

## **Analysis of the circadian transcriptome of the Antarctic krill *Euphausia superba***

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**Supplementary Table 5. Gene Ontology analysis of genes with a sinusoidal expression pattern in LD.**

Classification of annotated genes with sinusoidal expression patterns throughout the 24-hour cycle in LD regime (1,485 genes). <sup>a</sup>ID: accession number of krill master transcriptome<sup>23</sup>; <sup>b</sup>Annotation = description of the gene; <sup>c</sup>GO term: gene ontology biological process; <sup>d</sup>GO child term: most fitting gene ontology child term to further refine the functional annotation.

| ID                                     | Annotation  | GO term                         | Go child term              |
|--|---|---------------------------------|----------------------------|
| <b>Cellular component organization</b> |   |                                 |                            |
| M108674                                |   | Cellular component organization | Chromosome organization    |
| M17873                                 |   | Cellular component organization | Chromosome organization    |
| N18234                                 | PREDICTED: <i>Nasonia vitripennis</i> imitation SWI (Iswi), mRNA                                    | Cellular component organization | Chromosome organization    |
| N22970                                 | hypothetical protein CAEBREN_26312 [Caenorhabditis brenneri]  | Cellular component organization | Chromosome organization    |
| N23421                                 | PREDICTED: H2A histone family, member Y-like [Saccoglossus kowalevskii]                             | Cellular component organization | Chromosome organization    |
| N23850                                 | PREDICTED: H1 histone family, member O-like [Saccoglossus kowalevskii]                              | Cellular component organization | Chromosome organization    |
| N24637                                 |   | Cellular component organization | Chromosome organization    |
| N26441                                 | histone H1 orphon [Xenoturbella bocki]  | Cellular component organization | Chromosome organization    |
| N26710                                 |   | Cellular component organization | Chromosome organization    |
| N33184                                 | unknown [Dendroctonus ponderosae]   | Cellular component organization | Chromosome organization    |
| N41202                                 | PREDICTED: histone H1-delta-like [Aplysia californica]  | Cellular component organization | Chromosome organization    |
| N50496                                 | Branchiostoma floridae hypothetical protein, mRNA   | Cellular component organization | Chromosome organization    |
| N55793                                 |   | Cellular component organization | Chromosome organization    |
| E2934                                  | RecName: Full=Tubulin alpha-3 chain; AltName: Full=Alpha-III tubulin >gi 1562539 g                  | Cellular component organization | Cytoskeleton organization  |
| E4642                                  | hypothetical protein AMTR_s00032p00056500 [Amborella trichopoda]                                    | Cellular component organization | Cytoskeleton organization  |
| M10012                                 | Haliotis diversicolor putative tubulin beta chain (TUBB) mRNA, complete cds                         | Cellular component organization | Cytoskeleton organization  |
| M108155                                | hypothetical protein AaeL_AAELO08947 [Aedes aegypti] >gi 108875003 gb EAT3922                       | Cellular component organization | Cytoskeleton organization  |
| M1452                                  | Scylla paramamosain suppressor of profilin 2 mRNA, partial cds                                      | Cellular component organization | Cytoskeleton organization  |
| M19065                                 |   | Cellular component organization | Cytoskeleton organization  |
| M19725                                 | PREDICTED: kinectin isoform 5 [Ceratotherium simum simum]   | Cellular component organization | Cytoskeleton organization  |
| M22315                                 | Strongyloides stercoralis beta-tubulin (btub) gene, complete cds                                    | Cellular component organization | Cytoskeleton organization  |
| M31074                                 | profilin [Penaeus monodon]  | Cellular component organization | Cytoskeleton organization  |
| M35289                                 | Rattus norvegicus TLOAAA47YN11 mRNA sequence  | Cellular component organization | Cytoskeleton organization  |
| M3685                                  | PREDICTED: F-actin-capping protein subunit beta-like [Nasonia vitripennis]                          | Cellular component organization | Cytoskeleton organization  |
| M5119                                  | hypothetical protein DAPPUDRAFT_305421 [Daphnia pulex]  | Cellular component organization | Cytoskeleton organization  |
| M523                                   | Dugesia japonica Djtuba mRNA for tubulin alpha chain, complete cds                                  | Cellular component organization | Cytoskeleton organization  |
| M56592                                 | PREDICTED: kinesin-like protein KIF3A-like isoform X2 [Oreochromis niloticus]                       | Cellular component organization | Cytoskeleton organization  |
| M58034                                 | Nematostella vectensis predicted protein (NEMVEDRAFT_v1g188665) partial mRNA                        | Cellular component organization | Cytoskeleton organization  |
| M59795                                 | conserved hypothetical protein [Pediculus humanus corporis] >gi 212513136 gb EEF                    | Cellular component organization | Cytoskeleton organization  |
| M71966                                 | beta-tubulin [Oxymonadida environmental sample]   | Cellular component organization | Cytoskeleton organization  |
| M7549                                  |   | Cellular component organization | Cytoskeleton organization  |
| N16988                                 | hypothetical protein BRAFLDRAFT_90471 [Branchiostoma floridae] >gi 229274973 g                      | Cellular component organization | Cytoskeleton organization  |
| N18342                                 |   | Cellular component organization | Cytoskeleton organization  |
| N18728                                 |   | Cellular component organization | Cytoskeleton organization  |
| N19790                                 | Cryptocercus punctulatus alpha-tubulin (Atub) mRNA, partial cds                                     | Cellular component organization | Cytoskeleton organization  |
| N20018                                 | Caenorhabditis remanei CRE-MEC-7 protein (Cre-mec-7) mRNA, complete cds                             | Cellular component organization | Cytoskeleton organization  |
| N20366                                 | hypothetical protein BRAFLDRAFT_114859 [Branchiostoma floridae] >gi 229277313                       | Cellular component organization | Cytoskeleton organization  |
| N22526                                 | conserved hypothetical protein [Pediculus humanus corporis] >gi 212515782 gb EEF                    | Cellular component organization | Cytoskeleton organization  |
| N22966                                 | hypothetical protein AND_08724 [Anopheles darlingi]   | Cellular component organization | Cytoskeleton organization  |
| N26915                                 | hypothetical protein BRAFLDRAFT_67536 [Branchiostoma floridae] >gi 229291637 g                      | Cellular component organization | Cytoskeleton organization  |
| N27135                                 | kinesin 2B [Nasonia vitripennis] >gi 299782459 ref NP_001177680.1  kinesin 2B [N                    | Cellular component organization | Cytoskeleton organization  |
| N32668                                 | Dystroglycan [Acromyrmex echinatior]  | Cellular component organization | Cytoskeleton organization  |
| N35788                                 | hypothetical protein CAPTEDRAFT_219709 [Capitella teleta]   | Cellular component organization | Cytoskeleton organization  |
| N51300                                 | PREDICTED: actin-related protein 2-like isoform 1 [Megachile rotundata]                             | Cellular component organization | Cytoskeleton organization  |
| N7610                                  |   | Cellular component organization | Cytoskeleton organization  |
| N9729                                  | PREDICTED: <i>Monodelphis domestica</i> tubulin alpha-1B chain-like (LOC100010347), m               | Cellular component organization | Cytoskeleton organization  |
| M92476                                 | RecName: Full=Tropomin T; Short=TnT >gi 4928474 gb AAD33603.1 AF133520_1 trc                        | Cellular component organization | Mitochondrion organization |
| N26226                                 | peroxisomal biogenesis factor 16 [Acyrthosiphon pisum] >gi 239792324 dbj BAH725                     | Cellular component organization | Other                      |
| <b>Cellular Process</b>                |   |                                 |                            |
| M112844                                | thrombospondin [Aedes aegypti] >gi 108875947 gb EAT40172.1  AAEL008062-PA, $\zeta$ Cellular Process | Cellular Process                | Cell adhesion              |
| M14137                                 | thrombospondin, putative [Ixodes scapularis] >gi 215497762 gb EEC07256.1  thron                     | Cellular Process                | Cell adhesion              |
| M3277                                  | myosin heavy chain isoform 3 [Daphnia pulex]  | Cellular Process                | Cell adhesion              |
| M88841                                 | PREDICTED: protocadherin Fat 1 isoform X5 [Xenopus (Silurana) tropicalis]                           | Cellular Process                | Cell adhesion              |
| N20755                                 | PREDICTED: Apis mellifera vinculin (Vinc), mRNA   | Cellular Process                | Cell adhesion              |
| N3255                                  | hypothetical protein BRAFLDRAFT_69086 [Branchiostoma floridae] >gi 229280755 g                      | Cellular Process                | Cell adhesion              |
| N37791                                 | conserved hypothetical protein [Pediculus humanus corporis] >gi 212510848 gb EEF                    | Cellular Process                | Cell adhesion              |
| N43256                                 | hypothetical protein DAPPUDRAFT_212574 [Daphnia pulex]  | Cellular Process                | Cell adhesion              |
| N54977                                 | hypothetical protein DAPPUDRAFT_321186 [Daphnia pulex]  | Cellular Process                | Cell adhesion              |
| N56021                                 | hypothetical protein DAPPUDRAFT_329129 [Daphnia pulex]  | Cellular Process                | Cell adhesion              |
| M11225                                 | PREDICTED: protein ECT2-like [Megachile rotundata]  | Cellular Process                | Cell cycle                 |
| M114824                                | U3 snoRNP-associated protein, putative [Ixodes scapularis] >gi 215499878 gb EEC05                   | Cellular Process                | Cell cycle                 |
| M1163                                  | PREDICTED: ubiquitin-conjugating enzyme E2 C-like [Nasonia vitripennis]                             | Cellular Process                | Cell cycle                 |
| M12125                                 | PREDICTED: anaphase-promoting complex subunit 4-like [Bombyx mori]                                  | Cellular Process                | Cell cycle                 |
| M22224                                 | Pediculus humanus corporis mitosis protein dim1, putative, mRNA                                     | Cellular Process                | Cell cycle                 |
| M2312                                  | hypothetical protein BRAFLDRAFT_124509 [Branchiostoma floridae] >gi 229275705                       | Cellular Process                | Cell cycle                 |
| M47744                                 | Homarus americanus beta-I tubulin mRNA, complete cds  | Cellular Process                | Cell cycle                 |
| M748                                   | hypothetical protein CAPTEDRAFT_218074 [Capitella teleta]   | Cellular Process                | Cell cycle                 |
| M79039                                 | PREDICTED: <i>Apis florea</i> polyubiquitin-A-like (LOC100869991), miscRNA                          | Cellular Process                | Cell cycle                 |
| M9135                                  |   | Cellular Process                | Cell cycle                 |
| M918                                   |   | Cellular Process                | Cell cycle                 |
| M98302                                 | cyclin K [Artemia parthenogenetica]   | Cellular Process                | Cell cycle                 |

| ID                           | Annotation  | GO term               | Go child term                        |
|------------------------------|---|-----------------------|--------------------------------------|
| M98593                       | conserved hypothetical protein [Trichinella spiralis] >gi 316979321 gb EFV62128.1       | Cellular Process      | Cell cycle                           |
| N18186                       |   | Cellular Process      | Cell cycle                           |
| N18390                       | hypothetical protein BRAFLDRAFT_123390 [Branchiostoma floridae] >gi 229283692           | Cellular Process      | Cell cycle                           |
| N18723                       | Structural maintenance of chromosomes protein 5 [Acromyrmex echinatior]                 | Cellular Process      | Cell cycle                           |
| N19234                       | PREDICTED: origin recognition complex subunit 4 [Sorex araneus]                         | Cellular Process      | Cell cycle                           |
| N19240                       | PREDICTED: hypothetical protein LOC100124009 [Nasonia vitripennis]                      | Cellular Process      | Cell cycle                           |
| N20073                       | viral A-type inclusion protein [Trichomonas vaginalis G3] >gi 121915630 gb EAY204       | Cellular Process      | Cell cycle                           |
| N20707                       | hypothetical protein CAPTEDRAFT_140107, partial [Capitella teleta]                      | Cellular Process      | Cell cycle                           |
| N22167                       | PREDICTED: Saccoglossus kowalevskii mps one binder kinase activator-like 3-like (LOC    | Cellular Process      | Cell cycle                           |
| N22972                       | PREDICTED: similar to g1/s-specific cyclin c [Tribolium castaneum] >gi 270003157 gb     | Cellular Process      | Cell cycle                           |
| N39027                       | PREDICTED: DIX domain containing 1-like [Saccoglossus kowalevskii]                      | Cellular Process      | Cell cycle                           |
| N51170                       | hypothetical protein DAPPUDRAFT_202549 [Daphnia pulex]                                  | Cellular Process      | Cell cycle                           |
| M110026                      | Schistosoma mansoni strain Puerto Rico chromosome 1, complete genome                    | Cellular Process      | Cell death                           |
| M3851                        | PREDICTED: hypothetical protein LOC100118119 [Nasonia vitripennis]                      | Cellular Process      | Cell death                           |
| M39101                       | Anopheles gambiae str. PEST AGAP001971-PA (AgaP_AGAP001971) mRNA, complete              | Cellular Process      | Cell death                           |
| M4821                        | GalNAc/Gal-specific lectin [Crenomytilus grayanus]                                      | Cellular Process      | Cell death                           |
| M96949                       | Armigeres subalbatus ASAP ID: 43771 cytosolic small ribosomal subunit 27A mRNA se       | Cellular Process      | Cell death                           |
| N19301                       | p63-like transcription factor [Saccoglossus kowalevskii] >gi 268054253 gb ACY9261       | Cellular Process      | Cell death                           |
| N19348                       |   | Cellular Process      | Cell death                           |
| N25552                       | DNA fragmentation factor subunit beta [Esox lucius]                                     | Cellular Process      | Cell death                           |
| N31320                       | PREDICTED: NADPH dependent diflavin oxidoreductase 1-like [Saccoglossus kowalevs        | Cellular Process      | Cell death                           |
| N34633                       | PREDICTED: G2/M phase-specific E3 ubiquitin-protein ligase [Nomascus leucogenys]        | Cellular Process      | Cell death                           |
| N36400                       | GL14252 [Drosophila persimilis] >gi 194103844 gb EDW25887.1  GL14252 [Drosop            | Cellular Process      | Cell death                           |
| N36730                       | hypothetical protein DAPPUDRAFT_304833 [Daphnia pulex]                                  | Cellular Process      | Cell death                           |
| N36763                       | GalNAc/Gal-specific lectin [Crenomytilus grayanus]                                      | Cellular Process      | Cell death                           |
| N36782                       | dynamin associated protein 160, isoform H [Drosophila melanogaster] >gi 44021403        | Cellular Process      | Cell differentiation                 |
| N6778                        |   | Cellular Process      | Cell differentiation                 |
| M1516                        |   | Cellular Process      | Cell growth                          |
| M9307                        |   | Cellular Process      | Cell growth                          |
| N11186                       | secreted protein, putative [Ixodes scapularis] >gi 215504738 gb EEC14232.1  secret      | Cellular Process      | Cell growth                          |
| N20944                       |   | Cellular Process      | Cell growth                          |
| N22228                       | hypothetical protein DAPPUDRAFT_305543 [Daphnia pulex]                                  | Cellular Process      | Cell growth                          |
| N32590                       | single IB domain protein [Litopenaeus vannamei]   | Cellular Process      | Cell growth                          |
| M58051                       | RecName: Full=Protein 60A; AltName: Full=Protein glass bottom boat; Flags: Precursc     | Cellular Process      | Cell proliferation                   |
| N18361                       | M-phase inducer phosphatase 2 [Culex quinquefasciatus] >gi 167867878 gb EDS312          | Cellular Process      | Cell proliferation                   |
| N12719                       | PREDICTED: similar to dre4 CG1828-PA [Tribolium castaneum] >gi 270007613 gb EF.         | Cellular Process      | Other                                |
| N12909                       | hypothetical protein BRAFLDRAFT_217557 [Branchiostoma floridae] >gi 229279859           | Cellular Process      | Other                                |
| N38970                       | RING zinc finger-containing protein [Dictyostelium fasciculatum] >gi 328871844 gb       | Cellular Process      | Other                                |
| N7766                        | PREDICTED: similar to CG10576 CG10576-PA [Tribolium castaneum] >gi 270015297            | Cellular Process      | Other                                |
| <b>Developmental process</b> |   |                       |                                      |
| M16872                       | Penaeus monodon actin 1 (act1) mRNA, complete cds                                       | Developmental process | Embryo development                   |
| M21636                       |   | Developmental process | Embryo development                   |
| M33430                       | crustacean hematopoietic factor [Pacifastacus leniusculus]                              | Developmental process | Embryo development                   |
| N19897                       | hypothetical protein DAPPUDRAFT_302804 [Daphnia pulex]                                  | Developmental process | Embryo development                   |
| N22212                       | probable global transcription activator SNF2L1 [Danio rerio]                            | Developmental process | Embryo development                   |
| N42326                       | PREDICTED: COP9 signalosome complex subunit 3 [Ornithorhynchus anatinus]                | Developmental process | Embryo development                   |
| M18035                       | PREDICTED: Apis florea heterogeneous nuclear ribonucleoprotein Q-like (LOC100863        | Developmental process | Multicellular organismal development |
| M18892                       |   | Developmental process | Multicellular organismal development |
| N10625                       | HMGBa [Litopenaeus vannamei]  | Developmental process | Multicellular organismal development |
| N12758                       |   | Developmental process | Multicellular organismal development |
| N25016                       | engrailed-b homeobox protein [Sacculina carcinii]                                       | Developmental process | Multicellular organismal development |
| N25457                       | GE13571 [Drosophila yakuba] >gi 194177391 gb EDW91002.1  GE13571 [Drosophil             | Developmental process | Multicellular organismal development |
| N31644                       | PREDICTED: hypothetical protein LOC100118826 [Nasonia vitripennis]                      | Developmental process | Multicellular organismal development |
| N36333                       | PREDICTED: long-chain-fatty-acid-CoA ligase 3-like [Apis florea]                        | Developmental process | Multicellular organismal development |
| N38018                       | hypothetical protein YQE_09076, partial [Dendroctonus ponderosae] >gi 546684617         | Developmental process | Multicellular organismal development |
| N43005                       | dishevelled-like protein [Daphnia pulex]  | Developmental process | Multicellular organismal development |
| N19061                       | PREDICTED: aspartate-tRNA ligase, cytoplasmic-like [Megachile rotundata]                | Developmental process | Nervous system development           |
| N28214                       | neuferricin-like protein [Ascaris suum]   | Developmental process | Nervous system development           |
| N34395                       | hypothetical protein YQE_03768, partial [Dendroctonus ponderosae]                       | Developmental process | Nervous system development           |
| N43973                       | PREDICTED: DNA-directed RNA polymerase II subunit RPB9-like [Ceratitis capitata]        | Developmental process | Nervous system development           |
| N49669                       | PREDICTED: probable E3 ubiquitin-protein ligase makorin-2 isoform X3 [Danio rerio]      | Developmental process | Nervous system development           |
| N50963                       | hypothetical protein DAPPUDRAFT_217067 [Daphnia pulex]                                  | Developmental process | Nervous system development           |
| M10611                       | PREDICTED: cytoplasmic dynein 1 intermediate chain-like isoform X1 [Ceratitis capitata] | Developmental process | Other                                |
| M8825                        |   | Developmental process | Other                                |
| N22265                       | src tyrosine kinase, putative [Ixodes scapularis] >gi 215497797 gb EEC07291.1  src t    | Developmental process | Other                                |
| N55781                       | PREDICTED: exostosin-2-like [Aplysia californica]                                       | Developmental process | Other                                |
| <b>Metabolic process</b>     |   |                       |                                      |
| M68938                       | hypothetical protein DAPPUDRAFT_321839 [Daphnia pulex]                                  | Metabolic process     | Autofagy                             |
| N20139                       | WD repeat domain phosphoinositide-interacting protein, putative [Pediculus humani       | Metabolic process     | Autofagy                             |
| E4529                        | i-type lysozyme-like protein 1 [Penaeus monodon]  | Metabolic process     | Carbohydrate metabolic process       |
| E4652                        | PREDICTED: beta-1,4-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase        | Metabolic process     | Carbohydrate metabolic process       |
| E5180                        |   | Metabolic process     | Carbohydrate metabolic process       |
| M10239                       | cuticular protein, putative [Ixodes scapularis] >gi 215494596 gb EEC04237.1  cuticu     | Metabolic process     | Carbohydrate metabolic process       |
| M10340                       |   | Metabolic process     | Carbohydrate metabolic process       |
| M105964                      | PREDICTED: glycogen phosphorylase, liver form isoform X1 [Cavia porcellus]              | Metabolic process     | Carbohydrate metabolic process       |

| ID      | Annotation   | GO term           | Go child term                  |
|---------|--|-------------------|--------------------------------|
| M108    |  | Metabolic process | Carbohydrate metabolic process |
| M108205 |  | Metabolic process | Carbohydrate metabolic process |
| M109534 | hypothetical protein DAPPUDRAFT_62084 [Daphnia pulex]                                | Metabolic process | Carbohydrate metabolic process |
| M1135   | putative cuticle protein [Lepeophtheirus salmonis]                                   | Metabolic process | Carbohydrate metabolic process |
| M12607  | chitinase 2 [Penaeus monodon]  | Metabolic process | Carbohydrate metabolic process |
| M13238  | hypothetical protein TcasGA2_TC001169 [Tribolium castaneum]                          | Metabolic process | Carbohydrate metabolic process |
| M14811  |  | Metabolic process | Carbohydrate metabolic process |
| M16168  | chitinase-like protein, partial [Pandalopsis japonica]                               | Metabolic process | Carbohydrate metabolic process |
| M16221  | conserved hypothetical protein [Pediculus humanus corporis] >gi 212510636 gb EEF     | Metabolic process | Carbohydrate metabolic process |
| M16262  | chitinase 2 [Penaeus monodon]  | Metabolic process | Carbohydrate metabolic process |
| M16697  | i-type lysozyme-like protein 2 [Penaeus monodon]                                     | Metabolic process | Carbohydrate metabolic process |
| M1720   | GE21870 [Drosophila yakuba] >gi 194180626 gb EDW94237.1  GE21870 [Drosophil          | Metabolic process | Carbohydrate metabolic process |
| M17683  | n-acetylgalactosaminyltransferase [Aedes aegypti] >gi 108884053 gb EAT48278.1  /     | Metabolic process | Carbohydrate metabolic process |
| M18620  | putative fructose 1,6-bisphosphate aldolase [Oncometopia nigricans]                  | Metabolic process | Carbohydrate metabolic process |
| M18847  | hypothetical protein DAPPUDRAFT_218978 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| M18933  | chitin binding peritrophin-A, putative [Pediculus humanus corporis] >gi 212514415    | Metabolic process | Carbohydrate metabolic process |
| M19074  | hypothetical protein DAPPUDRAFT_188180 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| M19131  | hypothetical protein DAPPUDRAFT_218978 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| M19336  | unnamed protein product [Oikopleura dioica]  | Metabolic process | Carbohydrate metabolic process |
| M2028   |  | Metabolic process | Carbohydrate metabolic process |
| M2255   |  | Metabolic process | Carbohydrate metabolic process |
| M23222  | hypothetical protein DAPPUDRAFT_218978 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| M24012  | thrombospondin [Fenneropenaeus merguiensis]  | Metabolic process | Carbohydrate metabolic process |
| M26541  | hypothetical protein DAPPUDRAFT_310106 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| M2781   | chitin binding peritrophin-A, putative [Pediculus humanus corporis] >gi 212514415    | Metabolic process | Carbohydrate metabolic process |
| M2834   | alpha glucosidase [Litopenaeus vannamei]   | Metabolic process | Carbohydrate metabolic process |
| M31050  | chitin binding peritrophin-A, putative [Pediculus humanus corporis] >gi 212514415    | Metabolic process | Carbohydrate metabolic process |
| M31172  | hypothetical protein DAPPUDRAFT_223002 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| M3194   | lactate dehydrogenase [Litopenaeus vannamei] >gi 385211791 gb AFI47930.1  L-lat      | Metabolic process | Carbohydrate metabolic process |
| M3385   | PREDICTED: hypothetical protein [Saccoglossus kowalevskii]                           | Metabolic process | Carbohydrate metabolic process |
| M33902  |  | Metabolic process | Carbohydrate metabolic process |
| M3469   | mannosyltransferase 1, putative [Aedes aegypti] >gi 108883791 gb EAT48016.1  AA      | Metabolic process | Carbohydrate metabolic process |
| M35029  | hypothetical protein CAPTEDRAFT_149382 [Capitella teleta]                            | Metabolic process | Carbohydrate metabolic process |
| M36881  | peritrophin [Rimicaris exoculata]  | Metabolic process | Carbohydrate metabolic process |
| M3890   | kexokinase [Litopenaeus vannamei]  | Metabolic process | Carbohydrate metabolic process |
| M40107  | GJ15463 [Drosophila virilis] >gi 194141867 gb EDW58280.1  GJ15463 [Drosophila v      | Metabolic process | Carbohydrate metabolic process |
| M4050   |  | Metabolic process | Carbohydrate metabolic process |
| M41199  |  | Metabolic process | Carbohydrate metabolic process |
| M4184   | hypothetical protein DAPPUDRAFT_223002 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| M4573   | hypothetical protein DAPPUDRAFT_218978 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| M4996   |  | Metabolic process | Carbohydrate metabolic process |
| M5387   | thrombospondin [Marsupenaeus japonicus]  | Metabolic process | Carbohydrate metabolic process |
| M559    | hypothetical protein CGI_10022349 [Crassostrea gigas]                                | Metabolic process | Carbohydrate metabolic process |
| M55945  | hypothetical protein BRAFLDRAFT_262109 [Branchiostoma floridae] >gi 229298842        | Metabolic process | Carbohydrate metabolic process |
| M57268  | PREDICTED: carbohydrate sulfotransferase 9 isoform X1 [Chrysemys picta bellii] >gi 5 | Metabolic process | Carbohydrate metabolic process |
| M57844  | GE21870 [Drosophila yakuba] >gi 194180626 gb EDW94237.1  GE21870 [Drosophil          | Metabolic process | Carbohydrate metabolic process |
| M58927  |  | Metabolic process | Carbohydrate metabolic process |
| M60556  | hypothetical protein DAPPUDRAFT_307215 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| M63793  | PREDICTED: galactoside 2-alpha-L-fucosyltransferase 2-like [Echinops telfairii]      | Metabolic process | Carbohydrate metabolic process |
| M649    | hypothetical protein DAPPUDRAFT_194601 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| M67698  | hypothetical protein DAPPUDRAFT_198312 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| M71137  | Glutamine:fructose-6-phosphate aminotransferase 2 [Drosophila melanogaster] >gi      | Metabolic process | Carbohydrate metabolic process |
| M75519  |  | Metabolic process | Carbohydrate metabolic process |
| M7877   | i-type lysozyme-like protein 2 [Penaeus monodon]                                     | Metabolic process | Carbohydrate metabolic process |
| M81733  | defender against apoptotic death [Penaeus monodon]                                   | Metabolic process | Carbohydrate metabolic process |
| M91327  | trehalose-6-phosphate synthase [Fenneropenaeus chinensis]                            | Metabolic process | Carbohydrate metabolic process |
| M91486  | hypothetical protein EAG_15972 [Camponotus floridanus]                               | Metabolic process | Carbohydrate metabolic process |
| M93809  | PREDICTED: carbohydrate sulfotransferase 11-like [Nasonia vitripennis]               | Metabolic process | Carbohydrate metabolic process |
| M95016  | hypothetical protein DAPPUDRAFT_313010 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| M96176  |  | Metabolic process | Carbohydrate metabolic process |
| N10288  | hypothetical protein TcasGA2_TC012734 [Tribolium castaneum]                          | Metabolic process | Carbohydrate metabolic process |
| N11908  | endoplasmic reticulum protein 57 [Penaeus monodon]                                   | Metabolic process | Carbohydrate metabolic process |
| N12153  | i-type lysozyme-like protein 2 [Penaeus monodon]                                     | Metabolic process | Carbohydrate metabolic process |
| N12205  | hypothetical protein DAPPUDRAFT_223002 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| N12995  | hypothetical protein DAPPUDRAFT_218978 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| N12999  | hypothetical protein DAPPUDRAFT_194601 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| N13000  | hypothetical protein DAPPUDRAFT_194601 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| N13131  | hypothetical protein CAPTEDRAFT_149382 [Capitella teleta]                            | Metabolic process | Carbohydrate metabolic process |
| N13249  |  | Metabolic process | Carbohydrate metabolic process |
| N13297  | hypothetical protein DAPPUDRAFT_209471 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| N13357  | hypothetical protein DAPPUDRAFT_218978 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| N13605  | hypothetical protein YQE_11184, partial [Dendroctonus ponderosae]                    | Metabolic process | Carbohydrate metabolic process |
| N13755  | hypothetical protein DAPPUDRAFT_309434 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| N13793  | peritrophin A, isoform A [Drosophila melanogaster] >gi 24643467 ref NP_728324.1      | Metabolic process | Carbohydrate metabolic process |
| N13919  | PREDICTED: hypothetical protein LOC100120260 [Nasonia vitripennis]                   | Metabolic process | Carbohydrate metabolic process |
| N14679  | hypothetical protein DAPPUDRAFT_223002 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |

