Table S1. Primer sequences used for qPCR

| Gene Name | Gene ID | Primer Start | Primer Sequence |
|---|---|---|---|
| thiolase | GB12182 | 843F | GAAACCAGCATTTGTTAAACCATATG |
| thiolase | GB12182 | 920R | GCTGCTGATGCACCATCAGT |
| CPT1 | GB11897 | 394F | CCGCATGGTCAAACTTCATTAA |
| CPT1 | GB11897 | 491R | ACACCATAACCATCATCAGCTACAG |
| lsd2 | GB14434 | 580F | CCAGTATCTGCCGATGAGAACA |
| lsd2 | GB14434 | 650R | GCGGTTTTCGTGGATAATTGTC |
| Vg | ApisVg- | 492F | AGTTCCGACCGACGACG |
| Vg | ApisVg- | 554R | TTCCCTCCCACGGAGTCC |
| JHE | GB15327 | 23F | TTCTTTCTTCTCTTGTGACTTTTGGTT |
| JHE | GB15327 | 101R | CCCTTAATTGCACCTAAAGGAGTTT |
| JHEH | GB10771 | 454F | TTAACAAAACCTTGGCCTAATCAAA |
| JHEH | GB10771 | 528R | GGAGAAACCGTATCCAGGAAGTG |
| ilp2 | GB10174 | 9F | CCAATATTATGGTCGAACTTTGTCA |
| ilp2 | GB10174 | 74R | CGAGAATTATAAACACTACCGCACAT |
| inR1 | GB30322 | 1907F | TTCCGTGTACCACGGCAGA |
| inR1 | GB30322 | 1979R | GGTGCAAAGTACGCGTGAGA |
| npfR | GB30377 | 232F | AATTTGGCATTGAGCGATGTT |
| npfR | GB30377 | 302R | CCGAGGAACGTGTACAATGGT |
| akhR | GB16857 | 291F | TTGGGCGATCACTGTTTCCT |
| akhR | GB16857 | 377R | GATGATAAGTACAGGCCAAACATTCTAA |
| eIFIII-S8 | GB12747 | 1637F | TGAGTGTCTGCTATGGATTGCAA |
| eIFIII-S8 | GB12747 | 1718R | TCGCGGCTCGTGGTAAA |

Table S2. Gene Ontology terms with a directional bias toward foragers (F)>nurses (N)

| Term | *P* Value | Category F>N | Category N<F | Total F>N | Total N<F |
|---|---|---|---|---|---|
| GO:0065007~biological regulation | 7.91E-05 | 147 | 60 | 591 | 410 |
| GO:0051179~localization | 2.51E-04 | 182 | 84 | 591 | 410 |
| GO:0048749~compound eye development | 5.98E-04 | 28 | 3 | 591 | 410 |
| GO:0007243~protein kinase cascade | 9.20E-04 | 18 | 0 | 591 | 410 |
| GO:0001745~compound eye morphogenesis | 1.00E-03 | 24 | 2 | 591 | 410 |
| GO:0051234~establishment of localization | 1.08E-03 | 152 | 70 | 591 | 410 |
| GO:0050896~response to stimulus | 1.11E-03 | 99 | 39 | 591 | 410 |
| GO:0007560~imaginal disc morphogenesis | 1.26E-03 | 36 | 7 | 591 | 410 |
| GO:0006810~transport | 1.60E-03 | 150 | 70 | 591 | 410 |
| GO:0002164~larval development | 1.68E-03 | 44 | 11 | 591 | 410 |
| GO:0002117~larval development (sensu Amphibia) | 1.96E-03 | 37 | 8 | 591 | 410 |
| GO:0007552~metamorphosis | 1.96E-03 | 37 | 8 | 591 | 410 |
| GO:0050789~regulation of biological process | 1.99E-03 | 124 | 55 | 591 | 410 |
| GO:0001654~eye development | 2.02E-03 | 30 | 5 | 591 | 410 |
| GO:0050793~regulation of developmental process | 2.35E-03 | 22 | 2 | 591 | 410 |
| GO:0048592~eye morphogenesis | 2.50E-03 | 27 | 4 | 591 | 410 |
| GO:0016043~cellular component organization and biogenesis | 2.71E-03 | 165 | 81 | 591 | 410 |
| GO:0032502~developmental process | 2.89E-03 | 155 | 75 | 591 | 410 |
| GO:0007444~imaginal disc development | 3.03E-03 | 40 | 10 | 591 | 410 |
| GO:0051188~cofactor biosynthetic process | 3.03E-03 | 24 | 3 | 591 | 410 |
| GO:0006796~phosphate metabolic process | 3.22E-03 | 71 | 26 | 591 | 410 |
| GO:0006793~phosphorus metabolic process | 3.22E-03 | 71 | 26 | 591 | 410 |
| GO:0042221~response to chemical stimulus | 3.56E-03 | 33 | 7 | 591 | 410 |
| GO:0006119~oxidative phosphorylation | 4.61E-03 | 30 | 6 | 591 | 410 |
| GO:0007423~sensory organ development | 4.97E-03 | 32 | 7 | 591 | 410 |
| GO:0000165~MAPKKK cascade | 6.29E-03 | 14 | 0 | 591 | 410 |
| GO:0009887~organ morphogenesis | 7.59E-03 | 43 | 13 | 591 | 410 |
| GO:0051641~cellular localization | 8.21E-03 | 67 | 26 | 591 | 410 |
| GO:0065008~regulation of biological quality | 9.50E-03 | 30 | 7 | 591 | 410 |
| GO:0000902~cell morphogenesis | 9.82E-03 | 44 | 14 | 591 | 410 |
| GO:0032989~cellular structure morphogenesis | 9.82E-03 | 44 | 14 | 591 | 410 |
| GO:0009790~embryonic development | 1.01E-02 | 38 | 11 | 591 | 410 |
| GO:0009653~anatomical structure morphogenesis | 1.09E-02 | 78 | 33 | 591 | 410 |
| GO:0007275~multicellular organismal development | 1.09E-02 | 128 | 63 | 591 | 410 |
| GO:0035214~eye-antennal disc development | 1.18E-02 | 25 | 5 | 591 | 410 |
| GO:0007455~eye-antennal disc morphogenesis | 1.18E-02 | 25 | 5 | 591 | 410 |
| GO:0001751~compound eye photoreceptor cell differentiation | 1.19E-02 | 18 | 2 | 591 | 410 |
| GO:0030154~cell differentiation | 1.32E-02 | 89 | 40 | 591 | 410 |
| GO:0007610~behavior | 1.35E-02 | 33 | 9 | 591 | 410 |
| GO:0009108~coenzyme biosynthetic process | 1.39E-02 | 20 | 3 | 591 | 410 |
| GO:0048869~cellular developmental process | 1.50E-02 | 90 | 41 | 591 | 410 |
| GO:0007254~JNK cascade | 1.60E-02 | 12 | 0 | 591 | 410 |
| GO:0031098~stress-activated protein kinase signaling pathway | 1.60E-02 | 12 | 0 | 591 | 410 |
| GO:0016192~vesicle-mediated transport | 1.60E-02 | 44 | 15 | 591 | 410 |
| GO:0042775~organelle ATP synthesis coupled electron transport | 1.76E-02 | 17 | 2 | 591 | 410 |
| GO:0042773~ATP synthesis coupled electron transport | 1.76E-02 | 17 | 2 | 591 | 410 |
| GO:0051649~establishment of cellular localization | 1.95E-02 | 63 | 26 | 591 | 410 |
| GO:0046530~photoreceptor cell differentiation | 2.00E-02 | 19 | 3 | 591 | 410 |
| GO:0032501~multicellular organismal process | 2.04E-02 | 151 | 80 | 591 | 410 |
| GO:0015672~monovalent inorganic cation transport | 2.17E-02 | 21 | 4 | 591 | 410 |
| GO:0048468~cell development | 2.25E-02 | 76 | 34 | 591 | 410 |
| GO:0006811~ion transport | 2.34E-02 | 33 | 10 | 591 | 410 |
| GO:0006457~protein folding | 2.35E-02 | 25 | 6 | 591 | 410 |
| GO:0045165~cell fate commitment | 2.35E-02 | 25 | 6 | 591 | 410 |
| GO:0006139~nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | 2.50E-02 | 126 | 65 | 591 | 410 |
| GO:0048856~anatomical structure development | 2.50E-02 | 110 | 55 | 591 | 410 |
| GO:0022604~regulation of cell morphogenesis | 2.52E-02 | 11 | 0 | 591 | 410 |
| GO:0022603~regulation of anatomical structure morphogenesis | 2.52E-02 | 11 | 0 | 591 | 410 |
| GO:0008360~regulation of cell shape | 2.52E-02 | 11 | 0 | 591 | 410 |
| GO:0009607~response to biotic stimulus | 2.85E-02 | 18 | 3 | 591 | 410 |
| GO:0001754~eye photoreceptor cell differentiation | 2.85E-02 | 18 | 3 | 591 | 410 |
| GO:0006952~defense response | 2.98E-02 | 34 | 11 | 591 | 410 |
| GO:0035220~wing disc development | 3.03E-02 | 20 | 4 | 591 | 410 |
| GO:0050794~regulation of cellular process | 3.14E-02 | 94 | 46 | 591 | 410 |
| GO:0006812~cation transport | 3.17E-02 | 28 | 8 | 591 | 410 |
| GO:0043412~biopolymer modification | 3.24E-02 | 79 | 37 | 591 | 410 |
| GO:0019953~sexual reproduction | 3.25E-02 | 50 | 20 | 591 | 410 |
| GO:0007276~gamete generation | 3.25E-02 | 50 | 20 | 591 | 410 |
| GO:0003006~reproductive developmental process | 3.26E-02 | 13 | 1 | 591 | 410 |

| | | | | | |
|---|---|---|---|---|---|
| GO:0046034~ATP metabolic process | 3.26E-02 | 13 | 1 | 591 | 410 |
| GO:0046907~intracellular transport | 3.95E-02 | 56 | 24 | 591 | 410 |
| GO:0016311~dephosphorylation | 4.03E-02 | 17 | 3 | 591 | 410 |
| GO:0048731~system development | 4.05E-02 | 94 | 47 | 591 | 410 |
| GO:0016310~phosphorylation | 4.17E-02 | 54 | 23 | 591 | 410 |
| GO:0030707~ovarian follicle cell development | 4.20E-02 | 19 | 4 | 591 | 410 |
| GO:0006464~protein modification process | 4.54E-02 | 77 | 37 | 591 | 410 |
| GO:0043283~biopolymer metabolic process | 4.58E-02 | 162 | 91 | 591 | 410 |
| GO:0006754~ATP biosynthetic process | 4.86E-02 | 12 | 1 | 591 | 410 |
| GO:0006753~nucleoside phosphate metabolic process | 4.86E-02 | 12 | 1 | 591 | 410 |
| GO:0015992~proton transport | 4.86E-02 | 12 | 1 | 591 | 410 |
| GO:0042048~olfactory behavior | 4.86E-02 | 12 | 1 | 591 | 410 |
| GO:0006399~tRNA metabolic process | 4.86E-02 | 12 | 1 | 591 | 410 |
| GO:0007635~chemosensory behavior | 4.86E-02 | 12 | 1 | 591 | 410 |
| GO:0006818~hydrogen transport | 4.86E-02 | 12 | 1 | 591 | 410 |
| GO:0048513~organ development | 5.11E-02 | 73 | 35 | 591 | 410 |
| GO:0016477~cell migration | 5.44E-02 | 26 | 8 | 591 | 410 |
| GO:0048522~positive regulation of cellular process | 5.75E-02 | 18 | 4 | 591 | 410 |
| GO:0007476~imaginal disc-derived wing morphogenesis | 5.75E-02 | 18 | 4 | 591 | 410 |
| GO:0007472~wing disc morphogenesis | 5.75E-02 | 18 | 4 | 591 | 410 |
| GO:0000003~reproduction | 5.76E-02 | 54 | 24 | 591 | 410 |
| GO:0048737~imaginal disc-derived appendage development | 5.76E-02 | 20 | 5 | 591 | 410 |
| GO:0048736~appendage development | 5.76E-02 | 20 | 5 | 591 | 410 |
| GO:0035114~imaginal disc-derived appendage morphogenesis | 5.76E-02 | 20 | 5 | 591 | 410 |
| GO:0035107~appendage morphogenesis | 5.76E-02 | 20 | 5 | 591 | 410 |
| GO:0043687~post-translational protein modification | 5.80E-02 | 59 | 27 | 591 | 410 |
| GO:0002165~instar larval or pupal development | 6.09E-02 | 52 | 23 | 591 | 410 |
| GO:0009791~post-embryonic development | 6.09E-02 | 52 | 23 | 591 | 410 |
| GO:0006928~cell motility | 6.22E-02 | 31 | 11 | 591 | 410 |
| GO:0051674~localization of cell | 6.22E-02 | 31 | 11 | 591 | 410 |
| GO:0007242~intracellular signaling cascade | 6.67E-02 | 43 | 18 | 591 | 410 |
| GO:0010324~membrane invagination | 6.77E-02 | 27 | 9 | 591 | 410 |
| GO:0006897~endocytosis | 6.77E-02 | 27 | 9 | 591 | 410 |
| GO:0015986~ATP synthesis coupled proton transport | 7.16E-02 | 11 | 1 | 591 | 410 |
| GO:0006120~mitochondrial electron transport, NADH to ubiquinone | 7.16E-02 | 11 | 1 | 591 | 410 |
| GO:0007154~cell communication | 7.34E-02 | 101 | 54 | 591 | 410 |
| GO:0016044~membrane organization and biogenesis | 7.45E-02 | 32 | 12 | 591 | 410 |
| GO:0051707~response to other organism | 7.80E-02 | 15 | 3 | 591 | 410 |
| GO:0051704~multi-organism process | 7.80E-02 | 15 | 3 | 591 | 410 |
| GO:0045045~secretory pathway | 8.61E-02 | 26 | 9 | 591 | 410 |
| GO:0046903~secretion | 8.61E-02 | 26 | 9 | 591 | 410 |
| GO:0032940~secretion by cell | 8.61E-02 | 26 | 9 | 591 | 410 |
| GO:0002376~immune system process | 9.41E-02 | 22 | 7 | 591 | 410 |
| GO:0009617~response to bacterium | 9.48E-02 | 8 | 0 | 591 | 410 |
| GO:0042742~defense response to bacterium | 9.48E-02 | 8 | 0 | 591 | 410 |

## Table S3. Gene Ontology terms with a directional bias toward nurses (N)>foragers (F)

| Term | P Value | Category F>N | Category N>F | Total F>N | Total N>F |
|---|---|---|---|---|---|
| GO:0006412~translation | 9.83E-11 | 33 | 79 | 588 | 413 |
| GO:0009059~macromolecule biosynthetic process | 1.13E-08 | 46 | 85 | 588 | 413 |
| GO:0044249~cellular biosynthetic process | 1.42E-07 | 84 | 116 | 588 | 413 |
| GO:0009058~biosynthetic process | 1.23E-06 | 99 | 124 | 588 | 413 |
| GO:0010467~gene expression | 1.32E-04 | 101 | 113 | 588 | 413 |
| GO:0006631~fatty acid metabolic process | 1.44E-04 | 4 | 20 | 588 | 413 |
| GO:0044260~cellular macromolecule metabolic process | 1.47E-03 | 168 | 157 | 588 | 413 |
| GO:0044238~primary metabolic process | 3.82E-03 | 354 | 284 | 588 | 413 |
| GO:0044267~cellular protein metabolic process | 6.51E-03 | 167 | 150 | 588 | 413 |
| GO:0006629~lipid metabolic process | 7.47E-03 | 31 | 41 | 588 | 413 |
| GO:0032787~monocarboxylic acid metabolic process | 1.11E-02 | 12 | 22 | 588 | 413 |
| GO:0008152~metabolic process | 1.14E-02 | 416 | 320 | 588 | 413 |
| GO:0044255~cellular lipid metabolic process | 1.31E-02 | 25 | 34 | 588 | 413 |
| GO:0019538~protein metabolic process | 2.38E-02 | 177 | 151 | 588 | 413 |
| GO:0009124~nucleoside monophosphate biosynthetic process | 2.91E-02 | 1 | 8 | 588 | 413 |
| GO:0009123~nucleoside monophosphate metabolic process | 2.91E-02 | 1 | 8 | 588 | 413 |
| GO:0006635~fatty acid beta-oxidation | 3.43E-02 | 2 | 9 | 588 | 413 |
| GO:0019395~fatty acid oxidation | 3.43E-02 | 2 | 9 | 588 | 413 |
| GO:0006044~N-acetylglucosamine metabolic process | 3.80E-02 | 3 | 10 | 588 | 413 |
| GO:0006041~glucosamine metabolic process | 3.80E-02 | 3 | 10 | 588 | 413 |
| GO:0006040~amino sugar metabolic process | 3.80E-02 | 3 | 10 | 588 | 413 |
| GO:0006637~acyl-CoA metabolic process | 4.61E-02 | 0 | 6 | 588 | 413 |
| GO:0043170~macromolecule metabolic process | 4.82E-02 | 278 | 219 | 588 | 413 |
| GO:0009161~ribonucleoside monophosphate metabolic process | 5.66E-02 | 1 | 7 | 588 | 413 |
| GO:0009156~ribonucleoside monophosphate biosynthetic process | 5.66E-02 | 1 | 7 | 588 | 413 |
| GO:0006030~chitin metabolic process | 5.66E-02 | 1 | 7 | 588 | 413 |
| GO:0044237~cellular metabolic process | 9.45E-02 | 373 | 280 | 588 | 413 |

Table S4. Quantitative proteomic analyses of protein abundance in the fat bodies of bees fed rich vs. poor diet

| Description | *P*-value | logFC protein (F-N) | logFC RNA (F-N) |
|---|---|---|---|
| GB12681-RA [PREDICTED: Apis mellifera similar to Aldehyde dehydrogenase type III CG11140-PI, isoform I (LOC411822), mRNA] | 1.29E-04 | -1.14 | -0.14 |
| GB14361-RA [PREDICTED: Apis mellifera similar to Larval serum protein 2 CG6806-PA (LOC551648), mRNA] | 5.64E-04 | -3.82 | -4.22 |
| GB18917-RA [PREDICTED: Apis mellifera similar to Cofilin/actin-depolymerizing factor homolog (Protein D61) (Protein twinstar) (LOC725718), mRNA] | 3.13E-03 | 0.36 | 0.34 |
| GB14791-RA [PREDICTED: Apis mellifera similar to bellwether CG3612-PA, transcript variant 1 (LOC409114), mRNA] | 6.54E-03 | 1.05 | 0.02 |
| GB12797-RA [PREDICTED: Apis mellifera similar to Trehalose-6-phosphate synthase 1 CG4104-PA (LOC408867), partial mRNA] | 8.94E-03 | 1.23 | 0.61 |
| GB12855-RA [PREDICTED: Apis mellifera similar to Neural conserved at 73EF CG11661-PA, isoform A, transcript variant 1 (LOC408286), mRNA] | 9.10E-03 | 1.37 | 0.29 |
| GB13999-RA [Apis mellifera vitellogenin (Vg), mRNA] | 1.50E-02 | -3.26 | -3.12 |
| GB16568-RA [PREDICTED: Apis mellifera similar to CG11015-PA (LOC552610), mRNA] | 1.58E-02 | 2.09 | 0.18 |
| GB12741-RA [PREDICTED: Apis mellifera similar to Aldehyde dehydrogenase CG3752-PA, transcript variant 1 (LOC550687), mRNA] | 1.96E-02 | 0.57 | 0.36 |
| GB16903-RA [PREDICTED: Apis mellifera similar to cathD CG1548-PA (LOC409341), mRNA] | 2.05E-02 | -0.89 | -0.80 |
| GB13073-RA [PREDICTED: Apis mellifera similar to CG5214-PA (LOC409155), mRNA] | 2.90E-02 | 1.14 | 0.14 |
| GB14852-RA [PREDICTED: Apis mellifera similar to heat shock protein 8, transcript variant 1 (LOC409418), mRNA] | 3.31E-02 | 0.25 | 0.09 |
| GB19166-RA [PREDICTED: Apis mellifera similar to Rab-protein 1 CG3320-PA, isoform A (LOC409456), mRNA] | 3.44E-02 | -0.74 | 0.10 |
| GB10973-RA [Apis mellifera arginine kinase (Argk), mRNA] | 4.86E-02 | 1.00 | -0.07 |
| GB10695-RA [PREDICTED: Apis mellifera similar to Pyruvate kinase CG7070-PB, isoform B (LOC552007), mRNA] | 5.14E-02 | 0.99 | 0.26 |
| GB11059-RA [PREDICTED: Apis mellifera similar to Retinoid- and fatty-acid binding protein CG11064-PA, transcript variant 1 (LOC408961), mRNA] | 5.40E-02 | -1.35 | NA |
| GB18969-RA [PREDICTED: Apis mellifera similar to 60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 kDa chaperonin) (CPN60) (Heat shock protein 60) (HSP-60) (Mitochondrial matrix protein P1) (LOC409384), mRNA] | 5.63E-02 | -0.49 | -0.15 |
| GB15049-RB [PREDICTED: Apis mellifera similar to CG7470-PA (LOC412948), mRNA] | 5.94E-02 | 1.09 | 0.91 |
| GB13058-RA [PREDICTED: Apis mellifera similar to dihydroxyacetone kinase 2 (LOC413697), mRNA] | 5.96E-02 | -1.24 | -1.70 |
| GB12488-RA [PREDICTED: Apis mellifera similar to Aconitase CG9244-PB (LOC408446), mRNA] | 5.98E-02 | 1.23 | 0.27 |
| GB14517-RA [PREDICTED: Apis mellifera similar to Isocitrate dehydrogenase CG7176-PC, isoform C, transcript variant 2 (LOC551276), mRNA] | 6.23E-02 | -0.41 | -0.29 |
| GB13596-RA [PREDICTED: Apis mellifera similar to ATP synthase- CG11154-PA, isoform A (LOC551766), mRNA] | 6.34E-02 | 1.14 | 0.12 |
| GB20017-RA [PREDICTED: Apis mellifera similar to TER94 CG2331-PA, isoform A, transcript variant 1 (LOC409377), mRNA] | 6.42E-02 | -0.20 | 0.04 |
| GB14284-RA [PREDICTED: Apis mellifera similar to Sorbitol dehydrogenase-2 CG4649-PA (LOC408871), mRNA] | 7.40E-02 | -0.66 | -0.93 |
| GB19171-RA [PREDICTED: Apis mellifera similar to Vacuolar H+-ATPase 55kD B subunit CG17369-PB, isoform B (LOC551721), mRNA] | 7.44E-02 | 0.77 | 0.41 |
| GB12113-RA [PREDICTED: Apis mellifera similar to porin CG6647-PA, isoform A (LOC551325), mRNA] | 8.30E-02 | 1.89 | NA |
| GB10477-RA [PREDICTED: Apis mellifera similar to B-cell receptor-associated protein 37 (LOC551944), mRNA] | 8.39E-02 | 0.55 | -0.38 |
| GB11385-RA [PREDICTED: Apis mellifera similar to CG3731-PB, isoform B (LOC410022), mRNA] | 8.54E-02 | 1.86 | 0.29 |
| GB13368-RA [PREDICTED: Apis mellifera lambda crystallin-like protein, transcript variant 1 (Cryl1), partial mRNA] | 8.56E-02 | 0.60 | 0.94 |
| GB14798-RA [PREDICTED: Apis mellifera similar to Glyceraldehyde 3 phosphate dehydrogenase 1 CG12055-PA, isoform A, transcript variant 2 (LOC410122), mRNA] | 8.96E-02 | 0.48 | 0.17 |
| GB17663-RA [PREDICTED: Apis mellifera similar to CG5065-PA (LOC411910), mRNA] | 9.65E-02 | -2.80 | -0.86 |
| GB18004-RA [PREDICTED: Apis mellifera similar to CG31075-PA (LOC408559), mRNA] | 1.17E-01 | -1.41 | -1.44 |
| GB13508-RA [PREDICTED: Apis mellifera similar to ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (LOC411183), mRNA] | 1.18E-01 | 2.02 | 0.04 |
| GB19247-RA [PREDICTED: Apis mellifera similar to Elongation factor 2 (EF-2), transcript variant 1 (LOC409167), mRNA] | 1.22E-01 | -0.53 | -0.08 |
| GB18737-RA [PREDICTED: Apis mellifera similar to 15-hydroxyprostaglandin dehydrogenase (LOC551423), mRNA] | 1.34E-01 | -2.19 | -1.71 |
| GB20117-RA [PREDICTED: Apis mellifera hypothetical LOC552391 (LOC552391), mRNA] | 1.41E-01 | -2.14 | -0.19 |
| GB15629-RA [PREDICTED: Apis mellifera similar to ATP synthase O subunit, mitochondrial precursor (Oligomycin sensitivity conferral protein) (OSCP) (LOC409236), mRNA] | 1.45E-01 | 0.89 | 0.02 |
| GB11503-RA [PREDICTED: Apis mellifera similar to CG5195-PA (LOC724779), mRNA] | 1.45E-01 | 0.50 | 1.33 |
| GB17626-RA [PREDICTED: Apis mellifera similar to CG7430-PA, transcript variant 1 (LOC551039), mRNA] | 1.49E-01 | 0.59 | 0.03 |
| GB14205-RA [PREDICTED: Apis mellifera similar to CG11267-PA (LOC552531), mRNA] | 1.64E-01 | 0.48 | 0.09 |
| GB10312-RA [PREDICTED: Apis mellifera similar to CG7461-PA (LOC412025), mRNA] | 1.67E-01 | -0.69 | -0.24 |
| GB16443-RA [PREDICTED: Apis mellifera similar to lethal (1) G0334 CG7010-PD, isoform D, transcript variant 1 (LOC551103), mRNA] | 1.83E-01 | 0.84 | -0.09 |
| GB19860-RA [PREDICTED: Apis mellifera similar to Heat shock protein cognate 5 CG8542-PA (LOC408605), mRNA] | 1.92E-01 | 0.74 | 0.24 |
| GB18300-RA [PREDICTED: Apis mellifera similar to yellow-h CG1629-PA (LOC724293), mRNA] | 1.93E-01 | 0.63 | 0.96 |
| GB12573-RA [PREDICTED: Apis mellifera similar to lethal (1) G0030 CG3861-PA, isoform A (LOC410059), mRNA] | 1.96E-01 | 1.17 | 0.36 |
| GB18162-RA [PREDICTED: Apis mellifera similar to Peroxisomal multifunctional enzyme type 2 (MFE-2) (D-bifunctional protein) (DBP) (17-beta-hydroxysteroid dehydrogenase 4) (17-beta-HSD 4) (LOC409986), mRNA] | 1.98E-01 | -0.44 | -0.19 |
| GB16448-RA [PREDICTED: Apis mellifera similar to Annexin-B9 (Annexin-9) (Annexin IX), transcript variant 1 (LOC409533), mRNA] | 1.99E-01 | 0.59 | 0.76 |
| GB15716-RA [PREDICTED: Apis mellifera similar to CG5028-PA (LOC410396), mRNA] | 2.00E-01 | 1.88 | 0.11 |
| GB16526-RA [PREDICTED: Apis mellifera similar to Proteasome subunit alpha type 5 (Proteasome zeta chain) (Macropain zeta chain) (Multicatalytic endopeptidase complex zeta chain) (LOC551956), mRNA] | 2.02E-01 | -0.38 | -0.04 |
| GB13680-RA [PREDICTED: Apis mellifera similar to 3-hydroxyacyl-CoA dehydrogenase type-2 (3-hydroxyacyl-CoA dehydrogenase type II) (Type II HADH) (3-hydroxy-2-methylbutyryl-CoA dehydrogenase) (Scully protein) (LOC725274), mRNA] | 2.02E-01 | -1.89 | -0.85 |
| GB12526-RA [PREDICTED: Apis mellifera similar to lethal (2) k05713 CG8256-PC, isoform C (LOC551904), mRNA] | 2.09E-01 | 1.52 | 0.69 |
| GB16951-RA [PREDICTED: Apis mellifera similar to Malic enzyme CG10120-PB, isoform B, transcript variant 1 | 2.11E-01 | -0.88 | -0.44 |

