Science AAAS

Single-Cell Genomics Reveals Organismal Interactions in Uncultivated Marine Protists

Hwan Su Yoon, *et al.*

Science **332**, 714 (2011);
DOI: 10.1126/science.1203163

Science (print ISSN 0036-8075; online ISSN 1095-9203) is published weekly, except the last week in December, by the American Association for the Advancement of Science, 1200 New York Avenue NW, Washington, DC 20005.

Single-Cell Genomics Reveals Organismal Interactions in Uncultivated Marine Protists

Hwan Su Yoon,[1,2]* Dana C. Price,[3]* Ramunas Stepanauskas,[1] Veeran D. Rajah,[3] Michael E. Sieracki,[1] William H. Wilson,[1] Eun Chan Yang,[1] Siobain Duffy,[3] Debashish Bhattacharya[3]†

Whole-genome shotgun sequence data from three individual cells isolated from seawater, followed by analysis of ribosomal DNA, indicated that the cells represented three divergent clades of picobiliphytes. In contrast with the recent description of this phylum, we found no evidence of plastid DNA nor of nuclear-encoded plastid-targeted proteins, which suggests that these picobiliphytes are heterotrophs. Genome data from one cell were dominated by sequences from a widespread single-stranded DNA virus. This virus was absent from the other two cells, both of which contained non-eukaryote DNA derived from marine Bacteroidetes and large DNA viruses. By using shotgun sequencing of uncultured marine picobiliphytes, we revealed the distinct interactions of individual cells.

Culture-independent analyses of environmental ribosomal DNA (rDNA) clone libraries and metagenomes can uncover unexpected microbial species and gene diversity (e.g., *1*–*3*). These methods cannot, however, reveal in situ interactions among organisms. To achieve this level of resolution, genome data from single cells captured from the wild environment are needed. We used single-cell genomics (*4*–*7*) to study the marine plankton group Picobiliphyta, recently described as a previously unknown lineage of pigmented eukaryotes with a phylogenetic affinity to cryptophytes and katablepharids (*8*, *9*). The cells were originally identified microscopically with the use of 18*S* rDNA-based fluorescent in situ hybridization probes. Although their ultrastructure is unknown, previous studies using autofluorescence and 4′,6-diamidino-2-phenylindole staining data (*9*, *10*) appeared to show that picobiliphytes contain a plastid derived from a cryptophyte alga (owing to the presence of phycobilin proteins; hence the phylum name) and the associated remnant nucleus (nucleomorph). These taxa have not yet been successfully cultivated, leaving open the possibility that the plastid and nucleomorph may not be permanent acquisitions but rather come from a klepto-plastid or a cryptophyte alga

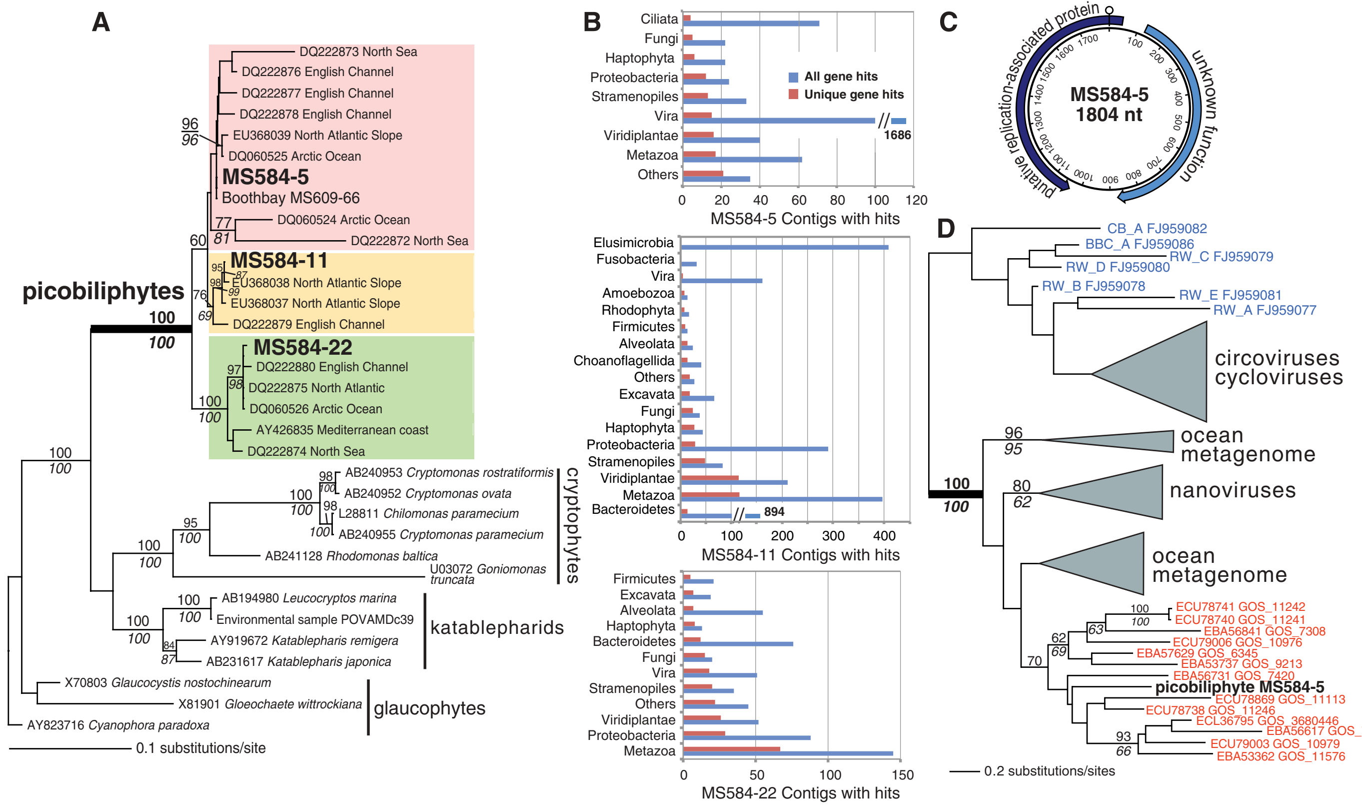

Fig. 1. (**A**) Randomized accelerated maximum likelihood (RAxML) phylogenetic tree of picobiliphyte SSU rDNA coding regions. RAxML bootstrap values are above the branches, and those derived from maximum parsimony (when nodes are shared) are below the branches. Only bootstrap values ≥60% are shown. Sequenced genomes are in bold. GenBank numbers are shown for each taxon. (**B**) Analysis of the taxonomic distribution of BLASTx hits using as query the 454-derived contigs from each SAG assembly (when ≥10; if ≤10, the different hits were grouped under "Others"). The total number of hits (blue bars) and the unique gene hits (red bars) are shown for MS584-5, MS584-11, and MS584-22. Some taxa are overrepresented, such as virus hits in MS584-5 and Bacteroidetes in MS584-22 that are probably explained by MDA bias. (**C**) Genome structure of the previously unknown ssDNA virus. (**D**) Simplified RAxML tree of Rep proteins from representative ssDNA viruses, showing the phylogenetic position of the MS584-5 sequence. Rep from marine ssDNA viruses is shown in blue, whereas sequences derived from ocean metagenome data are shown in red. The bootstrap values (when ≥60%) above the branches are from RAxML, whereas those below are from PhyML. The full tree is shown in fig. S2A.

---

[1] Bigelow Laboratory for Ocean Sciences, West Boothbay Harbor, ME 04575, USA. [2] Department of Biological Sciences, Sungkyunkwan University, Suwon 440-746, South Korea. [3] Department of Ecology, Evolution and Natural Resources, Rutgers University, New Brunswick, NJ 08901, USA.

*These authors contributed equally to this work.

†To whom correspondence should be addressed. E-mail: bhattacharya@aesop.rutgers.edu

captured as food. Picobiliphytes are distributed in variable physicochemical habitats (4 to 89 m in depth, 5° to 30°C in temperature) over broad geographical ranges from the Arctic Ocean to the Sargasso Sea and the Mediterranean coast (*8*, *9*, *11*).

We used fluorescence-activated cell sorting to separate individual heterotrophic (lacking chlorophyll fluorescence) protist cells <10 μm in diameter from a single 50-ml seawater sample collected at Boothbay Harbor in the Gulf of Maine. The temperature, amount of chlorophyll, and composition of the microbial community were typical for midsummer at this site (table S1). After whole-genome amplification using multiple displacement amplification (MDA), the taxonomic identity of each single-cell amplified genome (SAG) was determined by sequencing the 18*S* rDNA gene. Of 35 protist SAGs that were analyzed, 6 (17%) were picobiliphytes (*12*) representing three evolutionarily divergent clades, all of which have been previously regarded as photosynthetic (Fig. 1A). The finding of picobiliphytes in the heterotrophic fraction is consistent with the results of another study of 109 SAGs derived from fluorescent and nonfluorescent protists isolated from Boothbay Harbor (table S2). In that analysis of SAG rDNA sequences, picobiliphytes were present only among cells that lacked chlorophyll fluorescence.

Shotgun sequencing of picobiliphyte SAGs MS584-5, MS584-11, and MS584-22 was done using Roche 454 FLX Titanium series reagents and resulted in ~90 mega–base pairs (Mbp) of individual reads and ~5 Mbp of assembled contigs per SAG (table S3). A BLASTx analysis of contigs (Fig. 1B) and unassembled singletons (fig. S1A) revealed many top hits in different eukaryotes. For MS584-5, the majority [85%; 1686 out of 1995 (1686/1995)] of total contig hits were to viral genes. To reduce the impact of possible amplification bias introduced by MDA (*7*, *13*), we reduced the picobiliphyte lists to unique gene hits in each phylum. This was done by reducing multiple hits to the same protein within a single species in our database (table S4) to a single entry. This assumed that each of the duplicated hits represented the same DNA fragment that was overrepresented because of MDA bias. This procedure reduced the overrepresentation of sequences from particular phyla [for example, Elusimicrobia (408 hits to a PBSX phage terminase in *Elusimicrobium minutum* Pei191) and Bacteroidetes in MS584-11] and increased the relative number of hits to Metazoa, Viridiplantae, and Stramenopiles (Fig. 1B and fig. S1A).

Taxonomic analysis of MS584-5 contigs indicated that this SAG contains a previously uncharacterized virus absent in the other two cells (fig. S1A). The assembled genome of this virus (1804 nt; Fig. 1C) was used in a BLASTx search against the NCBI RefSeq viral repository. This showed that the genome encoded a putative replication-associated protein (Rep), with all 58 hits being to Rep proteins in single-stranded DNA (ssDNA) nanoviruses of plants and circoviruses of animals. The top hit was the Rep protein in the Faba bean necrotic yellows virus [expect (*e*) value that by chance another alignment exists with a higher probability = 6.00×10^{-24}; see fig. S1B]. A BLASTn analysis of the individual 454 reads derived from MS584-5 using the assembled viral genome sequence as a query identified 109,748 reads (46.2% of the total data from this SAG) with an *e* value $\leq 1 \times 10^{-20}$, consistent with the large number of virus-derived contigs in this cell. The sequence coverage across this genome was relatively uniform (mean = 22740; standard deviation = 3396). Given the high abundance of shotgun reads spanning the entire genome of a single "nanovirus" genotype in picobiliphyte MS584-5, our data probably indicate virus infection captured in situ by single-cell sequencing. The MS584-5 Rep protein shares no similarity with plasmids of the red alga *Porphyra pulchra* or ssDNA viruses of diatoms (*14*, *15*) or organelle DNA. The virus is larger than any characterized nanovirus genome segment and has a second open reading frame in the opposite sense to Rep (Fig. 1C). Analysis of the Global Ocean Survey metagenome data (*16*) showed that related Rep protein sequences are abundant in the ocean (Fig. 1D).

Contig and singleton BLASTx hits to non-eukaryote DNA from MS584-11 included marine Bacteroidetes, Proteobacteria, and Firmicutes (Fig. 1B and fig. S1A). MS584-22 harbored a diverse range of larger double-stranded DNA viruses, phages, and Proteobacteria (Fig. 1B and

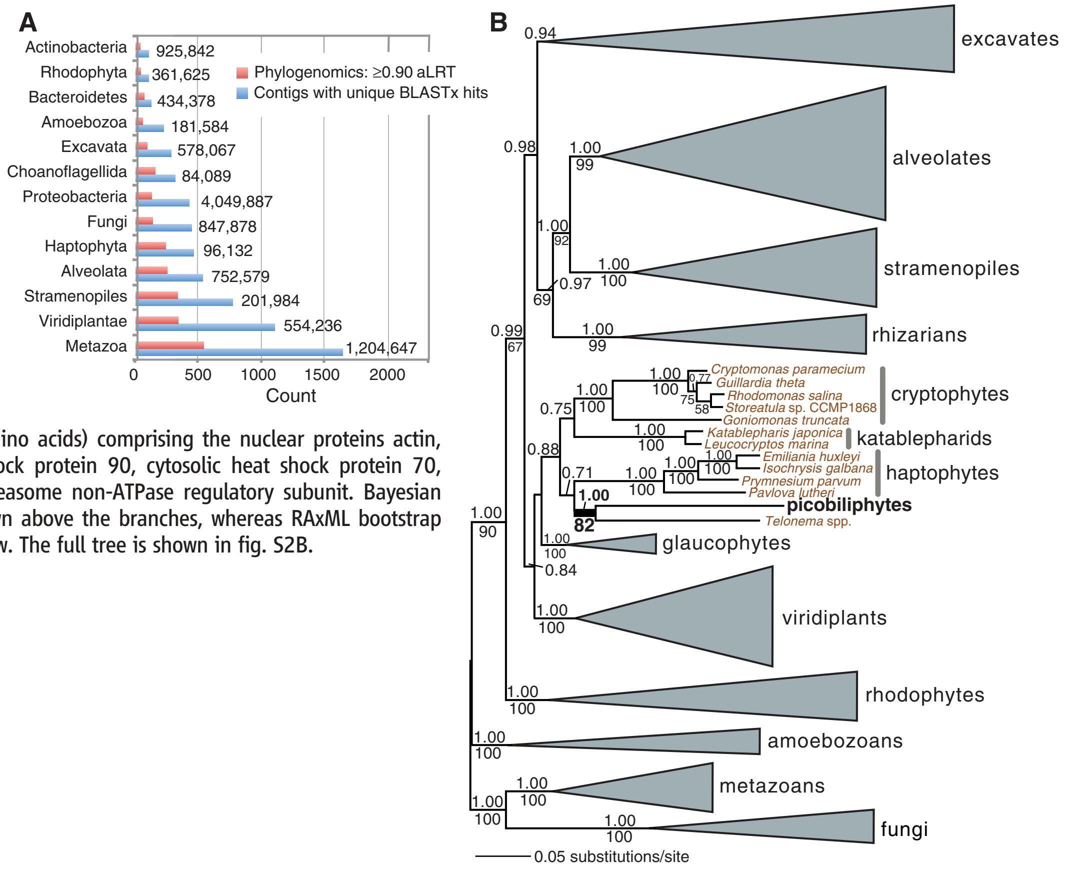

Fig. 2. (**A**) Analysis of the taxonomic distribution of unique BLASTx hits (blue bars) using as query the contigs from the 454 + Illumina assembly of MS584-11. Only phyla with >100 hits are shown. The red bars show the phylogenetic distribution of MS584-11 proteins in PhyML trees at aLRT ≥0.90. The value at the right of the bars is the total number of proteins representing each phylum in our database. (**B**) Simplified phylogeny inferred with Bayesian inference, showing the phylogenetic position of picobiliphytes. This tree was built using a concatenated alignment (2594 amino acids) comprising the nuclear proteins actin, alpha-tubulin, beta-tubulin, heat shock protein 90, cytosolic heat shock protein 70, ribosomal protein L3, and 26*S* proteasome non-ATPase regulatory subunit. Bayesian posterior probability values are shown above the branches, whereas RAxML bootstrap values (when ≥60%) are shown below. The full tree is shown in fig. S2B.

fig. S1A). Presumably, the picobiliphytes feed on Proteobacteria, Bacteroidetes (some apparently phage-infected), and large DNA viruses (*17*), although attachment of viral and bacterial DNA to the picobiliphyte cell surface cannot be ruled out with our approach.

To address the possibility that the picobiliphytes we studied might contain a plastid (*9*) and were sorted as heterotrophs because of a loss of autofluorescence as a result of damage caused by photobleaching, we searched the SAG data for hits to plastid- and mitochondrion-encoded proteins. BLASTx analysis identified 62, 3646, and 102 hits to mitochondrial proteins in the sequence reads from MS584-5, MS584-11, and MS584-22, respectively, but failed to recover plastid proteins (contig hits are shown in table S5). We then generated an additional ~3 Gbp of data from MS584-11 using an Illumina GAIIx sequencer. These data (29.3 million paired-end reads) were coassembled with the existing 454 data, resulting in ~28 Mbp of contigs. Assessment of the two sets of sequence data showed that 94% of the 454 data mapped (at ≤3 mismatches in a 53-bp sliding window of comparison) to the Illumina reads. BLASTx analysis of the combined assembly again failed to identify plastid DNA. As a final step, we generated ~9 Gbp of Illumina data from MS584-22 and used BLASTx to search the assembled ~27 Mbp of contigs for hits to plastid genes; none were found except for a hit to a site-specific DNA endonuclease and to a hypothetical protein that are plastid-encoded in two different green algae (table S6). To assess our ability to identify plastid genes in a SAG-MDA sample, we examined Illumina data derived from a photosynthetic amoeba, *Paulinella chromatophora* [for details, see (*S24*)]. This analysis showed that over one-half of the *P. chromatophora* plastid-encoded genes could be successfully retrieved with BLASTx.

The 454 + Illumina draft genome assembly for MS584-11 afforded assessment of the level of gene homology between the poorly understood picobiliphytes and other eukaryotes. The MS584-11 data were initially analyzed with BLASTx to determine the number of hits of MS584-11 contigs to the total set of predicted proteins in the sequenced genomes of brewer's yeast *Saccharomyces cerevisae* S288c and the model diatom *Phaeodactylum tricornutum* CCAP 1055/1. Using the cutoff *e* value $\leq 1 \times 10^{-5}$, 1866/5863 (31.8%) and 2792/9488 (29.4%) of proteins in the yeast and the diatom, respectively, had hits to picobiliphyte contigs. This suggests that ~2000 picobiliphyte proteins shared detectable similarity with sequences in other eukaryotes. We searched annotations for all diatom protein hits to the picobiliphyte data, now at the more stringent *e* value $\leq 1 \times 10^{-10}$ (1687 proteins) for putative nuclear-encoded plastid-targeted proteins in MS584-11. This analysis turned up a weak hit to a putative chloroplast-targeted nuclear-encoded recombinase and a plastidic inositol phosphatase in *P. tricornutum* (GenBank identification nos. 219111175 and 219110535, respectively). The picobiliphyte recombinase homolog was, however, of bacterial origin, and the inositol phosphatase was of eukaryotic provenance but related to nonplastidic forms of the enzyme. A BLASTx analysis of the MS584-11 contigs against our local database (Fig. 2A) found more unique hits to eukaryote genes in this SAG (with most hits to Metazoa, Viridiplantae, and Stramenopiles) than to prokaryote genes. The large number of hits to Metazoa probably reflects the size of our database (>1.2 million proteins, Fig. 2A), combined with an absence of data from genomes that are closely related to picobiliphytes (Figs. 1A and 2B). Summing the lengths of all MS584-11 contigs with significant BLASTx hits to eukaryote proteins gave an estimate of 7.9 Mbp of detectable, gene-encoding regions of the picobiliphyte genome in our assembly. Given that other pico-sized eukaryotes such as *Ostreococcus* sp. and *Micromonas* spp. have genome sizes of ~12 to 22 Mbp (*18*), and that picobiliphyte-specific proteins will not be detected by our approach, the MS548-11 assembly probably covers a minimum of 50% of the picobiliphyte genome.

The predicted proteins from the MS584-11 assembly that had significant BLASTx hits (8334 proteins) were used as input for a phylogenomic analysis against our local genome database (see the supporting online material) (*19*). The picobiliphyte data included many highly conserved eukaryotic proteins such as beta-tubulin (contig21336_2; average coverage = 457x) and the second-largest subunit of DNA-directed RNA polymerase I (contig20686_4; average coverage = 11x). We concatenated seven conserved proteins present in the picobiliphyte genome data [actin, alpha-tubulin, beta-tubulin, heat shock protein 90, cytosolic heat shock protein 70, ribosomal protein L3, and 26*S* proteasome non–adenosine triphosphatase (non-ATPase) regulatory subunit] to infer their position in the tree of life. This Bayesian phylogeny (Fig. 2B) shows picobiliphytes to comprise an ancient divergence among eukaryotes with a putative phylogenetic relationship to the plastid-lacking telonemids. The picobiliphyte-telonemid clade is sister to the photosynthetic haptophytes and cryptophytes and the plastid-lacking katablepharids. The union of plastid-containing and plastid-lacking taxa suggests the possibility that picobiliphytes may once have been photosynthetic, as has been suggested for ciliates (*20*) and telonemids (*21*).

Phylogenomics using the MS584-11 data returned 5231 maximum likelihood (PhyML) trees that were sorted (*22*) to determine the taxonomic affinities of the different picobiliphyte proteins at the approximate likelihood-ratio test (aLRT) (*23*) cutoff ≥0.90 (Fig. 2A). This analysis showed that 2228 picobiliphyte proteins (3242 at aLRT ≥0.70) are monophyletic with the eukaryotes tested in our analysis (table S7), which is consistent with the BLASTx analysis described above using the yeast and diatom genome data. Phylogenomics provided a robust estimate of the number of eukaryotic proteins in the MS548-11 data set because it relied on maximum likelihood phylogenetic analysis to assess gene affiliation. The finding that 338, 335, and 240 picobiliphyte proteins group at aLRT ≥0.90 with the Viridiplantae, Stramenopiles, and Haptophyta (table S7), respectively, is consistent with a possible photosynthetic ancestry for picobiliphytes (Fig. 2B). An example of a PhyML tree returned by our pipeline (showing members of the major facilitator superfamily of transporters) that supports a close association of MS584-11 with photosynthetic lineages is shown in fig. S3.

In a final attempt to find potential plastid-targeted proteins in MS584-11, we collected all of the maximum likelihood trees resulting from the phylogenomic analysis that grouped the picobiliphytes with Stramenopiles at aLRT ≥0.70 (1683 individual proteins) and generated gene ontology annotations for these sequences (table S8). Again, we found no evidence for nuclear-encoded plastid-targeted proteins (such as photosystem or light-harvesting proteins) in this data set that included nuclear genome data from photosynthetic diatoms and the pelagophyte *Aureococcus anophagefferens*, which are known to contain these genes. We interpret these different lines of evidence as arguing against a photosynthetic lifestyle for the picobiliphyte SAGs we have studied.

In this study, SAG analysis allowed us to generate significant genome data from three individual, related cells found in a single 50-ml coastal seawater sample. This revealed complex biotic interactions among previously uncharacterized marine microorganisms, with each cell undergoing distinct types of interaction. Our single-cell sequencing approach opens novel opportunities to study protist, prokaryote, and viral interactions in situ, without cultivation artifacts, and has biomedical applications; for example, in determining DNA differences between healthy and diseased cells. The ability to generate substantial amounts of genome data from single cells also opens the possibility of reconstructing the eukaryotic tree of life, using a multitude of uncultured taxa isolated directly from their natural environment.

References and Notes

1. B. J. Baker *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* **107**, 8806 (2010).
2. I. Bodaker *et al.*, *ISME J.* **4**, 399 (2010).
3. P. A. Vaishampayan *et al.*, *Genome Biol. Evol.* **2**, 53 (2010).
4. K. Zhang *et al.*, *Nat. Biotechnol.* **24**, 680 (2006).
5. Y. Marcy *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* **104**, 11889 (2007).
6. R. Stepanauskas, M. E. Sieracki, *Proc. Natl. Acad. Sci. U.S.A.* **104**, 9052 (2007).
7. T. Woyke *et al.*, *PLoS ONE* **4**, e5299 (2009).
8. M. L. Cuvelier *et al.*, *Environ. Microbiol.* **10**, 1621 (2008).
9. F. Not *et al.*, *Science* **315**, 253 (2007).
10. E. Kim *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* **108**, 1496 (2011).
11. C. Lovejoy, R. Massana, C. Pedrós-Alió, *Appl. Environ. Microbiol.* **72**, 3085 (2006).
12. J. L. Heywood, M. E. Sieracki, W. Bellows, N. J. Poulton, R. Stepanauskas, *ISME J.* **5**, 674 (2011).
13. S. Rodrigue *et al.*, *PLoS ONE* **4**, e6864 (2009).
14. D. A. Moon, L. J. Goff, *Curr. Genet.* **32**, 132 (1997).
15. Y. Shirai *et al.*, *Appl. Environ. Microbiol.* **74**, 4022 (2008).
16. S. J. Williamson *et al.*, *PLoS ONE* **3**, e1456 (2008).

17. C. Evans, W. H. Wilson, *Limnol. Oceanogr.* **53**, 2035 (2008).
18. A. Z. Worden *et al.*, *Science* **324**, 268 (2009).
19. A. Moustafa *et al.*, *Science* **324**, 1724 (2009).
20. A. Reyes-Prieto, A. Moustafa, D. Bhattacharya, *Curr. Biol.* **18**, 956 (2008).
21. N. Okamoto, C. Chantangsi, A. Horák, B. S. Leander, P. J. Keeling, *PLoS ONE* **4**, e7080 (2009).
22. A. Moustafa, D. Bhattacharya, *BMC Evol. Biol.* **8**, 6 (2008).
23. M. Anisimova, O. Gascuel, *Syst. Biol.* **55**, 539 (2006).

Acknowledgments: This project was supported by NSF grants EF-0827023, DEB-0936884, OCE-0821374, and OCE-0623288, and by Next-Generation BioGreen 21 (SSAC, 2011), Rural Development Administration, South Korea. The authors thank J. Heywood and N. Poulton for technical support. The genome sequence of the MS584-5 virus is available in GenBank under the accession number HQ322117, whereas the 454 sequence data from SAG MS584-5 and 454 + Illumina reads from MS584-11 and MS584-22 are available at the NCBI Sequence Read Archive under the accession numbers SRR068243.1, SRR068244.2, and SRR068245.2, respectively. The assembled contigs for each SAG, the phylogenomic results (alignments and trees), singleton hit lists, annotations for the 8334 proteins in the MS584-11 joint assembly, protein alignments used for the trees presented in the paper, and the *Paulinella chromatophora* plastid sequence and Illumina genome data used to determine the frequency of plastid genes recovered from these reads are freely available at http://dbdata.rutgers.edu/data/pico.

Supporting Online Material

www.sciencemag.org/cgi/content/full/332/6030/714/DC1
Materials and Methods
SOM Text
Figs. S1 to S3
Tables S1 to S8
References

21 January 2011; accepted 1 April 2011
10.1126/science.1203163

A Family of IFN-γ–Inducible 65-kD GTPases Protects Against Bacterial Infection

Bae-Hoon Kim,[1] Avinash R. Shenoy,[1] Pradeep Kumar,[1] Rituparna Das,[1,2] Sangeeta Tiwari,[1] John D. MacMicking[1]*

Immune interferon gamma (IFN-γ) is essential for mammalian host defense against intracellular pathogens. IFN-γ induces nearly 2000 host genes, yet few have any assigned function. Here, we examined a complete mouse 65-kilodalton (kD) guanylate-binding protein (Gbp) gene family as part of a 43-member IFN-γ–inducible guanosine triphosphatase (GTPase) superfamily in mouse and human genomes. Family-wide loss-of-function analysis found that at least four Gbps—Gbp1, Gbp6, Gbp7, and Gbp10—conferred cell-autonomous immunity to listerial or mycobacterial infection within macrophages and gene-deficient animals. These Gbps solicited host defense proteins, including the phagocyte oxidase, antimicrobial peptides, and autophagy effectors, to kill intracellular bacteria. Thus, specific 65-kD Gbps coordinate a potent oxidative and vesicular trafficking program to protect the host from infection.

Immune interferon gamma (IFN-γ) is critical for resistance to infection, exerting its effects through broad transcriptional programs involving ~2000 genes, many of which remain uncharacterized (*1*, *2*). Prominent within this transcriptional signature are several families of guanosine triphosphatases (GTPases). These include the 47-kD immunity-related GTPases (p47 IRGs), 65- to 73-kD guanylate-binding proteins (p65 Gbps), and 285-kD very large inducible GTPases (Vligs/Gvins) (*2*).

Recent mapping efforts have uncovered 43 members of this IFN-γ–inducible GTPase superfamily within mouse and human genomes (*3*–*7*) (fig. S1, A and B). p47 IRGs represent the largest subgroup (~18 to 21 genes) important for host defense (*8*–*12*). These GTPases bind phosphoinositides, cardiolipin, soluble NSF attachment protein receptor adaptor proteins, and other p47 IRGs to direct their membrane regulatory activities against compartmentalized bacteria and protozoa (*10*–*12*). In contrast, little is known about the p65 Gbp and Gvin subfamilies, despite accounting for ~20% of the relative abundance of all proteins induced by IFN-γ (*2*). Weak antiviral or antibacterial properties have been ascribed individually to Gbp1, Gbp2, and Gbp5 (*13*–*15*); however, integrated family contributions remain untested (*2*, *5*).

We thus conducted loss-of-function screens across the complete 11-member mouse *Gbp* family in macrophages where it is strongly induced by IFN-γ compared with other IFNs (IFN-αβ, IFN-λ, and IFN-Z) and Toll-like receptor (TLR) ligands (fig. S1, C and D) (*6*). These immune cells were infected with two intracellular bacteria particularly sensitive to IFN-γ–mediated killing: *Listeria monocytogenes* (*Lm*), a gram-positive bacterium responsible for food-borne infection in humans, or *Mycobacterium bovis* BCG (*Mb* BCG), which causes lethal mycobacteriosis in IFNγR-deficient patients (*1*). Using short 21-bp (base pair) Gbp small interfering RNA (siRNA) duplexes that gave robust gene-specific silencing (fig. S2, A and B), we found that Gbp1, Gbp6, Gbp7, and Gbp10 were critical for control of virulent *Lm* (EGD strain) or *Mb* BCG (Phipps strain). In resting RAW264.7 macrophages, *Lm* multiplied by a factor of ~85 (log$10^{1.9}$ growth) over 6 hours after uptake. IFN-γ activation, however, curtailed replication (to a factor of ~18, or log$10^{1.2}$ growth), a restriction that was reversed with siRNAs for Gbp1, Gbp6, Gbp7, Gbp10 and to a lesser extent Gbp5 (to a factor of 39 to 58 or ~log$10^{1.5-1.75}$ growth; $P < 0.0062$) (Fig. 1A and fig. S3A). Protective Gbps functioned cooperatively, with siRNA combinations exacerbating the loss of IFN-γ–induced killing (Fig. 1A and fig. S3A). siRNA phenotypes were not attributable to single- and double-stranded RNA sensing. Primary bone-marrow–derived macrophages (BMMs) and RAW264.7 cells defective in either TLR (MyD88$^{-/-}$Trif$^{-/-}$) or Rig-1/Mda5/Ips-1–dependent RNA recognition (expressing the viral Rig-1/Mda5/Ips-1 inhibitor, NS34A) yielded comparable results (Fig. 1A and fig. S3A).

Mb BCG challenge showed similar Gbp-dependent resistance. In short 48-hour killing assays that were necessitated by waning siRNA effectiveness at 96 hours, IFN-γ reduced *Mb* BCG by ~log$10^{0.8}$ [72 to 77% reduction in colony-forming units (CFU)] in untreated and scrambled RNA (scRNA)–treated macrophages. Inhibition was partly reversed by Gbp1, Gbp5, Gbp7, or Gbp6/Gbp10 siRNAs (56 to 64% CFU reduction) but not siRNAs for the remaining *Gbp* genes (77 to 82%; $P < 0.0112$) (Fig. 1A and fig. S3B).

To amplify the smaller phenotypes for slow-growing *Mb* BCG, we devised a system of long-term Gbp inhibition. Dominant-negative (DN) mutants were identified and stably expressed under tetracycline-repressible control [tTA-TRE2-Gbp (DN)] to avoid polyketide antibiotics during infection. Two conserved P-loop residues (GxxH/RxKS) required for nucleotide-dependent self-assembly or a C-terminal CaaX box (CVIL) used for C_{20} isoprenyl membrane tethering were mutated (*16*, *17*). All Gbp1 (Gbp1$^{\mathrm{H48P}}$, Gbp1$^{\mathrm{S52N}}$, and Gbp1$^{\mathrm{SVIL}}$) and Gbp7 (Gbp7$^{\mathrm{R48P}}$ and Gbp7$^{\mathrm{S52N}}$) mutants failed to target vesicle membranes; however, those of Gbp10 (Gbp10$^{\mathrm{R46P}}$ and Gbp10$^{\mathrm{S50N}}$) showed a less robust phenotype and were not pursued further as potential DN candidates (fig. S4A). Stable expression of Gbp1 and Gbp7 P-loop (S52N) mutants disrupted endogenous Gbp vesicle localization in IFN-γ–activated macrophages (fig. S4B), underscoring their DN action by binding wild-type partners for incorporation into "dead-end" multimeric complexes (fig. S5, A to C). This resembles dynamin-1 P-loop (S52N)

---

[1] Section of Microbial Pathogenesis, Boyer Centre for Molecular Medicine, Yale University School of Medicine, New Haven, CT 06510, USA. [2] Department of Internal Medicine, Division of Infectious Diseases, Yale University School of Medicine, New Haven, CT 06510, USA.

*To whom correspondence should be addressed. E-mail: john.macmicking@yale.edu

Correction: 9 May 2011

www.sciencemag.org/cgi/content/full/332/6030/714/DC1

Supporting Online Material for

Single-Cell Genomics Reveals Organismal Interactions in Uncultivated Marine Protists

Hwan Su Yoon, Dana C. Price, Ramunas Stepanauskas, Veeran D. Rajah, Michael E. Sieracki, William H. Wilson, Eun Chan Yang, Siobain Duffy, Debashish Bhattacharya*

*To whom correspondence should be addressed. E-mail: bhattacharya@aesop.rutgers.edu

Published 6 May 2011, *Science* **332**, 714 (2011)
DOI: 10.1126/science.1203163

This PDF file includes:

- Materials and Methods
- SOM Text
- Figs. S1 to S3
- Tables S1 to S8
- References

Correction: Tables S1 to S8 were added to the SOM file.

REPORT

Single-cell genomics reveals organismal interactions in uncultivated marine protists

Hwan Su Yoon, Dana C. Price, Ramunas Stepanauskas, Veeran D. Rajah, Michael E. Sieracki, William H. Wilson, Eun Chan Yang, Siobain Duffy, Debashish Bhattacharya

Supporting Online Material

Analysis of Plastid Genes in *Paulinella chromatophora*

To determine whether the inability to identify plastid DNA in the picobiliphytes, in spite of extensive genome sampling of MS584-11 and MS584-22, may reflect an unknown bias associated with our approach, we searched for plastid DNA in SAG-MDA derived Illumina genome data from a 50-cell sample of the photosynthetic amoeba *Paulinella chromatophora* FK01 for which the plastid genome sequence is known (*S24*). We chose this species because the genome data for *P. chromatophora* were generated using the same approach as for the picobiliphytes and therefore provided a direct test of the idea that plastid genes can be successfully recovered from SAG-MDA derived Illumina sequence reads. Ten bins of unassembled data, each totaling 80 Mbp (theoretical 1x coverage of the amoeba nuclear genome), were created by randomly retrieving 640,000 reads of length 125 bp from a 3.1 Gbp *P. chromatophora* Illumina-generated DNA library. The bins were then each used as a BLASTx query (*e-value* ≤ 1e-20) against a protein database containing all FK01 plastid proteins. Using this approach, we identified an average of 149 matches per bin to the 841 distinct proteins on the FK01 organelle genome. A total of 459/841 plastid proteins had matches over the ten bins of data (the *P. chromatophora* plastid sequence and Illumina genome data used to determine the frequency of plastid genes recovered from these reads are freely available at http://dbdata.rutgers.edu/data/pico). Although the *P. chromatophora* plastid genome is ~5-6-fold larger than in a typical alga (*S24*), and we sampled pooled DNA from a culture, our data suggest that if present, plastid DNA should have been identified among the ~3 Gbp and ~9 Gbp of total data from MS584-11 and MS584-22, respectively.

Materials and Methods

A 50 mL coastal water sample was collected from 1 m depth in Boothbay Harbor in the Gulf of Maine, U.S.A. (43°50'39.76"N, 69°38'27.76"W). Sampling was at high tide (8:15 am) on July 25th, 2007. Water temperature was 18°C. Samples were kept in the dark at *in situ* temperature until processing (< 6h). Subsamples (3 mL) were incubated for 10 min with Lysotracker Green DND-26 (75 nmol.L^{-1}; Invitrogen), a pH-sensitive green fluorescing probe that stains food vacuoles in protists (*S25*). Target cells were identified and sorted using a MoFlo™ (Beckman-Coulter) flow cytometer equipped with a 488 nm laser for excitation. Prior to sorting, the cytometer was cleaned thoroughly with bleach: all tubes, plates, and buffers were UV-treated prior to use to remove any DNA contamination: a 1% NaCl solution (0.2 µm filtered and UV treated) was used as sheath fluid (*S26*).

Heterotrophic protists were identified by the presence of Lysotracker fluorescence and absence of chlorophyll fluorescence. Side scatter was used to select protists <10 µm in diameter that were deposited into 96 well plates, with some wells dedicated to positive (10 cells/well) and negative controls (0 cells/well). All wells on the microplates contained 5 µL 1 x PBS (sample labels starting with MS584) or Lyse-N-Go (Pierce) (sample labels starting with MS609). Samples were centrifuged briefly and stored at -80ºC. Processing of a cell to generate a single cell amplified genome (SAG) using multiple displacement amplification (MDA) was done as previously described (*S25*). The PCR survey of the SAGs included 18S rDNA, actin, alpha-, and beta-tubulin all of which returned positive gene products. DNA from four picobiliphyte SAGs (MS584-5, MS584-11, MS584-22, and MS609-66) were re-amplified using the Repli-G midi kit (Qiagen) using the manufacturer's instructions. The products of the second MDA reaction were de-branched with S1 nuclease to reduce chimeric sequences during MDA (*S27*) and purified with a spin column (QIAquick PCR Purification Kit, Qiagen).

About 5 µg of genomic DNA derived from each SAG with the A260/280 ratio of 1.85 were used for shotgun sequencing with the GS-FLX Titanium platform (Roche) at the DNA Facility at the University of Iowa (http://dna-9.int-med.uiowa.edu/). One-quarter of a picotitre plate was used to generate sequence data from each picobiliphyte SAG resulting in over 230,000 reads per SAG. The individual sequence reads were assembled using *Celera* wgs-6.0 beta (see http://sourceforge.net/apps/mediawiki/wgs-assembler/index.php?title=Main_Page) using default settings (see table S3 for assembly output).

Thereafter about 10 μg of MDA-derived total DNA from MS584-11 and MS584-22 were each used to construct a library (sheared DNA fragments were of size 500 bp) for 100 bp x 100 bp paired-end sequencing using an Illumina GAIIx instrument in the Bhattacharya lab. Standard Illumina protocols (http://www.illumina.com/) were used to generate the library. We generated 29,286,431 reads totaling nearly 3 Gbp for MS584-11 and 68,757,098 reads totaling 9.5 Gbp for MS584-22. The MS584-11 Illumina data were co-assembled with the 454 reads from this SAG-using the proprietary software in *CLC Genomics Workbench* (http://www.clcbio.com/) resulting in 73,286 contigs with a total size 27.6 Mbp and a N50 of 638 bp. Assembly of only the Illumina data from MS584-22 using the *CLC Genomics Workbench* resulted in 74,660 contigs with a total size 29.4 Mbp and a N50 of 506 bp.

A local database was used to analyze the singletons and contigs resulting from the picobiliphyte 454-derived single cell genome assemblies. This database is described in Moustafa et al. (*S28*) and is composed of predicted and annotated proteins from RefSeq (Release 42), the genome of the red alga *Cyanidioschyzon merolae* (*S29*), diatom and green algal genomes available from the Joint Genome Institute, and partial EST data from protists such as dinoflagellates and cryptophytes available from other public repositories. The singleton analysis was done from each SAG 454 assembly to determine the phylogenetic origins of the unassembled reads. Using a BLASTx cut-off value of $E \leq 1e^{-10}$ and the database described above, we found hits to 14402, 17671, and 2244 singletons in MS584-5, MS584-11, and MS584 -22, respectively (list of singleton hits for each SAG available at http://dbdata.rutgers.edu/data/pico). BLASTx analysis with a threshold value of $E \leq 1e^{-5}$ identified 62, 3646, and 102 hits to mitochondrial DNA in the contigs of MS584-5, MS584-11, and MS584-22, respectively. Phylogenomic analysis was done as described in Moustafa et al. (*S28*). Resulting alignments were analyzed using PhyML (*S30*) with the approximate likelihood ratio test (aLRT) SH-like support values (*S31*) to infer ML trees under the WAG model. These trees were filtered with PhyloSort (*S32*) by searching for the monophyly of picobiliphytes with other eukaryotic and prokaryotic groups of interest with aLRT support score ≥0.90, or ≥0.70. For the trees presented in the main text paper we also used

RAxML (*S33*) with the WAG + Γ + I model of amino acid evolution to generate the trees. One hundred bootstrap replicates were used with RAxML, PhyML, or maximum parsimony (for rDNA) to assess the stability of nodes in these phylogenies (e.g., *S34*)

References and Notes

S24. A. Reyes-Prieto *et al., Mol Biol Evol* **27**, 1530 (2010).

S25. J. M. Rose, D. A. Caron, M. E. Sieracki, N. Poulton, *Aquat Micob Ecol* **34**, 263 (2004).

S26. R. Stepanauskas, M. E. Sieracki, *Proc Natl Acad Sci U S A* **104**, 9052 (2007).

S27. K. Zhang *et al.*, *Nature Biotechnol* **24**, 680 (2006).

S28. A. Moustafa *et al.*, *Science* **324**, 1724 (2009).

S29. M. Matsuzaki *et al.*, *Nature* **428**, 653 (2004).

S30. S. Guindon, O. Gascuel, *Syst Biol* **52**, 696 (2003).

S31. M. Anisimova, O. Gascuel, *Syst Biol* **55**, 539 (2006).

S32. A. Moustafa, D. Bhattacharya, *BMC Evol Biol* **8**, 6 (2008).

S33. A. Stamatakis, T. Ludwig, H. Meier, *Bioinformatics* **21**, 456 (2005).

S34. J. D. Hackett *et al.*, *Mol Biol Evol* **24**, 1702 (2007).

S35. S. Q. Le, O. Gascuel, *Mol Biol Evol* **25**, 1307 (2008).

S36. J. P. Huelsenbeck, M. A. Suchard, *Syst Biol* **56**, 975 (2007).

Figure Legends

Figure S1. Analysis of genome data from picobiliphyte SAGs. (A) The bar graphs on the left are the results of analysis of the taxonomic distribution of total and unique BLASTx hits for genes in eukaryotic phyla using as query the 454-derived singleton reads from each SAG assembly. The total number of singletons analyzed for MS584-5, MS584-11, and MS584-22 is shown. The pie charts on the right of the bar graphs show the total number of hits to viral or bacterial phyla. (B) Distribution of the total number of BLASTx hits to different ssDNA virus sequences using as query contigs derived from the assembly of 454 data from MS584-5.

Figure S2. Phylogeny of picobiliphyte sequences. (A) Maximum likelihood (RAxML) tree of Rep proteins from representative ssDNA viruses showing the phylogenetic position of the MS584-5 Rep. RAxML bootstrap values are above the branches and those derived from PhyML (when nodes are shared) are below the branches. Only bootstrap values ≥60% are shown. Circoviruses and their proposed sister group cycloviruses are in maroon text and nanoviruses in green. Rep from marine ssDNA viruses are shown in blue, whereas sequences derived from ocean metagenome data is in red. RW viruses are from reclaimed water, CB from Chesapeake Bay, and BCC from the coast of British Columbia. (B) Bayesian phylogeny inferred using a concatenated alignment (2594 aa) of the nuclear proteins actin, alpha-tubulin, beta-tubulin, heat shock protein 90, cytosolic heat shock protein 70, ribosomal protein L3, and 26S proteasome non-ATPase regulatory subunit. This is the most-likely tree derived from Phylobayes (V3.2e) analysis under the LG rate matrix (*S35*). Rates across sites were modeled under a Dirichlet process (*S36*). Four independent chains were run for 43,191 cycles each, until the mean discrepancy (meandiff) across all bipartitions was < 0.0015 (burnin = 20%). Bayesian posterior probability values are shown above the branches, whereas RAxML bootstrap values (when ≥60%) are shown below.

Figure S3. Maximum likelihood (PhyML) tree returned by the phylogenomics pipeline that shows members of the major facilitator superfamily (MFS) of membrane transporters. MFS proteins are single-polypeptide secondary carriers that facilitate the transport across cytoplasmic or internal membranes of a variety of small metabolites. The aLRT values (when ≥0.500) are shown at the branches. GenBank numbers are shown for each taxon. Viridiplantae are shown in green text, chromalveolates are shown in brown text, and Cyanobacteria in blue.

Table S1. Temperature, chlorophyll *a* (Chl), and microbe abundances (by flow cytometry) in the 25 July 2007 sample, compared to the 10-year average for week number 30 in Boothbay Harbor, ME. Abbreviations: HBac: heterotrophic bacteria, Syn: *Synechococcus*, PPROT: phototrophic protists (<20µm), Crypt: cryptophytes, HPROT: heterotrophic protists (<20µm).

Table S2. Results of rDNA analysis of SAG DNA generated using FACS-MDA. The SAG data shown in black text were derived from cells sorted using Lysotracker Green DND-26 to identify heterotrophs. The SAG data shown in green text were derived from cells sorted using chlorophyll autoflourescence to identify phototrophs. The SAG data shown in red text had intermediate autoflourescence levels. Note that picobiliphytes occur only in the heterotrophic fraction in these SAG data.

Table S3. Results of the *Celera* wgs-6.0 beta draft genome assembly using as input 454 pyrosequencing reads from SAGs MS584-5, MS584-11, and MS584-22.

Table S4. The number of protein sequences in our local database that was used for the BLASTx and phylogenomic analyses (based on phyla).

Table S5. Annotation of representative BLASTx hits to mtDNA and ptDNA (in gray background) using as query, translated 454-derived picobiliphyte genome contigs (utg [unitig] under *Celera*) from MS584-5, MS584-11, and MS584-22.

Table S6. BLASTx top hits to contigs derived from the MS584-22 Illumina assembly using the *CLC Genomics Workbench*. Proteins with plastid-encoded homologs in other taxa are shown with the green background and mitochondrial proteins with the red background.

Table S7. Results of the phylogenomic analysis of contigs generated from the assembly of 454+Illumina data from MS584-11. The putative proteins were predicted using BLASTx, which were then used as a query against our local database and the output analyzed with *PhyloSort* (*S9*) to identify the different monophyletic groups. A total of 5231 maximum likelihood (PhyML) trees were returned by the pipeline.

Table S8. Gene ontology (GO) annotations of the 1683 Stramenopiles proteins that grouped at aLRT≥0.70 (using PhyML) with proteins encoded on MS584-11 contigs (454+Illumina assembly). The maximum likelihood phylogenetic approach provides strong evidence that the Stramenopiles and picobiliphyte proteins are putative homologs.

Figure S1

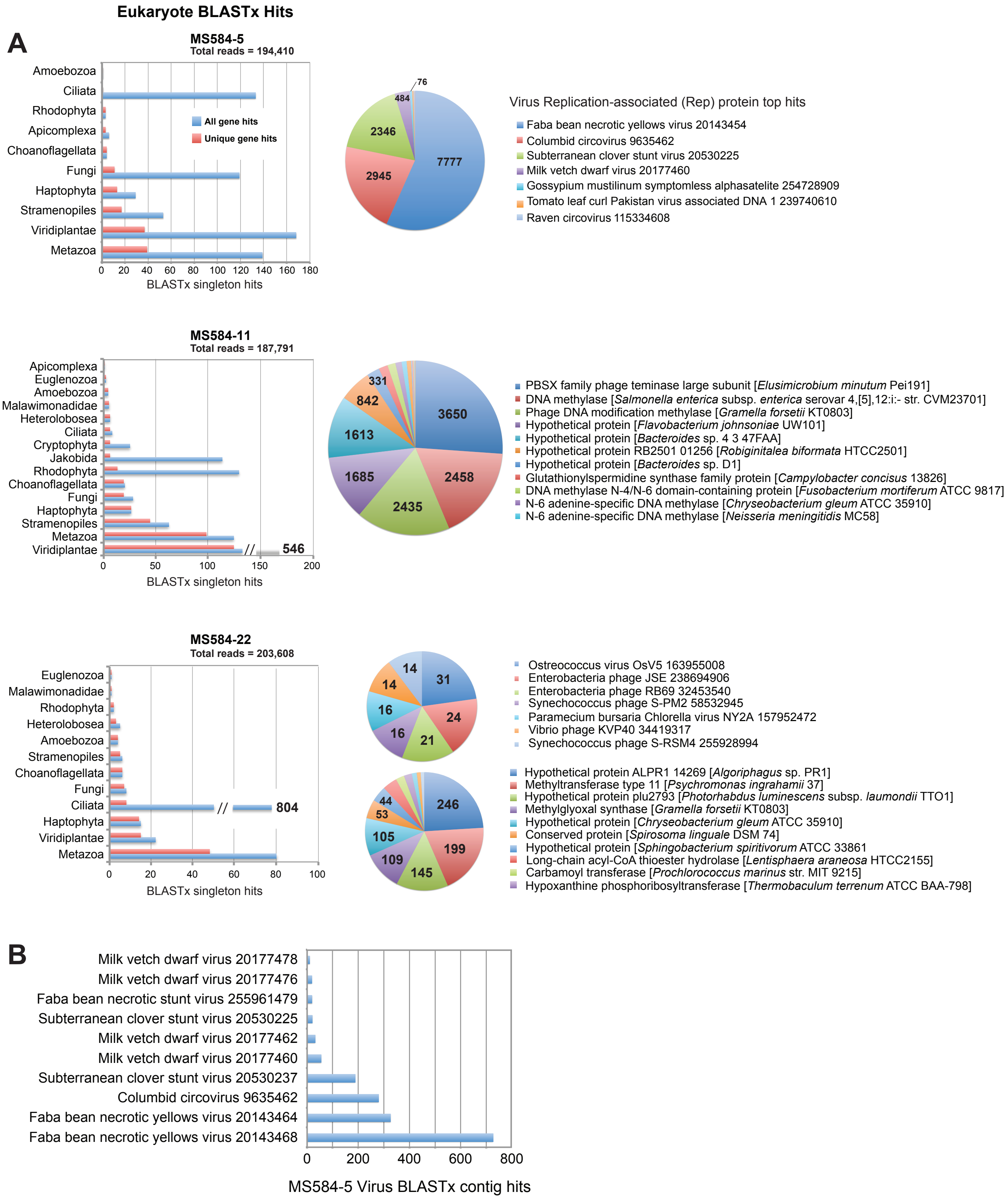
Eukaryote BLASTx Hits
A
MS584-5
Total reads = 194,410
Amoebozoa
Ciliata
Rhodophyta
Apicomplexa
Choanoflagellata
Fungi
Haptophyta
Stramenopiles
Viridiplantae
Metazoa
All gene hits
Unique gene hits
0 20 40 60 80 100 120 140 160 180
BLASTx singleton hits
76
484
2346
2945
7777
Virus Replication-associated (Rep) protein top hits
Faba bean necrotic yellows virus 20143454
Columbid circovirus 9635462
Subterranean clover stunt virus 20530225
Milk vetch dwarf virus 20177460
Gossypium mustilinum symptomless alphasatelite 254728909
Tomato leaf curl Pakistan virus associated DNA 1 239740610
Raven circovirus 115334608
MS584-11
Total reads = 187,791
Apicomplexa
Euglenozoa
Amoebozoa
Malawimonadidae
Heterolobosea
Ciliata
Cryptophyta
Jakobida
Rhodophyta
Choanoflagellata
Fungi
Haptophyta
Stramenopiles
Metazoa
Viridiplantae
546
0 50 100 150 200
BLASTx singleton hits
331
842
3650
1613
1685
2458
2435
PBSX family phage teminase large subunit [*Elusimicrobium minutum* Pei191]
DNA methylase [*Salmonella enterica* subsp. *enterica* serovar 4,[5],12:i:- str. CVM23701]
Phage DNA modification methylase [*Gramella forsetii* KT0803]
Hypothetical protein [*Flavobacterium johnsoniae* UW101]
Hypothetical protein [*Bacteroides* sp. 4 3 47FAA]
Hypothetical protein RB2501 01256 [*Robiginitalea biformata* HTCC2501]
Hypothetical protein [*Bacteroides* sp. D1]
Glutathionylspermidine synthase family protein [*Campylobacter concisus* 13826]
DNA methylase N-4/N-6 domain-containing protein [*Fusobacterium mortiferum* ATCC 9817]
N-6 adenine-specific DNA methylase [*Chryseobacterium gleum* ATCC 35910]
N-6 adenine-specific DNA methylase [*Neisseria meningitidis* MC58]
MS584-22
Total reads = 203,608
Euglenozoa
Malawimonadidae
Rhodophyta
Heterolobosea
Amoebozoa
Stramenopiles
Choanoflagellata
Fungi
Ciliata
Haptophyta
Viridiplantae
Metazoa
804
0 20 40 60 80 100
BLASTx singleton hits
14
31
14
24
16
16
21
Ostreococcus virus OsV5 163955008
Enterobacteria phage JSE 238694906
Enterobacteria phage RB69 32453540
Synechococcus phage S-PM2 58532945
Paramecium bursaria Chlorella virus NY2A 157952472
Vibrio phage KVP40 34419317
Synechococcus phage S-RSM4 255928994
44
53
246
105
199
109
145
Hypothetical protein ALPR1 14269 [*Algoriphagus* sp. PR1]
Methyltransferase type 11 [*Psychromonas ingrahamii* 37]
Hypothetical protein plu2793 [*Photorhabdus luminescens* subsp. *laumondii* TTO1]
Methylglyoxal synthase [*Gramella forsetii* KT0803]
Hypothetical protein [*Chryseobacterium gleum* ATCC 35910]
Conserved protein [*Spirosoma linguale* DSM 74]
Hypothetical protein [*Sphingobacterium spiritivorum* ATCC 33861]
Long-chain acyl-CoA thioester hydrolase [*Lentisphaera araneosa* HTCC2155]
Carbamoyl transferase [*Prochlorococcus marinus* str. MIT 9215]
Hypoxanthine phosphoribosyltransferase [*Thermobaculum terrenum* ATCC BAA-798]
B
Milk vetch dwarf virus 20177478
Milk vetch dwarf virus 20177476
Faba bean necrotic stunt virus 255961479
Subterranean clover stunt virus 20530225
Milk vetch dwarf virus 20177462
Milk vetch dwarf virus 20177460
Subterranean clover stunt virus 20530237
Columbid circovirus 9635462
Faba bean necrotic yellows virus 20143464
Faba bean necrotic yellows virus 20143468
0 200 400 600 800
MS584-5 Virus BLASTx contig hits

Figure S2

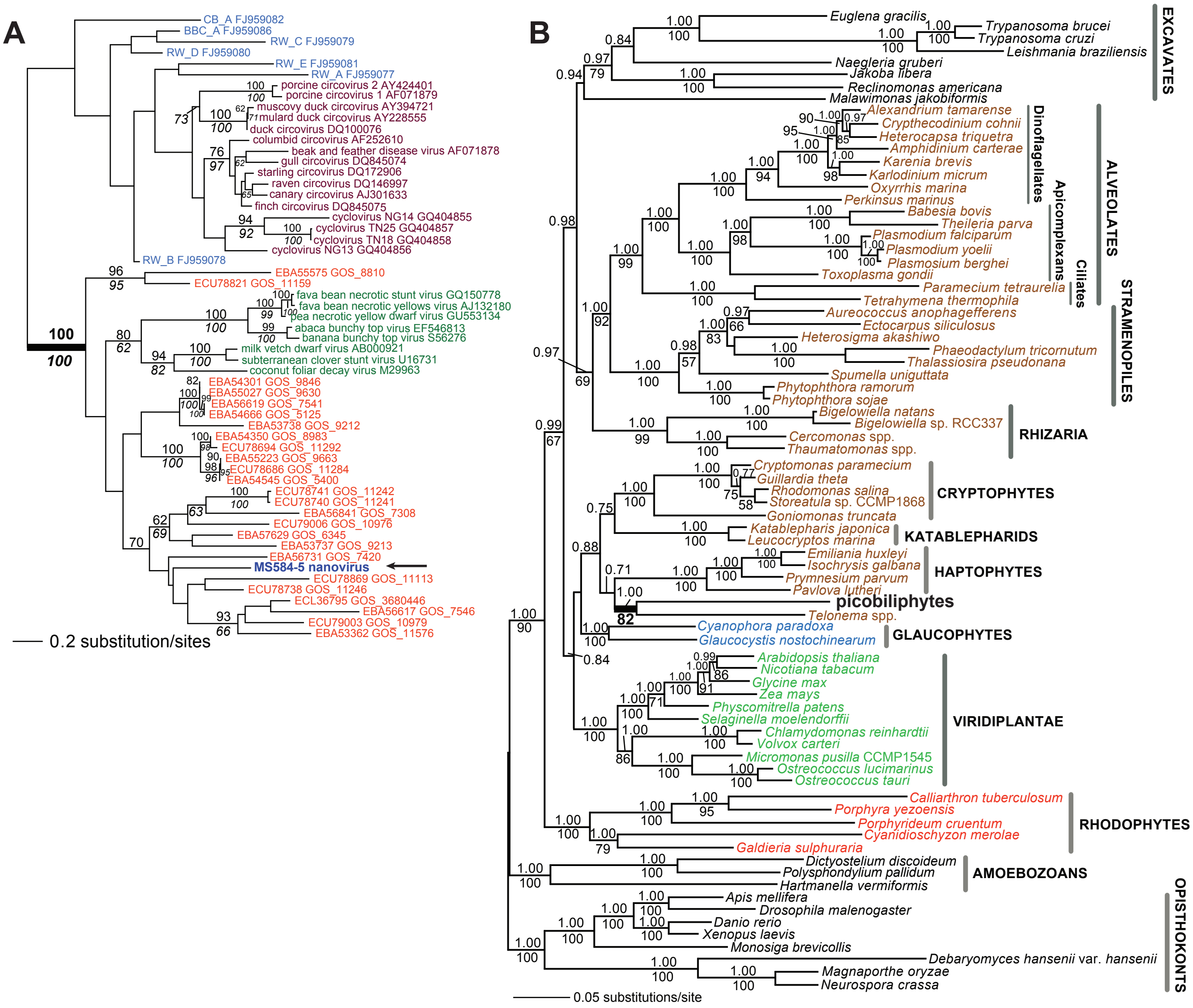
A
CB_A FJ959082
BBC_A FJ959086
RW_C FJ959079
RW_D FJ959080
RW_E FJ959081
RW_A FJ959077
porcine circovirus 2 AY424401
porcine circovirus 1 AF071879
muscovy duck circovirus AY394721
mulard duck circovirus AY228555
duck circovirus DQ100076
columbid circovirus AF252610
beak and feather disease virus AF071878
gull circovirus DQ845074
starling circovirus DQ172906
raven circovirus DQ146997
canary circovirus AJ301633
finch circovirus DQ845075
cyclovirus NG14 GQ404855
cyclovirus TN25 GQ404857
cyclovirus TN18 GQ404858
cyclovirus NG13 GQ404856
RW_B FJ959078
EBA55575 GOS_8810
ECU78821 GOS_11159
fava bean necrotic stunt virus GQ150778
fava bean necrotic yellows virus AJ132180
pea necrotic yellow dwarf virus GU553134
abaca bunchy top virus EF546813
banana bunchy top virus S56276
milk vetch dwarf virus AB000921
subterranean clover stunt virus U16731
coconut foliar decay virus M29963
EBA54301 GOS_9846
EBA55027 GOS_9630
EBA56619 GOS_7541
EBA54666 GOS_5125
EBA53738 GOS_9212
EBA54350 GOS_8983
ECU78694 GOS_11292
EBA55223 GOS_9663
ECU78686 GOS_11284
EBA54545 GOS_5400
ECU78741 GOS_11242
ECU78740 GOS_11241
EBA56841 GOS_7308
ECU79006 GOS_10976
EBA57629 GOS_6345
EBA53737 GOS_9213
EBA56731 GOS_7420
MS584-5 nanovirus
ECU78869 GOS_11113
ECU78738 GOS_11246
ECL36795 GOS_3680446
EBA56617 GOS_7546
ECU79003 GOS_10979
EBA53362 GOS_11576
100
100
0.2 substitution/sites
B
Euglena gracilis
Trypanosoma brucei
Trypanosoma cruzi
Leishmania braziliensis
Naegleria gruberi
Jakoba libera
Reclinomonas americana
Malawimonas jakobiformis
EXCAVATES
Alexandrium tamarense
Crypthecodinium cohnii
Heterocapsa triquetra
Amphidinium carterae
Karenia brevis
Karlodinium micrum
Oxyrrhis marina
Perkinsus marinus
Dinoflagellates
Babesia bovis
Theileria parva
Plasmodium falciparum
Plasmodium yoelii
Plasmosium berghei
Toxoplasma gondii
Apicomplexans
Paramecium tetraurelia
Tetrahymena thermophila
Ciliates
ALVEOLATES
Aureococcus anophagefferens
Ectocarpus siliculosus
Heterosigma akashiwo
Phaeodactylum tricornutum
Thalassiosira pseudonana
Spumella uniguttata
Phytophthora ramorum
Phytophthora sojae
STRAMENOPILES
Bigelowiella natans
Bigelowiella sp. RCC337
Cercomonas spp.
Thaumatomonas spp.
RHIZARIA
Cryptomonas paramecium
Guillardia theta
Rhodomonas salina
Storeatula sp. CCMP1868
Goniomonas truncata
CRYPTOPHYTES
Katablepharis japonica
Leucocryptos marina
KATABLEPHARIDS
Emiliania huxleyi
Isochrysis galbana
Prymnesium parvum
Pavlova lutheri
HAPTOPHYTES
picobiliphytes
82
Telonema spp.
Cyanophora paradoxa
Glaucocystis nostochinearum
GLAUCOPHYTES
Arabidopsis thaliana
Nicotiana tabacum
Glycine max
Zea mays
Physcomitrella patens
Selaginella moelendorffii
Chlamydomonas reinhardtii
Volvox carteri
Micromonas pusilla CCMP1545
Ostreococcus lucimarinus
Ostreococcus tauri
VIRIDIPLANTAE
Calliarthron tuberculosum
Porphyra yezoensis
Porphyrideum cruentum
Cyanidioschyzon merolae
Galdieria sulphuraria
RHODOPHYTES
Dictyostelium discoideum
Polysphondylium pallidum
Hartmanella vermiformis
AMOEBOZOANS
Apis mellifera
Drosophila malenogaster
Danio rerio
Xenopus laevis
Monosiga brevicollis
Debaryomyces hansenii var. hansenii
Magnaporthe oryzae
Neurospora crassa
OPISTHOKONTS
0.05 substitutions/site

Figure S3

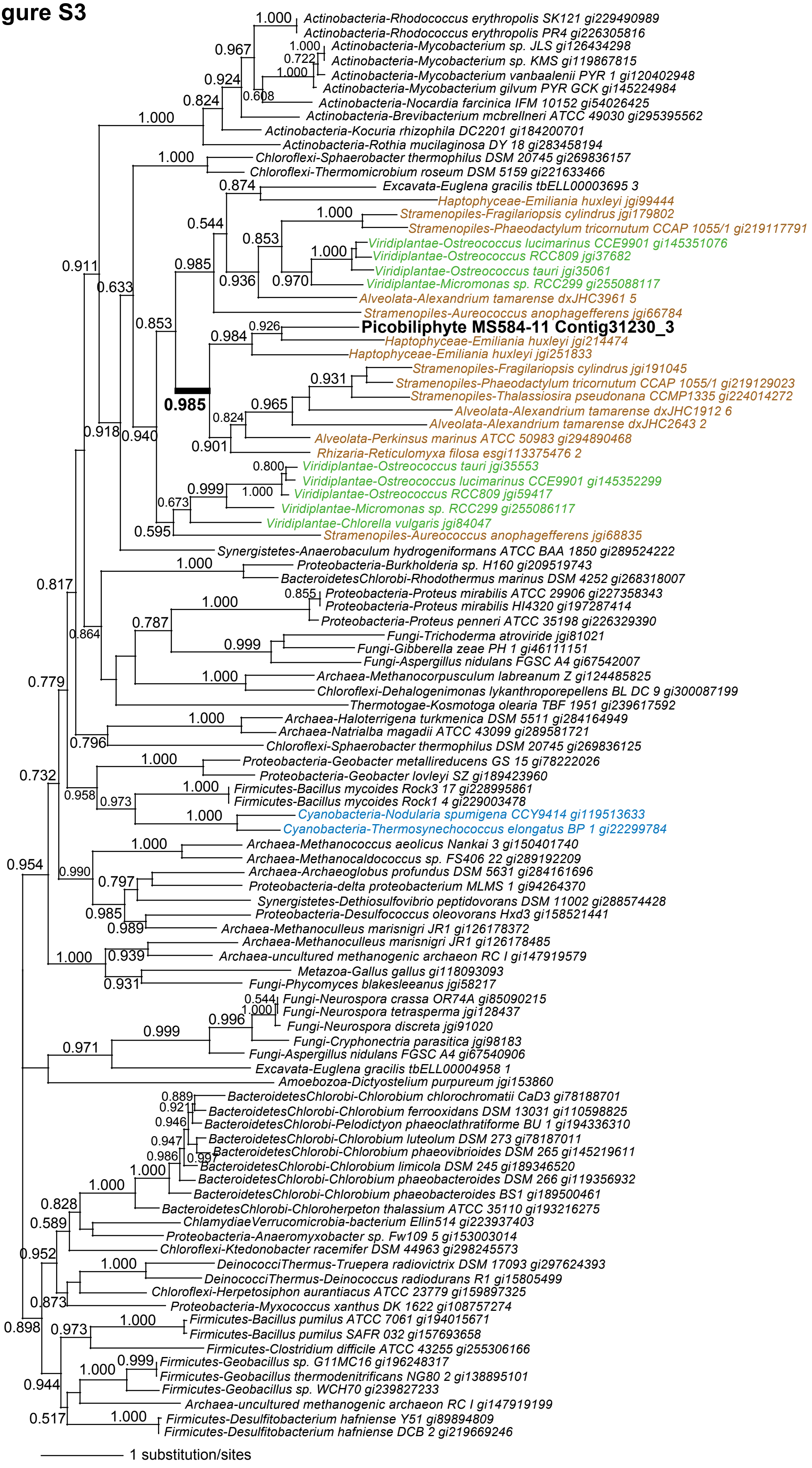
1.000
Actinobacteria-Rhodococcus erythropolis SK121 gi229490989
Actinobacteria-Rhodococcus erythropolis PR4 gi226305816
0.967
1.000
Actinobacteria-Mycobacterium sp. JLS gi126434298
0.722
Actinobacteria-Mycobacterium sp. KMS gi119867815
1.000
Actinobacteria-Mycobacterium vanbaalenii PYR 1 gi120402948
0.924
Actinobacteria-Mycobacterium gilvum PYR GCK gi145224984
0.608
0.824
Actinobacteria-Nocardia farcinica IFM 10152 gi54026425
1.000
Actinobacteria-Brevibacterium mcbrellneri ATCC 49030 gi295395562
Actinobacteria-Kocuria rhizophila DC2201 gi184200701
Actinobacteria-Rothia mucilaginosa DY 18 gi283458194
1.000
Chloroflexi-Sphaerobacter thermophilus DSM 20745 gi269836157
Chloroflexi-Thermomicrobium roseum DSM 5159 gi221633466
0.874
Excavata-Euglena gracilis tbELL00003695 3
Haptophyceae-Emiliania huxleyi jgi99444
0.544
1.000
Stramenopiles-Fragilariopsis cylindrus jgi179802
Stramenopiles-Phaeodactylum tricornutum CCAP 1055/1 gi219117791
0.853
1.000
Viridiplantae-Ostreococcus lucimarinus CCE9901 gi145351076
Viridiplantae-Ostreococcus RCC809 jgi37682
0.911
0.985
Viridiplantae-Ostreococcus tauri jgi35061
0.633
0.936
0.970
Viridiplantae-Micromonas sp. RCC299 gi255088117
Alveolata-Alexandrium tamarense dxJHC3961 5
Stramenopiles-Aureococcus anophagefferens jgi66784
0.853
0.926
Picobiliphyte MS584-11 Contig31230_3
0.984
Haptophyceae-Emiliania huxleyi jgi214474
Haptophyceae-Emiliania huxleyi jgi251833
Stramenopiles-Fragilariopsis cylindrus jgi191045
0.931
Stramenopiles-Phaeodactylum tricornutum CCAP 1055/1 gi219129023
Stramenopiles-Thalassiosira pseudonana CCMP1335 gi224014272
0.985
0.965
Alveolata-Alexandrium tamarense dxJHC1912 6
0.824
Alveolata-Alexandrium tamarense dxJHC2643 2
0.918
0.940
Alveolata-Perkinsus marinus ATCC 50983 gi294890468
0.901
Rhizaria-Reticulomyxa filosa esgi113375476 2
0.800
Viridiplantae-Ostreococcus tauri jgi35553
Viridiplantae-Ostreococcus lucimarinus CCE9901 gi145352299
0.999
1.000
Viridiplantae-Ostreococcus RCC809 jgi59417
0.673
Viridiplantae-Micromonas sp. RCC299 gi255086117
Viridiplantae-Chlorella vulgaris jgi84047
0.595
Stramenopiles-Aureococcus anophagefferens jgi68835
Synergistetes-Anaerobaculum hydrogeniformans ATCC BAA 1850 gi289524222
1.000
Proteobacteria-Burkholderia sp. H160 gi209519743
BacteroidetesChlorobi-Rhodothermus marinus DSM 4252 gi268318007
0.817
0.855
Proteobacteria-Proteus mirabilis ATCC 29906 gi227358343
1.000
Proteobacteria-Proteus mirabilis HI4320 gi197287414
0.787
Proteobacteria-Proteus penneri ATCC 35198 gi226329390
0.864
Fungi-Trichoderma atroviride jgi81021
0.999
Fungi-Gibberella zeae PH 1 gi46111151
Fungi-Aspergillus nidulans FGSC A4 gi67542007
0.779
1.000
Archaea-Methanocorpusculum labreanum Z gi124485825
Chloroflexi-Dehalogenimonas lykanthroporepellens BL DC 9 gi300087199
Thermotogae-Kosmotoga olearia TBF 1951 gi239617592
1.000
Archaea-Haloterrigena turkmenica DSM 5511 gi284164949
Archaea-Natrialba magadii ATCC 43099 gi289581721
0.796
Chloroflexi-Sphaerobacter thermophilus DSM 20745 gi269836125
1.000
Proteobacteria-Geobacter metallireducens GS 15 gi78222026
0.732
Proteobacteria-Geobacter lovleyi SZ gi189423960
1.000
0.958
Firmicutes-Bacillus mycoides Rock3 17 gi228995861
0.973
Firmicutes-Bacillus mycoides Rock1 4 gi229003478
1.000
Cyanobacteria-Nodularia spumigena CCY9414 gi119513633
Cyanobacteria-Thermosynechococcus elongatus BP 1 gi22299784
1.000
Archaea-Methanococcus aeolicus Nankai 3 gi150401740
0.954
Archaea-Methanocaldococcus sp. FS406 22 gi289192209
0.990
Archaea-Archaeoglobus profundus DSM 5631 gi284161696
0.797
Proteobacteria-delta proteobacterium MLMS 1 gi94264370
Synergistetes-Dethiosulfovibrio peptidovorans DSM 11002 gi288574428
0.985
Proteobacteria-Desulfococcus oleovorans Hxd3 gi158521441
0.989
Archaea-Methanoculleus marisnigri JR1 gi126178372
Archaea-Methanoculleus marisnigri JR1 gi126178485
1.000
0.939
Archaea-uncultured methanogenic archaeon RC I gi147919579
Metazoa-Gallus gallus gi118093093
0.931
Fungi-Phycomyces blakesleeanus jgi58217
0.544
Fungi-Neurospora crassa OR74A gi85090215
1.000
Fungi-Neurospora tetrasperma jgi128437
0.996
Fungi-Neurospora discreta jgi91020
0.999
Fungi-Cryphonectria parasitica jgi98183
0.971
Fungi-Aspergillus nidulans FGSC A4 gi67540906
Excavata-Euglena gracilis tbELL00004958 1
Amoebozoa-Dictyostelium purpureum jgi153860
0.889
BacteroidetesChlorobi-Chlorobium chlorochromatii CaD3 gi78188701
0.921
BacteroidetesChlorobi-Chlorobium ferrooxidans DSM 13031 gi110598825
0.946
BacteroidetesChlorobi-Pelodictyon phaeoclathratiforme BU 1 gi194336310
0.947
BacteroidetesChlorobi-Chlorobium luteolum DSM 273 gi78187011
BacteroidetesChlorobi-Chlorobium phaeovibrioides DSM 265 gi145219611
0.986
0.997
BacteroidetesChlorobi-Chlorobium limicola DSM 245 gi189346520
1.000
BacteroidetesChlorobi-Chlorobium phaeobacteroides DSM 266 gi119356932
1.000
BacteroidetesChlorobi-Chlorobium phaeobacteroides BS1 gi189500461
0.828
BacteroidetesChlorobi-Chloroherpeton thalassium ATCC 35110 gi193216275
0.589
ChlamydiaeVerrucomicrobia-bacterium Ellin514 gi223937403
Proteobacteria-Anaeromyxobacter sp. Fw109 5 gi153003014
0.952
Chloroflexi-Ktedonobacter racemifer DSM 44963 gi298245573
1.000
DeinococciThermus-Truepera radiovictrix DSM 17093 gi297624393
DeinococciThermus-Deinococcus radiodurans R1 gi15805499
0.873
Chloroflexi-Herpetosiphon aurantiacus ATCC 23779 gi159897325
Proteobacteria-Myxococcus xanthus DK 1622 gi108757274
0.898
0.973
1.000
Firmicutes-Bacillus pumilus ATCC 7061 gi194015671
Firmicutes-Bacillus pumilus SAFR 032 gi157693658
Firmicutes-Clostridium difficile ATCC 43255 gi255306166
0.999
Firmicutes-Geobacillus sp. G11MC16 gi196248317
1.000
Firmicutes-Geobacillus thermodenitrificans NG80 2 gi138895101
0.944
Firmicutes-Geobacillus sp. WCH70 gi239827233
Archaea-uncultured methanogenic archaeon RC I gi147919199
0.517
1.000
Firmicutes-Desulfitobacterium hafniense Y51 gi89894809
Firmicutes-Desulfitobacterium hafniense DCB 2 gi219669246
1 substitution/sites

Table S1. Temperature, chlorophyll *a* (Chl), and microbe abundances (by flow cytometry) in the 25 July 2007 sample, compared to the 10-year average for week number 30 in Boothbay Harbor, ME. Abbreviations: HBac: heterotrophic bacteria, Syn: *Synechococcus*, PPROT: phototrophic protists (<20µm), Crypt: cryptophytes, HPROT: heterotrophic protists (<20µm).

	Temp °C	Chl µgL^{-1}	Chl <20µm %	HBac mL^{-1}	Syn mL^{-1}	PPROT mL^{-1}	Crypt mL^{-1}	HPROT mL^{-1}
25-Jul-07	18.1	2.65	96.2	3.06×10^6	39825	30506	786	2219
Average	19.1	2.60	90.8	3.11×10^6	25256	37823	577	2689

Table S2. Results of rDNA analysis of SAG DNA generated using FACS-MDA. The SAG data shown in black text were derived from cells sorted using Lysotracker Green DND-26 to identify heterotrophs. The SAG data shown in green text were derived from cells sorted using chlorophyll autoflourescence to identify phototrophs. The SAG data shown in red text had intermediate autoflourescence levels. Note that picobiliphytes occur only in the heterotrophic fraction in these SAG data.

Container	Well (row:column)	Eukaryotic "supergroup"	Division	Class	Order	Family	Genus	Clade
AAA071	B:3	Archaeplastida	Rhodophyta	Florideophyceae	Florideophyceae	Corallinales	*Neogoniolithon*	
AAA071	A:2	Chromalveolata	Alveolata	Dinophyceae	Syndiniales	Dino-Group II		Dino-Group II-Clade 2
AAA071	B:5	Chromalveolata	Alveolata	Dinophyceae	Syndiniales	Dino-Group II		Dino-Group II-Clade 1
AAA071	C:7	Chromalveolata	Alveolata	Dinophyceae	Syndiniales	Dino-Group II		Dino-Group II-Clade 33
AAA071	G:14	Chromalveolata	Alveolata	Dinophyceae	Syndiniales	Dino-Group II		Dino-Group II-Clade 1
AAA071	I:11	Chromalveolata	Alveolata	Dinophyceae	Syndiniales	Dino-Group II		Dino-Group II-Clade 1
AAA071	I:14	Chromalveolata	Alveolata	Dinophyceae	Syndiniales	Dino-Group II		Dino-Group II-Clade 2
AAA071	J:15	Chromalveolata	Alveolata	Dinophyceae	Syndiniales	Dino-Group II		Dino-Group II-Clade 2
AAA071	M:8	Chromalveolata	Alveolata	Dinophyceae	Syndiniales	Dino-Group II		Dino-Group II-Clade 1
AAA071	M:9	Chromalveolata	Alveolata	Dinophyceae	Syndiniales	Dino-Group II		Dino-Group II-Clade 2
AAA071	M:19	Chromalveolata	Alveolata	Dinophyceae	Syndiniales	Dino-Group II	*Alexandrium*	Dino-Group II-Clade 4
AAA071	N:17	Chromalveolata	Alveolata	Dinophyceae	Syndiniales	Dino-Group II		Dino-Group II-Clade 2
AAA071	O:10	Chromalveolata	Alveolata	Dinophyceae	Syndiniales	Dino-Group II		Dino-Group II-Clade 1
AAA071	N:8	Chromalveolata	Katablepharidophyta	Katablepharidaceae	Katablepharidales			
AAA071	**F:5**	**Chromalveolata**	**Picobiliphyta**	**Picobiliphyta**	**Picobiliphyta**			
AAA071	**J:7**	**Chromalveolata**	**Picobiliphyta**	**Picobiliphyta**	**Picobiliphyta**	**Monopisthocotylea**		
AAA071	**L:9**	**Chromalveolata**	**Picobiliphyta**	**Picobiliphyta**	**Picobiliphyta**			
AAA071	A:3	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Hibberdiales_Chrysosphaerales_Ochromonadales		
AAA071	E:3	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Hibberdiales_Chrysosphaerales_Ochromonadales		
AAA071	E:16	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		Novel Ochromonadales 1
AAA071	G:7	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		
AAA071	J:21	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Paraphysomonadales		Paraphysomonas group 1
AAA071	K:4	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		
AAA071	K:20	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae			
AAA071	L:13	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Oikomonadales		Oikomonas group 1
AAA071	M:11	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae			
AAA071	O:2	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		Novel Ochromonadales 1
AAA071	F:22	Chromalveolata	Stramenopiles	Labyrinthulida	Thraustochytriidae			
AAA071	B:18	Chromalveolata	Stramenopiles	MAST-4	MAST-4			
AAA071	C:5	Chromalveolata	Stramenopiles	MAST-4	MAST-4			
AAA071	E:17	Chromalveolata	Stramenopiles	MAST-4	MAST-4			
AAA071	M:18	Chromalveolata	Stramenopiles	MAST-4	MAST-4			
AAA071	E:15	Opisthokonta	Choanoflagellida	Choanoflagellida	Choanoflagellida			
AAA071	I:17	Opisthokonta	Choanoflagellida	Choanoflagellida	Choanoflagellida	Hydrozoa		
AAA071	L:17	Opisthokonta	Choanoflagellida	Choanoflagellida	Choanoflagellida			
AAA071	J:3	Opisthokonta	Fungi	Ascomycota	Pezizomycotina	Eurotiomycetes		
AAA071	M:5	Opisthokonta	Fungi	Ascomycota	Pezizomycotina	Dothideomycetes		
AAA071	G:13	Rhizaria	Cercozoa	Thecofilosea	Thecofilosea	Thecofilosea		
AAA071	G:16	Rhizaria	Cercozoa	Thecofilosea	Thecofilosea	Thecofilosea		
AAA071	I:23	Rhizaria	Cercozoa	Thecofilosea	Thecofilosea	Thecofilosea		
AAA172	A:6	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Bathycoccus*	
AAA172	A:21	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Ostreococcus*	Ostreo Clade A
AAA172	B:3	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Ostreococcus*	Ostreo Clade A
AAA172	B:6	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Micromonas*	Mpusilla Clade B.E.3
AAA172	B:13	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Bathycoccus*	
AAA172	B:18	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Ostreococcus*	Ostreo Clade A
AAA172	D:15	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Ostreococcus*	
AAA172	D:20	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Micromonas*	Mpusilla Clade A.ABC.1-2
AAA172	D:23	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Ostreococcus*	
AAA172	E:3	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Ostreococcus*	
AAA172	E:5	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Bathycoccus*	
AAA172	E:6	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Ostreococcus*	Ostreo Clade A
AAA172	F:6	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Ostreococcus*	Ostreo Clade A
AAA172	F:14	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Ostreococcus*	
AAA172	J:3	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Micromonas*	Mpusilla Clade C.D.5
AAA172	J:9	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Ostreococcus*	Ostreo Clade A
AAA172	J:15	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Micromonas*	Mpusilla Clade C.D.5
AAA172	K:5	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Ostreococcus*	
AAA172	K:19	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Micromonas*	Mpusilla Clade C.D.5
AAA172	M:14	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Ostreococcus*	
AAA172	N:13	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Ostreococcus*	
AAA172	O:9	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Ostreococcus*	Ostreo Clade A
AAA172	O:11	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Ostreococcus*	Ostreo Clade A
AAA172	O:17	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Micromonas*	Mpusilla Clade C.D.5
AAA172	P:3	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Micromonas*	Mpusilla Clade B.E.3
AAA172	P:11	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Ostreococcus*	
AAA172	P:13	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Bathycoccus*	
AAA172	P:15	Archaeplastida	Chlorophyta	Prasinophyceae	Mamiellales	Mamiellaceae	*Ostreococcus*	
AAA074	E:3	Chromalveolata	Stramenopiles	Bacillariophyta	Pennate diatoms			
AAA074	A:2	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		Novel Ochromonadales 1

AAA074	A:3	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		Novel Ochromonadales 1
AAA074	B:9	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		Novel Ochromonadales 1
AAA074	B:18	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		Novel Ochromonadales 1
AAA074	C:5	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae			
AAA074	C:18	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae			
AAA074	C:20	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae			
AAA074	D:10	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae			
AAA074	D:18	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		Novel Ochromonadales 1
AAA074	E:4	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae			
AAA074	E:5	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		Novel Ochromonadales 1
AAA074	E:14	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		
AAA074	E:17	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		Novel Ochromonadales 1
AAA074	E:19	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae			
AAA074	F:10	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		
AAA074	G:15	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		Novel Ochromonadales 1
AAA074	I:5	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae			
AAA074	I:10	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		Novel Ochromonadales 1
AAA074	I:11	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae			
AAA074	I:13	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		Novel Ochromonadales 1
AAA074	I:15	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae			
AAA074	I:16	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae			
AAA074	I:17	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		Novel Ochromonadales 1
AAA074	J:7	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		Novel Ochromonadales 1
AAA074	J:15	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		Novel Ochromonadales 1
AAA074	J:18	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae			
AAA074	J:19	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae			
AAA074	K:17	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae			
AAA074	L:7	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		Novel Ochromonadales 1
AAA074	L:13	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		Novel Ochromonadales 1
AAA074	M:18	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		Novel Ochromonadales 1
AAA074	M:19	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		Novel Ochromonadales 1
AAA074	M:20	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		Novel Ochromonadales 1
AAA074	N:15	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		Novel Ochromonadales 1
AAA074	N:17	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		Novel Ochromonadales 1
AAA074	O:2	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae	Ochromonadales		
AAA074	P:18	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae			
AAA074	P:22	Chromalveolata	Stramenopiles	Chrysophyceae and Synurophyceae	Chrysophyceae and Synurophyceae			
AAA074	K:6	Chromalveolata	Stramenopiles	MAST-4	MAST-4			
AAA074	M:7	Opisthokonta	Fungi	Basidiomycota	Agaricomycotina	Agaricomycetes		

Table S3. Results of the *Celera* wgs-6.0 beta draft genome assembly using as input 454 pyrosequencing reads from SAGs MS584-5, MS584-11, and MS584-22.

***Celera* wgs-6.0 beta output**	**Boothbay MS584-5**	**Boothbay MS583-11**	**Boothbay MS584-22**
Total usable reads	231,979	241,297	253,002
Average read length (bases)	391	372	355
Number of Contigs	123	472	268
Contig length (bases)	233,941	860,593	483,234
Number of Degenerate contigs	8,779	9,886	7,652
Degenerate contig length (bases)	4,545,717	5,327,645	4,049,336
Singleton reads	194,410 (83.8%)	187,795 (77.8%)	203,611 (80.5%)
Singleton length (bases)	74,000,433	67,073,167	68,590,052
Contig coverage	6.2X	4.6X	5.3X
GC-content	55.6%	53.8%	47.4%

Table S4. The number of protein sequences in our local database that was used for the BLASTx and phylogenomic analyses (based on phyla).

	Grouping	Species/Strain	RefSeq	JGI	EST[1]	Independent[2]	Total
PROKARYOTES	Archaea	121	225,867	0	0	0	225,867
	Bact-Actinobacteria	282	994,292	0	0	0	994,292
	Bact-Aquificae	10	19,325	0	0	0	19,325
	Bact-BacteroidetesChlorobi	141	450,081	0	0	0	450,081
	Bact-ChlamydiaeVerrucomicrobia	38	79,759	0	0	0	79,759
	Bact-Chloroflexi	15	52,585	0	0	0	52,585
	Bact-Cyanobacteria	68	225,555	0	0	0	225,555
	Bact-Deferribacteres	2	5,338	0	0	0	5,338
	Bact-Deinococci	12	26,191	0	0	0	26,191
	Bact-Dictyoglomi	2	3,656	0	0	0	3,656
	Bact-Elusimicrobia	2	2,305	0	0	0	2,305
	Bact-Environmental	2	408	0	0	0	408
	Bact-FibrobacteresAcidobacteria	6	28,629	0	0	0	28,629
	Bact-Firmicutes	759	2,099,809	0	0	0	2,099,809
	Bact-Fusobacteria	25	59,335	0	0	0	59,335
	Bact-Gemmatimonadetes	1	3,935	0	0	0	3,935
	Bact-Nitrospirae	3	6,366	0	0	0	6,366
	Bact-Planctomycetes	6	36,794	0	0	0	36,794
	Bact-Proteobacteria	1239	4,251,165	0	0	0	4,251,165
	Bact-Spirochaetes	44	72,342	0	0	0	72,342
	Bact-Synergistetes	6	13,162	0	0	0	13,162
	Bact-Tenericutes	55	32,455	0	0	0	32,455
	Bact-Thermotogae	11	20,807	0	0	0	20,807
	Bact-Unclassified	9	17,518	0	0	0	17,518
EUKARYOTES	Alveolata	70	167,836	0	584,904	0	752,740
	Amoebozoa	22	30,550	12,410	138,624	0	181,584
	Cryptophyta	8	1,419	0	40,320	0	41,739
	Excavata	30	134,643	0	443,424	0	578,067
	Haptophyta	5	140	39,124	56,868	0	96,132
	Opisthokonta-Choanoflagellida	4	9,203	0	74,886	0	84,089
	Opisthokonta-Fungi	186	569,377	212,456	132,168	0	914,001
	Opisthokonta-Metazoa	2120	1,067,024	140,855	30,108	0	1,237,987
	Opisthokonta-Others	4	0	0	46,494	0	46,494
	Plantae-Glaucophyta	3	149	0	57,696	0	57,845
	Plantae-Rhodophyta	23	1,168	0	331,482	28,975	361,625
	Plantae-Viridiplantae	228	385,435	114,102	114,294	0	613,831
	Rhizaria	5	1,211	0	29,112	0	30,323
	Stramenopiles	47	41,980	81,762	96,078	0	219,820
	Vira	2475	84,202	0	0	0	84,202
	Others	39	1,062	0	0	0	1,062
	Total	**8,128**	**11,223,078**	**600,709**	**2,176,458**	**28,975**	**14,029,220**

[1] The actual numbers of EST contigs are the numbers in this column divided by 6 due to six-frame translations.

[2] These data represent protein models from *Cyanidioschyzon merolae* and *Calliarthron tuberculosum*.

Table S5. Annotation of representative BLASTx hits to mtDNA and ptDNA (in gray background) using as query, translated picobiliphyte genome contigs (utg [unitig] under *Celera*) from MS584-5, MS584-11, and MS584-22.

Picobiliphyte Unitig ID	Top Hit Organism	Putative Annotation
utg7180000000001	Viridiplantae-Chara vulgaris mt 38638282	>NP 943685 NADH dehydrogenase subunit 4 [Chara vulgaris].
utg7180000000002	Viridiplantae-Chlorokybus atmophyticus mt 150406468	>YP 001315136 NADH dehydrogenase subunit 2 [Chlorokybus atmophyticus].
utg7180000000003	Cryptophyta-Rhodomonas salina mt 11466601	>NP 066491 cytochrome c oxidase subunit 1 [Rhodomonas salina].
utg7180000000003	Cryptophyta-Rhodomonas salina mt 11466601	>NP 066491 cytochrome c oxidase subunit 1 [Rhodomonas salina].
utg7180000000004	Rhodophyta-Porphyra purpurea mt 11465632	>NP 049303 NADH dehydrogenase subunit 1 [Porphyra purpurea].
utg7180000000006	Viridiplantae-Chlorokybus atmophyticus mt 150406471	>YP 001315130 NADH dehydrogenase subunit 5 [Chlorokybus atmophyticus].
utg7180000000007	Viridiplantae-Chlorokybus atmophyticus mt 150406468	>YP 001315136 NADH dehydrogenase subunit 2 [Chlorokybus atmophyticus].
utg7180000000008	Viridiplantae-Chlorokybus atmophyticus mt 150406466	>YP 001315135 NADH dehydrogenase subunit 1 [Chlorokybus atmophyticus].
utg7180000000009	Viridiplantae-Ostreococcus tauri mt 113170503	>YP 717294 Atp6 [Ostreococcus tauri].
utg7180000000010	Jakobida-Reclinomonas americana mt 11466560	>NP 044809 cytochrome c oxidase subunit 2 [Reclinomonas americana].
utg7180000000011	Planctomycetes-Planctomyces maris DSM 8797 149179536	>ZP 01858077 30S ribosomal protein S12 [Planctomyces maris DSM 8797].
utg7180000000012	Cryptophyta-Hemiselmis andersenii mt 186920131	>YP 001874785 NADH dehydrogenase subunit 6 [Hemiselmis andersenii].
utg7180000000013	Proteobacteria-Erythrobacter sp SD-21 149184321	>ZP 01862639 LSU ribosomal protein L14P [Erythrobacter sp. SD-21].
utg7180000000014	Gemmatimonadetes-Gemmatimonas aurantiaca T-27 226226286	>YP 002760392 50S ribosomal protein L16 [Gemmatimonas aurantiaca T-27].
utg7180000000015	Heterokonta-Phytophthora ramorum mt 145932460	>YP 001165372 ribosomal protein S14 [Phytophthora ramorum].
utg7180000000016	Metazoa-Hydra magnipapillata 221130316	>XP 002162613 PREDICTED: similar to predicted protein [Hydra magnipapillata].
utg7180000000017	Viridiplantae-Chara vulgaris mt 38638280	>NP 943686 NADH dehydrogenase subunit 2 [Chara vulgaris].
utg7180000000018	Viridiplantae-Chara vulgaris mt 38638280	>NP 943686 NADH dehydrogenase subunit 2 [Chara vulgaris].
utg7180000000019	Viridiplantae-Marchantia polymorpha mt 11467101	>NP 054402 NADH dehydrogenase subunit 2 [Marchantia polymorpha].
utg7180000000020	Viridiplantae-Chlorokybus atmophyticus mt 150406468	>YP 001315136 NADH dehydrogenase subunit 2 [Chlorokybus atmophyticus].
utg7180000000021	Viridiplantae-Chlorokybus atmophyticus mt 150406468	>YP 001315136 NADH dehydrogenase subunit 2 [Chlorokybus atmophyticus].
utg7180000000022	Viridiplantae-Nephroselmis olivacea mt 110225675	>YP 665681 cytochrome c oxidase subunit 3 [Nephroselmis olivacea].
utg7180000000023	Viridiplantae-Nephroselmis olivacea mt 110225675	>YP 665681 cytochrome c oxidase subunit 3 [Nephroselmis olivacea].
utg7180000000024	Viridiplantae-Physcomitrella patens mt 91208858	>YP 539019 NADH dehydrogenase subunit 2 [Physcomitrella patens].

utg7180000000025	Viridiplantae-Physcomitrella patens mt 91208857	>YP 539018 NADH dehydrogenase subunit 4 [Physcomitrella patens].
utg7180000000026	Rhodophyta-Chondrus crispus mt 9653246	>NP 062492 NADH dehydrogenase subunit 3 [Chondrus crispus].
utg7180000000027	Rhodophyta-Porphyra purpurea mt 11465632	>NP 049303 NADH dehydrogenase subunit 1 [Porphyra purpurea].
utg7180000000028	Rhodophyta-Cyanidioschyzon merolae strain 10D CMW021C	>NP 059359 NADH dehydrogenase subunit 1 [Cyanidioschyzon merolae]
utg7180000000028	Rhodophyta-Cyanidioschyzon merolae strain 10D CMW021C	
utg7180000000028	Rhodophyta-Cyanidioschyzon merolae strain 10D CMW021C	
utg7180000000029	Viridiplantae-Chara vulgaris mt 38638282	>NP 943685 NADH dehydrogenase subunit 4 [Chara vulgaris].
utg7180000000030	Viridiplantae-Chara vulgaris mt 38638282	>NP 943685 NADH dehydrogenase subunit 4 [Chara vulgaris].
utg7180000000031	Viridiplantae-Chara vulgaris mt 38638282	>NP 943685 NADH dehydrogenase subunit 4 [Chara vulgaris].
utg7180000000032	Viridiplantae-Ostreococcus tauri mt 113170508	>YP 717299 nad4 [Ostreococcus tauri].
utg7180000000033	Viridiplantae-Ostreococcus tauri mt 113170508	>YP 717299 nad4 [Ostreococcus tauri].
utg7180000000034	Viridiplantae-Chaetosphaeridium globosum mt 22550336	>NP 689386 cytochrome c oxidase subunit 1 [Chaetosphaeridium globosum].
utg7180000000035	Viridiplantae-Nephroselmis olivacea mt 110225658	>YP 665664 cytochrome c oxidase subunit 1 [Nephroselmis olivacea].
utg7180000000036	Choanoflagellata-Monosiga brevicollis ATCC 50154 mt 23464621	>NP 696989 apocytochrome b [Monosiga brevicollis ATCC 50154].
utg7180000000037	Jakobida-Reclinomonas americana mt 11466551	>NP 044800 NADH dehydrogenase subunit 5 [Reclinomonas americana].
utg7180000000038	Jakobida-Reclinomonas americana mt 11466551	>NP 044800 NADH dehydrogenase subunit 5 [Reclinomonas americana].
utg7180000000039	Viridiplantae-Mesostigma viride mt 110225699	>YP 665704 cytochrome c oxidase subunit 2 [Mesostigma viride].
utg7180000000040	Heterokonta-Phytophthora infestans mt 9695376	>NP 037598 cytochrome c oxidase subunit 2 [Phytophthora infestans].
utg7180000000041	Viridiplantae-Mesostigma viride mt 110225699	>YP 665704 cytochrome c oxidase subunit 2 [Mesostigma viride].
utg7180000000042	Viridiplantae-Chlorokybus atmophyticus mt 150406471	>YP 001315130 NADH dehydrogenase subunit 5 [Chlorokybus atmophyticus].
utg7180000000043	Jakobida-Reclinomonas americana mt 11466550	>NP 044799 NADH dehydrogenase subunit 4L [Reclinomonas americana].
utg7180000000044	Viridiplantae-Ostreococcus tauri mt 113170509	>YP 717300 nad5 [Ostreococcus tauri].
utg7180000000044	Viridiplantae-Ostreococcus tauri mt 113170509	>YP 717300 nad5 [Ostreococcus tauri].
utg7180000000045	Heterokonta-Phytophthora ramorum mt 145932460	>YP 001165372 ribosomal protein S14 [Phytophthora ramorum].
utg7180000000000	Choanoflagellata-Monosiga brevicollis ATCC 50154 mt 23464621	>NP 696989 apocytochrome b [Monosiga brevicollis ATCC 50154].
utg7180000000001	Planctomycetes-Planctomyces maris DSM 8797 149179536	>ZP 01858077 30S ribosomal protein S12 [Planctomyces maris DSM 8797].
utg7180000000002	Verrucomicrobia-Akkermansia muciniphila ATCC BAA-835 187734946	>YP 001877058 ribosomal protein S13 [Akkermansia muciniphila ATCC BAA-835].
utg7180000000003	Gemmatimonadetes-Gemmatimonas	>YP 002760392 50S ribosomal protein

	aurantiaca T-27 226226286	L16 [Gemmatimonas aurantiaca T-27].
utg7180000000004	Proteobacteria-Erythrobacter sp SD-21 149184321	>ZP 01862639 LSU ribosomal protein L14P [Erythrobacter sp. SD-21].
utg7180000000005	Proteobacteria-Agrobacterium tumefaciens str C58 159184736	>NP 354381 30S ribosomal protein S2 [Agrobacterium tumefaciens str. C58].
utg7180000000006	Heterokonta-Phytophthora sojae jgi108909	
utg7180000000007	Viridiplantae-Vitis vinifera 225426230	>XP 002263323 PREDICTED: hypothetical protein [Vitis vinifera].
utg7180000000008	Heterokonta-Phytophthora capsici jgi95944	
utg7180000000008	Heterokonta-Phytophthora capsici jgi95944	
utg7180000000009	Viridiplantae-Micromonas sp RCC299 255070073	>XP 002507118 heat shock binding protein 70, ER luminal [Micromonas sp. RCC299].
utg7180000000009	Viridiplantae-Micromonas sp RCC299 255070073	>XP 002507118 heat shock binding protein 70, ER luminal [Micromonas sp. RCC299].
utg7180000000009	Viridiplantae-Micromonas sp RCC299 255070073	>XP 002507118 heat shock binding protein 70, ER luminal [Micromonas sp. RCC299].
utg7180000000010	Viridiplantae-Chlorella sp NC64A jgi29643	
utg7180000000011	Viridiplantae-Coccomyxa sp C-169 jgi34760	
utg7180000000012	Fungi-Schizosaccharomyces japonicus yFS275 213408811	>XP 002175176 heat shock protein [Schizosaccharomyces japonicus yFS275].
utg7180000000013	Proteobacteria-Rhodospirillum centenum SW 209964055	>YP 002296970 50S ribosomal protein L6 [Rhodospirillum centenum SW].

Table S6. BLASTx top hits to contigs derived from the MS584-22 Illumina assembly using the *CLC Genomics Workbench*. Proteins with plastid-encoded homologs in other taxa are shown with the green background and mitochondrial proteins with the red background.