| ID     | Annotation   | GO term           | Go child term                  |
|--------|--|-------------------|--------------------------------|
| N14843 | cuticular protein [Artemia franciscana]  | Metabolic process | Carbohydrate metabolic process |
| N16657 | hypothetical protein DAPPUDRAFT_52904 [Daphnia pulex]                                | Metabolic process | Carbohydrate metabolic process |
| N18219 | hypothetical protein DAPPUDRAFT_300811 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| N18281 | Culex quinquefasciatus glycogen phosphorylase, mRNA                                  | Metabolic process | Carbohydrate metabolic process |
| N18293 | hypothetical protein BRAFLDRAFT_107076 [Branchiostoma floridae] >gi 229281129        | Metabolic process | Carbohydrate metabolic process |
| N1840  | chitin binding peritrophin-A, putative [Pediculus humanus corporis] >gi 212514415    | Metabolic process | Carbohydrate metabolic process |
| N18460 | hypothetical protein DAPPUDRAFT_303417 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| N18608 | PREDICTED: Loxodonta africana dolichyl-diphosphooligosaccharide--protein glycosylt   | Metabolic process | Carbohydrate metabolic process |
| N18791 | hypothetical protein DAPPUDRAFT_218978 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| N18846 | Chondroitin sulfate synthase, putative [Pediculus humanus corporis] >gi 212507482    | Metabolic process | Carbohydrate metabolic process |
| N18880 | chitin deacetylase 1 precursor [Cherax quadricarinatus]                              | Metabolic process | Carbohydrate metabolic process |
| N18901 | hypothetical protein DAPPUDRAFT_58801 [Daphnia pulex]                                | Metabolic process | Carbohydrate metabolic process |
| N18962 | pyruvate kinase 2 [Litopenaeus vannamei]   | Metabolic process | Carbohydrate metabolic process |
| N19079 |  | Metabolic process | Carbohydrate metabolic process |
| N19338 | putative triacylglycerol lipase [Daphnia pulex]                                      | Metabolic process | Carbohydrate metabolic process |
| N19626 | PREDICTED: dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa s   | Metabolic process | Carbohydrate metabolic process |
| N19873 | endo-beta-1,4-glucanase [Coptotermes formosanus]                                     | Metabolic process | Carbohydrate metabolic process |
| N20273 | trehalose-6-phosphate synthase [Fenneropenaeus chinensis]                            | Metabolic process | Carbohydrate metabolic process |
| N20547 | hypothetical protein TcasGA2_TC003876 [Tribolium castaneum]                          | Metabolic process | Carbohydrate metabolic process |
| N20763 |  | Metabolic process | Carbohydrate metabolic process |
| N21844 | PREDICTED: 6-phosphofructokinase-like isoform 3 [Acyrtosiphon pisum]                 | Metabolic process | Carbohydrate metabolic process |
| N21964 | cuticular protein [Artemia franciscana]  | Metabolic process | Carbohydrate metabolic process |
| N22117 | PREDICTED: beta-hexosaminidase subunit alpha-like [Ciona intestinalis]               | Metabolic process | Carbohydrate metabolic process |
| N22304 | PREDICTED: hexokinase-1-like [Megachile rotundata]                                   | Metabolic process | Carbohydrate metabolic process |
| N22459 | thrombospondin protein [Penaeus monodon]   | Metabolic process | Carbohydrate metabolic process |
| N22982 | PREDICTED: carbohydrate sulfotransferase 9 isoform X1 [Chrysemys picta bellii] >gi 5 | Metabolic process | Carbohydrate metabolic process |
| N23226 | Carbohydrate sulfotransferase 14 [Camponotus floridanus]                             | Metabolic process | Carbohydrate metabolic process |
| N23374 | hypothetical protein BRAFLDRAFT_123545 [Branchiostoma floridae] >gi 229277020        | Metabolic process | Carbohydrate metabolic process |
| N2465  | hypothetical protein TcasGA2_TC009890 [Tribolium castaneum]                          | Metabolic process | Carbohydrate metabolic process |
| N2481  | hypothetical protein TcasGA2_TC009890 [Tribolium castaneum]                          | Metabolic process | Carbohydrate metabolic process |
| N2485  |  | Metabolic process | Carbohydrate metabolic process |
| N25384 |  | Metabolic process | Carbohydrate metabolic process |
| N26189 | hypothetical protein DAPPUDRAFT_223002 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| N28597 |  | Metabolic process | Carbohydrate metabolic process |
| N28954 | Carbohydrate sulfotransferase 11 [Crassostrea gigas]                                 | Metabolic process | Carbohydrate metabolic process |
| N29090 | cuticular protein [Artemia franciscana]  | Metabolic process | Carbohydrate metabolic process |
| N2914  | chitin binding peritrophin-A, putative [Pediculus humanus corporis] >gi 212514415    | Metabolic process | Carbohydrate metabolic process |
| N30067 |  | Metabolic process | Carbohydrate metabolic process |
| N30228 |  | Metabolic process | Carbohydrate metabolic process |
| N30602 |  | Metabolic process | Carbohydrate metabolic process |
| N30729 |  | Metabolic process | Carbohydrate metabolic process |
| N31102 |  | Metabolic process | Carbohydrate metabolic process |
| N31446 | trehalose-6-phosphate synthase [Fenneropenaeus chinensis]                            | Metabolic process | Carbohydrate metabolic process |
| N31465 |  | Metabolic process | Carbohydrate metabolic process |
| N32999 | Heparan sulfate glucosamine 3-O-sulfotransferase 5 [Tupaia chinensis]                | Metabolic process | Carbohydrate metabolic process |
| N34711 | PREDICTED: chitinase-3-like protein 1 isoform X1 [Capra hircus]                      | Metabolic process | Carbohydrate metabolic process |
| N36122 | hypothetical protein CAPTEDRAFT_218878 [Capitella teleta]                            | Metabolic process | Carbohydrate metabolic process |
| N3717  |  | Metabolic process | Carbohydrate metabolic process |
| N3718  |  | Metabolic process | Carbohydrate metabolic process |
| N3728  |  | Metabolic process | Carbohydrate metabolic process |
| N3740  |  | Metabolic process | Carbohydrate metabolic process |
| N38910 | PREDICTED: carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8-like [Saccog  | Metabolic process | Carbohydrate metabolic process |
| N39090 | Beta-1,4-galactosyltransferase 3 [Chelonia mydas]                                    | Metabolic process | Carbohydrate metabolic process |
| N39451 | cuticular protein [Artemia franciscana]  | Metabolic process | Carbohydrate metabolic process |
| N41283 | PREDICTED: similar to n-acetylgalactosaminyltransferase [Tribolium castaneum] >gi 2  | Metabolic process | Carbohydrate metabolic process |
| N41735 | hypothetical protein DAPPUDRAFT_327753 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| N43379 | hypothetical protein TRIADDRAFT_51036 [Trichoplax adhaerens] >gi 190580249 gb        | Metabolic process | Carbohydrate metabolic process |
| N47191 | hypothetical protein DAPPUDRAFT_218978 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| N48559 | chitinase [Pandalopsis japonica]   | Metabolic process | Carbohydrate metabolic process |
| N58260 | chondroitin 4-sulfotransferase [Aedes aegypti] >gi 108873718 gb EAT37943.1  AAE      | Metabolic process | Carbohydrate metabolic process |
| N60524 | PREDICTED: chitotriosidase-1-like [Nasonia vitripennis]                              | Metabolic process | Carbohydrate metabolic process |
| N61129 | hypothetical protein DAPPUDRAFT_49320 [Daphnia pulex]                                | Metabolic process | Carbohydrate metabolic process |
| N6335  | hypothetical protein DAPPUDRAFT_218978 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| N6572  |  | Metabolic process | Carbohydrate metabolic process |
| N6715  | cuticular protein [Artemia franciscana]  | Metabolic process | Carbohydrate metabolic process |
| N6991  | hypothetical protein DAPPUDRAFT_307182 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| N7213  |  | Metabolic process | Carbohydrate metabolic process |
| N7300  | chitin binding peritrophin-A domain containing protein [Coptotermes formosanus]      | Metabolic process | Carbohydrate metabolic process |
| N8629  | hypothetical protein TcasGA2_TC012734 [Tribolium castaneum]                          | Metabolic process | Carbohydrate metabolic process |
| N8631  | hypothetical protein DAPPUDRAFT_235148 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| N9216  | cuticular protein, putative [Ixodes scapularis] >gi 215494596 gb EEC04237.1  cuticu  | Metabolic process | Carbohydrate metabolic process |
| N9218  | i-type lysozyme-like protein 2 [Penaeus monodon]                                     | Metabolic process | Carbohydrate metabolic process |
| N9427  | hypothetical protein DAPPUDRAFT_218978 [Daphnia pulex]                               | Metabolic process | Carbohydrate metabolic process |
| N9476  | Gasterosteus aculeatus clone CFW246-H10 mRNA sequence                                | Metabolic process | Carbohydrate metabolic process |
| N9500  | hypothetical protein TcasGA2_TC012734 [Tribolium castaneum]                          | Metabolic process | Carbohydrate metabolic process |
| N9745  |  | Metabolic process | Carbohydrate metabolic process |

| ID      | Annotation   | GO term           | Go child term                         |
|---------|--|-------------------|---------------------------------------|
| N9749   | hypothetical protein CAPTEDRAFT_167427 [Capitella teleta]  | Metabolic process | Carbohydrate metabolic process        |
| N9752   | hypothetical protein BRAFLDRAFT_70494 [Branchiostoma floridae] >gi 229289185 g   | Metabolic process | Carbohydrate metabolic process        |
| N9845   |  | Metabolic process | Carbohydrate metabolic process        |
| M109440 | Asparaginyl-tRNA synthetase, isoform A [Drosophila melanogaster] >gi 442628315 r   | Metabolic process | Cellular amino acid metabolic process |
| M1168   | hypothetical protein DAPPUDRAFT_191289 [Daphnia pulex]   | Metabolic process | Cellular amino acid metabolic process |
| M13834  | PREDICTED: LOW QUALITY PROTEIN: TP53-regulating kinase [Callithrix jacchus]  | Metabolic process | Cellular amino acid metabolic process |
| M14316  | Libinia emarginata isolate 11_12 voucher LemMALA alpha-spectrin mRNA, partial cds: Arginine kinase 2 [Neocaridina denticulata] | Metabolic process | Cellular amino acid metabolic process |
| M1680   |  | Metabolic process | Cellular amino acid metabolic process |
| M18723  | putative ATP synthase oligomycin sensitivity conferral protein [Coptotermes formosa  | Metabolic process | Cellular amino acid metabolic process |
| M18942  | hypothetical protein BRAFLDRAFT_78594 [Branchiostoma floridae] >gi 229295124 g   | Metabolic process | Cellular amino acid metabolic process |
| M2035   | PREDICTED: uncharacterized protein LOC101860265 isoform X1 [Aplysia californica]   | Metabolic process | Cellular amino acid metabolic process |
| M21     |  | Metabolic process | Cellular amino acid metabolic process |
| M23144  | glycine N-methyltransferase-like [Nasonia vitripennis]   | Metabolic process | Cellular amino acid metabolic process |
| M25     | hypothetical protein BRAFLDRAFT_63907 [Branchiostoma floridae] >gi 229296831 g   | Metabolic process | Cellular amino acid metabolic process |
| M26420  | hypothetical protein BRAFLDRAFT_72748 [Branchiostoma floridae] >gi 229278397 g   | Metabolic process | Cellular amino acid metabolic process |
| M288    | hypothetical protein DAPPUDRAFT_214647 [Daphnia pulex]   | Metabolic process | Cellular amino acid metabolic process |
| M3130   | Fumarylacetoacetate [Crassostrea gigas]  | Metabolic process | Cellular amino acid metabolic process |
| M378    | conserved hypothetical protein [Pediculus humanus corporis] >gi 212516655 gb EEF   | Metabolic process | Cellular amino acid metabolic process |
| M3801   | hypothetical protein DAPPUDRAFT_52799 [Daphnia pulex]  | Metabolic process | Cellular amino acid metabolic process |
| M4015   |  | Metabolic process | Cellular amino acid metabolic process |
| M4120   | hypothetical protein DAPPUDRAFT_318250 [Daphnia pulex]   | Metabolic process | Cellular amino acid metabolic process |
| M4436   | hypothetical protein BRAFLDRAFT_130501 [Branchiostoma floridae] >gi 229280180  | Metabolic process | Cellular amino acid metabolic process |
| M47556  | betaine homocysteine methyl transferase-like protein [Homarus americanus]  | Metabolic process | Cellular amino acid metabolic process |
| M5020   | PREDICTED: glycine cleavage system H protein, mitochondrial [Orcinus orca]   | Metabolic process | Cellular amino acid metabolic process |
| M5185   | hypothetical protein BRAFLDRAFT_103698 [Branchiostoma floridae] >gi 229280206  | Metabolic process | Cellular amino acid metabolic process |
| M545    | hypothetical protein DAPPUDRAFT_56817 [Daphnia pulex]  | Metabolic process | Cellular amino acid metabolic process |
| M56721  | L-aspartate dehydrogenase [Caligus clemensi]   | Metabolic process | Cellular amino acid metabolic process |
| M59782  | arginase [Hyriopsis cumingii]  | Metabolic process | Cellular amino acid metabolic process |
| M61204  | PREDICTED: Cricetulus griseus methylmalonyl-Coenzyme A mutase (Mut), mRNA  | Metabolic process | Cellular amino acid metabolic process |
| M61546  | homogentisate 1,2-dioxygenase HgmA [Capsaspora owczarzaki ATCC 30864] >gi 320:   | Metabolic process | Cellular amino acid metabolic process |
| M61757  | hypothetical protein DAPPUDRAFT_65532 [Daphnia pulex]  | Metabolic process | Cellular amino acid metabolic process |
| M63222  | hypothetical protein DAPPUDRAFT_308482 [Daphnia pulex]   | Metabolic process | Cellular amino acid metabolic process |
| M66867  | hypothetical protein CAPTEDRAFT_43016, partial [Capitella teleta]  | Metabolic process | Cellular amino acid metabolic process |
| M6768   | lactate dehydrogenase [Litopenaeus vannamei] >gi 385211791 gb AFI47930.1  L-lac  | Metabolic process | Cellular amino acid metabolic process |
| M70102  | GG11794 [Drosophila erecta] >gi 190655748 gb EDV52980.1  GG11794 [Drosophila   | Metabolic process | Cellular amino acid metabolic process |
| M7047   | hypothetical protein DAPPUDRAFT_22132 [Daphnia pulex]  | Metabolic process | Cellular amino acid metabolic process |
| M71240  | PREDICTED: RNA guanylyltransferase and 5-phosphatase-like [Saccoglossus kowalevskii]   | Metabolic process | Cellular amino acid metabolic process |
| M7237   | tryptophanyl-tRNA synthetase [Coccidioides posadasii str. Silveira]  | Metabolic process | Cellular amino acid metabolic process |
| M7360   | PREDICTED: valyl-tRNA synthetase-like [Saccoglossus kowalevskii]   | Metabolic process | Cellular amino acid metabolic process |
| M79250  | hypothetical protein DAPPUDRAFT_299913 [Daphnia pulex]   | Metabolic process | Cellular amino acid metabolic process |
| M86357  | betaine homocysteine methyl transferase-like protein [Homarus americanus]  | Metabolic process | Cellular amino acid metabolic process |
| M87594  | PREDICTED: tryptophan 2,3-dioxygenase [Nomascus leucogenys]  | Metabolic process | Cellular amino acid metabolic process |
| M93328  |  | Metabolic process | Cellular amino acid metabolic process |
| M94977  | Adenosylhomocysteinase [Lepeophtheirus salmonis]   | Metabolic process | Cellular amino acid metabolic process |
| M96624  | Glutaminase kidney isoform, mitochondrial [Acromyrmex echinatior]  | Metabolic process | Cellular amino acid metabolic process |
| M96944  | PREDICTED: argininosuccinate lyase-like [Apis mellifera]   | Metabolic process | Cellular amino acid metabolic process |
| M97234  | hypothetical protein DAPPUDRAFT_220733 [Daphnia pulex]   | Metabolic process | Cellular amino acid metabolic process |
| M9776   | PREDICTED: MGC80816 protein-like [Saccoglossus kowalevskii]  | Metabolic process | Cellular amino acid metabolic process |
| M9982   | hypothetical protein DAPPUDRAFT_318167 [Daphnia pulex]   | Metabolic process | Cellular amino acid metabolic process |
| N12862  | glutamine-oxaloacetic transaminase [Daphnia magna] >gi 224486260 gb ACN51895   | Metabolic process | Cellular amino acid metabolic process |
| N12875  | hypothetical protein DAPPUDRAFT_204767 [Daphnia pulex]   | Metabolic process | Cellular amino acid metabolic process |
| N13019  | cysteinyl-tRNA synthetase (predicted), isoform CRA_a [Rattus norvegicus]   | Metabolic process | Cellular amino acid metabolic process |
| N14451  | hematopoietic prostaglandin D synthase [Penaeus monodon]   | Metabolic process | Cellular amino acid metabolic process |
| N18205  | hypothetical protein DAPPUDRAFT_316089 [Daphnia pulex]   | Metabolic process | Cellular amino acid metabolic process |
| N18243  | hypothetical protein DAPPUDRAFT_318233 [Daphnia pulex]   | Metabolic process | Cellular amino acid metabolic process |
| N18290  | hypothetical protein DAPPUDRAFT_305406 [Daphnia pulex]   | Metabolic process | Cellular amino acid metabolic process |
| N18415  | glycyl-tRNA synthetase, putative [Pediculus humanus corporis] >gi 212518378 gb EE  | Metabolic process | Cellular amino acid metabolic process |
| N18485  | hypothetical protein BRAFLDRAFT_117885 [Branchiostoma floridae] >gi 229296009  | Metabolic process | Cellular amino acid metabolic process |
| N18645  | PREDICTED: threonine synthase-like 1 [Xenopus (Silurana) tropicalis]   | Metabolic process | Cellular amino acid metabolic process |
| N18663  | hypothetical protein CAPTEDRAFT_148401 [Capitella teleta]  | Metabolic process | Cellular amino acid metabolic process |
| N18692  | aldehyde dehydrogenase, putative [Ixodes scapularis] >gi 215502496 gb EEC11990.  | Metabolic process | Cellular amino acid metabolic process |
| N18769  | hypothetical protein DAPPUDRAFT_327265 [Daphnia pulex]   | Metabolic process | Cellular amino acid metabolic process |
| N18874  | lysyl-tRNA synthetase [Aedes aegypti] >gi 108868817 gb EAT33042.1  AAEL014702-   | Metabolic process | Cellular amino acid metabolic process |
| N18918  | phenylalanine-tRNA ligase alpha subunit [Danio rerio] >gi 146345522 sp Q1JPX3.2  | Metabolic process | Cellular amino acid metabolic process |
| N19176  | lactate dehydrogenase [Litopenaeus vannamei] >gi 385211791 gb AFI47930.1  L-lac  | Metabolic process | Cellular amino acid metabolic process |
| N19287  | hypothetical protein BRAFLDRAFT_124526 [Branchiostoma floridae] >gi 229275740  | Metabolic process | Cellular amino acid metabolic process |
| N19921  |  | Metabolic process | Cellular amino acid metabolic process |
| N19992  | PREDICTED: arginase-1-like [Loxodonta africana]  | Metabolic process | Cellular amino acid metabolic process |
| N20540  | PREDICTED: UPF0436 protein C9orf6-like [Monodelphis domestica]   | Metabolic process | Cellular amino acid metabolic process |
| N20761  | hypothetical protein DAPPUDRAFT_211091 [Daphnia pulex]   | Metabolic process | Cellular amino acid metabolic process |
| N20765  | Wormaldia moesta voucher Wmo2 putative enolase protein mRNA, partial cds:  | Metabolic process | Cellular amino acid metabolic process |
| N22201  | hypothetical protein DAPPUDRAFT_220335 [Daphnia pulex]   | Metabolic process | Cellular amino acid metabolic process |
| N23228  | glutathione S-transferases [Macrobrachium nipponense]  | Metabolic process | Cellular amino acid metabolic process |
| N27726  | hypothetical protein BRAFLDRAFT_183632 [Branchiostoma floridae] >gi 229277195  | Metabolic process | Cellular amino acid metabolic process |
| N31813  | lactate dehydrogenase [Litopenaeus vannamei]   | Metabolic process | Cellular amino acid metabolic process |
| N51830  | hypothetical protein DAPPUDRAFT_309832 [Daphnia pulex]   | Metabolic process | Cellular amino acid metabolic process |