| | | | |
|---|---|---|---|
| (LOC411813), partial mRNA] | | | |
| GB17876-RA [PREDICTED: Apis mellifera similar to Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type (Calcium pump), transcript variant 1 (LOC410371), mRNA] | 2.43E-01 | 0.83 | 0.36 |
| GB15079-RA [PREDICTED: Apis mellifera similar to Glutamate dehydrogenase CG5320-PF, isoform F, transcript variant 1 (LOC409253), mRNA] | 2.50E-01 | 1.58 | -0.21 |
| GB12327-RA [PREDICTED: Apis mellifera similar to aldehyde dehydrogenase 1 family, member L2 (LOC551401), mRNA] | 2.53E-01 | 0.36 | 1.23 |
| GB18647-RA [PREDICTED: Apis mellifera similar to lethal (2) 37Cc CG10691-PA, isoform A (LOC408412), mRNA] | 2.54E-01 | 0.38 | -0.14 |
| GB10989-RA [PREDICTED: Apis mellifera similar to Vacuolar ATP synthase catalytic subunit A, osteoclast isoform (V-ATPase subunit A 2) (Vacuolar proton pump alpha subunit 2) (V-ATPase 69 kDa subunit 2) (Isoform HO68), transcript variant 1 (LOC551093), mRNA | 2.54E-01 | 1.01 | 0.15 |
| GB19380-RA [PREDICTED: Apis mellifera similar to thioredoxin peroxidase 1 CG1633-PA, isoform A, transcript variant 1 (LOC409954), mRNA] | 2.71E-01 | 0.22 | 0.36 |
| GB14677-RA [PREDICTED: Apis mellifera similar to CG11089-PA (LOC412467), mRNA] | 2.79E-01 | -0.76 | -0.33 |
| GB17549-RA [PREDICTED: Apis mellifera similar to Putative Achaete Scute Target 1 CG6148-PB, isoform B (LOC413012), mRNA] | 2.99E-01 | 0.66 | 0.04 |
| GB17255-RA [PREDICTED: Apis mellifera similar to lethal (1) G0230 CG2968-PA (LOC552682), mRNA] | 3.34E-01 | 0.26 | 0.03 |
| GB11431-RA [PREDICTED: Apis mellifera similar to Nucleosome remodeling factor – 38kD CG4634-PA (LOC409774), mRNA] | 3.36E-01 | 0.21 | 0.01 |
| GB14758-RA [PREDICTED: Apis mellifera similar to heat shock protein 90-alpha, transcript variant 1 (LOC408928), mRNA] | 3.38E-01 | 0.39 | 0.17 |
| GB17223-RA [PREDICTED: Apis mellifera similar to CG5590-PA (LOC552717), mRNA] | 3.48E-01 | -0.84 | -0.16 |
| GB12338-RA [PREDICTED: Apis mellifera similar to 60S acidic ribosomal protein P0 (DNA-(apurinic or apyrimidinic site) lyase) (Apurinic-apyrimidinic endonuclease), transcript variant 1 (LOC550711), mRNA] | 3.57E-01 | -0.18 | -0.41 |
| GB14849-RA [PREDICTED: Apis mellifera similar to Putative deoxyribose-phosphate aldolase (Phosphodeoxyriboaldolase) (Deoxyriboaldolase) (DERA) (LOC551986), mRNA] | 3.60E-01 | -0.67 | -0.51 |
| GB15016-RA [PREDICTED: Apis mellifera similar to Heat shock protein cognate 3 CG4147-PA, isoform A (LOC409587), mRNA] | 3.69E-01 | 0.20 | 0.41 |
| GB13160-RA [PREDICTED: Apis mellifera similar to pugilist CG4067-PA, isoform A, transcript variant 1 (LOC550749), mRNA] | 3.85E-01 | 0.82 | 0.24 |
| GB13427-RA [PREDICTED: Apis mellifera similar to CG17337-PA, transcript variant 1 (LOC412393), mRNA] | 3.91E-01 | 0.55 | 0.55 |
| GB10514-RA [PREDICTED: Apis mellifera similar to Tubulin alpha-1 chain (LOC408388), mRNA] | 3.92E-01 | 0.31 | 0.24 |
| GB15172-RA [PREDICTED: Apis mellifera similar to lethal (1) G0255 CG4094-PA, isoform A (LOC724321), mRNA] | 4.06E-01 | 0.22 | 0.06 |
| GB12364-RA [PREDICTED: Apis mellifera similar to fumarylacetoacetate hydrolase domain containing 2A, transcript variant 2 (LOC410635), mRNA] | 4.08E-01 | 1.09 | 0.17 |
| GB18557-RA [PREDICTED: Apis mellifera similar to Spectrin alpha chain (LOC551291), mRNA] | 4.16E-01 | 0.58 | 0.20 |
| GB11665-RA [PREDICTED: Apis mellifera similar to Imaginal disc growth factor 4 CG1780-PA, isoform A (LOC413324), mRNA] | 4.31E-01 | 0.83 | 0.91 |
| GB10133-RA [PREDICTED: Apis mellifera CuZn superoxide dismutase, transcript variant 1 (Sod1), mRNA] | 4.33E-01 | -0.19 | -0.10 |
| GB11973-RA [Apis mellifera cytochrome P450 monooxygenase (Cyp4g11), mRNA] | 4.37E-01 | -0.53 | -0.61 |
| GB10275-RA [PREDICTED: Apis mellifera similar to –Tubulin at 56D CG9277-PB, isoform B (LOC408782), mRNA] | 4.46E-01 | 0.10 | 0.38 |
| GB10238-RA [PREDICTED: Apis mellifera similar to ERp60 CG8983-PA, isoform A, transcript variant 2 (LOC409911), mRNA] | 4.46E-01 | -0.30 | 0.17 |
| GB16485-RA [PREDICTED: Apis mellifera similar to ATP synthase D chain, mitochondrial (LOC410557), mRNA] | 4.50E-01 | 0.50 | 0.39 |
| GB18497-RA [PREDICTED: Apis mellifera similar to Elongation factor Tu mitochondrial CG6050-PA, transcript variant 2 (LOC408328), mRNA] | 4.65E-01 | 0.85 | -0.12 |
| GB10992-RA [PREDICTED: Apis mellifera similar to ATP citrate lyase CG8322-PA, isoform A, transcript variant 2 (LOC550686), mRNA] | 4.80E-01 | -0.35 | -0.26 |
| GB15619-RA [PREDICTED: Apis mellifera similar to CG8036-PB, isoform B, transcript variant 1 (LOC550804), mRNA] | 4.93E-01 | 0.72 | 0.28 |
| GB15039-RA [PREDICTED: Apis mellifera similar to Enolase CG17654-PA, isoform A (LOC552678), partial mRNA] | 5.05E-01 | 0.31 | 0.10 |
| GB19460-RA [PREDICTED: Apis mellifera similar to Aldolase CG6058-PF, isoform F (LOC550785), mRNA] | 5.07E-01 | 0.36 | -0.45 |
| GB12951-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG17870-PC, isoform C, transcript variant 1 (LOC408289), mRNA] | 5.10E-01 | -0.32 | 0.22 |
| GB12951-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG17870-PC, isoform C, transcript variant 1 (LOC408289), mRNA] | 5.10E-01 | -0.32 | 0.22 |
| GB12951-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG17870-PC, isoform C, transcript variant 1 (LOC408289), mRNA] | 5.10E-01 | -0.32 | 0.22 |
| GB18760-RA [PREDICTED: Apis mellifera similar to L-xylulose reductase (XR) (Dicarbonyl/L-xylulose reductase) (LOC413567), mRNA] | 5.44E-01 | 0.98 | -0.68 |
| GB11461-RA [PREDICTED: Apis mellifera similar to UGP CG4347-PA, isoform A, transcript variant 1 (LOC412069), mRNA] | 6.19E-01 | 0.19 | 0.58 |
| GB13967-RA [Apis mellifera venom protein 2 (LOC503505), mRNA] | 6.31E-01 | -0.32 | -0.28 |
| GB17681-RA [PREDICTED: Apis mellifera actin, transcript variant 2 (LOC406122), mRNA] | 6.61E-01 | 0.14 | 0.28 |
| GB18719-RA [PREDICTED: Apis mellifera similar to R04B5.5 (LOC410167), mRNA] | 6.69E-01 | -0.14 | -0.04 |
| GB18727-RA [PREDICTED: Apis mellifera similar to CG5362-PA, transcript variant 1 (LOC411014), mRNA] | 7.20E-01 | -0.15 | -0.11 |
| GB13045-RA [PREDICTED: Apis mellifera similar to CG4685-PA, isoform A (LOC412305), mRNA] | 7.25E-01 | 0.13 | -0.17 |
| GB12182-RA [PREDICTED: Apis mellifera similar to Thiolase CG4581-PA (LOC551775), mRNA] | 7.47E-01 | 0.08 | -0.47 |
| GB10498-RA [PREDICTED: Apis mellifera similar to Peroxiredoxin 2540 CG11765-PA (LOC551975), mRNA] | 7.62E-01 | 0.11 | -0.28 |
| GB18498-RA [PREDICTED: Apis mellifera enoyl Coenzyme A hydratase, short chain, 1, mitochondrial (Echs1), mRNA] | 7.92E-01 | -0.12 | -0.72 |
| GB16132-RA [PREDICTED: Apis mellifera similar to CG7834-PA, isoform A (LOC410308), mRNA] | 7.99E-01 | -0.03 | -0.47 |
| GB16464-RA [PREDICTED: Apis mellifera similar to mitochondrial malate dehydrogenase precursor, transcript variant 1 (LOC408950), mRNA] | 8.15E-01 | 0.05 | NA |
| GB19745-RA [Apis mellifera transferrin (Trf), mRNA] | 8.22E-01 | -0.13 | -1.00 |
| GB16882-RA [PREDICTED: Apis mellifera similar to walrus CG8996-PB, isoform B, transcript variant 1 (LOC551710), mRNA] | 8.65E-01 | 0.12 | -0.82 |
| GB17499-RA [Apis mellifera ADP/ATP translocase (Ant), mRNA] | 8.93E-01 | -0.10 | 0.14 |
| GB15662-RA [PREDICTED: Apis mellifera similar to CG10962-PB, isoform B (LOC724721), mRNA] | 9.17E-01 | -0.06 | 0.37 |

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|---|---|---|---|
| GB19030-RA [PREDICTED: Apis mellifera similar to CG10638-PA, isoform A, transcript variant 1 (LOC552018), mRNA] | 9.46E-01 | -0.02 | 0.69 |
| GB12956-RA [PREDICTED: Apis mellifera similar to yippee interacting protein 2 CG4600-PA (LOC408291), mRNA] | 9.64E-01 | 0.03 | -0.81 |
| GB15718-RA [PREDICTED: Apis mellifera similar to CG14207-PB, isoform B, transcript variant 1 (LOC408875), mRNA] | 9.72E-01 | 0.02 | 0.10 |
| GB16864-RA [PREDICTED: Apis mellifera similar to CG4389-PA, isoform A (LOC410325), mRNA] | 9.79E-01 | -0.01 | -0.23 |
| GB10411-RA [PREDICTED: Apis mellifera similar to Proteasome subunit alpha type 7-1 (Proteasome 28 kDa subunit 1) (PROS-Dm28.1), transcript variant 1 (LOC410095), mRNA] | 1.00E+00 | 0.00 | 0.18 |

Table S5. Gene Ontology with a directional bias toward poor diet (P)>rich diet (R)

| Term | *P* Value | Category P>R | Category R>P | Total P>R | Total R>P |
|---|---|---|---|---|---|
| GO:0050794~regulation of cellular process | 3.82E-12 | 126 | 61 | 511 | 653 |
| GO:0009653~anatomical structure morphogenesis | 3.87E-12 | 112 | 49 | 511 | 653 |
| GO:0050789~regulation of biological process | 5.08E-11 | 150 | 88 | 511 | 653 |
| GO:0032502~developmental process | 7.05E-11 | 182 | 121 | 511 | 653 |
| GO:0048856~anatomical structure development | 7.53E-11 | 144 | 83 | 511 | 653 |
| GO:0048731~system development | 5.41E-10 | 124 | 68 | 511 | 653 |
| GO:0007275~multicellular organismal development | 1.30E-09 | 158 | 103 | 511 | 653 |
| GO:0048869~cellular developmental process | 2.76E-09 | 113 | 61 | 511 | 653 |
| GO:0032501~multicellular organismal process | 4.58E-09 | 178 | 127 | 511 | 653 |
| GO:0065007~biological regulation | 6.17E-09 | 165 | 114 | 511 | 653 |
| GO:0030154~cell differentiation | 7.11E-09 | 111 | 61 | 511 | 653 |
| GO:0000902~cell morphogenesis | 9.09E-09 | 68 | 25 | 511 | 653 |
| GO:0032989~cellular structure morphogenesis | 9.09E-09 | 68 | 25 | 511 | 653 |
| GO:0048513~organ development | 9.80E-09 | 97 | 49 | 511 | 653 |
| GO:0031323~regulation of cellular metabolic process | 2.68E-08 | 81 | 37 | 511 | 653 |
| GO:0019222~regulation of metabolic process | 3.85E-08 | 85 | 41 | 511 | 653 |
| GO:0006350~transcription | 4.03E-08 | 79 | 36 | 511 | 653 |
| GO:0019219~regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | 5.45E-08 | 76 | 34 | 511 | 653 |
| GO:0007444~imaginal disc development | 5.92E-08 | 51 | 15 | 511 | 653 |
| GO:0007154~cell communication | 6.26E-08 | 125 | 79 | 511 | 653 |
| GO:0007165~signal transduction | 1.20E-07 | 109 | 65 | 511 | 653 |
| GO:0010468~regulation of gene expression | 1.50E-07 | 74 | 34 | 511 | 653 |
| GO:0010467~gene expression | 1.53E-07 | 156 | 113 | 511 | 653 |
| GO:0045449~regulation of transcription | 3.56E-07 | 65 | 28 | 511 | 653 |
| GO:0043283~biopolymer metabolic process | 8.39E-07 | 186 | 151 | 511 | 653 |
| GO:0007560~imaginal disc morphogenesis | 9.47E-07 | 42 | 12 | 511 | 653 |
| GO:0009887~organ morphogenesis | 9.51E-07 | 49 | 17 | 511 | 653 |
| GO:0006351~transcription, DNA-dependent | 2.32E-06 | 66 | 32 | 511 | 653 |
| GO:0032774~RNA biosynthetic process | 2.32E-06 | 66 | 32 | 511 | 653 |
| GO:0002117~larval development (sensu Amphibia) | 2.76E-06 | 43 | 14 | 511 | 653 |
| GO:0007552~metamorphosis | 2.76E-06 | 43 | 14 | 511 | 653 |
| GO:0006355~regulation of transcription, DNA-dependent | 2.80E-06 | 56 | 24 | 511 | 653 |
| GO:0048468~cell development | 5.85E-06 | 85 | 51 | 511 | 653 |
| GO:0016070~RNA metabolic process | 7.20E-06 | 100 | 66 | 511 | 653 |
| GO:0007242~intracellular signaling cascade | 1.36E-05 | 54 | 25 | 511 | 653 |
| GO:0007399~nervous system development | 3.56E-05 | 60 | 32 | 511 | 653 |
| GO:0016043~cellular component organization and biogenesis | 6.58E-05 | 173 | 152 | 511 | 653 |
| GO:0007423~sensory organ development | 7.21E-05 | 37 | 14 | 511 | 653 |
| GO:0048523~negative regulation of cellular process | 1.07E-04 | 40 | 17 | 511 | 653 |
| GO:0051301~cell division | 1.62E-04 | 26 | 7 | 511 | 653 |
| GO:0009790~embryonic development | 1.85E-04 | 46 | 23 | 511 | 653 |
| GO:0048519~negative regulation of biological process | 1.94E-04 | 40 | 18 | 511 | 653 |
| GO:0001654~eye development | 2.15E-04 | 31 | 11 | 511 | 653 |
| GO:0000003~reproduction | 2.46E-04 | 51 | 28 | 511 | 653 |
| GO:0007010~cytoskeleton organization and biogenesis | 2.57E-04 | 52 | 29 | 511 | 653 |
| GO:0048736~appendage development | 2.89E-04 | 25 | 7 | 511 | 653 |
| GO:0006357~regulation of transcription from RNA polymerase II promoter | 2.90E-04 | 33 | 13 | 511 | 653 |
| GO:0048749~compound eye development | 3.08E-04 | 29 | 10 | 511 | 653 |
| GO:0007276~gamete generation | 3.23E-04 | 47 | 25 | 511 | 653 |
| GO:0019953~sexual reproduction | 3.23E-04 | 47 | 25 | 511 | 653 |
| GO:0022008~neurogenesis | 3.37E-04 | 40 | 19 | 511 | 653 |
| GO:0035107~appendage morphogenesis | 5.10E-04 | 24 | 7 | 511 | 653 |
| GO:0007292~female gamete generation | 5.30E-04 | 39 | 19 | 511 | 653 |
| GO:0048477~oogenesis | 5.30E-04 | 39 | 19 | 511 | 653 |
| GO:0048699~generation of neurons | 5.30E-04 | 39 | 19 | 511 | 653 |
| GO:0002165~instar larval or pupal development | 5.95E-04 | 51 | 30 | 511 | 653 |
| GO:0006366~transcription from RNA polymerase II promoter | 6.42E-04 | 42 | 22 | 511 | 653 |
| GO:0002164~larval development | 6.77E-04 | 43 | 23 | 511 | 653 |
| GO:0007476~imaginal disc-derived wing morphogenesis | 7.15E-04 | 22 | 6 | 511 | 653 |
| GO:0007472~wing disc morphogenesis | 7.15E-04 | 22 | 6 | 511 | 653 |
| GO:0035214~eye-antennal disc development | 7.50E-04 | 26 | 9 | 511 | 653 |
| GO:0000904~cellular morphogenesis during differentiation | 8.25E-04 | 38 | 19 | 511 | 653 |
| GO:0048737~imaginal disc-derived appendage development | 8.91E-04 | 23 | 7 | 511 | 653 |
| GO:0030030~cell projection organization and biogenesis | 1.20E-03 | 36 | 18 | 511 | 653 |
| GO:0032990~cell part morphogenesis | 1.20E-03 | 36 | 18 | 511 | 653 |
| GO:0048858~cell projection morphogenesis | 1.20E-03 | 36 | 18 | 511 | 653 |
| GO:0006996~organelle organization and biogenesis | 1.21E-03 | 84 | 65 | 511 | 653 |
| GO:0048592~eye morphogenesis | 1.26E-03 | 25 | 9 | 511 | 653 |

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|---|---|---|---|---|---|
| GO:0007455~eye-antennal disc morphogenesis | 1.26E-03 | 25 | 9 | 511 | 653 |
| GO:0043170~macromolecule metabolic process | 1.45E-03 | 276 | 293 | 511 | 653 |
| GO:0035220~wing disc development | 1.54E-03 | 22 | 7 | 511 | 653 |
| GO:0035114~imaginal disc-derived appendage morphogenesis | 1.54E-03 | 22 | 7 | 511 | 653 |
| GO:0048812~neurite morphogenesis | 1.62E-03 | 33 | 16 | 511 | 653 |
| GO:0048667~neuron morphogenesis during differentiation | 1.62E-03 | 33 | 16 | 511 | 653 |
| GO:0031175~neurite development | 1.62E-03 | 33 | 16 | 511 | 653 |
| GO:0045165~cell fate commitment | 1.64E-03 | 27 | 11 | 511 | 653 |
| GO:0009791~post-embryonic development | 1.94E-03 | 51 | 33 | 511 | 653 |
| GO:0007166~cell surface receptor linked signal transduction | 1.96E-03 | 52 | 34 | 511 | 653 |
| GO:0007049~cell cycle | 2.13E-03 | 38 | 21 | 511 | 653 |
| GO:0030036~actin cytoskeleton organization and biogenesis | 2.39E-03 | 25 | 10 | 511 | 653 |
| GO:0030029~actin filament-based process | 2.39E-03 | 25 | 10 | 511 | 653 |
| GO:0008283~cell proliferation | 2.39E-03 | 25 | 10 | 511 | 653 |
| GO:0048518~positive regulation of biological process | 2.63E-03 | 21 | 7 | 511 | 653 |
| GO:0048666~neuron development | 2.66E-03 | 33 | 17 | 511 | 653 |
| GO:0030182~neuron differentiation | 2.80E-03 | 34 | 18 | 511 | 653 |
| GO:0022402~cell cycle process | 2.94E-03 | 35 | 19 | 511 | 653 |
| GO:0001745~compound eye morphogenesis | 3.05E-03 | 22 | 8 | 511 | 653 |
| GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway | 3.06E-03 | 12 | 1 | 511 | 653 |
| GO:0006928~cell motility | 3.64E-03 | 30 | 15 | 511 | 653 |
| GO:0006259~DNA metabolic process | 4.39E-03 | 34 | 19 | 511 | 653 |
| GO:0050793~regulation of developmental process | 4.61E-03 | 26 | 12 | 511 | 653 |
| GO:0016477~cell migration | 4.95E-03 | 27 | 13 | 511 | 653 |
| GO:0007409~axonogenesis | 5.04E-03 | 21 | 8 | 511 | 653 |
| GO:0007369~gastrulation | 6.03E-03 | 11 | 1 | 511 | 653 |
| GO:0007350~blastoderm segmentation | 6.03E-03 | 11 | 1 | 511 | 653 |
| GO:0051674~localization of cell | 6.08E-03 | 31 | 17 | 511 | 653 |
| GO:0009888~tissue development | 7.19E-03 | 25 | 12 | 511 | 653 |
| GO:0003006~reproductive developmental process | 7.28E-03 | 9 | 0 | 511 | 653 |
| GO:0007163~establishment and/or maintenance of cell polarity | 7.81E-03 | 15 | 4 | 511 | 653 |
| GO:0043687~post-translational protein modification | 8.97E-03 | 60 | 47 | 511 | 653 |
| GO:0007243~protein kinase cascade | 9.32E-03 | 16 | 5 | 511 | 653 |
| GO:0022403~cell cycle phase | 9.77E-03 | 22 | 10 | 511 | 653 |
| GO:0000278~mitotic cell cycle | 9.77E-03 | 22 | 10 | 511 | 653 |
| GO:0051276~chromosome organization and biogenesis | 1.04E-02 | 23 | 11 | 511 | 653 |
| GO:0003008~system process | 1.05E-02 | 41 | 28 | 511 | 653 |
| GO:0007411~axon guidance | 1.07E-02 | 17 | 6 | 511 | 653 |
| GO:0008356~asymmetric cell division | 1.17E-02 | 10 | 1 | 511 | 653 |
| GO:0051248~negative regulation of protein metabolic process | 1.17E-02 | 10 | 1 | 511 | 653 |
| GO:0051246~regulation of protein metabolic process | 1.20E-02 | 18 | 7 | 511 | 653 |
| GO:0006139~nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | 1.27E-02 | 139 | 138 | 511 | 653 |
| GO:0040007~growth | 1.42E-02 | 20 | 9 | 511 | 653 |
| GO:0001703~gastrulation with mouth forming first | 1.50E-02 | 8 | 0 | 511 | 653 |
| GO:0010004~gastrulation involving germ band extension | 1.50E-02 | 8 | 0 | 511 | 653 |
| GO:0048754~branching morphogenesis of a tube | 1.50E-02 | 8 | 0 | 511 | 653 |
| GO:0001763~morphogenesis of a branching structure | 1.50E-02 | 8 | 0 | 511 | 653 |
| GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | 1.59E-02 | 11 | 2 | 511 | 653 |
| GO:0016071~mRNA metabolic process | 1.88E-02 | 27 | 16 | 511 | 653 |
| GO:0048522~positive regulation of cellular process | 1.93E-02 | 17 | 7 | 511 | 653 |
| GO:0007067~mitosis | 1.93E-02 | 17 | 7 | 511 | 653 |
| GO:0000087~M phase of mitotic cell cycle | 1.93E-02 | 17 | 7 | 511 | 653 |
| GO:0009408~response to heat | 1.97E-02 | 12 | 3 | 511 | 653 |
| GO:0035282~segmentation | 1.97E-02 | 12 | 3 | 511 | 653 |
| GO:0031325~positive regulation of cellular metabolic process | 1.97E-02 | 12 | 3 | 511 | 653 |
| GO:0009893~positive regulation of metabolic process | 1.97E-02 | 12 | 3 | 511 | 653 |
| GO:0001738~morphogenesis of a polarized epithelium | 1.97E-02 | 12 | 3 | 511 | 653 |
| GO:0046530~photoreceptor cell differentiation | 2.08E-02 | 18 | 8 | 511 | 653 |
| GO:0043412~biopolymer modification | 2.11E-02 | 75 | 67 | 511 | 653 |
| GO:0009966~regulation of signal transduction | 2.21E-02 | 19 | 9 | 511 | 653 |
| GO:0003012~muscle system process | 2.24E-02 | 9 | 1 | 511 | 653 |
| GO:0006936~muscle contraction | 2.24E-02 | 9 | 1 | 511 | 653 |
| GO:0009266~response to temperature stimulus | 2.31E-02 | 13 | 4 | 511 | 653 |
| GO:0000226~microtubule cytoskeleton organization and biogenesis | 2.31E-02 | 13 | 4 | 511 | 653 |
| GO:0048646~anatomical structure formation | 2.42E-02 | 21 | 11 | 511 | 653 |
| GO:0045941~positive regulation of transcription | 2.88E-02 | 10 | 2 | 511 | 653 |
| GO:0048589~developmental growth | 2.88E-02 | 10 | 2 | 511 | 653 |
| GO:0016055~Wnt receptor signaling pathway | 2.88E-02 | 10 | 2 | 511 | 653 |
| GO:0040008~regulation of growth | 2.88E-02 | 10 | 2 | 511 | 653 |

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|---|---|---|---|---|---|
| GO:0007446~imaginal disc growth | 3.05E-02 | 7 | 0 | 511 | 653 |
| GO:0016570~histone modification | 3.05E-02 | 7 | 0 | 511 | 653 |
| GO:0016569~covalent chromatin modification | 3.05E-02 | 7 | 0 | 511 | 653 |
| GO:0001754~eye photoreceptor cell differentiation | 3.06E-02 | 16 | 7 | 511 | 653 |
| GO:0001751~compound eye photoreceptor cell differentiation | 3.06E-02 | 16 | 7 | 511 | 653 |
| GO:0006325~establishment and/or maintenance of chromatin architecture | 3.23E-02 | 17 | 8 | 511 | 653 |
| GO:0006323~DNA packaging | 3.23E-02 | 17 | 8 | 511 | 653 |
| GO:0007264~small GTPase mediated signal transduction | 3.23E-02 | 17 | 8 | 511 | 653 |
| GO:0022414~reproductive process | 3.42E-02 | 11 | 3 | 511 | 653 |
| GO:0007164~establishment of tissue polarity | 3.42E-02 | 11 | 3 | 511 | 653 |
| GO:0001736~establishment of planar polarity | 3.42E-02 | 11 | 3 | 511 | 653 |
| GO:0048598~embryonic morphogenesis | 3.51E-02 | 19 | 10 | 511 | 653 |
| GO:0009607~response to biotic stimulus | 3.51E-02 | 19 | 10 | 511 | 653 |
| GO:0000279~M phase | 3.51E-02 | 19 | 10 | 511 | 653 |
| GO:0009628~response to abiotic stimulus | 3.61E-02 | 20 | 11 | 511 | 653 |
| GO:0006397~mRNA processing | 3.83E-02 | 24 | 15 | 511 | 653 |
| GO:0000165~MAPKKK cascade | 4.22E-02 | 13 | 5 | 511 | 653 |
| GO:0051726~regulation of cell cycle | 4.51E-02 | 14 | 6 | 511 | 653 |
| GO:0000074~regulation of progression through cell cycle | 4.51E-02 | 14 | 6 | 511 | 653 |
| GO:0009987~cellular process | 4.61E-02 | 452 | 554 | 511 | 653 |
| GO:0007167~enzyme linked receptor protein signaling pathway | 4.74E-02 | 15 | 7 | 511 | 653 |
| GO:0007517~muscle development | 5.08E-02 | 17 | 9 | 511 | 653 |
| GO:0051049~regulation of transport | 5.10E-02 | 9 | 2 | 511 | 653 |
| GO:0006396~RNA processing | 5.26E-02 | 28 | 20 | 511 | 653 |
| GO:0001700~embryonic development via the syncytial blastoderm | 5.37E-02 | 21 | 13 | 511 | 653 |
| GO:0007610~behavior | 5.37E-02 | 21 | 13 | 511 | 653 |
| GO:0050896~response to stimulus | 5.61E-02 | 73 | 70 | 511 | 653 |
| GO:0008361~regulation of cell size | 5.78E-02 | 10 | 3 | 511 | 653 |
| GO:0000910~cytokinesis | 5.78E-02 | 10 | 3 | 511 | 653 |
| GO:0051252~regulation of RNA metabolic process | 5.78E-02 | 10 | 3 | 511 | 653 |
| GO:0006464~protein modification process | 6.05E-02 | 70 | 67 | 511 | 653 |
| GO:0050877~neurological system process | 6.23E-02 | 35 | 28 | 511 | 653 |
| GO:0016568~chromatin modification | 6.30E-02 | 11 | 4 | 511 | 653 |
| GO:0007398~ectoderm development | 6.99E-02 | 13 | 6 | 511 | 653 |
| GO:0042221~response to chemical stimulus | 7.19E-02 | 26 | 19 | 511 | 653 |
| GO:0035239~tube morphogenesis | 7.21E-02 | 14 | 7 | 511 | 653 |
| GO:0007498~mesoderm development | 7.21E-02 | 14 | 7 | 511 | 653 |
| GO:0006468~protein amino acid phosphorylation | 7.27E-02 | 25 | 18 | 511 | 653 |
| GO:0030707~ovarian follicle cell development | 7.37E-02 | 15 | 8 | 511 | 653 |
| GO:0009792~embryonic development ending in birth or egg hatching | 7.54E-02 | 21 | 14 | 511 | 653 |
| GO:0042127~regulation of cell proliferation | 7.71E-02 | 7 | 1 | 511 | 653 |
| GO:0009968~negative regulation of signal transduction | 8.79E-02 | 8 | 2 | 511 | 653 |
| GO:0007267~cell-cell signaling | 9.26E-02 | 27 | 21 | 511 | 653 |
| GO:0003002~regionalization | 9.43E-02 | 26 | 20 | 511 | 653 |
| GO:0007389~pattern specification process | 9.43E-02 | 26 | 20 | 511 | 653 |
| GO:0007265~Ras protein signal transduction | 9.53E-02 | 9 | 3 | 511 | 653 |
| GO:0019226~transmission of nerve impulse | 9.59E-02 | 25 | 19 | 511 | 653 |