ConsensusfromContig1371Viridiplantae-Pseudendoclonium_akinetum_pt_gi108796958	1.60E-13	>YP_636258 putative site-specific DNA endonuclease [Pseudendoclonium akinetum].
ConsensusfromContig3444Viridiplantae-Zygnema_circumcarinatum_pt_gi108796758	1.50E-14	>YP_636502 hypothetical protein ZyciCp036 [Zygnema circumcarinatum].
ConsensusfromContig1270Metazoa-Chondrilla_aff_nucula_CHOND_mt_gi164421148	7.80E-17	>YP_001648550 NADH dehydrogenase subunit 5 [Chondrilla aff. nucula CHOND].
ConsensusfromContig1758Viridiplantae-Marchantia_polymorpha_mt_gi11467101	3.20E-12	>NP_054402 NADH dehydrogenase subunit 2 [Marchantia polymorpha].
ConsensusfromContig1941Viridiplantae-Chara_vulgaris_mt_gi38638282	6.40E-42	>NP_943685 NADH dehydrogenase subunit 4 [Chara vulgaris].
ConsensusfromContig2304Viridiplantae-Physcomitrella_patens_mt_gi171259158	3.20E-59	>YP_539000 cytochrome c oxidase subunit 1 [Physcomitrella patens].
ConsensusfromContig2497Viridiplantae-Ostreococcus_tauri_mt_gi113170508	1.20E-42	>YP_717299 nad4 [Ostreococcus tauri].
ConsensusfromContig2800Viridiplantae-Chlorokybus_atmophyticus_mt_gi150406468	2.40E-31	>YP_001315136 NADH dehydrogenase subunit 2 [Chlorokybus atmophyticus].
ConsensusfromContig2800Viridiplantae-Chlorokybus_atmophyticus_mt_gi150406468	2.40E-31	>YP_001315136 NADH dehydrogenase subunit 2 [Chlorokybus atmophyticus].
ConsensusfromContig3132Stramenopiles-Chattonella_marina_mt_gi289065169	6.70E-57	>YP_003434221 cytochrome c oxidase subunit II [Chattonella marina].
ConsensusfromContig3242Viridiplantae-Chlorokybus_atmophyticus_mt_gi150406504	4.90E-30	>YP_001315110 putative reverse transcriptase and intron maturase [Chlorokybus atmophyticus].
ConsensusfromContig3415Viridiplantae-Chlorokybus_atmophyticus_mt_gi150406502	2.30E-11	>YP_001315104 hypothetical protein Chatpmp20 [Chlorokybus atmophyticus].
ConsensusfromContig3427Viridiplantae-Nicotiana_tabacum_mt_gi57013882	2.50E-15	>YP_173356 hypothetical protein NitaMp008 [Nicotiana tabacum].
ConsensusfromContig3651Viridiplantae-Chlorokybus_atmophyticus_mt_gi150406504	5.90E-16	>YP_001315110 putative reverse transcriptase and intron maturase [Chlorokybus atmophyticus].
ConsensusfromContig4776Viridiplantae-Chlorokybus_atmophyticus_mt_gi150406468	1.40E-13	>YP_001315136 NADH dehydrogenase subunit 2 [Chlorokybus atmophyticus].
ConsensusfromContig5133Excavata-Reclinomonas_americana_mt_gi11466551	3.10E-196	>NP_044800 NADH dehydrogenase subunit 5 [Reclinomonas americana].
ConsensusfromContig5218Viridiplantae-Nephroselmis_olivacea_mt_gi110225658	1.30E-167	>YP_665664 cytochrome c oxidase subunit 1 [Nephroselmis olivacea].
ConsensusfromContig5435Excavata-Reclinomonas_americana_mt_gi11466552	1.10E-152	>NP_044801 NADH dehydrogenase subunit 4 [Reclinomonas americana].
ConsensusfromContig5445Viridiplantae-Nicotiana_tabacum_mt_gi57013882	1.70E-16	>YP_173356 hypothetical protein NitaMp008 [Nicotiana tabacum].
ConsensusfromContig5455Viridiplantae-Chaetosphaeridium_globosum_mt_gi22550335	5.50E-112	>NP_689380 apocytochrome b [Chaetosphaeridium globosum].
ConsensusfromContig5680Viridiplantae-Nephroselmis_olivacea_mt_gi110225658	8.60E-37	>YP_665664 cytochrome c oxidase subunit 1 [Nephroselmis olivacea].
ConsensusfromContig5680Viridiplantae-Nephroselmis_olivacea_mt_gi110225658	8.60E-37	>YP_665664 cytochrome c oxidase subunit 1 [Nephroselmis olivacea].
ConsensusfromContig6133Viridiplantae-Chlorokybus_atmophyticus_mt_gi150406504	3.30E-23	>YP_001315110 putative reverse transcriptase and intron maturase [Chlorokybus atmophyticus].
ConsensusfromContig6150Excavata-Reclinomonas_americana_mt_gi11466505	1.50E-46	>NP_044754 NADH dehydrogenase subunit 1 [Reclinomonas americana].
ConsensusfromContig6189Stramenopiles-Phytophthora_ramorum_mt_gi145932439	8.30E-13	>YP_001165351 NADH dehydrogenase subunit 2 [Phytophthora ramorum].
ConsensusfromContig6189Stramenopiles-Phytophthora_ramorum_mt_gi145932439	8.30E-13	>YP_001165351 NADH dehydrogenase subunit 2 [Phytophthora ramorum].
ConsensusfromContig6262Viridiplantae-Marchantia_polymorpha_mt_gi11467101	7.20E-30	>NP_054402 NADH dehydrogenase subunit 2 [Marchantia polymorpha].
ConsensusfromContig6474Metazoa-Topsentia_ophiraphidites_mt_gi164421007	5.60E-12	>YP_001648502 cytochrome c oxidase subunit III [Topsentia ophiraphidites].
ConsensusfromContig6150Excavata-Reclinomonas_americana_mt_gi11466505	1.50E-46	>NP_044754 NADH dehydrogenase subunit 1 [Reclinomonas americana].
ConsensusfromContig6686Excavata-Reclinomonas_americana_mt_gi11466533	5.10E-17	>NP_044782 NADH dehydrogenase subunit 7 [Reclinomonas americana].
ConsensusfromContig7094Viridiplantae-Chara_vulgaris_mt_gi38638279	3.80E-68	>NP_943693 NADH dehydrogenase subunit 1 [Chara vulgaris].
ConsensusfromContig7137Viridiplantae-Prototheca_wickerhamii_mt_gi11497477	7.20E-26	>NP_042267 NADH dehydrogenase (ubiquinone), subunit 4L [Prototheca wickerhamii].
ConsensusfromContig7346Viridiplantae-Nephroselmis_olivacea_mt_gi110225675	5.60E-14	>YP_665681 cytochrome c oxidase subunit 3 [Nephroselmis olivacea].
ConsensusfromContig2348Actinobacteria-Actinosynnema_mirum_DSM_43827_gi256375186	1.60E-19	>YP_003098846 Alpha-galactosidase [Actinosynnema mirum DSM 43827].
ConsensusfromContig2079Actinobacteria-Actinosynnema_mirum_DSM_43827_gi256377304	4.80E-14	>YP_003100964 hypothetical protein Amir_3209 [Actinosynnema mirum DSM 43827].
ConsensusfromContig5170Actinobacteria-Beutenbergia_cavernae_DSM_12333_gi229818998	7.30E-12	>YP_002880524 major facilitator superfamily MFS_1 [Beutenbergia cavernae DSM 12333].
ConsensusfromContig3429Actinobacteria-Beutenbergia_cavernae_DSM_12333_gi229819432	1.50E-22	>YP_002880958 Phytanoyl-CoA dioxygenase [Beutenbergia cavernae DSM 12333].
ConsensusfromContig7558Actinobacteria-Catenulispora_acidiphila_DSM_44928_gi256394790	9.20E-13	>YP_003116354 Beta-N-acetylhexosaminidase [Catenulispora acidiphila DSM 44928].
ConsensusfromContig5161Actinobacteria-Conexibacter_woesei_DSM_14684_gi284044319	2.90E-48	>YP_003394659 domain of unknown function DUF1731 [Conexibacter woesei DSM 14684].
ConsensusfromContig2298Actinobacteria-Cryptobacterium_curtum_DSM_15641_gi256826780	1.70E-18	>YP_003150739 serine/threonine protein kinase [Cryptobacterium curtum DSM 15641].
ConsensusfromContig2398Actinobacteria-Frankia_sp_EUN1f_gi288916463	1.00E-14	>ZP_06410841 AAA ATPase central domain protein [Frankia sp. EUN1f].
ConsensusfromContig2433Actinobacteria-Frankia_sp_EUN1f_gi288917371	4.00E-17	>ZP_06411738 Hydroxyacylglutathione hydrolase [Frankia sp. EUN1f].
ConsensusfromContig2417Actinobacteria-Frankia_symbiont_of_Datisca_glomerata_gi289641839	6.80E-26	>ZP_06473996 Ferroxidase [Frankia symbiont of Datisca glomerata].
ConsensusfromContig5226Actinobacteria-Frankia_symbiont_of_Datisca_glomerata_gi289644143	1.40E-41	>ZP_06476236 short-chain dehydrogenase/reductase SDR [Frankia symbiont of Datisca glomerata].
ConsensusfromContig1989Actinobacteria-Geodermatophilus_obscurus_DSM_43160_gi284992406	2.40E-14	>YP_003410960 endonuclease/exonuclease/phosphatase [Geodermatophilus obscurus DSM 43160].
ConsensusfromContig1946Actinobacteria-Janibacter_sp_HTCC2649_gi84498585	5.80E-11	>ZP_00997348 putative long-chain fatty-acid CoA ligase [Janibacter sp. HTCC2649].
ConsensusfromContig4623Actinobacteria-Kineococcus_radiotolerans_SRS30216_gi152966274	2.60E-12	>YP_001362058 hypothetical protein Krad_2313 [Kineococcus radiotolerans SRS30216].
ConsensusfromContig4715Actinobacteria-Kribbella_flavida_DSM_17836_gi284030564	2.90E-11	>YP_003380495 alpha-L-rhamnosidase [Kribbella flavida DSM 17836].
ConsensusfromContig1923Actinobacteria-Kribbella_flavida_DSM_17836_gi284032401	9.20E-11	>YP_003382332 glycoside hydrolase family 2 sugar binding protein [Kribbella flavida DSM 17836].
ConsensusfromContig1949Actinobacteria-Kribbella_flavida_DSM_17836_gi284032401	3.80E-32	>YP_003382332 glycoside hydrolase family 2 sugar binding protein [Kribbella flavida DSM 17836].
ConsensusfromContig6978Actinobacteria-Kribbella_flavida_DSM_17836_gi284032401	1.10E-19	>YP_003382332 glycoside hydrolase family 2 sugar binding protein [Kribbella flavida DSM 17836].
ConsensusfromContig5921Actinobacteria-marine_actinobacterium_PHSC20C1_gi88856654	9.10E-30	>ZP_01131310 hypothetical protein A20C1_10745 [marine actinobacterium PHSC20C1].
ConsensusfromContig2272Actinobacteria-Micromonospora_sp_L5_gi288791739	1.70E-17	>ZP_06397482 Glycoside hydrolase family 59 [Micromonospora sp. L5].
ConsensusfromContig3168Actinobacteria-Mycobacterium_parascrofulaceum_ATCC_BAA_614_gi296171002	2.90E-11	>ZP_06852486 conserved hypothetical protein [Mycobacterium parascrofulaceum ATCC BAA-614].
ConsensusfromContig5966Actinobacteria-Mycobacterium_tuberculosis_02_1987_gi289746734	9.50E-11	>ZP_06506112 phenolpthiocerol synthesis type-I polyketide synthase ppsd [Mycobacterium tuberculosis 02_1987].
ConsensusfromContig2025Actinobacteria-Nocardiopsis_dassonvillei_subsp_dassonvillei_DSM_43111_gi297562438	9.70E-16	>YP_003681412 acyltransferase 3 [Nocardiopsis dassonvillei subsp. dassonvillei DSM 43111].
ConsensusfromContig4762Actinobacteria-Propionibacterium_acnes_KPA171202_gi50841908	1.90E-12	>YP_055135 hypothetical protein PPA2398 [Propionibacterium acnes KPA171202].
ConsensusfromContig2576Actinobacteria-Propionibacterium_freudenreichii_subsp_shermanii_CIRM_BIA1_gi297626729	2.70E-11	>YP_003688492 hypothetical protein PFREUD_15690 [Propionibacterium freudenreichii subsp. shermanii CIRM-BIA1].
ConsensusfromContig2576Actinobacteria-Propionibacterium_freudenreichii_subsp_shermanii_CIRM_BIA1_gi297626729	2.70E-11	>YP_003688492 hypothetical protein PFREUD_15690 [Propionibacterium freudenreichii subsp. shermanii CIRM-BIA1].
ConsensusfromContig5329Actinobacteria-Rhodococcus_erythropolis_SK121_gi229492866	6.80E-32	>ZP_04386662 conserved hypothetical protein [Rhodococcus erythropolis SK121].
ConsensusfromContig5461Actinobacteria-Rhodococcus_erythropolis_SK121_gi229492866	9.30E-13	>ZP_04386662 conserved hypothetical protein [Rhodococcus erythropolis SK121].
ConsensusfromContig7378Actinobacteria-Saccharomonospora_viridis_DSM_43017_gi257055466	2.80E-14	>YP_003133298 beta-galactosidase/beta-glucuronidase [Saccharomonospora viridis DSM 43017].
ConsensusfromContig2229Actinobacteria-Saccharomonospora_viridis_DSM_43017_gi257057184	8.90E-14	>YP_003135016 tetratricopeptide repeat protein [Saccharomonospora viridis DSM 43017].
ConsensusfromContig2100Actinobacteria-Saccharopolyspora_erythraea_NRRL_2338_gi134103490	3.00E-15	>YP_001109151 putative alpha-galactosidase [Saccharopolyspora erythraea NRRL 2338].
ConsensusfromContig3139Actinobacteria-Salinispora_tropica_CNB_440_gi145596123	3.40E-12	>YP_001160420 glyoxalase/bleomycin resistance protein/dioxygenase [Salinispora tropica CNB-440].
ConsensusfromContig4959Actinobacteria-Sanguibacter_keddieii_DSM_10542_gi269794916	6.50E-13	>YP_003314371 nucleoside-diphosphate-sugar epimerase [Sanguibacter keddieii DSM 10542].
ConsensusfromContig2391Actinobacteria-Stackebrandtia_nassauensis_DSM_44728_gi291300871	6.30E-26	>YP_003512149 Phytanoyl-CoA dioxygenase [Stackebrandtia nassauensis DSM 44728].
ConsensusfromContig1945Actinobacteria-Streptomyces_avermitilis_MA_4680_gi29830182	9.00E-26	>NP_824816 thioesterase [Streptomyces avermitilis MA-4680].
ConsensusfromContig2408Actinobacteria-Streptomyces_clavuligerus_ATCC_27064_gi294811519	1.50E-11	>ZP_06770162 Alginate_lyase domain-containing protein [Streptomyces clavuligerus ATCC 27064].
ConsensusfromContig3557Actinobacteria-Streptomyces_flavogriseus_ATCC_33331_gi260456612	1.50E-13	>ZP_05804989 Beta-galactosidase [Streptomyces flavogriseus ATCC 33331].
ConsensusfromContig3557Actinobacteria-Streptomyces_flavogriseus_ATCC_33331_gi260456612	1.50E-13	>ZP_05804989 Beta-galactosidase [Streptomyces flavogriseus ATCC 33331].
ConsensusfromContig3436Actinobacteria-Streptomyces_griseus_subsp_griseus_NBRC_13350_gi182434427	8.50E-11	>YP_001822146 putative StrG-like protein [Streptomyces griseus subsp. griseus NBRC 13350].
ConsensusfromContig2366Actinobacteria-Streptomyces_hygroscopicus_ATCC_53653_gi256782365	2.90E-21	>ZP_05520828 carbon-nitrogen family hydrolase [Streptomyces hygroscopicus ATCC 53653].
ConsensusfromContig3166Actinobacteria-Streptomyces_sp_Mg1_gi254386939	1.70E-11	>ZP_05002222 hypothetical protein SSAG_06535 [Streptomyces sp. Mg1].
ConsensusfromContig5870Actinobacteria-Streptomyces_sviceus_ATCC_29083_gi297197084	5.80E-14	>ZP_06914481 secreted alpha-galactosidase [Streptomyces sviceus ATCC 29083].
ConsensusfromContig2186Actinobacteria-Streptomyces_sviceus_ATCC_29083_gi297197804	1.30E-23	>ZP_06915201 alpha-galactosidase [Streptomyces sviceus ATCC 29083].
ConsensusfromContig3341Actinobacteria-Streptomyces_sviceus_ATCC_29083_gi297197858	7.30E-15	>ZP_06915255 alpha-N-arabinofuranosidase [Streptomyces sviceus ATCC 29083].
ConsensusfromContig2238Actinobacteria-Streptosporangium_roseum_DSM_43021_gi271967420	9.50E-35	>YP_003341616 hypothetical protein Sros_6143 [Streptosporangium roseum DSM 43021].
ConsensusfromContig5148Actinobacteria-Thermobispora_bispora_DSM_43833_gi296269863	3.40E-25	>YP_003652495 sulfatase [Thermobispora bispora DSM 43833].
ConsensusfromContig1976Actinobacteria-Xylanimonas_cellulosilytica_DSM_15894_gi269957876	4.70E-25	>YP_003327665 putative lipoprotein [Xylanimonas cellulosilytica DSM 15894].
ConsensusfromContig7225Alveolata-Alexandrium_catenella_esContig331_2	2.80E-17	
ConsensusfromContig2284Alveolata-Alexandrium_catenella_esContig391_1	3.90E-18	
ConsensusfromContig5371Alveolata-Alexandrium_catenella_esgi186952784_2	4.00E-13	>EX455521 sqb5cb7a69 Alexandrium catenella ACC07 expressed sequence tags Alexandrium catenella cDNA, mRNA sequence.
ConsensusfromContig1171Alveolata-Alexandrium_catenella_esgi186952817_1	3.20E-12	>EX456919 sqb822ee3e Alexandrium catenella ACC07 expressed sequence tags Alexandrium catenella cDNA, mRNA sequence.
ConsensusfromContig6575Alveolata-Alexandrium_catenella_esgi186952817_3	1.30E-14	>EX456919 sqb822ee3e Alexandrium catenella ACC07 expressed sequence tags Alexandrium catenella cDNA, mRNA sequence.
ConsensusfromContig2400Alveolata-Alexandrium_catenella_esgi186953118_3	3.00E-28	>EX456980 sqd7b27f48 Alexandrium catenella ACC07 expressed sequence tags Alexandrium catenella cDNA, mRNA sequence.
ConsensusfromContig2400Alveolata-Alexandrium_catenella_esgi186953118_3	3.00E-28	>EX456980 sqd7b27f48 Alexandrium catenella ACC07 expressed sequence tags Alexandrium catenella cDNA, mRNA sequence.
ConsensusfromContig7111Alveolata-Alexandrium_catenella_esgi186954472_1	2.70E-15	>EX457048 sqefaa85b4 Alexandrium catenella ACC07 expressed sequence tags Alexandrium catenella cDNA, mRNA sequence.
ConsensusfromContig7451Alveolata-Alexandrium_catenella_esgi186954520_3	2.90E-11	>EX455028 sqf01d6b8c Alexandrium catenella ACC07 expressed sequence tags Alexandrium catenella cDNA, mRNA sequence.
ConsensusfromContig6930Alveolata-Alexandrium_catenella_esgi186959833_2	6.00E-53	>EX460209 sq389ed421 Alexandrium catenella ACC07 expressed sequence tags Alexandrium catenella cDNA, mRNA sequence.
ConsensusfromContig8166Alveolata-Alexandrium_catenella_esgi186959912_2	1.60E-15	>EX463603 sq29cf6a0e Alexandrium catenella ACC07 expressed sequence tags Alexandrium catenella cDNA, mRNA sequence.
ConsensusfromContig3765Alveolata-Alexandrium_catenella_esgi186959912_2	3.30E-41	>EX463603 sq29cf6a0e Alexandrium catenella ACC07 expressed sequence tags Alexandrium catenella cDNA, mRNA sequence.
ConsensusfromContig7079Alveolata-Alexandrium_catenella_esgi186961616_1	3.40E-23	>EX462325 sq5576dd57 Alexandrium catenella ACC07 expressed sequence tags Alexandrium catenella cDNA, mRNA sequence.
ConsensusfromContig2297Alveolata-Alexandrium_catenella_esgi186962952_2	1.60E-29	>EX456752 sqf83493d3 Alexandrium catenella ACC07 expressed sequence tags Alexandrium catenella cDNA, mRNA sequence.
ConsensusfromContig5789Alveolata-Alexandrium_catenella_esgi186962952_2	1.40E-23	>EX456752 sqf83493d3 Alexandrium catenella ACC07 expressed sequence tags Alexandrium catenella cDNA, mRNA sequence.
ConsensusfromContig7155Alveolata-Alexandrium_catenella_esgi186963545_1	1.70E-25	>EX458658 sqc19531fc Alexandrium catenella ACC07 expressed sequence tags Alexandrium catenella cDNA, mRNA sequence.
ConsensusfromContig7079Alveolata-Alexandrium_minutum_esContig1129_3	1.30E-15	

ConsensusfromContig5147Alveolata-Alexandrium_minutum_esContig1293_1	2.00E-12	
ConsensusfromContig5126Alveolata-Alexandrium_minutum_esContig1437_5	6.40E-23	
ConsensusfromContig5664Alveolata-Alexandrium_minutum_esContig1829_6	4.50E-26	
ConsensusfromContig7432Alveolata-Alexandrium_minutum_esContig2510_4	4.60E-12	
ConsensusfromContig2072Alveolata-Alexandrium_minutum_esContig2597_2	1.10E-33	
ConsensusfromContig2030Alveolata-Alexandrium_minutum_esContig2779_4	5.10E-17	
ConsensusfromContig2000Alveolata-Alexandrium_minutum_esContig2872_2	6.20E-49	
ConsensusfromContig6333Alveolata-Alexandrium_minutum_esContig3122_1	7.40E-14	
ConsensusfromContig2303Alveolata-Alexandrium_minutum_esContig3131_1	7.80E-50	
ConsensusfromContig2863Alveolata-Alexandrium_minutum_esContig3131_1	3.00E-32	
ConsensusfromContig2115Alveolata-Alexandrium_minutum_esContig354_6	1.10E-12	
ConsensusfromContig2976Alveolata-Alexandrium_minutum_esgi297637419_2	9.60E-14	>GW795302 AmnE011001P0035A12.y_phred13_vc Alexandrium minutum normalized EST library Alexandrium minutum cDNA, mRNA sequence.
ConsensusfromContig4847Alveolata-Alexandrium_minutum_esgi297642649_3	8.70E-11	>GW802226 AmnE011001P0086G23.x_phred13_vc Alexandrium minutum normalized EST library Alexandrium minutum cDNA, mRNA sequence.
ConsensusfromContig5141Alveolata-Alexandrium_minutum_esgi297644712_1	3.80E-31	>GW810253 AmnE011001P0151E04.y_phred13_vc Alexandrium minutum normalized EST library Alexandrium minutum cDNA, mRNA sequence.
ConsensusfromContig2159Alveolata-Alexandrium_minutum_esgi297650009_2	1.20E-13	>GW798786 AmnE011001P0066H12.y_phred13_vc Alexandrium minutum normalized EST library Alexandrium minutum cDNA, mRNA sequence.
ConsensusfromContig3145Alveolata-Alexandrium_tamarense_dxContig1417_4	1.60E-12	
ConsensusfromContig6958Alveolata-Alexandrium_tamarense_dxContig1494_2	1.20E-15	
ConsensusfromContig8618Alveolata-Alexandrium_tamarense_dxJHC1057_5	1.20E-16	
ConsensusfromContig3124Alveolata-Alexandrium_tamarense_dxJHC10717_3	1.50E-25	
ConsensusfromContig9369Alveolata-Alexandrium_tamarense_dxJHC11278_6	9.40E-12	
ConsensusfromContig3194Alveolata-Alexandrium_tamarense_dxJHC12328_1	3.90E-12	
ConsensusfromContig2056Alveolata-Alexandrium_tamarense_dxJHC13435_5	1.70E-11	
ConsensusfromContig6639Alveolata-Alexandrium_tamarense_dxJHC13522_1	4.60E-18	
ConsensusfromContig2139Alveolata-Alexandrium_tamarense_dxJHC1425_3	9.60E-15	
ConsensusfromContig1973Alveolata-Alexandrium_tamarense_dxJHC14755_4	2.60E-23	
ConsensusfromContig3944Alveolata-Alexandrium_tamarense_dxJHC16214_3	4.70E-16	
ConsensusfromContig4922Alveolata-Alexandrium_tamarense_dxJHC16214_3	4.90E-22	
ConsensusfromContig5108Alveolata-Alexandrium_tamarense_dxJHC1640_3	3.40E-12	
ConsensusfromContig5213Alveolata-Alexandrium_tamarense_dxJHC16667_5	1.40E-23	
ConsensusfromContig2419Alveolata-Alexandrium_tamarense_dxJHC17473_2	2.20E-54	
ConsensusfromContig5114Alveolata-Alexandrium_tamarense_dxJHC1838_6	2.70E-17	
ConsensusfromContig6220Alveolata-Alexandrium_tamarense_dxJHC21402_5	2.00E-20	
ConsensusfromContig2446Alveolata-Alexandrium_tamarense_dxJHC21770_4	1.40E-11	
ConsensusfromContig6515Alveolata-Alexandrium_tamarense_dxJHC22214_6	7.80E-11	
ConsensusfromContig4616Alveolata-Alexandrium_tamarense_dxJHC22368_4	1.30E-11	
ConsensusfromContig7104Alveolata-Alexandrium_tamarense_dxJHC22987_6	2.80E-12	
ConsensusfromContig1947Alveolata-Alexandrium_tamarense_dxJHC23483_4	6.00E-16	
ConsensusfromContig3122Alveolata-Alexandrium_tamarense_dxJHC23483_4	1.00E-13	
ConsensusfromContig5339Alveolata-Alexandrium_tamarense_dxJHC23483_4	8.70E-15	
ConsensusfromContig5446Alveolata-Alexandrium_tamarense_dxJHC23483_4	2.00E-18	
ConsensusfromContig4574Alveolata-Alexandrium_tamarense_dxJHC24619_6	3.70E-19	
ConsensusfromContig6272Alveolata-Alexandrium_tamarense_dxJHC2719_2	7.40E-54	
ConsensusfromContig2602Alveolata-Alexandrium_tamarense_dxJHC3083_2	2.90E-12	
ConsensusfromContig1712Alveolata-Alexandrium_tamarense_dxJHC3440_5	4.10E-17	
ConsensusfromContig3105Alveolata-Alexandrium_tamarense_dxJHC36417_3	1.30E-12	
ConsensusfromContig3707Alveolata-Alexandrium_tamarense_dxJHC41885_5	2.70E-14	
ConsensusfromContig3707Alveolata-Alexandrium_tamarense_dxJHC41885_5	2.70E-14	
ConsensusfromContig7120Alveolata-Alexandrium_tamarense_dxJHC4388_1	3.30E-15	
ConsensusfromContig6962Alveolata-Alexandrium_tamarense_dxJHC5122_1	8.50E-20	
ConsensusfromContig6477Alveolata-Alexandrium_tamarense_dxJHC5950_2	3.20E-12	
ConsensusfromContig1602Alveolata-Alexandrium_tamarense_dxJHC6243_3	9.60E-11	
ConsensusfromContig3922Alveolata-Alexandrium_tamarense_dxJHC714_3	6.60E-12	
ConsensusfromContig5369Alveolata-Alexandrium_tamarense_dxJHC714_3	1.80E-22	
ConsensusfromContig852 Alveolata-Alexandrium_tamarense_dxJHC7147_1	2.00E-16	
ConsensusfromContig2065Alveolata-Alexandrium_tamarense_dxJHC7448_2	2.00E-11	
ConsensusfromContig6290Alveolata-Alexandrium_tamarense_dxJHC8955_1	1.30E-14	
ConsensusfromContig3549Alveolata-Alexandrium_tamarense_dxJHC8955_3	3.90E-25	
ConsensusfromContig1592Alveolata-Alexandrium_tamarense_dxJHC9820_5	4.90E-12	
ConsensusfromContig2382Alveolata-Amphidinium_carterae_esgi39542533_2	9.20E-17	>CF064837 Ac1462r Amphidinium carterae Amphidinium carterae cDNA clone Ac1462r 5', mRNA sequence.
ConsensusfromContig2246Alveolata-Amphidinium_carterae_esgi39544170_3	1.40E-12	>CF066474 Ac4258 Amphidinium carterae Amphidinium carterae cDNA clone Ac4258 3', mRNA sequence.
ConsensusfromContig5259Alveolata-Amphidinium_carterae_esgi39544267_3	8.80E-23	>CF066571 Ac4412 Amphidinium carterae Amphidinium carterae cDNA clone Ac4412 3', mRNA sequence.
ConsensusfromContig2002Alveolata-Amphidinium_carterae_esgi39545286_3	1.50E-11	>CF067590 Ac766 Amphidinium carterae Amphidinium carterae cDNA clone Ac766 3', mRNA sequence.
ConsensusfromContig2386Alveolata-Anophryoides_haemophila_tbAHL00000492_2	1.50E-39	
ConsensusfromContig5929Alveolata-Anophryoides_haemophila_tbAHL00000492_2	4.00E-40	
ConsensusfromContig1762Alveolata-Babesia_bovis_T2Bo_gi156089535	5.30E-15	>XP_001612174 ribosomal protein L21 [Babesia bovis T2Bo].
ConsensusfromContig4645Alveolata-Cryptosporidium_hominis_TU502_gi67616500	1.30E-23	>XP_667490 hypothetical protein [Cryptosporidium hominis TU502].
ConsensusfromContig2124Alveolata-Heterocapsa_triquetra_tbHTL00000727_2	9.80E-27	
ConsensusfromContig5841Alveolata-Heterocapsa_triquetra_tbHTL00000727_2	3.10E-17	
ConsensusfromContig6163Alveolata-Heterocapsa_triquetra_tbHTL00000727_2	1.30E-13	
ConsensusfromContig5400Alveolata-Heterocapsa_triquetra_tbHTL00001443_1	1.60E-17	
ConsensusfromContig2489Alveolata-Karenia_brevis_esContig1462_3	3.80E-13	
ConsensusfromContig4065Alveolata-Karenia_brevis_esContig2024_2	1.60E-12	
ConsensusfromContig5923Alveolata-Karenia_brevis_esContig2024_2	3.80E-16	
ConsensusfromContig2655Alveolata-Karenia_brevis_esContig228_3	3.10E-20	
ConsensusfromContig1936Alveolata-Karenia_brevis_esContig3516_3	1.50E-123	
ConsensusfromContig1961Alveolata-Karenia_brevis_esContig3516_3	1.10E-127	
ConsensusfromContig2846Alveolata-Karenia_brevis_esContig3589_4	6.50E-20	
ConsensusfromContig7171Alveolata-Karenia_brevis_esContig3961_2	9.10E-28	
ConsensusfromContig3653Alveolata-Karenia_brevis_esContig3969_1	2.00E-17	
ConsensusfromContig2965Alveolata-Karenia_brevis_esContig4085_3	1.00E-23	
ConsensusfromContig2215Alveolata-Karenia_brevis_esContig4106_4	2.90E-24	
ConsensusfromContig5198Alveolata-Karenia_brevis_esContig4839_2	1.00E-15	
ConsensusfromContig5386Alveolata-Karenia_brevis_esContig4994_5	2.60E-31	
ConsensusfromContig1969Alveolata-Karenia_brevis_esContig5086_5	2.30E-25	
ConsensusfromContig4951Alveolata-Karenia_brevis_esContig5086_5	4.20E-23	
ConsensusfromContig5156Alveolata-Karenia_brevis_esContig5086_5	9.70E-35	
ConsensusfromContig3529Alveolata-Karenia_brevis_esContig5371_4	6.20E-11	
ConsensusfromContig1953Alveolata-Karenia_brevis_esContig5598_2	2.60E-39	
ConsensusfromContig5153Alveolata-Karenia_brevis_esContig5866_2	1.50E-45	
ConsensusfromContig2075Alveolata-Karenia_brevis_esContig6192_6	1.40E-18	
ConsensusfromContig5113Alveolata-Karenia_brevis_esContig6480_5	4.80E-26	
ConsensusfromContig6989Alveolata-Karenia_brevis_esContig6565_2	8.20E-37	
ConsensusfromContig6974Alveolata-Karenia_brevis_esContig6681_3	7.60E-21	
ConsensusfromContig1939Alveolata-Karenia_brevis_esContig6868_5	3.10E-24	
ConsensusfromContig2219Alveolata-Karenia_brevis_esContig6868_5	9.90E-24	
ConsensusfromContig2021Alveolata-Karenia_brevis_esContig7132_1	7.40E-14	
ConsensusfromContig3127Alveolata-Karenia_brevis_esContig7132_1	2.30E-15	
ConsensusfromContig1634Alveolata-Karenia_brevis_esContig7267_2	3.50E-13	
ConsensusfromContig6945Alveolata-Karenia_brevis_esContig7403_6	2.30E-23	
ConsensusfromContig7433Alveolata-Karenia_brevis_esContig7789_5	2.20E-11	

ConsensusfromContig5106	Alveolata-Karenia_brevis_esContig7875_6	3.50E-16	
ConsensusfromContig2143	Alveolata-Karenia_brevis_esContig7977_4	1.10E-14	
ConsensusfromContig3397	Alveolata-Karenia_brevis_esContig8090_3	1.80E-17	
ConsensusfromContig2019	Alveolata-Karenia_brevis_esContig8254_2	1.90E-85	
ConsensusfromContig7093	Alveolata-Karenia_brevis_esContig8316_6	5.00E-21	
ConsensusfromContig1972	Alveolata-Karenia_brevis_esContig8440_2	3.60E-20	
ConsensusfromContig4413	Alveolata-Karenia_brevis_esContig8528_3	1.10E-11	
ConsensusfromContig2015	Alveolata-Karenia_brevis_esContig8544_1	3.10E-18	
ConsensusfromContig3409	Alveolata-Karenia_brevis_esContig8654_4	8.00E-13	
ConsensusfromContig5349	Alveolata-Karenia_brevis_esContig8654_4	1.00E-21	
ConsensusfromContig2065	Alveolata-Karenia_brevis_esContig8824_1	1.10E-18	
ConsensusfromContig2975	Alveolata-Karenia_brevis_esContig8824_1	2.10E-11	
ConsensusfromContig5391	Alveolata-Karenia_brevis_esContig8824_1	2.10E-25	
ConsensusfromContig6572	Alveolata-Karenia_brevis_esContig8824_1	4.80E-11	
ConsensusfromContig6980	Alveolata-Karenia_brevis_esContig8824_1	7.50E-34	
ConsensusfromContig2112	Alveolata-Karenia_brevis_esContig8846_1	4.80E-14	
ConsensusfromContig7000	Alveolata-Karenia_brevis_esContig8917_3	9.90E-28	
ConsensusfromContig6145	Alveolata-Karenia_brevis_esContig9198_1	6.20E-15	
ConsensusfromContig4193	Alveolata-Karenia_brevis_esContig9346_3	1.90E-14	
ConsensusfromContig6979	Alveolata-Karenia_brevis_esContig9422_3	3.10E-17	
ConsensusfromContig2197	Alveolata-Karenia_brevis_esContig9685_2	2.90E-14	
ConsensusfromContig5418	Alveolata-Karenia_brevis_esContig9685_2	1.00E-15	
ConsensusfromContig5104	Alveolata-Karenia_brevis_esContig9697_2	1.80E-16	
ConsensusfromContig3027	Alveolata-Karenia_brevis_esgi158890876_1	2.00E-16	>EX865128 AUAO1176.fwd AUAO Karenia brevis Karbr Dark-phase Karenia brevis cDNA clone AUAO1176 5', mRNA sequence.
ConsensusfromContig5168	Alveolata-Karenia_brevis_esgi158893293_2	4.40E-15	>EX867545 AUAO2482.fwd AUAO Karenia brevis Karbr Dark-phase Karenia brevis cDNA clone AUAO2482 5', mRNA sequence.
ConsensusfromContig1231	Alveolata-Karenia_brevis_esgi158895501_2	2.20E-14	>EX869753 AUAO3689.fwd AUAO Karenia brevis Karbr Dark-phase Karenia brevis cDNA clone AUAO3689 5', mRNA sequence.
ConsensusfromContig2449	Alveolata-Karenia_brevis_esgi158902093_2	1.10E-52	>EX876345 AUAO7216.fwd AUAO Karenia brevis Karbr Dark-phase Karenia brevis cDNA clone AUAO7216 5', mRNA sequence.
ConsensusfromContig6951	Alveolata-Karenia_brevis_esgi158902332_1	1.80E-18	>EX876584 AUAO7342.fwd AUAO Karenia brevis Karbr Dark-phase Karenia brevis cDNA clone AUAO7342 5', mRNA sequence.
ConsensusfromContig2160	Alveolata-Karenia_brevis_esgi158904645_5	1.60E-16	>EX878897 AUAO957.rev AUAO Karenia brevis Karbr Dark-phase Karenia brevis cDNA clone AUAO957 3', mRNA sequence.
ConsensusfromContig7246	Alveolata-Karenia_brevis_esgi158904646_1	7.20E-31	>EX878898 AUAO957.fwd AUAO Karenia brevis Karbr Dark-phase Karenia brevis cDNA clone AUAO957 5', mRNA sequence.
ConsensusfromContig3201	Alveolata-Karenia_brevis_esgi159001026_5	1.30E-18	>EX957364 CAGO10471.rev CAGO Karenia brevis Karbr Stressed (light+5 combined stress conditions) Karenia brevis cDNA clone CAGO10471 3', mRNA sequence.
ConsensusfromContig5181	Alveolata-Karenia_brevis_esgi159001026_5	6.30E-11	>EX957364 CAGO10471.rev CAGO Karenia brevis Karbr Stressed (light+5 combined stress conditions) Karenia brevis cDNA clone CAGO10471 3', mRNA sequence.
ConsensusfromContig1396	Alveolata-Karenia_brevis_esgi159004799_3	2.00E-11	>EX961233 CAGO12488.fwd CAGO Karenia brevis Karbr Stressed (light+5 combined stress conditions) Karenia brevis cDNA clone CAGO12488 5', mRNA sequence.
ConsensusfromContig2202	Alveolata-Karenia_brevis_esgi159004799_3	4.40E-33	>EX961233 CAGO12488.fwd CAGO Karenia brevis Karbr Stressed (light+5 combined stress conditions) Karenia brevis cDNA clone CAGO12488 5', mRNA sequence.
ConsensusfromContig6968	Alveolata-Karenia_brevis_esgi159004799_3	7.20E-17	>EX961233 CAGO12488.fwd CAGO Karenia brevis Karbr Stressed (light+5 combined stress conditions) Karenia brevis cDNA clone CAGO12488 5', mRNA sequence.
ConsensusfromContig7028	Alveolata-Karenia_brevis_esgi159005895_1	1.60E-22	>EX962232 CAGO13015.fwd CAGO Karenia brevis Karbr Stressed (light+5 combined stress conditions) Karenia brevis cDNA clone CAGO13015 5', mRNA sequence.
ConsensusfromContig2382	Alveolata-Karenia_brevis_esgi159008517_1	1.30E-15	>EX965177 CAGO2167.fwd CAGO Karenia brevis Karbr Stressed (light+5 combined stress conditions) Karenia brevis cDNA clone CAGO2167 5', mRNA sequence.
ConsensusfromContig1987	Alveolata-Karenia_brevis_esgi159010104_2	1.70E-30	>EX966468 CAGO2878.fwd CAGO Karenia brevis Karbr Stressed (light+5 combined stress conditions) Karenia brevis cDNA clone CAGO2878 5', mRNA sequence.
ConsensusfromContig5104	Alveolata-Karenia_brevis_esgi159012758_1	1.30E-20	>EX968844 CAGO4171.fwd CAGO Karenia brevis Karbr Stressed (light+5 combined stress conditions) Karenia brevis cDNA clone CAGO4171 5', mRNA sequence.
ConsensusfromContig2522	Alveolata-Karenia_brevis_esgi194480572_1	3.10E-17	>FK838091 K01111E10 Karenia brevis Multi-strain Library Karenia brevis cDNA 5', mRNA sequence.
ConsensusfromContig2522	Alveolata-Karenia_brevis_esgi194480572_1	3.10E-17	>FK838091 K01111E10 Karenia brevis Multi-strain Library Karenia brevis cDNA 5', mRNA sequence.
ConsensusfromContig3260	Alveolata-Karenia_brevis_esgi194482810_3	6.60E-13	>FK840470 K05191F05 Karenia brevis Multi-strain Library Karenia brevis cDNA 5', mRNA sequence.
ConsensusfromContig1293	Alveolata-Karenia_brevis_esgi194489544_1	3.40E-12	>FK850253 K10031B05 Karenia brevis Multi-strain Library Karenia brevis cDNA 5', mRNA sequence.
ConsensusfromContig1293	Alveolata-Karenia_brevis_esgi194489544_1	3.40E-12	>FK850253 K10031B05 Karenia brevis Multi-strain Library Karenia brevis cDNA 5', mRNA sequence.
ConsensusfromContig1787	Alveolata-Karenia_brevis_esgi194489544_1	1.90E-16	>FK850253 K10031B05 Karenia brevis Multi-strain Library Karenia brevis cDNA 5', mRNA sequence.
ConsensusfromContig1519	Alveolata-Karenia_brevis_esgi194489645_1	1.50E-21	>FK848899 K06051F02 Karenia brevis Multi-strain Library Karenia brevis cDNA 5', mRNA sequence.
ConsensusfromContig1591	Alveolata-Karenia_brevis_esgi194491422_2	1.70E-23	>FK847630 K05451F02 Karenia brevis Multi-strain Library Karenia brevis cDNA 5', mRNA sequence.
ConsensusfromContig5111	Alveolata-Karenia_brevis_esgi194493219_2	3.30E-38	>FK852054 K20041E07 Karenia brevis Multi-strain Library Karenia brevis cDNA 5', mRNA sequence.
ConsensusfromContig2519	Alveolata-Karenia_brevis_esgi48701791_2	5.60E-18	>CO059622 est_k_brevis5851 Karenia brevis EST Library (L99-05) Karenia brevis cDNA, mRNA sequence.
ConsensusfromContig7317	Alveolata-Karenia_brevis_esgi48703904_2	6.90E-12	>CO061735 est_k_brevis1311 Karenia brevis EST Library (L99-05) Karenia brevis cDNA, mRNA sequence.
ConsensusfromContig7119	Alveolata-Karenia_brevis_esgi48704326_3	1.40E-21	>CO062157 est_k_brevis1734 Karenia brevis EST Library (L99-05) Karenia brevis cDNA, mRNA sequence.
ConsensusfromContig1064	Alveolata-Karenia_brevis_esgi48706915_2	1.70E-16	>CO064746 est_k_brevis4357 Karenia brevis EST Library (L99-05) Karenia brevis cDNA, mRNA sequence.
ConsensusfromContig3560	Alveolata-Karenia_brevis_esgi48706972_1	7.50E-23	>CO064803 est_k_brevis4414 Karenia brevis EST Library (L99-05) Karenia brevis cDNA, mRNA sequence.
ConsensusfromContig3560	Alveolata-Karenia_brevis_esgi48706972_1	7.50E-23	>CO064803 est_k_brevis4414 Karenia brevis EST Library (L99-05) Karenia brevis cDNA, mRNA sequence.
ConsensusfromContig7233	Alveolata-Karlodinium_micrum_tbKML00001964_3	1.60E-18	
ConsensusfromContig2874	Alveolata-Karlodinium_micrum_tbKML00003142_2	3.80E-24	
ConsensusfromContig1932	Alveolata-Karlodinium_micrum_tbKML00003276_3	2.40E-26	
ConsensusfromContig5199	Alveolata-Karlodinium_micrum_tbKML00003276_3	5.10E-18	
ConsensusfromContig6266	Alveolata-Karlodinium_micrum_tbKML00003276_3	9.20E-17	
ConsensusfromContig3	Alveolata-Karlodinium_micrum_tbKML00005491_3	3.70E-18	
ConsensusfromContig5267	Alveolata-Karlodinium_micrum_tbKML00006501_2	5.10E-12	
ConsensusfromContig2369	Alveolata-Karlodinium_micrum_tbKML00006732_3	1.00E-13	
ConsensusfromContig4626	Alveolata-Karlodinium_micrum_tbKML00007083_2	2.60E-19	
ConsensusfromContig2465	Alveolata-Karlodinium_micrum_tbKML00007350_1	1.50E-11	
ConsensusfromContig7319	Alveolata-Karlodinium_micrum_tbKML00007350_1	2.60E-17	
ConsensusfromContig1205	Alveolata-Karlodinium_micrum_tbKML00007752_3	6.50E-17	
ConsensusfromContig2273	Alveolata-Karlodinium_micrum_tbKML00010921_3	7.10E-24	
ConsensusfromContig1292	Alveolata-Karlodinium_micrum_tbKML00011946_1	8.40E-11	
ConsensusfromContig2046	Alveolata-Lingulodinium_polyedrum_esgi39541194_1	1.10E-51	>CD809870 575 Lingulodinium polyedrum Lingulodinium polyedrum cDNA clone Lp2384, mRNA sequence.
ConsensusfromContig2222	Alveolata-Lingulodinium_polyedrum_esgi39541212_6	3.70E-11	>CD809888 593 Lingulodinium polyedrum Lingulodinium polyedrum cDNA clone Lp2447, mRNA sequence.
ConsensusfromContig5145	Alveolata-Lingulodinium_polyedrum_esgi39541779_1	1.00E-28	>CD810440 1190 Lingulodinium polyedrum Lingulodinium polyedrum cDNA clone Lp489, mRNA sequence.
ConsensusfromContig3141	Alveolata-Lingulodinium_polyedrum_esgi53884415_1	3.60E-16	>BP742195 BP742195 Lingulodinium polyedrum cDNA Lingulodinium polyedrum cDNA clone LP13EST03A03, mRNA sequence.
ConsensusfromContig1159	Alveolata-Lingulodinium_polyedrum_esgi53885473_1	1.70E-15	>BP743253 BP743253 Lingulodinium polyedrum cDNA Lingulodinium polyedrum cDNA clone LP13EST26E09, mRNA sequence.
ConsensusfromContig5175	Alveolata-Lingulodinium_polyedrum_esgi53885560_1	1.00E-42	>BP743340 BP743340 Lingulodinium polyedrum cDNA Lingulodinium polyedrum cDNA clone LP13EST28G09, mRNA sequence.
ConsensusfromContig2110	Alveolata-Lingulodinium_polyedrum_esgi53885898_2	3.30E-16	>BP743678 BP743678 Lingulodinium polyedrum cDNA Lingulodinium polyedrum cDNA clone LP13EST37C08, mRNA sequence.
ConsensusfromContig7084	Alveolata-Lingulodinium_polyedrum_esgi53886334_3	1.10E-22	>BP744114 BP744114 Lingulodinium polyedrum cDNA Lingulodinium polyedrum cDNA clone LP13EST49B03, mRNA sequence.
ConsensusfromContig3000	Alveolata-Paramecium_tetraurelia_strain_d4_2_gi145476441	1.40E-25	>XP_001424243 hypothetical protein [Paramecium tetraurelia strain d4-2].
ConsensusfromContig2293	Alveolata-Paramecium_tetraurelia_strain_d4_2_gi145480475	1.40E-24	>XP_001426260 hypothetical protein [Paramecium tetraurelia strain d4-2].
ConsensusfromContig5119	Alveolata-Paramecium_tetraurelia_strain_d4_2_gi145484499	3.20E-71	>XP_001428259 hypothetical protein [Paramecium tetraurelia strain d4-2].
ConsensusfromContig5133	Alveolata-Paramecium_tetraurelia_strain_d4_2_gi145502321	5.70E-53	>XP_001437139 hypothetical protein [Paramecium tetraurelia strain d4-2].
ConsensusfromContig6926	Alveolata-Paramecium_tetraurelia_strain_d4_2_gi145513136	5.50E-28	>XP_001442479 hypothetical protein [Paramecium tetraurelia strain d4-2].
ConsensusfromContig4781	Alveolata-Paramecium_tetraurelia_strain_d4_2_gi145513478	6.60E-18	>XP_001442650 hypothetical protein [Paramecium tetraurelia strain d4-2].
ConsensusfromContig1991	Alveolata-Paramecium_tetraurelia_strain_d4_2_gi145518051	1.80E-72	>XP_001444903 hypothetical protein [Paramecium tetraurelia strain d4-2].
ConsensusfromContig1992	Alveolata-Paramecium_tetraurelia_strain_d4_2_gi145518051	2.10E-168	>XP_001444903 hypothetical protein [Paramecium tetraurelia strain d4-2].
ConsensusfromContig2309	Alveolata-Paramecium_tetraurelia_strain_d4_2_gi145520060	1.80E-12	>XP_001445891 hypothetical protein [Paramecium tetraurelia strain d4-2].
ConsensusfromContig5225	Alveolata-Paramecium_tetraurelia_strain_d4_2_gi145546368	9.60E-11	>XP_001458867 hypothetical protein [Paramecium tetraurelia strain d4-2].
ConsensusfromContig1949	Alveolata-Paramecium_tetraurelia_strain_d4_2_gi145553124	3.50E-13	>XP_001462237 hypothetical protein [Paramecium tetraurelia strain d4-2].
ConsensusfromContig2247	Alveolata-Perkinsus_marinus_ATCC_50983_gi294868102	2.00E-17	>XP_002765382 hypothetical protein Pmar_PMAR002378 [Perkinsus marinus ATCC 50983].
ConsensusfromContig2811	Alveolata-Perkinsus_marinus_ATCC_50983_gi294876389	5.70E-15	>XP_002767659 hypothetical protein Pmar_PMAR008603 [Perkinsus marinus ATCC 50983].
ConsensusfromContig2074	Alveolata-Perkinsus_marinus_ATCC_50983_gi294879611	3.90E-65	>XP_002768734 nexus protein 1, putative [Perkinsus marinus ATCC 50983].
ConsensusfromContig2272	Alveolata-Perkinsus_marinus_ATCC_50983_gi294885969	2.30E-64	>XP_002771492 cAMP-dependent protein kinase catalytic subunit isoform 2, putative [Perkinsus marinus ATCC 50983].
ConsensusfromContig7447	Alveolata-Perkinsus_marinus_ATCC_50983_gi294887509	1.50E-13	>XP_002772145 amp dependent ligase/synthetase, putative [Perkinsus marinus ATCC 50983].
ConsensusfromContig3129	Alveolata-Perkinsus_marinus_ATCC_50983_gi294889481	4.90E-94	>XP_002772834 beta-tubulin, putative [Perkinsus marinus ATCC 50983].
ConsensusfromContig1944	Alveolata-Perkinsus_marinus_ATCC_50983_gi294894141	6.00E-24	>XP_002774744 hypothetical protein Pmar_PMAR020309 [Perkinsus marinus ATCC 50983].
ConsensusfromContig2035	Alveolata-Perkinsus_marinus_ATCC_50983_gi294894669	7.40E-28	>XP_002774908 membrane associated RING finger, putative [Perkinsus marinus ATCC 50983].
ConsensusfromContig2488	Alveolata-Perkinsus_marinus_ATCC_50983_gi294911603	1.40E-11	>XP_002778018 peroxisomal abc transporter, putative [Perkinsus marinus ATCC 50983].
ConsensusfromContig3184	Alveolata-Perkinsus_marinus_ATCC_50983_gi294917444	4.80E-22	>XP_002778466 cyclophilin, putative [Perkinsus marinus ATCC 50983].
ConsensusfromContig5789	Alveolata-Perkinsus_marinus_ATCC_50983_gi294931439	1.30E-15	>XP_002779875 hypothetical protein Pmar_PMAR002273 [Perkinsus marinus ATCC 50983].
ConsensusfromContig1950	Alveolata-Perkinsus_marinus_ATCC_50983_gi294932263	2.90E-32	>XP_002780185 hypothetical protein Pmar_PMAR019084 [Perkinsus marinus ATCC 50983].
ConsensusfromContig7490	Alveolata-Perkinsus_marinus_ATCC_50983_gi294932732	1.50E-64	>XP_002780414 heat shock protein 70, putative [Perkinsus marinus ATCC 50983].

ConsensusfromContig1963Alveolata-Perkinsus_marinus_ATCC_50983_gi294935707	1.70E-72	>XP_002781499 hypothetical protein Pmar_PMAR015892 [Perkinsus marinus ATCC 50983].
ConsensusfromContig6638Alveolata-Perkinsus_marinus_ATCC_50983_gi294947886	6.50E-25	>XP_002785509 vacuole membrane protein, putative [Perkinsus marinus ATCC 50983].
ConsensusfromContig1506Alveolata-Perkinsus_marinus_ATCC_50983_gi294953203	6.00E-14	>XP_002787646 sodium/calcium exchanger, putative [Perkinsus marinus ATCC 50983].
ConsensusfromContig7273Alveolata-Plasmodium_berghei_str_ANKA_gi68076327	3.60E-16	>XP_680083 hypothetical protein [Plasmodium berghei strain ANKA].
ConsensusfromContig2280Alveolata-Symbiodinium_sp_C3_esContig322_1	1.20E-15	
ConsensusfromContig2202Alveolata-Symbiodinium_sp_C3_esContig529_1	1.10E-54	
ConsensusfromContig5547Alveolata-Symbiodinium_sp_C3_esgi186955945_3	4.40E-24	>FE865971 ZooX20011I16.g_056 Symbiodinium normalized stress library Lambda ZAP II Symbiodinium sp. C3 cDNA 5', mRNA sequence.
ConsensusfromContig5209Alveolata-Symbiodinium_sp_C3_esgi186959088_5	2.70E-27	>FE865756 ZooX20011D21.g_093 Symbiodinium normalized stress library Lambda ZAP II Symbiodinium sp. C3 cDNA 5', mRNA sequence.
ConsensusfromContig6931Alveolata-Symbiodinium_sp_C3_esgi186963101_1	1.20E-25	>FE865810 ZooX20009M18.g_067 Symbiodinium normalized stress library Lambda ZAP II Symbiodinium sp. C3 cDNA 5', mRNA sequence.
ConsensusfromContig2475Alveolata-Symbiodinium_sp_C3_esgi186963953_6	1.30E-14	>FE865500 ZooX20008A17.g_079 Symbiodinium normalized stress library Lambda ZAP II Symbiodinium sp. C3 cDNA 5', mRNA sequence.
ConsensusfromContig2896Alveolata-Symbiodinium_sp_C3_esgi186963953_6	7.60E-17	>FE865500 ZooX20008A17.g_079 Symbiodinium normalized stress library Lambda ZAP II Symbiodinium sp. C3 cDNA 5', mRNA sequence.
ConsensusfromContig1048Alveolata-Tetrahymena_thermophila_gi118346309	1.20E-14	>XP_976852 ubiquitin-activating enzyme E1 family protein [Tetrahymena thermophila].
ConsensusfromContig6842Alveolata-Tetrahymena_thermophila_gi118348690	2.60E-16	>XP_001007820 U-box domain containing protein [Tetrahymena thermophila].
ConsensusfromContig7402Alveolata-Tetrahymena_thermophila_gi118348690	1.50E-33	>XP_001007820 U-box domain containing protein [Tetrahymena thermophila].
ConsensusfromContig5412Alveolata-Tetrahymena_thermophila_gi118356530	1.10E-16	>XP_001011521 hypothetical protein TTHERM_00784630 [Tetrahymena thermophila].
ConsensusfromContig5412Alveolata-Tetrahymena_thermophila_gi118356530	1.10E-16	>XP_001011521 hypothetical protein TTHERM_00784630 [Tetrahymena thermophila].
ConsensusfromContig2342Alveolata-Tetrahymena_thermophila_gi118362306	1.10E-24	>XP_001014380 hypothetical protein TTHERM_00522020 [Tetrahymena thermophila].
ConsensusfromContig3522Alveolata-Tetrahymena_thermophila_gi118373016	6.90E-17	>XP_001019702 Tubulin-tyrosine ligase family protein [Tetrahymena thermophila].
ConsensusfromContig2973Alveolata-Tetrahymena_thermophila_gi118377189	8.90E-14	>XP_001021775 ABC transporter family protein [Tetrahymena thermophila].
ConsensusfromContig4147Alveolata-Tetrahymena_thermophila_gi146164110	5.60E-12	>XP_001013003 Phosphatidylinositol 3- and 4-kinase family protein [Tetrahymena thermophila].
ConsensusfromContig4953Alveolata-Tetrahymena_thermophila_gi146178978	1.40E-12	>XP_001470898 Serine/threonine-protein kinase, putative [Tetrahymena thermophila].
ConsensusfromContig3298Alveolata-Tetrahymena_thermophila_SB210_gi118382267	5.20E-21	>XP_001024292 hypothetical protein [Tetrahymena thermophila SB210].
ConsensusfromContig5488Alveolata-Tetrahymena_thermophila_SB210_gi118382267	2.30E-36	>XP_001024292 hypothetical protein [Tetrahymena thermophila SB210].
ConsensusfromContig8095Alveolata-Tetrahymena_thermophila_SB210_gi118393302	3.20E-14	>XP_001029114 hypothetical protein [Tetrahymena thermophila SB210].
ConsensusfromContig3283Alveolata-Tetrahymena_thermophila_SB210_gi118393302	2.30E-12	>XP_001029114 hypothetical protein [Tetrahymena thermophila SB210].
ConsensusfromContig3952Alveolata-Tetrahymena_thermophila_SB210_gi118393302	1.80E-21	>XP_001029114 hypothetical protein [Tetrahymena thermophila SB210].
ConsensusfromContig5690Alveolata-Tetrahymena_thermophila_SB210_gi118393302	1.40E-17	>XP_001029114 hypothetical protein [Tetrahymena thermophila SB210].
ConsensusfromContig3781Alveolata-Toxoplasma_gondii_ME49_gi237831795	3.00E-15	>XP_002365195 folate/methotrexate transporter, putative [Toxoplasma gondii ME49].
ConsensusfromContig1364Alveolata-Toxoplasma_gondii_ME49_gi237833937	1.70E-12	>XP_002366266 cAMP-dependent protein kinase catalytic subunit, putative [Toxoplasma gondii ME49].
ConsensusfromContig2216Alveolata-Toxoplasma_gondii_ME49_gi237840331	2.50E-13	>XP_002369463 zinc transporter ZIP domain-containing protein [Toxoplasma gondii ME49].
ConsensusfromContig712 Alveolata-Toxoplasma_gondii_ME49_gi237841907	1.10E-14	>XP_002370251 type I fatty acid synthase, putative [Toxoplasma gondii ME49].
ConsensusfromContig1932Alveolata-Toxoplasma_gondii_ME49_gi237841907	3.30E-156	>XP_002370251 type I fatty acid synthase, putative [Toxoplasma gondii ME49].
ConsensusfromContig2312Alveolata-Toxoplasma_gondii_ME49_gi237841907	1.70E-11	>XP_002370251 type I fatty acid synthase, putative [Toxoplasma gondii ME49].
ConsensusfromContig2312Alveolata-Toxoplasma_gondii_ME49_gi237841907	1.70E-11	>XP_002370251 type I fatty acid synthase, putative [Toxoplasma gondii ME49].
ConsensusfromContig2021Amoebozoa-Acanthamoeba_castellanii_tbACL00000192_1	1.10E-34	
ConsensusfromContig7400Amoebozoa-Acanthamoeba_castellanii_tbACL00002330_3	2.00E-17	
ConsensusfromContig2170Amoebozoa-Acanthamoeba_castellanii_tbACL00004442_1	1.30E-52	
ConsensusfromContig2135Amoebozoa-Acanthamoeba_castellanii_tbACL00004658_3	1.20E-42	
ConsensusfromContig6927Amoebozoa-Acanthamoeba_castellanii_tbACL00009058_2	2.50E-33	
ConsensusfromContig1242Amoebozoa-Acanthamoeba_castellanii_tbACL00009431_4	1.60E-13	
ConsensusfromContig1936Amoebozoa-Dictyostelium_discoideum_AX4_gi111226606	8.60E-29	>XP_641288 hypothetical protein DDB_G0280375 [Dictyostelium discoideum AX4].
ConsensusfromContig5110Amoebozoa-Dictyostelium_discoideum_AX4_gi111226606	9.50E-18	>XP_641288 hypothetical protein DDB_G0280375 [Dictyostelium discoideum AX4].
ConsensusfromContig5115Amoebozoa-Dictyostelium_discoideum_AX4_gi66801758	3.60E-18	>XP_629800 hypothetical protein DDB_G0292060 [Dictyostelium discoideum AX4].
ConsensusfromContig4537Amoebozoa-Dictyostelium_discoideum_AX4_gi66802514	4.70E-29	>XP_635129 serine hydroxymethyltransferase [Dictyostelium discoideum AX4].
ConsensusfromContig9912Amoebozoa-Dictyostelium_discoideum_AX4_gi66802578	2.20E-15	>XP_635161 chaperonin containing TCP1 beta subunit [Dictyostelium discoideum AX4].
ConsensusfromContig1994Amoebozoa-Dictyostelium_discoideum_AX4_gi66802974	3.00E-17	>XP_635330 hypothetical protein DDB_G0291688 [Dictyostelium discoideum AX4].
ConsensusfromContig5174Amoebozoa-Dictyostelium_discoideum_AX4_gi66802974	1.50E-16	>XP_635330 hypothetical protein DDB_G0291688 [Dictyostelium discoideum AX4].
ConsensusfromContig2105Amoebozoa-Dictyostelium_discoideum_AX4_gi66802990	3.80E-29	>XP_635338 hypothetical protein DDB_G0291223 [Dictyostelium discoideum AX4].
ConsensusfromContig2678Amoebozoa-Dictyostelium_discoideum_AX4_gi66806459	1.20E-13	>XP_636952 hypothetical protein DDB_G0288041 [Dictyostelium discoideum AX4].
ConsensusfromContig1936Amoebozoa-Dictyostelium_discoideum_AX4_gi66807841	2.30E-19	>XP_637643 vacuolar protein sorting-associated protein 13 family protein [Dictyostelium discoideum AX4].
ConsensusfromContig3049Amoebozoa-Dictyostelium_discoideum_AX4_gi66808855	2.20E-28	>XP_638150 WD40 repeat-containing protein [Dictyostelium discoideum AX4].
ConsensusfromContig3049Amoebozoa-Dictyostelium_discoideum_AX4_gi66808855	2.20E-28	>XP_638150 WD40 repeat-containing protein [Dictyostelium discoideum AX4].
ConsensusfromContig4040Amoebozoa-Dictyostelium_discoideum_AX4_gi66810313	2.30E-20	>XP_638880 actin-like protein [Dictyostelium discoideum AX4].
ConsensusfromContig2114Amoebozoa-Dictyostelium_discoideum_AX4_gi66813336	9.20E-35	>XP_640847 kinesin family member 3 [Dictyostelium discoideum AX4].
ConsensusfromContig5170Amoebozoa-Dictyostelium_discoideum_AX4_gi66814490	2.70E-49	>XP_641424 myosin light chain kinase [Dictyostelium discoideum AX4].
ConsensusfromContig7069Amoebozoa-Dictyostelium_discoideum_AX4_gi66814490	1.10E-14	>XP_641424 myosin light chain kinase [Dictyostelium discoideum AX4].
ConsensusfromContig2175Amoebozoa-Dictyostelium_discoideum_AX4_gi66815339	3.20E-43	>XP_641686 protein kinase A regulatory subunit [Dictyostelium discoideum AX4].
ConsensusfromContig1942Amoebozoa-Dictyostelium_discoideum_AX4_gi66815909	2.90E-12	>XP_641971 IPT/TIG domain-containing protein [Dictyostelium discoideum AX4].
ConsensusfromContig6923Amoebozoa-Dictyostelium_discoideum_AX4_gi66819701	1.50E-18	>XP_643509 hypothetical protein DDB_G0275443 [Dictyostelium discoideum AX4].
ConsensusfromContig2867Amoebozoa-Dictyostelium_discoideum_AX4_gi66820400	2.40E-17	>XP_643820 phosphatidylinositol-4,5-diphosphate 3-kinase [Dictyostelium discoideum AX4].
ConsensusfromContig2624Amoebozoa-Dictyostelium_discoideum_AX4_gi66821367	4.70E-19	>XP_644171 class VII unconventional myosin [Dictyostelium discoideum AX4].
ConsensusfromContig2624Amoebozoa-Dictyostelium_discoideum_AX4_gi66821367	4.70E-19	>XP_644171 class VII unconventional myosin [Dictyostelium discoideum AX4].
ConsensusfromContig6959Amoebozoa-Dictyostelium_discoideum_AX4_gi66824483	1.80E-60	>XP_645596 hypothetical protein DDB_G0271550 [Dictyostelium discoideum AX4].
ConsensusfromContig1954Amoebozoa-Dictyostelium_discoideum_AX4_gi66825131	6.80E-90	>XP_645920 P-type ATPase [Dictyostelium discoideum AX4].
ConsensusfromContig7872Amoebozoa-Dictyostelium_discoideum_AX4_gi66825447	9.80E-29	>XP_646078 hypothetical protein DDB_G0269194 [Dictyostelium discoideum AX4].
ConsensusfromContig6120Amoebozoa-Dictyostelium_discoideum_AX4_gi66825643	7.30E-37	>XP_646176 transcription factor jumonji, jmjC domain-containing protein [Dictyostelium discoideum AX4].
ConsensusfromContig3751Amoebozoa-Dictyostelium_discoideum_AX4_gi66826965	6.70E-11	>XP_646837 hypothetical protein DDB_G0268922 [Dictyostelium discoideum AX4].
ConsensusfromContig1972Amoebozoa-Dictyostelium_discoideum_AX4_gi66827587	1.90E-31	>XP_647148 hypothetical protein DDB_G0267588 [Dictyostelium discoideum AX4].
ConsensusfromContig2960Amoebozoa-Dictyostelium_purpureum_jgi11305	5.20E-17	
ConsensusfromContig1934Amoebozoa-Dictyostelium_purpureum_jgi12712	3.30E-13	
ConsensusfromContig1520Amoebozoa-Dictyostelium_purpureum_jgi148338	3.20E-17	
ConsensusfromContig4238Amoebozoa-Dictyostelium_purpureum_jgi148338	4.90E-22	
ConsensusfromContig6969Amoebozoa-Dictyostelium_purpureum_jgi149505	1.90E-65	
ConsensusfromContig1940Amoebozoa-Dictyostelium_purpureum_jgi154579	6.30E-67	
ConsensusfromContig5539Amoebozoa-Dictyostelium_purpureum_jgi155311	4.10E-13	
ConsensusfromContig1984Amoebozoa-Dictyostelium_purpureum_jgi156766	1.30E-16	
ConsensusfromContig3237Amoebozoa-Dictyostelium_purpureum_jgi158675	1.40E-52	
ConsensusfromContig3586Amoebozoa-Dictyostelium_purpureum_jgi27799	2.90E-14	
ConsensusfromContig599 Amoebozoa-Dictyostelium_purpureum_jgi32017	7.50E-24	
ConsensusfromContig5355Amoebozoa-Dictyostelium_purpureum_jgi33395	2.20E-46	
ConsensusfromContig3303Amoebozoa-Dictyostelium_purpureum_jgi36746	7.10E-14	
ConsensusfromContig2068Amoebozoa-Dictyostelium_purpureum_jgi38363	2.30E-13	
ConsensusfromContig2113Amoebozoa-Dictyostelium_purpureum_jgi38363	6.00E-21	
ConsensusfromContig2314Amoebozoa-Dictyostelium_purpureum_jgi38363	7.50E-15	
ConsensusfromContig1996Amoebozoa-Dictyostelium_purpureum_jgi41242	6.10E-22	
ConsensusfromContig2025Amoebozoa-Dictyostelium_purpureum_jgi41316	1.30E-47	
ConsensusfromContig6938Amoebozoa-Dictyostelium_purpureum_jgi46365	4.10E-17	
ConsensusfromContig6284Amoebozoa-Dictyostelium_purpureum_jgi47412	1.00E-12	
ConsensusfromContig1957Amoebozoa-Dictyostelium_purpureum_jgi52275	6.10E-158	
ConsensusfromContig2691Amoebozoa-Dictyostelium_purpureum_jgi52275	7.50E-12	
ConsensusfromContig5714Amoebozoa-Dictyostelium_purpureum_jgi57034	2.70E-39	
ConsensusfromContig1976Amoebozoa-Dictyostelium_purpureum_jgi57851	9.50E-99	
ConsensusfromContig6598Amoebozoa-Dictyostelium_purpureum_jgi59022	1.50E-19	
ConsensusfromContig1944Amoebozoa-Dictyostelium_purpureum_jgi80926	3.90E-50	
ConsensusfromContig5222Amoebozoa-Dictyostelium_purpureum_jgi9137	1.80E-34	
ConsensusfromContig1950Amoebozoa-Dictyostelium_purpureum_jgi97064	1.90E-61	
ConsensusfromContig7194Amoebozoa-Entamoeba_histolytica_HM_1_IMSS_gi183234913	1.60E-14	>XP_001914113 hypothetical protein [Entamoeba histolytica HM-1:IMSS].
ConsensusfromContig2232Amoebozoa-Entamoeba_histolytica_HM_1_IMSS_gi67473696	5.70E-29	>XP_652598 Rab family GTPase [Entamoeba histolytica HM-1:IMSS].
ConsensusfromContig2057Amoebozoa-Hartmannella_vermiformis_tbHVL00000742_3	5.40E-13	
ConsensusfromContig6517Amoebozoa-Hartmannella_vermiformis_tbHVL00001466_1	1.00E-17	

ConsensusfromContig2646Amoebozoa-Hartmannella_vermiformis_tbHVL00001568_3	3.40E-38	
ConsensusfromContig2350Amoebozoa-Hartmannella_vermiformis_tbHVL00002403_2	1.20E-11	
ConsensusfromContig3654Amoebozoa-Hartmannella_vermiformis_tbHVL00004220_3	4.90E-32	
ConsensusfromContig687 Amoebozoa-Hartmannella_vermiformis_tbHVL00004644_3	3.60E-15	
ConsensusfromContig2665Amoebozoa-Hyperamoeba_dachnaya_tbHDL00000478_5	1.90E-14	
ConsensusfromContig6949Amoebozoa-Hyperamoeba_sp_tbHSL00000441_4	1.20E-16	
ConsensusfromContig2410Amoebozoa-Hyperamoeba_sp_tbHSL00000707_6	1.90E-25	
ConsensusfromContig5970Amoebozoa-Hyperamoeba_sp_tbHSL00000775_2	1.50E-26	
ConsensusfromContig2103Amoebozoa-Hyperamoeba_sp_tbHSL00001902_6	7.30E-21	
ConsensusfromContig5138Amoebozoa-Hyperamoeba_sp_tbHSL00001902_6	1.80E-11	
ConsensusfromContig7104Amoebozoa-Mastigamoeba_balamuthi_tbMBL00001750_1	5.80E-12	
ConsensusfromContig5156Amoebozoa-Mastigamoeba_balamuthi_tbMBL00003306_3	3.80E-22	
ConsensusfromContig9493Amoebozoa-Mastigamoeba_balamuthi_tbMBL00004046_2	3.00E-16	
ConsensusfromContig9493Amoebozoa-Mastigamoeba_balamuthi_tbMBL00004046_2	3.00E-16	
ConsensusfromContig9493Amoebozoa-Mastigamoeba_balamuthi_tbMBL00004046_2	3.00E-16	
ConsensusfromContig5148Amoebozoa-Mastigamoeba_balamuthi_tbMBL00005987_1	1.10E-29	
ConsensusfromContig1317Amoebozoa-Physarum_polycephalum_tbPPL00000552_5	4.50E-11	
ConsensusfromContig2191Amoebozoa-Physarum_polycephalum_tbPPL00001279_3	6.90E-11	
ConsensusfromContig2397Amoebozoa-Physarum_polycephalum_tbPPL00001286_1	2.10E-34	
ConsensusfromContig1180Amoebozoa-Physarum_polycephalum_tbPPL00001990_2	1.10E-12	
ConsensusfromContig5656Amoebozoa-Physarum_polycephalum_tbPPL00002323_1	2.80E-16	
ConsensusfromContig2754Amoebozoa-Physarum_polycephalum_tbPPL00002834_2	3.20E-12	
ConsensusfromContig3682Amoebozoa-Physarum_polycephalum_tbPPL00002990_3	6.20E-19	
ConsensusfromContig4275Amoebozoa-Physarum_polycephalum_tbPPL00003133_1	1.60E-15	
ConsensusfromContig5294Amoebozoa-Physarum_polycephalum_tbPPL00003133_1	2.00E-21	
ConsensusfromContig5769Amoebozoa-Polysphondylium_pallidum_tbPSL00000136_3	7.60E-25	
ConsensusfromContig2320Amoebozoa-Polysphondylium_pallidum_tbPSL00000449_1	3.10E-16	
ConsensusfromContig3256Archaea-Aciduliprofundum_boonei_T469_gi254167226	7.60E-12	>ZP_04874079 pyrrolidone-carboxylate peptidase [Aciduliprofundum boonei T469].
ConsensusfromContig7348Archaea-Haloterrigena_turkmenica_DSM_5511_gi284167239	5.20E-12	>YP_003405517 hypothetical protein Htur_3996 [Haloterrigena turkmenica DSM 5511].
ConsensusfromContig4958Archaea-Methanosarcina_barkeri_str_Fusaro_gi73669489	1.10E-14	>YP_305504 cell surface protein [Methanosarcina barkeri str. Fusaro].
ConsensusfromContig2132Archaea-Nitrosopumilus_maritimus_SCM1_gi161527665	6.00E-16	>YP_001581491 helix-turn-helix domain-containing protein [Nitrosopumilus maritimus SCM1].
ConsensusfromContig6447Archaea-Sulfolobus_islandicus_YN1551_gi229582572	6.30E-16	>YP_002840971 Ankyrin [Sulfolobus islandicus Y.N.15.51].
ConsensusfromContig2072BacteriaUnclassified-Candidatus_Cloacamonas_acidaminovorans_gi218961083	2.80E-14	>YP_001740858 Peptidylarginine deiminase precursor (modular protein) [Candidatus Cloacamonas acidaminovorans].
ConsensusfromContig5315BacteriaUnclassified-Candidatus_Cloacamonas_acidaminovorans_gi218961083	3.00E-30	>YP_001740858 Peptidylarginine deiminase precursor (modular protein) [Candidatus Cloacamonas acidaminovorans].
ConsensusfromContig5343BacteriaUnclassified-Candidatus_Poribacteria_sp_WGA_A3_gi284097424	6.80E-13	>ZP_06385534 conserved hypothetical protein [Candidatus Poribacteria sp. WGA-A3].
ConsensusfromContig2094BacteriaUnclassified-Candidatus_Poribacteria_sp_WGA_A3_gi284097512	3.10E-11	>ZP_06385593 hypothetical protein POR_0182 [Candidatus Poribacteria sp. WGA-A3].
ConsensusfromContig3471BacteriaUnclassified-Candidatus_Poribacteria_sp_WGA_A3_gi284097512	1.90E-23	>ZP_06385593 hypothetical protein POR_0182 [Candidatus Poribacteria sp. WGA-A3].
ConsensusfromContig6982BacteriaUnclassified-Candidatus_Poribacteria_sp_WGA_A3_gi284097512	2.50E-24	>ZP_06385593 hypothetical protein POR_0182 [Candidatus Poribacteria sp. WGA-A3].
ConsensusfromContig6982BacteriaUnclassified-Candidatus_Poribacteria_sp_WGA_A3_gi284097512	2.50E-24	>ZP_06385593 hypothetical protein POR_0182 [Candidatus Poribacteria sp. WGA-A3].
ConsensusfromContig2331BacteriaUnclassified-Candidatus_Poribacteria_sp_WGA_A3_gi284104059	5.10E-22	>ZP_06386125 conserved hypothetical protein [Candidatus Poribacteria sp. WGA-A3].
ConsensusfromContig5718BacteriaUnclassified-Candidatus_Poribacteria_sp_WGA_A3_gi284114311	3.40E-17	>ZP_06386663 phytanoyl-CoA dioxygenase family protein [Candidatus Poribacteria sp. WGA-A3].
ConsensusfromContig5361BacteriaUnclassified-Candidatus_Poribacteria_sp_WGA_A3_gi284126006	1.70E-14	>ZP_06386997 hypothetical protein POR_1603 [Candidatus Poribacteria sp. WGA-A3].
ConsensusfromContig4810BacteriaUnclassified-Thermobaculum_terrenum_ATCC_BAA_798_gi269839625	9.70E-14	>YP_003324317 NAD-dependent epimerase/dehydratase [Thermobaculum terrenum ATCC BAA-798].
ConsensusfromContig5100BacteriaUnclassified-Thermobaculum_terrenum_ATCC_BAA_798_gi269926788	1.20E-25	>YP_003323411 serine/threonine protein kinase [Thermobaculum terrenum ATCC BAA-798].
ConsensusfromContig3369BacteriaUnclassified-Thermobaculum_terrenum_ATCC_BAA_798_gi269926789	1.30E-19	>YP_003323412 serine/threonine protein kinase [Thermobaculum terrenum ATCC BAA-798].
ConsensusfromContig1783BacteroidetesChlorobi-Algoriphagus_sp_PR1_gi126646890	9.30E-20	>ZP_01719400 probable ribonucleoside-diphosphate reductase small chain [Algoriphagus sp. PR1].
ConsensusfromContig1981BacteroidetesChlorobi-Algoriphagus_sp_PR1_gi126648424	2.40E-87	>ZP_01720911 hypothetical protein ALPR1_08448 [Algoriphagus sp. PR1].
ConsensusfromContig5149BacteroidetesChlorobi-Bacteroides_cellulosilyticus_DSM_14838_gi224536577	1.10E-19	>ZP_03677116 hypothetical protein BACCELL_01452 [Bacteroides cellulosilyticus DSM 14838].
ConsensusfromContig2313BacteroidetesChlorobi-Bacteroides_cellulosilyticus_DSM_14838_gi224539787	7.10E-40	>ZP_03680326 hypothetical protein BACCELL_04696 [Bacteroides cellulosilyticus DSM 14838].
ConsensusfromContig5099BacteroidetesChlorobi-Bacteroides_cellulosilyticus_DSM_14838_gi224540408	9.60E-23	>ZP_03680947 hypothetical protein BACCELL_05321 [Bacteroides cellulosilyticus DSM 14838].
ConsensusfromContig6988BacteroidetesChlorobi-Bacteroides_finegoldii_DSM_17565_gi255690205	1.80E-18	>ZP_05413880 xylosidase/arabinosidase [Bacteroides finegoldii DSM 17565].
ConsensusfromContig1958BacteroidetesChlorobi-Bacteroides_fragilis_3_1_12_gi255010034	2.50E-51	>ZP_05282160 putative alpha-L-arabinofuranosidase [Bacteroides fragilis 3_1_12].
ConsensusfromContig3903BacteroidetesChlorobi-Bacteroides_fragilis_NCTC_9343_gi60680313	9.20E-16	>YP_210457 putative glycosyl hydrolase [Bacteroides fragilis NCTC 9343].
ConsensusfromContig1256BacteroidetesChlorobi-Bacteroides_intestinalis_DSM_17393_gi189466638	3.90E-27	>ZP_03015423 hypothetical protein BACINT_03013 [Bacteroides intestinalis DSM 17393].
ConsensusfromContig2419BacteroidetesChlorobi-Bacteroides_intestinalis_DSM_17393_gi189467437	7.20E-20	>ZP_03016222 hypothetical protein BACINT_03826 [Bacteroides intestinalis DSM 17393].
ConsensusfromContig1960BacteroidetesChlorobi-Bacteroides_plebeius_DSM_17135_gi198275801	2.80E-13	>ZP_03208332 hypothetical protein BACPLE_01976 [Bacteroides plebeius DSM 17135].
ConsensusfromContig4703BacteroidetesChlorobi-Bacteroides_sp_1_1_6_gi253571091	9.60E-12	>ZP_04848498 glutaminase [Bacteroides sp. 1_1_6].
ConsensusfromContig2026BacteroidetesChlorobi-Bacteroides_sp_2_1_33B_gi262380955	1.60E-24	>ZP_06074093 PBSX family phage terminase, large subunit [Bacteroides sp. 2_1_33B].
ConsensusfromContig2178BacteroidetesChlorobi-Bacteroides_sp_2_1_33B_gi262380955	1.80E-56	>ZP_06074093 PBSX family phage terminase, large subunit [Bacteroides sp. 2_1_33B].
ConsensusfromContig7218BacteroidetesChlorobi-Bacteroides_sp_2_1_33B_gi262381464	1.60E-15	>ZP_06074602 endoribonuclease L-PSP [Bacteroides sp. 2_1_33B].
ConsensusfromContig4796BacteroidetesChlorobi-Bacteroides_sp_3_1_19_gi298377335	1.10E-12	>ZP_06987288 alpha-rhamnosidase [Bacteroides sp. 3_1_19].
ConsensusfromContig2761BacteroidetesChlorobi-Bacteroides_sp_3_2_5_gi253564229	7.00E-27	>ZP_04841686 coagulation factor 5/8 type [Bacteroides sp. 3_2_5].
ConsensusfromContig1752BacteroidetesChlorobi-Bacteroides_sp_4_3_47FAA_gi254881475	3.50E-12	>ZP_05254185 alpha-galactosidase [Bacteroides sp. 4_3_47FAA].
ConsensusfromContig3171BacteroidetesChlorobi-Bacteroides_sp_9_1_42FAA_gi237709027	8.60E-31	>ZP_04539508 alpha-L-fucosidase [Bacteroides sp. 9_1_42FAA].
ConsensusfromContig5134BacteroidetesChlorobi-Bacteroides_sp_D2_gi260172557	1.50E-15	>ZP_05758969 Alpha-galactosidase [Bacteroides sp. D2].
ConsensusfromContig5126BacteroidetesChlorobi-Bacteroides_sp_D2_gi260172974	1.50E-21	>ZP_05759386 hypothetical protein BacD2_13978 [Bacteroides sp. D2].
ConsensusfromContig2010BacteroidetesChlorobi-Bacteroides_sp_D22_gi298481303	5.30E-52	>ZP_06999496 conserved hypothetical protein [Bacteroides sp. D22].
ConsensusfromContig2635BacteroidetesChlorobi-Bacteroides_uniformis_ATCC_8492_gi160890689	4.40E-14	>ZP_02071692 hypothetical protein BACUNI_03134 [Bacteroides uniformis ATCC 8492].
ConsensusfromContig6815BacteroidetesChlorobi-Bacteroidetes_oral_taxon_274_str_F0058_gi298372182	3.30E-18	>ZP_06982172 TPR repeat protein [Bacteroidetes oral taxon 274 str. F0058].
ConsensusfromContig1728BacteroidetesChlorobi-Capnocytophaga_gingivalis_ATCC_33624_gi228471550	5.40E-36	>ZP_04056325 ABC transporter, ATP-binding protein, MsbA family [Capnocytophaga gingivalis ATCC 33624].
ConsensusfromContig2030BacteroidetesChlorobi-Chitinophaga_pinensis_DSM_2588_gi256423975	8.90E-11	>YP_003124628 Beta-N-acetylhexosaminidase [Chitinophaga pinensis DSM 2588].
ConsensusfromContig7260BacteroidetesChlorobi-Chlorobium_chlorochromatii_CaD3_gi78188168	6.80E-17	>YP_378506 glutamate synthase subunit beta [Chlorobium chlorochromatii CaD3].
ConsensusfromContig6600BacteroidetesChlorobi-Chryseobacterium_gleum_ATCC_35910_gi227367629	2.70E-11	>ZP_03851159 conserved hypothetical protein [Chryseobacterium gleum ATCC 35910].
ConsensusfromContig1408BacteroidetesChlorobi-Croceibacter_atlanticus_HTCC2559_gi298207669	5.20E-34	>YP_003715848 hypothetical protein CA2559_05425 [Croceibacter atlanticus HTCC2559].
ConsensusfromContig2302BacteroidetesChlorobi-Dokdonia_donghaensis_MED134_gi86132154	1.60E-14	>ZP_01050750 hypothetical protein MED134_12246 [Dokdonia donghaensis MED134].
ConsensusfromContig5159BacteroidetesChlorobi-Dyadobacter_fermentans_DSM_18053_gi255034294	7.10E-19	>YP_003084915 selenocysteine synthase (seryl-tRNASer selenium transferase)-like protein [Dyadobacter fermentans DSM 18053].
ConsensusfromContig2136BacteroidetesChlorobi-Dyadobacter_fermentans_DSM_18053_gi255035681	6.00E-15	>YP_003086302 Phytanoyl-CoA dioxygenase [Dyadobacter fermentans DSM 18053].
ConsensusfromContig6811BacteroidetesChlorobi-Dyadobacter_fermentans_DSM_18053_gi255036059	1.30E-25	>YP_003086680 alpha-L-rhamnosidase [Dyadobacter fermentans DSM 18053].
ConsensusfromContig4853BacteroidetesChlorobi-Dyadobacter_fermentans_DSM_18053_gi255036060	1.00E-14	>YP_003086681 Phytanoyl-CoA dioxygenase [Dyadobacter fermentans DSM 18053].
ConsensusfromContig5103BacteroidetesChlorobi-Dyadobacter_fermentans_DSM_18053_gi255036060	5.50E-30	>YP_003086681 Phytanoyl-CoA dioxygenase [Dyadobacter fermentans DSM 18053].
ConsensusfromContig7238BacteroidetesChlorobi-Dyadobacter_fermentans_DSM_18053_gi255036202	5.50E-15	>YP_003086823 selenocysteine synthase (seryl-tRNASer selenium transferase)-like protein [Dyadobacter fermentans DSM 18053].
ConsensusfromContig2196BacteroidetesChlorobi-Dyadobacter_fermentans_DSM_18053_gi255036622	3.30E-15	>YP_003087243 hypothetical protein Dfer_2863 [Dyadobacter fermentans DSM 18053].
ConsensusfromContig2866BacteroidetesChlorobi-Flavobacteria_bacterium_BAL38_gi126662511	1.70E-11	>ZP_01733510 glycosyl hydrolase [Flavobacteria bacterium BAL38].
ConsensusfromContig1118BacteroidetesChlorobi-Flavobacteriales_bacterium_ALC_1_gi163786628	1.10E-27	>ZP_02181076 ribonucleoside-diphosphate reductase , beta subunit 1 [Flavobacteriales bacterium ALC-1].
ConsensusfromContig7295BacteroidetesChlorobi-Flavobacteriales_bacterium_HTCC2170_gi88710902	4.00E-22	>ZP_01104990 hypothetical protein FB2170_02290 [Flavobacteriales bacterium HTCC2170].
ConsensusfromContig2663BacteroidetesChlorobi-Flavobacteriales_bacterium_HTCC2170_gi88711390	2.00E-18	>ZP_01105478 hypothetical protein FB2170_04730 [Flavobacteriales bacterium HTCC2170].
ConsensusfromContig3124BacteroidetesChlorobi-Flavobacteriales_bacterium_HTCC2170_gi88711509	2.80E-28	>ZP_01105597 hypothetical protein FB2170_05325 [Flavobacteriales bacterium HTCC2170].
ConsensusfromContig2102BacteroidetesChlorobi-Flavobacteriales_bacterium_HTCC2170_gi88713912	2.80E-26	>ZP_01107992 hypothetical protein FB2170_01387 [Flavobacteriales bacterium HTCC2170].
ConsensusfromContig5174BacteroidetesChlorobi-Flavobacteriales_bacterium_HTCC2170_gi88713912	2.20E-21	>ZP_01107992 hypothetical protein FB2170_01387 [Flavobacteriales bacterium HTCC2170].
ConsensusfromContig4607BacteroidetesChlorobi-Flavobacterium_johnsoniae_UW101_gi146301131	1.40E-11	>YP_001195722 glycoside hydrolase family 3 protein [Flavobacterium johnsoniae UW101].
ConsensusfromContig2002BacteroidetesChlorobi-Flavobacterium_johnsoniae_UW101_gi146301288	3.80E-38	>YP_001195879 hypothetical protein Fjoh_3546 [Flavobacterium johnsoniae UW101].
ConsensusfromContig5112BacteroidetesChlorobi-Gramella_forsetii_KT0803_gi120436187	4.10E-55	>YP_861873 hyalin domain-containing protein [Gramella forsetii KT0803].
ConsensusfromContig2179BacteroidetesChlorobi-Gramella_forsetii_KT0803_gi120436806	3.10E-45	>YP_862492 phage DNA modification methylase [Gramella forsetii KT0803].
ConsensusfromContig1940BacteroidetesChlorobi-Kordia_algicida_OT_1_gi163755917	2.70E-49	>ZP_02163034 Cell wall hydrolase/autolysin [Kordia algicida OT-1].
ConsensusfromContig2136BacteroidetesChlorobi-Microscilla_marina_ATCC_23134_gi124002164	2.60E-56	>ZP_01687018 membrane-associated lipoprotein precurser [Microscilla marina ATCC 23134].
ConsensusfromContig5714BacteroidetesChlorobi-Microscilla_marina_ATCC_23134_gi124002164	4.70E-30	>ZP_01687018 membrane-associated lipoprotein precurser [Microscilla marina ATCC 23134].
ConsensusfromContig5767BacteroidetesChlorobi-Microscilla_marina_ATCC_23134_gi124002164	1.50E-13	>ZP_01687018 membrane-associated lipoprotein precurser [Microscilla marina ATCC 23134].
ConsensusfromContig2067BacteroidetesChlorobi-Parabacteroides_johnsonii_DSM_18315_gi218258437	2.90E-22	>ZP_03474816 hypothetical protein PRABACTJOHN_00471 [Parabacteroides johnsonii DSM 18315].
ConsensusfromContig6164BacteroidetesChlorobi-Parabacteroides_merdae_ATCC_43184_gi154489987	1.40E-28	>ZP_02030248 hypothetical protein PARMER_00216 [Parabacteroides merdae ATCC 43184].
ConsensusfromContig5359BacteroidetesChlorobi-Parabacteroides_merdae_ATCC_43184_gi154492008	6.10E-20	>ZP_02031634 hypothetical protein PARMER_01639 [Parabacteroides merdae ATCC 43184].

ConsensusfromContig2680BacteroidetesChlorobi-Pedobacter_heparinus_DSM_2366_gi255530878	7.60E-11	>YP_003091250 hypothetical protein Phep_0966 [Pedobacter heparinus DSM 2366].
ConsensusfromContig6041BacteroidetesChlorobi-Pedobacter_heparinus_DSM_2366_gi255531479	6.10E-15	>YP_003091851 Phytanoyl-CoA dioxygenase [Pedobacter heparinus DSM 2366].
ConsensusfromContig2387BacteroidetesChlorobi-Pedobacter_heparinus_DSM_2366_gi255532585	4.40E-15	>YP_003092957 glycosyl hydrolase family 88 [Pedobacter heparinus DSM 2366].
ConsensusfromContig1108BacteroidetesChlorobi-Pedobacter_heparinus_DSM_2366_gi255532869	3.40E-11	>YP_003093241 NHL repeat containing protein [Pedobacter heparinus DSM 2366].
ConsensusfromContig2099BacteroidetesChlorobi-Pedobacter_heparinus_DSM_2366_gi255533375	8.30E-26	>YP_003093747 hypothetical protein Phep_3494 [Pedobacter heparinus DSM 2366].
ConsensusfromContig5096BacteroidetesChlorobi-Pedobacter_sp_BAL39_gi149279048	5.00E-26	>ZP_01885182 peptidase S15 [Pedobacter sp. BAL39].
ConsensusfromContig2371BacteroidetesChlorobi-Polaribacter_irgensii_23_P_gi88801469	7.00E-17	>ZP_01116997 AAA ATPase, CDC48 [Polaribacter irgensii 23-P].
ConsensusfromContig5109BacteroidetesChlorobi-Polaribacter_irgensii_23_P_gi88802112	2.40E-64	>ZP_01117640 sulfate transporter [Polaribacter irgensii 23-P].
ConsensusfromContig3540BacteroidetesChlorobi-Prevotella_melaninogenica_ATCC_25845_gi252120629	1.30E-15	>ZP_04834251 surface antigen BspA [Prevotella melaninogenica ATCC 25845].
ConsensusfromContig1959BacteroidetesChlorobi-Psychroflexus_torquis_ATCC_700755_gi91219288	2.40E-15	>ZP_01255997 hypothetical protein P700755_21651 [Psychroflexus torquis ATCC 700755].
ConsensusfromContig9743BacteroidetesChlorobi-Psychroflexus_torquis_ATCC_700755_gi91219368	5.30E-14	>ZP_01256050 hypothetical protein P700755_24321 [Psychroflexus torquis ATCC 700755].
ConsensusfromContig9743BacteroidetesChlorobi-Psychroflexus_torquis_ATCC_700755_gi91219368	5.30E-14	>ZP_01256050 hypothetical protein P700755_24321 [Psychroflexus torquis ATCC 700755].
ConsensusfromContig5189BacteroidetesChlorobi-Psychroflexus_torquis_ATCC_700755_gi91221878	5.30E-23	>ZP_01257512 hypothetical protein P700755_29183 [Psychroflexus torquis ATCC 700755].
ConsensusfromContig6954BacteroidetesChlorobi-Rhodothermus_marinus_DSM_4252_gi268315846	5.10E-17	>YP_003289565 hypothetical protein Rmar_0271 [Rhodothermus marinus DSM 4252].
ConsensusfromContig1027BacteroidetesChlorobi-Rhodothermus_marinus_DSM_4252_gi268316196	4.20E-14	>YP_003289915 phenazine biosynthesis protein PhzF family [Rhodothermus marinus DSM 4252].
ConsensusfromContig1982BacteroidetesChlorobi-Robiginitalea_biformata_HTCC2501_gi260061206	3.10E-15	>YP_003194286 hypothetical protein RB2501_06395 [Robiginitalea biformata HTCC2501].
ConsensusfromContig3558BacteroidetesChlorobi-Robiginitalea_biformata_HTCC2501_gi260061943	2.10E-12	>YP_003195023 putative secreted protein [Robiginitalea biformata HTCC2501].
ConsensusfromContig6450BacteroidetesChlorobi-Robiginitalea_biformata_HTCC2501_gi260061943	6.30E-11	>YP_003195023 putative secreted protein [Robiginitalea biformata HTCC2501].
ConsensusfromContig7099BacteroidetesChlorobi-Robiginitalea_biformata_HTCC2501_gi260062594	1.20E-29	>YP_003195674 hypothetical protein RB2501_13424 [Robiginitalea biformata HTCC2501].
ConsensusfromContig2240BacteroidetesChlorobi-Robiginitalea_biformata_HTCC2501_gi260063394	2.90E-29	>YP_003196474 hypothetical protein RB2501_01256 [Robiginitalea biformata HTCC2501].
ConsensusfromContig5464BacteroidetesChlorobi-Salinibacter_ruber_DSM_13855_gi83815052	1.70E-12	>YP_445269 penicillin amidase superfamily protein [Salinibacter ruber DSM 13855].
ConsensusfromContig6414BacteroidetesChlorobi-Spirosoma_linguale_DSM_74_gi284005864	2.70E-12	>YP_003391683 oxidoreductase molybdopterin binding protein [Spirosoma linguale DSM 74].
ConsensusfromContig2063BacteroidetesChlorobi-Spirosoma_linguale_DSM_74_gi284035814	9.20E-12	>YP_003385744 glycosyl transferase family 2 [Spirosoma linguale DSM 74].
ConsensusfromContig2510BacteroidetesChlorobi-Spirosoma_linguale_DSM_74_gi284036118	4.50E-12	>YP_003386048 fumarylacetoacetate (FAA) hydrolase [Spirosoma linguale DSM 74].
ConsensusfromContig4349BacteroidetesChlorobi-Spirosoma_linguale_DSM_74_gi284036262	1.60E-12	>YP_003386192 hypothetical protein Slin_1343 [Spirosoma linguale DSM 74].
ConsensusfromContig4558BacteroidetesChlorobi-Spirosoma_linguale_DSM_74_gi284036262	3.60E-15	>YP_003386192 hypothetical protein Slin_1343 [Spirosoma linguale DSM 74].
ConsensusfromContig2006BacteroidetesChlorobi-Spirosoma_linguale_DSM_74_gi284036778	4.80E-46	>YP_003386708 protein of unknown function DUF323 [Spirosoma linguale DSM 74].
ConsensusfromContig1955BacteroidetesChlorobi-Spirosoma_linguale_DSM_74_gi284037515	6.80E-18	>YP_003387445 glycosyl hydrolase BNR repeat-containing protein [Spirosoma linguale DSM 74].
ConsensusfromContig3158BacteroidetesChlorobi-Spirosoma_linguale_DSM_74_gi284037859	4.70E-22	>YP_003387789 hypothetical protein Slin_2978 [Spirosoma linguale DSM 74].
ConsensusfromContig3176BacteroidetesChlorobi-Spirosoma_linguale_DSM_74_gi284037859	2.20E-12	>YP_003387789 hypothetical protein Slin_2978 [Spirosoma linguale DSM 74].
ConsensusfromContig2420BacteroidetesChlorobi-Spirosoma_linguale_DSM_74_gi284038456	4.90E-17	>YP_003388386 alpha-L-rhamnosidase [Spirosoma linguale DSM 74].
ConsensusfromContig7117BacteroidetesChlorobi-Spirosoma_linguale_DSM_74_gi284038898	3.10E-23	>YP_003388828 glycoside hydrolase family 2 sugar binding protein [Spirosoma linguale DSM 74].
ConsensusfromContig2309BacteroidetesChlorobi-Zunongwangia_profunda_SM_A87_gi295133599	5.00E-14	>YP_003584275 selenocysteine synthase (seryl-tRNASer selenium transferase) [Zunongwangia profunda SM-A87].
ConsensusfromContig2439BacteroidetesChlorobi-Zunongwangia_profunda_SM_A87_gi295134875	3.00E-11	>YP_003585551 beta-glucosidase [Zunongwangia profunda SM-A87].
ConsensusfromContig4507ChlamydiaeVerrucomicrobia-bacterium_Ellin514_gi223935677	1.00E-16	>ZP_03627593 Sel1 domain protein repeat-containing protein [bacterium Ellin514].
ConsensusfromContig5133ChlamydiaeVerrucomicrobia-bacterium_Ellin514_gi223936752	1.30E-78	>ZP_03628662 putative esterase [bacterium Ellin514].
ConsensusfromContig5192ChlamydiaeVerrucomicrobia-bacterium_Ellin514_gi223937316	2.30E-29	>ZP_03629222 hypothetical protein Cflav_PD3526 [bacterium Ellin514].
ConsensusfromContig2261ChlamydiaeVerrucomicrobia-bacterium_Ellin514_gi223937347	4.70E-23	>ZP_03629252 conserved hypothetical protein [bacterium Ellin514].
ConsensusfromContig2870ChlamydiaeVerrucomicrobia-bacterium_Ellin514_gi223937347	8.30E-23	>ZP_03629252 conserved hypothetical protein [bacterium Ellin514].
ConsensusfromContig6967ChlamydiaeVerrucomicrobia-bacterium_Ellin514_gi223937634	1.00E-11	>ZP_03629536 alpha-L-rhamnosidase [bacterium Ellin514].
ConsensusfromContig4602ChlamydiaeVerrucomicrobia-bacterium_Ellin514_gi223939786	1.50E-11	>ZP_03631657 acetylornithine and succinylornithine aminotransferase [bacterium Ellin514].
ConsensusfromContig4781ChlamydiaeVerrucomicrobia-bacterium_Ellin514_gi223939786	7.30E-24	>ZP_03631657 acetylornithine and succinylornithine aminotransferase [bacterium Ellin514].
ConsensusfromContig1990ChlamydiaeVerrucomicrobia-Chlamydia_muridarum_Nigg_gi29337301	1.70E-18	>NP_296498 hypothetical protein TC0114 [Chlamydia muridarum Nigg].
ConsensusfromContig1963ChlamydiaeVerrucomicrobia-Chlamydophila_caviae_GPIC_gi29839958	6.90E-16	>NP_829064 30S ribosomal protein S7 [Chlamydophila caviae GPIC].
ConsensusfromContig1941ChlamydiaeVerrucomicrobia-Chthoniobacter_flavus_Ellin428_gi196228361	9.20E-14	>ZP_03127228 Exo-poly-alpha-galacturonosidase [Chthoniobacter flavus Ellin428].
ConsensusfromContig6591ChlamydiaeVerrucomicrobia-Chthoniobacter_flavus_Ellin428_gi196228954	6.30E-16	>ZP_03127820 beta-lactamase [Chthoniobacter flavus Ellin428].
ConsensusfromContig1802ChlamydiaeVerrucomicrobia-Chthoniobacter_flavus_Ellin428_gi196230743	1.10E-25	>ZP_03129604 protein of unknown function DUF1501 [Chthoniobacter flavus Ellin428].
ConsensusfromContig1802ChlamydiaeVerrucomicrobia-Chthoniobacter_flavus_Ellin428_gi196230743	1.10E-25	>ZP_03129604 protein of unknown function DUF1501 [Chthoniobacter flavus Ellin428].
ConsensusfromContig2039ChlamydiaeVerrucomicrobia-Chthoniobacter_flavus_Ellin428_gi196232211	6.40E-12	>ZP_03131065 hypothetical protein CfE428DRAFT_4231 [Chthoniobacter flavus Ellin428].
ConsensusfromContig2637ChlamydiaeVerrucomicrobia-Chthoniobacter_flavus_Ellin428_gi196232340	7.60E-12	>ZP_03131194 putative secreted protein, putative xanthan lyase related [Chthoniobacter flavus Ellin428].
ConsensusfromContig5224ChlamydiaeVerrucomicrobia-Chthoniobacter_flavus_Ellin428_gi196232861	4.10E-22	>ZP_03131711 Phytanoyl-CoA dioxygenase [Chthoniobacter flavus Ellin428].
ConsensusfromContig7122ChlamydiaeVerrucomicrobia-Chthoniobacter_flavus_Ellin428_gi196233916	6.90E-11	>ZP_03132753 hypothetical protein CfE428DRAFT_5921 [Chthoniobacter flavus Ellin428].
ConsensusfromContig5134ChlamydiaeVerrucomicrobia-Coraliomargarita_akajimensis_DSM_45221_gi294053897	4.00E-51	>YP_003547555 hypothetical protein Caka_0360 [Coraliomargarita akajimensis DSM 45221].
ConsensusfromContig7012ChlamydiaeVerrucomicrobia-Coraliomargarita_akajimensis_DSM_45221_gi294056641	1.80E-67	>YP_003550299 hypothetical protein Caka_3116 [Coraliomargarita akajimensis DSM 45221].
ConsensusfromContig2307ChlamydiaeVerrucomicrobia-Lentisphaera_araneosa_HTCC2155_gi149196027	1.70E-18	>ZP_01873083 hypothetical protein LNTAR_22814 [Lentisphaera araneosa HTCC2155].
ConsensusfromContig3055ChlamydiaeVerrucomicrobia-Lentisphaera_araneosa_HTCC2155_gi149196027	6.10E-18	>ZP_01873083 hypothetical protein LNTAR_22814 [Lentisphaera araneosa HTCC2155].
ConsensusfromContig5182ChlamydiaeVerrucomicrobia-Lentisphaera_araneosa_HTCC2155_gi149196298	2.70E-16	>ZP_01873353 hypothetical protein LNTAR_14112 [Lentisphaera araneosa HTCC2155].
ConsensusfromContig5438ChlamydiaeVerrucomicrobia-Lentisphaera_araneosa_HTCC2155_gi149198007	3.40E-50	>ZP_01875055 hypothetical protein LNTAR_21460 [Lentisphaera araneosa HTCC2155].
ConsensusfromContig5249ChlamydiaeVerrucomicrobia-Lentisphaera_araneosa_HTCC2155_gi149198102	9.00E-22	>ZP_01875149 beta-glucanase precursor [Lentisphaera araneosa HTCC2155].
ConsensusfromContig2426ChlamydiaeVerrucomicrobia-Lentisphaera_araneosa_HTCC2155_gi149198979	1.50E-58	>ZP_01876020 sucrose-6-phosphate hydrolase [Lentisphaera araneosa HTCC2155].
ConsensusfromContig6992ChlamydiaeVerrucomicrobia-Methylacidiphilum_infernorum_V4_gi189218158	1.00E-53	>YP_001938800 SAM-dependent methyltransferase [Methylacidiphilum infernorum V4].
ConsensusfromContig1969ChlamydiaeVerrucomicrobia-Opitutaceae_bacterium_TAV2_gi225155800	5.30E-23	>ZP_03724287 alpha-L-rhamnosidase [Opitutaceae bacterium TAV2].
ConsensusfromContig1031ChlamydiaeVerrucomicrobia-Opitutaceae_bacterium_TAV2_gi225159363	1.40E-13	>ZP_03725660 hypothetical protein ObacDRAFT_7513 [Opitutaceae bacterium TAV2].
ConsensusfromContig5175ChlamydiaeVerrucomicrobia-Opitutaceae_bacterium_TAV2_gi225165732	7.30E-20	>ZP_03727527 hypothetical protein ObacDRAFT_5992 [Opitutaceae bacterium TAV2].
ConsensusfromContig2348ChlamydiaeVerrucomicrobia-Opitutaceae_bacterium_TAV2_gi225165944	5.70E-14	>ZP_03727705 hypothetical protein ObacDRAFT_5458 [Opitutaceae bacterium TAV2].
ConsensusfromContig2243ChlamydiaeVerrucomicrobia-Opitutaceae_bacterium_TAV2_gi225166080	3.40E-11	>ZP_03727817 sialic acid-specific 9-O-acetylesterase [Opitutaceae bacterium TAV2].
ConsensusfromContig1991ChlamydiaeVerrucomicrobia-Opitutus_terrae_PB90_1_gi182413780	3.60E-87	>YP_001818846 Beta-ketoacyl synthase [Opitutus terrae PB90-1].
ConsensusfromContig5120ChlamydiaeVerrucomicrobia-Opitutus_terrae_PB90_1_gi182414669	3.80E-13	>YP_001819735 SMP-30/gluconolaconase/LRE domain-containing protein [Opitutus terrae PB90-1].
ConsensusfromContig2077ChlamydiaeVerrucomicrobia-Opitutus_terrae_PB90_1_gi182414787	1.30E-60	>YP_001819853 Alpha-L-fucosidase [Opitutus terrae PB90-1].
ConsensusfromContig2033ChlamydiaeVerrucomicrobia-Parachlamydia_acanthamoebae_str_Halls_coccus_gi282891348	6.50E-35	>ZP_06299850 hypothetical protein pah_c050o147 [Parachlamydia acanthamoebae str. Hall's coccus].
ConsensusfromContig1963ChlamydiaeVerrucomicrobia-Verrucomicrobiae_bacterium_DG1235_gi254446605	2.00E-26	>ZP_05060081 oxidoreductase, aldo/keto reductase family [Verrucomicrobiae bacterium DG1235].
ConsensusfromContig2291ChlamydiaeVerrucomicrobia-Verrucomicrobium_spinosum_DSM_4136_gi171910146	4.70E-14	>ZP_02925616 hypothetical protein VspiD_03220 [Verrucomicrobium spinosum DSM 4136].
ConsensusfromContig5192ChlamydiaeVerrucomicrobia-Verrucomicrobium_spinosum_DSM_4136_gi171910726	3.00E-39	>ZP_02926196 O-acetylhomoserine/O-acetylserine sulfhydrylase [Verrucomicrobium spinosum DSM 4136].
ConsensusfromContig6122ChlamydiaeVerrucomicrobia-Verrucomicrobium_spinosum_DSM_4136_gi171910726	2.50E-69	>ZP_02926196 O-acetylhomoserine/O-acetylserine sulfhydrylase [Verrucomicrobium spinosum DSM 4136].
ConsensusfromContig2092ChlamydiaeVerrucomicrobia-Verrucomicrobium_spinosum_DSM_4136_gi171911014	7.00E-11	>ZP_02926484 Sialidase [Verrucomicrobium spinosum DSM 4136].
ConsensusfromContig3326ChlamydiaeVerrucomicrobia-Verrucomicrobium_spinosum_DSM_4136_gi171911961	1.70E-14	>ZP_02927431 cobalamin synthesis protein, P47K [Verrucomicrobium spinosum DSM 4136].
ConsensusfromContig5541ChlamydiaeVerrucomicrobia-Verrucomicrobium_spinosum_DSM_4136_gi171911977	7.40E-20	>ZP_02927447 hypothetical protein VspiD_12395 [Verrucomicrobium spinosum DSM 4136].
ConsensusfromContig2382ChlamydiaeVerrucomicrobia-Verrucomicrobium_spinosum_DSM_4136_gi171912546	3.70E-20	>ZP_02928016 putative esterase [Verrucomicrobium spinosum DSM 4136].
ConsensusfromContig2114ChlamydiaeVerrucomicrobia-Verrucomicrobium_spinosum_DSM_4136_gi171913349	5.80E-14	>ZP_02928819 hypothetical protein VspiD_19255 [Verrucomicrobium spinosum DSM 4136].
ConsensusfromContig2098ChlamydiaeVerrucomicrobia-Victivallis_vadensis_ATCC_BAA_548_gi281355473	8.70E-18	>ZP_06241967 hypothetical protein Vvad_PD3579 [Victivallis vadensis ATCC BAA-548].
ConsensusfromContig4675ChlamydiaeVerrucomicrobia-Victivallis_vadensis_ATCC_BAA_548_gi281355474	5.50E-14	>ZP_06241968 hypothetical protein Vvad_PD3580 [Victivallis vadensis ATCC BAA-548].
ConsensusfromContig4675ChlamydiaeVerrucomicrobia-Victivallis_vadensis_ATCC_BAA_548_gi281355474	5.50E-14	>ZP_06241968 hypothetical protein Vvad_PD3580 [Victivallis vadensis ATCC BAA-548].
ConsensusfromContig5741ChlamydiaeVerrucomicrobia-Victivallis_vadensis_ATCC_BAA_548_gi281355474	5.50E-24	>ZP_06241968 hypothetical protein Vvad_PD3580 [Victivallis vadensis ATCC BAA-548].
ConsensusfromContig2029ChlamydiaeVerrucomicrobia-Victivallis_vadensis_ATCC_BAA_548_gi281355786	5.10E-22	>ZP_06242280 Beta-agarase [Victivallis vadensis ATCC BAA-548].
ConsensusfromContig2962ChlamydiaeVerrucomicrobia-Victivallis_vadensis_ATCC_BAA_548_gi281355786	8.70E-28	>ZP_06242280 Beta-agarase [Victivallis vadensis ATCC BAA-548].
ConsensusfromContig2402ChlamydiaeVerrucomicrobia-Victivallis_vadensis_ATCC_BAA_548_gi281356363	4.00E-17	>ZP_06242855 hypothetical protein Vvad_PD1734 [Victivallis vadensis ATCC BAA-548].
ConsensusfromContig5125ChlamydiaeVerrucomicrobia-Victivallis_vadensis_ATCC_BAA_548_gi281356371	1.60E-30	>ZP_06242863 Alpha-galactosidase [Victivallis vadensis ATCC BAA-548].
ConsensusfromContig6653ChlamydiaeVerrucomicrobia-Victivallis_vadensis_ATCC_BAA_548_gi281356918	1.40E-20	>ZP_06243408 hypothetical protein Vvad_PD1436 [Victivallis vadensis ATCC BAA-548].
ConsensusfromContig5205Chloroflexi-Chloroflexus_aggregans_DSM_9485_gi219847607	8.90E-60	>YP_002462040 regulator of chromosome condensation RCC1 [Chloroflexus aggregans DSM 9485].
ConsensusfromContig2001Chloroflexi-Chloroflexus_aggregans_DSM_9485_gi219848899	9.20E-32	>YP_002463332 Na-Ca exchanger/integrin-beta4 [Chloroflexus aggregans DSM 9485].
ConsensusfromContig2750Chloroflexi-Herpetosiphon_aurantiacus_ATCC_23779_gi159899678	4.50E-12	>YP_001545925 hypothetical protein Haur_3160 [Herpetosiphon aurantiacus ATCC 23779].
ConsensusfromContig2024Chloroflexi-Ktedonobacter_racemifer_DSM_44963_gi298242984	1.90E-11	>ZP_06966791 Amidase [Ktedonobacter racemifer DSM 44963].
ConsensusfromContig7148Chloroflexi-Ktedonobacter_racemifer_DSM_44963_gi298242984	1.60E-27	>ZP_06966791 Amidase [Ktedonobacter racemifer DSM 44963].
ConsensusfromContig2350Chloroflexi-Ktedonobacter_racemifer_DSM_44963_gi298243025	2.10E-27	>ZP_06966832 Phytanoyl-CoA dioxygenase [Ktedonobacter racemifer DSM 44963].
ConsensusfromContig5128Chloroflexi-Roseiflexus_castenholzii_DSM_13941_gi156741854	4.40E-52	>YP_001431983 alpha-L-rhamnosidase [Roseiflexus castenholzii DSM 13941].
ConsensusfromContig5634Chloroflexi-Roseiflexus_castenholzii_DSM_13941_gi156742824	4.70E-11	>YP_001432953 polymorphic outer membrane protein [Roseiflexus castenholzii DSM 13941].
ConsensusfromContig6946Chloroflexi-Roseiflexus_castenholzii_DSM_13941_gi156743320	2.10E-12	>YP_001433449 serine/threonine protein kinase [Roseiflexus castenholzii DSM 13941].
ConsensusfromContig7024Chloroflexi-Roseiflexus_castenholzii_DSM_13941_gi156743776	1.30E-30	>YP_001433905 hypothetical protein Rcas_3850 [Roseiflexus castenholzii DSM 13941].
ConsensusfromContig4839Chloroflexi-Roseiflexus_castenholzii_DSM_13941_gi156744335	1.60E-15	>YP_001434464 asparaginase [Roseiflexus castenholzii DSM 13941].
ConsensusfromContig2364Chloroflexi-Roseiflexus_sp_RS_1_gi148656852	1.30E-16	>YP_001277057 alpha-L-rhamnosidase [Roseiflexus sp. RS-1].

ConsensusfromContig2116	Chloroflexi-Sphaerobacter_thermophilus_DSM_20745_gi269838065	6.50E-46	>YP_003320293 X-Pro dipeptidyl-peptidase domain protein [Sphaerobacter thermophilus DSM 20745].
ConsensusfromContig2258	Chloroflexi-Sphaerobacter_thermophilus_DSM_20745_gi269838241	1.20E-14	>YP_003320469 transcriptional regulator, GntR family with aminotransferase domain protein [Sphaerobacter thermophilus DSM 20745].
ConsensusfromContig8823	Choanoflagellida-Monosiga_brevicollis_MX1_gi167515406	2.50E-14	>XP_001742044 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig3430	Choanoflagellida-Monosiga_brevicollis_MX1_gi167515406	7.00E-21	>XP_001742044 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig7115	Choanoflagellida-Monosiga_brevicollis_MX1_gi167515406	1.20E-65	>XP_001742044 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig1181	Choanoflagellida-Monosiga_brevicollis_MX1_gi167515678	6.90E-13	>XP_001742180 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig1005	Choanoflagellida-Monosiga_brevicollis_MX1_gi167515698	5.80E-19	>XP_001742190 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig9651	Choanoflagellida-Monosiga_brevicollis_MX1_gi167516278	4.50E-27	>XP_001742480 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig1706	Choanoflagellida-Monosiga_brevicollis_MX1_gi167516278	2.20E-12	>XP_001742480 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig1974	Choanoflagellida-Monosiga_brevicollis_MX1_gi167516278	9.70E-75	>XP_001742480 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2498	Choanoflagellida-Monosiga_brevicollis_MX1_gi167516278	1.30E-33	>XP_001742480 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2887	Choanoflagellida-Monosiga_brevicollis_MX1_gi167516278	4.30E-20	>XP_001742480 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2887	Choanoflagellida-Monosiga_brevicollis_MX1_gi167516278	4.30E-20	>XP_001742480 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig6241	Choanoflagellida-Monosiga_brevicollis_MX1_gi167516504	5.00E-13	>XP_001742593 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig4812	Choanoflagellida-Monosiga_brevicollis_MX1_gi167516638	9.50E-22	>XP_001742660 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5179	Choanoflagellida-Monosiga_brevicollis_MX1_gi167516638	5.30E-18	>XP_001742660 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig1934	Choanoflagellida-Monosiga_brevicollis_MX1_gi167516790	4.60E-21	>XP_001742736 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2107	Choanoflagellida-Monosiga_brevicollis_MX1_gi167516910	2.20E-18	>XP_001742796 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5140	Choanoflagellida-Monosiga_brevicollis_MX1_gi167516910	4.00E-51	>XP_001742796 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2052	Choanoflagellida-Monosiga_brevicollis_MX1_gi167517187	5.00E-58	>XP_001742934 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5312	Choanoflagellida-Monosiga_brevicollis_MX1_gi167517243	4.80E-23	>XP_001742962 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig1952	Choanoflagellida-Monosiga_brevicollis_MX1_gi167517727	2.90E-134	>XP_001743204 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig1996	Choanoflagellida-Monosiga_brevicollis_MX1_gi167517957	6.40E-20	>XP_001743319 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig1999	Choanoflagellida-Monosiga_brevicollis_MX1_gi167518017	2.50E-26	>XP_001743349 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig1940	Choanoflagellida-Monosiga_brevicollis_MX1_gi167518241	1.70E-14	>XP_001743461 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig1949	Choanoflagellida-Monosiga_brevicollis_MX1_gi167518241	1.80E-27	>XP_001743461 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig6635	Choanoflagellida-Monosiga_brevicollis_MX1_gi167518490	7.00E-11	>XP_001743585 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig7054	Choanoflagellida-Monosiga_brevicollis_MX1_gi167518568	5.60E-29	>XP_001743624 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5128	Choanoflagellida-Monosiga_brevicollis_MX1_gi167518696	4.30E-29	>XP_001743688 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig6928	Choanoflagellida-Monosiga_brevicollis_MX1_gi167518918	1.20E-72	>XP_001743799 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2784	Choanoflagellida-Monosiga_brevicollis_MX1_gi167518938	1.80E-11	>XP_001743809 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig1963	Choanoflagellida-Monosiga_brevicollis_MX1_gi167519278	5.00E-56	>XP_001743979 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5151	Choanoflagellida-Monosiga_brevicollis_MX1_gi167519278	9.40E-15	>XP_001743979 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5451	Choanoflagellida-Monosiga_brevicollis_MX1_gi167519278	4.00E-38	>XP_001743979 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2179	Choanoflagellida-Monosiga_brevicollis_MX1_gi167519332	8.10E-34	>XP_001744006 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5606	Choanoflagellida-Monosiga_brevicollis_MX1_gi167519433	3.40E-12	>XP_001744056 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig4926	Choanoflagellida-Monosiga_brevicollis_MX1_gi167519809	4.10E-17	>XP_001744244 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig3752	Choanoflagellida-Monosiga_brevicollis_MX1_gi167519969	5.10E-12	>XP_001744324 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5198	Choanoflagellida-Monosiga_brevicollis_MX1_gi167519969	3.80E-41	>XP_001744324 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig6202	Choanoflagellida-Monosiga_brevicollis_MX1_gi167520276	2.70E-20	>XP_001744477 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig4639	Choanoflagellida-Monosiga_brevicollis_MX1_gi167520280	6.70E-11	>XP_001744479 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2502	Choanoflagellida-Monosiga_brevicollis_MX1_gi167520300	1.90E-25	>XP_001744489 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2585	Choanoflagellida-Monosiga_brevicollis_MX1_gi167520300	1.90E-31	>XP_001744489 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2502	Choanoflagellida-Monosiga_brevicollis_MX1_gi167520300	1.90E-25	>XP_001744489 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig4557	Choanoflagellida-Monosiga_brevicollis_MX1_gi167520300	1.00E-15	>XP_001744489 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig4557	Choanoflagellida-Monosiga_brevicollis_MX1_gi167520300	1.00E-15	>XP_001744489 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig6934	Choanoflagellida-Monosiga_brevicollis_MX1_gi167520300	4.00E-63	>XP_001744489 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig6977	Choanoflagellida-Monosiga_brevicollis_MX1_gi167520300	2.60E-27	>XP_001744489 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5220	Choanoflagellida-Monosiga_brevicollis_MX1_gi167520392	7.90E-111	>XP_001744535 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig7129	Choanoflagellida-Monosiga_brevicollis_MX1_gi167521455	3.20E-15	>XP_001745066 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2817	Choanoflagellida-Monosiga_brevicollis_MX1_gi167521664	4.60E-13	>XP_001745170 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5112	Choanoflagellida-Monosiga_brevicollis_MX1_gi167521808	2.30E-51	>XP_001745242 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2051	Choanoflagellida-Monosiga_brevicollis_MX1_gi167521882	1.40E-11	>XP_001745279 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5109	Choanoflagellida-Monosiga_brevicollis_MX1_gi167522441	9.20E-75	>XP_001745558 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2095	Choanoflagellida-Monosiga_brevicollis_MX1_gi167522539	8.70E-15	>XP_001745607 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5131	Choanoflagellida-Monosiga_brevicollis_MX1_gi167522583	8.70E-99	>XP_001745629 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2437	Choanoflagellida-Monosiga_brevicollis_MX1_gi167522609	2.00E-27	>XP_001745642 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2883	Choanoflagellida-Monosiga_brevicollis_MX1_gi167522609	2.50E-15	>XP_001745642 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig3717	Choanoflagellida-Monosiga_brevicollis_MX1_gi167522609	3.00E-11	>XP_001745642 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig1824	Choanoflagellida-Monosiga_brevicollis_MX1_gi167522719	3.10E-11	>XP_001745697 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2048	Choanoflagellida-Monosiga_brevicollis_MX1_gi167522846	3.00E-38	>XP_001745760 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2379	Choanoflagellida-Monosiga_brevicollis_MX1_gi167522846	1.30E-52	>XP_001745760 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig3908	Choanoflagellida-Monosiga_brevicollis_MX1_gi167522846	1.40E-18	>XP_001745760 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig4214	Choanoflagellida-Monosiga_brevicollis_MX1_gi167522846	5.80E-13	>XP_001745760 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5156	Choanoflagellida-Monosiga_brevicollis_MX1_gi167522846	1.70E-30	>XP_001745760 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5182	Choanoflagellida-Monosiga_brevicollis_MX1_gi167522846	8.50E-70	>XP_001745760 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2059	Choanoflagellida-Monosiga_brevicollis_MX1_gi167523062	7.90E-37	>XP_001745868 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5283	Choanoflagellida-Monosiga_brevicollis_MX1_gi167523062	1.60E-13	>XP_001745868 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig1026	Choanoflagellida-Monosiga_brevicollis_MX1_gi167523521	5.80E-11	>XP_001746097 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig1979	Choanoflagellida-Monosiga_brevicollis_MX1_gi167523521	2.00E-16	>XP_001746097 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig1979	Choanoflagellida-Monosiga_brevicollis_MX1_gi167523521	2.00E-16	>XP_001746097 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2194	Choanoflagellida-Monosiga_brevicollis_MX1_gi167523521	8.50E-27	>XP_001746097 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2673	Choanoflagellida-Monosiga_brevicollis_MX1_gi167523521	1.20E-11	>XP_001746097 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2798	Choanoflagellida-Monosiga_brevicollis_MX1_gi167523521	6.30E-18	>XP_001746097 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig4987	Choanoflagellida-Monosiga_brevicollis_MX1_gi167523521	1.00E-11	>XP_001746097 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5514	Choanoflagellida-Monosiga_brevicollis_MX1_gi167523521	5.90E-15	>XP_001746097 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig7051	Choanoflagellida-Monosiga_brevicollis_MX1_gi167523521	6.90E-22	>XP_001746097 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig7104	Choanoflagellida-Monosiga_brevicollis_MX1_gi167523521	1.70E-28	>XP_001746097 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig3041	Choanoflagellida-Monosiga_brevicollis_MX1_gi167523731	2.20E-24	>XP_001746202 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2030	Choanoflagellida-Monosiga_brevicollis_MX1_gi167523735	1.10E-14	>XP_001746204 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig3888	Choanoflagellida-Monosiga_brevicollis_MX1_gi167523735	6.70E-21	>XP_001746204 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig7257	Choanoflagellida-Monosiga_brevicollis_MX1_gi167523735	1.50E-23	>XP_001746204 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5388	Choanoflagellida-Monosiga_brevicollis_MX1_gi167523775	4.70E-27	>XP_001746224 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig42	Choanoflagellida-Monosiga_brevicollis_MX1_gi167523877	1.50E-17	>XP_001746275 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig3890	Choanoflagellida-Monosiga_brevicollis_MX1_gi167523877	9.50E-33	>XP_001746275 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig4526	Choanoflagellida-Monosiga_brevicollis_MX1_gi167523877	4.00E-51	>XP_001746275 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig6550	Choanoflagellida-Monosiga_brevicollis_MX1_gi167523877	2.20E-22	>XP_001746275 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig7027	Choanoflagellida-Monosiga_brevicollis_MX1_gi167523877	3.20E-33	>XP_001746275 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig6959	Choanoflagellida-Monosiga_brevicollis_MX1_gi167524240	1.20E-38	>XP_001746456 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig4200	Choanoflagellida-Monosiga_brevicollis_MX1_gi167524284	5.20E-14	>XP_001746478 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig3894	Choanoflagellida-Monosiga_brevicollis_MX1_gi167524308	2.10E-12	>XP_001746490 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5136	Choanoflagellida-Monosiga_brevicollis_MX1_gi167524340	2.60E-27	>XP_001746506 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig6951	Choanoflagellida-Monosiga_brevicollis_MX1_gi167524340	8.60E-32	>XP_001746506 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig6952	Choanoflagellida-Monosiga_brevicollis_MX1_gi167524356	7.00E-19	>XP_001746514 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig6989	Choanoflagellida-Monosiga_brevicollis_MX1_gi167524356	2.30E-24	>XP_001746514 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2055	Choanoflagellida-Monosiga_brevicollis_MX1_gi167524366	9.80E-35	>XP_001746519 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2503	Choanoflagellida-Monosiga_brevicollis_MX1_gi167524366	5.30E-11	>XP_001746519 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5570	Choanoflagellida-Monosiga_brevicollis_MX1_gi167524366	5.70E-12	>XP_001746519 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig7743	Choanoflagellida-Monosiga_brevicollis_MX1_gi167524457	2.90E-14	>XP_001746564 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig3007	Choanoflagellida-Monosiga_brevicollis_MX1_gi167524805	6.50E-20	>XP_001746738 hypothetical protein [Monosiga brevicollis MX1].