| ID      | Annotation   | GO term           | Go child term                           |
|---------|--|-------------------|---|
| N53005  | betaine homocysteine methyl transferase-like protein [Homarus americanus]            | Metabolic process | Cellular amino acid metabolic process   |
| N55506  | 4-aminobutyrate aminotransferase [Aedes aegypti] >gi 108870984 gb EAT35209.1         | Metabolic process | Cellular amino acid metabolic process   |
| N56643  | mRNA-capping enzyme [Camponotus floridanus]  | Metabolic process | Cellular amino acid metabolic process   |
| N59606  | tyrosine hydroxylase isoform A [Manduca sexta]                                       | Metabolic process | Cellular amino acid metabolic process   |
| E5781   | mitochondrial ATP synthase epsilon subunit precursor [Litopenaeus vannamei]          | Metabolic process | Generation of precursor metabolites and |
| M10290  | glyceraldehyde-3-phosphate dehydrogenase [Procambarus clarkii]                       | Metabolic process | Generation of precursor metabolites and |
| M113051 | Euphausia superba voucher 760M mitochondrion, partial genome                         | Metabolic process | Generation of precursor metabolites and |
| M13619  | hypothetical protein DAPPUDRAFT_50463 [Daphnia pulex]                                | Metabolic process | Generation of precursor metabolites and |
| M14565  | mitochondrial ATP synthase gamma subunit precursor [Litopenaeus vannamei]            | Metabolic process | Generation of precursor metabolites and |
| M17951  | PREDICTED: glycogen debranching enzyme-like [Nasonia vitripennis]                    | Metabolic process | Generation of precursor metabolites and |
| M18729  | PREDICTED: Otolemur garnettii succinate-CoA ligase, alpha subunit (SUCLG1), mRNA     | Metabolic process | Generation of precursor metabolites and |
| M18821  | mitochondrial ATP synthase coupling factor 6 precursor [Ochlerotatus taeniorhynchus] | Metabolic process | Generation of precursor metabolites and |
| M18904  | hypothetical protein DAPPUDRAFT_230269 [Daphnia pulex]                               | Metabolic process | Generation of precursor metabolites and |
| M2029   | putative glycogen synthase [Daphnia pulex]   | Metabolic process | Generation of precursor metabolites and |
| M21528  | hypothetical protein DAPPUDRAFT_231048 [Daphnia pulex]                               | Metabolic process | Generation of precursor metabolites and |
| M21548  |  | Metabolic process | Generation of precursor metabolites and |
| M23287  | cytochrome c oxidase-like protein [Glyptapanteles flavicoxis]                        | Metabolic process | Generation of precursor metabolites and |
| M24954  | Euphausia superba mitochondrion, partial genome                                      | Metabolic process | Generation of precursor metabolites and |
| M31032  | mitochondrial cytochrome c oxidase subunit Va [Litopenaeus vannamei]                 | Metabolic process | Generation of precursor metabolites and |
| M42144  | Euphausia superba voucher 760M mitochondrion, partial genome                         | Metabolic process | Generation of precursor metabolites and |
| M46863  | Euphausia superba voucher 760M mitochondrion, partial genome                         | Metabolic process | Generation of precursor metabolites and |
| M5551   |  | Metabolic process | Generation of precursor metabolites and |
| M55970  | Euphausia superba voucher 702K mitochondrion, partial genome                         | Metabolic process | Generation of precursor metabolites and |
| M57202  | mitochondrial cytochrome c oxidase subunit IV [Litopenaeus vannamei]                 | Metabolic process | Generation of precursor metabolites and |
| M63042  | S-adenosylmethionine synthetase [Candida tropicalis MYA-3404] >gi 240132872 gb       | Metabolic process | Generation of precursor metabolites and |
| M70684  | hypothetical protein DAPPUDRAFT_308310 [Daphnia pulex]                               | Metabolic process | Generation of precursor metabolites and |
| M785    | PREDICTED: glycogen debranching enzyme [Megachile rotundata]                         | Metabolic process | Generation of precursor metabolites and |
| M8823   | hypothetical protein DAPPUDRAFT_64425 [Daphnia pulex]                                | Metabolic process | Generation of precursor metabolites and |
| M8882   | 1,4-alpha-glucan-branching enzyme [Trichinella spiralis] >gi 316967211 gb EFV5167    | Metabolic process | Generation of precursor metabolites and |
| N11963  |  | Metabolic process | Generation of precursor metabolites and |
| N18402  | phosphoenolpyruvate carboxykinase [Litopenaeus vannamei]                             | Metabolic process | Generation of precursor metabolites and |
| N20906  |  | Metabolic process | Generation of precursor metabolites and |
| N27804  | mitochondrial ubiquinol-cytochrome c reductase complex 11 kDa protein [Scylla para   | Metabolic process | Generation of precursor metabolites and |
| N3133   | PREDICTED: S-adenosylmethionine synthase-like isoform 2 [Nasonia vitripennis]        | Metabolic process | Generation of precursor metabolites and |
| N31394  | cytochrome c oxidase subunit VIIA putative [Scylla paramamosain]                     | Metabolic process | Generation of precursor metabolites and |
| N3151   | PREDICTED: S-adenosylmethionine synthase-like isoform 1 [Nasonia vitripennis]        | Metabolic process | Generation of precursor metabolites and |
| N36505  | vacuolar proton translocating ATPase 116 kDa subunit A isoform, putative [Pediculus  | Metabolic process | Generation of precursor metabolites and |
| N9508   | mitochondrial cytochrome c oxidase subunit IV [Litopenaeus vannamei]                 | Metabolic process | Generation of precursor metabolites and |
| M10403  | ankyrin-1, putative [Pediculus humanus corporis] >gi 212518141 gb EEB19933.1  ar     | Metabolic process | Generation of precursor metabolites and |
| M16759  | hypothetical protein DAPPUDRAFT_305782 [Daphnia pulex]                               | Metabolic process | Lipid metabolic process                 |
| M1878   | Homo sapiens peroxisomal D3,D2-enoyl-CoA isomerase [synthetic construct] >gi 606     | Metabolic process | Lipid metabolic process                 |
| M3079   | PREDICTED: similar to CG9914 CG9914-PA isoform 1 [Tribolium castaneum] >gi 2700      | Metabolic process | Lipid metabolic process                 |
| M32708  | putative triacylglycerol lipase [Daphnia pulex]                                      | Metabolic process | Lipid metabolic process                 |
| M5575   | proteasome 26S non-ATPase subunit 10 [Xenopus (Silurana) tropicalis] >gi 89266984    | Metabolic process | Lipid metabolic process                 |
| M57812  | hypothetical protein DAPPUDRAFT_300931 [Daphnia pulex]                               | Metabolic process | Lipid metabolic process                 |
| M58225  | hypothetical protein DAPPUDRAFT_300149 [Daphnia pulex]                               | Metabolic process | Lipid metabolic process                 |
| M58882  | PREDICTED: phospholipase A2-like [Bombbyx mori]                                      | Metabolic process | Lipid metabolic process                 |
| M61209  | Diacylglycerol kinase zeta, putative [Pediculus humanus corporis] >gi 212508871 gb   | Metabolic process | Lipid metabolic process                 |
| M64386  | ras, putative [Pediculus humanus corporis] >gi 212509170 gb EEB12638.1  ras, put     | Metabolic process | Lipid metabolic process                 |
| M64437  | hypothetical protein BRAFLDRAFT_232211 [Branchiostoma floridae] >gi 229281209        | Metabolic process | Lipid metabolic process                 |
| M67472  | hypothetical protein DAPPUDRAFT_56898 [Daphnia pulex]                                | Metabolic process | Lipid metabolic process                 |
| M71319  | Ldlr2-a protein [Xenopus laevis] >gi 213626297 gb AAI70522.1  Ldlr2-a protein [Xer   | Metabolic process | Lipid metabolic process                 |
| M735    | oxidoreductase [alpha proteobacterium BAL199] >gi 15917770 gb EDP62321.1  sh         | Metabolic process | Lipid metabolic process                 |
| M75326  | PREDICTED: LOW QUALITY PROTEIN: alkaline ceramidase 2 [Dasypus novemcinctus]         | Metabolic process | Lipid metabolic process                 |
| M775    | hypothetical protein DAPPUDRAFT_231244 [Daphnia pulex]                               | Metabolic process | Lipid metabolic process                 |
| M86465  | PREDICTED: galactose-3-O-sulfotransferase 1-like [Saccoglossus kowalevskii]          | Metabolic process | Lipid metabolic process                 |
| M90544  | sphingomyelin phosphodiesterase [Cherax quadricarinatus]                             | Metabolic process | Lipid metabolic process                 |
| M91179  | hypothetical protein DAPPUDRAFT_199604 [Daphnia pulex]                               | Metabolic process | Lipid metabolic process                 |
| N12095  | 7-dehydrocholesterol reductase [Lepeophtheirus salmonis] >gi 290462921 gb ADD2       | Metabolic process | Lipid metabolic process                 |
| N13719  |  | Metabolic process | Lipid metabolic process                 |
| N14473  | PREDICTED: decaprenyl-diphosphate synthase subunit 1-like [Nasonia vitripennis]      | Metabolic process | Lipid metabolic process                 |
| N18980  | hypothetical protein BRAFLDRAFT_115040 [Branchiostoma floridae] >gi 229274202        | Metabolic process | Lipid metabolic process                 |
| N19597  | PREDICTED: uncharacterized protein LOC100904803 [Metaseiulus occidentalis]           | Metabolic process | Lipid metabolic process                 |
| N19820  | hypothetical protein CAPTEDRAFT_160702 [Capitella teleta]                            | Metabolic process | Lipid metabolic process                 |
| N19986  | hypothetical protein DAPPUDRAFT_319865 [Daphnia pulex]                               | Metabolic process | Lipid metabolic process                 |
| N20177  | hypothetical protein DAPPUDRAFT_31637 [Daphnia pulex]                                | Metabolic process | Lipid metabolic process                 |
| N21911  | salivary alkaline phosphatase [Daphnia pulex]  | Metabolic process | Lipid metabolic process                 |
| N22590  | hypothetical protein DAPPUDRAFT_307575 [Daphnia pulex]                               | Metabolic process | Lipid metabolic process                 |
| N22794  | geranylgeranyl pyrophosphate synthase/polyprenyl synthetase, putative [Ixodes scap   | Metabolic process | Lipid metabolic process                 |
| N23066  | crustacyanin subunit A [Fenneropenaeus merguiensis]                                  | Metabolic process | Lipid metabolic process                 |
| N24872  | Inositol monophosphatase 3 [Caligus clemensi]  | Metabolic process | Lipid metabolic process                 |
| N36501  |  | Metabolic process | Lipid metabolic process                 |
| N37214  | Alkaline phosphatase, tissue-nonspecific isozyme precursor, putative [Pediculus hum  | Metabolic process | Lipid metabolic process                 |
| N45199  | period [Eurydice pulchra]  | Metabolic process | Lipid metabolic process                 |
| N7648   |  | Metabolic process | Lipid metabolic process                 |
| M109012 | PREDICTED: agmatinase, mitochondrial-like [Strongylocentrotus purpuratus]            | Metabolic process | Nitrogen compound metabolic process     |

| ID      | Annotation  | GO term           | Go child term                        |
|---------|---|-------------------|--------------------------------------|
| M2380   |   | Metabolic process | Nitrogen compound metabolic process  |
| M35901  | hypothetical protein BRAFLDRAFT_78594 [Branchiostoma floridae] >gi 229295124 g                        | Metabolic process | Nitrogen compound metabolic process  |
| M94914  | glycosyl-phosphatidylinositol-linked carbonic anhydrase [Litopenaeus vannamei]                        | Metabolic process | Nitrogen compound metabolic process  |
| N10315  | hypothetical protein DAPPUDRAFT_306977 [Daphnia pulex]  | Metabolic process | Nitrogen compound metabolic process  |
| N32147  | PREDICTED: peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase [Sarcophil Metabolic process   | Metabolic process | Nitrogen compound metabolic process  |
| N34523  | agmatinase [Pseudomonas] >gi 395337156 gb EFJ69014.1  agmatinase [Pseudomonas] Metabolic process      | Metabolic process | Nitrogen compound metabolic process  |
| N45146  | hypothetical protein BRAFLDRAFT_95006 [Branchiostoma floridae] >gi 229286520 g                        | Metabolic process | Nitrogen compound metabolic process  |
| N9798   | glycosyl-phosphatidylinositol-linked carbonic anhydrase [Litopenaeus vannamei]                        | Metabolic process | Nitrogen compound metabolic process  |
| E2163   | oncoprotein nm23 [Litopenaeus vannamei]   | Metabolic process | Nucleobase-containing compound metab |
| M101631 |   | Metabolic process | Nucleobase-containing compound metab |
| M14480  | PREDICTED: Saccoglossus kowalevskii DNA directed RNA polymerase II polypeptide E- Metabolic process   | Metabolic process | Nucleobase-containing compound metab |
| M22464  | RNA polymerase I/III 16Kd polypeptide, putative [Ixodes scapularis] >gi 215493414 g                   | Metabolic process | Nucleobase-containing compound metab |
| M2790   | putative myosin head [Trichinella spiralis] >gi 316971212 gb EFV55023.1  putative i                   | Metabolic process | Nucleobase-containing compound metab |
| M3981   | PREDICTED: similar to adenine phosphoribosyltransferase [Tribolium castaneum] >gi                     | Metabolic process | Nucleobase-containing compound metab |
| M40599  | oncoprotein nm23 [Litopenaeus vannamei]   | Metabolic process | Nucleobase-containing compound metab |
| M4174   | hypothetical protein DAPPUDRAFT_306425 [Daphnia pulex]  | Metabolic process | Nucleobase-containing compound metab |
| M5074   |   | Metabolic process | Nucleobase-containing compound metab |
| M56219  | Pseudouridylate synthase 7-like protein [Harpegnathos saltator]                                       | Metabolic process | Nucleobase-containing compound metab |
| M56287  | hypothetical protein DAPPUDRAFT_304334 [Daphnia pulex]  | Metabolic process | Nucleobase-containing compound metab |
| M56865  | PREDICTED: inosine-5'-monophosphate dehydrogenase isoform 1 [Apis mellifera] >gi                      | Metabolic process | Nucleobase-containing compound metab |
| M6211   | DNA-directed RNA polymerase [Coptotermes formosanus]  | Metabolic process | Nucleobase-containing compound metab |
| M62133  |   | Metabolic process | Nucleobase-containing compound metab |
| M62739  | ABC protein, subfamily ABCA [Daphnia pulex]   | Metabolic process | Nucleobase-containing compound metab |
| M78121  | hypothetical protein TcasGA2_TC014142 [Tribolium castaneum]   | Metabolic process | Nucleobase-containing compound metab |
| M8921   | NME/NM23 family member 7 [Xenopus (Silurana) tropicalis] >gi 38181932 gb AAH6                         | Metabolic process | Nucleobase-containing compound metab |
| N10324  | PREDICTED: UDP-galactose-4-epimerase [Oryctolagus cuniculus]  | Metabolic process | Nucleobase-containing compound metab |
| N12873  |   | Metabolic process | Nucleobase-containing compound metab |
| N18215  | conserved hypothetical protein [Pediculus humanus corporis] >gi 212508370 gb EEF                      | Metabolic process | Nucleobase-containing compound metab |
| N18669  | hypothetical protein BRAFLDRAFT_76524 [Branchiostoma floridae] >gi 229275470 g                        | Metabolic process | Nucleobase-containing compound metab |
| N18936  | PREDICTED: bifunctional purine biosynthesis protein PURH [Nasonia vitripennis]                        | Metabolic process | Nucleobase-containing compound metab |
| N18959  | exonuclease 3'-5' domain containing 2 [Xenopus laevis]  | Metabolic process | Nucleobase-containing compound metab |
| N19230  | hypothetical protein DAPPUDRAFT_307202 [Daphnia pulex]  | Metabolic process | Nucleobase-containing compound metab |
| N19588  | PREDICTED: adenylosuccinate lyase-like [Nasonia vitripennis]  | Metabolic process | Nucleobase-containing compound metab |
| N20154  | purine biosynthesis protein 6, pur6, putative [Pediculus humanus corporis] >gi 21251Metabolic process | Metabolic process | Nucleobase-containing compound metab |
| N20270  | Caenorhabditis briggsae Hypothetical protein CBG16623 (CBG16623) mRNA, complet                        | Metabolic process | Nucleobase-containing compound metab |
| N20569  | glycynamide ribonucleotide synthetase-aminoimidazole ribonucleotide synthetase-gly                    | Metabolic process | Nucleobase-containing compound metab |
| N21697  |   | Metabolic process | Nucleobase-containing compound metab |
| N24180  | hypothetical protein DAPPUDRAFT_305695 [Daphnia pulex]  | Metabolic process | Nucleobase-containing compound metab |
| N25611  | hypothetical protein DAPPUDRAFT_202914 [Daphnia pulex]  | Metabolic process | Nucleobase-containing compound metab |
| N29027  | hypothetical protein BRAFLDRAFT_116233 [Branchiostoma floridae] >gi 229290860                         | Metabolic process | Nucleobase-containing compound metab |
| N30083  | PREDICTED: adenylate cyclase type 9-like [Megachile rotundata]  | Metabolic process | Nucleobase-containing compound metab |
| N39678  | hypothetical protein DAPPUDRAFT_230475 [Daphnia pulex]  | Metabolic process | Nucleobase-containing compound metab |
| N43051  | hypothetical protein BRAFLDRAFT_129513 [Branchiostoma floridae] >gi 229291355                         | Metabolic process | Nucleobase-containing compound metab |
| N44520  | PREDICTED: exonuclease 3'-5' domain-containing protein 2 [Condylura cristata]                         | Metabolic process | Nucleobase-containing compound metab |
| N52606  | Inosine triphosphate pyrophosphatase [Salmo salar] >gi 197632311 gb ACH70879.1                        | Metabolic process | Nucleobase-containing compound metab |
| N60051  | adenyls kinase, putative [Ixodes scapularis] >gi 215491529 gb ECC01170.1  ac                          | Metabolic process | Nucleobase-containing compound metab |
| N7920   | sodium potassium-transporting ATPase subunit beta [Litopenaeus vannamei]                              | Metabolic process | Nucleobase-containing compound metab |
| N9290   | hypothetical protein DAPPUDRAFT_331571 [Daphnia pulex]  | Metabolic process | Nucleobase-containing compound metab |
| E1475   | guanine nucleotide-binding protein, putative [Ixodes scapularis] >gi 215507555 gb E                   | Metabolic process | Nucleobase-containing compound metab |
| E4140   | unknown [Dendroctonus ponderosae]   | Metabolic process | Other                                |
| M101952 | PREDICTED: long-chain-fatty-acid-CoA ligase 1-like [Megachile rotundata]                              | Metabolic process | Other                                |
| M103670 | hypothetical protein BRAFLDRAFT_126836 [Branchiostoma floridae] >gi 229295634                         | Metabolic process | Other                                |
| M108336 | protein kinase C and casein kinase substrate in neurons protein, putative [Pediculus h                | Metabolic process | Other                                |
| M108370 | hypothetical protein BRAFLDRAFT_89744 [Branchiostoma floridae] >gi 229273995 g                        | Metabolic process | Other                                |
| M11883  | PREDICTED: acyl-CoA synthetase family member 3, mitochondrial-like isoform X1 [Ap                     | Metabolic process | Other                                |
| M1220   | PREDICTED: methylenetetrahydrofolate dehydrogenase 1-like [Saccoglossus kowalev:                      | Metabolic process | Other                                |
| M12227  | PREDICTED: cytochrome c-type heme lyase-like [Strongylocentrotus purpuratus]                          | Metabolic process | Other                                |
| M12718  | PREDICTED: WD repeat domain-containing protein 83-like [Strongylocentrotus purpu                      | Metabolic process | Other                                |
| M1473   | PREDICTED: long-chain fatty acid transport protein 4-like [Aplysia californica]                       | Metabolic process | Other                                |
| M14744  | PREDICTED: similar to mandelate racemase [Tribolium castaneum] >gi 270013803 g                        | Metabolic process | Other                                |
| M16328  | hypothetical protein CAPTEDRAFT_176070 [Capitella teleta]   | Metabolic process | Other                                |
| M1672   | hypothetical protein DAPPUDRAFT_51170 [Daphnia pulex]   | Metabolic process | Other                                |
| M1775   | hypothetical protein DAPPUDRAFT_200081 [Daphnia pulex]  | Metabolic process | Other                                |
| M18842  | PREDICTED: similar to AGAP004744-PA [Tribolium castaneum]   | Metabolic process | Other                                |
| M33255  | hypothetical protein BRAFLDRAFT_120483 [Branchiostoma floridae] >gi 229282046                         | Metabolic process | Other                                |
| M3693   | WD-repeat protein, putative [Ixodes scapularis] >gi 215505822 gb EEC15316.1  WD                       | Metabolic process | Other                                |
| M3796   | hypothetical protein DAPPUDRAFT_299821 [Daphnia pulex]  | Metabolic process | Other                                |
| M383    | PREDICTED: similar to tan CG12120-PA [Tribolium castaneum] >gi 270004130 gb EF.                       | Metabolic process | Other                                |
| M4676   | SEL-1, putative [Ixodes scapularis] >gi 215509773 gb EEC19226.1  SEL-1, putative [I:                  | Metabolic process | Other                                |
| M5130   | hypothetical protein AaeL_AAELO08679 [Aedes aegypti] >gi 122105719 sp Q16Y34.: Metabolic process      | Metabolic process | Other                                |
| M58016  | Diacylglycerol O-acyltransferase, putative [Pediculus humanus corporis] >gi 2125152                   | Metabolic process | Other                                |
| M586    | Cytosolic Fe-S cluster assembly factor NUBP1-like protein [Crassostrea gigas]                         | Metabolic process | Other                                |
| M58842  | hypothetical protein DAPPUDRAFT_306312 [Daphnia pulex]  | Metabolic process | Other                                |
| M652    | hypothetical protein DAPPUDRAFT_303807 [Daphnia pulex]  | Metabolic process | Other                                |
| M65529  | putative serine palmitoyltransferase [Hottentotta judaicus]   | Metabolic process | Other                                |
| M69422  |   | Metabolic process | Other                                |

