**Supplemental Table 1**. Transcripts with differential expression patterns in fully expanded trifoliate 4 (T4) and growing trifoliate 6 (T6) soybean leaves. Annotations are based first on the BLASTX hit of the 3′ end EST if sequence information was available, and second on the 5′ end EST.

| **ID** | **Description** | **F** | **p** | **T6/T4** |
|---|---|---|---|---|
| Gm-r1088-8190 | No Hits | 48.07 | 0.0001204 | 0.286 |
| Gm-r1088-7918 | GA [Pisum sativum] | 64.79 | 4.179E-05 | 0.335 |
| Gm-r1070-6153 | ferric reductase [Oryza sativa (japonica cultivar-group)] | 24.00 | 0.0027141 | 0.345 |
| Gm-r1070-3422 | type 1 metallothionein [Glycine max] | 19.28 | 0.0046108 | 0.354 |
| Gm-r1088-5264 | plasma membrane polypeptide [Nicotiana tabacum] | 52.15 | 9.053E-05 | 0.362 |
| Gm-r1088-8183 | CCR protein [x Citrofortunella mitis] | 25.47 | 0.0009935 | 0.376 |
| Gm-r1088-8332 | No Hits | 65.05 | 4.119E-05 | 0.376 |
| Gm-r1088-7127 | Unknown | 26.91 | 0.0008349 | 0.384 |
| Gm-r1088-4055 | Unknown | 31.12 | 0.0005233 | 0.388 |
| Gm-r1088-8135 | Unknown | 37.39 | 0.0002849 | 0.389 |
| Gm-r1070-7748 | granule-bound starch synthase Ib precursor [Phaseolus vulgaris] | 25.06 | 0.0024372 | 0.395 |
| Gm-r1070-470 | myo inositol 1-phosphate synthase [Phaseolus vulgaris] | 20.72 | 0.0038845 | 0.404 |
| Gm-r1070-5201 | Inositol-3-phosphate synthase | 18.62 | 0.0050066 | 0.416 |
| Gm-r1070-2762 | drought responsive element binding protein [Glycine soja] | 19.90 | 0.0042792 | 0.427 |
| Gm-r1070-610 | No Hits | 6.69 | 0.0413548 | 0.433 |
| Gm-r1070-3635 | AT3g15840 [Arabidopsis thaliana] | 34.05 | 0.0011155 | 0.436 |
| Gm-r1088-8755 | mitochondrial pyruvate dehydrogenase kinase isoform 1 [Glycine max] | 30.31 | 0.0005699 | 0.440 |
| Gm-r1088-7770 | cytochrome P450 [Helianthus tuberosus] | 5.45 | 0.0478987 | 0.444 |
| Gm-r1088-6355 | Inositol-3-phosphate synthase (Myo-inositol-1-phosphate synthase) (IPS) | 16.03 | 0.0039325 | 0.461 |
| Gm-r1088-8748 | amidohydrolase family [Arabidopsis thaliana] | 67.81 | 3.545E-05 | 0.475 |
| Gm-r1070-3592 | cysteine proteinase [Glycine max] | 25.53 | 0.0023267 | 0.479 |
| Gm-r1088-2998 | unknown [Arabidopsis thaliana] | 14.04 | 0.0056507 | 0.486 |
| Gm-r1088-7764 | No Hits | 15.80 | 0.0040929 | 0.487 |
| Gm-r1088-7549 | putative arm repeat-containing protein [Oryza sativa (japonica cultivar-group)] | 37.99 | 0.0002699 | 0.488 |
| Gm-r1088-7948 | No Hits | 6.32 | 0.0361724 | 0.491 |
| Gm-r1088-8357 | AAA-type ATPase family protein [Arabidopsis thaliana] | 40.71 | 0.0002136 | 0.492 |
| Gm-r1088-1645 | unknown protein [Arabidopsis thaliana] | 28.11 | 0.0007265 | 0.495 |

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|---|---|---|---|---|
| Gm-r1070-3990 | No Hits | 8.35 | 0.02768 | 0.495 |
| Gm-r1088-8492 | Ammonium transporter [Lotus japonicus] | 52.18 | 9.036E-05 | 0.496 |
| Gm-r1088-8552 | No Hits | 37.49 | 0.0002822 | 0.500 |
| Gm-r1070-5440 | plasma membrane intrinsic polypeptide [Cicer arietinum] | 20.97 | 0.0037713 | 0.503 |
| Gm-r1070-7310 | AT3g15840 [Arabidopsis thaliana] | 46.82 | 0.0004791 | 0.505 |
| Gm-r1088-4151 | OSJNBa0088I22.7 [Oryza sativa (japonica cultivar-group)] | 29.43 | 0.0006273 | 0.508 |
| Gm-r1070-2546 | No Hits | 36.68 | 0.0009185 | 0.512 |
| Gm-r1070-1025 | photosystem II 23kDa polypeptide [Nicotiana tabacum] | 8.30 | 0.0280449 | 0.514 |
| Gm-r1070-5969 | copper chaperone homolog CCH [Glycine max] | 32.79 | 0.0012307 | 0.515 |
| Gm-r1088-1954 | At1g06690/F4H5_17 [Arabidopsis thaliana] | 20.59 | 0.0019055 | 0.517 |
| Gm-r1070-3118 | putative ripening-related protein [Vitis vinifera] | 9.22 | 0.0229213 | 0.520 |
| Gm-r1088-7824 | At1g71710/F14O23_9 [Arabidopsis thaliana] | 16.62 | 0.0035481 | 0.521 |
| Gm-r1088-8259 | No Hits | 71.94 | 2.86E-05 | 0.521 |
| Gm-r1088-7762 | No Hits | 45.04 | 0.0001509 | 0.524 |
| Gm-r1088-8691 | No Hits | 36.74 | 0.0003021 | 0.525 |
| Gm-r1070-2115 | No Hits | 19.48 | 0.0045008 | 0.527 |
| Gm-r1070-473 | At2g19670 [Arabidopsis thaliana] | 13.13 | 0.0110465 | 0.531 |
| Gm-r1070-1376 | ferredoxin--NADP(+) reductase [Nicotiana tabacum] | 47.90 | 0.0004504 | 0.534 |
| Gm-r1070-7879 | Unknown | 31.39 | 0.0013775 | 0.535 |
| Gm-r1070-2860 | No Hits | 24.54 | 0.0025689 | 0.536 |
| Gm-r1088-8472 | No Hits | 10.65 | 0.0114606 | 0.540 |
| Gm-r1070-8526 | grr1 [Glycine max] | 12.38 | 0.0125468 | 0.540 |
| Gm-r1070-4236 | cysteine proteinase [Glycine max] | 62.51 | 0.0002172 | 0.540 |
| Gm-r1088-3680 | alpha 1,4-glucan phosphorylase type H [Vicia faba var. minor] | 20.28 | 0.0019921 | 0.541 |
| Gm-r1088-8504 | No Hits | 26.48 | 0.0008787 | 0.542 |
| Gm-r1070-7203 | At1g54990/F14C21_5 [Arabidopsis thaliana] | 15.67 | 0.0074653 | 0.546 |
| Gm-r1070-1367 | Unknown | 8.15 | 0.0289671 | 0.547 |
| Gm-r1070-1450 | putative RNA binding protein [Arabidopsis thaliana] | 11.15 | 0.0156412 | 0.552 |
| Gm-r1088-8086 | At1g52190/F9I5_4 [Arabidopsis thaliana] | 11.94 | 0.0086274 | 0.553 |
| Gm-r1070-6230 | No Hits | 10.80 | 0.0166948 | 0.554 |
| Gm-r1088-8188 | thiol protease isoform B [Glycine max] | 60.08 | 5.478E-05 | 0.555 |
| Gm-r1070-269 | chloroplast oxygen-evolving enhancer protein [Manihot esculenta] | 6.73 | 0.0410129 | 0.559 |
| Gm-r1070-2347 | putative RNA recognition motif (RRM)-containing protein [Oryza sativa] | 40.74 | 0.0006955 | 0.560 |
| Gm-r1070-2003 | unknown protein [Arabidopsis thaliana] | 14.65 | 0.0086846 | 0.560 |

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|---|---|---|---|---|
| Gm-r1070-2666 | No Hits | 18.49 | 0.0050916 | 0.561 |
| Gm-r1070-1591 | probable ubiquitin-like protein [imported] - Arabidopsis thaliana | 17.96 | 0.0054495 | 0.564 |
| Gm-r1070-712 | No Hits | 7.20 | 0.0363897 | 0.565 |
| Gm-r1088-8359 | At5g49760 [Oryza sativa (japonica cultivar-group)] | 40.21 | 0.0002227 | 0.565 |
| Gm-r1070-6028 | putative leucine-rich repeat family protein [Gossypium hirsutum] | 9.33 | 0.0224019 | 0.567 |
| Gm-r1070-6232 | No Hits | 22.37 | 0.0032246 | 0.568 |
| Gm-r1070-5643 | No Hits | 15.81 | 0.0073147 | 0.568 |
| Gm-r1088-3307 | TGA-type basic leucine zipper protein TGA2.2 [Phaseolus vulgaris] | 10.45 | 0.0120138 | 0.569 |
| Gm-r1088-2959 | No Hits | 7.31 | 0.0269341 | 0.569 |
| Gm-r1070-3845 | No Hits | 28.87 | 0.0017071 | 0.569 |
| Gm-r1088-1421 | auxin-induced protein [Mesembryanthemum crystallinum] | 19.20 | 0.0023446 | 0.570 |
| Gm-r1088-6822 | ubiquitin carboxyl-terminal hydrolase [Arabidopsis thaliana] | 10.64 | 0.0114986 | 0.570 |
| Gm-r1070-442 | hypothetical protein [Gossypium hirsutum] | 7.89 | 0.0308031 | 0.579 |
| Gm-r1070-2653 | putative cinnamoyl-CoA reductase [Solanum demissum] | 38.15 | 0.000828 | 0.580 |
| Gm-r1088-873 | No Hits | 25.71 | 0.000964 | 0.582 |
| Gm-r1088-7720 | cysteine proteinase inhibitor [Glycine max] | 22.81 | 0.001397 | 0.583 |
| Gm-r1088-8186 | 1-aminocyclopropane-1-carboxylic acid oxidase [Phaseolus lunatus] | 17.25 | 0.0031925 | 0.583 |
| Gm-r1088-2763 | clathrin binding protein-like [Arabidopsis thaliana] | 9.51 | 0.0150305 | 0.584 |
| Gm-r1088-8736 | plastoglobule associated protein PG1 precursor [Pisum sativum] | 12.41 | 0.0078162 | 0.586 |
| Gm-r1088-8206 | putative potassium transporter AtKT1p [Arabidopsis thaliana] | 13.08 | 0.0068095 | 0.586 |
| Gm-r1088-5712 | ubiquitin-like protein [Arabidopsis thaliana] | 11.89 | 0.0087098 | 0.587 |
| Gm-r1088-2052 | unknown [Arabidopsis thaliana] | 8.45 | 0.0196627 | 0.588 |
| Gm-r1088-4384 | phi-1 [Nicotiana tabacum] | 14.99 | 0.0047283 | 0.591 |
| Gm-r1070-3836 | remorin 1 [Lycopersicon esculentum] | 10.01 | 0.0194751 | 0.591 |
| Gm-r1088-8939 | starch branching enzyme I [Pisum sativum] | 21.96 | 0.0015683 | 0.592 |
| Gm-r1088-8633 | alpha 1,4-glucan phosphorylase type H [Vicia faba var. minor] | 7.24 | 0.0274947 | 0.595 |
| Gm-r1070-239 | unnamed protein product [Arabidopsis thaliana] | 10.18 | 0.0188103 | 0.598 |
| Gm-r1070-2965 | Ca2+/H+-exchanging protein - mung bean | 132.44 | 2.587E-05 | 0.600 |
| Gm-r1088-8241 | No Hits | 8.03 | 0.0219968 | 0.601 |
| Gm-r1070-474 | No Hits | 10.49 | 0.0177097 | 0.602 |
| Gm-r1070-7508 | ubiquitin-like protein SMT3 [Phaseolus vulgaris] | 8.28 | 0.0281562 | 0.602 |
| Gm-r1070-3547 | putative purple acid phosphatase precursor [Phaseolus vulgaris] | 17.85 | 0.0055346 | 0.606 |
| Gm-r1088-8588 | sigma factor [Spinacia oleracea] | 22.47 | 0.0014635 | 0.607 |
| Gm-r1088-1226 | glycerophosphodiester phosphodiesterase-like protein [Manihot esculenta] | 5.86 | 0.0417947 | 0.608 |

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|---|---|---|---|---|
| Gm-r1088-442 | No Hits | 11.65 | 0.0091782 | 0.608 |
| Gm-r1088-7954 | methionine sulfoxide reductase A [Populus balsamifera] | 22.19 | 0.0015203 | 0.609 |
| Gm-r1088-2032 | Unknown | 7.74 | 0.0238759 | 0.609 |
| Gm-r1088-9138 | No Hits | 6.19 | 0.0376536 | 0.612 |
| Gm-r1088-2764 | CTF2A [Arabidopsis thaliana] | 13.49 | 0.0062885 | 0.613 |
| Gm-r1088-7612 | putative At5g37260 [Lycopersicon peruvianum] | 14.69 | 0.0050014 | 0.613 |
| Gm-r1088-6745 | OSJNBa0088A01.20 protein | 10.57 | 0.0116749 | 0.613 |
| Gm-r1088-3066 | expressed protein [Arabidopsis thaliana] | 7.77 | 0.0236656 | 0.614 |
| Gm-r1088-2292 | methionyl-tRNA synthetase [Oryza sativa (japonica cultivar-group)] | 8.91 | 0.0174778 | 0.615 |
| Gm-r1088-8400 | F4N2.16 [Arabidopsis thaliana] | 6.84 | 0.0308321 | 0.616 |
| Gm-r1088-6209 | putative At5g37260 [Lycopersicon peruvianum] | 13.18 | 0.0066846 | 0.616 |
| Gm-r1070-3076 | NHL repeat-containing protein-like [Oryza sativa (japonica cultivar-group)] | 36.24 | 0.000948 | 0.616 |
| Gm-r1070-6591 | AtABCA1 [Arabidopsis thaliana] | 6.67 | 0.0416389 | 0.618 |
| Gm-r1088-8931 | putative diacylglycerol kinase [Arabidopsis thaliana] | 14.59 | 0.0050962 | 0.620 |
| Gm-r1070-5454 | No Hits | 21.00 | 0.00376 | 0.621 |
| Gm-r1070-1948 | No Hits | 35.41 | 0.0010072 | 0.621 |
| Gm-r1088-7551 | Citrate synthase, glyoxysomal precursor (GCS) | 13.20 | 0.0066526 | 0.621 |
| Gm-r1088-8152 | T23G18.9 [Arabidopsis thaliana] | 37.74 | 0.0002759 | 0.622 |
| Gm-r1070-5971 | IAA21 [Arabidopsis thaliana] | 7.93 | 0.0305358 | 0.622 |
| Gm-r1070-1856 | No Hits | 14.70 | 0.0086225 | 0.623 |
| Gm-r1088-8301 | At5g38640 [Arabidopsis thaliana] | 48.47 | 0.000117 | 0.623 |
| Gm-r1088-1951 | DnaJ protein homolog ANJ1 | 14.17 | 0.0055081 | 0.624 |
| Gm-r1070-110 | ultraviolet-B-repressible protein [Gossypium hirsutum] | 19.57 | 0.0044541 | 0.629 |
| Gm-r1070-4114 | No Hits | 21.24 | 0.0036582 | 0.629 |
| Gm-r1088-6955 | Similar to nodulins and lipase homolog from Arabidopsis thaliana | 6.69 | 0.0323083 | 0.630 |
| Gm-r1088-9067 | short chain alcohol dehydrogenase [Nicotiana tabacum] | 36.31 | 0.0003144 | 0.631 |
| Gm-r1088-1742 | unknown protein [Arabidopsis thaliana] | 16.29 | 0.0037573 | 0.631 |
| Gm-r1070-3626 | putative protein [Arabidopsis thaliana] | 11.38 | 0.0149766 | 0.631 |
| Gm-r1088-2817 | unnamed protein product [Arabidopsis thaliana] | 11.46 | 0.0095699 | 0.633 |
| Gm-r1070-5251 | transcription factor EIL2 [Vigna radiata] | 14.18 | 0.009336 | 0.633 |
| Gm-r1070-1614 | At1g70820 [Arabidopsis thaliana] | 15.33 | 0.0078436 | 0.633 |
| Gm-r1070-4111 | No Hits | 19.92 | 0.0042702 | 0.633 |
| Gm-r1070-4995 | No Hits | 9.32 | 0.0224259 | 0.635 |
| Gm-r1070-7330 | copper chaperone homolog CCH [Glycine max] | 25.50 | 0.0023347 | 0.635 |