ConsensusfromContig7319Choanoflagellida-Monosiga_brevicollis_MX1_gi167524813	6.20E-17	>XP_001746742 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig6932Choanoflagellida-Monosiga_brevicollis_MX1_gi167525098	7.70E-68	>XP_001746884 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig1961Choanoflagellida-Monosiga_brevicollis_MX1_gi167525174	7.40E-51	>XP_001746922 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig6000Choanoflagellida-Monosiga_brevicollis_MX1_gi167525250	5.10E-20	>XP_001746960 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2045Choanoflagellida-Monosiga_brevicollis_MX1_gi167525274	3.00E-16	>XP_001746972 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig916 Choanoflagellida-Monosiga_brevicollis_MX1_gi167525649	8.70E-28	>XP_001747159 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig916 Choanoflagellida-Monosiga_brevicollis_MX1_gi167525649	8.70E-28	>XP_001747159 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig6934Choanoflagellida-Monosiga_brevicollis_MX1_gi167526088	2.00E-47	>XP_001747378 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig7376Choanoflagellida-Monosiga_brevicollis_MX1_gi167526375	4.00E-14	>XP_001747521 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig7046Choanoflagellida-Monosiga_brevicollis_MX1_gi167526642	2.90E-11	>XP_001747654 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig883 Choanoflagellida-Monosiga_brevicollis_MX1_gi167526963	3.00E-25	>XP_001747814 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5334Choanoflagellida-Monosiga_brevicollis_MX1_gi167527177	1.50E-27	>XP_001747921 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5654Choanoflagellida-Monosiga_brevicollis_MX1_gi167527177	3.20E-11	>XP_001747921 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig7024Choanoflagellida-Monosiga_brevicollis_MX1_gi167527328	8.10E-17	>XP_001747996 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig4636Choanoflagellida-Monosiga_brevicollis_MX1_gi167527442	6.40E-17	>XP_001748053 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2875Choanoflagellida-Monosiga_brevicollis_MX1_gi167533023	6.50E-29	>XP_001748192 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig8803Choanoflagellida-Monosiga_brevicollis_MX1_gi167533053	8.60E-14	>XP_001748207 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig8803Choanoflagellida-Monosiga_brevicollis_MX1_gi167533053	8.60E-14	>XP_001748207 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2639Choanoflagellida-Monosiga_brevicollis_MX1_gi167533053	3.00E-15	>XP_001748207 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig4316Choanoflagellida-Monosiga_brevicollis_MX1_gi167533053	4.10E-34	>XP_001748207 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig1603Choanoflagellida-Monosiga_brevicollis_MX1_gi167533389	1.70E-18	>XP_001748374 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2504Choanoflagellida-Monosiga_brevicollis_MX1_gi167533389	4.90E-26	>XP_001748374 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5208Choanoflagellida-Monosiga_brevicollis_MX1_gi167533616	3.10E-29	>XP_001748487 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5909Choanoflagellida-Monosiga_brevicollis_MX1_gi167534266	9.10E-15	>XP_001748811 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5909Choanoflagellida-Monosiga_brevicollis_MX1_gi167534266	9.10E-15	>XP_001748811 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig1295Choanoflagellida-Monosiga_brevicollis_MX1_gi167534373	6.30E-16	>XP_001748862 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig6950Choanoflagellida-Monosiga_brevicollis_MX1_gi167534587	8.70E-71	>XP_001748969 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5099Choanoflagellida-Monosiga_brevicollis_MX1_gi167534724	2.30E-43	>XP_001749037 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2154Choanoflagellida-Monosiga_brevicollis_MX1_gi167534874	2.10E-19	>XP_001749112 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig3376Choanoflagellida-Monosiga_brevicollis_MX1_gi167534874	5.90E-18	>XP_001749112 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig3786Choanoflagellida-Monosiga_brevicollis_MX1_gi167534874	4.80E-13	>XP_001749112 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig4546Choanoflagellida-Monosiga_brevicollis_MX1_gi167534874	5.80E-13	>XP_001749112 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig6001Choanoflagellida-Monosiga_brevicollis_MX1_gi167534874	1.10E-19	>XP_001749112 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig7222Choanoflagellida-Monosiga_brevicollis_MX1_gi167534874	9.00E-13	>XP_001749112 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5327Choanoflagellida-Monosiga_brevicollis_MX1_gi167534965	2.80E-42	>XP_001749157 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2134Choanoflagellida-Monosiga_brevicollis_MX1_gi167535035	7.40E-14	>XP_001749192 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig3061Choanoflagellida-Monosiga_brevicollis_MX1_gi167535035	5.20E-25	>XP_001749192 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig3278Choanoflagellida-Monosiga_brevicollis_MX1_gi167535133	2.20E-34	>XP_001749241 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig3513Choanoflagellida-Monosiga_brevicollis_MX1_gi167535637	1.00E-11	>XP_001749492 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5424Choanoflagellida-Monosiga_brevicollis_MX1_gi167535637	4.90E-25	>XP_001749492 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig4597Choanoflagellida-Monosiga_brevicollis_MX1_gi167535718	1.60E-23	>XP_001749532 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig3054Choanoflagellida-Monosiga_brevicollis_MX1_gi167535834	5.00E-29	>XP_001749590 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig3771Choanoflagellida-Monosiga_brevicollis_MX1_gi167535834	7.30E-12	>XP_001749590 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2069Choanoflagellida-Monosiga_brevicollis_MX1_gi167535902	3.60E-12	>XP_001749624 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig6943Choanoflagellida-Monosiga_brevicollis_MX1_gi167536186	2.30E-20	>XP_001749765 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5196Choanoflagellida-Monosiga_brevicollis_MX1_gi167536505	9.40E-44	>XP_001749924 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2081Choanoflagellida-Monosiga_brevicollis_MX1_gi167536527	3.10E-16	>XP_001749935 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig4725Choanoflagellida-Monosiga_brevicollis_MX1_gi167536865	6.30E-12	>XP_001750103 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2563Choanoflagellida-Monosiga_brevicollis_MX1_gi167537582	7.20E-13	>XP_001750459 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5564Choanoflagellida-Monosiga_brevicollis_MX1_gi167537582	8.00E-16	>XP_001750459 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5200Choanoflagellida-Monosiga_brevicollis_MX1_gi167537751	1.20E-72	>XP_001750543 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2008Choanoflagellida-Monosiga_brevicollis_MX1_gi167538519	5.90E-32	>XP_001750923 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig3868Choanoflagellida-Monosiga_brevicollis_MX1_gi167538519	1.60E-27	>XP_001750923 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig3868Choanoflagellida-Monosiga_brevicollis_MX1_gi167538519	1.60E-27	>XP_001750923 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig6075Choanoflagellida-Monosiga_brevicollis_MX1_gi167538519	1.90E-23	>XP_001750923 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig1945Choanoflagellida-Monosiga_brevicollis_MX1_gi167538687	2.80E-64	>XP_001751005 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig2820Choanoflagellida-Monosiga_brevicollis_MX1_gi167538687	1.30E-13	>XP_001751005 hypothetical protein [Monosiga brevicollis MX1].
ConsensusfromContig5152Choanoflagellida-Monosiga_ovata_esContig1251_1	3.70E-18	
ConsensusfromContig5967Choanoflagellida-Monosiga_ovata_esContig1361_3	2.30E-19	
ConsensusfromContig5967Choanoflagellida-Monosiga_ovata_esContig1361_3	2.30E-19	
ConsensusfromContig5190Choanoflagellida-Monosiga_ovata_esContig1486_1	9.40E-16	
ConsensusfromContig1597Choanoflagellida-Monosiga_ovata_esContig1674_5	4.10E-12	
ConsensusfromContig2058Choanoflagellida-Monosiga_ovata_esContig1679_1	8.00E-12	
ConsensusfromContig1709Choanoflagellida-Monosiga_ovata_esContig170_5	9.30E-11	
ConsensusfromContig2777Choanoflagellida-Monosiga_ovata_esContig170_5	4.10E-13	
ConsensusfromContig4289Choanoflagellida-Monosiga_ovata_esContig1807_2	7.70E-15	
ConsensusfromContig3595Choanoflagellida-Monosiga_ovata_esContig1845_3	1.20E-13	
ConsensusfromContig4163Choanoflagellida-Monosiga_ovata_esContig1906_5	7.30E-16	
ConsensusfromContig3570Choanoflagellida-Monosiga_ovata_esContig1960_2	6.20E-23	
ConsensusfromContig1584Choanoflagellida-Monosiga_ovata_esContig2321_1	1.80E-14	
ConsensusfromContig1584Choanoflagellida-Monosiga_ovata_esContig2321_1	1.80E-14	
ConsensusfromContig5943Choanoflagellida-Monosiga_ovata_esContig2423_2	4.50E-11	
ConsensusfromContig6093Choanoflagellida-Monosiga_ovata_esContig2768_2	5.10E-11	
ConsensusfromContig4794Choanoflagellida-Monosiga_ovata_esContig277_2	5.20E-13	
ConsensusfromContig2626Choanoflagellida-Monosiga_ovata_esContig278_2	1.00E-14	
ConsensusfromContig5210Choanoflagellida-Monosiga_ovata_esContig2793_2	7.40E-43	
ConsensusfromContig7110Choanoflagellida-Monosiga_ovata_esContig2793_2	1.90E-20	
ConsensusfromContig8385Choanoflagellida-Monosiga_ovata_esContig288_2	1.30E-15	
ConsensusfromContig1952Choanoflagellida-Monosiga_ovata_esContig331_3	2.60E-58	
ConsensusfromContig6964Choanoflagellida-Monosiga_ovata_esContig3359_4	8.80E-26	
ConsensusfromContig5803Choanoflagellida-Monosiga_ovata_esContig3422_3	1.50E-17	
ConsensusfromContig2179Choanoflagellida-Monosiga_ovata_esContig3539_6	3.90E-29	
ConsensusfromContig2310Choanoflagellida-Monosiga_ovata_esContig3539_6	6.30E-11	
ConsensusfromContig4282Choanoflagellida-Monosiga_ovata_esContig3539_6	5.20E-11	
ConsensusfromContig5193Choanoflagellida-Monosiga_ovata_esContig3772_4	5.10E-65	
ConsensusfromContig5123Choanoflagellida-Monosiga_ovata_esContig381_1	1.10E-34	
ConsensusfromContig5180Choanoflagellida-Monosiga_ovata_esContig3830_1	4.70E-20	
ConsensusfromContig7436Choanoflagellida-Monosiga_ovata_esContig4156_2	2.70E-12	
ConsensusfromContig2683Choanoflagellida-Monosiga_ovata_esContig4452_5	6.20E-18	
ConsensusfromContig3008Choanoflagellida-Monosiga_ovata_esContig4503_1	8.80E-19	
ConsensusfromContig4179Choanoflagellida-Monosiga_ovata_esContig4632_1	6.10E-12	
ConsensusfromContig2651Choanoflagellida-Monosiga_ovata_esContig4733_1	2.30E-12	
ConsensusfromContig5408Choanoflagellida-Monosiga_ovata_esContig4733_1	2.20E-13	
ConsensusfromContig1999Choanoflagellida-Monosiga_ovata_esContig5386_3	2.50E-26	
ConsensusfromContig2372Choanoflagellida-Monosiga_ovata_esContig664_3	5.20E-16	
ConsensusfromContig2059Choanoflagellida-Monosiga_ovata_esContig678_3	1.70E-53	
ConsensusfromContig2173Choanoflagellida-Monosiga_ovata_esContig806_3	8.90E-17	
ConsensusfromContig2048Choanoflagellida-Monosiga_ovata_esgi106846431_2	8.50E-11	>EC164808 MNE00006923 Monosiga ovata Non-normalized Monosiga ovata cDNA, mRNA sequence.
ConsensusfromContig2142Choanoflagellida-Monosiga_ovata_esgi106848547_1	1.70E-12	>EC166924 MNE00001537 Monosiga ovata Non-normalized Monosiga ovata cDNA, mRNA sequence.
ConsensusfromContig7285Choanoflagellida-Monosiga_ovata_esgi106849269_1	8.10E-13	>EC167646 MNE00003933 Monosiga ovata Non-normalized Monosiga ovata cDNA, mRNA sequence.

ConsensusfromContig5875Choanoflagellida-Monosiga_ovata_esgi106850223_1	5.20E-13	>EC168600 MNE00001837 Monosiga ovata Non-normalized Monosiga ovata cDNA, mRNA sequence.
ConsensusfromContig6970Choanoflagellida-Monosiga_ovata_esgi106850389_3	8.90E-13	>EC168766 MNE00004915 Monosiga ovata Non-normalized Monosiga ovata cDNA, mRNA sequence.
ConsensusfromContig5206Choanoflagellida-Monosiga_ovata_esgi163006043_5	3.20E-12	>DC470945 DC470945 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-030H24 3', mRNA sequence.
ConsensusfromContig2110Choanoflagellida-Monosiga_ovata_esgi163009823_4	9.40E-25	>DC482175 DC482175 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-046M07 3', mRNA sequence.
ConsensusfromContig5130Choanoflagellida-Monosiga_ovata_esgi163009823_4	1.30E-38	>DC482175 DC482175 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-046M07 3', mRNA sequence.
ConsensusfromContig5109Choanoflagellida-Monosiga_ovata_esgi163013020_6	1.80E-28	>DC484589 DC484589 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-050D17 3', mRNA sequence.
ConsensusfromContig6956Choanoflagellida-Monosiga_ovata_esgi163019752_4	7.90E-23	>DC474565 DC474565 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-035L11 3', mRNA sequence.
ConsensusfromContig2983Choanoflagellida-Monosiga_ovata_esgi163020132_2	8.50E-17	>DC474917 DC474917 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-036D13 5', mRNA sequence.
ConsensusfromContig2415Choanoflagellida-Monosiga_ovata_esgi163026715_2	2.70E-41	>DC452793 DC452793 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-004B04 5', mRNA sequence.
ConsensusfromContig1985Choanoflagellida-Monosiga_ovata_esgi163026716_4	1.30E-38	>DC452794 DC452794 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-004B04 3', mRNA sequence.
ConsensusfromContig2052Choanoflagellida-Monosiga_ovata_esgi163026716_4	3.10E-43	>DC452794 DC452794 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-004B04 3', mRNA sequence.
ConsensusfromContig3938Choanoflagellida-Monosiga_ovata_esgi163026716_4	5.20E-12	>DC452794 DC452794 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-004B04 3', mRNA sequence.
ConsensusfromContig4150Choanoflagellida-Monosiga_ovata_esgi163032254_3	2.40E-19	>DC456449 DC456449 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-009G22 5', mRNA sequence.
ConsensusfromContig6194Choanoflagellida-Monosiga_ovata_esgi163041826_1	7.90E-11	>DC465568 DC465568 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-022J20 5', mRNA sequence.
ConsensusfromContig2177Choanoflagellida-Monosiga_ovata_esgi163043037_1	2.40E-15	>DC465623 DC465623 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-022L04 5', mRNA sequence.
ConsensusfromContig3170Choanoflagellida-Monosiga_ovata_esgi163060895_5	4.70E-24	>DC486748 DC486748 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-053F06 3', mRNA sequence.
ConsensusfromContig6292Choanoflagellida-Monosiga_ovata_esgi163061733_3	3.60E-11	>DC486802 DC486802 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-053G13 5', mRNA sequence.
ConsensusfromContig1939Choanoflagellida-Monosiga_ovata_esgi163062545_2	2.60E-21	>DC489199 DC489199 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-056N21 5', mRNA sequence.
ConsensusfromContig6958Choanoflagellida-Monosiga_ovata_esgi163067102_4	7.90E-17	>DC490765 DC490765 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-059B08 3', mRNA sequence.
ConsensusfromContig6958Choanoflagellida-Monosiga_ovata_esgi163067102_4	7.90E-17	>DC490765 DC490765 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-059B08 3', mRNA sequence.
ConsensusfromContig3645Choanoflagellida-Monosiga_ovata_esgi163073358_1	8.70E-14	>DC498890 DC498890 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-070N10 5', mRNA sequence.
ConsensusfromContig5126Choanoflagellida-Monosiga_ovata_esgi163073358_1	1.80E-17	>DC498890 DC498890 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-070N10 5', mRNA sequence.
ConsensusfromContig6198Choanoflagellida-Monosiga_ovata_esgi163073358_1	7.30E-23	>DC498890 DC498890 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-070N10 5', mRNA sequence.
ConsensusfromContig2937Choanoflagellida-Monosiga_ovata_esgi163075532_1	2.00E-11	>DC499806 DC499806 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-072C10 5', mRNA sequence.
ConsensusfromContig2983Choanoflagellida-Monosiga_ovata_esgi163075563_4	8.50E-11	>DC499837 DC499837 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-072D02 3', mRNA sequence.
ConsensusfromContig2173Choanoflagellida-Monosiga_ovata_esgi163079557_1	2.90E-12	>DC503112 DC503112 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-076P11 5', mRNA sequence.
ConsensusfromContig3317Choanoflagellida-Monosiga_ovata_esgi163079557_1	8.30E-12	>DC503112 DC503112 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-076P11 5', mRNA sequence.
ConsensusfromContig2475Choanoflagellida-Monosiga_ovata_esgi163079658_1	4.60E-25	>DC502513 DC502513 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-076B14 5', mRNA sequence.
ConsensusfromContig7066Choanoflagellida-Monosiga_ovata_esgi163081252_1	3.40E-14	>DC502049 DC502049 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-075G15 5', mRNA sequence.
ConsensusfromContig3714Choanoflagellida-Monosiga_ovata_esgi163081253_5	2.20E-11	>DC502050 DC502050 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-075G15 3', mRNA sequence.
ConsensusfromContig3714Choanoflagellida-Monosiga_ovata_esgi163081253_5	2.20E-11	>DC502050 DC502050 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-075G15 3', mRNA sequence.
ConsensusfromContig6948Choanoflagellida-Monosiga_ovata_esgi163083499_1	1.90E-62	>DC504833 DC504833 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-079H04 5', mRNA sequence.
ConsensusfromContig2136Choanoflagellida-Monosiga_ovata_esgi163086042_3	8.30E-17	>DC505436 DC505436 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-080E20 5', mRNA sequence.
ConsensusfromContig4722Choanoflagellida-Monosiga_ovata_esgi163086043_5	2.00E-16	>DC505437 DC505437 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-080E20 3', mRNA sequence.
ConsensusfromContig6878Choanoflagellida-Monosiga_ovata_esgi163088817_1	4.00E-16	>DC507352 DC507352 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-083B07 5', mRNA sequence.
ConsensusfromContig1675Choanoflagellida-Monosiga_ovata_esgi163088839_3	8.50E-14	>DC507360 DC507360 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-083B11 5', mRNA sequence.
ConsensusfromContig4809Choanoflagellida-Monosiga_ovata_esgi163091366_2	5.50E-14	>DC511147 DC511147 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-088I19 5', mRNA sequence.
ConsensusfromContig5170Choanoflagellida-Monosiga_ovata_esgi163093125_2	1.50E-26	>DC512182 DC512182 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-090A20 5', mRNA sequence.
ConsensusfromContig7063Choanoflagellida-Monosiga_ovata_esgi163099406_1	2.50E-11	>DC517172 DC517172 Full length cDNA Library, Monosiga ovata, MOC Monosiga ovata cDNA clone MOC-097D19 5', mRNA sequence.
ConsensusfromContig5130Choanoflagellida-Proterospongia_sp_tbPRL00000146_5	1.50E-24	
ConsensusfromContig3740Choanoflagellida-Proterospongia_sp_tbPRL00000195_5	4.40E-16	
ConsensusfromContig5933Choanoflagellida-Proterospongia_sp_tbPRL00000238_1	6.80E-14	
ConsensusfromContig5637Cryptophyta-Goniomonas_cf_pacifica_esgi148275991_3	2.20E-39	>ES558581 GA0d5M13R_G10.ab1 GONIO-CCMP-05 Goniomonas cf. pacifica cDNA 3', mRNA sequence.
ConsensusfromContig4542Cryptophyta-Goniomonas_cf_pacifica_esgi148276158_4	4.90E-14	>ES558748 GA0a12T3_A08.ab15190519ABI GONIO-CCMP-05 Goniomonas cf. pacifica cDNA 3', mRNA sequence.
ConsensusfromContig2113Cryptophyta-Guillardia_theta_tbGTL00001041_2	5.40E-56	
ConsensusfromContig3171Cryptophyta-Guillardia_theta_tbGTL00001060_2	8.00E-14	
ConsensusfromContig7099Cryptophyta-Guillardia_theta_tbGTL00001239_3	1.30E-29	
ConsensusfromContig2409Cryptophyta-Guillardia_theta_tbGTL00001704_2	1.40E-17	
ConsensusfromContig2734Cryptophyta-Guillardia_theta_tbGTL00001925_1	9.90E-22	
ConsensusfromContig2891Cryptophyta-Guillardia_theta_tbGTL00001925_1	1.90E-17	
ConsensusfromContig3615Cryptophyta-Guillardia_theta_tbGTL00002387_1	5.70E-17	
ConsensusfromContig1579Cryptophyta-Guillardia_theta_tbGTL00002928_1	9.10E-12	
ConsensusfromContig2254Cryptophyta-Guillardia_theta_tbGTL00003585_2	1.10E-14	
ConsensusfromContig2950Cryptophyta-Guillardia_theta_tbGTL00003937_1	1.90E-17	
ConsensusfromContig3549Cryptophyta-Guillardia_theta_tbGTL00003937_1	5.70E-15	
ConsensusfromContig5164Cryptophyta-Guillardia_theta_tbGTL00003937_1	1.90E-21	
ConsensusfromContig2078Cryptophyta-Guillardia_theta_tbGTL00005896_1	1.10E-17	
ConsensusfromContig5444Cyanobacteria-Acaryochloris_marina_MBIC11017_gi158334417	1.20E-15	>YP_001515589 FG-GAP repeat- calx-beta domain-containing protein [Acaryochloris marina MBIC11017].
ConsensusfromContig5968Cyanobacteria-Acaryochloris_marina_MBIC11017_gi158334954	1.00E-18	>YP_001516126 peptidylprolyl isomerase, FKBP type [Acaryochloris marina MBIC11017].
ConsensusfromContig2242Cyanobacteria-Acaryochloris_marina_MBIC11017_gi158335052	1.10E-21	>YP_001516224 hypothetical protein AM1_1890 [Acaryochloris marina MBIC11017].
ConsensusfromContig2017Cyanobacteria-Acaryochloris_marina_MBIC11017_gi158336249	4.40E-25	>YP_001517423 appr-1-p processing enzyme family protein [Acaryochloris marina MBIC11017].
ConsensusfromContig3945Cyanobacteria-Acaryochloris_marina_MBIC11017_gi158339495	5.20E-12	>YP_001520884 non-ribosomal peptide synthetase [Acaryochloris marina MBIC11017].
ConsensusfromContig2034Cyanobacteria-Arthrospira_maxima_CS_328_gi209522900	3.20E-25	>ZP_03271457 peptidylprolyl isomerase FKBP-type [Arthrospira maxima CS-328].
ConsensusfromContig7075Cyanobacteria-Arthrospira_platensis_str_Paraca_gi284052294	1.80E-12	>ZP_06382504 hypothetical protein AplaP_12573 [Arthrospira platensis str. Paraca].
ConsensusfromContig6960Cyanobacteria-Arthrospira_platensis_str_Paraca_gi284052505	1.10E-24	>ZP_06382715 cobalamin synthesis protein P47K [Arthrospira platensis str. Paraca].
ConsensusfromContig1961Cyanobacteria-Arthrospira_platensis_str_Paraca_gi284053593	4.40E-19	>ZP_06383803 magnesium and cobalt transport protein CorA [Arthrospira platensis str. Paraca].
ConsensusfromContig1514Cyanobacteria-Cyanothece_sp_CCY0110_gi126661643	1.20E-31	>ZP_01732662 hypothetical protein CY0110_00950 [Cyanothece sp. CCY0110].
ConsensusfromContig1514Cyanobacteria-Cyanothece_sp_CCY0110_gi126661643	1.20E-31	>ZP_01732662 hypothetical protein CY0110_00950 [Cyanothece sp. CCY0110].
ConsensusfromContig6105Cyanobacteria-Cyanothece_sp_PCC_7424_gi218437453	2.90E-12	>YP_002375782 folate/biopterin transporter [Cyanothece sp. PCC 7424].
ConsensusfromContig862 Cyanobacteria-Cyanothece_sp_PCC_7424_gi218437509	5.20E-14	>YP_002375838 peptidylprolyl isomerase FKBP-type [Cyanothece sp. PCC 7424].
ConsensusfromContig4238Cyanobacteria-Cyanothece_sp_PCC_7425_gi220909173	2.00E-11	>YP_002484484 hypothetical protein Cyan7425_3804 [Cyanothece sp. PCC 7425].
ConsensusfromContig6560Cyanobacteria-Cyanothece_sp_PCC_7822_gi196257654	9.20E-16	>ZP_03156190 TPR repeat-containing protein [Cyanothece sp. PCC 7822].
ConsensusfromContig5251Cyanobacteria-Gloeobacter_violaceus_PCC_7421_gi37520209	2.30E-33	>NP_923586 glucosamine-6-sulfatase [Gloeobacter violaceus PCC 7421].
ConsensusfromContig7193Cyanobacteria-Gloeobacter_violaceus_PCC_7421_gi37521848	1.40E-16	>NP_925225 hypothetical protein glr2279 [Gloeobacter violaceus PCC 7421].
ConsensusfromContig5476Cyanobacteria-Lyngbya_sp_PCC_8106_gi119487492	4.00E-11	>ZP_01621102 Rab family protein [Lyngbya sp. PCC 8106].
ConsensusfromContig5403Cyanobacteria-Lyngbya_sp_PCC_8106_gi119492179	2.60E-21	>ZP_01623589 NAD-dependent epimerase/dehydratase [Lyngbya sp. PCC 8106].
ConsensusfromContig7121Cyanobacteria-Microcoleus_chthonoplastes_PCC_7420_gi254409456	2.10E-17	>ZP_05023237 Penicillin amidase superfamily [Microcoleus chthonoplastes PCC 7420].
ConsensusfromContig2948Cyanobacteria-Microcoleus_chthonoplastes_PCC_7420_gi254409724	2.70E-11	>ZP_05023505 tetratricopeptide repeat domain protein [Microcoleus chthonoplastes PCC 7420].
ConsensusfromContig2948Cyanobacteria-Microcoleus_chthonoplastes_PCC_7420_gi254409724	2.70E-11	>ZP_05023505 tetratricopeptide repeat domain protein [Microcoleus chthonoplastes PCC 7420].
ConsensusfromContig5435Cyanobacteria-Microcoleus_chthonoplastes_PCC_7420_gi254410261	9.90E-28	>ZP_05024041 C-5 cytosine-specific DNA methylase superfamily [Microcoleus chthonoplastes PCC 7420].
ConsensusfromContig4449Cyanobacteria-Microcoleus_chthonoplastes_PCC_7420_gi254411467	1.00E-14	>ZP_05025244 Leucine Rich Repeat domain protein [Microcoleus chthonoplastes PCC 7420].
ConsensusfromContig2372Cyanobacteria-Microcoleus_chthonoplastes_PCC_7420_gi254414742	3.50E-12	>ZP_05028507 hypothetical protein MC7420_3763 [Microcoleus chthonoplastes PCC 7420].
ConsensusfromContig2978Cyanobacteria-Microcoleus_chthonoplastes_PCC_7420_gi254416421	7.00E-11	>ZP_05030174 Leucine Rich Repeat domain protein [Microcoleus chthonoplastes PCC 7420].
ConsensusfromContig3020Cyanobacteria-Microcoleus_chthonoplastes_PCC_7420_gi254416421	4.50E-12	>ZP_05030174 Leucine Rich Repeat domain protein [Microcoleus chthonoplastes PCC 7420].
ConsensusfromContig5446Cyanobacteria-Microcoleus_chthonoplastes_PCC_7420_gi254416421	3.70E-28	>ZP_05030174 Leucine Rich Repeat domain protein [Microcoleus chthonoplastes PCC 7420].
ConsensusfromContig5451Cyanobacteria-Microcoleus_chthonoplastes_PCC_7420_gi254416421	4.00E-33	>ZP_05030174 Leucine Rich Repeat domain protein [Microcoleus chthonoplastes PCC 7420].
ConsensusfromContig3129Cyanobacteria-Microcoleus_chthonoplastes_PCC_7420_gi254417561	3.20E-36	>ZP_05031299 dienelactone hydrolase family [Microcoleus chthonoplastes PCC 7420].
ConsensusfromContig2020Cyanobacteria-Nodularia_spumigena_CCY9414_gi119512692	3.80E-35	>ZP_01631765 hypothetical protein N9414_14523 [Nodularia spumigena CCY9414].
ConsensusfromContig5108Cyanobacteria-Nostoc_azollae_0708_gi298492814	3.20E-35	>YP_003722991 hypothetical protein Aazo_4641 ['Nostoc azollae' 0708].
ConsensusfromContig2064Cyanobacteria-Nostoc_punctiforme_PCC_73102_gi186681165	2.30E-17	>YP_001864361 TPR repeat-containing protein [Nostoc punctiforme PCC 73102].
ConsensusfromContig6999Cyanobacteria-Nostoc_punctiforme_PCC_73102_gi186681869	1.40E-14	>YP_001865065 hypothetical protein Npun_F1415 [Nostoc punctiforme PCC 73102].
ConsensusfromContig7015Cyanobacteria-Nostoc_punctiforme_PCC_73102_gi186681869	3.30E-16	>YP_001865065 hypothetical protein Npun_F1415 [Nostoc punctiforme PCC 73102].
ConsensusfromContig2953Cyanobacteria-Nostoc_punctiforme_PCC_73102_gi186682447	6.60E-21	>YP_001865643 beta-ketoacyl synthase [Nostoc punctiforme PCC 73102].
ConsensusfromContig5989Cyanobacteria-Nostoc_punctiforme_PCC_73102_gi186683375	1.50E-40	>YP_001866571 beta-ketoacyl synthase [Nostoc punctiforme PCC 73102].
ConsensusfromContig5987Cyanobacteria-Nostoc_punctiforme_PCC_73102_gi186683584	7.50E-11	>YP_001866780 beta-ketoacyl synthase [Nostoc punctiforme PCC 73102].
ConsensusfromContig2516Cyanobacteria-Nostoc_punctiforme_PCC_73102_gi186686830	1.70E-13	>YP_001870023 TPR repeat-containing protein [Nostoc punctiforme PCC 73102].
ConsensusfromContig8466Cyanobacteria-Nostoc_sp_PCC_7120_gi17230171	1.10E-11	>NP_486719 polyketide synthase [Nostoc sp. PCC 7120].
ConsensusfromContig7015Cyanobacteria-Prochlorococcus_marinus_str_MIT_9211_gi159904079	1.80E-15	>YP_001551423 hypothetical protein P9211_15381 [Prochlorococcus marinus str. MIT 9211].
ConsensusfromContig26 Cyanobacteria-Prochlorococcus_marinus_str_MIT_9301_gi126696593	1.00E-23	>YP_001091479 hypothetical protein P9301_12551 [Prochlorococcus marinus str. MIT 9301].
ConsensusfromContig1962Cyanobacteria-Synechococcus_elongatus_PCC_7942_gi81300390	1.70E-47	>YP_400598 peptidase M14, carboxypeptidase A [Synechococcus elongatus PCC 7942].

ConsensusfromContig2740Cyanobacteria-Synechococcus_sp_JA_2_3Ba_2_13__gi86609330	4.20E-18	>YP_478092 isopenicillin N-epimerase [Synechococcus sp. JA-2-3B'a(2-13)].
ConsensusfromContig3024Cyanobacteria-Synechococcus_sp_PCC_7335_gi254424572	2.00E-19	>ZP_05038290 Miro-like protein [Synechococcus sp. PCC 7335].
ConsensusfromContig2106Cyanobacteria-Synechococcus_sp_PCC_7335_gi254425464	1.40E-12	>ZP_05039181 Cna protein B-type domain [Synechococcus sp. PCC 7335].
ConsensusfromContig2106Cyanobacteria-Synechococcus_sp_PCC_7335_gi254425464	1.40E-12	>ZP_05039181 Cna protein B-type domain [Synechococcus sp. PCC 7335].
ConsensusfromContig3117Cyanobacteria-Synechococcus_sp_WH_5701_gi87300681	2.90E-17	>ZP_01083523 hypothetical protein WH5701_04515 [Synechococcus sp. WH 5701].
ConsensusfromContig7054Cyanobacteria-Synechococcus_sp_WH_5701_gi87302673	2.10E-12	>ZP_01085484 possible CsgA C-factor signaling protein [Synechococcus sp. WH 5701].
ConsensusfromContig6996Cyanobacteria-Synechococcus_sp_WH_7803_gi148240388	1.40E-26	>YP_001225775 oxidoreductase [Synechococcus sp. WH 7803].
ConsensusfromContig2084Cyanobacteria-Thermosynechococcus_elongatus_BP_1_gi22298150	2.00E-37	>NP_681397 putative oxidoreductase [Thermosynechococcus elongatus BP-1].
ConsensusfromContig3658Cyanobacteria-Trichodesmium_erythraeum_IMS101_gi113475094	4.60E-28	>YP_721155 peptidase S9, prolyl oligopeptidase active site region [Trichodesmium erythraeum IMS101].
ConsensusfromContig2009Cyanobacteria-Trichodesmium_erythraeum_IMS101_gi113477275	4.10E-54	>YP_723336 beta-ketoacyl synthase [Trichodesmium erythraeum IMS101].
ConsensusfromContig6080Cyanobacteria-Trichodesmium_erythraeum_IMS101_gi113477277	9.30E-25	>YP_723338 beta-ketoacyl synthase [Trichodesmium erythraeum IMS101].
ConsensusfromContig5009Cyanobacteria-Trichodesmium_erythraeum_IMS101_gi113478270	1.40E-12	>YP_724331 cyclic nucleotide-binding protein [Trichodesmium erythraeum IMS101].
ConsensusfromContig7211DeinococciThermus-Deinococcus_deserti_VCD115_gi226357403	9.10E-17	>YP_002787143 NAD dependent epimerase/dehydratase [Deinococcus deserti VCD115].
ConsensusfromContig5447DeinococciThermus-Deinococcus_geothermalis_DSM_11300_gi158421569	1.00E-13	>YP_001527796 SegD-like phage related protein [Deinococcus geothermalis DSM 11300].
ConsensusfromContig3128DeinococciThermus-Meiothermus_ruber_DSM_1279_gi291294603	3.50E-22	>YP_003506001 ribosylpyrimidine nucleosidase [Meiothermus ruber DSM 1279].
ConsensusfromContig4224DeinococciThermus-Meiothermus_ruber_DSM_1279_gi291295592	4.70E-13	>YP_003506990 peptidase S10 serine carboxypeptidase [Meiothermus ruber DSM 1279].
ConsensusfromContig2002DeinococciThermus-Meiothermus_silvanus_DSM_9946_gi297565194	7.70E-21	>YP_003684166 agmatinase [Meiothermus silvanus DSM 9946].
ConsensusfromContig6212DeinococciThermus-Thermus_thermophilus_HB27_gi46255233	7.80E-14	>YP_006145 ribonucleotide-diphosphate reductase subunit alpha [Thermus thermophilus HB27].
ConsensusfromContig2174DeinococciThermus-Truepera_radiovictrix_DSM_17093_gi297622358	1.10E-13	>YP_003703792 ribonucleoside-diphosphate reductase, alpha chain [Truepera radiovictrix DSM 17093].
ConsensusfromContig2018Dictyoglomi-Dictyoglomus_thermophilum_H_6_12_gi206900611	6.30E-14	>YP_002250229 laminarinase [Dictyoglomus thermophilum H-6-12].
ConsensusfromContig2277Dictyoglomi-Dictyoglomus_thermophilum_H_6_12_gi206901822	7.40E-15	>YP_002250172 alpha-rhamnosidase [Dictyoglomus thermophilum H-6-12].
ConsensusfromContig2154Excavata-Astasia_longa_tbALL00000054_3	1.30E-25	
ConsensusfromContig2658Excavata-Euglena_gracilis_tbELL00000319_1	2.20E-13	
ConsensusfromContig2497Excavata-Euglena_gracilis_tbELL00000560_1	1.80E-49	
ConsensusfromContig2777Excavata-Euglena_gracilis_tbELL00000933_2	1.20E-12	
ConsensusfromContig1952Excavata-Euglena_gracilis_tbELL00001898_2	3.20E-12	
ConsensusfromContig7425Excavata-Euglena_gracilis_tbELL00002054_3	2.60E-27	
ConsensusfromContig3199Excavata-Euglena_gracilis_tbELL00002086_3	7.10E-18	
ConsensusfromContig4852Excavata-Euglena_gracilis_tbELL00002260_2	1.50E-14	
ConsensusfromContig6752Excavata-Euglena_gracilis_tbELL00002338_3	2.70E-11	
ConsensusfromContig6936Excavata-Euglena_gracilis_tbELL00002868_1	2.50E-12	
ConsensusfromContig6933Excavata-Euglena_gracilis_tbELL00003263_3	5.00E-29	
ConsensusfromContig9390Excavata-Euglena_gracilis_tbELL00003397_1	3.20E-14	
ConsensusfromContig5777Excavata-Euglena_gracilis_tbELL00004982_2	3.10E-13	
ConsensusfromContig1918Excavata-Euglena_gracilis_tbELL00006259_3	5.20E-11	
ConsensusfromContig2791Excavata-Euglena_gracilis_tbELL00006630_1	2.20E-30	
ConsensusfromContig5236Excavata-Giardia_lamblia_ATCC_50803_gi159112398	5.10E-16	>XP_001706428 Dynein light chain [Giardia lamblia ATCC 50803].
ConsensusfromContig1890Excavata-Giardia_lamblia_ATCC_50803_gi159119436	1.90E-11	>XP_001709936 Dynein heavy chain [Giardia lamblia ATCC 50803].
ConsensusfromContig1864Excavata-Histiona_aroides_tbHAL00000935_2	6.90E-13	
ConsensusfromContig1986Excavata-Histiona_aroides_tbHAL00000935_2	1.00E-25	
ConsensusfromContig5201Excavata-Histiona_aroides_tbHAL00001599_1	4.90E-30	
ConsensusfromContig5902Excavata-Jakoba_bahamiensis_tbJBL00000423_2	1.70E-16	
ConsensusfromContig4096Excavata-Jakoba_bahamiensis_tbJBL00000773_1	1.70E-25	
ConsensusfromContig4096Excavata-Jakoba_bahamiensis_tbJBL00000773_1	1.70E-25	
ConsensusfromContig3124Excavata-Jakoba_bahamiensis_tbJBL00001118_1	1.40E-38	
ConsensusfromContig3596Excavata-Jakoba_bahamiensis_tbJBL00001352_2	1.70E-11	
ConsensusfromContig2045Excavata-Jakoba_bahamiensis_tbJBL00001557_2	5.60E-14	
ConsensusfromContig1848Excavata-Jakoba_bahamiensis_tbJBL00002014_2	7.20E-11	
ConsensusfromContig2543Excavata-Jakoba_libera_tbJLL00000046_3	8.70E-17	
ConsensusfromContig3006Excavata-Jakoba_libera_tbJLL00000048_4	2.20E-13	
ConsensusfromContig3246Excavata-Jakoba_libera_tbJLL00000110_3	4.00E-17	
ConsensusfromContig5464Excavata-Jakoba_libera_tbJLL00000527_2	2.20E-14	
ConsensusfromContig5283Excavata-Jakoba_libera_tbJLL00000733_2	1.80E-20	
ConsensusfromContig2102Excavata-Jakoba_libera_tbJLL00000772_2	1.00E-125	
ConsensusfromContig3103Excavata-Jakoba_libera_tbJLL00001235_1	6.70E-11	
ConsensusfromContig3830Excavata-Leishmania_braziliensis_MHOM/BR/75/M2904_gi154334765	6.40E-12	>XP_001563629 histone acethyltransferase-like protein [Leishmania braziliensis MHOM/BR/75/M2904].
ConsensusfromContig1383Excavata-Leishmania_braziliensis_MHOM/BR/75/M2904_gi154342546	4.80E-14	>XP_001567221 succinyl-diaminopimelate desuccinylase-like protein [Leishmania braziliensis MHOM/BR/75/M2904].
ConsensusfromContig2019Excavata-Leishmania_braziliensis_MHOM/BR/75/M2904_gi154343315	1.50E-11	>XP_001567603 membrane associated protein-like protein [Leishmania braziliensis MHOM/BR/75/M2904].
ConsensusfromContig3210Excavata-Leishmania_braziliensis_MHOM/BR/75/M2904_gi154344449	7.20E-16	>XP_001568166 proteophosphoglycan ppg4 [Leishmania braziliensis MHOM/BR/75/M2904].
ConsensusfromContig5106Excavata-Leishmania_braziliensis_MHOM/BR/75/M2904_gi154344449	4.90E-17	>XP_001568166 proteophosphoglycan ppg4 [Leishmania braziliensis MHOM/BR/75/M2904].
ConsensusfromContig6929Excavata-Leishmania_braziliensis_MHOM/BR/75/M2904_gi154344451	1.00E-11	>XP_001568167 proteophosphoglycan ppg4 [Leishmania braziliensis MHOM/BR/75/M2904].
ConsensusfromContig5176Excavata-Leishmania_infantum_JPCM5_gi146076105	5.10E-21	>XP_001462839 pteridine transporter (truncated) [Leishmania infantum JPCM5].
ConsensusfromContig1949Excavata-Leishmania_infantum_JPCM5_gi146081619	1.70E-11	>XP_001464297 kinesin K39 [Leishmania infantum JPCM5].
ConsensusfromContig6944Excavata-Leishmania_infantum_JPCM5_gi146089119	3.10E-15	>XP_001466240 hypothetical protein [Leishmania infantum JPCM5].
ConsensusfromContig2084Excavata-Leishmania_major_strain_Friedlin_gi157865947	1.30E-16	>XP_001681680 surface antigen protein [Leishmania major strain Friedlin].
ConsensusfromContig5142Excavata-Leishmania_major_strain_Friedlin_gi157867349	2.00E-12	>XP_001682229 kinesin [Leishmania major strain Friedlin].
ConsensusfromContig3058Excavata-Leishmania_major_strain_Friedlin_gi157867524	1.40E-12	>XP_001682316 hypothetical protein [Leishmania major strain Friedlin].
ConsensusfromContig1944Excavata-Leishmania_major_strain_Friedlin_gi72547023	3.10E-19	>XP_843162 proteophosphoglycan ppg4 [Leishmania major strain Friedlin].
ConsensusfromContig1959Excavata-Leishmania_major_strain_Friedlin_gi72547023	2.20E-16	>XP_843162 proteophosphoglycan ppg4 [Leishmania major strain Friedlin].
ConsensusfromContig3126Excavata-Leishmania_major_strain_Friedlin_gi72547023	5.80E-12	>XP_843162 proteophosphoglycan ppg4 [Leishmania major strain Friedlin].
ConsensusfromContig3128Excavata-Leishmania_major_strain_Friedlin_gi72547023	8.90E-13	>XP_843162 proteophosphoglycan ppg4 [Leishmania major strain Friedlin].
ConsensusfromContig5101Excavata-Leishmania_major_strain_Friedlin_gi72547023	6.80E-17	>XP_843162 proteophosphoglycan ppg4 [Leishmania major strain Friedlin].
ConsensusfromContig5127Excavata-Leishmania_major_strain_Friedlin_gi72547023	1.40E-12	>XP_843162 proteophosphoglycan ppg4 [Leishmania major strain Friedlin].
ConsensusfromContig1966Excavata-Leishmania_major_strain_Friedlin_gi72547036	8.50E-14	>XP_843163 proteophosphoglycan 5 [Leishmania major strain Friedlin].
ConsensusfromContig6924Excavata-Leishmania_major_strain_Friedlin_gi72547036	2.30E-11	>XP_843163 proteophosphoglycan 5 [Leishmania major strain Friedlin].
ConsensusfromContig3016Excavata-Malawimonas_californiana_tbMCL00000127_3	2.10E-19	
ConsensusfromContig1952Excavata-Malawimonas_californiana_tbMCL00000245_2	1.90E-48	
ConsensusfromContig1960Excavata-Malawimonas_californiana_tbMCL00001730_1	6.60E-12	
ConsensusfromContig2637Excavata-Malawimonas_californiana_tbMCL00002202_3	4.10E-15	
ConsensusfromContig5977Excavata-Malawimonas_californiana_tbMCL00002297_2	7.40E-14	
ConsensusfromContig2894Excavata-Malawimonas_jakobiformis_tbMJL00000816_2	1.70E-22	
ConsensusfromContig3503Excavata-Malawimonas_jakobiformis_tbMJL00001256_3	9.20E-11	
ConsensusfromContig3629Excavata-Malawimonas_jakobiformis_tbMJL00001256_3	1.90E-12	
ConsensusfromContig2367Excavata-Malawimonas_jakobiformis_tbMJL00001276_2	6.00E-18	
ConsensusfromContig2103Excavata-Malawimonas_jakobiformis_tbMJL00002721_1	1.50E-30	
ConsensusfromContig5103Excavata-Malawimonas_jakobiformis_tbMJL00003571_3	6.90E-24	
ConsensusfromContig5121Excavata-Naegleria_gruberi_strain_NEG_M_gi290973659	3.40E-39	>XP_002669565 phosphatidylserine synthase [Naegleria gruberi].
ConsensusfromContig1937Excavata-Naegleria_gruberi_strain_NEG_M_gi290974128	9.50E-29	>XP_002669798 predicted protein [Naegleria gruberi].
ConsensusfromContig1947Excavata-Naegleria_gruberi_strain_NEG_M_gi290974128	2.10E-49	>XP_002669798 predicted protein [Naegleria gruberi].
ConsensusfromContig1997Excavata-Naegleria_gruberi_strain_NEG_M_gi290974128	5.70E-24	>XP_002669798 predicted protein [Naegleria gruberi].
ConsensusfromContig2029Excavata-Naegleria_gruberi_strain_NEG_M_gi290974128	1.90E-71	>XP_002669798 predicted protein [Naegleria gruberi].
ConsensusfromContig3140Excavata-Naegleria_gruberi_strain_NEG_M_gi290974128	2.20E-32	>XP_002669798 predicted protein [Naegleria gruberi].
ConsensusfromContig5170Excavata-Naegleria_gruberi_strain_NEG_M_gi290974128	7.30E-71	>XP_002669798 predicted protein [Naegleria gruberi].
ConsensusfromContig5200Excavata-Naegleria_gruberi_strain_NEG_M_gi290974128	4.30E-19	>XP_002669798 predicted protein [Naegleria gruberi].
ConsensusfromContig5201Excavata-Naegleria_gruberi_strain_NEG_M_gi290974128	4.80E-12	>XP_002669798 predicted protein [Naegleria gruberi].
ConsensusfromContig5443Excavata-Naegleria_gruberi_strain_NEG_M_gi290974128	1.20E-19	>XP_002669798 predicted protein [Naegleria gruberi].
ConsensusfromContig5455Excavata-Naegleria_gruberi_strain_NEG_M_gi290974128	1.50E-17	>XP_002669798 predicted protein [Naegleria gruberi].
ConsensusfromContig5767Excavata-Naegleria_gruberi_strain_NEG_M_gi290974128	5.60E-11	>XP_002669798 predicted protein [Naegleria gruberi].
ConsensusfromContig6934Excavata-Naegleria_gruberi_strain_NEG_M_gi290974128	2.70E-79	>XP_002669798 predicted protein [Naegleria gruberi].
ConsensusfromContig6960Excavata-Naegleria_gruberi_strain_NEG_M_gi290974128	7.90E-80	>XP_002669798 predicted protein [Naegleria gruberi].

ConsensusfromContig5128	Excavata-Naegleria_gruberi_strain_NEG_M_gi290978417	1.10E-34	>XP_002671932 predicted protein [Naegleria gruberi].
ConsensusfromContig2015	Excavata-Naegleria_gruberi_strain_NEG_M_gi290978957	9.50E-13	>XP_002672201 predicted protein [Naegleria gruberi].
ConsensusfromContig1942	Excavata-Naegleria_gruberi_strain_NEG_M_gi290979914	2.80E-17	>XP_002672678 predicted protein [Naegleria gruberi].
ConsensusfromContig2928	Excavata-Naegleria_gruberi_strain_NEG_M_gi290980695	2.60E-11	>XP_002673067 predicted protein [Naegleria gruberi].
ConsensusfromContig4840	Excavata-Naegleria_gruberi_strain_NEG_M_gi290981736	2.70E-15	>XP_002673587 predicted protein [Naegleria gruberi].
ConsensusfromContig4840	Excavata-Naegleria_gruberi_strain_NEG_M_gi290981736	2.70E-15	>XP_002673587 predicted protein [Naegleria gruberi].
ConsensusfromContig1535	Excavata-Naegleria_gruberi_strain_NEG_M_gi290984568	2.00E-27	>XP_002674999 poly ADP-ribose polymerase family, member 14-like protein [Naegleria gruberi].
ConsensusfromContig2005	Excavata-Naegleria_gruberi_strain_NEG_M_gi290984568	2.30E-27	>XP_002674999 poly ADP-ribose polymerase family, member 14-like protein [Naegleria gruberi].
ConsensusfromContig2438	Excavata-Naegleria_gruberi_strain_NEG_M_gi290984809	1.20E-14	>XP_002675119 predicted protein [Naegleria gruberi].
ConsensusfromContig3101	Excavata-Naegleria_gruberi_strain_NEG_M_gi290986675	1.60E-13	>XP_002676049 histone demethlylase [Naegleria gruberi].
ConsensusfromContig2043	Excavata-Naegleria_gruberi_strain_NEG_M_gi290987293	1.20E-15	>XP_002676357 predicted protein [Naegleria gruberi].
ConsensusfromContig5318	Excavata-Naegleria_gruberi_strain_NEG_M_gi290987567	1.80E-23	>XP_002676494 hypothetical protein NAEGRDRAFT_68477 [Naegleria gruberi].
ConsensusfromContig5132	Excavata-Naegleria_gruberi_strain_NEG_M_gi290990672	2.30E-42	>XP_002677960 ATP-dependent DNA ligase IV [Naegleria gruberi].
ConsensusfromContig5207	Excavata-Naegleria_gruberi_strain_NEG_M_gi290992999	6.70E-17	>XP_002679121 set domain-containing protein [Naegleria gruberi].
ConsensusfromContig2169	Excavata-Naegleria_gruberi_strain_NEG_M_gi291000230	1.10E-18	>XP_002682682 predicted protein [Naegleria gruberi].
ConsensusfromContig3126	Excavata-Naegleria_gruberi_strain_NEG_M_gi291000230	4.00E-40	>XP_002682682 predicted protein [Naegleria gruberi].
ConsensusfromContig6386	Excavata-Naegleria_gruberi_strain_NEG_M_gi291000248	7.00E-16	>XP_002682691 predicted protein [Naegleria gruberi].
ConsensusfromContig6437	Excavata-Naegleria_gruberi_strain_NEG_M_gi291001209	2.00E-14	>XP_002683171 predicted protein [Naegleria gruberi].
ConsensusfromContig2092	Excavata-Naegleria_gruberi_strain_NEG_M_gi291001341	1.80E-38	>XP_002683237 rab family small GTPase [Naegleria gruberi].
ConsensusfromContig4507	Excavata-Reclinomonas_americana_tbRAL00000634_1	1.70E-18	
ConsensusfromContig1974	Excavata-Reclinomonas_americana_tbRAL00001303_2	3.10E-19	
ConsensusfromContig2464	Excavata-Reclinomonas_americana_tbRAL00003137_1	1.20E-29	
ConsensusfromContig2464	Excavata-Reclinomonas_americana_tbRAL00003137_1	1.20E-29	
ConsensusfromContig2213	Excavata-Reclinomonas_americana_tbRAL00006189_2	1.90E-24	
ConsensusfromContig1998	Excavata-Reclinomonas_americana_tbRAL00006305_2	2.50E-30	
ConsensusfromContig8913	Excavata-Reclinomonas_americana_tbRAL00006330_1	2.50E-11	
ConsensusfromContig1993	Excavata-Seculamonas_ecuadoriensis_tbSEL00000214_2	1.70E-17	
ConsensusfromContig3304	Excavata-Seculamonas_ecuadoriensis_tbSEL00000424_2	4.90E-17	
ConsensusfromContig2038	Excavata-Seculamonas_ecuadoriensis_tbSEL00000602_1	7.70E-12	
ConsensusfromContig2266	Excavata-Seculamonas_ecuadoriensis_tbSEL00000741_1	3.20E-53	
ConsensusfromContig1507	Excavata-Seculamonas_ecuadoriensis_tbSEL00001931_2	2.90E-14	
ConsensusfromContig2311	Excavata-Stachyamoeba_lipophora_tbSLL00001107_2	5.00E-14	
ConsensusfromContig3201	Excavata-Trichomonas_vaginalis_G3_gi123397103	2.60E-63	>XP_001301026 hypothetical protein [Trichomonas vaginalis G3].
ConsensusfromContig2301	Excavata-Trichomonas_vaginalis_G3_gi123398905	1.80E-31	>XP_001301368 ankyrin repeat protein [Trichomonas vaginalis G3].
ConsensusfromContig6801	Excavata-Trichomonas_vaginalis_G3_gi123408691	1.70E-11	>XP_001303246 surface antigen BspA-like [Trichomonas vaginalis G3].
ConsensusfromContig5422	Excavata-Trichomonas_vaginalis_G3_gi123411526	1.20E-25	>XP_001303902 hypothetical protein [Trichomonas vaginalis G3].
ConsensusfromContig6965	Excavata-Trichomonas_vaginalis_G3_gi123438302	6.20E-28	>XP_001309937 C2 domain containing protein [Trichomonas vaginalis G3].
ConsensusfromContig2327	Excavata-Trichomonas_vaginalis_G3_gi123453498	3.70E-64	>XP_001314730 ankyrin repeat protein [Trichomonas vaginalis G3].
ConsensusfromContig5224	Excavata-Trichomonas_vaginalis_G3_gi123473584	1.10E-20	>XP_001319979 hypothetical protein [Trichomonas vaginalis G3].
ConsensusfromContig4291	Excavata-Trichomonas_vaginalis_G3_gi154411809	7.30E-16	>XP_001578939 surface antigen BspA-like [Trichomonas vaginalis G3].
ConsensusfromContig1984	Excavata-Trichomonas_vaginalis_G3_gi154416369	1.10E-72	>XP_001581207 CAMK family protein kinase [Trichomonas vaginalis G3].
ConsensusfromContig5210	Excavata-Trichomonas_vaginalis_G3_gi154418773	7.00E-11	>XP_001582404 viral A-type inclusion protein [Trichomonas vaginalis G3].
ConsensusfromContig2237	Excavata-Trimastix_pyriformis_tbTPL00001196_1	4.90E-47	
ConsensusfromContig1881	Excavata-Trimastix_pyriformis_tbTPL00001510_1	4.10E-12	
ConsensusfromContig6974	Excavata-Trimastix_pyriformis_tbTPL00001510_1	1.70E-17	
ConsensusfromContig2542	Excavata-Trimastix_pyriformis_tbTPL00001760_2	1.70E-27	
ConsensusfromContig2331	Excavata-Trimastix_pyriformis_tbTPL00002376_3	2.10E-38	
ConsensusfromContig2849	Excavata-Trypanosoma_brucei_TREU927_gi72388916	2.10E-11	>XP_844753 casein kinase I, epsilon isoform [Trypanosoma brucei TREU927].
ConsensusfromContig2629	Excavata-Trypanosoma_brucei_TREU927_gi72389737	2.10E-32	>XP_845163 peptidase M20/M25/M40 [Trypanosoma brucei TREU927].
ConsensusfromContig3313	Excavata-Trypanosoma_brucei_TREU927_gi72390579	1.90E-39	>XP_845584 hypothetical protein [Trypanosoma brucei TREU927].
ConsensusfromContig3530	Excavata-Trypanosoma_cruzi_strain_CL_Brener_gi71406035	2.30E-40	>XP_805588 serine/threonine-protein phosphatase 2A, catalytic subunit [Trypanosoma cruzi strain CL Brener].
ConsensusfromContig6958	FibrobacteresAcidobacteria-Acidobacterium_capsulatum_ATCC_51196_gi225872508	1.20E-63	>YP_002753963 hypothetical protein ACP_0852 [Acidobacterium capsulatum ATCC 51196].
ConsensusfromContig2294	FibrobacteresAcidobacteria-Acidobacterium_capsulatum_ATCC_51196_gi225873198	1.60E-14	>YP_002754657 glycosyl hydrolase, family 39 [Acidobacterium capsulatum ATCC 51196].
ConsensusfromContig2205	FibrobacteresAcidobacteria-Acidobacterium_sp_MP5ACTX8_gi299136609	2.90E-18	>ZP_07029792 conserved hypothetical protein [Acidobacterium sp. MP5ACTX8].
ConsensusfromContig5117	FibrobacteresAcidobacteria-Acidobacterium_sp_MP5ACTX8_gi299137242	3.60E-11	>ZP_07030424 Fibronectin type III domain protein [Acidobacterium sp. MP5ACTX8].
ConsensusfromContig38	FibrobacteresAcidobacteria-Acidobacterium_sp_MP5ACTX8_gi299139613	8.00E-16	>ZP_07032787 putative esterase [Acidobacterium sp. MP5ACTX8].
ConsensusfromContig2263	FibrobacteresAcidobacteria-Acidobacterium_sp_MP5ACTX8_gi299139960	4.90E-11	>ZP_07033131 conserved hypothetical protein [Acidobacterium sp. MP5ACTX8].
ConsensusfromContig3462	FibrobacteresAcidobacteria-Candidatus_Koribacter_versatilis_Ellin345_gi94967927	4.10E-25	>YP_589975 Alpha-glucosidase [Candidatus Koribacter versatilis Ellin345].
ConsensusfromContig3123	FibrobacteresAcidobacteria-Candidatus_Koribacter_versatilis_Ellin345_gi94970276	8.00E-19	>YP_592324 glycoside hydrolase, clan GH-D [Candidatus Koribacter versatilis Ellin345].
ConsensusfromContig5119	FibrobacteresAcidobacteria-Candidatus_Solibacter_usitatus_Ellin6076_gi116619336	2.00E-16	>YP_821492 exo-alpha-sialidase [Candidatus Solibacter usitatus Ellin6076].
ConsensusfromContig7407	FibrobacteresAcidobacteria-Candidatus_Solibacter_usitatus_Ellin6076_gi116619343	1.30E-22	>YP_821499 hypothetical protein Acid_0200 [Candidatus Solibacter usitatus Ellin6076].
ConsensusfromContig1985	FibrobacteresAcidobacteria-Candidatus_Solibacter_usitatus_Ellin6076_gi116619958	1.70E-84	>YP_822114 peptidase S15 [Candidatus Solibacter usitatus Ellin6076].
ConsensusfromContig5135	FibrobacteresAcidobacteria-Candidatus_Solibacter_usitatus_Ellin6076_gi116619958	1.30E-79	>YP_822114 peptidase S15 [Candidatus Solibacter usitatus Ellin6076].
ConsensusfromContig6935	FibrobacteresAcidobacteria-Candidatus_Solibacter_usitatus_Ellin6076_gi116619958	2.30E-35	>YP_822114 peptidase S15 [Candidatus Solibacter usitatus Ellin6076].
ConsensusfromContig1971	FibrobacteresAcidobacteria-Candidatus_Solibacter_usitatus_Ellin6076_gi116620173	8.80E-64	>YP_822329 HpcH/HpaI aldolase [Candidatus Solibacter usitatus Ellin6076].
ConsensusfromContig2928	FibrobacteresAcidobacteria-Candidatus_Solibacter_usitatus_Ellin6076_gi116620173	1.80E-30	>YP_822329 HpcH/HpaI aldolase [Candidatus Solibacter usitatus Ellin6076].
ConsensusfromContig8155	FibrobacteresAcidobacteria-Candidatus_Solibacter_usitatus_Ellin6076_gi116622321	2.50E-26	>YP_824477 putative esterase [Candidatus Solibacter usitatus Ellin6076].
ConsensusfromContig2086	FibrobacteresAcidobacteria-Candidatus_Solibacter_usitatus_Ellin6076_gi116622764	5.40E-29	>YP_824920 phytanoyl-CoA dioxygenase [Candidatus Solibacter usitatus Ellin6076].
ConsensusfromContig5347	FibrobacteresAcidobacteria-Candidatus_Solibacter_usitatus_Ellin6076_gi116623080	3.30E-12	>YP_825236 hypothetical protein Acid_3984 [Candidatus Solibacter usitatus Ellin6076].
ConsensusfromContig2066	FibrobacteresAcidobacteria-Candidatus_Solibacter_usitatus_Ellin6076_gi116625203	1.70E-27	>YP_827359 selenocysteine synthase-like protein [Candidatus Solibacter usitatus Ellin6076].
ConsensusfromContig2413	FibrobacteresAcidobacteria-Candidatus_Solibacter_usitatus_Ellin6076_gi116625203	4.40E-12	>YP_827359 selenocysteine synthase-like protein [Candidatus Solibacter usitatus Ellin6076].
ConsensusfromContig2807	FibrobacteresAcidobacteria-Candidatus_Solibacter_usitatus_Ellin6076_gi116625211	9.80E-11	>YP_827367 hypothetical protein Acid_6156 [Candidatus Solibacter usitatus Ellin6076].
ConsensusfromContig6088	FibrobacteresAcidobacteria-Candidatus_Solibacter_usitatus_Ellin6076_gi116625211	1.90E-48	>YP_827367 hypothetical protein Acid_6156 [Candidatus Solibacter usitatus Ellin6076].
ConsensusfromContig2256	FibrobacteresAcidobacteria-Candidatus_Solibacter_usitatus_Ellin6076_gi116626332	4.00E-24	>YP_828488 hypothetical protein Acid_7292 [Candidatus Solibacter usitatus Ellin6076].
ConsensusfromContig2514	Firmicutes-Abiotrophia_defectiva_ATCC_49176_gi229826180	5.80E-16	>ZP_04452249 hypothetical protein GCWU000182_01552 [Abiotrophia defectiva ATCC 49176].
ConsensusfromContig2915	Firmicutes-Ammonifex_degensii_KC4_gi260891938	3.70E-17	>YP_003238035 SNO glutamine amidotransferase [Ammonifex degensii KC4].
ConsensusfromContig2082	Firmicutes-Bacillus_amyloliquefaciens_FZB42_gi154687458	1.90E-42	>YP_001422619 YvgN [Bacillus amyloliquefaciens FZB42].
ConsensusfromContig5300	Firmicutes-Bacillus_cellulosilyticus_DSM_2522_gi283848060	4.50E-16	>ZP_06365477 D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding [Bacillus cellulosilyticus DSM 2522].
ConsensusfromContig2204	Firmicutes-Bacillus_cereus_BDRD_ST196_gi229133742	8.40E-15	>ZP_04262568 Ankyrin repeat protein [Bacillus cereus BDRD-ST196].
ConsensusfromContig7100	Firmicutes-Bacillus_cereus_W_gi196036338	1.80E-11	>ZP_03103736 methyltransferase, FkbM family protein [Bacillus cereus W].
ConsensusfromContig5462	Firmicutes-Bacillus_pumilus_ATCC_7061_gi194015228	2.90E-37	>ZP_03053844 DNA methylase [Bacillus pumilus ATCC 7061].
ConsensusfromContig6702	Firmicutes-Bacillus_pumilus_ATCC_7061_gi194015228	9.60E-27	>ZP_03053844 DNA methylase [Bacillus pumilus ATCC 7061].
ConsensusfromContig5123	Firmicutes-Bacillus_sp_NRRL_B_14911_gi89098301	3.00E-13	>ZP_01171185 acetyltransferase, GNAT family protein [Bacillus sp. NRRL B-14911].
ConsensusfromContig2917	Firmicutes-Bacillus_sp_NRRL_B_14911_gi89098430	9.90E-17	>ZP_01171314 stage V sporulation protein K [Bacillus sp. NRRL B-14911].
ConsensusfromContig6070	Firmicutes-Bacillus_weihenstephanensis_KBAB4_gi163937911	1.80E-16	>YP_001642797 phage minor structural protein [Bacillus weihenstephanensis KBAB4].
ConsensusfromContig2596	Firmicutes-Caldicellulosiruptor_saccharolyticus_DSM_8903_gi146297401	2.30E-22	>YP_001181172 glycoside hydrolase family protein [Caldicellulosiruptor saccharolyticus DSM 8903].
ConsensusfromContig2080	Firmicutes-Caldicellulosiruptor_saccharolyticus_DSM_8903_gi146297523	6.80E-24	>YP_001181294 hypothetical protein Csac_2528 [Caldicellulosiruptor saccharolyticus DSM 8903].
ConsensusfromContig6961	Firmicutes-Clostridiales_bacterium_1_7_47FAA_gi239628103	7.50E-49	>ZP_04671134 D-mannonate dehydratase [Clostridiales bacterium 1_7_47_FAA].
ConsensusfromContig1958	Firmicutes-Clostridium_botulinum_B_str_Eklund_17B_gi187934575	7.50E-14	>YP_001885133 DNA methyltransferase [Clostridium botulinum B str. Eklund 17B].
ConsensusfromContig6925	Firmicutes-Clostridium_botulinum_B_str_Eklund_17B_gi187934575	4.20E-19	>YP_001885133 DNA methyltransferase [Clostridium botulinum B str. Eklund 17B].
ConsensusfromContig2165	Firmicutes-Clostridium_butyricum_5521_gi182418782	1.10E-27	>ZP_02950050 stage V sporulation protein K [Clostridium butyricum 5521].
ConsensusfromContig1961	Firmicutes-Clostridium_cellulolyticum_H10_gi220929020	1.50E-37	>YP_002505929 glycoside hydrolase clan GH-D [Clostridium cellulolyticum H10].
ConsensusfromContig1935	Firmicutes-Clostridium_difficile_QCD_63q42_gi255103003	3.70E-31	>ZP_05331980 DNA methylase N-4/N-6 domain-containing protein [Clostridium difficile QCD-63q42].
ConsensusfromContig2303	Firmicutes-Clostridium_difficile_QCD_63q42_gi255103003	4.70E-17	>ZP_05331980 DNA methylase N-4/N-6 domain-containing protein [Clostridium difficile QCD-63q42].
ConsensusfromContig5154	Firmicutes-Clostridium_leptum_DSM_753_gi160934207	7.00E-36	>ZP_02081594 hypothetical protein CLOLEP_03078 [Clostridium leptum DSM 753].
ConsensusfromContig5155	Firmicutes-Clostridium_methylpentosum_DSM_5476_gi225017953	8.60E-13	>ZP_03707145 hypothetical protein CLOSTMETH_01888 [Clostridium methylpentosum DSM 5476].
ConsensusfromContig6103	Firmicutes-Clostridium_methylpentosum_DSM_5476_gi225018998	1.80E-17	>ZP_03708190 hypothetical protein CLOSTMETH_02949 [Clostridium methylpentosum DSM 5476].
ConsensusfromContig2010	Firmicutes-Clostridium_perfringens_C_str_JGS1495_gi169342803	2.10E-18	>ZP_02863837 putative sporulation protein [Clostridium perfringens C str. JGS1495].
ConsensusfromContig2377	Firmicutes-Desulfotomaculum_acetoxidans_DSM_771_gi258515056	1.60E-30	>YP_003191278 Nitrilase/cyanide hydratase and apolipoprotein N- acyltransferase [Desulfotomaculum acetoxidans DSM 771].
ConsensusfromContig2898	Firmicutes-Desulfotomaculum_acetoxidans_DSM_771_gi258516949	8.20E-15	>YP_003193171 pyruvate phosphate dikinase PEP/pyruvate- binding [Desulfotomaculum acetoxidans DSM 771].

ConsensusfromContig3838	Firmicutes-Eubacterium_siraeum_DSM_15702_gi167751650	1.30E-15	>ZP_02423777 hypothetical protein EUBSIR_02655 [Eubacterium siraeum DSM 15702].
ConsensusfromContig4225	Firmicutes-Eubacterium_siraeum_DSM_15702_gi167751650	1.40E-13	>ZP_02423777 hypothetical protein EUBSIR_02655 [Eubacterium siraeum DSM 15702].
ConsensusfromContig1889	Firmicutes-Exiguobacterium_sibiricum_255_15_gi172057190	1.20E-13	>YP_001813650 ABC transporter related [Exiguobacterium sibiricum 255-15].
ConsensusfromContig2348	Firmicutes-Exiguobacterium_sibiricum_255_15_gi172057190	1.20E-16	>YP_001813650 ABC transporter related [Exiguobacterium sibiricum 255-15].
ConsensusfromContig4848	Firmicutes-Geobacillus_sp_Y41MC1_gi255332763	7.70E-20	>ZP_05373760 ATP-dependent DNA helicase PcrA [Geobacillus sp. Y4.1MC1].
ConsensusfromContig6056	Firmicutes-Geobacillus_thermodenitrificans_NG80_2_gi138895762	2.10E-14	>YP_001126215 methylglyoxal synthase [Geobacillus thermodenitrificans NG80-2].
ConsensusfromContig2984	Firmicutes-Lactobacillus_rhamnosus_LMS2_1_gi229553373	6.00E-11	>ZP_04442098 beta-galactosidase [Lactobacillus rhamnosus LMS2-1].
ConsensusfromContig4226	Firmicutes-Leuconostoc_kimchii_IMSNU_11154_gi296111465	6.00E-12	>YP_003621847 Hemolysin-type calcium-binding region:RTX N-terminal domain protein [Leuconostoc kimchii IMSNU 11154].
ConsensusfromContig2088	Firmicutes-Leuconostoc_mesenteroides_subsp_cremoris_ATCC_19254_gi227431774	5.60E-18	>ZP_03913801 adenine-specific methyltransferase [Leuconostoc mesenteroides subsp. cremoris ATCC 19254].
ConsensusfromContig1948	Firmicutes-Lysinibacillus_fusiformis_ZC1_gi299536085	1.50E-21	>ZP_07049402 cellulosome anchoring protein cohesin region [Lysinibacillus fusiformis ZC1].
ConsensusfromContig1955	Firmicutes-Lysinibacillus_fusiformis_ZC1_gi299536085	6.20E-27	>ZP_07049402 cellulosome anchoring protein cohesin region [Lysinibacillus fusiformis ZC1].
ConsensusfromContig1976	Firmicutes-Lysinibacillus_fusiformis_ZC1_gi299536085	3.50E-22	>ZP_07049402 cellulosome anchoring protein cohesin region [Lysinibacillus fusiformis ZC1].
ConsensusfromContig1989	Firmicutes-Lysinibacillus_fusiformis_ZC1_gi299536085	2.10E-19	>ZP_07049402 cellulosome anchoring protein cohesin region [Lysinibacillus fusiformis ZC1].
ConsensusfromContig2980	Firmicutes-Lysinibacillus_fusiformis_ZC1_gi299536085	2.10E-21	>ZP_07049402 cellulosome anchoring protein cohesin region [Lysinibacillus fusiformis ZC1].
ConsensusfromContig3231	Firmicutes-Lysinibacillus_fusiformis_ZC1_gi299536085	3.70E-28	>ZP_07049402 cellulosome anchoring protein cohesin region [Lysinibacillus fusiformis ZC1].
ConsensusfromContig5269	Firmicutes-Lysinibacillus_fusiformis_ZC1_gi299536085	4.90E-25	>ZP_07049402 cellulosome anchoring protein cohesin region [Lysinibacillus fusiformis ZC1].
ConsensusfromContig5605	Firmicutes-Lysinibacillus_fusiformis_ZC1_gi299536085	2.20E-14	>ZP_07049402 cellulosome anchoring protein cohesin region [Lysinibacillus fusiformis ZC1].
ConsensusfromContig5977	Firmicutes-Lysinibacillus_fusiformis_ZC1_gi299536085	6.90E-13	>ZP_07049402 cellulosome anchoring protein cohesin region [Lysinibacillus fusiformis ZC1].
ConsensusfromContig5605	Firmicutes-Lysinibacillus_fusiformis_ZC1_gi299536085	2.20E-14	>ZP_07049402 cellulosome anchoring protein cohesin region [Lysinibacillus fusiformis ZC1].
ConsensusfromContig4283	Firmicutes-Moorella_thermoacetica_ATCC_39073_gi83590730	5.10E-11	>YP_430739 hypothetical protein Moth_1896 [Moorella thermoacetica ATCC 39073].
ConsensusfromContig2269	Firmicutes-Paenibacillus_sp_JDR_2_gi251794383	1.60E-25	>YP_003009114 6-phosphogluconolactonase [Paenibacillus sp. JDR-2].
ConsensusfromContig2088	Firmicutes-Paenibacillus_sp_JDR_2_gi251794554	4.20E-12	>YP_003009285 hypothetical protein Pjdr2_0518 [Paenibacillus sp. JDR-2].
ConsensusfromContig2089	Firmicutes-Paenibacillus_sp_JDR_2_gi251794554	1.60E-22	>YP_003009285 hypothetical protein Pjdr2_0518 [Paenibacillus sp. JDR-2].
ConsensusfromContig2086	Firmicutes-Paenibacillus_sp_JDR_2_gi251794782	1.80E-40	>YP_003009513 Alpha-galactosidase [Paenibacillus sp. JDR-2].
ConsensusfromContig2127	Firmicutes-Paenibacillus_sp_JDR_2_gi251794963	1.30E-13	>YP_003009694 Parallel beta-helix repeat protein [Paenibacillus sp. JDR-2].
ConsensusfromContig2227	Firmicutes-Paenibacillus_sp_JDR_2_gi251794963	6.90E-16	>YP_003009694 Parallel beta-helix repeat protein [Paenibacillus sp. JDR-2].
ConsensusfromContig2274	Firmicutes-Paenibacillus_sp_JDR_2_gi251795753	1.30E-21	>YP_003010484 oxidoreductase domain protein [Paenibacillus sp. JDR-2].
ConsensusfromContig1952	Firmicutes-Paenibacillus_sp_JDR_2_gi251797225	9.50E-16	>YP_003011956 Phytanoyl-CoA dioxygenase [Paenibacillus sp. JDR-2].
ConsensusfromContig7344	Firmicutes-Paenibacillus_sp_JDR_2_gi251797225	7.20E-16	>YP_003011956 Phytanoyl-CoA dioxygenase [Paenibacillus sp. JDR-2].
ConsensusfromContig6955	Firmicutes-Paenibacillus_sp_JDR_2_gi251799202	1.20E-11	>YP_003013933 Beta-galactosidase [Paenibacillus sp. JDR-2].
ConsensusfromContig5478	Firmicutes-Roseburia_intestinalis_L1_82_gi240147466	4.70E-16	>ZP_04746067 conserved hypothetical protein [Roseburia intestinalis L1-82].
ConsensusfromContig5645	Firmicutes-Roseburia_intestinalis_L1_82_gi240147466	9.00E-13	>ZP_04746067 conserved hypothetical protein [Roseburia intestinalis L1-82].
ConsensusfromContig5790	Firmicutes-Roseburia_intestinalis_L1_82_gi240147466	4.80E-13	>ZP_04746067 conserved hypothetical protein [Roseburia intestinalis L1-82].
ConsensusfromContig1938	Firmicutes-Roseburia_intestinalis_L1_82_gi257413708	1.40E-16	>ZP_04743935 conserved hypothetical protein [Roseburia intestinalis L1-82].
ConsensusfromContig4352	Firmicutes-Shuttleworthia_satelles_DSM_14600_gi229829458	1.80E-11	>ZP_04455527 hypothetical protein GCWU000342_01548 [Shuttleworthia satelles DSM 14600].
ConsensusfromContig4369	Firmicutes-Shuttleworthia_satelles_DSM_14600_gi229829458	2.50E-12	>ZP_04455527 hypothetical protein GCWU000342_01548 [Shuttleworthia satelles DSM 14600].
ConsensusfromContig5100	Firmicutes-Staphylococcus_aureus_gi10956164	4.10E-27	>NP_052693 hypothetical protein pC221_p2 [Staphylococcus aureus].
ConsensusfromContig1315	Firmicutes-Staphylococcus_aureus_gi10956172	5.80E-33	>NP_048341 replication protein [Staphylococcus aureus].
ConsensusfromContig2013	Firmicutes-Staphylococcus_aureus_subsp_aureus_MW2_gi21283455	8.40E-23	>NP_646543 hypothetical protein MW1726 [Staphylococcus aureus subsp. aureus MW2].
ConsensusfromContig3236	Firmicutes-Staphylococcus_capitis_SK14_gi223043397	3.00E-24	>ZP_03613443 DNA gyrase, A subunit [Staphylococcus capitis SK14].
ConsensusfromContig2019	Firmicutes-Streptococcus_pneumoniae_ATCC_700669_gi221232510	4.90E-12	>YP_002511663 cell wall surface anchored protein [Streptococcus pneumoniae ATCC 700669].
ConsensusfromContig5296	Firmicutes-Streptococcus_pneumoniae_ATCC_700669_gi221232510	1.70E-15	>YP_002511663 cell wall surface anchored protein [Streptococcus pneumoniae ATCC 700669].
ConsensusfromContig6926	Firmicutes-Streptococcus_pneumoniae_ATCC_700669_gi221232510	8.20E-18	>YP_002511663 cell wall surface anchored protein [Streptococcus pneumoniae ATCC 700669].
ConsensusfromContig6922	Firmicutes-Streptococcus_pneumoniae_Hungary19A_6_gi169833528	6.30E-33	>YP_001695146 cell wall surface anchor family protein [Streptococcus pneumoniae Hungary19A-6].
ConsensusfromContig2021	Firmicutes-Streptococcus_pneumoniae_Hungary19A_6_gi169834073	1.10E-11	>YP_001694194 hypothetical protein SPH_0827 [Streptococcus pneumoniae Hungary19A-6].
ConsensusfromContig1941	Firmicutes-Symbiobacterium_thermophilum_IAM_14863_gi51892303	3.50E-67	>YP_074994 S-adenosylmethionine:tRNA-ribosyltransferase- isomerase [Symbiobacterium thermophilum IAM 14863].
ConsensusfromContig6171	Firmicutes-Symbiobacterium_thermophilum_IAM_14863_gi51893875	7.80E-29	>YP_076566 glycerophosphodiester phosphodiesterase [Symbiobacterium thermophilum IAM 14863].
ConsensusfromContig2053	Firmicutes-Thermoanaerobacter_pseudethanolicus_ATCC_33223_gi167038355	1.80E-30	>YP_001665933 D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding [Thermoanaerobacter pseudethanolicus ATCC 33223].
ConsensusfromContig5137	Fungi-Ajellomyces_capsulatus_NAm1_gi154269571	1.50E-13	>XP_001535753 hypothetical protein HCAG_09330 [Ajellomyces capsulatus NAm1].
ConsensusfromContig3146	Fungi-Ajellomyces_capsulatus_NAm1_gi154269709	2.80E-25	>XP_001535788 hypothetical protein HCAG_09286 [Ajellomyces capsulatus NAm1].
ConsensusfromContig5485	Fungi-Ajellomyces_capsulatus_NAm1_gi154269709	5.20E-29	>XP_001535788 hypothetical protein HCAG_09286 [Ajellomyces capsulatus NAm1].
ConsensusfromContig7267	Fungi-Ajellomyces_capsulatus_NAm1_gi154271826	4.90E-17	>XP_001536766 hypothetical protein HCAG_08548 [Ajellomyces capsulatus NAm1].
ConsensusfromContig1989	Fungi-Ajellomyces_capsulatus_NAm1_gi154273452	9.10E-17	>XP_001537578 predicted protein [Ajellomyces capsulatus NAm1].
ConsensusfromContig7090	Fungi-Ajellomyces_capsulatus_NAm1_gi154274333	1.20E-16	>XP_001538018 conserved hypothetical protein [Ajellomyces capsulatus NAm1].
ConsensusfromContig2131	Fungi-Ajellomyces_capsulatus_NAm1_gi154275976	7.90E-50	>XP_001538833 hypothetical protein HCAG_06438 [Ajellomyces capsulatus NAm1].
ConsensusfromContig6083	Fungi-Ajellomyces_capsulatus_NAm1_gi154275976	3.10E-45	>XP_001538833 hypothetical protein HCAG_06438 [Ajellomyces capsulatus NAm1].
ConsensusfromContig2191	Fungi-Ajellomyces_capsulatus_NAm1_gi154283975	2.90E-21	>XP_001542783 conserved hypothetical protein [Ajellomyces capsulatus NAm1].
ConsensusfromContig2204	Fungi-Ajellomyces_capsulatus_NAm1_gi154284878	4.90E-27	>XP_001543234 hypothetical protein HCAG_00280 [Ajellomyces capsulatus NAm1].
ConsensusfromContig1955	Fungi-Allomyces_macrogynus_tbAML00000113_1	4.60E-20	
ConsensusfromContig1776	Fungi-Allomyces_macrogynus_tbAML00000523_1	1.30E-12	
ConsensusfromContig2415	Fungi-Alternaria_brassicicola_jgiAB00940	4.90E-11	
ConsensusfromContig2506	Fungi-Alternaria_brassicicola_jgiAB03271	1.20E-12	
ConsensusfromContig7166	Fungi-Alternaria_brassicicola_jgiAB03458	1.70E-21	
ConsensusfromContig5838	Fungi-Arthroderma_otae_CBS_113480_gi296826646	1.20E-26	>XP_002851011 calnexin [Arthroderma otae CBS 113480].
ConsensusfromContig7138	Fungi-Aspergillus_flavus_NRRL3357_gi238500782	3.10E-21	>XP_002381625 conserved hypothetical protein [Aspergillus flavus NRRL3357].
ConsensusfromContig5163	Fungi-Aspergillus_flavus_NRRL3357_gi238509435	1.30E-13	>XP_002385618 LINE-1 retrotransposon-like element, putative [Aspergillus flavus NRRL3357].
ConsensusfromContig2463	Fungi-Aspergillus_nidulans_FGSC_A4_gi67537634	5.60E-14	>XP_662591 KAPR_EMENI CAMP-DEPENDENT PROTEIN KINASE REGULATORY CHAIN [Aspergillus nidulans FGSC A4].
ConsensusfromContig3139	Fungi-Aspergillus_nidulans_FGSC_A4_gi67537634	8.60E-20	>XP_662591 KAPR_EMENI CAMP-DEPENDENT PROTEIN KINASE REGULATORY CHAIN [Aspergillus nidulans FGSC A4].
ConsensusfromContig1152	Fungi-Aspergillus_nidulans_FGSC_A4_gi67539890	5.70E-11	>XP_663719 hypothetical protein AN6115.2 [Aspergillus nidulans FGSC A4].
ConsensusfromContig1152	Fungi-Aspergillus_nidulans_FGSC_A4_gi67539890	5.70E-11	>XP_663719 hypothetical protein AN6115.2 [Aspergillus nidulans FGSC A4].
ConsensusfromContig63	Fungi-Aspergillus_nidulans_FGSC_A4_gi67902558	1.10E-16	>XP_681535 hypothetical protein AN8266.2 [Aspergillus nidulans FGSC A4].
ConsensusfromContig3774	Fungi-Aspergillus_niger_CBS_51388_gi145240643	1.70E-25	>XP_001392968 hypothetical protein An08g08550 [Aspergillus niger].
ConsensusfromContig1959	Fungi-Aspergillus_oryzae_RIB40_gi169785713	8.10E-34	>XP_001827317 hypothetical protein [Aspergillus oryzae RIB40].
ConsensusfromContig2336	Fungi-Aspergillus_terreus_NIH2624_gi115443450	5.30E-23	>XP_001218532 predicted protein [Aspergillus terreus NIH2624].
ConsensusfromContig5580	Fungi-Batrachochytrium_dendrobatidis_jgi20825	1.40E-62	
ConsensusfromContig5177	Fungi-Batrachochytrium_dendrobatidis_jgi34181	8.30E-77	
ConsensusfromContig3031	Fungi-Batrachochytrium_dendrobatidis_jgi35515	3.10E-11	
ConsensusfromContig1564	Fungi-Batrachochytrium_dendrobatidis_jgi36288	8.90E-21	
ConsensusfromContig4678	Fungi-Batrachochytrium_dendrobatidis_jgi86343	9.10E-13	
ConsensusfromContig6923	Fungi-Batrachochytrium_dendrobatidis_jgi9753	9.60E-179	
ConsensusfromContig5117	Fungi-Batrachochytrium_dendrobatidis_tbBDL00000061_4	4.30E-53	
ConsensusfromContig7128	Fungi-Batrachochytrium_dendrobatidis_tbBDL00002363_5	1.60E-33	
ConsensusfromContig3146	Fungi-Botryotinia_fuckeliana_B0510_gi154290730	3.20E-31	>XP_001545956 hypothetical protein BC1G_15284 [Botryotinia fuckeliana B05.10].
ConsensusfromContig5112	Fungi-Botryotinia_fuckeliana_B0510_gi154290730	1.00E-48	>XP_001545956 hypothetical protein BC1G_15284 [Botryotinia fuckeliana B05.10].
ConsensusfromContig6818	Fungi-Botryotinia_fuckeliana_B0510_gi154310168	2.10E-11	>XP_001554416 hypothetical protein BC1G_07004 [Botryotinia fuckeliana B05.10].
ConsensusfromContig2360	Fungi-Botryotinia_fuckeliana_B0510_gi154314528	7.00E-19	>XP_001556588 calmodulin [Botryotinia fuckeliana B05.10].
ConsensusfromContig6966	Fungi-Botryotinia_fuckeliana_B0510_gi154321217	7.70E-28	>XP_001559924 hypothetical protein BC1G_01483 [Botryotinia fuckeliana B05.10].
ConsensusfromContig5375	Fungi-Candida_albicans_SC5314_gi68492489	3.00E-13	>XP_710003 hypothetical protein CaO19.564 [Candida albicans SC5314].
ConsensusfromContig3149	Fungi-Candida_dubliniensis_CD36_gi241956792	6.30E-28	>XP_002421116 retrotransposon reverse transcriptase, pseudogene, putative [Candida dubliniensis CD36].
ConsensusfromContig6929	Fungi-Candida_glabrata_CBS_138_gi50294163	1.70E-13	>XP_449493 hypothetical protein [Candida glabrata CBS 138].
ConsensusfromContig1647	Fungi-Chaetomium_globosum_CBS_14851_gi116191741	7.80E-15	>XP_001221683 hypothetical protein CHGG_05588 [Chaetomium globosum CBS 148.51].
ConsensusfromContig4536	Fungi-Chaetomium_globosum_CBS_14851_gi116191741	1.30E-14	>XP_001221683 hypothetical protein CHGG_05588 [Chaetomium globosum CBS 148.51].
ConsensusfromContig6257	Fungi-Chaetomium_globosum_CBS_14851_gi116191741	2.70E-16	>XP_001221683 hypothetical protein CHGG_05588 [Chaetomium globosum CBS 148.51].
ConsensusfromContig3161	Fungi-Clavispora_lusitaniae_ATCC_42720_gi260940779	2.20E-29	>XP_002615229 hypothetical protein CLUG_04111 [Clavispora lusitaniae ATCC 42720].
ConsensusfromContig5256	Fungi-Clavispora_lusitaniae_ATCC_42720_gi260940779	1.40E-31	>XP_002615229 hypothetical protein CLUG_04111 [Clavispora lusitaniae ATCC 42720].
ConsensusfromContig3147	Fungi-Coccidioides_immitis_RS_gi119189289	9.30E-16	>XP_001245251 hypothetical protein CIMG_04692 [Coccidioides immitis RS].
ConsensusfromContig3403	Fungi-Coccidioides_immitis_RS_gi119189373	2.40E-16	>XP_001245293 hypothetical protein CIMG_04734 [Coccidioides immitis RS].
ConsensusfromContig1955	Fungi-Coccidioides_immitis_RS_gi119193496	4.30E-47	>XP_001247354 hypothetical protein CIMG_01125 [Coccidioides immitis RS].
ConsensusfromContig5217	Fungi-Coccidioides_immitis_RS_gi119193496	3.70E-13	>XP_001247354 hypothetical protein CIMG_01125 [Coccidioides immitis RS].
ConsensusfromContig2869	Fungi-Coccidioides_immitis_RS_gi119196989	4.00E-12	>XP_001249098 kinesin heavy chain [Coccidioides immitis RS].

ConsensusfromContig6942Fungi-Coccidioides_immitis_RS_gi119197189	1.90E-11	>XP_001249196 hypothetical protein CIMG_10358 [Coccidioides immitis RS].
ConsensusfromContig3135Fungi-Cochliobolus_heterostrophus_C5_jgi83460	6.70E-51	
ConsensusfromContig1980Fungi-Coprinopsis_cinerea_okayama7#130_gi299739478	1.20E-85	>XP_001835316 transcriptional factor B3 [Coprinopsis cinerea okayama7#130].
ConsensusfromContig5122Fungi-Coprinopsis_cinerea_okayama7#130_gi299739478	1.50E-92	>XP_001835316 transcriptional factor B3 [Coprinopsis cinerea okayama7#130].
ConsensusfromContig5397Fungi-Coprinopsis_cinerea_okayama7#130_gi299739478	4.50E-21	>XP_001835316 transcriptional factor B3 [Coprinopsis cinerea okayama7#130].
ConsensusfromContig1987Fungi-Coprinopsis_cinerea_okayama7#130_gi299750808	5.70E-29	>XP_001829840 ankyrin repeat domain-containing protein 44 [Coprinopsis cinerea okayama7#130].
ConsensusfromContig5370Fungi-Cryphonectria_parasitica_jgi43125	2.60E-27	
ConsensusfromContig5370Fungi-Cryphonectria_parasitica_jgi43125	2.60E-27	
ConsensusfromContig5141Fungi-Cryptococcus_neoformans_var_neoformans_B_3501A_gi134111348	3.10E-69	>XP_775816 hypothetical protein CNBD5450 [Cryptococcus neoformans var. neoformans B-3501A].
ConsensusfromContig5229Fungi-Cryptococcus_neoformans_var_neoformans_B_3501A_gi134112920	2.70E-68	>XP_775003 hypothetical protein CNBF1660 [Cryptococcus neoformans var. neoformans B-3501A].
ConsensusfromContig3302Fungi-Cryptococcus_neoformans_var_neoformans_B_3501A_gi134119038	9.30E-18	>XP_771821 hypothetical protein CNBN1990 [Cryptococcus neoformans var. neoformans B-3501A].
ConsensusfromContig2213Fungi-Cryptococcus_neoformans_var_neoformans_JEC21_gi58260596	6.90E-16	>XP_567708 hypothetical protein [Cryptococcus neoformans var. neoformans JEC21].
ConsensusfromContig4085Fungi-Cryptococcus_neoformans_var_neoformans_JEC21_gi58266612	6.70E-15	>XP_570462 DNA supercoiling [Cryptococcus neoformans var. neoformans JEC21].
ConsensusfromContig2276Fungi-Cryptococcus_neoformans_var_neoformans_JEC21_gi58266776	3.10E-39	>XP_570544 hypothetical protein [Cryptococcus neoformans var. neoformans JEC21].
ConsensusfromContig7156Fungi-Cryptococcus_neoformans_var_neoformans_JEC21_gi58268442	3.70E-11	>XP_571377 retrotransposon nucleocapsid protein [Cryptococcus neoformans var. neoformans JEC21].
ConsensusfromContig2166Fungi-Gibberella_zeae_PH_1_gi46107866	1.20E-12	>XP_380992 hypothetical protein FG00816.1 [Gibberella zeae PH-1].
ConsensusfromContig5351Fungi-Gibberella_zeae_PH_1_gi46122427	5.40E-13	>XP_385767 hypothetical protein FG05591.1 [Gibberella zeae PH-1].
ConsensusfromContig4625Fungi-Heterobasidion_annosum_jgi169479	1.60E-12	
ConsensusfromContig1955Fungi-Heterobasidion_annosum_jgi50655	4.10E-47	
ConsensusfromContig2389Fungi-Heterobasidion_annosum_jgi59609	1.20E-13	
ConsensusfromContig1189Fungi-Kluyveromyces_lactis_gi50312713	8.00E-17	>XP_453840 unnamed protein product [Kluyveromyces lactis].
ConsensusfromContig7041Fungi-Laccaria_bicolor_S238N_H82_gi170112043	2.40E-17	>XP_001887224 reverse transcriptase-RNase H-integrase [Laccaria bicolor S238N-H82].
ConsensusfromContig6147Fungi-Laccaria_bicolor_S238N_H82_gi170114191	1.50E-12	>XP_001888293 predicted protein [Laccaria bicolor S238N-H82].
ConsensusfromContig1554Fungi-Lodderomyces_elongisporus_NRRL_YB_4239_gi149244356	6.60E-15	>XP_001526721 chromo domain protein 1 [Lodderomyces elongisporus NRRL YB-4239].
ConsensusfromContig5127Fungi-Lodderomyces_elongisporus_NRRL_YB_4239_gi149247889	1.70E-31	>XP_001528332 conserved hypothetical protein [Lodderomyces elongisporus NRRL YB-4239].
ConsensusfromContig5443Fungi-Magnaporthe_oryzae_70_15_gi145603835	6.00E-49	>XP_001404878 hypothetical protein MGG_13314 [Magnaporthe oryzae 70-15].
ConsensusfromContig5424Fungi-Magnaporthe_oryzae_70_15_gi145610651	6.70E-31	>XP_368232 hypothetical protein MGG_01012 [Magnaporthe oryzae 70-15].
ConsensusfromContig5408Fungi-Magnaporthe_oryzae_70_15_gi145613313	5.50E-28	>XP_363810 hypothetical protein MGG_11154 [Magnaporthe oryzae 70-15].
ConsensusfromContig5438Fungi-Magnaporthe_oryzae_70_15_gi145615171	3.60E-109	>XP_001414325 hypothetical protein MGG_13051 [Magnaporthe oryzae 70-15].
ConsensusfromContig2039Fungi-Magnaporthe_oryzae_70_15_gi39942232	2.30E-14	>XP_360653 hypothetical protein MGG_03196 [Magnaporthe oryzae 70-15].
ConsensusfromContig5722Fungi-Magnaporthe_oryzae_70_15_gi39975845	7.60E-29	>XP_369313 conserved hypothetical protein [Magnaporthe oryzae 70-15].
ConsensusfromContig2395Fungi-Malassezia_globosa_CBS_7966_gi164656665	1.40E-22	>XP_001729460 hypothetical protein MGL_3495 [Malassezia globosa CBS 7966].
ConsensusfromContig3126Fungi-Malassezia_globosa_CBS_7966_gi164657554	8.40E-24	>XP_001729903 hypothetical protein MGL_2889 [Malassezia globosa CBS 7966].
ConsensusfromContig6416Fungi-Moniliophthora_perniciosa_FA553_gi238576146	7.20E-11	>XP_002387931 hypothetical protein MPER_13116 [Moniliophthora perniciosa FA553].
ConsensusfromContig789 Fungi-Moniliophthora_perniciosa_FA553_gi238576153	7.50E-15	>XP_002387934 hypothetical protein MPER_13114 [Moniliophthora perniciosa FA553].
ConsensusfromContig3348Fungi-Moniliophthora_perniciosa_FA553_gi238576601	4.40E-13	>XP_002388093 hypothetical protein MPER_12935 [Moniliophthora perniciosa FA553].
ConsensusfromContig6936Fungi-Moniliophthora_perniciosa_FA553_gi238577208	5.90E-12	>XP_002388312 hypothetical protein MPER_12682 [Moniliophthora perniciosa FA553].
ConsensusfromContig3220Fungi-Moniliophthora_perniciosa_FA553_gi238577539	2.10E-16	>XP_002388424 hypothetical protein MPER_12556 [Moniliophthora perniciosa FA553].
ConsensusfromContig5512Fungi-Moniliophthora_perniciosa_FA553_gi238577539	2.40E-18	>XP_002388424 hypothetical protein MPER_12556 [Moniliophthora perniciosa FA553].
ConsensusfromContig7151Fungi-Moniliophthora_perniciosa_FA553_gi238577539	2.40E-17	>XP_002388424 hypothetical protein MPER_12556 [Moniliophthora perniciosa FA553].
ConsensusfromContig2188Fungi-Moniliophthora_perniciosa_FA553_gi238577728	2.00E-33	>XP_002388489 hypothetical protein MPER_12484 [Moniliophthora perniciosa FA553].
ConsensusfromContig2231Fungi-Moniliophthora_perniciosa_FA553_gi238580509	1.80E-11	>XP_002389308 hypothetical protein MPER_11577 [Moniliophthora perniciosa FA553].
ConsensusfromContig4024Fungi-Moniliophthora_perniciosa_FA553_gi238599279	8.40E-18	>XP_002394837 hypothetical protein MPER_05211 [Moniliophthora perniciosa FA553].
ConsensusfromContig4273Fungi-Moniliophthora_perniciosa_FA553_gi238603774	8.20E-14	>XP_002396037 hypothetical protein MPER_03807 [Moniliophthora perniciosa FA553].
ConsensusfromContig4273Fungi-Moniliophthora_perniciosa_FA553_gi238603774	8.20E-14	>XP_002396037 hypothetical protein MPER_03807 [Moniliophthora perniciosa FA553].
ConsensusfromContig5296Fungi-Moniliophthora_perniciosa_FA553_gi238603774	2.30E-13	>XP_002396037 hypothetical protein MPER_03807 [Moniliophthora perniciosa FA553].
ConsensusfromContig6986Fungi-Moniliophthora_perniciosa_FA553_gi238603774	1.20E-16	>XP_002396037 hypothetical protein MPER_03807 [Moniliophthora perniciosa FA553].
ConsensusfromContig7016Fungi-Mortierella_verticillata_tbMAL00000241_4	2.10E-16	
ConsensusfromContig4230Fungi-Mortierella_verticillata_tbMAL00000741_1	9.40E-13	
ConsensusfromContig4230Fungi-Mortierella_verticillata_tbMAL00000741_1	9.40E-13	
ConsensusfromContig4939Fungi-Mortierella_verticillata_tbMAL00001125_1	1.70E-17	
ConsensusfromContig2536Fungi-Mucor_circinelloides_jgi11746	6.80E-11	
ConsensusfromContig1203Fungi-Mucor_circinelloides_jgi13132	1.40E-27	
ConsensusfromContig6845Fungi-Mucor_circinelloides_jgi20333	5.70E-15	
ConsensusfromContig2109Fungi-Mucor_circinelloides_jgi34535	7.10E-15	
ConsensusfromContig5204Fungi-Mucor_circinelloides_jgi38919	5.70E-39	
ConsensusfromContig5403Fungi-Mucor_circinelloides_jgi39988	8.90E-17	
ConsensusfromContig5403Fungi-Mucor_circinelloides_jgi39988	8.90E-17	
ConsensusfromContig5879Fungi-Mucor_circinelloides_jgi42263	2.50E-26	
ConsensusfromContig5879Fungi-Mucor_circinelloides_jgi42263	2.50E-26	
ConsensusfromContig5138Fungi-Mucor_circinelloides_jgi50294	1.20E-62	
ConsensusfromContig2101Fungi-Mucor_circinelloides_jgi72163	2.70E-24	
ConsensusfromContig1952Fungi-Mucor_circinelloides_jgi73988	2.00E-22	
ConsensusfromContig5143Fungi-Mucor_circinelloides_jgi74618	5.30E-18	
ConsensusfromContig1976Fungi-Mucor_circinelloides_jgi80571	4.20E-20	
ConsensusfromContig1990Fungi-Mucor_circinelloides_jgi87738	6.30E-157	
ConsensusfromContig6963Fungi-Mucor_circinelloides_jgi93043	6.40E-11	
ConsensusfromContig1954Fungi-Mucor_circinelloides_jgi93125	2.70E-89	
ConsensusfromContig5120Fungi-Mucor_circinelloides_jgi9707	3.90E-17	
ConsensusfromContig2384Fungi-Mycosphaerella_graminicola_jgi107669	1.20E-66	
ConsensusfromContig1950Fungi-Mycosphaerella_graminicola_jgi37396	6.50E-12	
ConsensusfromContig2915Fungi-Neurospora_crassa_OR74A_gi164424025	3.60E-21	>XP_963276 hypothetical protein NCU08404 [Neurospora crassa OR74A].
ConsensusfromContig2566Fungi-Neurospora_crassa_OR74A_gi164429217	6.60E-11	>XP_962002 sulfite reductase beta subunit [Neurospora crassa OR74A].
ConsensusfromContig2123Fungi-Neurospora_discreta_jgi100584	1.10E-12	
ConsensusfromContig7091Fungi-Penicillium_marneffei_ATCC_18224_gi212528198	2.10E-17	>XP_002144256 cAMP-dependent protein kinase regulatory subunit PkaR [Penicillium marneffei ATCC 18224].
ConsensusfromContig3133Fungi-Penicillium_marneffei_ATCC_18224_gi212536790	7.40E-18	>XP_002148551 conserved hypothetical protein [Penicillium marneffei ATCC 18224].
ConsensusfromContig2345Fungi-Phaeosphaeria_nodorum_SN15_gi169623203	1.40E-16	>XP_001805009 hypothetical protein SNOG_14834 [Phaeosphaeria nodorum SN15].
ConsensusfromContig5586Fungi-Phanerochaete_chrysosporium_jgi10655	1.00E-11	
ConsensusfromContig5586Fungi-Phanerochaete_chrysosporium_jgi10655	1.00E-11	
ConsensusfromContig7098Fungi-Phanerochaete_chrysosporium_jgi1398	1.90E-11	
ConsensusfromContig2039Fungi-Phanerochaete_chrysosporium_jgi29618	1.80E-54	
ConsensusfromContig2260Fungi-Phanerochaete_chrysosporium_jgi33698	2.60E-15	
ConsensusfromContig5456Fungi-Phanerochaete_chrysosporium_jgi33720	3.20E-22	
ConsensusfromContig2479Fungi-Phanerochaete_chrysosporium_jgi42809	2.00E-15	
ConsensusfromContig7033Fungi-Phanerochaete_chrysosporium_jgi42809	1.40E-20	
ConsensusfromContig1961Fungi-Phycomyces_blakesleeanus_jgi23346	7.00E-16	
ConsensusfromContig1994Fungi-Phycomyces_blakesleeanus_jgi23346	7.40E-15	
ConsensusfromContig2130Fungi-Phycomyces_blakesleeanus_jgi23346	2.20E-25	
ConsensusfromContig2462Fungi-Phycomyces_blakesleeanus_jgi23346	3.10E-39	
ConsensusfromContig2553Fungi-Phycomyces_blakesleeanus_jgi23346	2.80E-11	
ConsensusfromContig3121Fungi-Phycomyces_blakesleeanus_jgi23346	4.20E-65	
ConsensusfromContig5111Fungi-Phycomyces_blakesleeanus_jgi23346	3.70E-45	
ConsensusfromContig5158Fungi-Phycomyces_blakesleeanus_jgi23346	2.00E-29	
ConsensusfromContig6460Fungi-Phycomyces_blakesleeanus_jgi23346	9.40E-14	
ConsensusfromContig6943Fungi-Phycomyces_blakesleeanus_jgi23346	1.10E-39	
ConsensusfromContig7001Fungi-Phycomyces_blakesleeanus_jgi23346	1.60E-56	
ConsensusfromContig6947Fungi-Phycomyces_blakesleeanus_jgi3230	2.60E-68	
ConsensusfromContig5816Fungi-Phycomyces_blakesleeanus_jgi34593	1.20E-32	
ConsensusfromContig2017Fungi-Phycomyces_blakesleeanus_jgi36382	6.60E-76	
ConsensusfromContig1957Fungi-Phycomyces_blakesleeanus_jgi4	2.70E-24	

ConsensusfromContig5170Fungi-Phycomyces_blakesleeanus_jgi4628	6.50E-16	
ConsensusfromContig2133Fungi-Phycomyces_blakesleeanus_jgi70142	9.90E-16	
ConsensusfromContig6950Fungi-Phycomyces_blakesleeanus_jgi76840	3.70E-29	
ConsensusfromContig8454Fungi-Phycomyces_blakesleeanus_jgi77729	1.10E-20	
ConsensusfromContig4517Fungi-Pichia_pastoris_GS115_gi254572892	1.00E-12	>XP_002493555 hypothetical protein [Pichia pastoris GS115].
ConsensusfromContig5662Fungi-Podospora_anserina_S_mat+_gi171684235	1.10E-16	>XP_001907059 hypothetical protein [Podospora anserina S mat+].
ConsensusfromContig5662Fungi-Podospora_anserina_S_mat+_gi171684235	1.10E-16	>XP_001907059 hypothetical protein [Podospora anserina S mat+].
ConsensusfromContig6127Fungi-Podospora_anserina_S_mat+_gi171685532	2.70E-11	>XP_001907707 hypothetical protein [Podospora anserina S mat+].
ConsensusfromContig3216Fungi-Podospora_anserina_S_mat+_gi171689846	2.40E-13	>XP_001909863 hypothetical protein [Podospora anserina S mat+].
ConsensusfromContig2710Fungi-Pyrenophora_tritici_repentis_Pt_1C_BFP_gi189209021	2.20E-22	>XP_001940843 vegetative incompatibility protein HET-E-1 [Pyrenophora tritici-repentis Pt-1C-BFP].
ConsensusfromContig1602Fungi-Rhizopus_oryzae_tbROL00000282_1	3.80E-12	
ConsensusfromContig6101Fungi-Rhizopus_oryzae_tbROL00002999_3	1.40E-27	
ConsensusfromContig6048Fungi-Rhizopus_oryzae_tbROL00003706_6	1.50E-15	
ConsensusfromContig6424Fungi-Rhizopus_oryzae_tbROL00003723_6	7.50E-11	
ConsensusfromContig4315Fungi-Rhizopus_oryzae_tbROL00004639_3	8.80E-27	
ConsensusfromContig4646Fungi-Schizosaccharomyces_pombe_gi19114853	2.80E-12	>NP_593941 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) methylideneamino]imidazole-4-carboxamide isomerase (predicted) [Schizosaccharomyces pombe 972h-].
ConsensusfromContig3953Fungi-Sclerotinia_sclerotiorum_1980_UF_70_gi156035777	2.80E-17	>XP_001586000 hypothetical protein SS1G_13092 [Sclerotinia sclerotiorum 1980].
ConsensusfromContig5118Fungi-Sclerotinia_sclerotiorum_1980_UF_70_gi156050243	5.90E-12	>XP_001591083 hypothetical protein SS1G_07708 [Sclerotinia sclerotiorum 1980].
ConsensusfromContig5986Fungi-Sclerotinia_sclerotiorum_1980_UF_70_gi156051526	1.90E-17	>XP_001591724 hypothetical protein SS1G_07170 [Sclerotinia sclerotiorum 1980].
ConsensusfromContig2462Fungi-Sclerotinia_sclerotiorum_1980_UF_70_gi156059422	1.20E-30	>XP_001595634 hypothetical protein SS1G_03723 [Sclerotinia sclerotiorum 1980].
ConsensusfromContig5081Fungi-Sclerotinia_sclerotiorum_1980_UF_70_gi156060563	2.10E-11	>XP_001596204 hypothetical protein SS1G_02421 [Sclerotinia sclerotiorum 1980].
ConsensusfromContig3166Fungi-Sclerotinia_sclerotiorum_1980_UF_70_gi156065843	1.20E-18	>XP_001598843 hypothetical protein SS1G_00932 [Sclerotinia sclerotiorum 1980].
ConsensusfromContig7112Fungi-Spizellomyces_punctatus_tbSPL00000110_1	4.50E-12	
ConsensusfromContig2695Fungi-Spizellomyces_punctatus_tbSPL00000992_2	3.00E-11	
ConsensusfromContig1990Fungi-Sporobolomyces_roseus_jgi14468	4.60E-30	
ConsensusfromContig5102Fungi-Sporobolomyces_roseus_jgi14592	4.60E-93	
ConsensusfromContig6489Fungi-Sporobolomyces_roseus_jgi15328	5.60E-17	
ConsensusfromContig3127Fungi-Sporobolomyces_roseus_jgi1929	2.00E-23	
ConsensusfromContig7298Fungi-Sporobolomyces_roseus_jgi33323	6.60E-23	
ConsensusfromContig6354Fungi-Sporobolomyces_roseus_jgi8244	3.00E-18	
ConsensusfromContig5118Fungi-Sporotrichum_thermophile_jgi25766	2.00E-14	
ConsensusfromContig5249Fungi-Talaromyces_stipitatus_ATCC_10500_gi242761183	2.30E-14	>XP_002340131 G-protein beta WD-40 repeats containing protein, putative [Talaromyces stipitatus ATCC 10500].
ConsensusfromContig2143Fungi-Tremella_mesenterica_jgi26115	6.70E-14	
ConsensusfromContig3249Fungi-Tremella_mesenterica_jgi26115	1.10E-12	
ConsensusfromContig3129Fungi-Tremella_mesenterica_jgi27051	1.10E-53	
ConsensusfromContig2092Fungi-Tremella_mesenterica_jgi32265	1.80E-25	
ConsensusfromContig6916Fungi-Tremella_mesenterica_jgi36119	6.50E-26	
ConsensusfromContig3992Fungi-Tremella_mesenterica_jgi63092	2.60E-12	
ConsensusfromContig1967Fungi-Trichoderma_atroviride_jgi24644	3.00E-26	
ConsensusfromContig2346Fungi-Trichoderma_atroviride_jgi83589	1.80E-16	
ConsensusfromContig1966Fungi-Trichoderma_atroviride_jgi86734	1.10E-13	
ConsensusfromContig6753Fungi-Trichoderma_reesei_jgi34413	5.90E-15	
ConsensusfromContig6995Fungi-Trichoderma_virens_jgi24364	1.40E-16	
ConsensusfromContig7243Fungi-Trichoderma_virens_jgi68192	4.00E-13	
ConsensusfromContig3139Fungi-Trichoderma_virens_jgi69203	7.40E-20	
ConsensusfromContig2153Fungi-Trichoderma_virens_jgi85812	1.70E-21	
ConsensusfromContig1039Fungi-Tuber_melanosporum_Mel28_gi296412815	1.00E-12	>XP_002836115 hypothetical protein [Tuber melanosporum Mel28].
ConsensusfromContig2645Fungi-Ustilago_maydis_521_gi71005136	7.90E-15	>XP_757234 hypothetical protein UM01087.1 [Ustilago maydis 521].
ConsensusfromContig2799Fungi-Ustilago_maydis_521_gi71014070	1.10E-27	>XP_758692 hypothetical protein UM02545.1 [Ustilago maydis 521].
ConsensusfromContig2359Fungi-Ustilago_maydis_521_gi71018379	6.10E-17	>XP_759420 hypothetical protein UM03273.1 [Ustilago maydis 521].
ConsensusfromContig5963Fungi-Ustilago_maydis_521_gi71022033	9.10E-11	>XP_761247 hypothetical protein UM05100.1 [Ustilago maydis 521].
ConsensusfromContig3129Fungi-Ustilago_maydis_521_gi71024365	1.60E-24	>XP_762412 hypothetical protein UM06265.1 [Ustilago maydis 521].
ConsensusfromContig5139Fungi-Ustilago_maydis_521_gi71024365	1.10E-21	>XP_762412 hypothetical protein UM06265.1 [Ustilago maydis 521].
ConsensusfromContig2045Fungi-Yarrowia_lipolytica_CLIB122_gi50555167	9.10E-24	>XP_504992 YALI0F04422p [Yarrowia lipolytica].
ConsensusfromContig2000Fusobacteria-Fusobacterium_sp_1_1_41FAA_gi294782215	3.40E-33	>ZP_06747541 phage-associated terminase large subunit [Fusobacterium sp. 1_1_41FAA].
ConsensusfromContig1142Glaucophyta-Cyanophora_paradoxa_dxContig124_4	8.10E-14	
ConsensusfromContig5474Glaucophyta-Cyanophora_paradoxa_dxContig22_1	2.00E-26	
ConsensusfromContig2129Glaucophyta-Cyanophora_paradoxa_dxContig237_5	1.00E-240	
ConsensusfromContig7183Glaucophyta-Cyanophora_paradoxa_dxContig465_2	1.30E-50	
ConsensusfromContig2709Glaucophyta-Cyanophora_paradoxa_dxContig465_6	1.20E-14	
ConsensusfromContig2393Glaucophyta-Cyanophora_paradoxa_dxContig721_2	8.10E-13	
ConsensusfromContig3963Glaucophyta-Cyanophora_paradoxa_dxContig790_2	1.00E-36	
ConsensusfromContig3850Glaucophyta-Cyanophora_paradoxa_dxContig857_1	1.50E-20	
ConsensusfromContig3385Glaucophyta-Cyanophora_paradoxa_dxContig880_4	8.40E-61	
ConsensusfromContig2716Glaucophyta-Cyanophora_paradoxa_dxUIcontig2742_4	3.10E-12	
ConsensusfromContig3544Glaucophyta-Cyanophora_paradoxa_tbCDL00001664_3	6.50E-60	
ConsensusfromContig5149Glaucophyta-Cyanophora_paradoxa_tbCDL00002429_1	1.10E-41	
ConsensusfromContig6113Glaucophyta-Cyanophora_paradoxa_tbCPL00000344_1	3.50E-20	
ConsensusfromContig1997Glaucophyta-Cyanophora_paradoxa_tbCPL00000457_2	5.90E-238	
ConsensusfromContig6016Glaucophyta-Cyanophora_paradoxa_tbCPL00001026_4	1.60E-21	
ConsensusfromContig5097Glaucophyta-Glaucocystis_nostochinearum_esContig356_2	1.90E-17	
ConsensusfromContig2306Glaucophyta-Glaucocystis_nostochinearum_esContig534_3	1.00E-17	
ConsensusfromContig5107Glaucophyta-Glaucocystis_nostochinearum_esContig668_1	2.00E-21	
ConsensusfromContig4642Glaucophyta-Glaucocystis_nostochinearum_esContig798_1	1.20E-34	
ConsensusfromContig2807Glaucophyta-Glaucocystis_nostochinearum_esContig815_5	7.90E-16	
ConsensusfromContig2022Glaucophyta-Glaucocystis_nostochinearum_esContig969_2	8.50E-91	
ConsensusfromContig5965Haptophyceae-Emiliania_huxleyi_jgi100471	4.10E-14	
ConsensusfromContig2454Haptophyceae-Emiliania_huxleyi_jgi100487	1.40E-18	
ConsensusfromContig2345Haptophyceae-Emiliania_huxleyi_jgi101482	1.70E-11	
ConsensusfromContig2436Haptophyceae-Emiliania_huxleyi_jgi101482	7.80E-19	
ConsensusfromContig5578Haptophyceae-Emiliania_huxleyi_jgi102338	1.10E-16	
ConsensusfromContig2440Haptophyceae-Emiliania_huxleyi_jgi102453	5.10E-12	
ConsensusfromContig2992Haptophyceae-Emiliania_huxleyi_jgi102453	1.70E-12	
ConsensusfromContig5145Haptophyceae-Emiliania_huxleyi_jgi102453	1.60E-26	
ConsensusfromContig2892Haptophyceae-Emiliania_huxleyi_jgi102665	2.20E-13	
ConsensusfromContig5135Haptophyceae-Emiliania_huxleyi_jgi103044	2.40E-57	
ConsensusfromContig5951Haptophyceae-Emiliania_huxleyi_jgi103561	6.00E-20	
ConsensusfromContig5951Haptophyceae-Emiliania_huxleyi_jgi103561	6.00E-20	
ConsensusfromContig1973Haptophyceae-Emiliania_huxleyi_jgi103855	1.10E-37	
ConsensusfromContig3107Haptophyceae-Emiliania_huxleyi_jgi104030	8.50E-13	
ConsensusfromContig2005Haptophyceae-Emiliania_huxleyi_jgi104746	3.70E-55	
ConsensusfromContig2288Haptophyceae-Emiliania_huxleyi_jgi105876	2.90E-23	
ConsensusfromContig1933Haptophyceae-Emiliania_huxleyi_jgi106292	9.10E-18	
ConsensusfromContig8206Haptophyceae-Emiliania_huxleyi_jgi106804	7.20E-19	
ConsensusfromContig3771Haptophyceae-Emiliania_huxleyi_jgi107359	3.80E-11	
ConsensusfromContig5144Haptophyceae-Emiliania_huxleyi_jgi107359	1.50E-91	
ConsensusfromContig7147Haptophyceae-Emiliania_huxleyi_jgi108038	4.70E-14	
ConsensusfromContig2958Haptophyceae-Emiliania_huxleyi_jgi108458	3.90E-22	
ConsensusfromContig1780Haptophyceae-Emiliania_huxleyi_jgi111295	4.50E-11	
ConsensusfromContig7160Haptophyceae-Emiliania_huxleyi_jgi111890	1.50E-14	