| ID      | Annotation   | GO term           | Go child term               |
|---------|--|-------------------|-----------------------------|
| M72726  | hypothetical protein CAPTEDRAFT_161927 [Capitella teleta]  | Metabolic process | Other                       |
| M78789  | RB13-6 antigen, putative [Ixodes scapularis] >gi 215507372 gb EEC16864.1  RB13-6                         | Metabolic process | Other                       |
| M848    | PREDICTED: molybdopterin synthase catalytic subunit-like [Amphimedon queenslandi]                        | Metabolic process | Other                       |
| M93902  | PREDICTED: UDP-N-acetylhexosamine pyrophosphorylase-like [Metaseiulus occidentalis]                      | Metabolic process | Other                       |
| M941    | hypothetical protein BRAFLDRAFT_128896 [Branchiostoma floridae] >gi 229297143                            | Metabolic process | Other                       |
| N10610  | hypothetical protein DAPPUDRAFT_221341 [Daphnia pulex]   | Metabolic process | Other                       |
| N11132  | aldehyde-activating protein [Rhizobium]  | Metabolic process | Other                       |
| N11504  | fatty acid synthase [Litopenaeus vannamei]   | Metabolic process | Other                       |
| N11532  | GMP synthase, putative [Pediculus humanus corporis] >gi 212512030 gb EEB14877                            | Metabolic process | Other                       |
| N11915  | hypothetical protein DAPPUDRAFT_203975 [Daphnia pulex]   | Metabolic process | Other                       |
| N13137  | hypothetical protein BRAFLDRAFT_118764 [Branchiostoma floridae] >gi 229298782                            | Metabolic process | Other                       |
| N13439  | 3-hydroxybutyrate dehydrogenase [Branchiostoma floridae] >gi 229297934 gb EEN                            | Metabolic process | Other                       |
| N18287  | PREDICTED: long-chain-fatty-acid-CoA ligase 3-like [Megachile rotundata]                                 | Metabolic process | Other                       |
| N18322  | JHE-like carboxylesterase 1 [Pandalopsis japonica]   | Metabolic process | Other                       |
| N18351  | Histone acetyltransferase KAT2B [Crassostrea gigas]  | Metabolic process | Other                       |
| N18659  | tetratricopeptide repeat protein, putative [Ixodes scapularis] >gi 215491239 gb EEC                      | Metabolic process | Other                       |
| N18686  |  | Metabolic process | Other                       |
| N19473  | putative hemomucin [Schistocerca gregaria]   | Metabolic process | Other                       |
| N19692  |  | Metabolic process | Other                       |
| N19981  | PREDICTED: similar to glucosyl/glucuronosyl transferases [Tribolium castaneum]                           | Metabolic process | Other                       |
| N19988  | hypothetical protein DAPPUDRAFT_190063 [Daphnia pulex]   | Metabolic process | Other                       |
| N20264  | PREDICTED: tissue specific transplantation antigen P35B-like [Saccoglossus kowalevskii]                  | Metabolic process | Other                       |
| N20465  | glucosyl/glucuronosyl transferases [Aedes aegypti] >gi 108881419 gb EAT45644.1                           | Metabolic process | Other                       |
| N20470  | PREDICTED: 1-acyl-sn-glycerol-3-phosphate acyltransferase gamma-like [Nasonia vitripennis]               | Metabolic process | Other                       |
| N20529  | gem-associated protein, putative [Ixodes scapularis] >gi 215498896 gb EEC08390.1                         | Metabolic process | Other                       |
| N20590  | Phosphotriesterase-related protein [Crassostrea gigas]   | Metabolic process | Other                       |
| N21023  | hypothetical protein [alpha proteobacterium SCGG AAA015-N04]   | Metabolic process | Other                       |
| N21249  | hypothetical protein DAPPUDRAFT_97952 [Daphnia pulex]  | Metabolic process | Other                       |
| N21899  | hypothetical protein DAPPUDRAFT_302220 [Daphnia pulex]   | Metabolic process | Other                       |
| N22108  | hypothetical protein DAPPUDRAFT_306348 [Daphnia pulex]   | Metabolic process | Other                       |
| N22272  | hypothetical protein DAPPUDRAFT_231053 [Daphnia pulex]   | Metabolic process | Other                       |
| N22649  | hypothetical protein DAPPUDRAFT_327533 [Daphnia pulex]   | Metabolic process | Other                       |
| N22872  | hypothetical protein DAPPUDRAFT_210509 [Daphnia pulex]   | Metabolic process | Other                       |
| N23265  | PREDICTED: hypothetical protein [Saccoglossus kowalevskii]   | Metabolic process | Other                       |
| N25112  | PREDICTED: uncharacterized protein LOC100877790 [Megachile rotundata]                                    | Metabolic process | Other                       |
| N25254  | hypothetical protein TRIADDRDRAFT_56199 [Trichoplax adhaerens] >gi 190584349 gb                          | Metabolic process | Other                       |
| N25668  | PREDICTED: molybdenum cofactor biosynthesis protein 1 isoform X1 [Cavia porcellus]                       | Metabolic process | Other                       |
| N26353  | hypothetical protein BRAFLDRAFT_101015 [Branchiostoma floridae] >gi 229290895                            | Metabolic process | Other                       |
| N26424  | hypothetical protein DAPPUDRAFT_307317 [Daphnia pulex]   | Metabolic process | Other                       |
| N27420  | PREDICTED: methylglutaconyl-CoA hydratase, mitochondrial-like [Ceratitis capitata]                       | Metabolic process | Other                       |
| N29868  | alkaline phosphatase, partial [Macrobrachium rosenbergii]  | Metabolic process | Other                       |
| N30129  |  | Metabolic process | Other                       |
| N32142  | tRNA 2-thiocytidine biosynthesis protein ttcA [Lepeophtheirus salmonis]                                  | Metabolic process | Other                       |
| N34674  | PREDICTED: hypothetical protein LOC100117960 [Nasonia vitripennis]                                       | Metabolic process | Other                       |
| N40837  | hypothetical protein BRAFLDRAFT_77131 [Branchiostoma floridae] >gi 229295502 g                           | Metabolic process | Other                       |
| N41594  | hypothetical protein TRIADDRDRAFT_14880 [Trichoplax adhaerens] >gi 190586970 gb                          | Metabolic process | Other                       |
| N49965  | hypothetical protein BRAFLDRAFT_126580 [Branchiostoma floridae] >gi 229272947                            | Metabolic process | Other                       |
| N50248  |  | Metabolic process | Other                       |
| N50663  | hypothetical protein DAPPUDRAFT_316454 [Daphnia pulex]   | Metabolic process | Other                       |
| N51392  | PREDICTED: acyl-CoA synthetase short-chain family member 1-like [Saccoglossus kowalevskii]               | Metabolic process | Other                       |
| N57795  | nitric oxide synthase [Litopenaeus vannamei]   | Metabolic process | Other                       |
| N60366  | hypothetical protein EAI_00199 [Harpegnathos saltator]   | Metabolic process | Other                       |
| N7968   | PREDICTED: Caenorhabditis Epsilon Oxide Hydrolase family member (ceeh-1)-like [Saccoglossus kowalevskii] | Metabolic process | Other                       |
| N9043   | PREDICTED: inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase [Metabolic process]  | Metabolic process | Other                       |
| E3439   | Xanthine dehydrogenase/oxidase [Salmo salar]   | Metabolic process | Oxidation-reduction process |
| E3651   | extracellular superoxide dismutase precursor [Pacifastacus leniusculus]                                  | Metabolic process | Oxidation-reduction process |
| M111084 | Euphausia superba mitochondrion, partial genome  | Metabolic process | Oxidation-reduction process |
| M13711  | extracellular superoxide dismutase precursor [Pacifastacus leniusculus]                                  | Metabolic process | Oxidation-reduction process |
| M18084  | Alkylated DNA repair protein alkB-like protein 8 [Camponotus floridanus]                                 | Metabolic process | Oxidation-reduction process |
| M19061  | PREDICTED: Saccoglossus kowalevskii NADH dehydrogenase iron-sulfur protein 8, mitochondrial              | Metabolic process | Oxidation-reduction process |
| M19104  |  | Metabolic process | Oxidation-reduction process |
| M1958   | hypothetical protein DAPPUDRAFT_315212 [Daphnia pulex]   | Metabolic process | Oxidation-reduction process |
| M21476  | protein disulfide isomerase [Litopenaeus vannamei]   | Metabolic process | Oxidation-reduction process |
| M33821  | ubiquitin [Schizosaccharomyces cryophilus OY26]  | Metabolic process | Oxidation-reduction process |
| M37562  |  | Metabolic process | Oxidation-reduction process |
| M4807   | carbonyl reductase [Daphnia pulex]   | Metabolic process | Oxidation-reduction process |
| M5066   | hypothetical protein DAPPUDRAFT_304354 [Daphnia pulex]   | Metabolic process | Oxidation-reduction process |
| M56300  | hypothetical protein DAPPUDRAFT_306714 [Daphnia pulex]   | Metabolic process | Oxidation-reduction process |
| M57279  | PREDICTED: dehydrogenase/reductase SDR family member 11 [Pseudopodoces humilis]                          | Metabolic process | Oxidation-reduction process |
| M58100  | hypothetical protein DAPPUDRAFT_202746 [Daphnia pulex]   | Metabolic process | Oxidation-reduction process |
| M61083  | extracellular superoxide dismutase precursor [Pacifastacus leniusculus]                                  | Metabolic process | Oxidation-reduction process |
| M62474  | cytochrome P450 [Litopenaeus vannamei]   | Metabolic process | Oxidation-reduction process |
| M65385  | hypothetical protein DAPPUDRAFT_304184 [Daphnia pulex]   | Metabolic process | Oxidation-reduction process |
| M66353  | hypothetical protein DAPPUDRAFT_199005 [Daphnia pulex]   | Metabolic process | Oxidation-reduction process |
| M73880  | thromboxane A synthase [Penaeus monodon]   | Metabolic process | Oxidation-reduction process |
| M80754  | glyceraldehyde-3-phosphate dehydrogenase [Rimicaris exoculata]   | Metabolic process | Oxidation-reduction process |

| ID                             | Annotation   | GO term                 | Go child term                 |
|--------------------------------|--|-------------------------|-------------------------------|
| M83059                         | PREDICTED: cytochrome P450 2J2-like isoform 2 [Meleagris gallopavo]                                  | Metabolic process       | Oxidation-reduction process   |
| M9052                          | Retinol dehydrogenase 11 [Camponotus floridanus]   | Metabolic process       | Oxidation-reduction process   |
| M92656                         | hypothetical protein TRIADDRAFT_54215 [Trichoplax adhaerens] >gi 190586282 gb                        | Metabolic process       | Oxidation-reduction process   |
| M99381                         | hypothetical protein DAPPUDRAFT_251911 [Daphnia pulex]   | Metabolic process       | Oxidation-reduction process   |
| N10515                         | hypothetical protein TcasGA2_TC014229 [Tribolium castaneum]  | Metabolic process       | Oxidation-reduction process   |
| N10730                         | PREDICTED: Saccoglossus kowalevskii NADH dehydrogenase iron-sulfur protein 8, mit                    | Metabolic process       | Oxidation-reduction process   |
| N10779                         | peroxiredoxin [Litopenaeus vannamei]   | Metabolic process       | Oxidation-reduction process   |
| N11974                         | hypothetical protein CAPTEDRAFT_167094 [Capitella teleta]  | Metabolic process       | Oxidation-reduction process   |
| N12985                         | hypothetical protein DAPPUDRAFT_188248 [Daphnia pulex]   | Metabolic process       | Oxidation-reduction process   |
| N13222                         | hypothetical protein DAPPUDRAFT_50786 [Daphnia pulex]  | Metabolic process       | Oxidation-reduction process   |
| N16890                         | thromboxane A synthase [Penaeus monodon]   | Metabolic process       | Oxidation-reduction process   |
| N18385                         |  | Metabolic process       | Oxidation-reduction process   |
| N18632                         |  | Metabolic process       | Oxidation-reduction process   |
| N18655                         |  | Metabolic process       | Oxidation-reduction process   |
| N18760                         | protein disulfide isomerase A6 [Penaeus monodon]   | Metabolic process       | Oxidation-reduction process   |
| N19097                         | Anoplopoma fimbria clone afim-evh-016-151 NADH dehydrogenase iron-sulfur protein                     | Metabolic process       | Oxidation-reduction process   |
| N19130                         | PREDICTED: acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain-like [Saccoglossus kowalevskii] | Metabolic process       | Oxidation-reduction process   |
| N19275                         | hypothetical protein DAPPUDRAFT_188248 [Daphnia pulex]   | Metabolic process       | Oxidation-reduction process   |
| N21156                         | hypothetical protein DAPPUDRAFT_330720 [Daphnia pulex]   | Metabolic process       | Oxidation-reduction process   |
| N21406                         | cytochrome P450 [Bemisia tabaci]   | Metabolic process       | Oxidation-reduction process   |
| N21510                         | senecionine N-oxygenase, putative [Pediculus humanus corporis] >gi 212515735 gb                      | Metabolic process       | Oxidation-reduction process   |
| N22381                         | AAEL017133-PA [Aedes aegypti]  | Metabolic process       | Oxidation-reduction process   |
| N22914                         | CREG1 precursor [Caligus clemensi]   | Metabolic process       | Oxidation-reduction process   |
| N23050                         | hypothetical protein BRAFLDRAFT_129234 [Branchiostoma floridae] >gi 229295408                        | Metabolic process       | Oxidation-reduction process   |
| N24172                         | hypothetical protein DAPPUDRAFT_313254 [Daphnia pulex]   | Metabolic process       | Oxidation-reduction process   |
| N26026                         | hypothetical protein SINV_06374 [Solenopsis invicta]   | Metabolic process       | Oxidation-reduction process   |
| N28175                         | flavonol reductase/cinnamoyl-CoA reductase, putative [Ixodes scapularis] >gi 215497                  | Metabolic process       | Oxidation-reduction process   |
| N31519                         | aankyrin [Allbaculum stercoricanis]  | Metabolic process       | Oxidation-reduction process   |
| N32458                         | Allene oxide synthase-lipoxygenase protein [Crassostrea gigas]                                       | Metabolic process       | Oxidation-reduction process   |
| N34035                         | pacifastin heavy chain precursor [Pacificastacus leniusculus]  | Metabolic process       | Oxidation-reduction process   |
| N39784                         | hypothetical protein DAPPUDRAFT_315087 [Daphnia pulex]   | Metabolic process       | Oxidation-reduction process   |
| N40545                         | DnaJ-like protein subfamily C member 16 [Harpegnathos saltator]                                      | Metabolic process       | Oxidation-reduction process   |
| N43458                         | hypothetical protein CAPTEDRAFT_178407 [Capitella teleta]  | Metabolic process       | Oxidation-reduction process   |
| N44626                         | PREDICTED: similar to AGAP003652-PA [Tribolium castaneum] >gi 270002022 gb EE                        | Metabolic process       | Oxidation-reduction process   |
| N45271                         | hypothetical protein DAPPUDRAFT_300978 [Daphnia pulex]   | Metabolic process       | Oxidation-reduction process   |
| N46236                         | hypothetical protein BRAFLDRAFT_68404 [Branchiostoma floridae] >gi 229298781 g                       | Metabolic process       | Oxidation-reduction process   |
| N46564                         | hypothetical protein BRAFLDRAFT_202728 [Branchiostoma floridae] >gi 229295985                        | Metabolic process       | Oxidation-reduction process   |
| N5097                          | protein disulfide isomerase 2 [Fenneropenaeus chinensis]   | Metabolic process       | Oxidation-reduction process   |
| N59367                         | hypothetical protein DAPPUDRAFT_98658 [Daphnia pulex]  | Metabolic process       | Oxidation-reduction process   |
| N59550                         | PREDICTED: thioredoxin domain containing like [Saccoglossus kowalevskii]                             | Metabolic process       | Oxidation-reduction process   |
| N6078                          | protaglandin reductase 1 [Penaeus monodon]   | Metabolic process       | Oxidation-reduction process   |
| N9128                          | Trx1 [Eriocheir sinensis]  | Metabolic process       | Oxidation-reduction process   |
| N9447                          | PREDICTED: Bombus impatiens glutamate dehydrogenase, mitochondrial-like (LOC101928500)               | Metabolic process       | Oxidation-reduction process   |
| N9461                          | PREDICTED: magnesium transporter protein 1-like [Nasonia vitripennis]                                | Metabolic process       | Oxidation-reduction process   |
| <b>Nucleic acid metabolism</b> |  |                         |                               |
| M61659                         | three-prime repair exonuclease 1 [Phascolarctos cinereus]  | Nucleic acid metabolism | DNA metabolic process         |
| N10823                         |  | Nucleic acid metabolism | DNA metabolic process         |
| N12689                         | PREDICTED: Taeniopygia guttata topoisomerase (DNA) II beta 180kDa (TOP2B), mRNA                      | Nucleic acid metabolism | DNA metabolic process         |
| N18165                         | hypothetical protein D910_02572 [Dendroctonus ponderosae]  | Nucleic acid metabolism | DNA metabolic process         |
| M2033                          | PREDICTED: DNA polymerase V-like [Nasonia vitripennis]   | Nucleic acid metabolism | DNA replication               |
| M6756                          | hypothetical protein DAPPUDRAFT_227571 [Daphnia pulex]   | Nucleic acid metabolism | DNA replication               |
| M85198                         | F121229p1 [Drosophila melanogaster]  | Nucleic acid metabolism | DNA replication               |
| N11858                         | hypothetical protein YQE_03506, partial [Dendroctonus ponderosae]                                    | Nucleic acid metabolism | DNA replication               |
| N19216                         | hypothetical protein BRAFLDRAFT_113525 [Branchiostoma floridae] >gi 229296827                        | Nucleic acid metabolism | DNA replication               |
| N40254                         | predicted protein [Nematostella vectensis] >gi 156221198 gb EDO42056.1  predict                      | Nucleic acid metabolism | DNA replication               |
| M10621                         | PREDICTED: zinc finger protein 782-like [Sus scrofa]   | Nucleic acid metabolism | Regulation of gene expression |
| M11678                         | CREB-binding protein [Zootermopsis nevadensis]   | Nucleic acid metabolism | Regulation of gene expression |
| M2134                          | conserved hypothetical protein [Pediculus humanus corporis] >gi 212510168 gb EE                      | Nucleic acid metabolism | Regulation of gene expression |
| M55626                         | conserved hypothetical protein [Pediculus humanus corporis] >gi 212508735 gb EE                      | Nucleic acid metabolism | Regulation of gene expression |
| M5576                          | conserved hypothetical protein [Pediculus humanus corporis] >gi 212511742 gb EE                      | Nucleic acid metabolism | Regulation of gene expression |
| M600                           | PREDICTED: similar to histidine triad protein member [Tribolium castaneum]                           | Nucleic acid metabolism | Regulation of gene expression |
| M7241                          | PREDICTED: zinc finger protein 358-like, partial [Ornithorhynchus anatinus]                          | Nucleic acid metabolism | Regulation of gene expression |
| N12903                         |  | Nucleic acid metabolism | Regulation of gene expression |
| N17291                         | Zinc finger protein 84 [Tupaia chinensis]  | Nucleic acid metabolism | Regulation of gene expression |
| N18441                         | PREDICTED: LOW QUALITY PROTEIN: ets DNA-binding protein pokkuri-like [Nasonia vitripennis]           | Nucleic acid metabolism | Regulation of gene expression |
| N18444                         | LIM class homeobox transcription factor Lmx [Mnemiopsis leidyi]                                      | Nucleic acid metabolism | Regulation of gene expression |
| N19004                         | PREDICTED: similar to AGAP009141-PA [Tribolium castaneum] >gi 270005569 gb EF                        | Nucleic acid metabolism | Regulation of gene expression |
| N19425                         |  | Nucleic acid metabolism | Regulation of gene expression |
| N20174                         |  | Nucleic acid metabolism | Regulation of gene expression |
| N22626                         | Cyclic AMP-dependent transcription factor ATF-6 beta, putative [Pediculus humanus corporis]          | Nucleic acid metabolism | Regulation of gene expression |
| N28291                         | PREDICTED: zinc finger protein 600 isoform X1 [Homo sapiens] >gi 119592502 gb EF                     | Nucleic acid metabolism | Regulation of gene expression |
| N28717                         | protein groucho, putative [Pediculus humanus corporis] >gi 212511585 gb EEB1451                      | Nucleic acid metabolism | Regulation of gene expression |
| N31082                         | Protein bunched, class 2 isoform [Camponotus floridanus]   | Nucleic acid metabolism | Regulation of gene expression |
| N34881                         | PREDICTED: transcriptional enhancer factor TEF-1 isoform X3 [Chinchilla lanigera]                    | Nucleic acid metabolism | Regulation of gene expression |
| N37283                         | PREDICTED: zinc finger protein Xfin-like [Strongylocentrotus purpuratus]                             | Nucleic acid metabolism | Regulation of gene expression |
| N39148                         | ETS-related transcription factor Elf-3 [Crassostrea gigas]   | Nucleic acid metabolism | Regulation of gene expression |

| ID                        | Annotation   | GO term                 | Go child term                             |
|---------------------------|--|-------------------------|---|
| N53807                    | ETS factor [Trichinella spiralis] >gi 316978761 gb EFV61692.1  ETS factor [Trichinell; Nucleic acid metabolism |                         | Regulation of gene expression             |
| N60094                    | RecName: Full=Zinc finger Y-chromosomal protein 1; Short=ZFY-1 >gi 65269 emb C/ Nucleic acid metabolism        | Nucleic acid metabolism | Regulation of gene expression             |
| N8399                     |  | Nucleic acid metabolism | Regulation of gene expression             |
| M121                      | PREDICTED: hypothetical protein LOC100122935 [Nasonia vitripennis]   | Nucleic acid metabolism | Regulation of gene expression, epigenetic |
| M1844                     | PREDICTED: mediator of RNA polymerase II transcription subunit 8-like [Hyalella azteca]                        | Nucleic acid metabolism | RNA metabolic process                     |
| M20226                    |  | Nucleic acid metabolism | RNA metabolic process                     |
| M2517                     | hypothetical protein DAPPUDRAFT_191515 [Daphnia pulex]   | Nucleic acid metabolism | RNA metabolic process                     |
| M338                      | PREDICTED: pre-rRNA-processing protein TSR2 homolog [Aplysia californica]                                      | Nucleic acid metabolism | RNA metabolic process                     |
| M4435                     | hypothetical protein CAPTEDRAFT_220697 [Capitella teleta]  | Nucleic acid metabolism | RNA metabolic process                     |
| M5050                     | hypothetical protein DAPPUDRAFT_52884 [Daphnia pulex]  | Nucleic acid metabolism | RNA metabolic process                     |
| M56294                    | PREDICTED: CDK5RAP1-like protein-like [Apis florea]  | Nucleic acid metabolism | RNA metabolic process                     |
| M61831                    | Protein suppressor of forked [Camponotus floridanus]   | Nucleic acid metabolism | RNA metabolic process                     |
| M64830                    | PREDICTED: similar to spliceosome associated protein [Tribolium castaneum] >gi 270  Nucleic acid metabolism    | Nucleic acid metabolism | RNA metabolic process                     |
| M66915                    | PREDICTED: ATP-dependent RNA helicase DDX39A-like [Monodelphis domestica]                                      | Nucleic acid metabolism | RNA metabolic process                     |
| N10539                    |  | Nucleic acid metabolism | RNA metabolic process                     |
| N12725                    | eukaryotic translation initiation factor 4 gamma, putative [Pediculus humanus corporis]                        | Nucleic acid metabolism | RNA metabolic process                     |
| N12797                    |  | Nucleic acid metabolism | RNA metabolic process                     |
| N12849                    | hypothetical protein DAPPUDRAFT_198197 [Daphnia pulex]   | Nucleic acid metabolism | RNA metabolic process                     |
| N13217                    | hypothetical protein DAPPUDRAFT_331348 [Daphnia pulex]   | Nucleic acid metabolism | RNA metabolic process                     |
| N13861                    | conserved hypothetical protein [Pediculus humanus corporis] >gi 212508823 gb EEf  Nucleic acid metabolism      | Nucleic acid metabolism | RNA metabolic process                     |
| N15767                    | hypothetical protein DAPPUDRAFT_220519 [Daphnia pulex]   | Nucleic acid metabolism | RNA metabolic process                     |
| N18079                    | PREDICTED: transcription elongation factor SPT6-like [Megachile rotundata]                                     | Nucleic acid metabolism | RNA metabolic process                     |
| N18176                    | RRP5-like protein [Crassostrea gigas]  | Nucleic acid metabolism | RNA metabolic process                     |
| N18306                    |  | Nucleic acid metabolism | RNA metabolic process                     |
| N18313                    |  | Nucleic acid metabolism | RNA metabolic process                     |
| N18423                    | PREDICTED: putative rRNA methyltransferase 3-like [Nasonia vitripennis]  | Nucleic acid metabolism | RNA metabolic process                     |
| N18993                    | Acyrthosiphon pisum protein arginine n-methyltransferase 1, putative (LOC10016585) Nucleic acid metabolism     | Nucleic acid metabolism | RNA metabolic process                     |
| N19013                    | hypothetical protein DAPPUDRAFT_306325 [Daphnia pulex]   | Nucleic acid metabolism | RNA metabolic process                     |
| N19354                    | Leukocyte receptor cluster member 9 [Caligus rogercresseyi]  | Nucleic acid metabolism | RNA metabolic process                     |
| N19375                    | Nematostella vectensis predicted protein (NEMVEDRAFT_v1g185061) partial mRNA                                   | Nucleic acid metabolism | RNA metabolic process                     |
| N19697                    | PREDICTED: poly(A)-specific ribonuclease PARN isoform X1 [Danio rerio]   | Nucleic acid metabolism | RNA metabolic process                     |
| N19884                    | hypothetical protein DAPPUDRAFT_300423 [Daphnia pulex]   | Nucleic acid metabolism | RNA metabolic process                     |
| N20041                    | conserved hypothetical protein [Pediculus humanus corporis] >gi 212517197 gb EEf  Nucleic acid metabolism      | Nucleic acid metabolism | RNA metabolic process                     |
| N20316                    | hypothetical protein BRAFLDRAFT_276703 [Branchiostoma floridae] >gi 229285781  Nucleic acid metabolism         | Nucleic acid metabolism | RNA metabolic process                     |
| N21545                    | Nucleolar protein 66 [Crassostrea gigas]   | Nucleic acid metabolism | RNA metabolic process                     |
| N22415                    | PREDICTED: transcription elongation factor SPT5-like [Megachile rotundata]                                     | Nucleic acid metabolism | RNA metabolic process                     |
| N23046                    | hypothetical protein BRAFLDRAFT_201261 [Branchiostoma floridae] >gi 229279415  Nucleic acid metabolism         | Nucleic acid metabolism | RNA metabolic process                     |
| N23545                    | mediator of RNA polymerase II transcription subunit 15 [Zootermopsis nevadensis]                               | Nucleic acid metabolism | RNA metabolic process                     |
| N23615                    | hypothetical protein BRAFLDRAFT_111011 [Branchiostoma floridae] >gi 229270902  Nucleic acid metabolism         | Nucleic acid metabolism | RNA metabolic process                     |
| N24228                    | PREDICTED: elongator complex protein 4-like [Aplysia californica]  | Nucleic acid metabolism | RNA metabolic process                     |
| N27329                    | hypothetical protein TcasGA2_TC015113 [Tribolium castaneum]  | Nucleic acid metabolism | RNA metabolic process                     |
| N27855                    | PREDICTED: mediator of RNA polymerase II transcription subunit 19-like isoform 1 [N                            | Nucleic acid metabolism | RNA metabolic process                     |
| N29611                    | PREDICTED: WD repeat-containing protein 36 [Trichechus manatus latirostris]                                    | Nucleic acid metabolism | RNA metabolic process                     |
| N30373                    |  | Nucleic acid metabolism | RNA metabolic process                     |
| N33717                    | PREDICTED: CCR4-NOT transcription complex, subunit 1-like [Saccoglossus kowalevskii]                           | Nucleic acid metabolism | RNA metabolic process                     |
| N35076                    | PREDICTED: hypothetical protein LOC100679578 [Nasonia vitripennis]   | Nucleic acid metabolism | RNA metabolic process                     |
| N38517                    | hypothetical protein DAPPUDRAFT_304474 [Daphnia pulex]   | Nucleic acid metabolism | RNA metabolic process                     |
| N43700                    | Ribonuclease P/MRP protein subunit POPS [Camponotus floridanus]  | Nucleic acid metabolism | RNA metabolic process                     |
| N45734                    | PREDICTED: probable methyltransferase C20orf7 homolog, mitochondrial-like isoform                              | Nucleic acid metabolism | RNA metabolic process                     |
| N46206                    | PREDICTED: RNA-binding protein 28 [Sarcophilus harrisii]   | Nucleic acid metabolism | RNA metabolic process                     |
| N47138                    | conserved hypothetical protein [Pediculus humanus corporis] >gi 212510210 gb EEf  Nucleic acid metabolism      | Nucleic acid metabolism | RNA metabolic process                     |
| N49298                    | hypothetical protein CAPTEDRAFT_135802, partial [Capitella teleta]   | Nucleic acid metabolism | RNA metabolic process                     |
| N61350                    | PREDICTED: alanyl-tRNA editing protein Aarsd1 [Sarcophilus harrisii]   | Nucleic acid metabolism | RNA metabolic process                     |
| N7721                     | PREDICTED: RNA-binding protein 39-like isoform 1 [Megachile rotundata]   | Nucleic acid metabolism | RNA metabolic process                     |
| M16005                    | DNA-directed RNA polymerase I subunit RPA1 [Crassostrea gigas]   | Nucleic acid metabolism | Transcription, DNA-dependent              |
| M67221                    | hypothetical protein DAPPUDRAFT_209553 [Daphnia pulex]   | Nucleic acid metabolism | Transcription, DNA-dependent              |
| N21123                    | PREDICTED: DNA-directed RNA polymerase I subunit RPA43-like [Nasonia vitripennis]                              | Nucleic acid metabolism | Transcription, DNA-dependent              |
| N28651                    | hypothetical protein BRAFLDRAFT_117854 [Branchiostoma floridae] >gi 229295938  Nucleic acid metabolism         | Nucleic acid metabolism | Transcription, DNA-dependent              |
| <b>Protein metabolism</b> |  |                         |   |
| M112647                   | hypothetical protein DAPPUDRAFT_51930 [Daphnia pulex]  | Protein metabolism      | Cellular protein modification process     |
| M15039                    | Ixodes scapularis traf2 and nck interacting kinase, tnk, putative, mRNA  | Protein metabolism      | Cellular protein modification process     |
| M15628                    | PREDICTED: hypothetical protein LOC100118283 [Nasonia vitripennis]   | Protein metabolism      | Cellular protein modification process     |
| M16593                    | PREDICTED: dual specificity protein phosphatase CDC14A isoform 3 [Trichechus manatus]                          | Protein metabolism      | Cellular protein modification process     |
| M1798                     | hypothetical protein DAPPUDRAFT_188007 [Daphnia pulex]   | Protein metabolism      | Cellular protein modification process     |
| M181                      | PREDICTED: polyserape-2-like [Acyrthosiphon pisum]   | Protein metabolism      | Cellular protein modification process     |
| M2135                     | protein phosphatase 2 (formerly 2A), catalytic subunit [Strigomonas culicis]                                   | Protein metabolism      | Cellular protein modification process     |
| M21763                    |  | Protein metabolism      | Cellular protein modification process     |
| M2429                     | PREDICTED: uncharacterized protein LOC100879681 [Megachile rotundata]  | Protein metabolism      | Cellular protein modification process     |
| M5442                     | PREDICTED: dual specificity protein phosphatase 12-like [Nasonia vitripennis]                                  | Protein metabolism      | Cellular protein modification process     |
| M59191                    | projectin [Procambarus clarkii]  | Protein metabolism      | Cellular protein modification process     |
| M59923                    | hypothetical protein BRAFLDRAFT_63881 [Branchiostoma floridae] >gi 229296855 g  Protein metabolism             | Protein metabolism      | Cellular protein modification process     |
| M619                      | PREDICTED: cyclin-dependent kinase 7-like [Megachile rotundata]  | Protein metabolism      | Cellular protein modification process     |
| M62125                    | phosphorylase kinase gamma subunit, putative [Ixodes scapularis] >gi 215491336 gt  Protein metabolism          | Protein metabolism      | Cellular protein modification process     |
| M62372                    | PREDICTED: endothelin-converting enzyme 2 [Ciona intestinalis]   | Protein metabolism      | Cellular protein modification process     |
| M63916                    | PREDICTED: p90 ribosomal S6 kinase-like [Saccoglossus kowalevskii]   | Protein metabolism      | Cellular protein modification process     |
| M66217                    | Diphthamide biosynthesis protein 2 [Dicentrarchus labrax]  | Protein metabolism      | Cellular protein modification process     |