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|---|---|---|---|---|
| Gm-r1070-2954 | expressed protein [Arabidopsis thaliana] | 10.29 | 0.0184158 | 0.637 |
| Gm-r1070-783 | putative nodule membrane protein [Medicago sativa] | 6.38 | 0.044946 | 0.637 |
| Gm-r1070-8298 | adenosine 5'-phosphosulfate reductase [Glycine max] | 22.69 | 0.0031156 | 0.638 |
| Gm-r1088-2989 | unknown [Arabidopsis thaliana] | 15.45 | 0.004356 | 0.639 |
| Gm-r1088-8532 | hypothetical protein At2g26200 [imported] - Arabidopsis thaliana | 13.62 | 0.0061207 | 0.639 |
| Gm-r1070-1765 | adenosine 5' phosphosulfate reductase [Physcomitrella patens] | 39.93 | 0.0007337 | 0.640 |
| Gm-r1088-7024 | Contains similarity to an unknown protein F7A7_100 gi\|7327817 from Arabidopsis thaliana | 9.02 | 0.0169946 | 0.641 |
| Gm-r1070-4120 | At2g27385 [Arabidopsis thaliana] | 15.35 | 0.0078185 | 0.641 |
| Gm-r1088-8162 | unnamed protein product [Arabidopsis thaliana] | 9.41 | 0.015398 | 0.642 |
| Gm-r1070-6975 | No Hits | 22.65 | 0.0031284 | 0.642 |
| Gm-r1070-2393 | ABC transporter family protein [Arabidopsis thaliana] | 9.42 | 0.0219855 | 0.642 |
| Gm-r1088-7326 | trehalose-6-phosphate synthase [Ginkgo biloba] | 22.28 | 0.0015029 | 0.642 |
| Gm-r1088-8263 | aminotransferase 1 [Cucumis melo] | 11.35 | 0.0098044 | 0.642 |
| Gm-r1088-2765 | No Hits | 8.01 | 0.0221328 | 0.642 |
| Gm-r1088-2351 | OSJNBb0072N21.10 [Oryza sativa (japonica cultivar-group)] | 15.81 | 0.0040857 | 0.642 |
| Gm-r1070-6300 | No Hits | 37.28 | 0.0008801 | 0.643 |
| Gm-r1088-1453 | No Hits | 12.33 | 0.0079432 | 0.643 |
| Gm-r1088-8694 | No Hits | 10.98 | 0.0106411 | 0.644 |
| Gm-r1088-8388 | transketolase [Craterostigma plantagineum] | 23.76 | 0.0012324 | 0.645 |
| Gm-r1088-2014 | No Hits | 11.34 | 0.0098321 | 0.646 |
| Gm-r1088-5481 | expressed protein [Arabidopsis thaliana] | 26.84 | 0.0008423 | 0.647 |
| Gm-r1070-4830 | At1g02300/T6A9_10 [Arabidopsis thaliana] | 35.67 | 0.000988 | 0.647 |
| Gm-r1070-6198 | No Hits | 35.18 | 0.0010242 | 0.648 |
| Gm-r1070-4035 | Sali3-2 [Glycine max] | 32.31 | 0.001278 | 0.648 |
| Gm-r1070-4267 | carbonic anhydrase 2 [Flaveria bidentis] | 27.18 | 0.0019895 | 0.651 |
| Gm-r1070-3823 | xanthine dehydrogenase, putative [Arabidopsis thaliana] | 18.89 | 0.0048438 | 0.652 |
| Gm-r1088-1858 | phospholipid glutathione peroxidase [Pisum sativum] | 10.32 | 0.0123904 | 0.652 |
| Gm-r1070-237 | No Hits | 8.39 | 0.0274362 | 0.653 |
| Gm-r1088-8160 | No Hits | 17.67 | 0.0029805 | 0.653 |
| Gm-r1070-1388 | clp protease [Arabidopsis thaliana] | 7.89 | 0.030827 | 0.654 |
| Gm-r1088-5622 | zinc-finger protein [Oryza sativa (japonica cultivar-group)] | 35.27 | 0.0003464 | 0.654 |
| Gm-r1088-5837 | unknown protein [Oryza sativa (japonica cultivar-group)] | 11.82 | 0.0088573 | 0.655 |
| Gm-r1088-8165 | auxin response factor 10 [Oryza sativa] | 19.69 | 0.0021762 | 0.655 |

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|---|---|---|---|---|
| Gm-r1070-586 | No Hits | 7.71 | 0.0321415 | 0.655 |
| Gm-r1070-4422 | No Hits | 26.37 | 0.0021467 | 0.658 |
| Gm-r1070-391 | nine-cis-epoxycarotenoid dioxygenase1 [Pisum sativum] | 7.23 | 0.0360649 | 0.658 |
| Gm-r1088-8289 | No Hits | 9.44 | 0.0152733 | 0.658 |
| Gm-r1088-8198 | No Hits | 22.53 | 0.001452 | 0.660 |
| Gm-r1088-1641 | expressed protein [Arabidopsis thaliana] | 14.02 | 0.0056657 | 0.660 |
| Gm-r1088-4703 | putative leucine-rich repeat protein [Oryza sativa (japonica cultivar-group)] | 9.07 | 0.0167664 | 0.661 |
| Gm-r1088-8142 | photosystem I subunit PSI-E [Nicotiana sylvestris] | 35.26 | 0.0003465 | 0.661 |
| Gm-r1088-9131 | OSJNBa0039C07.7 [Oryza sativa (japonica cultivar-group)] | 42.88 | 0.0001788 | 0.662 |
| Gm-r1088-1860 | chloroplast protease [Capsicum annuum] | 8.51 | 0.019386 | 0.663 |
| Gm-r1070-5393 | Ca2+/H+-exchanging protein - mung bean | 29.73 | 0.0015836 | 0.663 |
| Gm-r1088-4056 | unknown [Hyacinthus orientalis] | 54.30 | 7.851E-05 | 0.665 |
| Gm-r1088-1628 | selenium binding protein [Medicago sativa] | 9.12 | 0.0165622 | 0.666 |
| Gm-r1088-2795 | hypothetical protein At2g39470 [imported] - Arabidopsis thaliana | 10.04 | 0.0132332 | 0.666 |
| Gm-r1070-1970 | No Hits | 21.95 | 0.0033791 | 0.667 |
| Gm-r1070-5793 | alpha glucosidase-like protein [Arabidopsis thaliana] | 29.62 | 0.001598 | 0.668 |
| Gm-r1088-7241 | No Hits | 14.86 | 0.0048459 | 0.669 |
| Gm-r1088-899 | At5g13180/T19L5_140 [Arabidopsis thaliana] | 10.29 | 0.0124584 | 0.669 |
| Gm-r1070-801 | unnamed protein product [Homo sapiens] | 18.62 | 0.0050125 | 0.669 |
| Gm-r1070-5787 | microsomal omega-3 fatty acid desaturase [Glycine max] | 12.31 | 0.0126861 | 0.670 |
| Gm-r1088-1383 | unknown protein [Oryza sativa (japonica cultivar-group)] | 5.84 | 0.0420371 | 0.670 |
| Gm-r1088-6179 | transcription factor EIL1 [Vigna radiata] | 7.01 | 0.0293263 | 0.671 |
| Gm-r1088-7533 | unknown protein [Arabidopsis thaliana] | 22.97 | 0.0013675 | 0.671 |
| Gm-r1088-7900 | chlorophyll a/b-binding protein CP26 precursor - maize [Oryza sativa] | 11.12 | 0.0103186 | 0.672 |
| Gm-r1088-5225 | similar to squamosa-promoter binding protein 1 isolog gi\|1707009 [Arabidopsis thaliana] | 6.08 | 0.0389438 | 0.672 |
| Gm-r1088-5070 | ubiquitin carrier protein | 6.53 | 0.0339066 | 0.673 |
| Gm-r1088-8013 | putative ZEITLUPE [Oryza sativa (japonica cultivar-group)] | 13.72 | 0.0060095 | 0.673 |
| Gm-r1070-3136 | At5g13560 [Arabidopsis thaliana] | 14.19 | 0.0093264 | 0.674 |
| Gm-r1088-4851 | Pathogenesis-related genes transcriptional activator PTI5 (PTO-interacting protein 5) | 10.91 | 0.0108037 | 0.674 |
| Gm-r1070-6007 | hypothetical protein At2g39050 [imported] - Arabidopsis thaliana | 11.15 | 0.0156192 | 0.674 |
| Gm-r1088-8328 | No Hits | 36.42 | 0.000311 | 0.676 |
| Gm-r1070-2956 | phenylalkylamine binding protein homolog [Arabidopsis thaliana] | 9.59 | 0.0211951 | 0.676 |

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|---|---|---|---|---|
| Gm-r1070-3887 | No Hits | 7.66 | 0.0325088 | 0.676 |
| Gm-r1088-32 | TGF-beta receptor-interacting protein 1 [Phaseolus vulgaris] | 6.72 | 0.0320243 | 0.677 |
| Gm-r1088-8681 | No Hits | 33.56 | 0.0004083 | 0.678 |
| Gm-r1070-6262 | unknown protein [Arabidopsis thaliana] | 18.47 | 0.0051037 | 0.678 |
| Gm-r1088-6820 | type 2 metallothionein [Glycine max] | 11.62 | 0.0092407 | 0.678 |
| Gm-r1070-2234 | putative glutamate decarboxylase [Glycine max] | 9.51 | 0.0215638 | 0.678 |
| Gm-r1070-2810 | No Hits | 7.34 | 0.0351595 | 0.679 |
| Gm-r1070-1413 | class II knotted-like homeodomain protein [Lycopersicon esculentum] | 21.56 | 0.003527 | 0.679 |
| Gm-r1088-5613 | FtsH-like protein Pftf precursor [Nicotiana tabacum] | 5.84 | 0.0420568 | 0.679 |
| Gm-r1070-480 | No Hits | 8.57 | 0.0263557 | 0.680 |
| Gm-r1088-8115 | At5g50320/MXI22_3 [Arabidopsis thaliana] | 11.93 | 0.0086468 | 0.680 |
| Gm-r1070-798 | unknown [Arabidopsis thaliana] | 21.41 | 0.0035902 | 0.681 |
| Gm-r1088-8334 | No Hits | 18.35 | 0.0026758 | 0.681 |
| Gm-r1070-2990 | unnamed protein product [Arabidopsis thaliana] | 29.09 | 0.0016746 | 0.681 |
| Gm-r1070-5791 | Enod8.2 [Medicago truncatula] | 16.28 | 0.006846 | 0.682 |
| Gm-r1070-5835 | transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] | 25.77 | 0.0022739 | 0.682 |
| Gm-r1088-5835 | hypothetical protein [Arabidopsis thaliana] | 17.00 | 0.0033304 | 0.683 |
| Gm-r1070-6782 | At1g02300/T6A9_10 [Arabidopsis thaliana] | 14.87 | 0.0083981 | 0.683 |
| Gm-r1088-4110 | No Hits | 12.84 | 0.007153 | 0.683 |
| Gm-r1088-3170 | somatic embryogenesis receptor kinase 1 [Medicago truncatula] | 7.47 | 0.0257186 | 0.683 |
| Gm-r1088-8284 | No Hits | 17.82 | 0.0029118 | 0.684 |
| Gm-r1070-5188 | subtilisin-like protease C1 [Glycine max] | 10.91 | 0.0163558 | 0.684 |
| Gm-r1088-3083 | unknown protein [Arabidopsis thaliana] | 6.74 | 0.031828 | 0.684 |
| Gm-r1088-8585 | protein phosphatase 2c [Medicago sativa] | 15.42 | 0.0043739 | 0.684 |
| Gm-r1070-8296 | putative cinnamoyl-CoA reductase [Solanum demissum] | 8.30 | 0.0280212 | 0.684 |
| Gm-r1070-972 | No Hits | 21.16 | 0.0036938 | 0.684 |
| Gm-r1070-6923 | lipoic acid synthase-like protein [Arabidopsis thaliana] | 8.59 | 0.026267 | 0.685 |
| Gm-r1088-439 | proline-rich family protein [Arabidopsis thaliana] | 9.42 | 0.0153615 | 0.685 |
| Gm-r1088-5620 | putative cytochrome P450 [Glycine max] | 9.35 | 0.0156245 | 0.685 |
| Gm-r1070-5241 | hypothetical protein [Oryza sativa (japonica cultivar-group)] | 36.03 | 0.0009621 | 0.685 |
| Gm-r1088-5258 | unknown protein [Oryza sativa (japonica cultivar-group)] | 18.46 | 0.0026278 | 0.686 |
| Gm-r1088-8293 | ripening-related protein-like; contains similarity to pectinesterase [Arabidopsis thaliana] | 30.15 | 0.0005797 | 0.686 |
| Gm-r1070-3472 | abscisic stress ripening-like protein [Prunus persica] | 9.18 | 0.0230959 | 0.686 |

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| Gm-r1088-2893 | glycine hydroxymethyltransferase [Solanum tuberosum] | 19.76 | 0.0021513 | 0.686 |
| Gm-r1070-3503 | No Hits | 15.21 | 0.0079806 | 0.686 |
| Gm-r1088-7553 | putative WD-40 repeat protein [Arabidopsis thaliana] | 29.94 | 0.0005929 | 0.686 |
| Gm-r1070-622 | No Hits | 14.27 | 0.0092081 | 0.687 |
| Gm-r1088-8398 | copia-type polyprotein, putative [Arabidopsis thaliana] | 5.96 | 0.0404667 | 0.687 |
| Gm-r1088-8119 | unknown [Arabidopsis thaliana] | 14.24 | 0.0054415 | 0.687 |
| Gm-r1070-5970 | hypothetical protein At2g03890 [imported] - Arabidopsis thaliana | 10.63 | 0.0172344 | 0.687 |
| Gm-r1088-6604 | MATE efflux family protein [Arabidopsis thaliana] | 14.00 | 0.0056912 | 0.687 |
| Gm-r1070-2163 | No Hits | 12.88 | 0.0115257 | 0.688 |
| Gm-r1088-1852 | No Hits | 6.79 | 0.0313507 | 0.688 |
| Gm-r1088-5277 | No Hits | 8.87 | 0.0176456 | 0.688 |
| Gm-r1088-8338 | No Hits | 11.17 | 0.0102069 | 0.690 |
| Gm-r1070-968 | No Hits | 11.91 | 0.0136163 | 0.690 |
| Gm-r1088-4901 | hypothetical protein [Arabidopsis thaliana] | 11.72 | 0.0090495 | 0.690 |
| Gm-r1070-2390 | No Hits | 28.34 | 0.0017884 | 0.691 |
| Gm-r1088-2814 | unknown protein [Arabidopsis thaliana] | 5.91 | 0.0410881 | 0.692 |
| Gm-r1088-8291 | No Hits | 7.73 | 0.0239 | 0.692 |
| Gm-r1088-2832 | cytosol aminopeptidase family protein [Arabidopsis thaliana] | 6.24 | 0.037067 | 0.692 |
| Gm-r1088-3896 | At2g15890 [Arabidopsis thaliana] | 13.21 | 0.0066425 | 0.692 |
| Gm-r1070-4490 | expressed protein [Arabidopsis thaliana] | 7.43 | 0.0344061 | 0.692 |
| Gm-r1088-7728 | At3g24420 [Arabidopsis thaliana] | 13.29 | 0.0065372 | 0.693 |
| Gm-r1088-7667 | No Hits | 8.71 | 0.0183902 | 0.693 |
| Gm-r1070-1073 | No Hits | 22.61 | 0.0031429 | 0.693 |
| Gm-r1088-7761 | unknown protein [Arabidopsis thaliana] | 9.08 | 0.0167294 | 0.694 |
| Gm-r1070-6056 | BEL1-related homeotic protein 29 [Solanum tuberosum] | 20.16 | 0.0041461 | 0.695 |
| Gm-r1088-5341 | No Hits | 12.74 | 0.0073004 | 0.696 |
| Gm-r1088-2558 | protein kinase (APK1b) [Arabidopsis thaliana] | 8.00 | 0.0222 | 0.696 |
| Gm-r1070-6243 | BEL1-related homeotic protein 29 [Solanum tuberosum] | 13.20 | 0.0109265 | 0.697 |
| Gm-r1088-2324 | No Hits | 8.25 | 0.0207427 | 0.697 |
| Gm-r1088-1470 | cysteine synthase [Nicotiana tabacum] | 17.76 | 0.0029375 | 0.697 |
| Gm-r1088-2794 | putative lipoic acid synthase LIP1 [Arabidopsis thaliana] | 6.20 | 0.0375798 | 0.697 |
| Gm-r1070-3844 | protein P21 | 30.56 | 0.0014755 | 0.698 |
| Gm-r1088-8361 | DNA-binding protein PD1 [Pisum sativum] | 27.40 | 0.0007886 | 0.698 |
| Gm-r1070-8317 | RAB1Y [Lotus corniculatus var. japonicus] | 11.95 | 0.0135076 | 0.698 |

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| Gm-r1088-8915 | No Hits | 34.28 | 0.0003806 | 0.699 |
| Gm-r1088-3561 | unknown protein [Arabidopsis thaliana] | 5.35 | 0.0494677 | 0.699 |
| Gm-r1070-1172 | unknown [Arabidopsis thaliana] | 14.43 | 0.0089772 | 0.699 |
| Gm-r1088-5075 | At4g16650/dl4350w [Arabidopsis thaliana] | 5.82 | 0.0424113 | 0.700 |
| Gm-r1088-1281 | unknown protein [Arabidopsis thaliana] | 11.39 | 0.009718 | 0.700 |
| Gm-r1070-475 | LHCII type III chlorophyll a/b binding protein [Vigna radiata] | 11.56 | 0.0144838 | 0.700 |
| Gm-r1070-669 | chlorophyll a/b-binding protein type I [Malus x domestica] | 28.15 | 0.00182 | 0.700 |
| Gm-r1070-3096 | hypothetical protein [Cicer arietinum] | 23.19 | 0.0029525 | 0.700 |
| Gm-r1070-472 | No Hits | 7.46 | 0.0340946 | 0.700 |
| Gm-r1070-985 | No Hits | 16.09 | 0.0070282 | 0.701 |
| Gm-r1070-8342 | Plastid-lipid associated protein, chloroplast precursor (CitPAP) | 12.04 | 0.0132976 | 0.701 |
| Gm-r1088-4855 | unnamed protein product [Arabidopsis thaliana] | 13.51 | 0.0062643 | 0.701 |
| Gm-r1070-1121 | putative mitochondrial dicarboxylate carrier protein [Arabidopsis thaliana] | 9.07 | 0.0236314 | 0.702 |
| Gm-r1070-5817 | No Hits | 7.88 | 0.0308848 | 0.702 |
| Gm-r1088-1230 | dihydrofolate synthetase/folylpolyglutamate synthetase [Arabidopsis thaliana] | 12.29 | 0.0080047 | 0.702 |
| Gm-r1088-8171 | NAM-like protein [Prunus persica] | 20.07 | 0.002055 | 0.703 |
| Gm-r1088-2903 | unknown protein [Arabidopsis thaliana] | 13.09 | 0.0068029 | 0.703 |
| Gm-r1088-8387 | putative protein [Arabidopsis thaliana] | 22.20 | 0.0015182 | 0.703 |
| Gm-r1070-991 | No Hits | 10.18 | 0.0188069 | 0.704 |
| Gm-r1070-1115 | No Hits | 8.72 | 0.0255123 | 0.704 |
| Gm-r1070-5187 | No Hits | 7.56 | 0.0333345 | 0.705 |
| Gm-r1088-8348 | No Hits | 18.97 | 0.0024293 | 0.705 |
| Gm-r1088-458 | ferredoxin thioredoxin reductase precursor [Glycine max] | 15.58 | 0.0042548 | 0.706 |
| Gm-r1070-6071 | transaldolase [Pseudomonas putida KT2440] | 14.05 | 0.009523 | 0.706 |
| Gm-r1070-6962 | hypothetical protein At2g31380 [imported] - Arabidopsis thaliana | 17.81 | 0.0055572 | 0.706 |
| Gm-r1070-2392 | No Hits | 8.74 | 0.0254121 | 0.707 |
| Gm-r1088-7820 | No Hits | 9.65 | 0.014521 | 0.707 |
| Gm-r1088-8138 | No Hits | 19.95 | 0.0020931 | 0.707 |
| Gm-r1070-1402 | No Hits | 8.86 | 0.0247638 | 0.707 |
| Gm-r1070-6206 | CcmE/CycJ protein [Nitrosomonas eutropha C71] | 17.80 | 0.0055694 | 0.708 |
| Gm-r1070-1771 | aminoacyl-t-RNA synthetase, putative [Arabidopsis thaliana] | 8.20 | 0.0286677 | 0.708 |
| Gm-r1070-5577 | No Hits | 9.56 | 0.0213431 | 0.708 |
| Gm-r1088-8933 | hypothetical protein [Oryza sativa (japonica cultivar-group)] | 7.01 | 0.0293604 | 0.709 |
| Gm-r1088-34 | No Hits | 5.63 | 0.0450892 | 0.710 |