ConsensusfromContig1532Haptophyceae-Emiliania_huxleyi_jgi112129	1.70E-29
ConsensusfromContig5429Haptophyceae-Emiliania_huxleyi_jgi114705	1.90E-16
ConsensusfromContig1977Haptophyceae-Emiliania_huxleyi_jgi114959	1.10E-16
ConsensusfromContig5195Haptophyceae-Emiliania_huxleyi_jgi115340	4.80E-16
ConsensusfromContig6366Haptophyceae-Emiliania_huxleyi_jgi116982	1.10E-21
ConsensusfromContig2582Haptophyceae-Emiliania_huxleyi_jgi118044	5.80E-11
ConsensusfromContig6027Haptophyceae-Emiliania_huxleyi_jgi118389	4.20E-21
ConsensusfromContig2079Haptophyceae-Emiliania_huxleyi_jgi118844	3.30E-18
ConsensusfromContig6176Haptophyceae-Emiliania_huxleyi_jgi120758	6.20E-13
ConsensusfromContig5126Haptophyceae-Emiliania_huxleyi_jgi121687	3.20E-23
ConsensusfromContig7094Haptophyceae-Emiliania_huxleyi_jgi122142	9.30E-12
ConsensusfromContig4539Haptophyceae-Emiliania_huxleyi_jgi122517	5.20E-11
ConsensusfromContig3825Haptophyceae-Emiliania_huxleyi_jgi124916	9.90E-14
ConsensusfromContig5238Haptophyceae-Emiliania_huxleyi_jgi193771	4.40E-73
ConsensusfromContig1462Haptophyceae-Emiliania_huxleyi_jgi194364	6.40E-13
ConsensusfromContig2046Haptophyceae-Emiliania_huxleyi_jgi194364	1.10E-47
ConsensusfromContig3483Haptophyceae-Emiliania_huxleyi_jgi194364	6.80E-47
ConsensusfromContig1989Haptophyceae-Emiliania_huxleyi_jgi194410	4.00E-55
ConsensusfromContig2353Haptophyceae-Emiliania_huxleyi_jgi194410	7.40E-24
ConsensusfromContig5128Haptophyceae-Emiliania_huxleyi_jgi194410	3.00E-52
ConsensusfromContig5289Haptophyceae-Emiliania_huxleyi_jgi194410	2.80E-26
ConsensusfromContig2600Haptophyceae-Emiliania_huxleyi_jgi194414	4.60E-15
ConsensusfromContig5619Haptophyceae-Emiliania_huxleyi_jgi195267	5.90E-19
ConsensusfromContig2161Haptophyceae-Emiliania_huxleyi_jgi195332	8.80E-29
ConsensusfromContig5829Haptophyceae-Emiliania_huxleyi_jgi195332	9.50E-21
ConsensusfromContig2927Haptophyceae-Emiliania_huxleyi_jgi195350	2.40E-27
ConsensusfromContig2451Haptophyceae-Emiliania_huxleyi_jgi196059	5.30E-14
ConsensusfromContig2583Haptophyceae-Emiliania_huxleyi_jgi197111	1.20E-23
ConsensusfromContig2002Haptophyceae-Emiliania_huxleyi_jgi197156	7.10E-24
ConsensusfromContig7078Haptophyceae-Emiliania_huxleyi_jgi197783	2.20E-12
ConsensusfromContig2795Haptophyceae-Emiliania_huxleyi_jgi199401	1.10E-22
ConsensusfromContig4897Haptophyceae-Emiliania_huxleyi_jgi199401	1.30E-11
ConsensusfromContig4897Haptophyceae-Emiliania_huxleyi_jgi199401	1.30E-11
ConsensusfromContig6935Haptophyceae-Emiliania_huxleyi_jgi199401	1.20E-20
ConsensusfromContig2760Haptophyceae-Emiliania_huxleyi_jgi199722	5.00E-22
ConsensusfromContig2218Haptophyceae-Emiliania_huxleyi_jgi199723	2.60E-22
ConsensusfromContig2218Haptophyceae-Emiliania_huxleyi_jgi199723	2.60E-22
ConsensusfromContig3122Haptophyceae-Emiliania_huxleyi_jgi199862	3.00E-36
ConsensusfromContig1670Haptophyceae-Emiliania_huxleyi_jgi201091	4.80E-11
ConsensusfromContig2919Haptophyceae-Emiliania_huxleyi_jgi201091	8.20E-11
ConsensusfromContig1995Haptophyceae-Emiliania_huxleyi_jgi202055	4.70E-33
ConsensusfromContig5980Haptophyceae-Emiliania_huxleyi_jgi202055	1.60E-15
ConsensusfromContig5980Haptophyceae-Emiliania_huxleyi_jgi202055	1.60E-15
ConsensusfromContig6952Haptophyceae-Emiliania_huxleyi_jgi202762	1.60E-40
ConsensusfromContig6960Haptophyceae-Emiliania_huxleyi_jgi203571	2.40E-13
ConsensusfromContig3172Haptophyceae-Emiliania_huxleyi_jgi203844	1.30E-14
ConsensusfromContig2005Haptophyceae-Emiliania_huxleyi_jgi203865	3.60E-21
ConsensusfromContig6975Haptophyceae-Emiliania_huxleyi_jgi203982	1.90E-37
ConsensusfromContig1718Haptophyceae-Emiliania_huxleyi_jgi205377	5.30E-12
ConsensusfromContig1933Haptophyceae-Emiliania_huxleyi_jgi205415	5.00E-132
ConsensusfromContig2176Haptophyceae-Emiliania_huxleyi_jgi207406	5.10E-16
ConsensusfromContig2634Haptophyceae-Emiliania_huxleyi_jgi207406	7.40E-23
ConsensusfromContig6981Haptophyceae-Emiliania_huxleyi_jgi207426	2.00E-21
ConsensusfromContig6022Haptophyceae-Emiliania_huxleyi_jgi208078	1.60E-20
ConsensusfromContig2144Haptophyceae-Emiliania_huxleyi_jgi208941	8.70E-28
ConsensusfromContig5225Haptophyceae-Emiliania_huxleyi_jgi209550	3.30E-13
ConsensusfromContig6169Haptophyceae-Emiliania_huxleyi_jgi210275	3.90E-19
ConsensusfromContig6994Haptophyceae-Emiliania_huxleyi_jgi211563	3.10E-137
ConsensusfromContig2009Haptophyceae-Emiliania_huxleyi_jgi212222	6.20E-13
ConsensusfromContig6253Haptophyceae-Emiliania_huxleyi_jgi212280	2.50E-21
ConsensusfromContig7097Haptophyceae-Emiliania_huxleyi_jgi212280	2.80E-30
ConsensusfromContig1962Haptophyceae-Emiliania_huxleyi_jgi213155	2.50E-43
ConsensusfromContig3178Haptophyceae-Emiliania_huxleyi_jgi213256	4.20E-11
ConsensusfromContig1681Haptophyceae-Emiliania_huxleyi_jgi213721	1.10E-20
ConsensusfromContig1681Haptophyceae-Emiliania_huxleyi_jgi213721	1.10E-20
ConsensusfromContig7084Haptophyceae-Emiliania_huxleyi_jgi213721	1.00E-16
ConsensusfromContig5176Haptophyceae-Emiliania_huxleyi_jgi215588	1.60E-27
ConsensusfromContig5216Haptophyceae-Emiliania_huxleyi_jgi215588	5.00E-15
ConsensusfromContig5388Haptophyceae-Emiliania_huxleyi_jgi215588	2.40E-19
ConsensusfromContig7001Haptophyceae-Emiliania_huxleyi_jgi215588	3.90E-82
ConsensusfromContig2791Haptophyceae-Emiliania_huxleyi_jgi216501	3.30E-15
ConsensusfromContig5525Haptophyceae-Emiliania_huxleyi_jgi216512	1.70E-17
ConsensusfromContig2234Haptophyceae-Emiliania_huxleyi_jgi217103	1.90E-33
ConsensusfromContig1786Haptophyceae-Emiliania_huxleyi_jgi217453	1.10E-18
ConsensusfromContig2052Haptophyceae-Emiliania_huxleyi_jgi218522	1.20E-52
ConsensusfromContig2499Haptophyceae-Emiliania_huxleyi_jgi219373	2.10E-19
ConsensusfromContig5120Haptophyceae-Emiliania_huxleyi_jgi219900	7.90E-12
ConsensusfromContig7221Haptophyceae-Emiliania_huxleyi_jgi219900	6.70E-11
ConsensusfromContig1088Haptophyceae-Emiliania_huxleyi_jgi221122	9.60E-26
ConsensusfromContig7026Haptophyceae-Emiliania_huxleyi_jgi222125	1.60E-17
ConsensusfromContig5121Haptophyceae-Emiliania_huxleyi_jgi222319	1.10E-12
ConsensusfromContig3106Haptophyceae-Emiliania_huxleyi_jgi223963	4.00E-12
ConsensusfromContig4341Haptophyceae-Emiliania_huxleyi_jgi224232	1.20E-43
ConsensusfromContig7377Haptophyceae-Emiliania_huxleyi_jgi225855	5.20E-18
ConsensusfromContig5104Haptophyceae-Emiliania_huxleyi_jgi226207	7.30E-14
ConsensusfromContig5132Haptophyceae-Emiliania_huxleyi_jgi226709	1.80E-46
ConsensusfromContig2289Haptophyceae-Emiliania_huxleyi_jgi227739	6.80E-13
ConsensusfromContig2400Haptophyceae-Emiliania_huxleyi_jgi227739	1.20E-15
ConsensusfromContig2865Haptophyceae-Emiliania_huxleyi_jgi227739	1.70E-17
ConsensusfromContig5331Haptophyceae-Emiliania_huxleyi_jgi227739	8.00E-13
ConsensusfromContig5285Haptophyceae-Emiliania_huxleyi_jgi229198	1.70E-56
ConsensusfromContig6046Haptophyceae-Emiliania_huxleyi_jgi230887	4.90E-36
ConsensusfromContig7141Haptophyceae-Emiliania_huxleyi_jgi230887	7.30E-54
ConsensusfromContig1388Haptophyceae-Emiliania_huxleyi_jgi231423	2.30E-20
ConsensusfromContig1543Haptophyceae-Emiliania_huxleyi_jgi232674	1.70E-11
ConsensusfromContig2241Haptophyceae-Emiliania_huxleyi_jgi232880	1.50E-59
ConsensusfromContig2734Haptophyceae-Emiliania_huxleyi_jgi233645	4.90E-22
ConsensusfromContig7109Haptophyceae-Emiliania_huxleyi_jgi235099	1.70E-19
ConsensusfromContig1934Haptophyceae-Emiliania_huxleyi_jgi236180	2.90E-57
ConsensusfromContig5127Haptophyceae-Emiliania_huxleyi_jgi236180	3.00E-17

ConsensusfromContig6927	Haptophyceae-Emiliania_huxleyi_jgi236180	1.30E-80
ConsensusfromContig5625	Haptophyceae-Emiliania_huxleyi_jgi236372	3.50E-16
ConsensusfromContig1701	Haptophyceae-Emiliania_huxleyi_jgi236565	1.00E-11
ConsensusfromContig2074	Haptophyceae-Emiliania_huxleyi_jgi236565	3.80E-66
ConsensusfromContig5332	Haptophyceae-Emiliania_huxleyi_jgi236565	7.90E-18
ConsensusfromContig4074	Haptophyceae-Emiliania_huxleyi_jgi236678	5.10E-15
ConsensusfromContig6071	Haptophyceae-Emiliania_huxleyi_jgi238572	4.50E-13
ConsensusfromContig5218	Haptophyceae-Emiliania_huxleyi_jgi238947	3.50E-17
ConsensusfromContig1533	Haptophyceae-Emiliania_huxleyi_jgi239508	1.70E-19
ConsensusfromContig1297	Haptophyceae-Emiliania_huxleyi_jgi239509	6.60E-24
ConsensusfromContig1052	Haptophyceae-Emiliania_huxleyi_jgi240215	2.70E-15
ConsensusfromContig2529	Haptophyceae-Emiliania_huxleyi_jgi241996	4.10E-18
ConsensusfromContig2646	Haptophyceae-Emiliania_huxleyi_jgi243617	9.60E-45
ConsensusfromContig5456	Haptophyceae-Emiliania_huxleyi_jgi243676	3.10E-11
ConsensusfromContig2385	Haptophyceae-Emiliania_huxleyi_jgi244098	4.30E-16
ConsensusfromContig2013	Haptophyceae-Emiliania_huxleyi_jgi244383	2.20E-14
ConsensusfromContig6947	Haptophyceae-Emiliania_huxleyi_jgi248062	1.10E-65
ConsensusfromContig5187	Haptophyceae-Emiliania_huxleyi_jgi248116	3.70E-26
ConsensusfromContig5163	Haptophyceae-Emiliania_huxleyi_jgi248959	9.40E-50
ConsensusfromContig5124	Haptophyceae-Emiliania_huxleyi_jgi250638	1.50E-84
ConsensusfromContig1940	Haptophyceae-Emiliania_huxleyi_jgi253414	9.30E-41
ConsensusfromContig2899	Haptophyceae-Emiliania_huxleyi_jgi254981	1.80E-11
ConsensusfromContig3635	Haptophyceae-Emiliania_huxleyi_jgi255773	2.30E-36
ConsensusfromContig5924	Haptophyceae-Emiliania_huxleyi_jgi259753	7.80E-24
ConsensusfromContig5167	Haptophyceae-Emiliania_huxleyi_jgi260479	7.90E-23
ConsensusfromContig2433	Haptophyceae-Emiliania_huxleyi_jgi308227	1.50E-16
ConsensusfromContig5123	Haptophyceae-Emiliania_huxleyi_jgi310779	4.90E-26
ConsensusfromContig2662	Haptophyceae-Emiliania_huxleyi_jgi350751	2.80E-15
ConsensusfromContig1111	Haptophyceae-Emiliania_huxleyi_jgi356053	6.60E-12
ConsensusfromContig2367	Haptophyceae-Emiliania_huxleyi_jgi357673	3.00E-12
ConsensusfromContig1973	Haptophyceae-Emiliania_huxleyi_jgi358739	3.70E-19
ConsensusfromContig2049	Haptophyceae-Emiliania_huxleyi_jgi362345	1.10E-23
ConsensusfromContig3223	Haptophyceae-Emiliania_huxleyi_jgi363343	2.20E-20
ConsensusfromContig3998	Haptophyceae-Emiliania_huxleyi_jgi365635	6.60E-17
ConsensusfromContig5359	Haptophyceae-Emiliania_huxleyi_jgi366539	1.90E-11
ConsensusfromContig1990	Haptophyceae-Emiliania_huxleyi_jgi368722	9.00E-67
ConsensusfromContig2037	Haptophyceae-Emiliania_huxleyi_jgi415715	3.60E-32
ConsensusfromContig2343	Haptophyceae-Emiliania_huxleyi_jgi416895	1.40E-29
ConsensusfromContig3950	Haptophyceae-Emiliania_huxleyi_jgi420372	1.40E-11
ConsensusfromContig2034	Haptophyceae-Emiliania_huxleyi_jgi427647	4.80E-22
ConsensusfromContig5386	Haptophyceae-Emiliania_huxleyi_jgi431771	4.80E-25
ConsensusfromContig1129	Haptophyceae-Emiliania_huxleyi_jgi432589	2.50E-14
ConsensusfromContig5188	Haptophyceae-Emiliania_huxleyi_jgi432907	8.80E-14
ConsensusfromContig1454	Haptophyceae-Emiliania_huxleyi_jgi433441	2.50E-14
ConsensusfromContig2007	Haptophyceae-Emiliania_huxleyi_jgi433441	6.20E-22
ConsensusfromContig5124	Haptophyceae-Emiliania_huxleyi_jgi433441	1.20E-64
ConsensusfromContig1527	Haptophyceae-Emiliania_huxleyi_jgi433479	3.70E-14
ConsensusfromContig1454	Haptophyceae-Emiliania_huxleyi_jgi435533	6.60E-15
ConsensusfromContig1943	Haptophyceae-Emiliania_huxleyi_jgi436192	1.70E-69
ConsensusfromContig5979	Haptophyceae-Emiliania_huxleyi_jgi438457	7.60E-13
ConsensusfromContig4772	Haptophyceae-Emiliania_huxleyi_jgi438669	2.00E-14
ConsensusfromContig5271	Haptophyceae-Emiliania_huxleyi_jgi438669	1.40E-58
ConsensusfromContig3113	Haptophyceae-Emiliania_huxleyi_jgi439255	9.90E-11
ConsensusfromContig5366	Haptophyceae-Emiliania_huxleyi_jgi439968	3.40E-15
ConsensusfromContig2821	Haptophyceae-Emiliania_huxleyi_jgi441558	1.40E-15
ConsensusfromContig2082	Haptophyceae-Emiliania_huxleyi_jgi442922	1.00E-26
ConsensusfromContig1980	Haptophyceae-Emiliania_huxleyi_jgi442986	1.40E-12
ConsensusfromContig2455	Haptophyceae-Emiliania_huxleyi_jgi443003	2.90E-36
ConsensusfromContig5186	Haptophyceae-Emiliania_huxleyi_jgi443137	2.50E-20
ConsensusfromContig5109	Haptophyceae-Emiliania_huxleyi_jgi444197	2.40E-37
ConsensusfromContig5109	Haptophyceae-Emiliania_huxleyi_jgi444197	2.40E-37
ConsensusfromContig2061	Haptophyceae-Emiliania_huxleyi_jgi447989	2.60E-13
ConsensusfromContig5157	Haptophyceae-Emiliania_huxleyi_jgi447998	2.50E-44
ConsensusfromContig2886	Haptophyceae-Emiliania_huxleyi_jgi448407	3.70E-36
ConsensusfromContig1127	Haptophyceae-Emiliania_huxleyi_jgi448687	1.10E-16
ConsensusfromContig1127	Haptophyceae-Emiliania_huxleyi_jgi448687	1.10E-16
ConsensusfromContig2088	Haptophyceae-Emiliania_huxleyi_jgi450538	2.30E-21
ConsensusfromContig2036	Haptophyceae-Emiliania_huxleyi_jgi451521	1.10E-37
ConsensusfromContig5117	Haptophyceae-Emiliania_huxleyi_jgi451639	2.60E-17
ConsensusfromContig5188	Haptophyceae-Emiliania_huxleyi_jgi451639	1.50E-18
ConsensusfromContig5141	Haptophyceae-Emiliania_huxleyi_jgi452247	3.80E-32
ConsensusfromContig1978	Haptophyceae-Emiliania_huxleyi_jgi452510	2.30E-18
ConsensusfromContig2128	Haptophyceae-Emiliania_huxleyi_jgi453008	3.40E-31
ConsensusfromContig5184	Haptophyceae-Emiliania_huxleyi_jgi454057	2.40E-30
ConsensusfromContig7349	Haptophyceae-Emiliania_huxleyi_jgi454930	2.50E-11
ConsensusfromContig1934	Haptophyceae-Emiliania_huxleyi_jgi455791	4.90E-65
ConsensusfromContig6943	Haptophyceae-Emiliania_huxleyi_jgi456239	1.20E-23
ConsensusfromContig6895	Haptophyceae-Emiliania_huxleyi_jgi457819	1.30E-12
ConsensusfromContig3334	Haptophyceae-Emiliania_huxleyi_jgi458067	3.00E-11
ConsensusfromContig5162	Haptophyceae-Emiliania_huxleyi_jgi459414	8.10E-15
ConsensusfromContig2210	Haptophyceae-Emiliania_huxleyi_jgi460130	8.20E-12
ConsensusfromContig1032	Haptophyceae-Emiliania_huxleyi_jgi460348	9.60E-27
ConsensusfromContig5440	Haptophyceae-Emiliania_huxleyi_jgi461539	1.00E-82
ConsensusfromContig4924	Haptophyceae-Emiliania_huxleyi_jgi461645	1.00E-23
ConsensusfromContig5378	Haptophyceae-Emiliania_huxleyi_jgi461647	8.80E-53
ConsensusfromContig7074	Haptophyceae-Emiliania_huxleyi_jgi461715	8.10E-12
ConsensusfromContig781	Haptophyceae-Emiliania_huxleyi_jgi462184	8.00E-33
ConsensusfromContig1981	Haptophyceae-Emiliania_huxleyi_jgi462184	1.20E-127
ConsensusfromContig7401	Haptophyceae-Emiliania_huxleyi_jgi462780	2.10E-13
ConsensusfromContig5136	Haptophyceae-Emiliania_huxleyi_jgi462792	5.80E-11
ConsensusfromContig5421	Haptophyceae-Emiliania_huxleyi_jgi463630	1.00E-25
ConsensusfromContig6273	Haptophyceae-Emiliania_huxleyi_jgi463630	8.00E-20
ConsensusfromContig2042	Haptophyceae-Emiliania_huxleyi_jgi464278	6.70E-19
ConsensusfromContig1110	Haptophyceae-Emiliania_huxleyi_jgi465373	1.70E-19
ConsensusfromContig1717	Haptophyceae-Emiliania_huxleyi_jgi465373	5.90E-11
ConsensusfromContig1717	Haptophyceae-Emiliania_huxleyi_jgi465373	5.90E-11
ConsensusfromContig4802	Haptophyceae-Emiliania_huxleyi_jgi465373	1.50E-18
ConsensusfromContig6938	Haptophyceae-Emiliania_huxleyi_jgi466221	1.60E-40
ConsensusfromContig2465	Haptophyceae-Emiliania_huxleyi_jgi466294	8.40E-58
ConsensusfromContig1237	Haptophyceae-Emiliania_huxleyi_jgi466319	4.00E-17

ConsensusfromContig1237	Haptophyceae-Emiliania_huxleyi_jgi466319	4.00E-17	
ConsensusfromContig4412	Haptophyceae-Emiliania_huxleyi_jgi466469	2.00E-20	
ConsensusfromContig1093	Haptophyceae-Emiliania_huxleyi_jgi468499	3.80E-14	
ConsensusfromContig2029	Haptophyceae-Emiliania_huxleyi_jgi468499	1.50E-15	
ConsensusfromContig2073	Haptophyceae-Emiliania_huxleyi_jgi468597	9.30E-87	
ConsensusfromContig2046	Haptophyceae-Emiliania_huxleyi_jgi469884	4.10E-62	
ConsensusfromContig6468	Haptophyceae-Emiliania_huxleyi_jgi470091	1.90E-34	
ConsensusfromContig1986	Haptophyceae-Emiliania_huxleyi_jgi47359	1.20E-15	
ConsensusfromContig1940	Haptophyceae-Emiliania_huxleyi_jgi50066	6.10E-30	
ConsensusfromContig5191	Haptophyceae-Emiliania_huxleyi_jgi54516	8.40E-13	
ConsensusfromContig5940	Haptophyceae-Emiliania_huxleyi_jgi55001	4.40E-23	
ConsensusfromContig2249	Haptophyceae-Emiliania_huxleyi_jgi62301	8.00E-31	
ConsensusfromContig5351	Haptophyceae-Emiliania_huxleyi_jgi62301	5.00E-44	
ConsensusfromContig2243	Haptophyceae-Emiliania_huxleyi_jgi62379	1.30E-65	
ConsensusfromContig2568	Haptophyceae-Emiliania_huxleyi_jgi64727	1.90E-14	
ConsensusfromContig2932	Haptophyceae-Emiliania_huxleyi_jgi65641	2.10E-13	
ConsensusfromContig1970	Haptophyceae-Emiliania_huxleyi_jgi69471	2.30E-15	
ConsensusfromContig2609	Haptophyceae-Emiliania_huxleyi_jgi69905	3.20E-13	
ConsensusfromContig2934	Haptophyceae-Emiliania_huxleyi_jgi69905	1.70E-37	
ConsensusfromContig4777	Haptophyceae-Emiliania_huxleyi_jgi69905	3.20E-13	
ConsensusfromContig1550	Haptophyceae-Emiliania_huxleyi_jgi73204	5.60E-11	
ConsensusfromContig2010	Haptophyceae-Emiliania_huxleyi_jgi73553	1.20E-62	
ConsensusfromContig7067	Haptophyceae-Emiliania_huxleyi_jgi73777	1.70E-17	
ConsensusfromContig6067	Haptophyceae-Emiliania_huxleyi_jgi73824	3.50E-17	
ConsensusfromContig2080	Haptophyceae-Emiliania_huxleyi_jgi75898	3.30E-53	
ConsensusfromContig2080	Haptophyceae-Emiliania_huxleyi_jgi75898	3.30E-53	
ConsensusfromContig9520	Haptophyceae-Emiliania_huxleyi_jgi76857	4.70E-11	
ConsensusfromContig2612	Haptophyceae-Emiliania_huxleyi_jgi95007	7.20E-12	
ConsensusfromContig2023	Haptophyceae-Emiliania_huxleyi_jgi95026	2.30E-42	
ConsensusfromContig2704	Haptophyceae-Emiliania_huxleyi_jgi95026	4.90E-23	
ConsensusfromContig5111	Haptophyceae-Emiliania_huxleyi_jgi95026	9.40E-121	
ConsensusfromContig5153	Haptophyceae-Emiliania_huxleyi_jgi96138	1.10E-25	
ConsensusfromContig2241	Haptophyceae-Emiliania_huxleyi_jgi97161	3.80E-16	
ConsensusfromContig5865	Haptophyceae-Emiliania_huxleyi_jgi97161	2.20E-16	
ConsensusfromContig2196	Haptophyceae-Emiliania_huxleyi_jgi97544	7.10E-29	
ConsensusfromContig3759	Haptophyceae-Emiliania_huxleyi_jgi97544	6.50E-11	
ConsensusfromContig6939	Haptophyceae-Emiliania_huxleyi_jgi98220	1.10E-23	
ConsensusfromContig6800	Haptophyceae-Emiliania_huxleyi_jgi98869	7.40E-13	
ConsensusfromContig2003	Haptophyceae-Emiliania_huxleyi_jgi99009	7.40E-125	
ConsensusfromContig1820	Haptophyceae-Emiliania_huxleyi_jgi99421	1.60E-13	
ConsensusfromContig4323	Haptophyceae-Emiliania_huxleyi_jgi99509	5.10E-17	
ConsensusfromContig7321	Haptophyceae-Emiliania_huxleyi_jgi99509	1.30E-13	
ConsensusfromContig2044	Haptophyceae-Emiliania_huxleyi_jgi99558	3.40E-54	
ConsensusfromContig7142	Haptophyceae-Isochrysis_galbana_tbISL00000054_3	1.60E-56	
ConsensusfromContig6941	Haptophyceae-Isochrysis_galbana_tbISL00000482_1	9.50E-14	
ConsensusfromContig1893	Haptophyceae-Isochrysis_galbana_tbISL00000711_2	1.20E-42	
ConsensusfromContig2954	Haptophyceae-Isochrysis_galbana_tbISL00000716_3	4.90E-22	
ConsensusfromContig4808	Haptophyceae-Isochrysis_galbana_tbISL00000830_3	1.50E-12	
ConsensusfromContig2868	Haptophyceae-Isochrysis_galbana_tbISL00001220_2	1.10E-13	
ConsensusfromContig6988	Haptophyceae-Isochrysis_galbana_tbISL00001535_1	8.40E-15	
ConsensusfromContig5938	Haptophyceae-Isochrysis_galbana_tbISL00002225_3	1.80E-21	
ConsensusfromContig2073	Haptophyceae-Isochrysis_galbana_tbISL00002317_2	1.60E-27	
ConsensusfromContig2073	Haptophyceae-Isochrysis_galbana_tbISL00002317_2	1.60E-27	
ConsensusfromContig2313	Haptophyceae-Isochrysis_galbana_tbISL00002317_2	4.70E-11	
ConsensusfromContig5115	Haptophyceae-Isochrysis_galbana_tbISL00002317_2	7.10E-31	
ConsensusfromContig5171	Haptophyceae-Isochrysis_galbana_tbISL00002317_2	9.50E-16	
ConsensusfromContig1947	Haptophyceae-Isochrysis_galbana_tbISL00002332_2	6.70E-12	
ConsensusfromContig2208	Haptophyceae-Isochrysis_galbana_tbISL00002365_2	3.10E-38	
ConsensusfromContig3317	Haptophyceae-Isochrysis_galbana_tbISL00002426_1	4.70E-20	
ConsensusfromContig5455	Haptophyceae-Isochrysis_galbana_tbISL00003649_2	5.20E-17	
ConsensusfromContig4279	Haptophyceae-Isochrysis_galbana_tbISL00003931_2	6.20E-19	
ConsensusfromContig1938	Haptophyceae-Isochrysis_galbana_tbISL00004212_1	8.10E-11	
ConsensusfromContig2069	Haptophyceae-Isochrysis_galbana_tbISL00004546_3	1.30E-46	
ConsensusfromContig5513	Haptophyceae-Isochrysis_galbana_tbISL00007307_1	1.40E-13	
ConsensusfromContig6549	Haptophyceae-Pavlova_lutheri_tbPLL00000075_6	2.70E-11	
ConsensusfromContig1934	Haptophyceae-Pavlova_lutheri_tbPLL00000270_3	1.30E-14	
ConsensusfromContig2951	Haptophyceae-Pavlova_lutheri_tbPLL00000345_1	1.70E-37	
ConsensusfromContig5361	Haptophyceae-Pavlova_lutheri_tbPLL00000345_1	3.80E-20	
ConsensusfromContig7128	Haptophyceae-Pavlova_lutheri_tbPLL00001356_2	5.30E-13	
ConsensusfromContig4760	Haptophyceae-Pavlova_lutheri_tbPLL00001525_2	2.20E-12	
ConsensusfromContig2277	Haptophyceae-Pavlova_lutheri_tbPLL00001598_3	7.90E-14	
ConsensusfromContig6992	Haptophyceae-Pavlova_lutheri_tbPLL00002602_2	1.30E-13	
ConsensusfromContig1869	Haptophyceae-Pavlova_lutheri_tbPLL00002635_1	2.60E-11	
ConsensusfromContig5174	Metazoa-Acyrthosiphon_pisum_gi193596410	3.60E-12	>XP_001948769 PREDICTED: similar to proteasome (prosome, macropain) 26S subunit, non-ATPase, 10 [Acyrthosiphon pisum].
ConsensusfromContig4123	Metazoa-Acyrthosiphon_pisum_gi193596679	6.60E-13	>XP_001947322 PREDICTED: similar to predicted protein [Acyrthosiphon pisum].
ConsensusfromContig2272	Metazoa-Acyrthosiphon_pisum_gi193618024	7.80E-61	>XP_001950544 PREDICTED: similar to elongation factor 2 [Acyrthosiphon pisum].
ConsensusfromContig2152	Metazoa-Acyrthosiphon_pisum_gi193620339	4.80E-12	>XP_001947526 PREDICTED: similar to zinc finger protein [Acyrthosiphon pisum].
ConsensusfromContig6985	Metazoa-Acyrthosiphon_pisum_gi193624968	2.00E-16	>XP_001945316 PREDICTED: similar to cleavage and polyadenylation specific factor 4 [Acyrthosiphon pisum].
ConsensusfromContig3523	Metazoa-Acyrthosiphon_pisum_gi193652654	7.30E-24	>XP_001944369 PREDICTED: similar to zinc finger protein, partial [Acyrthosiphon pisum].
ConsensusfromContig2956	Metazoa-Acyrthosiphon_pisum_gi193654871	4.00E-41	>XP_001946776 PREDICTED: similar to predicted protein [Acyrthosiphon pisum].
ConsensusfromContig5908	Metazoa-Acyrthosiphon_pisum_gi193666950	1.70E-15	>XP_001944697 PREDICTED: similar to sodium/hydrogen exchanger 8 [Acyrthosiphon pisum].
ConsensusfromContig3129	Metazoa-Acyrthosiphon_pisum_gi193690850	5.10E-26	>XP_001946682 PREDICTED: similar to novel KRAB box and zinc finger, C2H2 type domain containing protein [Acyrthosiphon pisum].
ConsensusfromContig3138	Metazoa-Acyrthosiphon_pisum_gi193704592	1.20E-16	>XP_001942535 PREDICTED: similar to KRAB-A domain containing 2, partial [Acyrthosiphon pisum].
ConsensusfromContig736	Metazoa-Acyrthosiphon_pisum_gi193704634	1.80E-11	>XP_001944542 PREDICTED: similar to Multidrug-Resistance like Protein 1 CG6214-PK [Acyrthosiphon pisum].
ConsensusfromContig6930	Metazoa-Acyrthosiphon_pisum_gi193716098	1.70E-18	>XP_001952595 PREDICTED: similar to myosin-X, partial [Acyrthosiphon pisum].
ConsensusfromContig1274	Metazoa-Aedes_aegypti_gi157105151	6.20E-13	>XP_001648739 kinesin-like protein Klp10A [Aedes aegypti].
ConsensusfromContig1385	Metazoa-Aedes_aegypti_gi157106769	5.70E-17	>XP_001649474 ankyrin 2,3/unc44 [Aedes aegypti].
ConsensusfromContig6930	Metazoa-Aedes_aegypti_gi157112757	4.40E-41	>XP_001651857 superoxide dismutase [Aedes aegypti].
ConsensusfromContig2476	Metazoa-Aedes_aegypti_gi157114411	4.20E-31	>XP_001652258 succinyl-CoA synthetase small subunit, putative [Aedes aegypti].
ConsensusfromContig2141	Metazoa-Aedes_aegypti_gi157119028	1.60E-14	>XP_001659301 poly(adp-ribose) glycohydrolase [Aedes aegypti].
ConsensusfromContig3470	Metazoa-Aedes_aegypti_gi157120352	9.00E-18	>XP_001653621 regulator of telomere elongation helicase 1 rtel1 [Aedes aegypti].
ConsensusfromContig2050	Metazoa-Aedes_aegypti_gi157127870	1.10E-18	>XP_001655059 cubulin [Aedes aegypti].
ConsensusfromContig1934	Metazoa-Aedes_aegypti_gi157128919	1.10E-68	>XP_001661548 voltage-dependent p/q type calcium channel [Aedes aegypti].
ConsensusfromContig7448	Metazoa-Aedes_aegypti_gi157134658	3.40E-12	>XP_001663334 transcription factor IIB, putative [Aedes aegypti].
ConsensusfromContig2264	Metazoa-Aedes_aegypti_gi157136853	1.40E-53	>XP_001656940 wd-repeat protein [Aedes aegypti].
ConsensusfromContig1135	Metazoa-Amphimedon_queenslandica_jgiAqu1200959	2.40E-13	
ConsensusfromContig2993	Metazoa-Amphimedon_queenslandica_jgiAqu1200959	1.50E-11	
ConsensusfromContig5163	Metazoa-Amphimedon_queenslandica_jgiAqu1200971	5.40E-11	
ConsensusfromContig6019	Metazoa-Amphimedon_queenslandica_jgiAqu1201032	2.90E-37	
ConsensusfromContig1933	Metazoa-Amphimedon_queenslandica_jgiAqu1201944	1.60E-62	

ConsensusfromContig2424	Metazoa-Amphimedon_queenslandica_jgiAqu1201944	3.00E-26	
ConsensusfromContig6168	Metazoa-Amphimedon_queenslandica_jgiAqu1201944	5.80E-16	
ConsensusfromContig5496	Metazoa-Amphimedon_queenslandica_jgiAqu1202371	2.40E-51	
ConsensusfromContig7018	Metazoa-Amphimedon_queenslandica_jgiAqu1202371	2.00E-36	
ConsensusfromContig4235	Metazoa-Amphimedon_queenslandica_jgiAqu1203830	5.10E-11	
ConsensusfromContig1975	Metazoa-Amphimedon_queenslandica_jgiAqu1204904	3.80E-19	
ConsensusfromContig5157	Metazoa-Amphimedon_queenslandica_jgiAqu1205599	4.30E-21	
ConsensusfromContig3201	Metazoa-Amphimedon_queenslandica_jgiAqu1206218	3.40E-30	
ConsensusfromContig5758	Metazoa-Amphimedon_queenslandica_jgiAqu1207561	1.10E-11	
ConsensusfromContig3146	Metazoa-Amphimedon_queenslandica_jgiAqu1208670	3.30E-12	
ConsensusfromContig5326	Metazoa-Amphimedon_queenslandica_jgiAqu1209041	6.20E-25	
ConsensusfromContig6334	Metazoa-Amphimedon_queenslandica_jgiAqu1209041	7.00E-11	
ConsensusfromContig6476	Metazoa-Amphimedon_queenslandica_jgiAqu1209041	1.90E-26	
ConsensusfromContig5213	Metazoa-Amphimedon_queenslandica_jgiAqu1209161	3.00E-27	
ConsensusfromContig5132	Metazoa-Amphimedon_queenslandica_jgiAqu1209589	9.80E-21	
ConsensusfromContig2200	Metazoa-Amphimedon_queenslandica_jgiAqu1209937	4.00E-23	
ConsensusfromContig6925	Metazoa-Amphimedon_queenslandica_jgiAqu1209937	2.60E-33	
ConsensusfromContig6933	Metazoa-Amphimedon_queenslandica_jgiAqu1210295	4.20E-12	
ConsensusfromContig2022	Metazoa-Amphimedon_queenslandica_jgiAqu1210513	8.30E-13	
ConsensusfromContig2588	Metazoa-Amphimedon_queenslandica_jgiAqu1210513	1.70E-12	
ConsensusfromContig3620	Metazoa-Amphimedon_queenslandica_jgiAqu1210513	6.20E-19	
ConsensusfromContig3620	Metazoa-Amphimedon_queenslandica_jgiAqu1210513	6.20E-19	
ConsensusfromContig5176	Metazoa-Amphimedon_queenslandica_jgiAqu1211417	9.40E-26	
ConsensusfromContig2424	Metazoa-Amphimedon_queenslandica_jgiAqu1211786	5.40E-11	
ConsensusfromContig5345	Metazoa-Amphimedon_queenslandica_jgiAqu1212388	6.50E-13	
ConsensusfromContig2159	Metazoa-Amphimedon_queenslandica_jgiAqu1212846	1.90E-15	
ConsensusfromContig7257	Metazoa-Amphimedon_queenslandica_jgiAqu1212957	5.20E-12	
ConsensusfromContig1976	Metazoa-Amphimedon_queenslandica_jgiAqu1215172	5.60E-68	
ConsensusfromContig2777	Metazoa-Amphimedon_queenslandica_jgiAqu1215837	1.70E-28	
ConsensusfromContig2777	Metazoa-Amphimedon_queenslandica_jgiAqu1215837	1.70E-28	
ConsensusfromContig7718	Metazoa-Amphimedon_queenslandica_jgiAqu1216257	3.20E-12	
ConsensusfromContig1952	Metazoa-Amphimedon_queenslandica_jgiAqu1216257	7.80E-42	
ConsensusfromContig5372	Metazoa-Amphimedon_queenslandica_jgiAqu1216257	1.90E-18	
ConsensusfromContig2035	Metazoa-Amphimedon_queenslandica_jgiAqu1216481	1.70E-24	
ConsensusfromContig5168	Metazoa-Amphimedon_queenslandica_jgiAqu1216481	4.00E-14	
ConsensusfromContig2000	Metazoa-Amphimedon_queenslandica_jgiAqu1217862	1.80E-24	
ConsensusfromContig6979	Metazoa-Amphimedon_queenslandica_jgiAqu1217965	4.10E-44	
ConsensusfromContig3035	Metazoa-Amphimedon_queenslandica_jgiAqu1218520	3.00E-12	
ConsensusfromContig6155	Metazoa-Amphimedon_queenslandica_jgiAqu1220415	6.90E-29	
ConsensusfromContig2092	Metazoa-Amphimedon_queenslandica_jgiAqu1220630	8.10E-60	
ConsensusfromContig6964	Metazoa-Amphimedon_queenslandica_jgiAqu1220826	2.80E-28	
ConsensusfromContig6978	Metazoa-Amphimedon_queenslandica_jgiAqu1221992	7.40E-78	
ConsensusfromContig697	Metazoa-Amphimedon_queenslandica_jgiAqu1222279	1.80E-11	
ConsensusfromContig3963	Metazoa-Amphimedon_queenslandica_jgiAqu1222291	1.20E-35	
ConsensusfromContig5898	Metazoa-Amphimedon_queenslandica_jgiAqu1222465	1.10E-14	
ConsensusfromContig3125	Metazoa-Amphimedon_queenslandica_jgiAqu1222648	1.70E-19	
ConsensusfromContig6987	Metazoa-Amphimedon_queenslandica_jgiAqu1222870	5.90E-24	
ConsensusfromContig2083	Metazoa-Amphimedon_queenslandica_jgiAqu1223590	2.20E-11	
ConsensusfromContig2380	Metazoa-Amphimedon_queenslandica_jgiAqu1223647	2.30E-12	
ConsensusfromContig7134	Metazoa-Amphimedon_queenslandica_jgiAqu1223720	9.10E-29	
ConsensusfromContig6923	Metazoa-Amphimedon_queenslandica_jgiAqu1224260	1.30E-109	
ConsensusfromContig2044	Metazoa-Amphimedon_queenslandica_jgiAqu1224483	5.40E-13	
ConsensusfromContig7460	Metazoa-Amphimedon_queenslandica_jgiAqu1224483	2.00E-24	
ConsensusfromContig5146	Metazoa-Amphimedon_queenslandica_jgiAqu1224535	9.00E-15	
ConsensusfromContig1073	Metazoa-Amphimedon_queenslandica_jgiAqu1224825	2.80E-12	
ConsensusfromContig1073	Metazoa-Amphimedon_queenslandica_jgiAqu1224825	2.80E-12	
ConsensusfromContig6399	Metazoa-Amphimedon_queenslandica_jgiAqu1225526	4.90E-21	
ConsensusfromContig5212	Metazoa-Amphimedon_queenslandica_jgiAqu1225745	1.70E-72	
ConsensusfromContig2098	Metazoa-Amphimedon_queenslandica_jgiAqu1225929	2.60E-60	
ConsensusfromContig5159	Metazoa-Amphimedon_queenslandica_jgiAqu1225929	8.20E-74	
ConsensusfromContig7298	Metazoa-Amphimedon_queenslandica_jgiAqu1226427	1.60E-18	
ConsensusfromContig2104	Metazoa-Amphimedon_queenslandica_jgiAqu1226462	1.20E-41	
ConsensusfromContig7080	Metazoa-Amphimedon_queenslandica_jgiAqu1226841	7.90E-11	
ConsensusfromContig5125	Metazoa-Amphimedon_queenslandica_jgiAqu1226914	1.60E-17	
ConsensusfromContig2302	Metazoa-Amphimedon_queenslandica_jgiAqu1227146	1.70E-25	
ConsensusfromContig6999	Metazoa-Amphimedon_queenslandica_jgiAqu1227234	4.60E-23	
ConsensusfromContig3744	Metazoa-Amphimedon_queenslandica_jgiAqu1227481	6.20E-11	
ConsensusfromContig2118	Metazoa-Amphimedon_queenslandica_jgiAqu1227564	2.70E-11	
ConsensusfromContig5110	Metazoa-Amphimedon_queenslandica_jgiAqu1227740	8.30E-93	
ConsensusfromContig1432	Metazoa-Amphimedon_queenslandica_jgiAqu1227741	2.50E-22	
ConsensusfromContig2172	Metazoa-Amphimedon_queenslandica_jgiAqu1227741	5.80E-24	
ConsensusfromContig1239	Metazoa-Amphimedon_queenslandica_jgiAqu1227952	8.50E-15	
ConsensusfromContig1955	Metazoa-Amphimedon_queenslandica_jgiAqu1228390	4.00E-21	
ConsensusfromContig2406	Metazoa-Amphimedon_queenslandica_jgiAqu1228433	1.40E-36	
ConsensusfromContig4362	Metazoa-Amphimedon_queenslandica_jgiAqu1228433	7.40E-24	
ConsensusfromContig2441	Metazoa-Amphimedon_queenslandica_jgiAqu1228464	1.60E-32	
ConsensusfromContig1995	Metazoa-Amphimedon_queenslandica_jgiAqu1228909	7.20E-15	
ConsensusfromContig5639	Metazoa-Amphimedon_queenslandica_jgiAqu1228909	3.50E-13	
ConsensusfromContig5178	Metazoa-Amphimedon_queenslandica_jgiAqu1229267	1.20E-13	
ConsensusfromContig3051	Metazoa-Amphimedon_queenslandica_jgiAqu1229503	4.90E-18	
ConsensusfromContig1073	Metazoa-Amphimedon_queenslandica_jgiAqu1229724	2.80E-13	
ConsensusfromContig5341	Metazoa-Amphimedon_queenslandica_jgiAqu1230002	2.80E-15	
ConsensusfromContig5372	Metazoa-Amphimedon_queenslandica_jgiAqu1230091	1.10E-11	
ConsensusfromContig5112	Metazoa-Anopheles_gambiae_str_PEST_gi118794899	2.80E-26	>XP_321804 AGAP001341-PA [Anopheles gambiae str. PEST].
ConsensusfromContig1947	Metazoa-Anopheles_gambiae_str_PEST_gi158284773	8.90E-43	>XP_307859 AGAP009446-PA [Anopheles gambiae str. PEST].
ConsensusfromContig6137	Metazoa-Anopheles_gambiae_str_PEST_gi158286795	2.10E-24	>XP_308929 AGAP006817-PA [Anopheles gambiae str. PEST].
ConsensusfromContig2313	Metazoa-Anopheles_gambiae_str_PEST_gi158288775	5.10E-12	>XP_310614 AGAP000478-PA [Anopheles gambiae str. PEST].
ConsensusfromContig2468	Metazoa-Anopheles_gambiae_str_PEST_gi158289428	1.70E-22	>XP_001687752 AGAP000003-PA [Anopheles gambiae str. PEST].
ConsensusfromContig2496	Metazoa-Anopheles_gambiae_str_PEST_gi158289428	4.20E-11	>XP_001687752 AGAP000003-PA [Anopheles gambiae str. PEST].
ConsensusfromContig3157	Metazoa-Anopheles_gambiae_str_PEST_gi158289428	2.00E-12	>XP_001687752 AGAP000003-PA [Anopheles gambiae str. PEST].
ConsensusfromContig3538	Metazoa-Anopheles_gambiae_str_PEST_gi158289428	9.40E-11	>XP_001687752 AGAP000003-PA [Anopheles gambiae str. PEST].
ConsensusfromContig5531	Metazoa-Anopheles_gambiae_str_PEST_gi158289428	8.10E-21	>XP_001687752 AGAP000003-PA [Anopheles gambiae str. PEST].
ConsensusfromContig7084	Metazoa-Anopheles_gambiae_str_PEST_gi158289428	4.90E-16	>XP_001687752 AGAP000003-PA [Anopheles gambiae str. PEST].
ConsensusfromContig5332	Metazoa-Anopheles_gambiae_str_PEST_gi158289979	4.70E-11	>XP_001230815 AGAP010372-PA [Anopheles gambiae str. PEST].
ConsensusfromContig5464	Metazoa-Anopheles_gambiae_str_PEST_gi158296123	7.20E-20	>XP_316621 AGAP006594-PA [Anopheles gambiae str. PEST].
ConsensusfromContig2334	Metazoa-Anopheles_gambiae_str_PEST_gi58392495	4.30E-13	>XP_319412 AGAP010224-PA [Anopheles gambiae str. PEST].
ConsensusfromContig5132	Metazoa-Apis_mellifera_gi48130459	5.60E-34	>XP_393319 PREDICTED: similar to F-box and leucine-rich repeat protein 20 isoform 1 [Apis mellifera].
ConsensusfromContig5120	Metazoa-Apis_mellifera_gi58585182	3.90E-22	>NP_001011619 hyaluronidase precursor [Apis mellifera].
ConsensusfromContig7313	Metazoa-Bombyx_mori_gi219362829	2.30E-11	>NP_001136443 clathrin heavy chain [Bombyx mori].
ConsensusfromContig7270	Metazoa-Bombyx_mori_gi255652865	8.40E-14	>NP_001157373 beta-galactosidase [Bombyx mori].

ConsensusfromContig1946Metazoa-Bos_taurus_gi119909988	3.60E-43	>XP_001256367 PREDICTED: ATP-binding cassette, sub-family C (CFTR/MRP), member 12-like [Bos taurus].
ConsensusfromContig5140Metazoa-Bos_taurus_gi119920738	8.70E-15	>XP_600615 PREDICTED: NIMA-related kinase 10 [Bos taurus].
ConsensusfromContig5554Metazoa-Bos_taurus_gi194676951	1.80E-29	>XP_001789733 PREDICTED: leucine carboxyl methyltransferase 2 (predicted)-like [Bos taurus].
ConsensusfromContig4882Metazoa-Branchiostoma_floridae_gi260782022	6.20E-11	>XP_002586092 hypothetical protein BRAFLDRAFT_139422 [Branchiostoma floridae].
ConsensusfromContig5349Metazoa-Branchiostoma_floridae_gi260782022	1.50E-11	>XP_002586092 hypothetical protein BRAFLDRAFT_139422 [Branchiostoma floridae].
ConsensusfromContig1578Metazoa-Branchiostoma_floridae_gi260782187	3.70E-14	>XP_002586172 hypothetical protein BRAFLDRAFT_109674 [Branchiostoma floridae].
ConsensusfromContig7415Metazoa-Branchiostoma_floridae_gi260782452	3.70E-23	>XP_002586301 hypothetical protein BRAFLDRAFT_82907 [Branchiostoma floridae].
ConsensusfromContig2332Metazoa-Branchiostoma_floridae_gi260782551	2.30E-15	>XP_002586349 hypothetical protein BRAFLDRAFT_108829 [Branchiostoma floridae].
ConsensusfromContig5768Metazoa-Branchiostoma_floridae_gi260784173	1.30E-11	>XP_002587143 hypothetical protein BRAFLDRAFT_61708 [Branchiostoma floridae].
ConsensusfromContig1125Metazoa-Branchiostoma_floridae_gi260784388	1.30E-13	>XP_002587249 hypothetical protein BRAFLDRAFT_270316 [Branchiostoma floridae].
ConsensusfromContig1961Metazoa-Branchiostoma_floridae_gi260785090	1.20E-30	>XP_002587596 hypothetical protein BRAFLDRAFT_230468 [Branchiostoma floridae].
ConsensusfromContig2504Metazoa-Branchiostoma_floridae_gi260786970	5.50E-17	>XP_002588529 hypothetical protein BRAFLDRAFT_79485 [Branchiostoma floridae].
ConsensusfromContig1275Metazoa-Branchiostoma_floridae_gi260787006	1.20E-21	>XP_002588547 hypothetical protein BRAFLDRAFT_122359 [Branchiostoma floridae].
ConsensusfromContig2181Metazoa-Branchiostoma_floridae_gi260788155	1.60E-24	>XP_002589116 hypothetical protein BRAFLDRAFT_144886 [Branchiostoma floridae].
ConsensusfromContig5455Metazoa-Branchiostoma_floridae_gi260789934	6.90E-15	>XP_002589999 hypothetical protein BRAFLDRAFT_135646 [Branchiostoma floridae].
ConsensusfromContig7110Metazoa-Branchiostoma_floridae_gi260791673	4.70E-19	>XP_002590853 hypothetical protein BRAFLDRAFT_125711 [Branchiostoma floridae].
ConsensusfromContig4275Metazoa-Branchiostoma_floridae_gi260791904	2.00E-15	>XP_002590967 hypothetical protein BRAFLDRAFT_69482 [Branchiostoma floridae].
ConsensusfromContig2053Metazoa-Branchiostoma_floridae_gi260791928	4.60E-17	>XP_002590979 hypothetical protein BRAFLDRAFT_69470 [Branchiostoma floridae].
ConsensusfromContig2053Metazoa-Branchiostoma_floridae_gi260791928	4.60E-17	>XP_002590979 hypothetical protein BRAFLDRAFT_69470 [Branchiostoma floridae].
ConsensusfromContig5978Metazoa-Branchiostoma_floridae_gi260791928	5.30E-11	>XP_002590979 hypothetical protein BRAFLDRAFT_69470 [Branchiostoma floridae].
ConsensusfromContig6959Metazoa-Branchiostoma_floridae_gi260791928	1.00E-17	>XP_002590979 hypothetical protein BRAFLDRAFT_69470 [Branchiostoma floridae].
ConsensusfromContig2852Metazoa-Branchiostoma_floridae_gi260793206	3.80E-15	>XP_002591603 hypothetical protein BRAFLDRAFT_223487 [Branchiostoma floridae].
ConsensusfromContig7049Metazoa-Branchiostoma_floridae_gi260794374	1.10E-12	>XP_002592184 hypothetical protein BRAFLDRAFT_88079 [Branchiostoma floridae].
ConsensusfromContig4638Metazoa-Branchiostoma_floridae_gi260794631	9.80E-11	>XP_002592312 hypothetical protein BRAFLDRAFT_207041 [Branchiostoma floridae].
ConsensusfromContig5382Metazoa-Branchiostoma_floridae_gi260794631	2.10E-12	>XP_002592312 hypothetical protein BRAFLDRAFT_207041 [Branchiostoma floridae].
ConsensusfromContig5404Metazoa-Branchiostoma_floridae_gi260796177	4.90E-16	>XP_002593081 hypothetical protein BRAFLDRAFT_72844 [Branchiostoma floridae].
ConsensusfromContig5129Metazoa-Branchiostoma_floridae_gi260800285	5.00E-95	>XP_002595064 hypothetical protein BRAFLDRAFT_60124 [Branchiostoma floridae].
ConsensusfromContig7379Metazoa-Branchiostoma_floridae_gi260800285	3.30E-13	>XP_002595064 hypothetical protein BRAFLDRAFT_60124 [Branchiostoma floridae].
ConsensusfromContig1943Metazoa-Branchiostoma_floridae_gi260803459	3.80E-26	>XP_002596607 hypothetical protein BRAFLDRAFT_280249 [Branchiostoma floridae].
ConsensusfromContig8782Metazoa-Branchiostoma_floridae_gi260803521	2.80E-11	>XP_002596638 hypothetical protein BRAFLDRAFT_219218 [Branchiostoma floridae].
ConsensusfromContig7227Metazoa-Branchiostoma_floridae_gi260803521	4.80E-18	>XP_002596638 hypothetical protein BRAFLDRAFT_219218 [Branchiostoma floridae].
ConsensusfromContig1563Metazoa-Branchiostoma_floridae_gi260803838	2.80E-13	>XP_002596796 hypothetical protein BRAFLDRAFT_211833 [Branchiostoma floridae].
ConsensusfromContig2228Metazoa-Branchiostoma_floridae_gi260803838	8.20E-44	>XP_002596796 hypothetical protein BRAFLDRAFT_211833 [Branchiostoma floridae].
ConsensusfromContig2181Metazoa-Branchiostoma_floridae_gi260804277	6.10E-31	>XP_002597015 hypothetical protein BRAFLDRAFT_215938 [Branchiostoma floridae].
ConsensusfromContig2181Metazoa-Branchiostoma_floridae_gi260804277	6.10E-31	>XP_002597015 hypothetical protein BRAFLDRAFT_215938 [Branchiostoma floridae].
ConsensusfromContig5258Metazoa-Branchiostoma_floridae_gi260804277	4.70E-17	>XP_002597015 hypothetical protein BRAFLDRAFT_215938 [Branchiostoma floridae].
ConsensusfromContig2434Metazoa-Branchiostoma_floridae_gi260804447	2.40E-11	>XP_002597099 hypothetical protein BRAFLDRAFT_121315 [Branchiostoma floridae].
ConsensusfromContig2034Metazoa-Branchiostoma_floridae_gi260806492	1.70E-25	>XP_002598118 hypothetical protein BRAFLDRAFT_85664 [Branchiostoma floridae].
ConsensusfromContig3132Metazoa-Branchiostoma_floridae_gi260806591	2.20E-12	>XP_002598167 hypothetical protein BRAFLDRAFT_114725 [Branchiostoma floridae].
ConsensusfromContig5786Metazoa-Branchiostoma_floridae_gi260806599	7.00E-12	>XP_002598171 hypothetical protein BRAFLDRAFT_119101 [Branchiostoma floridae].
ConsensusfromContig7053Metazoa-Branchiostoma_floridae_gi260806599	9.50E-14	>XP_002598171 hypothetical protein BRAFLDRAFT_119101 [Branchiostoma floridae].
ConsensusfromContig2164Metazoa-Branchiostoma_floridae_gi260809500	8.00E-12	>XP_002599543 hypothetical protein BRAFLDRAFT_217776 [Branchiostoma floridae].
ConsensusfromContig4970Metazoa-Branchiostoma_floridae_gi260809656	1.50E-26	>XP_002599621 hypothetical protein BRAFLDRAFT_77720 [Branchiostoma floridae].
ConsensusfromContig2672Metazoa-Branchiostoma_floridae_gi260811335	2.20E-24	>XP_002600378 hypothetical protein BRAFLDRAFT_170475 [Branchiostoma floridae].
ConsensusfromContig7225Metazoa-Branchiostoma_floridae_gi260811335	2.60E-20	>XP_002600378 hypothetical protein BRAFLDRAFT_170475 [Branchiostoma floridae].
ConsensusfromContig6951Metazoa-Branchiostoma_floridae_gi260812916	7.90E-35	>XP_002601166 hypothetical protein BRAFLDRAFT_75615 [Branchiostoma floridae].
ConsensusfromContig4010Metazoa-Branchiostoma_floridae_gi260812974	4.30E-11	>XP_002601195 hypothetical protein BRAFLDRAFT_75637 [Branchiostoma floridae].
ConsensusfromContig7385Metazoa-Branchiostoma_floridae_gi260812974	3.70E-11	>XP_002601195 hypothetical protein BRAFLDRAFT_75637 [Branchiostoma floridae].
ConsensusfromContig5921Metazoa-Branchiostoma_floridae_gi260814147	3.60E-19	>XP_002601777 hypothetical protein BRAFLDRAFT_121174 [Branchiostoma floridae].
ConsensusfromContig7098Metazoa-Branchiostoma_floridae_gi260814494	2.30E-14	>XP_002601950 hypothetical protein BRAFLDRAFT_86434 [Branchiostoma floridae].
ConsensusfromContig2005Metazoa-Branchiostoma_floridae_gi260815375	1.60E-50	>XP_002602449 hypothetical protein BRAFLDRAFT_63459 [Branchiostoma floridae].
ConsensusfromContig2022Metazoa-Branchiostoma_floridae_gi260815375	5.60E-97	>XP_002602449 hypothetical protein BRAFLDRAFT_63459 [Branchiostoma floridae].
ConsensusfromContig2017Metazoa-Branchiostoma_floridae_gi260816819	9.00E-39	>XP_002603285 hypothetical protein BRAFLDRAFT_226384 [Branchiostoma floridae].
ConsensusfromContig1080Metazoa-Branchiostoma_floridae_gi260817774	3.60E-20	>XP_002603760 hypothetical protein BRAFLDRAFT_86588 [Branchiostoma floridae].
ConsensusfromContig2170Metazoa-Branchiostoma_floridae_gi260821499	5.00E-25	>XP_002606070 hypothetical protein BRAFLDRAFT_92090 [Branchiostoma floridae].
ConsensusfromContig5495Metazoa-Branchiostoma_floridae_gi260821499	3.80E-34	>XP_002606070 hypothetical protein BRAFLDRAFT_92090 [Branchiostoma floridae].
ConsensusfromContig2165Metazoa-Branchiostoma_floridae_gi260821639	8.80E-41	>XP_002606140 hypothetical protein BRAFLDRAFT_88051 [Branchiostoma floridae].
ConsensusfromContig1572Metazoa-Branchiostoma_floridae_gi260821780	2.90E-15	>XP_002606281 hypothetical protein BRAFLDRAFT_67520 [Branchiostoma floridae].
ConsensusfromContig4158Metazoa-Branchiostoma_floridae_gi260823118	4.10E-16	>XP_002604030 hypothetical protein BRAFLDRAFT_71680 [Branchiostoma floridae].
ConsensusfromContig1967Metazoa-Branchiostoma_floridae_gi260823352	5.20E-18	>XP_002604147 hypothetical protein BRAFLDRAFT_208101 [Branchiostoma floridae].
ConsensusfromContig2340Metazoa-Branchiostoma_floridae_gi260824189	5.90E-23	>XP_002607050 hypothetical protein BRAFLDRAFT_68168 [Branchiostoma floridae].
ConsensusfromContig7373Metazoa-Branchiostoma_floridae_gi260824523	1.40E-17	>XP_002607217 hypothetical protein BRAFLDRAFT_67985 [Branchiostoma floridae].
ConsensusfromContig5225Metazoa-Branchiostoma_floridae_gi260824890	1.90E-45	>XP_002607400 hypothetical protein BRAFLDRAFT_204961 [Branchiostoma floridae].
ConsensusfromContig1977Metazoa-Branchiostoma_floridae_gi260826470	6.00E-37	>XP_002608188 hypothetical protein BRAFLDRAFT_125860 [Branchiostoma floridae].
ConsensusfromContig2375Metazoa-Branchiostoma_floridae_gi260826470	7.90E-22	>XP_002608188 hypothetical protein BRAFLDRAFT_125860 [Branchiostoma floridae].
ConsensusfromContig6130Metazoa-Branchiostoma_floridae_gi260826470	1.70E-53	>XP_002608188 hypothetical protein BRAFLDRAFT_125860 [Branchiostoma floridae].
ConsensusfromContig1196Metazoa-Branchiostoma_floridae_gi260827166	2.10E-14	>XP_002608536 hypothetical protein BRAFLDRAFT_92365 [Branchiostoma floridae].
ConsensusfromContig4234Metazoa-Branchiostoma_floridae_gi260827166	7.50E-13	>XP_002608536 hypothetical protein BRAFLDRAFT_92365 [Branchiostoma floridae].
ConsensusfromContig5695Metazoa-Branchiostoma_floridae_gi260828999	1.20E-21	>XP_002609450 hypothetical protein BRAFLDRAFT_226607 [Branchiostoma floridae].
ConsensusfromContig5789Metazoa-Branchiostoma_floridae_gi260829331	4.20E-14	>XP_002609615 hypothetical protein BRAFLDRAFT_125029 [Branchiostoma floridae].
ConsensusfromContig7133Metazoa-Branchiostoma_floridae_gi260831430	8.10E-14	>XP_002610662 hypothetical protein BRAFLDRAFT_202192 [Branchiostoma floridae].
ConsensusfromContig1946Metazoa-Branchiostoma_floridae_gi260832882	2.60E-15	>XP_002611386 hypothetical protein BRAFLDRAFT_73217 [Branchiostoma floridae].
ConsensusfromContig2100Metazoa-Branchiostoma_floridae_gi260833024	3.50E-23	>XP_002611457 hypothetical protein BRAFLDRAFT_63910 [Branchiostoma floridae].
ConsensusfromContig1840Metazoa-Branchiostoma_floridae_gi260833144	2.20E-16	>XP_002611517 hypothetical protein BRAFLDRAFT_117190 [Branchiostoma floridae].
ConsensusfromContig2938Metazoa-Branchiostoma_floridae_gi260833935	1.30E-15	>XP_002611967 hypothetical protein BRAFLDRAFT_91852 [Branchiostoma floridae].
ConsensusfromContig1623Metazoa-Branchiostoma_floridae_gi260835695	9.40E-13	>XP_002612843 hypothetical protein BRAFLDRAFT_67209 [Branchiostoma floridae].
ConsensusfromContig6496Metazoa-Branchiostoma_floridae_gi260835699	7.70E-26	>XP_002612845 hypothetical protein BRAFLDRAFT_118409 [Branchiostoma floridae].
ConsensusfromContig3650Metazoa-Branchiostoma_floridae_gi260839820	1.40E-14	>XP_002613780 hypothetical protein BRAFLDRAFT_124169 [Branchiostoma floridae].
ConsensusfromContig5780Metazoa-Branchiostoma_floridae_gi261289479	8.50E-19	>XP_002604716 hypothetical protein BRAFLDRAFT_80311 [Branchiostoma floridae].
ConsensusfromContig5107Metazoa-Brugia_malayi_gi170579958	2.00E-11	>XP_001895056 Histidine-rich glycoprotein precursor [Brugia malayi].
ConsensusfromContig2351Metazoa-Buddenbrockia_plumatellae_tbBPL00000348_2	1.20E-35	
ConsensusfromContig2351Metazoa-Buddenbrockia_plumatellae_tbBPL00000348_2	1.20E-35	
ConsensusfromContig6677Metazoa-Caenorhabditis_briggsae_gi268558352	4.20E-17	>XP_002637166 C. briggsae CBR-GSP-1 protein [Caenorhabditis briggsae].
ConsensusfromContig3553Metazoa-Caenorhabditis_briggsae_gi268561144	3.30E-12	>XP_002638248 Hypothetical protein CBG15910 [Caenorhabditis briggsae].
ConsensusfromContig3615Metazoa-Caenorhabditis_briggsae_gi268565247	3.40E-11	>XP_002639383 Hypothetical protein CBG03970 [Caenorhabditis briggsae].
ConsensusfromContig6907Metazoa-Caenorhabditis_briggsae_gi268567884	6.90E-26	>XP_002647896 Hypothetical protein CBG23762 [Caenorhabditis briggsae].
ConsensusfromContig4650Metazoa-Caenorhabditis_briggsae_gi268572907	1.20E-11	>XP_002649075 Hypothetical protein CBG22566 [Caenorhabditis briggsae].
ConsensusfromContig3437Metazoa-Caenorhabditis_elegans_gi17534697	2.70E-12	>NP_495214 hypothetical protein H12I13.3 [Caenorhabditis elegans].
ConsensusfromContig1153Metazoa-Caenorhabditis_elegans_gi17541656	2.20E-12	>NP_501984 Na/Ca eXchangers family member (ncx-3) [Caenorhabditis elegans].
ConsensusfromContig3335Metazoa-Caenorhabditis_elegans_gi17550776	1.50E-18	>NP_510803 hypothetical protein C33E10.6 [Caenorhabditis elegans].
ConsensusfromContig4126Metazoa-Caenorhabditis_elegans_gi17550776	1.20E-17	>NP_510803 hypothetical protein C33E10.6 [Caenorhabditis elegans].
ConsensusfromContig1465Metazoa-Caenorhabditis_elegans_gi71985768	3.00E-18	>NP_001022573 Elongation Factor Kinase family member (efk-1) [Caenorhabditis elegans].
ConsensusfromContig1441Metazoa-Callithrix_jacchus_gi296190105	2.30E-12	>XP_002743054 PREDICTED: WD40 repeat-containing protein SMU1 isoform 2 [Callithrix jacchus].
ConsensusfromContig2356Metazoa-Callithrix_jacchus_gi296193364	1.30E-25	>XP_002744490 PREDICTED: mitotic spindle assembly checkpoint protein MAD1 [Callithrix jacchus].
ConsensusfromContig5839Metazoa-Callithrix_jacchus_gi296194950	3.90E-13	>XP_002745185 PREDICTED: hypothetical protein LOC100389613 [Callithrix jacchus].
ConsensusfromContig5100Metazoa-Callithrix_jacchus_gi296219315	5.60E-126	>XP_002755841 PREDICTED: ATP-binding cassette sub-family A member 3 isoform 1 [Callithrix jacchus].
ConsensusfromContig3502Metazoa-Callithrix_jacchus_gi296232479	2.00E-14	>XP_002761610 PREDICTED: hypothetical protein LOC100412928, partial [Callithrix jacchus].
ConsensusfromContig3502Metazoa-Callithrix_jacchus_gi296232479	2.00E-14	>XP_002761610 PREDICTED: hypothetical protein LOC100412928, partial [Callithrix jacchus].
ConsensusfromContig1999Metazoa-Canis_lupus_familiaris_gi73977360	1.60E-165	>XP_864115 PREDICTED: similar to Chromodomain-helicase-DNA-binding protein 8 (CHD-8) (Helicase with SNF2 domain 1) isoform 3 [Canis familiaris].
ConsensusfromContig5185Metazoa-Canis_lupus_familiaris_gi73980394	6.20E-25	>XP_532876 PREDICTED: similar to Protein disulfide-isomerase A6 precursor (Thioredoxin domain containing protein 7) [Canis familiaris].

ConsensusfromContig3347Metazoa-Canis_lupus_familiaris_gi73986826	2.40E-22	>XP_868230 PREDICTED: similar to eukaryotic translation initiation factor 3, subunit 4 (delta) (predicted) isoform 5 [Canis familiaris].
ConsensusfromContig2365Metazoa-Canis_lupus_familiaris_gi74007402	6.20E-15	>XP_538035 PREDICTED: similar to calcium channel, voltage-dependent, alpha 1F subunit [Canis familiaris].
ConsensusfromContig1009Metazoa-Cavia_porcellus_gi290491236	2.80E-19	>NP_001166492 hyaluronidase PH-20 [Cavia porcellus].
ConsensusfromContig7116Metazoa-Ciona_intestinalis_gi198415822	7.40E-23	>XP_002122214 PREDICTED: similar to LOC495686 protein, partial [Ciona intestinalis].
ConsensusfromContig6781Metazoa-Ciona_intestinalis_gi198415937	5.80E-11	>XP_002120127 PREDICTED: similar to notch homolog 1b [Ciona intestinalis].
ConsensusfromContig5101Metazoa-Ciona_intestinalis_gi198416740	2.90E-18	>XP_002126259 PREDICTED: similar to predicted protein [Ciona intestinalis].
ConsensusfromContig6940Metazoa-Ciona_intestinalis_gi198417017	4.70E-18	>XP_002122361 PREDICTED: similar to thrombospondin type 1 repeat containing protein [Ciona intestinalis].
ConsensusfromContig2227Metazoa-Ciona_intestinalis_gi198418315	9.10E-19	>XP_002120274 PREDICTED: similar to WD repeat domain 52, partial [Ciona intestinalis].
ConsensusfromContig7074Metazoa-Ciona_intestinalis_gi198419005	2.10E-32	>XP_002130105 PREDICTED: similar to LOC792966 protein [Ciona intestinalis].
ConsensusfromContig1655Metazoa-Ciona_intestinalis_gi198423606	1.10E-12	>XP_002121556 PREDICTED: similar to dumpy CG33196-PB [Ciona intestinalis].
ConsensusfromContig2148Metazoa-Ciona_intestinalis_gi198423992	1.40E-18	>XP_002130823 PREDICTED: hemicentin-like [Ciona intestinalis].
ConsensusfromContig2333Metazoa-Ciona_intestinalis_gi198423992	7.90E-19	>XP_002130823 PREDICTED: hemicentin-like [Ciona intestinalis].
ConsensusfromContig2333Metazoa-Ciona_intestinalis_gi198423992	7.90E-19	>XP_002130823 PREDICTED: hemicentin-like [Ciona intestinalis].
ConsensusfromContig2750Metazoa-Ciona_intestinalis_gi198426451	3.70E-11	>XP_002127605 PREDICTED: similar to Double C2-like domain-containing protein beta (Doc2-beta) [Ciona intestinalis].
ConsensusfromContig7374Metazoa-Ciona_intestinalis_gi198431525	2.20E-11	>XP_002121157 PREDICTED: similar to multicopper oxidase 1 [Ciona intestinalis].
ConsensusfromContig2305Metazoa-Ciona_intestinalis_gi198433100	2.90E-18	>XP_002120805 PREDICTED: similar to Cytoplasmic dynein 2 heavy chain 1 (Dynein heavy chain isotype 1B) [Ciona intestinalis].
ConsensusfromContig2872Metazoa-Ciona_intestinalis_gi198433100	7.10E-18	>XP_002120805 PREDICTED: similar to Cytoplasmic dynein 2 heavy chain 1 (Dynein heavy chain isotype 1B) [Ciona intestinalis].
ConsensusfromContig6332Metazoa-Ciona_intestinalis_gi198437238	2.50E-24	>XP_002124766 PREDICTED: similar to predicted protein [Ciona intestinalis].
ConsensusfromContig3136Metazoa-Ciona_intestinalis_gi198437622	3.60E-59	>XP_002128501 PREDICTED: similar to SV2 related protein [Ciona intestinalis].
ConsensusfromContig9861Metazoa-Ciona_intestinalis_gi198438122	7.70E-17	>XP_002124590 PREDICTED: similar to cytosolic sialic acid 9-O-acetylesterase homolog [Ciona intestinalis].
ConsensusfromContig2997Metazoa-Ciona_intestinalis_gi198438487	7.00E-34	>XP_002126221 PREDICTED: similar to Dynein heavy chain 5, axonemal (Axonemal beta dynein heavy chain 5) (Ciliary dynein heavy chain 5) [Ciona intestinalis].
ConsensusfromContig2095Metazoa-Ciona_intestinalis_gi74096053	5.50E-20	>NP_001027639 cGMP phosphodiesterase delta subunit [Ciona intestinalis].
ConsensusfromContig5204Metazoa-Culex_quinquefasciatus_gi170028940	1.40E-65	>XP_001842352 conserved hypothetical protein [Culex quinquefasciatus].
ConsensusfromContig1192Metazoa-Culex_quinquefasciatus_gi170049041	2.90E-22	>XP_001853968 histone H3.2 [Culex quinquefasciatus].
ConsensusfromContig5389Metazoa-Culex_quinquefasciatus_gi170050914	3.40E-12	>XP_001861526 conserved hypothetical protein [Culex quinquefasciatus].
ConsensusfromContig4250Metazoa-Culex_quinquefasciatus_gi170051445	5.60E-14	>XP_001861766 conserved hypothetical protein [Culex quinquefasciatus].
ConsensusfromContig1663Metazoa-Culex_quinquefasciatus_gi170056016	6.40E-43	>XP_001863841 crumbs [Culex quinquefasciatus].
ConsensusfromContig5285Metazoa-Culex_quinquefasciatus_gi170056240	3.90E-11	>XP_001863941 conserved hypothetical protein [Culex quinquefasciatus].
ConsensusfromContig1869Metazoa-Culex_quinquefasciatus_gi170061186	3.50E-11	>XP_001866126 disulfide isomerase [Culex quinquefasciatus].
ConsensusfromContig3185Metazoa-Danio_rerio_gi125805421	7.60E-16	>XP_694621 PREDICTED: LReO_3-like [Danio rerio].
ConsensusfromContig3219Metazoa-Danio_rerio_gi125805421	2.10E-15	>XP_694621 PREDICTED: LReO_3-like [Danio rerio].
ConsensusfromContig5481Metazoa-Danio_rerio_gi125805421	3.70E-19	>XP_694621 PREDICTED: LReO_3-like [Danio rerio].
ConsensusfromContig5865Metazoa-Danio_rerio_gi125853949	6.10E-11	>XP_688608 PREDICTED: lysosomal alpha-N-acetyl glucosaminidase-like [Danio rerio].
ConsensusfromContig2241Metazoa-Danio_rerio_gi189518832	4.20E-29	>XP_001919541 PREDICTED: hypothetical protein [Danio rerio].
ConsensusfromContig5452Metazoa-Danio_rerio_gi189527797	2.90E-28	>XP_688600 PREDICTED: LReO_3-like [Danio rerio].
ConsensusfromContig3202Metazoa-Danio_rerio_gi292610095	8.70E-14	>XP_001920404 PREDICTED: hypothetical protein, partial [Danio rerio].
ConsensusfromContig6924Metazoa-Danio_rerio_gi292610537	1.90E-33	>XP_001344452 PREDICTED: hypothetical protein [Danio rerio].
ConsensusfromContig5209Metazoa-Danio_rerio_gi292612046	9.80E-39	>XP_002661295 PREDICTED: LReO_3-like [Danio rerio].
ConsensusfromContig5471Metazoa-Danio_rerio_gi292613347	1.00E-23	>XP_002661892 PREDICTED: LReO_3-like [Danio rerio].
ConsensusfromContig7067Metazoa-Danio_rerio_gi292615051	5.70E-12	>XP_002662530 PREDICTED: LReO_3-like [Danio rerio].
ConsensusfromContig7449Metazoa-Danio_rerio_gi292615299	9.20E-15	>XP_002662599 PREDICTED: tubulin, alpha 4-like [Danio rerio].
ConsensusfromContig3480Metazoa-Danio_rerio_gi292617066	8.80E-16	>XP_001338510 PREDICTED: LReO_3-like [Danio rerio].
ConsensusfromContig3480Metazoa-Danio_rerio_gi292617066	8.80E-16	>XP_001338510 PREDICTED: LReO_3-like [Danio rerio].
ConsensusfromContig2068Metazoa-Danio_rerio_gi292619560	1.20E-34	>XP_002664009 PREDICTED: LReO_3-like [Danio rerio].
ConsensusfromContig7009Metazoa-Danio_rerio_gi292623727	2.40E-23	>XP_002665394 PREDICTED: LReO_3-like [Danio rerio].
ConsensusfromContig7221Metazoa-Danio_rerio_gi292623803	6.50E-14	>XP_001922111 PREDICTED: RETRotransposon-like family member (retr-1)-like [Danio rerio].
ConsensusfromContig1951Metazoa-Danio_rerio_gi292624627	2.40E-57	>XP_695977 PREDICTED: LReO_3-like [Danio rerio].
ConsensusfromContig2077Metazoa-Danio_rerio_gi292626487	2.70E-20	>XP_689703 PREDICTED: reverse transcriptase/ribonuclease H/putative methyltransferase-like [Danio rerio].
ConsensusfromContig6427Metazoa-Danio_rerio_gi292627110	2.40E-12	>XP_002666541 PREDICTED: catalytic phosphatidylinositol 3-kinase delta-like [Danio rerio].
ConsensusfromContig3264Metazoa-Danio_rerio_gi292627550	3.40E-15	>XP_002666673 PREDICTED: RETRotransposon-like family member (retr-1)-like [Danio rerio].
ConsensusfromContig6668Metazoa-Danio_rerio_gi292627864	2.20E-17	>XP_002666774 PREDICTED: dynein, axonemal, heavy chain 3-like [Danio rerio].
ConsensusfromContig6943Metazoa-Danio_rerio_gi42415501	5.60E-27	>NP_963872 26S proteasome non-ATPase regulatory subunit 12 [Danio rerio].
ConsensusfromContig1946Metazoa-Danio_rerio_gi48762662	4.20E-37	>NP_956520 ribonuclease H2 subunit A [Danio rerio].
ConsensusfromContig1935Metazoa-Danio_rerio_gi68399910	5.90E-51	>XP_684355 PREDICTED: polyprotein-like [Danio rerio].
ConsensusfromContig3214Metazoa-Danio_rerio_gi68399910	1.90E-15	>XP_684355 PREDICTED: polyprotein-like [Danio rerio].
ConsensusfromContig2725Metazoa-Danio_rerio_gi71834674	1.80E-11	>NP_001025439 calcium-binding protein 2 [Danio rerio].
ConsensusfromContig4466Metazoa-Danio_rerio_gi89886293	4.80E-11	>NP_001034899 DNA polymerase delta catalytic subunit [Danio rerio].
ConsensusfromContig2557Metazoa-Daphnia_pulex_jgi187752	4.60E-12	
ConsensusfromContig2396Metazoa-Daphnia_pulex_jgi29116	2.80E-64	
ConsensusfromContig1178Metazoa-Daphnia_pulex_jgi310458	1.80E-16	
ConsensusfromContig5110Metazoa-Daphnia_pulex_jgi333049	1.10E-50	
ConsensusfromContig2030Metazoa-Daphnia_pulex_jgi40660	2.50E-37	
ConsensusfromContig1971Metazoa-Daphnia_pulex_jgi5678	4.60E-13	
ConsensusfromContig5150Metazoa-Drosophila_ananassae_gi194753720	2.80E-21	>XP_001959158 GF12744 [Drosophila ananassae].
ConsensusfromContig5614Metazoa-Drosophila_erecta_gi194879342	8.00E-11	>XP_001974221 GG21615 [Drosophila erecta].
ConsensusfromContig7238Metazoa-Drosophila_erecta_gi194879342	1.20E-11	>XP_001974221 GG21615 [Drosophila erecta].
ConsensusfromContig6513Metazoa-Drosophila_melanogaster_gi24665543	1.30E-17	>NP_730201 CG9674, isoform B [Drosophila melanogaster].
ConsensusfromContig2040Metazoa-Drosophila_mojavensis_gi195108217	2.90E-17	>XP_001998689 GI24108 [Drosophila mojavensis].
ConsensusfromContig2508Metazoa-Drosophila_mojavensis_gi195116485	4.00E-20	>XP_002002785 GI17572 [Drosophila mojavensis].
ConsensusfromContig6615Metazoa-Drosophila_sechellia_gi195355441	1.90E-17	>XP_002044200 GM22522 [Drosophila sechellia].
ConsensusfromContig6615Metazoa-Drosophila_sechellia_gi195355441	1.90E-17	>XP_002044200 GM22522 [Drosophila sechellia].
ConsensusfromContig5448Metazoa-Drosophila_sechellia_gi195357340	1.50E-25	>XP_002045008 GM24059 [Drosophila sechellia].
ConsensusfromContig5356Metazoa-Drosophila_virilis_gi195376481	7.90E-15	>XP_002047025 GJ12156 [Drosophila virilis].
ConsensusfromContig4469Metazoa-Drosophila_virilis_gi195378490	1.60E-27	>XP_002048017 GJ13737 [Drosophila virilis].
ConsensusfromContig6947Metazoa-Drosophila_willistoni_gi195437510	1.70E-97	>XP_002066683 GK24436 [Drosophila willistoni].
ConsensusfromContig2356Metazoa-Drosophila_yakuba_gi195498604	6.20E-30	>XP_002096594 GE25752 [Drosophila yakuba].
ConsensusfromContig1972Metazoa-Equus_caballus_gi149756942	3.90E-49	>XP_001488967 PREDICTED: Wolf-Hirschhorn syndrome candidate 1 [Equus caballus].
ConsensusfromContig1978Metazoa-Equus_caballus_gi194219404	2.60E-54	>XP_001915343 PREDICTED: similar to calcium channel, voltage-dependent, T type, alpha 1H subunit [Equus caballus].
ConsensusfromContig5953Metazoa-Gallus_gallus_gi118087963	2.80E-17	>XP_001234831 PREDICTED: similar to putative elicitin protein RAM6 [Gallus gallus].
ConsensusfromContig2001Metazoa-Gallus_gallus_gi118096218	0	>XP_001232348 PREDICTED: splicing factor 3b, subunit 3, 130kDa [Gallus gallus].
ConsensusfromContig2146Metazoa-Gallus_gallus_gi118098210	9.90E-11	>XP_424526 PREDICTED: hypothetical protein [Gallus gallus].
ConsensusfromContig30 Metazoa-Gallus_gallus_gi118099779	7.40E-19	>XP_425382 PREDICTED: similar to arylsulfatase G [Gallus gallus].
ConsensusfromContig6989Metazoa-Gallus_gallus_gi47604954	4.60E-12	>NP_990406 ubiquitin-60S ribosomal protein L40 [Gallus gallus].
ConsensusfromContig7048Metazoa-Gallus_gallus_gi50730955	1.10E-47	>XP_417097 PREDICTED: hypothetical protein [Gallus gallus].
ConsensusfromContig3128Metazoa-Helobdella_robusta_jgi130122	5.10E-18	
ConsensusfromContig5321Metazoa-Helobdella_robusta_jgi172904	7.70E-22	
ConsensusfromContig1947Metazoa-Helobdella_robusta_jgi188679	2.40E-13	
ConsensusfromContig4154Metazoa-Helobdella_robusta_jgi66624	3.50E-18	
ConsensusfromContig7146Metazoa-Helobdella_robusta_jgi74931	1.20E-20	
ConsensusfromContig2206Metazoa-Helobdella_robusta_jgi75686	8.10E-18	
ConsensusfromContig3122Metazoa-Helobdella_robusta_jgi82032	2.30E-33	
ConsensusfromContig7432Metazoa-Helobdella_robusta_jgi83982	3.40E-17	
ConsensusfromContig6291Metazoa-Helobdella_robusta_jgi98272	2.20E-13	
ConsensusfromContig5204Metazoa-Homo_sapiens_gi291045294	9.30E-34	>NP_001122307 trafficking protein particle complex subunit 2 isoform 2 [Homo sapiens].
ConsensusfromContig4687Metazoa-Hydra_magnipapillata_gi221091156	7.00E-14	>XP_002170041 PREDICTED: similar to Y26D4A.9, partial [Hydra magnipapillata].
ConsensusfromContig5442Metazoa-Hydra_magnipapillata_gi221102232	2.10E-122	>XP_002169170 PREDICTED: similar to predicted protein [Hydra magnipapillata].
ConsensusfromContig1324Metazoa-Hydra_magnipapillata_gi221103318	4.60E-12	>XP_002169660 PREDICTED: similar to predicted protein [Hydra magnipapillata].
ConsensusfromContig3344Metazoa-Hydra_magnipapillata_gi221103899	5.10E-24	>XP_002170695 PREDICTED: similar to predicted protein [Hydra magnipapillata].
ConsensusfromContig2497Metazoa-Hydra_magnipapillata_gi221104863	9.40E-16	>XP_002169253 PREDICTED: similar to predicted protein, partial [Hydra magnipapillata].
ConsensusfromContig2097Metazoa-Hydra_magnipapillata_gi221105278	1.10E-58	>XP_002163140 PREDICTED: similar to predicted protein [Hydra magnipapillata].

ConsensusfromContig5997Metazoa-Hydra_magnipapillata_gi221105471	1.10E-12	>XP_002168097 PREDICTED: similar to predicted protein [Hydra magnipapillata].
ConsensusfromContig1935Metazoa-Hydra_magnipapillata_gi221106115	4.70E-167	>XP_002169350 PREDICTED: similar to Y26D4A.9 [Hydra magnipapillata].
ConsensusfromContig2121Metazoa-Hydra_magnipapillata_gi221106115	6.40E-81	>XP_002169350 PREDICTED: similar to Y26D4A.9 [Hydra magnipapillata].
ConsensusfromContig2064Metazoa-Hydra_magnipapillata_gi221107582	9.10E-14	>XP_002160398 PREDICTED: similar to F59H6.5, partial [Hydra magnipapillata].
ConsensusfromContig4227Metazoa-Hydra_magnipapillata_gi221107774	2.30E-16	>XP_002167750 PREDICTED: similar to predicted protein [Hydra magnipapillata].
ConsensusfromContig3003Metazoa-Hydra_magnipapillata_gi221108705	1.10E-19	>XP_002161804 PREDICTED: similar to predicted protein [Hydra magnipapillata].
ConsensusfromContig2523Metazoa-Hydra_magnipapillata_gi221109375	1.10E-25	>XP_002169683 PREDICTED: similar to predicted protein, partial [Hydra magnipapillata].
ConsensusfromContig3126Metazoa-Hydra_magnipapillata_gi221109375	2.60E-20	>XP_002169683 PREDICTED: similar to predicted protein, partial [Hydra magnipapillata].
ConsensusfromContig3132Metazoa-Hydra_magnipapillata_gi221109375	1.30E-20	>XP_002169683 PREDICTED: similar to predicted protein, partial [Hydra magnipapillata].
ConsensusfromContig5446Metazoa-Hydra_magnipapillata_gi221109375	3.00E-43	>XP_002169683 PREDICTED: similar to predicted protein, partial [Hydra magnipapillata].
ConsensusfromContig5457Metazoa-Hydra_magnipapillata_gi221109375	7.00E-27	>XP_002169683 PREDICTED: similar to predicted protein, partial [Hydra magnipapillata].
ConsensusfromContig6553Metazoa-Hydra_magnipapillata_gi221109375	1.00E-14	>XP_002169683 PREDICTED: similar to predicted protein, partial [Hydra magnipapillata].
ConsensusfromContig7013Metazoa-Hydra_magnipapillata_gi221109375	2.60E-35	>XP_002169683 PREDICTED: similar to predicted protein, partial [Hydra magnipapillata].
ConsensusfromContig2097Metazoa-Hydra_magnipapillata_gi221110375	3.00E-56	>XP_002168688 PREDICTED: similar to C33E10.6 [Hydra magnipapillata].
ConsensusfromContig6326Metazoa-Hydra_magnipapillata_gi221112046	7.00E-20	>XP_002167680 PREDICTED: similar to predicted protein [Hydra magnipapillata].
ConsensusfromContig3267Metazoa-Hydra_magnipapillata_gi221113511	7.20E-11	>XP_002168130 PREDICTED: similar to predicted protein [Hydra magnipapillata].
ConsensusfromContig3398Metazoa-Hydra_magnipapillata_gi221113663	3.20E-24	>XP_002161586 PREDICTED: similar to predicted protein [Hydra magnipapillata].
ConsensusfromContig5173Metazoa-Hydra_magnipapillata_gi221116061	6.10E-30	>XP_002157149 PREDICTED: similar to predicted protein, partial [Hydra magnipapillata].
ConsensusfromContig4215Metazoa-Hydra_magnipapillata_gi221116289	6.60E-18	>XP_002157705 PREDICTED: similar to predicted protein, partial [Hydra magnipapillata].
ConsensusfromContig3417Metazoa-Hydra_magnipapillata_gi221118425	6.80E-15	>XP_002158142 PREDICTED: similar to Y26D4A.9 [Hydra magnipapillata].
ConsensusfromContig6080Metazoa-Hydra_magnipapillata_gi221119096	8.70E-39	>XP_002155697 PREDICTED: similar to predicted protein, partial [Hydra magnipapillata].
ConsensusfromContig2690Metazoa-Hydra_magnipapillata_gi221120612	1.10E-22	>XP_002154080 PREDICTED: similar to predicted protein [Hydra magnipapillata].
ConsensusfromContig6616Metazoa-Hydra_magnipapillata_gi221120920	5.00E-12	>XP_002161712 PREDICTED: similar to predicted protein [Hydra magnipapillata].
ConsensusfromContig3284Metazoa-Hydra_magnipapillata_gi221124930	2.80E-13	>XP_002158979 PREDICTED: similar to predicted protein [Hydra magnipapillata].
ConsensusfromContig3288Metazoa-Hydra_magnipapillata_gi221124930	3.20E-11	>XP_002158979 PREDICTED: similar to predicted protein [Hydra magnipapillata].
ConsensusfromContig6208Metazoa-Hydra_magnipapillata_gi221125257	3.10E-18	>XP_002167505 PREDICTED: similar to predicted protein [Hydra magnipapillata].
ConsensusfromContig5368Metazoa-Hydra_magnipapillata_gi221126873	3.20E-36	>XP_002159034 PREDICTED: similar to predicted protein [Hydra magnipapillata].
ConsensusfromContig2395Metazoa-Hydra_magnipapillata_gi221129179	1.90E-16	>XP_002166860 PREDICTED: similar to eukaryotic translation initiation factor 4, gamma 1, partial [Hydra magnipapillata].
ConsensusfromContig6931Metazoa-Hydra_magnipapillata_gi221131319	7.10E-13	>XP_002160828 PREDICTED: similar to Peptidyl-glycine alpha-amidating monooxygenase B [Hydra magnipapillata].
ConsensusfromContig4470Metazoa-Hydra_magnipapillata_jgiHma2201196	7.60E-17	
ConsensusfromContig3967Metazoa-Hydra_magnipapillata_jgiHma2208631	1.40E-11	
ConsensusfromContig7038Metazoa-Hydra_magnipapillata_jgiHma2221205	4.90E-29	
ConsensusfromContig5439Metazoa-Hydra_magnipapillata_jgiHma2222285	6.20E-12	
ConsensusfromContig5576Metazoa-Hydra_magnipapillata_jgiHma2225930	1.90E-19	
ConsensusfromContig6704Metazoa-Hydra_magnipapillata_jgiHma2226105	2.40E-20	
ConsensusfromContig5506Metazoa-Hydra_magnipapillata_jgiHma2227650	2.10E-14	
ConsensusfromContig3135Metazoa-Hydra_magnipapillata_jgiHma2227669	6.80E-56	
ConsensusfromContig5458Metazoa-Hydra_magnipapillata_jgiHma2227669	4.80E-30	
ConsensusfromContig7269Metazoa-Hydra_magnipapillata_jgiHma2227669	2.40E-20	
ConsensusfromContig4017Metazoa-Hydra_magnipapillata_jgiHma2227827	1.40E-12	
ConsensusfromContig4481Metazoa-Hydra_magnipapillata_jgiHma2227827	1.90E-18	
ConsensusfromContig6832Metazoa-Hydra_magnipapillata_jgiHma2227827	1.40E-12	
ConsensusfromContig2011Metazoa-Hydra_magnipapillata_jgiHma2228394	5.00E-26	
ConsensusfromContig2099Metazoa-Hydra_magnipapillata_jgiHma2228394	7.80E-16	
ConsensusfromContig5801Metazoa-Hydra_magnipapillata_jgiHma2228394	5.60E-15	
ConsensusfromContig2948Metazoa-Hydra_magnipapillata_jgiHma2230779	3.50E-22	
ConsensusfromContig3782Metazoa-Hydra_magnipapillata_jgiHma2231595	4.60E-19	
ConsensusfromContig2270Metazoa-Hydra_magnipapillata_jgiHma2234376	4.20E-13	
ConsensusfromContig5142Metazoa-Ixodes_scapularis_gi241157998	6.00E-72	>XP_002408179 conserved hypothetical protein [Ixodes scapularis].
ConsensusfromContig5163Metazoa-Ixodes_scapularis_gi241260138	4.70E-46	>XP_002404924 beta-transducin, putative [Ixodes scapularis].
ConsensusfromContig2263Metazoa-Ixodes_scapularis_gi241636951	1.20E-15	>XP_002410669 conserved hypothetical protein [Ixodes scapularis].
ConsensusfromContig2271Metazoa-Ixodes_scapularis_gi241636951	2.10E-12	>XP_002410669 conserved hypothetical protein [Ixodes scapularis].
ConsensusfromContig2016Metazoa-Ixodes_scapularis_gi241757317	2.50E-15	>XP_002401506 voltage-gated calcium channel, putative [Ixodes scapularis].
ConsensusfromContig3990Metazoa-Ixodes_scapularis_gi241830518	8.00E-32	>XP_002414810 conserved hypothetical protein [Ixodes scapularis].
ConsensusfromContig4115Metazoa-Ixodes_scapularis_gi241997716	1.30E-20	>XP_002433507 conserved hypothetical protein [Ixodes scapularis].
ConsensusfromContig2089Metazoa-Ixodes_scapularis_gi242046504	4.30E-42	>XP_002399627 protein farnesyltransferase beta subunit, putative [Ixodes scapularis].
ConsensusfromContig3083Metazoa-Lottia_gigantea_jgi115648	7.40E-22	
ConsensusfromContig6944Metazoa-Lottia_gigantea_jgi117637	1.20E-26	
ConsensusfromContig3572Metazoa-Lottia_gigantea_jgi125375	1.80E-12	
ConsensusfromContig5111Metazoa-Lottia_gigantea_jgi126614	2.80E-29	
ConsensusfromContig3093Metazoa-Lottia_gigantea_jgi131176	5.30E-15	
ConsensusfromContig2386Metazoa-Lottia_gigantea_jgi143229	4.10E-40	
ConsensusfromContig2884Metazoa-Lottia_gigantea_jgi158685	1.40E-35	
ConsensusfromContig7183Metazoa-Lottia_gigantea_jgi158797	5.60E-23	
ConsensusfromContig6942Metazoa-Lottia_gigantea_jgi159918	3.00E-30	
ConsensusfromContig7276Metazoa-Lottia_gigantea_jgi161662	3.90E-19	
ConsensusfromContig7276Metazoa-Lottia_gigantea_jgi161662	3.90E-19	
ConsensusfromContig5591Metazoa-Lottia_gigantea_jgi164605	1.30E-13	
ConsensusfromContig2207Metazoa-Lottia_gigantea_jgi174010	8.00E-15	
ConsensusfromContig5126Metazoa-Lottia_gigantea_jgi174010	1.90E-65	
ConsensusfromContig6930Metazoa-Lottia_gigantea_jgi174338	8.90E-173	
ConsensusfromContig3442Metazoa-Lottia_gigantea_jgi184255	1.70E-11	
ConsensusfromContig6561Metazoa-Lottia_gigantea_jgi188889	1.30E-11	
ConsensusfromContig5322Metazoa-Lottia_gigantea_jgi190164	4.00E-13	
ConsensusfromContig3129Metazoa-Lottia_gigantea_jgi195251	1.50E-33	
ConsensusfromContig1797Metazoa-Lottia_gigantea_jgi197664	1.70E-31	
ConsensusfromContig7401Metazoa-Lottia_gigantea_jgi208936	5.10E-13	
ConsensusfromContig2064Metazoa-Lottia_gigantea_jgi214893	2.00E-31	
ConsensusfromContig5121Metazoa-Lottia_gigantea_jgi216279	2.90E-41	
ConsensusfromContig5391Metazoa-Lottia_gigantea_jgi228577	7.60E-13	
ConsensusfromContig7061Metazoa-Lottia_gigantea_jgi228908	7.90E-26	
ConsensusfromContig5440Metazoa-Lottia_gigantea_jgi229509	5.20E-14	
ConsensusfromContig5440Metazoa-Lottia_gigantea_jgi229509	5.20E-14	
ConsensusfromContig4876Metazoa-Lottia_gigantea_jgi231605	9.50E-11	
ConsensusfromContig5445Metazoa-Lottia_gigantea_jgi232580	7.00E-21	
ConsensusfromContig6975Metazoa-Lottia_gigantea_jgi234457	7.70E-14	
ConsensusfromContig2159Metazoa-Lottia_gigantea_jgi234925	3.50E-26	
ConsensusfromContig3082Metazoa-Lottia_gigantea_jgi236362	1.10E-12	
ConsensusfromContig5102Metazoa-Lottia_gigantea_jgi70151	8.80E-13	
ConsensusfromContig3399Metazoa-Lottia_gigantea_jgi76922	1.30E-12	
ConsensusfromContig2288Metazoa-Lottia_gigantea_jgi92651	5.50E-14	
ConsensusfromContig3609Metazoa-Lottia_gigantea_jgi95501	9.10E-13	
ConsensusfromContig3969Metazoa-Lottia_gigantea_jgi95501	4.60E-26	
ConsensusfromContig2042Metazoa-Lottia_gigantea_jgi96811	4.60E-19	
ConsensusfromContig6935Metazoa-Macaca_mulatta_gi109088110	9.40E-18	>XP_001104766 PREDICTED: calmodulin-like 5 [Macaca mulatta].
ConsensusfromContig6218Metazoa-Macaca_mulatta_gi297260195	6.90E-19	>XP_001111152 PREDICTED: uncharacterized protein C20orf194-like [Macaca mulatta].
ConsensusfromContig2452Metazoa-Macaca_mulatta_gi297262255	2.80E-12	>XP_001104802 PREDICTED: ADP-ribosylation factor 3-like isoform 3 [Macaca mulatta].
ConsensusfromContig6668Metazoa-Macaca_mulatta_gi297267277	5.40E-13	>XP_002799508 PREDICTED: zinc finger protein 91-like [Macaca mulatta].
ConsensusfromContig5329Metazoa-Macaca_mulatta_gi297269899	2.70E-18	>XP_002799976 PREDICTED: hypothetical protein LOC100426959, partial [Macaca mulatta].
ConsensusfromContig7108Metazoa-Macaca_mulatta_gi297281240	4.80E-17	>XP_002808305 PREDICTED: LOW QUALITY PROTEIN: hemicentin-1-like [Macaca mulatta].

ConsensusfromContig3361Metazoa-Macaca_mulatta_gi297298311	2.30E-12	>XP_002805170 PREDICTED: putative uncharacterized protein C8orf49-like [Macaca mulatta].
ConsensusfromContig2095Metazoa-Monodelphis_domestica_gi126282424	3.00E-46	>XP_001372720 PREDICTED: similar to galactosylceramidase, [Monodelphis domestica].
ConsensusfromContig5718Metazoa-Monodelphis_domestica_gi126290345	2.50E-26	>XP_001368072 PREDICTED: similar to rabkinesin6 [Monodelphis domestica].
ConsensusfromContig5261Metazoa-Monodelphis_domestica_gi126294274	3.20E-34	>XP_001371438 PREDICTED: similar to crumbs homolog 2 (Drosophila), [Monodelphis domestica].
ConsensusfromContig1522Metazoa-Monodelphis_domestica_gi126310040	3.40E-16	>XP_001364391 PREDICTED: similar to Cullin-7 (CUL-7) [Monodelphis domestica].
ConsensusfromContig5196Metazoa-Monodelphis_domestica_gi126310054	6.70E-44	>XP_001362696 PREDICTED: similar to RNA polymerase I subunit hRPA39 [Monodelphis domestica].
ConsensusfromContig3080Metazoa-Monodelphis_domestica_gi126330778	9.50E-14	>XP_001373365 PREDICTED: similar to malignant fibrous histiocytoma amplified sequence 1 [Monodelphis domestica].
ConsensusfromContig2078Metazoa-Monodelphis_domestica_gi126335115	5.20E-44	>XP_001365236 PREDICTED: similar to asparagine-linked glycosylation 2 homolog (S. cerevisiae, alpha-1,3-mannosyltransferase) [Monodelphis domestica].
ConsensusfromContig2078Metazoa-Monodelphis_domestica_gi126335115	5.20E-44	>XP_001365236 PREDICTED: similar to asparagine-linked glycosylation 2 homolog (S. cerevisiae, alpha-1,3-mannosyltransferase) [Monodelphis domestica].
ConsensusfromContig5139Metazoa-Mus_musculus_gi125656171	1.30E-43	>NP_033842 arylsulfatase B precursor [Mus musculus].
ConsensusfromContig4095Metazoa-Mus_musculus_gi133778924	5.50E-22	>NP_038491 alpha-galactosidase A [Mus musculus].
ConsensusfromContig2147Metazoa-Mus_musculus_gi149275105	2.80E-17	>XP_001003060 PREDICTED: hypothetical protein [Mus musculus].
ConsensusfromContig9800Metazoa-Mus_musculus_gi154350232	1.90E-12	>NP_573502 crumbs homolog 1 precursor [Mus musculus].
ConsensusfromContig6930Metazoa-Mus_musculus_gi164698506	1.40E-116	>NP_033216 vacuolar protein sorting-associated protein 4B [Mus musculus].
ConsensusfromContig5164Metazoa-Mus_musculus_gi282154801	5.10E-50	>NP_064429 NFU1 iron-sulfur cluster scaffold homolog, mitochondrial isoform 2 precursor [Mus musculus].
ConsensusfromContig6968Metazoa-Mus_musculus_gi31980962	1.40E-32	>NP_062519 WW domain-containing oxidoreductase [Mus musculus].
ConsensusfromContig4377Metazoa-Mus_musculus_gi6680868	2.40E-11	>NP_031657 G1/S-specific cyclin-D1 [Mus musculus].
ConsensusfromContig1938Metazoa-Mus_musculus_gi7106425	1.50E-35	>NP_035622 serine/threonine-protein kinase 11 [Mus musculus].
ConsensusfromContig2274Metazoa-Nasonia_vitripennis_gi156539003	4.60E-19	>XP_001602819 PREDICTED: hypothetical protein, partial [Nasonia vitripennis].
ConsensusfromContig3993Metazoa-Nasonia_vitripennis_gi156539683	1.60E-15	>XP_001600228 PREDICTED: hypothetical protein, partial [Nasonia vitripennis].
ConsensusfromContig2392Metazoa-Nasonia_vitripennis_gi156539693	3.20E-32	>XP_001602154 PREDICTED: hypothetical protein [Nasonia vitripennis].
ConsensusfromContig2126Metazoa-Nasonia_vitripennis_gi156539705	1.90E-12	>XP_001602768 PREDICTED: similar to retrotransposon protein, putative, Ty3-gypsy subclass [Nasonia vitripennis].
ConsensusfromContig5154Metazoa-Nasonia_vitripennis_gi156540037	1.20E-19	>XP_001599370 PREDICTED: hypothetical protein [Nasonia vitripennis].
ConsensusfromContig3436Metazoa-Nasonia_vitripennis_gi156540207	2.70E-12	>XP_001602640 PREDICTED: hypothetical protein [Nasonia vitripennis].
ConsensusfromContig3891Metazoa-Nasonia_vitripennis_gi156540207	2.70E-12	>XP_001602640 PREDICTED: hypothetical protein [Nasonia vitripennis].
ConsensusfromContig4064Metazoa-Nasonia_vitripennis_gi156540439	3.20E-14	>XP_001601554 PREDICTED: hypothetical protein [Nasonia vitripennis].
ConsensusfromContig6920Metazoa-Nasonia_vitripennis_gi156540439	2.60E-12	>XP_001601554 PREDICTED: hypothetical protein [Nasonia vitripennis].
ConsensusfromContig2310Metazoa-Nasonia_vitripennis_gi156540764	4.40E-28	>XP_001599249 PREDICTED: hypothetical protein [Nasonia vitripennis].
ConsensusfromContig2677Metazoa-Nasonia_vitripennis_gi156540764	8.40E-33	>XP_001599249 PREDICTED: hypothetical protein [Nasonia vitripennis].
ConsensusfromContig3025Metazoa-Nasonia_vitripennis_gi156540764	5.00E-14	>XP_001599249 PREDICTED: hypothetical protein [Nasonia vitripennis].
ConsensusfromContig3487Metazoa-Nasonia_vitripennis_gi156540764	6.90E-18	>XP_001599249 PREDICTED: hypothetical protein [Nasonia vitripennis].
ConsensusfromContig4992Metazoa-Nasonia_vitripennis_gi156540764	2.20E-11	>XP_001599249 PREDICTED: hypothetical protein [Nasonia vitripennis].
ConsensusfromContig4992Metazoa-Nasonia_vitripennis_gi156540764	2.20E-11	>XP_001599249 PREDICTED: hypothetical protein [Nasonia vitripennis].
ConsensusfromContig6999Metazoa-Nasonia_vitripennis_gi156540768	6.30E-24	>XP_001599745 PREDICTED: similar to Peptidase, cysteine peptidase active site; Zinc finger, CCHC-type; Peptidase aspartic, catalytic; Polynucleotidyl transferase, Ribonuclease H fold [Nasonia vitripennis].
ConsensusfromContig5596Metazoa-Nasonia_vitripennis_gi156541164	9.90E-13	>XP_001603663 PREDICTED: hypothetical protein [Nasonia vitripennis].
ConsensusfromContig3265Metazoa-Nasonia_vitripennis_gi156541471	1.70E-11	>XP_001599618 PREDICTED: hypothetical protein [Nasonia vitripennis].
ConsensusfromContig5874Metazoa-Nasonia_vitripennis_gi156541471	1.80E-27	>XP_001599618 PREDICTED: hypothetical protein [Nasonia vitripennis].
ConsensusfromContig3563Metazoa-Nasonia_vitripennis_gi156541506	5.80E-16	>XP_001599293 PREDICTED: similar to pol polyprotein [Nasonia vitripennis].
ConsensusfromContig6352Metazoa-Nasonia_vitripennis_gi156541748	1.40E-15	>XP_001602742 PREDICTED: hypothetical protein [Nasonia vitripennis].
ConsensusfromContig1582Metazoa-Nasonia_vitripennis_gi156541819	3.80E-19	>XP_001600338 PREDICTED: similar to beta-hexosaminidase b [Nasonia vitripennis].
ConsensusfromContig5162Metazoa-Nasonia_vitripennis_gi156546928	4.20E-15	>XP_001603288 PREDICTED: similar to phosphatidylethanolamine-binding protein isoform 3 [Nasonia vitripennis].
ConsensusfromContig1147Metazoa-Nasonia_vitripennis_gi156548518	4.60E-19	>XP_001606139 PREDICTED: similar to serine/threonine-protein kinase rio1 (rio kinase 1) [Nasonia vitripennis].
ConsensusfromContig7115Metazoa-Nasonia_vitripennis_gi156552601	8.20E-14	>XP_001601671 PREDICTED: similar to CG15094-PA [Nasonia vitripennis].
ConsensusfromContig1989Metazoa-Nematostella_vectensis_gi156322155	9.60E-47	>XP_001618299 hypothetical protein NEMVEDRAFT_v1g225297 [Nematostella vectensis].
ConsensusfromContig7027Metazoa-Nematostella_vectensis_gi156331255	4.10E-12	>XP_001619177 hypothetical protein NEMVEDRAFT_v1g152156 [Nematostella vectensis].
ConsensusfromContig8906Metazoa-Nematostella_vectensis_gi156331289	7.00E-11	>XP_001619186 hypothetical protein NEMVEDRAFT_v1g224413 [Nematostella vectensis].
ConsensusfromContig4347Metazoa-Nematostella_vectensis_gi156348360	2.00E-22	>XP_001621820 hypothetical protein NEMVEDRAFT_v1g888 [Nematostella vectensis].
ConsensusfromContig1938Metazoa-Nematostella_vectensis_gi156349180	1.30E-20	>XP_001621950 hypothetical protein NEMVEDRAFT_v1g143091 [Nematostella vectensis].
ConsensusfromContig2515Metazoa-Nematostella_vectensis_gi156351201	8.90E-22	>XP_001622405 hypothetical protein NEMVEDRAFT_v1g141385 [Nematostella vectensis].
ConsensusfromContig5139Metazoa-Nematostella_vectensis_gi156352985	1.00E-75	>XP_001622861 predicted protein [Nematostella vectensis].
ConsensusfromContig4319Metazoa-Nematostella_vectensis_gi156354102	3.70E-12	>XP_001623241 predicted protein [Nematostella vectensis].
ConsensusfromContig3172Metazoa-Nematostella_vectensis_gi156356009	6.30E-37	>XP_001623724 predicted protein [Nematostella vectensis].
ConsensusfromContig3322Metazoa-Nematostella_vectensis_gi156359506	8.40E-31	>XP_001624809 predicted protein [Nematostella vectensis].
ConsensusfromContig6957Metazoa-Nematostella_vectensis_gi156359983	9.80E-15	>XP_001625042 predicted protein [Nematostella vectensis].
ConsensusfromContig7097Metazoa-Nematostella_vectensis_gi156360668	2.60E-31	>XP_001625148 predicted protein [Nematostella vectensis].
ConsensusfromContig5120Metazoa-Nematostella_vectensis_gi156363477	5.40E-27	>XP_001626070 predicted protein [Nematostella vectensis].
ConsensusfromContig5313Metazoa-Nematostella_vectensis_gi156365616	2.70E-28	>XP_001626740 predicted protein [Nematostella vectensis].
ConsensusfromContig2952Metazoa-Nematostella_vectensis_gi156365935	6.80E-12	>XP_001626897 predicted protein [Nematostella vectensis].
ConsensusfromContig1734Metazoa-Nematostella_vectensis_gi156368443	1.10E-20	>XP_001627703 predicted protein [Nematostella vectensis].
ConsensusfromContig2238Metazoa-Nematostella_vectensis_gi156371714	2.30E-50	>XP_001628907 predicted protein [Nematostella vectensis].
ConsensusfromContig6619Metazoa-Nematostella_vectensis_gi156373810	6.70E-11	>XP_001629503 predicted protein [Nematostella vectensis].
ConsensusfromContig1953Metazoa-Nematostella_vectensis_gi156376779	5.80E-74	>XP_001630536 predicted protein [Nematostella vectensis].
ConsensusfromContig6233Metazoa-Nematostella_vectensis_gi156378552	1.30E-11	>XP_001631206 predicted protein [Nematostella vectensis].
ConsensusfromContig2456Metazoa-Nematostella_vectensis_gi156379266	5.00E-13	>XP_001631379 predicted protein [Nematostella vectensis].
ConsensusfromContig3164Metazoa-Nematostella_vectensis_gi156379266	2.70E-21	>XP_001631379 predicted protein [Nematostella vectensis].
ConsensusfromContig5465Metazoa-Nematostella_vectensis_gi156379266	9.20E-14	>XP_001631379 predicted protein [Nematostella vectensis].
ConsensusfromContig7058Metazoa-Nematostella_vectensis_gi156379266	2.50E-12	>XP_001631379 predicted protein [Nematostella vectensis].
ConsensusfromContig5419Metazoa-Nematostella_vectensis_gi156379313	1.60E-20	>XP_001631402 predicted protein [Nematostella vectensis].
ConsensusfromContig6939Metazoa-Nematostella_vectensis_gi156379682	4.30E-30	>XP_001631585 predicted protein [Nematostella vectensis].
ConsensusfromContig5543Metazoa-Nematostella_vectensis_gi156380006	2.00E-11	>XP_001631746 predicted protein [Nematostella vectensis].
ConsensusfromContig5449Metazoa-Nematostella_vectensis_gi156380437	5.20E-14	>XP_001631775 predicted protein [Nematostella vectensis].
ConsensusfromContig3770Metazoa-Nematostella_vectensis_gi156380489	7.10E-14	>XP_001631801 predicted protein [Nematostella vectensis].
ConsensusfromContig3326Metazoa-Nematostella_vectensis_gi156383694	6.60E-19	>XP_001632968 predicted protein [Nematostella vectensis].
ConsensusfromContig3382Metazoa-Nematostella_vectensis_gi156383694	5.30E-17	>XP_001632968 predicted protein [Nematostella vectensis].
ConsensusfromContig1287Metazoa-Nematostella_vectensis_gi156383902	9.00E-32	>XP_001633071 predicted protein [Nematostella vectensis].
ConsensusfromContig2040Metazoa-Nematostella_vectensis_gi156383902	8.20E-23	>XP_001633071 predicted protein [Nematostella vectensis].
ConsensusfromContig6381Metazoa-Nematostella_vectensis_gi156383902	3.30E-16	>XP_001633071 predicted protein [Nematostella vectensis].
ConsensusfromContig6381Metazoa-Nematostella_vectensis_gi156383902	3.30E-16	>XP_001633071 predicted protein [Nematostella vectensis].
ConsensusfromContig7327Metazoa-Nematostella_vectensis_gi156383902	1.30E-11	>XP_001633071 predicted protein [Nematostella vectensis].
ConsensusfromContig5221Metazoa-Nematostella_vectensis_gi156384966	4.10E-34	>XP_001633403 predicted protein [Nematostella vectensis].
ConsensusfromContig2317Metazoa-Nematostella_vectensis_gi156385286	3.80E-18	>XP_001633562 predicted protein [Nematostella vectensis].
ConsensusfromContig5330Metazoa-Nematostella_vectensis_gi156385301	2.10E-79	>XP_001633569 predicted protein [Nematostella vectensis].
ConsensusfromContig3225Metazoa-Nematostella_vectensis_gi156385478	6.40E-15	>XP_001633657 predicted protein [Nematostella vectensis].
ConsensusfromContig1937Metazoa-Nematostella_vectensis_gi156385510	4.00E-151	>XP_001633673 predicted protein [Nematostella vectensis].
ConsensusfromContig5198Metazoa-Nematostella_vectensis_gi156386220	3.30E-13	>XP_001633811 predicted protein [Nematostella vectensis].
ConsensusfromContig2429Metazoa-Nematostella_vectensis_gi156387693	1.60E-37	>XP_001634337 predicted protein [Nematostella vectensis].
ConsensusfromContig5217Metazoa-Nematostella_vectensis_gi156387910	7.60E-11	>XP_001634445 predicted protein [Nematostella vectensis].
ConsensusfromContig5217Metazoa-Nematostella_vectensis_gi156387910	7.60E-11	>XP_001634445 predicted protein [Nematostella vectensis].
ConsensusfromContig5417Metazoa-Nematostella_vectensis_gi156388853	2.20E-15	>XP_001634707 predicted protein [Nematostella vectensis].
ConsensusfromContig3012Metazoa-Nematostella_vectensis_gi156389623	2.70E-13	>XP_001635090 predicted protein [Nematostella vectensis].
ConsensusfromContig2946Metazoa-Nematostella_vectensis_gi156392674	3.50E-18	>XP_001636173 predicted protein [Nematostella vectensis].
ConsensusfromContig5463Metazoa-Nematostella_vectensis_gi156392674	5.70E-41	>XP_001636173 predicted protein [Nematostella vectensis].
ConsensusfromContig7091Metazoa-Nematostella_vectensis_gi156394133	2.00E-42	>XP_001636681 predicted protein [Nematostella vectensis].
ConsensusfromContig1713Metazoa-Nematostella_vectensis_gi156395260	2.90E-41	>XP_001637029 predicted protein [Nematostella vectensis].
ConsensusfromContig2013Metazoa-Nematostella_vectensis_gi156395388	8.90E-17	>XP_001637093 predicted protein [Nematostella vectensis].
ConsensusfromContig1409Metazoa-Nematostella_vectensis_gi156398190	6.40E-20	>XP_001638072 predicted protein [Nematostella vectensis].
ConsensusfromContig3131Metazoa-Nematostella_vectensis_gi156398391	4.30E-184	>XP_001638172 predicted protein [Nematostella vectensis].
ConsensusfromContig3131Metazoa-Nematostella_vectensis_gi156398391	1.90E-157	>XP_001638172 predicted protein [Nematostella vectensis].
ConsensusfromContig3147Metazoa-Nematostella_vectensis_gi156398391	5.00E-205	>XP_001638172 predicted protein [Nematostella vectensis].
ConsensusfromContig3256Metazoa-Nematostella_vectensis_gi156398391	8.90E-115	>XP_001638172 predicted protein [Nematostella vectensis].