| ID     | Annotation   | GO term            | Go child term                         |
|--------|--|--------------------|---------------------------------------|
| M66985 | guanylate cyclase PGC-M2 precursor [Procambarus clarkii]   | Protein metabolism | Cellular protein modification process |
| M683   | sumo-1-activating enzyme E1a, putative [Pediculus humanus corporis] >gi 21251422 Protein metabolism                                    | Protein metabolism | Cellular protein modification process |
| M68569 | hypothetical protein YQE_02518, partial [Dendroctonus ponderosae]  | Protein metabolism | Cellular protein modification process |
| M7056  | hypothetical protein DAPPUDRAFT_305261 [Daphnia pulex]   | Protein metabolism | Cellular protein modification process |
| M72356 |  | Protein metabolism | Cellular protein modification process |
| M8240  | PITSLRE serine/threonine-protein kinase CDC2L1 [Camponotus floridanus]   | Protein metabolism | Cellular protein modification process |
| M9345  | hypothetical protein DAPPUDRAFT_52407 [Daphnia pulex]  | Protein metabolism | Cellular protein modification process |
| M96600 | AGAPO11030-PA [Anopheles gambiae str. PEST] >gi 157019323 gb EAL41443.3  AG Protein metabolism   | Protein metabolism | Cellular protein modification process |
| M97294 | PREDICTED: serine/threonine-protein kinase Warts-like [Nasonia vitripennis]  | Protein metabolism | Cellular protein modification process |
| M99514 | hypothetical protein CAPTEDRAFT_166676 [Capitella teleta]  | Protein metabolism | Cellular protein modification process |
| M9972  | zinc metalloproteinase, putative [Pediculus humanus corporis] >gi 212510824 gb EE Protein metabolism                                   | Protein metabolism | Cellular protein modification process |
| N11822 |  | Protein metabolism | Cellular protein modification process |
| N11830 |  | Protein metabolism | Cellular protein modification process |
| N11977 | PREDICTED: protein phosphatase 1B-like [Saccoglossus kowalevskii]  | Protein metabolism | Cellular protein modification process |
| N11990 | PREDICTED: similar to CG1973 CG1973-PA [Tribolium castaneum]   | Protein metabolism | Cellular protein modification process |
| N12755 | PREDICTED: similar to transglutaminase [Tribolium castaneum] >gi 270007058 gb El Protein metabolism                                    | Protein metabolism | Cellular protein modification process |
| N12811 |  | Protein metabolism | Cellular protein modification process |
| N13007 | checkpoint kinase 1 [Daphnia pulex]  | Protein metabolism | Cellular protein modification process |
| N13499 | PREDICTED: uncharacterized protein LOC100883185 isoform 2 [Megachile rotundata]  | Protein metabolism | Cellular protein modification process |
| N13597 | signal peptidase complex, subunit SPC25, putative [Ixodes scapularis] >gi 215501946 Protein metabolism                                 | Protein metabolism | Cellular protein modification process |
| N13653 | hypothetical protein DAPPUDRAFT_319998 [Daphnia pulex]   | Protein metabolism | Cellular protein modification process |
| N18162 | PREDICTED: DNA (cytosine-5)-methyltransferase PlmCI-like [Megachile rotundata]   | Protein metabolism | Cellular protein modification process |
| N18208 |  | Protein metabolism | Cellular protein modification process |
| N18262 | PREDICTED: LOW QUALITY PROTEIN: myosin-IIIa [Nasonia vitripennis]  | Protein metabolism | Cellular protein modification process |
| N18288 | casein kinase 1 epsilon [Eurydice pulchra]   | Protein metabolism | Cellular protein modification process |
| N18484 | hypothetical protein DAPPUDRAFT_305996 [Daphnia pulex]   | Protein metabolism | Cellular protein modification process |
| N18549 | PREDICTED: lipoyltransferase 1, mitochondrial-like [Nasonia vitripennis]   | Protein metabolism | Cellular protein modification process |
| N18839 | PREDICTED: LOW QUALITY PROTEIN: myosin-IIIa [Nasonia vitripennis]  | Protein metabolism | Cellular protein modification process |
| N18948 | PREDICTED: serine/threonine-protein kinase RIO2-like [Megachile rotundata]   | Protein metabolism | Cellular protein modification process |
| N19391 | diphthine synthase-like protein [Cricetulus griseus]   | Protein metabolism | Cellular protein modification process |
| N19601 | hypothetical protein YQE_12968, partial [Dendroctonus ponderosae]  | Protein metabolism | Cellular protein modification process |
| N19788 | cAMP-dependent protein kinase catalytic subunit, putative [Pediculus humanus corporis]   | Protein metabolism | Cellular protein modification process |
| N20205 | hypothetical protein DAPPUDRAFT_301830 [Daphnia pulex]   | Protein metabolism | Cellular protein modification process |
| N20268 | PREDICTED: wee1-like protein kinase-like [Nasonia vitripennis]   | Protein metabolism | Cellular protein modification process |
| N21051 | hypothetical protein DAPPUDRAFT_305360 [Daphnia pulex]   | Protein metabolism | Cellular protein modification process |
| N22641 |  | Protein metabolism | Cellular protein modification process |
| N28061 | hypothetical protein DAPPUDRAFT_303533 [Daphnia pulex]   | Protein metabolism | Cellular protein modification process |
| N28399 | GJ12403 [Drosophila virilis] >gi 194153739 gb EDW68923.1  GJ12403 [Drosophila virilis] >gi 194153739 gb EDW68923.1  Protein metabolism | Protein metabolism | Cellular protein modification process |
| N28864 | leucine-rich transmembrane protein, putative [Pediculus humanus corporis] >gi 212511266 gb El Protein metabolism                       | Protein metabolism | Cellular protein modification process |
| N30386 | PREDICTED: similar to transglutaminase [Tribolium castaneum] >gi 270004163 gb El Protein metabolism                                    | Protein metabolism | Cellular protein modification process |
| N32407 | protein purity of essence, putative [Pediculus humanus corporis] >gi 212511266 gb Protein metabolism                                   | Protein metabolism | Cellular protein modification process |
| N32909 | hypothetical protein DAPPUDRAFT_39456 [Daphnia pulex]  | Protein metabolism | Cellular protein modification process |
| N33379 | PREDICTED: similar to Nedd4 CG7555-PC [Tribolium castaneum]  | Protein metabolism | Cellular protein modification process |
| N34569 | PREDICTED: tyrosine-protein kinase Fer [Sorex araneus]   | Protein metabolism | Cellular protein modification process |
| N36697 | PREDICTED: dual specificity testis-specific protein kinase 1-like [Chrysemys picta bellii]   | Protein metabolism | Cellular protein modification process |
| N38023 | hypothetical protein DAPPUDRAFT_300590 [Daphnia pulex]   | Protein metabolism | Cellular protein modification process |
| N38468 | PREDICTED: leucine rich repeat containing 7-like, partial [Saccoglossus kowalevskii]   | Protein metabolism | Cellular protein modification process |
| N39683 | hypothetical protein DAPPUDRAFT_128092 [Daphnia pulex]   | Protein metabolism | Cellular protein modification process |
| N55712 | diphthamide biosynthesis protein 2 [Danio rerio] >gi 160010406 sp A4QN59.1 DPH Protein metabolism                                      | Protein metabolism | Cellular protein modification process |
| N61180 | PREDICTED: hypothetical protein LOC100115038 [Nasonia vitripennis]   | Protein metabolism | Cellular protein modification process |
| M4643  | centromere/kinetochore protein zw10 [Xenopus laevis] >gi 159155457 gb AAI5496 Protein metabolism                                       | Protein metabolism | Macromolecular complex assembly       |
| N14373 | lethal (1) G0136, isoform A [Drosophila melanogaster] >gi 194894350 ref XP_00197 Protein metabolism                                    | Protein metabolism | Macromolecular complex assembly       |
| N23242 | PREDICTED: similar to inner membrane protein COX18, mitochondrial [Tribolium castaneum]  | Protein metabolism | Macromolecular complex assembly       |
| M18846 | Drosophila willistoni GK16371 (Dwil\GK16371), mRNA   | Protein metabolism | Other                                 |
| M2290  | PREDICTED: similar to bone morphogenetic protein [Tribolium castaneum] >gi 27000 Protein metabolism                                    | Protein metabolism | Other                                 |
| M23640 |  | Protein metabolism | Other                                 |
| M3285  |  | Protein metabolism | Other                                 |
| M43606 | Branchiostoma floridae hypothetical protein, mRNA  | Protein metabolism | Other                                 |
| M4415  | salivary plasminogen activator beta precursor, putative [Pediculus humanus corporis]   | Protein metabolism | Other                                 |
| M62299 | caspase [Fenneropenaeus chinensis]   | Protein metabolism | Other                                 |
| M6427  | RNA recognition motif containing protein [Brugia malayi] >gi 158594962 gb EDP335 Protein metabolism                                    | Protein metabolism | Other                                 |
| M64325 | PREDICTED: CG10098-like [Saccoglossus kowalevskii]   | Protein metabolism | Other                                 |
| M6499  | PREDICTED: plasma kallikrein [Dasypus novemcinctus]  | Protein metabolism | Other                                 |
| M70652 | procollagen-lysine2-oxoglutarate 5-dioxygenase [Schistosoma mansoni] >gi 3600448 Protein metabolism                                    | Protein metabolism | Other                                 |
| M7795  | prophenoloxidase-activating enzyme 2 [Penaeus monodon]   | Protein metabolism | Other                                 |
| M7880  | RecName: Full=Chymotrypsin Bl; Flags: Precursor >gi 10089 emb CAA47046.1  prep Protein metabolism                                      | Protein metabolism | Other                                 |
| M9196  |  | Protein metabolism | Other                                 |
| M96180 | PREDICTED: papilin-like [Aplysia californica]  | Protein metabolism | Other                                 |
| N12301 |  | Protein metabolism | Other                                 |
| N12905 |  | Protein metabolism | Other                                 |
| N12959 | hypothetical protein DAPPUDRAFT_65345 [Daphnia pulex]  | Protein metabolism | Other                                 |
| N13751 | Trichoplax adhaerens conserved hypothetical protein, mRNA  | Protein metabolism | Other                                 |
| N15411 | PREDICTED: protein SpAN-like [Strongylocentrotus purpuratus]   | Protein metabolism | Other                                 |
| N19096 | hypothetical protein DAPPUDRAFT_307138 [Daphnia pulex]   | Protein metabolism | Other                                 |
| N19304 | hypothetical protein DAPPUDRAFT_303947 [Daphnia pulex]   | Protein metabolism | Other                                 |
| N19403 | PC2-like protein [Penaeus monodon]   | Protein metabolism | Other                                 |

| ID      | Annotation   | GO term            | Go child term   |
|---------|--|--------------------|-----------------|
| N19422  | hypothetical protein D910_10828 [Dendroctonus ponderosae]  | Protein metabolism | Other           |
| N19526  | hypothetical protein DAPPUDRAFT_307836 [Daphnia pulex]   | Protein metabolism | Other           |
| N19665  | hypothetical protein YQE_09353, partial [Dendroctonus ponderosae]                                    | Protein metabolism | Other           |
| N21736  | hypothetical protein BRAFLDRAFT_279226 [Branchiostoma floridae] >gi 229281678                        | Protein metabolism | Other           |
| N23820  | hypothetical protein DAPPUDRAFT_120652 [Daphnia pulex]   | Protein metabolism | Other           |
| N24379  | hypothetical protein DAPPUDRAFT_306867 [Daphnia pulex]   | Protein metabolism | Other           |
| N25394  | pro-phenoloxidase activating enzyme-I precursor [Holotrichia diomphalia]                             | Protein metabolism | Other           |
| N27616  | prophenoloxidase activating enzyme [Litopenaeus vannamei]  | Protein metabolism | Other           |
| N29559  |  | Protein metabolism | Other           |
| N29592  |  | Protein metabolism | Other           |
| N32282  | hypothetical protein CAPTEDRAFT_175182, partial [Capitella teleta]                                   | Protein metabolism | Other           |
| N34957  | polyc binding protein, putative [Pediculus humanus corporis] >gi 212516622 gb EE                     | Protein metabolism | Other           |
| N35496  | prophenoloxide activating enzyme III [Macrobrachium rosenbergii]                                     | Protein metabolism | Other           |
| N36733  | Probable glutamyl-tRNA(Gln) amidotransferase subunit B, mitochondrial [Camponotus floridanus]        | Protein metabolism | Other           |
| N52929  |  | Protein metabolism | Other           |
| N5373   | PREDICTED: Nasonia vitripennis 26S protease regulatory subunit 4-like (LOC10011828)                  | Protein metabolism | Other           |
| N6315   |  | Protein metabolism | Other           |
| N8848   | trypsinogen 1 [Litopenaeus vannamei]   | Protein metabolism | Other           |
| M18705  | Portunus trituberculatus heat shock protein 60 (HSP60) mRNA, complete cds                            | Protein metabolism | Protein folding |
| M19227  | Pediculus humanus corporis Hsp60 protein, putative, mRNA   | Protein metabolism | Protein folding |
| M2216   | GrpE protein [Cherax quadricarinatus]  | Protein metabolism | Protein folding |
| M3122   | calnexin [Penaeus monodon]   | Protein metabolism | Protein folding |
| M3608   | PREDICTED: uncharacterized protein LOC100879476 [Megachile rotundata]                                | Protein metabolism | Protein folding |
| M49636  | Der f Mal f 6 allergen [Dermatophagoides farinae]  | Protein metabolism | Protein folding |
| M55225  | protein disulfide-isomerase TXNDC10 precursor, putative [Pediculus humanus corporis]                 | Protein metabolism | Protein folding |
| M60388  | hypothetical protein DAPPUDRAFT_306744 [Daphnia pulex]   | Protein metabolism | Protein folding |
| M65353  | related to FPR2-FK506/rapamycin-binding protein of the ER [Ustilago hordei]                          | Protein metabolism | Protein folding |
| M66780  |  | Protein metabolism | Protein folding |
| M82401  | hypothetical protein GUILTHDRAFT_83873, partial [Guillardia theta CCMP2712]                          | Protein metabolism | Protein folding |
| M84945  | hypothetical protein DAPPUDRAFT_299901 [Daphnia pulex]   | Protein metabolism | Protein folding |
| M84968  | myosin heavy chain type b [Marsupenaeus japonicus]   | Protein metabolism | Protein folding |
| N11842  | heat shock protein 90 [Scylla paramamosain]  | Protein metabolism | Protein folding |
| N11929  |  | Protein metabolism | Protein folding |
| N13901  |  | Protein metabolism | Protein folding |
| N13967  |  | Protein metabolism | Protein folding |
| N18807  |  | Protein metabolism | Protein folding |
| N19144  |  | Protein metabolism | Protein folding |
| N20244  |  | Protein metabolism | Protein folding |
| N22893  | hypothetical protein DAPPUDRAFT_299901 [Daphnia pulex]   | Protein metabolism | Protein folding |
| N23884  | prefoldin subunit 4-like protein [Coptotermes formosanus]  | Protein metabolism | Protein folding |
| N24711  | heat shock protein 10 [Scylla paramamosain]  | Protein metabolism | Protein folding |
| N3034   | hypothetical protein [Monosiga brevicollis MX1] >gi 163776367 gb EDQ89987.1  pr                      | Protein metabolism | Protein folding |
| N30735  | PREDICTED: peptidyl-prolyl cis-trans isomerase-like 1-like [Ceratitis capitata]                      | Protein metabolism | Protein folding |
| N43033  | hypothetical protein DAPPUDRAFT_306744 [Daphnia pulex]   | Protein metabolism | Protein folding |
| N54164  | serine/threonine-protein phosphatase 2A regulatory subunit B', putative [Pediculus humanus corporis] | Protein metabolism | Protein folding |
| N5465   | Fenneropenaeus chinensis calreticulin precursor (CRT) mRNA, complete cds                             | Protein metabolism | Protein folding |
| N6790   | chaperonin [Macrobrachium rosenbergii]   | Protein metabolism | Protein folding |
| N8142   |  | Protein metabolism | Protein repair  |
| N8143   |  | Protein metabolism | Protein repair  |
| E4164   | RecName: Full=Chymotrypsin Bl; Flags: Precursor >gi 10089 emb CAA47046.1  prep                       | Protein metabolism | Proteolysis     |
| E4182   | GJ23159 [Drosophila virilis] >gi 194148630 gb EDW64328.1  GJ23159 [Drosophila virilis]               | Protein metabolism | Proteolysis     |
| E6184   | hypothetical protein THAOC_18267 [Thalassiosira oceanica]  | Protein metabolism | Proteolysis     |
| E903    | PREDICTED: proteasome subunit alpha type-7-1-like isoform 1 [Apis mellifera] >gi 35161609 gb         | Protein metabolism | Proteolysis     |
| M102676 | trypsin 2 [Panulirus argus]  | Protein metabolism | Proteolysis     |
| M102744 | CUB-serine protease [Panulirus argus]  | Protein metabolism | Proteolysis     |
| M102785 | PREDICTED: ovochymase-1-like [Ceratitis capitata]  | Protein metabolism | Proteolysis     |
| M103525 | ubiquitin [Procamarbus clarkii]  | Protein metabolism | Proteolysis     |
| M103627 | hypothetical protein CAPTEDRAFT_195788 [Capitella teleta]  | Protein metabolism | Proteolysis     |
| M108894 | serine protease [Sinonovacula constricta]  | Protein metabolism | Proteolysis     |
| M109778 | CUB-serine protease [Panulirus argus]  | Protein metabolism | Proteolysis     |
| M111021 | CUB-serine protease [Panulirus argus]  | Protein metabolism | Proteolysis     |
| M111121 | CUB-serine protease [Panulirus argus]  | Protein metabolism | Proteolysis     |
| M11130  |  | Protein metabolism | Proteolysis     |
| M112845 | Chymotrypsin BlI [Litopenaeus vannamei]  | Protein metabolism | Proteolysis     |
| M12757  | serine proteinase [Portunus trituberculatus]   | Protein metabolism | Proteolysis     |
| M12833  | serine/threonine-protein kinase VRK1, putative [Pediculus humanus corporis] >gi 21134366 gb          | Protein metabolism | Proteolysis     |
| M15086  | GK25063 [Drosophila willistoni] >gi 194167670 gb EDW82571.1  GK25063 [Drosophila willistoni]         | Protein metabolism | Proteolysis     |
| M1538   | nucleotide excision repair protein [Marsupenaeus japonicus]  | Protein metabolism | Proteolysis     |
| M15560  |  | Protein metabolism | Proteolysis     |
| M16069  | hypothetical protein DICPUDRAFT_97266 [Dictyostelium purpureum] >gi 325083989 gb                     | Protein metabolism | Proteolysis     |
| M16330  | CUB-serine protease [Panulirus argus]  | Protein metabolism | Proteolysis     |
| M16754  | PREDICTED: similar to ubiquitin specific protease 7 [Tribolium castaneum]                            | Protein metabolism | Proteolysis     |
| M17359  | PREDICTED: membrane metallo-endopeptidase-like 1-like [Metaseiulus occidentalis]                     | Protein metabolism | Proteolysis     |
| M17428  | cathepsin A [Ericheir sinensis]  | Protein metabolism | Proteolysis     |
| M17495  | CUB-serine protease [Panulirus argus]  | Protein metabolism | Proteolysis     |
| M17539  |  | Protein metabolism | Proteolysis     |