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| Gm-r1070-1954 | histone H2B [Cicer arietinum] | 13.20 | 0.0109256 | 0.711 |
| Gm-r1070-1206 | unknown [Arabidopsis thaliana] | 11.39 | 0.014948 | 0.711 |
| Gm-r1070-6024 | MADS box transcription factor [Daucus carota subsp. sativus] | 23.64 | 0.0028166 | 0.712 |
| Gm-r1070-5231 | unknown protein [Arabidopsis thaliana] | 12.88 | 0.0115251 | 0.712 |
| Gm-r1070-3733 | 1-deoxy-D-xylulose 5-phosphate reductoisomerase [Pueraria montana var. lobata] | 11.67 | 0.0142209 | 0.712 |
| Gm-r1088-2001 | No Hits | 7.71 | 0.0240423 | 0.712 |
| Gm-r1070-5904 | Unknown protein [Arabidopsis thaliana] | 9.73 | 0.0205897 | 0.712 |
| Gm-r1088-1246 | putative protein [Arabidopsis thaliana] | 7.38 | 0.0264072 | 0.713 |
| Gm-r1088-7595 | Glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform (G6PD) | 10.15 | 0.0128772 | 0.713 |
| Gm-r1088-8522 | AT3g16950/K14A17_7 [Arabidopsis thaliana] | 18.57 | 0.0025831 | 0.713 |
| Gm-r1070-3855 | serine acetyltransferase [Glycine max] | 16.16 | 0.0069566 | 0.713 |
| Gm-r1088-7964 | No Hits | 8.07 | 0.0217568 | 0.714 |
| Gm-r1070-1738 | dehydrin [Glycine max] | 7.83 | 0.0312475 | 0.714 |
| Gm-r1088-634 | unknown [Arabidopsis thaliana] | 8.92 | 0.0174382 | 0.715 |
| Gm-r1070-3821 | putative von Hippel-Lindau binding protein [Arabidopsis thaliana] | 9.17 | 0.0231727 | 0.715 |
| Gm-r1070-2972 | No Hits | 6.87 | 0.0395655 | 0.715 |
| Gm-r1088-8365 | At1g16520 [Arabidopsis thaliana] | 16.96 | 0.0033523 | 0.716 |
| Gm-r1088-8350 | No Hits | 19.86 | 0.0021223 | 0.716 |
| Gm-r1070-2004 | No Hits | 13.23 | 0.0108627 | 0.717 |
| Gm-r1088-2958 | thioredoxin h [Pisum sativum] | 13.79 | 0.005921 | 0.717 |
| Gm-r1070-3597 | phosphoenolpyruvate carboxykinase [Flaveria pringlei] | 9.37 | 0.0221831 | 0.717 |
| Gm-r1070-655 | DNAJ PROTEIN HOMOLOG ATJ [Arabidopsis thaliana] | 26.31 | 0.0021589 | 0.717 |
| Gm-r1070-988 | No Hits | 11.51 | 0.0146348 | 0.717 |
| Gm-r1070-7575 | No Hits | 13.30 | 0.0107405 | 0.718 |
| Gm-r1070-5011 | No Hits | 6.33 | 0.0455625 | 0.718 |
| Gm-r1088-3018 | No Hits | 15.92 | 0.0040084 | 0.718 |
| Gm-r1088-8087 | Photosystem I reaction center subunit II, chloroplast precursor (PSI-D) (PS I subunit 5) | 17.97 | 0.0028407 | 0.718 |
| Gm-r1070-5291 | No Hits | 19.12 | 0.0047055 | 0.718 |
| Gm-r1070-917 | No Hits | 19.59 | 0.0044435 | 0.718 |
| Gm-r1070-8484 | Chain A, Crystal Structure Of Soybean Beta-Amylase Mutant (M51t) | 11.41 | 0.0148882 | 0.719 |
| Gm-r1088-5848 | phospholipase-like protein [Arabidopsis thaliana] | 9.05 | 0.016869 | 0.719 |
| Gm-r1070-6616 | cellulose synthase (EC 2.4.1.-) catalytic chain celA2 - upland cotton (fragment) | 10.68 | 0.0170728 | 0.719 |
| Gm-r1070-602 | No Hits | 9.11 | 0.023461 | 0.719 |

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| Gm-r1088-1998 | putative ATP synthase gamma chain 1, chloroplast (H(+)-transporting [Oryza sativa] | 13.12 | 0.0067672 | 0.719 |
| Gm-r1070-871 | No Hits | 19.91 | 0.0042711 | 0.719 |
| Gm-r1070-651 | No Hits | 10.41 | 0.0180008 | 0.720 |
| Gm-r1088-7614 | DnaJ-like protein [Phaseolus vulgaris] | 12.50 | 0.0076683 | 0.720 |
| Gm-r1088-5052 | Bax inhibitor 1 [Nicotiana tabacum] | 11.79 | 0.0089102 | 0.720 |
| Gm-r1088-3530 | unknown [Arabidopsis thaliana] | 29.67 | 0.000611 | 0.720 |
| Gm-r1088-8908 | No Hits | 16.47 | 0.0036389 | 0.720 |
| Gm-r1070-893 | No Hits | 12.93 | 0.0114208 | 0.721 |
| Gm-r1070-4047 | No Hits | 11.07 | 0.0158692 | 0.721 |
| Gm-r1088-1955 | unknown protein [Arabidopsis thaliana] | 6.16 | 0.0380061 | 0.721 |
| Gm-r1088-5025 | isoflavone reductase homolog 1 [Glycine max] | 25.60 | 0.0009769 | 0.722 |
| Gm-r1088-8489 | At1g16320/F3O9_12 [Arabidopsis thaliana] | 6.74 | 0.0317954 | 0.722 |
| Gm-r1070-5995 | unknown protein [Arabidopsis thaliana] | 8.68 | 0.0257674 | 0.722 |
| Gm-r1088-9110 | putative enoyl-CoA hydratase [Arabidopsis thaliana] | 36.84 | 0.0002994 | 0.723 |
| Gm-r1070-829 | No Hits | 11.73 | 0.0140573 | 0.723 |
| Gm-r1088-5323 | homeodomain leucine zipper protein HDZ2 [Phaseolus vulgaris] | 8.98 | 0.01715 | 0.724 |
| Gm-r1088-3468 | PREDICTED P0455F03.23 gene product [Oryza sativa (japonica cultivar-group)] | 7.99 | 0.0222403 | 0.724 |
| Gm-r1088-409 | eukaryotic translation initiation factor 2B family protein [Arabidopsis thaliana] | 13.06 | 0.0068431 | 0.725 |
| Gm-r1070-2523 | GCPE protein [Catharanthus roseus] | 35.05 | 0.0010345 | 0.725 |
| Gm-r1088-5627 | hypothetical protein - Arabidopsis thaliana | 10.10 | 0.0130238 | 0.725 |
| Gm-r1088-7846 | NIT4A [Lupinus angustifolius] | 5.73 | 0.0436617 | 0.726 |
| Gm-r1088-8283 | No Hits | 19.90 | 0.002108 | 0.726 |
| Gm-r1070-892 | glutaredoxin family protein [Arabidopsis thaliana] | 8.10 | 0.0293508 | 0.726 |
| Gm-r1088-8587 | zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] | 11.52 | 0.0094362 | 0.727 |
| Gm-r1070-4068 | No Hits | 18.73 | 0.0049435 | 0.727 |
| Gm-r1088-8140 | No Hits | 45.53 | 0.0001454 | 0.727 |
| Gm-r1088-3266 | Phosphoribulokinase, chloroplast precursor (Phosphopentokinase) (PRKase) (PRK) | 16.84 | 0.00342 | 0.728 |
| Gm-r1070-770 | No Hits | 8.00 | 0.0300103 | 0.729 |
| Gm-r1070-6170 | NAM-like protein [Prunus persica] | 20.16 | 0.0041498 | 0.729 |
| Gm-r1070-6201 | unknown protein [Arabidopsis thaliana] | 25.38 | 0.0023629 | 0.729 |
| Gm-r1070-1049 | No Hits | 8.30 | 0.0280309 | 0.729 |
| Gm-r1070-4232 | No Hits | 47.23 | 0.0004679 | 0.730 |

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| Gm-r1088-3048 | putative protein [Arabidopsis thaliana] | 6.03 | 0.0395946 | 0.730 |
| Gm-r1070-3296 | No Hits | 9.23 | 0.0228377 | 0.730 |
| Gm-r1088-7353 | unknown protein [Arabidopsis thaliana] | 6.66 | 0.0325926 | 0.730 |
| Gm-r1070-1749 | unnamed protein product [Pisum sativum] | 6.87 | 0.0395111 | 0.730 |
| Gm-r1088-3952 | unknown protein [Arabidopsis thaliana] | 11.16 | 0.0102272 | 0.731 |
| Gm-r1070-3688 | putative plastid glucose 6 phosphate/phosphate translocator [Glycine max] | 8.49 | 0.0268433 | 0.731 |
| Gm-r1088-38 | no apical meristem (NAM) protein-related [Arabidopsis thaliana] | 13.61 | 0.0061402 | 0.731 |
| Gm-r1088-807 | glycosyltransferase [Medicago truncatula] | 9.58 | 0.0147814 | 0.732 |
| Gm-r1070-899 | No Hits | 10.99 | 0.0160899 | 0.732 |
| Gm-r1070-1859 | adenosine 5'-phosphosulfate reductase [Glycine max] | 8.62 | 0.0260904 | 0.732 |
| Gm-r1070-1019 | No Hits | 19.04 | 0.0047531 | 0.732 |
| Gm-r1088-1999 | No Hits | 11.42 | 0.0096511 | 0.732 |
| Gm-r1070-671 | No Hits | 8.08 | 0.0294687 | 0.732 |
| Gm-r1070-796 | mRNA binding protein precursor-like [Arabidopsis thaliana] | 14.05 | 0.0095228 | 0.732 |
| Gm-r1088-8069 | receptor-like kinase Xa21-binding protein 3 [Oryza sativa] | 12.11 | 0.0083196 | 0.733 |
| Gm-r1070-3561 | No Hits | 8.26 | 0.0282963 | 0.733 |
| Gm-r1088-8392 | unknown protein [Arabidopsis thaliana] | 6.78 | 0.0313877 | 0.733 |
| Gm-r1088-8539 | No Hits | 9.11 | 0.0165984 | 0.733 |
| Gm-r1070-3131 | Fas-associated factor 1-like protein [Capsicum annuum] | 20.20 | 0.0041265 | 0.733 |
| Gm-r1088-8322 | putative p60 katanin [Oryza sativa (japonica cultivar-group)] | 12.95 | 0.0070004 | 0.733 |
| Gm-r1088-8529 | hydrolase-like [Oryza sativa (japonica cultivar-group)] | 7.85 | 0.0231256 | 0.734 |
| Gm-r1070-921 | No Hits | 9.91 | 0.0198489 | 0.735 |
| Gm-r1088-2842 | MAR-binding protein MFP1 homolog [Nicotiana tabacum] | 7.49 | 0.0255405 | 0.735 |
| Gm-r1088-80 | GHMYB38 [Gossypium hirsutum] | 6.98 | 0.0296214 | 0.735 |
| Gm-r1070-6138 | No Hits | 16.86 | 0.0063103 | 0.735 |
| Gm-r1070-6359 | invertase/pectin methylesterase inhibitor family protein [Arabidopsis thaliana] | 6.56 | 0.0428507 | 0.736 |
| Gm-r1070-854 | At4g34190/F28A23_50 [Arabidopsis thaliana] | 12.98 | 0.0113347 | 0.737 |
| Gm-r1088-8330 | putative protein [Arabidopsis thaliana] | 22.07 | 0.0015458 | 0.738 |
| Gm-r1088-6960 | predicted protein of unknown function [Arabidopsis thaliana] | 8.91 | 0.0174846 | 0.738 |
| Gm-r1088-2158 | unnamed protein product [Arabidopsis thaliana] | 12.31 | 0.0079734 | 0.738 |
| Gm-r1070-1013 | No Hits | 11.18 | 0.0155442 | 0.738 |
| Gm-r1088-1876 | unknown protein [Arabidopsis thaliana] | 11.77 | 0.0089365 | 0.738 |
| Gm-r1088-1228 | putative chlorophyll a/b-binding protein [Arabidopsis thaliana] | 6.66 | 0.0325591 | 0.738 |
| Gm-r1070-1666 | No Hits | 11.41 | 0.0149081 | 0.739 |

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| Gm-r1088-6616 | selenium binding protein [Medicago sativa] | 21.37 | 0.0017042 | 0.739 |
| Gm-r1070-2966 | 2-dehydro-3-deoxyphosphoheptonate aldolase [Arabidopsis thaliana] | 9.35 | 0.0223003 | 0.739 |
| Gm-r1088-2030 | early flowering 3 [Mesembryanthemum crystallinum] | 8.91 | 0.0174595 | 0.739 |
| Gm-r1088-653 | expressed protein [Arabidopsis thaliana] | 6.02 | 0.0396989 | 0.740 |
| Gm-r1070-2900 | No Hits | 14.52 | 0.0088554 | 0.740 |
| Gm-r1070-2022 | flavonol synthase [Allium cepa] | 11.22 | 0.015438 | 0.740 |
| Gm-r1070-795 | No Hits | 8.62 | 0.0260751 | 0.741 |
| Gm-r1070-4104 | No Hits | 11.86 | 0.0137332 | 0.741 |
| Gm-r1070-1996 | UDP-glucose glucosyltransferase [Catharanthus roseus] | 13.40 | 0.0105663 | 0.741 |
| Gm-r1070-6997 | remorin 1 [Lycopersicon esculentum] | 11.01 | 0.0160458 | 0.741 |
| Gm-r1088-3734 | hypothetical protein [Oryza sativa (japonica cultivar-group)] | 5.44 | 0.0479932 | 0.742 |
| Gm-r1070-5073 | unknown [Arabidopsis thaliana] | 9.63 | 0.0210201 | 0.743 |
| Gm-r1088-5210 | proline-rich protein | 10.40 | 0.0121586 | 0.743 |
| Gm-r1088-7783 | No Hits | 11.01 | 0.0105666 | 0.743 |
| Gm-r1070-3628 | protein kinase family protein [Arabidopsis thaliana] | 9.49 | 0.0216322 | 0.743 |
| Gm-r1070-4704 | zinc finger protein; WRKY1 [Pimpinella brachycarpa] | 6.79 | 0.0403723 | 0.744 |
| Gm-r1070-4037 | At1g55080 [Arabidopsis thaliana] | 10.01 | 0.0194587 | 0.745 |
| Gm-r1070-1029 | No Hits | 6.17 | 0.0475999 | 0.745 |
| Gm-r1088-7359 | protein kinase family protein [Arabidopsis thaliana] | 12.15 | 0.0082591 | 0.745 |
| Gm-r1070-3891 | No Hits | 16.47 | 0.0066676 | 0.745 |
| Gm-r1070-727 | No Hits | 8.36 | 0.0276327 | 0.746 |
| Gm-r1070-6535 | At4g12080/F16J13_150 [Arabidopsis thaliana] | 7.35 | 0.0350716 | 0.746 |
| Gm-r1088-2954 | putative protein [Arabidopsis thaliana] | 8.77 | 0.0181128 | 0.746 |
| Gm-r1088-5700 | No Hits | 7.20 | 0.027755 | 0.747 |
| Gm-r1088-4107 | pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] | 10.12 | 0.0129661 | 0.747 |
| Gm-r1088-8363 | unknown protein [Oryza sativa (japonica cultivar-group)] | 20.39 | 0.0019601 | 0.747 |
| Gm-r1070-6380 | harpin-induced protein 1 family (HIN1)-like [Oryza sativa (japonica cultivar-group)] | 18.43 | 0.0051302 | 0.747 |
| Gm-r1088-3516 | T12C24.17 [Arabidopsis thaliana] | 9.90 | 0.0136608 | 0.747 |
| Gm-r1088-2809 | unknown protein [Arabidopsis thaliana] | 7.70 | 0.0241059 | 0.748 |
| Gm-r1070-962 | No Hits | 11.61 | 0.0143652 | 0.748 |
| Gm-r1070-791 | oxygen evolving enhancer protein 1 precursor [Bruguiera gymnorrhiza] | 6.35 | 0.0452639 | 0.748 |
| Gm-r1088-6665 | putative phosphatase (with alternative splicing) [Oryza sativa (japonica cultivar-group)] | 9.70 | 0.0143506 | 0.748 |