Table S6. Gene Ontology terms with a directional bias toward rich diet (R)>poor diet (P)

| Term | *P* Value | Category P>R | Category R>P | Total P>R | Total R>P |
|---|---|---|---|---|---|
| GO:0019752~carboxylic acid metabolic process | 5.12E-11 | 14 | 89 | 506 | 658 |
| GO:0006082~organic acid metabolic process | 5.12E-11 | 14 | 89 | 506 | 658 |
| GO:0055086~nucleobase, nucleoside and nucleotide metabolic process | 3.41E-09 | 2 | 47 | 506 | 658 |
| GO:0009117~nucleotide metabolic process | 1.42E-07 | 2 | 40 | 506 | 658 |
| GO:0009058~biosynthetic process | 2.79E-07 | 67 | 167 | 506 | 658 |
| GO:0006725~aromatic compound metabolic process | 3.33E-07 | 1 | 35 | 506 | 658 |
| GO:0006807~nitrogen compound metabolic process | 6.28E-07 | 16 | 72 | 506 | 658 |
| GO:0006520~amino acid metabolic process | 7.92E-07 | 10 | 58 | 506 | 658 |
| GO:0009165~nucleotide biosynthetic process | 9.74E-07 | 1 | 33 | 506 | 658 |
| GO:0006119~oxidative phosphorylation | 9.74E-07 | 1 | 33 | 506 | 658 |
| GO:0051186~cofactor metabolic process | 9.82E-07 | 5 | 45 | 506 | 658 |
| GO:0009259~ribonucleotide metabolic process | 1.16E-06 | 0 | 29 | 506 | 658 |
| GO:0006519~amino acid and derivative metabolic process | 1.56E-06 | 12 | 61 | 506 | 658 |
| GO:0009260~ribonucleotide biosynthetic process | 2.02E-06 | 0 | 28 | 506 | 658 |
| GO:0009308~amine metabolic process | 2.05E-06 | 16 | 69 | 506 | 658 |
| GO:0006732~coenzyme metabolic process | 2.52E-06 | 5 | 43 | 506 | 658 |
| GO:0006163~purine nucleotide metabolic process | 3.52E-06 | 0 | 27 | 506 | 658 |
| GO:0006164~purine nucleotide biosynthetic process | 6.11E-06 | 0 | 26 | 506 | 658 |
| GO:0009150~purine ribonucleotide metabolic process | 6.11E-06 | 0 | 26 | 506 | 658 |
| GO:0006091~generation of precursor metabolites and energy | 9.72E-06 | 19 | 71 | 506 | 658 |
| GO:0009152~purine ribonucleotide biosynthetic process | 1.06E-05 | 0 | 25 | 506 | 658 |
| GO:0008152~metabolic process | 1.46E-05 | 334 | 509 | 506 | 658 |
| GO:0044249~cellular biosynthetic process | 2.51E-05 | 62 | 143 | 506 | 658 |
| GO:0006629~lipid metabolic process | 4.10E-05 | 15 | 59 | 506 | 658 |
| GO:0032787~monocarboxylic acid metabolic process | 5.72E-05 | 3 | 31 | 506 | 658 |
| GO:0006631~fatty acid metabolic process | 1.04E-04 | 2 | 27 | 506 | 658 |
| GO:0046483~heterocycle metabolic process | 1.78E-04 | 1 | 23 | 506 | 658 |
| GO:0009112~nucleobase metabolic process | 2.73E-04 | 0 | 19 | 506 | 658 |
| GO:0006118~electron transport | 3.44E-04 | 14 | 51 | 506 | 658 |
| GO:0051188~cofactor biosynthetic process | 4.84E-04 | 1 | 21 | 506 | 658 |
| GO:0009108~coenzyme biosynthetic process | 4.84E-04 | 1 | 21 | 506 | 658 |
| GO:0009205~purine ribonucleoside triphosphate metabolic process | 7.90E-04 | 0 | 17 | 506 | 658 |
| GO:0009199~ribonucleoside triphosphate metabolic process | 7.90E-04 | 0 | 17 | 506 | 658 |
| GO:0009144~purine nucleoside triphosphate metabolic process | 7.90E-04 | 0 | 17 | 506 | 658 |
| GO:0009141~nucleoside triphosphate metabolic process | 7.90E-04 | 0 | 17 | 506 | 658 |
| GO:0044255~cellular lipid metabolic process | 1.26E-03 | 15 | 49 | 506 | 658 |
| GO:0009206~purine ribonucleoside triphosphate biosynthetic process | 1.34E-03 | 0 | 16 | 506 | 658 |
| GO:0009201~ribonucleoside triphosphate biosynthetic process | 1.34E-03 | 0 | 16 | 506 | 658 |
| GO:0009145~purine nucleoside triphosphate biosynthetic process | 1.34E-03 | 0 | 16 | 506 | 658 |
| GO:0009142~nucleoside triphosphate biosynthetic process | 1.34E-03 | 0 | 16 | 506 | 658 |
| GO:0044271~nitrogen compound biosynthetic process | 1.75E-03 | 2 | 21 | 506 | 658 |
| GO:0009309~amine biosynthetic process | 1.75E-03 | 2 | 21 | 506 | 658 |
| GO:0044237~cellular metabolic process | 3.12E-03 | 303 | 447 | 506 | 658 |
| GO:0015992~proton transport | 3.77E-03 | 0 | 14 | 506 | 658 |
| GO:0006144~purine base metabolic process | 3.77E-03 | 0 | 14 | 506 | 658 |
| GO:0046034~ATP metabolic process | 3.77E-03 | 0 | 14 | 506 | 658 |
| GO:0006818~hydrogen transport | 3.77E-03 | 0 | 14 | 506 | 658 |
| GO:0008652~amino acid biosynthetic process | 4.29E-03 | 2 | 19 | 506 | 658 |
| GO:0044270~nitrogen compound catabolic process | 5.42E-03 | 1 | 16 | 506 | 658 |
| GO:0009310~amine catabolic process | 5.42E-03 | 1 | 16 | 506 | 658 |
| GO:0009063~amino acid catabolic process | 5.42E-03 | 1 | 16 | 506 | 658 |
| GO:0006754~ATP biosynthetic process | 6.28E-03 | 0 | 13 | 506 | 658 |
| GO:0006753~nucleoside phosphate metabolic process | 6.28E-03 | 0 | 13 | 506 | 658 |
| GO:0015986~ATP synthesis coupled proton transport | 1.04E-02 | 0 | 12 | 506 | 658 |
| GO:0009064~glutamine family amino acid metabolic process | 1.04E-02 | 0 | 12 | 506 | 658 |
| GO:0044248~cellular catabolic process | 1.14E-02 | 26 | 60 | 506 | 658 |
| GO:0045454~cell redox homeostasis | 1.36E-02 | 1 | 14 | 506 | 658 |
| GO:0042775~organelle ATP synthesis coupled electron transport | 1.36E-02 | 1 | 14 | 506 | 658 |
| GO:0042773~ATP synthesis coupled electron transport | 1.36E-02 | 1 | 14 | 506 | 658 |
| GO:0006635~fatty acid beta-oxidation | 1.72E-02 | 0 | 11 | 506 | 658 |
| GO:0019395~fatty acid oxidation | 1.72E-02 | 0 | 11 | 506 | 658 |
| GO:0009056~catabolic process | 1.87E-02 | 28 | 61 | 506 | 658 |
| GO:0022618~protein-RNA complex assembly | 2.14E-02 | 1 | 13 | 506 | 658 |
| GO:0022613~ribonucleoprotein complex biogenesis and assembly | 2.47E-02 | 4 | 19 | 506 | 658 |
| GO:0042440~pigment metabolic process | 2.81E-02 | 0 | 10 | 506 | 658 |
| GO:0006626~protein targeting to mitochondrion | 2.81E-02 | 0 | 10 | 506 | 658 |

| | | | | | |
|---|---|---|---|---|---|
| GO:0019748~secondary metabolic process | 3.32E-02 | 1 | 12 | 506 | 658 |
| GO:0007005~mitochondrion organization and biogenesis | 3.54E-02 | 2 | 14 | 506 | 658 |
| GO:0019725~cellular homeostasis | 4.47E-02 | 6 | 21 | 506 | 658 |
| GO:0042592~homeostatic process | 4.47E-02 | 6 | 21 | 506 | 658 |
| GO:0046148~pigment biosynthetic process | 4.56E-02 | 0 | 9 | 506 | 658 |
| GO:0009161~ribonucleoside monophosphate metabolic process | 4.56E-02 | 0 | 9 | 506 | 658 |
| GO:0009156~ribonucleoside monophosphate biosynthetic process | 4.56E-02 | 0 | 9 | 506 | 658 |
| GO:0009124~nucleoside monophosphate biosynthetic process | 4.56E-02 | 0 | 9 | 506 | 658 |
| GO:0009123~nucleoside monophosphate metabolic process | 4.56E-02 | 0 | 9 | 506 | 658 |
| GO:0006413~translational initiation | 5.09E-02 | 1 | 11 | 506 | 658 |
| GO:0006839~mitochondrial transport | 7.65E-02 | 2 | 12 | 506 | 658 |
| GO:0051187~cofactor catabolic process | 7.73E-02 | 1 | 10 | 506 | 658 |
| GO:0045333~cellular respiration | 7.73E-02 | 1 | 10 | 506 | 658 |
| GO:0006099~tricarboxylic acid cycle | 7.73E-02 | 1 | 10 | 506 | 658 |
| GO:0009109~coenzyme catabolic process | 7.73E-02 | 1 | 10 | 506 | 658 |
| GO:0009060~aerobic respiration | 7.73E-02 | 1 | 10 | 506 | 658 |
| GO:0046356~acetyl-CoA catabolic process | 7.73E-02 | 1 | 10 | 506 | 658 |
| GO:0044238~primary metabolic process | 8.73E-02 | 308 | 428 | 506 | 658 |
| GO:0006811~ion transport | 9.59E-02 | 17 | 36 | 506 | 658 |

Table S7. Quantitative proteomic analyses of protein abundance in the fat bodies of bees fed rich vs. poor diet

| Description | *P*-value | logFC protein (rich-poor) | logFC RNA (rich-poor) |
|---|---|---|---|
| GB12488-RA [PREDICTED: Apis mellifera similar to Aconitase CG9244-PB (LOC408446), mRNA] | 7.18E-04 | -0.22 | -0.20 |
| GB11056-RA [PREDICTED: Apis mellifera similar to Phosphoglycerate kinase, transcript variant 1 (LOC411576), mRNA] | 9.29E-04 | -0.28 | -0.08 |
| GB15116-RA [PREDICTED: Apis mellifera similar to CG9357-PA (LOC413705), mRNA] | 2.39E-03 | 1.40 | -0.48 |
| GB17503-RA [PREDICTED: Apis mellifera similar to CG8993-PA (LOC410120), mRNA] | 2.87E-03 | 0.64 | 0.13 |
| GB11810-RA [PREDICTED: Apis mellifera similar to Contactin CG1084-PA (LOC412312), mRNA] | 4.84E-03 | -0.19 | -0.03 |
| GB19832-RA [PREDICTED: Apis mellifera similar to CG9514-PA (LOC408603), mRNA] | 5.50E-03 | 1.10 | 1.25 |
| GB14424-RA [PREDICTED: Apis mellifera similar to Nidogen/entactin CG12908-PA, isoform A (LOC408797), mRNA] | 6.33E-03 | -0.40 | 0.30 |
| GB14284-RA [PREDICTED: Apis mellifera similar to Sorbitol dehydrogenase-2 CG4649-PA (LOC408871), mRNA] | 1.60E-02 | 0.71 | 2.31 |
| GB13401-RA [PREDICTED: Apis mellifera similar to Putative aldehyde dehydrogenase family 7 member A1 homolog (ALH-9) (LOC411140), mRNA] | 1.73E-02 | 0.93 | 1.62 |
| GB15716-RA [PREDICTED: Apis mellifera similar to CG5028-PA (LOC410396), mRNA] | 1.84E-02 | -1.03 | 0.33 |
| GB19293-RA [PREDICTED: Apis mellifera mitochondrial cytochrome C (CytC), mRNA] | 1.97E-02 | -0.28 | 0.05 |
| GB19247-RA [PREDICTED: Apis mellifera similar to Elongation factor 2 (EF-2), transcript variant 1 (LOC409167), mRNA] | 2.14E-02 | 0.37 | -0.25 |
| GB12283-RA [PREDICTED: Apis mellifera similar to MOCO sulphurase C-terminal domain containing 1 (LOC724919), mRNA] | 2.19E-02 | -0.29 | 0.16 |
| GB17376-RA [PREDICTED: Apis mellifera similar to CG17560-PA (LOC724560), partial mRNA] | 2.36E-02 | 1.05 | 0.33 |
| GB19030-RA [PREDICTED: Apis mellifera similar to CG10638-PA, isoform A, transcript variant 1 (LOC552018), mRNA] | 2.40E-02 | 0.66 | 0.77 |
| GB15016-RA [PREDICTED: Apis mellifera similar to Heat shock protein cognate 3 CG4147-PA, isoform A (LOC409587), mRNA] | 2.85E-02 | 0.39 | 0.16 |
| GB19004-RA [PREDICTED: Apis mellifera similar to CG4169-PA (LOC552671), mRNA] | 3.03E-02 | -1.36 | 0.16 |
| GB18969-RA [PREDICTED: Apis mellifera similar to 60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 kDa chaperonin) (CPN60) (Heat shock protein 60) (HSP-60) (Mitochondrial matrix protein P1) (LOC409384), mRNA] | 3.07E-02 | 0.47 | 1.11 |
| GB14813-RA [PREDICTED: Apis mellifera similar to Cytochrome b5 (CYTB5) (LOC726860), mRNA] | 3.25E-02 | 0.31 | -0.31 |
| GB11403-RA [PREDICTED: Apis mellifera similar to CG6414-PA (LOC408395), mRNA] | 3.28E-02 | 0.31 | 0.60 |
| GB19200-RA [PREDICTED: Apis mellifera similar to Pros5 CG12323-PA, isoform A (LOC411206), mRNA] | 3.41E-02 | 0.34 | 0.19 |
| GB14637-RA [PREDICTED: Apis mellifera similar to cAMP-dependent protein kinase R2 CG15862-PA, isoform A, transcript variant 1 (LOC409390), mRNA] | 3.44E-02 | 0.37 | -0.19 |
| GB12198-RA [PREDICTED: Apis mellifera similar to CG3523-PA (LOC412815), mRNA] | 3.47E-02 | 0.50 | -0.17 |
| GB16579-RA [PREDICTED: Apis mellifera similar to CG12262-PA (LOC408567), mRNA] | 3.48E-02 | 0.85 | 0.86 |
| [Antisense] GB13237-RA [PREDICTED: Apis mellifera similar to Phosphogluconate mutase CG5165-PA (LOC411897), mRNA] | 3.52E-02 | 0.17 | -0.13 |
| [Antisense] GB13237-RA [PREDICTED: Apis mellifera similar to Phosphogluconate mutase CG5165-PA (LOC411897), mRNA] | 3.52E-02 | 0.17 | 0.20 |
| GB13237-RA [PREDICTED: Apis mellifera similar to Phosphogluconate mutase CG5165-PA (LOC411897), mRNA] | 3.52E-02 | 0.17 | -0.13 |
| GB13237-RA [PREDICTED: Apis mellifera similar to Phosphogluconate mutase CG5165-PA (LOC411897), mRNA] | 3.52E-02 | 0.17 | 0.20 |
| GB19888-RA [PREDICTED: Apis mellifera similar to Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial precursor (ETF-QO) (ETF-ubiquinone oxidoreductase) (ETF dehydrogenase) (Electron-transferring-flavoprotein dehydrogenase), transcript | 3.54E-02 | 0.26 | 0.49 |
| GB14324-RA [PREDICTED: Apis mellifera similar to Adenosylhomocysteinase at 13 CG11654-PA (LOC408368), mRNA] | 3.56E-02 | 0.51 | 0.39 |
| GB19321-RA [PREDICTED: Apis mellifera similar to COP9 signalosome subunit 6 (LOC410195), mRNA] | 4.27E-02 | -0.28 | 0.17 |
| GB10695-RA [PREDICTED: Apis mellifera similar to Pyruvate kinase CG7070-PB, isoform B (LOC552007), mRNA] | 4.42E-02 | -0.45 | -0.14 |
| GB16459-RA [Apis mellifera major royal jelly protein 3 (Mrjp3), mRNA] | 4.46E-02 | 2.00 | -0.06 |
| GB15408-RA [PREDICTED: Apis mellifera similar to CG8798-PA, isoform A (LOC409459), mRNA] | 4.53E-02 | 0.33 | 0.54 |
| GB17876-RA [PREDICTED: Apis mellifera similar to Calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type (Calcium pump), transcript variant 1 (LOC410371), mRNA] | 4.73E-02 | -1.10 | -0.41 |
| GB11655-RA [PREDICTED: Apis mellifera similar to Succinyl coenzyme A synthetase subunit CG1065-PA (LOC551403), mRNA] | 4.74E-02 | -0.31 | -0.04 |
| GB16882-RA [PREDICTED: Apis mellifera similar to walrus CG8996-PB, isoform B, transcript variant 1 (LOC551710), mRNA] | 4.88E-02 | 0.50 | 0.43 |
| GB18719-RA [PREDICTED: Apis mellifera similar to R04B5.5 (LOC410167), mRNA] | 4.94E-02 | 0.84 | 1.05 |
| GB15052-RA [PREDICTED: Apis mellifera similar to Phosphoglyceromutase CG1721-PA, isoform A (LOC552736), mRNA] | 4.94E-02 | -0.27 | -0.28 |
| GB18162-RA [PREDICTED: Apis mellifera similar to Peroxisomal multifunctional enzyme type 2 (MFE-2) (D-bifunctional protein) (DBP) (17-beta-hydroxysteroid dehydrogenase 4) (17-beta-HSD 4) (LOC409986), mRNA] | 5.01E-02 | 0.76 | 0.20 |

| | | | |
|---|---|---|---|
| GB11059-RA [PREDICTED: Apis mellifera similar to Retinoid- and fatty-acid binding protein CG11064-PA, transcript variant 1 (LOC408961), mRNA] | 5.16E-02 | -0.17 | NA |
| GB19878-RA [PREDICTED: Apis mellifera similar to Rpt3 CG16916-PA (LOC410026), mRNA] | 5.17E-02 | 0.33 | -0.16 |
| GB18077-RA [PREDICTED: Apis mellifera similar to CG31004-PA, isoform A, transcript variant 1 (LOC408878), mRNA] | 5.19E-02 | -0.70 | -0.57 |
| GB11665-RA [PREDICTED: Apis mellifera similar to Imaginal disc growth factor 4 CG1780-PA, isoform A (LOC413324), mRNA] | 5.19E-02 | -0.47 | 0.75 |
| GB10771-RA [PREDICTED: Apis mellifera epoxide hydrolase (LOC406152), mRNA] | 5.23E-02 | 0.91 | 0.59 |
| GB12338-RA [PREDICTED: Apis mellifera similar to 60S acidic ribosomal protein P0 (DNA-(apurinic or apyrimidinic site) lyase) (Apurinic-apyrimidinic endonuclease), transcript variant 1 (LOC550711), mRNA] | 5.62E-02 | -0.84 | 0.04 |
| GB15518-RA [PREDICTED: Apis mellifera similar to CG9380-PA, isoform A (LOC552843), mRNA] | 5.74E-02 | -0.96 | -0.55 |
| GB12029-RA [PREDICTED: Apis mellifera similar to CG1532-PA (LOC552722), mRNA] | 5.93E-02 | 0.38 | 0.23 |
| GB16448-RA [PREDICTED: Apis mellifera similar to Annexin-B9 (Annexin-9) (Annexin IX), transcript variant 1 (LOC409533), mRNA] | 6.03E-02 | 0.47 | 0.27 |
| GB14517-RA [PREDICTED: Apis mellifera similar to Isocitrate dehydrogenase CG7176-PC, isoform C, transcript variant 2 (LOC551276), mRNA] | 6.26E-02 | 0.66 | 0.68 |
| GB10312-RA [PREDICTED: Apis mellifera similar to CG7461-PA (LOC412025), mRNA] | 6.32E-02 | 0.46 | 0.63 |
| GB13772-RA [PREDICTED: Apis mellifera similar to Puromycin sensitive aminopeptidase CG1009-PC, isoform C, transcript variant 1 (LOC410769), mRNA] | 6.45E-02 | 0.43 | 0.29 |
| GB14678-RA [PREDICTED: Apis mellifera similar to Tat-binding protein-1 CG10370-PA (LOC409198), mRNA] | 6.56E-02 | 0.23 | -0.20 |
| GB11385-RA [PREDICTED: Apis mellifera similar to CG3731-PB, isoform B (LOC410022), mRNA] | 6.58E-02 | -0.84 | 0.57 |
| GB13514-RA [PREDICTED: Apis mellifera similar to CG11790-PA, isoform A (LOC411255), mRNA] | 6.63E-02 | 0.23 | 0.07 |
| GB12741-RA [PREDICTED: Apis mellifera similar to Aldehyde dehydrogenase CG3752-PA, transcript variant 1 (LOC550687), mRNA] | 6.66E-02 | 0.60 | 1.84 |
| GB17035-RA [PREDICTED: Apis mellifera similar to CG15828-PB, isoform B (LOC410793), mRNA] | 6.73E-02 | -0.44 | -0.06 |
| GB15648-RA [PREDICTED: Apis mellifera similar to 60S ribosomal protein L9 (LOC551107), mRNA] | 6.90E-02 | -0.82 | -0.29 |
| GB15637-RA [PREDICTED: Apis mellifera similar to 40S ribosomal protein S3 (LOC551330), mRNA] | 7.07E-02 | -0.77 | -0.20 |
| GB17223-RA [PREDICTED: Apis mellifera similar to CG5590-PA (LOC552717), mRNA] | 7.11E-02 | 0.59 | 0.42 |
| GB11202-RA [PREDICTED: Apis mellifera similar to Laminin A CG10236-PA (LOC412663), partial mRNA] | 7.16E-02 | -0.68 | NA |
| [Antisense] GB17056-RA [PREDICTED: Apis mellifera similar to Cyclophilin 1 CG9916-PA (LOC409890), mRNA] | 7.18E-02 | 0.16 | 0.07 |
| [Antisense] GB17056-RA [PREDICTED: Apis mellifera similar to Cyclophilin 1 CG9916-PA (LOC409890), mRNA] | 7.18E-02 | 0.16 | 0.72 |
| [Antisense] GB17056-RA [PREDICTED: Apis mellifera similar to Cyclophilin 1 CG9916-PA (LOC409890), mRNA] | 7.18E-02 | 0.16 | 0.55 |
| GB17056-RA [PREDICTED: Apis mellifera similar to Cyclophilin 1 CG9916-PA (LOC409890), mRNA] | 7.18E-02 | 0.16 | 0.07 |
| GB17056-RA [PREDICTED: Apis mellifera similar to Cyclophilin 1 CG9916-PA (LOC409890), mRNA] | 7.18E-02 | 0.16 | 0.72 |
| GB17056-RA [PREDICTED: Apis mellifera similar to Cyclophilin 1 CG9916-PA (LOC409890), mRNA] | 7.18E-02 | 0.16 | 0.55 |
| GB17056-RA [PREDICTED: Apis mellifera similar to Cyclophilin 1 CG9916-PA (LOC409890), mRNA] | 7.18E-02 | 0.16 | 0.07 |
| GB17056-RA [PREDICTED: Apis mellifera similar to Cyclophilin 1 CG9916-PA (LOC409890), mRNA] | 7.18E-02 | 0.16 | 0.72 |
| GB17056-RA [PREDICTED: Apis mellifera similar to Cyclophilin 1 CG9916-PA (LOC409890), mRNA] | 7.18E-02 | 0.16 | 0.55 |
| GB18952-RA [PREDICTED: Apis mellifera similar to Acetyl-CoA acetyltransferase, mitochondrial precursor (Acetoacetyl-CoA thiolase) (LOC726218), mRNA] | 7.40E-02 | 0.36 | 0.66 |
| GB15113-RB [PREDICTED: Apis mellifera similar to hu li tai shao CG9325-PB, isoform B (LOC409713), mRNA] | 7.54E-02 | -0.27 | -0.34 |
| GB12681-RA [PREDICTED: Apis mellifera similar to Aldehyde dehydrogenase type III CG11140-PI, isoform I (LOC411822), mRNA] | 7.55E-02 | 0.86 | 0.75 |
| GB12956-RA [PREDICTED: Apis mellifera similar to yippee interacting protein 2 CG4600-PA (LOC408291), mRNA] | 7.64E-02 | 0.32 | 0.55 |
| GB13999-RA [Apis mellifera vitellogenin (Vg), mRNA] | 8.02E-02 | 1.64 | 3.50 |
| GB16864-RA [PREDICTED: Apis mellifera similar to CG4389-PA, isoform A (LOC410325), mRNA] | 8.95E-02 | 0.35 | 0.13 |
| GB18498-RA [PREDICTED: Apis mellifera enoyl Coenzyme A hydratase, short chain, 1, mitochondrial (Echs1), mRNA] | 9.00E-02 | 0.52 | 0.93 |
| GB14849-RA [PREDICTED: Apis mellifera similar to Putative deoxyribose-phosphate aldolase (Phosphodeoxyriboaldolase) (Deoxyriboaldolase) (DERA) (LOC551986), mRNA] | 9.01E-02 | 0.72 | 0.79 |
| GB12182-RA [PREDICTED: Apis mellifera similar to Thiolase CG4581-PA (LOC551775), mRNA] | 9.13E-02 | 0.54 | 0.21 |
| GB11749-RA [PREDICTED: Apis mellifera similar to Calcium-binding mitochondrial carrier Aralar1 (LOC408967), partial mRNA] | 9.22E-02 | -0.81 | 0.01 |
| GB16246-RA [Apis mellifera major royal jelly protein 2 (Mrjp2), mRNA] | 9.22E-02 | 2.89 | -0.50 |
| GB16246-RA [Apis mellifera major royal jelly protein 2 (Mrjp2), mRNA] | 9.22E-02 | 2.89 | 0.22 |

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|---|---|---|---|
| GB16246-RA [Apis mellifera major royal jelly protein 2 (Mrjp2), mRNA] | 9.22E-02 | 2.89 | -0.50 |
| GB16246-RA [Apis mellifera major royal jelly protein 2 (Mrjp2), mRNA] | 9.22E-02 | 2.89 | 0.22 |
| GB15664-RA [PREDICTED: Apis mellifera similar to karst CG12008-PA, isoform A (LOC413332), mRNA] | 1.00E-01 | -0.34 | -0.27 |
| GB13135-RA [PREDICTED: Apis mellifera similar to Ras-like GTP-binding protein Rho1, transcript variant 2 (LOC409910), mRNA] | 1.01E-01 | 1.05 | -0.21 |
| GB13135-RA [PREDICTED: Apis mellifera similar to Ras-like GTP-binding protein Rho1, transcript variant 2 (LOC409910), mRNA] | 1.01E-01 | 1.05 | -0.16 |
| GB13135-RA [PREDICTED: Apis mellifera similar to Ras-like GTP-binding protein Rho1, transcript variant 2 (LOC409910), mRNA] | 1.01E-01 | 1.05 | -0.21 |
| GB13135-RA [PREDICTED: Apis mellifera similar to Ras-like GTP-binding protein Rho1, transcript variant 2 (LOC409910), mRNA] | 1.01E-01 | 1.05 | -0.16 |
| GB10339-RA [PREDICTED: Apis mellifera similar to Protein lethal(2)essential for life (Protein Efl21), transcript variant 1 (LOC410857), mRNA] | 1.04E-01 | -0.91 | -0.53 |
| GB16526-RA [PREDICTED: Apis mellifera similar to Proteasome subunit alpha type 5 (Proteasome zeta chain) (Macropain zeta chain) (Multicatalytic endopeptidase complex zeta chain) (LOC551956), mRNA] | 1.07E-01 | 0.29 | 0.28 |
| GB16563-RA [PREDICTED: Apis mellifera similar to Trap1 CG3152-PA, transcript variant 1 (LOC550968), mRNA] | 1.11E-01 | 0.37 | 0.06 |
| GB13680-RA [PREDICTED: Apis mellifera similar to 3-hydroxyacyl-CoA dehydrogenase type-2 (3-hydroxyacyl-CoA dehydrogenase type II) (Type II HADH) (3-hydroxy-2-methylbutyryl-CoA dehydrogenase) (Scully protein) (LOC725274), mRNA] | 1.11E-01 | 0.53 | 0.87 |
| GB12732-RA [PREDICTED: Apis mellifera similar to Proteasome subunit alpha type 3 (Proteasome component C8) (Macropain subunit C8) (Multicatalytic endopeptidase complex subunit C8) (LOC408986), mRNA] | 1.13E-01 | 0.28 | 0.13 |
| GB19208-RA [PREDICTED: Apis mellifera similar to sar1 CG7073-PA, isoform A, transcript variant 2 (LOC409613), mRNA] | 1.14E-01 | 1.16 | 0.19 |
| GB17517-RA [PREDICTED: Apis mellifera similar to CG32702-PA (LOC411053), mRNA] | 1.16E-01 | -0.52 | 0.19 |
| GB15990-RA [Apis mellifera FABP-like protein (Fabp), mRNA] | 1.16E-01 | 0.70 | -0.14 |
| GB16184-RA [PREDICTED: Apis mellifera similar to lethal (2) 44DEa CG8732-PB, isoform B, transcript variant 1 (LOC409515), mRNA] | 1.17E-01 | 0.26 | -0.07 |
| GB19935-RA [PREDICTED: Apis mellifera similar to CG3609-PA (LOC552024), mRNA] | 1.18E-01 | 1.59 | 3.85 |
| GB15796-RA [PREDICTED: Apis mellifera similar to squid CG16901-PC, isoform C, transcript variant 1 (LOC408936), mRNA] | 1.18E-01 | -0.38 | 0.13 |
| GB14888-RA [Apis mellifera major royal jelly protein 1 (Mrjp1), mRNA] | 1.18E-01 | 2.30 | NA |
| GB16903-RA [PREDICTED: Apis mellifera similar to cathD CG1548-PA (LOC409341), mRNA] | 1.22E-01 | 0.57 | 0.02 |
| GB14205-RA [PREDICTED: Apis mellifera similar to CG11267-PA (LOC552531), mRNA] | 1.23E-01 | 0.34 | 1.16 |
| GB12383-RA [PREDICTED: Apis mellifera similar to Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial precursor (Somatic-type succinyl CoA:3-oxoacid CoA-transferase) (Scot-S) (LOC409157), mRNA] | 1.23E-01 | 0.32 | 0.07 |
| GB12841-RA [PREDICTED: Apis mellifera similar to CG7580-PA (LOC726747), mRNA] | 1.24E-01 | -1.00 | 0.16 |
| GB12125-RA [PREDICTED: Apis mellifera similar to CG6465-PA (LOC408969), mRNA] | 1.27E-01 | 0.73 | 0.76 |
| GB16803-RA [PREDICTED: Apis mellifera similar to Probable cytochrome P450 9f2 (CYPIXF2) (LOC410490), mRNA] | 1.28E-01 | 0.32 | 0.15 |
| GB12113-RA [PREDICTED: Apis mellifera similar to porin CG6647-PA, isoform A (LOC551325), mRNA] | 1.28E-01 | -1.56 | NA |
| GB12144-RA [PREDICTED: Apis mellifera similar to Vesicular-fusion protein Nsf1 (N-ethylmaleimide-sensitive fusion protein 1) (NEM-sensitive fusion protein 1) (dNsf-1) (Protein comatose), transcript variant 1 (LOC725680), mRNA] | 1.32E-01 | -0.19 | 0.22 |
| GB17531-RA [PREDICTED: Apis mellifera similar to Dihydropteridine reductase CG4665-PA, isoform A (LOC409160), mRNA] | 1.35E-01 | 0.43 | 0.57 |
| GB12049-RA [PREDICTED: Apis mellifera similar to Putative actin-interacting protein 1 (AIP1) (LOC412495), mRNA] | 1.35E-01 | 0.08 | 0.04 |
| GB11892-RA [PREDICTED: Apis mellifera similar to Glycogen phosphorylase, transcript variant 2 (LOC409267), mRNA] | 1.36E-01 | 0.40 | 0.10 |
| GB20013-RA [PREDICTED: Apis mellifera similar to Rpt4 CG3455-PA (LOC551386), mRNA] | 1.37E-01 | 0.29 | 0.14 |
| GB18042-RA [PREDICTED: Apis mellifera similar to Oligosaccharyltransferase 48kD subunit CG9022-PA, transcript variant 1 (LOC552051), mRNA] | 1.38E-01 | -0.56 | 0.42 |
| GB19380-RA [PREDICTED: Apis mellifera similar to thioredoxin peroxidase 1 CG1633-PA, isoform A, transcript variant 1 (LOC409954), mRNA] | 1.38E-01 | 0.57 | 0.32 |
| GB18667-RA [PREDICTED: Apis mellifera similar to CG1440-PA (LOC724901), mRNA] | 1.41E-01 | -0.45 | 0.06 |
| GB14141-RA [PREDICTED: Apis mellifera similar to cheerio CG3937-PD, isoform D (LOC409697), mRNA] | 1.45E-01 | -0.15 | 0.16 |
| GB12135-RA [PREDICTED: Apis mellifera similar to CG1213-PA, isoform A (LOC413575), mRNA] | 1.47E-01 | -0.96 | 0.07 |
| GB10469-RA [PREDICTED: Apis mellifera similar to klingon CG6669-PA (LOC409091), mRNA] | 1.49E-01 | -0.35 | 0.04 |
| GB15327-RA [Apis mellifera juvenile hormone esterase (Jhe), mRNA] | 1.49E-01 | 0.96 | 1.90 |
| GB14798-RA [PREDICTED: Apis mellifera similar to Glyceraldehyde 3 phosphate dehydrogenase 1 CG12055-PA, isoform A, transcript variant 2 (LOC410122), mRNA] | 1.49E-01 | -0.25 | -0.05 |
| GB13004-RA [PREDICTED: Apis mellifera similar to CG12163-PA, isoform A (LOC408851), mRNA] | 1.51E-01 | -0.48 | -0.30 |
| GB17353-RA [PREDICTED: Apis mellifera similar to CG7433-PA, isoform A, transcript variant 1 (LOC408955), mRNA] | 1.51E-01 | -0.53 | 0.13 |
| GB12230-RA [PREDICTED: Apis mellifera hypothetical protein LOC406120 (LOC406120), | 1.53E-01 | -0.61 | -0.23 |