| ID     | Annotation  | GO term            | Go child term |
|--------|---|--------------------|---------------|
| M17621 | mitochondrial inner membrane protease subunit [Aedes aegypti] >gi 108883262 gb                                    | Protein metabolism | Proteolysis   |
| M17735 |   | Protein metabolism | Proteolysis   |
| M18434 | CUB-serine protease [Panulirus argus]   | Protein metabolism | Proteolysis   |
| M18636 | trypsin [Marsupenaeus japonicus]  | Protein metabolism | Proteolysis   |
| M19247 | hypothetical protein KGM_10936 [Danaus plexippus]   | Protein metabolism | Proteolysis   |
| M19563 | CUB-serine protease [Panulirus argus]   | Protein metabolism | Proteolysis   |
| M19735 |   | Protein metabolism | Proteolysis   |
| M19739 | CUB-serine protease [Panulirus argus]   | Protein metabolism | Proteolysis   |
| M20312 | trypsinogen 1 [Litopenaeus vannamei]  | Protein metabolism | Proteolysis   |
| M20539 | serine proteinase [Portunus trituberculatus]  | Protein metabolism | Proteolysis   |
| M21562 | CUB-serine protease [Panulirus argus]   | Protein metabolism | Proteolysis   |
| M2230  | PREDICTED: metalloproteinase SpAN-like [Saccoglossus kowalevskii]   | Protein metabolism | Proteolysis   |
| M22603 | hypothetical protein DAPPUDRAFT_305996 [Daphnia pulex]  | Protein metabolism | Proteolysis   |
| M22635 | hypothetical protein BRAFLDRAFT_71828 [Branchiostoma floridae] >gi 229298917 g                                    | Protein metabolism | Proteolysis   |
| M229   |   | Protein metabolism | Proteolysis   |
| M23518 | hypothetical protein BRAFLDRAFT_71828 [Branchiostoma floridae] >gi 229298917 g                                    | Protein metabolism | Proteolysis   |
| M25374 | trypsin [Litopenaeus vannamei]  | Protein metabolism | Proteolysis   |
| M25636 | CUB-serine protease [Panulirus argus]   | Protein metabolism | Proteolysis   |
| M28491 | CUB-serine protease [Panulirus argus]   | Protein metabolism | Proteolysis   |
| M29577 | collagenolytic serine protease [Fenneropenaeus chinensis]   | Protein metabolism | Proteolysis   |
| M30344 | CUB-serine protease [Panulirus argus]   | Protein metabolism | Proteolysis   |
| M3153  | CUB-serine protease [Panulirus argus]   | Protein metabolism | Proteolysis   |
| M3294  | hypothetical protein DAPPUDRAFT_316896 [Daphnia pulex]  | Protein metabolism | Proteolysis   |
| M35708 | GI22815 [Drosophila mojavensis] >gi 193913962 gb EDW12829.1  GI22815 [Drosophila Protein metabolism               | Protein metabolism | Proteolysis   |
| M3619  | CUB-serine protease [Panulirus argus]   | Protein metabolism | Proteolysis   |
| M3764  | PREDICTED: similar to GA20276-PA [Tribolium castaneum] >gi 270010872 gb EFA07 Protein metabolism                  | Protein metabolism | Proteolysis   |
| M39522 | expressed hypothetical protein [Trichoplas adhaerens] >gi 190583179 gb EDV2325C Protein metabolism                | Protein metabolism | Proteolysis   |
| M39822 | CUB-serine protease [Panulirus argus]   | Protein metabolism | Proteolysis   |
| M40617 | Procamarbus clarkii clone pc-97 ubiquitin mRNA, complete cds  | Protein metabolism | Proteolysis   |
| M4163  | PREDICTED: aminopeptidase N-like [Nasonia vitripennis]  | Protein metabolism | Proteolysis   |
| M44980 | CUB-serine protease [Panulirus argus]   | Protein metabolism | Proteolysis   |
| M4677  | hypothetical protein DAPPUDRAFT_307535 [Daphnia pulex]  | Protein metabolism | Proteolysis   |
| M47110 | collagenolytic serine protease [Paralithodes camtschaticus]   | Protein metabolism | Proteolysis   |
| M55140 | CUB-serine protease [Panulirus argus]   | Protein metabolism | Proteolysis   |
| M56049 | hypothetical protein DAPPUDRAFT_63727 [Daphnia pulex]   | Protein metabolism | Proteolysis   |
| M5727  | serine protease [Aedes aegypti] >gi 108881966 gb EAT46191.1  AAEL002595-PA [Ae Protein metabolism                 | Protein metabolism | Proteolysis   |
| M57964 | CUB-serine protease [Panulirus argus]   | Protein metabolism | Proteolysis   |
| M59149 | trypsin [Marsupenaeus japonicus]  | Protein metabolism | Proteolysis   |
| M60471 | transmembrane serine protease 9, putative [Pediculus humanus corporis] >gi 21251 Protein metabolism               | Protein metabolism | Proteolysis   |
| M62145 | hypothetical protein DAPPUDRAFT_309332 [Daphnia pulex]  | Protein metabolism | Proteolysis   |
| M67255 | CUB-serine protease [Panulirus argus]   | Protein metabolism | Proteolysis   |
| M6843  |   | Protein metabolism | Proteolysis   |
| M71467 | cullin-3 [Danio rerio] >gi 37682167 gb AAQ98010.1  cullin 3 [Danio rerio]   | Protein metabolism | Proteolysis   |
| M71612 | CUB-serine protease [Panulirus argus]   | Protein metabolism | Proteolysis   |
| M73671 | trypsinogen 1 [Litopenaeus vannamei]  | Protein metabolism | Proteolysis   |
| M75323 | hypothetical protein DAPPUDRAFT_303785 [Daphnia pulex]  | Protein metabolism | Proteolysis   |
| M75818 | CUB-serine protease [Panulirus argus]   | Protein metabolism | Proteolysis   |
| M7669  |   | Protein metabolism | Proteolysis   |
| M85248 | hypothetical protein DAPPUDRAFT_314716 [Daphnia pulex]  | Protein metabolism | Proteolysis   |
| M85980 | GL16806 [Drosophila persimilis] >gi 194114159 gb EDW36202.1  GL16806 [Drosophila Protein metabolism               | Protein metabolism | Proteolysis   |
| M9145  | PREDICTED: transmembrane protease serine 9-like [Ceratitis capitata]  | Protein metabolism | Proteolysis   |
| M91709 | trypsin [Marsupenaeus japonicus]  | Protein metabolism | Proteolysis   |
| M9171  | hypothetical protein DAPPUDRAFT_300481 [Daphnia pulex]  | Protein metabolism | Proteolysis   |
| M931   | protease [Homarus americanus]   | Protein metabolism | Proteolysis   |
| M9318  | anaphase-promoting complex subunit, putative [Pediculus humanus corporis] >gi 21 Protein metabolism               | Protein metabolism | Proteolysis   |
| M94518 | Procamarbus clarkii clone pc-97 ubiquitin mRNA, complete cds  | Protein metabolism | Proteolysis   |
| M9678  | conserved hypothetical protein [Pediculus humanus corporis] >gi 212514364 gb EE Protein metabolism                | Protein metabolism | Proteolysis   |
| M97028 | Protein CBR-NAS-4 [Caenorhabditis briggsae]   | Protein metabolism | Proteolysis   |
| M98646 | trypsin, putative [Pediculus humanus corporis] >gi 212515418 gb EEB17565.1  tripsi Protein metabolism             | Protein metabolism | Proteolysis   |
| N10435 | Aminopeptidase N precursor, putative [Pediculus humanus corporis] >gi 212513794 Protein metabolism                | Protein metabolism | Proteolysis   |
| N10456 | PREDICTED: carboxypeptidase B-like [Apis florea]  | Protein metabolism | Proteolysis   |
| N11537 | hypothetical protein DAPPUDRAFT_130325 [Daphnia pulex]  | Protein metabolism | Proteolysis   |
| N11888 | PREDICTED: similar to masquerade-like serine proteinase homologue [Tribolium castaneum] Protein metabolism        | Protein metabolism | Proteolysis   |
| N11943 | CUB-serine protease [Panulirus argus]   | Protein metabolism | Proteolysis   |
| N11966 | Cytosolic non-specific dipeptidase [Lepeophtheirus salmonis]  | Protein metabolism | Proteolysis   |
| N12001 | PREDICTED: cullin-4B-like [Nasonia vitripennis]   | Protein metabolism | Proteolysis   |
| N12061 | meprin A metalloprotease, putative [Ixodes scapularis] >gi 215490952 gb EEC00593 Protein metabolism               | Protein metabolism | Proteolysis   |
| N12929 | meprin A metalloprotease, putative [Ixodes scapularis] >gi 215490952 gb EEC00593 Protein metabolism               | Protein metabolism | Proteolysis   |
| N13389 | CUB-serine protease [Panulirus argus]   | Protein metabolism | Proteolysis   |
| N13604 | ubiquitin protein ligase [Ixodes scapularis] >gi 215497661 gb EEC07155.1  ubiquitin Protein metabolism            | Protein metabolism | Proteolysis   |
| N13722 | proteasome alpha 3 [Penaeus monodon]  | Protein metabolism | Proteolysis   |
| N13773 | PREDICTED: Prolyl Carboxy Peptidase like family member (pcp-2)-like [Saccoglossus kowalevskii] Protein metabolism | Protein metabolism | Proteolysis   |
| N16100 | serine protease like protein [Graptosaltria nigrofuscata]   | Protein metabolism | Proteolysis   |
| N16740 | truncated cathepsin A [Eriocheir sinensis]  | Protein metabolism | Proteolysis   |
| N17787 |   | Protein metabolism | Proteolysis   |
| N18195 | ubiquitin-activating enzyme E1 [Eriocheir sinensis]   | Protein metabolism | Proteolysis   |

| ID      | Annotation  | GO term                           | Go child term                           |  |
|---------|---|-----------------------------------|---|--|
| N18470  | ubiquitin specific peptidase 25 [Xenopus (Silurana) tropicalis] >gi 89272530 emb CA                         | Protein metabolism                | Proteolysis                             |  |
| N18474  | PREDICTED: E3 ubiquitin-protein ligase hyd-like isoform 2 [Nasonia vitripennis]                             | Protein metabolism                | Proteolysis                             |  |
| N18522  |   | Protein metabolism                | Proteolysis                             |  |
| N18765  | hypothetical protein CAPTEDRAFT_180996 [Capitella teleta]   | Protein metabolism                | Proteolysis                             |  |
| N19197  |   | Protein metabolism                | Proteolysis                             |  |
| N19464  | Thimet oligopeptidase [Crassostrea gigas]   | Protein metabolism                | Proteolysis                             |  |
| N19798  | hypothetical protein DAPPUDRAFT_311166 [Daphnia pulex]  | Protein metabolism                | Proteolysis                             |  |
| N19821  | CUB-serine protease [Panulirus argus]   | Protein metabolism                | Proteolysis                             |  |
| N19857  | Naumovozyma castellii CBS 4309 hypothetical protein (NCASOF02300) mRNA, comple                              | Protein metabolism                | Proteolysis                             |  |
| N20124  | CUB-serine protease [Panulirus argus]   | Protein metabolism                | Proteolysis                             |  |
| N2087   | uncharacterized protein LOC641564 precursor [Danio rerio] >gi 82414856 gb AAI10                             | Protein metabolism                | Proteolysis                             |  |
| N21605  |   | Protein metabolism                | Proteolysis                             |  |
| N21939  | PREDICTED: cullin-3-A-like [Megachile rotundata]  | Protein metabolism                | Proteolysis                             |  |
| N22284  | hypothetical protein BRAFLDRAFT_275724 [Branchiostoma floridae] >gi 229278212                               | Protein metabolism                | Proteolysis                             |  |
| N23322  | hypothetical protein DAPPUDRAFT_230628 [Daphnia pulex]  | Protein metabolism                | Proteolysis                             |  |
| N23960  | hypothetical protein D910_11170 [Dendroctonus ponderosae]   | Protein metabolism                | Proteolysis                             |  |
| N30084  | CUB-serine protease [Panulirus argus]   | Protein metabolism                | Proteolysis                             |  |
| N39388  | hypothetical protein YQE_02808, partial [Dendroctonus ponderosae] >gi 546680994                             | Protein metabolism                | Proteolysis                             |  |
| N40575  | PREDICTED: LOW QUALITY PROTEIN: transmembrane protease serine 9-like [Monodelphis domestica]                | Protein metabolism                | Proteolysis                             |  |
| N44114  | PREDICTED: probable ubiquitin carboxyl-terminal hydrolase FAF-X [Strongylocentrotus purpuratus]             | Protein metabolism                | Proteolysis                             |  |
| N46473  | CUB-serine protease [Panulirus argus]   | Protein metabolism                | Proteolysis                             |  |
| N50100  | hypothetical protein DAPPUDRAFT_189791 [Daphnia pulex]  | Protein metabolism                | Proteolysis                             |  |
| N50173  | Kazal-type serine proteinase inhibitor 1 [Fenneropenaeus chinensis]   | Protein metabolism                | Proteolysis                             |  |
| N60298  | ubiquitin specific protease, putative [Ixodes scapularis] >gi 215507050 gb EEC16544                         | Protein metabolism                | Proteolysis                             |  |
| N62029  | hypothetical protein DAPPUDRAFT_307535 [Daphnia pulex]  | Protein metabolism                | Proteolysis                             |  |
| N62093  | masquerade, isoform C [Drosophila melanogaster] >gi 440215292 gb AGB94103.1                                 | Protein metabolism                | Proteolysis                             |  |
| N6903   | PREDICTED: aminopeptidase N-like [Nasonia vitripennis]  | Protein metabolism                | Proteolysis                             |  |
| N7956   | cathepsin C [Fenneropenaeus chinensis]  | Protein metabolism                | Proteolysis                             |  |
| N9093   | CUB-serine protease [Panulirus argus]   | Protein metabolism                | Proteolysis                             |  |
| N9470   | RecName: Full=Blastula protease 10; Flags: Precursor >gi 10929 emb CAA39673.1                               | Protein metabolism                | Proteolysis                             |  |
| E1597   | RecName: Full=Elongation factor 1-alpha; Short=EF-1-alpha >gi 168380 gb AAA3342                             | Protein metabolism                | Regulation of translational elongation  |  |
| E1735   | elongation factor 1-beta', putative [Pediculus humanus corporis] >gi 212507797 gb                           | Protein metabolism                | Regulation of translational elongation  |  |
| E2094   | eukaryotic translation elongation factor 1 alpha 1 [Saccoglossus kowalevskii]                               | Protein metabolism                | Regulation of translational elongation  |  |
| E2187   | RecName: Full=Elongation factor 1-alpha; Short=EF-1-alpha >gi 168380 gb AAA3342                             | Protein metabolism                | Regulation of translational elongation  |  |
| E2510   | eukaryotic translation elongation factor 1 alpha 1 [Saccoglossus kowalevskii]                               | Protein metabolism                | Regulation of translational elongation  |  |
| E2602   | eukaryotic translation elongation factor 1 alpha 1 [Saccoglossus kowalevskii]                               | Protein metabolism                | Regulation of translational elongation  |  |
| M30255  | Euphausia mutica 18S small subunit ribosomal RNA gene, partial sequence                                     | Protein metabolism                | Regulation of translational elongation  |  |
| M45229  | RecName: Full=Elongation factor 1-alpha; Short=EF-1-alpha >gi 168380 gb AAA3342                             | Protein metabolism                | Regulation of translational elongation  |  |
| M4937   | ORM1-like protein 3 [Danio rerio] >gi 81174971 sp Q5XR6.1 ORML3_DANRE                                       | RecName: Protein metabolism       | Regulation of translational elongation  |  |
| M66668  | hypothetical protein, partial [Herbaspirillum seropediae]   | Protein metabolism                | Regulation of translational elongation  |  |
| N14265  | hypothetical protein CAPTEDRAFT_228652 [Capitella teleta]   | Protein metabolism                | Regulation of translational elongation  |  |
| N18254  |   | Protein metabolism                | Regulation of translational elongation  |  |
| N57382  | transcription elongation factor [Plasmodium cynomolgi strain B] >gi 389583820 dbj                           | Protein metabolism                | Regulation of translational elongation  |  |
| N7888   | PREDICTED: similar to Elongation factor 1 beta CG6341-PA [Tribolium castaneum] >gi 212507797 gb             | Protein metabolism                | Regulation of translational elongation  |  |
| M2529   | unknown [Dendroctonus ponderosae] >gi 478259386 gb ENN79282.1   | hypothetical                      | Protein metabolism                      | Regulation of translational initiation |
| M3245   | hypothetical protein DAPPUDRAFT_226467 [Daphnia pulex]  | Protein metabolism                | Regulation of translational initiation  |  |
| M69321  |   | Protein metabolism                | Regulation of translational initiation  |  |
| M7737   | eukaryotic initiation factor 1 [Coptotermes formosanus]   | Protein metabolism                | Regulation of translational initiation  |  |
| N10357  | PREDICTED: eukaryotic translation initiation factor 2 subunit 2-like [Ornithorhynchus anatinus]             | Protein metabolism                | Regulation of translational initiation  |  |
| N11874  | hypothetical protein DAPPUDRAFT_303630 [Daphnia pulex]  | Protein metabolism                | Regulation of translational initiation  |  |
| N12435  | eukaryotic initiation factor 1 [Coptotermes formosanus]   | Protein metabolism                | Regulation of translational initiation  |  |
| N14083  | putative accessory gland protein [Gryllus firmus]   | Protein metabolism                | Regulation of translational initiation  |  |
| N18953  | PREDICTED: eukaryotic translation initiation factor 3 subunit D-like [Megachile rotundata] >gi 212507797 gb | Protein metabolism                | Regulation of translational initiation  |  |
| N20448  | hypothetical protein DAPPUDRAFT_304176 [Daphnia pulex]  | Protein metabolism                | Regulation of translational initiation  |  |
| N21322  | hypothetical protein DAPPUDRAFT_189030 [Daphnia pulex]  | Protein metabolism                | Regulation of translational initiation  |  |
| N23182  | eukaryotic translation initiation factor 4E type, putative [Pediculus humanus corporis]                     | Protein metabolism                | Regulation of translational initiation  |  |
| N24811  | eIF2B-alpha protein [Daphnia pulex]   | Protein metabolism                | Regulation of translational initiation  |  |
| N33237  | PREDICTED: tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6 [Danio rerio]               | Protein metabolism                | Regulation of translational initiation  |  |
| N40609  | hypothetical protein YQE_10251, partial [Dendroctonus ponderosae] >gi 546673857 gb                          | Protein metabolism                | Regulation of translational initiation  |  |
| N8842   | eukaryotic initiation factor 2 subunit alpha [Litopenaeus vannamei]   | Protein metabolism                | Regulation of translational initiation  |  |
| N18344  | PREDICTED: Megachile rotundata eukaryotic peptide chain release factor subunit 1-lil                        | Protein metabolism                | Regulation of translational termination |  |
| E1939   | PREDICTED: 60S ribosomal protein L11-1-like [Vitis vinifera]  | Protein metabolism                | Ribosome biogenesis                     |  |
| E2054   | ribosomal protein L37 [Acartia pacifica]  | Protein metabolism                | Ribosome biogenesis                     |  |
| E2203   | PREDICTED: 60S ribosomal protein L11-1-like [Vitis vinifera]  | Protein metabolism                | Ribosome biogenesis                     |  |
| E2397   | 60S ribosomal protein L37, putative [Pediculus humanus corporis] >gi 212506270 gb                           | Protein metabolism                | Ribosome biogenesis                     |  |
| E2487   | 40S ribosomal protein S2 [Artemia franciscana]  | Protein metabolism                | Ribosome biogenesis                     |  |
| E2530   | GH21709 [Drosophila grimshawi] >gi 193903065 gb EDW01932.1  | GH21709 [Drosophila melanogaster] | Protein metabolism                      | Ribosome biogenesis                    |
| E2609   | hypothetical protein BRAFLDRAFT_114866 [Branchiostoma floridae] >gi 229277362                               | Protein metabolism                | Ribosome biogenesis                     |  |
| E2641   | ribosomal protein L44 [Procambarus clarkii]   | Protein metabolism                | Ribosome biogenesis                     |  |
| E2797   | RecName: Full=60S ribosomal protein L17 >gi 70909721 emb CAJ17286.1   | ribosomal                         | Protein metabolism                      | Ribosome biogenesis                    |
| E3016   |   | Protein metabolism                | Ribosome biogenesis                     |  |
| E3605   | ribosomal protein S3a [Fenneropenaeus merguiensis]  | Protein metabolism                | Ribosome biogenesis                     |  |
| E5221   | 40S ribosomal protein S2 [Artemia franciscana]  | Protein metabolism                | Ribosome biogenesis                     |  |
| M101526 | RecName: Full=60S ribosomal protein L38 >gi 62083499 gb AAX62474.1  | ribosomal                         | Protein metabolism                      | Ribosome biogenesis                    |
| M101760 | ribosomal protein S7 [Procambarus clarkii]  | Protein metabolism                | Ribosome biogenesis                     |  |
| M105642 | ribosomal protein rps13 [Scylla paramamosain]   | Protein metabolism                | Ribosome biogenesis                     |  |

| ID      | Annotation  | GO term            | Go child term       |
|---------|---|--------------------|---------------------|
| M107342 |   | Protein metabolism | Ribosome biogenesis |
| M108453 | 60S ribosomal protein L11 [Lepeophtheirus salmonis]                               | Protein metabolism | Ribosome biogenesis |
| M109487 | QM protein [Penaeus monodon] >gi 429843492 gb AGA16579.1  QM protein [Litop       | Protein metabolism | Ribosome biogenesis |
| M114084 |   | Protein metabolism | Ribosome biogenesis |
| M16453  | ribosome like protein [Marsupenaeus japonicus]                                    | Protein metabolism | Ribosome biogenesis |
| M18519  | hypothetical protein DAPPUDRAFT_299917 [Daphnia pulex]                            | Protein metabolism | Ribosome biogenesis |
| M18586  | ribosomal protein L19e [Coptotermes formosanus]                                   | Protein metabolism | Ribosome biogenesis |
| M19220  | PREDICTED: zinc finger protein 256-like [Megachile rotundata]                     | Protein metabolism | Ribosome biogenesis |
| M21269  | Palaemonetes varians ribosomal protein S14 mRNA, partial cds                      | Protein metabolism | Ribosome biogenesis |
| M21285  | RecName: Full=60S ribosomal protein L15 >gi 4530186 gb AAD21924.1  L15-like rib   | Protein metabolism | Ribosome biogenesis |
| M21399  | 60S ribosomal protein L6 [Coptotermes formosanus]                                 | Protein metabolism | Ribosome biogenesis |
| M21530  | PREDICTED: Megachile rotundata 40S ribosomal protein S3a-like (LOC100876732), ml  | Protein metabolism | Ribosome biogenesis |
| M21700  | ribosomal protein P1 [Palaemonetes varians]                                       | Protein metabolism | Ribosome biogenesis |
| M21789  | 60S ribosomal protein L38 [Titus discrepans]                                      | Protein metabolism | Ribosome biogenesis |
| M21834  |   | Protein metabolism | Ribosome biogenesis |
| M22249  |   | Protein metabolism | Ribosome biogenesis |
| M23963  | Trichophyton verrucosum HKI 0517 hypothetical protein, mRNA                       | Protein metabolism | Ribosome biogenesis |
| M2518   | hypothetical protein DAPPUDRAFT_193882 [Daphnia pulex]                            | Protein metabolism | Ribosome biogenesis |
| M27167  | Trichophyton verrucosum HKI 0517 hypothetical protein, mRNA                       | Protein metabolism | Ribosome biogenesis |
| M28821  | Procamarbarus clarkii clone pc-639 ribosomal protein S24 mRNA, complete cds       | Protein metabolism | Ribosome biogenesis |
| M33616  | Euphausia eximia voucher KCeux 28S large subunit ribosomal RNA gene, partial seqt | Protein metabolism | Ribosome biogenesis |
| M33880  | ribosomal protein L3 [Penaeus monodon]  | Protein metabolism | Ribosome biogenesis |
| M418    | mitochondrial ribosomal protein, L23, putative [Aedes aegypti] >gi 108879205 gb E | Protein metabolism | Ribosome biogenesis |
| M44196  | Hordeum vulgare subsp. vulgare cDNA clone: FLbaf103d03, mRNA sequence             | Protein metabolism | Ribosome biogenesis |
| M45683  |   | Protein metabolism | Ribosome biogenesis |
| M45899  | 60S ribosomal protein L37A, putative [Pediculus humanus corporis] >gi 212518389 g | Protein metabolism | Ribosome biogenesis |
| M46733  | ribosomal protein rps21 [Palaemonetes varians]                                    | Protein metabolism | Ribosome biogenesis |
| M47690  | putative 60S ribosomal protein RPL31 [Flustra foliacea]                           | Protein metabolism | Ribosome biogenesis |
| M49068  |   | Protein metabolism | Ribosome biogenesis |
| M55239  | PREDICTED: Nasonia vitripennis histone H2A-like (LOC100679332), mRNA              | Protein metabolism | Ribosome biogenesis |
| M61542  | Euphausia superba isolate DGGE band AntEuk13-5 18S ribosomal RNA gene, partial s  | Protein metabolism | Ribosome biogenesis |
| M64656  | ribosome like protein [Marsupenaeus japonicus]                                    | Protein metabolism | Ribosome biogenesis |
| M65348  | PREDICTED: 40S ribosomal protein S8-like [Nasonia vitripennis]                    | Protein metabolism | Ribosome biogenesis |
| M66561  | 40S ribosomal protein S6 [Schizosaccharomyces japonicus yFS275] >gi 212003034 gt  | Protein metabolism | Ribosome biogenesis |
| M66809  | ribosomal protein rps21 [Palaemonetes varians]                                    | Protein metabolism | Ribosome biogenesis |
| M67893  | ribosomal protein L10a [Fenneropenaeus merguiensis]                               | Protein metabolism | Ribosome biogenesis |
| M69255  | Heliconius erato control protein HCTL036 mRNA, partial cds                        | Protein metabolism | Ribosome biogenesis |
| M73104  | 60S ribosomal protein RPL23 [Palaemonetes varians]                                | Protein metabolism | Ribosome biogenesis |
| M74132  | ribosomal protein L44 [Procamarbarus clarkii]                                     | Protein metabolism | Ribosome biogenesis |
| M74190  | putative 60S ribosomal protein RPL17 [Phoronis muelleri]                          | Protein metabolism | Ribosome biogenesis |
| M74416  | ribosomal protein L10a [Fenneropenaeus merguiensis]                               | Protein metabolism | Ribosome biogenesis |
| M75744  | ribosomal protein L36 [Procamarbarus clarkii]                                     | Protein metabolism | Ribosome biogenesis |
| M7919   | putative 40S ribosomal protein S12 [Nephrops norvegicus]                          | Protein metabolism | Ribosome biogenesis |
| M81851  | putative ribosomal protein S23e [Scylla paramamosain]                             | Protein metabolism | Ribosome biogenesis |
| M82075  | putative 60S ribosomal protein RPL31 [Flustra foliacea]                           | Protein metabolism | Ribosome biogenesis |
| M8319   | 39S ribosomal protein L47, mitochondrial [Camponotus floridanus]                  | Protein metabolism | Ribosome biogenesis |
| M84006  | ribosomal protein S3 [Palaemonetes varians]                                       | Protein metabolism | Ribosome biogenesis |
| M84652  | Euphausia superba isolate DGGE band AntEuk13-5 18S ribosomal RNA gene, partial s  | Protein metabolism | Ribosome biogenesis |
| M87835  | ribosomal protein L19e [Scylla paramamosain]                                      | Protein metabolism | Ribosome biogenesis |
| M9073   | ribosomal protein S13 [synthetic construct]                                       | Protein metabolism | Ribosome biogenesis |
| M95582  | 60S ribosomal protein L18a [Caligus clemensi]                                     | Protein metabolism | Ribosome biogenesis |
| M99151  | PREDICTED: 40S ribosomal protein S13-like [Ornithorhynchus anatinus]              | Protein metabolism | Ribosome biogenesis |
| M99579  | ribosomal protein L18 [Litopenaeus vannamei]                                      | Protein metabolism | Ribosome biogenesis |
| M99801  | ribosomal protein L10a [Fenneropenaeus merguiensis]                               | Protein metabolism | Ribosome biogenesis |
| N10674  | 60S ribosomal protein L7A [Ixodes pacificus] >gi 67083827 gb AYA66848.1  60S rbc  | Protein metabolism | Ribosome biogenesis |
| N109    | Phoronis muelleri putative 40S ribosomal protein RPS20 mRNA, complete cds         | Protein metabolism | Ribosome biogenesis |
| N11207  | ribosomal protein S11 [Rimicaris exoculata]                                       | Protein metabolism | Ribosome biogenesis |
| N11420  | lymphoid organ expressed yellow head virus receptor protein [Penaeus monodon]     | Protein metabolism | Ribosome biogenesis |
| N11749  | ribosomal protein S6 [Procamarbarus clarkii]                                      | Protein metabolism | Ribosome biogenesis |
| N11803  | PREDICTED: 60S ribosomal protein L14-like [Aplysia californica]                   | Protein metabolism | Ribosome biogenesis |
| N13267  | hypothetical protein DAPPUDRAFT_306295 [Daphnia pulex]                            | Protein metabolism | Ribosome biogenesis |
| N13567  | ribosomal protein L24 [Azumapecten farreri]                                       | Protein metabolism | Ribosome biogenesis |
| N14540  | Palaemonetes varians ribosomal protein S3 mRNA, partial cds                       | Protein metabolism | Ribosome biogenesis |
| N16052  | ribosomal protein rpl35a [Lineus viridis]   | Protein metabolism | Ribosome biogenesis |
| N16225  | 60S ribosomal protein L37, putative [Pediculus humanus corporis] >gi 212506270 gb | Protein metabolism | Ribosome biogenesis |
| N16289  | 28S ribosomal protein S16, mitochondrial [Aedes aegypti] >gi 108874273 gb EAT38   | Protein metabolism | Ribosome biogenesis |
| N17629  |   | Protein metabolism | Ribosome biogenesis |
| N18966  | hypothetical protein CAPTEDRAFT_149919 [Capitella teleta]                         | Protein metabolism | Ribosome biogenesis |
| N20156  | hypothetical protein DAPPUDRAFT_308176 [Daphnia pulex]                            | Protein metabolism | Ribosome biogenesis |
| N2040   | 60S ribosomal protein L23 [Esox lucius]   | Protein metabolism | Ribosome biogenesis |
| N21176  | PREDICTED: similar to AGAP005615-PA [Tribolium castaneum] >gi 270006846 gb EF     | Protein metabolism | Ribosome biogenesis |
| N23227  | mitochondrial ribosomal protein L24 [Aedes aegypti] >gi 108871351 gb EAT35576.1   | Protein metabolism | Ribosome biogenesis |
| N28192  | putative ribosomal protein L34 [Diaphorina citri]                                 | Protein metabolism | Ribosome biogenesis |
| N29470  | PREDICTED: similar to GA18111-PA [Tribolium castaneum] >gi 270009430 gb EFA05     | Protein metabolism | Ribosome biogenesis |
| N31346  | hypothetical protein DAPPUDRAFT_306294 [Daphnia pulex]                            | Protein metabolism | Ribosome biogenesis |
| N34693  | mitochondrial ribosomal protein, L14, putative [Aedes aegypti] >gi 108879961 gb E | Protein metabolism | Ribosome biogenesis |