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|---|---|---|---|---|
| Gm-r1088-8143 | aldose 1-epimerase-like protein [Arabidopsis thaliana] | 9.15 | 0.0164282 | 0.749 |
| Gm-r1088-8091 | protein F15H18.11 [imported] - Arabidopsis thaliana | 5.62 | 0.0451715 | 0.749 |
| Gm-r1088-8311 | No Hits | 11.92 | 0.0086659 | 0.749 |
| Gm-r1070-3494 | pollen coat-like protein [Arabidopsis thaliana] | 6.16 | 0.0476655 | 0.750 |
| Gm-r1070-1385 | ribosomal RNA adenine dimethylase family protein [Arabidopsis thaliana] | 9.25 | 0.0227534 | 0.750 |
| Gm-r1070-2002 | unknown [Arabidopsis thaliana] | 8.52 | 0.0266448 | 0.750 |
| Gm-r1070-2021 | unknown protein [Arabidopsis thaliana] | 9.96 | 0.0196764 | 0.751 |
| Gm-r1070-6555 | hypothetical protein F22O13.20 - Arabidopsis thaliana | 15.84 | 0.007279 | 0.751 |
| Gm-r1070-9 | chloroplast ribosomal L1-like protein [Arabidopsis thaliana] | 6.38 | 0.0448871 | 0.751 |
| Gm-r1088-2736 | No Hits | 10.29 | 0.0124543 | 0.751 |
| Gm-r1088-4501 | At2g29510 [Arabidopsis thaliana] | 12.54 | 0.0076098 | 0.751 |
| Gm-r1088-7920 | No Hits | 21.24 | 0.0017364 | 0.751 |
| Gm-r1088-5486 | putative ripening-related protein [Vitis vinifera] | 11.81 | 0.0088769 | 0.752 |
| Gm-r1088-6177 | allene oxide cyclase [Medicago truncatula] | 6.38 | 0.035444 | 0.752 |
| Gm-r1088-678 | putative mucin [Oryza sativa] | 15.53 | 0.0042888 | 0.752 |
| Gm-r1070-2547 | No Hits | 8.75 | 0.0253515 | 0.752 |
| Gm-r1070-811 | No Hits | 16.00 | 0.0071161 | 0.752 |
| Gm-r1088-1979 | No Hits | 6.46 | 0.0346211 | 0.752 |
| Gm-r1070-5797 | P-protein [Flaveria anomala] | 10.64 | 0.017196 | 0.752 |
| Gm-r1088-9036 | No Hits | 6.79 | 0.0313675 | 0.752 |
| Gm-r1070-1976 | DNA-binding protein 4 [Nicotiana tabacum] | 7.78 | 0.0316071 | 0.752 |
| Gm-r1088-2356 | protein; similar to unknown protein [Arabidopsis thaliana] | 5.96 | 0.0404706 | 0.752 |
| Gm-r1088-6646 | phosphoglycerate kinase [Nicotiana tabacum] | 7.38 | 0.026397 | 0.752 |
| Gm-r1088-4669 | putative chromatin structure regulator (SUPT6H) from Homo sapiens | 8.05 | 0.0219229 | 0.753 |
| Gm-r1070-3980 | putative protein [Arabidopsis thaliana] | 7.15 | 0.0368469 | 0.753 |
| Gm-r1070-6647 | AT4g36780/C7A10_580 [Arabidopsis thaliana] | 9.27 | 0.0226705 | 0.753 |
| Gm-r1088-7527 | P0431G06.23 [Oryza sativa (japonica cultivar-group)] | 18.94 | 0.0024401 | 0.753 |
| Gm-r1088-8173 | protein kinase family protein [Arabidopsis thaliana] | 6.75 | 0.031698 | 0.753 |
| Gm-r1088-4693 | phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis thaliana] | 22.45 | 0.001468 | 0.754 |
| Gm-r1070-680 | No Hits | 8.18 | 0.0287684 | 0.754 |
| Gm-r1070-1427 | No Hits | 6.82 | 0.0400669 | 0.755 |
| Gm-r1070-994 | putative ubiquitin ligase SINAT5 [Oryza sativa (japonica cultivar-group)] | 12.06 | 0.01327 | 0.755 |
| Gm-r1070-823 | No Hits | 8.15 | 0.0289699 | 0.755 |
| Gm-r1088-4947 | No Hits | 12.89 | 0.0070802 | 0.755 |

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|---|---|---|---|---|
| Gm-r1070-3650 | unknown protein [Arabidopsis thaliana] | 10.08 | 0.0192149 | 0.756 |
| Gm-r1070-90 | glycinin G3 subunit [soybeans, Peptide, 484 aa] | 8.89 | 0.0246112 | 0.756 |
| Gm-r1088-8715 | putative protein [Arabidopsis thaliana] | 12.94 | 0.0070119 | 0.756 |
| Gm-r1070-616 | No Hits | 6.47 | 0.0438515 | 0.757 |
| Gm-r1088-9035 | molybdopterin synthase, large subunit [Arabidopsis thaliana] | 23.30 | 0.0013099 | 0.757 |
| Gm-r1070-608 | No Hits | 6.40 | 0.0447425 | 0.757 |
| Gm-r1070-3892 | DNA binding protein Rav [Capsicum annuum] | 12.06 | 0.0132504 | 0.757 |
| Gm-r1088-5511 | chloroplast ferredoxin I [Nicotiana tabacum] | 9.83 | 0.0139194 | 0.757 |
| Gm-r1070-2196 | subtilase family protein [Arabidopsis thaliana] | 6.25 | 0.0465193 | 0.757 |
| Gm-r1070-6388 | protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum] | 13.76 | 0.0099708 | 0.758 |
| Gm-r1070-1078 | No Hits | 7.90 | 0.030709 | 0.758 |
| Gm-r1070-1420 | unknown protein [Oryza sativa (japonica cultivar-group)] | 10.27 | 0.0184978 | 0.759 |
| Gm-r1088-7592 | tRNA/rRNA methyltransferase (SpoU) family protein [Arabidopsis thaliana] | 23.94 | 0.001205 | 0.759 |
| Gm-r1070-3509 | thioredoxin [Glycine max] | 8.36 | 0.0276295 | 0.759 |
| Gm-r1070-1009 | gibberellin-regulated protein GASA2 precursor [Arabidopsis thaliana] | 7.35 | 0.0350521 | 0.759 |
| Gm-r1070-1401 | No Hits | 12.84 | 0.0115923 | 0.760 |
| Gm-r1070-7197 | unknown protein [Arabidopsis thaliana] | 11.32 | 0.0151402 | 0.760 |
| Gm-r1070-8855 | putative splicing factor [Cicer arietinum] | 43.86 | 0.000571 | 0.760 |
| Gm-r1088-4159 | putative protein [Arabidopsis thaliana] | 9.12 | 0.0165798 | 0.761 |
| Gm-r1088-6830 | hypothetical protein 177O13.35 [Solanum bulbocastanum] | 11.05 | 0.0104809 | 0.761 |
| Gm-r1070-4274 | No Hits | 7.08 | 0.0375059 | 0.761 |
| Gm-r1088-5021 | unknown protein [Arabidopsis thaliana] | 5.36 | 0.049255 | 0.761 |
| Gm-r1070-2512 | putative Glucan 1,3-beta-glucosidase precursor [Oryza sativa (japonica cultivar-group)] | 8.35 | 0.0277066 | 0.761 |
| Gm-r1070-4098 | No Hits | 8.49 | 0.0268231 | 0.761 |
| Gm-r1088-7509 | No Hits | 6.57 | 0.0335294 | 0.761 |
| Gm-r1070-1966 | No Hits | 13.43 | 0.0105288 | 0.762 |
| Gm-r1088-5632 | glutathione S-transferase GST 9 [Glycine max] | 21.73 | 0.001621 | 0.762 |
| Gm-r1088-5452 | Ferritin 2, chloroplast precursor (SFerH-2) | 19.67 | 0.0021817 | 0.762 |
| Gm-r1070-4844 | No Hits | 14.05 | 0.0095241 | 0.762 |
| Gm-r1088-3012 | unnamed protein product [Pisum sativum] | 8.26 | 0.0207055 | 0.762 |
| Gm-r1070-654 | No Hits | 9.44 | 0.021895 | 0.762 |
| Gm-r1070-5423 | putative thioredoxin m2 [Pisum sativum] | 6.81 | 0.0401908 | 0.763 |
| Gm-r1088-8885 | EF-Tu [Glycine max] | 18.27 | 0.0027075 | 0.763 |

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| Gm-r1070-3310 | F11A17.16 [Arabidopsis thaliana] | 8.03 | 0.029836 | 0.764 |
| Gm-r1070-6964 | putative peroxisomal membrane protein PEX11-1 [Arabidopsis thaliana] | 19.68 | 0.0043924 | 0.764 |
| Gm-r1070-1622 | putative mitochondrial glyoxalase II [Cicer arietinum] | 7.63 | 0.0327542 | 0.764 |
| Gm-r1088-8319 | hypothetical protein FG00150.1 [Gibberella zeae PH-1] | 5.89 | 0.0413878 | 0.765 |
| Gm-r1070-1626 | F22L4.5 protein - Arabidopsis thaliana | 13.07 | 0.0111595 | 0.765 |
| Gm-r1070-3093 | copper-transporting P-type ATPase [Brassica napus] | 12.70 | 0.0118752 | 0.765 |
| Gm-r1088-4761 | unknown protein [Arabidopsis thaliana] | 6.83 | 0.0309852 | 0.765 |
| Gm-r1070-2576 | unknown protein [Arabidopsis thaliana] | 9.44 | 0.0218924 | 0.765 |
| Gm-r1070-7491 | glycosyl transferase family 20 protein / trehalose-phosphatase family protein [Arabidopsis thaliana] | 8.20 | 0.028655 | 0.765 |
| Gm-r1070-989 | No Hits | 9.11 | 0.0234664 | 0.765 |
| Gm-r1088-8101 | SUMO activating enzyme, putative [Arabidopsis thaliana] | 9.83 | 0.0139197 | 0.766 |
| Gm-r1088-3754 | putative protein [Arabidopsis thaliana] | 7.41 | 0.0261757 | 0.767 |
| Gm-r1088-8002 | No Hits | 6.75 | 0.0317154 | 0.767 |
| Gm-r1070-1034 | No Hits | 6.18 | 0.0474086 | 0.768 |
| Gm-r1088-8167 | NIN-like protein 1 [Lotus corniculatus var. japonicus] | 15.19 | 0.0045593 | 0.768 |
| Gm-r1088-642 | snap25a [Arabidopsis thaliana] | 19.04 | 0.0024017 | 0.768 |
| Gm-r1070-844 | XH/XS domain-containing protein / XS zinc finger domain-containing protein [Arabidopsis thaliana] | 21.56 | 0.0035268 | 0.768 |
| Gm-r1088-8568 | mRNA capping enzyme family protein [Arabidopsis thaliana] | 9.34 | 0.0156748 | 0.768 |
| Gm-r1088-660 | transporter-like protein [Arabidopsis thaliana] | 6.41 | 0.0351327 | 0.768 |
| Gm-r1088-604 | putative leucine-rich repeat disease resistance protein [Arabidopsis thaliana] | 8.72 | 0.0183231 | 0.769 |
| Gm-r1070-6590 | No Hits | 32.51 | 0.001258 | 0.769 |
| Gm-r1088-1416 | aspartic proteinase 1 [Glycine max] | 8.61 | 0.0188713 | 0.769 |
| Gm-r1088-7363 | No Hits | 18.93 | 0.0024421 | 0.769 |
| Gm-r1088-7375 | putative UOS1 [Oryza sativa (japonica cultivar-group)] | 19.60 | 0.0022052 | 0.770 |
| Gm-r1088-2556 | expressed protein [Oryza sativa (japonica cultivar-group)] | 7.92 | 0.0226967 | 0.770 |
| Gm-r1070-7145 | No Hits | 12.14 | 0.0130643 | 0.770 |
| Gm-r1070-414 | endomembrane protein 70, putative [Arabidopsis thaliana] | 7.15 | 0.0367933 | 0.770 |
| Gm-r1070-990 | No Hits | 7.87 | 0.0309628 | 0.770 |
| Gm-r1070-6837 | pherophorin-dz1 protein [Volvox carteri f. nagariensis] | 7.01 | 0.0381127 | 0.771 |
| Gm-r1088-3384 | Plastocyanin From Spinach | 7.08 | 0.0287474 | 0.771 |
| Gm-r1088-3776 | ENSANGP00000027831 [Anopheles gambiae str. PEST] | 12.52 | 0.0076388 | 0.771 |
| Gm-r1088-8071 | F-box protein family, AtFBX5 [Arabidopsis thaliana] | 8.82 | 0.0178603 | 0.771 |

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| Gm-r1070-6622 | unnamed protein product [Arabidopsis thaliana] | 7.44 | 0.0343131 | 0.771 |
| Gm-r1088-8895 | putative protein [Arabidopsis thaliana] | 6.04 | 0.0394445 | 0.772 |
| Gm-r1088-2850 | PPF-1 protein [Pisum sativum] | 5.41 | 0.0485212 | 0.772 |
| Gm-r1070-3781 | putative protein [Arabidopsis thaliana] | 12.14 | 0.0130759 | 0.772 |
| Gm-r1070-4803 | fiber protein Fb12 [Gossypium barbadense] | 8.02 | 0.0298843 | 0.772 |
| Gm-r1070-1935 | At1g75460/F1B16_22 [Arabidopsis thaliana] | 6.63 | 0.0421118 | 0.773 |
| Gm-r1088-8893 | putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Oryza sativa (japonica cultivar-group)] | 17.35 | 0.0031427 | 0.773 |
| Gm-r1088-1420 | Narf-like protein [Medicago truncatula] | 11.05 | 0.0104813 | 0.773 |
| Gm-r1088-5123 | F23M19.3 [Arabidopsis thaliana] | 6.62 | 0.0329705 | 0.773 |
| Gm-r1070-997 | No Hits | 13.31 | 0.010722 | 0.773 |
| Gm-r1070-3264 | No Hits | 12.20 | 0.0129421 | 0.773 |
| Gm-r1070-7727 | No Hits | 23.86 | 0.0027527 | 0.773 |
| Gm-r1088-8728 | CTF2A [Arabidopsis thaliana] | 7.09 | 0.0286792 | 0.774 |
| Gm-r1088-8910 | 2-oxoglutarate-dependent dioxygenase [Lycopersicon esculentum] | 15.69 | 0.0041681 | 0.774 |
| Gm-r1088-1560 | chloroplast drought-induced stress protein, putative [Arabidopsis thaliana] | 10.81 | 0.0110569 | 0.774 |
| Gm-r1070-7604 | At1g36050 [Arabidopsis thaliana] | 12.02 | 0.0133571 | 0.774 |
| Gm-r1070-847 | putative quinone reductase [Vitis vinifera] | 6.92 | 0.0390357 | 0.775 |
| Gm-r1088-8072 | No Hits | 7.19 | 0.027831 | 0.775 |
| Gm-r1070-3551 | BEL1-related homeotic protein 29 [Solanum tuberosum] | 6.48 | 0.0437096 | 0.775 |
| Gm-r1088-9114 | No Hits | 6.42 | 0.0350149 | 0.775 |
| Gm-r1070-1932 | NIP3 [Medicago truncatula] | 6.60 | 0.0424002 | 0.775 |
| Gm-r1088-8009 | patatin family protein [Arabidopsis thaliana] | 11.48 | 0.0095161 | 0.775 |
| Gm-r1088-4092 | fis1 [Linum usitatissimum] | 11.09 | 0.0103788 | 0.777 |
| Gm-r1088-7781 | unknown protein [Arabidopsis thaliana] | 8.97 | 0.0171959 | 0.777 |
| Gm-r1088-6826 | No Hits | 8.73 | 0.0183105 | 0.777 |
| Gm-r1088-8299 | unknown protein [Arabidopsis thaliana] | 5.76 | 0.043168 | 0.777 |
| Gm-r1088-8575 | putative pathogenesis related protein 1 precursor [Vitis vinifera] | 5.85 | 0.0419321 | 0.777 |
| Gm-r1088-7564 | putative zinc finger protein [Oryza sativa (japonica cultivar-group)] | 24.91 | 0.0010648 | 0.778 |
| Gm-r1088-8163 | putative cellulose synthase [Arabidopsis thaliana] | 13.52 | 0.0062474 | 0.778 |
| Gm-r1070-6748 | No Hits | 9.33 | 0.0223693 | 0.778 |
| Gm-r1070-2400 | AT4g15470/dl3775w [Arabidopsis thaliana] | 17.56 | 0.0057461 | 0.778 |
| Gm-r1088-8700 | phytoene synthase [Adonis palaestina] | 6.24 | 0.0370112 | 0.779 |
| Gm-r1088-8157 | hypothetical protein At2g47960 [imported] - Arabidopsis thaliana | 13.35 | 0.0064583 | 0.779 |

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| Gm-r1088-3382 | unknown [Arabidopsis thaliana] | 7.79 | 0.0235339 | 0.779 |
| Gm-r1070-802 | No Hits | 8.08 | 0.0294474 | 0.779 |
| Gm-r1070-5468 | MYB-like DNA-binding protein [Catharanthus roseus] | 44.08 | 0.0005635 | 0.779 |
| Gm-r1088-7507 | ubiquitin carrier protein [Populus tomentosa] | 23.14 | 0.001337 | 0.779 |
| Gm-r1070-2772 | F-box family protein [Arabidopsis thaliana] | 9.18 | 0.0231167 | 0.779 |
| Gm-r1070-1570 | unknown [Arabidopsis thaliana] | 6.62 | 0.0421317 | 0.780 |
| Gm-r1088-8971 | squalene monooxygenase 2 [Medicago truncatula] | 8.90 | 0.0174917 | 0.780 |
| Gm-r1088-8193 | unnamed protein product [Arabidopsis thaliana] | 15.72 | 0.0041507 | 0.780 |
| Gm-r1088-2892 | preprotein translocase secA precursor - spinach | 5.85 | 0.0419348 | 0.781 |
| Gm-r1088-4663 | putative p53 binding protein [Oryza sativa (japonica cultivar-group)] | 20.32 | 0.0019817 | 0.781 |
| Gm-r1070-2544 | No Hits | 18.90 | 0.0048387 | 0.781 |
| Gm-r1070-5593 | L-galactose-1-phosphate phosphatase [Actinidia deliciosa] | 6.88 | 0.0394609 | 0.782 |
| Gm-r1088-8335 | MutT domain protein-like [Oryza sativa (japonica cultivar-group)] | 6.63 | 0.032873 | 0.782 |
| Gm-r1070-3608 | unknown [Arabidopsis thaliana] | 7.71 | 0.0321507 | 0.782 |
| Gm-r1070-919 | No Hits | 10.07 | 0.0192531 | 0.782 |
| Gm-r1088-8355 | F15H18.5 [Arabidopsis thaliana] | 11.76 | 0.0089702 | 0.782 |
| Gm-r1088-1250 | No Hits | 7.32 | 0.026833 | 0.783 |
| Gm-r1070-2391 | AT5g57360/MSF19_2 [Arabidopsis thaliana] | 10.22 | 0.0186718 | 0.783 |
| Gm-r1070-5852 | No Hits | 10.48 | 0.0177495 | 0.783 |
| Gm-r1070-9041 | expressed protein [Arabidopsis thaliana] | 8.96 | 0.0242094 | 0.784 |
| Gm-r1070-4559 | one helix protein [Ipomoea nil] | 8.39 | 0.0274809 | 0.784 |
| Gm-r1088-2928 | unknown protein [Arabidopsis thaliana] | 9.08 | 0.0167481 | 0.784 |
| Gm-r1088-3240 | starch phosphorylase (EC 2.4.1.1) isoform L precursor, chloroplast - fava bean | 5.49 | 0.0471666 | 0.784 |
| Gm-r1070-3272 | hydrolase-like [Oryza sativa (japonica cultivar-group)] | 7.84 | 0.0311283 | 0.785 |
| Gm-r1088-2694 | unknown protein [Arabidopsis thaliana] | 12.18 | 0.0082016 | 0.785 |
| Gm-r1070-1904 | glycosyl hydrolase family protein 27 / alpha-galactosidase family protein [Arabidopsis thaliana] | 6.06 | 0.0490238 | 0.785 |
| Gm-r1088-5307 | putative growth-on protein GRO10 [Oryza sativa (japonica cultivar-group)] | 14.81 | 0.0048847 | 0.785 |
| Gm-r1070-462 | SPF1 protein [Ipomoea batatas] | 15.09 | 0.0081244 | 0.785 |
| Gm-r1070-852 | acid phosphatase [Glycine max] | 6.37 | 0.0450374 | 0.786 |
| Gm-r1070-6020 | linoleoyl desaturase | 12.61 | 0.0120606 | 0.787 |
| Gm-r1070-2906 | At2g43020/MFL8.12 [Arabidopsis thaliana] | 19.80 | 0.0043279 | 0.787 |
| Gm-r1070-7983 | glutathione S-transferase GST 5 [Glycine max] | 14.99 | 0.0082472 | 0.787 |
| Gm-r1070-1651 | No Hits | 9.66 | 0.0208821 | 0.787 |