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|---|---|---|---|
| mRNA] | | | |
| GB12326-RA [PREDICTED: Apis mellifera similar to Ornithine aminotransferase precursor CG8782-PA (LOC410583), mRNA] | 1.54E-01 | 0.73 | 0.31 |
| GB16951-RA [PREDICTED: Apis mellifera similar to Malic enzyme CG10120-PB, isoform B, transcript variant 1 (LOC411813), partial mRNA] | 1.55E-01 | 0.88 | 0.07 |
| GB13058-RA [PREDICTED: Apis mellifera similar to dihydroxyacetone kinase 2 (LOC413697), mRNA] | 1.57E-01 | 0.56 | 1.34 |
| GB19460-RA [PREDICTED: Apis mellifera similar to Aldolase CG6058-PF, isoform F (LOC550785), mRNA] | 1.57E-01 | 0.27 | 0.51 |
| GB19460-RA [PREDICTED: Apis mellifera similar to Aldolase CG6058-PF, isoform F (LOC550785), mRNA] | 1.57E-01 | 0.27 | 0.40 |
| GB19460-RA [PREDICTED: Apis mellifera similar to Aldolase CG6058-PF, isoform F (LOC550785), mRNA] | 1.57E-01 | 0.27 | 0.51 |
| GB19460-RA [PREDICTED: Apis mellifera similar to Aldolase CG6058-PF, isoform F (LOC550785), mRNA] | 1.57E-01 | 0.27 | 0.40 |
| GB14138-RA [PREDICTED: Apis mellifera putative thioredoxin peroxidase (Gtpx-1), mRNA] | 1.57E-01 | 0.24 | -0.02 |
| GB15053-RA [PREDICTED: Apis mellifera similar to Rpt1 CG1341-PA (LOC551343), mRNA] | 1.58E-01 | 0.24 | 0.32 |
| GB18955-RA [PREDICTED: Apis mellifera similar to Phospholipid hydroperoxide glutathione peroxidase, mitochondrial precursor (PHGPx) (GPX-4) (LOC726269), mRNA] | 1.64E-01 | -0.19 | -0.39 |
| GB11846-RA [PREDICTED: Apis mellifera similar to Neuroglian CG1634-PA, isoform A (LOC411829), mRNA] | 1.64E-01 | -0.51 | -0.01 |
| GB19498-RA [PREDICTED: Apis mellifera similar to bendless CG18319-PA (LOC409386), mRNA] | 1.65E-01 | 0.36 | 0.08 |
| GB10560-RA [Apis mellifera translation elongation factor eEF-1 alpha chain (LOC408385), mRNA] | 1.66E-01 | -0.28 | 0.40 |
| GB19166-RA [PREDICTED: Apis mellifera similar to Rab-protein 1 CG3320-PA, isoform A (LOC409456), mRNA] | 1.71E-01 | 0.61 | -0.20 |
| GB11973-RA [Apis mellifera cytochrome P450 monooxygenase (Cyp4g11), mRNA] | 1.73E-01 | 0.78 | -0.18 |
| GB11431-RA [PREDICTED: Apis mellifera similar to Nucleosome remodeling factor - 38kD CG4634-PA (LOC409774), mRNA] | 1.77E-01 | 0.66 | 0.46 |
| GB17377-RA [PREDICTED: Apis mellifera similar to CG2604-PA, isoform A, transcript variant 1 (LOC552075), mRNA] | 1.81E-01 | 0.73 | -0.02 |
| GB20017-RA [PREDICTED: Apis mellifera similar to TER94 CG2331-PA, isoform A, transcript variant 1 (LOC409377), mRNA] | 1.81E-01 | 0.17 | 0.43 |
| GB15619-RA [PREDICTED: Apis mellifera similar to CG8036-PB, isoform B, transcript variant 1 (LOC550804), mRNA] | 1.83E-01 | 0.68 | 0.65 |
| GB20012-RA [PREDICTED: Apis mellifera similar to CG10664-PA, isoform A (LOC412396), mRNA] | 1.85E-01 | -0.95 | -0.04 |
| GB18647-RA [PREDICTED: Apis mellifera similar to lethal (2) 37Cc CG10691-PA, isoform A (LOC408412), mRNA] | 1.86E-01 | -0.54 | 0.33 |
| GB12567-RA [PREDICTED: Apis mellifera similar to bubblegum CG4501-PA (LOC551837), partial mRNA] | 1.87E-01 | 0.21 | -0.29 |
| GB10238-RA [PREDICTED: Apis mellifera similar to ERp60 CG8983-PA, isoform A, transcript variant 2 (LOC409911), mRNA] | 1.88E-01 | 0.37 | 0.12 |
| GB18109-RA [PREDICTED: Apis mellifera similar to CG6084-PA, isoform A, transcript variant 1 (LOC551968), mRNA] | 1.89E-01 | 0.87 | 1.60 |
| GB19351-RA | 1.91E-01 | 0.41 | 0.32 |
| GB19082-RA [PREDICTED: Apis mellifera similar to stubarista CG14792-PA, isoform A (LOC410486), mRNA] | 1.92E-01 | -0.68 | -0.46 |
| GB11482-RA [PREDICTED: Apis mellifera similar to Proteasome subunit alpha type 4 (Proteasome component C9) (Macropain subunit C9) (Multicatalytic endopeptidase complex subunit C9) (Proteasome subunit L) (LOC413757), mRNA] | 1.95E-01 | 0.31 | 0.00 |
| GB11786-RA [PREDICTED: Apis mellifera similar to CG2947-PA, isoform A, transcript variant 1 (LOC411171), mRNA] | 1.97E-01 | 0.61 | 0.41 |
| GB14621-RA [PREDICTED: Apis mellifera similar to Protein lethal(2)essential for life (Protein Efl21) (LOC724488), mRNA] | 1.98E-01 | -0.83 | 0.72 |
| GB16443-RA [PREDICTED: Apis mellifera similar to lethal (1) G0334 CG7010-PD, isoform D, transcript variant 1 (LOC551103), mRNA] | 1.98E-01 | 0.60 | -0.20 |
| GB18045-RA [PREDICTED: Apis mellifera glutathione-S-transferase 1 (Gst1), mRNA] | 2.01E-01 | 0.52 | 0.31 |
| GB12855-RA [PREDICTED: Apis mellifera similar to Neural conserved at 73EF CG11661-PA, isoform A, transcript variant 1 (LOC408286), mRNA] | 2.05E-01 | -0.09 | -0.06 |
| GB20080-RA [PREDICTED: Apis mellifera similar to T-complex protein 1 subunit alpha (TCP-1-alpha) (CCT-alpha), transcript variant 1 (LOC409134), mRNA] | 2.06E-01 | -0.37 | 0.12 |
| GB14972-RA [PREDICTED: Apis mellifera thioredoxin reductase, transcript variant 2 (Trxr-1), mRNA] | 2.07E-01 | 0.46 | 0.07 |
| GB17548-RA [PREDICTED: Apis mellifera similar to CG3603-PA (LOC552493), mRNA] | 2.09E-01 | 0.27 | 0.83 |
| GB15779-RA [PREDICTED: Apis mellifera similar to Zwischenferment CG12529-PA, isoform A (LOC725325), mRNA] | 2.10E-01 | 0.54 | 0.03 |
| GB15629-RA [PREDICTED: Apis mellifera similar to ATP synthase O subunit, mitochondrial precursor (Oligomycin sensitivity conferral protein) (OSCP) (LOC409236), mRNA] | 2.12E-01 | -0.44 | -0.02 |
| GB15807-RA [PREDICTED: Apis mellifera similar to CG17896-PB, isoform B (LOC409736), mRNA] | 2.18E-01 | 0.83 | 0.83 |
| GB13045-RA [PREDICTED: Apis mellifera similar to CG4685-PA, isoform A (LOC412305), mRNA] | 2.19E-01 | -0.21 | 0.60 |
| GB10973-RA [Apis mellifera arginine kinase (Argk), mRNA] | 2.22E-01 | -0.22 | 0.58 |
| GB19724-RA [PREDICTED: Apis mellifera similar to Eukaryotic initiation factor 4A (ATP-dependent RNA helicase eIF4A) (eIF-4A), transcript variant 2 (LOC411989), mRNA] | 2.28E-01 | -0.13 | 0.05 |

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|---|---|---|---|
| GB14852-RA [PREDICTED: Apis mellifera similar to heat shock protein 8, transcript variant 1 (LOC409418), mRNA] | 2.33E-01 | 0.44 | -0.04 |
| GB10992-RA [PREDICTED: Apis mellifera similar to ATP citrate lyase CG8322-PA, isoform A, transcript variant 2 (LOC550686), mRNA] | 2.34E-01 | 0.26 | -0.47 |
| GB16547-RA | 2.36E-01 | -0.27 | 0.23 |
| GB10699-RA [PREDICTED: Apis mellifera similar to CG7033-PA, isoform A, transcript variant 1 (LOC409809), mRNA] | 2.37E-01 | -0.38 | 0.20 |
| GB16335-RA [PREDICTED: Apis mellifera similar to Nucleoplasmin CG7917-PA, transcript variant 1 (LOC410710), mRNA] | 2.37E-01 | -0.88 | -0.13 |
| GB18440-RA [PREDICTED: Apis mellifera similar to Proteasome p44.5 subunit CG10149-PB, isoform B, transcript variant 1 (LOC408397), mRNA] | 2.38E-01 | 0.21 | 0.21 |
| GB11076-RA [PREDICTED: Apis mellifera similar to Guanine nucleotide-binding protein subunit beta-like protein (Receptor of activated protein kinase C homolog), transcript variant 1 (LOC409450), mRNA] | 2.41E-01 | -0.59 | -0.27 |
| GB18404-RA [PREDICTED: Apis mellifera similar to CG2862-PA, isoform A (LOC552670), mRNA] | 2.41E-01 | 0.45 | 0.34 |
| GB20055-RA [PREDICTED: Apis mellifera similar to Na pump subunit CG5670-PG, isoform G, transcript variant 2 (LOC408832), mRNA] | 2.41E-01 | -0.53 | -0.20 |
| GB20055-RA [PREDICTED: Apis mellifera similar to Na pump subunit CG5670-PG, isoform G, transcript variant 2 (LOC408832), mRNA] | 2.41E-01 | -0.53 | 0.25 |
| GB20055-RB | 2.41E-01 | -0.53 | -0.20 |
| GB20055-RB | 2.41E-01 | -0.53 | 0.25 |
| GB10800-RA [PREDICTED: Apis mellifera similar to T-complex protein 1 subunit gamma (TCP-1-gamma) (CCT-gamma) (LOC409296), mRNA] | 2.43E-01 | -0.47 | 0.04 |
| GB18578-RA [PREDICTED: Apis mellifera similar to CG1240-PA (LOC408520), mRNA] | 2.45E-01 | -1.23 | 0.17 |
| GB18905-RA [PREDICTED: Apis mellifera similar to proteasome (prosome, macropain) subunit, beta type, 6 (LOC409831), mRNA] | 2.45E-01 | 0.39 | 0.34 |
| GB14970-RA [PREDICTED: Apis mellifera similar to Muscle-specific protein 300 CG33715-PB, isoform B (LOC551356), mRNA] | 2.46E-01 | -0.68 | -0.16 |
| GB10228-RA [PREDICTED: Apis mellifera similar to CG1444-PA (LOC725258), mRNA] | 2.46E-01 | 0.41 | -0.54 |
| GB20002-RA [PREDICTED: Apis mellifera similar to CG10527-PA (LOC412543), mRNA] | 2.47E-01 | -0.48 | 0.70 |
| GB16452-RA [PREDICTED: Apis mellifera similar to CG5525-PA, transcript variant 1 (LOC551275), mRNA] | 2.50E-01 | -0.28 | 0.17 |
| GB11373-RA [PREDICTED: Apis mellifera similar to Ras-related protein Rac1, transcript variant 1 (LOC551554), mRNA] | 2.52E-01 | -0.21 | 0.36 |
| GB12797-RA [PREDICTED: Apis mellifera similar to Trehalose-6-phosphate synthase 1 CG4104-PA (LOC408867), partial mRNA] | 2.53E-01 | -0.91 | 0.18 |
| GB10337-RA [PREDICTED: Apis mellifera similar to Ank2 CG7462-PB, isoform B (LOC409051), mRNA] | 2.53E-01 | -0.37 | -0.98 |
| GB18233-RA [PREDICTED: Apis mellifera similar to ergic53 CG6822-PA, isoform A, transcript variant 1 (LOC550798), mRNA] | 2.54E-01 | -0.27 | 0.42 |
| GB18497-RA [PREDICTED: Apis mellifera similar to Elongation factor Tu mitochondrial CG6050-PA, transcript variant 2 (LOC408328), mRNA] | 2.57E-01 | -0.62 | 0.07 |
| GB13982-RA [PREDICTED: Apis mellifera similar to Fumarylacetoacetase (Fumarylacetoacetate hydrolase) (Beta-diketonase) (FAA) (LOC552210), mRNA] | 2.58E-01 | 0.43 | 0.83 |
| GB11407-RA [PREDICTED: Apis mellifera similar to Spectrin beta chain (LOC411744), mRNA] | 2.64E-01 | -0.25 | -0.57 |
| GB14710-RA [PREDICTED: Apis mellifera similar to CG4572-PB, isoform B (LOC410451), mRNA] | 2.64E-01 | -0.23 | -0.04 |
| GB17555-RA [PREDICTED: Apis mellifera similar to Limpet CG32171-PD, isoform D (LOC410211), mRNA] | 2.65E-01 | -0.96 | 0.14 |
| GB17555-RA [PREDICTED: Apis mellifera similar to Limpet CG32171-PD, isoform D (LOC410211), mRNA] | 2.65E-01 | -0.96 | -0.60 |
| GB17555-RA [PREDICTED: Apis mellifera similar to Limpet CG32171-PD, isoform D (LOC410211), mRNA] | 2.65E-01 | -0.96 | 0.35 |
| GB17555-RA [PREDICTED: Apis mellifera similar to Limpet CG32171-PD, isoform D (LOC410211), mRNA] | 2.65E-01 | -0.96 | 0.14 |
| GB17555-RA [PREDICTED: Apis mellifera similar to Limpet CG32171-PD, isoform D (LOC410211), mRNA] | 2.65E-01 | -0.96 | -0.60 |
| GB17555-RA [PREDICTED: Apis mellifera similar to Limpet CG32171-PD, isoform D (LOC410211), mRNA] | 2.65E-01 | -0.96 | 0.35 |
| GB17555-RA [PREDICTED: Apis mellifera similar to Limpet CG32171-PD, isoform D (LOC410211), mRNA] | 2.65E-01 | -0.96 | 0.14 |
| GB17555-RA [PREDICTED: Apis mellifera similar to Limpet CG32171-PD, isoform D (LOC410211), mRNA] | 2.65E-01 | -0.96 | -0.60 |
| GB17555-RA [PREDICTED: Apis mellifera similar to Limpet CG32171-PD, isoform D (LOC410211), mRNA] | 2.65E-01 | -0.96 | 0.35 |
| GB12180-RA [PREDICTED: Apis mellifera similar to metalloprotease 1 (LOC413657), mRNA] | 2.66E-01 | 0.20 | -0.06 |
| [Antisense] GB17673-RA [PREDICTED: Apis mellifera similar to rhea CG6831-PA (LOC408396), partial mRNA] | 2.66E-01 | -0.18 | 0.47 |
| [Antisense] GB17673-RA [PREDICTED: Apis mellifera similar to rhea CG6831-PA (LOC408396), partial mRNA] | 2.66E-01 | -0.18 | -0.03 |
| [Antisense] GB17673-RA [PREDICTED: Apis mellifera similar to rhea CG6831-PA (LOC408396), partial mRNA] | 2.66E-01 | -0.18 | -0.27 |
| GB17673-RA [PREDICTED: Apis mellifera similar to rhea CG6831-PA (LOC408396), partial mRNA] | 2.66E-01 | -0.18 | 0.47 |
| GB17673-RA [PREDICTED: Apis mellifera similar to rhea CG6831-PA (LOC408396), partial | 2.66E-01 | -0.18 | -0.03 |

| | | | |
|---|---|---|---|
| mRNA] | | | |
| GB17673-RA [PREDICTED: Apis mellifera similar to rhea CG6831-PA (LOC408396), partial mRNA] | 2.66E-01 | -0.18 | -0.27 |
| GB17673-RA [PREDICTED: Apis mellifera similar to rhea CG6831-PA (LOC408396), partial mRNA] | 2.66E-01 | -0.18 | 0.47 |
| GB17673-RA [PREDICTED: Apis mellifera similar to rhea CG6831-PA (LOC408396), partial mRNA] | 2.66E-01 | -0.18 | -0.03 |
| GB17673-RA [PREDICTED: Apis mellifera similar to rhea CG6831-PA (LOC408396), partial mRNA] | 2.66E-01 | -0.18 | -0.27 |
| GB16792-RA [PREDICTED: Apis mellifera similar to Lamin CG6944-PA (LOC413222), partial mRNA] | 2.73E-01 | -0.42 | -0.06 |
| GB15662-RA [PREDICTED: Apis mellifera similar to CG10962-PB, isoform B (LOC724721), mRNA] | 2.73E-01 | -0.28 | -0.73 |
| GB10732-RA [PREDICTED: Apis mellifera similar to CG2918-PA (LOC551763), mRNA] | 2.74E-01 | 0.39 | -0.06 |
| GB14791-RA [PREDICTED: Apis mellifera similar to bellwether CG3612-PA, transcript variant 1 (LOC409114), mRNA] | 2.77E-01 | -0.35 | 0.29 |
| GB13160-RA [PREDICTED: Apis mellifera similar to pugilist CG4067-PA, isoform A, transcript variant 1 (LOC550749), mRNA] | 2.79E-01 | 0.32 | 1.68 |
| GB12526-RA [PREDICTED: Apis mellifera similar to lethal (2) k05713 CG8256-PC, isoform C (LOC551904), mRNA] | 2.82E-01 | -0.20 | 0.20 |
| GB19347-RA [PREDICTED: Apis mellifera similar to pericardin CG5700-PB (LOC724749), mRNA] | 2.93E-01 | -0.30 | 2.38 |
| GB19582-RA [PREDICTED: Apis mellifera similar to Serine protease inhibitor 5 CG18525-PA, isoform A (LOC413749), mRNA] | 2.96E-01 | -0.34 | 0.31 |
| GB19078-RA [PREDICTED: Apis mellifera similar to phosphoserine aminotransferase 1 isoform 1 (LOC412670), mRNA] | 2.97E-01 | 0.77 | 1.68 |
| GB19465-RA [PREDICTED: Apis mellifera similar to CG3195-PA, isoform A (LOC550715), mRNA] | 3.01E-01 | -0.61 | 0.08 |
| GB15225-RA [PREDICTED: Apis mellifera similar to Ribosomal protein S7 CG1883-PA, isoform A (LOC552564), mRNA] | 3.03E-01 | 0.50 | -0.23 |
| GB12364-RA [PREDICTED: Apis mellifera similar to fumarylacetoacetate hydrolase domain containing 2A, transcript variant 2 (LOC410635), mRNA] | 3.10E-01 | 0.34 | 0.99 |
| GB19305-RA [PREDICTED: Apis mellifera similar to Ribosomal protein S4 CG11276-PA, isoform A, transcript variant 1 (LOC550651), mRNA] | 3.11E-01 | -0.80 | 0.01 |
| GB11744-RA [PREDICTED: Apis mellifera similar to CG12876-PA (LOC412662), mRNA] | 3.16E-01 | 0.16 | 0.12 |
| GB16881-RA [Apis mellifera troponin T (TpnT), mRNA] | 3.17E-01 | -0.88 | -0.19 |
| GB17684-RA [PREDICTED: Apis mellifera similar to CG11198-PA, isoform A, transcript variant 2 (LOC552286), mRNA] | 3.18E-01 | 0.07 | -0.06 |
| GB18819-RA [Apis mellifera antennal-specific protein 3c precursor (Asp3c), mRNA] | 3.18E-01 | 0.37 | -0.17 |
| GB18292-RA [PREDICTED: Apis mellifera similar to 26S protease regulatory subunit 8, transcript variant 1 (LOC550794), mRNA] | 3.19E-01 | 0.17 | -0.10 |
| GB12633-RA [PREDICTED: Apis mellifera similar to Ribosomal protein L23 CG3661-PA (LOC409294), mRNA] | 3.21E-01 | -0.64 | 0.01 |
| GB15172-RA [PREDICTED: Apis mellifera similar to lethal (1) G0255 CG4094-PA, isoform A (LOC724321), mRNA] | 3.24E-01 | -0.53 | 0.42 |
| GB17282-RA [PREDICTED: Apis mellifera similar to Calreticulin CG9429-PA, transcript variant 1 (LOC409165), mRNA] | 3.27E-01 | 0.17 | 0.22 |
| GB18737-RA [PREDICTED: Apis mellifera similar to 15-hydroxyprostaglandin dehydrogenase (LOC551423), mRNA] | 3.28E-01 | 2.01 | 0.99 |
| GB10139-RA [PREDICTED: Apis mellifera similar to Glutamine synthetase 2 CG1743-PC, isoform C (LOC410066), mRNA] | 3.29E-01 | -0.46 | 0.40 |
| GB11643-RA [PREDICTED: Apis mellifera similar to ribosomal protein L7a (LOC409528), mRNA] | 3.32E-01 | -0.61 | -0.12 |
| GB17626-RA [PREDICTED: Apis mellifera similar to CG7430-PA, transcript variant 1 (LOC551039), mRNA] | 3.33E-01 | -0.22 | 0.16 |
| GB12562-RA [PREDICTED: Apis mellifera similar to CG10513-PA, transcript variant 1 (LOC408421), mRNA] | 3.36E-01 | 0.26 | 0.09 |
| GB20152-RA [PREDICTED: Apis mellifera similar to CG6370-PA (LOC412045), mRNA] | 3.37E-01 | -0.28 | 0.18 |
| GB13730-RA [PREDICTED: Apis mellifera similar to GDP dissociation inhibitor CG4422-PA (LOC411765), mRNA] | 3.38E-01 | 0.19 | 0.44 |
| GB11283-RA [PREDICTED: Apis mellifera similar to transaldolase 1 (LOC413867), mRNA] | 3.41E-01 | 0.82 | 0.31 |
| GB18920-RA [PREDICTED: Apis mellifera similar to Pdsw CG8844-PA, isoform A (LOC552424), mRNA] | 3.48E-01 | -1.07 | 0.05 |
| GB13791-RA [PREDICTED: Apis mellifera similar to CG31954-PA (LOC413645), mRNA] | 3.53E-01 | -0.46 | -0.83 |
| GB17499-RA [Apis mellifera ADP/ATP translocase (Ant), mRNA] | 3.55E-01 | -0.67 | -0.17 |
| GB11840-RA [PREDICTED: Apis mellifera similar to Vha100-2 CG18617-PB, isoform B, transcript variant 1 (LOC412810), mRNA] | 3.56E-01 | -0.46 | -0.42 |
| GB17630-RA [PREDICTED: Apis mellifera similar to Mitochondrial import inner membrane translocase subunit Tim13 (LOC725705), mRNA] | 3.57E-01 | 0.45 | 0.45 |
| GB13596-RA [PREDICTED: Apis mellifera similar to ATP synthase- CG11154-PA, isoform A (LOC551766), mRNA] | 3.59E-01 | -0.26 | 0.48 |
| GB18874-RA [PREDICTED: Apis mellifera similar to CG1458-PA (LOC410636), mRNA] | 3.61E-01 | 0.06 | 0.40 |
| GB10796-RA [PREDICTED: Apis mellifera similar to 26S proteasome non-ATPase regulatory subunit 8 (26S proteasome regulatory subunit S14) (p31) (LOC552838), mRNA] | 3.65E-01 | 0.25 | 0.16 |
| GB10107-RA [PREDICTED: Apis mellifera similar to CG6459-PA (LOC413762), mRNA] | 3.75E-01 | 0.32 | 0.35 |
| GB16844-RA [Apis mellifera elongation factor 1-alpha (EF1-alpha), mRNA] | 3.75E-01 | -0.15 | 0.10 |
| GB10133-RA [PREDICTED: Apis mellifera CuZn superoxide dismutase, transcript variant 1 | 3.76E-01 | 0.29 | 0.03 |

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|---|---|---|---|
| (Sod1), mRNA] | | | |
| GB13427-RA [PREDICTED: Apis mellifera similar to CG17337-PA, transcript variant 1 (LOC412393), mRNA] | 3.76E-01 | -0.21 | 0.33 |
| GB10294-RA [PREDICTED: Apis mellifera similar to CG5731-PA (LOC725899), mRNA] | 3.76E-01 | 0.48 | -0.20 |
| GB10294-RA [PREDICTED: Apis mellifera similar to CG5731-PA (LOC725899), mRNA] | 3.76E-01 | 0.48 | -0.24 |
| GB10294-RA [PREDICTED: Apis mellifera similar to CG5731-PA (LOC725899), mRNA] | 3.76E-01 | 0.48 | -0.20 |
| GB10294-RA [PREDICTED: Apis mellifera similar to CG5731-PA (LOC725899), mRNA] | 3.76E-01 | 0.48 | -0.24 |
| GB12573-RA [PREDICTED: Apis mellifera similar to lethal (1) G0030 CG3861-PA, isoform A (LOC410059), mRNA] | 3.81E-01 | -0.37 | 0.12 |
| GB12614-RA [PREDICTED: Apis mellifera similar to Actin-87E, transcript variant 2 (LOC410075), mRNA] | 3.81E-01 | 0.83 | -0.07 |
| GB10675-RA [PREDICTED: Apis mellifera similar to ADP ribosylation factor 79F CG8385-PB, isoform B, transcript variant 1 (LOC409481), mRNA] | 3.82E-01 | 0.09 | 0.19 |
| GB13229-RA [PREDICTED: Apis mellifera similar to CG30084-PC, isoform C (LOC410204), mRNA] | 3.84E-01 | -0.32 | -0.28 |
| GB12586-RA [PREDICTED: Apis mellifera similar to Protein disulfide-isomerase precursor (PDI) (LOC551435), partial mRNA] | 3.84E-01 | 0.58 | 0.78 |
| GB11177-RA [PREDICTED: Apis mellifera similar to Probable elongation factor 1-delta (EF-1-delta) (LOC409015), mRNA] | 3.84E-01 | 0.09 | 0.38 |
| GB16464-RA [PREDICTED: Apis mellifera similar to mitochondrial malate dehydrogenase precursor, transcript variant 1 (LOC408950), mRNA] | 3.85E-01 | 0.14 | NA |
| GB15582-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG31196-PC, isoform C, transcript variant 1 (LOC408951), mRNA] | 3.90E-01 | -0.19 | -0.07 |
| GB18004-RA [PREDICTED: Apis mellifera similar to CG31075-PA (LOC408559), mRNA] | 3.95E-01 | 0.34 | 0.66 |
| GB13882-RA [PREDICTED: Apis mellifera similar to Ecdysone-inducible gene L3 CG10160-PA (LOC411188), mRNA] | 3.97E-01 | 0.22 | 0.02 |
| GB17793-RA [PREDICTED: Apis mellifera similar to Probable cytochrome P450 9f2 (CYPIXF2) (LOC408452), mRNA] | 3.98E-01 | -0.79 | 0.20 |
| GB19171-RA [PREDICTED: Apis mellifera similar to Vacuolar H+-ATPase 55kD B subunit CG17369-PB, isoform B (LOC551721), mRNA] | 4.00E-01 | -0.32 | 0.39 |
| GB19048-RA [PREDICTED: Apis mellifera similar to CG16935-PA (LOC411662), mRNA] | 4.01E-01 | 0.11 | 0.55 |
| GB11461-RA [PREDICTED: Apis mellifera similar to UGP CG4347-PA, isoform A, transcript variant 1 (LOC412069), mRNA] | 4.04E-01 | 0.06 | 0.59 |
| GB12860-RA [PREDICTED: Apis mellifera similar to Tudor-SN CG7008-PA (LOC552259), mRNA] | 4.07E-01 | -0.28 | 0.33 |
| GB19207-RA [PREDICTED: Apis mellifera hypothetical LOC408695 (LOC408695), mRNA] | 4.08E-01 | -0.24 | -0.40 |
| GB13602-RA | 4.12E-01 | 0.77 | -0.10 |
| GB10498-RA [PREDICTED: Apis mellifera similar to Peroxiredoxin 2540 CG11765-PA (LOC551975), mRNA] | 4.13E-01 | 0.58 | 0.68 |
| GB19503-RA [PREDICTED: Apis mellifera similar to heat shock protein 8, transcript variant 1 (LOC410620), mRNA] | 4.15E-01 | 0.20 | -0.06 |
| GB19797-RA [PREDICTED: Apis mellifera similar to Cytochrome P450 6a2 (CYPVIA2) (P450-B1) (LOC724211), mRNA] | 4.15E-01 | 0.21 | -0.34 |
| GB16965-RA [PREDICTED: Apis mellifera similar to CG7217-PB, isoform B (LOC552429), mRNA] | 4.15E-01 | 0.43 | 0.05 |
| GB11217-RA [PREDICTED: Apis mellifera similar to CG31974-PA (LOC724536), mRNA] | 4.17E-01 | -0.35 | -0.59 |
| GB17084-RA [PREDICTED: Apis mellifera similar to Fasciclin-3 precursor (Fasciclin III) (FAS III) (LOC724243), mRNA] | 4.18E-01 | -0.58 | -0.21 |
| GB17549-RA [PREDICTED: Apis mellifera similar to Putative Achaete Scute Target 1 CG6148-PB, isoform B (LOC413012), mRNA] | 4.21E-01 | -0.14 | 0.00 |
| GB19193-RA [PREDICTED: Apis mellifera similar to Protein translation factor SUI1 homolog (LOC409076), mRNA] | 4.22E-01 | -0.13 | 0.02 |
| GB11227-RA [PREDICTED: Apis mellifera similar to Ribosomal protein S27A CG5271-PA (LOC413884), mRNA] | 4.28E-01 | -0.74 | -0.03 |
| GB17108-RA [PREDICTED: Apis mellifera similar to 60S acidic ribosomal protein P2 (Acidic ribosomal protein RPA1) (LOC725884), mRNA] | 4.28E-01 | -0.08 | -0.19 |
| GB12747-RA [PREDICTED: Apis mellifera similar to eIF3-S8 CG4954-PA (LOC551184), mRNA] | 4.35E-01 | 0.25 | -0.08 |
| GB10060-RA [PREDICTED: Apis mellifera similar to ARMET-like protein precursor (LOC552645), mRNA] | 4.36E-01 | -0.16 | -0.23 |
| GB19606-RA [PREDICTED: Apis mellifera similar to Muscle LIM protein at 84B CG1019-PA, isoform A, transcript variant 1 (LOC411285), mRNA] | 4.37E-01 | -0.32 | -0.28 |
| GB17255-RA [PREDICTED: Apis mellifera similar to lethal (1) G0230 CG2968-PA (LOC552682), mRNA] | 4.38E-01 | -0.22 | 0.14 |
| GB18300-RA [PREDICTED: Apis mellifera similar to yellow-h CG1629-PA (LOC724293), mRNA] | 4.38E-01 | -0.27 | 0.55 |
| GB12913-RA [PREDICTED: Apis mellifera similar to Vacuolar ATP synthase subunit E (V-ATPase E subunit) (Vacuolar proton pump E subunit) (V-ATPase 28 kDa subunit) (LOC552720), mRNA] | 4.40E-01 | -0.30 | 0.07 |
| GB13368-RA [PREDICTED: Apis mellifera lambda crystallin-like protein, transcript variant 1 (Cryl1), partial mRNA] | 4.42E-01 | 0.47 | 1.18 |
| GB15605-RA [PREDICTED: Apis mellifera similar to 40S ribosomal protein S12 (LOC552266), mRNA] | 4.43E-01 | -0.63 | -0.12 |
| GB13559-RA [PREDICTED: Apis mellifera similar to CG7460-PB, transcript variant 1 (LOC413478), mRNA] | 4.46E-01 | -0.21 | 0.50 |
| GB18172-RA [PREDICTED: Apis mellifera similar to CG18143-PA (LOC727293), mRNA] | 4.47E-01 | -0.05 | 1.17 |
| GB19422-RA [PREDICTED: Apis mellifera similar to lethal (1) G0156 CG12233-PA, isoform | 4.47E-01 | 0.21 | 0.31 |

