |
| 248381_at | At5g51830 | fructokinase 1; supported by cDNA: gi_13878052_gb_AF370289.1_AF370289 | 1.755 |
| 252652_at | At3g44720 | putative chloroplast prephenate dehydratase similar to bacterial PheA gene products | 1.754 |
| 264005_at | At2g22470 | unknown protein; supported by cDNA: gi_3883121_gb_AF082299.1_AF082299 | 1.754 |
| 245788_at | At1g32120 | hypothetical protein similar to hypothetical protein GB:AAD27684 GI:4680504 from [Oryza sativa] | 1.753 |
| 252414_at | At3g47420 | putative protein sn-glycerol-3-phosphate permease - Haemophilus influenzae,PID:g3603157; supported by cDNA: gi_13430515_gb_AF360170.1_AF360170 | 1.751 |
| 256266_at | At3g12310 | unknown protein; supported by cDNA: gi_15293280_gb_AY051074.1_ | 1.751 |
| 260015_at | At1g67980 | putative S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase similar to S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase GB:AAA62426 [Arabidopsis thaliana] (function=disease resistance); supported by cDNA: gi_682727_gb_L40031.1_ATHORF | 1.745 |
| 245151_at | At2g47550 | putative pectinesterase ;supported by full-length cDNA: Ceres:111254. | 1.742 |
| 265276_at | At2g28400 | hypothetical protein predicted by genscan and genefinder | 1.731 |
| 255502_at | At4g02410 | contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 166.20) and to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 139.32) | 1.730 |
| 253628_at | At4g30280 | xyloglucan endo-1,4-beta-D-glucanase-like protein xyloglucan endo-1,4-beta-D-glucanase (EC 3.2.1.-) XTR-3 - Arabidopsis thaliana,PIR2:S71222;supported by full-length cDNA: Ceres:142204. | 1.725 |
| 264867_at | At1g24150 | Formin homologue 4 (ATFH4); encodes a group I formin. Localized to cell junctions. Polymerizes actin. Binds profilin. | 1.724 |
| 264645_at | At1g08940 | unknown protein Similar to Saccharomyces hypothetical protein YDR051c (gb\|Z49209). ESTs gb\|T44436,gb\|42252 come from this gene | 1.723 |
| 251479_at | At3g59700 | serine/threonine-specific kinase lecRK1 precursor,lectin receptor-like | 1.717 |
| 244953_s_at | nad6 | NADH dehydrogenase subunit 6 | 1.715 |
| 245119_at | At2g41640 | unknown protein; supported by cDNA: gi_16930450_gb_AF419579.1_AF419579 | 1.715 |
| 251061_at | At5g01830 | putative protein hypothetical protein ARC1 - Brassica napus, PIR:T08872 | 1.710 |
| 249032_at | At5g44910 | putative protein contains similarity to disease resistance protein | 1.709 |
| 248327_at | At5g52750 | putative protein similar to unknown protein (emb\|CAA71173.1);supported by full-length cDNA: Ceres:19542. | 1.707 |
| 259479_at | At1g19015 | Expressed protein; supported by full-length cDNA: Ceres: 31015. | 1.706 |
| 248322_at | At5g52760 | heavy-metal-associated domain-containing protein; similar to heavy-metal-associated domain-containing protein [Arabidopsis thaliana] (TAIR:AT5G52750.1) | 1.704 |
| 262381_at | At1g72900 | virus resistance protein, putative similar to virus resistance protein GI:558886 from [Nicotiana glutinosa] | 1.704 |
| 252739_at | At3g43250 | cell cycle control protein-related; similar to cell cycle control protein-related [Arabidopsis thaliana] (TAIR:AT2G32050.1) | 1.699 |
| 266821_at | At2g44840 | putative ethylene response element binding protein (EREBP) ;supported by full-length cDNA: Ceres:6397. | 1.698 |
| 252278_at | At3g49530 | NAC2-like protein NAC2 - Arabidopsis thaliana, EMBL:AF201456; supported by cDNA: gi_16604578_gb_AY059734.1_ | 1.697 |
| 263800_at | At2g24600 | hypothetical protein predicted by genscan; supported by cDNA: gi_15810330_gb_AY056204.1_ | 1.697 |
| 265675_at | At2g32120 | 70kD heat shock protein ;supported by full-length cDNA: Ceres:98979. | 1.694 |
| 246340_s_at | At3g44860 | AtPP -like protein AtPP protein, Brassica napus, EMBL:BNA245479; supported by cDNA: gi_15293070_gb_AY050969.1_ | 1.683 |
| 246418_at | At5g16960 | quinone oxidoreductase -like protein probable quinone oxidoreductase (EC 1.6.5.5) P1, Arabidopsis thaliana, PIR:S57611;supported by full-length cDNA: Ceres:7898. | 1.677 |
| 257751_at | At3g18690 | hypothetical protein predicted by genemark.hmm;supported by full-length cDNA: Ceres:104278. | 1.674 |