| ID                        | Annotation  | GO term            | Go child term                |
|---------------------------|---|--------------------|------------------------------|
| N35222                    | ribosomal protein S4e [Mycetophagus quadripustulatus]                                 | Protein metabolism | Ribosome biogenesis          |
| N3623                     | ribosomal protein S26 [Branchiostoma belcheri]  | Protein metabolism | Ribosome biogenesis          |
| N3958                     | ribosomal protein S15 (RpS15) mRNA, complete cds                                      | Protein metabolism | Ribosome biogenesis          |
| N4202                     | Heliconius melpomene cythera ribosomal protein S15 (RpS15) mRNA, complete cds         | Protein metabolism | Ribosome biogenesis          |
| N43805                    | RecName: Full=40S ribosomal protein S27 >gi 1835724 gb AAB46716.1  40S ribosor        | Protein metabolism | Ribosome biogenesis          |
| N48510                    | putative ribosomal protein S23e [Scylla paramamosain]                                 | Protein metabolism | Ribosome biogenesis          |
| N49331                    |   | Protein metabolism | Ribosome biogenesis          |
| N5213                     |   | Protein metabolism | Ribosome biogenesis          |
| N5488                     | expressed hypothetical protein [Trichoplax adhaerens] >gi 190586310 gb EDV26363       | Protein metabolism | Ribosome biogenesis          |
| N59348                    | hypothetical protein DAPPUDRAFT_194445 [Daphnia pulex]                                | Protein metabolism | Ribosome biogenesis          |
| N6199                     | ribosomal protein L9 [Procambarus clarkii]  | Protein metabolism | Ribosome biogenesis          |
| N62587                    | 60S ribosomal protein L39 [Caligus rogercresseyi]                                     | Protein metabolism | Ribosome biogenesis          |
| N6662                     | Hordeum vulgare subsp. vulgare cDNA clone: Flbaf103d03, mRNA sequence                 | Protein metabolism | Ribosome biogenesis          |
| N6847                     | ribosomal protein S24 [Marsupenaeus japonicus]  | Protein metabolism | Ribosome biogenesis          |
| N8057                     | Branchiostoma floridae hypothetical protein, mRNA                                     | Protein metabolism | Ribosome biogenesis          |
| N8695                     | Litopenaeus vannamei clone C060 ribosomal protein S23e-like mRNA, partial sequenc     | Protein metabolism | Ribosome biogenesis          |
| N8742                     | ribosomal protein L28-like protein [Maconellicoccus hirsutus]                         | Protein metabolism | Ribosome biogenesis          |
| N8901                     | 60S ribosomal protein L30 [Haplopelma schmidti]                                       | Protein metabolism | Ribosome biogenesis          |
| N8903                     | 60S ribosomal protein L30 [Haplopelma schmidti]                                       | Protein metabolism | Ribosome biogenesis          |
| N9172                     | PREDICTED: Oreochromis niloticus 60S ribosomal protein L4-B-like (LOC100694481), i    | Protein metabolism | Ribosome biogenesis          |
| N9292                     | PREDICTED: Strongylocentrotus purpuratus 40S ribosomal protein S16-like, transcript   | Protein metabolism | Ribosome biogenesis          |
| N9387                     | putative 60S ribosomal protein RPL31 [Flustra foliacea]                               | Protein metabolism | Ribosome biogenesis          |
| <b>Response to stress</b> |   |                    |                              |
| M101679                   |   | Response to stress | Defence responce             |
| M18271                    | PREDICTED: DNA-directed RNA polymerase III subunit RPC4 [Sarcophilus harrisii]        | Response to stress | Defence responce             |
| M18811                    | PREDICTED: similar to DNA replication licensing factor MCM3 [Tribolium castaneum]     | Response to stress | Defence responce             |
| M28143                    | crustacyanin subunit C [Fenneropenaeus merguiensis]                                   | Response to stress | Defence responce             |
| M38819                    | hypothetical protein CB1_000307002 [Camelus ferus]                                    | Response to stress | Defence responce             |
| M7368                     | guanine nucleotide-binding protein alpha subunit [Calliphora vicina]                  | Response to stress | Defence responce             |
| N19055                    | hypothetical protein BRAFLDRAFT_231177 [Branchiostoma floridae] >gi 229293953         | Response to stress | Defence responce             |
| N19308                    | PREDICTED: similar to Cytochrome P450 9b2 (CYP1B2) [Tribolium castaneum]              | Response to stress | Defence responce             |
| N19696                    | Aplysia californica alpha tubulin 2 (LOC100533261), mRNA >gi 20069088 gb AF4810       | Response to stress | Defence responce             |
| N25269                    | Putative ferric-chelate reductase 1 [Crassostrea gigas]                               | Response to stress | Defence responce             |
| N41485                    | PREDICTED: similar to AGAP003789-PA [Tribolium castaneum] >gi 270008459 gb EF         | Response to stress | Defence responce             |
| N6533                     |   | Response to stress | Defence responce             |
| M12331                    | 6-4 photolyase [Eurydice pulchra]   | Response to stress | DNA repair                   |
| M3134                     | PREDICTED: F-box and WD repeat domain containing 7-like [Saccoglossus kowalevskii]    | Response to stress | DNA repair                   |
| M38460                    | hypothetical protein DAPPUDRAFT_210135 [Daphnia pulex]                                | Response to stress | DNA repair                   |
| M78537                    | predicted protein [Nematostella vectensis] >gi 156216845 gb EDO37773.1  predict       | Response to stress | DNA repair                   |
| N20425                    | hypothetical protein BRAFLDRAFT_131216 [Branchiostoma floridae] >gi 229273875         | Response to stress | DNA repair                   |
| N21905                    | TFIIB basal transcription factor complex p52 subunit, putative [Pediculus humanus co  | Response to stress | DNA repair                   |
| N22411                    | hypothetical protein BRAFLDRAFT_277469 [Branchiostoma floridae] >gi 229298852         | Response to stress | DNA repair                   |
| N23030                    | Fanconi anemia group J protein [Crassostrea gigas]                                    | Response to stress | DNA repair                   |
| N26975                    | PREDICTED: N-methylpurine-DNA glycosylase-like [Saccoglossus kowalevskii]             | Response to stress | DNA repair                   |
| N27521                    | hypothetical protein BRAFLDRAFT_91042 [Branchiostoma floridae] >gi 229294428 g        | Response to stress | DNA repair                   |
| N29406                    | PREDICTED: DNA mismatch repair protein Msh6-like [Strongylocentrotus purpuratus]      | Response to stress | DNA repair                   |
| N31585                    | PREDICTED: checkpoint protein HUS1-like [Ornithorhynchus anatinus]                    | Response to stress | DNA repair                   |
| N34663                    | PREDICTED: structural maintenance of chromosomes protein 6-like [Apis mellifera]      | Response to stress | DNA repair                   |
| N35298                    | AGAP008939-PA [Anopheles gambiae str. PEST] >gi 157013593 gb EAA14799.5  AG           | Response to stress | DNA repair                   |
| M12535                    | PREDICTED: long-chain fatty acid transport protein 4-like [Megachile rotundata]       | Response to stress | Other                        |
| M18908                    | eukaryotic translation initiation factor 2A [Bos taurus] >gi 151556051 gb AAI49971    | Response to stress | Other                        |
| M5628                     | Armandia brevis histone H3 gene, partial cds  | Response to stress | Other                        |
| M62214                    | toll, putative [Ixodes scapularis] >gi 215504708 gb EEC14202.1  toll, putative [Ixode | Response to stress | Other                        |
| M709                      | heat shock protein 70 (hsp70)-interacting protein [Aedes aegypti] >gi 108880263 gb    | Response to stress | Other                        |
| N18366                    | heat shock protein 40 [Marsupenaeus japonicus]  | Response to stress | Other                        |
| N18621                    | PREDICTED: similar to Bm44 [Tribolium castaneum] >gi 270002597 gb EEZ99044.1          | Response to stress | Other                        |
| N45454                    | DnaJ domain-containing protein [Synecchococcus sp. JA-2-3B'a(2-13)] >gi 499753257     | Response to stress | Other                        |
| N61357                    | PREDICTED: long-chain fatty acid transport protein 1 [Sarcophilus harrisii]           | Response to stress | Other                        |
| M104807                   | hypothetical protein DAPPUDRAFT_301956 [Daphnia pulex]                                | Response to stress | Response to oxidative stress |
| M30619                    | PREDICTED: uncharacterized protein LOC100899356 [Metaseiulus occidentalis]            | Response to stress | Response to oxidative stress |
| M4522                     | peroxinectin, putative [Ixodes scapularis] >gi 215500805 gb EEC10299.1  peroxinect    | Response to stress | Response to oxidative stress |
| M4728                     | hypothetical protein TcasGA2_TC015234 [Tribolium castaneum]                           | Response to stress | Response to oxidative stress |
| M61329                    | peroxinectin [Penaeus monodon]  | Response to stress | Response to oxidative stress |
| M66423                    | peroxinectin [Eriocheir sinensis]   | Response to stress | Response to oxidative stress |
| M74305                    | peroxinectin [Fenneropenaeus chinensis]   | Response to stress | Response to oxidative stress |
| M96899                    | Peroxidasin [Acromyrmex echinatior]   | Response to stress | Response to oxidative stress |
| N14121                    | putative peroxidasin, partial [Latrodectus hesperus]                                  | Response to stress | Response to oxidative stress |
| N19074                    | hypothetical protein DAPPUDRAFT_42141 [Daphnia pulex]                                 | Response to stress | Response to oxidative stress |
| N21683                    | oxidase/peroxidase, putative [Ixodes scapularis] >gi 215494874 gb EEC04515.1  oxi     | Response to stress | Response to oxidative stress |
| N22567                    | peroxinectin [Penaeus monodon]  | Response to stress | Response to oxidative stress |
| N23464                    | glutathione peroxidase [Haemaphysalis longicornis]                                    | Response to stress | Response to oxidative stress |
| N25658                    | hypothetical protein BRAFLDRAFT_123508 [Branchiostoma floridae] >gi 229286043         | Response to stress | Response to oxidative stress |
| N28628                    | peroxinectin [Fenneropenaeus chinensis]   | Response to stress | Response to oxidative stress |
| N46318                    | peroxinectin [Penaeus monodon]  | Response to stress | Response to oxidative stress |
| N47292                    | peroxinectin [Fenneropenaeus chinensis]   | Response to stress | Response to oxidative stress |
| N5524                     | glutathione peroxidase [Metapenaeus ensis] >gi 171189513 gb ACB42237.1  glutat        | Response to stress | Response to oxidative stress |

| ID                         | Annotation  | GO term             | Go child term                     |
|----------------------------|---|---------------------|-----------------------------------|
| N9090                      | Chorion peroxidase [Camponotus floridanus]  | Response to stress  | Response to oxidative stress      |
| N9588                      | selenium-dependent glutathione peroxidase [Macrobrachium rosenbergii]   | Response to stress  | Response to oxidative stress      |
| <b>Signal transduction</b> |   |                     |                                   |
| N22913                     | Sorting nexin-12 [Camponotus floridanus]  | Signal transduction | Cell communication                |
| M3501                      |   | Signal transduction | Cell-cell signaling               |
| M80075                     | ionotropic glutamate receptor subunit [Homarus americanus]  | Signal transduction | Cell-cell signaling               |
| M96025                     | PREDICTED: synapsin-like [Megachile rotundata]  | Signal transduction | Cell-cell signaling               |
| N12768                     | innexin 1 [Cancer borealis]   | Signal transduction | Cell-cell signaling               |
| N12787                     |   | Signal transduction | Cell-cell signaling               |
| N13835                     | GM19962 [Drosophila sechellia] >gi 194126289 gb EDW48332.1  GM19962 [Drosophila sechellia] >gi 194126289 gb EDW48332.1  Signal transduction                   | Signal transduction | Cell-cell signaling               |
| N18727                     | hypothetical protein DAPPUDRAFT_301948 [Daphnia pulex]  | Signal transduction | Cell-cell signaling               |
| M10547                     | PREDICTED: hypothetical protein LOC100426888 [Macaca mulatta]   | Signal transduction | Intracellular signal transduction |
| M11721                     | myosin-IX, putative [Ixodes scapularis] >gi 215505558 gb EEC15052.1  myosin-IX, putative [Ixodes scapularis] >gi 215505558 gb EEC15052.1  Signal transduction | Signal transduction | Intracellular signal transduction |
| M71681                     | hypothetical protein DAPPUDRAFT_304508 [Daphnia pulex]  | Signal transduction | Intracellular signal transduction |
| M7219                      | cAMP-dependent protein kinase catalytic subunit, putative [Pediculus humanus corporis]  | Signal transduction | Intracellular signal transduction |
| M77475                     | PREDICTED: CDC42 binding protein kinase alpha-like [Saccoglossus kowalevskii]   | Signal transduction | Intracellular signal transduction |
| N17078                     | cAMP-dependent protein kinase catalytic subunit, putative [Pediculus humanus corporis]  | Signal transduction | Intracellular signal transduction |
| N18741                     | PREDICTED: hypothetical protein LOC100678008 [Nasonia vitripennis]  | Signal transduction | Intracellular signal transduction |
| N23230                     | RAC protein kinase DRAC-PK85, putative [Pediculus humanus corporis] >gi 21251675 gb EEB12477.1  Signal transduction   | Signal transduction | Intracellular signal transduction |
| N26112                     | PREDICTED: protein kinase C, brain isozyme-like isoform 1 [Nasonia vitripennis]   | Signal transduction | Intracellular signal transduction |
| N29301                     | hypothetical protein DAPPUDRAFT_315683 [Daphnia pulex]  | Signal transduction | Intracellular signal transduction |
| N35561                     | phospholipid phospholipase C beta isoform [Homarus americanus]  | Signal transduction | Intracellular signal transduction |
| N47703                     | phospholipid phospholipase C beta isoform [Homarus americanus]  | Signal transduction | Intracellular signal transduction |
| M10870                     | CG13830-PA-like protein [Daphnia pulex]   | Signal transduction | Intracellular signal transduction |
| M110018                    | RecName: Full=Compound eye opsin BCRH1 >gi 829043 gb BAA09132.1  opsin BcR Signal transduction  | Signal transduction | Other                             |
| M11327                     | cAMP-dependent protein kinase catalytic subunit, putative [Pediculus humanus corporis]  | Signal transduction | Other                             |
| M11904                     | PREDICTED: LOW QUALITY PROTEIN: TBC1 domain family member CG11727 [Apis mellifera]  | Signal transduction | Other                             |
| M16660                     | pigment-dispersing hormone 3 [Marsupenaeus japonicus]   | Signal transduction | Other                             |
| M19175                     | pigment dispersing hormone precursor [Litopenaeus vannamei]   | Signal transduction | Other                             |
| M2709                      |   | Signal transduction | Other                             |
| M28764                     | cuticle protein CUT8 [Portunus pelagicus]   | Signal transduction | Other                             |
| M31314                     | RecName: Full=Compound eye opsin BCRH1 >gi 829043 gb BAA09132.1  opsin BcR Signal transduction  | Signal transduction | Other                             |
| M34439                     | RecName: Full=Compound eye opsin BCRH2 >gi 829045 gb BAA09133.1  opsin BcR Signal transduction  | Signal transduction | Other                             |
| M5422                      | arrestin [Libelloides macaronius]   | Signal transduction | Other                             |
| M55453                     | hypothetical protein CAPTEDRAFT_173251 [Capitella teleta]   | Signal transduction | Other                             |
| M55919                     | hypothetical protein DAPPUDRAFT_44292 [Daphnia pulex]   | Signal transduction | Other                             |
| M56179                     | hypothetical protein DAPPUDRAFT_301966 [Daphnia pulex]  | Signal transduction | Other                             |
| M56268                     | class B secretin-like G-protein coupled receptor GPRcal2, putative [Pediculus humanus corporis]   | Signal transduction | Other                             |
| M66480                     | PREDICTED: peroxisomal membrane protein PEX14 isoform X1 [Columba livia]  | Signal transduction | Other                             |
| M669                       | PREDICTED: similar to chilling-inducible protein, putative [Tribolium castaneum] >gi 212511528 gb EEB12477.1  Signal transduction                             | Signal transduction | Other                             |
| M6816                      | hypothetical protein DAPPUDRAFT_223163 [Daphnia pulex]  | Signal transduction | Other                             |
| M68573                     | phosrestin I, putative [Pediculus humanus corporis] >gi 212508943 gb EEB12477.1  Signal transduction  | Signal transduction | Other                             |
| M73551                     | hypothetical protein AaeL_AAEL004819 [Aedes aegypti] >gi 108879555 gb EAT4378  Signal transduction  | Signal transduction | Other                             |
| M74855                     | RecName: Full=Techylectin-5A; Flags: Precursor >gi 5851893 gb BAA84188.1  tech  Signal transduction   | Signal transduction | Other                             |
| M77959                     | PREDICTED: stromal membrane-associated protein 1-like [Megachile rotundata]   | Signal transduction | Other                             |
| M8094                      | ubiquitin-protein ligase EDD1, putative [Pediculus humanus corporis] >gi 212511528 gb EEB12477.1  Signal transduction   | Signal transduction | Other                             |
| M81405                     | 130 kDa phosphatidylinositol 4,5-biphosphate-dependent ARF1 GTPase-activating protein BcR Signal transduction   | Signal transduction | Other                             |
| M8285                      | RecName: Full=Compound eye opsin BCRH2 >gi 829045 gb BAA09133.1  opsin BcR Signal transduction  | Signal transduction | Other                             |
| M85776                     | signal transducer and activator of transcription [Fenneropenaeus chinensis]   | Signal transduction | Other                             |
| M88373                     | arrestin [Libelloides macaronius]   | Signal transduction | Other                             |
| M93343                     | PREDICTED: apoptosis regulatory protein Siva isoform X2 [Mesocricetus auratus]  | Signal transduction | Other                             |
| M94605                     | protein kinase, putative [Ixodes scapularis] >gi 215496277 gb EEC05917.1  protein   Signal transduction   | Signal transduction | Other                             |
| M95757                     | Val-1 SIFamide [Homarus americanus]   | Signal transduction | Other                             |
| M98592                     |   | Signal transduction | Other                             |
| N10393                     |   | Signal transduction | Other                             |
| N11520                     |   | Signal transduction | Other                             |
| N11936                     | PREDICTED: arrestin homolog [Bombus terrestris]   | Signal transduction | Other                             |
| N12955                     | PREDICTED: ATP-dependent RNA helicase DDX54 [Xenopus (Silurana) tropicalis]   | Signal transduction | Other                             |
| N13913                     | RecName: Full=Compound eye opsin BCRH2 >gi 829045 gb BAA09133.1  opsin BcR Signal transduction  | Signal transduction | Other                             |
| N14135                     | hypothetical protein DAPPUDRAFT_324178 [Daphnia pulex]  | Signal transduction | Other                             |
| N15417                     | PREDICTED: rab3 GTPase-activating protein catalytic subunit isoform 2 [Cavia porcellus]   | Signal transduction | Other                             |
| N17953                     | retinoid X receptor isoform 2 [Crangon crangon]   | Signal transduction | Other                             |
| N18394                     |   | Signal transduction | Other                             |
| N19184                     |   | Signal transduction | Other                             |
| N19969                     | RecName: Full=Arrestin homolog >gi 298756 gb AAB25860.1  arrestin homolog [Loewi apertus]   | Signal transduction | Other                             |
| N20346                     | opsin protein [Charybdis japonica]  | Signal transduction | Other                             |
| N20549                     | Marsupenaeus japonicus MjGo mRNA for GTP binding protein alpha subunit Go, com  | Signal transduction | Other                             |
| N20954                     | hypothetical protein CAPTEDRAFT_180983 [Capitella teleta]   | Signal transduction | Other                             |
| N21098                     | hypothetical protein DAPPUDRAFT_44292 [Daphnia pulex]   | Signal transduction | Other                             |
| N21529                     | hypothetical protein YQE_11312, partial [Dendroctonus ponderosae] >gi 546681223 gb EEB12477.1  Signal transduction  | Signal transduction | Other                             |
| N21988                     | bride of sevenless [Tribolium castaneum]  | Signal transduction | Other                             |
| N22768                     |   | Signal transduction | Other                             |
| N23914                     | hypothetical protein CRE_08567 [Caenorhabditis remanei] >gi 308253586 gb EFO97  Signal transduction   | Signal transduction | Other                             |
| N24013                     | PREDICTED: RAS protein activator like 2-like [Saccoglossus kowalevskii]   | Signal transduction | Other                             |
| N24867                     |   | Signal transduction | Other                             |
| N25485                     |   | Signal transduction | Other                             |