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|---|---|---|---|
| A (LOC409292), mRNA] | | | |
| GB19093-RA [PREDICTED: Apis mellifera similar to Guanine nucleotide-binding protein G(o) subunit alpha 47A (LOC726858), partial mRNA] | 4.54E-01 | -0.31 | 0.30 |
| GB17641-RA [PREDICTED: Apis mellifera similar to CG1640-PA, isoform A, transcript variant 1 (LOC409196), mRNA] | 4.63E-01 | 0.04 | 0.56 |
| GB18683-RA [PREDICTED: Apis mellifera similar to Annexin-B9 (Annexin-9) (Annexin IX) (LOC412487), partial mRNA] | 4.64E-01 | 0.29 | 0.60 |
| GB16429-RA [PREDICTED: Apis mellifera similar to Glucose-6-phosphate isomerase (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (LOC551154), mRNA] | 4.70E-01 | 0.13 | 0.17 |
| GB10590-RA [PREDICTED: Apis mellifera similar to vibrator CG5269-PA (LOC552183), mRNA] | 4.74E-01 | -0.70 | 0.35 |
| GB19777-RA [PREDICTED: Apis mellifera similar to Proteasome subunit beta type 4 precursor (Proteasome beta chain) (Macropain beta chain) (Multicatalytic endopeptidase complex beta chain) (Proteasome chain 3) (LOC411520), mRNA] | 4.81E-01 | 0.27 | 0.38 |
| GB17736-RA [PREDICTED: Apis mellifera similar to Protein disulfide-isomerase precursor (PDI) (LOC726142), partial mRNA] | 4.89E-01 | 0.56 | 0.40 |
| GB15226-RA [PREDICTED: Apis mellifera similar to Vacuolar ATP synthase subunit D 1 (V-ATPase D subunit 1) (Vacuolar proton pump D subunit 1) (dV-ATPase D), transcript variant 1 (LOC411295), mRNA] | 4.89E-01 | -0.27 | 0.20 |
| GB15457-RA [PREDICTED: Apis mellifera similar to Thioredoxin-like CG5495-PA, transcript variant 1 (LOC550734), mRNA] | 4.92E-01 | 0.39 | 0.11 |
| GB14321-RA [PREDICTED: Apis mellifera similar to ATP synthase B chain, mitochondrial precursor (FO-ATP synthase subunit B) (LOC551923), mRNA] | 4.96E-01 | -0.20 | 0.42 |
| GB18760-RA [PREDICTED: Apis mellifera similar to L-xylulose reductase (XR) (Dicarbonyl/L-xylulose reductase) (LOC413567), mRNA] | 4.97E-01 | 0.29 | 0.56 |
| GB10989-RA [PREDICTED: Apis mellifera similar to Vacuolar ATP synthase catalytic subunit A, osteoclast isoform (V-ATPase subunit A 2) (Vacuolar proton pump alpha subunit 2) (V-ATPase 69 kDa subunit 2) (Isoform HO68), transcript variant 1 (LOC551093), mRNA | 4.99E-01 | -0.16 | 0.06 |
| GB16245-RA [PREDICTED: Apis mellifera similar to CG9342-PA (LOC551250), mRNA] | 5.01E-01 | 0.21 | 0.45 |
| GB10477-RA [PREDICTED: Apis mellifera similar to B-cell receptor-associated protein 37 (LOC551944), mRNA] | 5.05E-01 | -0.35 | 0.16 |
| GB12510-RA [PREDICTED: Apis mellifera similar to CG4769-PA (LOC413605), mRNA] | 5.08E-01 | -0.36 | 0.15 |
| GB16028-RA [PREDICTED: Apis mellifera similar to CG9674-PA, isoform A, transcript variant 1 (LOC413372), mRNA] | 5.08E-01 | 0.55 | 0.01 |
| GB18917-RA [PREDICTED: Apis mellifera similar to Cofilin/actin-depolymerizing factor homolog (Protein D61) (Protein twinstar) (LOC725718), mRNA] | 5.11E-01 | 0.28 | 0.01 |
| GB11282-RA [PREDICTED: Apis mellifera similar to Moesin CG10701-PD, isoform D (LOC412799), mRNA] | 5.13E-01 | -0.39 | 0.05 |
| GB17380-RA [PREDICTED: Apis mellifera similar to failed axon connections CG4609-PA, isoform A, transcript variant 1 (LOC409643), mRNA] | 5.13E-01 | -0.41 | 0.12 |
| GB18415-RA [PREDICTED: Apis mellifera similar to CG5065-PA (LOC411910), mRNA] | 5.14E-01 | 0.40 | 0.68 |
| GB14059-RA [PREDICTED: Apis mellifera similar to Nucleosome assembly protein 1-like 1 (NAP-1-related protein) (hNRP), transcript variant 1 (LOC550824), mRNA] | 5.31E-01 | -0.10 | 0.00 |
| GB10836-RA [PREDICTED: Apis mellifera similar to Hsc70Cb CG6603-PA, isoform A, transcript variant 1 (LOC408706), mRNA] | 5.35E-01 | 0.14 | 0.02 |
| GB17251-RA [PREDICTED: Apis mellifera similar to Nucleoside diphosphate kinase (NDK) (NDP kinase) (Abnormal wing disks protein) (Killer of prune protein) (LOC409861), mRNA] | 5.36E-01 | 0.32 | 0.23 |
| GB10382-RA [PREDICTED: Apis mellifera similar to lethal (1) G0022 CG8231-PA (LOC551295), partial mRNA] | 5.40E-01 | -0.10 | 0.28 |
| GB15291-RA [PREDICTED: Apis mellifera similar to ATP synthase gamma chain, mitochondrial precursor (LOC552699), mRNA] | 5.43E-01 | -0.53 | 0.31 |
| GB16959-RA [PREDICTED: Apis mellifera similar to Glutathione S transferase S1 CG8938-PA, isoform A (LOC552304), mRNA] | 5.50E-01 | 0.61 | 0.39 |
| GB11251-RA [PREDICTED: Apis mellifera similar to CG3902-PA (LOC409712), mRNA] | 5.52E-01 | 0.28 | 1.67 |
| GB10275-RA [PREDICTED: Apis mellifera similar to -Tubulin at 56D CG9277-PB, isoform B (LOC408782), mRNA] | 5.55E-01 | 0.25 | 0.32 |
| GB13821-RA [PREDICTED: Apis mellifera similar to CG3609-PA (LOC412231), mRNA] | 5.56E-01 | 0.05 | 0.07 |
| GB16568-RA [PREDICTED: Apis mellifera similar to CG11015-PA (LOC552610), mRNA] | 5.58E-01 | -0.12 | 0.27 |
| GB10717-RA [PREDICTED: Apis mellifera similar to Muscle protein 20 CG4696-PA, isoform A (LOC408972), mRNA] | 5.61E-01 | -0.25 | -0.76 |
| GB16525-RA [PREDICTED: Apis mellifera similar to proteasome (prosome, macropain) 26S subunit, non-ATPase, 10 (LOC551954), mRNA] | 5.63E-01 | -0.22 | 0.20 |
| GB12951-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG17870-PC, isoform C, transcript variant 1 (LOC408289), mRNA] | 5.66E-01 | 0.24 | 0.02 |
| GB12951-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG17870-PC, isoform C, transcript variant 1 (LOC408289), mRNA] | 5.66E-01 | 0.24 | 0.05 |
| GB12951-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG17870-PC, isoform C, transcript variant 1 (LOC408289), mRNA] | 5.66E-01 | 0.24 | 0.00 |
| GB12951-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG17870-PC, isoform C, transcript variant 1 (LOC408289), mRNA] | 5.66E-01 | 0.24 | 0.02 |
| GB12951-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG17870-PC, isoform C, transcript variant 1 (LOC408289), mRNA] | 5.66E-01 | 0.24 | 0.05 |
| GB12951-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG17870-PC, isoform C, transcript variant 1 (LOC408289), mRNA] | 5.66E-01 | 0.24 | 0.00 |
| GB12951-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG17870-PC, isoform C, transcript variant 1 (LOC408289), mRNA] | 5.66E-01 | 0.24 | 0.02 |

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|---|---|---|---|
| GB12951-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG17870-PC, isoform C, transcript variant 1 (LOC408289), mRNA] | 5.66E-01 | 0.24 | 0.05 |
| GB12951-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG17870-PC, isoform C, transcript variant 1 (LOC408289), mRNA] | 5.66E-01 | 0.24 | 0.00 |
| GB14409-RA [PREDICTED: Apis mellifera similar to CG9119-PA (LOC411385), mRNA] | 5.70E-01 | -0.19 | 0.61 |
| GB13595-RA [PREDICTED: Apis mellifera similar to CG11771-PA (LOC412154), mRNA] | 5.72E-01 | 0.26 | -0.04 |
| GB15168-RA [PREDICTED: Apis mellifera similar to VAMP (vesicle-associated membrane protein)-associated protein A (LOC409934), mRNA] | 5.73E-01 | -0.18 | 0.07 |
| GB10282-RA [PREDICTED: Apis mellifera similar to Adenylate kinase-2 CG3140-PA (LOC551523), mRNA] | 5.77E-01 | -0.13 | 0.21 |
| GB15619-RA [PREDICTED: Apis mellifera similar to CG8036-PB, isoform B, transcript variant 1 (LOC550804), mRNA] | 5.78E-01 | 0.29 | 0.65 |
| GB10598-RA [PREDICTED: Apis mellifera similar to CG6852-PA (LOC727309), mRNA] | 5.79E-01 | 0.07 | 0.32 |
| GB12140-RA [PREDICTED: Apis mellifera similar to Ribosomal protein S18 CG8900-PA, isoform A (LOC552726), mRNA] | 5.84E-01 | -0.20 | -0.21 |
| GB11503-RA [PREDICTED: Apis mellifera similar to CG5195-PA (LOC724779), mRNA] | 5.92E-01 | -0.08 | 0.11 |
| GB19286-RA [PREDICTED: Apis mellifera similar to Rpn2 CG11888-PA (LOC409699), mRNA] | 6.05E-01 | 0.11 | 0.37 |
| GB12840-RA [PREDICTED: Apis mellifera similar to squid CG16901-PC, isoform C (LOC725626), mRNA] | 6.09E-01 | -0.27 | 0.01 |
| GB14261-RA [PREDICTED: Apis mellifera hypothetical protein LOC724386 (LOC724386), mRNA] | 6.11E-01 | 0.23 | 0.95 |
| GB16132-RA [PREDICTED: Apis mellifera similar to CG7834-PA, isoform A (LOC410308), mRNA] | 6.13E-01 | 0.13 | 0.78 |
| GB19501-RA [PREDICTED: Apis mellifera similar to CG5023-PA (LOC408532), mRNA] | 6.19E-01 | -0.22 | 0.01 |
| GB11028-RA [PREDICTED: Apis mellifera similar to Alpha-actinin, sarcomeric (F-actin cross linking protein) (LOC725782), mRNA] | 6.34E-01 | -0.09 | -0.24 |
| GB15307-RA [PREDICTED: Apis mellifera similar to Guanine nucleotide-binding protein subunit beta 1, transcript variant 1 (LOC410497), mRNA] | 6.38E-01 | -0.13 | -0.04 |
| GB13224-RA [PREDICTED: Apis mellifera similar to Multidrug resistance protein homolog 49 (P-glycoprotein 49) (LOC551167), mRNA] | 6.40E-01 | -0.39 | -0.12 |
| GB17125-RA [PREDICTED: Apis mellifera similar to leukotriene B4 12-hydroxydehydrogenase (LOC411378), mRNA] | 6.42E-01 | 0.17 | -0.06 |
| GB13073-RA [PREDICTED: Apis mellifera similar to CG5214-PA (LOC409155), mRNA] | 6.45E-01 | -0.08 | 0.46 |
| GB19820-RA [PREDICTED: Apis mellifera similar to Probable cytochrome P450 9f2 (CYPIXF2) (LOC410492), mRNA] | 6.47E-01 | 0.21 | 0.10 |
| GB10827-RA [PREDICTED: Apis mellifera similar to Kinesin heavy chain CG7765-PA, transcript variant 1 (LOC411769), mRNA] | 6.48E-01 | -0.14 | -0.06 |
| GB18313-RA [Apis mellifera prophenoloxidase (LOC406155), mRNA] | 6.49E-01 | 0.04 | 0.23 |
| GB17764-RA [PREDICTED: Apis mellifera similar to Rab-protein 11 CG5771-PB, isoform B (LOC551603), mRNA] | 6.53E-01 | -0.05 | 0.05 |
| GB10901-RA | 6.53E-01 | -0.14 | -0.13 |
| GB18557-RA [PREDICTED: Apis mellifera similar to Spectrin alpha chain (LOC551291), mRNA] | 6.58E-01 | -0.16 | -0.32 |
| GB14269-RA [PREDICTED: Apis mellifera similar to CG15117-PA, isoform A (LOC409814), mRNA] | 6.62E-01 | 0.25 | 0.53 |
| GB10411-RA [PREDICTED: Apis mellifera similar to Proteasome subunit alpha type 7-1 (Proteasome 28 kDa subunit 1) (PROS-Dm28.1), transcript variant 1 (LOC410095), mRNA] | 6.71E-01 | 0.09 | -0.02 |
| GB16807-RA [PREDICTED: Apis mellifera similar to CG9518-PA (LOC410733), mRNA] | 6.72E-01 | -0.21 | 0.15 |
| GB10587-RA [PREDICTED: Apis mellifera similar to T-complex Chaperonin 5 CG8439-PA, isoform A (LOC409825), mRNA] | 6.76E-01 | -0.17 | 0.18 |
| GB13082-RA [PREDICTED: Apis mellifera similar to esterase D/formylglutathione hydrolase (LOC412193), mRNA] | 6.78E-01 | 0.03 | 0.40 |
| GB14607-RA [Apis mellifera short-chain dehydrogenase/reductase (LOC406147), mRNA] | 6.91E-01 | -0.13 | -0.68 |
| GB12949-RA [PREDICTED: Apis mellifera similar to 6-phosphogluconate dehydrogenase, decarboxylating (LOC552712), partial mRNA] | 6.98E-01 | 0.14 | 0.04 |
| GB17379-RA [PREDICTED: Apis mellifera similar to CG4567-PA, transcript variant 1 (LOC411351), mRNA] | 7.05E-01 | -0.01 | 0.26 |
| GB19860-RA [PREDICTED: Apis mellifera similar to Heat shock protein cognate 5 CG8542-PA (LOC408605), mRNA] | 7.23E-01 | 0.21 | 0.46 |
| GB15202-RA [PREDICTED: Apis mellifera similar to dj-1 CG1349-PA (LOC551882), mRNA] | 7.24E-01 | -0.05 | -0.11 |
| GB15692-RA [PREDICTED: Apis mellifera similar to ribosomal protein S13 (LOC551867), mRNA] | 7.32E-01 | -0.27 | 0.09 |
| GB16272-RA [PREDICTED: Apis mellifera similar to CG7145-PA, isoform A (LOC551113), mRNA] | 7.34E-01 | -0.08 | 0.13 |
| GB18727-RA [PREDICTED: Apis mellifera similar to CG5362-PA, transcript variant 1 (LOC411014), mRNA] | 7.45E-01 | 0.12 | 0.27 |
| GB15299-RA [Apis mellifera fatty acid binding protein (Fabp), mRNA] | 7.47E-01 | 0.05 | 0.00 |
| GB19429-RA [PREDICTED: Apis mellifera similar to CG17838-PE, isoform E (LOC408775), mRNA] | 7.49E-01 | 0.03 | 0.19 |
| GB19003-RA [PREDICTED: Apis mellifera similar to Proteasome subunit beta type 3 (Proteasome theta chain) (Proteasome chain 13) (Proteasome component C10-II) (LOC552579), mRNA] | 7.55E-01 | 0.15 | 0.27 |
| GB11284-RA [PREDICTED: Apis mellifera similar to Proteasome subunit alpha type 1 (Proteasome component C2) (Macropain subunit C2) (Multicatalytic endopeptidase complex subunit C2) (Proteasome nu chain) (LOC552654), mRNA] | 7.58E-01 | -0.06 | 0.09 |

| | | | |
|---|---|---|---|
| GB14499-RA [PREDICTED: Apis mellifera similar to CG33105-PA (LOC412554), mRNA] | 7.69E-01 | -0.23 | -0.15 |
| GB16485-RA [PREDICTED: Apis mellifera similar to ATP synthase D chain, mitochondrial (LOC410557), mRNA] | 7.83E-01 | -0.10 | 0.07 |
| GB15044-RA [PREDICTED: Apis mellifera similar to CG6180-PA, transcript variant 1 (LOC408516), mRNA] | 7.83E-01 | 0.06 | 0.30 |
| GB20117-RA [PREDICTED: Apis mellifera hypothetical LOC552391 (LOC552391), mRNA] | 8.01E-01 | 0.23 | 0.99 |
| GB14603-RA [PREDICTED: Apis mellifera similar to CG7142-PA (LOC726372), mRNA] | 8.02E-01 | -0.18 | -0.08 |
| GB10614-RA [PREDICTED: Apis mellifera similar to Sc2 CG10849-PA (LOC725146), mRNA] | 8.14E-01 | -0.16 | 0.01 |
| GB14758-RA [PREDICTED: Apis mellifera similar to heat shock protein 90-alpha, transcript variant 1 (LOC408928), mRNA] | 8.16E-01 | -0.07 | 0.66 |
| GB14012-RA [PREDICTED: Apis mellifera similar to CG9090-PA, transcript variant 1 (LOC413517), mRNA] | 8.19E-01 | -0.03 | 0.01 |
| GB10939-RA [PREDICTED: Apis mellifera similar to Tropomyosin 2 CG4843-PB, isoform B (LOC408414), mRNA] | 8.21E-01 | -0.18 | -0.06 |
| GB10514-RA [PREDICTED: Apis mellifera similar to Tubulin alpha-1 chain (LOC408388), mRNA] | 8.27E-01 | 0.09 | 0.02 |
| GB13236-RA [PREDICTED: Apis mellifera similar to CG5958-PA (LOC552447), mRNA] | 8.33E-01 | -0.03 | -0.21 |
| GB10576-RA [PREDICTED: Apis mellifera similar to CG33519-PB, transcript variant 1 (LOC408830), mRNA] | 8.34E-01 | -0.05 | -0.38 |
| GB19359-RA [PREDICTED: Apis mellifera similar to Clathrin heavy chain CG9012-PA, isoform A, transcript variant 1 (LOC550716), mRNA] | 8.35E-01 | -0.05 | 0.01 |
| GB16412-RA [PREDICTED: Apis mellifera similar to Translationally controlled tumor protein CG4800-PA, transcript variant 1 (LOC411832), mRNA] | 8.37E-01 | -0.10 | -0.24 |
| GB10584-RA [PREDICTED: Apis mellifera similar to glucocerebrosidase precursor, transcript variant 2 (LOC409708), mRNA] | 8.38E-01 | -0.45 | -0.03 |
| GB19425-RA [PREDICTED: Apis mellifera similar to Hsp70/Hsp90 organizing protein homolog CG2720-PA, transcript variant 1 (LOC411002), mRNA] | 8.41E-01 | -0.08 | 0.29 |
| GB18204-RA [PREDICTED: Apis mellifera similar to CG8839-PA, isoform A (LOC727034), partial mRNA] | 8.56E-01 | 0.07 | 0.30 |
| GB12721-RA [PREDICTED: Apis mellifera similar to Pterin-4-alpha-carbinolamine dehydratase 2 (PHS 2) (4-alpha-hydroxy-tetrahydropterin dehydratase 2) (DcoH-like protein DCoHm) (Dimerization cofactor of hepatocyte nuclear factor 1 from muscle) (HNF1-alpha d | 8.64E-01 | -0.05 | 0.37 |
| GB11412-RA [PREDICTED: Apis mellifera similar to CG1443-PA, transcript variant 1 (LOC411983), mRNA] | 8.66E-01 | 0.14 | -1.34 |
| GB10390-RA [PREDICTED: Apis mellifera similar to Proteasome 25kD subunit CG5266-PA (LOC409802), mRNA] | 8.71E-01 | -0.04 | -0.02 |
| GB15039-RA [PREDICTED: Apis mellifera similar to Enolase CG17654-PA, isoform A (LOC552678), partial mRNA] | 8.72E-01 | 0.02 | -0.41 |
| GB15030-RA [PREDICTED: Apis mellifera similar to -Esterase-7 CG1112-PA, isoform A (LOC726134), mRNA] | 8.73E-01 | 0.06 | 0.84 |
| GB15079-RA [PREDICTED: Apis mellifera similar to Glutamate dehydrogenase CG5320-PF, isoform F, transcript variant 1 (LOC409253), mRNA] | 8.75E-01 | -0.10 | 0.38 |
| GB19923-RA [PREDICTED: Apis mellifera similar to Cathepsin L precursor (Cysteine proteinase 1) (LOC552756), mRNA] | 8.79E-01 | -0.05 | 0.21 |
| GB13033-RA [PREDICTED: Apis mellifera similar to CG8258-PA (LOC551436), mRNA] | 8.86E-01 | 0.02 | 0.16 |
| GB10441-RA [PREDICTED: Apis mellifera similar to CG14516-PA, isoform A (LOC551180), partial mRNA] | 9.11E-01 | -0.03 | -0.77 |
| GB10855-RA [PREDICTED: Apis mellifera similar to plasma glutamate carboxypeptidase, transcript variant 1 (LOC410149), mRNA] | 9.12E-01 | -0.07 | -0.03 |
| GB10467-RA [PREDICTED: Apis mellifera similar to aspartate aminotransferase 2 precursor, transcript variant 1 (LOC412675), mRNA] | 9.13E-01 | 0.06 | 0.28 |
| GB20101-RA [PREDICTED: Apis mellifera similar to CG4893-PA, transcript variant 1 (LOC411570), mRNA] | 9.27E-01 | -0.05 | 0.41 |
| GB15718-RA [PREDICTED: Apis mellifera similar to CG14207-PB, isoform B, transcript variant 1 (LOC408875), mRNA] | 9.28E-01 | -0.04 | 0.44 |
| GB16189-RA [PREDICTED: Apis mellifera similar to 26S proteasome non-ATPase regulatory subunit 4 (26S proteasome regulatory subunit S5A) (Multiubiquitin chain-binding protein) (54 kDa subunit of mu particle) (p54) (LOC409609), mRNA] | 9.35E-01 | 0.07 | -0.13 |
| GB19811-RA [Apis mellifera take-out-like carrier protein (JHBP-1), mRNA] | 9.37E-01 | -0.04 | 0.97 |
| GB18764-RA [PREDICTED: Apis mellifera similar to translation elongation factor 1-gamma, transcript variant 2 (LOC551211), mRNA] | 9.39E-01 | 0.02 | -0.01 |
| GB13536-RA [PREDICTED: Apis mellifera similar to CG11963-PA (LOC551958), mRNA] | 9.43E-01 | -0.02 | 0.08 |
| GB17439-RA [PREDICTED: Apis mellifera similar to succinate dehydrogenase complex, subunit A, flavoprotein (Fp), transcript variant 1 (LOC550667), mRNA] | 9.49E-01 | -0.01 | 0.27 |
| GB15989-RA [PREDICTED: Apis mellifera similar to downstream of receptor kinase CG6033-PA, isoform A (LOC550857), mRNA] | 9.51E-01 | 0.02 | 0.18 |
| GB19846-RA [PREDICTED: Apis mellifera similar to CG5255-PA (LOC410894), mRNA] | 9.55E-01 | 0.04 | -1.34 |
| GB12122-RA [PREDICTED: Apis mellifera similar to CG11333-PA (LOC410420), mRNA] | 9.57E-01 | 0.01 | 0.70 |
| GB20070-RA [Apis mellifera alpha-glucosidase (Hbg2), mRNA] | 9.57E-01 | 0.01 | 0.09 |
| GB12607-RA [Apis mellifera alpha-glucosidase (Hbg1), mRNA] | 9.69E-01 | 0.01 | -1.31 |
| GB14191-RA [PREDICTED: Apis mellifera similar to Proteasome subunit beta type 1 (Proteasome 26 kDa subunit) (LOC411695), mRNA] | 9.71E-01 | -0.01 | 0.09 |
| GB19745-RA [Apis mellifera transferrin (Trf), mRNA] | 9.83E-01 | 0.01 | 0.59 |
| GB19444-RA [PREDICTED: Apis mellifera similar to NADPH--cytochrome P450 reductase (CPR) (P450R) (LOC724870), mRNA] | 9.84E-01 | 0.00 | 0.38 |

| | | | |
|---|---|---|---|
| GB10176-RA [PREDICTED: Apis mellifera hypothetical LOC552071 (LOC552071), mRNA] | 9.85E-01 | 0.01 | 0.24 |
| GB20037-RA [PREDICTED: Apis mellifera similar to CG4666-PA (LOC552211), mRNA] | 9.85E-01 | 0.01 | -0.08 |
| GB18844-RA [PREDICTED: Apis mellifera similar to Glutamate oxaloacetate transaminase 1 CG8430-PA, isoform A (LOC726943), partial mRNA] | 9.87E-01 | 0.01 | 0.74 |
| GB11587-RA [PREDICTED: Apis mellifera similar to proteasome (prosome, macropain) 26S subunit, non-ATPase, 2 (LOC409475), mRNA] | 9.89E-01 | 0.00 | -0.03 |
| GB10561-RA [PREDICTED: Apis mellifera similar to CG8351-PA, transcript variant 1 (LOC550694), mRNA] | 9.93E-01 | 0.00 | 0.31 |
| GB12420-RA [PREDICTED: Apis mellifera similar to CG1129-PA, isoform A (LOC409329), mRNA] | 9.93E-01 | 0.00 | 0.42 |
| GB14642-RA [PREDICTED: Apis mellifera similar to sallimus CG1915-PC, isoform C (LOC551181), mRNA] | 9.96E-01 | 0.00 | -0.41 |

Table S8. Gene Ontology terms with a directional bias toward *vg* RNAi (V)>control (C)

| Term | *P*-value | Category V>C | Category C>V | Total V>C | Total C>V |
|---|---|---|---|---|---|
| GO:0019538~protein metabolic process | 4.16E–06 | 125 | 91 | 336 | 418 |
| GO:0044267~cellular protein metabolic process | 3.05E–05 | 116 | 87 | 336 | 418 |
| GO:0043170~macromolecule metabolic process | 3.35E–05 | 185 | 167 | 336 | 418 |
| GO:0044260~cellular macromolecule metabolic process | 7.65E–05 | 118 | 92 | 336 | 418 |
| GO:0016043~cellular component organization and biogenesis | 9.20E–04 | 112 | 94 | 336 | 418 |
| GO:0033036~macromolecule localization | 1.98E–03 | 43 | 25 | 336 | 418 |
| GO:0022607~cellular component assembly | 2.07E–03 | 34 | 17 | 336 | 418 |
| GO:0043283~biopolymer metabolic process | 2.17E–03 | 100 | 84 | 336 | 418 |
| GO:0010467~gene expression | 2.29E–03 | 87 | 70 | 336 | 418 |
| GO:0008104~protein localization | 2.74E–03 | 40 | 23 | 336 | 418 |
| GO:0006911~phagocytosis, engulfment | 3.55E–03 | 22 | 8 | 336 | 418 |
| GO:0065003~macromolecular complex assembly | 5.81E–03 | 27 | 13 | 336 | 418 |
| GO:0045184~establishment of protein localization | 8.13E–03 | 35 | 21 | 336 | 418 |
| GO:0009987~cellular process | 8.61E–03 | 297 | 342 | 336 | 418 |
| GO:0016070~RNA metabolic process | 8.95E–03 | 51 | 37 | 336 | 418 |
| GO:0006909~phagocytosis | 1.13E–02 | 22 | 10 | 336 | 418 |
| GO:0015031~protein transport | 1.17E–02 | 34 | 21 | 336 | 418 |
| GO:0046907~intracellular transport | 1.23E–02 | 38 | 25 | 336 | 418 |
| GO:0006996~organelle organization and biogenesis | 1.60E–02 | 51 | 39 | 336 | 418 |
| GO:0016311~dephosphorylation | 1.63E–02 | 8 | 0 | 336 | 418 |
| GO:0006508~proteolysis | 1.64E–02 | 32 | 20 | 336 | 418 |
| GO:0009059~macromolecule biosynthetic process | 1.68E–02 | 46 | 34 | 336 | 418 |
| GO:0022618~protein–RNA complex assembly | 1.76E–02 | 11 | 2 | 336 | 418 |
| GO:0006413~translational initiation | 1.76E–02 | 11 | 2 | 336 | 418 |
| GO:0007292~female gamete generation | 1.93E–02 | 23 | 12 | 336 | 418 |
| GO:0048477~oogenesis | 1.93E–02 | 23 | 12 | 336 | 418 |
| GO:0006886~intracellular protein transport | 2.30E–02 | 30 | 19 | 336 | 418 |
| GO:0006605~protein targeting | 2.65E–02 | 20 | 10 | 336 | 418 |
| GO:0051641~cellular localization | 3.02E–02 | 43 | 33 | 336 | 418 |
| GO:0006412~translation | 3.05E–02 | 42 | 32 | 336 | 418 |
| GO:0044237~cellular metabolic process | 3.09E–02 | 227 | 253 | 336 | 418 |
| GO:0065007~biological regulation | 3.21E–02 | 89 | 84 | 336 | 418 |
| GO:0019953~sexual reproduction | 3.23E–02 | 29 | 19 | 336 | 418 |
| GO:0010324~membrane invagination | 3.23E–02 | 29 | 19 | 336 | 418 |
| GO:0006897~endocytosis | 3.23E–02 | 29 | 19 | 336 | 418 |
| GO:0007276~gamete generation | 3.23E–02 | 29 | 19 | 336 | 418 |
| GO:0000003~reproduction | 3.25E–02 | 33 | 23 | 336 | 418 |
| GO:0016044~membrane organization and biogenesis | 3.25E–02 | 32 | 22 | 336 | 418 |
| GO:0051704~multi-organism process | 4.24E–02 | 12 | 4 | 336 | 418 |
| GO:0022403~cell cycle phase | 4.65E–02 | 13 | 5 | 336 | 418 |
| GO:0022613~ribonucleoprotein complex biogenesis and assembly | 4.99E–02 | 14 | 6 | 336 | 418 |
| GO:0051649~establishment of cellular localization | 5.18E–02 | 41 | 33 | 336 | 418 |
| GO:0048592~eye morphogenesis | 5.27E–02 | 15 | 7 | 336 | 418 |
| GO:0016192~vesicle-mediated transport | 5.42E–02 | 38 | 30 | 336 | 418 |
| GO:0006366~transcription from RNA polymerase II promoter | 5.68E–02 | 17 | 9 | 336 | 418 |
| GO:0007389~pattern specification process | 6.02E–02 | 20 | 12 | 336 | 418 |
| GO:0006470~protein amino acid dephosphorylation | 6.46E–02 | 6 | 0 | 336 | 418 |
| GO:0050789~regulation of biological process | 6.77E–02 | 80 | 78 | 336 | 418 |
| GO:0000279~M phase | 7.32E–02 | 12 | 5 | 336 | 418 |
| GO:0006457~protein folding | 7.94E–02 | 14 | 7 | 336 | 418 |
| GO:0001745~compound eye morphogenesis | 7.94E–02 | 14 | 7 | 336 | 418 |
| GO:0048468~cell development | 8.01E–02 | 42 | 36 | 336 | 418 |
| GO:0051276~chromosome organization and biogenesis | 8.29E–02 | 16 | 9 | 336 | 418 |
| GO:0006139~nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | 8.97E–02 | 75 | 74 | 336 | 418 |
| GO:0044238~primary metabolic process | 9.27E–02 | 216 | 247 | 336 | 418 |