ConsensusfromContig4315Metazoa-Nematostella_vectensis_gi156398391	1.50E-26	>XP_001638172 predicted protein [Nematostella vectensis].
ConsensusfromContig4584Metazoa-Nematostella_vectensis_gi156398391	1.10E-14	>XP_001638172 predicted protein [Nematostella vectensis].
ConsensusfromContig5103Metazoa-Nematostella_vectensis_gi156398391	1.50E-226	>XP_001638172 predicted protein [Nematostella vectensis].
ConsensusfromContig5108Metazoa-Nematostella_vectensis_gi156398391	2.30E-220	>XP_001638172 predicted protein [Nematostella vectensis].
ConsensusfromContig5111Metazoa-Nematostella_vectensis_gi156398391	3.00E-243	>XP_001638172 predicted protein [Nematostella vectensis].
ConsensusfromContig5221Metazoa-Nematostella_vectensis_gi156398391	1.30E-241	>XP_001638172 predicted protein [Nematostella vectensis].
ConsensusfromContig5442Metazoa-Nematostella_vectensis_gi156398391	4.80E-101	>XP_001638172 predicted protein [Nematostella vectensis].
ConsensusfromContig5615Metazoa-Nematostella_vectensis_gi156398391	3.70E-22	>XP_001638172 predicted protein [Nematostella vectensis].
ConsensusfromContig5840Metazoa-Nematostella_vectensis_gi156398391	4.00E-41	>XP_001638172 predicted protein [Nematostella vectensis].
ConsensusfromContig5959Metazoa-Nematostella_vectensis_gi156398391	4.80E-14	>XP_001638172 predicted protein [Nematostella vectensis].
ConsensusfromContig6236Metazoa-Nematostella_vectensis_gi156398391	1.40E-11	>XP_001638172 predicted protein [Nematostella vectensis].
ConsensusfromContig6480Metazoa-Nematostella_vectensis_gi156398391	2.30E-11	>XP_001638172 predicted protein [Nematostella vectensis].
ConsensusfromContig6762Metazoa-Nematostella_vectensis_gi156398391	3.90E-17	>XP_001638172 predicted protein [Nematostella vectensis].
ConsensusfromContig6929Metazoa-Nematostella_vectensis_gi156398391	3.20E-158	>XP_001638172 predicted protein [Nematostella vectensis].
ConsensusfromContig2072Metazoa-Nematostella_vectensis_gi156399337	7.70E-12	>XP_001638458 predicted protein [Nematostella vectensis].
ConsensusfromContig3262Metazoa-Nematostella_vectensis_gi156399451	1.10E-11	>XP_001638515 predicted protein [Nematostella vectensis].
ConsensusfromContig3329Metazoa-Nematostella_vectensis_gi156399451	2.20E-11	>XP_001638515 predicted protein [Nematostella vectensis].
ConsensusfromContig3577Metazoa-Nematostella_vectensis_gi156399451	7.10E-13	>XP_001638515 predicted protein [Nematostella vectensis].
ConsensusfromContig3849Metazoa-Nematostella_vectensis_gi156399451	1.60E-14	>XP_001638515 predicted protein [Nematostella vectensis].
ConsensusfromContig4744Metazoa-Nematostella_vectensis_gi156399451	1.40E-14	>XP_001638515 predicted protein [Nematostella vectensis].
ConsensusfromContig5195Metazoa-Nematostella_vectensis_gi156399451	2.00E-13	>XP_001638515 predicted protein [Nematostella vectensis].
ConsensusfromContig5498Metazoa-Nematostella_vectensis_gi156399451	2.40E-20	>XP_001638515 predicted protein [Nematostella vectensis].
ConsensusfromContig5865Metazoa-Nematostella_vectensis_gi156399451	1.50E-33	>XP_001638515 predicted protein [Nematostella vectensis].
ConsensusfromContig5916Metazoa-Nematostella_vectensis_gi156399451	9.10E-16	>XP_001638515 predicted protein [Nematostella vectensis].
ConsensusfromContig2300Metazoa-Nematostella_vectensis_gi156399690	3.60E-26	>XP_001638634 predicted protein [Nematostella vectensis].
ConsensusfromContig2025Metazoa-Nematostella_vectensis_gi156399861	1.30E-74	>XP_001638719 predicted protein [Nematostella vectensis].
ConsensusfromContig3139Metazoa-Nematostella_vectensis_gi156400904	1.00E-41	>XP_001639032 predicted protein [Nematostella vectensis].
ConsensusfromContig1318Metazoa-Nematostella_vectensis_gi156402578	6.30E-19	>XP_001639667 predicted protein [Nematostella vectensis].
ConsensusfromContig5836Metazoa-Nematostella_vectensis_gi156402848	9.80E-15	>XP_001639802 predicted protein [Nematostella vectensis].
ConsensusfromContig6930Metazoa-Nematostella_vectensis_gi156403861	1.20E-21	>XP_001640126 predicted protein [Nematostella vectensis].
ConsensusfromContig3137Metazoa-Nematostella_vectensis_gi156405862	6.00E-15	>XP_001640950 predicted protein [Nematostella vectensis].
ConsensusfromContig2053Metazoa-Nematostella_vectensis_gi156406717	2.20E-22	>XP_001641191 predicted protein [Nematostella vectensis].
ConsensusfromContig3122Metazoa-Nematostella_vectensis_gi156406717	5.60E-41	>XP_001641191 predicted protein [Nematostella vectensis].
ConsensusfromContig5289Metazoa-Nematostella_vectensis_gi156406717	2.90E-12	>XP_001641191 predicted protein [Nematostella vectensis].
ConsensusfromContig2772Metazoa-Ornithorhynchus_anatinus_gi149410532	1.10E-13	>XP_001505256 PREDICTED: similar to 5, 10-methenyltetrahydrofolate synthetase [Ornithorhynchus anatinus].
ConsensusfromContig4934Metazoa-Ornithorhynchus_anatinus_gi149572340	1.10E-12	>XP_001515777 PREDICTED: similar to cytoplasmic dynein heavy chain 2, partial [Ornithorhynchus anatinus].
ConsensusfromContig2048Metazoa-Ornithorhynchus_anatinus_gi149588168	3.10E-11	>XP_001507616 PREDICTED: similar to DRAK1 [Ornithorhynchus anatinus].
ConsensusfromContig5117Metazoa-Ornithorhynchus_anatinus_gi149611552	2.70E-92	>XP_001521337 PREDICTED: similar to SMARCA4, partial [Ornithorhynchus anatinus].
ConsensusfromContig2323Metazoa-Ornithorhynchus_anatinus_gi149640752	5.80E-23	>XP_001507899 PREDICTED: hypothetical protein [Ornithorhynchus anatinus].
ConsensusfromContig6924Metazoa-Oryctolagus_cuniculus_gi291384075	1.60E-21	>XP_002708680 PREDICTED: Ester hydrolase C11orf54-like isoform 1 [Oryctolagus cuniculus].
ConsensusfromContig7090Metazoa-Oryctolagus_cuniculus_gi291389906	1.50E-25	>XP_002711457 PREDICTED: FAD-dependent oxidoreductase domain containing 2 [Oryctolagus cuniculus].
ConsensusfromContig2051Metazoa-Oryctolagus_cuniculus_gi291401149	1.20E-24	>XP_002716962 PREDICTED: transmembrane protein 184C [Oryctolagus cuniculus].
ConsensusfromContig3400Metazoa-Oryctolagus_cuniculus_gi291412335	1.20E-11	>XP_002722440 PREDICTED: protein disulfide isomerase A6 [Oryctolagus cuniculus].
ConsensusfromContig2110Metazoa-Oryctolagus_cuniculus_gi291414029	1.90E-24	>XP_002723268 PREDICTED: solute carrier family 25, member 29-like [Oryctolagus cuniculus].
ConsensusfromContig2769Metazoa-Oryzias_latipes_gi238054054	2.00E-34	>NP_001153904 cell division cycle 20 [Oryzias latipes].
ConsensusfromContig5404Metazoa-Pan_troglodytes_gi114600137	2.60E-48	>XP_517751 PREDICTED: cAMP-specific phosphodiesterase 4D isoform 9 [Pan troglodytes].
ConsensusfromContig2436Metazoa-Pan_troglodytes_gi114662366	2.20E-12	>XP_001163394 PREDICTED: ATP-binding cassette protein C12 isoform 3 [Pan troglodytes].
ConsensusfromContig2320Metazoa-Pan_troglodytes_gi114681829	1.80E-14	>XP_001137585 PREDICTED: hypothetical protein LOC735483 isoform 3 [Pan troglodytes].
ConsensusfromContig6734Metazoa-Papio_anubis_gi281183376	2.50E-14	>NP_001162315 LRRGT00196 [Papio anubis].
ConsensusfromContig5135Metazoa-Pediculus_humanus_corporis_gi242011892	4.10E-16	>XP_002426677 conserved hypothetical protein [Pediculus humanus corporis].
ConsensusfromContig1061Metazoa-Pediculus_humanus_corporis_gi242014808	1.20E-24	>XP_002428077 sodium/potassium-transporting ATPase alpha-1 chain, putative [Pediculus humanus corporis].
ConsensusfromContig3138Metazoa-Pediculus_humanus_corporis_gi242022148	3.60E-21	>XP_002431503 enzymatic polyprotein; Endonuclease; Reverse transcriptase, putative [Pediculus humanus corporis].
ConsensusfromContig5175Metazoa-Pongo_abelii_gi297668160	4.40E-17	>XP_002812323 PREDICTED: hypothetical protein LOC100455595 [Pongo abelii].
ConsensusfromContig4571Metazoa-Pongo_abelii_gi297681028	1.30E-31	>XP_002818285 PREDICTED: putative uncharacterized protein CXorf62-like [Pongo abelii].
ConsensusfromContig5893Metazoa-Pongo_abelii_gi297701890	8.50E-15	>XP_002827939 PREDICTED: hypothetical protein LOC100447275 [Pongo abelii].
ConsensusfromContig2038Metazoa-Pongo_abelii_gi297715167	3.10E-11	>XP_002833962 PREDICTED: hypothetical protein LOC100433421, partial [Pongo abelii].
ConsensusfromContig7262Metazoa-Pongo_abelii_gi297715167	1.00E-12	>XP_002833962 PREDICTED: hypothetical protein LOC100433421, partial [Pongo abelii].
ConsensusfromContig5175Metazoa-Rattus_norvegicus_gi109462094	1.70E-23	>XP_001058176 PREDICTED: OTU domain containing 7-like [Rattus norvegicus].
ConsensusfromContig2176Metazoa-Rattus_norvegicus_gi189181728	2.30E-16	>NP_001032739 nephrocystin-4 [Rattus norvegicus].
ConsensusfromContig2176Metazoa-Rattus_norvegicus_gi189181728	2.30E-16	>NP_001032739 nephrocystin-4 [Rattus norvegicus].
ConsensusfromContig6323Metazoa-Rattus_norvegicus_gi293341005	7.30E-11	>XP_002724830 PREDICTED: predicted protein-like [Rattus norvegicus].
ConsensusfromContig3246Metazoa-Rattus_norvegicus_gi293345664	5.60E-18	>XP_002742492 PREDICTED: hypothetical protein LOC100360267 [Rattus norvegicus].
ConsensusfromContig1703Metazoa-Rattus_norvegicus_gi293351131	2.70E-28	>XP_001056402 PREDICTED: cyclin-dependent kinase 11B-like [Rattus norvegicus].
ConsensusfromContig1810Metazoa-Saccoglossus_kowalevskii_gi291222171	2.40E-11	>XP_002731091 PREDICTED: hypothetical protein, partial [Saccoglossus kowalevskii].
ConsensusfromContig2026Metazoa-Saccoglossus_kowalevskii_gi291222542	2.30E-12	>XP_002731275 PREDICTED: cyclic nucleotide gated channel beta 1-like [Saccoglossus kowalevskii].
ConsensusfromContig2326Metazoa-Saccoglossus_kowalevskii_gi291222699	2.90E-11	>XP_002731355 PREDICTED: CDW92 antigen-like [Saccoglossus kowalevskii].
ConsensusfromContig2077Metazoa-Saccoglossus_kowalevskii_gi291222967	5.80E-18	>XP_002731491 PREDICTED: expressed hypothetical protein-like [Saccoglossus kowalevskii].
ConsensusfromContig2110Metazoa-Saccoglossus_kowalevskii_gi291225743	5.80E-11	>XP_002732858 PREDICTED: SPRY domain containing 3-like [Saccoglossus kowalevskii].
ConsensusfromContig1144Metazoa-Saccoglossus_kowalevskii_gi291225763	2.20E-36	>XP_002732866 PREDICTED: CG12263-like [Saccoglossus kowalevskii].
ConsensusfromContig5483Metazoa-Saccoglossus_kowalevskii_gi291226101	2.20E-15	>XP_002733037 PREDICTED: predicted protein-like [Saccoglossus kowalevskii].
ConsensusfromContig225 Metazoa-Saccoglossus_kowalevskii_gi291226248	1.20E-11	>XP_002733106 PREDICTED: vacuolar proton ATPase, putative-like, partial [Saccoglossus kowalevskii].
ConsensusfromContig2434Metazoa-Saccoglossus_kowalevskii_gi291226747	1.50E-13	>XP_002733351 PREDICTED: hypothetical protein [Saccoglossus kowalevskii].
ConsensusfromContig2022Metazoa-Saccoglossus_kowalevskii_gi291228382	2.20E-29	>XP_002734149 PREDICTED: RecQ protein-like (DNA helicase Q1-like)-like [Saccoglossus kowalevskii].
ConsensusfromContig2831Metazoa-Saccoglossus_kowalevskii_gi291229598	1.40E-11	>XP_002734760 PREDICTED: CG15270-like [Saccoglossus kowalevskii].
ConsensusfromContig2831Metazoa-Saccoglossus_kowalevskii_gi291229598	1.40E-11	>XP_002734760 PREDICTED: CG15270-like [Saccoglossus kowalevskii].
ConsensusfromContig5092Metazoa-Saccoglossus_kowalevskii_gi291229661	3.10E-12	>XP_002734791 PREDICTED: iduronate-2-sulfatase-like [Saccoglossus kowalevskii].
ConsensusfromContig5165Metazoa-Saccoglossus_kowalevskii_gi291229661	2.10E-28	>XP_002734791 PREDICTED: iduronate-2-sulfatase-like [Saccoglossus kowalevskii].
ConsensusfromContig7410Metazoa-Saccoglossus_kowalevskii_gi291229915	3.10E-14	>XP_002734916 PREDICTED: jumonji domain containing 6-like [Saccoglossus kowalevskii].
ConsensusfromContig2347Metazoa-Saccoglossus_kowalevskii_gi291229979	1.10E-25	>XP_002734950 PREDICTED: hypothetical protein [Saccoglossus kowalevskii].
ConsensusfromContig2266Metazoa-Saccoglossus_kowalevskii_gi291230109	3.20E-16	>XP_002735012 PREDICTED: CG4525-like [Saccoglossus kowalevskii].
ConsensusfromContig5120Metazoa-Saccoglossus_kowalevskii_gi291230346	3.50E-18	>XP_002735128 PREDICTED: hypothetical protein [Saccoglossus kowalevskii].
ConsensusfromContig3903Metazoa-Saccoglossus_kowalevskii_gi291231206	2.00E-17	>XP_002735556 PREDICTED: galactosamine (N-acetyl)-6-sulfate sulfatase-like [Saccoglossus kowalevskii].
ConsensusfromContig6038Metazoa-Saccoglossus_kowalevskii_gi291231206	3.00E-23	>XP_002735556 PREDICTED: galactosamine (N-acetyl)-6-sulfate sulfatase-like [Saccoglossus kowalevskii].
ConsensusfromContig2162Metazoa-Saccoglossus_kowalevskii_gi291233895	7.50E-36	>XP_002736893 PREDICTED: hypothetical protein [Saccoglossus kowalevskii].
ConsensusfromContig5104Metazoa-Saccoglossus_kowalevskii_gi291234019	6.30E-204	>XP_002736950 PREDICTED: neurogenic locus notch homolog protein 2-like [Saccoglossus kowalevskii].
ConsensusfromContig5475Metazoa-Saccoglossus_kowalevskii_gi291234021	2.10E-18	>XP_002736951 PREDICTED: neurogenic locus notch homolog protein 2-like [Saccoglossus kowalevskii].
ConsensusfromContig1985Metazoa-Saccoglossus_kowalevskii_gi291234025	8.00E-247	>XP_002736953 PREDICTED: neurogenic locus notch homolog protein 2-like [Saccoglossus kowalevskii].
ConsensusfromContig4609Metazoa-Saccoglossus_kowalevskii_gi291235937	7.00E-12	>XP_002737909 PREDICTED: thioredoxin domain containing 5-like [Saccoglossus kowalevskii].
ConsensusfromContig1996Metazoa-Saccoglossus_kowalevskii_gi291236187	9.30E-18	>XP_002738022 PREDICTED: Phospholipase B1, membrane-associated-like [Saccoglossus kowalevskii].
ConsensusfromContig1996Metazoa-Saccoglossus_kowalevskii_gi291236187	9.30E-18	>XP_002738022 PREDICTED: Phospholipase B1, membrane-associated-like [Saccoglossus kowalevskii].
ConsensusfromContig2085Metazoa-Saccoglossus_kowalevskii_gi291236560	7.80E-20	>XP_002738207 PREDICTED: hypothetical protein [Saccoglossus kowalevskii].
ConsensusfromContig5164Metazoa-Saccoglossus_kowalevskii_gi291236809	1.60E-17	>XP_002738330 PREDICTED: hCG27481-like, partial [Saccoglossus kowalevskii].
ConsensusfromContig745 Metazoa-Saccoglossus_kowalevskii_gi291237031	2.10E-11	>XP_002738447 PREDICTED: chitobiase, di-N-acetyl--like [Saccoglossus kowalevskii].
ConsensusfromContig2185Metazoa-Saccoglossus_kowalevskii_gi291237733	2.40E-28	>XP_002738787 PREDICTED: arylsulfatase G-like [Saccoglossus kowalevskii].
ConsensusfromContig5151Metazoa-Saccoglossus_kowalevskii_gi291237733	3.80E-39	>XP_002738787 PREDICTED: arylsulfatase G-like [Saccoglossus kowalevskii].
ConsensusfromContig2249Metazoa-Saccoglossus_kowalevskii_gi291238094	5.80E-16	>XP_002738966 PREDICTED: hypothetical protein [Saccoglossus kowalevskii].
ConsensusfromContig6891Metazoa-Saccoglossus_kowalevskii_gi291238094	9.80E-11	>XP_002738966 PREDICTED: hypothetical protein [Saccoglossus kowalevskii].
ConsensusfromContig7162Metazoa-Saccoglossus_kowalevskii_gi291238094	6.40E-11	>XP_002738966 PREDICTED: hypothetical protein [Saccoglossus kowalevskii].
ConsensusfromContig3130Metazoa-Saccoglossus_kowalevskii_gi291239314	2.40E-14	>XP_002739568 PREDICTED: polyprotein-like [Saccoglossus kowalevskii].
ConsensusfromContig3184Metazoa-Saccoglossus_kowalevskii_gi291239314	1.20E-11	>XP_002739568 PREDICTED: polyprotein-like [Saccoglossus kowalevskii].

ConsensusfromContig2423Metazoa-Saccoglossus_kowalevskii_gi291239510	3.30E-26	>XP_002739666 PREDICTED: fatty acid desaturase 2-like [Saccoglossus kowalevskii].
ConsensusfromContig5510Metazoa-Saccoglossus_kowalevskii_gi291239947	5.10E-19	>XP_002739884 PREDICTED: predicted protein-like, partial [Saccoglossus kowalevskii].
ConsensusfromContig2002Metazoa-Saccoglossus_kowalevskii_gi291240811	2.50E-105	>XP_002740311 PREDICTED: neurogenic locus notch homolog protein 2-like [Saccoglossus kowalevskii].
ConsensusfromContig2314Metazoa-Saccoglossus_kowalevskii_gi291242505	1.70E-18	>XP_002741147 PREDICTED: WD repeat domain 52-like [Saccoglossus kowalevskii].
ConsensusfromContig7790Metazoa-Saccoglossus_kowalevskii_gi291242676	7.70E-11	>XP_002741233 PREDICTED: regulatory associated protein of MTOR, complex 1 [Saccoglossus kowalevskii].
ConsensusfromContig2002Metazoa-Saccoglossus_kowalevskii_gi291244357	4.40E-28	>XP_002742059 PREDICTED: sperm flagellar protein 2-like [Saccoglossus kowalevskii].
ConsensusfromContig1560Metazoa-Saccoglossus_kowalevskii_gi291244373	8.20E-13	>XP_002742071 PREDICTED: neurogenic locus notch protein homolog [Saccoglossus kowalevskii].
ConsensusfromContig2061Metazoa-Salmo_salar_gi213513131	1.50E-54	>NP_001133389 NOP14 nucleolar protein homolog [Salmo salar].
ConsensusfromContig3106Metazoa-Salmo_salar_gi213515020	6.90E-13	>NP_001133830 fucose-1-phosphate guanylyltransferase [Salmo salar].
ConsensusfromContig4216Metazoa-Salmo_salar_gi213515528	4.50E-27	>NP_001133235 elongation factor 1 gamma [Salmo salar].
ConsensusfromContig6981Metazoa-Schistosoma_mansoni_gi256076783	5.50E-47	>XP_002574689 stromal antigen [Schistosoma mansoni].
ConsensusfromContig2339Metazoa-Schistosoma_mansoni_gi256080938	3.10E-20	>XP_002576732 ER lumen protein retaining receptor [Schistosoma mansoni].
ConsensusfromContig2430Metazoa-Schistosoma_mansoni_gi256083202	7.30E-12	>XP_002577838 prion interactor pint1 [Schistosoma mansoni].
ConsensusfromContig1607Metazoa-Schistosoma_mansoni_gi256087010	1.10E-16	>XP_002579673 serine/threonine protein kinase [Schistosoma mansoni].
ConsensusfromContig6557Metazoa-Schistosoma_mansoni_gi256088913	1.80E-13	>XP_002580566 hypothetical protein [Schistosoma mansoni].
ConsensusfromContig1241Metazoa-Strongylocentrotus_purpuratus_gi115611345	8.40E-14	>XP_001199441 PREDICTED: similar to WD repeat domain 52, partial [Strongylocentrotus purpuratus].
ConsensusfromContig2868Metazoa-Strongylocentrotus_purpuratus_gi115615210	4.60E-25	>XP_784839 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus].
ConsensusfromContig5215Metazoa-Strongylocentrotus_purpuratus_gi115621288	2.70E-13	>XP_001198299 PREDICTED: similar to polyprotein [Strongylocentrotus purpuratus].
ConsensusfromContig5142Metazoa-Strongylocentrotus_purpuratus_gi115629154	5.10E-18	>XP_001178621 PREDICTED: similar to Prefoldin 5 [Strongylocentrotus purpuratus].
ConsensusfromContig5917Metazoa-Strongylocentrotus_purpuratus_gi115634755	7.90E-14	>XP_798028 PREDICTED: similar to Notch homolog Scalloped wings [Strongylocentrotus purpuratus].
ConsensusfromContig2217Metazoa-Strongylocentrotus_purpuratus_gi115634757	2.90E-48	>XP_791473 PREDICTED: similar to ENSANGP00000005397 [Strongylocentrotus purpuratus].
ConsensusfromContig7303Metazoa-Strongylocentrotus_purpuratus_gi115634787	2.70E-12	>XP_786094 PREDICTED: similar to FRAP-related protein [Strongylocentrotus purpuratus].
ConsensusfromContig5042Metazoa-Strongylocentrotus_purpuratus_gi115643117	1.20E-15	>XP_001191555 PREDICTED: similar to ankyrin 2,3/unc44 [Strongylocentrotus purpuratus].
ConsensusfromContig2025Metazoa-Strongylocentrotus_purpuratus_gi115643659	4.50E-20	>XP_001198886 PREDICTED: similar to sulfatase 1 precursor, partial [Strongylocentrotus purpuratus].
ConsensusfromContig3284Metazoa-Strongylocentrotus_purpuratus_gi115644512	9.00E-11	>XP_786096 PREDICTED: similar to zinc finger protein [Strongylocentrotus purpuratus].
ConsensusfromContig4001Metazoa-Strongylocentrotus_purpuratus_gi115644512	1.80E-11	>XP_786096 PREDICTED: similar to zinc finger protein [Strongylocentrotus purpuratus].
ConsensusfromContig1956Metazoa-Strongylocentrotus_purpuratus_gi115644637	7.80E-19	>XP_001186730 PREDICTED: similar to fibropellin Ia, partial [Strongylocentrotus purpuratus].
ConsensusfromContig2018Metazoa-Strongylocentrotus_purpuratus_gi115664471	1.30E-51	>XP_001204386 PREDICTED: similar to ankyrin 2,3/unc44 [Strongylocentrotus purpuratus].
ConsensusfromContig2888Metazoa-Strongylocentrotus_purpuratus_gi115676828	2.20E-12	>XP_001181433 PREDICTED: similar to ankyrin 2,3/unc44, partial [Strongylocentrotus purpuratus].
ConsensusfromContig5822Metazoa-Strongylocentrotus_purpuratus_gi115676946	3.20E-14	>XP_001186732 PREDICTED: similar to zinc finger protein [Strongylocentrotus purpuratus].
ConsensusfromContig5822Metazoa-Strongylocentrotus_purpuratus_gi115676946	3.20E-14	>XP_001186732 PREDICTED: similar to zinc finger protein [Strongylocentrotus purpuratus].
ConsensusfromContig2219Metazoa-Strongylocentrotus_purpuratus_gi115683360	8.10E-31	>XP_001203096 PREDICTED: similar to EGF-like protein [Strongylocentrotus purpuratus].
ConsensusfromContig6967Metazoa-Strongylocentrotus_purpuratus_gi115692054	2.70E-11	>XP_001186857 PREDICTED: similar to Os11g0297800 [Strongylocentrotus purpuratus].
ConsensusfromContig5241Metazoa-Strongylocentrotus_purpuratus_gi115698606	8.40E-11	>XP_001180085 PREDICTED: similar to PDI-like protein, partial [Strongylocentrotus purpuratus].
ConsensusfromContig7280Metazoa-Strongylocentrotus_purpuratus_gi115700271	1.30E-12	>XP_788391 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus].
ConsensusfromContig3503Metazoa-Strongylocentrotus_purpuratus_gi115728557	9.20E-17	>XP_782020 PREDICTED: similar to fibropellin Ib [Strongylocentrotus purpuratus].
ConsensusfromContig1954Metazoa-Strongylocentrotus_purpuratus_gi115737728	5.00E-12	>XP_001203833 PREDICTED: similar to polyprotein [Strongylocentrotus purpuratus].
ConsensusfromContig1978Metazoa-Strongylocentrotus_purpuratus_gi115737728	7.20E-23	>XP_001203833 PREDICTED: similar to polyprotein [Strongylocentrotus purpuratus].
ConsensusfromContig3131Metazoa-Strongylocentrotus_purpuratus_gi115737728	1.20E-18	>XP_001203833 PREDICTED: similar to polyprotein [Strongylocentrotus purpuratus].
ConsensusfromContig3904Metazoa-Strongylocentrotus_purpuratus_gi115741825	1.20E-11	>XP_796347 PREDICTED: similar to arylsulfatase B [Strongylocentrotus purpuratus].
ConsensusfromContig5750Metazoa-Strongylocentrotus_purpuratus_gi115744121	5.40E-18	>XP_786592 PREDICTED: similar to PMS2 protein [Strongylocentrotus purpuratus].
ConsensusfromContig2130Metazoa-Strongylocentrotus_purpuratus_gi115744320	4.80E-23	>XP_797963 PREDICTED: similar to endonuclease-reverse transcriptase [Strongylocentrotus purpuratus].
ConsensusfromContig2386Metazoa-Strongylocentrotus_purpuratus_gi115750442	8.40E-50	>XP_001202596 PREDICTED: similar to Leucine rich repeat containing 49, partial [Strongylocentrotus purpuratus].
ConsensusfromContig2827Metazoa-Strongylocentrotus_purpuratus_gi115752629	9.80E-12	>XP_789646 PREDICTED: similar to fibropellin III [Strongylocentrotus purpuratus].
ConsensusfromContig7423Metazoa-Strongylocentrotus_purpuratus_gi115758050	1.40E-15	>XP_001198714 PREDICTED: similar to fibropellin Ib [Strongylocentrotus purpuratus].
ConsensusfromContig6782Metazoa-Strongylocentrotus_purpuratus_gi115758167	5.50E-13	>XP_785057 PREDICTED: similar to putative chloride channel, partial [Strongylocentrotus purpuratus].
ConsensusfromContig6977Metazoa-Strongylocentrotus_purpuratus_gi115761356	4.00E-29	>XP_001196672 PREDICTED: similar to fibropellin Ia, partial [Strongylocentrotus purpuratus].
ConsensusfromContig5379Metazoa-Strongylocentrotus_purpuratus_gi115762612	1.30E-20	>XP_788668 PREDICTED: similar to neurogenic locus notch (notch) [Strongylocentrotus purpuratus].
ConsensusfromContig4635Metazoa-Strongylocentrotus_purpuratus_gi115762734	3.20E-16	>XP_785296 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus].
ConsensusfromContig2021Metazoa-Strongylocentrotus_purpuratus_gi115764748	1.50E-140	>XP_797229 PREDICTED: similar to receptor protein Notch1 [Strongylocentrotus purpuratus].
ConsensusfromContig3129Metazoa-Strongylocentrotus_purpuratus_gi115764748	1.50E-72	>XP_797229 PREDICTED: similar to receptor protein Notch1 [Strongylocentrotus purpuratus].
ConsensusfromContig5114Metazoa-Strongylocentrotus_purpuratus_gi115764748	4.00E-114	>XP_797229 PREDICTED: similar to receptor protein Notch1 [Strongylocentrotus purpuratus].
ConsensusfromContig6963Metazoa-Strongylocentrotus_purpuratus_gi115768345	3.00E-70	>XP_001186266 PREDICTED: similar to argininosuccinate lyase (EC 4.3.2.1) - bullfrog, partial [Strongylocentrotus purpuratus].
ConsensusfromContig5761Metazoa-Strongylocentrotus_purpuratus_gi115774532	1.30E-12	>XP_786001 PREDICTED: similar to ankyrin 2,3/unc44 [Strongylocentrotus purpuratus].
ConsensusfromContig1955Metazoa-Strongylocentrotus_purpuratus_gi115803132	3.70E-14	>XP_001198853 PREDICTED: similar to endonuclease-reverse transcriptase [Strongylocentrotus purpuratus].
ConsensusfromContig3125Metazoa-Strongylocentrotus_purpuratus_gi115803132	2.80E-16	>XP_001198853 PREDICTED: similar to endonuclease-reverse transcriptase [Strongylocentrotus purpuratus].
ConsensusfromContig5130Metazoa-Strongylocentrotus_purpuratus_gi115803132	1.10E-12	>XP_001198853 PREDICTED: similar to endonuclease-reverse transcriptase [Strongylocentrotus purpuratus].
ConsensusfromContig5169Metazoa-Strongylocentrotus_purpuratus_gi115803132	3.80E-24	>XP_001198853 PREDICTED: similar to endonuclease-reverse transcriptase [Strongylocentrotus purpuratus].
ConsensusfromContig5232Metazoa-Strongylocentrotus_purpuratus_gi115803132	9.60E-14	>XP_001198853 PREDICTED: similar to endonuclease-reverse transcriptase [Strongylocentrotus purpuratus].
ConsensusfromContig6953Metazoa-Strongylocentrotus_purpuratus_gi115841655	2.00E-52	>XP_796968 PREDICTED: similar to chloride channel 7 [Strongylocentrotus purpuratus].
ConsensusfromContig2861Metazoa-Strongylocentrotus_purpuratus_gi115893469	4.20E-39	>XP_001199314 PREDICTED: similar to fibrosurfin [Strongylocentrotus purpuratus].
ConsensusfromContig2403Metazoa-Strongylocentrotus_purpuratus_gi115894456	9.70E-21	>XP_789829 PREDICTED: similar to LOC446948 protein [Strongylocentrotus purpuratus].
ConsensusfromContig5083Metazoa-Strongylocentrotus_purpuratus_gi115894456	2.20E-27	>XP_789829 PREDICTED: similar to LOC446948 protein [Strongylocentrotus purpuratus].
ConsensusfromContig3417Metazoa-Strongylocentrotus_purpuratus_gi115901570	7.40E-19	>XP_783551 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus].
ConsensusfromContig5252Metazoa-Strongylocentrotus_purpuratus_gi115901733	4.10E-14	>XP_796756 PREDICTED: similar to endonuclease-reverse transcriptase, partial [Strongylocentrotus purpuratus].
ConsensusfromContig5252Metazoa-Strongylocentrotus_purpuratus_gi115901733	4.10E-14	>XP_796756 PREDICTED: similar to endonuclease-reverse transcriptase, partial [Strongylocentrotus purpuratus].
ConsensusfromContig6971Metazoa-Strongylocentrotus_purpuratus_gi115903744	1.30E-19	>XP_001180711 PREDICTED: similar to endonuclease-reverse transcriptase [Strongylocentrotus purpuratus].
ConsensusfromContig1959Metazoa-Strongylocentrotus_purpuratus_gi115923432	2.70E-15	>XP_780534 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus].
ConsensusfromContig6884Metazoa-Strongylocentrotus_purpuratus_gi115926458	2.50E-12	>XP_001180763 PREDICTED: similar to ankyrin 2,3/unc44 [Strongylocentrotus purpuratus].
ConsensusfromContig6462Metazoa-Strongylocentrotus_purpuratus_gi115965015	5.10E-23	>XP_001178383 PREDICTED: similar to fibropellin Ib isoform 3 [Strongylocentrotus purpuratus].
ConsensusfromContig5219Metazoa-Strongylocentrotus_purpuratus_gi72006009	2.80E-106	>XP_801879 PREDICTED: similar to Hydroxymethylglutaryl-CoA synthase, cytoplasmic (HMG-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A synthase) isoform 4 [Strongylocentrotus purpuratus].
ConsensusfromContig5940Metazoa-Strongylocentrotus_purpuratus_gi72006830	2.20E-11	>XP_785133 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus].
ConsensusfromContig1974Metazoa-Strongylocentrotus_purpuratus_gi72070127	1.90E-12	>XP_799176 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus].
ConsensusfromContig1956Metazoa-Strongylocentrotus_purpuratus_gi72099679	1.70E-11	>XP_790269 PREDICTED: similar to Double C2, beta [Strongylocentrotus purpuratus].
ConsensusfromContig1937Metazoa-Strongylocentrotus_purpuratus_gi72108971	5.70E-24	>XP_795222 PREDICTED: hypothetical protein, partial [Strongylocentrotus purpuratus].
ConsensusfromContig60 Metazoa-Strongylocentrotus_purpuratus_gi72111462	4.20E-21	>XP_790164 PREDICTED: hypothetical protein [Strongylocentrotus purpuratus].
ConsensusfromContig5653Metazoa-Taeniopygia_guttata_gi224058363	1.30E-19	>XP_002198815 PREDICTED: dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase [Taeniopygia guttata].
ConsensusfromContig4896Metazoa-Taeniopygia_guttata_gi224061685	2.10E-19	>XP_002191458 PREDICTED: hypothetical protein [Taeniopygia guttata].
ConsensusfromContig2387Metazoa-Taeniopygia_guttata_gi224098132	3.30E-20	>XP_002198163 PREDICTED: myotubularin 1 [Taeniopygia guttata].
ConsensusfromContig5404Metazoa-Taeniopygia_guttata_gi224172195	4.00E-19	>XP_002199415 PREDICTED: protein phosphatase 1, catalytic subunit, beta isoform, partial [Taeniopygia guttata].
ConsensusfromContig7124Metazoa-Tribolium_castaneum_gi189234037	6.90E-29	>XP_001808080 PREDICTED: similar to protease, reverse transcriptase, ribonuclease H, integrase [Tribolium castaneum].
ConsensusfromContig5408Metazoa-Tribolium_castaneum_gi189236883	1.10E-15	>XP_001807231 PREDICTED: similar to orf [Tribolium castaneum].
ConsensusfromContig6137Metazoa-Tribolium_castaneum_gi189239408	1.00E-34	>XP_973885 PREDICTED: similar to AGAP003925-PA [Tribolium castaneum].
ConsensusfromContig2019Metazoa-Tribolium_castaneum_gi189241070	2.00E-17	>XP_001808548 PREDICTED: similar to AGAP007135-PA [Tribolium castaneum].
ConsensusfromContig6928Metazoa-Tribolium_castaneum_gi189241946	9.30E-32	>XP_001810658 PREDICTED: similar to Y26D4A.11 [Tribolium castaneum].
ConsensusfromContig3562Metazoa-Tribolium_castaneum_gi189242099	1.90E-14	>XP_001806948 PREDICTED: similar to predicted protein, partial [Tribolium castaneum].
ConsensusfromContig2130Metazoa-Tribolium_castaneum_gi91079142	3.70E-16	>XP_975469 PREDICTED: similar to factor inhibiting HIF-1 [Tribolium castaneum].
ConsensusfromContig2440Metazoa-Tribolium_castaneum_gi91081929	1.60E-14	>XP_966547 PREDICTED: similar to leucine zipper protein [Tribolium castaneum].
ConsensusfromContig1562Metazoa-Tribolium_castaneum_gi91088413	9.00E-16	>XP_966659 PREDICTED: similar to TATA-binding protein-associated factor 172 [Tribolium castaneum].
ConsensusfromContig5950Metazoa-Tribolium_castaneum_gi91094105	2.90E-15	>XP_967378 PREDICTED: similar to conserved hypothetical protein [Tribolium castaneum].
ConsensusfromContig2278Metazoa-Trichoplax_adhaerens_gi195998123	2.20E-31	>XP_002108930 hypothetical protein TRIADDRAFT_18642 [Trichoplax adhaerens].
ConsensusfromContig5640Metazoa-Trichoplax_adhaerens_gi195998858	5.20E-22	>XP_002109297 hypothetical protein TRIADDRAFT_21526 [Trichoplax adhaerens].
ConsensusfromContig5640Metazoa-Trichoplax_adhaerens_gi195998858	5.20E-22	>XP_002109297 hypothetical protein TRIADDRAFT_21526 [Trichoplax adhaerens].
ConsensusfromContig5640Metazoa-Trichoplax_adhaerens_gi195998858	5.20E-22	>XP_002109297 hypothetical protein TRIADDRAFT_21526 [Trichoplax adhaerens].
ConsensusfromContig7300Metazoa-Trichoplax_adhaerens_gi196001407	5.50E-20	>XP_002110571 predicted protein [Trichoplax adhaerens].
ConsensusfromContig3034Metazoa-Trichoplax_adhaerens_gi196002789	8.90E-12	>XP_002111262 hypothetical protein TRIADDRAFT_22287 [Trichoplax adhaerens].
ConsensusfromContig5622Metazoa-Trichoplax_adhaerens_gi196002833	3.10E-46	>XP_002111284 hypothetical protein TRIADDRAFT_22861 [Trichoplax adhaerens].
ConsensusfromContig2962Metazoa-Trichoplax_adhaerens_gi196003334	1.20E-42	>XP_002111534 hypothetical protein TRIADDRAFT_24000 [Trichoplax adhaerens].
ConsensusfromContig2199Metazoa-Trichoplax_adhaerens_gi196003640	1.90E-33	>XP_002111687 hypothetical protein TRIADDRAFT_55968 [Trichoplax adhaerens].
ConsensusfromContig2999Metazoa-Trichoplax_adhaerens_gi196006391	3.60E-12	>XP_002113062 hypothetical protein TRIADDRAFT_25812 [Trichoplax adhaerens].

ConsensusfromContig7418	Metazoa-Trichoplax_adhaerens_gi196006429	1.80E-14	>XP_002113081 hypothetical protein TRIADDRAFT_25138 [Trichoplax adhaerens].
ConsensusfromContig5214	Metazoa-Trichoplax_adhaerens_gi196006517	9.40E-33	>XP_002113125 hypothetical protein TRIADDRAFT_37778 [Trichoplax adhaerens].
ConsensusfromContig4078	Metazoa-Trichoplax_adhaerens_gi196006531	2.20E-11	>XP_002113132 hypothetical protein TRIADDRAFT_50347 [Trichoplax adhaerens].
ConsensusfromContig2236	Metazoa-Trichoplax_adhaerens_gi196007192	6.10E-79	>XP_002113462 hypothetical protein TRIADDRAFT_50429 [Trichoplax adhaerens].
ConsensusfromContig7439	Metazoa-Trichoplax_adhaerens_gi196007806	4.00E-40	>XP_002113769 hypothetical protein TRIADDRAFT_57533 [Trichoplax adhaerens].
ConsensusfromContig3588	Metazoa-Trichoplax_adhaerens_gi196008331	3.70E-12	>XP_002114031 hypothetical protein TRIADDRAFT_58077 [Trichoplax adhaerens].
ConsensusfromContig7115	Metazoa-Trichoplax_adhaerens_gi196009971	2.00E-20	>XP_002114850 expressed hypothetical protein [Trichoplax adhaerens].
ConsensusfromContig2207	Metazoa-Trichoplax_adhaerens_gi196010744	7.30E-50	>XP_002115236 hypothetical protein TRIADDRAFT_28979 [Trichoplax adhaerens].
ConsensusfromContig7280	Metazoa-Trichoplax_adhaerens_gi196012036	2.40E-37	>XP_002115881 hypothetical protein TRIADDRAFT_30006 [Trichoplax adhaerens].
ConsensusfromContig5118	Metazoa-Trichoplax_adhaerens_gi196013711	1.10E-68	>XP_002116716 hypothetical protein TRIADDRAFT_31346 [Trichoplax adhaerens].
ConsensusfromContig2127	Metazoa-Xenopus__Silurana__tropicalis_gi187607465	2.60E-52	>NP_001120428 WD repeat domain 63 [Xenopus (Silurana) tropicalis].
ConsensusfromContig3824	Metazoa-Xenopus__Silurana__tropicalis_gi56118404	2.20E-26	>NP_001008196 C-terminal binding protein 2 [Xenopus (Silurana) tropicalis].
ConsensusfromContig3824	Metazoa-Xenopus__Silurana__tropicalis_gi56118404	2.20E-26	>NP_001008196 C-terminal binding protein 2 [Xenopus (Silurana) tropicalis].
ConsensusfromContig2643	Metazoa-Xenopus__Silurana__tropicalis_gi58332848	3.50E-24	>NP_001011500 di-N-acetylchitobiase [Xenopus (Silurana) tropicalis].
ConsensusfromContig1958	Metazoa-Xenopus__Silurana__tropicalis_gi71896271	6.00E-45	>NP_001025550 hydrogen/potassium-exchanging ATPase 4A [Xenopus (Silurana) tropicalis].
ConsensusfromContig2012	Metazoa-Xenopus_laevis_gi147898757	8.30E-55	>NP_001085150 cell differentiation protein RCD1 homolog [Xenopus laevis].
ConsensusfromContig3174	Metazoa-Xenopus_laevis_gi147899475	8.30E-126	>NP_001085069 polyadenylate-binding protein 1-B [Xenopus laevis].
ConsensusfromContig1997	Metazoa-Xenopus_laevis_gi147901169	7.30E-26	>NP_001087187 U6 snRNA-associated Sm-like protein LSm5 [Xenopus laevis].
ConsensusfromContig6297	Metazoa-Xenopus_laevis_gi147901815	8.40E-15	>NP_001086246 erlin-2-B [Xenopus laevis].
ConsensusfromContig1982	Metazoa-Xenopus_laevis_gi147902154	5.80E-107	>NP_001080604 3-ketoacyl-CoA thiolase, peroxisomal [Xenopus laevis].
ConsensusfromContig1243	Metazoa-Xenopus_laevis_gi147903651	1.20E-11	>NP_001088991 X-epilectin [Xenopus laevis].
ConsensusfromContig2431	Metazoa-Xenopus_laevis_gi147904671	7.10E-23	>NP_001086853 fatty acid desaturase 2 [Xenopus laevis].
ConsensusfromContig2010	Metazoa-Xenopus_laevis_gi147905101	8.80E-38	>NP_001086599 DENN/MADD domain containing 2D [Xenopus laevis].
ConsensusfromContig5131	Metazoa-Xenopus_laevis_gi148223415	1.00E-49	>NP_001079220 calcium/calmodulin-dependent protein kinase IV [Xenopus laevis].
ConsensusfromContig2018	Metazoa-Xenopus_laevis_gi148225748	6.90E-27	>NP_001088845 poly (ADP-ribose) polymerase family, member 3 [Xenopus laevis].
ConsensusfromContig2003	Metazoa-Xenopus_laevis_gi148229814	5.60E-42	>NP_001086557 B9 domain-containing protein 1 [Xenopus laevis].
ConsensusfromContig6972	Metazoa-Xenopus_laevis_gi148232962	8.70E-32	>NP_001086442 helicase, lymphoid-specific [Xenopus laevis].
ConsensusfromContig2969	Metazoa-Xenopus_laevis_gi207028423	1.30E-16	>NP_001128709 anoctamin 1, calcium activated chloride channel [Xenopus laevis].
ConsensusfromContig3150	Nucleariidae-Nuclearia_simplex_str4_tbNSL00000188_2	4.50E-81	
ConsensusfromContig6768	Nucleariidae-Nuclearia_simplex_str4_tbNSL00000639_3	3.10E-12	
ConsensusfromContig2124	Opisthokonta-Capsaspora_owczarzaki_tbNUL00000647_3	8.60E-40	
ConsensusfromContig2766	Opisthokonta-Capsaspora_owczarzaki_tbNUL00000907_4	1.70E-11	
ConsensusfromContig4836	Opisthokonta-Capsaspora_owczarzaki_tbNUL00001857_3	5.50E-11	
ConsensusfromContig4836	Opisthokonta-Capsaspora_owczarzaki_tbNUL00001857_3	5.50E-11	
ConsensusfromContig5746	Opisthokonta-Sphaeroforma_arctica_tbSAL00000005_6	6.90E-12	
ConsensusfromContig3124	Opisthokonta-Sphaeroforma_arctica_tbSAL00000285_6	5.00E-11	
ConsensusfromContig5172	Opisthokonta-Sphaeroforma_arctica_tbSAL00000298_3	9.10E-73	
ConsensusfromContig2017	Opisthokonta-Sphaeroforma_arctica_tbSAL00001185_3	3.50E-17	
ConsensusfromContig2081	Opisthokonta-Sphaeroforma_arctica_tbSAL00002534_4	2.00E-14	
ConsensusfromContig1104	Planctomycetes-Blastopirellula_marina_DSM_3645_gi87306849	2.30E-23	>ZP_01088995 serine/threonine protein kinase [Blastopirellula marina DSM 3645].
ConsensusfromContig6002	Planctomycetes-Blastopirellula_marina_DSM_3645_gi87308132	1.60E-11	>ZP_01090274 Lipolytic enzyme, G-D-S-L family protein [Blastopirellula marina DSM 3645].
ConsensusfromContig7134	Planctomycetes-Blastopirellula_marina_DSM_3645_gi87309449	3.00E-11	>ZP_01091584 arylsulfatase A (precursor) [Blastopirellula marina DSM 3645].
ConsensusfromContig7018	Planctomycetes-Blastopirellula_marina_DSM_3645_gi87312143	4.00E-27	>ZP_01094248 putative membrane protein-putative a permease [Blastopirellula marina DSM 3645].
ConsensusfromContig7222	Planctomycetes-Blastopirellula_marina_DSM_3645_gi87312143	1.50E-18	>ZP_01094248 putative membrane protein-putative a permease [Blastopirellula marina DSM 3645].
ConsensusfromContig2174	Planctomycetes-Gemmata_obscuriglobus_UQM_2246_gi168699530	1.10E-13	>ZP_02731807 MlrC domain protein [Gemmata obscuriglobus UQM 2246].
ConsensusfromContig2193	Planctomycetes-Gemmata_obscuriglobus_UQM_2246_gi168699606	6.80E-24	>ZP_02731883 hypothetical protein GobsU_08794 [Gemmata obscuriglobus UQM 2246].
ConsensusfromContig7081	Planctomycetes-Gemmata_obscuriglobus_UQM_2246_gi168699862	4.40E-24	>ZP_02732139 hypothetical protein GobsU_10078 [Gemmata obscuriglobus UQM 2246].
ConsensusfromContig5107	Planctomycetes-Gemmata_obscuriglobus_UQM_2246_gi168704247	8.30E-31	>ZP_02736524 hypothetical protein GobsU_32224 [Gemmata obscuriglobus UQM 2246].
ConsensusfromContig7220	Planctomycetes-Gemmata_obscuriglobus_UQM_2246_gi168704750	1.10E-38	>ZP_02737027 peptidase S15 [Gemmata obscuriglobus UQM 2246].
ConsensusfromContig1000	Planctomycetes-Pirellula_staleyi_DSM_6068_gi283779179	7.20E-11	>YP_003369934 hypothetical protein Psta_1398 [Pirellula staleyi DSM 6068].
ConsensusfromContig7036	Planctomycetes-Pirellula_staleyi_DSM_6068_gi283779236	1.20E-13	>YP_003369991 sulfatase [Pirellula staleyi DSM 6068].
ConsensusfromContig5143	Planctomycetes-Pirellula_staleyi_DSM_6068_gi283780458	3.30E-67	>YP_003371213 Phytanoyl-CoA dioxygenase [Pirellula staleyi DSM 6068].
ConsensusfromContig1971	Planctomycetes-Pirellula_staleyi_DSM_6068_gi283782174	3.90E-19	>YP_003372929 protein of unknown function DUF303 acetylesterase putative [Pirellula staleyi DSM 6068].
ConsensusfromContig1685	Planctomycetes-Planctomyces_limnophilus_DSM_3776_gi296120941	3.30E-11	>YP_003628719 Phytanoyl-CoA dioxygenase [Planctomyces limnophilus DSM 3776].
ConsensusfromContig1934	Planctomycetes-Planctomyces_maris_DSM_8797_gi149173071	3.20E-30	>ZP_01851702 hypothetical protein PM8797T_27814 [Planctomyces maris DSM 8797].
ConsensusfromContig3135	Planctomycetes-Planctomyces_maris_DSM_8797_gi149173071	1.30E-58	>ZP_01851702 hypothetical protein PM8797T_27814 [Planctomyces maris DSM 8797].
ConsensusfromContig6062	Planctomycetes-Planctomyces_maris_DSM_8797_gi149173071	5.20E-17	>ZP_01851702 hypothetical protein PM8797T_27814 [Planctomyces maris DSM 8797].
ConsensusfromContig1180	Planctomycetes-Planctomyces_maris_DSM_8797_gi149173765	1.70E-18	>ZP_01852394 Amidohydrolase 2 [Planctomyces maris DSM 8797].
ConsensusfromContig2104	Planctomycetes-Planctomyces_maris_DSM_8797_gi149174292	8.10E-19	>ZP_01852919 YclG [Planctomyces maris DSM 8797].
ConsensusfromContig5132	Planctomycetes-Planctomyces_maris_DSM_8797_gi149174292	6.80E-32	>ZP_01852919 YclG [Planctomyces maris DSM 8797].
ConsensusfromContig5161	Planctomycetes-Planctomyces_maris_DSM_8797_gi149174292	1.90E-27	>ZP_01852919 YclG [Planctomyces maris DSM 8797].
ConsensusfromContig5132	Planctomycetes-Planctomyces_maris_DSM_8797_gi149174292	6.80E-32	>ZP_01852919 YclG [Planctomyces maris DSM 8797].
ConsensusfromContig5178	Planctomycetes-Planctomyces_maris_DSM_8797_gi149174292	1.50E-14	>ZP_01852919 YclG [Planctomyces maris DSM 8797].
ConsensusfromContig6931	Planctomycetes-Planctomyces_maris_DSM_8797_gi149174292	6.90E-35	>ZP_01852919 YclG [Planctomyces maris DSM 8797].
ConsensusfromContig7044	Planctomycetes-Planctomyces_maris_DSM_8797_gi149174292	8.20E-15	>ZP_01852919 YclG [Planctomyces maris DSM 8797].
ConsensusfromContig4415	Planctomycetes-Planctomyces_maris_DSM_8797_gi149174409	3.20E-11	>ZP_01853035 hypothetical protein PM8797T_09059 [Planctomyces maris DSM 8797].
ConsensusfromContig3157	Planctomycetes-Planctomyces_maris_DSM_8797_gi149174416	1.30E-52	>ZP_01853042 putative secreted protein [Planctomyces maris DSM 8797].
ConsensusfromContig2101	Planctomycetes-Planctomyces_maris_DSM_8797_gi149175673	1.10E-20	>ZP_01854292 hypothetical protein PM8797T_31148 [Planctomyces maris DSM 8797].
ConsensusfromContig5119	Planctomycetes-Planctomyces_maris_DSM_8797_gi149175673	2.10E-19	>ZP_01854292 hypothetical protein PM8797T_31148 [Planctomyces maris DSM 8797].
ConsensusfromContig2935	Planctomycetes-Planctomyces_maris_DSM_8797_gi149175934	3.00E-17	>ZP_01854551 hypothetical protein PM8797T_03745 [Planctomyces maris DSM 8797].
ConsensusfromContig5339	Planctomycetes-Planctomyces_maris_DSM_8797_gi149175934	3.90E-24	>ZP_01854551 hypothetical protein PM8797T_03745 [Planctomyces maris DSM 8797].
ConsensusfromContig2119	Planctomycetes-Planctomyces_maris_DSM_8797_gi149177204	1.50E-43	>ZP_01855810 hypothetical protein PM8797T_17107 [Planctomyces maris DSM 8797].
ConsensusfromContig2459	Planctomycetes-Planctomyces_maris_DSM_8797_gi149177204	6.60E-17	>ZP_01855810 hypothetical protein PM8797T_17107 [Planctomyces maris DSM 8797].
ConsensusfromContig2449	Planctomycetes-Planctomyces_maris_DSM_8797_gi149177619	1.10E-48	>ZP_01856221 hypothetical protein PM8797T_00392 [Planctomyces maris DSM 8797].
ConsensusfromContig2449	Planctomycetes-Planctomyces_maris_DSM_8797_gi149177619	1.10E-48	>ZP_01856221 hypothetical protein PM8797T_00392 [Planctomyces maris DSM 8797].
ConsensusfromContig5962	Planctomycetes-Planctomyces_maris_DSM_8797_gi149177619	1.70E-14	>ZP_01856221 hypothetical protein PM8797T_00392 [Planctomyces maris DSM 8797].
ConsensusfromContig9682	Planctomycetes-Planctomyces_maris_DSM_8797_gi149178070	2.60E-15	>ZP_01856666 hypothetical protein PM8797T_02314 [Planctomyces maris DSM 8797].
ConsensusfromContig6780	Planctomycetes-Planctomyces_maris_DSM_8797_gi149178070	2.40E-13	>ZP_01856666 hypothetical protein PM8797T_02314 [Planctomyces maris DSM 8797].
ConsensusfromContig5119	Planctomycetes-Planctomyces_maris_DSM_8797_gi149178290	1.60E-16	>ZP_01856882 hypothetical protein PM8797T_01034 [Planctomyces maris DSM 8797].
ConsensusfromContig5204	Planctomycetes-Planctomyces_maris_DSM_8797_gi149178353	1.70E-12	>ZP_01856944 hypothetical protein PM8797T_08389 [Planctomyces maris DSM 8797].
ConsensusfromContig3354	Planctomycetes-Planctomyces_maris_DSM_8797_gi149179549	3.80E-12	>ZP_01858088 hypothetical protein PM8797T_10349 [Planctomyces maris DSM 8797].
ConsensusfromContig7214	Planctomycetes-Rhodopirellula_baltica_SH_1_gi32470725	1.60E-12	>NP_863718 cysteine proteinase [Rhodopirellula baltica SH 1].
ConsensusfromContig2083	Planctomycetes-Rhodopirellula_baltica_SH_1_gi32471040	4.20E-15	>NP_864033 alfa-L-rhamnosidase [Rhodopirellula baltica SH 1].
ConsensusfromContig2040	Planctomycetes-Rhodopirellula_baltica_SH_1_gi32473109	1.30E-17	>NP_866103 hypothetical protein RB4444 [Rhodopirellula baltica SH 1].
ConsensusfromContig6700	Planctomycetes-Rhodopirellula_baltica_SH_1_gi32474093	2.70E-15	>NP_867087 hypothetical protein RB6145 [Rhodopirellula baltica SH 1].
ConsensusfromContig7235	Planctomycetes-Rhodopirellula_baltica_SH_1_gi32475430	3.20E-13	>NP_868424 uridylate kinase [Rhodopirellula baltica SH 1].
ConsensusfromContig5123	Planctomycetes-Rhodopirellula_baltica_SH_1_gi32477770	3.20E-11	>NP_870764 hypothetical protein RB12890 [Rhodopirellula baltica SH 1].
ConsensusfromContig2618	Proteobacteria-Acidovorax_avenae_subsp_avenae_ATCC_19860_gi270491821	3.70E-26	>ZP_06208884 aldo/keto reductase [Acidovorax avenae subsp. avenae ATCC 19860].
ConsensusfromContig6201	Proteobacteria-Acidovorax_avenae_subsp_avenae_ATCC_19860_gi270492445	4.00E-23	>ZP_06209506 NCS1 nucleoside transporter family [Acidovorax avenae subsp. avenae ATCC 19860].
ConsensusfromContig5243	Proteobacteria-Actinobacillus_minor_202_gi257464835	5.00E-53	>ZP_05629206 ribonucleotide-diphosphate reductase subunit alpha [Actinobacillus minor 202].
ConsensusfromContig6926	Proteobacteria-Actinobacillus_succinogenes_130Z_gi152978827	1.70E-57	>YP_001344456 gluconate 5-dehydrogenase [Actinobacillus succinogenes 130Z].
ConsensusfromContig5203	Proteobacteria-Aeromonas_hydrophila_subsp_hydrophila_ATCC_7966_gi117619339	6.90E-40	>YP_856959 sodium/proton antiporter [Aeromonas hydrophila subsp. hydrophila ATCC 7966].
ConsensusfromContig2941	Proteobacteria-Alcanivorax_borkumensis_SK2_gi110833673	2.40E-14	>YP_692532 CAIB/BAIF family protein [Alcanivorax borkumensis SK2].
ConsensusfromContig2941	Proteobacteria-Alcanivorax_borkumensis_SK2_gi110833673	2.40E-14	>YP_692532 CAIB/BAIF family protein [Alcanivorax borkumensis SK2].
ConsensusfromContig2345	Proteobacteria-alpha_proteobacterium_BAL199_gi163794749	7.90E-28	>ZP_02188719 hypothetical protein BAL199_27356 [alpha proteobacterium BAL199].
ConsensusfromContig2055	Proteobacteria-alpha_proteobacterium_BAL199_gi163795829	7.40E-28	>ZP_02189793 putative alpha-ketoglutarate-dependent taurine dioxygenase oxidoreductase protein [alpha proteobacterium BAL199].
ConsensusfromContig2447	Proteobacteria-alpha_proteobacterium_BAL199_gi163796304	3.70E-43	>ZP_02190265 Amidohydrolase [alpha proteobacterium BAL199].
ConsensusfromContig2027	Proteobacteria-alpha_proteobacterium_BAL199_gi163796515	4.40E-23	>ZP_02190474 Acyl-CoA transferase/carnitine dehydratase [alpha proteobacterium BAL199].
ConsensusfromContig5412	Proteobacteria-Alteromonadales_bacterium_TW_7_gi119468231	8.30E-24	>ZP_01611357 aconitate hydratase [Alteromonadales bacterium TW-7].
ConsensusfromContig7497	Proteobacteria-Alteromonas_macleodii_Deep_ecotype_gi196158406	8.40E-13	>YP_002127895 Type I site-specific restriction-modification system, R (restriction) subunit and related helicase [Alteromonas macleodii 'Deep ecotype'].

ConsensusfromContig6962Proteobacteria-Anaeromyxobacter_dehalogenans_2CP_1_gi220916418	1.20E-11	>YP_002491722 hypothetical protein A2cp1_1312 [Anaeromyxobacter dehalogenans 2CP-1].
ConsensusfromContig1438Proteobacteria-Anaeromyxobacter_sp_Fw109_5_gi153005739	1.50E-27	>YP_001380064 hypothetical protein Anae109_2880 [Anaeromyxobacter sp. Fw109-5].
ConsensusfromContig5165Proteobacteria-Anaeromyxobacter_sp_Fw109_5_gi153005739	1.10E-31	>YP_001380064 hypothetical protein Anae109_2880 [Anaeromyxobacter sp. Fw109-5].
ConsensusfromContig6957Proteobacteria-Anaeromyxobacter_sp_Fw109_5_gi153005739	1.20E-39	>YP_001380064 hypothetical protein Anae109_2880 [Anaeromyxobacter sp. Fw109-5].
ConsensusfromContig2042Proteobacteria-Anaeromyxobacter_sp_Fw109_5_gi153005784	2.50E-16	>YP_001380109 hypothetical protein Anae109_2925 [Anaeromyxobacter sp. Fw109-5].
ConsensusfromContig5174Proteobacteria-Anaeromyxobacter_sp_K_gi197124590	7.50E-143	>YP_002136541 hypothetical protein AnaeK_4209 [Anaeromyxobacter sp. K].
ConsensusfromContig3136Proteobacteria-Azoarcus_sp_BH72_gi119898285	7.40E-11	>YP_933498 2-dehydropantoate 2-reductase [Azoarcus sp. BH72].
ConsensusfromContig5608Proteobacteria-Azorhizobium_caulinodans_ORS_571_gi158421738	2.10E-11	>YP_001523030 NADH flavin oxidoreductase [Azorhizobium caulinodans ORS 571].
ConsensusfromContig2980Proteobacteria-Azorhizobium_caulinodans_ORS_571_gi158424298	1.30E-15	>YP_001525590 phenylhydantoinase [Azorhizobium caulinodans ORS 571].
ConsensusfromContig1994Proteobacteria-Azospirillum_sp_B510_gi288963197	3.50E-23	>YP_003453476 TPR repeat-containing protein [Azospirillum sp. B510].
ConsensusfromContig1942Proteobacteria-Bdellovibrio_bacteriovorus_HD100_gi42523439	1.60E-12	>NP_968819 putative V8-like Glu-specific endopeptidase [Bdellovibrio bacteriovorus HD100].
ConsensusfromContig2343Proteobacteria-Bdellovibrio_bacteriovorus_HD100_gi42524003	8.90E-12	>NP_969383 hypothetical protein Bd2581 [Bdellovibrio bacteriovorus HD100].
ConsensusfromContig6956Proteobacteria-Bordetella_bronchiseptica_RB50_gi33600733	3.60E-21	>NP_888293 short chain dehydrogenase [Bordetella bronchiseptica RB50].
ConsensusfromContig6936Proteobacteria-Bordetella_bronchiseptica_RB50_gi33600980	6.30E-59	>NP_888540 hypothetical protein BB1995 [Bordetella bronchiseptica RB50].
ConsensusfromContig2880Proteobacteria-Bordetella_petrii_DSM_12804_gi163855911	1.30E-12	>YP_001630209 hypothetical protein Bpet1601 [Bordetella petrii DSM 12804].
ConsensusfromContig2282Proteobacteria-Bradyrhizobium_japonicum_USDA_110_gi27380745	5.00E-15	>NP_772274 putative 3-oxoacyl-[acyl-carrier-protein] reductase [Bradyrhizobium japonicum USDA 110].
ConsensusfromContig2684Proteobacteria-Burkholderia_ambifaria_MC40_6_gi172064546	7.60E-22	>YP_001812196 hypothetical protein BamMC406_6522 [Burkholderia ambifaria MC40-6].
ConsensusfromContig2558Proteobacteria-Burkholderia_oklahomensis_EO147_gi167566383	2.00E-32	>ZP_02359299 hypothetical protein BoklE_27754 [Burkholderia oklahomensis EO147].
ConsensusfromContig6316Proteobacteria-Burkholderia_phymatum_STM815_gi186472826	2.90E-15	>YP_001860168 nitroreductase [Burkholderia phymatum STM815].
ConsensusfromContig5129Proteobacteria-Burkholderia_pseudomallei_DM98_gi167721025	2.20E-15	>ZP_02404261 type I polyketide synthase WcbR [Burkholderia pseudomallei DM98].
ConsensusfromContig6927Proteobacteria-Burkholderia_pseudomallei_K96243_gi53717750	1.30E-87	>YP_106736 putative carbon-nitrogen hydrolase [Burkholderia pseudomallei K96243].
ConsensusfromContig1391Proteobacteria-Burkholderia_sp_CCGE1001_gi282883412	4.70E-35	>ZP_06292001 protein of unknown function DUF839 [Burkholderia sp. CCGE1001].
ConsensusfromContig6621Proteobacteria-Burkholderia_sp_Ch1_1_gi296163597	4.30E-13	>ZP_06846332 RNA-directed DNA polymerase (Reverse transcriptase) [Burkholderia sp. Ch1-1].
ConsensusfromContig3357Proteobacteria-Burkholderia_sp_H160_gi209517614	6.80E-11	>ZP_03266452 LamG domain protein jellyroll fold domain protein [Burkholderia sp. H160].
ConsensusfromContig5238Proteobacteria-Burkholderia_sp_H160_gi209517651	1.90E-11	>ZP_03266489 conserved hypothetical protein [Burkholderia sp. H160].
ConsensusfromContig5930Proteobacteria-Burkholderia_ubonensis_Bu_gi167587199	6.30E-11	>ZP_02379587 high-affinity nickel-transporter [Burkholderia ubonensis Bu].
ConsensusfromContig5930Proteobacteria-Burkholderia_ubonensis_Bu_gi167587199	6.30E-11	>ZP_02379587 high-affinity nickel-transporter [Burkholderia ubonensis Bu].
ConsensusfromContig1577Proteobacteria-Burkholderia_vietnamiensis_G4_gi134291637	8.20E-31	>YP_001115406 putative transcriptional regulator [Burkholderia vietnamiensis G4].
ConsensusfromContig5459Proteobacteria-Campylobacter_upsaliensis_RM3195_gi57242195	1.70E-61	>ZP_00370134 adenine specific DNA methyltransferase (MFOKI) [Campylobacter upsaliensis RM3195].
ConsensusfromContig3021Proteobacteria-Candidatus_Accumulibacter_phosphatis_clade_IIA_str_UW_1_gi257092579	3.10E-20	>YP_003166220 acyltransferase 3 [Candidatus Accumulibacter phosphatis clade IIA str. UW-1].
ConsensusfromContig6052Proteobacteria-Candidatus_Accumulibacter_phosphatis_clade_IIA_str_UW_1_gi257093883	1.90E-21	>YP_003167524 Glutathione S-transferase domain protein [Candidatus Accumulibacter phosphatis clade IIA str. UW-1].
ConsensusfromContig2370Proteobacteria-Candidatus_Puniceispirillum_marinum_IMCC1322_gi294084336	1.60E-14	>YP_003551094 phytanoyl-CoA dioxygenase [Candidatus Puniceispirillum marinum IMCC1322].
ConsensusfromContig1359Proteobacteria-Candidatus_Puniceispirillum_marinum_IMCC1322_gi294084337	1.20E-49	>YP_003551095 diaminopropionate ammonia-lyase [Candidatus Puniceispirillum marinum IMCC1322].
ConsensusfromContig6935Proteobacteria-Caulobacter_segnis_ATCC_21756_gi295688577	1.30E-46	>YP_003592270 cobalamin synthesis protein P47K [Caulobacter segnis ATCC 21756].
ConsensusfromContig6503Proteobacteria-Cellvibrio_japonicus_Ueda107_gi192361044	1.90E-15	>YP_001981834 CAIB/BAIF family protein [Cellvibrio japonicus Ueda107].
ConsensusfromContig1944Proteobacteria-Colwellia_psychrerythraea_34H_gi71282552	2.30E-13	>YP_270567 serine protease [Colwellia psychrerythraea 34H].
ConsensusfromContig8314Proteobacteria-Comamonas_sp_CNB_1_gi190571980	2.50E-11	>YP_001967706 transposase Tn3 [Comamonas sp. CNB-1].
ConsensusfromContig922 Proteobacteria-Comamonas_sp_CNB_1_gi190571980	7.40E-24	>YP_001967706 transposase Tn3 [Comamonas sp. CNB-1].
ConsensusfromContig2362Proteobacteria-Comamonas_testosteroni_KF_1_gi221068722	1.70E-12	>ZP_03544827 Sel1 domain protein repeat-containing protein [Comamonas testosteroni KF-1].
ConsensusfromContig2362Proteobacteria-Comamonas_testosteroni_KF_1_gi221068722	1.70E-12	>ZP_03544827 Sel1 domain protein repeat-containing protein [Comamonas testosteroni KF-1].
ConsensusfromContig3267Proteobacteria-Comamonas_testosteroni_S44_gi299530332	6.70E-16	>ZP_07043757 bacteriophage protein [Comamonas testosteroni S44].
ConsensusfromContig2075Proteobacteria-Congregibacter_litoralis_KT71_gi88704759	8.00E-18	>ZP_01102472 peptidase yuxL [Congregibacter litoralis KT71].
ConsensusfromContig9894Proteobacteria-Cupriavidus_metallidurans_CH34_gi56130724	4.90E-22	>YP_145627 general secretion pathway protein [Ralstonia metallidurans CH34].
ConsensusfromContig6663Proteobacteria-Cupriavidus_metallidurans_CH34_gi56130724	5.50E-23	>YP_145627 general secretion pathway protein [Ralstonia metallidurans CH34].
ConsensusfromContig1515Proteobacteria-Cupriavidus_metallidurans_CH34_gi94313422	2.00E-19	>YP_586631 ferric siderophore receptor protein (TonB-dependent siderophore receptor) [Cupriavidus metallidurans CH34].
ConsensusfromContig6683Proteobacteria-Cupriavidus_metallidurans_CH34_gi94314012	4.80E-18	>YP_587221 N-acyl-D-amino-acid deacylase [Cupriavidus metallidurans CH34].
ConsensusfromContig2415Proteobacteria-Cupriavidus_taiwanensis_gi188591457	4.60E-25	>YP_001796056 hypothetical protein pRALTA_0165 [Cupriavidus taiwanensis].
ConsensusfromContig1624Proteobacteria-Cupriavidus_taiwanensis_gi194289609	2.10E-12	>YP_002005516 conserved hypothetical protein, ankyrin repeat domain; putative exported protein [Cupriavidus taiwanensis].
ConsensusfromContig3052Proteobacteria-Delftia_acidovorans_SPH_1_gi160895891	5.80E-35	>YP_001561473 LysR family transcriptional regulator [Delftia acidovorans SPH-1].
ConsensusfromContig5128Proteobacteria-Delftia_acidovorans_SPH_1_gi160899935	1.90E-42	>YP_001565517 aspartate racemase [Delftia acidovorans SPH-1].
ConsensusfromContig6795Proteobacteria-Delftia_acidovorans_SPH_1_gi160900929	1.30E-22	>YP_001566511 preprotein translocase subunit SecA [Delftia acidovorans SPH-1].
ConsensusfromContig4544Proteobacteria-Delftia_acidovorans_SPH_1_gi160901225	3.80E-13	>YP_001566807 hypothetical protein Daci_5794 [Delftia acidovorans SPH-1].
ConsensusfromContig2244Proteobacteria-Desulfatibacillum_alkenivorans_AK_01_gi218779512	2.00E-17	>YP_002430830 D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding [Desulfatibacillum alkenivorans AK-01].
ConsensusfromContig1959Proteobacteria-Desulfatibacillum_alkenivorans_AK_01_gi218781705	3.80E-53	>YP_002433023 3-hydroxybutyryl-CoA dehydrogenase [Desulfatibacillum alkenivorans AK-01].
ConsensusfromContig3128Proteobacteria-Desulfococcus_oleovorans_Hxd3_gi158522297	1.00E-14	>YP_001530167 YadA domain-containing protein [Desulfococcus oleovorans Hxd3].
ConsensusfromContig2567Proteobacteria-Desulfohalobium_retbaense_DSM_5692_gi258406639	4.20E-27	>YP_003199380 transcriptional regulator, XRE family [Desulfohalobium retbaense DSM 5692].
ConsensusfromContig6927Proteobacteria-Desulfotalea_psychrophila_LSv54_gi51244085	7.00E-57	>YP_063969 calcium/proton antiporter [Desulfotalea psychrophila LSv54].
ConsensusfromContig5108Proteobacteria-Desulfovibrio_desulfuricans_subsp_desulfuricans_str_ATCC_27774_gi220905497	1.40E-29	>YP_002480809 hypothetical protein Ddes_2235 [Desulfovibrio desulfuricans subsp. desulfuricans str. ATCC 27774].
ConsensusfromContig2121Proteobacteria-Desulfovibrio_sp_FW1012B_gi283852716	2.70E-11	>ZP_06369981 cyclic nucleotide-regulated small mechanosensitive ion channel [Desulfovibrio sp. FW1012B].
ConsensusfromContig2415Proteobacteria-Desulfovibrio_vulgaris_str_Hildenborough_gi46579286	1.30E-27	>YP_010094 elongation factor Ts [Desulfovibrio vulgaris str. Hildenborough].
ConsensusfromContig5380Proteobacteria-Desulfurivibrio_alkaliphilus_AHT2_gi297568852	5.00E-13	>YP_003690196 domain of unknown function DUF1745 [Desulfurivibrio alkaliphilus AHT2].
ConsensusfromContig7375Proteobacteria-Dickeya_zeae_Ech1591_gi251791300	7.00E-11	>YP_003006021 amine oxidase [Dickeya zeae Ech1591].
ConsensusfromContig1253Proteobacteria-Ehrlichia_chaffeensis_str_Sapulpa_gi68171923	5.90E-15	>ZP_00545241 Cytochrome b/b6, C-terminal [Ehrlichia chaffeensis str. Sapulpa].
ConsensusfromContig2820Proteobacteria-Ehrlichia_chaffeensis_str_Sapulpa_gi68171923	6.50E-16	>ZP_00545241 Cytochrome b/b6, C-terminal [Ehrlichia chaffeensis str. Sapulpa].
ConsensusfromContig5429Proteobacteria-Francisella_philomiragia_subsp_philomiragia_ATCC_25015_gi254876751	1.20E-16	>ZP_05249461 FAD binding family protein [Francisella philomiragia subsp. philomiragia ATCC 25015].
ConsensusfromContig2259Proteobacteria-gamma_proteobacterium_NOR51_B_gi254282757	1.50E-27	>ZP_04957725 aminomethyltransferase [gamma proteobacterium NOR51-B].
ConsensusfromContig2259Proteobacteria-gamma_proteobacterium_NOR51_B_gi254282757	1.50E-27	>ZP_04957725 aminomethyltransferase [gamma proteobacterium NOR51-B].
ConsensusfromContig1819Proteobacteria-Geobacter_lovleyi_SZ_gi189425489	1.20E-14	>YP_001952666 hypothetical protein Glov_2432 [Geobacter lovleyi SZ].
ConsensusfromContig2024Proteobacteria-Geobacter_sp_M18_gi255057344	3.40E-40	>ZP_05309520 tail sheath protein [Geobacter sp. M18].
ConsensusfromContig2862Proteobacteria-Geobacter_uraniireducens_Rf4_gi148264042	9.00E-13	>YP_001230748 Sel1 domain-containing protein [Geobacter uraniireducens Rf4].
ConsensusfromContig1997Proteobacteria-Gluconacetobacter_hansenii_ATCC_23769_gi296114143	3.90E-47	>ZP_06832798 putative cytoplasmic protein [Gluconacetobacter hansenii ATCC 23769].
ConsensusfromContig4449Proteobacteria-Haemophilus_parasuis_SH0165_gi219871495	4.60E-20	>YP_002475870 ribonucleotide-diphosphate reductase alpha subunit [Haemophilus parasuis SH0165].
ConsensusfromContig2373Proteobacteria-Haemophilus_somnus_129PT_gi113461606	3.40E-12	>YP_719675 hypothetical protein HS_1465 [Haemophilus somnus 129PT].
ConsensusfromContig5693Proteobacteria-Haliangium_ochraceum_DSM_14365_gi262194098	3.10E-24	>YP_003265307 amino acid adenylation domain protein [Haliangium ochraceum DSM 14365].
ConsensusfromContig2096Proteobacteria-Haliangium_ochraceum_DSM_14365_gi262196757	1.10E-14	>YP_003267966 Glutaryl-7-aminocephalosporanic-acid acylase [Haliangium ochraceum DSM 14365].
ConsensusfromContig2038Proteobacteria-Haliangium_ochraceum_DSM_14365_gi262197238	1.00E-14	>YP_003268447 Phytanoyl-CoA dioxygenase [Haliangium ochraceum DSM 14365].
ConsensusfromContig6376Proteobacteria-Haliangium_ochraceum_DSM_14365_gi262198178	5.60E-16	>YP_003269387 peptidase M20 [Haliangium ochraceum DSM 14365].
ConsensusfromContig7440Proteobacteria-Herbaspirillum_seropedicae_SmR1_gi300311980	3.40E-18	>YP_003776072 Fe-S protein [Herbaspirillum seropedicae SmR1].
ConsensusfromContig1029Proteobacteria-Herbaspirillum_seropedicae_SmR1_gi300312509	2.90E-18	>YP_003776601 arabinose efflux permease [Herbaspirillum seropedicae SmR1].
ConsensusfromContig6995Proteobacteria-Hirschia_baltica_ATCC_49814_gi254294104	3.30E-11	>YP_003060127 NADH-ubiquinone/plastoquinone oxidoreductase chain 3 [Hirschia baltica ATCC 49814].
ConsensusfromContig5268Proteobacteria-Hirschia_baltica_ATCC_49814_gi254294854	2.50E-13	>YP_003060877 hypothetical protein Hbal_2505 [Hirschia baltica ATCC 49814].
ConsensusfromContig5343Proteobacteria-Hoeflea_phototrophica_DFL_43_gi163757603	2.50E-23	>ZP_02164692 putative TolB-like protein [Hoeflea phototrophica DFL-43].
ConsensusfromContig5034Proteobacteria-Idiomarina_loihiensis_L2TR_gi56459240	7.00E-16	>YP_154521 hypothetical protein IL0129 [Idiomarina loihiensis L2TR].
ConsensusfromContig1310Proteobacteria-Idiomarina_loihiensis_L2TR_gi56459588	8.30E-37	>YP_154869 GTPase ObgE [Idiomarina loihiensis L2TR].
ConsensusfromContig6892Proteobacteria-Idiomarina_loihiensis_L2TR_gi56460271	4.00E-21	>YP_155552 Outer membrane protein [Idiomarina loihiensis L2TR].
ConsensusfromContig1298Proteobacteria-Idiomarina_loihiensis_L2TR_gi56460322	2.20E-37	>YP_155603 transposase Tra5 related protein [Idiomarina loihiensis L2TR].
ConsensusfromContig1325Proteobacteria-Idiomarina_loihiensis_L2TR_gi56460770	2.60E-45	>YP_156051 2OG-Fe(II) oxygenase superfamily protein [Idiomarina loihiensis L2TR].
ConsensusfromContig1098Proteobacteria-Idiomarina_loihiensis_L2TR_gi56460984	5.80E-40	>YP_156265 acyltransferase [Idiomarina loihiensis L2TR].
ConsensusfromContig4290Proteobacteria-Idiomarina_loihiensis_L2TR_gi56460991	4.30E-35	>YP_156272 DNA-directed RNA polymerase subunit alpha [Idiomarina loihiensis L2TR].
ConsensusfromContig1324Proteobacteria-Idiomarina_loihiensis_L2TR_gi56461053	1.00E-36	>YP_156334 DNA topoisomerase IV subunit A [Idiomarina loihiensis L2TR].
ConsensusfromContig1588Proteobacteria-Idiomarina_loihiensis_L2TR_gi56461093	1.20E-37	>YP_156374 NAD-dependent aldehyde dehydrogenase [Idiomarina loihiensis L2TR].
ConsensusfromContig6673Proteobacteria-Idiomarina_loihiensis_L2TR_gi56461267	1.30E-12	>YP_156548 PerM family permease [Idiomarina loihiensis L2TR].
ConsensusfromContig1214Proteobacteria-Idiomarina_loihiensis_L2TR_gi56461386	4.30E-30	>YP_156667 acetyl-CoA carboxylase biotin carboxylase subunit [Idiomarina loihiensis L2TR].
ConsensusfromContig6622Proteobacteria-Idiomarina_loihiensis_L2TR_gi56461418	3.60E-17	>YP_156699 bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein [Idiomarina loihiensis L2TR].
ConsensusfromContig6707Proteobacteria-Idiomarina_loihiensis_L2TR_gi56461436	2.80E-16	>YP_156717 Zn-dependent peptidase [Idiomarina loihiensis L2TR].
ConsensusfromContig5097Proteobacteria-Idiomarina_loihiensis_L2TR_gi56461495	1.50E-22	>YP_156776 amino acid transporter [Idiomarina loihiensis L2TR].
ConsensusfromContig3404Proteobacteria-Janthinobacterium_sp_Marseille_gi152979769	6.10E-11	>YP_001352747 mandelate racemase/muconate lactonizing enzyme family protein [Janthinobacterium sp. Marseille].
ConsensusfromContig2350Proteobacteria-Kingella_oralis_ATCC_51147_gi238022230	9.40E-12	>ZP_04602656 hypothetical protein GCWU000324_02137 [Kingella oralis ATCC 51147].
ConsensusfromContig6182Proteobacteria-Klebsiella_pneumoniae_subsp_rhinoscleromatis_ATCC_13884_gi262042515	3.50E-11	>ZP_06015673 conserved hypothetical protein [Klebsiella pneumoniae subsp. rhinoscleromatis ATCC 13884].
ConsensusfromContig4416Proteobacteria-Labrenzia_aggregata_IAM_12614_gi118590869	7.10E-18	>ZP_01548269 probable D-lactate dehydrogenase [Stappia aggregata IAM 12614].

ConsensusfromContig2550Proteobacteria-Labrenzia_aggregata_IAM_12614_gi118591994	4.40E-15	>ZP_01549388 hydroxymethylglutaryl-CoA lyase [Stappia aggregata IAM 12614].
ConsensusfromContig6954Proteobacteria-Labrenzia_alexandrii_DFL_11_gi254500804	4.30E-27	>ZP_05112955 conserved hypothetical protein [Labrenzia alexandrii DFL-11].
ConsensusfromContig6431Proteobacteria-Labrenzia_alexandrii_DFL_11_gi254500841	3.10E-12	>ZP_05112992 Glutathione S-transferase, N-terminal domain protein [Labrenzia alexandrii DFL-11].
ConsensusfromContig7018Proteobacteria-Legionella_longbeachae_NSW150_gi289166470	1.90E-18	>YP_003456608 lipopolysaccharide core biosynthesis protein [Legionella longbeachae NSW150].
ConsensusfromContig1635Proteobacteria-Leptothrix_cholodnii_SP_6_gi171057149	4.60E-30	>YP_001789498 YceI family protein [Leptothrix cholodnii SP-6].
ConsensusfromContig4985Proteobacteria-Leptothrix_cholodnii_SP_6_gi171057750	3.20E-28	>YP_001790099 oxidoreductase domain-containing protein [Leptothrix cholodnii SP-6].
ConsensusfromContig5704Proteobacteria-Magnetococcus_sp_MC_1_gi117923677	4.70E-22	>YP_864294 TPR repeat-containing protein [Magnetococcus sp. MC-1].
ConsensusfromContig7021Proteobacteria-Magnetococcus_sp_MC_1_gi117923677	9.90E-11	>YP_864294 TPR repeat-containing protein [Magnetococcus sp. MC-1].
ConsensusfromContig2070Proteobacteria-Magnetococcus_sp_MC_1_gi117924771	2.80E-13	>YP_865388 hypothetical protein Mmc1_1473 [Magnetococcus sp. MC-1].
ConsensusfromContig1078Proteobacteria-Magnetospirillum_magnetotacticum_MS_1_gi23010342	7.20E-12	>ZP_00051064 COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Magnetospirillum magnetotacticum MS-1].
ConsensusfromContig1503Proteobacteria-Magnetospirillum_magnetotacticum_MS_1_gi23010798	7.70E-11	>ZP_00051366 COG0365: Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases [Magnetospirillum magnetotacticum MS-1].
ConsensusfromContig5124Proteobacteria-Magnetospirillum_magnetotacticum_MS_1_gi23016336	1.70E-58	>ZP_00056093 COG1024: Enoyl-CoA hydratase/carnithine racemase [Magnetospirillum magnetotacticum MS-1].
ConsensusfromContig2536Proteobacteria-Magnetospirillum_magnetotacticum_MS_1_gi46202253	1.10E-14	>ZP_00208451 COG2873: O-acetylhomoserine sulfhydrylase [Magnetospirillum magnetotacticum MS-1].
ConsensusfromContig5138Proteobacteria-Mannheimia_haemolytica_PHL213_gi254362874	2.30E-13	>ZP_04978949 hypothetical bacteriophage protein [Mannheimia haemolytica PHL213].
ConsensusfromContig3122Proteobacteria-Maricaulis_maris_MCS10_gi114571321	7.10E-22	>YP_758001 outer membrane autotransporter [Maricaulis maris MCS10].
ConsensusfromContig5899Proteobacteria-marine_gamma_proteobacterium_HTCC2080_gi119503827	3.10E-18	>ZP_01625909 cobalamin synthesis protein/P47K family protein [marine gamma proteobacterium HTCC2080].
ConsensusfromContig1941Proteobacteria-marine_gamma_proteobacterium_HTCC2080_gi119504988	3.70E-39	>ZP_01627065 hypothetical protein MGP2080_05220 [marine gamma proteobacterium HTCC2080].
ConsensusfromContig5117Proteobacteria-marine_gamma_proteobacterium_HTCC2143_gi119476053	6.50E-14	>ZP_01616405 hypothetical protein GP2143_05670 [marine gamma proteobacterium HTCC2143].
ConsensusfromContig941 Proteobacteria-marine_gamma_proteobacterium_HTCC2143_gi119476878	3.20E-22	>ZP_01617159 hypothetical protein GP2143_10007 [marine gamma proteobacterium HTCC2143].
ConsensusfromContig2102Proteobacteria-marine_gamma_proteobacterium_HTCC2143_gi119476878	2.70E-14	>ZP_01617159 hypothetical protein GP2143_10007 [marine gamma proteobacterium HTCC2143].
ConsensusfromContig6164Proteobacteria-marine_gamma_proteobacterium_HTCC2143_gi119476878	1.20E-14	>ZP_01617159 hypothetical protein GP2143_10007 [marine gamma proteobacterium HTCC2143].
ConsensusfromContig6955Proteobacteria-marine_gamma_proteobacterium_HTCC2143_gi119476878	4.90E-31	>ZP_01617159 hypothetical protein GP2143_10007 [marine gamma proteobacterium HTCC2143].
ConsensusfromContig3122Proteobacteria-marine_gamma_proteobacterium_HTCC2143_gi119478730	6.60E-11	>ZP_01618588 hypothetical protein GP2143_12396 [marine gamma proteobacterium HTCC2143].
ConsensusfromContig2629Proteobacteria-marine_gamma_proteobacterium_HTCC2148_gi254480517	2.40E-11	>ZP_05093764 Bacterial Na+/H+ antiporter B superfamily protein [marine gamma proteobacterium HTCC2148].
ConsensusfromContig6929Proteobacteria-Marinobacter_aquaeolei_VT8_gi120553259	9.10E-36	>YP_957610 FAD dependent oxidoreductase [Marinobacter aquaeolei VT8].
ConsensusfromContig2366Proteobacteria-Mesorhizobium_opportunistum_WSM2075_gi260461172	2.00E-24	>ZP_05809421 short-chain dehydrogenase/reductase SDR [Mesorhizobium opportunistum WSM2075].
ConsensusfromContig6525Proteobacteria-Mesorhizobium_opportunistum_WSM2075_gi260461818	3.90E-15	>ZP_05810064 beta-lactamase [Mesorhizobium opportunistum WSM2075].
ConsensusfromContig6206Proteobacteria-Mesorhizobium_opportunistum_WSM2075_gi260462413	5.70E-16	>ZP_05810621 transcriptional regulator, MucR family [Mesorhizobium opportunistum WSM2075].
ConsensusfromContig1651Proteobacteria-Mesorhizobium_opportunistum_WSM2075_gi260462639	5.00E-17	>ZP_05810845 isochorismatase hydrolase [Mesorhizobium opportunistum WSM2075].
ConsensusfromContig1651Proteobacteria-Mesorhizobium_opportunistum_WSM2075_gi260462639	5.00E-17	>ZP_05810845 isochorismatase hydrolase [Mesorhizobium opportunistum WSM2075].
ConsensusfromContig2689Proteobacteria-Methylobacterium_extorquens_AM1_gi240137570	7.80E-40	>YP_002962041 NADH-quinone oxidoreductase chain M (NADH dehydrogenase I, chain M) [Methylobacterium extorquens AM1].
ConsensusfromContig2548Proteobacteria-Methylobacterium_radiotolerans_JCM_2831_gi170749984	1.70E-12	>YP_001756244 MerR family transcriptional regulator [Methylobacterium radiotolerans JCM 2831].
ConsensusfromContig6961Proteobacteria-Methylobacterium_radiotolerans_JCM_2831_gi170750810	1.00E-18	>YP_001757070 Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase [Methylobacterium radiotolerans JCM 2831].
ConsensusfromContig3073Proteobacteria-Methylobacterium_radiotolerans_JCM_2831_gi170751012	3.30E-12	>YP_001757272 phosphoglyceromutase [Methylobacterium radiotolerans JCM 2831].
ConsensusfromContig2097Proteobacteria-Methylobacterium_sp_4_46_gi170738805	3.70E-37	>YP_001767460 Asp/Glu/hydantoin racemase [Methylobacterium sp. 4-46].
ConsensusfromContig5114Proteobacteria-Methylobacterium_sp_4_46_gi170740907	1.50E-168	>YP_001769562 AMP-dependent synthetase and ligase [Methylobacterium sp. 4-46].
ConsensusfromContig2031Proteobacteria-Moraxella_catarrhalis_RH4_gi296112621	4.10E-59	>YP_003626559 aconitase [Moraxella catarrhalis RH4].
ConsensusfromContig1970Proteobacteria-Moritella_sp_PE36_gi149912414	3.30E-15	>ZP_01900956 hypothetical protein PE36_09853 [Moritella sp. PE36].
ConsensusfromContig2026Proteobacteria-Myxococcus_xanthus_DK_1622_gi108757284	1.10E-46	>YP_635333 putative lipoprotein [Myxococcus xanthus DK 1622].
ConsensusfromContig5488Proteobacteria-Myxococcus_xanthus_DK_1622_gi108758432	4.30E-15	>YP_633599 hypothetical protein MXAN_5456 [Myxococcus xanthus DK 1622].
ConsensusfromContig1954Proteobacteria-Myxococcus_xanthus_DK_1622_gi108758524	2.10E-23	>YP_633405 putative acetylpolyamine aminohydrolase [Myxococcus xanthus DK 1622].
ConsensusfromContig4676Proteobacteria-Myxococcus_xanthus_DK_1622_gi108761023	1.80E-16	>YP_629150 RCC1 repeat-containing protein [Myxococcus xanthus DK 1622].
ConsensusfromContig5703Proteobacteria-Myxococcus_xanthus_DK_1622_gi108762272	7.40E-19	>YP_629357 efflux ABC transporter permease/ATP-binding protein [Myxococcus xanthus DK 1622].
ConsensusfromContig5703Proteobacteria-Myxococcus_xanthus_DK_1622_gi108762272	7.40E-19	>YP_629357 efflux ABC transporter permease/ATP-binding protein [Myxococcus xanthus DK 1622].
ConsensusfromContig5125Proteobacteria-Neisseria_lactamica_ATCC_23970_gi269214533	5.10E-19	>ZP_05986767 endoribonuclease L-PSP family protein [Neisseria lactamica ATCC 23970].
ConsensusfromContig7295Proteobacteria-Neisseria_subflava_NJ9703_gi261381445	2.20E-13	>ZP_05986018 retrovirus-related Pol polyprotein LINE-1 [Neisseria subflava NJ9703].
ConsensusfromContig3976Proteobacteria-Neptuniibacter_caesariensis_gi89092652	1.10E-17	>ZP_01165605 positive regulator of gcv operon [Oceanospirillum sp. MED92].
ConsensusfromContig2430Proteobacteria-Nitrococcus_mobilis_Nb_231_gi88811099	2.10E-30	>ZP_01126355 hypothetical protein NB231_09863 [Nitrococcus mobilis Nb-231].
ConsensusfromContig2192Proteobacteria-Nitrococcus_mobilis_Nb_231_gi88813583	4.30E-28	>ZP_01128815 hypothetical protein NB231_13636 [Nitrococcus mobilis Nb-231].
ConsensusfromContig2877Proteobacteria-Nitrococcus_mobilis_Nb_231_gi88813583	2.70E-27	>ZP_01128815 hypothetical protein NB231_13636 [Nitrococcus mobilis Nb-231].
ConsensusfromContig7310Proteobacteria-Nitrosococcus_halophilus_Nc4_gi292493473	1.60E-17	>YP_003528912 Ferroxidase [Nitrosococcus halophilus Nc4].
ConsensusfromContig2813Proteobacteria-Nitrosococcus_watsoni_C_113_gi300112987	5.00E-11	>YP_003759562 S-isoprenylcysteine methyltransferase-like protein [Nitrosococcus watsoni C-113].
ConsensusfromContig2506Proteobacteria-Nitrosomonas_eutropha_C91_gi114330585	6.70E-12	>YP_746807 50S ribosomal protein L5 [Nitrosomonas eutropha C91].
ConsensusfromContig3445Proteobacteria-Oceanicaulis_alexandrii_HTCC2633_gi83860017	3.30E-13	>ZP_00953537 short chain dehydrogenase [Oceanicaulis alexandrii HTCC2633].
ConsensusfromContig1946Proteobacteria-Oceanicola_granulosus_HTCC2516_gi89067639	4.70E-12	>ZP_01155093 hypothetical protein OG2516_00519 [Oceanicola granulosus HTCC2516].
ConsensusfromContig1848Proteobacteria-Ochrobactrum_anthropi_ATCC_49188_gi153010011	1.60E-16	>YP_001371226 Fe-S metabolism associated SufE [Ochrobactrum anthropi ATCC 49188].
ConsensusfromContig5398Proteobacteria-Octadecabacter_antarcticus_238_gi254453303	2.10E-25	>ZP_05066740 ATP-dependent protease La [Octadecabacter antarcticus 238].
ConsensusfromContig5207Proteobacteria-Oxalobacter_formigenes_OXCC13_gi237748373	1.10E-51	>ZP_04578853 glycosyltransferase tibC [Oxalobacter formigenes OXCC13].
ConsensusfromContig7389Proteobacteria-Oxalobacter_formigenes_OXCC13_gi237748501	1.20E-30	>ZP_04578981 DNA polymerase III subunit epsilon [Oxalobacter formigenes OXCC13].
ConsensusfromContig7318Proteobacteria-Parvibaculum_lavamentivorans_DS_1_gi154251187	7.10E-27	>YP_001412011 short chain dehydrogenase [Parvibaculum lavamentivorans DS-1].
ConsensusfromContig7318Proteobacteria-Parvibaculum_lavamentivorans_DS_1_gi154251187	7.10E-27	>YP_001412011 short chain dehydrogenase [Parvibaculum lavamentivorans DS-1].
ConsensusfromContig2085Proteobacteria-Parvibaculum_lavamentivorans_DS_1_gi154251294	1.30E-34	>YP_001412118 taurine dioxygenase [Parvibaculum lavamentivorans DS-1].
ConsensusfromContig3133Proteobacteria-Parvularcula_bermudensis_HTCC2503_gi84703794	9.90E-19	>ZP_01017622 ribonuclease D [Parvularcula bermudensis HTCC2503].
ConsensusfromContig3819Proteobacteria-Photorhabdus_luminescens_subsp_laumondii_TTO1_gi37526683	2.80E-11	>NP_930027 hypothetical protein plu2793 [Photorhabdus luminescens subsp. laumondii TTO1].
ConsensusfromContig6874Proteobacteria-Photorhabdus_luminescens_subsp_laumondii_TTO1_gi37526683	5.70E-18	>NP_930027 hypothetical protein plu2793 [Photorhabdus luminescens subsp. laumondii TTO1].
ConsensusfromContig2342Proteobacteria-Plesiocystis_pacifica_SIR_1_gi149919684	1.30E-14	>ZP_01908162 major facilitator family transporter [Plesiocystis pacifica SIR-1].
ConsensusfromContig1181Proteobacteria-Plesiocystis_pacifica_SIR_1_gi149921341	1.50E-15	>ZP_01909795 hypothetical protein PPSIR1_17300 [Plesiocystis pacifica SIR-1].
ConsensusfromContig2098Proteobacteria-Plesiocystis_pacifica_SIR_1_gi149921401	2.90E-21	>ZP_01909854 K+ transporter, Kef-type [Plesiocystis pacifica SIR-1].
ConsensusfromContig5149Proteobacteria-Plesiocystis_pacifica_SIR_1_gi149922903	1.20E-23	>ZP_01911324 Periplasmic protein TonB links inner and outer membranes-like protein [Plesiocystis pacifica SIR-1].
ConsensusfromContig3052Proteobacteria-Pseudoalteromonas_atlantica_T6c_gi109899091	1.10E-11	>YP_662346 glucose-methanol-choline oxidoreductase [Pseudoalteromonas atlantica T6c].
ConsensusfromContig6851Proteobacteria-Pseudoalteromonas_atlantica_T6c_gi109900292	1.90E-15	>YP_663547 glutaryl-CoA dehydrogenase [Pseudoalteromonas atlantica T6c].
ConsensusfromContig6963Proteobacteria-Pseudomonas_fluorescens_Pf_5_gi70729138	9.20E-45	>YP_258874 glutathione S-transferase [Pseudomonas fluorescens Pf-5].
ConsensusfromContig2022Proteobacteria-Pseudomonas_fluorescens_Pf0_1_gi77456388	2.20E-29	>YP_345893 BNR repeat-containing glycosyl hydrolase [Pseudomonas fluorescens Pf0-1].
ConsensusfromContig2420Proteobacteria-Pseudomonas_mendocina_ymp_gi146306566	4.60E-35	>YP_001187031 monooxygenase, FAD-binding [Pseudomonas mendocina ymp].
ConsensusfromContig2361Proteobacteria-Pseudovibrio_sp_JE062_gi254471506	3.40E-33	>ZP_05084908 FAD dependent oxidoreductase, putative [Pseudovibrio sp. JE062].
ConsensusfromContig6783Proteobacteria-Psychromonas_ingrahamii_37_gi119947061	1.20E-11	>YP_944741 methyltransferase type 11 [Psychromonas ingrahamii 37].
ConsensusfromContig1736Proteobacteria-Ralstonia_eutropha_H16_gi113868817	6.30E-26	>YP_727306 glutathione S-transferase [Ralstonia eutropha H16].
ConsensusfromContig1736Proteobacteria-Ralstonia_eutropha_H16_gi113868817	6.30E-26	>YP_727306 glutathione S-transferase [Ralstonia eutropha H16].
ConsensusfromContig1600Proteobacteria-Ralstonia_eutropha_H16_gi116695274	9.50E-30	>YP_840850 hypothetical protein H16_B1330 [Ralstonia eutropha H16].
ConsensusfromContig7113Proteobacteria-Ralstonia_eutropha_JMP134_gi72383794	2.60E-20	>YP_293148 L-carnitine dehydratase/bile acid-inducible protein F [Ralstonia eutropha JMP134].
ConsensusfromContig1126Proteobacteria-Ralstonia_eutropha_JMP134_gi73538475	8.30E-11	>YP_298842 Beta-lactamase [Ralstonia eutropha JMP134].
ConsensusfromContig7424Proteobacteria-Ralstonia_pickettii_12D_gi241589596	6.60E-28	>YP_002979621 Ribonucleotide reductase alpha subunit-like protein [Ralstonia pickettii 12D].
ConsensusfromContig1735Proteobacteria-Ralstonia_pickettii_12D_gi241589600	7.70E-35	>YP_002979625 hypothetical protein Rpic12D_4735 [Ralstonia pickettii 12D].
ConsensusfromContig2751Proteobacteria-Ralstonia_pickettii_12D_gi241589606	1.10E-41	>YP_002979631 hypothetical protein Rpic12D_4742 [Ralstonia pickettii 12D].
ConsensusfromContig1707Proteobacteria-Ralstonia_pickettii_12D_gi241589617	6.00E-33	>YP_002979642 AAA ATPase central domain protein [Ralstonia pickettii 12D].
ConsensusfromContig1239Proteobacteria-Ralstonia_pickettii_12D_gi241589621	3.00E-16	>YP_002979646 hypothetical protein Rpic12D_4757 [Ralstonia pickettii 12D].
ConsensusfromContig2526Proteobacteria-Ralstonia_pickettii_12D_gi241589736	7.10E-16	>YP_002979761 hypothetical protein Rpic12D_4873 [Ralstonia pickettii 12D].
ConsensusfromContig1832Proteobacteria-Ralstonia_pickettii_12J_gi187926948	4.80E-26	>YP_001893293 flagellar hook-associated protein FlgK [Ralstonia pickettii 12J].
ConsensusfromContig4352Proteobacteria-Ralstonia_pickettii_12J_gi187928252	5.80E-18	>YP_001898739 glycosyl transferase group 1 [Ralstonia pickettii 12J].
ConsensusfromContig3001Proteobacteria-Ralstonia_pickettii_12J_gi187928594	3.80E-35	>YP_001899081 conserved hypothetical protein [Ralstonia pickettii 12J].
ConsensusfromContig1765Proteobacteria-Ralstonia_pickettii_12J_gi187928653	7.40E-24	>YP_001899140 putative DNA helicase [Ralstonia pickettii 12J].
ConsensusfromContig2835Proteobacteria-Ralstonia_pickettii_12J_gi187928655	1.50E-18	>YP_001899142 conserved hypothetical protein [Ralstonia pickettii 12J].
ConsensusfromContig6875Proteobacteria-Ralstonia_pickettii_12J_gi187928693	1.10E-25	>YP_001899180 hypothetical protein Rpic_1610 [Ralstonia pickettii 12J].
ConsensusfromContig1400Proteobacteria-Ralstonia_pickettii_12J_gi187929276	1.60E-42	>YP_001899763 acyl-CoA dehydrogenase domain protein [Ralstonia pickettii 12J].
ConsensusfromContig5050Proteobacteria-Ralstonia_pickettii_12J_gi187930181	2.30E-44	>YP_001900668 amidohydrolase [Ralstonia pickettii 12J].
ConsensusfromContig1251Proteobacteria-Ralstonia_solanacearum_GMI1000_gi17546576	7.70E-18	>NP_519978 putative transcription regulator protein [Ralstonia solanacearum GMI1000].
ConsensusfromContig2024Proteobacteria-Ralstonia_solanacearum_GMI1000_gi17549705	5.50E-142	>NP_523045 hypothetical protein RS03057 [Ralstonia solanacearum GMI1000].
ConsensusfromContig6629Proteobacteria-Ralstonia_solanacearum_MolK2_gi207724489	8.60E-15	>YP_002254886 hypothetical protein RSMK02773 [Ralstonia solanacearum MolK2].
ConsensusfromContig5141Proteobacteria-Rhizobium_etli_Brasil_5_gi218507754	2.90E-21	>ZP_03505632 probable cobalamin biosynthesis protein [Rhizobium etli Brasil 5].
ConsensusfromContig2196Proteobacteria-Rhodobacter_capsulatus_SB_1003_gi294676516	5.80E-20	>YP_003577131 hypothetical protein RCAP_rcc00961 [Rhodobacter capsulatus SB 1003].