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| Gm-r1070-32 | unknown [Arabidopsis thaliana] | 7.29 | 0.0356063 | 0.788 |
| Gm-r1088-8717 | ribulose-5-phosphate-3-epimerase [Pisum sativum] | 6.72 | 0.0319965 | 0.788 |
| Gm-r1070-5999 | No Hits | 19.63 | 0.0044188 | 0.788 |
| Gm-r1088-2564 | unknown protein; 10-1710 [Arabidopsis thaliana] | 7.54 | 0.0252089 | 0.789 |
| Gm-r1088-3142 | methyltransferase-related [Arabidopsis thaliana] | 7.71 | 0.0240387 | 0.789 |
| Gm-r1088-1038 | No Hits | 19.03 | 0.0024048 | 0.789 |
| Gm-r1070-1296 | expressed protein [Arabidopsis thaliana] | 14.23 | 0.0092606 | 0.790 |
| Gm-r1070-2941 | vacuolar H+-ATPase c subunit [Citrus unshiu] | 6.87 | 0.039577 | 0.790 |
| Gm-r1088-5621 | unknown protein [Arabidopsis thaliana] | 10.19 | 0.0127668 | 0.790 |
| Gm-r1088-7388 | No Hits | 5.68 | 0.0443789 | 0.790 |
| Gm-r1088-9077 | Serine Carboxypeptidase II-like protein [Arabidopsis thaliana] | 6.82 | 0.0310636 | 0.791 |
| Gm-r1070-645 | putative formate--tetrahydrofolate ligase [Oryza sativa (japonica cultivar-group)] | 10.58 | 0.0174015 | 0.791 |
| Gm-r1088-5216 | SPBPJ4664.02 [Schizosaccharomyces pombe] | 9.19 | 0.0162627 | 0.792 |
| Gm-r1070-1630 | 31.2 kDa small heat shock family protein / hsp20 family protein [Arabidopsis thaliana] | 7.02 | 0.0380239 | 0.792 |
| Gm-r1070-2719 | No Hits | 6.87 | 0.0395147 | 0.792 |
| Gm-r1070-3459 | omega-3 fatty acid desaturase (EC 1.14.99.-) GMD [similarity] - soybean | 7.20 | 0.0363824 | 0.792 |
| Gm-r1070-1098 | No Hits | 11.19 | 0.0155139 | 0.793 |
| Gm-r1070-2551 | glycosyl hydrolase family 20 protein [Arabidopsis thaliana] | 7.50 | 0.033831 | 0.793 |
| Gm-r1088-7597 | HECT-domain-containing protein / ubiquitin-transferase family protein [Arabidopsis thaliana] | 10.55 | 0.0117481 | 0.794 |
| Gm-r1088-3022 | unknown [Arabidopsis thaliana] | 7.73 | 0.0238926 | 0.795 |
| Gm-r1088-4951 | unnamed protein product [Arabidopsis thaliana] | 8.06 | 0.0218602 | 0.796 |
| Gm-r1088-8265 | At3g03380/T21P5_20 [Arabidopsis thaliana] | 10.78 | 0.0111387 | 0.796 |
| Gm-r1088-8682 | expressed protein [Arabidopsis thaliana] | 10.48 | 0.0119263 | 0.796 |
| Gm-r1088-7796 | two-pore calcium channel [Nicotiana tabacum] | 7.72 | 0.0239596 | 0.796 |
| Gm-r1070-3675 | No Hits | 17.87 | 0.0055163 | 0.796 |
| Gm-r1070-1002 | Rubisco large subunit N-methyltransferase, chloroplast precursor | 10.30 | 0.0183949 | 0.796 |
| Gm-r1088-4263 | protein phosphatase 2C [Arabidopsis thaliana] | 9.85 | 0.0138439 | 0.796 |
| Gm-r1088-8156 | putative DegP2 protease [Oryza sativa (japonica cultivar-group)] | 6.27 | 0.0367026 | 0.797 |
| Gm-r1088-2613 | No Hits | 5.55 | 0.0461872 | 0.798 |
| Gm-r1088-5625 | No Hits | 8.47 | 0.0196047 | 0.798 |
| Gm-r1070-3284 | No Hits | 8.54 | 0.0265496 | 0.798 |
| Gm-r1088-5321 | SPCP1 protein - soybean | 7.34 | 0.0266962 | 0.798 |

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| Gm-r1070-5467 | No Hits | 6.48 | 0.0438032 | 0.799 |
| Gm-r1088-2185 | No Hits | 6.27 | 0.0367103 | 0.799 |
| Gm-r1070-6955 | putative protein [Arabidopsis thaliana] | 12.30 | 0.0127235 | 0.799 |
| Gm-r1070-6915 | nsGRP-2 [Nicotiana sylvestris] | 8.24 | 0.0284228 | 0.799 |
| Gm-r1070-6021 | MtN3-like protein [Arabidopsis thaliana] | 10.26 | 0.0185186 | 0.800 |
| Gm-r1070-7497 | tubby-like protein [Cicer arietinum] | 7.55 | 0.0333683 | 0.800 |
| Gm-r1070-6484 | ATP synthase (gamma subunit) [Pisum sativum] | 30.16 | 0.0015271 | 0.800 |
| Gm-r1070-261 | protein phosphatase type 2C [Lotus japonicus] | 10.98 | 0.0161307 | 0.800 |
| Gm-r1070-419 | GTP-binding protein TypA [Trifolium pratense] | 6.93 | 0.0389041 | 0.800 |
| Gm-r1088-8342 | putative glutamate decarboxylase [Glycine max] | 23.25 | 0.0013191 | 0.801 |
| Gm-r1070-2140 | No Hits | 9.17 | 0.0231569 | 0.802 |
| Gm-r1070-996 | cytochrome P450-like protein [Arabidopsis thaliana] | 6.32 | 0.0456738 | 0.802 |
| Gm-r1070-6474 | unknown protein [Arabidopsis thaliana] | 7.57 | 0.0332463 | 0.802 |
| Gm-r1070-7313 | endoxyloglucan transferase [Daucus carota] | 7.24 | 0.0360341 | 0.802 |
| Gm-r1088-8178 | lipoxygenase [Citrus jambhiri] | 6.16 | 0.03794 | 0.803 |
| Gm-r1088-9045 | disease resistance-responsive family protein [Arachis hypogaea] | 7.34 | 0.0267168 | 0.803 |
| Gm-r1088-5117 | At5g25752 [Arabidopsis thaliana] | 6.41 | 0.0351724 | 0.803 |
| Gm-r1070-7008 | phospholipid glutathione peroxidase [Pisum sativum] | 6.18 | 0.0474782 | 0.804 |
| Gm-r1070-4238 | fiber protein E6 (clone CKE6-4A) - upland cotton | 14.99 | 0.0082449 | 0.805 |
| Gm-r1070-4609 | No Hits | 7.51 | 0.0337274 | 0.805 |
| Gm-r1088-8550 | hypothetical protein At2g44920 [imported] - Arabidopsis thaliana | 6.17 | 0.0378822 | 0.805 |
| Gm-r1088-2416 | AAA-type ATPase family protein [Arabidopsis thaliana] | 13.67 | 0.0060622 | 0.805 |
| Gm-r1070-4877 | protein kinase (EC 2.7.1.37) 5 [Arabidopsis thaliana] | 11.92 | 0.0135932 | 0.805 |
| Gm-r1070-7189 | low affinity sulphate transporter [Stylosanthes hamata] | 6.17 | 0.0475555 | 0.805 |
| Gm-r1070-1672 | unnamed protein product [Arabidopsis thaliana] | 7.05 | 0.0377287 | 0.807 |
| Gm-r1070-1051 | No Hits | 6.79 | 0.0403217 | 0.807 |
| Gm-r1070-9006 | palmitoyl-acyl carrier protein thioesterase [Gossypium hirsutum] | 11.76 | 0.0139866 | 0.808 |
| Gm-r1088-2960 | unknown protein [Oryza sativa (japonica cultivar-group)] | 10.02 | 0.0132713 | 0.808 |
| Gm-r1070-7899 | No Hits | 6.83 | 0.0399049 | 0.809 |
| Gm-r1088-1057 | neutral leucine aminopeptidase preprotein [Lycopersicon esculentum] | 6.78 | 0.0313958 | 0.809 |
| Gm-r1088-6577 | hypothetical protein [Arabidopsis thaliana] | 6.03 | 0.0395621 | 0.811 |
| Gm-r1070-2926 | pectinesterase (EC 3.1.1.11) [imported] - Salix gilgiana | 9.63 | 0.0210428 | 0.811 |
| Gm-r1070-821 | Type II chlorophyll a/b binding protein from photosystem I [Pisum sativum] | 12.09 | 0.0131917 | 0.811 |
| Gm-r1070-3898 | unknown protein [Oryza sativa (japonica cultivar-group)] | 9.93 | 0.0197953 | 0.812 |

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| Gm-r1070-1101 | allene-oxide cyclase [Medicago truncatula] | 8.52 | 0.0266862 | 0.812 |
| Gm-r1088-2964 | unknown protein [Oryza sativa (japonica cultivar-group)] | 6.72 | 0.0320091 | 0.813 |
| Gm-r1070-326 | AT5g02940/F9G14_250 [Arabidopsis thaliana] | 8.65 | 0.0259239 | 0.813 |
| Gm-r1088-2407 | T22J18.6 [Arabidopsis thaliana] | 10.66 | 0.0114421 | 0.813 |
| Gm-r1070-1390 | UDP-glucose 4-epimerase (Galactowaldenase) (UDP-galactose 4-epimerase) | 11.89 | 0.0136533 | 0.813 |
| Gm-r1070-2296 | putative receptor-like protein kinase [Oryza sativa (japonica cultivar-group)] | 10.52 | 0.0176272 | 0.813 |
| Gm-r1088-8349 | unknown protein [Oryza sativa (japonica cultivar-group)] | 26.52 | 0.000875 | 0.814 |
| Gm-r1070-7005 | kinase-like protein [Arabidopsis thaliana] | 7.72 | 0.0320693 | 0.814 |
| Gm-r1088-8169 | At3g05090/T12H1_5 [Arabidopsis thaliana] | 18.61 | 0.0025678 | 0.815 |
| Gm-r1088-5889 | phox (PX) domain-containing protein [Arabidopsis thaliana] | 9.18 | 0.0163025 | 0.815 |
| Gm-r1088-6853 | 9-cis-epoxycarotenoid dioxygenase [Phaseolus vulgaris] | 5.63 | 0.0450783 | 0.815 |
| Gm-r1070-6442 | pollen 2-phosphoglycerate dehydrogenase 2 precursor [Cynodon dactylon] | 11.79 | 0.0139093 | 0.816 |
| Gm-r1070-39 | Similar to phosphoribosylanthranilate transferase from Pisum sativum | 8.29 | 0.0280598 | 0.816 |
| Gm-r1070-6002 | No Hits | 10.71 | 0.0169638 | 0.816 |
| Gm-r1088-3791 | Isocitrate lyase 2 (Isocitrase 2) (Isocitratase 2) (ICL 2) | 9.61 | 0.0146791 | 0.817 |
| Gm-r1088-8271 | leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana] | 5.49 | 0.0472284 | 0.817 |
| Gm-r1088-5419 | putative peroxisomal membrane protein PEX11-1 [Arabidopsis thaliana] | 11.18 | 0.0101693 | 0.817 |
| Gm-r1088-5217 | unknown protein [Oryza sativa (japonica cultivar-group)] | 20.29 | 0.0019902 | 0.818 |
| Gm-r1070-822 | No Hits | 9.29 | 0.0225888 | 0.819 |
| Gm-r1070-3870 | No Hits | 11.31 | 0.0151843 | 0.820 |
| Gm-r1088-6653 | No Hits | 7.76 | 0.023721 | 0.821 |
| Gm-r1070-7595 | LHY protein [Phaseolus vulgaris] | 7.07 | 0.0376052 | 0.821 |
| Gm-r1088-4504 | Dreg-2 like protein [Oryza sativa (japonica cultivar-group)] | 5.91 | 0.0411764 | 0.822 |
| Gm-r1088-7877 | maturation-associated protein MAT1 - soybean | 5.36 | 0.0493155 | 0.822 |
| Gm-r1088-2526 | hypothetical protein [Arabidopsis thaliana] | 9.10 | 0.0166537 | 0.822 |
| Gm-r1070-8759 | No Hits | 7.73 | 0.0319982 | 0.822 |
| Gm-r1088-4116 | putative protein [Arabidopsis thaliana] | 8.38 | 0.0200358 | 0.823 |
| Gm-r1070-7139 | hypothetical protein - tomato | 6.14 | 0.0478817 | 0.823 |
| Gm-r1070-4296 | putative CBL-interacting protein kinase 23 [Oryza sativa (japonica cultivar-group)] | 26.42 | 0.0021365 | 0.823 |
| Gm-r1070-797 | No Hits | 6.12 | 0.0481475 | 0.825 |
| Gm-r1088-4301 | unknown protein [Arabidopsis thaliana] | 6.53 | 0.0338964 | 0.825 |
| Gm-r1088-4446 | putative hypersensitive-induced response protein [Oryza sativa (japonica cultivar-group)] | 7.80 | 0.0234729 | 0.825 |
| Gm-r1088-7756 | cationic peroxidase | 10.89 | 0.0108634 | 0.825 |

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| Gm-r1088-7554 | putative membrane associated protein [Arabidopsis thaliana] | 12.58 | 0.0075482 | 0.825 |
| Gm-r1070-7060 | No Hits | 6.16 | 0.0477281 | 0.826 |
| Gm-r1088-4150 | At4g39470/F23K16_100 [Arabidopsis thaliana] | 8.84 | 0.0177658 | 0.826 |
| Gm-r1070-7172 | No Hits | 7.39 | 0.0347182 | 0.826 |
| Gm-r1070-2259 | putative ethanolamine kinase 1 [Oryza sativa (japonica cultivar-group)] | 10.26 | 0.0185165 | 0.826 |
| Gm-r1088-9115 | oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana] | 7.82 | 0.0233019 | 0.827 |
| Gm-r1088-7723 | At1g23780/F5O8_31 [Arabidopsis thaliana] | 9.12 | 0.0165707 | 0.828 |
| Gm-r1088-1190 | myosin XI [Nicotiana tabacum] | 8.96 | 0.0172361 | 0.828 |
| Gm-r1070-1862 | nine-cis-epoxycarotenoid dioxygenase1 [Pisum sativum] | 9.37 | 0.0221985 | 0.829 |
| Gm-r1088-7922 | No Hits | 7.88 | 0.022964 | 0.830 |
| Gm-r1070-5039 | receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris] | 8.11 | 0.0292838 | 0.830 |
| Gm-r1070-3907 | unnamed protein product [Arabidopsis thaliana] | 6.53 | 0.0431333 | 0.831 |
| Gm-r1070-4116 | No Hits | 7.79 | 0.0315532 | 0.831 |
| Gm-r1088-2908 | GPI transamidase component family protein / Gaa1-like family protein [Arabidopsis thaliana] | 5.64 | 0.0449025 | 0.832 |
| Gm-r1088-8397 | unknown protein [Arabidopsis thaliana] | 7.29 | 0.0270567 | 0.832 |
| Gm-r1070-3338 | photosystem I subunit PSI-E [Nicotiana sylvestris] | 6.11 | 0.048401 | 0.833 |
| Gm-r1088-8217 | No Hits | 5.67 | 0.0444534 | 0.834 |
| Gm-r1070-280 | shock protein SRC2 - soybean | 7.23 | 0.0360716 | 0.835 |
| Gm-r1088-2534 | cellulose synthase family protein [Arabidopsis thaliana] | 10.52 | 0.0118112 | 0.835 |
| Gm-r1088-8302 | putative RNA helicase [Oryza sativa (japonica cultivar-group)] | 6.17 | 0.0378988 | 0.835 |
| Gm-r1070-2528 | No Hits | 8.22 | 0.0285377 | 0.835 |
| Gm-r1088-7505 | bZIP [Phaseolus acutifolius] | 5.96 | 0.0404601 | 0.837 |
| Gm-r1070-284 | calcium/calmodulin-dependent protein kinase CaMK3 [Arabidopsis thaliana] | 10.23 | 0.018619 | 0.838 |
| Gm-r1088-4853 | type-A response regulator [Catharanthus roseus] | 9.06 | 0.0168131 | 0.838 |
| Gm-r1070-6966 | transcription factor EIL1 [Vigna radiata] | 19.61 | 0.0044312 | 0.839 |
| Gm-r1088-864 | expressed protein [Arabidopsis thaliana] | 8.69 | 0.0184715 | 0.839 |
| Gm-r1070-5874 | unknown protein [Arabidopsis thaliana] | 16.26 | 0.0068621 | 0.840 |
| Gm-r1070-6781 | At1g26660/T24P13_4 [Arabidopsis thaliana] | 9.18 | 0.0231122 | 0.840 |
| Gm-r1088-7763 | phosphogluconate dehydrogenase (decarboxylating) (EC 1.1.1.44) - soybean | 11.20 | 0.0101253 | 0.841 |
| Gm-r1070-5180 | No Hits | 7.06 | 0.0376935 | 0.843 |
| Gm-r1070-241 | putative protein [Arabidopsis thaliana] | 12.71 | 0.0118439 | 0.844 |
| Gm-r1088-6557 | trihelix DNA-binding protein, putative [Arabidopsis thaliana] | 9.54 | 0.01492 | 0.845 |
| Gm-r1070-4149 | thylakoid lumen protein, chloroplast precursor [Arabidopsis thaliana] | 7.68 | 0.0323923 | 0.846 |