| 260662_at | At1g19540 | 2-hydroxyisoflavone reductase, putative similar to PIR:T08106 from [Betula pendula] | 1.669 |
| 262369_at | At1g73010 | phosphoric monoester hydrolase; similar to phosphoric monoester hydrolase [Arabidopsis thaliana] (TAIR:AT1G17710.1);supported by full-length cDNA: Ceres:19976. | 1.665 |
| 256050_at | At1g07000 | leucine zipper protein, putative similar to leucine zipper protein GI:10177020 from [Arabidopsis thaliana] | 1.663 |

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| 246631_at | At1g50740 | unknown protein; supported by full-length cDNA: Ceres: 34587. | 1.661 |
| 249260_at | At5g41680 | Pto kinase interactor 1-like protein | 1.659 |
| 264757_at | At1g61360 | receptor protein kinase (IRK1), putative similar to receptor protein kinase (IRK1) GI:836953 from [Ipomoea trifida] | 1.658 |
| 247240_at | At5g64660 | U-box domain-containing protein | 1.655 |
| 258752_at | At3g09520 | ATEXO70H4; a member of EXO70 gene family, putative exocyst subunits, conserved in land plants. | 1.650 |
| 252234_at | At3g49780 | Phytosulfokine 3 precursor (ATPSK4), coding for a unique plant peptide growth factor; supported by full-length cDNA: Ceres: 40302. | 1.647 |
| 257785_at | At3g26980 | geranylgeranylated protein, putative similar to ATGP4 GB:AAD00115 from [Arabidopsis thaliana] | 1.643 |
| 249485_at | At5g39020 | receptor protein kinase - like protein receptor-protein kinase-like protein, Arabidopsis thaliana, PIR:T45786 | 1.642 |
| 258941_at | At3g09940 | putative monodehydroascorbate reductase (NADH) similar to monodehydroascorbate reductase (NADH) GB:JU0182 [Cucumis sativus]; supported by full-length cDNA: Ceres: 11160. | 1.638 |
| 255512_at | At3g05710 | SYNTAXIN 43 (SYP43); member of SYP4 Gene Family; supported by cDNA: gi_5059351_gb_AF154574.1_AF154574 | 1.635 |
| 249072_at | At5g44060 | putative protein similar to unknown protein (gb\|AAD10670.1) | 1.635 |
| 254256_at | At4g23180 | serine/threonine kinase -like protein serine/threonine kinase, Brassica oleracea; supported by cDNA: gi_13506744_gb_AF224705.1_AF224705 | 1.635 |
| 251336_at | At3g61190 | Bon association protein 1 (BAP1); encodes a protein with a C2 domain that binds to BON1 in yeast two hybrid analyses. ;supported by full-length cDNA: Ceres:30454. | 1.631 |
| 252827_at | At4g39950 | cytochrome P450 - like protein cytochrome P450, Sinapis alba, AF069494; supported by cDNA: gi_15028134_gb_AY046017.1_ | 1.630 |
| 247532_at | At5g61560 | putative protein disease resistance protein kinase Pto, Lycopersiocon esculentum, PIR:A49332 | 1.629 |
| 249078_at | At5g44070 | phytochelatin synthase (gb\|AAD41794.1); supported by cDNA: gi_14532653_gb_AY039951.1_ | 1.629 |
| 256793_at | At3g22160 | VQ motif-containing protein; similar to VQ motif-containing protein [Arabidopsis thaliana] (TAIR:AT4G15120.1); supported by full-length cDNA: Ceres:8081. | 1.629 |
| 255549_at | At4g01950 | Glycerol-3-phosphate acyltransferase 3 (gpat3); encodes a member of a family of proteins with glycerol-3-phosphate acyltransferase activity | 1.627 |
| 260206_at | At1g70740 | putative protein kinase contains Pfam profile: PF00069 Eukaryotic protein kinase domain | 1.618 |
| 251603_at | At3g57760 | putative protein wall-associated kinase 1, Arabidopsis thaliana, AJ009696; supported by cDNA: gi_13937221_gb_AF372966.1_AF372966 | 1.614 |
| 265620_at | At2g27310 | F-box family protein; similar to F-box family protein [Arabidopsis thaliana] (TAIR:AT2G36090.1) | 1.611 |
| 261718_at | At1g18390 | wall-associated kinase, putative similar to wall-associated kinase 2 GB:CAB42872 GI:4826399 from [Arabidopsis thaliana] | 1.609 |
| 247708_at | At5g59550 | putative protein COP1-interacting protein CIP8, Arabidopsis thaliana, EMBL:AF162150; supported by cDNA: gi_15450686_gb_AY052711.1_ | 1.608 |
| 245329_at | At4g14360 | dehydration-responsive protein-related; similar to dehydration-responsive protein-related [Arabidopsis thaliana] (TAIR:AT1G04430.1); supported by full-length cDNA: Ceres: 37809. | 1.608 |
| 247026_at | At5g67080 | protein kinase-like protein | 1.607 |