Table S9. Gene Ontology terms with directional bias toward control (C)>*vg* RNAi (V)

| Term | *P*-value | Category V>C | Category C>V | Total V>C | Total C>V |
|---|---|---|---|---|---|
| GO:0006732~coenzyme metabolic process | 1.71E-04 | 4 | 30 | 335 | 419 |
| GO:0006629~lipid metabolic process | 4.83E-04 | 13 | 46 | 335 | 419 |
| GO:0051186~cofactor metabolic process | 7.85E-04 | 6 | 31 | 335 | 419 |
| GO:0044255~cellular lipid metabolic process | 1.19E-03 | 9 | 36 | 335 | 419 |
| GO:0044262~cellular carbohydrate metabolic process | 2.62E-03 | 5 | 26 | 335 | 419 |
| GO:0005975~carbohydrate metabolic process | 3.56E-03 | 14 | 42 | 335 | 419 |
| GO:0009056~catabolic process | 8.68E-03 | 20 | 49 | 335 | 419 |
| GO:0044248~cellular catabolic process | 1.41E-02 | 18 | 44 | 335 | 419 |
| GO:0051188~cofactor biosynthetic process | 2.91E-02 | 2 | 14 | 335 | 419 |
| GO:0009108~coenzyme biosynthetic process | 2.91E-02 | 2 | 14 | 335 | 419 |
| GO:0044275~cellular carbohydrate catabolic process | 2.91E-02 | 2 | 14 | 335 | 419 |
| GO:0008610~lipid biosynthetic process | 2.91E-02 | 2 | 14 | 335 | 419 |
| GO:0006091~generation of precursor metabolites and energy | 3.93E-02 | 18 | 40 | 335 | 419 |
| GO:0009064~glutamine family amino acid metabolic process | 3.98E-02 | 0 | 9 | 335 | 419 |
| GO:0032787~monocarboxylic acid metabolic process | 4.03E-02 | 4 | 17 | 335 | 419 |
| GO:0016052~carbohydrate catabolic process | 4.25E-02 | 3 | 15 | 335 | 419 |
| GO:0006096~glycolysis | 4.37E-02 | 1 | 11 | 335 | 419 |
| GO:0006066~alcohol metabolic process | 4.40E-02 | 7 | 22 | 335 | 419 |
| GO:0046164~alcohol catabolic process | 4.40E-02 | 2 | 13 | 335 | 419 |
| GO:0046365~monosaccharide catabolic process | 4.40E-02 | 2 | 13 | 335 | 419 |
| GO:0019320~hexose catabolic process | 4.40E-02 | 2 | 13 | 335 | 419 |
| GO:0006007~glucose catabolic process | 4.40E-02 | 2 | 13 | 335 | 419 |
| GO:0006006~glucose metabolic process | 4.40E-02 | 2 | 13 | 335 | 419 |
| GO:0044265~cellular macromolecule catabolic process | 5.39E-02 | 8 | 23 | 335 | 419 |
| GO:0003008~system process | 5.58E-02 | 17 | 37 | 335 | 419 |
| GO:0016310~phosphorylation | 7.02E-02 | 17 | 36 | 335 | 419 |
| GO:0005996~monosaccharide metabolic process | 8.07E-02 | 4 | 15 | 335 | 419 |
| GO:0019318~hexose metabolic process | 8.07E-02 | 4 | 15 | 335 | 419 |
| GO:0009057~macromolecule catabolic process | 8.69E-02 | 11 | 26 | 335 | 419 |
| GO:0006936~muscle contraction | 9.63E-02 | 2 | 11 | 335 | 419 |
| GO:0030534~adult behavior | 9.63E-02 | 2 | 11 | 335 | 419 |
| GO:0003012~muscle system process | 9.63E-02 | 2 | 11 | 335 | 419 |

Table S10. Gene Ontology terms with directional bias toward control (C)>QMP (Q)

| Term | *P*-value | Category C>Q | Category Q>C | Total C>Q | Total Q>C |
|---|---|---|---|---|---|
| GO:0006520~amino acid metabolic process | 3.27E–03 | 12 | 1 | 50 | 56 |
| GO:0006519~amino acid and derivative metabolic process | 3.27E–03 | 12 | 1 | 50 | 56 |
| GO:0006807~nitrogen compound metabolic process | 1.23E–02 | 13 | 3 | 50 | 56 |
| GO:0009309~amine biosynthetic process | 1.77E–02 | 8 | 0 | 50 | 56 |
| GO:0044271~nitrogen compound biosynthetic process | 1.77E–02 | 8 | 0 | 50 | 56 |
| GO:0008652~amino acid biosynthetic process | 1.77E–02 | 8 | 0 | 50 | 56 |
| GO:0009308~amine metabolic process | 2.26E–02 | 12 | 3 | 50 | 56 |
| GO:0006082~organic acid metabolic process | 2.63E–02 | 13 | 4 | 50 | 56 |
| GO:0019752~carboxylic acid metabolic process | 2.63E–02 | 13 | 4 | 50 | 56 |
| GO:0009064~glutamine family amino acid metabolic process | 7.19E–02 | 6 | 0 | 50 | 56 |

Table S11. Gene Ontology terms with directional bias toward QMP (Q)>control (C)

| Term | *P* Value | Category C>Q | Category Q>C | Total C>Q | Total Q>C |
|---|---|---|---|---|---|
| GO:0044260~cellular macromolecule metabolic process | 9.52E-06 | 3 | 26 | 50 | 56 |
| GO:0044267~cellular protein metabolic process | 9.52E-06 | 3 | 26 | 50 | 56 |
| GO:0019538~protein metabolic process | 9.52E-06 | 3 | 26 | 50 | 56 |
| GO:0009057~macromolecule catabolic process | 2.97E-03 | 0 | 12 | 50 | 56 |
| GO:0044265~cellular macromolecule catabolic process | 5.80E-03 | 0 | 11 | 50 | 56 |
| GO:0006508~proteolysis | 9.87E-03 | 2 | 14 | 50 | 56 |
| GO:0009987~cellular process | 1.03E-02 | 33 | 49 | 50 | 56 |
| GO:0043285~biopolymer catabolic process | 1.11E-02 | 0 | 10 | 50 | 56 |
| GO:0030163~protein catabolic process | 1.11E-02 | 0 | 10 | 50 | 56 |
| GO:0043170~macromolecule metabolic process | 1.23E-02 | 14 | 30 | 50 | 56 |
| GO:0044257~cellular protein catabolic process | 2.08E-02 | 0 | 9 | 50 | 56 |
| GO:0019941~modification-dependent protein catabolic process | 2.08E-02 | 0 | 9 | 50 | 56 |
| GO:0006511~ubiquitin-dependent protein catabolic process | 2.08E-02 | 0 | 9 | 50 | 56 |
| GO:0051603~proteolysis involved in cellular protein catabolic process | 2.08E-02 | 0 | 9 | 50 | 56 |
| GO:0043632~modification-dependent macromolecule catabolic process | 2.08E-02 | 0 | 9 | 50 | 56 |
| GO:0043283~biopolymer metabolic process | 2.91E-02 | 6 | 18 | 50 | 56 |
| GO:0043412~biopolymer modification | 5.98E-02 | 1 | 9 | 50 | 56 |
| GO:0006464~protein modification process | 5.98E-02 | 1 | 9 | 50 | 56 |

Table S12. Quantitative proteomic analyses of protein abundance in the hemolymph of foragers and nurses

| Description | *P*-value | logFC protein (F-N) | logFC RNA (F-N) |
|---|---|---|---|
| GB12364-RA [PREDICTED: Apis mellifera similar to fumarylacetoacetate hydrolase domain containing 2A, transcript variant 2 (LOC410635), mRNA] | 1.49E-03 | 1.12 | 0.17 |
| GB19860-RA [PREDICTED: Apis mellifera similar to Heat shock protein cognate 5 CG8542-PA (LOC408605), mRNA] | 1.61E-03 | 1.54 | 0.24 |
| GB12113-RA [PREDICTED: Apis mellifera similar to porin CG6647-PA, isoform A (LOC551325), mRNA] | 3.39E-03 | 0.71 | NA |
| GB16443-RA [PREDICTED: Apis mellifera similar to lethal (1) G0334 CG7010-PD, isoform D, transcript variant 1 (LOC551103), mRNA] | 4.54E-03 | 1.61 | -0.09 |
| GB12526-RA [PREDICTED: Apis mellifera similar to lethal (2) k05713 CG8256-PC, isoform C (LOC551904), mRNA] | 4.95E-03 | 1.84 | 0.69 |
| GB16464-RA [PREDICTED: Apis mellifera similar to mitochondrial malate dehydrogenase precursor, transcript variant 1 (LOC408950), mRNA] | 5.00E-03 | 1.57 | NA |
| GB15172-RA [PREDICTED: Apis mellifera similar to lethal (1) G0255 CG4094-PA, isoform A (LOC724321), mRNA] | 7.70E-03 | 2.03 | 0.06 |
| GB15039-RA [PREDICTED: Apis mellifera similar to Enolase CG17654-PA, isoform A (LOC552678), partial mRNA] | 7.77E-03 | 0.71 | 0.10 |
| GB20012-RA [PREDICTED: Apis mellifera similar to CG10664-PA, isoform A (LOC412396), mRNA] | 9.14E-03 | 1.29 | 0.12 |
| GB16485-RA [PREDICTED: Apis mellifera similar to ATP synthase D chain, mitochondrial (LOC410557), mRNA] | 9.24E-03 | 1.54 | 0.39 |
| GB18363-RA [Apis mellifera odorant binding protein 13 (Obp13), mRNA] | 9.40E-03 | -3.56 | -2.13 |
| GB15252-RA [PREDICTED: Apis mellifera similar to CG5548-PA (LOC724827), mRNA] | 9.71E-03 | 1.38 | -0.06 |
| GB14247-RA [PREDICTED: Apis mellifera similar to easter CG4920-PA (LOC726256), mRNA] | 1.07E-02 | -1.41 | 1.46 |
| GB16568-RA [PREDICTED: Apis mellifera similar to CG11015-PA (LOC552610), mRNA] | 1.14E-02 | 1.92 | 0.18 |
| GB16927-RA [PREDICTED: Apis mellifera hypothetical LOC408280 (LOC408280), mRNA] | 1.25E-02 | 1.75 | 2.17 |
| GB19460-RA [PREDICTED: Apis mellifera similar to Aldolase CG6058-PF, isoform F (LOC550785), mRNA] | 1.26E-02 | 1.45 | -0.45 |
| GB19460-RA [PREDICTED: Apis mellifera similar to Aldolase CG6058-PF, isoform F (LOC550785), mRNA] | 1.26E-02 | 1.45 | -0.46 |
| GB11655-RA [PREDICTED: Apis mellifera similar to Succinyl coenzyme A synthetase subunit CG1065-PA (LOC551403), mRNA] | 1.30E-02 | 2.44 | -0.21 |
| GB14791-RA [PREDICTED: Apis mellifera similar to bellwether CG3612-PA, transcript variant 1 (LOC409114), mRNA] | 1.42E-02 | 1.69 | 0.02 |
| GB17538-RA [Apis mellifera hymenoptaecin (LOC406142), mRNA] | 1.45E-02 | 1.74 | 2.35 |
| GB13223-RA [PREDICTED: Apis mellifera similar to Ferritin 2 light chain homologue CG1469-PA, isoform A (LOC551684), mRNA] | 1.53E-02 | -2.28 | -0.01 |
| GB14361-RA [PREDICTED: Apis mellifera similar to Larval serum protein 2 CG6806-PA (LOC551648), mRNA] | 1.64E-02 | -2.27 | -4.22 |
| GB18955-RA [PREDICTED: Apis mellifera similar to Phospholipid hydroperoxide glutathione peroxidase, mitochondrial precursor (PHGPx) (GPX-4) (LOC726269), mRNA] | 1.96E-02 | -2.95 | 0.17 |
| GB13073-RA [PREDICTED: Apis mellifera similar to CG5214-PA (LOC409155), mRNA] | 1.99E-02 | 1.84 | 0.14 |
| GB13928-RA [PREDICTED: Apis mellifera similar to lethal (2) 35Di CG13240-PA, isoform A (LOC725712), mRNA] | 2.04E-02 | 2.24 | 0.06 |
| GB17626-RA [PREDICTED: Apis mellifera similar to CG7430-PA, transcript variant 1 (LOC551039), mRNA] | 2.34E-02 | 1.54 | 0.03 |
| GB16552-RA [PREDICTED: Apis mellifera similar to CG9796-PA (LOC552600), mRNA] | 2.43E-02 | -3.07 | -3.28 |
| GB13320-RA [PREDICTED: Apis mellifera hypothetical LOC551541 (LOC551541), mRNA] | 2.52E-02 | 1.93 | 0.24 |
| GB10717-RA [PREDICTED: Apis mellifera similar to Muscle protein 20 CG4696-PA, isoform A (LOC408972), mRNA] | 2.54E-02 | 0.53 | 0.14 |
| GB10972-RA [PREDICTED: Apis mellifera thioredoxin peroxidase, transcript variant 1 (Tpx-3), mRNA] | 2.59E-02 | 1.90 | -0.16 |
| GB13508-RA [PREDICTED: Apis mellifera similar to ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (LOC411183), mRNA] | 2.73E-02 | 2.14 | 0.04 |
| GB15716-RA [PREDICTED: Apis mellifera similar to CG5028-PA (LOC410396), mRNA] | 2.78E-02 | 2.23 | 0.11 |
| GB15696-RA [PREDICTED: Apis mellifera hypothetical protein LOC726734 (LOC726734), mRNA] | 2.85E-02 | 1.63 | 1.68 |
| GB12573-RA [PREDICTED: Apis mellifera similar to lethal (1) G0030 CG3861-PA, isoform A (LOC410059), mRNA] | 2.96E-02 | 1.95 | 0.36 |
| GB12855-RA [PREDICTED: Apis mellifera similar to Neural conserved at 73EF CG11661-PA, isoform A, transcript variant 1 (LOC408286), mRNA] | 3.16E-02 | 2.28 | 0.29 |
| GB14645-RA [PREDICTED: Apis mellifera similar to CG6124-PA (LOC724421), mRNA] | 3.35E-02 | 1.30 | 0.41 |
| GB13536-RA [PREDICTED: Apis mellifera similar to CG11963-PA (LOC551958), mRNA] | 3.59E-02 | 2.19 | 0.29 |
| GB11846-RA [PREDICTED: Apis mellifera similar to Neuroglian CG1634-PA, isoform A (LOC411829), mRNA] | 3.61E-02 | -1.34 | -0.17 |
| GB17852-RA [PREDICTED: Apis mellifera similar to Ect3 CG3132-PA (LOC725756), mRNA] | 3.86E-02 | -1.42 | -0.38 |
| GB19745-RA [Apis mellifera transferrin (Trf), mRNA] | 4.20E-02 | -1.13 | -1.00 |
| GB19422-RA [PREDICTED: Apis mellifera similar to lethal (1) G0156 CG12233-PA, isoform A (LOC409292), mRNA] | 4.49E-02 | 1.36 | 0.10 |
| GB11431-RA [PREDICTED: Apis mellifera similar to Nucleosome remodeling factor – 38kD CG4634-PA (LOC409774), mRNA] | 4.49E-02 | 1.23 | 0.01 |
| GB14607-RA [Apis mellifera short-chain dehydrogenase/reductase (LOC406147), mRNA] | 4.64E-02 | -3.30 | 0.90 |
| GB10069-RA [PREDICTED: Apis mellifera similar to Thor CG8846-PA (LOC725039), mRNA] | 4.81E-02 | 0.67 | -0.13 |
| GB12488-RA [PREDICTED: Apis mellifera similar to Aconitase CG9244-PB (LOC408446), mRNA] | 5.25E-02 | 1.49 | 0.27 |
| GB10695-RA [PREDICTED: Apis mellifera similar to Pyruvate kinase CG7070-PB, isoform B (LOC552007), mRNA] | 5.49E-02 | 1.37 | 0.26 |
| GB14798-RA [PREDICTED: Apis mellifera similar to Glyceraldehyde 3 phosphate dehydrogenase 1 CG12055-PA, isoform A, transcript variant 2 (LOC410122), mRNA] | 5.63E-02 | 1.64 | 0.17 |
| GB14710-RA [PREDICTED: Apis mellifera similar to CG4572-PB, isoform B (LOC410451), mRNA] | 5.70E-02 | -0.94 | -0.35 |
| GB16494-RA [PREDICTED: Apis mellifera similar to ATPase coupling factor 6 CG4412-PA (LOC726120), mRNA] | 5.94E-02 | 2.17 | 0.25 |
| GB17699-RA [PREDICTED: Apis mellifera similar to CG8680-PA (LOC412328), mRNA] | 6.05E-02 | 2.26 | 0.14 |

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| GB11056-RA [PREDICTED: Apis mellifera similar to Phosphoglycerate kinase, transcript variant 1 (LOC411576), mRNA] | 6.07E-02 | 1.41 | 0.24 |
| GB13999-RA [Apis mellifera vitellogenin (Vg), mRNA] | 6.15E-02 | -2.07 | -3.12 |
| GB16459-RA [Apis mellifera major royal jelly protein 3 (Mrjp3), mRNA] | 6.61E-02 | -1.91 | 0.14 |
| GB19501-RA [PREDICTED: Apis mellifera similar to CG5023-PA (LOC408532), mRNA] | 6.61E-02 | 0.77 | 0.47 |
| GB14490-RA [PREDICTED: Apis mellifera similar to ciboulot CG4944-PB, isoform B (LOC551528), mRNA] | 6.81E-02 | -2.21 | -0.42 |
| GB17499-RA [Apis mellifera ADP/ATP translocase (Ant), mRNA] | 6.91E-02 | 1.49 | 0.14 |
| GB11022-RA [Apis mellifera major royal jelly protein 7 (Mrjp7), mRNA] | 6.95E-02 | -2.13 | -0.23 |
| GB10514-RA [PREDICTED: Apis mellifera similar to Tubulin alpha-1 chain (LOC408388), mRNA] | 7.11E-02 | -0.73 | 0.24 |
| GB10869-RA [Apis mellifera hexamerin 70b (LOC406117), mRNA] | 7.72E-02 | -3.49 | 0.10 |
| GB13596-RA [PREDICTED: Apis mellifera similar to ATP synthase- CG11154-PA, isoform A (LOC551766), mRNA] | 7.77E-02 | 1.35 | 0.12 |
| GB17503-RA [PREDICTED: Apis mellifera similar to CG8993-PA (LOC410120), mRNA] | 7.79E-02 | 1.02 | -0.01 |
| GB18917-RA [PREDICTED: Apis mellifera similar to Cofilin/actin-depolymerizing factor homolog (Protein D61) (Protein twinstar) (LOC725718), mRNA] | 8.16E-02 | -1.07 | 0.34 |
| GB16445-RA [PREDICTED: Apis mellifera similar to CG12859-PA (LOC725315), mRNA] | 8.45E-02 | 0.99 | 0.25 |
| GB19380-RA [PREDICTED: Apis mellifera similar to thioredoxin peroxidase 1 CG1633-PA, isoform A, transcript variant 1 (LOC409954), mRNA] | 8.48E-02 | 0.80 | 0.36 |
| GB10139-RA [PREDICTED: Apis mellifera similar to Glutamine synthetase 2 CG1743-PC, isoform C (LOC410066), mRNA] | 8.76E-02 | 0.53 | -0.10 |
| GB19293-RA [PREDICTED: Apis mellifera mitochondrial cytochrome C (CytC), mRNA] | 8.77E-02 | 1.18 | 1.21 |
| GB17444-RA [PREDICTED: Apis mellifera similar to CG32521-PA, isoform A (LOC725926), mRNA] | 8.82E-02 | 0.19 | 0.97 |
| GB10836-RA [PREDICTED: Apis mellifera similar to Hsc70Cb CG6603-PA, isoform A, transcript variant 1 (LOC408706), mRNA] | 8.95E-02 | 0.44 | 0.36 |
| GB10284-RA [PREDICTED: Apis mellifera similar to CG6463-PA (LOC413014), mRNA] | 9.10E-02 | 1.79 | 0.15 |
| GB10855-RA [PREDICTED: Apis mellifera similar to plasma glutamate carboxypeptidase, transcript variant 1 (LOC410149), mRNA] | 9.12E-02 | -1.06 | 0.11 |
| GB18969-RA [PREDICTED: Apis mellifera similar to 60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 kDa chaperonin) (CPN60) (Heat shock protein 60) (HSP-60) (Mitochondrial matrix protein P1) (LOC409384), mRNA] | 9.51E-02 | 0.75 | -0.15 |
| GB16153-RA [PREDICTED: Apis mellifera similar to Papilin CG33103-PB, isoform B, transcript variant 1 (LOC413021), mRNA] | 1.01E-01 | -0.67 | -0.05 |
| GB11059-RA [PREDICTED: Apis mellifera similar to Retinoid- and fatty-acid binding protein CG11064-PA, transcript variant 1 (LOC408961), mRNA] | 1.03E-01 | -1.25 | NA |
| GB11892-RA [PREDICTED: Apis mellifera similar to Glycogen phosphorylase, transcript variant 2 (LOC409267), mRNA] | 1.04E-01 | 1.38 | -0.07 |
| GB12841-RA [PREDICTED: Apis mellifera similar to CG7580-PA (LOC726747), mRNA] | 1.05E-01 | 2.26 | 0.05 |
| GB12375-RA [PREDICTED: Apis mellifera similar to Chd64 CG14996-PB (LOC408572), mRNA] | 1.05E-01 | -0.54 | 0.23 |
| GB17056-RA [PREDICTED: Apis mellifera similar to Cyclophilin 1 CG9916-PA (LOC409890), mRNA] | 1.06E-01 | -0.70 | 0.11 |
| GB17056-RA [PREDICTED: Apis mellifera similar to Cyclophilin 1 CG9916-PA (LOC409890), mRNA] | 1.06E-01 | -0.70 | -0.09 |
| [Antisense] GB17056-RA [PREDICTED: Apis mellifera similar to Cyclophilin 1 CG9916-PA (LOC409890), mRNA] | 1.06E-01 | -0.70 | -0.15 |
| GB13279-RA [PREDICTED: Apis mellifera similar to Tropomyosin-2 (Tropomyosin I) (LOC413204), mRNA] | 1.07E-01 | 1.41 | NA |
| GB10708-RA [PREDICTED: Apis mellifera hypothetical LOC408807 (LOC408807), mRNA] | 1.08E-01 | 1.34 | 1.89 |
| GB18819-RA [Apis mellifera antennal-specific protein 3c precursor (Asp3c), mRNA] | 1.10E-01 | -2.28 | -0.85 |
| GB19935-RA [PREDICTED: Apis mellifera similar to CG3609-PA (LOC552024), mRNA] | 1.10E-01 | -1.87 | -2.17 |
| GB11768-RA [Apis mellifera major royal jelly protein 4 (Mrjp4), mRNA] | 1.10E-01 | -2.87 | -0.54 |
| GB11768-RA [Apis mellifera major royal jelly protein 4 (Mrjp4), mRNA] | 1.10E-01 | -2.87 | -0.04 |
| GB19030-RA [PREDICTED: Apis mellifera similar to CG10638-PA, isoform A, transcript variant 1 (LOC552018), mRNA] | 1.18E-01 | 0.65 | 0.69 |
| GB14888-RA [Apis mellifera major royal jelly protein 1 (Mrjp1), mRNA] | 1.20E-01 | -1.86 | NA |
| GB10973-RA [Apis mellifera arginine kinase (Argk), mRNA] | 1.21E-01 | -0.55 | -0.07 |
| GB12700-RA [PREDICTED: Apis mellifera similar to Histone H1 (LOC725238), mRNA] | 1.24E-01 | -0.47 | 0.10 |
| GB16246-RA [Apis mellifera major royal jelly protein 2 (Mrjp2), mRNA] | 1.25E-01 | -2.32 | 0.61 |
| GB16246-RA [Apis mellifera major royal jelly protein 2 (Mrjp2), mRNA] | 1.25E-01 | -2.32 | 0.28 |
| GB11461-RA [PREDICTED: Apis mellifera similar to UGP CG4347-PA, isoform A, transcript variant 1 (LOC412069), mRNA] | 1.25E-01 | 0.80 | 0.58 |
| GB11983-RA [PREDICTED: Apis mellifera similar to Angiotensin converting enzyme CG8827-PA, isoform A (LOC410074), mRNA] | 1.27E-01 | -0.67 | 0.15 |
| GB12495-RA [PREDICTED: Apis mellifera hypothetical LOC552459 (LOC552459), mRNA] | 1.27E-01 | 1.33 | 1.53 |
| GB10275-RA [PREDICTED: Apis mellifera similar to –Tubulin at 56D CG9277-PB, isoform B (LOC408782), mRNA] | 1.45E-01 | -0.46 | 0.38 |
| GB15044-RA [PREDICTED: Apis mellifera similar to CG6180-PA, transcript variant 1 (LOC408516), mRNA] | 1.53E-01 | -0.25 | -0.58 |
| GB20014-RA [PREDICTED: Apis mellifera similar to Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic (GPD-C) (GPDH-C) (LOC551955), partial mRNA] | 1.56E-01 | 1.41 | -0.06 |
| GB17439-RA [PREDICTED: Apis mellifera similar to succinate dehydrogenase complex, subunit A, flavoprotein (Fp), transcript variant 1 (LOC550667), mRNA] | 1.60E-01 | 1.25 | 0.00 |
| GB19068-RA [PREDICTED: Apis mellifera similar to Lysosomal Pro-X carboxypeptidase precursor (Prolylcarboxypeptidase) (PRCP) (Proline carboxypeptidase) (Angiotensinase C) (Lysosomal carboxypeptidase C) (LOC551273), mRNA] | 1.61E-01 | -1.64 | -0.24 |
| GB10133-RA [PREDICTED: Apis mellifera CuZn superoxide dismutase, transcript variant 1 (Sod1), mRNA] | 1.63E-01 | 0.80 | -0.10 |
| GB14261-RA [PREDICTED: Apis mellifera hypothetical protein LOC724386 (LOC724386), mRNA] | 1.63E-01 | -2.04 | -1.52 |
| GB10282-RA [PREDICTED: Apis mellifera similar to Adenylate kinase-2 CG3140-PA (LOC551523), mRNA] | 1.70E-01 | 1.51 | -0.05 |
| GB19503-RA [PREDICTED: Apis mellifera similar to heat shock protein 8, transcript variant 1 (LOC410620), mRNA] | 1.71E-01 | 1.29 | 0.04 |
| GB14832-RA [PREDICTED: Apis mellifera similar to Succinate dehydrogenase B CG3283-PA (LOC551169), | 1.73E-01 | 1.63 | 0.10 |

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| mRNA] | | | |
| GB11658-RA [PREDICTED: Apis mellifera hypothetical LOC408608 (LOC408608), mRNA] | 1.73E-01 | 1.91 | 0.05 |
| GB13365-RA [PREDICTED: Apis mellifera similar to CG17292-PA, isoform A (LOC727193), partial mRNA] | 1.74E-01 | 1.67 | -1.20 |
| GB15079-RA [PREDICTED: Apis mellifera similar to Glutamate dehydrogenase CG5320-PF, isoform F, transcript variant 1 (LOC409253), mRNA] | 1.95E-01 | 0.94 | -0.21 |
| GB19509-RA [PREDICTED: Apis mellifera similar to SRY interacting protein 1 CG10939-PA (LOC413207), mRNA] | 2.07E-01 | 0.78 | 0.21 |
| GB15052-RA [PREDICTED: Apis mellifera similar to Phosphoglyceromutase CG1721-PA, isoform A (LOC552736), mRNA] | 2.09E-01 | 1.03 | 0.24 |
| GB15629-RA [PREDICTED: Apis mellifera similar to ATP synthase O subunit, mitochondrial precursor (Oligomycin sensitivity conferral protein) (OSCP) (LOC409236), mRNA] | 2.13E-01 | 1.30 | 0.02 |
| GB20117-RA [PREDICTED: Apis mellifera hypothetical LOC552391 (LOC552391), mRNA] | 2.14E-01 | -1.05 | -0.19 |
| GB19247-RA [PREDICTED: Apis mellifera similar to Elongation factor 2 (EF-2), transcript variant 1 (LOC409167), mRNA] | 2.27E-01 | 0.28 | -0.08 |
| GB12628-RA [PREDICTED: Apis mellifera similar to Oscillin CG6957-PA, isoform A, transcript variant 1 (LOC409520), mRNA] | 2.32E-01 | -0.65 | -0.16 |
| GB18109-RA [PREDICTED: Apis mellifera similar to CG6084-PA, isoform A, transcript variant 1 (LOC551968), mRNA] | 2.37E-01 | 0.78 | 0.26 |
| GB15619-RA [PREDICTED: Apis mellifera similar to CG8036-PB, isoform B, transcript variant 1 (LOC550804), mRNA] | 2.38E-01 | 0.45 | 0.28 |
| GB14284-RA [PREDICTED: Apis mellifera similar to Sorbitol dehydrogenase-2 CG4649-PA (LOC408871), mRNA] | 2.44E-01 | -1.15 | -0.93 |
| GB12951-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG17870-PC, isoform C, transcript variant 1 (LOC408289), mRNA] | 2.50E-01 | -0.55 | 0.21 |
| GB12951-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG17870-PC, isoform C, transcript variant 1 (LOC408289), mRNA] | 2.50E-01 | -0.55 | 0.22 |
| GB12951-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG17870-PC, isoform C, transcript variant 1 (LOC408289), mRNA] | 2.50E-01 | -0.55 | 0.17 |
| GB17035-RA [PREDICTED: Apis mellifera similar to CG15828-PB, isoform B (LOC410793), mRNA] | 2.59E-01 | -1.03 | 0.20 |
| GB10889-RA [PREDICTED: Apis mellifera similar to CG5080-PB, isoform B (LOC413792), partial mRNA] | 2.64E-01 | -0.41 | -0.34 |
| GB13004-RA [PREDICTED: Apis mellifera similar to CG12163-PA, isoform A (LOC408851), mRNA] | 2.65E-01 | -0.67 | 0.11 |
| GB17500-RA [PREDICTED: Apis mellifera hypothetical protein LOC725960 (LOC725960), mRNA] | 2.66E-01 | 0.34 | 0.42 |
| GB11503-RA [PREDICTED: Apis mellifera similar to CG5195-PA (LOC724779), mRNA] | 2.68E-01 | -0.88 | 1.33 |
| GB11040-RA [PREDICTED: Apis mellifera similar to CG14476-PB, isoform B, transcript variant 2 (LOC551205), mRNA] | 2.70E-01 | -1.18 | 0.18 |
| GB10477-RA [PREDICTED: Apis mellifera similar to B-cell receptor-associated protein 37 (LOC551944), mRNA] | 2.73E-01 | 0.68 | -0.38 |
| GB15536-RA [PREDICTED: Apis mellifera similar to CG5397-PA (LOC410187), mRNA] | 2.75E-01 | -1.51 | -0.28 |
| GB15299-RA [Apis mellifera fatty acid binding protein (Fabp), mRNA] | 2.80E-01 | -0.78 | -0.92 |
| GB12384-RA [PREDICTED: Apis mellifera similar to CG10467-PA (LOC552086), mRNA] | 2.89E-01 | -1.07 | -0.97 |
| GB15291-RA [PREDICTED: Apis mellifera similar to ATP synthase gamma chain, mitochondrial precursor (LOC552699), mRNA] | 2.90E-01 | 0.80 | -0.02 |
| GB16429-RA [PREDICTED: Apis mellifera similar to Glucose-6-phosphate isomerase (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (LOC551154), mRNA] | 2.96E-01 | 0.83 | -0.01 |
| GB18404-RA [PREDICTED: Apis mellifera similar to CG2862-PA, isoform A (LOC552670), mRNA] | 2.97E-01 | 0.65 | 0.12 |
| GB12913-RA [PREDICTED: Apis mellifera similar to Vacuolar ATP synthase subunit E (V-ATPase E subunit) (Vacuolar proton pump E subunit) (V-ATPase 28 kDa subunit) (LOC552720), mRNA] | 3.03E-01 | 0.96 | 0.19 |
| GB19582-RA [PREDICTED: Apis mellifera similar to Serine protease inhibitor 5 CG18525-PA, isoform A (LOC413749), mRNA] | 3.06E-01 | -0.58 | 1.00 |
| GB19819-RA [PREDICTED: Apis mellifera similar to Peroxidase CG3477-PA (LOC408953), mRNA] | 3.14E-01 | -1.15 | -0.15 |
| GB10622-RA [Apis mellifera major royal jelly protein 5 (Mrjp5), mRNA] | 3.16E-01 | -0.59 | 1.50 |
| GB19171-RA [PREDICTED: Apis mellifera similar to Vacuolar H+-ATPase 55kD B subunit CG17369-PB, isoform B (LOC551721), mRNA] | 3.30E-01 | 0.98 | 0.41 |
| GB10498-RA [PREDICTED: Apis mellifera similar to Peroxiredoxin 2540 CG11765-PA (LOC551975), mRNA] | 3.33E-01 | -1.52 | -0.28 |
| GB18498-RA [PREDICTED: Apis mellifera enoyl Coenzyme A hydratase, short chain, 1, mitochondrial (Echs1), mRNA] | 3.40E-01 | -0.56 | -0.72 |
| GB16500-RA [PREDICTED: Apis mellifera similar to 40S ribosomal protein S3a (C3 protein) (LOC413296), mRNA] | 3.44E-01 | -1.24 | -0.51 |
| GB19452-RA | 3.45E-01 | -0.35 | -0.98 |
| GB19832-RA [PREDICTED: Apis mellifera similar to CG9514-PA (LOC408603), mRNA] | 3.46E-01 | -0.60 | 0.06 |
| GB16903-RA [PREDICTED: Apis mellifera similar to cathD CG1548-PA (LOC409341), mRNA] | 3.66E-01 | -1.66 | -0.80 |
| GB18381-RA [PREDICTED: Apis mellifera similar to Uev1A CG10640-PA, isoform A, transcript variant 1 (LOC409920), mRNA] | 3.69E-01 | 0.31 | 0.01 |
| GB14758-RA [PREDICTED: Apis mellifera similar to heat shock protein 90-alpha, transcript variant 1 (LOC408928), mRNA] | 3.75E-01 | -0.12 | 0.17 |
| GB17879-RA [PREDICTED: Apis mellifera similar to Peptidoglycan recognition protein SA CG11709-PA (LOC727472), mRNA] | 3.83E-01 | -0.78 | 0.14 |
| GB15919-RA [PREDICTED: Apis mellifera similar to CG9977-PA (LOC551762), mRNA] | 3.87E-01 | 2.16 | -0.08 |
| GB13559-RA [PREDICTED: Apis mellifera similar to CG7460-PB, transcript variant 1 (LOC413478), mRNA] | 3.92E-01 | -0.23 | 1.38 |
| GB19017-RA [Apis mellifera alpha-glucosidase (LOC406131), mRNA] | 3.96E-01 | -0.88 | 0.09 |
| GB15718-RA [PREDICTED: Apis mellifera similar to CG14207-PB, isoform B, transcript variant 1 (LOC408875), mRNA] | 4.03E-01 | 0.36 | 0.10 |
| GB20070-RA [Apis mellifera alpha-glucosidase (Hbg2), mRNA] | 4.40E-01 | -0.42 | 0.71 |
| GB18767-RA [PREDICTED: Apis mellifera similar to CG9372-PA (LOC726126), mRNA] | 4.43E-01 | -0.52 | -0.36 |
| GB12797-RA [PREDICTED: Apis mellifera similar to Trehalose-6-phosphate synthase 1 CG4104-PA (LOC408867), partial mRNA] | 4.55E-01 | 0.20 | 0.61 |
| GB17255-RA [PREDICTED: Apis mellifera similar to lethal (1) G0230 CG2968-PA (LOC552682), mRNA] | 4.63E-01 | 1.96 | 0.03 |