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| Gm-r1088-4090 | putative beta-galactosidase [Glycine max] | 8.30 | 0.0204892 | 0.847 |
| Gm-r1070-3497 | No Hits | 9.71 | 0.0206689 | 0.848 |
| Gm-r1088-5244 | unnamed protein product [Arabidopsis thaliana] | 22.15 | 0.0015283 | 0.851 |
| Gm-r1088-5430 | unknown protein [Arabidopsis thaliana] | 9.15 | 0.0164572 | 0.851 |
| Gm-r1088-664 | aminoacyl-tRNA synthetase family protein [Arabidopsis thaliana] | 7.62 | 0.0246671 | 0.852 |
| Gm-r1088-1612 | unknown protein [Arabidopsis thaliana] | 5.39 | 0.0487294 | 0.854 |
| Gm-r1088-1779 | malate dehydrogenase (NADP+) [Pisum sativum] | 6.22 | 0.0373148 | 0.857 |
| Gm-r1070-812 | No Hits | 9.27 | 0.0226663 | 0.857 |
| Gm-r1088-694 | deetiolated 1-like protein [Solanum tuberosum] | 8.43 | 0.0197992 | 0.861 |
| Gm-r1070-2922 | No Hits | 7.00 | 0.0382932 | 0.867 |
| Gm-r1088-1431 | No Hits | 7.25 | 0.0273589 | 0.870 |
| Gm-r1070-5646 | No Hits | 6.21 | 0.0470331 | 0.870 |
| Gm-r1088-2898 | ankyrin-repeat protein - Arabidopsis thaliana | 5.92 | 0.0409773 | 0.872 |
| Gm-r1088-8712 | At5g26800 [Arabidopsis thaliana] | 5.58 | 0.0457665 | 0.872 |
| Gm-r1070-6775 | cytosolic glutamine synthetase GSbeta1 [Glycine max] | 6.33 | 0.0455839 | 0.874 |
| Gm-r1088-6614 | TPA: putative ABC transporter 1; AtABC1 [Arabidopsis thaliana] | 7.24 | 0.0274885 | 0.874 |
| Gm-r1088-4058 | At1g54990/F14C21_5 [Arabidopsis thaliana] | 11.47 | 0.009554 | 0.875 |
| Gm-r1070-3967 | No Hits | 9.09 | 0.0235682 | 0.875 |
| Gm-r1088-114 | F12A21.24 [Arabidopsis thaliana] | 8.27 | 0.020649 | 0.876 |
| Gm-r1070-3911 | ribosomal protein S5 [Spinacia oleracea] | 9.59 | 0.0212055 | 0.880 |
| Gm-r1088-1756 | unnamed protein product [Arabidopsis thaliana] | 6.59 | 0.0332521 | 0.881 |
| Gm-r1070-1020 | Similar to dTDP-D-glucose 4,6-dehydratase [Arabidopsis thaliana] | 8.45 | 0.0270798 | 0.881 |
| Gm-r1070-5991 | dehydration responsive element-binding protein 3 [Glycine max] | 6.33 | 0.0455892 | 0.882 |
| Gm-r1070-7452 | NAC2 protein [Glycine max] | 6.14 | 0.0479341 | 0.884 |
| Gm-r1088-836 | Putative finger family protein [Brassica oleracea] | 5.44 | 0.0480506 | 0.885 |
| Gm-r1088-1827 | At5g02250 [Arabidopsis thaliana] | 5.56 | 0.0460809 | 0.885 |
| Gm-r1088-6769 | unnamed protein product [Arabidopsis thaliana] | 6.80 | 0.0312073 | 0.899 |
| Gm-r1070-1793 | expressed protein [Arabidopsis thaliana] | 6.63 | 0.042023 | 0.900 |
| Gm-r1088-432 | At5g61670/k11j9_190 [Arabidopsis thaliana] | 6.22 | 0.037338 | 0.906 |
| Gm-r1088-3790 | At1g05140 [Arabidopsis thaliana] | 6.40 | 0.0352979 | 0.910 |
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| Gm-r1070-7418 | putative zinc finger transcription factor ZFP30 [Oryza sativa (japonica cultivar-group)] | 11.05 | 0.0159278 | 1.119 |

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| Gm-r1088-4164 | dynamin homolog [Astragalus sinicus] | 6.64 | 0.0328151 | 1.119 |
| Gm-r1070-5700 | putative acetyltransferase [Arabidopsis thaliana] | 5.99 | 0.0499283 | 1.125 |
| Gm-r1070-5948 | unknown protein [Oryza sativa (japonica cultivar-group)] | 9.60 | 0.021163 | 1.130 |
| Gm-r1070-7050 | pfkB-type carbohydrate kinase family protein [Arabidopsis thaliana] | 8.16 | 0.0289169 | 1.132 |
| Gm-r1070-3130 | chaperonin precursor [Pisum sativum] | 14.88 | 0.0083849 | 1.140 |
| Gm-r1088-5814 | At3g62310 [Arabidopsis thaliana] | 7.33 | 0.0267856 | 1.150 |
| Gm-r1088-4493 | non-repetitive/WGA-negative nucleoporin family protein [Arabidopsis thaliana] | 6.85 | 0.0307453 | 1.157 |
| Gm-r1070-7254 | AT5g41690/MBK23_23 [Arabidopsis thaliana] | 7.13 | 0.036981 | 1.158 |
| Gm-r1070-7474 | unnamed protein product [Arabidopsis thaliana] | 7.16 | 0.0367203 | 1.160 |
| Gm-r1088-8965 | B1088C09.17 [Oryza sativa (japonica cultivar-group)] | 6.31 | 0.0363123 | 1.162 |
| Gm-r1088-4540 | At5g36290 [Arabidopsis thaliana] | 12.81 | 0.0071991 | 1.166 |
| Gm-r1070-7480 | Phytochrome B | 27.39 | 0.00195 | 1.166 |
| Gm-r1070-1281 | ribosomal protein S19 | 19.59 | 0.0044398 | 1.167 |
| Gm-r1088-3274 | unknown protein; 16040-11188 [Arabidopsis thaliana] | 6.12 | 0.0385108 | 1.173 |
| Gm-r1070-6086 | unknown protein [Oryza sativa (japonica cultivar-group)] | 15.15 | 0.00805 | 1.174 |
| Gm-r1088-5415 | At5g26743 [Arabidopsis thaliana] | 5.40 | 0.0486963 | 1.178 |
| Gm-r1088-1634 | putative protein [Arabidopsis thaliana] | 6.61 | 0.0330828 | 1.179 |
| Gm-r1070-1337 | type IIIa membrane protein cp-wap13 [Vigna unguiculata] | 6.23 | 0.046832 | 1.193 |
| Gm-r1088-2587 | nicastrin-related [Arabidopsis thaliana] | 5.70 | 0.0440107 | 1.194 |
| Gm-r1070-4773 | endoplasmic reticulum HSC70-cognate binding protein precursor [Glycine max] | 6.51 | 0.0434184 | 1.201 |
| Gm-r1070-4798 | OSJNBa0019J05.15 [Oryza sativa (japonica cultivar-group)] | 6.53 | 0.0431671 | 1.208 |
| Gm-r1070-6312 | No Hits | 7.60 | 0.0329587 | 1.216 |
| Gm-r1070-6192 | wound-inducible basic protein - kidney bean | 9.81 | 0.0202597 | 1.218 |
| Gm-r1088-5229 | No Hits | 12.79 | 0.0072255 | 1.219 |
| Gm-r1070-7982 | putative small nuclear ribonucleoprotein polypeptide E [Oryza sativa (japonica cultivar-group)] | 6.58 | 0.0426631 | 1.220 |
| Gm-r1070-6700 | phi-1-like protein [Arabidopsis thaliana] | 6.63 | 0.0420704 | 1.220 |
| Gm-r1088-491 | putative chaperonin containing TCP1, subunit 3 (gamma) [Oryza sativa (japonica cultivar-group)] | 7.78 | 0.0235731 | 1.223 |
| Gm-r1070-6325 | putative extensin [Oryza sativa (japonica cultivar-group)] | 8.47 | 0.0269636 | 1.223 |
| Gm-r1088-5656 | UDP-N-acetylglucosamine O-acyltransferase-like protein [Arabidopsis thaliana] | 6.28 | 0.0365828 | 1.224 |
| Gm-r1070-4491 | No Hits | 6.42 | 0.0444509 | 1.227 |
| Gm-r1070-8633 | At5g22100 [Arabidopsis thaliana] | 9.83 | 0.0201824 | 1.228 |
| Gm-r1070-7846 | unknown [Arabidopsis thaliana] | 6.03 | 0.0494012 | 1.233 |

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| Gm-r1088-2981 | ribosomal protein L17, chloroplast - common tobacco | 10.79 | 0.011109 | 1.235 |
| Gm-r1088-4060 | unknown protein; 13339-10119 [Arabidopsis thaliana] | 7.14 | 0.0283054 | 1.236 |
| Gm-r1088-5982 | cationic peroxidase 2 [Glycine max] | 5.90 | 0.0412932 | 1.236 |
| Gm-r1088-8343 | putative 60S ribosomal protein L39 [Oryza sativa (japonica cultivar-group)] | 5.38 | 0.0488907 | 1.239 |
| Gm-r1070-8620 | MAP kinase PsMAPK2 [Pisum sativum] | 22.39 | 0.0032175 | 1.241 |
| Gm-r1070-1137 | unknown [Brassica napus] | 12.03 | 0.0133334 | 1.241 |
| Gm-r1070-6272 | No Hits | 15.86 | 0.0072638 | 1.241 |
| Gm-r1088-6225 | root nodule extensin [Pisum sativum] | 6.55 | 0.0337223 | 1.241 |
| Gm-r1070-6638 | eIF3e [Arabidopsis thaliana] | 18.07 | 0.0053749 | 1.243 |
| Gm-r1070-4972 | putative elicitor-inducible cytochrome P450 [Oryza sativa (japonica cultivar-group)] | 7.49 | 0.0338503 | 1.243 |
| Gm-r1070-8984 | No Hits | 12.11 | 0.0131548 | 1.245 |
| Gm-r1070-426 | No Hits | 6.64 | 0.0419185 | 1.245 |
| Gm-r1070-1066 | Gip1-like protein [Populus tomentosa] | 8.61 | 0.0261286 | 1.248 |
| Gm-r1070-5320 | expressed protein [Arabidopsis thaliana] | 13.57 | 0.0102818 | 1.248 |
| Gm-r1088-3331 | putative GDP-L-fucose synthetase [Arabidopsis thaliana] | 9.25 | 0.0160326 | 1.252 |
| Gm-r1070-6808 | putative GDSL-motif lipase/acylhydrolase [Arabidopsis thaliana] | 16.41 | 0.006722 | 1.252 |
| Gm-r1088-2953 | ribosomal protein S1 [Spinacia oleracea] | 7.56 | 0.0250794 | 1.255 |
| Gm-r1088-9032 | ubiquitin extension protein [Lupinus albus] | 5.88 | 0.0414721 | 1.257 |
| Gm-r1070-5946 | expressed protein [Arabidopsis thaliana] | 8.46 | 0.0270314 | 1.259 |
| Gm-r1088-93 | glycoside hydrolase family 28 protein / polygalacturonase family [Arabidopsis thaliana] | 9.52 | 0.0150049 | 1.259 |
| Gm-r1088-4113 | unknown protein [Arabidopsis thaliana] | 5.69 | 0.0441889 | 1.261 |
| Gm-r1070-6846 | NADPH-protochlorophyllide oxidoreductase [Cucumis sativus] | 6.66 | 0.04176 | 1.262 |
| Gm-r1070-1458 | OSJNBa0022H21.3 [Oryza sativa (japonica cultivar-group)] | 7.23 | 0.0361439 | 1.262 |
| Gm-r1088-4450 | No Hits | 7.80 | 0.0234395 | 1.263 |
| Gm-r1070-5130 | putative GDSL-motif lipase/acylhydrolase [Arabidopsis thaliana] | 20.22 | 0.0041201 | 1.264 |
| Gm-r1088-5623 | ribosomal protein L44 isoform b [Gossypium hirsutum] | 6.75 | 0.031748 | 1.265 |
| Gm-r1070-5316 | No Hits | 14.60 | 0.0087547 | 1.266 |
| Gm-r1070-3442 | No Hits | 6.94 | 0.0388286 | 1.268 |
| Gm-r1070-7373 | At4g02590/T10P11_13 [Arabidopsis thaliana] | 11.15 | 0.0156401 | 1.268 |
| Gm-r1070-5906 | putative protein [Arabidopsis thaliana] | 10.19 | 0.0187825 | 1.269 |
| Gm-r1070-7873 | putative ribosomal protein L10a [Oryza sativa (japonica cultivar-group)] | 11.09 | 0.0158116 | 1.270 |
| Gm-r1070-5123 | No Hits | 7.27 | 0.0357302 | 1.270 |

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| Gm-r1088-1607 | AT4g01050/F2N1_31 [Arabidopsis thaliana] | 5.52 | 0.0467499 | 1.271 |
| Gm-r1070-2152 | No Hits | 8.95 | 0.0242928 | 1.271 |
| Gm-r1070-8622 | hypothetical protein [Cicer arietinum] | 17.79 | 0.0055748 | 1.272 |
| Gm-r1088-3291 | At5g04800/MUK11_12 [Arabidopsis thaliana] | 5.47 | 0.047527 | 1.272 |
| Gm-r1070-5896 | No Hits | 11.89 | 0.0136662 | 1.273 |
| Gm-r1070-7903 | No Hits | 15.70 | 0.0074372 | 1.274 |
| Gm-r1088-226 | No Hits | 10.91 | 0.010808 | 1.274 |
| Gm-r1070-7859 | putative DNA-binding protein GBP16 [Oryza sativa (japonica cultivar-group)] | 8.23 | 0.0284971 | 1.275 |
| Gm-r1088-8380 | No Hits | 15.59 | 0.0042489 | 1.276 |
| Gm-r1070-5227 | putative lipid transfer protein GPI-anchored [Cicer arietinum] | 6.20 | 0.0472263 | 1.279 |
| Gm-r1070-7399 | unknown protein [Arabidopsis thaliana] | 11.71 | 0.0141066 | 1.281 |
| Gm-r1088-4158 | protein kinase family protein [Arabidopsis thaliana] | 8.02 | 0.0220578 | 1.282 |
| Gm-r1070-7785 | At1g11760 [Arabidopsis thaliana] | 24.15 | 0.0026728 | 1.283 |
| Gm-r1088-4167 | Very similar to helicases [Arabidopsis thaliana] | 27.50 | 0.0007792 | 1.283 |
| Gm-r1070-8056 | unknown protein [Arabidopsis thaliana] | 11.29 | 0.0152311 | 1.285 |
| Gm-r1088-4507 | AGL15 [Glycine max] | 8.82 | 0.0178796 | 1.285 |
| Gm-r1070-7534 | 4-coumarate-CoA ligase-like protein [Arabidopsis thaliana] | 8.74 | 0.0254125 | 1.286 |
| Gm-r1070-2921 | putative ribosomal protein L7 [Arabidopsis thaliana] | 23.93 | 0.0027344 | 1.287 |
| Gm-r1070-8504 | putative alpha7 proteasome subunit [Nicotiana tabacum] | 14.63 | 0.0087104 | 1.295 |
| Gm-r1088-126 | alpha tubulin [Anemia phyllitidis] | 5.44 | 0.0480458 | 1.296 |
| Gm-r1070-1710 | Adenylate kinase B (ATP-AMP transphosphorylase) | 24.50 | 0.0025782 | 1.297 |
| Gm-r1070-2055 | No Hits | 11.23 | 0.015384 | 1.298 |
| Gm-r1088-6033 | MYB-like DNA-binding protein [Catharanthus roseus] | 7.68 | 0.024262 | 1.301 |
| Gm-r1088-7708 | putative Spo76 protein [Oryza sativa (japonica cultivar-group)] | 7.43 | 0.0260199 | 1.303 |
| Gm-r1088-5213 | At2g33775 [Arabidopsis thaliana] | 10.36 | 0.012273 | 1.306 |
| Gm-r1070-7670 | putative ribosomal protein L21 [Oryza sativa (japonica cultivar-group)] | 9.11 | 0.0234529 | 1.307 |
| Gm-r1088-695 | 40S ribosomal protein S30-like [Oryza sativa (japonica cultivar-group)] | 6.42 | 0.0350466 | 1.308 |
| Gm-r1088-6026 | 40S ribosome protein S7 [Avicennia marina] | 13.88 | 0.005826 | 1.309 |
| Gm-r1070-9104 | At4g02930 [Arabidopsis thaliana] | 6.44 | 0.0441749 | 1.310 |
| Gm-r1088-2144 | No Hits | 10.32 | 0.0123768 | 1.311 |
| Gm-r1070-8832 | ribosomal protein L7 | 9.34 | 0.0223493 | 1.311 |
| Gm-r1070-8698 | Hypothetical protein [Arabidopsis thaliana] | 18.40 | 0.0051516 | 1.314 |
| Gm-r1088-3343 | plastid ribosomal protein S9 precursor [Spinacia oleracea] | 8.55 | 0.0191845 | 1.314 |
| Gm-r1088-4037 | S-adenosyl-L-methionine Mg-protoporphyrin IX methyltranserase [Nicotiana | 7.62 | 0.0246534 | 1.315 |