ConsensusfromContig6924Proteobacteria-Rhodobacteraceae_bacterium_KLH11_gi254513300	1.20E-24	>ZP_05125365 MlrC domain protein [Rhodobacteraceae bacterium KLH11].
ConsensusfromContig1541Proteobacteria-Rhodobacterales_bacterium_HTCC2150_gi126727058	6.20E-24	>ZP_01742896 hypothetical protein RB2150_18262 [Rhodobacterales bacterium HTCC2150].
ConsensusfromContig3140Proteobacteria-Rhodobacterales_bacterium_HTCC2654_gi84684134	6.00E-23	>ZP_01012036 molybdenum cofactor biosynthesis domain protein [Maritimibacter alkaliphilus HTCC2654].
ConsensusfromContig2279Proteobacteria-Rhodoferax_ferrireducens_T118_gi89899782	1.50E-13	>YP_522253 N-acyl-D-amino-acid deacylase [Rhodoferax ferrireducens T118].
ConsensusfromContig4106Proteobacteria-Rhodoferax_ferrireducens_T118_gi89900973	7.20E-13	>YP_523444 beta-lactamase [Rhodoferax ferrireducens T118].
ConsensusfromContig2410Proteobacteria-Rhodopseudomonas_palustris_BisA53_gi115526369	1.10E-11	>YP_783280 ATPase-like protein [Rhodopseudomonas palustris BisA53].
ConsensusfromContig5160Proteobacteria-Rhodopseudomonas_palustris_DX_1_gi283842040	5.50E-38	>ZP_06359579 2-dehydropantoate 2-reductase [Rhodopseudomonas palustris DX-1].
ConsensusfromContig6940Proteobacteria-Rhodospirillum_centenum_SW_gi209965023	5.10E-51	>YP_002297938 low specificity L-threonine aldolase [Rhodospirillum centenum SW].
ConsensusfromContig6051Proteobacteria-Rhodospirillum_rubrum_ATCC_11170_gi83592897	3.00E-24	>YP_426649 respiratory-chain NADH dehydrogenase, subunit 1 [Rhodospirillum rubrum ATCC 11170].
ConsensusfromContig1776Proteobacteria-Rhodospirillum_rubrum_ATCC_11170_gi83593349	5.10E-14	>YP_427101 twin-arginine translocation pathway signal [Rhodospirillum rubrum ATCC 11170].
ConsensusfromContig3132Proteobacteria-Roseomonas_cervicalis_ATCC_49957_gi296533570	1.60E-28	>ZP_06896139 methyltransferase [Roseomonas cervicalis ATCC 49957].
ConsensusfromContig4372Proteobacteria-Roseomonas_cervicalis_ATCC_49957_gi296533581	4.30E-14	>ZP_06896149 ATP-dependent hsl protease ATP-binding subunit HslU [Roseomonas cervicalis ATCC 49957].
ConsensusfromContig3446Proteobacteria-Roseomonas_cervicalis_ATCC_49957_gi296536768	1.30E-32	>ZP_06898823 3-hydroxybutyryl-CoA dehydrogenase [Roseomonas cervicalis ATCC 49957].
ConsensusfromContig2113Proteobacteria-Roseovarius_nubinhibens_ISM_gi83951734	2.80E-23	>ZP_00960466 hydroxymethylglutaryl-CoA lyase [Roseovarius nubinhibens ISM].
ConsensusfromContig3214Proteobacteria-Roseovarius_sp_HTCC2601_gi114765660	2.00E-25	>ZP_01444759 keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase [Pelagibaca bermudensis HTCC2601].
ConsensusfromContig1964Proteobacteria-Ruegeria_pomeroyi_DSS_3_gi56696583	3.00E-16	>YP_166941 hypothetical protein SPO1702 [Ruegeria pomeroyi DSS-3].
ConsensusfromContig1038Proteobacteria-Ruegeria_sp_R11_gi254475257	1.30E-21	>ZP_05088643 ectoine utilization protein EutD [Ruegeria sp. R11].
ConsensusfromContig4460Proteobacteria-Ruegeria_sp_TM1040_gi99081029	1.00E-18	>YP_613183 ABC transporter related [Ruegeria sp. TM1040].
ConsensusfromContig3720Proteobacteria-Saccharophagus_degradans_2_40_gi90021240	6.60E-13	>YP_527067 ribosomal protein S32 [Saccharophagus degradans 2-40].
ConsensusfromContig2204Proteobacteria-Saccharophagus_degradans_2_40_gi90022148	6.80E-13	>YP_527975 hypothetical protein Sde_2503 [Saccharophagus degradans 2-40].
ConsensusfromContig3006Proteobacteria-Saccharophagus_degradans_2_40_gi90022708	1.30E-37	>YP_528535 transglutaminase-like [Saccharophagus degradans 2-40].
ConsensusfromContig3148Proteobacteria-Saccharophagus_degradans_2_40_gi90023340	1.20E-40	>YP_529167 response regulator receiver domain-containing protein [Saccharophagus degradans 2-40].
ConsensusfromContig1987Proteobacteria-Salmonella_enterica_subsp_enterica_serovar_4,[5],12_i___str_CVM23701_gi205	3.50E-54	>ZP_03223900 DNA methylase [Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. CVM23701].
ConsensusfromContig5157Proteobacteria-Shewanella_amazonensis_SB2B_gi119774239	1.60E-27	>YP_926979 ATPase [Shewanella amazonensis SB2B].
ConsensusfromContig5955Proteobacteria-Shewanella_benthica_KT99_gi163750291	6.50E-15	>ZP_02157532 acetyltransferase, GNAT family protein [Shewanella benthica KT99].
ConsensusfromContig5157Proteobacteria-Shewanella_sp_MR_7_gi114046475	3.70E-12	>YP_737025 DNA-N1-methyladenine dioxygenase [Shewanella sp. MR-7].
ConsensusfromContig6950Proteobacteria-Shigella_flexneri_5_str_8401_gi110804179	6.30E-131	>YP_687699 bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase [Shigella flexneri 5 str. 8401].
ConsensusfromContig5108Proteobacteria-Silicibacter_sp_TrichCH4B_gi259418700	4.30E-25	>ZP_05742617 hypothetical protein SCH4B_4104 [Silicibacter sp. TrichCH4B].
ConsensusfromContig2054Proteobacteria-Sorangium_cellulosum_So_ce_56_gi162449238	1.30E-14	>YP_001611605 aldose 1-epimerase [Sorangium cellulosum 'So ce 56'].
ConsensusfromContig3168Proteobacteria-Sorangium_cellulosum_So_ce_56_gi162450991	1.80E-17	>YP_001613358 hypothetical protein sce2719 [Sorangium cellulosum 'So ce 56'].
ConsensusfromContig938 Proteobacteria-Sorangium_cellulosum_So_ce_56_gi162451321	1.10E-37	>YP_001613688 putative secreted protein [Sorangium cellulosum 'So ce 56'].
ConsensusfromContig3256Proteobacteria-Sorangium_cellulosum_So_ce_56_gi162451571	1.00E-10	>YP_001613938 latent transforming growth factor beta binding protein [Sorangium cellulosum 'So ce 56'].
ConsensusfromContig2014Proteobacteria-Sorangium_cellulosum_So_ce_56_gi162452868	5.90E-29	>YP_001615235 Alpha-L-arabinofuranosidase precursor [Sorangium cellulosum 'So ce 56'].
ConsensusfromContig1774Proteobacteria-Sorangium_cellulosum_So_ce_56_gi162453251	1.00E-12	>YP_001615618 putative secreted protein [Sorangium cellulosum 'So ce 56'].
ConsensusfromContig2036Proteobacteria-Sorangium_cellulosum_So_ce_56_gi162453650	3.00E-27	>YP_001616017 hypothetical protein sce5374 [Sorangium cellulosum 'So ce 56'].
ConsensusfromContig1951Proteobacteria-Sorangium_cellulosum_So_ce_56_gi162455207	9.40E-68	>YP_001617574 hypothetical protein sce6925 [Sorangium cellulosum 'So ce 56'].
ConsensusfromContig2238Proteobacteria-Sorangium_cellulosum_So_ce_56_gi162455865	2.20E-12	>YP_001618232 hypothetical protein sce7583 [Sorangium cellulosum 'So ce 56'].
ConsensusfromContig7108Proteobacteria-Sorangium_cellulosum_So_ce_56_gi162455885	2.00E-12	>YP_001618252 protein kinase [Sorangium cellulosum 'So ce 56'].
ConsensusfromContig5102Proteobacteria-Sorangium_cellulosum_So_ce_56_gi162456120	1.20E-19	>YP_001618487 hypothetical protein sce7837 [Sorangium cellulosum 'So ce 56'].
ConsensusfromContig5101Proteobacteria-Sphingobium_japonicum_UT26S_gi294011955	8.70E-22	>YP_003545415 protein involved in biosynthesis of mitomycin antibiotics/polyketide fumonisin [Sphingobium japonicum UT26S].
ConsensusfromContig3176Proteobacteria-Sphingomonas_wittichii_RW1_gi148556005	3.10E-11	>YP_001263587 hypothetical protein Swit_3100 [Sphingomonas wittichii RW1].
ConsensusfromContig3039Proteobacteria-Stigmatella_aurantiaca_DW4/3_1_gi115374805	8.70E-18	>ZP_01462080 aminotransferase, class III family [Stigmatella aurantiaca DW4/3-1].
ConsensusfromContig3089Proteobacteria-Teredinibacter_turnerae_T7901_gi254785966	6.40E-20	>YP_003073395 aconitate hydratase 2 [Teredinibacter turnerae T7901].
ConsensusfromContig5146Proteobacteria-Thioalkalivibrio_sp_K90mix_gi289209458	7.60E-23	>YP_003461524 Calcineurin phosphoesterase domain protein [Thioalkalivibrio sp. K90mix].
ConsensusfromContig7056Proteobacteria-Vibrio_harveyi_ATCC_BAA_1116_gi156936742	6.40E-17	>YP_001436093 hypothetical protein VIBHAR_p08226 [Vibrio harveyi ATCC BAA-1116].
ConsensusfromContig1676Proteobacteria-Vibrio_harveyi_ATCC_BAA_1116_gi156978121	8.80E-53	>YP_001449027 esterase [Vibrio harveyi ATCC BAA-1116].
ConsensusfromContig6470Proteobacteria-Vibrio_sp_AND4_gi163803336	2.10E-20	>ZP_02197213 bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase [Vibrio sp. AND4].
ConsensusfromContig1943Proteobacteria-Vibrio_vulnificus_YJ016_gi37678811	5.80E-30	>NP_933420 hypothetical protein VV0627 [Vibrio vulnificus YJ016].
ConsensusfromContig5691Proteobacteria-Wolbachia_endosymbiont_of_Drosophila_ananassae_gi58700186	6.30E-12	>ZP_00374686 ankyrin repeat domain protein [Wolbachia endosymbiont of Drosophila ananassae].
ConsensusfromContig3132Proteobacteria-Wolbachia_endosymbiont_of_Drosophila_willistoni_TSC#14030_081124_gi99035	1.40E-11	>ZP_01314984 hypothetical protein Wendoof_01000169 [Wolbachia endosymbiont of Drosophila willistoni TSC#14030-0811.24].
ConsensusfromContig7398Proteobacteria-Wolinella_succinogenes_DSM_1740_gi34558454	8.20E-32	>NP_908269 putative sugar nucleotidyltransferase [Wolinella succinogenes DSM 1740].
ConsensusfromContig6989Proteobacteria-Xanthomonas_albilineans_gi285018721	3.30E-14	>YP_003376432 hypothetical protein XALc_1954 [Xanthomonas albilineans].
ConsensusfromContig6054Proteobacteria-Xanthomonas_campestris_pv_musacearum_NCPPB4381_gi289671170	1.40E-20	>ZP_06492245 succinyl-diaminopimelate desuccinylase [Xanthomonas campestris pv. musacearum NCPPB4381].
ConsensusfromContig2952Proteobacteria-Xanthomonas_oryzae_pv_oryzae_KACC10331_gi58582326	3.40E-11	>YP_201342 N-ethylammeline chlorohydrolase [Xanthomonas oryzae pv. oryzae KACC10331].
ConsensusfromContig7195Proteobacteria-Xylella_fastidiosa_9a5c_gi15837693	1.40E-11	>NP_298381 hypothetical protein XF1091 [Xylella fastidiosa 9a5c].
ConsensusfromContig4886Proteobacteria-Yersinia_kristensenii_ATCC_33638_gi238762250	3.00E-12	>ZP_04623222 hypothetical protein ykris0001_1670 [Yersinia kristensenii ATCC 33638].
ConsensusfromContig4842Proteobacteria-Yersinia_mollaretii_ATCC_43969_gi238798198	5.00E-14	>ZP_04641684 FAD binding-monooxygenase family protein [Yersinia mollaretii ATCC 43969].
ConsensusfromContig2228Proteobacteria-Yersinia_rohdei_ATCC_43380_gi238753114	8.90E-17	>ZP_04614563 LPS glycosyltransferase family protein [Yersinia rohdei ATCC 43380].
ConsensusfromContig2100Rhizaria-Bigelowiella_natans_tbBNL00000036_1	5.80E-50	
ConsensusfromContig5412Rhizaria-Bigelowiella_natans_tbBNL00000530_1	2.60E-23	
ConsensusfromContig1085Rhizaria-Bigelowiella_natans_tbBNL00000683_3	2.20E-11	
ConsensusfromContig1509Rhizaria-Bigelowiella_natans_tbBNL00000693_2	5.60E-14	
ConsensusfromContig6715Rhizaria-Bigelowiella_natans_tbBNL00001108_1	1.60E-11	
ConsensusfromContig3984Rhizaria-Bigelowiella_natans_tbBNL00001117_2	2.90E-15	
ConsensusfromContig2609Rhizaria-Bigelowiella_natans_tbBNL00001313_1	1.90E-15	
ConsensusfromContig9081Rhizaria-Bigelowiella_natans_tbBNL00001498_3	4.50E-11	
ConsensusfromContig1939Rhizaria-Bigelowiella_natans_tbBNL00001553_3	5.30E-20	
ConsensusfromContig2088Rhizaria-Bigelowiella_natans_tbBNL00001553_3	7.50E-12	
ConsensusfromContig2166Rhizaria-Bigelowiella_natans_tbBNL00001864_3	1.30E-16	
ConsensusfromContig2196Rhizaria-Paracercomonas_marina_ATCC50319_tbCLL00000123_3	7.00E-90	
ConsensusfromContig3316Rhizaria-Paracercomonas_marina_ATCC50319_tbCLL00000488_6	3.30E-19	
ConsensusfromContig1940Rhizaria-Reticulomyxa_filosa_esgi113375496_2	3.40E-18	>EE664911 33445_re1399 R. filosa cDNA library Reticulomyxa filosa cDNA clone 33445_re1399, mRNA sequence.
ConsensusfromContig2138Rhizaria-Reticulomyxa_filosa_esgi113376273_3	6.50E-16	>EE665688 30533_re598 R. filosa cDNA library Reticulomyxa filosa cDNA clone 30533_re598, mRNA sequence.
ConsensusfromContig6108Rhodophyta-Calliarthron_tuberculosum_IDg1570t1	6.90E-15	
ConsensusfromContig5277Rhodophyta-Calliarthron_tuberculosum_IDg17584t1	9.60E-16	
ConsensusfromContig2807Rhodophyta-Calliarthron_tuberculosum_IDg20200t1	4.20E-14	
ConsensusfromContig7431Rhodophyta-Calliarthron_tuberculosum_IDg22049t1	1.90E-11	
ConsensusfromContig7143Rhodophyta-Calliarthron_tuberculosum_IDg23404t1	1.80E-32	
ConsensusfromContig1814Rhodophyta-Calliarthron_tuberculosum_IDg23596t1	2.60E-34	
ConsensusfromContig3125Rhodophyta-Calliarthron_tuberculosum_IDg2445t1	1.90E-26	
ConsensusfromContig5228Rhodophyta-Calliarthron_tuberculosum_IDg2445t1	9.20E-27	
ConsensusfromContig5440Rhodophyta-Calliarthron_tuberculosum_IDg2445t1	3.30E-34	
ConsensusfromContig5393Rhodophyta-Calliarthron_tuberculosum_IDg262t1	1.20E-42	
ConsensusfromContig2827Rhodophyta-Calliarthron_tuberculosum_IDg3440t1	9.90E-33	
ConsensusfromContig5121Rhodophyta-Calliarthron_tuberculosum_IDg4660t1	2.80E-21	
ConsensusfromContig5438Rhodophyta-Calliarthron_tuberculosum_IDg4660t1	4.80E-35	
ConsensusfromContig1034Rhodophyta-Calliarthron_tuberculosum_IDg6619t1	9.40E-41	
ConsensusfromContig2785Rhodophyta-Calliarthron_tuberculosum_IDg7093t1	2.20E-15	
ConsensusfromContig5774Rhodophyta-Cyanidioschyzon_merolae_CME146C	2.90E-45	
ConsensusfromContig1997Rhodophyta-Cyanidioschyzon_merolae_CMJ200C	2.90E-18	
ConsensusfromContig5218Rhodophyta-Cyanidioschyzon_merolae_CMK078C	1.90E-59	
ConsensusfromContig5152Rhodophyta-Cyanidioschyzon_merolae_CML205C	2.50E-64	
ConsensusfromContig5420Rhodophyta-Galdieria_sulphuraria_dxA45G05_1	7.20E-36	
ConsensusfromContig5420Rhodophyta-Galdieria_sulphuraria_dxA45G05_1	7.20E-36	
ConsensusfromContig5349Rhodophyta-Galdieria_sulphuraria_dxHET35E04_2	1.90E-20	
ConsensusfromContig3055Rhodophyta-Galdieria_sulphuraria_dxHET37E03_1	7.30E-20	
ConsensusfromContig2783Rhodophyta-Gracilaria_changii_esContig313_3	8.10E-22	
ConsensusfromContig6796Rhodophyta-Gracilaria_changii_esgi120458900_5	9.20E-24	>DV965948 GC03939 Gracilaria changii cDNA library Gracilaria changii cDNA clone HCL_PLATE1_D11_07, mRNA sequence.
ConsensusfromContig3089Rhodophyta-Gracilaria_changii_esgi120461283_2	5.90E-18	>DV969038 GC07045 Gracilaria changii cDNA library Gracilaria changii cDNA clone HCL_PLATE52_F07_11.AB1.seq.noA, mRNA sequence.
ConsensusfromContig6606Rhodophyta-Gracilaria_changii_esgi120463256_2	3.60E-14	>DV964071 GC02054 Gracilaria changii cDNA library Gracilaria changii cDNA clone 157-A05-T3, mRNA sequence.

ConsensusfromContig2003	Rhodophyta-Gracilaria_changii_esgi120464947_1	2.50E-17	>DV967588 GC05579 Gracilaria changii cDNA library Gracilaria changii cDNA clone HCL_PLATE36_C02_06, mRNA sequence.
ConsensusfromContig2996	Rhodophyta-Porphyra_haitanensis_esContig461_1	1.90E-22	
ConsensusfromContig6220	Rhodophyta-Porphyra_haitanensis_esgi115287323_1	4.20E-23	>EG016848 EST01558_0906 Sporophyte cDNA Library Porphyra haitanensis cDNA 5', mRNA sequence.
ConsensusfromContig3773	Rhodophyta-Porphyra_haitanensis_esgi115288425_1	4.20E-23	>EG017950 EST00044_0906 Sporophyte cDNA Library Porphyra haitanensis cDNA 5', mRNA sequence.
ConsensusfromContig5437	Rhodophyta-Porphyra_yezoensis_esContig1865_3	8.50E-193	
ConsensusfromContig2381	Rhodophyta-Porphyra_yezoensis_esContig197_2	1.90E-14	
ConsensusfromContig7033	Rhodophyta-Porphyra_yezoensis_esContig264_1	5.10E-39	
ConsensusfromContig3022	Rhodophyta-Porphyra_yezoensis_esContig54_1	7.20E-12	
ConsensusfromContig3061	Rhodophyta-Porphyra_yezoensis_esContig54_1	3.80E-12	
ConsensusfromContig3391	Rhodophyta-Porphyra_yezoensis_esContig54_1	2.50E-12	
ConsensusfromContig3819	Rhodophyta-Porphyra_yezoensis_esContig54_1	2.30E-11	
ConsensusfromContig2385	Rhodophyta-Porphyra_yezoensis_esContig875_3	1.30E-11	
ConsensusfromContig5118	Rhodophyta-Porphyra_yezoensis_esgi8590709_2	2.20E-12	>AV435484 AV435484 Porphyra yezoensis TU-1 Porphyra yezoensis cDNA clone PM058a12_r 5', mRNA sequence.
ConsensusfromContig2609	Rhodophyta-Porphyra_yezoensis_esgi8593856_2	2.30E-14	>AV438631 AV438631 Porphyra yezoensis TU-1 Porphyra yezoensis cDNA clone PS038h07_r 5', mRNA sequence.
ConsensusfromContig2678	Rhodophyta-Porphyridium_cruentum_dxContig10037_2	3.00E-12	
ConsensusfromContig2322	Rhodophyta-Porphyridium_cruentum_dxContig10686_6	5.60E-12	
ConsensusfromContig7258	Rhodophyta-Porphyridium_cruentum_dxContig11529_3	5.40E-38	
ConsensusfromContig2795	Rhodophyta-Porphyridium_cruentum_dxContig12579_5	1.90E-15	
ConsensusfromContig6992	Rhodophyta-Porphyridium_cruentum_dxContig15796_1	5.00E-11	
ConsensusfromContig3246	Rhodophyta-Porphyridium_cruentum_dxContig392_3	2.10E-35	
ConsensusfromContig5336	Rhodophyta-Porphyridium_cruentum_dxContig4559_1	9.20E-25	
ConsensusfromContig6661	Rhodophyta-Porphyridium_cruentum_dxContig4917_1	1.00E-11	
ConsensusfromContig6281	Rhodophyta-Porphyridium_cruentum_dxContig5143_4	1.70E-11	
ConsensusfromContig2702	Rhodophyta-Porphyridium_cruentum_dxContig5969_6	1.80E-27	
ConsensusfromContig3179	Rhodophyta-Porphyridium_cruentum_dxContig5969_6	1.40E-24	
ConsensusfromContig2698	Rhodophyta-Porphyridium_cruentum_dxGCDJ7DB01CJ88X_2	2.60E-16	
ConsensusfromContig5783	Rhodophyta-Porphyridium_cruentum_dxGCDJ7DB01DAFE2_1	1.60E-14	
ConsensusfromContig3097	Rhodophyta-Porphyridium_cruentum_dxGCDJ7DB01DFHXZ_5	4.00E-20	
ConsensusfromContig7140	Rhodophyta-Porphyridium_cruentum_dxGCDJ7DB01DXIJR_3	1.20E-23	
ConsensusfromContig4131	Rhodophyta-Porphyridium_cruentum_dxGCDJ7DB01ED4LS_2	6.60E-14	
ConsensusfromContig2527	Rhodophyta-Porphyridium_cruentum_dxGCDJ7DB01EEM8F_2	8.00E-13	
ConsensusfromContig5408	Spirochaetes-Brachyspira_murdochii_DSM_12563_gi296126560	2.30E-82	>YP_003633812 DNA-cytosine methyltransferase [Brachyspira murdochii DSM 12563].
ConsensusfromContig2061	Spirochaetes-Leptospira_biflexa_serovar_Patoc_strain_Patoc_1__Ames__gi189911350	4.40E-18	>YP_001962905 cyclic nucleotide-binding protein [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Ames)'].
ConsensusfromContig5117	Spirochaetes-Leptospira_biflexa_serovar_Patoc_strain_Patoc_1__Ames__gi189911350	2.10E-25	>YP_001962905 cyclic nucleotide-binding protein [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Ames)'].
ConsensusfromContig6931	Spirochaetes-Leptospira_biflexa_serovar_Patoc_strain_Patoc_1__Ames__gi189911350	7.30E-14	>YP_001962905 cyclic nucleotide-binding protein [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Ames)'].
ConsensusfromContig3638	Spirochaetes-Leptospira_biflexa_serovar_Patoc_strain_Patoc_1__Paris__gi183220609	6.80E-26	>YP_001838605 hypothetical protein LEPBI_I1215 [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Paris)'].
ConsensusfromContig3717	Spirochaetes-Leptospira_biflexa_serovar_Patoc_strain_Patoc_1__Paris__gi183220609	2.50E-11	>YP_001838605 hypothetical protein LEPBI_I1215 [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Paris)'].
ConsensusfromContig3951	Spirochaetes-Leptospira_biflexa_serovar_Patoc_strain_Patoc_1__Paris__gi183220609	1.80E-14	>YP_001838605 hypothetical protein LEPBI_I1215 [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Paris)'].
ConsensusfromContig4310	Spirochaetes-Leptospira_biflexa_serovar_Patoc_strain_Patoc_1__Paris__gi183220609	4.30E-16	>YP_001838605 hypothetical protein LEPBI_I1215 [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Paris)'].
ConsensusfromContig6197	Spirochaetes-Leptospira_interrogans_serovar_Lai_str_56601_gi24213817	9.50E-17	>NP_711298 hypothetical protein LA_1118 [Leptospira interrogans serovar Lai str. 56601].
ConsensusfromContig2503	Stramenopiles-Aureococcus_anophagefferens_jgi10217	4.80E-51	
ConsensusfromContig2395	Stramenopiles-Aureococcus_anophagefferens_jgi10939	6.40E-18	
ConsensusfromContig5358	Stramenopiles-Aureococcus_anophagefferens_jgi12663	1.20E-13	
ConsensusfromContig5121	Stramenopiles-Aureococcus_anophagefferens_jgi12804	2.10E-127	
ConsensusfromContig4338	Stramenopiles-Aureococcus_anophagefferens_jgi12951	2.60E-13	
ConsensusfromContig5219	Stramenopiles-Aureococcus_anophagefferens_jgi14200	3.40E-48	
ConsensusfromContig6678	Stramenopiles-Aureococcus_anophagefferens_jgi16	1.20E-21	
ConsensusfromContig2039	Stramenopiles-Aureococcus_anophagefferens_jgi18666	7.00E-26	
ConsensusfromContig6931	Stramenopiles-Aureococcus_anophagefferens_jgi18923	4.20E-46	
ConsensusfromContig1940	Stramenopiles-Aureococcus_anophagefferens_jgi19213	3.80E-13	
ConsensusfromContig782	Stramenopiles-Aureococcus_anophagefferens_jgi19576	8.50E-11	
ConsensusfromContig6870	Stramenopiles-Aureococcus_anophagefferens_jgi19876	1.10E-14	
ConsensusfromContig6852	Stramenopiles-Aureococcus_anophagefferens_jgi21131	1.00E-26	
ConsensusfromContig2761	Stramenopiles-Aureococcus_anophagefferens_jgi21146	8.60E-24	
ConsensusfromContig5946	Stramenopiles-Aureococcus_anophagefferens_jgi21841	8.10E-25	
ConsensusfromContig1355	Stramenopiles-Aureococcus_anophagefferens_jgi23523	3.10E-12	
ConsensusfromContig3673	Stramenopiles-Aureococcus_anophagefferens_jgi23523	6.90E-17	
ConsensusfromContig5954	Stramenopiles-Aureococcus_anophagefferens_jgi2359	3.50E-34	
ConsensusfromContig4138	Stramenopiles-Aureococcus_anophagefferens_jgi23593	1.90E-17	
ConsensusfromContig2132	Stramenopiles-Aureococcus_anophagefferens_jgi23831	3.20E-43	
ConsensusfromContig2803	Stramenopiles-Aureococcus_anophagefferens_jgi24160	2.40E-60	
ConsensusfromContig6966	Stramenopiles-Aureococcus_anophagefferens_jgi25028	5.00E-11	
ConsensusfromContig3050	Stramenopiles-Aureococcus_anophagefferens_jgi2521	5.70E-29	
ConsensusfromContig3155	Stramenopiles-Aureococcus_anophagefferens_jgi25371	2.30E-25	
ConsensusfromContig5224	Stramenopiles-Aureococcus_anophagefferens_jgi26320	1.50E-12	
ConsensusfromContig2230	Stramenopiles-Aureococcus_anophagefferens_jgi26908	2.00E-24	
ConsensusfromContig1335	Stramenopiles-Aureococcus_anophagefferens_jgi27315	3.50E-20	
ConsensusfromContig2221	Stramenopiles-Aureococcus_anophagefferens_jgi27787	3.80E-16	
ConsensusfromContig2221	Stramenopiles-Aureococcus_anophagefferens_jgi27787	3.80E-16	
ConsensusfromContig1059	Stramenopiles-Aureococcus_anophagefferens_jgi27794	5.40E-21	
ConsensusfromContig1909	Stramenopiles-Aureococcus_anophagefferens_jgi27862	3.80E-14	
ConsensusfromContig5421	Stramenopiles-Aureococcus_anophagefferens_jgi27956	7.00E-28	
ConsensusfromContig1554	Stramenopiles-Aureococcus_anophagefferens_jgi28349	1.50E-14	
ConsensusfromContig2437	Stramenopiles-Aureococcus_anophagefferens_jgi28349	3.40E-15	
ConsensusfromContig5165	Stramenopiles-Aureococcus_anophagefferens_jgi28349	1.40E-39	
ConsensusfromContig5101	Stramenopiles-Aureococcus_anophagefferens_jgi28381	1.60E-60	
ConsensusfromContig3071	Stramenopiles-Aureococcus_anophagefferens_jgi28918	8.10E-40	
ConsensusfromContig3947	Stramenopiles-Aureococcus_anophagefferens_jgi29612	1.80E-28	
ConsensusfromContig2995	Stramenopiles-Aureococcus_anophagefferens_jgi29805	1.20E-17	
ConsensusfromContig5273	Stramenopiles-Aureococcus_anophagefferens_jgi29980	1.30E-63	
ConsensusfromContig3143	Stramenopiles-Aureococcus_anophagefferens_jgi30070	1.70E-102	
ConsensusfromContig5165	Stramenopiles-Aureococcus_anophagefferens_jgi30278	2.20E-30	
ConsensusfromContig5696	Stramenopiles-Aureococcus_anophagefferens_jgi30696	3.40E-11	
ConsensusfromContig5152	Stramenopiles-Aureococcus_anophagefferens_jgi33640	1.50E-52	
ConsensusfromContig6922	Stramenopiles-Aureococcus_anophagefferens_jgi34330	3.20E-11	
ConsensusfromContig2748	Stramenopiles-Aureococcus_anophagefferens_jgi39152	8.80E-12	
ConsensusfromContig1522	Stramenopiles-Aureococcus_anophagefferens_jgi39233	1.90E-11	
ConsensusfromContig1158	Stramenopiles-Aureococcus_anophagefferens_jgi4638	3.10E-15	
ConsensusfromContig7292	Stramenopiles-Aureococcus_anophagefferens_jgi4752	2.20E-11	
ConsensusfromContig2262	Stramenopiles-Aureococcus_anophagefferens_jgi5150	5.40E-54	
ConsensusfromContig1092	Stramenopiles-Aureococcus_anophagefferens_jgi52627	3.80E-53	
ConsensusfromContig1079	Stramenopiles-Aureococcus_anophagefferens_jgi53176	1.30E-16	
ConsensusfromContig5155	Stramenopiles-Aureococcus_anophagefferens_jgi53176	2.20E-86	
ConsensusfromContig5159	Stramenopiles-Aureococcus_anophagefferens_jgi53176	9.90E-45	
ConsensusfromContig7040	Stramenopiles-Aureococcus_anophagefferens_jgi53176	1.30E-51	
ConsensusfromContig2366	Stramenopiles-Aureococcus_anophagefferens_jgi58625	2.20E-24	
ConsensusfromContig2192	Stramenopiles-Aureococcus_anophagefferens_jgi59335	4.40E-23	
ConsensusfromContig2230	Stramenopiles-Aureococcus_anophagefferens_jgi60103	1.40E-47	
ConsensusfromContig7393	Stramenopiles-Aureococcus_anophagefferens_jgi60295	5.00E-12	
ConsensusfromContig1998	Stramenopiles-Aureococcus_anophagefferens_jgi60648	3.50E-40	

ConsensusfromContig6986	Stramenopiles-Aureococcus_anophagefferens_jgi60668	1.10E-44
ConsensusfromContig2635	Stramenopiles-Aureococcus_anophagefferens_jgi60794	8.20E-23
ConsensusfromContig4016	Stramenopiles-Aureococcus_anophagefferens_jgi60794	1.00E-18
ConsensusfromContig6959	Stramenopiles-Aureococcus_anophagefferens_jgi60794	4.40E-42
ConsensusfromContig5182	Stramenopiles-Aureococcus_anophagefferens_jgi60815	5.20E-13
ConsensusfromContig884	Stramenopiles-Aureococcus_anophagefferens_jgi60931	9.20E-68
ConsensusfromContig6470	Stramenopiles-Aureococcus_anophagefferens_jgi60931	1.30E-15
ConsensusfromContig2370	Stramenopiles-Aureococcus_anophagefferens_jgi60984	7.70E-11
ConsensusfromContig5116	Stramenopiles-Aureococcus_anophagefferens_jgi61008	1.20E-32
ConsensusfromContig5959	Stramenopiles-Aureococcus_anophagefferens_jgi6107	1.70E-26
ConsensusfromContig1996	Stramenopiles-Aureococcus_anophagefferens_jgi61180	1.10E-14
ConsensusfromContig6936	Stramenopiles-Aureococcus_anophagefferens_jgi61364	7.00E-11
ConsensusfromContig1308	Stramenopiles-Aureococcus_anophagefferens_jgi61422	2.00E-21
ConsensusfromContig3393	Stramenopiles-Aureococcus_anophagefferens_jgi61422	9.50E-11
ConsensusfromContig5215	Stramenopiles-Aureococcus_anophagefferens_jgi6143	9.80E-55
ConsensusfromContig2023	Stramenopiles-Aureococcus_anophagefferens_jgi61721	1.10E-27
ConsensusfromContig6940	Stramenopiles-Aureococcus_anophagefferens_jgi61870	8.60E-11
ConsensusfromContig5100	Stramenopiles-Aureococcus_anophagefferens_jgi62035	2.00E-13
ConsensusfromContig1947	Stramenopiles-Aureococcus_anophagefferens_jgi62507	9.50E-13
ConsensusfromContig2173	Stramenopiles-Aureococcus_anophagefferens_jgi62513	3.60E-18
ConsensusfromContig5153	Stramenopiles-Aureococcus_anophagefferens_jgi62551	3.30E-24
ConsensusfromContig7781	Stramenopiles-Aureococcus_anophagefferens_jgi63054	3.70E-12
ConsensusfromContig3910	Stramenopiles-Aureococcus_anophagefferens_jgi63054	7.90E-57
ConsensusfromContig3910	Stramenopiles-Aureococcus_anophagefferens_jgi63054	7.90E-57
ConsensusfromContig1072	Stramenopiles-Aureococcus_anophagefferens_jgi63286	2.50E-11
ConsensusfromContig2467	Stramenopiles-Aureococcus_anophagefferens_jgi63286	2.80E-12
ConsensusfromContig2018	Stramenopiles-Aureococcus_anophagefferens_jgi63340	1.50E-18
ConsensusfromContig2054	Stramenopiles-Aureococcus_anophagefferens_jgi63340	4.70E-26
ConsensusfromContig4845	Stramenopiles-Aureococcus_anophagefferens_jgi63340	5.10E-24
ConsensusfromContig1977	Stramenopiles-Aureococcus_anophagefferens_jgi63520	3.30E-24
ConsensusfromContig1951	Stramenopiles-Aureococcus_anophagefferens_jgi63581	4.20E-14
ConsensusfromContig5395	Stramenopiles-Aureococcus_anophagefferens_jgi63946	1.10E-33
ConsensusfromContig7069	Stramenopiles-Aureococcus_anophagefferens_jgi63946	6.00E-30
ConsensusfromContig1998	Stramenopiles-Aureococcus_anophagefferens_jgi64125	4.30E-50
ConsensusfromContig2069	Stramenopiles-Aureococcus_anophagefferens_jgi64125	1.20E-18
ConsensusfromContig3122	Stramenopiles-Aureococcus_anophagefferens_jgi64125	6.20E-23
ConsensusfromContig1763	Stramenopiles-Aureococcus_anophagefferens_jgi64764	6.70E-11
ConsensusfromContig2412	Stramenopiles-Aureococcus_anophagefferens_jgi64808	8.60E-11
ConsensusfromContig5110	Stramenopiles-Aureococcus_anophagefferens_jgi64808	9.20E-39
ConsensusfromContig2094	Stramenopiles-Aureococcus_anophagefferens_jgi64875	4.90E-32
ConsensusfromContig5151	Stramenopiles-Aureococcus_anophagefferens_jgi64875	5.50E-51
ConsensusfromContig1356	Stramenopiles-Aureococcus_anophagefferens_jgi64885	6.40E-16
ConsensusfromContig4879	Stramenopiles-Aureococcus_anophagefferens_jgi64885	3.50E-11
ConsensusfromContig1210	Stramenopiles-Aureococcus_anophagefferens_jgi64968	8.60E-13
ConsensusfromContig6294	Stramenopiles-Aureococcus_anophagefferens_jgi64968	2.70E-15
ConsensusfromContig2155	Stramenopiles-Aureococcus_anophagefferens_jgi6503	5.90E-18
ConsensusfromContig6936	Stramenopiles-Aureococcus_anophagefferens_jgi65133	4.30E-44
ConsensusfromContig1114	Stramenopiles-Aureococcus_anophagefferens_jgi65313	4.50E-14
ConsensusfromContig1114	Stramenopiles-Aureococcus_anophagefferens_jgi65313	4.50E-14
ConsensusfromContig2271	Stramenopiles-Aureococcus_anophagefferens_jgi65313	6.00E-29
ConsensusfromContig2300	Stramenopiles-Aureococcus_anophagefferens_jgi65313	1.00E-12
ConsensusfromContig2016	Stramenopiles-Aureococcus_anophagefferens_jgi65636	1.50E-31
ConsensusfromContig6931	Stramenopiles-Aureococcus_anophagefferens_jgi65638	1.10E-11
ConsensusfromContig5781	Stramenopiles-Aureococcus_anophagefferens_jgi6566	2.50E-18
ConsensusfromContig3246	Stramenopiles-Aureococcus_anophagefferens_jgi65813	9.60E-11
ConsensusfromContig5198	Stramenopiles-Aureococcus_anophagefferens_jgi66027	7.20E-30
ConsensusfromContig7022	Stramenopiles-Aureococcus_anophagefferens_jgi66270	1.00E-65
ConsensusfromContig1936	Stramenopiles-Aureococcus_anophagefferens_jgi66355	6.70E-47
ConsensusfromContig2260	Stramenopiles-Aureococcus_anophagefferens_jgi66355	1.50E-21
ConsensusfromContig4706	Stramenopiles-Aureococcus_anophagefferens_jgi67187	1.10E-16
ConsensusfromContig2907	Stramenopiles-Aureococcus_anophagefferens_jgi67214	4.20E-23
ConsensusfromContig1895	Stramenopiles-Aureococcus_anophagefferens_jgi67274	8.70E-11
ConsensusfromContig5364	Stramenopiles-Aureococcus_anophagefferens_jgi67681	5.90E-19
ConsensusfromContig5198	Stramenopiles-Aureococcus_anophagefferens_jgi67726	3.10E-13
ConsensusfromContig3141	Stramenopiles-Aureococcus_anophagefferens_jgi67882	7.30E-43
ConsensusfromContig2335	Stramenopiles-Aureococcus_anophagefferens_jgi67925	4.50E-19
ConsensusfromContig5113	Stramenopiles-Aureococcus_anophagefferens_jgi67937	3.80E-18
ConsensusfromContig2085	Stramenopiles-Aureococcus_anophagefferens_jgi67940	7.20E-19
ConsensusfromContig6987	Stramenopiles-Aureococcus_anophagefferens_jgi68050	4.90E-24
ConsensusfromContig5397	Stramenopiles-Aureococcus_anophagefferens_jgi68595	5.60E-14
ConsensusfromContig2252	Stramenopiles-Aureococcus_anophagefferens_jgi68860	1.10E-11
ConsensusfromContig2047	Stramenopiles-Aureococcus_anophagefferens_jgi68993	7.40E-17
ConsensusfromContig2272	Stramenopiles-Aureococcus_anophagefferens_jgi68993	3.50E-22
ConsensusfromContig9003	Stramenopiles-Aureococcus_anophagefferens_jgi69060	7.20E-12
ConsensusfromContig1326	Stramenopiles-Aureococcus_anophagefferens_jgi69603	1.30E-14
ConsensusfromContig6305	Stramenopiles-Aureococcus_anophagefferens_jgi70731	2.40E-21
ConsensusfromContig2548	Stramenopiles-Aureococcus_anophagefferens_jgi70872	2.50E-14
ConsensusfromContig2031	Stramenopiles-Aureococcus_anophagefferens_jgi71496	1.40E-19
ConsensusfromContig5163	Stramenopiles-Aureococcus_anophagefferens_jgi71885	1.00E-25
ConsensusfromContig5173	Stramenopiles-Aureococcus_anophagefferens_jgi71885	5.50E-22
ConsensusfromContig3140	Stramenopiles-Aureococcus_anophagefferens_jgi71909	5.00E-23
ConsensusfromContig5310	Stramenopiles-Aureococcus_anophagefferens_jgi72156	2.10E-28
ConsensusfromContig2273	Stramenopiles-Aureococcus_anophagefferens_jgi72622	7.80E-16
ConsensusfromContig2892	Stramenopiles-Aureococcus_anophagefferens_jgi72622	1.60E-30
ConsensusfromContig7331	Stramenopiles-Aureococcus_anophagefferens_jgi72622	2.30E-26
ConsensusfromContig1989	Stramenopiles-Aureococcus_anophagefferens_jgi72645	2.00E-54
ConsensusfromContig2325	Stramenopiles-Aureococcus_anophagefferens_jgi72645	9.40E-18
ConsensusfromContig5402	Stramenopiles-Aureococcus_anophagefferens_jgi72645	6.00E-12
ConsensusfromContig2337	Stramenopiles-Aureococcus_anophagefferens_jgi72703	4.30E-27
ConsensusfromContig988	Stramenopiles-Aureococcus_anophagefferens_jgi72852	2.50E-22
ConsensusfromContig3140	Stramenopiles-Aureococcus_anophagefferens_jgi72852	2.90E-14
ConsensusfromContig1936	Stramenopiles-Aureococcus_anophagefferens_jgi7935	1.30E-46
ConsensusfromContig6909	Stramenopiles-Aureococcus_anophagefferens_jgi8334	2.20E-11
ConsensusfromContig2900	Stramenopiles-Blastocystis_hominis_tbBHL00001929_2	2.50E-16
ConsensusfromContig2900	Stramenopiles-Blastocystis_hominis_tbBHL00001929_2	2.50E-16
ConsensusfromContig2402	Stramenopiles-Fragilariopsis_cylindrus_jgi149139	1.30E-23
ConsensusfromContig5439	Stramenopiles-Fragilariopsis_cylindrus_jgi163093	1.90E-12
ConsensusfromContig6636	Stramenopiles-Fragilariopsis_cylindrus_jgi166097	7.10E-13
ConsensusfromContig5163	Stramenopiles-Fragilariopsis_cylindrus_jgi177704	1.70E-28
ConsensusfromContig2077	Stramenopiles-Fragilariopsis_cylindrus_jgi187472	1.50E-52

ConsensusfromContig6142	Stramenopiles-Fragilariopsis_cylindrus_jgi187472	3.60E-25	
ConsensusfromContig2400	Stramenopiles-Fragilariopsis_cylindrus_jgi191111	1.30E-11	
ConsensusfromContig5146	Stramenopiles-Fragilariopsis_cylindrus_jgi196614	1.30E-21	
ConsensusfromContig6387	Stramenopiles-Fragilariopsis_cylindrus_jgi207688	1.50E-11	
ConsensusfromContig5108	Stramenopiles-Fragilariopsis_cylindrus_jgi219434	4.50E-19	
ConsensusfromContig3763	Stramenopiles-Fragilariopsis_cylindrus_jgi224808	5.90E-29	
ConsensusfromContig3763	Stramenopiles-Fragilariopsis_cylindrus_jgi224808	5.90E-29	
ConsensusfromContig3005	Stramenopiles-Fragilariopsis_cylindrus_jgi225275	1.00E-17	
ConsensusfromContig2761	Stramenopiles-Fragilariopsis_cylindrus_jgi228566	8.10E-16	
ConsensusfromContig1830	Stramenopiles-Fragilariopsis_cylindrus_jgi228695	6.20E-11	
ConsensusfromContig2118	Stramenopiles-Fragilariopsis_cylindrus_jgi232497	4.60E-37	
ConsensusfromContig2090	Stramenopiles-Fragilariopsis_cylindrus_jgi232650	1.60E-12	
ConsensusfromContig2099	Stramenopiles-Fragilariopsis_cylindrus_jgi234116	5.20E-43	
ConsensusfromContig5375	Stramenopiles-Fragilariopsis_cylindrus_jgi234116	1.60E-16	
ConsensusfromContig767	Stramenopiles-Fragilariopsis_cylindrus_jgi234336	4.70E-31	
ConsensusfromContig2763	Stramenopiles-Fragilariopsis_cylindrus_jgi234336	1.10E-24	
ConsensusfromContig4411	Stramenopiles-Fragilariopsis_cylindrus_jgi234336	1.90E-11	
ConsensusfromContig6405	Stramenopiles-Fragilariopsis_cylindrus_jgi234764	6.30E-11	
ConsensusfromContig2111	Stramenopiles-Fragilariopsis_cylindrus_jgi238110	3.60E-50	
ConsensusfromContig2035	Stramenopiles-Fragilariopsis_cylindrus_jgi243335	3.60E-98	
ConsensusfromContig1948	Stramenopiles-Fragilariopsis_cylindrus_jgi247245	4.60E-13	
ConsensusfromContig3124	Stramenopiles-Fragilariopsis_cylindrus_jgi248830	2.30E-37	
ConsensusfromContig3370	Stramenopiles-Fragilariopsis_cylindrus_jgi249362	1.40E-44	
ConsensusfromContig2150	Stramenopiles-Fragilariopsis_cylindrus_jgi259247	8.90E-14	
ConsensusfromContig6696	Stramenopiles-Fragilariopsis_cylindrus_jgi259666	2.40E-20	
ConsensusfromContig6696	Stramenopiles-Fragilariopsis_cylindrus_jgi259666	2.40E-20	
ConsensusfromContig2115	Stramenopiles-Fragilariopsis_cylindrus_jgi259847	3.40E-15	
ConsensusfromContig3406	Stramenopiles-Fragilariopsis_cylindrus_jgi260621	1.20E-14	
ConsensusfromContig1587	Stramenopiles-Fragilariopsis_cylindrus_jgi260637	1.40E-17	
ConsensusfromContig2213	Stramenopiles-Fragilariopsis_cylindrus_jgi261883	6.80E-12	
ConsensusfromContig5705	Stramenopiles-Fragilariopsis_cylindrus_jgi262908	2.00E-23	
ConsensusfromContig7044	Stramenopiles-Fragilariopsis_cylindrus_jgi262908	3.10E-26	
ConsensusfromContig2778	Stramenopiles-Fragilariopsis_cylindrus_jgi269973	3.40E-20	
ConsensusfromContig6303	Stramenopiles-Fragilariopsis_cylindrus_jgi274417	7.30E-17	
ConsensusfromContig3150	Stramenopiles-Phaeodactylum_tricornutum_CCAP_1055/1_gi219110117	6.70E-17	>XP_002176810 arylsulfatase [Phaeodactylum tricornutum CCAP 1055/1].
ConsensusfromContig3150	Stramenopiles-Phaeodactylum_tricornutum_CCAP_1055/1_gi219110117	6.70E-17	>XP_002176810 arylsulfatase [Phaeodactylum tricornutum CCAP 1055/1].
ConsensusfromContig1497	Stramenopiles-Phaeodactylum_tricornutum_CCAP_1055/1_gi219110419	4.50E-23	>XP_002176961 predicted protein [Phaeodactylum tricornutum CCAP 1055/1].
ConsensusfromContig6089	Stramenopiles-Phaeodactylum_tricornutum_CCAP_1055/1_gi219112549	3.50E-41	>XP_002178026 predicted protein [Phaeodactylum tricornutum CCAP 1055/1].
ConsensusfromContig5401	Stramenopiles-Phaeodactylum_tricornutum_CCAP_1055/1_gi219116084	2.80E-13	>XP_002178837 predicted protein [Phaeodactylum tricornutum CCAP 1055/1].
ConsensusfromContig1974	Stramenopiles-Phaeodactylum_tricornutum_CCAP_1055/1_gi219116811	5.00E-12	>XP_002179200 predicted protein [Phaeodactylum tricornutum CCAP 1055/1].
ConsensusfromContig2115	Stramenopiles-Phaeodactylum_tricornutum_CCAP_1055/1_gi219117666	2.30E-28	>XP_002179624 predicted protein [Phaeodactylum tricornutum CCAP 1055/1].
ConsensusfromContig2004	Stramenopiles-Phaeodactylum_tricornutum_CCAP_1055/1_gi219117689	3.40E-27	>XP_002179635 predicted protein [Phaeodactylum tricornutum CCAP 1055/1].
ConsensusfromContig3138	Stramenopiles-Phaeodactylum_tricornutum_CCAP_1055/1_gi219118567	4.90E-15	>XP_002180053 silent information regulator protein Sir2 [Phaeodactylum tricornutum CCAP 1055/1].
ConsensusfromContig7101	Stramenopiles-Phaeodactylum_tricornutum_CCAP_1055/1_gi219119139	8.20E-30	>XP_002180336 predicted protein [Phaeodactylum tricornutum CCAP 1055/1].
ConsensusfromContig2040	Stramenopiles-Phaeodactylum_tricornutum_CCAP_1055/1_gi219119328	1.30E-33	>XP_002180427 galactosyl transferase [Phaeodactylum tricornutum CCAP 1055/1].
ConsensusfromContig2415	Stramenopiles-Phaeodactylum_tricornutum_CCAP_1055/1_gi219123837	7.70E-13	>XP_002182223 predicted protein [Phaeodactylum tricornutum CCAP 1055/1].
ConsensusfromContig1980	Stramenopiles-Phaeodactylum_tricornutum_CCAP_1055/1_gi219126383	2.70E-24	>XP_002183438 predicted protein [Phaeodactylum tricornutum CCAP 1055/1].
ConsensusfromContig5122	Stramenopiles-Phaeodactylum_tricornutum_CCAP_1055/1_gi219126613	2.00E-75	>XP_002183547 predicted protein [Phaeodactylum tricornutum CCAP 1055/1].
ConsensusfromContig1983	Stramenopiles-Phaeodactylum_tricornutum_CCAP_1055/1_gi219130619	3.00E-13	>XP_002185459 predicted protein [Phaeodactylum tricornutum CCAP 1055/1].
ConsensusfromContig7207	Stramenopiles-Phytophthora_brassicae_esContig1252_1	1.80E-32	
ConsensusfromContig8449	Stramenopiles-Phytophthora_brassicae_esContig1888_1	1.40E-35	
ConsensusfromContig8055	Stramenopiles-Phytophthora_brassicae_esContig290_2	8.40E-14	
ConsensusfromContig6628	Stramenopiles-Phytophthora_brassicae_esgi144591313_2	6.30E-13	>ES281650 PP022G05.XT7 non-sporulating culture of P. brassicae Phytophthora brassicae cDNA, mRNA sequence.
ConsensusfromContig1975	Stramenopiles-Phytophthora_brassicae_esgi144592214_3	2.10E-35	>ES282551 PP4.T7X.H01 non-sporulating culture of P. brassicae Phytophthora brassicae cDNA, mRNA sequence.
ConsensusfromContig6941	Stramenopiles-Phytophthora_brassicae_esgi144597094_2	8.70E-94	>ES287431 PT034C08.XT7 in vitro interaction, P. brassicae Phytophthora brassicae cDNA, mRNA sequence.
ConsensusfromContig2320	Stramenopiles-Phytophthora_capsici_jgi105594	1.30E-20	
ConsensusfromContig6022	Stramenopiles-Phytophthora_capsici_jgi107879	3.90E-12	
ConsensusfromContig2498	Stramenopiles-Phytophthora_capsici_jgi109685	7.50E-32	
ConsensusfromContig6697	Stramenopiles-Phytophthora_capsici_jgi112967	4.80E-18	
ConsensusfromContig5432	Stramenopiles-Phytophthora_capsici_jgi113866	1.30E-25	
ConsensusfromContig5721	Stramenopiles-Phytophthora_capsici_jgi115021	7.80E-90	
ConsensusfromContig5417	Stramenopiles-Phytophthora_capsici_jgi115180	2.00E-23	
ConsensusfromContig1868	Stramenopiles-Phytophthora_capsici_jgi115893	3.10E-15	
ConsensusfromContig7376	Stramenopiles-Phytophthora_capsici_jgi123360	7.40E-19	
ConsensusfromContig5144	Stramenopiles-Phytophthora_capsici_jgi124370	1.90E-48	
ConsensusfromContig5169	Stramenopiles-Phytophthora_capsici_jgi20194	2.50E-20	
ConsensusfromContig1941	Stramenopiles-Phytophthora_capsici_jgi20394	1.20E-33	
ConsensusfromContig3127	Stramenopiles-Phytophthora_capsici_jgi20394	1.20E-30	
ConsensusfromContig3127	Stramenopiles-Phytophthora_capsici_jgi21318	3.20E-13	
ConsensusfromContig3146	Stramenopiles-Phytophthora_capsici_jgi21318	6.30E-16	
ConsensusfromContig2492	Stramenopiles-Phytophthora_capsici_jgi24540	6.50E-15	
ConsensusfromContig5127	Stramenopiles-Phytophthora_capsici_jgi24562	7.80E-77	
ConsensusfromContig3569	Stramenopiles-Phytophthora_capsici_jgi27789	2.60E-15	
ConsensusfromContig2149	Stramenopiles-Phytophthora_capsici_jgi3288	3.40E-18	
ConsensusfromContig1403	Stramenopiles-Phytophthora_capsici_jgi34217	1.50E-11	
ConsensusfromContig3308	Stramenopiles-Phytophthora_capsici_jgi599	8.00E-23	
ConsensusfromContig1545	Stramenopiles-Phytophthora_capsici_jgi71568	2.20E-15	
ConsensusfromContig2232	Stramenopiles-Phytophthora_capsici_jgi73057	3.40E-26	
ConsensusfromContig1964	Stramenopiles-Phytophthora_capsici_jgi76252	2.70E-12	
ConsensusfromContig7122	Stramenopiles-Phytophthora_capsici_jgi76252	9.90E-17	
ConsensusfromContig2772	Stramenopiles-Phytophthora_capsici_jgi832	3.80E-25	
ConsensusfromContig2812	Stramenopiles-Phytophthora_capsici_jgi832	1.40E-24	
ConsensusfromContig1943	Stramenopiles-Phytophthora_capsici_jgi89700	5.70E-12	
ConsensusfromContig3170	Stramenopiles-Phytophthora_capsici_jgi89700	5.50E-32	
ConsensusfromContig7462	Stramenopiles-Phytophthora_parasitica_esgi222389680_4	3.80E-19	>FK934669 ppo3h07c08t.1 Phytophthora parasitica appressorium cDNA library Phytophthora parasitica cDNA, mRNA sequence.
ConsensusfromContig6956	Stramenopiles-Phytophthora_parasitica_esgi222413723_2	5.10E-12	>FK936523 ppo3h11n24t.1 Phytophthora parasitica appressorium cDNA library Phytophthora parasitica cDNA, mRNA sequence.
ConsensusfromContig5354	Stramenopiles-Phytophthora_parasitica_esgi68417099_1	6.60E-11	>DR439022 EST149_28_G08_T3 myc-149 Phytophthora parasitica cDNA clone EST149_28_G08 5', mRNA sequence.
ConsensusfromContig2238	Stramenopiles-Phytophthora_parasitica_esgi68419409_3	2.10E-21	>DR440922 EST149_28_B05_T3 myc-149 Phytophthora parasitica cDNA clone EST149_28_B05 5', mRNA sequence.
ConsensusfromContig1522	Stramenopiles-Phytophthora_ramorum_jgi38850	2.50E-14	
ConsensusfromContig4072	Stramenopiles-Phytophthora_ramorum_jgi38850	6.60E-14	
ConsensusfromContig6804	Stramenopiles-Phytophthora_ramorum_jgi38850	3.50E-16	
ConsensusfromContig7189	Stramenopiles-Phytophthora_ramorum_jgi40214	2.20E-16	
ConsensusfromContig1953	Stramenopiles-Phytophthora_ramorum_jgi50480	8.10E-25	
ConsensusfromContig1960	Stramenopiles-Phytophthora_ramorum_jgi50564	1.00E-82	
ConsensusfromContig6979	Stramenopiles-Phytophthora_ramorum_jgi71021	3.80E-30	
ConsensusfromContig5408	Stramenopiles-Phytophthora_ramorum_jgi72143	1.70E-28	
ConsensusfromContig5224	Stramenopiles-Phytophthora_ramorum_jgi72460	1.30E-83	
ConsensusfromContig1041	Stramenopiles-Phytophthora_ramorum_jgi72686	3.30E-37	
ConsensusfromContig3142	Stramenopiles-Phytophthora_ramorum_jgi75833	5.50E-19	
ConsensusfromContig6348	Stramenopiles-Phytophthora_ramorum_jgi75891	1.80E-25	

ConsensusfromContig6966	Stramenopiles-Phytophthora_ramorum_jgi75991	4.70E-27	
ConsensusfromContig6940	Stramenopiles-Phytophthora_ramorum_jgi76087	2.60E-25	
ConsensusfromContig1953	Stramenopiles-Phytophthora_ramorum_jgi76511	4.30E-46	
ConsensusfromContig5435	Stramenopiles-Phytophthora_ramorum_jgi77422	1.10E-15	
ConsensusfromContig2000	Stramenopiles-Phytophthora_ramorum_jgi78419	2.40E-27	
ConsensusfromContig2017	Stramenopiles-Phytophthora_ramorum_jgi82804	7.90E-22	
ConsensusfromContig5129	Stramenopiles-Phytophthora_ramorum_jgi83738	6.90E-15	
ConsensusfromContig5240	Stramenopiles-Phytophthora_ramorum_jgi84155	2.50E-28	
ConsensusfromContig1944	Stramenopiles-Phytophthora_ramorum_jgi84487	1.60E-35	
ConsensusfromContig1822	Stramenopiles-Phytophthora_ramorum_jgi84788	1.70E-12	
ConsensusfromContig4035	Stramenopiles-Phytophthora_ramorum_jgi85980	1.40E-13	
ConsensusfromContig2420	Stramenopiles-Phytophthora_ramorum_jgi86730	9.40E-21	
ConsensusfromContig5227	Stramenopiles-Phytophthora_ramorum_jgi94226	2.60E-27	
ConsensusfromContig6308	Stramenopiles-Phytophthora_ramorum_jgi94629	1.70E-23	
ConsensusfromContig6970	Stramenopiles-Phytophthora_ramorum_jgi95519	1.10E-13	
ConsensusfromContig2408	Stramenopiles-Phytophthora_ramorum_jgi96407	1.30E-17	
ConsensusfromContig923	Stramenopiles-Phytophthora_ramorum_jgi96955	6.60E-28	
ConsensusfromContig5168	Stramenopiles-Phytophthora_sojae_jgi108418	2.50E-22	
ConsensusfromContig1307	Stramenopiles-Phytophthora_sojae_jgi108909	2.60E-15	
ConsensusfromContig1307	Stramenopiles-Phytophthora_sojae_jgi108909	2.60E-15	
ConsensusfromContig3528	Stramenopiles-Phytophthora_sojae_jgi109096	2.30E-32	
ConsensusfromContig3528	Stramenopiles-Phytophthora_sojae_jgi109096	2.30E-32	
ConsensusfromContig2579	Stramenopiles-Phytophthora_sojae_jgi109150	1.60E-24	
ConsensusfromContig5531	Stramenopiles-Phytophthora_sojae_jgi109310	4.00E-14	
ConsensusfromContig3083	Stramenopiles-Phytophthora_sojae_jgi109343	1.70E-26	
ConsensusfromContig3135	Stramenopiles-Phytophthora_sojae_jgi109738	2.70E-13	
ConsensusfromContig3123	Stramenopiles-Phytophthora_sojae_jgi110545	3.20E-49	
ConsensusfromContig3123	Stramenopiles-Phytophthora_sojae_jgi110545	3.20E-49	
ConsensusfromContig2544	Stramenopiles-Phytophthora_sojae_jgi112609	3.80E-11	
ConsensusfromContig2741	Stramenopiles-Phytophthora_sojae_jgi120578	1.50E-21	
ConsensusfromContig2089	Stramenopiles-Phytophthora_sojae_jgi120633	7.60E-53	
ConsensusfromContig6478	Stramenopiles-Phytophthora_sojae_jgi123290	5.90E-33	
ConsensusfromContig1983	Stramenopiles-Phytophthora_sojae_jgi127244	1.90E-47	
ConsensusfromContig6075	Stramenopiles-Phytophthora_sojae_jgi127490	4.60E-56	
ConsensusfromContig679	Stramenopiles-Phytophthora_sojae_jgi127522	1.50E-37	
ConsensusfromContig2480	Stramenopiles-Phytophthora_sojae_jgi127909	3.10E-33	
ConsensusfromContig5123	Stramenopiles-Phytophthora_sojae_jgi128237	7.20E-39	
ConsensusfromContig3074	Stramenopiles-Phytophthora_sojae_jgi128674	1.70E-12	
ConsensusfromContig1954	Stramenopiles-Phytophthora_sojae_jgi128698	1.20E-31	
ConsensusfromContig3155	Stramenopiles-Phytophthora_sojae_jgi131304	9.20E-20	
ConsensusfromContig3432	Stramenopiles-Phytophthora_sojae_jgi131304	6.70E-16	
ConsensusfromContig5206	Stramenopiles-Phytophthora_sojae_jgi131304	5.90E-47	
ConsensusfromContig5288	Stramenopiles-Phytophthora_sojae_jgi131304	8.50E-31	
ConsensusfromContig1962	Stramenopiles-Phytophthora_sojae_jgi132210	2.20E-63	
ConsensusfromContig2941	Stramenopiles-Phytophthora_sojae_jgi133266	3.40E-14	
ConsensusfromContig1967	Stramenopiles-Phytophthora_sojae_jgi134863	8.70E-24	
ConsensusfromContig2283	Stramenopiles-Phytophthora_sojae_jgi134881	1.30E-53	
ConsensusfromContig2558	Stramenopiles-Phytophthora_sojae_jgi134881	3.50E-13	
ConsensusfromContig3132	Stramenopiles-Phytophthora_sojae_jgi136047	2.40E-65	
ConsensusfromContig8065	Stramenopiles-Phytophthora_sojae_jgi136424	2.20E-15	
ConsensusfromContig6922	Stramenopiles-Phytophthora_sojae_jgi137106	1.50E-53	
ConsensusfromContig3763	Stramenopiles-Phytophthora_sojae_jgi137435	1.60E-18	
ConsensusfromContig5130	Stramenopiles-Phytophthora_sojae_jgi138056	6.20E-29	
ConsensusfromContig5846	Stramenopiles-Phytophthora_sojae_jgi139358	1.60E-18	
ConsensusfromContig1998	Stramenopiles-Phytophthora_sojae_jgi139928	1.90E-46	
ConsensusfromContig5234	Stramenopiles-Phytophthora_sojae_jgi139928	2.20E-18	
ConsensusfromContig3086	Stramenopiles-Phytophthora_sojae_jgi140134	3.40E-22	
ConsensusfromContig3086	Stramenopiles-Phytophthora_sojae_jgi140134	3.40E-22	
ConsensusfromContig1976	Stramenopiles-Phytophthora_sojae_jgi140978	7.20E-22	
ConsensusfromContig7006	Stramenopiles-Phytophthora_sojae_jgi141480	1.40E-21	
ConsensusfromContig4789	Stramenopiles-Phytophthora_sojae_jgi141842	7.10E-12	
ConsensusfromContig7019	Stramenopiles-Phytophthora_sojae_jgi142568	3.70E-16	
ConsensusfromContig2715	Stramenopiles-Phytophthora_sojae_jgi142783	1.10E-37	
ConsensusfromContig2025	Stramenopiles-Phytophthora_sojae_jgi145353	1.00E-20	
ConsensusfromContig3449	Stramenopiles-Phytophthora_sojae_jgi156183	7.70E-12	
ConsensusfromContig7264	Stramenopiles-Phytophthora_sojae_jgi157656	4.20E-16	
ConsensusfromContig2503	Stramenopiles-Sargassum_binderi_esgi120455275_3	8.10E-20	>DV668945 SB00315 Sargassum binderi cDNA Library Sargassum binderi cDNA clone 105-C08-T3, mRNA sequence.
ConsensusfromContig3003	Stramenopiles-Sargassum_binderi_esgi120455275_3	3.40E-17	>DV668945 SB00315 Sargassum binderi cDNA Library Sargassum binderi cDNA clone 105-C08-T3, mRNA sequence.
ConsensusfromContig4632	Stramenopiles-Sargassum_binderi_esgi120455275_3	8.70E-18	>DV668945 SB00315 Sargassum binderi cDNA Library Sargassum binderi cDNA clone 105-C08-T3, mRNA sequence.
ConsensusfromContig5816	Stramenopiles-Sargassum_binderi_esgi120455275_3	7.80E-17	>DV668945 SB00315 Sargassum binderi cDNA Library Sargassum binderi cDNA clone 105-C08-T3, mRNA sequence.
ConsensusfromContig2495	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi223992843	1.70E-21	>XP_002286105 hypothetical protein THAPSDRAFT_267977 [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig5136	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi223993229	1.90E-45	>XP_002286298 predicted protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig5947	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi223995005	7.90E-13	>XP_002287186 hypothetical protein THAPSDRAFT_21161 [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig7036	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi223995005	1.40E-21	>XP_002287186 hypothetical protein THAPSDRAFT_21161 [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig4497	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi223996001	7.00E-19	>XP_002287674 member of the inositol monophosphatase protein family [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig5133	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi223996097	1.80E-55	>XP_002287722 hypothetical protein THAPSDRAFT_16605 [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig2971	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi223996827	4.40E-13	>XP_002288087 predicted protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig7186	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi223997364	1.40E-62	>XP_002288355 predicted protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig3081	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi223998927	1.00E-11	>XP_002289136 predicted protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig2045	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224000015	1.80E-19	>XP_002289680 cold-shock DNA-binding domain-containing protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig6425	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224000387	1.60E-36	>XP_002289866 alpha enolase [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig6996	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224000387	1.50E-72	>XP_002289866 alpha enolase [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig6846	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224001336	2.30E-12	>XP_002290340 predicted protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig2205	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224003733	1.80E-20	>XP_002291538 predicted protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig2391	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224004206	7.00E-13	>XP_002295754 predicted protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig2323	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224005430	5.60E-36	>XP_002296366 predicted protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig3065	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224005430	6.10E-49	>XP_002296366 predicted protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig7430	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224005430	2.30E-19	>XP_002296366 predicted protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig4318	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224007533	3.20E-14	>XP_002292726 predicted protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig6649	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224009732	7.90E-12	>XP_002293824 predicted protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig2061	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224010217	8.40E-19	>XP_002294066 hypothetical protein THAPSDRAFT_10111 [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig1985	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224010653	3.20E-29	>XP_002294284 predicted protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig7616	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224015006	1.40E-42	>XP_002297164 predicted protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig8469	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224015006	4.10E-26	>XP_002297164 predicted protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig1641	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224015006	1.50E-65	>XP_002297164 predicted protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig2310	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224015006	4.60E-37	>XP_002297164 predicted protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig2926	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224015006	8.80E-36	>XP_002297164 predicted protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig3535	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224015006	4.70E-13	>XP_002297164 predicted protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig4759	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224015006	1.20E-15	>XP_002297164 predicted protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig5194	Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224015006	2.90E-83	>XP_002297164 predicted protein [Thalassiosira pseudonana CCMP1335].

ConsensusfromContig5304Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224015006	4.20E-51	>XP_002297164 predicted protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig7055Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224015006	8.00E-60	>XP_002297164 predicted protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig5706Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224015210	1.20E-25	>XP_002297263 udp-galactose transporter-like protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig1205Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224015271	1.50E-12	>XP_002297293 predicted protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig5166Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224015271	1.10E-15	>XP_002297293 predicted protein [Thalassiosira pseudonana CCMP1335].
ConsensusfromContig3366Thermotogae-Thermosipho_africanus_TCF52B_gi217076847	7.50E-14	>YP_002334563 GTPase ObgE [Thermosipho africanus TCF52B].
ConsensusfromContig1964Thermotogae-Thermotoga_maritima_MSB8_gi15644466	7.60E-28	>NP_229518 DNA mismatch repair protein MutS [Thermotoga maritima MSB8].
ConsensusfromContig5748Thermotogae-Thermotoga_sp_RQ2_gi170288447	1.80E-13	>YP_001738685 ABC transporter transmembrane region [Thermotoga sp. RQ2].
ConsensusfromContig1939Vira-Acanthamoeba_polyphaga_mimivirus_gi55819085	2.70E-12	>YP_142560 helicase III/ VV D5-type ATPase (C-term) [Acanthamoeba polyphaga mimivirus].
ConsensusfromContig1981Vira-Acanthamoeba_polyphaga_mimivirus_gi55819085	2.60E-14	>YP_142560 helicase III/ VV D5-type ATPase (C-term) [Acanthamoeba polyphaga mimivirus].
ConsensusfromContig6949Vira-Acanthamoeba_polyphaga_mimivirus_gi55819085	1.80E-15	>YP_142560 helicase III/ VV D5-type ATPase (C-term) [Acanthamoeba polyphaga mimivirus].
ConsensusfromContig6957Vira-Ambystoma_tigrinum_virus_gi45686029	2.50E-44	>YP_003792 cytosine DNA methyltransferase [Ambystoma tigrinum virus].
ConsensusfromContig1949Vira-Flavobacterium_phage_11b_gi53793627	1.70E-64	>YP_112527 hypothetical protein PHG11b_51 [Flavobacterium phage 11b].
ConsensusfromContig5447Vira-Marseillevirus_gi284504057	6.00E-50	>YP_003406772 Dam-like adenine-specific DNA methylase [Marseillevirus].
ConsensusfromContig2041Vira-Ostreococcus_tauri_virus_1_gi290343528	4.70E-20	>YP_003494895 hypothetical protein OTV1_055 [Ostreococcus tauri virus 1].
ConsensusfromContig6985Vira-Ostreococcus_tauri_virus_1_gi290343528	1.20E-50	>YP_003494895 hypothetical protein OTV1_055 [Ostreococcus tauri virus 1].
ConsensusfromContig1982Vira-Ostreococcus_virus_OsV5_gi163955071	1.00E-20	>YP_001648175 hypothetical protein OsV5_098r [Ostreococcus virus OsV5].
ConsensusfromContig6939Vira-Ostreococcus_virus_OsV5_gi163955071	1.10E-18	>YP_001648175 hypothetical protein OsV5_098r [Ostreococcus virus OsV5].
ConsensusfromContig2271Vira-Ostreococcus_virus_OsV5_gi163955097	1.40E-62	>YP_001648201 hypothetical protein OsV5_124f [Ostreococcus virus OsV5].
ConsensusfromContig4297Vira-Paramecium_bursaria_Chlorella_virus_1_gi9631723	1.50E-13	>NP_048502 hypothetical protein PBCV1_A154L [Paramecium bursaria Chlorella virus 1].
ConsensusfromContig5593Vira-Paramecium_bursaria_Chlorella_virus_1_gi9631723	2.90E-13	>NP_048502 hypothetical protein PBCV1_A154L [Paramecium bursaria Chlorella virus 1].
ConsensusfromContig2146Vira-Paramecium_bursaria_Chlorella_virus_NY2A_gi157952703	1.80E-67	>YP_001497595 hypothetical protein NY2A_B399R [Paramecium bursaria Chlorella virus NY2A].
ConsensusfromContig3135Vira-Paramecium_bursaria_Chlorella_virus_NY2A_gi157952712	1.40E-30	>YP_001497604 hypothetical protein NY2A_B408R [Paramecium bursaria Chlorella virus NY2A].
ConsensusfromContig5192Vira-Paramecium_bursaria_Chlorella_virus_NY2A_gi157952712	1.70E-20	>YP_001497604 hypothetical protein NY2A_B408R [Paramecium bursaria Chlorella virus NY2A].
ConsensusfromContig6299Vira-Paramecium_bursaria_Chlorella_virus_NY2A_gi157952847	1.90E-14	>YP_001497739 hypothetical protein NY2A_B543L [Paramecium bursaria Chlorella virus NY2A].
ConsensusfromContig6981Vira-Prochlorococcus_phage_P_SSM2_gi61805950	3.80E-64	>YP_214310 hypothetical protein PSSM2_078 [Prochlorococcus phage P-SSM2].
ConsensusfromContig2076Vira-Prochlorococcus_phage_P_SSM2_gi61806058	1.40E-64	>YP_214418 DNA primase-helicase [Prochlorococcus phage P-SSM2].
ConsensusfromContig3688Vira-Pseudomonas_phage_D3112_gi38229130	3.10E-13	>NP_938225 hypothetical protein D3112p18 [Pseudomonas phage D3112].
ConsensusfromContig7965Viridiplantae-Arabidopsis_lyrata_jgi909113	1.20E-23	
ConsensusfromContig4576Viridiplantae-Arabidopsis_lyrata_jgi917605	1.40E-29	
ConsensusfromContig7372Viridiplantae-Arabidopsis_lyrata_subsp_lyrata_gi297791891	1.40E-11	>XP_002863830 hypothetical protein ARALYDRAFT_494835 [Arabidopsis lyrata subsp. lyrata].
ConsensusfromContig6968Viridiplantae-Arabidopsis_lyrata_subsp_lyrata_gi297807483	3.60E-16	>XP_002871625 hypothetical protein ARALYDRAFT_488306 [Arabidopsis lyrata subsp. lyrata].
ConsensusfromContig1988Viridiplantae-Arabidopsis_lyrata_subsp_lyrata_gi297812229	3.00E-49	>XP_002873998 predicted protein [Arabidopsis lyrata subsp. lyrata].
ConsensusfromContig5429Viridiplantae-Arabidopsis_lyrata_subsp_lyrata_gi297816236	4.00E-13	>XP_002876001 hypothetical protein ARALYDRAFT_485345 [Arabidopsis lyrata subsp. lyrata].
ConsensusfromContig7050Viridiplantae-Arabidopsis_lyrata_subsp_lyrata_gi297833172	6.20E-15	>XP_002884468 pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata].
ConsensusfromContig2012Viridiplantae-Arabidopsis_lyrata_subsp_lyrata_gi297837035	1.10E-81	>XP_002886399 F2K11.14 [Arabidopsis lyrata subsp. lyrata].
ConsensusfromContig3201Viridiplantae-Arabidopsis_lyrata_subsp_lyrata_gi297837451	5.80E-35	>XP_002886607 hypothetical protein ARALYDRAFT_893483 [Arabidopsis lyrata subsp. lyrata].
ConsensusfromContig6576Viridiplantae-Arabidopsis_thaliana_gi145326682	3.50E-13	>NP_001077788 protein kinase family protein [Arabidopsis thaliana].
ConsensusfromContig2054Viridiplantae-Arabidopsis_thaliana_gi15221781	4.40E-11	>NP_173866 polcalcin, putative / calcium-binding pollen allergen, putative [Arabidopsis thaliana].
ConsensusfromContig2751Viridiplantae-Arabidopsis_thaliana_gi15229253	7.40E-24	>NP_187074 SEC (secret agent); transferase, transferring glycosyl groups [Arabidopsis thaliana].
ConsensusfromContig5237Viridiplantae-Arabidopsis_thaliana_gi15241536	7.40E-76	>NP_196434 EMB1873 (EMBRYO DEFECTIVE 1873); agmatine deiminase [Arabidopsis thaliana].
ConsensusfromContig4295Viridiplantae-Arabidopsis_thaliana_gi18379060	1.10E-11	>NP_563676 splicing factor Prp18 family protein [Arabidopsis thaliana].
ConsensusfromContig6949Viridiplantae-Arabidopsis_thaliana_gi18400170	4.90E-29	>NP_566464 ATBFRUCT1; beta-fructofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana].
ConsensusfromContig6937Viridiplantae-Arabidopsis_thaliana_gi18405537	7.80E-12	>NP_564700 ATP binding / nucleotide binding / phenylalanine-tRNA ligase [Arabidopsis thaliana].
ConsensusfromContig3104Viridiplantae-Arabidopsis_thaliana_gi18420352	3.10E-15	>NP_568405 TSL (TOUSLED); kinase/ protein serine/threonine kinase [Arabidopsis thaliana].
ConsensusfromContig1418Viridiplantae-Arabidopsis_thaliana_gi238478996	1.50E-18	>NP_001154456 protein kinase family protein [Arabidopsis thaliana].
ConsensusfromContig1675Viridiplantae-Arabidopsis_thaliana_gi42569952	7.70E-11	>NP_182116 U-box domain-containing protein [Arabidopsis thaliana].
ConsensusfromContig3579Viridiplantae-Arabidopsis_thaliana_gi42572703	2.70E-17	>NP_974447 alpha-galactosidase, putative / melibiase, putative / alpha-D-galactoside galactohydrolase, putative [Arabidopsis thaliana].
ConsensusfromContig6367Viridiplantae-Chlamydomonas_reinhardtii_gi159462830	3.10E-18	>XP_001689645 predicted protein [Chlamydomonas reinhardtii].
ConsensusfromContig5104Viridiplantae-Chlamydomonas_reinhardtii_gi159462988	1.30E-58	>XP_001689724 flagellar associated protein [Chlamydomonas reinhardtii].
ConsensusfromContig6928Viridiplantae-Chlamydomonas_reinhardtii_gi159463184	6.70E-18	>XP_001689822 outer dynein arm-docking complex subunit 3 [Chlamydomonas reinhardtii].
ConsensusfromContig1988Viridiplantae-Chlamydomonas_reinhardtii_gi159463552	9.60E-16	>XP_001690006 alpha-galactosidase [Chlamydomonas reinhardtii].
ConsensusfromContig5298Viridiplantae-Chlamydomonas_reinhardtii_gi159463624	2.50E-45	>XP_001690042 ODA5-associated flagellar adenylate kinase [Chlamydomonas reinhardtii].
ConsensusfromContig2280Viridiplantae-Chlamydomonas_reinhardtii_gi159464257	9.30E-13	>XP_001690358 flagellar associated protein [Chlamydomonas reinhardtii].
ConsensusfromContig5143Viridiplantae-Chlamydomonas_reinhardtii_gi159464365	1.00E-54	>XP_001690412 hypothetical protein CHLREDRAFT_127918 [Chlamydomonas reinhardtii].
ConsensusfromContig2875Viridiplantae-Chlamydomonas_reinhardtii_gi159465629	8.10E-25	>XP_001691025 SNF2 superfamily protein [Chlamydomonas reinhardtii].
ConsensusfromContig2914Viridiplantae-Chlamydomonas_reinhardtii_gi159466756	1.10E-30	>XP_001691564 predicted protein [Chlamydomonas reinhardtii].
ConsensusfromContig5774Viridiplantae-Chlamydomonas_reinhardtii_gi159466778	2.40E-13	>XP_001691575 flagellar associated protein [Chlamydomonas reinhardtii].
ConsensusfromContig7376Viridiplantae-Chlamydomonas_reinhardtii_gi159466778	1.10E-25	>XP_001691575 flagellar associated protein [Chlamydomonas reinhardtii].
ConsensusfromContig2029Viridiplantae-Chlamydomonas_reinhardtii_gi159466868	2.30E-27	>XP_001691620 predicted protein [Chlamydomonas reinhardtii].
ConsensusfromContig2070Viridiplantae-Chlamydomonas_reinhardtii_gi159467701	2.00E-27	>XP_001692030 seryl-trna synthetase [Chlamydomonas reinhardtii].
ConsensusfromContig4125Viridiplantae-Chlamydomonas_reinhardtii_gi159468965	3.60E-26	>XP_001692638 splicing factor, component of the U4/U6-U5 snRNP complex [Chlamydomonas reinhardtii].
ConsensusfromContig2111Viridiplantae-Chlamydomonas_reinhardtii_gi159469339	2.80E-34	>XP_001692825 flagellar associated protein [Chlamydomonas reinhardtii].
ConsensusfromContig5335Viridiplantae-Chlamydomonas_reinhardtii_gi159471125	6.70E-23	>XP_001693707 membrane AAA-metalloprotease [Chlamydomonas reinhardtii].
ConsensusfromContig6137Viridiplantae-Chlamydomonas_reinhardtii_gi159471159	4.40E-13	>XP_001693724 hypothetical protein CHLREDRAFT_143431 [Chlamydomonas reinhardtii].
ConsensusfromContig6990Viridiplantae-Chlamydomonas_reinhardtii_gi159471159	6.50E-22	>XP_001693724 hypothetical protein CHLREDRAFT_143431 [Chlamydomonas reinhardtii].
ConsensusfromContig2297Viridiplantae-Chlamydomonas_reinhardtii_gi159471892	3.10E-14	>XP_001694090 xanthine dehydrogenase/oxidase [Chlamydomonas reinhardtii].
ConsensusfromContig2344Viridiplantae-Chlamydomonas_reinhardtii_gi159472581	2.40E-65	>XP_001694423 DNA polymerase zeta [Chlamydomonas reinhardtii].
ConsensusfromContig5454Viridiplantae-Chlamydomonas_reinhardtii_gi159472725	9.00E-13	>XP_001694495 predicted protein [Chlamydomonas reinhardtii].
ConsensusfromContig3144Viridiplantae-Chlamydomonas_reinhardtii_gi159474138	7.30E-48	>XP_001695186 predicted protein [Chlamydomonas reinhardtii].
ConsensusfromContig2236Viridiplantae-Chlamydomonas_reinhardtii_gi159475034	4.60E-32	>XP_001695628 hypothetical protein CHLREDRAFT_119255 [Chlamydomonas reinhardtii].
ConsensusfromContig2054Viridiplantae-Chlamydomonas_reinhardtii_gi159476220	1.70E-51	>XP_001696209 hypothetical protein CHLREDRAFT_97982 [Chlamydomonas reinhardtii].
ConsensusfromContig7361Viridiplantae-Chlamydomonas_reinhardtii_gi159479046	1.50E-19	>XP_001697609 CTP synthase [Chlamydomonas reinhardtii].
ConsensusfromContig3164Viridiplantae-Chlamydomonas_reinhardtii_gi159479968	1.60E-22	>XP_001698058 ubiquinone/menaquinone biosynthesis methyltransferase-like protein [Chlamydomonas reinhardtii].
ConsensusfromContig5109Viridiplantae-Chlamydomonas_reinhardtii_gi159481169	4.60E-74	>XP_001698654 peptidyl-prolyl cis-trans isomerase, cyclophilin-type [Chlamydomonas reinhardtii].
ConsensusfromContig5383Viridiplantae-Chlamydomonas_reinhardtii_gi159481524	4.50E-16	>XP_001698829 hypothetical protein CHLREDRAFT_193339 [Chlamydomonas reinhardtii].
ConsensusfromContig3245Viridiplantae-Chlamydomonas_reinhardtii_gi159481672	4.30E-65	>XP_001698902 flagellar associated protein [Chlamydomonas reinhardtii].
ConsensusfromContig2020Viridiplantae-Chlamydomonas_reinhardtii_gi159484978	3.10E-20	>XP_001700526 adenylate kinase 3 [Chlamydomonas reinhardtii].
ConsensusfromContig2187Viridiplantae-Chlamydomonas_reinhardtii_gi159486127	1.80E-26	>XP_001701095 glutathione S-transferase [Chlamydomonas reinhardtii].
ConsensusfromContig6193Viridiplantae-Chlamydomonas_reinhardtii_gi159486455	9.90E-26	>XP_001701255 beta-cop [Chlamydomonas reinhardtii].
ConsensusfromContig1988Viridiplantae-Chlamydomonas_reinhardtii_gi159486875	1.90E-132	>XP_001701462 TRP protein for ciliary function [Chlamydomonas reinhardtii].
ConsensusfromContig3129Viridiplantae-Chlamydomonas_reinhardtii_gi159486875	2.40E-52	>XP_001701462 TRP protein for ciliary function [Chlamydomonas reinhardtii].
ConsensusfromContig1949Viridiplantae-Chlamydomonas_reinhardtii_gi159488807	3.00E-11	>XP_001702394 hypothetical protein CHLREDRAFT_108061 [Chlamydomonas reinhardtii].
ConsensusfromContig2030Viridiplantae-Chlamydomonas_reinhardtii_gi159489044	4.40E-26	>XP_001702507 predicted protein [Chlamydomonas reinhardtii].
ConsensusfromContig2030Viridiplantae-Chlamydomonas_reinhardtii_gi159489044	4.40E-26	>XP_001702507 predicted protein [Chlamydomonas reinhardtii].
ConsensusfromContig3157Viridiplantae-Chlamydomonas_reinhardtii_gi159489398	2.30E-21	>XP_001702684 predicted protein [Chlamydomonas reinhardtii].
ConsensusfromContig5100Viridiplantae-Chlamydomonas_reinhardtii_gi159489398	3.20E-32	>XP_001702684 predicted protein [Chlamydomonas reinhardtii].
ConsensusfromContig5440Viridiplantae-Chlamydomonas_reinhardtii_gi159489398	6.90E-19	>XP_001702684 predicted protein [Chlamydomonas reinhardtii].
ConsensusfromContig5492Viridiplantae-Chlamydomonas_reinhardtii_gi159489398	5.50E-18	>XP_001702684 predicted protein [Chlamydomonas reinhardtii].
ConsensusfromContig2070Viridiplantae-Chlamydomonas_reinhardtii_gi159489894	6.30E-69	>XP_001702926 protein associated with central pair microtubule complex [Chlamydomonas reinhardtii].
ConsensusfromContig5154Viridiplantae-Chlorella_NC64A_jgi11287	2.10E-11	
ConsensusfromContig5154Viridiplantae-Chlorella_NC64A_jgi11287	2.10E-11	
ConsensusfromContig1938Viridiplantae-Chlorella_NC64A_jgi137433	6.90E-33	
ConsensusfromContig2198Viridiplantae-Chlorella_NC64A_jgi138020	9.20E-11	
ConsensusfromContig2374Viridiplantae-Chlorella_NC64A_jgi138531	5.10E-26	
ConsensusfromContig3000Viridiplantae-Chlorella_NC64A_jgi142022	6.50E-16	
ConsensusfromContig5393Viridiplantae-Chlorella_NC64A_jgi143607	6.60E-17	
ConsensusfromContig5212Viridiplantae-Chlorella_NC64A_jgi14696	5.50E-18	
ConsensusfromContig5171Viridiplantae-Chlorella_NC64A_jgi16754	3.10E-11	
ConsensusfromContig4737Viridiplantae-Chlorella_NC64A_jgi19238	1.00E-13	

ConsensusfromContig1293	Viridiplantae-Chlorella_NC64A_jgi22364	2.30E-16	
ConsensusfromContig4779	Viridiplantae-Chlorella_NC64A_jgi27284	1.70E-21	
ConsensusfromContig2007	Viridiplantae-Chlorella_NC64A_jgi27424	3.00E-77	
ConsensusfromContig2730	Viridiplantae-Chlorella_NC64A_jgi27424	3.70E-12	
ConsensusfromContig6924	Viridiplantae-Chlorella_NC64A_jgi29747	7.60E-108	
ConsensusfromContig2169	Viridiplantae-Chlorella_NC64A_jgi31062	1.20E-17	
ConsensusfromContig6934	Viridiplantae-Chlorella_NC64A_jgi33357	7.00E-84	
ConsensusfromContig3201	Viridiplantae-Chlorella_NC64A_jgi33359	1.10E-49	
ConsensusfromContig2145	Viridiplantae-Chlorella_NC64A_jgi33543	1.30E-48	
ConsensusfromContig5785	Viridiplantae-Chlorella_NC64A_jgi33771	1.00E-13	
ConsensusfromContig2031	Viridiplantae-Chlorella_NC64A_jgi36950	3.50E-16	
ConsensusfromContig3443	Viridiplantae-Chlorella_NC64A_jgi49216	1.40E-16	
ConsensusfromContig7093	Viridiplantae-Chlorella_NC64A_jgi58027	6.90E-21	
ConsensusfromContig5625	Viridiplantae-Chlorella_vulgaris_jgi15201	5.70E-15	
ConsensusfromContig5615	Viridiplantae-Chlorella_vulgaris_jgi26008	2.00E-16	
ConsensusfromContig2303	Viridiplantae-Chlorella_vulgaris_jgi28184	2.40E-57	
ConsensusfromContig3148	Viridiplantae-Chlorella_vulgaris_jgi30390	5.80E-31	
ConsensusfromContig5125	Viridiplantae-Chlorella_vulgaris_jgi38516	2.80E-19	
ConsensusfromContig7002	Viridiplantae-Chlorella_vulgaris_jgi39061	2.40E-92	
ConsensusfromContig5953	Viridiplantae-Chlorella_vulgaris_jgi42582	5.30E-39	
ConsensusfromContig2116	Viridiplantae-Chlorella_vulgaris_jgi42910	3.90E-16	
ConsensusfromContig2230	Viridiplantae-Chlorella_vulgaris_jgi59290	7.00E-11	
ConsensusfromContig3169	Viridiplantae-Chlorella_vulgaris_jgi59290	1.80E-14	
ConsensusfromContig55	Viridiplantae-Chlorella_vulgaris_jgi64152	1.80E-36	
ConsensusfromContig5232	Viridiplantae-Chlorella_vulgaris_jgi70067	9.90E-18	
ConsensusfromContig7126	Viridiplantae-Chlorella_vulgaris_jgi72307	1.30E-39	
ConsensusfromContig4613	Viridiplantae-Chlorella_vulgaris_jgi72314	8.00E-17	
ConsensusfromContig5488	Viridiplantae-Chlorella_vulgaris_jgi73177	9.30E-23	
ConsensusfromContig1993	Viridiplantae-Chlorella_vulgaris_jgi74507	3.80E-14	
ConsensusfromContig3390	Viridiplantae-Chlorella_vulgaris_jgi81272	1.30E-14	
ConsensusfromContig5301	Viridiplantae-Chlorella_vulgaris_jgi82458	1.10E-37	
ConsensusfromContig1007	Viridiplantae-Chlorella_vulgaris_jgi82806	1.50E-12	
ConsensusfromContig7103	Viridiplantae-Chlorella_vulgaris_jgi83828	2.90E-12	
ConsensusfromContig5219	Viridiplantae-Chlorella_vulgaris_jgi84104	1.90E-46	
ConsensusfromContig2423	Viridiplantae-Glycine_max_jgiGlyma01g01120	3.80E-31	
ConsensusfromContig3776	Viridiplantae-Glycine_max_jgiGlyma01g20680	9.00E-11	
ConsensusfromContig5510	Viridiplantae-Glycine_max_jgiGlyma01g20680	1.30E-22	
ConsensusfromContig7094	Viridiplantae-Glycine_max_jgiGlyma02g11240	4.50E-43	
ConsensusfromContig1995	Viridiplantae-Glycine_max_jgiGlyma03g22860	2.00E-26	
ConsensusfromContig1044	Viridiplantae-Glycine_max_jgiGlyma03g26620	9.50E-13	
ConsensusfromContig4409	Viridiplantae-Glycine_max_jgiGlyma03g41200	4.40E-22	
ConsensusfromContig5872	Viridiplantae-Glycine_max_jgiGlyma04g03210	3.10E-18	
ConsensusfromContig6673	Viridiplantae-Glycine_max_jgiGlyma05g30430	4.30E-15	
ConsensusfromContig4064	Viridiplantae-Glycine_max_jgiGlyma05g31270	6.90E-14	
ConsensusfromContig7129	Viridiplantae-Glycine_max_jgiGlyma05g34630	5.30E-36	
ConsensusfromContig1394	Viridiplantae-Glycine_max_jgiGlyma06g11040	5.30E-16	
ConsensusfromContig6785	Viridiplantae-Glycine_max_jgiGlyma06g19780	5.20E-19	
ConsensusfromContig5120	Viridiplantae-Glycine_max_jgiGlyma07g00430	4.70E-236	
ConsensusfromContig2435	Viridiplantae-Glycine_max_jgiGlyma07g16120	2.50E-66	
ConsensusfromContig2624	Viridiplantae-Glycine_max_jgiGlyma07g24440	1.70E-15	
ConsensusfromContig2723	Viridiplantae-Glycine_max_jgiGlyma09g07170	1.80E-11	
ConsensusfromContig6947	Viridiplantae-Glycine_max_jgiGlyma09g39270	3.50E-22	
ConsensusfromContig5104	Viridiplantae-Glycine_max_jgiGlyma09g40990	2.80E-52	
ConsensusfromContig5706	Viridiplantae-Glycine_max_jgiGlyma10g30050	4.40E-12	
ConsensusfromContig1989	Viridiplantae-Glycine_max_jgiGlyma10g43710	1.70E-16	
ConsensusfromContig5211	Viridiplantae-Glycine_max_jgiGlyma11g04150	3.20E-35	
ConsensusfromContig1088	Viridiplantae-Glycine_max_jgiGlyma11g11500	8.90E-17	
ConsensusfromContig2219	Viridiplantae-Glycine_max_jgiGlyma11g12120	4.40E-32	
ConsensusfromContig6937	Viridiplantae-Glycine_max_jgiGlyma11g33970	7.60E-15	
ConsensusfromContig1096	Viridiplantae-Glycine_max_jgiGlyma13g07460	7.40E-21	
ConsensusfromContig1198	Viridiplantae-Glycine_max_jgiGlyma13g24570	3.30E-12	
ConsensusfromContig2419	Viridiplantae-Glycine_max_jgiGlyma13g28290	9.90E-13	
ConsensusfromContig5967	Viridiplantae-Glycine_max_jgiGlyma14g00290	8.70E-12	
ConsensusfromContig6938	Viridiplantae-Glycine_max_jgiGlyma14g10850	7.80E-39	
ConsensusfromContig5116	Viridiplantae-Glycine_max_jgiGlyma15g15370	1.10E-79	
ConsensusfromContig6351	Viridiplantae-Glycine_max_jgiGlyma16g15820	9.60E-12	
ConsensusfromContig2731	Viridiplantae-Glycine_max_jgiGlyma16g31730	1.80E-23	
ConsensusfromContig5207	Viridiplantae-Glycine_max_jgiGlyma16g33510	1.30E-31	
ConsensusfromContig2163	Viridiplantae-Glycine_max_jgiGlyma18g02960	6.60E-104	
ConsensusfromContig1964	Viridiplantae-Glycine_max_jgiGlyma18g05080	2.30E-48	
ConsensusfromContig2484	Viridiplantae-Glycine_max_jgiGlyma18g14640	4.60E-13	
ConsensusfromContig6868	Viridiplantae-Glycine_max_jgiGlyma18g44210	7.70E-21	
ConsensusfromContig6994	Viridiplantae-Glycine_max_jgiGlyma18g46370	2.70E-11	
ConsensusfromContig1748	Viridiplantae-Glycine_max_jgiGlyma19g45310	1.20E-12	
ConsensusfromContig7367	Viridiplantae-Glycine_max_jgiGlyma20g20600	6.10E-15	
ConsensusfromContig6932	Viridiplantae-Glycine_max_jgiGlyma20g27760	7.90E-13	
ConsensusfromContig2020	Viridiplantae-Helicosporidium_sp_tbHEL00000431_3	7.30E-14	
ConsensusfromContig2020	Viridiplantae-Helicosporidium_sp_tbHEL00000431_3	7.30E-14	
ConsensusfromContig4080	Viridiplantae-Mesostigma_viride_esContig1584_3	4.60E-13	
ConsensusfromContig1512	Viridiplantae-Mesostigma_viride_esContig1911_1	4.50E-21	
ConsensusfromContig1547	Viridiplantae-Mesostigma_viride_esContig495_4	4.10E-11	
ConsensusfromContig5262	Viridiplantae-Mesostigma_viride_esgi60424227_2	1.60E-16	>DN255617 Meso02785 Mesostigma vegetative library Mesostigma viride cDNA clone Meso2a18e09.t7, mRNA sequence.
ConsensusfromContig4750	Viridiplantae-Mesostigma_viride_esgi60425116_1	5.30E-26	>DN256506 Meso01958 Mesostigma vegetative library Mesostigma viride cDNA clone Meso2a30b09.t7, mRNA sequence.
ConsensusfromContig1972	Viridiplantae-Micromonas_sp_RCC299_gi255070343	1.80E-37	>XP_002507253 dynein 18 kDa light chain, flagellar outer arm [Micromonas sp. RCC299].
ConsensusfromContig6926	Viridiplantae-Micromonas_sp_RCC299_gi255070981	2.90E-48	>XP_002507572 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig4145	Viridiplantae-Micromonas_sp_RCC299_gi255071527	9.90E-12	>XP_002499438 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig5401	Viridiplantae-Micromonas_sp_RCC299_gi255071609	3.60E-38	>XP_002499479 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig3439	Viridiplantae-Micromonas_sp_RCC299_gi255071795	7.50E-16	>XP_002499572 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig4549	Viridiplantae-Micromonas_sp_RCC299_gi255071803	1.70E-13	>XP_002499576 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig5138	Viridiplantae-Micromonas_sp_RCC299_gi255072315	7.60E-14	>XP_002499832 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig5243	Viridiplantae-Micromonas_sp_RCC299_gi255073039	3.60E-21	>XP_002500194 aminotransferase/S-adenosyl-L-homocysteine hydrolase [Micromonas sp. RCC299].
ConsensusfromContig6973	Viridiplantae-Micromonas_sp_RCC299_gi255073045	1.00E-23	>XP_002500197 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig2455	Viridiplantae-Micromonas_sp_RCC299_gi255073165	3.30E-14	>XP_002500257 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig1363	Viridiplantae-Micromonas_sp_RCC299_gi255073339	1.00E-28	>XP_002500344 dynein heavy chain [Micromonas sp. RCC299].
ConsensusfromContig2098	Viridiplantae-Micromonas_sp_RCC299_gi255074405	1.10E-27	>XP_002500877 voltage-gated ion channel superfamily [Micromonas sp. RCC299].
ConsensusfromContig2421	Viridiplantae-Micromonas_sp_RCC299_gi255074405	8.90E-17	>XP_002500877 voltage-gated ion channel superfamily [Micromonas sp. RCC299].
ConsensusfromContig5105	Viridiplantae-Micromonas_sp_RCC299_gi255074405	1.20E-34	>XP_002500877 voltage-gated ion channel superfamily [Micromonas sp. RCC299].
ConsensusfromContig6982	Viridiplantae-Micromonas_sp_RCC299_gi255074405	1.10E-14	>XP_002500877 voltage-gated ion channel superfamily [Micromonas sp. RCC299].
ConsensusfromContig5115	Viridiplantae-Micromonas_sp_RCC299_gi255074565	1.20E-22	>XP_002500957 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig2357	Viridiplantae-Micromonas_sp_RCC299_gi255074823	5.40E-17	>XP_002501086 predicted protein [Micromonas sp. RCC299].