| 250670_at | At5g06860 | polygalacturonase inhibiting protein 1; PGIP1 (gb\|AAF69827.1) ;supported by full-length cDNA: Ceres:5344. | 1.605 |
| 255568_at | At4g01250 | member of WRKY Transcription Factor; Group II-e, WRKY22 | 1.605 |
| 260411_at | At1g69890 | hypothetical protein similar to GB:AAB61488 [Arabidopsis thaliana];supported by full-length cDNA: Ceres:34864. | 1.604 |
| 256589_at | At3g28740 | cytochrome P450, putative contains Pfam profile: PF00067 cytochrome P450; supported by cDNA: gi_15292830_gb_AY050849.1_ | 1.601 |
| 246463_at | At5g16970 | quinone oxidoreductase -like protein probable quinone oxidoreductase (EC 1.6.5.5) P1, Arabidopsis thaliana, PIR:S57611 | 1.600 |
| 262238_at | At1g48300 | similar to soluble diacylglycerol acyltransferase [Arachis hypogaea] (GB:AAX62735.1) | -1.601 |
| 256598_at | At3g30180 | cytochrome P450 homolog, putative similar to cytochrome P450 homolog GB:U54770 GI:1421740 from [Lycopersicon esculentum];supported by full-length cDNA: Ceres:11278. | -1.620 |
| 266322_at | At2g46690 | putative auxin-regulated protein | -1.649 |
| 257008_at | At3g14210 | myrosinase-associated protein, putative similar to GB:CAA71238 from [Brassica napus], conatains Pfam profile:PF00657 Lipase/Acylhydrolase with GDSL-like motif; supported by cDNA: gi_15450434_gb_AY052318.1_ | -1.653 |
| 244932_at | AtCg01060 | PSI 9KDa protein | -1.654 |
| 263688_at | At1g26920 | unknown protein Location of EST 228A16T7A, gb\|N65686;supported by full-length cDNA: Ceres:24946. | -1.681 |
| 245861_at | At5g28300 | GTL1 - like protein GTL1, Arabidopsis thaliana, EMBL:ATAJ3215; supported by cDNA: gi_14423451_gb_AF386963.1_AF386963 | -1.690 |

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| 262682_at | At1g75900 | anter-specific proline-rich -like protein (APG-like) similar to anter-specific proline-rich protein (APG) SP:P40602 [Arabidopsis thaliana (Mouse-ear cress)]; supported by cDNA: gi_15054385_gb_AY028611.1_ | -1.698 |
| 263515_at | At2g21640 | unknown protein | -1.706 |
| 249850_at | At5g23240 | putative protein similar to unknown protein (gb\|AAD21732.1) | -1.718 |
| 252607_at | At3g44990 | xyloglucan endo-transglycosylase; supported by cDNA: gi_15810248_gb_AY056163.1_ | -1.726 |
| 249309_at | At5g41410 | Homeodomain protein involved in ovule morphogenesis, BEL1 | -1.735 |
| 248921_at | At5g45950 | GDSL-motif lipase/hydrolase-like protein | -1.798 |
| 255028_at | At4g09890 | putative protein Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence, gene T30B22.22, PID:g2529679 | -1.842 |
| 264042_at | At2g03760 | putative steroid sulfotransferase; supported by cDNA: gi_599639_emb_Z46823.1_ATTS4391 | -1.941 |
| 248961_at | At5g45650 | subtilisin-like protease | -1.992 |
| 267361_at | At2g39920 | acid phosphatase class B family protein; Identical to Hypothetical protein At2g39920 [Arabidopsis Thaliana] (GB:O04195); similar to acid phosphatase, putative [Arabidopsis thaliana] (TAIR:AT4G25150.1);supported by full-length cDNA: Ceres:33701. | -2.002 |
| 246275_at | At4g36540 | BEE2 (BR ENHANCED EXPRESSION 2); DNA binding / transcription factor; similar to basic helix-loop-helix (bHLH) family protein | -2.047 |
| 244972_at | AtCg00680 | PSII 47KDa protein | -2.079 |
| 252972_at | At4g38840 | auxin-induced protein - like auxin-inducible SAUR gene, Raphanus sativus,AB000708;supported by full-length cDNA: Ceres:10140. | -2.113 |
| 247252_at | At5g64770 | unknown protein | -2.115 |
| 263402_at | At2g04050 | MATE efflux family protein; similar to ATDTX1, antiporter/ multidrug efflux pump/ multidrug transporter/ transporter [Arabidopsis thaliana] (TAIR:AT2G04040.1) | -2.226 |
| 259790_s_at | At1g29430 | auxin-induced protein, putative similar to SP:P33083 from [Glycine max];supported by full-length cDNA: Ceres:4119. | -2.276 |
| 264014_at | At2g21210 | putative auxin-regulated protein | -2.386 |
| 252965_at | At4g38860 | putative auxin-induced protein auxin-induced protein 10A, Glycine max., PIR2:JQ1099 | -2.459 |
| 256060_at | At1g07050 | hypothetical protein contains similarity to photoperiod sensitivity quantitative trait locus (Hd1) GI:11094203 from [Oryza sativa];supported by full-length cDNA: Ceres:1955. | -2.476 |