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| | tabacum] | | | |
| Gm-r1070-5540 | No Hits | 7.23 | 0.0361258 | 1.316 |
| Gm-r1088-3747 | putative protein [Arabidopsis thaliana] | 8.78 | 0.0180594 | 1.318 |
| Gm-r1088-4917 | xyloglucan fucosyltransferase [Pisum sativum] | 5.90 | 0.041205 | 1.319 |
| Gm-r1070-7622 | No Hits | 14.87 | 0.0083959 | 1.319 |
| Gm-r1070-7772 | putative protein [Arabidopsis thaliana] | 12.19 | 0.0129617 | 1.320 |
| Gm-r1070-1818 | actin-depolymerizing factor 1 [Petunia x hybrida] | 11.64 | 0.0142886 | 1.321 |
| Gm-r1070-2194 | No Hits | 6.44 | 0.0442142 | 1.321 |
| Gm-r1070-5272 | No Hits | 11.86 | 0.0137346 | 1.322 |
| Gm-r1088-4721 | putative cytoplasmic ribosomal protein S15a [Arabidopsis thaliana] | 7.88 | 0.0229377 | 1.323 |
| Gm-r1070-5846 | No Hits | 9.38 | 0.0221621 | 1.324 |
| Gm-r1088-4840 | AT5g09860/MYH9_7 [Arabidopsis thaliana] | 5.51 | 0.0469004 | 1.324 |
| Gm-r1070-8184 | 20S proteasome beta subunit PBB2 [Arabidopsis thaliana] | 11.00 | 0.0160756 | 1.326 |
| Gm-r1070-8836 | ribosomal protein small subunit 28 [Helianthus annuus] | 9.91 | 0.0198529 | 1.327 |
| Gm-r1070-5287 | No Hits | 13.37 | 0.0106161 | 1.328 |
| Gm-r1070-8573 | SET domain-containing protein [Arabidopsis thaliana] | 21.63 | 0.003501 | 1.329 |
| Gm-r1088-9102 | putative oxidoreductase [Oryza sativa (japonica cultivar-group)] | 10.56 | 0.0117087 | 1.330 |
| Gm-r1070-4409 | phosphoethanolamine N-methyltransferase [Atriplex nummularia] | 11.88 | 0.0136896 | 1.332 |
| Gm-r1070-7424 | beta-galactosidase [Cicer arietinum] | 6.83 | 0.0399713 | 1.332 |
| Gm-r1088-5086 | unknown protein [Oryza sativa (japonica cultivar-group)] | 7.91 | 0.0227333 | 1.332 |
| Gm-r1088-4782 | putative dehydrogenase [Arabidopsis thaliana] | 5.90 | 0.0412288 | 1.334 |
| Gm-r1088-6208 | No Hits | 11.05 | 0.0104776 | 1.334 |
| Gm-r1088-489 | KOW domain-containing transcription factor family protein [Arabidopsis thaliana] | 8.95 | 0.0172859 | 1.334 |
| Gm-r1070-2542 | No Hits | 11.07 | 0.0158531 | 1.336 |
| Gm-r1070-2917 | chlorophyll a/b binding protein | 8.84 | 0.0248506 | 1.337 |
| Gm-r1070-279 | putative chaperonin [Oryza sativa (japonica cultivar-group)] | 15.25 | 0.0079411 | 1.338 |
| Gm-r1070-3000 | At3g53580/F4P12_280 [Arabidopsis thaliana] | 7.77 | 0.0316772 | 1.339 |
| Gm-r1070-4030 | No Hits | 7.97 | 0.0302256 | 1.339 |
| Gm-r1088-3981 | No Hits | 13.64 | 0.0061064 | 1.340 |
| Gm-r1088-8208 | 40s ribosomal protein S23 [Euphorbia esula] | 7.36 | 0.0265226 | 1.341 |
| Gm-r1070-5692 | putative proteasome regulatory non-ATPase subunit [Oryza sativa (japonica cultivar-group)] | 10.00 | 0.0195144 | 1.341 |
| Gm-r1088-6585 | 60S ribosomal protein L19 [Capsicum annuum] | 5.34 | 0.049688 | 1.342 |
| Gm-r1088-6610 | basic blue copper protein [Cicer arietinum] | 12.43 | 0.0077789 | 1.342 |

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| Gm-r1088-3597 | RNA-binding protein, putative [Arabidopsis thaliana] | 6.30 | 0.0363946 | 1.344 |
| Gm-r1070-5840 | unknown protein [Oryza sativa (japonica cultivar-group)] | 11.61 | 0.0143771 | 1.344 |
| Gm-r1070-1237 | putative 60S ribosomal protein L13, BBC1 protein [Arabidopsis thaliana] | 7.83 | 0.0312267 | 1.344 |
| Gm-r1088-3087 | vacuolar proton-inorganic pyrophosphatase [Hordeum vulgare subsp. vulgare] | 7.50 | 0.0254703 | 1.344 |
| Gm-r1070-7374 | At1g76400/F15M4_10 [Arabidopsis thaliana] | 12.97 | 0.011357 | 1.344 |
| Gm-r1070-4052 | No Hits | 9.23 | 0.022841 | 1.344 |
| Gm-r1070-8502 | unknown protein [Arabidopsis thaliana] | 11.64 | 0.0142969 | 1.345 |
| Gm-r1070-8375 | DNAJ protein-like [Arabidopsis thaliana] | 19.40 | 0.0045461 | 1.346 |
| Gm-r1070-8587 | calcium-binding EF hand-like protein [Oryza sativa (japonica cultivar-group)] | 26.76 | 0.0020674 | 1.348 |
| Gm-r1070-7767 | proteasome subunit [Spinacia oleracea] | 10.09 | 0.0191489 | 1.348 |
| Gm-r1088-8921 | hydroxyproline rich glycoprotein PsHRGP1 [Pisum sativum] | 6.40 | 0.0352389 | 1.348 |
| Gm-r1070-1487 | acidic ribosomal protein P0 [Glycine max] | 11.04 | 0.0159505 | 1.349 |
| Gm-r1070-3475 | unnamed protein product [Arabidopsis thaliana] | 6.94 | 0.0388629 | 1.350 |
| Gm-r1070-1021 | putative small nuclear ribonucleoprotein polypeptide F [Oryza sativa (japonica cultivar-group)] | 21.85 | 0.0034166 | 1.354 |
| Gm-r1070-4147 | AT5g55940/MYN21_5 [Arabidopsis thaliana] | 26.04 | 0.0022154 | 1.355 |
| Gm-r1070-1519 | Contains similarity to ycf37 gene product from Synechocystis | 8.21 | 0.0285957 | 1.357 |
| Gm-r1088-7357 | RNA polymerase alpha subunit [Vigna angularis] | 5.35 | 0.0494267 | 1.357 |
| Gm-r1070-3747 | DEAD BOX RNA helicase RH15 [Arabidopsis thaliana] | 10.73 | 0.0169299 | 1.358 |
| Gm-r1070-3663 | putative L24 ribosomal protein [Ipomoea batatas] | 17.80 | 0.0055708 | 1.358 |
| Gm-r1088-6075 | putative protein [Arabidopsis thaliana] | 6.15 | 0.0381449 | 1.360 |
| Gm-r1070-6880 | Citrate synthase, mitochondrial precursor | 8.80 | 0.0250683 | 1.361 |
| Gm-r1070-7936 | No Hits | 6.15 | 0.0478364 | 1.361 |
| Gm-r1088-4491 | beta-tubulin [Nicotiana attenuata] | 11.58 | 0.00931 | 1.362 |
| Gm-r1070-6604 | F20B24.7 [Arabidopsis thaliana] | 10.18 | 0.018816 | 1.363 |
| Gm-r1088-2912 | chloroplast inner envelope protein, 110 kD (IEP110) [Pisum sativum] | 13.82 | 0.0058904 | 1.364 |
| Gm-r1088-429 | At2g34480 [Arabidopsis thaliana] | 5.79 | 0.0427549 | 1.364 |
| Gm-r1070-6140 | putative RING3 protein [Oryza sativa (japonica cultivar-group)] | 7.05 | 0.0377762 | 1.367 |
| Gm-r1070-8192 | At1g75690 [Arabidopsis thaliana] | 8.70 | 0.0256397 | 1.369 |
| Gm-r1070-7732 | putative protein [Arabidopsis thaliana] | 11.61 | 0.014362 | 1.369 |
| Gm-r1070-7642 | hypothetical protein [Oryza sativa (japonica cultivar-group)] | 9.26 | 0.0227305 | 1.369 |
| Gm-r1070-3701 | GA [Pisum sativum] | 8.59 | 0.0262657 | 1.370 |
| Gm-r1070-8118 | BiP-isoform D [Glycine max] | 17.34 | 0.0059135 | 1.370 |
| Gm-r1088-7207 | calnexin [Glycine max] | 6.05 | 0.0392961 | 1.370 |

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| Gm-r1088-7247 | putative L5 ribosomal protein [Arabidopsis thaliana] | 7.59 | 0.0248923 | 1.372 |
| Gm-r1070-2299 | F1N21.7 [Arabidopsis thaliana] | 24.13 | 0.0026779 | 1.373 |
| Gm-r1088-3306 | acyl-CoA-binding protein [Ricinus communis] | 8.28 | 0.0206165 | 1.373 |
| Gm-r1070-7532 | transcriptional factor B3-like [Oryza sativa (japonica cultivar-group)] | 8.70 | 0.0256331 | 1.375 |
| Gm-r1088-3290 | No Hits | 10.03 | 0.0132675 | 1.375 |
| Gm-r1088-3345 | light-regulated chloroplast-localized protein [Solanum tuberosum] | 9.17 | 0.0163721 | 1.375 |
| Gm-r1088-5454 | ubiquitin precursor [Hevea brasiliensis] | 8.08 | 0.0217134 | 1.376 |
| Gm-r1070-4090 | dihydrolipoamide S-acetyltransferase [Arabidopsis thaliana] | 13.59 | 0.0102443 | 1.379 |
| Gm-r1070-8225 | LHCII type III chlorophyll a/b binding protein [Vigna radiata] | 11.83 | 0.0138083 | 1.380 |
| Gm-r1070-8553 | At4g34360 [Arabidopsis thaliana] | 14.44 | 0.0089732 | 1.381 |
| Gm-r1070-7579 | acyltransferase homolog [Petunia x hybrida] | 11.68 | 0.0141818 | 1.381 |
| Gm-r1070-5457 | At1g64520/F1N19_10 [Arabidopsis thaliana] | 13.84 | 0.0098526 | 1.381 |
| Gm-r1070-9004 | ubiquinol-cytochrome C reductase complex, putative / mitochondrial hinge protein | 6.84 | 0.0398176 | 1.383 |
| Gm-r1070-7932 | YABBY-like transcription factor GRAMINIFOLIA [Antirrhinum majus] | 9.60 | 0.0211656 | 1.387 |
| Gm-r1070-6471 | 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Vitis vinifera] | 7.85 | 0.0310887 | 1.388 |
| Gm-r1088-6417 | putative AT-hook DNA-binding protein [Arabidopsis thaliana] | 5.98 | 0.0402315 | 1.392 |
| Gm-r1070-7854 | putative plastid glucose 6 phosphate/phosphate translocator [Glycine max] | 8.70 | 0.0256202 | 1.392 |
| Gm-r1088-4767 | AP2/EREBP transcription factor BABY BOOM [Medicago truncatula] | 25.41 | 0.0010006 | 1.393 |
| Gm-r1070-5282 | eukaryotic initiation factor 4A [Pennisetum glaucum] | 8.48 | 0.0268972 | 1.394 |
| Gm-r1070-1846 | 60s acidic ribosomal protein [Hyacinthus orientalis] | 7.33 | 0.03519 | 1.395 |
| Gm-r1088-9167 | Csf-1 [Cucumis sativus] | 12.31 | 0.0079784 | 1.397 |
| Gm-r1088-3347 | gag/pol polyprotein [Pisum sativum] | 23.23 | 0.001322 | 1.398 |
| Gm-r1070-6350 | 60S ribosomal protein L10A [Phaseolus coccineus] | 10.39 | 0.0180469 | 1.399 |
| Gm-r1088-6328 | cellulose synthase [Populus tremula x Populus tremuloides] | 5.69 | 0.0441166 | 1.400 |
| Gm-r1088-953 | No Hits | 6.12 | 0.0384333 | 1.401 |
| Gm-r1070-4290 | putative ribosomal protein [Capsicum annuum] | 8.45 | 0.0271104 | 1.402 |
| Gm-r1070-8592 | 40S ribosomal protein S11 [Euphorbia esula] | 13.15 | 0.0110147 | 1.402 |
| Gm-r1070-8291 | putative ribosomal protein L19 [Arabidopsis thaliana] | 16.78 | 0.0063822 | 1.403 |
| Gm-r1070-8498 | aldose 1-epimerase-like protein [Arabidopsis thaliana] | 9.82 | 0.0202325 | 1.405 |
| Gm-r1088-7440 | Gip1-like protein [Populus tomentosa] | 10.87 | 0.0109026 | 1.407 |
| Gm-r1070-3049 | putative ATP synthase [Arabidopsis thaliana] | 7.50 | 0.0338014 | 1.408 |
| Gm-r1070-1505 | histone H3 | 11.43 | 0.0148413 | 1.409 |
| Gm-r1088-7449 | No Hits | 9.94 | 0.0135286 | 1.409 |
| Gm-r1070-1590 | GA [Pisum sativum] | 21.36 | 0.0036094 | 1.412 |

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| Gm-r1088-5902 | F23M19.3 [Arabidopsis thaliana] | 12.82 | 0.0071816 | 1.412 |
| Gm-r1070-7685 | WD40 [Cucumis melo] | 20.33 | 0.0040642 | 1.413 |
| Gm-r1088-4414 | Ferritin 3, chloroplast precursor (SFerH-3) | 5.55 | 0.046201 | 1.413 |
| Gm-r1088-1388 | unknown [Arabidopsis thaliana] | 11.28 | 0.0099551 | 1.415 |
| Gm-r1070-7925 | 26S proteasome regulatory particle non-ATPase subunit12 [Oryza sativa (japonica cultivar-group)] | 15.89 | 0.0072289 | 1.419 |
| Gm-r1088-3569 | ribosomal protein S8 [Vigna angularis] | 7.94 | 0.0225651 | 1.419 |
| Gm-r1088-2732 | fis1 [Linum usitatissimum] | 6.53 | 0.033888 | 1.420 |
| Gm-r1070-8303 | No Hits | 18.26 | 0.0052462 | 1.421 |
| Gm-r1070-7706 | putative transport protein subunit [Arabidopsis thaliana] | 18.79 | 0.0049057 | 1.421 |
| Gm-r1070-5575 | apyrase [Dolichos biflorus] | 13.12 | 0.0110687 | 1.422 |
| Gm-r1088-3467 | ankyrin repeat family protein / regulator of chromosome condensation family protein | 10.21 | 0.0126996 | 1.422 |
| Gm-r1070-8367 | putative small nuclear ribonucleoprotein polypeptide E [Oryza sativa (japonica cultivar-group)] | 13.20 | 0.010924 | 1.422 |
| Gm-r1088-8996 | ribosomal protein L36 [Triticum aestivum] | 10.91 | 0.0108178 | 1.424 |
| Gm-r1070-6479 | putative pre-mRNA splicing factor SF2 [Oryza sativa (japonica cultivar-group)] | 7.86 | 0.0310097 | 1.429 |
| Gm-r1088-4515 | No Hits | 11.27 | 0.0099852 | 1.430 |
| Gm-r1070-1854 | No Hits | 6.92 | 0.0390137 | 1.431 |
| Gm-r1070-3995 | ubiquitin-conjugating enzyme 2 [Arachis hypogaea] | 10.39 | 0.0180611 | 1.431 |
| Gm-r1088-6248 | AX110P-like protein [Arabidopsis thaliana] | 6.03 | 0.0395398 | 1.433 |
| Gm-r1070-5025 | Uroporphyrinogen-Iii Decarboxylase From Nicotiana Tabacum | 15.05 | 0.0081779 | 1.434 |
| Gm-r1070-4327 | 40S ribosomal protein S25 [Glycine max] | 11.54 | 0.0145589 | 1.435 |
| Gm-r1070-6566 | No Hits | 13.94 | 0.0097013 | 1.437 |
| Gm-r1088-150 | ribosomal protein S26 [Pisum sativum] | 17.02 | 0.0033187 | 1.437 |
| Gm-r1070-947 | polyphenol oxidase [Camellia sinensis] | 12.58 | 0.0121124 | 1.438 |
| Gm-r1088-4244 | Unknown | 6.25 | 0.0369424 | 1.438 |
| Gm-r1070-8478 | 60S ribosomal protein L19 [Capsicum annuum] | 17.09 | 0.0061189 | 1.438 |
| Gm-r1070-4391 | unknown protein [Oryza sativa (japonica cultivar-group)] | 7.03 | 0.0379651 | 1.441 |
| Gm-r1070-8140 | 26S proteasome subunit S3 (Nuclear antigen 21D7) | 12.42 | 0.0124599 | 1.442 |
| Gm-r1070-8263 | putative SSR alpha subunit [Oryza sativa (japonica cultivar-group)] | 11.70 | 0.0141231 | 1.442 |
| Gm-r1070-8612 | small nuclear ribonucleoprotein-like protein [Arabidopsis thaliana] | 29.07 | 0.0016769 | 1.442 |
| Gm-r1088-7017 | glycosyl hydrolase family 17 protein [Arabidopsis thaliana] | 5.54 | 0.0464269 | 1.446 |
| Gm-r1070-5748 | cell wall protein Exp1 precursor [Mirabilis jalapa] | 7.79 | 0.0315489 | 1.446 |

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| Gm-r1070-8537 | No Hits | 24.88 | 0.0024829 | 1.447 |
| Gm-r1070-1380 | putative histone H2A [Oryza sativa (japonica cultivar-group)] | 9.89 | 0.0199454 | 1.447 |
| Gm-r1088-5082 | lipid transfer protein-like protein [Retama raetam] | 5.42 | 0.0482306 | 1.448 |
| Gm-r1070-5655 | unknown protein [Arabidopsis thaliana] | 6.03 | 0.0493793 | 1.448 |
| Gm-r1070-7924 | histone H3 (H3-1.1) | 42.15 | 0.0006351 | 1.450 |
| Gm-r1088-3975 | MAR-binding protein MFP1 homolog [Nicotiana tabacum] | 15.39 | 0.0043979 | 1.451 |
| Gm-r1088-4765 | No Hits | 6.37 | 0.0355736 | 1.457 |
| Gm-r1070-1205 | ribonucleotide reductase R2 [Nicotiana tabacum] | 7.31 | 0.0353639 | 1.458 |
| Gm-r1070-9182 | 40S ribosomal protein S16 [Euphorbia esula] | 8.28 | 0.0281424 | 1.460 |
| Gm-r1070-8029 | ribosomal protein L17 [Triticum aestivum] | 7.40 | 0.0346213 | 1.463 |
| Gm-r1070-520 | No Hits | 47.19 | 0.0004689 | 1.465 |
| Gm-r1070-4876 | water channel-like protein [Arabidopsis thaliana] | 23.80 | 0.0027707 | 1.466 |
| Gm-r1070-4860 | ribosomal protein L44 isoform b [Gossypium hirsutum] | 13.70 | 0.0100733 | 1.467 |
| Gm-r1070-6536 | ribosomal protein L23a [Fritillaria agrestis] | 9.75 | 0.0205213 | 1.469 |
| Gm-r1070-6895 | Tubulin/FtsZ family, GTPase domain, putative [Oryza sativa (japonica cultivar-group)] | 8.91 | 0.0245051 | 1.469 |
| Gm-r1070-1582 | chaperonin precursor [Pisum sativum] | 16.54 | 0.0065959 | 1.471 |
| Gm-r1070-8513 | putative protein kinase ADK1 [Oryza sativa (japonica cultivar-group)] | 16.43 | 0.0067029 | 1.472 |
| Gm-r1088-6115 | ribosomal protein L37 [Glycine max] | 25.00 | 0.0010526 | 1.474 |
| Gm-r1070-8850 | plasma membrane intrinsic protein 2;5 [Mimosa pudica] | 18.59 | 0.0050315 | 1.475 |
| Gm-r1070-4710 | ribosomal protein L32 [Mercurialis annua] | 8.35 | 0.027692 | 1.476 |
| Gm-r1070-5309 | homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] | 6.51 | 0.0433927 | 1.478 |
| Gm-r1088-4274 | ribosomal protein [Petunia x hybrida] | 13.76 | 0.0059562 | 1.479 |
| Gm-r1070-2533 | No Hits | 8.72 | 0.0254895 | 1.479 |
| Gm-r1070-4302 | No Hits | 10.49 | 0.0176985 | 1.480 |
| Gm-r1070-4669 | No Hits | 7.43 | 0.034369 | 1.480 |
| Gm-r1070-5921 | TOM20 [Solanum tuberosum] | 6.60 | 0.0424299 | 1.481 |
| Gm-r1070-4666 | No Hits | 7.11 | 0.0372286 | 1.482 |
| Gm-r1070-7989 | BiP [Glycine max] | 68.54 | 0.0001681 | 1.487 |
| Gm-r1088-8351 | phospholipase [Citrullus lanatus] | 8.16 | 0.0212525 | 1.489 |
| Gm-r1070-8899 | glycine-rich RNA-binding protein PsGRBP [Pisum sativum] | 13.63 | 0.0101816 | 1.490 |
| Gm-r1070-8575 | unknown [Arabidopsis thaliana] | 6.67 | 0.0416658 | 1.491 |
| Gm-r1070-7617 | At1g74560/F1M20_24 [Arabidopsis thaliana] | 6.08 | 0.0487153 | 1.494 |
| Gm-r1070-8652 | plasma membrane intrinsic protein 2;3 [Mimosa pudica] | 6.01 | 0.0496344 | 1.498 |