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| GB20017-RA [PREDICTED: Apis mellifera similar to TER94 CG2331-PA, isoform A, transcript variant 1 (LOC409377), mRNA] | 4.71E-01 | -0.20 | 0.04 |
| GB16751-RA [PREDICTED: Apis mellifera similar to lethal (2) 06225 CG6105-PA (LOC726222), mRNA] | 4.88E-01 | 0.58 | 0.16 |
| GB18538-RA | 4.89E-01 | 0.46 | -0.27 |
| GB19961-RA [PREDICTED: Apis mellifera similar to Gram-negative bacteria binding protein 1 CG6895-PA (LOC725832), mRNA] | 4.96E-01 | 1.21 | 1.10 |
| GB10776-RA [PREDICTED: Apis mellifera similar to glycerol-3-phosphate dehydrogenase 1-like (LOC724574), mRNA] | 4.97E-01 | 0.75 | 0.00 |
| GB12951-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG17870-PC, isoform C, transcript variant 1 (LOC408289), mRNA] | 5.13E-01 | 0.43 | 0.21 |
| GB12951-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG17870-PC, isoform C, transcript variant 1 (LOC408289), mRNA] | 5.13E-01 | 0.43 | 0.22 |
| GB12951-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG17870-PC, isoform C, transcript variant 1 (LOC408289), mRNA] | 5.13E-01 | 0.43 | 0.17 |
| GB11665-RA [PREDICTED: Apis mellifera similar to Imaginal disc growth factor 4 CG1780-PA, isoform A (LOC413324), mRNA] | 5.20E-01 | -0.35 | 0.91 |
| GB19387-RA [PREDICTED: Apis mellifera similar to Hexokinase A CG3001-PA, isoform A (LOC551005), mRNA] | 5.23E-01 | 0.66 | 0.23 |
| GB14138-RA [PREDICTED: Apis mellifera putative thioredoxin peroxidase (Gtpx-1), mRNA] | 5.29E-01 | 0.26 | 0.22 |
| GB18313-RA [Apis mellifera prophenoloxidase (LOC406155), mRNA] | 5.30E-01 | -0.27 | -0.51 |
| GB12029-RA [PREDICTED: Apis mellifera similar to CG1532-PA (LOC552722), mRNA] | 5.65E-01 | 0.26 | 0.04 |
| GB10699-RA [PREDICTED: Apis mellifera similar to CG7033-PA, isoform A, transcript variant 1 (LOC409809), mRNA] | 6.01E-01 | 0.47 | -0.06 |
| GB12857-RA [PREDICTED: Apis mellifera similar to CG3009-PA (LOC409277), partial mRNA] | 6.34E-01 | 0.13 | 0.22 |
| GB16882-RA [PREDICTED: Apis mellifera similar to walrus CG8996-PB, isoform B, transcript variant 1 (LOC551710), mRNA] | 6.36E-01 | -0.45 | -0.82 |
| GB16582-RA [PREDICTED: Apis mellifera hypothetical protein LOC725175 (LOC725175), mRNA] | 6.41E-01 | 0.19 | 0.87 |
| GB16448-RA [PREDICTED: Apis mellifera similar to Annexin-B9 (Annexin-9) (Annexin IX), transcript variant 1 (LOC409533), mRNA] | 6.55E-01 | 0.22 | 0.76 |
| GB11150-RA [PREDICTED: Apis mellifera similar to CG3560-PA (LOC551757), mRNA] | 6.60E-01 | 0.44 | 0.11 |
| GB12562-RA [PREDICTED: Apis mellifera similar to CG10513-PA, transcript variant 1 (LOC408421), mRNA] | 6.65E-01 | 0.23 | 0.72 |
| GB14496-RA [PREDICTED: Apis mellifera similar to CG11034-PA (LOC410337), mRNA] | 6.70E-01 | 0.05 | 1.08 |
| GB19297-RA [PREDICTED: Apis mellifera hypothetical protein LOC725074 (LOC725074), mRNA] | 6.89E-01 | 0.60 | 0.90 |
| GB17736-RA [PREDICTED: Apis mellifera similar to Protein disulfide-isomerase precursor (PDI) (LOC726142), partial mRNA] | 7.09E-01 | -0.78 | 0.32 |
| GB14852-RA [PREDICTED: Apis mellifera similar to heat shock protein 8, transcript variant 1 (LOC409418), mRNA] | 7.11E-01 | 0.10 | 0.09 |
| GB10560-RA [Apis mellifera translation elongation factor eEF-1 alpha chain (LOC408385), mRNA] | 7.13E-01 | 0.25 | 0.13 |
| GB14205-RA [PREDICTED: Apis mellifera similar to CG11267-PA (LOC552531), mRNA] | 7.17E-01 | 0.26 | 0.09 |
| GB10989-RA [PREDICTED: Apis mellifera similar to Vacuolar ATP synthase catalytic subunit A, osteoclast isoform (V-ATPase subunit A 2) (Vacuolar proton pump alpha subunit 2) (V-ATPase 69 kDa subunit 2) (Isoform HO68), transcript variant 1 (LOC551093), mRNA | 7.22E-01 | 0.25 | 0.15 |
| GB13821-RA [PREDICTED: Apis mellifera similar to CG3609-PA (LOC412231), mRNA] | 7.26E-01 | 0.09 | -0.54 |
| GB16806-RA [PREDICTED: Apis mellifera similar to CG15040-PA (LOC725387), mRNA] | 7.29E-01 | -0.25 | 0.81 |
| GB12956-RA [PREDICTED: Apis mellifera similar to yippee interacting protein 2 CG4600-PA (LOC408291), mRNA] | 7.61E-01 | 0.13 | -0.81 |
| GB17645-RA [PREDICTED: Apis mellifera similar to CG7453-PB, isoform B (LOC724585), mRNA] | 7.82E-01 | 0.12 | 0.13 |
| GB12538-RA [PREDICTED: Apis mellifera similar to Tequila CG4821-PA, isoform A (LOC724971), mRNA] | 8.50E-01 | -0.08 | 0.74 |
| GB14517-RA [PREDICTED: Apis mellifera similar to Isocitrate dehydrogenase CG7176-PC, isoform C, transcript variant 2 (LOC551276), mRNA] | 8.66E-01 | 0.18 | -0.29 |
| GB11298-RA | 8.70E-01 | -0.19 | 1.35 |
| GB14107-RA [PREDICTED: Apis mellifera similar to germinal histone H4 (LOC726520), mRNA] | 8.76E-01 | -0.19 | -0.62 |
| GB19429-RA [PREDICTED: Apis mellifera similar to CG17838-PE, isoform E (LOC408775), mRNA] | 8.80E-01 | -0.06 | -0.04 |
| GB16889-RA [PREDICTED: Apis mellifera similar to CG4382-PA (LOC409801), mRNA] | 8.88E-01 | -0.07 | 0.15 |
| GB18637-RA [PREDICTED: Apis mellifera similar to F-actin capping protein subunit beta (LOC409581), mRNA] | 8.90E-01 | 0.07 | 0.23 |
| GB15202-RA [PREDICTED: Apis mellifera similar to dj-1 CG1349-PA (LOC551882), mRNA] | 9.01E-01 | 0.05 | 0.29 |
| GB15855-RA [PREDICTED: Apis mellifera similar to thioredoxin-2 CG31884-PA, isoform A (LOC409451), mRNA] | 9.08E-01 | -0.06 | 0.51 |
| GB15662-RA [PREDICTED: Apis mellifera similar to CG10962-PB, isoform B (LOC724721), mRNA] | 9.33E-01 | -0.10 | 0.37 |
| GB15016-RA [PREDICTED: Apis mellifera similar to Heat shock protein cognate 3 CG4147-PA, isoform A (LOC409587), mRNA] | 9.41E-01 | 0.03 | 0.41 |
| GB18727-RA [PREDICTED: Apis mellifera similar to CG5362-PA, transcript variant 1 (LOC411014), mRNA] | 9.44E-01 | 0.02 | -0.11 |
| GB16881-RA [Apis mellifera troponin T (TpnT), mRNA] | 9.59E-01 | 0.02 | -0.61 |
| GB19418-RA [Apis mellifera glucose oxidase (LOC406081), mRNA] | 9.69E-01 | 0.02 | NA |
| GB19418-RA [Apis mellifera glucose oxidase (LOC406081), mRNA] | 9.69E-01 | 0.02 | NA |
| GB11703-RA [PREDICTED: Apis mellifera similar to CG11550-PA (LOC413056), mRNA] | 9.89E-01 | 0.00 | -0.12 |
| GB15494-RA [PREDICTED: Apis mellifera hypothetical protein LOC724582 (LOC724582), mRNA] | 9.93E-01 | -0.01 | 0.85 |
| GB13368-RA [PREDICTED: Apis mellifera lambda crystallin-like protein, transcript variant 1 (Cryl1), partial mRNA] | 9.97E-01 | 0.00 | 0.94 |
| GB15518-RA [PREDICTED: Apis mellifera similar to CG9380-PA, isoform A (LOC552843), mRNA] | 9.98E-01 | 0.00 | 0.30 |
| GB10939-RA [PREDICTED: Apis mellifera similar to Tropomyosin 2 CG4843-PB, isoform B (LOC408414), mRNA] | 9.99E-01 | 0.00 | -0.09 |

Table S13. Quantitative proteomic analyses of protein abundance in the hemolymph of bees fed rich *vs* poor diet

| Description | *P*-value | logFC protein (rich-poor) | logFC RNA (rich-poor) |
|---|---|---|---|
| GB13999-RA [Apis mellifera vitellogenin (Vg), mRNA] | 7.09E-06 | 3.02 | 3.50 |
| GB20017-RA [PREDICTED: Apis mellifera similar to TER94 CG2331-PA, isoform A, transcript variant 1 (LOC409377), mRNA] | 6.71E-05 | -0.41 | 0.43 |
| GB18300-RA [PREDICTED: Apis mellifera similar to yellow-h CG1629-PA (LOC724293), mRNA] | 2.22E-04 | -0.60 | 0.55 |
| GB16445-RA [PREDICTED: Apis mellifera similar to CG12859-PA (LOC725315), mRNA] | 1.49E-03 | -0.85 | 0.28 |
| GB16485-RA [PREDICTED: Apis mellifera similar to ATP synthase D chain, mitochondrial (LOC410557), mRNA] | 3.19E-03 | -0.68 | 0.07 |
| GB18313-RA [Apis mellifera prophenoloxidase (LOC406155), mRNA] | 3.47E-03 | -0.07 | 0.23 |
| GB15291-RA [PREDICTED: Apis mellifera similar to ATP synthase gamma chain, mitochondrial precursor (LOC552699), mRNA] | 5.14E-03 | -0.82 | 0.31 |
| GB11040-RA [PREDICTED: Apis mellifera similar to CG14476-PB, isoform B, transcript variant 2 (LOC551205), mRNA] | 5.32E-03 | 0.17 | 0.39 |
| GB16568-RA [PREDICTED: Apis mellifera similar to CG11015-PA (LOC552610), mRNA] | 5.50E-03 | -0.97 | 0.27 |
| GB10253-RA [PREDICTED: Apis mellifera similar to CG17280-PA (LOC726042), mRNA] | 8.24E-03 | -1.05 | -0.01 |
| GB14791-RA [PREDICTED: Apis mellifera similar to bellwether CG3612-PA, transcript variant 1 (LOC409114), mRNA] | 9.14E-03 | -0.91 | 0.29 |
| GB10737-RA [PREDICTED: Apis mellifera hypothetical protein LOC727161 (LOC727161), mRNA] | 1.06E-02 | -2.07 | -0.88 |
| GB11508-RA [PREDICTED: Apis mellifera similar to CG5597-PA (LOC409695), mRNA] | 1.52E-02 | 0.22 | 0.01 |
| GB13320-RA [PREDICTED: Apis mellifera hypothetical LOC551541 (LOC551541), mRNA] | 1.71E-02 | -0.59 | -0.04 |
| GB16889-RA [PREDICTED: Apis mellifera similar to CG4382-PA (LOC409801), mRNA] | 1.77E-02 | 1.34 | 0.05 |
| GB14517-RA [PREDICTED: Apis mellifera similar to Isocitrate dehydrogenase CG7176-PC, isoform C, transcript variant 2 (LOC551276), mRNA] | 1.77E-02 | -0.15 | 0.68 |
| GB16443-RA [PREDICTED: Apis mellifera similar to lethal (1) G0334 CG7010-PD, isoform D, transcript variant 1 (LOC551103), mRNA] | 1.82E-02 | -0.88 | -0.20 |
| GB16751-RA [PREDICTED: Apis mellifera similar to lethal (2) 06225 CG6105-PA (LOC726222), mRNA] | 1.82E-02 | -1.01 | 0.06 |
| GB12526-RA [PREDICTED: Apis mellifera similar to lethal (2) k05713 CG8256-PC, isoform C (LOC551904), mRNA] | 1.84E-02 | -0.99 | 0.20 |
| GB14832-RA [PREDICTED: Apis mellifera similar to Succinate dehydrogenase B CG3283-PA (LOC551169), mRNA] | 1.87E-02 | -0.75 | 0.00 |
| GB12364-RA [PREDICTED: Apis mellifera similar to fumarylacetoacetate hydrolase domain containing 2A, transcript variant 2 (LOC410635), mRNA] | 1.91E-02 | -0.79 | 0.99 |
| GB14284-RA [PREDICTED: Apis mellifera similar to Sorbitol dehydrogenase-2 CG4649-PA (LOC408871), mRNA] | 1.91E-02 | 0.54 | 2.31 |
| GB13596-RA [PREDICTED: Apis mellifera similar to ATP synthase- CG11154-PA, isoform A (LOC551766), mRNA] | 1.97E-02 | -0.86 | 0.48 |
| GB19422-RA [PREDICTED: Apis mellifera similar to lethal (1) G0156 CG12233-PA, isoform A (LOC409292), mRNA] | 2.21E-02 | -1.19 | 0.31 |
| GB17439-RA [PREDICTED: Apis mellifera similar to succinate dehydrogenase complex, subunit A, flavoprotein (Fp), transcript variant 1 (LOC550667), mRNA] | 2.53E-02 | -0.77 | 0.27 |
| GB11658-RA [PREDICTED: Apis mellifera hypothetical LOC408608 (LOC408608), mRNA] | 2.66E-02 | 1.93 | 0.17 |
| GB10282-RA [PREDICTED: Apis mellifera similar to Adenylate kinase-2 CG3140-PA (LOC551523), mRNA] | 2.72E-02 | -0.65 | 0.21 |
| GB13261-RA [PREDICTED: Apis mellifera similar to echinoid CG12676-PA (LOC413423), mRNA] | 2.78E-02 | -0.24 | -0.15 |
| GB13223-RA [PREDICTED: Apis mellifera similar to Ferritin 2 light chain homologue CG1469-PA, isoform A (LOC551684), mRNA] | 2.93E-02 | -0.34 | 0.18 |
| GB16678-RA [PREDICTED: Apis mellifera similar to CG8029-PB, isoform B (LOC725661), mRNA] | 2.96E-02 | 0.26 | 0.32 |
| GB18969-RA [PREDICTED: Apis mellifera similar to 60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 kDa chaperonin) (CPN60) (Heat shock protein 60) (HSP-60) (Mitochondrial matrix protein P1) (LOC409384), mRNA] | 2.98E-02 | -0.61 | 1.11 |
| GB10477-RA [PREDICTED: Apis mellifera similar to B-cell receptor-associated protein 37 (LOC551944), mRNA] | 3.15E-02 | -0.72 | 0.16 |
| GB20117-RA [PREDICTED: Apis mellifera hypothetical LOC552391 (LOC552391), mRNA] | 3.20E-02 | 0.72 | 0.99 |
| GB19819-RA [PREDICTED: Apis mellifera similar to Peroxidase CG3477-PA (LOC408953), mRNA] | 3.45E-02 | 1.04 | 0.42 |
| GB15299-RA [Apis mellifera fatty acid binding protein (Fabp), mRNA] | 3.64E-02 | -0.17 | 0.00 |
| GB19297-RA [PREDICTED: Apis mellifera hypothetical protein LOC725074 (LOC725074), mRNA] | 3.83E-02 | 0.59 | 0.55 |
| GB16464-RA [PREDICTED: Apis mellifera similar to mitochondrial malate dehydrogenase precursor, transcript variant 1 (LOC408950), mRNA] | 3.86E-02 | -0.71 | NA |
| GB10708-RA [PREDICTED: Apis mellifera hypothetical LOC408807 (LOC408807), mRNA] | 3.87E-02 | 0.73 | -0.60 |
| GB12797-RA [PREDICTED: Apis mellifera similar to Trehalose-6-phosphate synthase 1 CG4104-PA (LOC408867), partial mRNA] | 4.19E-02 | -0.21 | 0.18 |
| GB12951-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG17870-PC, isoform C, transcript variant 1 (LOC408289), mRNA] | 4.21E-02 | -0.44 | 0.05 |
| GB12951-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG17870-PC, isoform C, transcript variant 1 (LOC408289), mRNA] | 4.21E-02 | -0.44 | 0.02 |
| GB12951-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG17870-PC, isoform C, transcript variant 1 (LOC408289), mRNA] | 4.21E-02 | -0.44 | 0.00 |
| GB18767-RA [PREDICTED: Apis mellifera similar to CG9372-PA (LOC726126), mRNA] | 4.28E-02 | 0.20 | -0.04 |
| GB17626-RA [PREDICTED: Apis mellifera similar to CG7430-PA, transcript variant 1 (LOC551039), mRNA] | 4.43E-02 | -0.91 | 0.16 |
| GB11655-RA [PREDICTED: Apis mellifera similar to Succinyl coenzyme A synthetase subunit CG1065-PA (LOC551403), mRNA] | 4.51E-02 | -0.53 | -0.04 |
| GB13692-RA [PREDICTED: Apis mellifera similar to Ribosomal protein S28b CG2998-PA (LOC724531), mRNA] | 4.54E-02 | 0.27 | 0.14 |

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|---|---|---|---|
| GB19860-RA [PREDICTED: Apis mellifera similar to Heat shock protein cognate 5 CG8542-PA (LOC408605), mRNA] | 4.68E-02 | -0.90 | 0.46 |
| GB11550-RA [PREDICTED: Apis mellifera hypothetical LOC552685 (LOC552685), mRNA] | 4.71E-02 | -0.79 | 0.54 |
| GB15716-RA [PREDICTED: Apis mellifera similar to CG5028-PA (LOC410396), mRNA] | 4.78E-02 | -0.62 | 0.33 |
| GB10628-RA | 4.78E-02 | -0.69 | -0.10 |
| GB10628-RA | 4.78E-02 | -0.69 | 0.05 |
| GB20012-RA [PREDICTED: Apis mellifera similar to CG10664-PA, isoform A (LOC412396), mRNA] | 5.00E-02 | -1.06 | -0.04 |
| GB17084-RA [PREDICTED: Apis mellifera similar to Fasciclin-3 precursor (Fasciclin III) (FAS III) (LOC724243), mRNA] | 5.01E-02 | -0.49 | -0.21 |
| GB17500-RA [PREDICTED: Apis mellifera hypothetical protein LOC725960 (LOC725960), mRNA] | 5.11E-02 | -0.60 | -0.66 |
| GB12488-RA [PREDICTED: Apis mellifera similar to Aconitase CG9244-PB (LOC408446), mRNA] | 5.30E-02 | -0.81 | -0.20 |
| GB18497-RA [PREDICTED: Apis mellifera similar to Elongation factor Tu mitochondrial CG6050-PA, transcript variant 2 (LOC408328), mRNA] | 5.33E-02 | -0.85 | 0.07 |
| GB12605-RA [PREDICTED: Apis mellifera similar to alpha-2-macroglobulin-like 1 (LOC408926), mRNA] | 5.55E-02 | 0.21 | 0.73 |
| GB13073-RA [PREDICTED: Apis mellifera similar to CG5214-PA (LOC409155), mRNA] | 5.55E-02 | -1.25 | 0.46 |
| GB14490-RA [PREDICTED: Apis mellifera similar to ciboulot CG4944-PB, isoform B (LOC551528), mRNA] | 6.23E-02 | 0.29 | 0.15 |
| GB19745-RA [Apis mellifera transferrin (Trf), mRNA] | 6.51E-02 | 0.38 | 0.59 |
| GB14803-RA [PREDICTED: Apis mellifera similar to Trehalase precursor (Alpha,alpha-trehalase) (Alpha,alpha-trehalose glucohydrolase) (LOC410484), mRNA] | 6.71E-02 | 0.96 | 0.31 |
| GB19387-RA [PREDICTED: Apis mellifera similar to Hexokinase A CG3001-PA, isoform A (LOC551005), mRNA] | 6.78E-02 | -0.57 | -0.24 |
| GB20070-RA [Apis mellifera alpha-glucosidase (Hbg2), mRNA] | 7.33E-02 | 0.47 | 0.09 |
| GB16587-RA [PREDICTED: Apis mellifera hypothetical LOC551077 (LOC551077), mRNA] | 7.56E-02 | 0.90 | 0.60 |
| GB15252-RA [PREDICTED: Apis mellifera similar to CG5548-PA (LOC724827), mRNA] | 7.91E-02 | -0.76 | -0.07 |
| GB10284-RA [PREDICTED: Apis mellifera similar to CG6463-PA (LOC413014), mRNA] | 7.94E-02 | -0.65 | -0.14 |
| GB11059-RA [PREDICTED: Apis mellifera similar to Retinoid- and fatty-acid binding protein CG11064-PA, transcript variant 1 (LOC408961), mRNA] | 8.02E-02 | 0.43 | NA |
| GB13917-RA [PREDICTED: Apis mellifera similar to Laminin B1 CG7123-PA, isoform A (LOC726736), mRNA] | 8.08E-02 | 0.60 | 0.18 |
| GB11431-RA [PREDICTED: Apis mellifera similar to Nucleosome remodeling factor – 38kD CG4634-PA (LOC409774), mRNA] | 8.40E-02 | -0.74 | 0.46 |
| GB12495-RA [PREDICTED: Apis mellifera hypothetical LOC552459 (LOC552459), mRNA] | 8.62E-02 | -0.50 | -0.14 |
| GB20014-RA [PREDICTED: Apis mellifera similar to Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic (GPD-C) (GPDH-C) (LOC551955), partial mRNA] | 8.73E-02 | -0.47 | 0.49 |
| GB12113-RA [PREDICTED: Apis mellifera similar to porin CG6647-PA, isoform A (LOC551325), mRNA] | 8.80E-02 | -0.81 | NA |
| GB18004-RA [PREDICTED: Apis mellifera similar to CG31075-PA (LOC408559), mRNA] | 9.01E-02 | -0.15 | 0.66 |
| GB12700-RA [PREDICTED: Apis mellifera similar to Histone H1 (LOC725238), mRNA] | 9.32E-02 | -0.43 | 0.04 |
| GB19171-RA [PREDICTED: Apis mellifera similar to Vacuolar H+-ATPase 55kD B subunit CG17369-PB, isoform B (LOC551721), mRNA] | 9.42E-02 | -0.40 | 0.39 |
| GB14496-RA [PREDICTED: Apis mellifera similar to CG11034-PA (LOC410337), mRNA] | 9.80E-02 | 0.24 | 0.74 |
| GB17852-RA [PREDICTED: Apis mellifera similar to Ect3 CG3132-PA (LOC725756), mRNA] | 9.80E-02 | -0.23 | 0.11 |
| GB15855-RA [PREDICTED: Apis mellifera similar to thioredoxin-2 CG31884-PA, isoform A (LOC409451), mRNA] | 9.84E-02 | 0.32 | 0.33 |
| GB18917-RA [PREDICTED: Apis mellifera similar to Cofilin/actin-depolymerizing factor homolog (Protein D61) (Protein twinstar) (LOC725718), mRNA] | 1.02E-01 | -0.28 | 0.01 |
| GB17499-RA [Apis mellifera ADP/ATP translocase (Ant), mRNA] | 1.05E-01 | -0.45 | -0.17 |
| GB12855-RA [PREDICTED: Apis mellifera similar to Neural conserved at 73EF CG11661-PA, isoform A, transcript variant 1 (LOC408286), mRNA] | 1.05E-01 | -0.99 | -0.06 |
| GB10695-RA [PREDICTED: Apis mellifera similar to Pyruvate kinase CG7070-PB, isoform B (LOC552007), mRNA] | 1.06E-01 | -0.56 | -0.14 |
| GB12600-RA [PREDICTED: Apis mellifera similar to Ccp84Ad CG2341-PA (LOC727197), mRNA] | 1.08E-01 | -0.59 | 0.01 |
| GB12600-RA [PREDICTED: Apis mellifera similar to Ccp84Ad CG2341-PA (LOC727197), mRNA] | 1.08E-01 | -0.59 | 0.15 |
| GB11933-RA [PREDICTED: Apis mellifera similar to acid alpha-glucosidase (LOC409365), mRNA] | 1.11E-01 | -0.36 | 0.06 |
| GB13536-RA [PREDICTED: Apis mellifera similar to CG11963-PA (LOC551958), mRNA] | 1.28E-01 | -0.64 | 0.08 |
| GB17804-RA [PREDICTED: Apis mellifera similar to tubulin-specific chaperone a (LOC412930), mRNA] | 1.29E-01 | 0.45 | 0.17 |
| GB12628-RA [PREDICTED: Apis mellifera similar to Oscillin CG6957-PA, isoform A, transcript variant 1 (LOC409520), mRNA] | 1.33E-01 | -0.27 | 0.32 |
| GB13928-RA [PREDICTED: Apis mellifera similar to lethal (2) 35Di CG13240-PA, isoform A (LOC725712), mRNA] | 1.35E-01 | -0.85 | -0.12 |
| GB19832-RA [PREDICTED: Apis mellifera similar to CG9514-PA (LOC408603), mRNA] | 1.42E-01 | 0.86 | 1.25 |
| GB16494-RA [PREDICTED: Apis mellifera similar to ATPase coupling factor 6 CG4412-PA (LOC726120), mRNA] | 1.43E-01 | -0.73 | 0.16 |
| GB16448-RA [PREDICTED: Apis mellifera similar to Annexin-B9 (Annexin-9) (Annexin IX), transcript variant 1 (LOC409533), mRNA] | 1.50E-01 | 0.20 | 0.27 |
| GB15039-RA [PREDICTED: Apis mellifera similar to Enolase CG17654-PA, isoform A (LOC552678), partial mRNA] | 1.54E-01 | -0.62 | -0.41 |
| GB13399-RA [PREDICTED: Apis mellifera similar to Myosin regulatory light chain 2 (MLC-2) (LOC409881), mRNA] | 1.59E-01 | 1.47 | 0.12 |
| GB15662-RA [PREDICTED: Apis mellifera similar to CG10962-PB, isoform B (LOC724721), mRNA] | 1.60E-01 | 0.54 | -0.73 |
| GB10453-RA [PREDICTED: Apis mellifera similar to CG3777-PB, isoform B (LOC408970), mRNA] | 1.62E-01 | -0.35 | 0.25 |
| GB12402-RA [PREDICTED: Apis mellifera similar to CG1707-PA (LOC551915), mRNA] | 1.63E-01 | -0.19 | 0.13 |
| GB12614-RA [PREDICTED: Apis mellifera similar to Actin-87E, transcript variant 2 (LOC410075), mRNA] | 1.69E-01 | -0.60 | -0.07 |