| ID               | Annotation   | GO term             | Go child term           |
|------------------|--|---------------------|-------------------------|
| N28300           | conserved hypothetical protein [Pediculus humanus corporis] >gi 212513821 gb EEF         | Signal transduction | Other                   |
| N28816           | signal transducer and activator of transcription [Penaeus monodon]                       | Signal transduction | Other                   |
| N30883           | HR3 nuclear receptor [Daphnia magna]   | Signal transduction | Other                   |
| N31199           |  | Signal transduction | Other                   |
| N31246           | integral membrane protein GPR177-B, putative [Ixodes scapularis] >gi 215506845 gb Signal | Signal transduction | Other                   |
| N32406           | hypothetical protein DAPPUDRAFT_316993 [Daphnia pulex]                                   | Signal transduction | Other                   |
| N33074           | PREDICTED: LOW QUALITY PROTEIN: ral guanine nucleotide dissociation stimulator-lil       | Signal transduction | Other                   |
| N34392           | RecName: Full=Arrestin, lateral eye >gi 475769 gb AAA82007.1  arrestin [Limulus p        | Signal transduction | Other                   |
| N35241           | peropsin [Cupiennius salei]  | Signal transduction | Other                   |
| N36102           | pigment dispersing hormone precursor [Litopenaeus vannamei]                              | Signal transduction | Other                   |
| N36343           |  | Signal transduction | Other                   |
| N36616           | hypothetical protein DAPPUDRAFT_321679 [Daphnia pulex]                                   | Signal transduction | Other                   |
| N40884           | hypothetical protein DAPPUDRAFT_64004 [Daphnia pulex]                                    | Signal transduction | Other                   |
| N45522           | RecName: Full=Compound eye opsin BCRH1 >gi 829043 gb BAA09132.1  opsin BcR               | Signal transduction | Other                   |
| N48998           | PREDICTED: disintegrin and metalloproteinase domain-containing protein 10-like isoform   | Signal transduction | Other                   |
| N51716           | PREDICTED: angiopoietin-like 2-like [Saccoglossus kowalevskii]                           | Signal transduction | Other                   |
| N55639           | TPA_inf: venus kinase receptor [Pediculus humanus corporis]                              | Signal transduction | Other                   |
| N57793           | RecName: Full=Arrestin homolog >gi 298756 gb AAB25860.1  arrestin homolog [Lo            | Signal transduction | Other                   |
| N59468           | nuclear receptor E75 protein [Fenneropenaeus chinensis]                                  | Signal transduction | Other                   |
| N61375           | PREDICTED: RUN and TBC1 domain containing 2-like [Saccoglossus kowalevskii]              | Signal transduction | Other                   |
| <b>Transport</b> |  |                     |                         |
| M55743           | GK22112 [Drosophila willistoni] >gi 300681124 sp B4MYA4.1 TRET1_DROWI                    | RecNa Transport     | Carbohydrate transport  |
| N49759           | sialin [Xenopus (Silurana) tropicalis] >gi 111305815 gb AAI21682.1  solute carrier fa    | Transport           | Carbohydrate transport  |
| N56030           | sugar transporter, putative [Ixodes scapularis] >gi 215499141 gb EEC08635.1  sugar       | Transport           | Carbohydrate transport  |
| M61              |  | Transport           | Intracellular transport |
| N13433           | hypothetical protein DAPPUDRAFT_304059 [Daphnia pulex]                                   | Transport           | Intracellular transport |
| N18258           |  | Transport           | Intracellular transport |
| E154             | voltage-gated calcium channel beta subunit transcript variant 6 [Scylla paramamosai      | Transport           | Ion transport           |
| E6444            | voltage-dependent non-L-type calcium channel alpha-1 subunit, partial [Cancer bore       | Transport           | Ion transport           |
| M10694           | hypothetical protein DAPPUDRAFT_226732 [Daphnia pulex]                                   | Transport           | Ion transport           |
| M107683          | Euphausia superba mitochondrion, partial genome  | Transport           | Ion transport           |
| M108201          | sodium-driven chloride bicarbonate exchanger, putative [Pediculus humanus corpori        | Transport           | Ion transport           |
| M112656          | hypothetical protein DAPPUDRAFT_40435 [Daphnia pulex]                                    | Transport           | Ion transport           |
| M14041           | sodium/hydrogen exchanger [Carcinus maenas]  | Transport           | Ion transport           |
| M15958           | Sideroflexin-1 [Lepeophtheirus salmonis]   | Transport           | Ion transport           |
| M1709            | hypothetical protein DAPPUDRAFT_308636 [Daphnia pulex]                                   | Transport           | Ion transport           |
| M19113           | NADH dehydrogenase, putative [Aedes aegypti] >gi 108875509 gb EAT39734.1  AA             | Transport           | Ion transport           |
| M19376           | Euphausia superba voucher 841M mitochondrion, partial genome                             | Transport           | Ion transport           |
| M2254            | Litopenaeus stylirostris Na+/K+-ATPase alpha subunit mRNA, complete cds                  | Transport           | Ion transport           |
| M26098           | mitochondrial ubiquinol-cytochrome c reductase complex 11 kDa protein [Scylla para       | Transport           | Ion transport           |
| M32986           | ferritin peptide [Fenneropenaeus indicus]  | Transport           | Ion transport           |
| M48035           |  | Transport           | Ion transport           |
| M55261           | PREDICTED: anion exchange protein 2 isoform X2 [Echinops telfairi]                       | Transport           | Ion transport           |
| M60197           | Euphausia superba voucher 841M mitochondrion, partial genome                             | Transport           | Ion transport           |
| M6504            | putative TRP channel protein [Periplaneta americana]                                     | Transport           | Ion transport           |
| M6590            | PREDICTED: ileal sodium/bile acid cotransporter-like isoform 1 [Nasonia vitripennis]     | Transport           | Ion transport           |
| M68570           | hypothetical protein LOAG_03365 [Loa loa]  | Transport           | Ion transport           |
| M69832           | conserved hypothetical protein [Culex quinquefasciatus] >gi 167873494 gb EDS368          | Transport           | Ion transport           |
| M70398           | sodium-driven chloride bicarbonate exchanger, putative [Pediculus humanus corpori        | Transport           | Ion transport           |
| M71335           | NADH dehydrogenase [Palaemonetes varians]  | Transport           | Ion transport           |
| M73935           | voltage-gated sodium channel [Cancer borealis]   | Transport           | Ion transport           |
| M81077           | PREDICTED: transient receptor potential protein-like [Megachile rotundata]               | Transport           | Ion transport           |
| M81910           | PREDICTED: anion exchange protein 3-like isoform 1 [Acyrthosiphon pisum]                 | Transport           | Ion transport           |
| M85975           | hypothetical protein TRIADDRAFT_21514 [Trichoplax adhaerens] >gi 190587887 gb            | Transport           | Ion transport           |
| M87362           | Nasonia vitripennis ATP synthase, H+ transporting, mitochondrial F0 complex, subunit     | Transport           | Ion transport           |
| M9551            | hypothetical protein CAPTEDRAFT_34319, partial [Capitella teleta]                        | Transport           | Ion transport           |
| N10536           | voltage-dependent anion-selective channel [Eriocheir sinensis]                           | Transport           | Ion transport           |
| N11826           | putative TRPL channel protein [Periplaneta americana]                                    | Transport           | Ion transport           |
| N14105           | Candida tropicalis MYA-3404 NADH-ubiquinone oxidoreductase 20 kDa subunit, mito          | Transport           | Ion transport           |
| N24331           | hypothetical protein DAPPUDRAFT_217456 [Daphnia pulex]                                   | Transport           | Ion transport           |
| N24758           | chloride channel, putative [Ixodes scapularis] >gi 215490978 gb EEC00619.1  chlorii      | Transport           | Ion transport           |
| N25724           | hypothetical protein DAPPUDRAFT_323725 [Daphnia pulex]                                   | Transport           | Ion transport           |
| N25984           | GE19913 [Drosophila yakuba] >gi 194181108 gb EDW94719.1  GE19913 [Drosophil              | Transport           | Ion transport           |
| N26495           | hypothetical protein CAPTEDRAFT_176070 [Capitella teleta]                                | Transport           | Ion transport           |
| N27782           | hypothetical protein BRAFLDRAFT_93126 [Branchiostoma floridae] >gi 229288904 g           | Transport           | Ion transport           |
| N28341           | voltage-dependent non-L-type calcium channel alpha-1 subunit, partial [Cancer bore       | Transport           | Ion transport           |
| N31065           | hypothetical protein DAPPUDRAFT_40908 [Daphnia pulex]                                    | Transport           | Ion transport           |
| N31753           | Probable NADH dehydrogenase 1 alpha subcomplex subunit 12 [Caligus rogercresseyi         | Transport           | Ion transport           |
| N33158           | copper chaperone Atox1 [Crassostrea ariakensis]  | Transport           | Ion transport           |
| N33931           | GD22775 [Drosophila simulans] >gi 194190001 gb EDX03577.1  GD22775 [Drosoph              | Transport           | Ion transport           |
| N36245           | Calcium-transporting ATPase type 2C member 1 [Crassostrea gigas]                         | Transport           | Ion transport           |
| N37259           | sodium-driven chloride bicarbonate exchanger, putative [Pediculus humanus corpori        | Transport           | Ion transport           |
| N37798           | PREDICTED: transient receptor potential-gamma protein-like [Metaseiulus occidental       | Transport           | Ion transport           |
| N39293           | hypothetical protein DAPPUDRAFT_40435 [Daphnia pulex]                                    | Transport           | Ion transport           |
| N40751           | hypothetical protein TcasGA2_TC010614 [Tribolium castaneum]                              | Transport           | Ion transport           |
| N42417           | ABC protein, subfamily ABCG [Daphnia pulex]  | Transport           | Ion transport           |

| ID      | Annotation  | GO term   | Go child term              |
|---------|---|-----------|----------------------------|
| N48362  | clottable protein [Marsupenaeus japonicus]  | Transport | Ion transport              |
| M2931   | PREDICTED: predicted protein-like [Saccoglossus kowalevskii]  | Transport | Lipid transport            |
| M83897  | PREDICTED: predicted protein-like [Saccoglossus kowalevskii]  | Transport | Lipid transport            |
| N10222  | hypothetical protein DAPPUDRAFT_220651 [Daphnia pulex]  | Transport | Lipid transport            |
| N11955  | hypothetical protein DAPPUDRAFT_332702 [Daphnia pulex]  | Transport | Lipid transport            |
| N21451  | PREDICTED: oxysterol-binding protein-related protein 6 [Papio anubis]   | Transport | Lipid transport            |
| M856    | CG8026, isoform B [Drosophila melanogaster] >gi 16648212 gb AAL25371.1  GH221Transport  | Transport | Mitochondrial transport    |
| N22878  | PREDICTED: peroxisomal membrane protein PMP34-like [Apis mellifera]   | Transport | Mitochondrial transport    |
| M103029 |   | Transport | Neurotransmitter transport |
| M74414  | PREDICTED: sodium- and chloride-dependent glycine transporter 1-like [Saccoglossus  | Transport | Neurotransmitter transport |
| N21981  | Sodium-dependent neutral amino acid transporter B(0) [Harpegnathos saltator]  | Transport | Neurotransmitter transport |
| N47183  | AGAP007367-PA [Anopheles gambiae str. PEST] >gi 157020163 gb EAA04277.4  AG   | Transport | Neurotransmitter transport |
| M110921 |   | Transport | Other                      |
| M111738 | PREDICTED: nuclear RNA export factor 1 isoform X1 [Oreochromis niloticus]   | Transport | Other                      |
| M12796  | hypothetical protein DAPPUDRAFT_230342 [Daphnia pulex]  | Transport | Other                      |
| M13825  | oligopeptide transporter [Aedes aegypti] >gi 108875616 gb EAT39841.1  AAELO083  | Transport | Other                      |
| M1536   | PREDICTED: nuclear pore complex protein Nup107-like isoform 2 [Strongylocentrotus   | Transport | Other                      |
| M16085  | hemoglobin [Carcinus maenas]  | Transport | Other                      |
| M21443  | hypothetical protein DAPPUDRAFT_308659 [Daphnia pulex]  | Transport | Other                      |
| M41629  | crustacyanin subunit A [Fenneropenaeus merguiensis]   | Transport | Other                      |
| M4464   |   | Transport | Other                      |
| M60000  | PREDICTED: apolipoprotein D-like [Aplysia californica]  | Transport | Other                      |
| M69167  | Canalicular multispecific organic anion transporter 1 [Tupaia chinensis]  | Transport | Other                      |
| M7110   |   | Transport | Other                      |
| M90499  | PREDICTED: hematopoietic stem/progenitor cells 176-like [Saccoglossus kowalevskii]  | Transport | Other                      |
| N13694  | PREDICTED: coatomer subunit zeta-1-like isoform 1 [Nasonia vitripennis]   | Transport | Other                      |
| N14537  | crustacyanin subunit A [Fenneropenaeus merguiensis]   | Transport | Other                      |
| N14811  | crustacyanin subunit C [Fenneropenaeus merguiensis]   | Transport | Other                      |
| N15675  | DD9B [Marsupenaeus japonicus]   | Transport | Other                      |
| N18559  | PREDICTED: similar to Protein SDA1 homolog (Mystery protein 45A) [Tribolium castaneum]  | Transport | Other                      |
| N19209  | hypothetical protein DAPPUDRAFT_22032 [Daphnia pulex]   | Transport | Other                      |
| N19781  | Transmembrane emp24 domain-containing protein 2 precursor [Lepeophtheirus salmonis]   | Transport | Other                      |
| N23540  | PREDICTED: similar to AGAP009835-PA [Tribolium castaneum]   | Transport | Other                      |
| N26082  | Solute carrier family 15 member 1 [Acromyrmex echinatior]   | Transport | Other                      |
| N27292  | PREDICTED: exocyst complex component 5-like [Apis mellifera]  | Transport | Other                      |
| N33902  | hypothetical protein DAPPUDRAFT_303543 [Daphnia pulex]  | Transport | Other                      |
| N41441  |   | Transport | Other                      |
| N48380  | Monosaccharide-transporting ATPase [Mesorhizobium sp. STM 4661] >gi 474662405   | Transport | Other                      |
| N54308  | nucleoside permease [uncultured SAR046 cluster bacterium HF0010_18013]  | Transport | Other                      |
| N57557  | PREDICTED: vesicle-trafficking protein SEC22b-B-like [Megachile rotundata]  | Transport | Other                      |
| N60720  | hemocyanin 2 [Pacifastacus leniusculus]   | Transport | Other                      |
| N61257  | PREDICTED: protein retinal degeneration B-like isoform X1 [Ceratitis capitata]  | Transport | Other                      |
| N7085   | crustacyanin-A2 precursor [Panulirus cygnus]  | Transport | Other                      |
| M1      | PREDICTED: importin-5 [Megachile rotundata]   | Transport | Protein transport          |
| M102512 | hypothetical protein CAPTEDRAFT_3285 [Capitella teleta]   | Transport | Protein transport          |
| M1086   | AP-3 complex subunit mu-1, putative [Pediculus humanus corporis] >gi 212511278 gb   | Transport | Protein transport          |
| M11116  | PREDICTED: similar to signal recognition particle receptor alpha subunit (sr-alpha) [Trichoplax adhaerens]  | Transport | Protein transport          |
| M14787  | hypothetical protein DAPPUDRAFT_308902 [Daphnia pulex]  | Transport | Protein transport          |
| M15168  | GJ20063 [Drosophila virilis] >gi 194145498 gb EDW61894.1  GJ20063 [Drosophila virilis]  | Transport | Protein transport          |
| M1524   |   | Transport | Protein transport          |
| M18819  | hypothetical protein DAPPUDRAFT_207615 [Daphnia pulex]  | Transport | Protein transport          |
| M3711   | PREDICTED: adaptor-related protein complex 2, beta 1 subunit-like [Saccoglossus kowalevskii]  | Transport | Protein transport          |
| M4131   | PREDICTED: hepatocyte growth factor-regulated tyrosine kinase substrate-like [Loxocarpus conserved hypothetical protein [Pediculus humanus corporis]] >gi 212510581 gb EEF1 | Transport | Protein transport          |
| M4292   | hypothetical protein DAPPUDRAFT_324067 [Daphnia pulex]  | Transport | Protein transport          |
| M58187  | Importin-7, putative [Pediculus humanus corporis] >gi 212517799 gb EEB19638.1  I  | Transport | Protein transport          |
| M61823  |   | Transport | Protein transport          |
| M65226  |   | Transport | Protein transport          |
| M729    | conserved hypothetical protein [Pediculus humanus corporis] >gi 212505671 gb EEF1   | Transport | Protein transport          |
| M73539  | PREDICTED: similar to AGAP006942-PA [Tribolium castaneum]   | Transport | Protein transport          |
| M7463   | AGAP004559-PA [Anopheles gambiae str. PEST] >gi 347972129 ref XP_001238827.3  | Transport | Protein transport          |
| M76166  | PREDICTED: similar to AGAP005934-PA [Tribolium castaneum] >gi 270003221 gb EEF1   | Transport | Protein transport          |
| M8947   | AP-3 complex subunit delta-1, putative [Ixodes scapularis] >gi 215498374 gb EEC07   | Transport | Protein transport          |
| M93600  |   | Transport | Protein transport          |
| N10239  | Coatomer subunit gamma-2, putative [Pediculus humanus corporis] >gi 212511156   | Transport | Protein transport          |
| N10417  |   | Transport | Protein transport          |
| N11893  |   | Transport | Protein transport          |
| N11897  |   | Transport | Protein transport          |
| N12003  | hypothetical protein CAPTEDRAFT_223046 [Capitella teleta]   | Transport | Protein transport          |
| N13263  | hypothetical protein DAPPUDRAFT_230571 [Daphnia pulex]  | Transport | Protein transport          |
| N13949  | Marsupenaeus japonicus Ras-related nuclear protein isoform (Ran-iso) mRNA, complementary  | Transport | Protein transport          |
| N14027  | conserved hypothetical protein [Pediculus humanus corporis] >gi 212508955 gb EEF1   | Transport | Protein transport          |
| N18153  | Importin-7 [Camponotus floridanus]  | Transport | Protein transport          |
| N18202  | hypothetical protein DAPPUDRAFT_306007 [Daphnia pulex]  | Transport | Protein transport          |
| N18212  | cellular apoptosis susceptibility protein [Fenneropenaeus chinensis]  | Transport | Protein transport          |
| N18311  | hypothetical protein DAPPUDRAFT_313075 [Daphnia pulex]  | Transport | Protein transport          |
| N18371  | PREDICTED: Nasonia vitripennis hypothetical protein LOC100121637 (LOC100121637)   | Transport | Protein transport          |

| ID      | Annotation  | GO term   | Go child term              |
|---------|---|-----------|----------------------------|
| N18464  | conserved hypothetical protein [Pediculus humanus corporis] >gi 212514278 gb EEF Transport    | Transport | Protein transport          |
| N18477  | PREDICTED: coatomer subunit delta [Sarcophilus harrisii]                                      | Transport | Protein transport          |
| N18709  | hypothetical protein DAPPUDRAFT_230883 [Daphnia pulex]  | Transport | Protein transport          |
| N18754  | Drosophila persimilis GL21499 (Dper\GL21499), mRNA  | Transport | Protein transport          |
| N18774  | nuclear pore complex protein Nup85 [Danio rerio] >gi 82182122 sp Q6DBY0.1 NUP Transport       | Transport | Protein transport          |
| N18912  | PREDICTED: signal recognition particle 72 kDa protein-like isoform 1 [Nasonia vitripennis]    | Transport | Protein transport          |
| N18978  |   | Transport | Protein transport          |
| N20490  | PREDICTED: extracellular matrix protein FRAS1 isoform X1 [Mustela putorius furo]              | Transport | Protein transport          |
| N20701  | PREDICTED: LOW QUALITY PROTEIN: metaxin-1-like [Nasonia vitripennis]                          | Transport | Protein transport          |
| N21371  | hypothetical protein DAPPUDRAFT_62579 [Daphnia pulex]   | Transport | Protein transport          |
| N21573  | GJ11573 [Drosophila virilis] >gi 194155190 gb EDW70374.1  GJ11573 [Drosophila v               | Transport | Protein transport          |
| N24163  | translocon-associated protein, gamma subunit, putative [Ixodes scapularis] >gi 2155 Transport | Transport | Protein transport          |
| N24480  |   | Transport | Protein transport          |
| N33152  | conserved hypothetical protein [Pediculus humanus corporis] >gi 212507534 gb EEF Transport    | Transport | Protein transport          |
| N34218  | conserved hypothetical protein [Pediculus humanus corporis] >gi 212505671 gb EEF Transport    | Transport | Protein transport          |
| N34390  | translocase of outer mitochondrial membrane 7 homolog [Tribolium castaneum]                   | Transport | Protein transport          |
| N40807  | hypothetical protein DAPPUDRAFT_39774 [Daphnia pulex]   | Transport | Protein transport          |
| N40945  | hypothetical protein BRAFLDRAFT_69266 [Branchiostoma floridae] >gi 229280680 g                | Transport | Protein transport          |
| N41658  | hypothetical protein BRAFLDRAFT_115215 [Branchiostoma floridae] >gi 229298493                 | Transport | Protein transport          |
| N42337  | hypothetical protein DAPPUDRAFT_216176 [Daphnia pulex]  | Transport | Protein transport          |
| N42390  | PREDICTED: transportin-1 [Nasonia vitripennis]  | Transport | Protein transport          |
| N45665  | Charged multivesicular body protein 2a [Caligus rogercresseyi]                                | Transport | Protein transport          |
| N8416   |   | Transport | Protein transport          |
| M103323 | uncharacterized protein LOC100123296 precursor [Nasonia vitripennis]                          | Transport | Transmembrane transport    |
| M104151 | hypothetical protein DAPPUDRAFT_301164 [Daphnia pulex]  | Transport | Transmembrane transport    |
| M17584  | hypothetical protein DAPPUDRAFT_312878 [Daphnia pulex]  | Transport | Transmembrane transport    |
| M18810  | Armigeres subalbatus ASAP ID: 38923 ATP/ADP antipporter mRNA sequence                         | Transport | Transmembrane transport    |
| M19423  | Litopenaeus vannamei adenine nucleotide translocase 2 (LVANT2) mRNA, complete c               | Transport | Transmembrane transport    |
| M64131  | conserved hypothetical protein [Pediculus humanus corporis] >gi 212507616 gb EEF Transport    | Transport | Transmembrane transport    |
| M65006  |   | Transport | Transmembrane transport    |
| M70222  | PREDICTED: protein spinster-like isoform 2 [Nasonia vitripennis]                              | Transport | Transmembrane transport    |
| M79487  | hypothetical protein BRAFLDRAFT_118384 [Branchiostoma floridae] >gi 229277890                 | Transport | Transmembrane transport    |
| M96963  | hypothetical protein DAPPUDRAFT_319730 [Daphnia pulex]  | Transport | Transmembrane transport    |
| N18984  | Chromaffin granule amine transporter, putative [Pediculus humanus corporis] >gi 21 Transport  | Transport | Transmembrane transport    |
| N21595  | PREDICTED: multidrug resistance-associated protein 1-like isoform 5 [Nasonia vitripennis]     | Transport | Transmembrane transport    |
| N22300  | GK22112 [Drosophila willistoni] >gi 300681124 sp B4MYA4.1 TRET1_DROWI RecNa                   | Transport | Transmembrane transport    |
| N27620  | Chromaffin granule amine transporter, putative [Pediculus humanus corporis] >gi 21 Transport  | Transport | Transmembrane transport    |
| N28367  | trehalose transporter 1 [Belsgica antarctica]   | Transport | Transmembrane transport    |
| N28608  | hypothetical protein DAPPUDRAFT_319730 [Daphnia pulex]  | Transport | Transmembrane transport    |
| N30097  | hypothetical protein BRAFLDRAFT_118384 [Branchiostoma floridae] >gi 229277890                 | Transport | Transmembrane transport    |
| N36354  | hypothetical protein SINV_05375 [Solenopsis invicta]  | Transport | Transmembrane transport    |
| N39369  | slalom [Tribolium castaneum]  | Transport | Transmembrane transport    |
| N40391  | hypothetical protein DAPPUDRAFT_312099 [Daphnia pulex]  | Transport | Transmembrane transport    |
| N44994  |   | Transport | Transmembrane transport    |
| N45206  | hypothetical protein BRAFLDRAFT_123511 [Branchiostoma floridae] >gi 229276954                 | Transport | Transmembrane transport    |
| N54348  | Xanthobacter autotrophicus Py2, complete genome   | Transport | Transmembrane transport    |
| N9533   | sugar transporter 16 [Nilaparvata lugens]   | Transport | Transmembrane transport    |
| N9534   | PREDICTED: similar to sugar transporter [Tribolium castaneum]                                 | Transport | Transmembrane transport    |
| M11860  | PREDICTED: ELMO domain-containing protein 2-like [Nasonia vitripennis]                        | Transport | Vesicle-mediated transport |
| M12077  | PREDICTED: vesicle transport protein SFT2A [Chrysemys picta bellii]                           | Transport | Vesicle-mediated transport |
| M56060  | PREDICTED: golgin subfamily A member 5 [Monodelphis domestica]                                | Transport | Vesicle-mediated transport |
| M99732  |   | Transport | Vesicle-mediated transport |
| N18389  | PREDICTED: dynamin-1-like protein-like isoform X1 [Ceratitis capitata] >gi 49898798           | Transport | Vesicle-mediated transport |
| N22080  | hypothetical protein DAPPUDRAFT_223164 [Daphnia pulex]  | Transport | Vesicle-mediated transport |
| N62075  | hypothetical protein DAPPUDRAFT_306117 [Daphnia pulex]  | Transport | Vesicle-mediated transport |







