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| Gm-r1088-4539 | At1g18610 [Arabidopsis thaliana] | 17.65 | 0.0029934 | 1.503 |
| Gm-r1070-3452 | ribosomal protein L35 [Arabidopsis thaliana] | 12.85 | 0.0115817 | 1.505 |
| Gm-r1088-5863 | ribosomal protein [Petunia x hybrida] | 18.25 | 0.002718 | 1.508 |
| Gm-r1088-5173 | 40s ribosomal protein S23 [Euphorbia esula] | 18.56 | 0.0025865 | 1.509 |
| Gm-r1070-8126 | putative ribosomal protein [Capsicum annuum] | 21.67 | 0.0034869 | 1.514 |
| Gm-r1070-8058 | ADP-ribosylation factor [Hyacinthus orientalis] | 15.86 | 0.0072628 | 1.516 |
| Gm-r1070-8639 | putative nascent polypeptide associated complex alpha chain [Oryza sativa] | 13.66 | 0.0101439 | 1.516 |
| Gm-r1088-5886 | glucosyltransferase-like protein [Arabidopsis thaliana] | 6.55 | 0.0337221 | 1.519 |
| Gm-r1070-420 | No Hits | 11.19 | 0.0155008 | 1.519 |
| Gm-r1070-7831 | TGB12K interacting protein 2 [Nicotiana tabacum] | 6.33 | 0.0455746 | 1.520 |
| Gm-r1070-1257 | 60S ribosomal protein L7A [Arabidopsis thaliana] | 18.69 | 0.0049675 | 1.521 |
| Gm-r1088-2161 | unnamed protein product [Pisum sativum] | 9.34 | 0.0156588 | 1.522 |
| Gm-r1088-4175 | serine carboxypeptidase S28 family protein [Arabidopsis thaliana] | 47.28 | 0.0001276 | 1.523 |
| Gm-r1070-8966 | putative histone H2A protein [Oryza sativa (japonica cultivar-group)] | 20.58 | 0.0039459 | 1.525 |
| Gm-r1088-2375 | No Hits | 9.63 | 0.0145942 | 1.528 |
| Gm-r1088-6691 | ribosomal protein L36 [Triticum aestivum] | 27.57 | 0.0007733 | 1.528 |
| Gm-r1070-7448 | alpha-expansin 3 [Cicer arietinum] | 9.93 | 0.019794 | 1.532 |
| Gm-r1070-9108 | At1g74560/F1M20_24 [Arabidopsis thaliana] | 33.12 | 0.0011988 | 1.534 |
| Gm-r1070-9090 | NADPH-protochlorophyllide oxidoreductase [Vigna radiata] | 13.95 | 0.0096742 | 1.534 |
| Gm-r1070-7790 | putative 60S ribosomal protein L10A (RPL10aC) [Oryza sativa (japonica cultivar-group)] | 18.35 | 0.0051873 | 1.538 |
| Gm-r1070-1266 | splicing factor 3B subunit 5-like protein [Oryza sativa (japonica cultivar-group)] | 8.45 | 0.0271126 | 1.538 |
| Gm-r1088-4318 | histone H2B [Cicer arietinum] | 20.91 | 0.0018197 | 1.541 |
| Gm-r1070-8744 | allantoinase [Robinia pseudoacacia] | 15.92 | 0.0072045 | 1.549 |
| Gm-r1088-6692 | chloroplast outer envelope protein 34 [Pisum sativum] | 17.89 | 0.002879 | 1.554 |
| Gm-r1070-9103 | protein phosphatase 2C [Medicago sativa] | 28.36 | 0.0017864 | 1.555 |
| Gm-r1070-6662 | unknown [Arabidopsis thaliana] | 23.30 | 0.0029192 | 1.556 |
| Gm-r1070-617 | No Hits | 7.47 | 0.0340524 | 1.559 |
| Gm-r1070-7098 | putative permease 1 [Arabidopsis thaliana] | 9.28 | 0.0226394 | 1.563 |
| Gm-r1088-3169 | unknown protein [Arabidopsis thaliana] | 12.30 | 0.0079891 | 1.571 |
| Gm-r1088-4861 | allergen-like protein BRSn20 [Arabidopsis thaliana] | 16.93 | 0.0033673 | 1.571 |
| Gm-r1070-8049 | putative protein [Arabidopsis thaliana] | 18.26 | 0.0052459 | 1.574 |
| Gm-r1070-8158 | ribosomal protein L14-like protein [Arabidopsis thaliana] | 9.41 | 0.022029 | 1.576 |
| Gm-r1070-5261 | No Hits | 22.31 | 0.0032474 | 1.579 |

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| Gm-r1070-7352 | fasciclin-like AGP 12 [Populus alba x Populus tremula] | 13.29 | 0.0107705 | 1.579 |
| Gm-r1070-4867 | 30S ribosomal protein S16-like [Oryza sativa (japonica cultivar-group)] | 13.66 | 0.0101322 | 1.580 |
| Gm-r1070-9110 | AT5g55220/MCO15_17 [Arabidopsis thaliana] | 13.84 | 0.0098531 | 1.580 |
| Gm-r1070-3763 | probable high mobility group protein HMG1 - sword bean | 16.64 | 0.0065094 | 1.583 |
| Gm-r1070-5619 | beta-primeverosidase [Camellia sinensis] | 19.60 | 0.0044339 | 1.583 |
| Gm-r1070-9185 | nucleoside diphosphate kinase [Glycine max] | 17.23 | 0.0060067 | 1.586 |
| Gm-r1070-3909 | ribosomal protein L11, putative [Arabidopsis thaliana] | 17.14 | 0.0060779 | 1.586 |
| Gm-r1088-44 | allergen-like protein BRSn20 [Arabidopsis thaliana] | 42.51 | 0.0001841 | 1.590 |
| Gm-r1088-164 | putative 40S ribosomal protein [Oryza sativa (japonica cultivar-group)] | 26.71 | 0.000855 | 1.590 |
| Gm-r1070-3312 | protoporphyrinogen oxidase I [Oryza sativa (japonica cultivar-group)] | 14.36 | 0.0090822 | 1.603 |
| Gm-r1088-5910 | CONSTANS-like protein 2 [Malus x domestica] | 5.43 | 0.0481578 | 1.605 |
| Gm-r1070-4596 | unknown protein [Arabidopsis thaliana] | 22.32 | 0.0032415 | 1.606 |
| Gm-r1088-4079 | matrix metalloproteinase MMP2 [Glycine max] | 20.15 | 0.0020333 | 1.617 |
| Gm-r1088-4729 | At5g25170 [Arabidopsis thaliana] | 15.42 | 0.0043741 | 1.620 |
| Gm-r1070-970 | histone H2A [Euphorbia esula] | 7.12 | 0.0370862 | 1.624 |
| Gm-r1070-3576 | ribosomal protein L37 [Glycine max] | 12.90 | 0.0114877 | 1.628 |
| Gm-r1070-4900 | Gip1-like protein [Populus tomentosa] | 11.67 | 0.0142064 | 1.631 |
| Gm-r1088-7068 | 60S ribosomal protein L13E [Picea abies] | 7.67 | 0.0243091 | 1.639 |
| Gm-r1070-5626 | putative ribosomal protein L19 [Oryza sativa (japonica cultivar-group)] | 22.99 | 0.003018 | 1.641 |
| Gm-r1088-4541 | tubulin family protein [Arabidopsis thaliana] | 10.33 | 0.0123594 | 1.646 |
| Gm-r1088-3139 | unnamed protein product [Homo sapiens] | 9.78 | 0.0140706 | 1.651 |
| Gm-r1088-7215 | ribosomal protein L15 [Petunia x hybrida] | 11.23 | 0.0100719 | 1.653 |
| Gm-r1070-8151 | 40S ribosomal protein S21, putative [Oryza sativa (japonica cultivar-group)] | 54.66 | 0.0003143 | 1.655 |
| Gm-r1070-8751 | ribosomal protein L29 [Panax ginseng] | 45.72 | 0.0005106 | 1.660 |
| Gm-r1070-7487 | enoyl-ACP reductase [Nicotiana tabacum] | 21.30 | 0.0036343 | 1.668 |
| Gm-r1070-7864 | dehydroascorbate reductase [Zinnia elegans] | 12.30 | 0.0127237 | 1.671 |
| Gm-r1088-3849 | putative methionine aminopeptidase [Arabidopsis thaliana] | 19.10 | 0.002379 | 1.673 |
| Gm-r1070-7659 | alpha-tubulin [Gossypium hirsutum] | 14.48 | 0.0089098 | 1.683 |
| Gm-r1070-8444 | ribosomal protein S26 [Pisum sativum] | 17.01 | 0.0061854 | 1.685 |
| Gm-r1070-5942 | subtilisin-like protease [Arabidopsis thaliana] | 13.69 | 0.0100844 | 1.686 |
| Gm-r1088-3273 | glutamate 1-semialdehyde aminotransferase | 9.74 | 0.0142138 | 1.697 |
| Gm-r1088-2119 | aquaporin 2 [Samanea saman] | 9.84 | 0.0138732 | 1.697 |
| Gm-r1070-4817 | ribosomal protein L7 | 31.44 | 0.0013716 | 1.703 |
| Gm-r1088-5951 | phosphatidylinositol transfer-like protein III [Lotus japonicus] | 8.74 | 0.0182286 | 1.704 |

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| Gm-r1088-8092 | No Hits | 9.40 | 0.0154434 | 1.708 |
| Gm-r1088-4320 | histone H2B1 [Gossypium hirsutum] | 6.22 | 0.0372701 | 1.711 |
| Gm-r1070-7446 | putative chaperon P13.9 [Castanea sativa] | 16.83 | 0.0063427 | 1.716 |
| Gm-r1088-4561 | No Hits | 10.75 | 0.0112024 | 1.717 |
| Gm-r1088-6263 | putative prunasin hydrolase isoform PHA precursor [Oryza sativa (japonica cultivar-group)] | 9.04 | 0.016888 | 1.730 |
| Gm-r1070-7870 | putative aquaporin PIP2-2 [Vitis berlandieri x Vitis rupestris] | 11.16 | 0.0156002 | 1.740 |
| Gm-r1070-9008 | 40S ribosomal protein S25 [Glycine max] | 14.28 | 0.0091912 | 1.740 |
| Gm-r1070-5307 | phosphate/phosphoenolpyruvate translocator precursor | 8.13 | 0.0291418 | 1.743 |
| Gm-r1070-4344 | No Hits | 6.77 | 0.0405599 | 1.744 |
| Gm-r1070-940 | ADR12-2 protein - soybean | 31.14 | 0.0014066 | 1.755 |
| Gm-r1088-8979 | putative ferrochelatase [Oryza sativa (japonica cultivar-group)] | 23.38 | 0.0012953 | 1.760 |
| Gm-r1070-8414 | 40S ribosomal protein S14 | 33.04 | 0.0012066 | 1.760 |
| Gm-r1088-741 | cationic peroxidase 2 [Glycine max] | 5.72 | 0.0436826 | 1.767 |
| Gm-r1088-4722 | unnamed protein product [Arabidopsis thaliana] | 12.10 | 0.0083335 | 1.779 |
| Gm-r1070-8326 | histone H2B-3 [Lycopersicon esculentum] | 17.70 | 0.0056382 | 1.780 |
| Gm-r1070-4628 | copper/topa quinone amine oxidase precursor [Lathyrus sativus] | 11.54 | 0.0145401 | 1.784 |
| Gm-r1070-4055 | PAC motif-containing protein [Arabidopsis thaliana] | 21.34 | 0.003617 | 1.785 |
| Gm-r1070-9066 | unknown protein [Arabidopsis thaliana] | 24.50 | 0.0025788 | 1.786 |
| Gm-r1070-6640 | At3g59540/T16L24_90 [Arabidopsis thaliana] | 45.75 | 0.0005098 | 1.799 |
| Gm-r1070-3758 | ribosomal protein small subunit 28 [Helianthus annuus] | 26.41 | 0.0021389 | 1.801 |
| Gm-r1088-7080 | 60S ribosomal protein L34 [Solanum demissum] | 11.78 | 0.0089328 | 1.820 |
| Gm-r1070-7322 | like heterochromatin protein LHP1 [Arabidopsis thaliana] | 29.86 | 0.0015659 | 1.821 |
| Gm-r1088-7618 | Stem 31 kDa glycoprotein precursor (Vegetative storage protein VSP25) | 10.78 | 0.011137 | 1.821 |
| Gm-r1070-4310 | No Hits | 23.32 | 0.002912 | 1.829 |
| Gm-r1070-5715 | T complex protein | 25.56 | 0.0023202 | 1.831 |
| Gm-r1070-5890 | 40S ribosome protein S7 [Avicennia marina] | 34.44 | 0.0010834 | 1.843 |
| Gm-r1070-1864 | fatty acid elongase-like protein [Arabidopsis thaliana] | 13.21 | 0.0109101 | 1.846 |
| Gm-r1070-1258 | Ser/Thr specific protein phosphatase [Medicago sativa subsp. x varia] | 6.93 | 0.03891 | 1.850 |
| Gm-r1070-806 | ADR12-2 protein - soybean | 12.51 | 0.0122734 | 1.861 |
| Gm-r1070-7481 | putative cytoplasmic ribosomal protein S15a [Arabidopsis thaliana] | 10.00 | 0.019498 | 1.862 |
| Gm-r1070-5480 | No Hits | 21.71 | 0.0034694 | 1.866 |
| Gm-r1070-6713 | At1g22780 [Arabidopsis thaliana] | 13.71 | 0.010058 | 1.883 |
| Gm-r1070-8254 | acidic ribosomal protein [Hyacinthus orientalis] | 21.80 | 0.0034332 | 1.908 |

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| Gm-r1070-5106 | unknown protein [Arabidopsis thaliana] | 33.62 | 0.0011528 | 1.926 |
| Gm-r1070-5505 | expansin [Pyrus communis] | 6.12 | 0.0481398 | 1.941 |
| Gm-r1088-2911 | At1g15340 [Arabidopsis thaliana] | 14.65 | 0.0050315 | 1.948 |
| Gm-r1070-5908 | allergen-like protein BRSn20 [Arabidopsis thaliana] | 26.31 | 0.0021574 | 1.952 |
| Gm-r1070-3344 | SDL5A | 29.87 | 0.0015642 | 1.952 |
| Gm-r1088-3220 | putative tropinone reductase [Arabidopsis thaliana] | 12.86 | 0.0071232 | 1.954 |
| Gm-r1070-5485 | At1g79600/F20B17_3 [Arabidopsis thaliana] | 22.68 | 0.0031196 | 1.955 |
| Gm-r1070-3852 | NBS-LRR type disease resistance protein RPG1-B [Glycine max] | 13.37 | 0.0106155 | 1.969 |
| Gm-r1070-831 | ADR12-2 protein - soybean | 26.16 | 0.0021889 | 1.976 |
| Gm-r1070-7787 | unnamed protein product [Medicago sativa] | 34.71 | 0.0010615 | 1.982 |
| Gm-r1088-2389 | dihydroxypolyprenylbenzoate methyltransferase [Arabidopsis thaliana] | 23.09 | 0.001347 | 1.985 |
| Gm-r1070-5741 | No Hits | 8.39 | 0.0274462 | 1.989 |
| Gm-r1070-8011 | unnamed protein product [Pisum sativum] | 8.02 | 0.0298661 | 2.006 |
| Gm-r1088-8783 | vegetative storage protein, 27K, precursor - soybean | 32.24 | 0.000466 | 2.009 |
| Gm-r1088-3593 | dehydroascorbate reductase [Glycine max] | 10.30 | 0.0124393 | 2.021 |
| Gm-r1070-5087 | unknown protein [Arabidopsis thaliana] | 40.68 | 0.0006984 | 2.021 |
| Gm-r1070-8979 | acidic ribosomal protein P0 [Glycine max] | 7.42 | 0.0344736 | 2.041 |
| Gm-r1070-6578 | No Hits | 11.89 | 0.0136569 | 2.051 |
| Gm-r1070-5465 | No Hits | 28.66 | 0.0017389 | 2.058 |
| Gm-r1070-1170 | No Hits | 12.96 | 0.0113614 | 2.179 |
| Gm-r1088-3798 | STYLOSA protein [Antirrhinum majus] | 9.79 | 0.0140252 | 2.241 |
| Gm-r1070-8599 | unnamed protein product [Arabidopsis thaliana] | 18.62 | 0.0050117 | 2.291 |
| Gm-r1070-2077 | unknown [Arabidopsis thaliana] | 23.67 | 0.0028067 | 2.309 |
| Gm-r1070-7220 | expressed protein [Arabidopsis thaliana] | 17.40 | 0.0058687 | 2.314 |
| Gm-r1070-1632 | ADR12-2 protein - soybean | 28.79 | 0.0017187 | 2.385 |
| Gm-r1070-9002 | 40S ribosomal protein S20-like protein [Arabidopsis thaliana] | 27.29 | 0.001968 | 2.416 |
| Gm-r1070-7450 | lipid tranfer protein II [Vigna radiata] | 30.46 | 0.0014877 | 2.538 |
| Gm-r1070-8777 | ly200 protein [Capsicum annuum] | 7.10 | 0.0372794 | 2.540 |
| Gm-r1070-1977 | F1N19.8 [Arabidopsis thaliana] | 21.27 | 0.0036477 | 2.547 |
| Gm-r1088-5079 | No Hits | 15.07 | 0.0046618 | 2.669 |
| Gm-r1070-5096 | proline-rich protein [Glycine max] | 22.83 | 0.0030694 | 3.279 |