ConsensusfromContig6924Viridiplantae-Micromonas_sp_RCC299_gi255074985	8.40E-101	>XP_002501167 mitochondrial carrier family [Micromonas sp. RCC299].
ConsensusfromContig3136Viridiplantae-Micromonas_sp_RCC299_gi255075035	1.40E-131	>XP_002501192 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig6975Viridiplantae-Micromonas_sp_RCC299_gi255075035	3.00E-47	>XP_002501192 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig6218Viridiplantae-Micromonas_sp_RCC299_gi255075773	3.00E-12	>XP_002501561 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig2000Viridiplantae-Micromonas_sp_RCC299_gi255076683	1.60E-42	>XP_002502014 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig2021Viridiplantae-Micromonas_sp_RCC299_gi255076683	6.70E-19	>XP_002502014 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig5381Viridiplantae-Micromonas_sp_RCC299_gi255076683	3.70E-16	>XP_002502014 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig1637Viridiplantae-Micromonas_sp_RCC299_gi255076922	9.20E-17	>XP_002502124 glycosyltransferase family 66 protein [Micromonas sp. RCC299].
ConsensusfromContig5101Viridiplantae-Micromonas_sp_RCC299_gi255077380	1.30E-17	>XP_002502332 voltage-gated ion channel superfamily [Micromonas sp. RCC299].
ConsensusfromContig6952Viridiplantae-Micromonas_sp_RCC299_gi255077976	9.00E-61	>XP_002502568 inositol monophosphatase [Micromonas sp. RCC299].
ConsensusfromContig4975Viridiplantae-Micromonas_sp_RCC299_gi255078036	1.20E-12	>XP_002502598 hypothetical protein MICPUN_113339 [Micromonas sp. RCC299].
ConsensusfromContig2815Viridiplantae-Micromonas_sp_RCC299_gi255078282	9.90E-17	>XP_002502721 voltage-gated ion channel superfamily [Micromonas sp. RCC299].
ConsensusfromContig5223Viridiplantae-Micromonas_sp_RCC299_gi255078282	2.60E-111	>XP_002502721 voltage-gated ion channel superfamily [Micromonas sp. RCC299].
ConsensusfromContig2946Viridiplantae-Micromonas_sp_RCC299_gi255078676	7.40E-11	>XP_002502918 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig2366Viridiplantae-Micromonas_sp_RCC299_gi255078758	7.80E-31	>XP_002502959 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig7132Viridiplantae-Micromonas_sp_RCC299_gi255079104	3.60E-11	>XP_002503132 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig3123Viridiplantae-Micromonas_sp_RCC299_gi255079270	3.90E-12	>XP_002503215 derlin-like protein [Micromonas sp. RCC299].
ConsensusfromContig1969Viridiplantae-Micromonas_sp_RCC299_gi255079404	6.40E-26	>XP_002503282 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig2446Viridiplantae-Micromonas_sp_RCC299_gi255079510	1.10E-29	>XP_002503335 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig1945Viridiplantae-Micromonas_sp_RCC299_gi255079708	5.90E-187	>XP_002503434 ATP-binding cassette superfamily [Micromonas sp. RCC299].
ConsensusfromContig5117Viridiplantae-Micromonas_sp_RCC299_gi255079954	5.10E-91	>XP_002503557 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig6384Viridiplantae-Micromonas_sp_RCC299_gi255079982	1.30E-11	>XP_002503571 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig1954Viridiplantae-Micromonas_sp_RCC299_gi255081134	8.60E-68	>XP_002507789 voltage-gated ion channel superfamily [Micromonas sp. RCC299].
ConsensusfromContig2334Viridiplantae-Micromonas_sp_RCC299_gi255081134	5.80E-12	>XP_002507789 voltage-gated ion channel superfamily [Micromonas sp. RCC299].
ConsensusfromContig3100Viridiplantae-Micromonas_sp_RCC299_gi255081134	5.00E-11	>XP_002507789 voltage-gated ion channel superfamily [Micromonas sp. RCC299].
ConsensusfromContig5208Viridiplantae-Micromonas_sp_RCC299_gi255081134	3.40E-23	>XP_002507789 voltage-gated ion channel superfamily [Micromonas sp. RCC299].
ConsensusfromContig2172Viridiplantae-Micromonas_sp_RCC299_gi255081600	1.20E-21	>XP_002508022 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig2873Viridiplantae-Micromonas_sp_RCC299_gi255081600	3.40E-15	>XP_002508022 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig7266Viridiplantae-Micromonas_sp_RCC299_gi255082011	1.30E-14	>XP_002508224 cytoplasmic dynein heavy chain 1b [Micromonas sp. RCC299].
ConsensusfromContig5623Viridiplantae-Micromonas_sp_RCC299_gi255082157	1.80E-17	>XP_002508297 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig5316Viridiplantae-Micromonas_sp_RCC299_gi255082548	4.50E-26	>XP_002504260 ATP-binding cassette superfamily [Micromonas sp. RCC299].
ConsensusfromContig5122Viridiplantae-Micromonas_sp_RCC299_gi255082742	2.00E-16	>XP_002504357 resistance-nodulation-cell division superfamily [Micromonas sp. RCC299].
ConsensusfromContig6946Viridiplantae-Micromonas_sp_RCC299_gi255082972	1.20E-26	>XP_002504472 voltage-gated ion channel superfamily [Micromonas sp. RCC299].
ConsensusfromContig1973Viridiplantae-Micromonas_sp_RCC299_gi255083008	6.10E-18	>XP_002504490 mRNA capping enzyme [Micromonas sp. RCC299].
ConsensusfromContig6936Viridiplantae-Micromonas_sp_RCC299_gi255084101	7.60E-27	>XP_002508625 ATP-binding cassette superfamily [Micromonas sp. RCC299].
ConsensusfromContig5114Viridiplantae-Micromonas_sp_RCC299_gi255084457	1.30E-68	>XP_002508803 voltage-gated ion channel superfamily [Micromonas sp. RCC299].
ConsensusfromContig6941Viridiplantae-Micromonas_sp_RCC299_gi255084457	3.90E-136	>XP_002508803 voltage-gated ion channel superfamily [Micromonas sp. RCC299].
ConsensusfromContig6992Viridiplantae-Micromonas_sp_RCC299_gi255084457	5.20E-22	>XP_002508803 voltage-gated ion channel superfamily [Micromonas sp. RCC299].
ConsensusfromContig2019Viridiplantae-Micromonas_sp_RCC299_gi255084469	1.60E-30	>XP_002508809 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig5169Viridiplantae-Micromonas_sp_RCC299_gi255084469	2.90E-27	>XP_002508809 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig2896Viridiplantae-Micromonas_sp_RCC299_gi255084810	1.50E-11	>XP_002504836 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig3126Viridiplantae-Micromonas_sp_RCC299_gi255085038	1.50E-33	>XP_002504950 voltage-gated ion channel superfamily [Micromonas sp. RCC299].
ConsensusfromContig5660Viridiplantae-Micromonas_sp_RCC299_gi255085088	1.80E-16	>XP_002504975 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig5157Viridiplantae-Micromonas_sp_RCC299_gi255085096	3.50E-17	>XP_002504979 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig6925Viridiplantae-Micromonas_sp_RCC299_gi255085476	3.10E-88	>XP_002505169 dynein, 70 kDa intermediate chain, flagellar outer arm [Micromonas sp. RCC299].
ConsensusfromContig6949Viridiplantae-Micromonas_sp_RCC299_gi255085476	2.10E-17	>XP_002505169 dynein, 70 kDa intermediate chain, flagellar outer arm [Micromonas sp. RCC299].
ConsensusfromContig5640Viridiplantae-Micromonas_sp_RCC299_gi255085682	2.40E-11	>XP_002505272 radial spoke protein 7 [Micromonas sp. RCC299].
ConsensusfromContig6999Viridiplantae-Micromonas_sp_RCC299_gi255085682	1.90E-36	>XP_002505272 radial spoke protein 7 [Micromonas sp. RCC299].
ConsensusfromContig5173Viridiplantae-Micromonas_sp_RCC299_gi255085907	1.20E-28	>XP_002508920 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig1980Viridiplantae-Micromonas_sp_RCC299_gi255085925	1.40E-11	>XP_002508929 voltage-gated ion channel superfamily [Micromonas sp. RCC299].
ConsensusfromContig3681Viridiplantae-Micromonas_sp_RCC299_gi255086407	1.60E-13	>XP_002509170 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig5667Viridiplantae-Micromonas_sp_RCC299_gi255087216	1.00E-17	>XP_002505531 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig5110Viridiplantae-Micromonas_sp_RCC299_gi255087500	1.20E-70	>XP_002505673 major facilitator superfamily [Micromonas sp. RCC299].
ConsensusfromContig2293Viridiplantae-Micromonas_sp_RCC299_gi255088199	7.80E-11	>XP_002506022 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig5236Viridiplantae-Micromonas_sp_RCC299_gi255088603	5.90E-53	>XP_002506224 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig4661Viridiplantae-Micromonas_sp_RCC299_gi255089244	2.00E-16	>XP_002506544 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig3037Viridiplantae-Micromonas_sp_RCC299_gi255089400	3.00E-16	>XP_002506622 dynein gamma chain, flagellar outer arm [Micromonas sp. RCC299].
ConsensusfromContig2050Viridiplantae-Micromonas_sp_RCC299_gi255089414	1.60E-18	>XP_002506629 predicted protein [Micromonas sp. RCC299].
ConsensusfromContig3713Viridiplantae-Oryza_sativa_Japonica_Group_gi115433976	1.30E-15	>NP_001041746 Os01g0102000 [Oryza sativa Japonica Group].
ConsensusfromContig5172Viridiplantae-Oryza_sativa_Japonica_Group_gi115436094	4.20E-24	>NP_001042805 Os01g0296200 [Oryza sativa Japonica Group].
ConsensusfromContig2276Viridiplantae-Oryza_sativa_Japonica_Group_gi115439209	2.60E-17	>NP_001043884 Os01g0681900 [Oryza sativa Japonica Group].
ConsensusfromContig5422Viridiplantae-Oryza_sativa_Japonica_Group_gi115439553	1.20E-50	>NP_001044056 Os01g0713900 [Oryza sativa Japonica Group].
ConsensusfromContig3043Viridiplantae-Oryza_sativa_Japonica_Group_gi115439761	1.90E-12	>NP_001044160 Os01g0733200 [Oryza sativa Japonica Group].
ConsensusfromContig2779Viridiplantae-Oryza_sativa_Japonica_Group_gi115445361	7.60E-13	>NP_001046460 Os02g0255000 [Oryza sativa Japonica Group].
ConsensusfromContig5118Viridiplantae-Oryza_sativa_Japonica_Group_gi115447363	4.20E-12	>NP_001047461 Os02g0621500 [Oryza sativa Japonica Group].
ConsensusfromContig6988Viridiplantae-Oryza_sativa_Japonica_Group_gi115448721	1.40E-12	>NP_001048140 Os02g0752200 [Oryza sativa Japonica Group].
ConsensusfromContig2006Viridiplantae-Oryza_sativa_Japonica_Group_gi115455785	8.10E-62	>NP_001051493 Os03g0786900 [Oryza sativa Japonica Group].
ConsensusfromContig2068Viridiplantae-Oryza_sativa_Japonica_Group_gi115461296	5.40E-60	>NP_001054248 Os04g0675500 [Oryza sativa Japonica Group].
ConsensusfromContig7057Viridiplantae-Oryza_sativa_Japonica_Group_gi115461651	5.70E-25	>NP_001054425 Os05g0107600 [Oryza sativa Japonica Group].
ConsensusfromContig6034Viridiplantae-Oryza_sativa_Japonica_Group_gi115462751	1.90E-12	>NP_001054975 Os05g0230600 [Oryza sativa Japonica Group].
ConsensusfromContig5239Viridiplantae-Oryza_sativa_Japonica_Group_gi115469764	4.70E-32	>NP_001058481 Os06g0701100 [Oryza sativa Japonica Group].
ConsensusfromContig6960Viridiplantae-Oryza_sativa_Japonica_Group_gi115471661	6.30E-96	>NP_001059429 Os07g0405100 [Oryza sativa Japonica Group].
ConsensusfromContig5106Viridiplantae-Oryza_sativa_Japonica_Group_gi115472935	1.30E-11	>NP_001060066 Os07g0573300 [Oryza sativa Japonica Group].
ConsensusfromContig5635Viridiplantae-Oryza_sativa_Japonica_Group_gi115474617	1.60E-30	>NP_001060905 Os08g0127700 [Oryza sativa Japonica Group].
ConsensusfromContig2047Viridiplantae-Oryza_sativa_Japonica_Group_gi115480025	6.40E-14	>NP_001063606 Os09g0506000 [Oryza sativa Japonica Group].
ConsensusfromContig1177Viridiplantae-Oryza_sativa_Japonica_Group_gi115489820	1.20E-16	>NP_001067397 Os12g0640800 [Oryza sativa Japonica Group].
ConsensusfromContig2560Viridiplantae-Oryza_sativa_Japonica_Group_gi297598845	8.60E-11	>NP_001046319 Os02g0220700 [Oryza sativa Japonica Group].
ConsensusfromContig5110Viridiplantae-Oryza_sativa_Japonica_Group_gi297607725	2.00E-43	>NP_001060485 Os07g0651500 [Oryza sativa Japonica Group].
ConsensusfromContig6813Viridiplantae-Oryza_sativa_Japonica_Group_gi297723699	1.80E-11	>NP_001174213 Os05g0143500 [Oryza sativa Japonica Group].
ConsensusfromContig2033Viridiplantae-Oryza_sativa_Japonica_Group_gi297727649	4.70E-22	>NP_001176188 Os10g0457932 [Oryza sativa Japonica Group].
ConsensusfromContig6668Viridiplantae-Ostreococcus_lucimarinus_CCE9901_gi145342057	1.90E-14	>XP_001416112 predicted protein [Ostreococcus lucimarinus CCE9901].
ConsensusfromContig2028Viridiplantae-Ostreococcus_lucimarinus_CCE9901_gi145342431	5.00E-23	>XP_001416186 Asparagine synthase (glutamine-hydrolyzing) related protein [Ostreococcus lucimarinus CCE9901].
ConsensusfromContig7006Viridiplantae-Ostreococcus_lucimarinus_CCE9901_gi145345433	2.90E-12	>XP_001417215 predicted protein [Ostreococcus lucimarinus CCE9901].
ConsensusfromContig1867Viridiplantae-Ostreococcus_lucimarinus_CCE9901_gi145345747	2.80E-30	>XP_001417362 predicted protein [Ostreococcus lucimarinus CCE9901].
ConsensusfromContig3517Viridiplantae-Ostreococcus_lucimarinus_CCE9901_gi145347643	3.40E-23	>XP_001418272 predicted protein [Ostreococcus lucimarinus CCE9901].
ConsensusfromContig5171Viridiplantae-Ostreococcus_lucimarinus_CCE9901_gi145350022	1.60E-41	>XP_001419423 predicted protein [Ostreococcus lucimarinus CCE9901].
ConsensusfromContig2267Viridiplantae-Ostreococcus_lucimarinus_CCE9901_gi145352193	1.60E-14	>XP_001420439 VIC family transporter: potassium ion channel subfamily H [Ostreococcus lucimarinus CCE9901].
ConsensusfromContig3040Viridiplantae-Ostreococcus_lucimarinus_CCE9901_gi145352433	8.40E-39	>XP_001420553 predicted protein [Ostreococcus lucimarinus CCE9901].
ConsensusfromContig2381Viridiplantae-Ostreococcus_lucimarinus_CCE9901_gi145353141	5.10E-28	>XP_001420883 predicted protein [Ostreococcus lucimarinus CCE9901].
ConsensusfromContig1711Viridiplantae-Ostreococcus_lucimarinus_CCE9901_gi145354210	9.60E-22	>XP_001421384 predicted protein [Ostreococcus lucimarinus CCE9901].
ConsensusfromContig4719Viridiplantae-Ostreococcus_lucimarinus_CCE9901_gi145356736	1.20E-26	>XP_001422582 predicted protein [Ostreococcus lucimarinus CCE9901].
ConsensusfromContig5853Viridiplantae-Ostreococcus_RCC809_jgi20242	7.90E-20	
ConsensusfromContig1958Viridiplantae-Ostreococcus_RCC809_jgi31045	1.60E-11	
ConsensusfromContig2738Viridiplantae-Ostreococcus_RCC809_jgi33474	8.20E-15	
ConsensusfromContig2137Viridiplantae-Ostreococcus_RCC809_jgi37803	1.30E-11	
ConsensusfromContig5709Viridiplantae-Ostreococcus_RCC809_jgi38046	9.10E-26	
ConsensusfromContig5183Viridiplantae-Ostreococcus_RCC809_jgi39140	7.20E-11	
ConsensusfromContig7120Viridiplantae-Ostreococcus_RCC809_jgi40186	1.30E-16	
ConsensusfromContig6957Viridiplantae-Ostreococcus_RCC809_jgi54958	2.70E-43	
ConsensusfromContig4521Viridiplantae-Ostreococcus_RCC809_jgi59036	2.70E-11	

ConsensusfromContig4521Viridiplantae-Ostreococcus_RCC809_jgi59036	2.70E-11	
ConsensusfromContig8205Viridiplantae-Ostreococcus_RCC809_jgi61040	3.40E-16	
ConsensusfromContig1968Viridiplantae-Ostreococcus_RCC809_jgi61285	8.80E-79	
ConsensusfromContig5387Viridiplantae-Ostreococcus_RCC809_jgi64013	8.10E-50	
ConsensusfromContig2703Viridiplantae-Ostreococcus_RCC809_jgi90882	1.70E-18	
ConsensusfromContig2100Viridiplantae-Ostreococcus_RCC809_jgi91452	1.10E-12	
ConsensusfromContig6960Viridiplantae-Ostreococcus_RCC809_jgi94531	1.10E-27	
ConsensusfromContig1961Viridiplantae-Ostreococcus_RCC809_jgi96587	5.70E-23	
ConsensusfromContig2262Viridiplantae-Ostreococcus_tauri_jgi11183	1.90E-11	
ConsensusfromContig5104Viridiplantae-Ostreococcus_tauri_jgi11263	1.90E-59	
ConsensusfromContig1991Viridiplantae-Ostreococcus_tauri_jgi13907	1.30E-13	
ConsensusfromContig1967Viridiplantae-Ostreococcus_tauri_jgi15076	1.10E-25	
ConsensusfromContig2572Viridiplantae-Ostreococcus_tauri_jgi15076	1.80E-26	
ConsensusfromContig4758Viridiplantae-Ostreococcus_tauri_jgi17421	4.40E-15	
ConsensusfromContig3486Viridiplantae-Ostreococcus_tauri_jgi20417	4.30E-19	
ConsensusfromContig7021Viridiplantae-Ostreococcus_tauri_jgi22334	8.40E-12	
ConsensusfromContig2047Viridiplantae-Ostreococcus_tauri_jgi24585	1.70E-13	
ConsensusfromContig5376Viridiplantae-Ostreococcus_tauri_jgi29311	3.70E-20	
ConsensusfromContig1970Viridiplantae-Ostreococcus_tauri_jgi32247	3.60E-12	
ConsensusfromContig1937Viridiplantae-Ostreococcus_tauri_jgi32559	1.70E-128	
ConsensusfromContig2200Viridiplantae-Ostreococcus_tauri_jgi32559	5.50E-35	
ConsensusfromContig2413Viridiplantae-Ostreococcus_tauri_jgi32640	1.70E-16	
ConsensusfromContig2386Viridiplantae-Ostreococcus_tauri_jgi36859	7.70E-14	
ConsensusfromContig5952Viridiplantae-Ostreococcus_tauri_jgi4500	5.60E-13	
ConsensusfromContig2746Viridiplantae-Ostreococcus_tauri_jgi5760	5.90E-20	
ConsensusfromContig1975Viridiplantae-Ostreococcus_tauri_jgi5986	5.10E-36	
ConsensusfromContig2391Viridiplantae-Ostreococcus_tauri_jgi917	1.80E-22	
ConsensusfromContig5108Viridiplantae-Ostreococcus_tauri_jgi9258	5.50E-27	
ConsensusfromContig7135Viridiplantae-Physcomitrella_patens_subsp_patens_gi167997261	2.10E-71	>XP_001751337 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig2649Viridiplantae-Physcomitrella_patens_subsp_patens_gi168003994	3.80E-16	>XP_001754697 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig2670Viridiplantae-Physcomitrella_patens_subsp_patens_gi168005774	2.40E-13	>XP_001755585 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig7010Viridiplantae-Physcomitrella_patens_subsp_patens_gi168018019	7.60E-15	>XP_001761544 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig7010Viridiplantae-Physcomitrella_patens_subsp_patens_gi168018019	7.60E-15	>XP_001761544 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig2892Viridiplantae-Physcomitrella_patens_subsp_patens_gi168018551	4.70E-26	>XP_001761809 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig5100Viridiplantae-Physcomitrella_patens_subsp_patens_gi168019895	4.00E-269	>XP_001762479 SWR1 complex protein, SNF2 family DNA-dependent ATPase [Physcomitrella patens subsp. patens].
ConsensusfromContig5129Viridiplantae-Physcomitrella_patens_subsp_patens_gi168022959	8.20E-24	>XP_001764006 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig5102Viridiplantae-Physcomitrella_patens_subsp_patens_gi168023077	2.30E-138	>XP_001764065 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig1962Viridiplantae-Physcomitrella_patens_subsp_patens_gi168023292	1.50E-26	>XP_001764172 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig750 Viridiplantae-Physcomitrella_patens_subsp_patens_gi168024352	3.20E-32	>XP_001764700 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig6757Viridiplantae-Physcomitrella_patens_subsp_patens_gi168025127	1.20E-15	>XP_001765086 ATP-binding cassette transporter, subfamily B, member 3, group TAP protein PpABCB3 [Physcomitrella patens subsp. patens].
ConsensusfromContig2222Viridiplantae-Physcomitrella_patens_subsp_patens_gi168025520	3.40E-29	>XP_001765282 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig2013Viridiplantae-Physcomitrella_patens_subsp_patens_gi168026035	1.30E-13	>XP_001765538 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig4304Viridiplantae-Physcomitrella_patens_subsp_patens_gi168026740	1.20E-11	>XP_001765889 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig2031Viridiplantae-Physcomitrella_patens_subsp_patens_gi168026772	9.80E-41	>XP_001765905 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig5100Viridiplantae-Physcomitrella_patens_subsp_patens_gi168027429	4.20E-14	>XP_001766232 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig2216Viridiplantae-Physcomitrella_patens_subsp_patens_gi168027493	7.20E-15	>XP_001766264 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig6214Viridiplantae-Physcomitrella_patens_subsp_patens_gi168027706	3.10E-19	>XP_001766370 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig2190Viridiplantae-Physcomitrella_patens_subsp_patens_gi168029847	5.60E-21	>XP_001767436 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig3127Viridiplantae-Physcomitrella_patens_subsp_patens_gi168030360	5.70E-103	>XP_001767691 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig4826Viridiplantae-Physcomitrella_patens_subsp_patens_gi168030396	3.00E-12	>XP_001767709 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig5178Viridiplantae-Physcomitrella_patens_subsp_patens_gi168032073	3.40E-55	>XP_001768544 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig5165Viridiplantae-Physcomitrella_patens_subsp_patens_gi168033971	2.50E-24	>XP_001769487 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig2445Viridiplantae-Physcomitrella_patens_subsp_patens_gi168036068	1.80E-19	>XP_001770530 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig5337Viridiplantae-Physcomitrella_patens_subsp_patens_gi168038680	2.10E-13	>XP_001771828 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig3239Viridiplantae-Physcomitrella_patens_subsp_patens_gi168038761	4.60E-23	>XP_001771868 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig6953Viridiplantae-Physcomitrella_patens_subsp_patens_gi168040912	7.50E-13	>XP_001772937 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig1691Viridiplantae-Physcomitrella_patens_subsp_patens_gi168041683	7.10E-18	>XP_001773320 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig7428Viridiplantae-Physcomitrella_patens_subsp_patens_gi168044454	3.70E-25	>XP_001774696 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig5238Viridiplantae-Physcomitrella_patens_subsp_patens_gi168047732	9.90E-32	>XP_001776323 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig2948Viridiplantae-Physcomitrella_patens_subsp_patens_gi168047754	1.50E-27	>XP_001776334 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig2372Viridiplantae-Physcomitrella_patens_subsp_patens_gi168049041	1.20E-23	>XP_001776973 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig6201Viridiplantae-Physcomitrella_patens_subsp_patens_gi168051272	9.20E-18	>XP_001778079 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig5436Viridiplantae-Physcomitrella_patens_subsp_patens_gi168054036	8.60E-21	>XP_001779439 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig6151Viridiplantae-Physcomitrella_patens_subsp_patens_gi168056699	1.20E-13	>XP_001780356 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig8228Viridiplantae-Physcomitrella_patens_subsp_patens_gi168057842	5.60E-43	>XP_001780921 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig2045Viridiplantae-Physcomitrella_patens_subsp_patens_gi168067594	4.00E-76	>XP_001785697 predicted protein [Physcomitrella patens subsp. patens].
ConsensusfromContig3078Viridiplantae-Polytomella_parva_tbPOL00001656_1	2.40E-14	
ConsensusfromContig3122Viridiplantae-Populus_trichocarpa_gi224053669	8.90E-44	>XP_002297920 predicted protein [Populus trichocarpa].
ConsensusfromContig5133Viridiplantae-Populus_trichocarpa_gi224062968	6.40E-14	>XP_002300953 predicted protein [Populus trichocarpa].
ConsensusfromContig3074Viridiplantae-Populus_trichocarpa_gi224063387	2.60E-30	>XP_002301123 predicted protein [Populus trichocarpa].
ConsensusfromContig2058Viridiplantae-Populus_trichocarpa_gi224068957	8.40E-91	>XP_002326240 predicted protein [Populus trichocarpa].
ConsensusfromContig2876Viridiplantae-Populus_trichocarpa_gi224081881	3.60E-12	>XP_002306513 predicted protein [Populus trichocarpa].
ConsensusfromContig2545Viridiplantae-Populus_trichocarpa_gi224082152	4.60E-11	>XP_002306583 predicted protein [Populus trichocarpa].
ConsensusfromContig6022Viridiplantae-Populus_trichocarpa_gi224083155	2.80E-28	>XP_002306955 calcium dependent protein kinase 27 [Populus trichocarpa].
ConsensusfromContig2638Viridiplantae-Populus_trichocarpa_gi224091769	6.30E-13	>XP_002309347 predicted protein [Populus trichocarpa].
ConsensusfromContig2041Viridiplantae-Populus_trichocarpa_gi224100361	7.40E-49	>XP_002311847 chromatin remodeling complex subunit [Populus trichocarpa].
ConsensusfromContig2222Viridiplantae-Populus_trichocarpa_gi224101049	1.20E-31	>XP_002312121 predicted protein [Populus trichocarpa].
ConsensusfromContig2087Viridiplantae-Populus_trichocarpa_gi224102637	4.00E-48	>XP_002312758 predicted protein [Populus trichocarpa].
ConsensusfromContig2077Viridiplantae-Populus_trichocarpa_gi224106716	2.90E-11	>XP_002314259 predicted protein [Populus trichocarpa].
ConsensusfromContig2438Viridiplantae-Populus_trichocarpa_gi224106986	1.90E-15	>XP_002314333 multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa].
ConsensusfromContig5195Viridiplantae-Populus_trichocarpa_gi224112120	9.50E-27	>XP_002316089 predicted protein [Populus trichocarpa].
ConsensusfromContig7043Viridiplantae-Populus_trichocarpa_gi224112467	1.30E-19	>XP_002316201 predicted protein [Populus trichocarpa].
ConsensusfromContig6980Viridiplantae-Populus_trichocarpa_gi224120122	4.70E-12	>XP_002318247 predicted protein [Populus trichocarpa].
ConsensusfromContig3804Viridiplantae-Populus_trichocarpa_gi224120178	1.10E-12	>XP_002318264 predicted protein [Populus trichocarpa].
ConsensusfromContig1981Viridiplantae-Populus_trichocarpa_gi224124420	1.70E-25	>XP_002319327 predicted protein [Populus trichocarpa].
ConsensusfromContig1939Viridiplantae-Populus_trichocarpa_gi224127294	1.20E-39	>XP_002329242 predicted protein [Populus trichocarpa].
ConsensusfromContig6938Viridiplantae-Populus_trichocarpa_gi224138670	4.10E-26	>XP_002322872 predicted protein [Populus trichocarpa].
ConsensusfromContig7098Viridiplantae-Populus_trichocarpa_gi224139002	4.60E-35	>XP_002322955 predicted protein [Populus trichocarpa].
ConsensusfromContig6287Viridiplantae-Populus_trichocarpa_gi224145796	1.40E-11	>XP_002336263 predicted protein [Populus trichocarpa].
ConsensusfromContig1169Viridiplantae-Prototheca_wickerhamii_tbPWL00001414_2	4.30E-11	
ConsensusfromContig2072Viridiplantae-Ricinus_communis_gi255556418	3.90E-33	>XP_002519243 conserved hypothetical protein [Ricinus communis].
ConsensusfromContig5367Viridiplantae-Ricinus_communis_gi255569438	7.70E-17	>XP_002525686 microfibril-associated protein, putative [Ricinus communis].
ConsensusfromContig5458Viridiplantae-Ricinus_communis_gi255570356	8.80E-18	>XP_002526137 ATP-binding cassette transporter, putative [Ricinus communis].
ConsensusfromContig2397Viridiplantae-Ricinus_communis_gi255573724	2.50E-24	>XP_002527783 phosphoglucomutase, putative [Ricinus communis].
ConsensusfromContig1564Viridiplantae-Ricinus_communis_gi255577258	7.20E-11	>XP_002529511 abc transporter, putative [Ricinus communis].
ConsensusfromContig2370Viridiplantae-Ricinus_communis_gi255580905	8.20E-18	>XP_002531271 conserved hypothetical protein [Ricinus communis].
ConsensusfromContig3806Viridiplantae-Ricinus_communis_gi255582350	9.80E-13	>XP_002531964 beta-hexosaminidase, putative [Ricinus communis].
ConsensusfromContig7007Viridiplantae-Ricinus_communis_gi255593791	1.90E-20	>XP_002535952 conserved hypothetical protein [Ricinus communis].
ConsensusfromContig7076Viridiplantae-Ricinus_communis_gi255606103	1.70E-11	>XP_002538503 hypothetical protein RCOM_1858570 [Ricinus communis].
ConsensusfromContig5134Viridiplantae-Scenedesmus_obliquus_tbSOL00000049_3	7.30E-23	

ConsensusfromContig3126Viridiplantae-Scenedesmus_obliquus_tbSOL00000053_1	9.40E-35	
ConsensusfromContig6937Viridiplantae-Scenedesmus_obliquus_tbSOL00001365_2	1.40E-16	
ConsensusfromContig3081Viridiplantae-Scenedesmus_obliquus_tbSOL00005756_3	6.80E-11	
ConsensusfromContig5147Viridiplantae-Sorghum_bicolor_gi242035709	6.50E-28	>XP_002465249 hypothetical protein SORBIDRAFT_01g034960 [Sorghum bicolor].
ConsensusfromContig2047Viridiplantae-Sorghum_bicolor_gi242036247	4.90E-97	>XP_002465518 hypothetical protein SORBIDRAFT_01g040400 [Sorghum bicolor].
ConsensusfromContig5368Viridiplantae-Sorghum_bicolor_gi242036247	2.80E-25	>XP_002465518 hypothetical protein SORBIDRAFT_01g040400 [Sorghum bicolor].
ConsensusfromContig5197Viridiplantae-Sorghum_bicolor_gi242040923	2.60E-29	>XP_002467856 hypothetical protein SORBIDRAFT_01g035280 [Sorghum bicolor].
ConsensusfromContig2032Viridiplantae-Sorghum_bicolor_gi242044156	4.70E-24	>XP_002459949 hypothetical protein SORBIDRAFT_02g018590 [Sorghum bicolor].
ConsensusfromContig2523Viridiplantae-Sorghum_bicolor_gi242044796	7.10E-42	>XP_002460269 hypothetical protein SORBIDRAFT_02g025730 [Sorghum bicolor].
ConsensusfromContig6935Viridiplantae-Sorghum_bicolor_gi242046940	2.00E-31	>XP_002461216 hypothetical protein SORBIDRAFT_02g042960 [Sorghum bicolor].
ConsensusfromContig7119Viridiplantae-Sorghum_bicolor_gi242059027	6.70E-25	>XP_002458659 hypothetical protein SORBIDRAFT_03g037600 [Sorghum bicolor].
ConsensusfromContig6925Viridiplantae-Sorghum_bicolor_gi242064454	3.90E-159	>XP_002453516 hypothetical protein SORBIDRAFT_04g007170 [Sorghum bicolor].
ConsensusfromContig2399Viridiplantae-Sorghum_bicolor_gi242068613	3.90E-15	>XP_002449583 hypothetical protein SORBIDRAFT_05g019600 [Sorghum bicolor].
ConsensusfromContig2006Viridiplantae-Sorghum_bicolor_gi242071841	2.60E-24	>XP_002451197 hypothetical protein SORBIDRAFT_05g025690 [Sorghum bicolor].
ConsensusfromContig1971Viridiplantae-Sorghum_bicolor_gi242074296	4.50E-17	>XP_002447084 hypothetical protein SORBIDRAFT_06g028280 [Sorghum bicolor].
ConsensusfromContig1950Viridiplantae-Sorghum_bicolor_gi242080665	3.00E-160	>XP_002445101 hypothetical protein SORBIDRAFT_07g004090 [Sorghum bicolor].
ConsensusfromContig5225Viridiplantae-Sorghum_bicolor_gi242081169	1.70E-25	>XP_002445353 hypothetical protein SORBIDRAFT_07g011900 [Sorghum bicolor].
ConsensusfromContig5040Viridiplantae-Sorghum_bicolor_gi242084560	6.50E-25	>XP_002442705 hypothetical protein SORBIDRAFT_08g001540 [Sorghum bicolor].
ConsensusfromContig5201Viridiplantae-Sorghum_bicolor_gi242086032	4.30E-19	>XP_002443441 hypothetical protein SORBIDRAFT_08g019540 [Sorghum bicolor].
ConsensusfromContig7143Viridiplantae-Sorghum_bicolor_gi242088309	2.10E-18	>XP_002439987 hypothetical protein SORBIDRAFT_09g023900 [Sorghum bicolor].
ConsensusfromContig1983Viridiplantae-Sorghum_bicolor_gi242090009	1.30E-67	>XP_002440837 hypothetical protein SORBIDRAFT_09g008040 [Sorghum bicolor].
ConsensusfromContig2465Viridiplantae-Sorghum_bicolor_gi242090009	1.10E-26	>XP_002440837 hypothetical protein SORBIDRAFT_09g008040 [Sorghum bicolor].
ConsensusfromContig2101Viridiplantae-Sorghum_bicolor_gi242090075	1.10E-16	>XP_002440870 hypothetical protein SORBIDRAFT_09g010571 [Sorghum bicolor].
ConsensusfromContig2346Viridiplantae-Sorghum_bicolor_gi242095258	1.40E-35	>XP_002438119 hypothetical protein SORBIDRAFT_10g008350 [Sorghum bicolor].
ConsensusfromContig3135Viridiplantae-Vitis_vinifera_gi225425786	1.50E-79	>XP_002264178 PREDICTED: hypothetical protein [Vitis vinifera].
ConsensusfromContig7088Viridiplantae-Vitis_vinifera_gi225425865	1.10E-18	>XP_002266225 PREDICTED: hypothetical protein [Vitis vinifera].
ConsensusfromContig3165Viridiplantae-Vitis_vinifera_gi225431635	2.50E-12	>XP_002263149 PREDICTED: hypothetical protein [Vitis vinifera].
ConsensusfromContig3165Viridiplantae-Vitis_vinifera_gi225431635	2.50E-12	>XP_002263149 PREDICTED: hypothetical protein [Vitis vinifera].
ConsensusfromContig2424Viridiplantae-Vitis_vinifera_gi225434032	3.60E-49	>XP_002273924 PREDICTED: hypothetical protein [Vitis vinifera].
ConsensusfromContig3211Viridiplantae-Vitis_vinifera_gi225435030	1.80E-35	>XP_002281312 PREDICTED: hypothetical protein [Vitis vinifera].
ConsensusfromContig3230Viridiplantae-Vitis_vinifera_gi225435030	5.00E-36	>XP_002281312 PREDICTED: hypothetical protein [Vitis vinifera].
ConsensusfromContig6307Viridiplantae-Vitis_vinifera_gi225444181	4.80E-15	>XP_002269427 PREDICTED: hypothetical protein [Vitis vinifera].
ConsensusfromContig5139Viridiplantae-Vitis_vinifera_gi225444239	1.50E-62	>XP_002272332 PREDICTED: hypothetical protein [Vitis vinifera].
ConsensusfromContig5189Viridiplantae-Vitis_vinifera_gi225445282	3.30E-17	>XP_002281184 PREDICTED: hypothetical protein [Vitis vinifera].
ConsensusfromContig1941Viridiplantae-Vitis_vinifera_gi225445786	4.90E-33	>XP_002273966 PREDICTED: hypothetical protein [Vitis vinifera].
ConsensusfromContig2275Viridiplantae-Vitis_vinifera_gi225448651	5.40E-14	>XP_002279730 PREDICTED: hypothetical protein [Vitis vinifera].
ConsensusfromContig5456Viridiplantae-Vitis_vinifera_gi225451104	6.70E-12	>XP_002264421 PREDICTED: hypothetical protein [Vitis vinifera].
ConsensusfromContig5223Viridiplantae-Vitis_vinifera_gi225451185	4.40E-167	>XP_002273273 PREDICTED: hypothetical protein [Vitis vinifera].
ConsensusfromContig1576Viridiplantae-Vitis_vinifera_gi225452974	6.50E-13	>XP_002284370 PREDICTED: hypothetical protein [Vitis vinifera].
ConsensusfromContig4253Viridiplantae-Vitis_vinifera_gi225453559	7.80E-25	>XP_002266064 PREDICTED: hypothetical protein [Vitis vinifera].
ConsensusfromContig2693Viridiplantae-Vitis_vinifera_gi225453660	4.30E-15	>XP_002268369 PREDICTED: hypothetical protein [Vitis vinifera].
ConsensusfromContig2585Viridiplantae-Vitis_vinifera_gi225457201	1.40E-12	>XP_002280750 PREDICTED: hypothetical protein [Vitis vinifera].
ConsensusfromContig1977Viridiplantae-Vitis_vinifera_gi225457500	5.10E-144	>XP_002269119 PREDICTED: hypothetical protein [Vitis vinifera].
ConsensusfromContig2653Viridiplantae-Vitis_vinifera_gi225458631	4.00E-12	>XP_002284804 PREDICTED: hypothetical protein [Vitis vinifera].
ConsensusfromContig7305Viridiplantae-Vitis_vinifera_gi225462143	5.60E-11	>XP_002265401 PREDICTED: hypothetical protein [Vitis vinifera].
ConsensusfromContig6939Viridiplantae-Vitis_vinifera_gi225463717	3.90E-28	>XP_002263359 PREDICTED: hypothetical protein [Vitis vinifera].
ConsensusfromContig2316Viridiplantae-Vitis_vinifera_gi225469218	2.10E-16	>XP_002264031 PREDICTED: hypothetical protein [Vitis vinifera].
ConsensusfromContig5221Viridiplantae-Vitis_vinifera_gi225470152	2.20E-30	>XP_002267295 PREDICTED: hypothetical protein [Vitis vinifera].
ConsensusfromContig5370Viridiplantae-Zea_mays_gi212275712	2.00E-36	>NP_001130324 hypothetical protein LOC100191418 [Zea mays].
ConsensusfromContig1932Viridiplantae-Zea_mays_gi226500950	1.20E-32	>NP_001148011 sialin [Zea mays].
ConsensusfromContig5144Viridiplantae-Zea_mays_gi226502935	6.60E-34	>NP_001149934 pyridoxal kinase [Zea mays].
ConsensusfromContig2024Viridiplantae-Zea_mays_gi293335337	4.50E-23	>NP_001168335 hypothetical protein LOC100382103 [Zea mays].
ConsensusfromContig2168Viridiplantae-Zea_mays_gi293336498	4.40E-11	>NP_001169721 hypothetical protein LOC100383602 [Zea mays].

Table S7. Results of the phylogenomic analysis of contigs generated from the assembly of 454+Illumina data from MS584-11. The putative proteins were predicted using BLASTx, which were then used as a query against our local database and the output analyzed with *PhyloSort* (*S9*) to identify the different monophyletic groups. A total of 5231 maximum likelihood (PhyML) trees were returned by the pipeline.

Taxonomic Affinity	**aLRT $\geq$ 0.90**	**aLRT $\geq$ 0.70**
Monophyly with Metazoa	538	670
Monophyly with Viridiplantae	338	480
Monophyly with Stramenopiles	335	479
Monophyly with Haptophyta	240	355
Monophyly with Alveolata	252	376
Monophyly with Choanoflagellida	158	228
Monophyly with Fungi	136	200
Monophyly with Excavata	93	179
Monophyly with Rhodophyta	43	91
Monophyly with Amoebozoa	57	105
Monophyly with Rhizaria	16	24
Monophyly with Cryptophyta	6	22
Monophyly with Glaucophyta	11	24
Monophyly with Opisthokonta	5	9
Monophyly with Proteobacteria	130	188
Monophyly with Bacteroidetes	69	81
Monophyly with Actinobacteria	39	53
Monophyly with Chlamydiae-Verrumicrobia	32	47
Monophyly with Firmicutes	35	47
Monophyly with Cyanobacteria	25	31
Monophyly with Planctomycetes	18	26
Monophyly with Chloroflexi	6	9
Nonophyly with Archaea	5	8
Monophyly with Fibrobacteres	2	3
Monophyly with Elusimicrobia	0	0