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|---|---|---|---|
| GB11117-RA [PREDICTED: Apis mellifera similar to LRP16 protein, transcript variant 2 (LOC408589), mRNA] | 1.69E-01 | -0.60 | -0.06 |
| GB15927-RA [PREDICTED: Apis mellifera similar to CG40500-PA.3 (LOC726309), mRNA] | 1.71E-01 | 0.82 | -0.33 |
| GB12951-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG17870-PC, isoform C, transcript variant 1 (LOC408289), mRNA] | 1.71E-01 | -0.30 | 0.05 |
| GB12951-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG17870-PC, isoform C, transcript variant 1 (LOC408289), mRNA] | 1.71E-01 | -0.30 | 0.02 |
| GB12951-RA [PREDICTED: Apis mellifera similar to 14-3-3 CG17870-PC, isoform C, transcript variant 1 (LOC408289), mRNA] | 1.71E-01 | -0.30 | 0.00 |
| GB18819-RA [Apis mellifera antennal-specific protein 3c precursor (Asp3c), mRNA] | 1.77E-01 | 1.31 | -0.17 |
| GB19923-RA [PREDICTED: Apis mellifera similar to Cathepsin L precursor (Cysteine proteinase 1) (LOC552756), mRNA] | 1.78E-01 | 0.68 | 0.21 |
| GB11983-RA [PREDICTED: Apis mellifera similar to Angiotensin converting enzyme CG8827-PA, isoform A (LOC410074), mRNA] | 1.79E-01 | 0.21 | 0.55 |
| GB11768-RA [Apis mellifera major royal jelly protein 4 (Mrjp4), mRNA] | 1.82E-01 | 1.51 | -0.02 |
| GB11768-RA [Apis mellifera major royal jelly protein 4 (Mrjp4), mRNA] | 1.82E-01 | 1.51 | -0.07 |
| GB12375-RA [PREDICTED: Apis mellifera similar to Chd64 CG14996-PB (LOC408572), mRNA] | 1.84E-01 | -0.26 | 0.25 |
| GB19961-RA [PREDICTED: Apis mellifera similar to Gram-negative bacteria binding protein 1 CG6895-PA (LOC725832), mRNA] | 1.88E-01 | 0.49 | 0.49 |
| GB14798-RA [PREDICTED: Apis mellifera similar to Glyceraldehyde 3 phosphate dehydrogenase 1 CG12055-PA, isoform A, transcript variant 2 (LOC410122), mRNA] | 1.89E-01 | -0.56 | -0.05 |
| GB11892-RA [PREDICTED: Apis mellifera similar to Glycogen phosphorylase, transcript variant 2 (LOC409267), mRNA] | 1.92E-01 | -0.55 | 0.10 |
| GB17761-RA [PREDICTED: Apis mellifera similar to CG30069-PA (LOC408677), mRNA] | 1.95E-01 | -0.43 | 0.12 |
| GB12857-RA [PREDICTED: Apis mellifera similar to CG3009-PA (LOC409277), partial mRNA] | 1.96E-01 | -0.34 | 0.10 |
| GB10776-RA [PREDICTED: Apis mellifera similar to glycerol-3-phosphate dehydrogenase 1-like (LOC724574), mRNA] | 1.96E-01 | -0.47 | 0.37 |
| GB15988-RA [PREDICTED: Apis mellifera similar to Collagen alpha-1(II) chain precursor (LOC410038), partial mRNA] | 2.03E-01 | 0.16 | -0.45 |
| GB16882-RA [PREDICTED: Apis mellifera similar to walrus CG8996-PB, isoform B, transcript variant 1 (LOC551710), mRNA] | 2.09E-01 | -0.83 | 0.43 |
| GB13613-RA [PREDICTED: Apis mellifera similar to Larval serum protein 2 CG6806-PA (LOC409354), mRNA] | 2.09E-01 | -0.43 | -0.06 |
| GB13004-RA [PREDICTED: Apis mellifera similar to CG12163-PA, isoform A (LOC408851), mRNA] | 2.19E-01 | 0.42 | -0.30 |
| GB19452-RA | 2.19E-01 | 0.24 | 0.46 |
| GB14141-RA [PREDICTED: Apis mellifera similar to cheerio CG3937-PD, isoform D (LOC409697), mRNA] | 2.22E-01 | -0.38 | 0.16 |
| GB17038-RA [PREDICTED: Apis mellifera similar to CG5703-PA (LOC409793), mRNA] | 2.28E-01 | -0.58 | 0.11 |
| GB18498-RA [PREDICTED: Apis mellifera enoyl Coenzyme A hydratase, short chain, 1, mitochondrial (Echs1), mRNA] | 2.30E-01 | -0.16 | 0.93 |
| GB15629-RA [PREDICTED: Apis mellifera similar to ATP synthase O subunit, mitochondrial precursor (Oligomycin sensitivity conferral protein) (OSCP) (LOC409236), mRNA] | 2.34E-01 | -0.70 | -0.02 |
| GB15494-RA [PREDICTED: Apis mellifera hypothetical protein LOC724582 (LOC724582), mRNA] | 2.34E-01 | 0.40 | 0.47 |
| GB19004-RA [PREDICTED: Apis mellifera similar to CG4169-PA (LOC552671), mRNA] | 2.51E-01 | -0.82 | 0.16 |
| GB15399-RA [PREDICTED: Apis mellifera similar to prefoldin subunit 2 (LOC726085), mRNA] | 2.53E-01 | -0.49 | -0.07 |
| GB16287-RA [PREDICTED: Apis mellifera similar to K06A9.1b (LOC408445), mRNA] | 2.58E-01 | -0.65 | -0.24 |
| GB12384-RA [PREDICTED: Apis mellifera similar to CG10467-PA (LOC552086), mRNA] | 2.59E-01 | 0.67 | 1.15 |
| GB11461-RA [PREDICTED: Apis mellifera similar to UGP CG4347-PA, isoform A, transcript variant 1 (LOC412069), mRNA] | 2.64E-01 | -0.32 | 0.59 |
| GB18404-RA [PREDICTED: Apis mellifera similar to CG2862-PA, isoform A (LOC552670), mRNA] | 2.64E-01 | -0.60 | 0.34 |
| GB19293-RA [PREDICTED: Apis mellifera mitochondrial cytochrome C (CytC), mRNA] | 2.66E-01 | -0.47 | 0.05 |
| GB19503-RA [PREDICTED: Apis mellifera similar to heat shock protein 8, transcript variant 1 (LOC410620), mRNA] | 2.66E-01 | -0.28 | -0.06 |
| GB18960-RA [PREDICTED: Apis mellifera similar to CG6439-PA (LOC552128), mRNA] | 2.67E-01 | -0.78 | 0.01 |
| GB19207-RA [PREDICTED: Apis mellifera hypothetical LOC408695 (LOC408695), mRNA] | 2.72E-01 | -0.39 | -0.40 |
| GB12718-RA [PREDICTED: Apis mellifera hypothetical protein LOC727264 (LOC727264), mRNA] | 2.77E-01 | 0.33 | 0.21 |
| GB17056-RA [PREDICTED: Apis mellifera similar to Cyclophilin 1 CG9916-PA (LOC409890), mRNA] | 2.80E-01 | 0.22 | 0.55 |
| GB17056-RA [PREDICTED: Apis mellifera similar to Cyclophilin 1 CG9916-PA (LOC409890), mRNA] | 2.80E-01 | 0.22 | 0.72 |
| [Antisense] GB17056-RA [PREDICTED: Apis mellifera similar to Cyclophilin 1 CG9916-PA (LOC409890), mRNA] | 2.80E-01 | 0.22 | 0.07 |
| GB10139-RA [PREDICTED: Apis mellifera similar to Glutamine synthetase 2 CG1743-PC, isoform C (LOC410066), mRNA] | 2.91E-01 | -0.47 | 0.40 |
| GB10514-RA [PREDICTED: Apis mellifera similar to Tubulin alpha-1 chain (LOC408388), mRNA] | 2.93E-01 | 0.63 | 0.02 |
| GB11056-RA [PREDICTED: Apis mellifera similar to Phosphoglycerate kinase, transcript variant 1 (LOC411576), mRNA] | 2.95E-01 | -0.54 | -0.08 |
| GB18538-RA | 2.96E-01 | 1.81 | -0.13 |
| GB18299-RA [PREDICTED: Apis mellifera similar to capricious CG11282-PA, isoform A (LOC726414), mRNA] | 2.97E-01 | 0.37 | -0.12 |
| GB11202-RA [PREDICTED: Apis mellifera similar to Laminin A CG10236-PA (LOC412663), partial mRNA] | 2.97E-01 | 0.28 | NA |
| GB11814-RA [PREDICTED: Apis mellifera similar to CG31974-PA (LOC725439), mRNA] | 2.99E-01 | -0.96 | 0.22 |
| GB19811-RA [Apis mellifera take-out-like carrier protein (JHBP-1), mRNA] | 3.01E-01 | 0.59 | 0.97 |
| GB10917-RA [PREDICTED: Apis mellifera similar to Protein-glutamine gamma-glutamyltransferase K (Transglutaminase K) (TGase K) (TGK) (TG(K)) (Transglutaminase-1) (Epidermal TGase) (LOC409425), mRNA] | 3.06E-01 | 0.25 | -0.37 |

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| GB10972-RA [PREDICTED: Apis mellifera thioredoxin peroxidase, transcript variant 1 (Tpx-3), mRNA] | 3.09E-01 | -0.57 | 0.30 |
| GB13559-RA [PREDICTED: Apis mellifera similar to CG7460-PB, transcript variant 1 (LOC413478), mRNA] | 3.10E-01 | 0.29 | 0.50 |
| GB14138-RA [PREDICTED: Apis mellifera putative thioredoxin peroxidase (Gtpx-1), mRNA] | 3.16E-01 | -0.21 | -0.02 |
| GB19460-RA [PREDICTED: Apis mellifera similar to Aldolase CG6058-PF, isoform F (LOC550785), mRNA] | 3.21E-01 | -3.32 | 0.51 |
| GB19460-RA [PREDICTED: Apis mellifera similar to Aldolase CG6058-PF, isoform F (LOC550785), mRNA] | 3.21E-01 | -3.32 | 0.40 |
| GB11022-RA [Apis mellifera major royal jelly protein 7 (Mrjp7), mRNA] | 3.29E-01 | 1.79 | 0.75 |
| GB19742-RA [PREDICTED: Apis mellifera similar to CG8369-PA (LOC408510), mRNA] | 3.32E-01 | 1.13 | -0.38 |
| GB13508-RA [PREDICTED: Apis mellifera similar to ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (LOC411183), mRNA] | 3.33E-01 | -0.42 | -0.11 |
| GB15718-RA [PREDICTED: Apis mellifera similar to CG14207-PB, isoform B, transcript variant 1 (LOC408875), mRNA] | 3.33E-01 | -0.21 | 0.44 |
| GB10855-RA [PREDICTED: Apis mellifera similar to plasma glutamate carboxypeptidase, transcript variant 1 (LOC410149), mRNA] | 3.34E-01 | 0.28 | -0.03 |
| GB19582-RA [PREDICTED: Apis mellifera similar to Serine protease inhibitor 5 CG18525-PA, isoform A (LOC413749), mRNA] | 3.41E-01 | 0.48 | 0.31 |
| GB17879-RA [PREDICTED: Apis mellifera similar to Peptidoglycan recognition protein SA CG11709-PA (LOC727472), mRNA] | 3.54E-01 | 0.51 | 1.84 |
| GB19200-RA [PREDICTED: Apis mellifera similar to Pros5 CG12323-PA, isoform A (LOC411206), mRNA] | 3.54E-01 | -0.14 | 0.19 |
| GB12231-RA [PREDICTED: Apis mellifera similar to Ferritin 1 heavy chain homologue CG2216-PE, isoform E (LOC551651), mRNA] | 3.56E-01 | -0.23 | 0.72 |
| GB14361-RA [PREDICTED: Apis mellifera similar to Larval serum protein 2 CG6806-PA (LOC551648), mRNA] | 3.60E-01 | 2.27 | 2.60 |
| GB12562-RA [PREDICTED: Apis mellifera similar to CG10513-PA, transcript variant 1 (LOC408421), mRNA] | 3.73E-01 | 0.43 | 0.09 |
| GB18637-RA [PREDICTED: Apis mellifera similar to F-actin capping protein subunit beta (LOC409581), mRNA] | 3.73E-01 | -0.22 | 0.38 |
| GB14317-RA [PREDICTED: Apis mellifera similar to sidekick CG5227-PA, isoform A, transcript variant 2 (LOC551168), mRNA] | 3.78E-01 | -0.21 | 0.63 |
| GB14382-RA [PREDICTED: Apis mellifera similar to Neurexin IV CG6827-PB, isoform B (LOC551807), mRNA] | 3.80E-01 | -0.12 | 0.07 |
| GB15052-RA [PREDICTED: Apis mellifera similar to Phosphoglyceromutase CG1721-PA, isoform A (LOC552736), mRNA] | 3.81E-01 | -0.42 | -0.28 |
| GB16246-RA [Apis mellifera major royal jelly protein 2 (Mrjp2), mRNA] | 3.88E-01 | 0.82 | 0.22 |
| GB16246-RA [Apis mellifera major royal jelly protein 2 (Mrjp2), mRNA] | 3.88E-01 | 0.82 | -0.50 |
| GB13821-RA [PREDICTED: Apis mellifera similar to CG3609-PA (LOC412231), mRNA] | 3.94E-01 | -0.18 | 0.07 |
| GB10275-RA [PREDICTED: Apis mellifera similar to –Tubulin at 56D CG9277-PB, isoform B (LOC408782), mRNA] | 3.95E-01 | -0.36 | 0.32 |
| GB14205-RA [PREDICTED: Apis mellifera similar to CG11267-PA (LOC552531), mRNA] | 3.95E-01 | -0.75 | 1.16 |
| GB18727-RA [PREDICTED: Apis mellifera similar to CG5362-PA, transcript variant 1 (LOC411014), mRNA] | 4.04E-01 | -0.14 | 0.27 |
| GB13967-RA [Apis mellifera venom protein 2 (LOC503505), mRNA] | 4.10E-01 | 0.21 | 0.40 |
| GB12230-RA [PREDICTED: Apis mellifera hypothetical protein LOC406120 (LOC406120), mRNA] | 4.15E-01 | 0.23 | -0.23 |
| GB15172-RA [PREDICTED: Apis mellifera similar to lethal (1) G0255 CG4094-PA, isoform A (LOC724321), mRNA] | 4.16E-01 | -0.56 | 0.42 |
| GB18892-RA [PREDICTED: Apis mellifera similar to hydroxyacylglutathione hydrolase, transcript variant 1 (LOC551059), mRNA] | 4.17E-01 | -0.68 | -0.14 |
| GB16881-RA [Apis mellifera troponin T (TpnT), mRNA] | 4.22E-01 | -0.59 | -0.19 |
| GB18764-RA [PREDICTED: Apis mellifera similar to translation elongation factor 1-gamma, transcript variant 2 (LOC551211), mRNA] | 4.26E-01 | -0.28 | -0.01 |
| GB12636-RA [PREDICTED: Apis mellifera hypothetical LOC409716 (LOC409716), mRNA] | 4.26E-01 | -0.24 | NA |
| GB12573-RA [PREDICTED: Apis mellifera similar to lethal (1) G0030 CG3861-PA, isoform A (LOC410059), mRNA] | 4.27E-01 | -0.47 | 0.12 |
| [Antisense] GB13237-RA [PREDICTED: Apis mellifera similar to Phosphogluconate mutase CG5165-PA (LOC411897), mRNA] | 4.28E-01 | -0.23 | -0.13 |
| GB13237-RA [PREDICTED: Apis mellifera similar to Phosphogluconate mutase CG5165-PA (LOC411897), mRNA] | 4.28E-01 | -0.23 | 0.20 |
| GB17035-RA [PREDICTED: Apis mellifera similar to CG15828-PB, isoform B (LOC410793), mRNA] | 4.33E-01 | 0.19 | -0.06 |
| GB17538-RA [Apis mellifera hymenoptaecin (LOC406142), mRNA] | 4.45E-01 | -0.66 | 0.20 |
| GB19380-RA [PREDICTED: Apis mellifera similar to thioredoxin peroxidase 1 CG1633-PA, isoform A, transcript variant 1 (LOC409954), mRNA] | 4.64E-01 | -0.19 | 0.32 |
| GB14424-RA [PREDICTED: Apis mellifera similar to Nidogen/entactin CG12908-PA, isoform A (LOC408797), mRNA] | 4.65E-01 | 0.36 | 0.30 |
| GB16429-RA [PREDICTED: Apis mellifera similar to Glucose-6-phosphate isomerase (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) (LOC551154), mRNA] | 4.67E-01 | -0.23 | 0.17 |
| GB16561-RA [PREDICTED: Apis mellifera similar to Saposin-related CG12070-PA, isoform A, transcript variant 1 (LOC408808), mRNA] | 4.72E-01 | 0.20 | -0.12 |
| GB17531-RA [PREDICTED: Apis mellifera similar to Dihydropteridine reductase CG4665-PA, isoform A (LOC409160), mRNA] | 4.82E-01 | 0.21 | 0.57 |
| GB18626-RA [PREDICTED: Apis mellifera similar to CG15006-PA (LOC552627), mRNA] | 4.90E-01 | -0.33 | -0.19 |
| [Antisense] GB18626-RA [PREDICTED: Apis mellifera similar to CG15006-PA (LOC552627), mRNA] | 4.90E-01 | -0.33 | 0.01 |
| GB18626-RA [PREDICTED: Apis mellifera similar to CG15006-PA (LOC552627), mRNA] | 4.90E-01 | -0.33 | -0.22 |

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| GB10498-RA [PREDICTED: Apis mellifera similar to Peroxiredoxin 2540 CG11765-PA (LOC551975), mRNA] | 5.07E-01 | 0.21 | 0.68 |
| GB14107-RA [PREDICTED: Apis mellifera similar to germinal histone H4 (LOC726520), mRNA] | 5.21E-01 | -0.17 | 0.36 |
| GB16459-RA [Apis mellifera major royal jelly protein 3 (Mrjp3), mRNA] | 5.41E-01 | 1.83 | -0.06 |
| GB16169-RA [PREDICTED: Apis mellifera similar to CG3305-PA, transcript variant 2 (LOC409495), mRNA] | 5.43E-01 | 0.29 | 0.07 |
| GB14852-RA [PREDICTED: Apis mellifera similar to heat shock protein 8, transcript variant 1 (LOC409418), mRNA] | 5.49E-01 | -0.09 | -0.04 |
| GB19509-RA [PREDICTED: Apis mellifera similar to SRY interacting protein 1 CG10939-PA (LOC413207), mRNA] | 5.58E-01 | -0.32 | 0.05 |
| GB19501-RA [PREDICTED: Apis mellifera similar to CG5023-PA (LOC408532), mRNA] | 5.62E-01 | 0.11 | 0.01 |
| GB16807-RA [PREDICTED: Apis mellifera similar to CG9518-PA (LOC410733), mRNA] | 5.81E-01 | 0.61 | 0.15 |
| GB15202-RA [PREDICTED: Apis mellifera similar to dj-1 CG1349-PA (LOC551882), mRNA] | 5.89E-01 | -0.20 | -0.11 |
| GB13279-RA [PREDICTED: Apis mellifera similar to Tropomyosin-2 (Tropomyosin I) (LOC413204), mRNA] | 5.96E-01 | -0.43 | NA |
| GB18109-RA [PREDICTED: Apis mellifera similar to CG6084-PA, isoform A, transcript variant 1 (LOC551968), mRNA] | 5.97E-01 | 0.22 | 1.60 |
| GB18955-RA [PREDICTED: Apis mellifera similar to Phospholipid hydroperoxide glutathione peroxidase, mitochondrial precursor (PHGPx) (GPX-4) (LOC726269), mRNA] | 6.07E-01 | -0.12 | -0.39 |
| GB16500-RA [PREDICTED: Apis mellifera similar to 40S ribosomal protein S3a (C3 protein) (LOC413296), mRNA] | 6.10E-01 | 0.36 | -0.29 |
| GB14710-RA [PREDICTED: Apis mellifera similar to CG4572-PB, isoform B (LOC410451), mRNA] | 6.13E-01 | 0.07 | -0.04 |
| GB15016-RA [PREDICTED: Apis mellifera similar to Heat shock protein cognate 3 CG4147-PA, isoform A (LOC409587), mRNA] | 6.20E-01 | 0.09 | 0.16 |
| GB17384-RA [PREDICTED: Apis mellifera similar to Ccp84Ag CG2342-PA (LOC409345), mRNA] | 6.21E-01 | 0.32 | -0.02 |
| GB17384-RA [PREDICTED: Apis mellifera similar to Ccp84Ag CG2342-PA (LOC409345), mRNA] | 6.21E-01 | 0.32 | -0.10 |
| GB16903-RA [PREDICTED: Apis mellifera similar to cathD CG1548-PA (LOC409341), mRNA] | 6.21E-01 | 0.06 | 0.02 |
| GB10133-RA [PREDICTED: Apis mellifera CuZn superoxide dismutase, transcript variant 1 (Sod1), mRNA] | 6.23E-01 | -0.17 | 0.03 |
| GB10351-RA [PREDICTED: Apis mellifera similar to CG17331-PA, transcript variant 1 (LOC409978), mRNA] | 6.23E-01 | -0.37 | 0.10 |
| GB16526-RA [PREDICTED: Apis mellifera similar to Proteasome subunit alpha type 5 (Proteasome zeta chain) (Macropain zeta chain) (Multicatalytic endopeptidase complex zeta chain) (LOC551956), mRNA] | 6.26E-01 | 0.06 | 0.28 |
| GB10973-RA [Apis mellifera arginine kinase (Argk), mRNA] | 6.38E-01 | -0.08 | 0.58 |
| GB20101-RA [PREDICTED: Apis mellifera similar to CG4893-PA, transcript variant 1 (LOC411570), mRNA] | 6.42E-01 | 0.44 | 0.41 |
| GB18905-RA [PREDICTED: Apis mellifera similar to proteasome (prosome, macropain) subunit, beta type, 6 (LOC409831), mRNA] | 6.56E-01 | -0.28 | 0.34 |
| GB17251-RA [PREDICTED: Apis mellifera similar to Nucleoside diphosphate kinase (NDK) (NDP kinase) (Abnormal wing disks protein) (Killer of prune protein) (LOC409861), mRNA] | 6.61E-01 | -0.21 | 0.23 |
| GB19075-RA [PREDICTED: Apis mellifera similar to CG3153-PB, isoform B (LOC725038), mRNA] | 6.65E-01 | 0.33 | -0.30 |
| GB10560-RA [Apis mellifera translation elongation factor eEF-1 alpha chain (LOC408385), mRNA] | 6.71E-01 | -0.13 | 0.40 |
| GB15536-RA [PREDICTED: Apis mellifera similar to CG5397-PA (LOC410187), mRNA] | 6.82E-01 | 0.09 | 0.27 |
| GB11150-RA [PREDICTED: Apis mellifera similar to CG3560-PA (LOC551757), mRNA] | 6.86E-01 | -0.26 | 0.09 |
| GB15619-RA [PREDICTED: Apis mellifera similar to CG8036-PB, isoform B, transcript variant 1 (LOC550804), mRNA] | 6.93E-01 | 0.11 | 0.65 |
| GB18363-RA [Apis mellifera odorant binding protein 13 (Obp13), mRNA] | 6.97E-01 | 0.15 | 0.43 |
| GB11665-RA [PREDICTED: Apis mellifera similar to Imaginal disc growth factor 4 CG1780-PA, isoform A (LOC413324), mRNA] | 7.10E-01 | 0.19 | 0.75 |
| GB16162-RA [PREDICTED: Apis mellifera similar to CG8498-PA (LOC411272), mRNA] | 7.10E-01 | 0.07 | 0.25 |
| GB14758-RA [PREDICTED: Apis mellifera similar to heat shock protein 90-alpha, transcript variant 1 (LOC408928), mRNA] | 7.12E-01 | -0.07 | 0.66 |
| GB19247-RA [PREDICTED: Apis mellifera similar to Elongation factor 2 (EF-2), transcript variant 1 (LOC409167), mRNA] | 7.26E-01 | -0.07 | -0.25 |
| GB16716-RA [PREDICTED: Apis mellifera similar to CG8561-PA (LOC725041), mRNA] | 7.37E-01 | 0.17 | 0.05 |
| GB12098-RA [PREDICTED: Apis mellifera similar to CG8773-PA (LOC550831), partial mRNA] | 7.38E-01 | -0.04 | 0.01 |
| GB16806-RA [PREDICTED: Apis mellifera similar to CG15040-PA (LOC725387), mRNA] | 7.40E-01 | 0.09 | 0.17 |
| GB14645-RA [PREDICTED: Apis mellifera similar to CG6124-PA (LOC724421), mRNA] | 7.41E-01 | -0.37 | 0.02 |
| GB14520-RA [PREDICTED: Apis mellifera similar to Fasciclin 2 CG3665-PB, isoform B, transcript variant 1 (LOC409849), mRNA] | 7.42E-01 | 0.18 | -0.24 |
| GB19017-RA [Apis mellifera alpha-glucosidase (LOC406131), mRNA] | 7.45E-01 | 0.41 | 0.10 |
| GB14705-RA [PREDICTED: Apis mellifera similar to Adenylosuccinate synthetase (IMP--aspartate ligase) (AdSS) (AMPSase) (LOC409299), mRNA] | 7.48E-01 | -0.12 | -0.04 |
| GB11846-RA [PREDICTED: Apis mellifera similar to Neuroglian CG1634-PA, isoform A (LOC411829), mRNA] | 7.92E-01 | -0.03 | -0.01 |
| GB17444-RA [PREDICTED: Apis mellifera similar to CG32521-PA, isoform A (LOC725926), mRNA] | 8.01E-01 | 0.04 | 0.64 |
| GB16582-RA [PREDICTED: Apis mellifera hypothetical protein LOC725175 (LOC725175), mRNA] | 8.02E-01 | -0.11 | 0.06 |
| GB14888-RA [Apis mellifera major royal jelly protein 1 (Mrjp1), mRNA] | 8.02E-01 | 0.50 | NA |
| GB10836-RA [PREDICTED: Apis mellifera similar to Hsc70Cb CG6603-PA, isoform A, transcript variant 1 (LOC408706), mRNA] | 8.02E-01 | -0.09 | 0.02 |
| GB10889-RA [PREDICTED: Apis mellifera similar to CG5080-PB, isoform B (LOC413792), partial mRNA] | 8.03E-01 | -0.04 | 0.72 |
| GB13668-RA [PREDICTED: Apis mellifera hypothetical LOC552675 (LOC552675), mRNA] | 8.04E-01 | -0.16 | -0.24 |
| GB13722-RA [PREDICTED: Apis mellifera similar to Y4C6B.6 (LOC409709), mRNA] | 8.07E-01 | 0.35 | -0.18 |
| GB19068-RA [PREDICTED: Apis mellifera similar to Lysosomal Pro-X carboxypeptidase precursor (Prolylcarboxypeptidase) (PRCP) (Proline carboxypeptidase) (Angiotensinase C) (Lysosomal | 8.08E-01 | 0.03 | 0.25 |

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| carboxypeptidase C) (LOC551273), mRNA] | | | |
| GB12956-RA [PREDICTED: Apis mellifera similar to yippee interacting protein 2 CG4600-PA (LOC408291), mRNA] | 8.10E-01 | -0.01 | 0.55 |
| GB14247-RA [PREDICTED: Apis mellifera similar to easter CG4920-PA (LOC726256), mRNA] | 8.14E-01 | 0.10 | 0.29 |
| GB19418-RA [Apis mellifera glucose oxidase (LOC406081), mRNA] | 8.19E-01 | 0.75 | NA |
| GB19418-RA [Apis mellifera glucose oxidase (LOC406081), mRNA] | 8.19E-01 | 0.75 | NA |
| GB16153-RA [PREDICTED: Apis mellifera similar to Papilin CG33103-PB, isoform B, transcript variant 1 (LOC413021), mRNA] | 8.21E-01 | -0.08 | -0.06 |
| GB15816-RA [PREDICTED: Apis mellifera similar to Cytochrome c oxidase polypeptide Va, mitochondrial precursor (LOC408837), mRNA] | 8.26E-01 | 0.62 | 0.17 |
| GB15044-RA [PREDICTED: Apis mellifera similar to CG6180-PA, transcript variant 1 (LOC408516), mRNA] | 8.30E-01 | -0.09 | 0.30 |
| GB17818-RA [PREDICTED: Apis mellifera hypothetical protein LOC724771 (LOC724771), mRNA] | 8.32E-01 | 0.02 | NA |
| GB13351-RA [Apis mellifera phospholipase A2 (Pla2), mRNA] | 8.41E-01 | 0.18 | 0.96 |
| GB16927-RA [PREDICTED: Apis mellifera hypothetical LOC408280 (LOC408280), mRNA] | 8.49E-01 | -0.06 | 0.66 |
| GB12538-RA [PREDICTED: Apis mellifera similar to Tequila CG4821-PA, isoform A (LOC724971), mRNA] | 8.54E-01 | 0.16 | 0.15 |
| GB18159-RA [PREDICTED: Apis mellifera similar to PTK7 protein tyrosine kinase 7 isoform a precursor (LOC410685), mRNA] | 8.58E-01 | -0.08 | NA |
| GB11298-RA | 8.62E-01 | 0.11 | 0.31 |
| GB10411-RA [PREDICTED: Apis mellifera similar to Proteasome subunit alpha type 7-1 (Proteasome 28 kDa subunit 1) (PROS-Dm28.1), transcript variant 1 (LOC410095), mRNA] | 8.70E-01 | 0.03 | -0.02 |
| GB11503-RA [PREDICTED: Apis mellifera similar to CG5195-PA (LOC724779), mRNA] | 8.81E-01 | 0.06 | 0.11 |
| GB13042-RA [PREDICTED: Apis mellifera similar to Flavin-containing monooxygenase 1 CG3006-PA (LOC410687), mRNA] | 8.84E-01 | -0.02 | 0.65 |
| GB10989-RA [PREDICTED: Apis mellifera similar to Vacuolar ATP synthase catalytic subunit A, osteoclast isoform (V-ATPase subunit A 2) (Vacuolar proton pump alpha subunit 2) (V-ATPase 69 kDa subunit 2) (Isoform HO68), transcript variant 1 (LOC551093), mRNA | 9.04E-01 | -0.02 | 0.06 |
| GB15518-RA [PREDICTED: Apis mellifera similar to CG9380-PA, isoform A (LOC552843), mRNA] | 9.06E-01 | -0.01 | -0.55 |
| GB14191-RA [PREDICTED: Apis mellifera similar to Proteasome subunit beta type 1 (Proteasome 26 kDa subunit) (LOC411695), mRNA] | 9.17E-01 | 0.08 | 0.09 |
| GB17645-RA [PREDICTED: Apis mellifera similar to CG7453-PB, isoform B (LOC724585), mRNA] | 9.18E-01 | 0.02 | 0.36 |
| [Antisense] GB16236-RA [PREDICTED: Apis mellifera similar to pericardin CG5700-PB (LOC552446), mRNA] | 9.42E-01 | -0.03 | NA |
| GB16236-RA [PREDICTED: Apis mellifera similar to pericardin CG5700-PB (LOC552446), mRNA] | 9.42E-01 | -0.03 | 0.83 |
| GB16236-RA [PREDICTED: Apis mellifera similar to pericardin CG5700-PB (LOC552446), mRNA] | 9.42E-01 | -0.03 | 0.78 |
| GB11810-RA [PREDICTED: Apis mellifera similar to Contactin CG1084-PA (LOC412312), mRNA] | 9.60E-01 | 0.00 | -0.03 |
| GB19030-RA [PREDICTED: Apis mellifera similar to CG10638-PA, isoform A, transcript variant 1 (LOC552018), mRNA] | 9.69E-01 | 0.01 | 0.77 |
| GB10717-RA [PREDICTED: Apis mellifera similar to Muscle protein 20 CG4696-PA, isoform A (LOC408972), mRNA] | 9.73E-01 | 0.01 | -0.76 |
| GB19425-RA [PREDICTED: Apis mellifera similar to Hsp70/Hsp90 organizing protein homolog CG2720-PA, transcript variant 1 (LOC411002), mRNA] | 9.89E-01 | -0.01 | 0.29 |
| GB16914-RA [PREDICTED: Apis mellifera similar to Ribosomal protein L14 CG6253-PA (LOC409290), mRNA] | 9.89E-01 | 0.00 | -0.59 |