Table S8. Gene ontology (GO) annotations of the 1683 Stramenopiles proteins that grouped at aLRT≥0.70 (using PhyML) with proteins encoded on MS584-11 contigs (454+Illumina assembly). The maximum likelihood phylogenetic approach provides strong evidence that the Stramenopiles and picobiliphyte proteins are putative homologs.

```
SeqName,length,score,eValue,hitName,GOs,Accession
Stramenopiles-Aureococcus_anophagefferens_jgi4399,257,283.493,1.62E-
74,gi|223996001|ref|XP_002287674.1|member of the inositol monophosphatase
protein family [Thalassiosira pseudonana CCMP1335] ,
GO:0004437,"XP_002287674.1,EED95117.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi223996001,274,567,8.25E-
160,gi|223996001|ref|XP_002287674.1|member of the inositol monophosphatase
protein family [Thalassiosira pseudonana CCMP1335] ,
GO:0004437,"XP_002287674.1,EED95117.1"
Stramenopiles-
Phytophthora_capsici_jgi123034,487,865.144,0,gi|301108605|ref|XP_002903384.1|ser
yl-tRNA synthetase [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0006412,GO:0005737,GO:0004812,GO:0006434,GO:0000166,GO:0006418,GO:
0004828","XP_002903384.1,EEY55808.1"
Stramenopiles-
Phytophthora_ramorum_jgi71791,408,773.467,0,gi|301122065|ref|XP_002908759.1|phos
phoglycerate kinase [Phytophthora infestans T30-4] ,"
GO:0016301,GO:0005737,GO:0016740,GO:0004618,GO:0006096","XP_002908759.1,EEY57573
.1"
Stramenopiles-
Phytophthora_capsici_jgi115330,429,807.364,0,gi|301122065|ref|XP_002908759.1|pho
sphoglycerate kinase [Phytophthora infestans T30-4] ,"
GO:0016301,GO:0005737,GO:0016740,GO:0004618,GO:0006096","XP_002908759.1,EEY57573
.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223997336,386,771.155,0,gi|223997336|ref|XP_
002288341.1|phosphoglycerate kinase [Thalassiosira pseudonana CCMP1335] ,"
GO:0016301,GO:0005737,GO:0016740,GO:0004618,GO:0006096","XP_002288341.1,EED93777
.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224003799,536,1103.97,0,gi|224003799|ref|XP_
002291571.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0050662,GO:0009082,GO:0004455,GO:0055114,GO:0016491,GO:0003824,GO:0008152,GO:
0008652,GO:0005488","XP_002291571.1,EED91678.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219113938,521,1074.69,0,gi|219113938|ref
|XP_002176152.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0050662,GO:0009082,GO:0004455,GO:0055114,GO:0016491,GO:0003824,GO:0008152,GO:
0008652,GO:0005488","XP_002176152.1,EEC42859.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi136663,492,383.645,2.65E-
104,"gi|301110280|ref|XP_002904220.1|beta-D-xylosidase, putative [Phytophthora
infestans T30-4] ","
GO:0004553,GO:0016787,GO:0008152,GO:0005975,GO:0016798","XP_002904220.1,EEY54398
.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi218338,261,301.982,4.07E-
80,gi|219121946|ref|XP_002181317.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0016740,GO:0009165,GO:0019205,GO:0005737,GO:0005524,GO:0019201,GO:0016301,GO:
0016776,GO:0006139,GO:0004017","XP_002181317.1,EEC47240.1"
```

```
Stramenopiles-Aureococcus_anophagefferens_jgi20832,99,84.3445,4.42E-
15,gi|218192553|gb|EEC74980.1|hypothetical protein OsI_11022 [Oryza sativa
Indica Group],,EEC74980.1
Stramenopiles-Aureococcus_anophagefferens_jgi21097,332,253.062,3.35E-
65,"gi|241950087|ref|XP_002417766.1|kinesin, putative [Candida dubliniensis
CD36] ","
GO:0005524,GO:0000166,GO:0003777,GO:0007018,GO:0003774,GO:0005874","XP_002417766
.1,CAX45479.1"
Stramenopiles-
Phytophthora_sojae_jgi158154,515,775.778,0,gi|301108970|ref|XP_002903566.1|conse
rved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0032313,GO:0005622,GO:0005097","XP_002903566.1,EEY55342.1"
Stramenopiles-Phytophthora_capsici_jgi39575,373,483.026,2.51E-
134,gi|301108970|ref|XP_002903566.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,"
GO:0032313,GO:0005622,GO:0005097","XP_002903566.1,EEY55342.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi224010,325,481.871,4.13E-
134,gi|224007837|ref|XP_002292878.1|hypothetical protein THAPSDRAFT_36419
[Thalassiosira pseudonana CCMP1335] ,"
GO:0032313,GO:0005622,GO:0005097","XP_002292878.1,EED90074.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224007837,326,681.789,0,gi|224007837|ref|XP_
002292878.1|hypothetical protein THAPSDRAFT_36419 [Thalassiosira pseudonana
CCMP1335] ," GO:0032313,GO:0005622,GO:0005097","XP_002292878.1,EED90074.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219117716,330,685.256,0,gi|219117716|ref
|XP_002179648.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0032313,GO:0005622,GO:0005097","XP_002179648.1,EEC48634.1"
Stramenopiles-Aureococcus_anophagefferens_jgi18383,342,296.59,3.04E-
78,gi|219117716|ref|XP_002179648.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0032313,GO:0005622,GO:0005097","XP_002179648.1,EEC48634.1"
Stramenopiles-Aureococcus_anophagefferens_jgi8566,98,95.1301,2.26E-
18,gi|307103743|gb|EFN52001.1|hypothetical protein CHLNCDRAFT_139531 [Chlorella
variabilis],,EFN52001.1
Stramenopiles-Fragilariopsis_cylindrus_jgi270431,216,285.034,3.46E-
75,gi|219129981|ref|XP_002185154.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002185154.1,EEC43286.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224014945,518,1080.47,0,gi|224014945|ref|XP_
002297134.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002297134.1,EED86602.1"
Stramenopiles-Aureococcus_anophagefferens_jgi14749,148,130.568,5.28E-
29,gi|302841807|ref|XP_002952448.1|hypothetical protein VOLCADRAFT_62482 [Volvox
carteri f. nagariensis] ,,"XP_002952448.1,EFJ46591.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219119917,282,575.089,2.51E-
162,gi|219119917|ref|XP_002180709.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0004358,GO:0006526","XP_002180709.1,EEC48117.1"
Stramenopiles-Aureococcus_anophagefferens_jgi13438,263,192.586,4.01E-
47,gi|303285434|ref|XP_003062007.1|voltage-gated ion channel superfamily
[Micromonas pusilla CCMP1545] ,"
GO:0005216,GO:0005245,GO:0005244,GO:0006816,GO:0016021,GO:0016020,GO:0006811,GO:
0006810,GO:0005262,GO:0055085,GO:0005891","XP_003062007.1,EEH53719.1"
Stramenopiles-
Phytophthora_ramorum_jgi80812,594,846.655,0,gi|301113500|ref|XP_002998520.1|cons
```

```
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002998520.1,EEY69873.1"
Stramenopiles-Phytophthora_sojae_jgi143093,670,547.74,1.59E-
153,gi|301113500|ref|XP_002998520.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002998520.1,EEY69873.1"
Stramenopiles-Phytophthora_capsici_jgi117939,284,479.174,1.98E-
133,gi|301113500|ref|XP_002998520.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002998520.1,EEY69873.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi188713,872,895.19,0,"gi|219124711|ref|XP_002182641.1
|P1B, P type ATPase [Phaeodactylum tricornutum CCAP 1055/1] ","
GO:0016021,GO:0016020,GO:0030001,GO:0015662,GO:0016787,GO:0000166,GO:0005524,GO:
0006754,GO:0003824,GO:0046872,GO:0008152,GO:0016820","XP_002182641.1,EEC45928.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219124711,710,1446.41,0,"gi|219124711|re
f|XP_002182641.1|P1B, P type ATPase [Phaeodactylum tricornutum CCAP 1055/1] ","
GO:0016021,GO:0016020,GO:0030001,GO:0015662,GO:0016787,GO:0000166,GO:0005524,GO:
0006754,GO:0003824,GO:0046872,GO:0008152,GO:0016820","XP_002182641.1,EEC45928.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223998022,699,1412.9,0,gi|223998022|ref|XP_0
02288684.1|heavy-metal transporter [Thalassiosira pseudonana CCMP1335] ,"
GO:0016021,GO:0016020,GO:0030001,GO:0015662,GO:0016787,GO:0000166,GO:0005524,GO:
0006754,GO:0003824,GO:0008551,GO:0046872,GO:0008152,GO:0016820","XP_002288684.1,
EED94120.1"
Stramenopiles-
Phytophthora_capsici_jgi37523,812,1540.4,0,gi|190574131|ref|YP_001971976.1|putat
ive copper-transporting P-type ATPase [Stenotrophomonas maltophilia K279a] ,"
GO:0005507,GO:0016021,GO:0004008,GO:0016020,GO:0030001,GO:0015662,GO:0016787,GO:
0005524,GO:0006754,GO:0003824,GO:0046873,GO:0006825,GO:0046872,GO:0008152,GO:001
6820","YP_001971976.1,CAQ45675.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224000419,634,1301.96,0,gi|224000419|ref|XP_
002289882.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0016192,GO:0005509,GO:0016021","XP_002289882.1,EED93419.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi53426,1457,909.057,0,gi|73989050|ref|XP_856765.1|
PREDICTED: similar to CG12149-PA isoform 5 [Canis familiaris],,XP_856765.1
Stramenopiles-Aureococcus_anophagefferens_jgi55227,1070,595.89,9.53E-
168,gi|147902762|ref|NP_001083293.1|hypothetical protein LOC398849 [Xenopus
laevis] ,"
GO:0016887,GO:0005524,GO:0000166,GO:0017111","NP_001083293.1,AAH59997.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi25816,939,689.108,0,gi|147902762|ref|NP_001083293
.1|hypothetical protein LOC398849 [Xenopus laevis] ,"
GO:0016887,GO:0005524,GO:0000166,GO:0017111","NP_001083293.1,AAH59997.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi169419,1217,867.455,0,gi|170035063|ref|XP_001845391.
1|conserved hypothetical protein [Culex quinquefasciatus] ,"
GO:0016887,GO:0005524,GO:0000166,GO:0017111","XP_001845391.1,EDS40232.1"
Stramenopiles-Sargassum_binderi_esgi120454329_3,258,363.999,7.64E-
99,gi|219129518|ref|XP_002184934.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0016887,GO:0005524","XP_002184934.1,EEC43670.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219129518,1312,2690.99,0,gi|219129518|re
```

```
f|XP_002184934.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0016887,GO:0005524","XP_002184934.1,EEC43670.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223996932,1763,3617.78,0,gi|223996932|ref|XP
_002288139.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0016887,GO:0005524,GO:0016020,GO:0055085,GO:0030001,GO:0046873","XP_002288139
.1,EED93575.1"
Stramenopiles-Phytophthora_brassicae_esgi144592094_2,248,405.601,2.09E-
111,gi|301117896|ref|XP_002906676.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002906676.1,EEY66077.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219126241,331,682.174,0,gi|219126241|ref
|XP_002183370.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0055114,GO:0016491","XP_002183370.1,EEC45070.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi168477,337,363.229,2.46E-
98,gi|219126241|ref|XP_002183370.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0055114,GO:0016491","XP_002183370.1,EEC45070.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224000109,333,682.559,0,gi|224000109|ref|XP_
002289727.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0055114,GO:0016491","XP_002289727.1,EED93264.1"
Stramenopiles-Aureococcus_anophagefferens_jgi67678,317,90.8929,1.88E-
16,"gi|257454177|ref|ZP_05619448.1|hydrolase, alpha/beta fold family
[Enhydrobacter aerosaccus SK60] ", GO:0016787,"ZP_05619448.1,EEV23410.1"
Stramenopiles-Aureococcus_anophagefferens_jgi67319,357,90.8929,2.38E-
16,"gi|257454177|ref|ZP_05619448.1|hydrolase, alpha/beta fold family
[Enhydrobacter aerosaccus SK60] ", GO:0016787,"ZP_05619448.1,EEV23410.1"
Stramenopiles-Phytophthora_capsici_jgi118634,134,276.559,5.54E-
73,"gi|301120402|ref|XP_002907928.1|eukaryotic translation initiation factor 5,
putative [Phytophthora infestans T30-4] ","
GO:0003677,GO:0005634,GO:0006413,GO:0045941,GO:0016070,GO:0005515,GO:0003743,GO:
0016563,GO:0005488","XP_002907928.1,EEY61011.1"
Stramenopiles-
Phytophthora_sojae_jgi108320,449,672.159,0,"gi|301120402|ref|XP_002907928.1|euka
ryotic translation initiation factor 5, putative [Phytophthora infestans T30-4]
","
GO:0003677,GO:0005634,GO:0006413,GO:0045941,GO:0016070,GO:0005515,GO:0003743,GO:
0016563,GO:0005488","XP_002907928.1,EEY61011.1"
Stramenopiles-Phytophthora_parasitica_esgi68417513_2,305,312.383,4.33E-
83,"gi|301120402|ref|XP_002907928.1|eukaryotic translation initiation factor 5,
putative [Phytophthora infestans T30-4] ","
GO:0003677,GO:0005634,GO:0006413,GO:0045941,GO:0016070,GO:0005515,GO:0003743,GO:
0016563,GO:0005488","XP_002907928.1,EEY61011.1"
Stramenopiles-Phytophthora_parasitica_esgi68417514_1,242,251.906,4.38E-
65,"gi|301120402|ref|XP_002907928.1|eukaryotic translation initiation factor 5,
putative [Phytophthora infestans T30-4] ","
GO:0003677,GO:0005634,GO:0006413,GO:0045941,GO:0016070,GO:0005515,GO:0003743,GO:
0016563,GO:0005488","XP_002907928.1,EEY61011.1"
Stramenopiles-Blastocystis_hominis_tbBHL00001500_2,389,619.772,1.72E-
175,gi|300176740|emb|CBK24405.2|unnamed protein product [Blastocystis hominis],"
GO:0004616,GO:0050662,GO:0050661,GO:0055114,GO:0006098,GO:0016491,GO:0003824,GO:
0008152,GO:0005488",CBK24405.2
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224000295,490,1013.06,0,gi|224000295|ref|XP_
002289820.1|6-phosphogluconate dehydrogenase [Thalassiosira pseudonana CCMP1335]
```

```
,"
GO:0004616,GO:0050662,GO:0050661,GO:0055114,GO:0006098,GO:0016491,GO:0003824,GO:
0008152,GO:0005488","XP_002289820.1,EED93357.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219121442,1041,2167.89,0,gi|219121442|re
f|XP_002185945.1|G6PDH/6PGDH fusion protein [Phaeodactylum tricornutum CCAP
1055/1] ,"
GO:0004616,GO:0050662,GO:0050661,GO:0055114,GO:0006098,GO:0005975,GO:0004345,GO:
0016491,GO:0003824,GO:0006006,GO:0008152,GO:0005488","XP_002185945.1,ACI65415.1"
Stramenopiles-
Phytophthora_ramorum_jgi71783,490,983.015,0,gi|301106971|ref|XP_002902568.1|6-
phosphogluconate dehydrogenase [Phytophthora infestans T30-4] ,"
GO:0004616,GO:0050662,GO:0050661,GO:0055114,GO:0006098,GO:0016491,GO:0003824,GO:
0008152,GO:0005488","XP_002902568.1,AAL76320.1,EEY56494.1"
Stramenopiles-
Phytophthora_brassicae_esContig1378_2,433,748.043,0,gi|301106971|ref|XP_00290256
8.1|6-phosphogluconate dehydrogenase [Phytophthora infestans T30-4] ,"
GO:0004616,GO:0050662,GO:0050661,GO:0055114,GO:0006098,GO:0016491,GO:0003824,GO:
0008152,GO:0005488","XP_002902568.1,AAL76320.1,EEY56494.1"
Stramenopiles-
Phytophthora_capsici_jgi57299,490,995.727,0,gi|301106971|ref|XP_002902568.1|6-
phosphogluconate dehydrogenase [Phytophthora infestans T30-4] ,"
GO:0004616,GO:0050662,GO:0050661,GO:0055114,GO:0006098,GO:0016491,GO:0003824,GO:
0008152,GO:0005488","XP_002902568.1,AAL76320.1,EEY56494.1"
Stramenopiles-
Phytophthora_sojae_jgi108585,490,990.719,0,gi|301106971|ref|XP_002902568.1|6-
phosphogluconate dehydrogenase [Phytophthora infestans T30-4] ,"
GO:0004616,GO:0050662,GO:0050661,GO:0055114,GO:0006098,GO:0016491,GO:0003824,GO:
0008152,GO:0005488","XP_002902568.1,AAL76320.1,EEY56494.1"
Stramenopiles-Phytophthora_parasitica_esContig888_1,349,462.996,2.09E-
128,gi|301106971|ref|XP_002902568.1|6-phosphogluconate dehydrogenase
[Phytophthora infestans T30-4] ,"
GO:0004616,GO:0050662,GO:0050661,GO:0055114,GO:0006098,GO:0016491,GO:0003824,GO:
0008152,GO:0005488","XP_002902568.1,AAL76320.1,EEY56494.1"
Stramenopiles-
Phytophthora_sojae_jgi157394,3272,6080.75,0,gi|301101074|ref|XP_002899626.1|dyne
in heavy chain [Phytophthora infestans T30-4] ,"
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018","X
P_002899626.1,EEY61986.1"
Stramenopiles-
Phytophthora_ramorum_jgi94629,3396,6338.06,0,gi|301101074|ref|XP_002899626.1|dyn
ein heavy chain [Phytophthora infestans T30-4] ,"
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018","X
P_002899626.1,EEY61986.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219113331,400,831.632,0,gi|219113331|ref
|XP_002186249.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0005488,GO:0016491,GO:0008152,GO:0003824","XP_002186249.1,ACI65719.1"
Stramenopiles-
Phytophthora_ramorum_jgi96286,1238,1097.03,0,gi|301118570|ref|XP_002907013.1|bar
det-Biedl syndrome 1 family protein [Phytophthora infestans T30-4]
,,"XP_002907013.1,EEY66414.1"
Stramenopiles-
Phytophthora_sojae_jgi136833,876,1107.05,0,gi|301118570|ref|XP_002907013.1|barde
```

```
t-Biedl syndrome 1 family protein [Phytophthora infestans T30-4]
,,"XP_002907013.1,EEY66414.1"
Stramenopiles-
Phytophthora_parasitica_esContig1400_1,454,747.273,0,gi|301107486|ref|XP_0029028
25.1|long-chain-fatty-acid-CoA ligase [Phytophthora infestans T30-4] ,"
GO:0016874,GO:0008152,GO:0003824","XP_002902825.1,EEY55995.1"
Stramenopiles-Phytophthora_brassicae_esContig829_2,333,585.489,2.57E-
165,gi|301107486|ref|XP_002902825.1|long-chain-fatty-acid-CoA ligase
[Phytophthora infestans T30-4] ,"
GO:0016874,GO:0008152,GO:0003824","XP_002902825.1,EEY55995.1"
Stramenopiles-Phytophthora_parasitica_esgi222380192_2,281,509.605,1.34E-
142,"gi|301121692|ref|XP_002908573.1|long-chain-fatty-acid-CoA ligase, putative
[Phytophthora infestans T30-4] ","
GO:0016874,GO:0008152,GO:0003824","XP_002908573.1,EEY61656.1"
Stramenopiles-
Phytophthora_sojae_jgi136217,1417,850.507,0,gi|301120155|ref|XP_002907805.1|spor
angia induced Bardet-Biedl syndrome 4 protein [Phytophthora infestans T30-4] ,
GO:0005488,"XP_002907805.1,EEY64369.1"
Stramenopiles-
Phytophthora_ramorum_jgi80509,393,644.81,0,gi|301120147|ref|XP_002907801.1|conse
rved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0051082,GO:0046872,GO:0005524,GO:0005737,GO:0006457,GO:0009408,GO:0031072","X
P_002907801.1,EEY64365.1"
Stramenopiles-Phytophthora_parasitica_esContig15_1,256,401.749,3.60E-
110,gi|301120147|ref|XP_002907801.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,"
GO:0051082,GO:0046872,GO:0005524,GO:0005737,GO:0006457,GO:0009408,GO:0031072","X
P_002907801.1,EEY64365.1"
Stramenopiles-
Phytophthora_capsici_jgi113846,389,654.44,0,gi|301120147|ref|XP_002907801.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0051082,GO:0046872,GO:0005524,GO:0005737,GO:0006457,GO:0009408,GO:0031072","X
P_002907801.1,EEY64365.1"
Stramenopiles-Phytophthora_brassicae_esgi144598969_2,240,415.616,2.21E-
114,gi|301106016|ref|XP_002902091.1|D-3-phosphoglycerate dehydrogenase
[Phytophthora infestans T30-4] ,"
GO:0051287,GO:0055114,GO:0016597,GO:0016616,GO:0016491,GO:0003824,GO:0048037,GO:
0008152,GO:0005488","XP_002902091.1,EEY56763.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223993205,452,919.457,0,gi|223993205|ref|XP_
002286286.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0030529,GO:0003676,GO:0000166,GO:0005525,GO:0005737,GO:0005524,GO:0031072,GO:
0009408,GO:0006457,GO:0003924,GO:0046872,GO:0051082","XP_002286286.1,EED95927.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219120919,447,914.835,0,gi|219120919|ref
|XP_002185691.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0051082,GO:0046872,GO:0005524,GO:0005737,GO:0006457,GO:0009408,GO:0031072","X
P_002185691.1,ACI65161.1"
Stramenopiles-Aureococcus_anophagefferens_jgi68202,734,243.817,5.22E-
62,gi|299471455|emb|CBN79406.1|conserved unknown protein [Ectocarpus
siliculosus],,CBN79406.1
Stramenopiles-Aureococcus_anophagefferens_jgi68227,540,240.35,4.95E-
61,gi|299471455|emb|CBN79406.1|conserved unknown protein [Ectocarpus
siliculosus],,CBN79406.1
```

```
Stramenopiles-Fragilariopsis_cylindrus_jgi240465,312,124.405,1.48E-
26,gi|167522583|ref|XP_001745629.1|hypothetical protein [Monosiga brevicollis
MX1] ," GO:0008152,GO:0003824,GO:0008484","XP_001745629.1,EDQ89600.1"
Stramenopiles-
Phytophthora_ramorum_jgi76390,513,833.173,0,gi|301120450|ref|XP_002907952.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002907952.1,EEY61035.1"
Stramenopiles-
Phytophthora_capsici_jgi13559,423,702.205,0,gi|301120450|ref|XP_002907952.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002907952.1,EEY61035.1"
Stramenopiles-
Phytophthora_sojae_jgi128942,530,868.611,0,gi|301120450|ref|XP_002907952.1|conse
rved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002907952.1,EEY61035.1"
Stramenopiles-Aureococcus_anophagefferens_jgi66010,1224,109.768,2.38E-
21,gi|308178988|ref|YP_003918394.1|putative RNA polymerase sigma factor
[Arthrobacter arilaitensis Re117] ,,"YP_003918394.1,CBT77423.1"
Stramenopiles-Phytophthora_sojae_jgi138218,288,540.036,1.18E-
151,gi|301110238|ref|XP_002904199.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002904199.1,EEY54377.1"
Stramenopiles-Phytophthora_capsici_jgi8092,295,507.679,6.71E-
142,gi|301110238|ref|XP_002904199.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002904199.1,EEY54377.1"
Stramenopiles-Phytophthora_ramorum_jgi81299,238,392.119,2.34E-
107,gi|301110238|ref|XP_002904199.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002904199.1,EEY54377.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi233182,388,169.859,5.04E-
40,gi|224001040|ref|XP_002290192.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,,"XP_002290192.1,EED91944.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219110473,380,789.645,0,gi|219110473|ref
|XP_002176988.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002176988.1,EEC51451.1"
Stramenopiles-Aureococcus_anophagefferens_jgi28349,301,332.413,3.57E-
89,gi|307545337|ref|YP_003897816.1|hypothetical protein HELO_2747 [Halomonas
elongata DSM 2581] ,,"YP_003897816.1,CBV42631.1"
Stramenopiles-
Phytophthora_ramorum_jgi79274,801,1124.77,0,gi|301119839|ref|XP_002907647.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002907647.1,EEY64211.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223998208,1222,2531.13,0,gi|223998208|ref|XP
_002288777.1|hypothetical protein THAPSDRAFT_268455 [Thalassiosira pseudonana
CCMP1335] , GO:0005488,"XP_002288777.1,EED94213.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi180589,1275,996.882,0,gi|219112405|ref|XP_002177954.
1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,
GO:0005488,"XP_002177954.1,EEC50768.1"
Stramenopiles-
Phytophthora_sojae_jgi135013,2990,4768.76,0,"gi|301119945|ref|XP_002907700.1|U3
small nucleolar RNA-associated protein, putative [Phytophthora infestans T30-4]
", GO:0005488,"XP_002907700.1,EEY64264.1"
Stramenopiles-
Phytophthora_capsici_jgi69341,2627,3496.83,0,"gi|301119945|ref|XP_002907700.1|U3
```

```
small nucleolar RNA-associated protein, putative [Phytophthora infestans T30-4]
", GO:0005488,"XP_002907700.1,EEY64264.1"
Stramenopiles-
Phytophthora_ramorum_jgi80598,2998,4711.75,0,"gi|301119945|ref|XP_002907700.1|U3
small nucleolar RNA-associated protein, putative [Phytophthora infestans T30-4]
", GO:0005488,"XP_002907700.1,EEY64264.1"
Stramenopiles-
Phytophthora_sojae_jgi135755,480,772.311,0,gi|301111536|ref|XP_002904847.1|conse
rved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002904847.1,EEY53229.1"
Stramenopiles-
Phytophthora_ramorum_jgi79860,477,767.689,0,gi|301111536|ref|XP_002904847.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002904847.1,EEY53229.1"
Stramenopiles-Aureococcus_anophagefferens_jgi68742,501,57.3806,5.36E-
06,gi|301111536|ref|XP_002904847.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002904847.1,EEY53229.1"
Stramenopiles-Aureococcus_anophagefferens_jgi70664,1557,172.17,4.36E-
40,gi|72077009|ref|XP_788875.1|PREDICTED: similar to elaC homolog 1
[Strongylocentrotus purpuratus] ,,"XP_788875.1,XP_001189573.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219115798,268,550.051,1.01E-
154,gi|219115798|ref|XP_002178694.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002178694.1,EEC49392.1"
Stramenopiles-
Phytophthora_ramorum_jgi96000,487,939.488,0,"gi|301117854|ref|XP_002906655.1|6-
phosphofructokinase, putative [Phytophthora infestans T30-4] ","
GO:0016301,GO:0005524,GO:0003872,GO:0006096,GO:0005945","XP_002906655.1,EEY66056
.1"
Stramenopiles-
Phytophthora_capsici_jgi92116,509,991.49,0,"gi|301117854|ref|XP_002906655.1|6-
phosphofructokinase, putative [Phytophthora infestans T30-4] ","
GO:0016301,GO:0005524,GO:0003872,GO:0006096,GO:0005945","XP_002906655.1,EEY66056
.1"
Stramenopiles-
Phytophthora_sojae_jgi134835,492,937.562,0,"gi|301117854|ref|XP_002906655.1|6-
phosphofructokinase, putative [Phytophthora infestans T30-4] ","
GO:0016301,GO:0005524,GO:0003872,GO:0006096,GO:0005945","XP_002906655.1,EEY66056
.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219130302,563,1159.44,0,gi|219130302|ref
|XP_002185307.1|pyrophosphate-dependent phosphofructose kinase [Phaeodactylum
tricornutum CCAP 1055/1] ,"
GO:0016301,GO:0005524,GO:0003872,GO:0006096,GO:0005945","XP_002185307.1,EEC43176
.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219130304,515,1065.45,0,gi|219130304|ref
|XP_002185308.1|phosphofructokinase [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0016301,GO:0005524,GO:0003872,GO:0006096,GO:0005945","XP_002185308.1,EEC43177
.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi149102,378,650.973,0,gi|219123551|ref|XP_002182086.1
|pyrophosphate-dependent phosphofructose kinase [Phaeodactylum tricornutum CCAP
1055/1] ,"
```

```
GO:0016301,GO:0005524,GO:0003872,GO:0006096,GO:0005945","XP_002182086.1,EEC46626
.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219123551,564,1182.55,0,gi|219123551|ref
|XP_002182086.1|pyrophosphate-dependent phosphofructose kinase [Phaeodactylum
tricornutum CCAP 1055/1] ,"
GO:0016301,GO:0005524,GO:0003872,GO:0006096,GO:0005945","XP_002182086.1,EEC46626
.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223992985,394,815.839,0,gi|223992985|ref|XP_
002286176.1|6-phosphofructokinase [Thalassiosira pseudonana CCMP1335] ,"
GO:0016301,GO:0005524,GO:0016740,GO:0047334,GO:0003872,GO:0006096,GO:0005945","X
P_002286176.1,EED95817.1"
Stramenopiles-Aureococcus_anophagefferens_jgi31362,484,514.612,1.12E-
143,gi|219123551|ref|XP_002182086.1|pyrophosphate-dependent phosphofructose
kinase [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0016301,GO:0005524,GO:0003872,GO:0006096,GO:0005945","XP_002182086.1,EEC46626
.1"
Stramenopiles-Aureococcus_anophagefferens_jgi2184,398,342.813,4.60E-
92,gi|225445037|ref|XP_002283274.1|PREDICTED: hypothetical protein [Vitis
vinifera],,XP_002283274.1
Stramenopiles-
Phytophthora_ramorum_jgi84880,1498,1481.46,0,gi|301102899|ref|XP_002900536.1|con
served hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0005509,GO:0005515","XP_002900536.1,EEY59851.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219113539,132,259.225,8.93E-
68,gi|219113539|ref|XP_002186353.1|calcium binding protein [Phaeodactylum
tricornutum CCAP 1055/1] , GO:0005509,"XP_002186353.1,ACI65823.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219129758,154,307.375,3.33E-
82,gi|219129758|ref|XP_002185048.1|calmodulin [Phaeodactylum tricornutum CCAP
1055/1] , GO:0005509,"XP_002185048.1,EEC43495.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224006039,518,1075.46,0,gi|224006039|ref|XP_
002291980.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0016491,GO:0005509","XP_002291980.1,EED90831.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi72359,745,681.019,0,gi|219124450|ref|XP_002182516
.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0055114,GO:0009331,GO:0016491,GO:0004368,GO:0006072","XP_002182516.1,EEC45803
.1"
Stramenopiles-Phytophthora_sojae_jgi144939,152,64.6994,3.86E-
09,gi|301109387|ref|XP_002903774.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,"
GO:0005509,GO:0004518,GO:0003677","XP_002903774.1,EEY54829.1"
Stramenopiles-
Phytophthora_ramorum_jgi75633,1515,2412.49,0,gi|301114397|ref|XP_002998968.1|con
served hypothetical protein [Phytophthora infestans T30-4] ,
GO:0005509,"XP_002998968.1,EEY69114.1"
Stramenopiles-Aureococcus_anophagefferens_jgi72273,733,86.6557,1.13E-
14,"gi|255567395|ref|XP_002524677.1|Anaphase-promoting complex subunit, putative
[Ricinus communis] ",,"XP_002524677.1,EEF37696.1"
Stramenopiles-
Phytophthora_capsici_jgi103670,465,771.926,0,"gi|301113914|ref|XP_002998727.1|ad
```

```
enylyl cyclase-associated protein, putative [Phytophthora infestans T30-4] ","
GO:0005488,GO:0003779,GO:0007010","XP_002998727.1,EEY70080.1"
Stramenopiles-
Phytophthora_ramorum_jgi79564,728,760.37,0,"gi|301113914|ref|XP_002998727.1|aden
ylyl cyclase-associated protein, putative [Phytophthora infestans T30-4] ","
GO:0005488,GO:0003779,GO:0007010","XP_002998727.1,EEY70080.1"
Stramenopiles-
Phytophthora_sojae_jgi158145,666,754.592,0,"gi|301113914|ref|XP_002998727.1|aden
ylyl cyclase-associated protein, putative [Phytophthora infestans T30-4] ","
GO:0005488,GO:0003779,GO:0007010","XP_002998727.1,EEY70080.1"
Stramenopiles-Phytophthora_brassicae_esContig1522_1,154,196.823,6.66E-
49,"gi|301115406|ref|XP_002905432.1|arginine biosynthesis bifunctional protein
argJ, putative [Phytophthora infestans T30-4] ","
GO:0005739,GO:0004358,GO:0016740,GO:0008415,GO:0005759,GO:0003824,GO:0008652,GO:
0006526","XP_002905432.1,D0N1U4.1,EEY68273.1"
Stramenopiles-
Phytophthora_sojae_jgi142184,467,879.782,0,"gi|301115406|ref|XP_002905432.1|argi
nine biosynthesis bifunctional protein argJ, putative [Phytophthora infestans
T30-4] ","
GO:0005739,GO:0004358,GO:0016740,GO:0008415,GO:0005759,GO:0003824,GO:0008652,GO:
0006526","XP_002905432.1,D0N1U4.1,EEY68273.1"
Stramenopiles-Phytophthora_parasitica_esgi222374224_5,184,281.182,3.35E-
74,"gi|301115406|ref|XP_002905432.1|arginine biosynthesis bifunctional protein
argJ, putative [Phytophthora infestans T30-4] ","
GO:0005739,GO:0004358,GO:0016740,GO:0008415,GO:0005759,GO:0003824,GO:0008652,GO:
0006526","XP_002905432.1,D0N1U4.1,EEY68273.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi185131,465,593.578,1.56E-
167,gi|223996635|ref|XP_002287991.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,"
GO:0005739,GO:0004358,GO:0016740,GO:0008415,GO:0005759,GO:0003824,GO:0008652,GO:
0006526","XP_002287991.1,B8BVB6.1,EED95434.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223996635,488,998.038,0,gi|223996635|ref|XP_
002287991.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0005739,GO:0004358,GO:0016740,GO:0008415,GO:0005759,GO:0003824,GO:0008652,GO:
0006526","XP_002287991.1,B8BVB6.1,EED95434.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi38538,1597,1872.06,0,gi|224009263|ref|XP_00229359
0.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0055114,GO:0006807,GO:0016491,GO:0008152,GO:0003824,GO:0015930,GO:0006537","X
P_002293590.1,EED89326.1"
Stramenopiles-
Phytophthora_ramorum_jgi71073,383,705.671,0,"gi|301114981|ref|XP_002999260.1|GTP
ase, putative [Phytophthora infestans T30-4] ","
GO:0005525,GO:0000166,GO:0005622","XP_002999260.1,EEY69406.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219109989,407,833.558,0,gi|219109989|ref
|XP_002176747.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0005525,GO:0000166,GO:0005622","XP_002176747.1,EEC51210.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224013052,377,783.097,0,gi|224013052|ref|XP_
002295178.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0005525,GO:0000166,GO:0005622","XP_002295178.1,EED87482.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219130227,373,776.163,0,gi|219130227|ref
```

```
|XP_002185271.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0005525,GO:0000166,GO:0005622","XP_002185271.1,EEC43140.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi198500,377,635.95,2.37E-
180,gi|219130227|ref|XP_002185271.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0005525,GO:0000166,GO:0005622","XP_002185271.1,EEC43140.1"
Stramenopiles-Aureococcus_anophagefferens_jgi29702,370,525.013,5.31E-
147,gi|219130227|ref|XP_002185271.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0005525,GO:0000166,GO:0005622","XP_002185271.1,EEC43140.1"
Stramenopiles-
Phytophthora_sojae_jgi108292,369,716.072,0,gi|301095226|ref|XP_002896714.1|devel
opmentally-regulated GTP-binding protein 1 [Phytophthora infestans T30-4] ,"
GO:0005525,GO:0000166,GO:0005622","XP_002896714.1,EEY66827.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223994011,385,787.334,0,gi|223994011|ref|XP_
002286689.1|hypothetical protein THAPSDRAFT_260852 [Thalassiosira pseudonana
CCMP1335] ,,"XP_002286689.1,EED96330.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219121021,455,939.873,0,gi|219121021|ref
|XP_002185742.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002185742.1,ACI65212.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi225224,367,350.517,1.64E-
94,gi|219121021|ref|XP_002185742.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002185742.1,ACI65212.1"
Stramenopiles-Phytophthora_ramorum_jgi51599,347,521.931,4.12E-
146,gi|301119119|ref|XP_002907287.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002907287.1,EEY63851.1"
Stramenopiles-Blastocystis_hominis_tbBHL00001824_1,321,493.426,1.55E-
137,gi|300121328|emb|CBK21708.2|unnamed protein product [Blastocystis hominis],"
GO:0006508,GO:0016787,GO:0008234,GO:0008233,GO:0004197",CBK21708.2
Stramenopiles-Aureococcus_anophagefferens_jgi21060,314,219.55,3.63E-
55,gi|157093355|gb|ABV22332.1|cysteine protease 1 [Noctiluca scintillans],"
GO:0006508,GO:0016787,GO:0008234,GO:0008233,GO:0004197",ABV22332.1
Stramenopiles-Phytophthora_capsici_jgi85800,305,467.233,8.74E-
130,gi|66270077|gb|AAY43368.1|cysteine protease [Phytophthora infestans],"
GO:0006508,GO:0008234,GO:0008233,GO:0004197",AAY43368.1
Stramenopiles-
Phytophthora_sojae_jgi142383,534,960.674,0,"gi|301116794|ref|XP_002906125.1|cyst
eine protease family C01A, putative [Phytophthora infestans T30-4] ","
GO:0006508,GO:0008234,GO:0008233,GO:0004197","XP_002906125.1,EEY65526.1"
Stramenopiles-
Phytophthora_brassicae_esContig702_3,391,650.973,0,"gi|301116794|ref|XP_00290612
5.1|cysteine protease family C01A, putative [Phytophthora infestans T30-4] ","
GO:0006508,GO:0008234,GO:0008233,GO:0004197","XP_002906125.1,EEY65526.1"
Stramenopiles-
Phytophthora_ramorum_jgi77898,537,958.362,0,"gi|301116794|ref|XP_002906125.1|cys
teine protease family C01A, putative [Phytophthora infestans T30-4] ","
GO:0006508,GO:0008234,GO:0008233,GO:0004197","XP_002906125.1,EEY65526.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219112639,360,757.673,0,gi|219112639|ref
|XP_002178071.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0006508,GO:0016787,GO:0008234,GO:0008233,GO:0004197","XP_002178071.1,EEC50885
.1"
Stramenopiles-Aureococcus_anophagefferens_jgi34120,166,123.635,6.88E-
27,gi|18481461|gb|AAL73456.1|AF451862_1endonuclease [Tetrahymena thermophila],"
```

```
GO:0006355,GO:0003676,GO:0016788,GO:0004519,GO:0005634,GO:0003700,GO:0003677",AA
L73456.1
Stramenopiles-Aureococcus_anophagefferens_jgi33571,166,127.102,6.07E-
28,gi|18481487|gb|AAL73479.1|AF451865_5endonuclease [Tetrahymena thermophila],"
GO:0006355,GO:0016788,GO:0004519,GO:0005634,GO:0003700,GO:0003677",AAL73479.1
Stramenopiles-Aureococcus_anophagefferens_jgi71879,757,153.295,1.14E-
34,gi|219119770|ref|XP_002180638.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002180638.1,EEC48046.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi259567,434,108.227,2.15E-
21,gi|219119770|ref|XP_002180638.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002180638.1,EEC48046.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219119770,326,681.789,0,gi|219119770|ref
|XP_002180638.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002180638.1,EEC48046.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi223995035,289,599.742,1.09E-
169,gi|223995035|ref|XP_002287201.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,,"XP_002287201.1,EED94644.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi273855,272,305.834,2.98E-
81,gi|219123561|ref|XP_002182091.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002182091.1,EEC46631.1"
Stramenopiles-Phytophthora_sojae_jgi137328,242,449.899,1.15E-
124,gi|301109944|ref|XP_002904052.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002904052.1,EEY54230.1"
Stramenopiles-Phytophthora_ramorum_jgi82193,241,442.965,1.21E-
122,gi|301109944|ref|XP_002904052.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002904052.1,EEY54230.1"
Stramenopiles-Phytophthora_capsici_jgi98918,240,453.751,7.57E-
126,gi|301109944|ref|XP_002904052.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002904052.1,EEY54230.1"
Stramenopiles-Phytophthora_ramorum_jgi74294,261,433.335,1.15E-
119,gi|301116339|ref|XP_002905898.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002905898.1,EEY67250.1"
Stramenopiles-
Phytophthora_sojae_jgi158217,1430,1725.68,0,gi|301113380|ref|XP_002998460.1|myot
ubularin-like protein [Phytophthora infestans T30-4] ,"
GO:0016791,GO:0016311,GO:0004725","XP_002998460.1,EEY69813.1"
Stramenopiles-Phytophthora_capsici_jgi96698,291,452.21,2.69E-
125,gi|301113384|ref|XP_002998462.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002998462.1,EEY69815.1"
Stramenopiles-
Phytophthora_ramorum_jgi95843,1303,1530,0,gi|301113380|ref|XP_002998460.1|myotub
ularin-like protein [Phytophthora infestans T30-4] ,"
GO:0016791,GO:0016311,GO:0004725","XP_002998460.1,EEY69813.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi179103,421,380.178,2.56E-
103,gi|86278368|gb|ABC88435.1|acid alpha galactosidase 2 [Cucumis sativus],"
GO:0004553,GO:0016787,GO:0008152,GO:0005975,GO:0043169,GO:0016798,GO:0003824,GO:
0004557",ABC88435.1
Stramenopiles-
Phytophthora_ramorum_jgi77908,697,1244.57,0,gi|301116820|ref|XP_002906138.1|clea
vage induced conserved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0046872,GO:0008270","XP_002906138.1,EEY65539.1"
Stramenopiles-
Phytophthora_sojae_jgi142373,699,1243.02,0,gi|301116820|ref|XP_002906138.1|cleav
```

```
age induced conserved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0046872,GO:0008270","XP_002906138.1,EEY65539.1"
Stramenopiles-
Phytophthora_sojae_jgi141860,689,997.653,0,gi|301121949|ref|XP_002908701.1|conse
rved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0046872,GO:0008270","XP_002908701.1,EEY57515.1"
Stramenopiles-Aureococcus_anophagefferens_jgi63725,3212,167.162,3.57E-
38,gi|167390078|ref|XP_001739198.1|Rho/RAC guanine nucleotide exchange factor
[Entamoeba dispar SAW760] ,"
GO:0046872,GO:0016740,GO:0005089,GO:0000285,GO:0035023,GO:0008270,GO:0005622,GO:
0005085","XP_001739198.1,EDR24412.1"
Stramenopiles-
Phytophthora_capsici_jgi113416,493,853.588,0,gi|301114603|ref|XP_002999071.1|con
served hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0046872,GO:0015485,GO:0017127,GO:0008270,GO:0006694","XP_002999071.1,EEY69217
.1"
Stramenopiles-
Phytophthora_ramorum_jgi96057,2151,1374.76,0,gi|301112847|ref|XP_002998194.1|con
served hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002998194.1,EEY70540.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219128950,151,315.849,7.78E-
85,gi|219128950|ref|XP_002184663.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] , GO:0016787,"XP_002184663.1,EEC43722.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi191760,158,222.246,1.21E-
56,gi|219128950|ref|XP_002184663.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] , GO:0016787,"XP_002184663.1,EEC43722.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi223992803,203,421.394,2.35E-
116,gi|223992803|ref|XP_002286085.1|hypothetical protein THAPSDRAFT_1165
[Thalassiosira pseudonana CCMP1335] , GO:0016787,"XP_002286085.1,EED95726.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi186913,229,279.641,1.56E-
73,gi|219113239|ref|XP_002186203.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] , GO:0016787,"XP_002186203.1,ACI65673.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi223994039,198,407.527,3.32E-
112,gi|223994039|ref|XP_002286703.1|predicted protein [Thalassiosira pseudonana
CCMP1335] , GO:0016787,"XP_002286703.1,EED96344.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219113239,199,410.994,3.18E-
113,gi|219113239|ref|XP_002186203.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] , GO:0016787,"XP_002186203.1,ACI65673.1"
Stramenopiles-Aureococcus_anophagefferens_jgi18344,229,273.863,9.77E-
72,gi|167538660|ref|XP_001750992.1|hypothetical protein [Monosiga brevicollis
MX1] , GO:0016787,"XP_001750992.1,EDQ84204.1"
Stramenopiles-Phytophthora_capsici_jgi115837,191,377.481,3.94E-
103,gi|301117860|ref|XP_002906658.1|inosine triphosphate pyrophosphatase
[Phytophthora infestans T30-4] , GO:0016787,"XP_002906658.1,EEY66059.1"
Stramenopiles-Phytophthora_ramorum_jgi71914,191,381.333,2.71E-
104,gi|301117860|ref|XP_002906658.1|inosine triphosphate pyrophosphatase
[Phytophthora infestans T30-4] , GO:0016787,"XP_002906658.1,EEY66059.1"
Stramenopiles-Phytophthora_sojae_jgi108811,191,380.563,4.82E-
104,gi|301117860|ref|XP_002906658.1|inosine triphosphate pyrophosphatase
[Phytophthora infestans T30-4] , GO:0016787,"XP_002906658.1,EEY66059.1"
Stramenopiles-
Phytophthora_capsici_jgi1707,623,1122.07,0,gi|301100780|ref|XP_002899479.1|Volta
ge-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
```

```
GO:0005249,GO:0016021,GO:0016020,GO:0055085,GO:0006813,GO:0006811,GO:0005216,GO:
0006810","XP_002899479.1,EEY61839.1"
Stramenopiles-
Phytophthora_ramorum_jgi96106,1152,1044.26,0,gi|301100780|ref|XP_002899479.1|Vol
tage-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0005249,GO:0016021,GO:0016020,GO:0055085,GO:0006813,GO:0006811,GO:0005216,GO:
0006810","XP_002899479.1,EEY61839.1"
Stramenopiles-Aureococcus_anophagefferens_jgi64816,823,225.328,2.41E-
56,gi|255073051|ref|XP_002500200.1|voltage-gated ion channel superfamily
[Micromonas sp. RCC299] ,"
GO:0005249,GO:0016021,GO:0016020,GO:0055085,GO:0006813,GO:0006811,GO:0005216,GO:
0006810","XP_002500200.1,ACO61458.1"
Stramenopiles-Aureococcus_anophagefferens_jgi67061,865,325.865,1.38E-
86,gi|303280485|ref|XP_003059535.1|voltage-gated ion channel superfamily
[Micromonas pusilla CCMP1545] ,"
GO:0005216,GO:0016021,GO:0016020,GO:0006813,GO:0006811,GO:0006810,GO:0055114,GO:
0016491,GO:0003824,GO:0055085,GO:0008152,GO:0005249,GO:0005488","XP_003059535.1,
EEH56667.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi191917,313,211.075,1.20E-
52,gi|219128283|ref|XP_002184346.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0055114,GO:0005488,GO:0008152,GO:0003824,GO:0004735,GO:0006561","XP_002184346
.1,EEC44095.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224004890,306,637.491,0,gi|224004890|ref|XP_
002296096.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0005488,GO:0008152,GO:0003824","XP_002296096.1,ACI64813.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219128283,339,700.279,0,gi|219128283|ref
|XP_002184346.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0055114,GO:0005488,GO:0008152,GO:0003824,GO:0004735,GO:0006561","XP_002184346
.1,EEC44095.1"
Stramenopiles-Phytophthora_parasitica_esgi68418750_1,267,461.07,6.05E-
128,"gi|301121660|ref|XP_002908557.1|enoyl-[acyl-carrier-protein] reductase
[NADH], putative [Phytophthora infestans T30-4] ","
GO:0055114,GO:0005488,GO:0016491,GO:0008152,GO:0004318,GO:0003824,GO:0006633","X
P_002908557.1,EEY61640.1"
Stramenopiles-Phytophthora_capsici_jgi19332,276,447.588,6.98E-
124,"gi|301121660|ref|XP_002908557.1|enoyl-[acyl-carrier-protein] reductase
[NADH], putative [Phytophthora infestans T30-4] ","
GO:0055114,GO:0005488,GO:0016491,GO:0008152,GO:0004318,GO:0003824,GO:0006633","X
P_002908557.1,EEY61640.1"
Stramenopiles-Phytophthora_ramorum_jgi45002,261,425.631,2.14E-
117,"gi|301121660|ref|XP_002908557.1|enoyl-[acyl-carrier-protein] reductase
[NADH], putative [Phytophthora infestans T30-4] ","
GO:0055114,GO:0005488,GO:0016491,GO:0008152,GO:0004318,GO:0003824,GO:0006633","X
P_002908557.1,EEY61640.1"
Stramenopiles-Phytophthora_brassicae_esContig625_3,249,397.127,8.42E-
109,"gi|301121660|ref|XP_002908557.1|enoyl-[acyl-carrier-protein] reductase
[NADH], putative [Phytophthora infestans T30-4] ","
GO:0055114,GO:0005488,GO:0016491,GO:0008152,GO:0004318,GO:0003824,GO:0006633","X
P_002908557.1,EEY61640.1"
Stramenopiles-Phytophthora_sojae_jgi137179,272,441.425,5.24E-
122,"gi|301121660|ref|XP_002908557.1|enoyl-[acyl-carrier-protein] reductase
[NADH], putative [Phytophthora infestans T30-4] ","
```

```
GO:0055114,GO:0005488,GO:0016491,GO:0008152,GO:0004318,GO:0003824,GO:0006633","X
P_002908557.1,EEY61640.1"
Stramenopiles-Aureococcus_anophagefferens_jgi12528,327,220.32,2.02E-
55,gi|41054147|ref|NP_956135.1|glucosamine (N-acetyl)-6-sulfatase b [Danio
rerio] ,"
GO:0005764,GO:0008152,GO:0008449,GO:0003824,GO:0008484","NP_956135.1,AAH45323.1,
AAI64157.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi157083,383,260.766,2.08E-
67,gi|163793311|ref|ZP_02187286.1|sulfatase [alpha proteobacterium BAL199] ,"
GO:0008152,GO:0008449,GO:0003824,GO:0008484,GO:0030203","ZP_02187286.1,EDP65628.
1"
Stramenopiles-Fragilariopsis_cylindrus_jgi247897,631,258.07,2.50E-
66,gi|167520137|ref|XP_001744408.1|hypothetical protein [Monosiga brevicollis
MX1] ,"
GO:0008152,GO:0008449,GO:0003824,GO:0008484,GO:0030203","XP_001744408.1,EDQ91111
.1"
Stramenopiles-Aureococcus_anophagefferens_jgi27956,448,296.59,3.66E-
78,gi|167521003|ref|XP_001744840.1|hypothetical protein [Monosiga brevicollis
MX1] ,"
GO:0005764,GO:0008152,GO:0008449,GO:0003824,GO:0008484,GO:0030203","XP_001744840
.1,EDQ90073.1"
Stramenopiles-Aureococcus_anophagefferens_jgi62077,538,237.269,4.17E-
60,gi|313224745|emb|CBY20536.1|unnamed protein product [Oikopleura
dioica],,CBY20536.1
Stramenopiles-Aureococcus_anophagefferens_jgi65345,268,116.701,2.21E-
24,gi|118469999|ref|YP_888676.1|phosphonoacetaldehyde hydrolase [Mycobacterium
smegmatis str. MC2 155] ,"
GO:0016787,GO:0008152,GO:0003824","YP_888676.1,ABK72182.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi223997872,295,605.134,2.57E-
171,gi|223997872|ref|XP_002288609.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ," GO:0008152,GO:0003824","XP_002288609.1,EED94045.1"
Stramenopiles-
Phytophthora_capsici_jgi105159,856,1466.06,0,gi|301103201|ref|XP_002900687.1|con
served hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0008270,GO:0005622","XP_002900687.1,EEY60002.1"
Stramenopiles-
Phytophthora_ramorum_jgi76587,810,1356.66,0,gi|301103201|ref|XP_002900687.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0008270,GO:0005622","XP_002900687.1,EEY60002.1"
Stramenopiles-
Phytophthora_ramorum_jgi79185,633,1201.81,0,"gi|301119661|ref|XP_002907558.1|sod
ium/glucose cotransporter, putative [Phytophthora infestans T30-4] ","
GO:0016021,GO:0016020,GO:0006814,GO:0055085,GO:0006811,GO:0006810,GO:0005215","X
P_002907558.1,EEY64122.1"
Stramenopiles-
Phytophthora_ramorum_jgi86098,542,987.638,0,"gi|301119661|ref|XP_002907558.1|sod
ium/glucose cotransporter, putative [Phytophthora infestans T30-4] ","
GO:0016021,GO:0016020,GO:0006814,GO:0055085,GO:0006811,GO:0006810,GO:0005215","X
P_002907558.1,EEY64122.1"
Stramenopiles-
Phytophthora_capsici_jgi100988,633,1230.31,0,"gi|301119661|ref|XP_002907558.1|so
dium/glucose cotransporter, putative [Phytophthora infestans T30-4] ","
GO:0016021,GO:0016020,GO:0006814,GO:0055085,GO:0006811,GO:0006810,GO:0005215","X
P_002907558.1,EEY64122.1"
```

```
Stramenopiles-
Phytophthora_sojae_jgi139077,643,1188.33,0,"gi|301119661|ref|XP_002907558.1|sodi
um/glucose cotransporter, putative [Phytophthora infestans T30-4] ","
GO:0016021,GO:0016020,GO:0006814,GO:0055085,GO:0006811,GO:0006810,GO:0005215","X
P_002907558.1,EEY64122.1"
Stramenopiles-Phytophthora_ramorum_jgi86366,398,301.212,1.47E-
79,"gi|157106769|ref|XP_001649474.1|ankyrin 2,3/unc44 [Aedes aegypti]
",,"XP_001649474.1,EAT33004.1"
Stramenopiles-Phytophthora_ramorum_jgi83969,398,300.827,1.80E-
79,"gi|157106769|ref|XP_001649474.1|ankyrin 2,3/unc44 [Aedes aegypti]
",,"XP_001649474.1,EAT33004.1"
Stramenopiles-Phytophthora_sojae_jgi131198,776,491.115,2.10E-
136,"gi|157106769|ref|XP_001649474.1|ankyrin 2,3/unc44 [Aedes aegypti]
",,"XP_001649474.1,EAT33004.1"
Stramenopiles-Phytophthora_ramorum_jgi83968,1017,619.387,7.10E-
175,"gi|115675516|ref|XP_798907.2|PREDICTED: similar to ankyrin 2,3/unc44,
partial [Strongylocentrotus purpuratus]",,XP_798907.2
Stramenopiles-Phytophthora_sojae_jgi131912,310,206.453,2.74E-
51,"gi|157106769|ref|XP_001649474.1|ankyrin 2,3/unc44 [Aedes aegypti]
",,"XP_001649474.1,EAT33004.1"
Stramenopiles-Phytophthora_sojae_jgi143949,1335,478.019,3.87E-
132,gi|301099225|ref|XP_002898704.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,"
GO:0005524,GO:0004672,GO:0006468,GO:0004674","XP_002898704.1,EEY62829.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223996291,853,1764.59,0,gi|223996291|ref|XP_
002287819.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0016021,GO:0016020,GO:0055085,GO:0006811,GO:0005216,GO:0006810","XP_002287819
.1,EED95262.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi197260,246,308.531,4.19E-
82,gi|219112943|ref|XP_002186055.1|bacterial type voltage activated sodium
channel [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0016021,GO:0016020,GO:0055085,GO:0006811,GO:0005216,GO:0006810","XP_002186055
.1,ACI65525.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219113409,718,1473.37,0,gi|219113409|ref
|XP_002186288.1|bacterial type voltage activated sodium channel [Phaeodactylum
tricornutum CCAP 1055/1] ,"
GO:0016021,GO:0016020,GO:0055085,GO:0006811,GO:0005216,GO:0006810","XP_002186288
.1,ACI65758.1"
Stramenopiles-Aureococcus_anophagefferens_jgi66966,1100,270.396,8.79E-
70,gi|301111810|ref|XP_002904984.1|Voltage-gated Ion Channel (VIC) Superfamily
[Phytophthora infestans T30-4] ,"
GO:0005509,GO:0016021,GO:0016020,GO:0055085,GO:0006811,GO:0005216,GO:0006810","X
P_002904984.1,EEY53366.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224009952,1149,2402.48,0,gi|224009952|ref|XP
_002293934.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0008270,GO:0005622","XP_002293934.1,EED88943.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi260416,1148,622.083,1.24E-
175,gi|224009952|ref|XP_002293934.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ," GO:0008270,GO:0005622","XP_002293934.1,EED88943.1"
Stramenopiles-
Phytophthora_capsici_jgi102948,448,785.793,0,gi|301115170|ref|XP_002905314.1|con
```

```
served hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0046872,GO:0008270,GO:0005515","XP_002905314.1,EEY68155.1"
Stramenopiles-
Phytophthora_ramorum_jgi93954,1045,1632.85,0,gi|301115170|ref|XP_002905314.1|con
served hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0046872,GO:0008270,GO:0005515","XP_002905314.1,EEY68155.1"
Stramenopiles-
Phytophthora_sojae_jgi156980,836,1305.04,0,gi|301115170|ref|XP_002905314.1|conse
rved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0046872,GO:0008270,GO:0005515","XP_002905314.1,EEY68155.1"
Stramenopiles-
Phytophthora_ramorum_jgi78460,427,832.402,0,gi|301091133|ref|XP_002895758.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002895758.1,EEY54722.1"
Stramenopiles-
Phytophthora_capsici_jgi118026,427,863.988,0,gi|301091133|ref|XP_002895758.1|con
served hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002895758.1,EEY54722.1"
Stramenopiles-
Phytophthora_sojae_jgi127940,427,842.803,0,gi|301091133|ref|XP_002895758.1|conse
rved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002895758.1,EEY54722.1"
Stramenopiles-
Phytophthora_brassicae_esContig460_1,406,779.245,0,gi|301091133|ref|XP_002895758
.1|conserved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002895758.1,EEY54722.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219119671,423,888.256,0,gi|219119671|ref
|XP_002180590.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002180590.1,EEC47998.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi225627,455,611.683,5.82E-
173,gi|219119671|ref|XP_002180590.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002180590.1,EEC47998.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224007084,468,978.008,0,gi|224007084|ref|XP_
002292502.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002292502.1,EED90477.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi260140,314,117.087,2.52E-
24,gi|195108805|ref|XP_001998983.1|GI24262 [Drosophila mojavensis] ,"
GO:0055114,GO:0005488,GO:0016491,GO:0008152,GO:0003824","XP_001998983.1,EDW14444
.1"
Stramenopiles-Phytophthora_sojae_jgi121880,310,360.147,1.91E-
97,"gi|301090920|ref|XP_002895656.1|glycoside hydrolase, putative [Phytophthora
infestans T30-4] ","
GO:0055114,GO:0005488,GO:0016491,GO:0016787,GO:0008152,GO:0003824","XP_002895656
.1,EEY55157.1"
Stramenopiles-Phytophthora_capsici_jgi70224,324,333.569,1.78E-
89,"gi|301090920|ref|XP_002895656.1|glycoside hydrolase, putative [Phytophthora
infestans T30-4] ","
GO:0055114,GO:0005488,GO:0016491,GO:0016787,GO:0008152,GO:0003824","XP_002895656
.1,EEY55157.1"
Stramenopiles-
Phytophthora_sojae_jgi137045,1912,2606.63,0,gi|301101690|ref|XP_002899933.1|ATP-
binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4] ,"
```

```
GO:0016887,GO:0005524,GO:0000166,GO:0016020,GO:0017111","XP_002899933.1,EEY60560
.1"
Stramenopiles-Phytophthora_ramorum_jgi82510,281,462.996,1.75E-
128,gi|301101692|ref|XP_002899934.1|ATP-binding Cassette (ABC) superfamily
[Phytophthora infestans T30-4] , GO:0005524,"XP_002899934.1,EEY60561.1"
Stramenopiles-Phytophthora_capsici_jgi50126,267,445.662,2.06E-
123,gi|301101692|ref|XP_002899934.1|ATP-binding Cassette (ABC) superfamily
[Phytophthora infestans T30-4] , GO:0005524,"XP_002899934.1,EEY60561.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224012787,698,1460.28,0,gi|224012787|ref|XP_
002295046.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002295046.1,EED87826.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224008891,514,1075.85,0,gi|224008891|ref|XP_
002293404.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002293404.1,EED89140.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi180822,439,343.199,3.54E-
92,gi|219129914|ref|XP_002185122.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002185122.1,EEC43254.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi193699,356,325.479,5.57E-
87,gi|219113773|ref|XP_002186470.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002186470.1,ACI65940.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219113773,715,1492.63,0,gi|219113773|ref
|XP_002186470.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002186470.1,ACI65940.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi193640,412,363.999,2.00E-
98,gi|219113773|ref|XP_002186470.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002186470.1,ACI65940.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi223998518,287,584.334,5.13E-
165,gi|223998518|ref|XP_002288932.1|hypothetical protein THAPSDRAFT_32880
[Thalassiosira pseudonana CCMP1335] ,"
GO:0001932,GO:0005952,GO:0008603","XP_002288932.1,EED94368.1"
Stramenopiles-Aureococcus_anophagefferens_jgi55450,409,376.326,3.20E-
102,gi|298715444|emb|CBJ34040.1|conserved unknown protein [Ectocarpus
siliculosus]," GO:0001932,GO:0005952,GO:0008603,GO:0007165",CBJ34040.1
Stramenopiles-
Phytophthora_ramorum_jgi95317,396,736.873,0,gi|301119699|ref|XP_002907577.1|cAMP
-dependent protein kinase regulatory subunit [Phytophthora infestans T30-4] ,"
GO:0016301,GO:0001932,GO:0005952,GO:0008603","XP_002907577.1,EEY64141.1"
Stramenopiles-
Phytophthora_capsici_jgi114285,614,743.036,0,gi|301119699|ref|XP_002907577.1|cAM
P-dependent protein kinase regulatory subunit [Phytophthora infestans T30-4] ,"
GO:0016301,GO:0001932,GO:0005952,GO:0008603","XP_002907577.1,EEY64141.1"
Stramenopiles-
Phytophthora_sojae_jgi139097,397,733.406,0,gi|301119699|ref|XP_002907577.1|cAMP-
dependent protein kinase regulatory subunit [Phytophthora infestans T30-4] ,"
GO:0016301,GO:0001932,GO:0005952,GO:0008603","XP_002907577.1,EEY64141.1"
Stramenopiles-Phytophthora_capsici_jgi108426,263,472.626,1.56E-
131,"gi|301093925|ref|XP_002997807.1|cAMP-dependent protein kinase regulatory
subunit, putative [Phytophthora infestans T30-4] ","
GO:0016301,GO:0001932,GO:0005952,GO:0008603","XP_002997807.1,EEY67945.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi232338,241,73.1738,2.98E-
11,gi|168005670|ref|XP_001755533.1|predicted protein [Physcomitrella patens
subsp. patens] ,"
```

```
GO:0016787,GO:0008152,GO:0007047,GO:0005975,GO:0016798,GO:0004650","XP_001755533
.1,EDQ79593.1"
Stramenopiles-Aureococcus_anophagefferens_jgi66106,2150,142.124,6.96E-
31,gi|255082564|ref|XP_002504268.1|predicted protein [Micromonas sp. RCC299] ,"
GO:0005488,GO:0016787","XP_002504268.1,ACO65526.1"
Stramenopiles-Phytophthora_sojae_jgi132480,335,160.614,2.13E-
37,gi|297743040|emb|CBI35907.3|unnamed protein product [Vitis
vinifera],,CBI35907.3
Stramenopiles-Phytophthora_ramorum_jgi75905,296,161.384,1.14E-
37,gi|297743040|emb|CBI35907.3|unnamed protein product [Vitis
vinifera],,CBI35907.3
Stramenopiles-Phytophthora_ramorum_jgi72774,331,635.18,2.68E-
180,gi|301122703|ref|XP_002909078.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002909078.1,EEY57892.1"
Stramenopiles-
Phytophthora_sojae_jgi130320,347,670.618,0,gi|301122703|ref|XP_002909078.1|conse
rved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002909078.1,EEY57892.1"
Stramenopiles-Aureococcus_anophagefferens_jgi539,734,418.698,1.29E-
114,gi|206901280|ref|YP_002250567.1|xylosidase/arabinosidase [Dictyoglomus
thermophilum H-6-12] ," GO:0004553,GO:0005975","YP_002250567.1,ACI19441.1"
Stramenopiles-Aureococcus_anophagefferens_jgi72811,710,110.923,5.28E-
22,gi|260786687|ref|XP_002588388.1|hypothetical protein BRAFLDRAFT_116982
[Branchiostoma floridae] ,"
GO:0006629,GO:0016787,GO:0008152","XP_002588388.1,EEN44399.1"
Stramenopiles-
Phytophthora_capsici_jgi37962,371,736.102,0,gi|254521355|ref|ZP_05133410.1|homos
erine O-acetyltransferase [Stenotrophomonas sp. SKA14] ,"
GO:0005737,GO:0016740,GO:0008415,GO:0004414,GO:0016413,GO:0008652,GO:0009086","Z
P_05133410.1,EED37471.1"
Stramenopiles-Phytophthora_parasitica_esgi68418339_3,219,206.838,1.29E-
51,"gi|301088968|ref|XP_002894846.1|homoserine O-acetyltransferase, putative
[Phytophthora infestans T30-4] ","
GO:0005737,GO:0016740,GO:0016413","XP_002894846.1,EEY64849.1"
Stramenopiles-Phytophthora_capsici_jgi116855,409,621.313,6.64E-
176,"gi|301088968|ref|XP_002894846.1|homoserine O-acetyltransferase, putative
[Phytophthora infestans T30-4] ","
GO:0005737,GO:0016740,GO:0016413","XP_002894846.1,EEY64849.1"
Stramenopiles-Phytophthora_ramorum_jgi81928,427,611.683,5.95E-
173,"gi|301088968|ref|XP_002894846.1|homoserine O-acetyltransferase, putative
[Phytophthora infestans T30-4] ","
GO:0005737,GO:0016740,GO:0016413","XP_002894846.1,EEY64849.1"
Stramenopiles-Phytophthora_sojae_jgi137199,731,458.373,1.43E-
126,"gi|301088968|ref|XP_002894846.1|homoserine O-acetyltransferase, putative
[Phytophthora infestans T30-4] ","
GO:0005737,GO:0016740,GO:0016413","XP_002894846.1,EEY64849.1"
Stramenopiles-Phytophthora_sojae_jgi127649,425,585.874,3.20E-
165,"gi|301088968|ref|XP_002894846.1|homoserine O-acetyltransferase, putative
[Phytophthora infestans T30-4] ","
GO:0005737,GO:0016740,GO:0016413","XP_002894846.1,EEY64849.1"
Stramenopiles-Phytophthora_sojae_jgi131940,430,619.387,2.55E-
175,"gi|301088968|ref|XP_002894846.1|homoserine O-acetyltransferase, putative
[Phytophthora infestans T30-4] ","
GO:0005737,GO:0016740,GO:0016413","XP_002894846.1,EEY64849.1"
```

```
Stramenopiles-Phytophthora_ramorum_jgi82452,291,490.73,7.67E-
137,gi|301123725|ref|XP_002909589.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002909589.1,EEY58403.1"
Stramenopiles-Phytophthora_capsici_jgi92544,299,492.271,2.87E-
137,gi|301123725|ref|XP_002909589.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002909589.1,EEY58403.1"
Stramenopiles-Phytophthora_sojae_jgi127220,283,459.914,1.21E-
127,gi|301123725|ref|XP_002909589.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002909589.1,EEY58403.1"
Stramenopiles-
Phytophthora_ramorum_jgi79515,1195,1400.19,0,"gi|301113792|ref|XP_002998666.1|tr
ansmembrane protein, putative [Phytophthora infestans T30-4] ",
GO:0016021,"XP_002998666.1,EEY70019.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219119117,809,1655.57,0,"gi|219119117|re
f|XP_002180325.1|P3A, P type ATPase [Phaeodactylum tricornutum CCAP 1055/1] ","
GO:0016021,GO:0016020,GO:0006812,GO:0015662,GO:0016787,GO:0000166,GO:0005524,GO:
0016887,GO:0006754,GO:0003824,GO:0008152,GO:0016820","XP_002180325.1,EEC48516.1"
Stramenopiles-
Phytophthora_capsici_jgi116830,1302,1912.5,0,"gi|301123081|ref|XP_002909267.1|pl
asma membrane H+-ATPase, putative [Phytophthora infestans T30-4] ","
GO:0016021,GO:0016020,GO:0006812,GO:0015662,GO:0016787,GO:0000166,GO:0005524,GO:
0016887,GO:0006754,GO:0003824,GO:0008152,GO:0016820","XP_002909267.1,EEY58081.1"
Stramenopiles-
Phytophthora_ramorum_jgi38850,849,1674.83,0,"gi|301123081|ref|XP_002909267.1|pla
sma membrane H+-ATPase, putative [Phytophthora infestans T30-4] ","
GO:0016021,GO:0016020,GO:0006812,GO:0015662,GO:0016787,GO:0000166,GO:0005524,GO:
0016887,GO:0006754,GO:0003824,GO:0008152,GO:0016820","XP_002909267.1,EEY58081.1"
Stramenopiles-
Phytophthora_sojae_jgi143361,965,1916.74,0,"gi|301123081|ref|XP_002909267.1|plas
ma membrane H+-ATPase, putative [Phytophthora infestans T30-4] ","
GO:0016021,GO:0016020,GO:0006812,GO:0015662,GO:0016787,GO:0000166,GO:0005524,GO:
0016887,GO:0006754,GO:0003824,GO:0008152,GO:0016820","XP_002909267.1,EEY58081.1"
Stramenopiles-Phytophthora_brassicae_esContig1306_1,244,488.419,2.76E-
136,"gi|301123081|ref|XP_002909267.1|plasma membrane H+-ATPase, putative
[Phytophthora infestans T30-4] ","
GO:0016021,GO:0016020,GO:0006812,GO:0015662,GO:0016787,GO:0000166,GO:0005524,GO:
0016887,GO:0006754,GO:0003824,GO:0008152,GO:0016820","XP_002909267.1,EEY58081.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi29805,868,846.655,0,"gi|301123081|ref|XP_00290926
7.1|plasma membrane H+-ATPase, putative [Phytophthora infestans T30-4] ","
GO:0016021,GO:0016020,GO:0006812,GO:0015662,GO:0016787,GO:0000166,GO:0005524,GO:
0016887,GO:0006754,GO:0003824,GO:0008152,GO:0016820","XP_002909267.1,EEY58081.1"
Stramenopiles-
Phytophthora_sojae_jgi156743,349,645.195,0,gi|301105679|ref|XP_002901923.1|conse
rved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002901923.1,EEY57313.1"
Stramenopiles-Aureococcus_anophagefferens_jgi61634,835,138.658,2.73E-
30,gi|303280379|ref|XP_003059482.1|predicted protein [Micromonas pusilla
CCMP1545] ,"
GO:0016791,GO:0016311,GO:0006470,GO:0008138","XP_003059482.1,EEH56614.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219127007,205,428.328,2.07E-
118,gi|219127007|ref|XP_002183736.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0016209,GO:0016151,GO:0004784","XP_002183736.1,EEC44918.1"
```

```
Stramenopiles-Fragilariopsis_cylindrus_jgi267154,206,340.117,7.58E-
92,gi|219127007|ref|XP_002183736.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0016209,GO:0016151,GO:0004784","XP_002183736.1,EEC44918.1"
Stramenopiles-Aureococcus_anophagefferens_jgi71563,1638,261.536,7.00E-
67,gi|71033369|ref|XP_766326.1|DNA repair protein Rad54 [Theileria parva strain
Muguga] ," GO:0004386,GO:0003676,GO:0005524,GO:0003677","XP_766326.1,EAN34043.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi247791,870,293.893,6.52E-
77,gi|298709934|emb|CBJ31658.1|conserved unknown protein [Ectocarpus
siliculosus],,CBJ31658.1
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223996567,613,1278.08,0,gi|223996567|ref|XP_
002287957.1|hypothetical protein THAPSDRAFT_261481 [Thalassiosira pseudonana
CCMP1335] ,,"XP_002287957.1,EED95400.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi232509,345,318.546,6.63E-
85,gi|149197564|ref|ZP_01874615.1|hypothetical protein LNTAR_01245 [Lentisphaera
araneosa HTCC2155] ,,"ZP_01874615.1,EDM27984.1"
Stramenopiles-Aureococcus_anophagefferens_jgi8504,104,103.99,5.77E-
21,gi|118779434|ref|XP_309303.3|AGAP011348-PA [Anopheles gambiae str. PEST] ,"
GO:0008152,GO:0003824,GO:0008484","XP_309303.3,EAA05277.3"
Stramenopiles-Aureococcus_anophagefferens_jgi27261,615,432.95,5.75E-
119,gi|298706368|emb|CBJ29377.1|Formylglycine-dependent sulfatase [Ectocarpus
siliculosus]," GO:0016787,GO:0008152,GO:0003824,GO:0008484",CBJ29377.1
Stramenopiles-Sargassum_binderi_esgi120455275_3,295,222.246,5.01E-
56,gi|298709363|emb|CBJ31297.1|conserved unknown protein [Ectocarpus
siliculosus]," GO:0005524,GO:0004672,GO:0006468,GO:0004674",CBJ31297.1
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224004054,1432,2982.59,0,gi|224004054|ref|XP
_002295678.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0005681,GO:0000398","XP_002295678.1,ACI64395.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223995765,1972,4109.29,0,gi|223995765|ref|XP
_002287556.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0005681,GO:0000398","XP_002287556.1,EED94999.1"
Stramenopiles-Blastocystis_hominis_tbBHL00002590_2,250,411.379,4.21E-
113,gi|300120898|emb|CBK21140.2|unnamed protein product [Blastocystis hominis],"
GO:0005681,GO:0000398",CBK21140.2
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224001454,933,1925.98,0,gi|224001454|ref|XP_
002290399.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002290399.1,EED92151.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi236403,1060,615.15,1.42E-
173,gi|224001454|ref|XP_002290399.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,,"XP_002290399.1,EED92151.1"
Stramenopiles-
Phytophthora_ramorum_jgi81826,2881,5674.36,0,gi|301112779|ref|XP_002998160.1|dyn
ein heavy chain [Phytophthora infestans T30-4] ,"
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018","X
P_002998160.1,EEY70506.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224009367,1154,2370.89,0,"gi|224009367|ref|X
P_002293642.1|ABC transporter, MRP family [Thalassiosira pseudonana CCMP1335]
","
GO:0016887,GO:0005524,GO:0016021,GO:0000166,GO:0042626,GO:0055085,GO:0017111,GO:
0006810","XP_002293642.1,EED89378.1"
```

```
Stramenopiles-
Aureococcus_anophagefferens_jgi30038,4494,6243.69,0,gi|298708134|emb|CBJ30475.1|
dynein heavy chain [Ectocarpus siliculosus],"
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018",CB
J30475.1
Stramenopiles-
Phytophthora_sojae_jgi136404,2049,3960.22,0,"gi|301098173|ref|XP_002898180.1|dyn
ein heavy chain, outer arm [Phytophthora infestans T30-4] ","
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018","X
P_002898180.1,EEY63593.1"
Stramenopiles-
Phytophthora_ramorum_jgi74125,4839,9036.38,0,"gi|301098173|ref|XP_002898180.1|dy
nein heavy chain, outer arm [Phytophthora infestans T30-4] ","
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018","X
P_002898180.1,EEY63593.1"
Stramenopiles-
Phytophthora_capsici_jgi10094,1839,3497.98,0,"gi|301098173|ref|XP_002898180.1|dy
nein heavy chain, outer arm [Phytophthora infestans T30-4] ","
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018","X
P_002898180.1,EEY63593.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi16,4439,5124.68,0,gi|301112779|ref|XP_002998160.1
|dynein heavy chain [Phytophthora infestans T30-4] ,"
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018","X
P_002998160.1,EEY70506.1"
Stramenopiles-
Phytophthora_ramorum_jgi84849,756,1306.58,0,gi|301102458|ref|XP_002900316.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,
GO:0005488,"XP_002900316.1,EEY60109.1"
Stramenopiles-
Phytophthora_sojae_jgi141520,750,1259.2,0,gi|301102472|ref|XP_002900323.1|conser
ved hypothetical protein [Phytophthora infestans T30-4] ,
GO:0005488,"XP_002900323.1,EEY60116.1"
Stramenopiles-Aureococcus_anophagefferens_jgi24760,153,160.614,4.54E-
38,gi|182413183|ref|YP_001818249.1|Beta-galactosidase [Opitutus terrae PB90-1]
,"
GO:0004565,GO:0004553,GO:0016787,GO:0008152,GO:0005975,GO:0043169,GO:0016798,GO:
0003824","YP_001818249.1,ACB74649.1"
Stramenopiles-Aureococcus_anophagefferens_jgi35927,378,328.176,9.78E-
88,gi|167522441|ref|XP_001745558.1|hypothetical protein [Monosiga brevicollis
MX1] ,"
GO:0004553,GO:0016787,GO:0008152,GO:0005975,GO:0043169,GO:0016798,GO:0003824","X
P_001745558.1,EDQ89529.1"
Stramenopiles-Sargassum_binderi_esContig165_1,402,144.436,2.13E-
32,gi|299472281|emb|CBN77251.1|peptidyl-prolyl cis-trans isomerase 1 [Ectocarpus
siliculosus]," GO:0003755,GO:0006457,GO:0016853",CBN77251.1
Stramenopiles-Fragilariopsis_cylindrus_jgi238385,588,318.546,1.37E-
84,gi|223998340|ref|XP_002288843.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,,"XP_002288843.1,EED94279.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223998340,319,660.218,0,gi|223998340|ref|XP_
002288843.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002288843.1,EED94279.1"
Stramenopiles-
Phytophthora_ramorum_jgi84730,1944,2006.49,0,gi|301090701|ref|XP_002895555.1|con
```

```
served hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002895555.1,EEY55870.1"
Stramenopiles-
Phytophthora_sojae_jgi127347,1955,2046.55,0,gi|301090701|ref|XP_002895555.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002895555.1,EEY55870.1"
Stramenopiles-Phytophthora_ramorum_jgi81567,328,545.428,3.01E-
153,"gi|301112873|ref|XP_002998207.1|FKBP-type peptidyl-prolyl cis-trans
isomerase, putative [Phytophthora infestans T30-4] ","
GO:0003755,GO:0006457,GO:0016853","XP_002998207.1,EEY70553.1"
Stramenopiles-Phytophthora_capsici_jgi62057,209,369.392,1.26E-
100,"gi|301112873|ref|XP_002998207.1|FKBP-type peptidyl-prolyl cis-trans
isomerase, putative [Phytophthora infestans T30-4] ","
GO:0003755,GO:0006457,GO:0016853","XP_002998207.1,EEY70553.1"
Stramenopiles-Phytophthora_sojae_jgi138654,327,534.258,6.80E-
150,"gi|301112873|ref|XP_002998207.1|FKBP-type peptidyl-prolyl cis-trans
isomerase, putative [Phytophthora infestans T30-4] ","
GO:0003755,GO:0006457,GO:0016853","XP_002998207.1,EEY70553.1"
Stramenopiles-Phytophthora_parasitica_esgi68419759_3,283,501.901,3.14E-
140,"gi|301112873|ref|XP_002998207.1|FKBP-type peptidyl-prolyl cis-trans
isomerase, putative [Phytophthora infestans T30-4] ","
GO:0003755,GO:0006457,GO:0016853","XP_002998207.1,EEY70553.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219128810,125,258.84,1.20E-
67,gi|219128810|ref|XP_002184597.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0003755,GO:0006457,GO:0016853","XP_002184597.1,EEC43996.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224006397,113,232.261,1.20E-
59,gi|224006397|ref|XP_002292159.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ," GO:0003755,GO:0006457,GO:0016853","XP_002292159.1,EED91010.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219128812,116,238.81,1.37E-
61,gi|219128812|ref|XP_002184598.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0003755,GO:0006457,GO:0016853","XP_002184598.1,EEC43997.1"
Stramenopiles-Aureococcus_anophagefferens_jgi30278,110,159.073,1.23E-
37,gi|219128812|ref|XP_002184598.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0003755,GO:0006457,GO:0016853","XP_002184598.1,EEC43997.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi185488,130,167.933,2.94E-
40,gi|219128812|ref|XP_002184598.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0003755,GO:0006457,GO:0016853","XP_002184598.1,EEC43997.1"
Stramenopiles-Blastocystis_hominis_tbBHL00000199_1,115,199.904,6.65E-
50,gi|300123577|emb|CBK24849.2|unnamed protein product [Blastocystis hominis],"
GO:0003755,GO:0006457,GO:0016853",CBK24849.2
Stramenopiles-
Phytophthora_capsici_jgi120994,654,1306.58,0,"gi|301117924|ref|XP_002906690.1|tR
NA wybutosine-synthesizing protein, putative [Phytophthora infestans T30-4] ","
GO:0055114,GO:0016491,GO:0005506,GO:0003824,GO:0010181,GO:0051536","XP_002906690
.1,EEY66091.1"
Stramenopiles-
Phytophthora_ramorum_jgi40791,631,1245.72,0,"gi|301117924|ref|XP_002906690.1|tRN
A wybutosine-synthesizing protein, putative [Phytophthora infestans T30-4] ","
GO:0055114,GO:0016491,GO:0005506,GO:0003824,GO:0010181,GO:0051536","XP_002906690
.1,EEY66091.1"
Stramenopiles-
Phytophthora_sojae_jgi108818,598,1147.88,0,"gi|301117924|ref|XP_002906690.1|tRNA
wybutosine-synthesizing protein, putative [Phytophthora infestans T30-4] ","
```

```
GO:0055114,GO:0016491,GO:0005506,GO:0003824,GO:0010181,GO:0051536","XP_002906690
.1,EEY66091.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224004152,564,1175.23,0,gi|224004152|ref|XP_
002295727.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0016491,GO:0003824,GO:0010181,GO:0051536","XP_002295727.1,ACI64444.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219122951,416,872.848,0,gi|219122951|ref
|XP_002181799.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0003824,GO:0051536","XP_002181799.1,EEC47013.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi181471,471,687.567,0,gi|219122951|ref|XP_002181799.1
|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0003824,GO:0051536","XP_002181799.1,EEC47013.1"
Stramenopiles-Aureococcus_anophagefferens_jgi21732,391,550.436,1.45E-
154,gi|219122951|ref|XP_002181799.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0003824,GO:0051536","XP_002181799.1,EEC47013.1"
Stramenopiles-
Phytophthora_capsici_jgi23962,414,835.099,0,gi|194365564|ref|YP_002028174.1|D-3-
phosphoglycerate dehydrogenase [Stenotrophomonas maltophilia R551-3] ,"
GO:0048037,GO:0005488,GO:0016597,GO:0008152,GO:0003824,GO:0016616,GO:0051287","Y
P_002028174.1,ACF51491.1"
Stramenopiles-
Phytophthora_sojae_jgi108653,455,875.93,0,gi|301106016|ref|XP_002902091.1|D-3-
phosphoglycerate dehydrogenase [Phytophthora infestans T30-4] ,"
GO:0051287,GO:0055114,GO:0016597,GO:0016616,GO:0016491,GO:0003824,GO:0048037,GO:
0008152,GO:0005488","XP_002902091.1,EEY56763.1"
Stramenopiles-
Phytophthora_capsici_jgi122113,452,871.307,0,gi|301106016|ref|XP_002902091.1|D-
3-phosphoglycerate dehydrogenase [Phytophthora infestans T30-4] ,"
GO:0051287,GO:0055114,GO:0016597,GO:0016616,GO:0016491,GO:0003824,GO:0048037,GO:
0008152,GO:0005488","XP_002902091.1,EEY56763.1"
Stramenopiles-
Phytophthora_ramorum_jgi71849,455,846.655,0,gi|301106016|ref|XP_002902091.1|D-3-
phosphoglycerate dehydrogenase [Phytophthora infestans T30-4] ,"
GO:0051287,GO:0055114,GO:0016597,GO:0016616,GO:0016491,GO:0003824,GO:0048037,GO:
0008152,GO:0005488","XP_002902091.1,EEY56763.1"
Stramenopiles-
Phytophthora_ramorum_jgi72455,455,846.655,0,gi|301106016|ref|XP_002902091.1|D-3-
phosphoglycerate dehydrogenase [Phytophthora infestans T30-4] ,"
GO:0051287,GO:0055114,GO:0016597,GO:0016616,GO:0016491,GO:0003824,GO:0048037,GO:
0008152,GO:0005488","XP_002902091.1,EEY56763.1"
Stramenopiles-Aureococcus_anophagefferens_jgi31432,515,380.948,2.09E-
103,gi|112143942|gb|ABI13180.1|hypothetical protein [Emiliania huxleyi],"
GO:0005525,GO:0003924,GO:0000166",ABI13180.1
Stramenopiles-Aureococcus_anophagefferens_jgi30262,438,440.269,2.10E-
121,"gi|298713481|emb|CBJ27036.1|RME1, RME-1/EHD family ATPase with a C-terminal
EH domain [Ectocarpus siliculosus]","
GO:0005525,GO:0003924,GO:0005509,GO:0000166",CBJ27036.1
Stramenopiles-Aureococcus_anophagefferens_jgi1666,383,323.553,2.74E-
86,"gi|298713481|emb|CBJ27036.1|RME1, RME-1/EHD family ATPase with a C-terminal
EH domain [Ectocarpus siliculosus]","
GO:0005525,GO:0003924,GO:0005509,GO:0000166",CBJ27036.1
Stramenopiles-
Fragilariopsis_cylindrus_jgi226667,568,908.286,0,gi|219128084|ref|XP_002184252.1
```

```
|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0005525,GO:0003924,GO:0005509","XP_002184252.1,EEC44430.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219128084,559,1140.95,0,gi|219128084|ref
|XP_002184252.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0005525,GO:0003924,GO:0005509","XP_002184252.1,EEC44430.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224009007,554,1138.25,0,gi|224009007|ref|XP_
002293462.1|receptor mediated endocytosis protein-like protein [Thalassiosira
pseudonana CCMP1335] ,"
GO:0005525,GO:0003924,GO:0005509,GO:0004872","XP_002293462.1,EED89198.1"
Stramenopiles-
Phytophthora_capsici_jgi82033,554,1009.59,0,gi|301100502|ref|XP_002899341.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0005525,GO:0003924,GO:0005509,GO:0000166","XP_002899341.1,EEY62310.1"
Stramenopiles-
Phytophthora_sojae_jgi109073,565,1011.13,0,gi|301100502|ref|XP_002899341.1|conse
rved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0005525,GO:0003924,GO:0005509,GO:0000166","XP_002899341.1,EEY62310.1"
Stramenopiles-
Phytophthora_ramorum_jgi52913,523,974.541,0,gi|301100502|ref|XP_002899341.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0005525,GO:0003924,GO:0005509,GO:0000166","XP_002899341.1,EEY62310.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi269305,226,56.6102,2.30E-
06,gi|15896255|ref|NP_349604.1|thymidylate synthase [Clostridium acetobutylicum
ATCC 824] ,"
GO:0009165,GO:0008168,GO:0005737,GO:0016740,GO:0006231,GO:0004799","NP_349604.1,
Q97EV3.1,AAK80944.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi54697,1148,748.429,0,gi|15237798|ref|NP_197752.1|
ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase familiy
protein [Arabidopsis thaliana] ,"
GO:0006875,GO:0009846,GO:0048867,GO:0016036,GO:0019829,GO:0005783,GO:0010152,GO:
0010073,GO:0005886","NP_197752.1,Q9LT02.1,BAA97238.1"
Stramenopiles-Aureococcus_anophagefferens_jgi27290,407,265.388,8.03E-
69,gi|260830940|ref|XP_002610418.1|hypothetical protein BRAFLDRAFT_277711
[Branchiostoma floridae] ,"
GO:0019752,GO:0003824,GO:0016831,GO:0030170,GO:0016829","XP_002610418.1,EEN66428
.1"
Stramenopiles-
Phytophthora_ramorum_jgi72686,609,1110.9,0,"gi|301122515|ref|XP_002908984.1|sphi
ngosine-1-phosphate lyase, putative [Phytophthora infestans T30-4] ","
GO:0019752,GO:0003824,GO:0016831,GO:0030170,GO:0016829","XP_002908984.1,EEY57798
.1"
Stramenopiles-Phytophthora_nicotianae_esgi40545120_2,216,359.762,1.10E-
97,"gi|301122515|ref|XP_002908984.1|sphingosine-1-phosphate lyase, putative
[Phytophthora infestans T30-4] ","
GO:0019752,GO:0003824,GO:0016831,GO:0030170,GO:0016829","XP_002908984.1,EEY57798
.1"
Stramenopiles-
Phytophthora_sojae_jgi130206,613,1117.84,0,"gi|301122515|ref|XP_002908984.1|sphi
ngosine-1-phosphate lyase, putative [Phytophthora infestans T30-4] ","
GO:0019752,GO:0003824,GO:0016831,GO:0030170,GO:0016829","XP_002908984.1,EEY57798
.1"
```

```
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219127490,442,921.383,0,gi|219127490|ref
|XP_002183967.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0019752,GO:0003824,GO:0016831,GO:0030170,GO:0016829","XP_002183967.1,EEC44636
.1"
Stramenopiles-
Phytophthora_ramorum_jgi87801,517,989.564,0,gi|301120111|ref|XP_002907783.1|keto
l-acid reductoisomerase [Phytophthora infestans T30-4] ,"
GO:0050662,GO:0009082,GO:0004455,GO:0055114,GO:0016491,GO:0003824,GO:0016853,GO:
0008152,GO:0008652,GO:0005488","XP_002907783.1,EEY64347.1"
Stramenopiles-
Phytophthora_capsici_jgi98884,516,1013.06,0,gi|301120111|ref|XP_002907783.1|keto
l-acid reductoisomerase [Phytophthora infestans T30-4] ,"
GO:0050662,GO:0009082,GO:0004455,GO:0055114,GO:0016491,GO:0003824,GO:0016853,GO:
0008152,GO:0008652,GO:0005488","XP_002907783.1,EEY64347.1"
Stramenopiles-
Phytophthora_sojae_jgi136278,516,1009.21,0,gi|301120111|ref|XP_002907783.1|ketol
-acid reductoisomerase [Phytophthora infestans T30-4] ,"
GO:0050662,GO:0009082,GO:0004455,GO:0055114,GO:0016491,GO:0003824,GO:0016853,GO:
0008152,GO:0008652,GO:0005488","XP_002907783.1,EEY64347.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219129854,539,1109.36,0,gi|219129854|ref
|XP_002185094.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0050662,GO:0009082,GO:0004455,GO:0055114,GO:0016491,GO:0003824,GO:0008152,GO:
0008652,GO:0005488","XP_002185094.1,EEC43541.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi166620,541,966.452,0,gi|219129854|ref|XP_002185094.1
|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0050662,GO:0009082,GO:0004455,GO:0055114,GO:0016491,GO:0003824,GO:0008152,GO:
0008652,GO:0005488","XP_002185094.1,EEC43541.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi160634,182,226.868,6.91E-
58,gi|294891272|ref|XP_002773506.1|phytanoyl-CoA dioxygenase domain containing
protein [Perkinsus marinus ATCC 50983] , GO:0016702,"XP_002773506.1,EER05322.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224007769,373,782.711,0,gi|224007769|ref|XP_
002292844.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002292844.1,EED90040.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi272003,162,48.1358,3.09E-
04,gi|167998196|ref|XP_001751804.1|predicted protein [Physcomitrella patens
subsp. patens] ," GO:0009055,GO:0005507","XP_001751804.1,EDQ83239.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi264955,223,53.1434,2.65E-
05,gi|159478102|ref|XP_001697143.1|hypothetical protein CHLREDRAFT_175974
[Chlamydomonas reinhardtii] ,,"XP_001697143.1,EDP00398.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi225537,326,339.347,3.36E-
91,gi|219130285|ref|XP_002185299.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0006342,GO:0070403,GO:0016811,GO:0045449,GO:0008270,GO:0006476","XP_002185299
.1,EEC43168.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219130285,264,545.428,2.15E-
153,gi|219130285|ref|XP_002185299.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0006342,GO:0070403,GO:0016811,GO:0045449,GO:0008270,GO:0006476","XP_002185299
.1,EEC43168.1"
```

```
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224006025,275,570.852,4.83E-
161,gi|224006025|ref|XP_002291973.1|sir2-like transcriptional regulatory protein
found in-like protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0006342,GO:0070403,GO:0016811,GO:0045449,GO:0008270,GO:0006476","XP_002291973
.1,EED90824.1"
Stramenopiles-Blastocystis_hominis_tbBHL00002755_3,97,162.155,1.84E-
38,gi|300120380|emb|CBK19934.2|unnamed protein product [Blastocystis hominis],"
GO:0006342,GO:0070403,GO:0016811,GO:0045449,GO:0008270,GO:0051287,GO:0006476",CB
K19934.2
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219113065,333,695.656,0,gi|219113065|ref
|XP_002186116.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002186116.1,ACI65586.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi184803,419,228.024,1.57E-
57,gi|283782174|ref|YP_003372929.1|protein of unknown function DUF303
acetylesterase putative [Pirellula staleyi DSM 6068] ,
GO:0016787,"YP_003372929.1,ADB19069.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223995025,837,1741.86,0,gi|223995025|ref|XP_
002287196.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,
GO:0005515,"XP_002287196.1,EED94639.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi196034,374,426.402,2.62E-
117,gi|219123017|ref|XP_002181829.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] , GO:0005515,"XP_002181829.1,EEC46369.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219123017,925,1934.07,0,gi|219123017|ref
|XP_002181829.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,
GO:0005515,"XP_002181829.1,EEC46369.1"
Stramenopiles-Aureococcus_anophagefferens_jgi5150,336,270.011,2.68E-
70,gi|256394010|ref|YP_003115574.1|Alpha-L-arabinofuranosidase B catalytic
[Catenulispora acidiphila DSM 44928] ,"
GO:0031221,GO:0046556","YP_003115574.1,ACU73733.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi244951,976,581.252,2.11E-
163,gi|223996447|ref|XP_002287897.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ," GO:0016624,GO:0008152","XP_002287897.1,EED95340.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219112671,468,978.778,0,gi|219112671|ref
|XP_002178087.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002178087.1,EEC50901.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223996447,814,1694.48,0,gi|223996447|ref|XP_
002287897.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0016624,GO:0008152","XP_002287897.1,EED95340.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219111705,613,1283.09,0,gi|219111705|ref
|XP_002177604.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002177604.1,EEC50418.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219112337,549,1153.27,0,gi|219112337|ref
|XP_002177920.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002177920.1,EEC50734.1"
Stramenopiles-Phytophthora_parasitica_esgi222375374_2,205,295.434,2.04E-
78,"gi|301112805|ref|XP_002998173.1|spindle assembly protein, putative
[Phytophthora infestans T30-4] ",,"XP_002998173.1,EEY70519.1"
```

```
Stramenopiles-Phytophthora_capsici_jgi48203,237,420.624,5.65E-
116,"gi|301112805|ref|XP_002998173.1|spindle assembly protein, putative
[Phytophthora infestans T30-4] ",,"XP_002998173.1,EEY70519.1"
Stramenopiles-Aureococcus_anophagefferens_jgi60767,441,189.504,6.06E-
46,gi|224001472|ref|XP_002290408.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,,"XP_002290408.1,EED92160.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223998456,568,1176.39,0,gi|223998456|ref|XP_
002288901.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,
GO:0016491,"XP_002288901.1,EED94337.1"
Stramenopiles-Aureococcus_anophagefferens_jgi72374,894,314.694,3.23E-
83,gi|301109731|ref|XP_002903946.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,"
GO:0045449,GO:0030528,GO:0005634","XP_002903946.1,EEY55001.1"
Stramenopiles-Aureococcus_anophagefferens_jgi55061,599,394.43,1.95E-
107,gi|170111503|ref|XP_001886955.1|predicted protein [Laccaria bicolor S238N-
H82] ," GO:0045449,GO:0030528,GO:0005634","XP_001886955.1,EDR02278.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219110195,107,222.246,1.30E-
56,gi|219110195|ref|XP_002176849.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0045449,GO:0030528,GO:0005634","XP_002176849.1,EEC51312.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi192974,76,150.984,3.56E-
35,gi|219110195|ref|XP_002176849.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0045449,GO:0030528,GO:0005634","XP_002176849.1,EEC51312.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224010858,140,293.123,6.48E-
78,gi|224010858|ref|XP_002294386.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ," GO:0045449,GO:0030528,GO:0005634","XP_002294386.1,EED88220.1"
Stramenopiles-Phytophthora_ramorum_jgi86442,436,407.527,1.73E-
111,gi|301109731|ref|XP_002903946.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,"
GO:0045449,GO:0030528,GO:0005634","XP_002903946.1,EEY55001.1"
Stramenopiles-
Phytophthora_capsici_jgi106782,613,936.791,0,gi|301109731|ref|XP_002903946.1|con
served hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0045449,GO:0030528,GO:0005634","XP_002903946.1,EEY55001.1"
Stramenopiles-
Phytophthora_sojae_jgi156463,927,938.332,0,gi|301109731|ref|XP_002903946.1|conse
rved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0045449,GO:0030528,GO:0005634","XP_002903946.1,EEY55001.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi210817,329,265.388,6.42E-
69,gi|219122488|ref|XP_002181576.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002181576.1,EEC46790.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219122488,310,637.106,0,gi|219122488|ref
|XP_002181576.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002181576.1,EEC46790.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi195507,396,178.718,1.14E-
42,gi|219122488|ref|XP_002181576.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002181576.1,EEC46790.1"
Stramenopiles-Sargassum_binderi_esgi120454435_2,277,265.003,6.85E-
69,gi|298707892|emb|CBJ30289.1|conserved unknown protein [Ectocarpus
siliculosus],,CBJ30289.1
Stramenopiles-Aureococcus_anophagefferens_jgi70546,932,191.43,4.09E-
46,gi|298707892|emb|CBJ30289.1|conserved unknown protein [Ectocarpus
siliculosus],,CBJ30289.1
```

```
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219129453,722,1506.89,0,gi|219129453|ref
|XP_002184903.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002184903.1,EEC43639.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi237325,724,983.786,0,gi|219129453|ref|XP_002184903.1
|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002184903.1,EEC43639.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224013341,589,1238.4,0,gi|224013341|ref|XP_0
02295322.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002295322.1,EED87388.1"
Stramenopiles-Aureococcus_anophagefferens_jgi68493,577,200.29,5.31E-
49,gi|299472005|emb|CBN80088.1|conserved unknown protein [Ectocarpus
siliculosus],,CBN80088.1
Stramenopiles-
Aureococcus_anophagefferens_jgi71551,1953,674.47,0,gi|299472005|emb|CBN80088.1|c
onserved unknown protein [Ectocarpus siliculosus],,CBN80088.1
Stramenopiles-
Phytophthora_capsici_jgi26673,366,687.952,0,gi|301117528|ref|XP_002906492.1|dyne
in heavy chain [Phytophthora infestans T30-4] ,"
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018,GO:
0005515","XP_002906492.1,EEY65893.1"
Stramenopiles-
Phytophthora_sojae_jgi156858,4071,7883.87,0,gi|301117528|ref|XP_002906492.1|dyne
in heavy chain [Phytophthora infestans T30-4] ,"
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018,GO:
0005515","XP_002906492.1,EEY65893.1"
Stramenopiles-
Phytophthora_ramorum_jgi94368,4097,7870.38,0,gi|301117528|ref|XP_002906492.1|dyn
ein heavy chain [Phytophthora infestans T30-4] ,"
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018,GO:
0005515","XP_002906492.1,EEY65893.1"
Stramenopiles-
Phytophthora_sojae_jgi137480,483,899.812,0,gi|301121454|ref|XP_002908454.1|dynei
n heavy chain [Phytophthora infestans T30-4] ,"
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018,GO:
0005515","XP_002908454.1,EEY61537.1"
Stramenopiles-
Phytophthora_capsici_jgi22599,470,890.952,0,gi|301121454|ref|XP_002908454.1|dyne
in heavy chain [Phytophthora infestans T30-4] ,"
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018,GO:
0005515","XP_002908454.1,EEY61537.1"
Stramenopiles-Aureococcus_anophagefferens_jgi63122,4491,235.728,1.06E-
58,gi|219129512|ref|XP_002184931.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002184931.1,EEC43667.1"
Stramenopiles-Aureococcus_anophagefferens_jgi62184,1051,141.354,6.51E-
31,gi|307108841|gb|EFN57080.1|hypothetical protein CHLNCDRAFT_143848 [Chlorella
variabilis],,EFN57080.1
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224012539,815,1714.89,0,gi|224012539|ref|XP_
002294922.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002294922.1,EED87702.1"
```

```
Stramenopiles-Phytophthora_ramorum_jgi74818,1338,360.147,1.24E-
96,gi|291190357|ref|NP_001167244.1|myotubularin [Salmo salar] ,"
GO:0016791,GO:0016311,GO:0016787,GO:0004725","NP_001167244.1,ACN11182.1"
Stramenopiles-Phytophthora_capsici_jgi122196,1268,369.007,2.27E-
99,gi|291190357|ref|NP_001167244.1|myotubularin [Salmo salar] ,"
GO:0016791,GO:0016311,GO:0016787,GO:0004725","NP_001167244.1,ACN11182.1"
Stramenopiles-Phytophthora_sojae_jgi141343,1343,362.073,2.99E-
97,gi|147899223|ref|NP_001089410.1|myotubularin [Xenopus laevis] ,"
GO:0016791,GO:0016311,GO:0016787,GO:0004725,GO:0004721","NP_001089410.1,Q52KU6.1
,AAH94184.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219115697,619,1268.83,0,gi|219115697|ref
|XP_002178644.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,
GO:0016021,"XP_002178644.1,EEC50309.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi260081,654,917.531,0,gi|219115697|ref|XP_002178644.1
|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,
GO:0016021,"XP_002178644.1,EEC50309.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224002460,610,1249.19,0,gi|224002460|ref|XP_
002290902.1|endomembrane protein EMP70 precusor [Thalassiosira pseudonana
CCMP1335] , GO:0016021,"XP_002290902.1,EED92654.1"
Stramenopiles-
Phytophthora_capsici_jgi222,1361,1137.48,0,"gi|301118310|ref|XP_002906883.1|endo
membrane protein 70-like protein, putative [Phytophthora infestans T30-4] ",
GO:0016021,"XP_002906883.1,EEY66284.1"
Stramenopiles-
Phytophthora_sojae_jgi157453,1540,1387.47,0,"gi|301118308|ref|XP_002906882.1|end
omembrane protein 70-like protein, putative [Phytophthora infestans T30-4]
",,"XP_002906882.1,EEY66283.1"
Stramenopiles-Phytophthora_ramorum_jgi85151,1983,418.698,3.59E-
114,gi|291221631|ref|XP_002730823.1|PREDICTED: Gap-Pol polyprotein-like
[Saccoglossus kowalevskii],,XP_002730823.1
Stramenopiles-Phytophthora_sojae_jgi136255,2557,590.112,1.36E-
165,gi|301123269|ref|XP_002909361.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ," GO:0006508,GO:0004190","XP_002909361.1,EEY58175.1"
Stramenopiles-Phytophthora_sojae_jgi133348,2211,590.112,1.23E-
165,gi|301123269|ref|XP_002909361.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ," GO:0006508,GO:0004190","XP_002909361.1,EEY58175.1"
Stramenopiles-Phytophthora_sojae_jgi132494,1800,510.76,7.49E-
142,gi|301123269|ref|XP_002909361.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ," GO:0006508,GO:0004190","XP_002909361.1,EEY58175.1"
Stramenopiles-Aureococcus_anophagefferens_jgi62784,1062,110.538,1.24E-
21,gi|149200144|ref|ZP_01877168.1|hypothetical protein LNTAR_03259 [Lentisphaera
araneosa HTCC2155] ,,"ZP_01877168.1,EDM25214.1"
Stramenopiles-Phytophthora_brassicae_esgi144588290_1,143,155.221,1.75E-
36,gi|301119119|ref|XP_002907287.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002907287.1,EEY63851.1"
Stramenopiles-Phytophthora_ramorum_jgi51813,399,521.931,4.66E-
146,gi|301119119|ref|XP_002907287.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002907287.1,EEY63851.1"
Stramenopiles-
Phytophthora_capsici_jgi3288,429,660.218,0,gi|301119119|ref|XP_002907287.1|conse
rved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002907287.1,EEY63851.1"
```

```
Stramenopiles-
Phytophthora_sojae_jgi128375,519,667.537,0,gi|301119119|ref|XP_002907287.1|conse
rved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002907287.1,EEY63851.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224011235,715,1471.83,0,gi|224011235|ref|XP_
002295392.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002295392.1,ACI64109.1"
Stramenopiles-Aureococcus_anophagefferens_jgi11416,333,274.633,1.04E-
71,gi|298704878|emb|CBJ28395.1|conserved unknown protein [Ectocarpus
siliculosus],,CBJ28395.1
Stramenopiles-
Phytophthora_capsici_jgi20595,609,862.448,0,gi|301117928|ref|XP_002906692.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002906692.1,EEY66093.1"
Stramenopiles-
Phytophthora_sojae_jgi134872,626,931.784,0,gi|301117928|ref|XP_002906692.1|conse
rved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002906692.1,EEY66093.1"
Stramenopiles-Aureococcus_anophagefferens_jgi20459,409,212.616,6.44E-
53,gi|29335747|dbj|BAC66445.1|alpha-galactosidase [Helianthus annuus],"
GO:0004553,GO:0016787,GO:0008152,GO:0005975,GO:0043169,GO:0016798,GO:0003824",BA
C66445.1
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219112825,384,797.734,0,gi|219112825|ref
|XP_002185996.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0005488,GO:0008152,GO:0003824","XP_002185996.1,ACI65466.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi226569,377,407.912,1.07E-
111,gi|223997386|ref|XP_002288366.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,"
GO:0005488,GO:0016491,GO:0008152,GO:0003824","XP_002288366.1,EED93802.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223997386,368,762.681,0,gi|223997386|ref|XP_
002288366.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0005488,GO:0016491,GO:0008152,GO:0003824","XP_002288366.1,EED93802.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224007146,396,820.076,0,gi|224007146|ref|XP_
002292533.1|hypothetical protein THAPSDRAFT_269459 [Thalassiosira pseudonana
CCMP1335] ,"
GO:0005488,GO:0016491,GO:0008152,GO:0003824","XP_002292533.1,EED90508.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224007144,439,912.138,0,gi|224007144|ref|XP_
002292532.1|hypothetical protein THAPSDRAFT_24060 [Thalassiosira pseudonana
CCMP1335] ,"
GO:0005488,GO:0016491,GO:0008152,GO:0003824","XP_002292532.1,EED90507.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi268182,234,413.305,1.10E-
113,gi|224007144|ref|XP_002292532.1|hypothetical protein THAPSDRAFT_24060
[Thalassiosira pseudonana CCMP1335] ,"
GO:0005488,GO:0016491,GO:0008152,GO:0003824","XP_002292532.1,EED90507.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219127313,1167,2419.81,0,gi|219127313|re
f|XP_002183882.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0005488,GO:0008152,GO:0003824","XP_002183882.1,EEC44551.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219115007,439,916.376,0,gi|219115007|ref
```

```
|XP_002178299.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0005488,GO:0008152,GO:0003824","XP_002178299.1,EEC49964.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi269966,370,538.88,4.00E-
151,gi|219115007|ref|XP_002178299.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0005488,GO:0008152,GO:0003824","XP_002178299.1,EEC49964.1"
Stramenopiles-Aureococcus_anophagefferens_jgi66270,387,347.436,1.55E-
93,gi|224007146|ref|XP_002292533.1|hypothetical protein THAPSDRAFT_269459
[Thalassiosira pseudonana CCMP1335] ,"
GO:0005488,GO:0016491,GO:0008152,GO:0003824","XP_002292533.1,EED90508.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224009648,960,1979.91,0,gi|224009648|ref|XP_
002293782.1|hypothetical protein THAPSDRAFT_264188 [Thalassiosira pseudonana
CCMP1335] ,"
GO:0046872,GO:0006508,GO:0003824,GO:0008270,GO:0004222","XP_002293782.1,EED88791
.1"
Stramenopiles-
Phytophthora_sojae_jgi143780,489,673.315,0,"gi|301104593|ref|XP_002901381.1|seri
ne protease family S08A, putative [Phytophthora infestans T30-4] ","
GO:0006508,GO:0004252,GO:0008233","XP_002901381.1,EEY58908.1"
Stramenopiles-
Phytophthora_sojae_jgi143289,489,685.641,0,"gi|301104593|ref|XP_002901381.1|seri
ne protease family S08A, putative [Phytophthora infestans T30-4] ","
GO:0006508,GO:0004252,GO:0008233","XP_002901381.1,EEY58908.1"
Stramenopiles-Phytophthora_capsici_jgi21939,334,505.753,2.82E-
141,"gi|301104593|ref|XP_002901381.1|serine protease family S08A, putative
[Phytophthora infestans T30-4] ","
GO:0006508,GO:0004252,GO:0008233","XP_002901381.1,EEY58908.1"
Stramenopiles-Phytophthora_brassicae_esgi144593721_5,247,317.39,8.98E-
85,"gi|301104593|ref|XP_002901381.1|serine protease family S08A, putative
[Phytophthora infestans T30-4] ","
GO:0006508,GO:0004252,GO:0008233","XP_002901381.1,EEY58908.1"
Stramenopiles-Phytophthora_brassicae_esgi144590221_4,127,164.851,2.24E-
39,"gi|301104593|ref|XP_002901381.1|serine protease family S08A, putative
[Phytophthora infestans T30-4] ","
GO:0006508,GO:0004252,GO:0008233","XP_002901381.1,EEY58908.1"
Stramenopiles-
Phytophthora_ramorum_jgi84204,535,814.683,0,"gi|301101239|ref|XP_002899708.1|ser
ine protease family S08A, putative [Phytophthora infestans T30-4] ","
GO:0006508,GO:0004252,GO:0008233","XP_002899708.1,EEY60762.1"
Stramenopiles-Phytophthora_sojae_jgi123724,331,469.929,1.73E-
130,"gi|301123077|ref|XP_002909265.1|serine protease family S08A, putative
[Phytophthora infestans T30-4] ","
GO:0006508,GO:0004252,GO:0008233","XP_002909265.1,EEY58079.1"
Stramenopiles-Phytophthora_ramorum_jgi38840,415,599.742,2.15E-
169,"gi|301123077|ref|XP_002909265.1|serine protease family S08A, putative
[Phytophthora infestans T30-4] ","
GO:0006508,GO:0004252,GO:0008233","XP_002909265.1,EEY58079.1"
Stramenopiles-Aureococcus_anophagefferens_jgi68573,1016,337.421,5.52E-
90,gi|285808340|gb|ADC35870.1|hypothetical protein [uncultured bacterium
92],,ADC35870.1
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223993279,658,1353.96,0,gi|223993279|ref|XP_
002286323.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0003852,GO:0016740,GO:0008152,GO:0046912,GO:0019752,GO:0003824,GO:0009098","X
P_002286323.1,EED95964.1"
```

```
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219115673,663,1363.59,0,gi|219115673|ref
|XP_002178632.1|2-isopropylmalate synthase [Phaeodactylum tricornutum CCAP
1055/1] ,"
GO:0003852,GO:0016740,GO:0008152,GO:0046912,GO:0019752,GO:0003824,GO:0009098","X
P_002178632.1,EEC50297.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi277320,628,993.801,0,gi|219115673|ref|XP_002178632.1
|2-isopropylmalate synthase [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0003852,GO:0016740,GO:0008152,GO:0046912,GO:0019752,GO:0003824,GO:0009098","X
P_002178632.1,EEC50297.1"
Stramenopiles-
Phytophthora_sojae_jgi108956,528,1031.55,0,gi|301118112|ref|XP_002906784.1|2-
isopropylmalate synthase [Phytophthora infestans T30-4] ,"
GO:0003852,GO:0016740,GO:0008152,GO:0046912,GO:0019752,GO:0003824,GO:0009098","X
P_002906784.1,EEY66185.1"
Stramenopiles-
Phytophthora_capsici_jgi95116,577,1106.28,0,gi|301118112|ref|XP_002906784.1|2-
isopropylmalate synthase [Phytophthora infestans T30-4] ,"
GO:0003852,GO:0016740,GO:0008152,GO:0046912,GO:0019752,GO:0003824,GO:0009098","X
P_002906784.1,EEY66185.1"
Stramenopiles-
Phytophthora_ramorum_jgi75281,577,1103.2,0,gi|301118112|ref|XP_002906784.1|2-
isopropylmalate synthase [Phytophthora infestans T30-4] ,"
GO:0003852,GO:0016740,GO:0008152,GO:0046912,GO:0019752,GO:0003824,GO:0009098","X
P_002906784.1,EEY66185.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi38625,617,829.321,0,gi|219115673|ref|XP_002178632
.1|2-isopropylmalate synthase [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0003852,GO:0016740,GO:0008152,GO:0046912,GO:0019752,GO:0003824,GO:0009098","X
P_002178632.1,EEC50297.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi54528,610,821.617,0,gi|219115673|ref|XP_002178632
.1|2-isopropylmalate synthase [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0003852,GO:0016740,GO:0008152,GO:0046912,GO:0019752,GO:0003824,GO:0009098","X
P_002178632.1,EEC50297.1"
Stramenopiles-Aureococcus_anophagefferens_jgi7873,133,112.079,1.91E-
23,gi|297828281|ref|XP_002882023.1|hypothetical protein ARALYDRAFT_904009
[Arabidopsis lyrata subsp. lyrata] ,,"XP_002882023.1,EFH58282.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi179112,252,144.436,1.01E-
32,gi|225713936|gb|ACO12814.1|FK506-binding protein 14 precursor [Lepeophtheirus
salmonis] ," GO:0005509,GO:0006457","ACO12814.1,ADD38568.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi209669,1048,1808.88,0,gi|219129893|ref|XP_002185112.
1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,
GO:0005488,"XP_002185112.1,EEC43244.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219129893,1045,2153.25,0,gi|219129893|re
f|XP_002185112.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,
GO:0005488,"XP_002185112.1,EEC43244.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223997554,975,2008.8,0,gi|223997554|ref|XP_0
02288450.1|hypothetical protein THAPSDRAFT_27556 [Thalassiosira pseudonana
CCMP1335] , GO:0005488,"XP_002288450.1,EED93886.1"
```

```
Stramenopiles-
Aureococcus_anophagefferens_jgi37713,1298,1670.98,0,gi|147905376|ref|NP_00108415
0.1|splicing factor 3B subunit 1 [Xenopus laevis] ,"
GO:0005681,GO:0005488,GO:0008380,GO:0006397,GO:0005634","NP_001084150.1,O57683.1
,CAA70201.1"
Stramenopiles-
Phytophthora_ramorum_jgi71523,1230,2307.33,0,gi|301113146|ref|XP_002998343.1|spl
icing factor 3B subunit 1 [Phytophthora infestans T30-4] ,
GO:0005488,"XP_002998343.1,EEY69696.1"
Stramenopiles-
Phytophthora_sojae_jgi109252,1263,2295,0,gi|301113146|ref|XP_002998343.1|splicin
g factor 3B subunit 1 [Phytophthora infestans T30-4] ,
GO:0005488,"XP_002998343.1,EEY69696.1"
Stramenopiles-Aureococcus_anophagefferens_jgi71230,2401,214.157,1.97E-
52,gi|298705070|emb|CBJ28529.1|conserved unknown protein [Ectocarpus
siliculosus]," GO:0030154,GO:0016779,GO:0016020",CBJ28529.1
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219121057,918,1876.68,0,gi|219121057|ref
|XP_002185760.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0016021,GO:0016020,GO:0008158","XP_002185760.1,ACI65230.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219121059,956,1960.27,0,gi|219121059|ref
|XP_002185761.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0016021,GO:0016020,GO:0008158","XP_002185761.1,ACI65231.1"
Stramenopiles-
Phytophthora_capsici_jgi87116,1563,1139.41,0,"gi|301094223|ref|XP_002997955.1|fa
tty acid synthase subunit alpha, putative [Phytophthora infestans T30-4] ","
GO:0016740,GO:0009059,GO:0006633,GO:0005737,GO:0055114,GO:0016491,GO:0003824,GO:
0004312,GO:0005835,GO:0008897,GO:0008152,GO:0000287,GO:0005488","XP_002997955.1,
EEY67793.1"
Stramenopiles-Aureococcus_anophagefferens_jgi21424,343,357.451,1.41E-
96,gi|256394010|ref|YP_003115574.1|Alpha-L-arabinofuranosidase B catalytic
[Catenulispora acidiphila DSM 44928] ,"
GO:0031221,GO:0046556","YP_003115574.1,ACU73733.1"
Stramenopiles-Aureococcus_anophagefferens_jgi1957,346,312.383,4.66E-
83,gi|256394010|ref|YP_003115574.1|Alpha-L-arabinofuranosidase B catalytic
[Catenulispora acidiphila DSM 44928] ,"
GO:0031221,GO:0046556","YP_003115574.1,ACU73733.1"
Stramenopiles-Aureococcus_anophagefferens_jgi2105,336,268.085,1.03E-
69,gi|256394010|ref|YP_003115574.1|Alpha-L-arabinofuranosidase B catalytic
[Catenulispora acidiphila DSM 44928] ,"
GO:0031221,GO:0046556","YP_003115574.1,ACU73733.1"
Stramenopiles-Phytophthora_sojae_jgi132315,352,577.015,9.59E-
163,gi|301114169|ref|XP_002998854.1|arabinofuranosidase [Phytophthora infestans
T30-4] ," GO:0031221,GO:0046556","XP_002998854.1,EEY69000.1"
Stramenopiles-Phytophthora_ramorum_jgi72148,357,580.867,8.45E-
164,gi|301114169|ref|XP_002998854.1|arabinofuranosidase [Phytophthora infestans
T30-4] ," GO:0031221,GO:0046556","XP_002998854.1,EEY69000.1"
Stramenopiles-Phytophthora_capsici_jgi24809,216,384.415,4.19E-
105,gi|301114169|ref|XP_002998854.1|arabinofuranosidase [Phytophthora infestans
T30-4] ," GO:0031221,GO:0046556","XP_002998854.1,EEY69000.1"
Stramenopiles-Phytophthora_capsici_jgi26231,361,621.313,5.60E-
176,gi|301114169|ref|XP_002998854.1|arabinofuranosidase [Phytophthora infestans
T30-4] ," GO:0031221,GO:0046556","XP_002998854.1,EEY69000.1"
```

```
Stramenopiles-Phytophthora_parasitica_esgi222414211_3,258,425.631,2.53E-
117,gi|301114169|ref|XP_002998854.1|arabinofuranosidase [Phytophthora infestans
T30-4] ," GO:0031221,GO:0046556","XP_002998854.1,EEY69000.1"
Stramenopiles-Phytophthora_sojae_jgi108620,362,437.573,1.21E-
120,gi|301114169|ref|XP_002998854.1|arabinofuranosidase [Phytophthora infestans
T30-4] ," GO:0031221,GO:0046556","XP_002998854.1,EEY69000.1"
Stramenopiles-
Phytophthora_sojae_jgi128108,729,754.207,0,gi|301102658|ref|XP_002900416.1|conse
rved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0005509,GO:0006457,GO:0005515","XP_002900416.1,EEY60209.1"
Stramenopiles-
Phytophthora_capsici_jgi85544,497,724.161,0,gi|301102658|ref|XP_002900416.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0005509,GO:0006457,GO:0005515","XP_002900416.1,EEY60209.1"
Stramenopiles-
Phytophthora_ramorum_jgi95158,706,736.102,0,gi|301102658|ref|XP_002900416.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0005509,GO:0006457,GO:0005515","XP_002900416.1,EEY60209.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219125257,477,992.645,0,gi|219125257|ref
|XP_002182901.1|delta 6 fatty acid desaturase [Phaeodactylum tricornutum CCAP
1055/1] ,"
GO:0006629,GO:0055114,GO:0016717,GO:0020037,GO:0016491,GO:0005506,GO:0006633","X
P_002182901.1,AAL92563.1,EEC45637.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224003715,484,1011.13,0,gi|224003715|ref|XP_
002291529.1|probable microsomal delta-6 desaturase [Thalassiosira pseudonana
CCMP1335] ,"
GO:0006629,GO:0055114,GO:0016717,GO:0020037,GO:0016491,GO:0005506,GO:0006633","X
P_002291529.1,AAX14505.1,EED91636.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi228533,489,709.138,0,gi|219125257|ref|XP_002182901.1
|delta 6 fatty acid desaturase [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0006629,GO:0055114,GO:0016717,GO:0020037,GO:0016491,GO:0005506,GO:0006633","X
P_002182901.1,AAL92563.1,EEC45637.1"
Stramenopiles-
Phytophthora_sojae_jgi108614,457,902.894,0,gi|111572541|gb|ABH10627.1|delta-6
desaturase [Phytophthora citrophthora],"
GO:0006629,GO:0055114,GO:0016717,GO:0020037,GO:0016491,GO:0005506,GO:0006633",AB
H10627.1
Stramenopiles-Phytophthora_capsici_jgi117744,274,520.776,5.32E-
146,gi|111572541|gb|ABH10627.1|delta-6 desaturase [Phytophthora citrophthora],"
GO:0006629,GO:0055114,GO:0016717,GO:0020037,GO:0016491,GO:0005506,GO:0006633",AB
H10627.1
Stramenopiles-Phytophthora_parasitica_esgi68418836_1,284,521.546,3.40E-
146,gi|111572541|gb|ABH10627.1|delta-6 desaturase [Phytophthora citrophthora],"
GO:0006629,GO:0055114,GO:0016717,GO:0020037,GO:0016491,GO:0005506,GO:0006633",AB
H10627.1
Stramenopiles-
Phytophthora_ramorum_jgi72056,457,879.396,0,gi|111572541|gb|ABH10627.1|delta-6
desaturase [Phytophthora citrophthora],"
GO:0006629,GO:0055114,GO:0016717,GO:0020037,GO:0016491,GO:0005506,GO:0006633",AB
H10627.1
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224006045,168,346.28,5.71E-
94,gi|224006045|ref|XP_002291983.1|predicted protein [Thalassiosira pseudonana
```

```
CCMP1335] ,"
GO:0055114,GO:0016705,GO:0005506,GO:0031418","XP_002291983.1,EED90834.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219123691,188,391.734,1.75E-
107,gi|219123691|ref|XP_002182153.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0055114,GO:0016705,GO:0005506,GO:0031418","XP_002182153.1,EEC46054.1"
Stramenopiles-Aureococcus_anophagefferens_jgi61447,318,144.436,1.49E-
32,gi|290243077|ref|YP_003494747.1|Procollagen-proline dioxygenase
[Thioalkalivibrio sp. K90mix] ,"
GO:0005506,GO:0031418,GO:0016705,GO:0016702,GO:0055114,GO:0006464,GO:0016491,GO:
0004656,GO:0004835","YP_003494747.1,ADC73280.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224012377,1164,2415.19,0,gi|224012377|ref|XP
_002294841.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0055114,GO:0016705,GO:0005506,GO:0031418","XP_002294841.1,EED87621.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224012759,194,408.683,1.39E-
112,gi|224012759|ref|XP_002295032.1|hypothetical protein THAPSDRAFT_264808
[Thalassiosira pseudonana CCMP1335] ,"
GO:0055114,GO:0016705,GO:0016491,GO:0005506,GO:0031418","XP_002295032.1,EED87812
.1"
Stramenopiles-Phytophthora_sojae_jgi145321,360,328.946,6.01E-
88,gi|301093292|ref|XP_002997494.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,"
GO:0055114,GO:0016705,GO:0016491,GO:0005506,GO:0031418","XP_002997494.1,EEY68688
.1"
Stramenopiles-Phytophthora_sojae_jgi133634,706,476.093,7.21E-
132,gi|301089064|ref|XP_002894876.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002894876.1,EEY64406.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224006375,394,825.469,0,gi|224006375|ref|XP_
002292148.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002292148.1,EED90999.1"
Stramenopiles-Aureococcus_anophagefferens_jgi62118,1700,142.895,3.18E-
31,gi|219113773|ref|XP_002186470.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002186470.1,ACI65940.1"
Stramenopiles-Aureococcus_anophagefferens_jgi63721,1207,135.576,3.52E-
29,gi|219113773|ref|XP_002186470.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002186470.1,ACI65940.1"
Stramenopiles-Aureococcus_anophagefferens_jgi70898,2365,330.872,1.40E-
87,"gi|91975071|ref|YP_567730.1|DNA helicase, putative [Rhodopseudomonas
palustris BisB5] ","
GO:0006355,GO:0004386,GO:0003711,GO:0003677","YP_567730.1,ABE37829.1"
Stramenopiles-Phytophthora_ramorum_jgi96093,304,561.992,2.94E-
158,gi|301100728|ref|XP_002899453.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,"
GO:0035091,GO:0007154,GO:0005515","XP_002899453.1,EEY61813.1"
Stramenopiles-Phytophthora_sojae_jgi156141,304,570.466,8.40E-
161,gi|301100728|ref|XP_002899453.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,"
GO:0035091,GO:0007154,GO:0005515","XP_002899453.1,EEY61813.1"
Stramenopiles-Blastocystis_hominis_tbBHL00001221_3,235,216.853,1.52E-
54,gi|300122044|emb|CBK22618.2|unnamed protein product [Blastocystis hominis],"
GO:0035091,GO:0007154,GO:0005515",CBK22618.2
```

```
Stramenopiles-
Phytophthora_ramorum_jgi81721,642,751.125,0,"gi|301100786|ref|XP_002899482.1|rib
onuclease H2 subunit A, putative [Phytophthora infestans T30-4] ","
GO:0007154,GO:0016787,GO:0003676,GO:0016070,GO:0003723,GO:0005515,GO:0004523,GO:
0035091,GO:0004519,GO:0004518","XP_002899482.1,EEY61842.1"
Stramenopiles-
Phytophthora_ramorum_jgi48825,641,1244.18,0,gi|301107486|ref|XP_002902825.1|long
-chain-fatty-acid-CoA ligase [Phytophthora infestans T30-4] ,"
GO:0016874,GO:0008152,GO:0003824","XP_002902825.1,EEY55995.1"
Stramenopiles-
Phytophthora_capsici_jgi89078,647,1274.61,0,gi|301107486|ref|XP_002902825.1|long
-chain-fatty-acid-CoA ligase [Phytophthora infestans T30-4] ,"
GO:0016874,GO:0008152,GO:0003824","XP_002902825.1,EEY55995.1"
Stramenopiles-
Phytophthora_sojae_jgi132768,647,1268.83,0,gi|301107486|ref|XP_002902825.1|long-
chain-fatty-acid-CoA ligase [Phytophthora infestans T30-4] ,"
GO:0016874,GO:0008152,GO:0003824","XP_002902825.1,EEY55995.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219117691,663,1377.84,0,gi|219117691|ref
|XP_002179636.1|long chain acyl-coa synthetase [Phaeodactylum tricornutum CCAP
1055/1] ,"
GO:0016874,GO:0004467,GO:0008152,GO:0003824","XP_002179636.1,EEC48622.1"
Stramenopiles-
Phytophthora_capsici_jgi18988,646,1094.34,0,"gi|301121716|ref|XP_002908585.1|lon
g-chain-fatty-acid-CoA ligase, putative [Phytophthora infestans T30-4] ","
GO:0016874,GO:0008152,GO:0003824","XP_002908585.1,EEY61668.1"
Stramenopiles-
Phytophthora_sojae_jgi109007,452,784.252,0,"gi|301121716|ref|XP_002908585.1|long
-chain-fatty-acid-CoA ligase, putative [Phytophthora infestans T30-4] ","
GO:0016874,GO:0008152,GO:0003824","XP_002908585.1,EEY61668.1"
Stramenopiles-
Phytophthora_ramorum_jgi77275,649,1088.95,0,"gi|301121716|ref|XP_002908585.1|lon
g-chain-fatty-acid-CoA ligase, putative [Phytophthora infestans T30-4] ","
GO:0016874,GO:0008152,GO:0003824","XP_002908585.1,EEY61668.1"
Stramenopiles-Aureococcus_anophagefferens_jgi10354,674,577.015,2.29E-
162,gi|308812292|ref|XP_003083453.1|MGC53673 protein (ISS) [Ostreococcus tauri]
," GO:0008152,GO:0003824","XP_003083453.1,CAL58002.1"
Stramenopiles-Blastocystis_hominis_tbBHL00000659_6,236,340.502,8.13E-
92,gi|300121230|emb|CBK21611.2|unnamed protein product [Blastocystis hominis],"
GO:0008152,GO:0003824",CBK21611.2
Stramenopiles-Aureococcus_anophagefferens_jgi52722,647,548.51,9.63E-
154,gi|167534933|ref|XP_001749141.1|hypothetical protein [Monosiga brevicollis
MX1] ," GO:0008152,GO:0003824","XP_001749141.1,EDQ85947.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219122411,437,915.605,0,gi|219122411|ref
|XP_002181539.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002181539.1,EEC46753.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi181416,418,276.944,3.23E-
72,gi|219122411|ref|XP_002181539.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002181539.1,EEC46753.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi238936,462,390.963,1.81E-
106,gi|219119296|ref|XP_002180411.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002180411.1,EEC47819.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219119296,420,875.159,0,gi|219119296|ref
```

```
|XP_002180411.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002180411.1,EEC47819.1"
Stramenopiles-Phytophthora_ramorum_jgi72332,171,340.887,3.06E-
92,gi|301113382|ref|XP_002998461.1|T-complex protein 1 subunit epsilon
[Phytophthora infestans T30-4] ,"
GO:0051082,GO:0044267,GO:0005524,GO:0005737,GO:0006457,GO:0000166,GO:0005515","X
P_002998461.1,EEY69814.1"
Stramenopiles-
Phytophthora_ramorum_jgi71707,537,1066.99,0,gi|301113382|ref|XP_002998461.1|T-
complex protein 1 subunit epsilon [Phytophthora infestans T30-4] ,"
GO:0051082,GO:0044267,GO:0005524,GO:0005737,GO:0006457,GO:0000166,GO:0005515","X
P_002998461.1,EEY69814.1"
Stramenopiles-Phytophthora_brassicae_esContig611_3,230,462.225,1.86E-
128,gi|301113382|ref|XP_002998461.1|T-complex protein 1 subunit epsilon
[Phytophthora infestans T30-4] ,"
GO:0051082,GO:0044267,GO:0005524,GO:0005737,GO:0006457,GO:0000166,GO:0005515","X
P_002998461.1,EEY69814.1"
Stramenopiles-
Phytophthora_sojae_jgi109330,537,1085.86,0,gi|301113382|ref|XP_002998461.1|T-
complex protein 1 subunit epsilon [Phytophthora infestans T30-4] ,"
GO:0051082,GO:0044267,GO:0005524,GO:0005737,GO:0006457,GO:0000166,GO:0005515","X
P_002998461.1,EEY69814.1"
Stramenopiles-
Phytophthora_capsici_jgi102249,537,1072.38,0,gi|301113382|ref|XP_002998461.1|T-
complex protein 1 subunit epsilon [Phytophthora infestans T30-4] ,"
GO:0051082,GO:0044267,GO:0005524,GO:0005737,GO:0006457,GO:0000166,GO:0005515","X
P_002998461.1,EEY69814.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi54967,646,869.766,0,gi|301113382|ref|XP_002998461
.1|T-complex protein 1 subunit epsilon [Phytophthora infestans T30-4] ,"
GO:0051082,GO:0044267,GO:0005524,GO:0005737,GO:0006457,GO:0000166,GO:0005515","X
P_002998461.1,EEY69814.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi26043,538,871.307,0,"gi|298705368|emb|CBJ28658.1|
T-complex protein, epsilon subunit [Ectocarpus siliculosus]","
GO:0051082,GO:0044267,GO:0005524,GO:0005737,GO:0006457,GO:0000166,GO:0005515",CB
J28658.1
Stramenopiles-
Fragilariopsis_cylindrus_jgi259523,554,835.099,0,gi|219122207|ref|XP_002181442.1
|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0051082,GO:0044267,GO:0005524,GO:0005737,GO:0006457,GO:0000166,GO:0005515","X
P_002181442.1,EEC47365.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219122207,541,1105.12,0,gi|219122207|ref
|XP_002181442.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0051082,GO:0044267,GO:0005524,GO:0005737,GO:0006457,GO:0000166,GO:0005515","X
P_002181442.1,EEC47365.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224002777,543,1113.21,0,"gi|224002777|ref|XP
_002291060.1|t-complex chaperonin protein, epsilon subunit [Thalassiosira
pseudonana CCMP1335] ","
GO:0051082,GO:0044267,GO:0005524,GO:0006457,GO:0000166,GO:0005515","XP_002291060
.1,EED91167.1"
Stramenopiles-
Phytophthora_sojae_jgi131452,5923,5217.51,0,gi|301118749|ref|XP_002907102.1|cons
```

```
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002907102.1,EEY63666.1"
Stramenopiles-
Phytophthora_ramorum_jgi73407,3008,5025.68,0,gi|301118749|ref|XP_002907102.1|con
served hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002907102.1,EEY63666.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224002394,3966,8272.92,0,gi|224002394|ref|XP
_002290869.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002290869.1,EED92621.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224009540,5245,10825.2,0,gi|224009540|ref|XP
_002293728.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002293728.1,EED88737.1"
Stramenopiles-
Phytophthora_sojae_jgi130084,717,711.835,0,"gi|301122279|ref|XP_002908866.1|cath
epsin, cysteine protease family C01A, putative [Phytophthora infestans T30-4]
"," GO:0006508,GO:0008234,GO:0008233","XP_002908866.1,EEY57680.1"
Stramenopiles-Phytophthora_capsici_jgi6086,305,582.793,1.48E-
164,"gi|301122279|ref|XP_002908866.1|cathepsin, cysteine protease family C01A,
putative [Phytophthora infestans T30-4] ","
GO:0006508,GO:0008234,GO:0008233","XP_002908866.1,EEY57680.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi163345,103,84.3445,4.36E-
15,gi|238059166|ref|ZP_04603875.1|tetratricopeptide TPR_4 [Micromonospora sp.
ATCC 39149] ," GO:0006952,GO:0005488","ZP_04603875.1,EEP69805.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224014166,291,613.224,9.35E-
174,gi|224014166|ref|XP_002296746.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,,"XP_002296746.1,EED86947.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224012343,723,1521.14,0,gi|224012343|ref|XP_
002294824.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002294824.1,EED87604.1"
Stramenopiles-
Phytophthora_sojae_jgi142831,593,999.964,0,"gi|301096651|ref|XP_002897422.1|lyso
somal Pro-X carboxypeptidase, putative [Phytophthora infestans T30-4] ","
GO:0006508,GO:0004180,GO:0008236","XP_002897422.1,EEY65165.1"
Stramenopiles-
Phytophthora_capsici_jgi106477,596,989.949,0,"gi|301096651|ref|XP_002897422.1|ly
sosomal Pro-X carboxypeptidase, putative [Phytophthora infestans T30-4] ","
GO:0006508,GO:0004180,GO:0008236","XP_002897422.1,EEY65165.1"
Stramenopiles-
Phytophthora_ramorum_jgi80328,590,962.6,0,"gi|301096651|ref|XP_002897422.1|lysos
omal Pro-X carboxypeptidase, putative [Phytophthora infestans T30-4] ","
GO:0006508,GO:0004180,GO:0008236","XP_002897422.1,EEY65165.1"
Stramenopiles-Aureococcus_anophagefferens_jgi71973,940,397.512,4.56E-
108,"gi|301096651|ref|XP_002897422.1|lysosomal Pro-X carboxypeptidase, putative
[Phytophthora infestans T30-4] ","
GO:0006508,GO:0004180,GO:0008236","XP_002897422.1,EEY65165.1"
Stramenopiles-
Phytophthora_capsici_jgi103354,537,937.947,0,"gi|301103554|ref|XP_002900863.1|ly
sosomal Pro-X carboxypeptidase, putative [Phytophthora infestans T30-4] ","
GO:0006508,GO:0004180,GO:0008236","XP_002900863.1,EEY59670.1"
Stramenopiles-Phytophthora_ramorum_jgi74753,191,269.626,1.20E-
70,"gi|301103554|ref|XP_002900863.1|lysosomal Pro-X carboxypeptidase, putative
```

```
[Phytophthora infestans T30-4] ","
GO:0006508,GO:0004180,GO:0008236","XP_002900863.1,EEY59670.1"
Stramenopiles-
Phytophthora_ramorum_jgi72987,567,895.96,0,"gi|301097471|ref|XP_002897830.1|lyso
somal Pro-X carboxypeptidase, putative [Phytophthora infestans T30-4] ","
GO:0006508,GO:0004180,GO:0008236","XP_002897830.1,EEY64630.1"
Stramenopiles-Aureococcus_anophagefferens_jgi28266,311,231.876,7.00E-
59,gi|224043680|ref|XP_002188561.1|PREDICTED: similar to prolylcarboxypeptidase
[Taeniopygia guttata],,XP_002188561.1
Stramenopiles-Aureococcus_anophagefferens_jgi2013,451,307.375,2.06E-
81,gi|14010871|ref|NP_114179.1|dipeptidyl peptidase 2 precursor [Rattus
norvegicus] ,"
GO:0016023,GO:0008239,GO:0005764,GO:0008236,GO:0005576,GO:0008233,GO:0006508,GO:
0005515,GO:0005829","NP_114179.1,Q9EPB1.1,BAB11691.1,BAB13500.1,AAH78783.1,EDL93
599.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi239498,509,289.656,6.51E-
76,gi|291234129|ref|XP_002737003.1|PREDICTED: prolylcarboxypeptidase isoform 1
preproprotein-like [Saccoglossus kowalevskii],,XP_002737003.1
Stramenopiles-Fragilariopsis_cylindrus_jgi193922,300,223.402,2.52E-
56,gi|219113425|ref|XP_002186296.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002186296.1,ACI65766.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219113425,311,626.32,1.36E-
177,gi|219113425|ref|XP_002186296.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002186296.1,ACI65766.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224005867,455,932.169,0,gi|224005867|ref|XP_
002291894.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,
GO:0016020,"XP_002291894.1,EED90745.1"
Stramenopiles-Aureococcus_anophagefferens_jgi70600,1261,400.208,8.34E-
109,gi|298706007|emb|CBJ29121.1|Mannitol dehydrogenase rossman domain family
[Ectocarpus siliculosus],"
GO:0055114,GO:0005488,GO:0016491,GO:0008152,GO:0003824,GO:0050662",CBJ29121.1
Stramenopiles-
Phytophthora_sojae_jgi108641,426,795.423,0,gi|301090360|ref|XP_002895398.1|fumar
ylacetoacetase [Phytophthora infestans T30-4] ,"
GO:0004334,GO:0008152,GO:0003824,GO:0009072","XP_002895398.1,EEY57057.1"
Stramenopiles-Phytophthora_capsici_jgi105774,121,236.884,4.72E-
61,gi|301090360|ref|XP_002895398.1|fumarylacetoacetase [Phytophthora infestans
T30-4] ,"
GO:0004334,GO:0008152,GO:0003824,GO:0009072","XP_002895398.1,EEY57057.1"
Stramenopiles-Phytophthora_sojae_jgi158615,296,540.036,1.09E-
151,gi|301112661|ref|XP_002998101.1|serine/threonine protein kinase
[Phytophthora infestans T30-4] ,"
GO:0016301,GO:0005524,GO:0004672,GO:0006468,GO:0004674","XP_002998101.1,EEY70447
.1"
Stramenopiles-Phytophthora_ramorum_jgi96144,511,536.954,2.22E-
150,gi|301112661|ref|XP_002998101.1|serine/threonine protein kinase
[Phytophthora infestans T30-4] ,"
GO:0016301,GO:0005524,GO:0004672,GO:0006468,GO:0004674","XP_002998101.1,EEY70447
.1"
Stramenopiles-Phytophthora_capsici_jgi22900,203,360.533,5.67E-
98,gi|301112661|ref|XP_002998101.1|serine/threonine protein kinase [Phytophthora
infestans T30-4] ,"
```

```
GO:0016301,GO:0005524,GO:0004672,GO:0006468,GO:0004674","XP_002998101.1,EEY70447
.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219129062,1038,2146.7,0,gi|219129062|ref
|XP_002184717.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0005524,GO:0004672,GO:0000166,GO:0006468,GO:0004674","XP_002184717.1,EEC43776
.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219117427,248,519.235,1.57E-
145,gi|219117427|ref|XP_002179508.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002179508.1,EEC49331.1"
Stramenopiles-Aureococcus_anophagefferens_jgi61543,207,97.4413,8.53E-
19,gi|219117427|ref|XP_002179508.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002179508.1,EEC49331.1"
Stramenopiles-Phytophthora_brassicae_esContig1888_1,227,301.982,2.85E-
80,gi|301113692|ref|XP_002998616.1|calmodulin [Phytophthora infestans T30-4] ,
GO:0005509,"XP_002998616.1,P27165.2,Q71UH5.1,AAG01043.1,AAA21424.1,ACG60663.1,EE
Y69969.1"
Stramenopiles-Phytophthora_sojae_jgi109328,150,296.59,5.65E-
79,gi|301113692|ref|XP_002998616.1|calmodulin [Phytophthora infestans T30-4] ,
GO:0005509,"XP_002998616.1,P27165.2,Q71UH5.1,AAG01043.1,AAA21424.1,ACG60663.1,EE
Y69969.1"
Stramenopiles-Phytophthora_parasitica_esContig918_2,229,300.442,9.58E-
80,gi|301113692|ref|XP_002998616.1|calmodulin [Phytophthora infestans T30-4] ,
GO:0005509,"XP_002998616.1,P27165.2,Q71UH5.1,AAG01043.1,AAA21424.1,ACG60663.1,EE
Y69969.1"
Stramenopiles-Aureococcus_anophagefferens_jgi71079,412,102.449,9.17E-
20,gi|260796519|ref|XP_002593252.1|hypothetical protein BRAFLDRAFT_124868
[Branchiostoma floridae] , GO:0005509,"XP_002593252.1,EEN49263.1"
Stramenopiles-
Phytophthora_ramorum_jgi80108,2730,1744.17,0,gi|301108984|ref|XP_002903573.1|nep
hrocystin-4-like protein [Phytophthora infestans T30-4] ,
GO:0005509,"XP_002903573.1,EEY55349.1"
Stramenopiles-
Phytophthora_capsici_jgi10024,2722,1544.25,0,gi|301108984|ref|XP_002903573.1|nep
hrocystin-4-like protein [Phytophthora infestans T30-4] ,
GO:0005509,"XP_002903573.1,EEY55349.1"
Stramenopiles-
Phytophthora_sojae_jgi140465,3114,1802.33,0,gi|301108984|ref|XP_002903573.1|neph
rocystin-4-like protein [Phytophthora infestans T30-4] ,
GO:0005509,"XP_002903573.1,EEY55349.1"
Stramenopiles-
Phytophthora_sojae_jgi137146,951,1789.62,0,"gi|301121630|ref|XP_002908542.1|seri
ne/threonine-protein phosphatase, putative [Phytophthora infestans T30-4] ","
GO:0005509,GO:0016787,GO:0004721","XP_002908542.1,EEY61625.1"
Stramenopiles-
Phytophthora_capsici_jgi19179,946,1791.93,0,"gi|301121630|ref|XP_002908542.1|ser
ine/threonine-protein phosphatase, putative [Phytophthora infestans T30-4] ","
GO:0005509,GO:0016787,GO:0004721","XP_002908542.1,EEY61625.1"
Stramenopiles-
Phytophthora_ramorum_jgi77307,942,1765.36,0,"gi|301121630|ref|XP_002908542.1|ser
ine/threonine-protein phosphatase, putative [Phytophthora infestans T30-4] ","
GO:0005509,GO:0016787,GO:0004721","XP_002908542.1,EEY61625.1"
```

```
Stramenopiles-Aureococcus_anophagefferens_jgi4337,234,171.4,7.20E-
41,gi|291232192|ref|XP_002736042.1|PREDICTED: phosphodiesterase 9A-like
[Saccoglossus kowalevskii],,XP_002736042.1
Stramenopiles-Aureococcus_anophagefferens_jgi12482,229,174.866,5.63E-
42,gi|126325421|ref|XP_001375398.1|PREDICTED: similar to PDE9A protein
[Monodelphis domestica],,XP_001375398.1
Stramenopiles-Aureococcus_anophagefferens_jgi2739,270,178.333,6.95E-
43,gi|194226286|ref|XP_001491056.2|PREDICTED: phosphodiesterase 9A [Equus
caballus],,XP_001491056.2
Stramenopiles-Fragilariopsis_cylindrus_jgi194811,410,470.7,1.43E-
130,gi|219115946|ref|XP_002178768.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0005524,GO:0005488,GO:0016740,GO:0008152,GO:0000166,GO:0003824","XP_002178768
.1,EEC49466.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223996857,388,801.971,0,gi|223996857|ref|XP_
002288102.1|hypothetical protein THAPSDRAFT_261602 [Thalassiosira pseudonana
CCMP1335] ,"
GO:0005524,GO:0005488,GO:0016740,GO:0008152,GO:0000166,GO:0003824","XP_002288102
.1,EED95545.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219115946,418,865.529,0,gi|219115946|ref
|XP_002178768.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0005524,GO:0005488,GO:0016740,GO:0008152,GO:0000166,GO:0003824","XP_002178768
.1,EEC49466.1"
Stramenopiles-Aureococcus_anophagefferens_jgi55300,404,278.87,6.89E-
73,gi|157106847|ref|XP_001649510.1|molybdopterin biosynthesis moeb protein
[Aedes aegypti] ,"
GO:0016740,GO:0008033,GO:0000166,GO:0005737,GO:0005524,GO:0016783,GO:0016779,GO:
0003824,GO:0006777,GO:0004792,GO:0046872,GO:0008152,GO:0005829,GO:0005488","XP_0
01649510.1,Q17CA7.1,EAT43968.1"
Stramenopiles-Phytophthora_sojae_jgi130255,475,437.573,1.68E-
120,"gi|301122607|ref|XP_002909030.1|molybdenum cofactor synthesis protein,
putative [Phytophthora infestans T30-4] ","
GO:0005488,GO:0008152,GO:0003824","XP_002909030.1,EEY57844.1"
Stramenopiles-Phytophthora_ramorum_jgi71032,424,373.244,2.86E-
101,"gi|301122607|ref|XP_002909030.1|molybdenum cofactor synthesis protein,
putative [Phytophthora infestans T30-4] ","
GO:0005488,GO:0008152,GO:0003824","XP_002909030.1,EEY57844.1"
Stramenopiles-Phytophthora_capsici_jgi3852,461,404.831,1.18E-
110,"gi|301122607|ref|XP_002909030.1|molybdenum cofactor synthesis protein,
putative [Phytophthora infestans T30-4] ","
GO:0005488,GO:0008152,GO:0003824","XP_002909030.1,EEY57844.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi257224,875,70.0922,1.53E-
09,gi|158148975|dbj|BAF82021.1|piggyBac transposase Uribo1 [Xenopus
borealis],,BAF82021.1
Stramenopiles-
Phytophthora_sojae_jgi138933,671,707.983,0,gi|301104417|ref|XP_002901293.1|conse
rved hypothetical protein [Phytophthora infestans T30-4] ,
GO:0004437,"XP_002901293.1,EEY58820.1"
Stramenopiles-
Phytophthora_capsici_jgi11648,645,659.833,0,gi|301104417|ref|XP_002901293.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,
GO:0004437,"XP_002901293.1,EEY58820.1"
```

```
Stramenopiles-
Phytophthora_ramorum_jgi79887,1534,1592.79,0,gi|301111602|ref|XP_002904880.1|con
served hypothetical protein [Phytophthora infestans T30-4] ,
GO:0004437,"XP_002904880.1,EEY53262.1"
Stramenopiles-
Phytophthora_sojae_jgi135769,1723,1594.33,0,gi|301111602|ref|XP_002904880.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,
GO:0004437,"XP_002904880.1,EEY53262.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219119779,322,672.159,0,gi|219119779|ref
|XP_002180642.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002180642.1,EEC48050.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219120807,451,937.562,0,gi|219120807|ref
|XP_002185635.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0016787,GO:0008152,GO:0007047,GO:0005975,GO:0016798,GO:0004650","XP_002185635
.1,ACI65105.1"
Stramenopiles-Aureococcus_anophagefferens_jgi2438,295,322.013,4.68E-
86,gi|219120807|ref|XP_002185635.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0016787,GO:0008152,GO:0007047,GO:0005975,GO:0016798,GO:0004650","XP_002185635
.1,ACI65105.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi223994361,223,457.218,4.90E-
127,gi|223994361|ref|XP_002286864.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ," GO:0009190,GO:0016849","XP_002286864.1,EED96505.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224008556,549,1136.71,0,gi|224008556|ref|XP_
002293237.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0009190,GO:0016849","XP_002293237.1,EED89698.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223999345,830,1723.75,0,gi|223999345|ref|XP_
002289345.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0009190,GO:0016849","XP_002289345.1,EED92882.1"
Stramenopiles-
Phytophthora_sojae_jgi140884,868,1447.95,0,gi|301113376|ref|XP_002998458.1|Volta
ge-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0009190,GO:0016849,GO:0016021,GO:0016020,GO:0055085,GO:0006811,GO:0005216,GO:
0006810","XP_002998458.1,EEY69811.1"
Stramenopiles-
Phytophthora_ramorum_jgi80869,740,1345.49,0,gi|301113376|ref|XP_002998458.1|Volt
age-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0009190,GO:0016849,GO:0016021,GO:0016020,GO:0055085,GO:0006811,GO:0005216,GO:
0006810","XP_002998458.1,EEY69811.1"
Stramenopiles-Aureococcus_anophagefferens_jgi71178,1197,600.512,4.80E-
169,gi|301113376|ref|XP_002998458.1|Voltage-gated Ion Channel (VIC) Superfamily
[Phytophthora infestans T30-4] ,"
GO:0009190,GO:0016849,GO:0016021,GO:0016020,GO:0055085,GO:0006811,GO:0005216,GO:
0006810","XP_002998458.1,EEY69811.1"
Stramenopiles-Aureococcus_anophagefferens_jgi31132,737,499.59,5.30E-
139,gi|301109349|ref|XP_002903755.1|Voltage-gated Ion Channel (VIC) Superfamily
[Phytophthora infestans T30-4] ,"
GO:0009190,GO:0016849","XP_002903755.1,EEY54810.1"
Stramenopiles-
Phytophthora_sojae_jgi130119,1302,1589.32,0,gi|301109349|ref|XP_002903755.1|Volt
```

```
age-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0009190,GO:0016849","XP_002903755.1,EEY54810.1"
Stramenopiles-
Phytophthora_capsici_jgi112552,709,781.171,0,gi|301109349|ref|XP_002903755.1|Vol
tage-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0009190,GO:0016849","XP_002903755.1,EEY54810.1"
Stramenopiles-
Phytophthora_ramorum_jgi74076,1353,1578.15,0,gi|301109349|ref|XP_002903755.1|Vol
tage-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0009190,GO:0016849","XP_002903755.1,EEY54810.1"
Stramenopiles-Aureococcus_anophagefferens_jgi69239,484,59.3066,1.07E-
06,gi|89891281|ref|ZP_01202788.1|conserved hypothetical protein [Flavobacteria
bacterium BBFL7] ," GO:0005102,GO:0007165","ZP_01202788.1,EAS19253.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi248235,179,168.703,2.31E-
40,gi|255078914|ref|XP_002503037.1|predicted protein [Micromonas sp. RCC299] ,"
GO:0045454,GO:0005783","XP_002503037.1,ACO64295.1"
Stramenopiles-Phytophthora_brassicae_esContig956_2,194,295.434,2.17E-
78,gi|119866043|gb|ABM05490.1|NUK7 [Phytophthora infestans],
GO:0045454,ABM05490.1
Stramenopiles-
Phytophthora_ramorum_jgi82203,423,660.218,0,gi|119866043|gb|ABM05490.1|NUK7
[Phytophthora infestans], GO:0045454,ABM05490.1
Stramenopiles-
Phytophthora_capsici_jgi113953,421,696.812,0,gi|119866043|gb|ABM05490.1|NUK7
[Phytophthora infestans], GO:0045454,ABM05490.1
Stramenopiles-
Phytophthora_sojae_jgi137340,425,666.381,0,gi|119866043|gb|ABM05490.1|NUK7
[Phytophthora infestans], GO:0045454,ABM05490.1
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223996751,541,1115.14,0,gi|223996751|ref|XP_
002288049.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0005488,GO:0008152,GO:0003824","XP_002288049.1,EED95492.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219115717,281,573.163,1.14E-
161,gi|219115717|ref|XP_002178654.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002178654.1,EEC50319.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi216468,259,460.685,6.58E-
128,gi|219115717|ref|XP_002178654.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002178654.1,EEC50319.1"
Stramenopiles-Aureococcus_anophagefferens_jgi65882,1500,431.409,4.26E-
118,gi|219115717|ref|XP_002178654.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002178654.1,EEC50319.1"
Stramenopiles-Phytophthora_ramorum_jgi85822,457,348.206,1.32E-
93,gi|301107712|ref|XP_002902938.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002902938.1,EEY56108.1"
Stramenopiles-Phytophthora_sojae_jgi131653,453,356.295,4.03E-
96,gi|301107712|ref|XP_002902938.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002902938.1,EEY56108.1"
Stramenopiles-Phytophthora_capsici_jgi34796,451,359.762,3.59E-
97,gi|301107712|ref|XP_002902938.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002902938.1,EEY56108.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi52441,763,684.485,0,gi|219125424|ref|XP_002182982
.1|channel voltage activated chloride channel [Phaeodactylum tricornutum CCAP
1055/1] ,"
```

```
GO:0006821,GO:0005247,GO:0016021,GO:0016020,GO:0055085,GO:0005216","XP_002182982
.1,EEC45718.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219120987,768,1580.46,0,gi|219120987|ref
|XP_002185725.1|voltage activated chloride channel CLC7 type [Phaeodactylum
tricornutum CCAP 1055/1] ,"
GO:0006821,GO:0005247,GO:0016020,GO:0055085,GO:0005216","XP_002185725.1,ACI65195
.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi213110,811,1003.05,0,gi|219120987|ref|XP_002185725.1
|voltage activated chloride channel CLC7 type [Phaeodactylum tricornutum CCAP
1055/1] ,"
GO:0006821,GO:0005247,GO:0016020,GO:0055085,GO:0005216","XP_002185725.1,ACI65195
.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi205516,798,1117.06,0,gi|219125424|ref|XP_002182982.1
|channel voltage activated chloride channel [Phaeodactylum tricornutum CCAP
1055/1] ,"
GO:0006821,GO:0005247,GO:0016021,GO:0016020,GO:0055085,GO:0005216","XP_002182982
.1,EEC45718.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219125424,693,1426.38,0,gi|219125424|ref
|XP_002182982.1|channel voltage activated chloride channel [Phaeodactylum
tricornutum CCAP 1055/1] ,"
GO:0006821,GO:0005247,GO:0016021,GO:0016020,GO:0055085,GO:0005216","XP_002182982
.1,EEC45718.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224013975,681,1405.96,0,gi|224013975|ref|XP_
002296651.1|chloride channel protein 7 [Thalassiosira pseudonana CCMP1335] ,"
GO:0006821,GO:0005247,GO:0016021,GO:0016020,GO:0055085,GO:0005216","XP_002296651
.1,EED87046.1"
Stramenopiles-
Phytophthora_capsici_jgi115302,1679,1762.66,0,gi|301107468|ref|XP_002902816.1|Ch
loride Channel (ClC) Family [Phytophthora infestans T30-4] ,"
GO:0006821,GO:0005247,GO:0016021,GO:0016020,GO:0055085,GO:0005216","XP_002902816
.1,EEY55986.1"
Stramenopiles-
Phytophthora_sojae_jgi132758,968,1774.22,0,gi|301107468|ref|XP_002902816.1|Chlor
ide Channel (ClC) Family [Phytophthora infestans T30-4] ,"
GO:0006821,GO:0005247,GO:0016021,GO:0016020,GO:0055085,GO:0005216","XP_002902816
.1,EEY55986.1"
Stramenopiles-
Phytophthora_ramorum_jgi79631,958,1772.29,0,gi|301107468|ref|XP_002902816.1|Chlo
ride Channel (ClC) Family [Phytophthora infestans T30-4] ,"
GO:0006821,GO:0005247,GO:0016021,GO:0016020,GO:0055085,GO:0005216","XP_002902816
.1,EEY55986.1"
Stramenopiles-
Phytophthora_ramorum_jgi39633,680,1129.01,0,gi|301098746|ref|XP_002898465.1|Chlo
ride Channel (ClC) Family [Phytophthora infestans T30-4] ,"
GO:0006821,GO:0005247,GO:0016021,GO:0016020,GO:0055085,GO:0005216","XP_002898465
.1,EEY62942.1"
Stramenopiles-
Phytophthora_sojae_jgi134892,649,1200.65,0,"gi|301117982|ref|XP_002906719.1|calc
ineurin-like phosphoesterase, putative [Phytophthora infestans T30-4] ","
GO:0046872,GO:0016787,GO:0003993","XP_002906719.1,EEY66120.1"
```

```
Stramenopiles-
Phytophthora_sojae_jgi133696,694,1117.06,0,"gi|301117982|ref|XP_002906719.1|calc
ineurin-like phosphoesterase, putative [Phytophthora infestans T30-4] ","
GO:0046872,GO:0016787,GO:0003993","XP_002906719.1,EEY66120.1"
Stramenopiles-Phytophthora_capsici_jgi114419,279,344.739,5.74E-
93,"gi|301117982|ref|XP_002906719.1|calcineurin-like phosphoesterase, putative
[Phytophthora infestans T30-4] ","
GO:0046872,GO:0016787,GO:0003993","XP_002906719.1,EEY66120.1"
Stramenopiles-
Phytophthora_capsici_jgi75766,663,969.148,0,"gi|301117020|ref|XP_002906238.1|cal
cineurin-like phosphoesterase, putative [Phytophthora infestans T30-4] ","
GO:0046872,GO:0016787,GO:0003993","XP_002906238.1,EEY65639.1"
Stramenopiles-
Phytophthora_ramorum_jgi84778,652,1182.16,0,"gi|301117982|ref|XP_002906719.1|cal
cineurin-like phosphoesterase, putative [Phytophthora infestans T30-4] ","
GO:0046872,GO:0016787,GO:0003993","XP_002906719.1,EEY66120.1"
Stramenopiles-
Phytophthora_ramorum_jgi84597,819,790.03,0,gi|301092936|ref|XP_002997318.1|kines
in-like protein [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0000166,GO:0003777,GO:0007018,GO:0003774,GO:0005874","XP_002997318
.1,EEY68890.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219130909,594,1237.63,0,gi|219130909|ref
|XP_002185595.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0009116,GO:0016740,GO:0009113,GO:0008152,GO:0004044","XP_002185595.1,EEC42893
.1"
Stramenopiles-Aureococcus_anophagefferens_jgi71078,1324,74.7146,9.96E-
11,gi|294872674|ref|XP_002766365.1|hypothetical protein Pmar_PMAR019730
[Perkinsus marinus ATCC 50983] , GO:0005509,"XP_002766365.1,EEQ99082.1"
Stramenopiles-Phytophthora_capsici_jgi28926,230,424.476,4.09E-
117,gi|301118522|ref|XP_002906989.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,"
GO:0006413,GO:0005488,GO:0006446,GO:0003743,GO:0005852,GO:0043022,GO:0005634","X
P_002906989.1,EEY66390.1"
Stramenopiles-Phytophthora_sojae_jgi136804,230,419.468,1.26E-
115,gi|301118522|ref|XP_002906989.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,"
GO:0006413,GO:0005488,GO:0006446,GO:0003743,GO:0005852,GO:0043022,GO:0005634","X
P_002906989.1,EEY66390.1"
Stramenopiles-Phytophthora_ramorum_jgi82310,230,428.713,2.24E-
118,gi|301118522|ref|XP_002906989.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,"
GO:0006413,GO:0005488,GO:0006446,GO:0003743,GO:0005852,GO:0043022,GO:0005634","X
P_002906989.1,EEY66390.1"
Stramenopiles-Aureococcus_anophagefferens_jgi68761,230,158.303,5.51E-
37,gi|255088603|ref|XP_002506224.1|predicted protein [Micromonas sp. RCC299] ,
GO:0003723,"XP_002506224.1,ACO67482.1"
Stramenopiles-Phytophthora_capsici_jgi101938,294,153.295,2.66E-
35,gi|291239634|ref|XP_002739727.1|PREDICTED: Luc7 homolog (S. cerevisiae)-like
[Saccoglossus kowalevskii],,XP_002739727.1
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223993001,450,927.932,0,gi|223993001|ref|XP_
002286184.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002286184.1,EED95825.1"
```

```
Stramenopiles-Fragilariopsis_cylindrus_jgi209432,488,311.997,1.12E-
82,gi|219120071|ref|XP_002180782.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002180782.1,EEC47434.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219120071,473,956.822,0,gi|219120071|ref
|XP_002180782.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002180782.1,EEC47434.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224004206,153,300.442,3.58E-
80,gi|224004206|ref|XP_002295754.1|predicted protein [Thalassiosira pseudonana
CCMP1335] , GO:0005509,"XP_002295754.1,ACI64471.1"
Stramenopiles-
Phytophthora_capsici_jgi87350,598,974.541,0,gi|301112499|ref|XP_002998020.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0008152,GO:0016758","XP_002998020.1,EEY70366.1"
Stramenopiles-
Phytophthora_sojae_jgi132514,627,1059.67,0,gi|301112499|ref|XP_002998020.1|conse
rved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0008152,GO:0016758","XP_002998020.1,EEY70366.1"
Stramenopiles-
Phytophthora_ramorum_jgi75924,619,1042.72,0,gi|301112499|ref|XP_002998020.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0008152,GO:0016758","XP_002998020.1,EEY70366.1"
Stramenopiles-
Phytophthora_capsici_jgi35696,552,759.214,0,gi|301100113|ref|XP_002899147.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0008152,GO:0016758","XP_002899147.1,EEY62511.1"
Stramenopiles-
Phytophthora_ramorum_jgi79867,558,771.541,0,gi|301100113|ref|XP_002899147.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0008152,GO:0016758","XP_002899147.1,EEY62511.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi224545,197,241.506,3.79E-
62,gi|219126281|ref|XP_002183389.1|hypothetical protein PHATRDRAFT_48891
[Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0055114,GO:0016705,GO:0016491,GO:0005506,GO:0031418","XP_002183389.1,EEC45089
.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219124513,193,408.683,1.53E-
112,gi|219124513|ref|XP_002182546.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0055114,GO:0016705,GO:0016491,GO:0005506,GO:0031418","XP_002182546.1,EEC45833
.1"
Stramenopiles-Aureococcus_anophagefferens_jgi39521,239,133.65,1.65E-
29,gi|310831339|ref|YP_003969982.1|putative prolyl 4-hydroxylase alpha subunit
[Cafeteria roenbergensis virus BV-PW1] ,,"YP_003969982.1,ADO67383.1"
Stramenopiles-Aureococcus_anophagefferens_jgi14928,182,265.003,2.22E-
69,gi|298712929|emb|CBJ26831.1|conserved unknown protein [Ectocarpus
siliculosus]," GO:0055114,GO:0016705,GO:0005506,GO:0031418",CBJ26831.1
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224008727,457,936.406,0,gi|224008727|ref|XP_
002293322.1|hypothetical protein THAPSDRAFT_269660 [Thalassiosira pseudonana
CCMP1335] ,,"XP_002293322.1,EED89058.1"
Stramenopiles-Aureococcus_anophagefferens_jgi3195,338,327.02,2.01E-
87,gi|301095607|ref|XP_002896903.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002896903.1,EEY66602.1"
```

```
Stramenopiles-
Phytophthora_ramorum_jgi81215,487,718.768,0,gi|301095607|ref|XP_002896903.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002896903.1,EEY66602.1"
Stramenopiles-Phytophthora_capsici_jgi67641,427,542.347,3.54E-
152,gi|301095607|ref|XP_002896903.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002896903.1,EEY66602.1"
Stramenopiles-
Phytophthora_sojae_jgi130604,492,743.421,0,gi|301095607|ref|XP_002896903.1|conse
rved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002896903.1,EEY66602.1"
Stramenopiles-
Phytophthora_ramorum_jgi75937,1296,1972.59,0,gi|301112451|ref|XP_002997996.1|con
served hypothetical protein [Phytophthora infestans T30-4] ,
GO:0005509,"XP_002997996.1,EEY70342.1"
Stramenopiles-
Phytophthora_sojae_jgi132531,1284,2002.64,0,gi|301112451|ref|XP_002997996.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,
GO:0005509,"XP_002997996.1,EEY70342.1"
Stramenopiles-
Phytophthora_capsici_jgi112236,463,672.544,0,gi|301112451|ref|XP_002997996.1|con
served hypothetical protein [Phytophthora infestans T30-4] ,
GO:0005509,"XP_002997996.1,EEY70342.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi183808,359,164.851,1.24E-
38,gi|223996037|ref|XP_002287692.1|hypothetical protein THAPSDRAFT_261258
[Thalassiosira pseudonana CCMP1335] ,"
GO:0046872,GO:0008270,GO:0005515","XP_002287692.1,EED95135.1"
Stramenopiles-Phytophthora_capsici_jgi121428,336,550.436,9.85E-
155,gi|301097730|ref|XP_002897959.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002897959.1,EEY64456.1"
Stramenopiles-Phytophthora_sojae_jgi156200,377,621.698,4.52E-
176,gi|301097730|ref|XP_002897959.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002897959.1,EEY64456.1"
Stramenopiles-Phytophthora_ramorum_jgi73728,383,627.091,9.10E-
178,gi|301097730|ref|XP_002897959.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002897959.1,EEY64456.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219118680,385,802.357,0,gi|219118680|ref
|XP_002180108.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002180108.1,EEC48299.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi246102,444,283.878,2.72E-
74,gi|219118680|ref|XP_002180108.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002180108.1,EEC48299.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224009820,332,689.108,0,gi|224009820|ref|XP_
002293868.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002293868.1,EED88877.1"
Stramenopiles-Phytophthora_ramorum_jgi95422,141,241.506,2.10E-
62,gi|301107380|ref|XP_002902772.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002902772.1,EEY55942.1"
Stramenopiles-
Phytophthora_capsici_jgi37321,450,721.079,0,gi|301103252|ref|XP_002900712.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0008168,GO:0006412","XP_002900712.1,EEY59519.1"
```

```
Stramenopiles-
Phytophthora_ramorum_jgi94164,443,731.48,0,gi|301103252|ref|XP_002900712.1|conse
rved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0008168,GO:0006412","XP_002900712.1,EEY59519.1"
Stramenopiles-Aureococcus_anophagefferens_jgi65154,304,245.358,5.20E-
63,gi|256675829|ref|ZP_05486140.1|short-chain dehydrogenase/reductase SDR
[Streptomyces sp. SPB78] ,"
GO:0055114,GO:0005488,GO:0016491,GO:0008152,GO:0003824","ZP_05486140.1,ZP_072706
88.1,EFK99056.1"
Stramenopiles-Phytophthora_capsici_jgi80203,399,493.426,1.83E-
137,"gi|301111726|ref|XP_002904942.1|oxidoreductase, putative [Phytophthora
infestans T30-4] ","
GO:0055114,GO:0005488,GO:0016491,GO:0008152,GO:0003824","XP_002904942.1,EEY53324
.1"
Stramenopiles-Phytophthora_ramorum_jgi95562,514,478.789,6.17E-
133,"gi|301111726|ref|XP_002904942.1|oxidoreductase, putative [Phytophthora
infestans T30-4] ","
GO:0055114,GO:0005488,GO:0016491,GO:0008152,GO:0003824","XP_002904942.1,EEY53324
.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219121710,1367,2810.02,0,gi|219121710|re
f|XP_002181204.1|non ribosomal peptide synthase [Phaeodactylum tricornutum CCAP
1055/1] ,"
GO:0055114,GO:0048037,GO:0005488,GO:0016491,GO:0000036,GO:0008152,GO:0003824,GO:
0004043","XP_002181204.1,EEC47127.1"
Stramenopiles-Aureococcus_anophagefferens_jgi52724,264,206.838,1.71E-
51,"gi|87312271|ref|ZP_01094370.1|oxidoreductase, short-chain
dehydrogenase/reductase family protein [Blastopirellula marina DSM 3645] ","
GO:0055114,GO:0005488,GO:0016491,GO:0008152,GO:0003824","ZP_01094370.1,EAQ76944.
1"
Stramenopiles-Phytophthora_capsici_jgi12414,511,512.686,4.75E-
143,gi|301095611|ref|XP_002896905.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002896905.1,EEY66604.1"
Stramenopiles-Phytophthora_capsici_jgi33944,526,474.167,1.82E-
131,gi|301095611|ref|XP_002896905.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002896905.1,EEY66604.1"
Stramenopiles-Phytophthora_sojae_jgi141704,543,498.819,6.87E-
139,gi|301095619|ref|XP_002896909.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002896909.1,EEY66608.1"
Stramenopiles-Aureococcus_anophagefferens_jgi62084,816,193.356,1.10E-
46,gi|301100019|ref|XP_002899100.1|Voltage-gated Ion Channel (VIC) Superfamily
[Phytophthora infestans T30-4] ,"
GO:0005249,GO:0016021,GO:0016020,GO:0055085,GO:0006813,GO:0006811,GO:0005216,GO:
0006810","XP_002899100.1,EEY62464.1"
Stramenopiles-Aureococcus_anophagefferens_jgi61180,822,196.438,1.14E-
47,gi|301111924|ref|XP_002905041.1|Voltage-gated Ion Channel (VIC) Superfamily
[Phytophthora infestans T30-4] ,"
GO:0005249,GO:0016021,GO:0016020,GO:0055085,GO:0006813,GO:0006811,GO:0005216,GO:
0006810","XP_002905041.1,EEY53423.1"
Stramenopiles-Phytophthora_capsici_jgi18241,424,497.278,1.58E-
138,gi|301101539|ref|XP_002899858.1|phosphatidylinositol-4-phosphate-5-kinase
(PIPK-D7/GPCR-PIPK) [Phytophthora infestans T30-4] ,"
GO:0016301,GO:0004888,GO:0046488,GO:0016307,GO:0016020,GO:0007166","XP_002899858
.1,EEY60912.1"
```

```
Stramenopiles-Phytophthora_ramorum_jgi85104,1235,1891.7,0,gi|301101539|ref|XP_002899858.1|phosphatidylinositol-4-phosphate-5-kinase (PIPK-D7/GPCR-PIPK) [Phytophthora infestans T30-4] ," GO:0016301,GO:0004888,GO:0046488,GO:0016307,GO:0016020,GO:0007166","XP_002899858.1,EEY60912.1"
Stramenopiles-Phytophthora_ramorum_jgi72755,1107,1642.09,0,gi|301122665|ref|XP_002909059.1|phosphatidylinositol-4-phosphate-5-kinase (Pi-PIPKD5) [Phytophthora infestans T30-4] ," GO:0016301,GO:0046488,GO:0016307,GO:0004930,GO:0016020,GO:0007186","XP_002909059.1,EEY57873.1"
Stramenopiles-Phytophthora_sojae_jgi130286,922,1658.27,0,gi|301122665|ref|XP_002909059.1|phosphatidylinositol-4-phosphate-5-kinase (Pi-PIPKD5) [Phytophthora infestans T30-4] ," GO:0016301,GO:0046488,GO:0016307,GO:0004930,GO:0016020,GO:0007186","XP_002909059.1,EEY57873.1"
Stramenopiles-Phytophthora_parasitica_esgi68418942_1,262,320.857,8.98E-86,gi|301122665|ref|XP_002909059.1|phosphatidylinositol-4-phosphate-5-kinase (Pi-PIPKD5) [Phytophthora infestans T30-4] ," GO:0016301,GO:0046488,GO:0016307,GO:0004930,GO:0016020,GO:0007186","XP_002909059.1,EEY57873.1"
Stramenopiles-Phytophthora_ramorum_jgi74484,1831,1679.46,0,gi|301105377|ref|XP_002901772.1|phosphatidylinositol-4-phosphate-5-kinase (Pi-PIPK-D2) [Phytophthora infestans T30-4] ," GO:0016301,GO:0004888,GO:0046488,GO:0016307,GO:0016020,GO:0007166","XP_002901772.1,EEY57162.1"
Stramenopiles-Phytophthora_sojae_jgi158495,1751,1736.85,0,gi|301105377|ref|XP_002901772.1|phosphatidylinositol-4-phosphate-5-kinase (Pi-PIPK-D2) [Phytophthora infestans T30-4] ," GO:0016301,GO:0004888,GO:0046488,GO:0016307,GO:0016020,GO:0007166","XP_002901772.1,EEY57162.1"
Stramenopiles-Phytophthora_sojae_jgi132410,865,856.284,0,gi|301101281|ref|XP_002899729.1|phosphatidylinositol-4-phosphate-5-kinase (PIPK-D6/GPCR-PIPK) [Phytophthora infestans T30-4] ," GO:0004888,GO:0016021,GO:0016020,GO:0016307,GO:0046488,GO:0004930,GO:0016301,GO:0007166,GO:0004872,GO:0007186","XP_002899729.1,EEY60783.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi183571,252,415.616,2.57E-114,gi|223995003|ref|XP_002287185.1|predicted protein [Thalassiosira pseudonana CCMP1335] ," GO:0007049,GO:0051301,GO:0005634","XP_002287185.1,EED94628.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi223995003,322,669.078,0,gi|223995003|ref|XP_002287185.1|predicted protein [Thalassiosira pseudonana CCMP1335] ," GO:0007049,GO:0051301,GO:0005634","XP_002287185.1,EED94628.1"
Stramenopiles-Phaeodactylum_tricornutum_CCAP_1055/1_gi219124659,222,458.759,1.97E-127,gi|219124659|ref|XP_002182616.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] , GO:0005634,"XP_002182616.1,EEC45903.1"
Stramenopiles-Phytophthora_capsici_jgi70750,317,588.956,2.11E-166,gi|301117658|ref|XP_002906557.1|conserved hypothetical protein [Phytophthora infestans T30-4] , GO:0005634,"XP_002906557.1,EEY65958.1"
```

```
Stramenopiles-Phytophthora_sojae_jgi134106,316,590.497,7.04E-
167,gi|301117658|ref|XP_002906557.1|conserved hypothetical protein [Phytophthora
infestans T30-4] , GO:0005634,"XP_002906557.1,EEY65958.1"
Stramenopiles-Phytophthora_ramorum_jgi81340,316,582.793,1.79E-
164,gi|301117658|ref|XP_002906557.1|conserved hypothetical protein [Phytophthora
infestans T30-4] , GO:0005634,"XP_002906557.1,EEY65958.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224002687,355,741.495,0,gi|224002687|ref|XP_
002291015.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0005488,GO:0008152,GO:0044237,GO:0003824,GO:0050662","XP_002291015.1,EED91122
.1"
Stramenopiles-
Phytophthora_ramorum_jgi73108,386,744.962,0,"gi|301114943|ref|XP_002999241.1|UDP
-glucose 4-epimerase, putative [Phytophthora infestans T30-4] ","
GO:0005488,GO:0008152,GO:0044237,GO:0003824,GO:0050662","XP_002999241.1,EEY69387
.1"
Stramenopiles-
Phytophthora_capsici_jgi102334,387,755.362,0,"gi|301114943|ref|XP_002999241.1|UD
P-glucose 4-epimerase, putative [Phytophthora infestans T30-4] ","
GO:0005488,GO:0008152,GO:0044237,GO:0003824,GO:0050662","XP_002999241.1,EEY69387
.1"
Stramenopiles-
Phytophthora_sojae_jgi129934,386,754.977,0,"gi|301114943|ref|XP_002999241.1|UDP-
glucose 4-epimerase, putative [Phytophthora infestans T30-4] ","
GO:0005488,GO:0008152,GO:0044237,GO:0003824,GO:0050662","XP_002999241.1,EEY69387
.1"
Stramenopiles-
Phytophthora_ramorum_jgi73107,371,727.628,0,"gi|301114945|ref|XP_002999242.1|UDP
-glucose 4-epimerase, putative [Phytophthora infestans T30-4] ","
GO:0005488,GO:0008152,GO:0044237,GO:0003824,GO:0050662","XP_002999242.1,EEY69388
.1"
Stramenopiles-
Phytophthora_parasitica_esContig1059_3,388,750.74,0,"gi|301114945|ref|XP_0029992
42.1|UDP-glucose 4-epimerase, putative [Phytophthora infestans T30-4] ","
GO:0005488,GO:0008152,GO:0044237,GO:0003824,GO:0050662","XP_002999242.1,EEY69388
.1"
Stramenopiles-
Phytophthora_sojae_jgi129935,371,750.355,0,"gi|301114945|ref|XP_002999242.1|UDP-
glucose 4-epimerase, putative [Phytophthora infestans T30-4] ","
GO:0005488,GO:0008152,GO:0044237,GO:0003824,GO:0050662","XP_002999242.1,EEY69388
.1"
Stramenopiles-Phytophthora_capsici_jgi102919,276,556.599,9.65E-
157,"gi|301114945|ref|XP_002999242.1|UDP-glucose 4-epimerase, putative
[Phytophthora infestans T30-4] ","
GO:0005488,GO:0008152,GO:0044237,GO:0003824,GO:0050662","XP_002999242.1,EEY69388
.1"
Stramenopiles-
Phytophthora_sojae_jgi108302,883,1649.41,0,gi|301097499|ref|XP_002897844.1|heat
shock protein 101 [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0006950,GO:0019538,GO:0000166,GO:0017111,GO:0005515","XP_002897844
.1,EEY64644.1"
Stramenopiles-
Phytophthora_ramorum_jgi71064,879,1637.47,0,gi|301097499|ref|XP_002897844.1|heat
shock protein 101 [Phytophthora infestans T30-4] ,"
```

```
GO:0005524,GO:0006950,GO:0019538,GO:0000166,GO:0017111,GO:0005515","XP_002897844
.1,EEY64644.1"
Stramenopiles-
Phytophthora_capsici_jgi118497,563,775.778,0,gi|301097499|ref|XP_002897844.1|hea
t shock protein 101 [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0006950,GO:0019538,GO:0000166,GO:0017111,GO:0005515","XP_002897844
.1,EEY64644.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219125089,887,1790.78,0,gi|219125089|ref
|XP_002182821.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0005524,GO:0019538,GO:0000166,GO:0017111,GO:0005515","XP_002182821.1,EEC45557
.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223997144,926,1871.67,0,gi|223997144|ref|XP_
002288245.1|member of the HSP104/clp superfamily [Thalassiosira pseudonana
CCMP1335] ,"
GO:0005524,GO:0019538,GO:0000166,GO:0017111,GO:0005515","XP_002288245.1,EED93681
.1"
Stramenopiles-Aureococcus_anophagefferens_jgi70780,1187,431.409,3.57E-
118,gi|303283942|ref|XP_003061262.1|predicted protein [Micromonas pusilla
CCMP1545] ," GO:0016779,GO:0008152","XP_003061262.1,EEH54912.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219129244,712,1470.29,0,gi|219129244|ref
|XP_002184804.1|precursor of phosphorylase udp-glucose diphosphorylase
[Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0016779,GO:0016740,GO:0003983,GO:0008152","XP_002184804.1,EEC43863.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi183667,641,951.044,0,gi|219129244|ref|XP_002184804.1
|precursor of phosphorylase udp-glucose diphosphorylase [Phaeodactylum
tricornutum CCAP 1055/1] ,"
GO:0016779,GO:0016740,GO:0003983,GO:0008152","XP_002184804.1,EEC43863.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224009484,608,1248.42,0,gi|224009484|ref|XP_
002293700.1|hypothetical protein THAPSDRAFT_42326 [Thalassiosira pseudonana
CCMP1335] ," GO:0016779,GO:0008152","XP_002293700.1,EED88709.1"
Stramenopiles-Aureococcus_anophagefferens_jgi22705,650,581.252,1.47E-
163,gi|299470261|emb|CBN79565.1|conserved unknown protein [Ectocarpus
siliculosus]," GO:0016779,GO:0008152",CBN79565.1
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219119007,600,1240.71,0,gi|219119007|ref
|XP_002180270.1|udp-n-acetylglucosamine diphosphorylase [Phaeodactylum
tricornutum CCAP 1055/1] ,"
GO:0016779,GO:0016740,GO:0008152,GO:0003977","XP_002180270.1,EEC48461.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi211962,635,704.516,0,gi|219119007|ref|XP_002180270.1
|udp-n-acetylglucosamine diphosphorylase [Phaeodactylum tricornutum CCAP 1055/1]
," GO:0016779,GO:0016740,GO:0008152,GO:0003977","XP_002180270.1,EEC48461.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224003733,600,1237.25,0,gi|224003733|ref|XP_
002291538.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0016779,GO:0008152","XP_002291538.1,EED91645.1"
Stramenopiles-Aureococcus_anophagefferens_jgi28944,616,535.413,7.71E-
150,gi|255079326|ref|XP_002503243.1|predicted protein [Micromonas sp. RCC299] ,"
GO:0016779,GO:0008152","XP_002503243.1,ACO64501.1"
```

```
Stramenopiles-Blastocystis_hominis_tbBHL00001171_3,220,273.478,1.02E-
71,gi|300123614|emb|CBK24886.2|unnamed protein product [Blastocystis hominis],"
GO:0016779,GO:0008152",CBK24886.2
Stramenopiles-
Phytophthora_sojae_jgi141803,999,1726.84,0,gi|301106332|ref|XP_002902249.1|conse
rved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002902249.1,EEY56921.1"
Stramenopiles-
Phytophthora_ramorum_jgi82041,991,1743.01,0,gi|301106332|ref|XP_002902249.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002902249.1,EEY56921.1"
Stramenopiles-Aureococcus_anophagefferens_jgi70759,1527,415.616,2.66E-
113,"gi|301105809|ref|XP_002901988.1|aldehyde dehydrogenase, putative
[Phytophthora infestans T30-4] ","
GO:0006081,GO:0055114,GO:0016491,GO:0008152,GO:0004030","XP_002901988.1,EEY57378
.1"
Stramenopiles-
Phytophthora_ramorum_jgi78368,663,684.871,0,gi|301103815|ref|XP_002900993.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002900993.1,EEY59383.1"
Stramenopiles-Phytophthora_capsici_jgi11692,560,611.683,8.32E-
173,gi|301103815|ref|XP_002900993.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002900993.1,EEY59383.1"
Stramenopiles-
Phytophthora_sojae_jgi144745,1732,2886.67,0,gi|301114397|ref|XP_002998968.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,
GO:0005509,"XP_002998968.1,EEY69114.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi276098,747,796.579,0,gi|219124450|ref|XP_002182516.1
|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0055114,GO:0009331,GO:0016491,GO:0004368,GO:0006072","XP_002182516.1,EEC45803
.1"
Stramenopiles-Aureococcus_anophagefferens_jgi66976,757,184.882,3.47E-
44,"gi|115941928|ref|XP_001178503.1|PREDICTED: hypothetical protein, partial
[Strongylocentrotus purpuratus]",,XP_001178503.1
Stramenopiles-
Fragilariopsis_cylindrus_jgi263777,574,683.33,0,gi|3283030|gb|AAD13804.1|silicon
transporter [Cylindrotheca fusiformis],,AAD13804.1
Stramenopiles-
Fragilariopsis_cylindrus_jgi212017,576,675.626,0,gi|3283036|gb|AAD13807.1|silico
n transporter [Cylindrotheca fusiformis],,AAD13807.1
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219128344,506,1030.78,0,gi|219128344|ref
|XP_002184375.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002184375.1,XP_002184376.1,ACJ65492.1,ACJ65493.1,EEC44124.1,EEC44125.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219128346,506,1030.78,0,gi|219128344|ref
|XP_002184375.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002184375.1,XP_002184376.1,ACJ65492.1,ACJ65493.1,EEC44124.1,EEC44125.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219126028,512,1046.57,0,gi|219126028|ref
|XP_002183269.1|silicon transporter [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002183269.1,ACJ65491.1,EEC45487.1"
```

```
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224004538,475,972.615,0,gi|82527195|gb|ABB81
826.1|silicon transporter [Thalassiosira pseudonana],,ABB81826.1
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224002056,464,947.577,0,gi|82527193|gb|ABB81
825.1|silicon transporter [Thalassiosira pseudonana],,ABB81825.1
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224003147,437,897.501,0,gi|82527197|gb|ABB81
827.1|silicon transporter [Thalassiosira pseudonana],,ABB81827.1
Stramenopiles-Fragilariopsis_cylindrus_jgi211148,553,529.25,5.16E-
148,gi|219128344|ref|XP_002184375.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1]
,,"XP_002184375.1,XP_002184376.1,ACJ65492.1,ACJ65493.1,EEC44124.1,EEC44125.1"
Stramenopiles-Phytophthora_capsici_jgi37307,343,344.739,8.00E-
93,"gi|301115672|ref|XP_002905565.1|RNA binding protein, putative [Phytophthora
infestans T30-4] "," GO:0003676,GO:0000166","XP_002905565.1,EEY68406.1"
Stramenopiles-Phytophthora_brassicae_esContig1945_2,388,474.937,6.91E-
132,"gi|301115672|ref|XP_002905565.1|RNA binding protein, putative [Phytophthora
infestans T30-4] "," GO:0003676,GO:0000166","XP_002905565.1,EEY68406.1"
Stramenopiles-Phytophthora_ramorum_jgi75500,343,540.421,1.15E-
151,"gi|301115672|ref|XP_002905565.1|RNA binding protein, putative [Phytophthora
infestans T30-4] "," GO:0003676,GO:0000166","XP_002905565.1,EEY68406.1"
Stramenopiles-Phytophthora_sojae_jgi141148,357,550.821,7.60E-
155,"gi|301115672|ref|XP_002905565.1|RNA binding protein, putative [Phytophthora
infestans T30-4] "," GO:0003676,GO:0000166","XP_002905565.1,EEY68406.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi171245,519,265.388,1.20E-
68,gi|298713553|emb|CBJ27081.1|conserved unknown protein [Ectocarpus
siliculosus]," GO:0003676,GO:0000166",CBJ27081.1
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224009309,189,391.734,1.86E-
107,gi|224009309|ref|XP_002293613.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ," GO:0003676,GO:0000166","XP_002293613.1,EED89349.1"
Stramenopiles-Blastocystis_hominis_tbBHL00000002_1,558,412.535,6.03E-
113,gi|300121714|emb|CBK22289.2|unnamed protein product [Blastocystis hominis],"
GO:0003735,GO:0003723,GO:0006412,GO:0030529,GO:0006396,GO:0005840,GO:0005622",CB
K22289.2
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219111803,76,154.451,3.62E-
36,gi|219111803|ref|XP_002177653.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0003676,GO:0000166","XP_002177653.1,EEC50467.1"
Stramenopiles-Aureococcus_anophagefferens_jgi32583,241,171.785,6.15E-
41,gi|299115572|emb|CBN75775.1|conserved unknown protein [Ectocarpus
siliculosus]," GO:0003676,GO:0000166",CBN75775.1
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219130905,222,456.447,9.45E-
127,gi|219130905|ref|XP_002185593.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0003676,GO:0000166","XP_002185593.1,EEC42891.1"
Stramenopiles-Aureococcus_anophagefferens_jgi37977,452,295.049,1.20E-
77,gi|255081020|ref|XP_002504076.1|thioredoxin [Micromonas sp. RCC299] ,"
GO:0045454,GO:0016491","XP_002504076.1,ACO65334.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi195876,142,131.339,3.29E-
29,gi|223995913|ref|XP_002287630.1|MYB DNA binding protein/ transcription
factor-like protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002287630.1,EED95073.1"
```

```
Stramenopiles-Fragilariopsis_cylindrus_jgi271054,280,146.747,2.75E-
33,gi|219119053|ref|XP_002180293.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] , GO:0045454,"XP_002180293.1,EEC48484.1"
Stramenopiles-Phytophthora_capsici_jgi123003,301,590.882,5.12E-
167,gi|301112272|ref|XP_002905215.1|WD domain-containing protein [Phytophthora
infestans T30-4] ,,"XP_002905215.1,EEY53597.1"
Stramenopiles-Phytophthora_sojae_jgi108359,301,601.668,3.23E-
170,gi|301112272|ref|XP_002905215.1|WD domain-containing protein [Phytophthora
infestans T30-4] ,,"XP_002905215.1,EEY53597.1"
Stramenopiles-Phytophthora_ramorum_jgi71484,301,587.03,7.33E-
166,gi|301112272|ref|XP_002905215.1|WD domain-containing protein [Phytophthora
infestans T30-4] ,,"XP_002905215.1,EEY53597.1"
Stramenopiles-Phytophthora_brassicae_esgi144592125_3,240,320.857,6.27E-
86,gi|301112272|ref|XP_002905215.1|WD domain-containing protein [Phytophthora
infestans T30-4] ,,"XP_002905215.1,EEY53597.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224005729,337,699.123,0,gi|224005729|ref|XP_
002291825.1|hypothetical protein THAPSDRAFT_41583 [Thalassiosira pseudonana
CCMP1335] ,,"XP_002291825.1,EED90676.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219121455,321,666.381,0,gi|219121455|ref
|XP_002185951.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002185951.1,ACI65421.1"
Stramenopiles-Aureococcus_anophagefferens_jgi22631,351,363.229,2.78E-
98,gi|299469791|emb|CBN76645.1|conserved unknown protein [Ectocarpus
siliculosus],,CBN76645.1
Stramenopiles-
Phytophthora_ramorum_jgi72910,1096,1066.99,0,gi|301123033|ref|XP_002909243.1|kin
esin-like protein [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0000166,GO:0003777,GO:0007018,GO:0003774,GO:0005874","XP_002909243
.1,EEY58057.1"
Stramenopiles-
Phytophthora_sojae_jgi158245,1136,1028.85,0,gi|301123033|ref|XP_002909243.1|kine
sin-like protein [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0000166,GO:0003777,GO:0007018,GO:0003774,GO:0005874","XP_002909243
.1,EEY58057.1"
Stramenopiles-
Phytophthora_ramorum_jgi51019,436,838.565,0,gi|301110312|ref|XP_002904236.1|kine
sin-like protein [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0000166,GO:0003777,GO:0007018,GO:0003774,GO:0005874","XP_002904236
.1,EEY54414.1"
Stramenopiles-
Phytophthora_sojae_jgi109123,349,706.057,0,gi|301110312|ref|XP_002904236.1|kines
in-like protein [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0000166,GO:0003777,GO:0007018,GO:0003774,GO:0005874","XP_002904236
.1,EEY54414.1"
Stramenopiles-Phytophthora_capsici_jgi118620,277,545.814,1.69E-
153,gi|301110312|ref|XP_002904236.1|kinesin-like protein [Phytophthora infestans
T30-4] ,"
GO:0005524,GO:0000166,GO:0003777,GO:0007018,GO:0003774,GO:0005874","XP_002904236
.1,EEY54414.1"
Stramenopiles-Aureococcus_anophagefferens_jgi1243,457,426.402,3.03E-
117,gi|301110312|ref|XP_002904236.1|kinesin-like protein [Phytophthora infestans
T30-4] ,"
```

```
GO:0005524,GO:0000166,GO:0003777,GO:0007018,GO:0003774,GO:0005874","XP_002904236
.1,EEY54414.1"
Stramenopiles-Phytophthora_ramorum_jgi40072,308,603.594,7.70E-
171,gi|301109070|ref|XP_002903616.1|kinesin-like protein [Phytophthora infestans
T30-4] ,"
GO:0005524,GO:0000166,GO:0003777,GO:0007018,GO:0003774,GO:0005874","XP_002903616
.1,EEY55392.1"
Stramenopiles-Phytophthora_sojae_jgi121724,308,620.928,5.50E-
176,gi|301109070|ref|XP_002903616.1|kinesin-like protein [Phytophthora infestans
T30-4] ,"
GO:0005524,GO:0000166,GO:0003777,GO:0007018,GO:0003774,GO:0005874","XP_002903616
.1,EEY55392.1"
Stramenopiles-Phytophthora_capsici_jgi17366,337,625.55,2.34E-
177,gi|301109070|ref|XP_002903616.1|kinesin-like protein [Phytophthora infestans
T30-4] ,"
GO:0005524,GO:0000166,GO:0003777,GO:0007018,GO:0003774,GO:0005874","XP_002903616
.1,EEY55392.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219121187,433,898.271,0,"gi|219121187|re
f|XP_002185822.1|glycosyl transferase, family 1 [Phaeodactylum tricornutum CCAP
1055/1] "," GO:0009058,GO:0016740","XP_002185822.1,ACI65292.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi183873,485,396.741,3.17E-
108,"gi|219121187|ref|XP_002185822.1|glycosyl transferase, family 1
[Phaeodactylum tricornutum CCAP 1055/1] ","
GO:0009058,GO:0016740","XP_002185822.1,ACI65292.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224010481,549,1149.04,0,gi|224010481|ref|XP_
002294198.1|glycosyltransferase [Thalassiosira pseudonana CCMP1335] ,"
GO:0009058,GO:0016740","XP_002294198.1,EED88553.1"
Stramenopiles-
Phytophthora_sojae_jgi108303,500,774.622,0,gi|301097485|ref|XP_002897837.1|conse
rved hypothetical protein [Phytophthora infestans T30-4] ,
GO:0009058,"XP_002897837.1,EEY64637.1"
Stramenopiles-Phytophthora_capsici_jgi91174,241,365.54,2.58E-
99,gi|301097485|ref|XP_002897837.1|conserved hypothetical protein [Phytophthora
infestans T30-4] , GO:0009058,"XP_002897837.1,EEY64637.1"
Stramenopiles-
Phytophthora_ramorum_jgi72993,492,772.311,0,gi|301097485|ref|XP_002897837.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,
GO:0009058,"XP_002897837.1,EEY64637.1"
Stramenopiles-Phytophthora_capsici_jgi91171,180,325.094,1.71E-
87,gi|301097485|ref|XP_002897837.1|conserved hypothetical protein [Phytophthora
infestans T30-4] , GO:0009058,"XP_002897837.1,EEY64637.1"
Stramenopiles-Blastocystis_hominis_tbBHL00002962_1,198,229.565,1.31E-
58,gi|300121242|emb|CBK21623.2|unnamed protein product [Blastocystis
hominis],,CBK21623.2
Stramenopiles-Aureococcus_anophagefferens_jgi2187,413,353.599,2.41E-
95,gi|156365753|ref|XP_001626808.1|predicted protein [Nematostella vectensis] ,
GO:0009058,"XP_001626808.1,EDO34708.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219115097,322,664.84,0,gi|219115097|ref|
XP_002178344.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0016433,GO:0006364,GO:0005737,GO:0000179,GO:0000154,GO:0008649","XP_002178344
.1,EEC50009.1"
```

```
Stramenopiles-Fragilariopsis_cylindrus_jgi188724,334,452.21,4.09E-
125,gi|224001108|ref|XP_002290226.1|dimethyladenosine transferase [Thalassiosira
pseudonana CCMP1335] ,"
GO:0016433,GO:0008168,GO:0006364,GO:0016740,GO:0000179,GO:0000154,GO:0008649","X
P_002290226.1,EED91978.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224001108,335,689.878,0,gi|224001108|ref|XP_
002290226.1|dimethyladenosine transferase [Thalassiosira pseudonana CCMP1335] ,"
GO:0016433,GO:0008168,GO:0006364,GO:0016740,GO:0000179,GO:0000154,GO:0008649","X
P_002290226.1,EED91978.1"
Stramenopiles-Aureococcus_anophagefferens_jgi60268,313,380.563,1.13E-
103,gi|301110310|ref|XP_002904235.1|dimethyladenosine transferase [Phytophthora
infestans T30-4] ,"
GO:0016433,GO:0006364,GO:0016740,GO:0000179,GO:0000154,GO:0008649","XP_002904235
.1,EEY54413.1"
Stramenopiles-Aureococcus_anophagefferens_jgi35437,192,257.684,4.22E-
67,gi|301110310|ref|XP_002904235.1|dimethyladenosine transferase [Phytophthora
infestans T30-4] ,"
GO:0016433,GO:0006364,GO:0016740,GO:0000179,GO:0000154,GO:0008649","XP_002904235
.1,EEY54413.1"
Stramenopiles-Phytophthora_ramorum_jgi71899,313,632.098,2.39E-
179,gi|301110310|ref|XP_002904235.1|dimethyladenosine transferase [Phytophthora
infestans T30-4] ,"
GO:0016433,GO:0006364,GO:0016740,GO:0000179,GO:0000154,GO:0008649","XP_002904235
.1,EEY54413.1"
Stramenopiles-Phytophthora_capsici_jgi38638,233,452.21,1.81E-
125,gi|301110310|ref|XP_002904235.1|dimethyladenosine transferase [Phytophthora
infestans T30-4] ,"
GO:0016433,GO:0006364,GO:0016740,GO:0000179,GO:0000154,GO:0008649","XP_002904235
.1,EEY54413.1"
Stramenopiles-Phytophthora_sojae_jgi109122,313,634.024,5.74E-
180,gi|301110310|ref|XP_002904235.1|dimethyladenosine transferase [Phytophthora
infestans T30-4] ,"
GO:0016433,GO:0006364,GO:0016740,GO:0000179,GO:0000154,GO:0008649","XP_002904235
.1,EEY54413.1"
Stramenopiles-Phytophthora_parasitica_esContig94_4,285,491.115,5.25E-
137,gi|301110310|ref|XP_002904235.1|dimethyladenosine transferase [Phytophthora
infestans T30-4] ,"
GO:0016433,GO:0006364,GO:0016740,GO:0000179,GO:0000154,GO:0008649","XP_002904235
.1,EEY54413.1"
Stramenopiles-
Phytophthora_sojae_jgi137358,477,698.353,0,gi|301109988|ref|XP_002904074.1|Drug/
Metabolite Transporter (DMT) Superfamily [Phytophthora infestans T30-4] ,"
GO:0016021,GO:0016020","XP_002904074.1,EEY54252.1"
Stramenopiles-
Phytophthora_capsici_jgi94797,488,751.51,0,gi|301109988|ref|XP_002904074.1|Drug/
Metabolite Transporter (DMT) Superfamily [Phytophthora infestans T30-4] ,"
GO:0016021,GO:0016020","XP_002904074.1,EEY54252.1"
Stramenopiles-
Phytophthora_ramorum_jgi82224,481,731.865,0,gi|301109988|ref|XP_002904074.1|Drug
/Metabolite Transporter (DMT) Superfamily [Phytophthora infestans T30-4] ,"
GO:0016021,GO:0016020","XP_002904074.1,EEY54252.1"
Stramenopiles-
Phytophthora_capsici_jgi69064,1090,1983.76,0,"gi|301113186|ref|XP_002998363.1|tr
```

```
ansmembrane protein, putative [Phytophthora infestans T30-4] ","
GO:0005509,GO:0016021","XP_002998363.1,EEY69716.1"
Stramenopiles-
Phytophthora_ramorum_jgi77447,1730,1973.36,0,"gi|301113186|ref|XP_002998363.1|tr
ansmembrane protein, putative [Phytophthora infestans T30-4] ","
GO:0005509,GO:0016021","XP_002998363.1,EEY69716.1"
Stramenopiles-
Phytophthora_sojae_jgi139975,1132,1993.01,0,"gi|301113186|ref|XP_002998363.1|tra
nsmembrane protein, putative [Phytophthora infestans T30-4] ","
GO:0005509,GO:0016021","XP_002998363.1,EEY69716.1"
Stramenopiles-
Phytophthora_sojae_jgi140001,1109,1808.88,0,gi|301111171|ref|XP_002904665.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,
GO:0005509,"XP_002904665.1,EEY54034.1"
Stramenopiles-
Phytophthora_ramorum_jgi77473,1145,1802.33,0,gi|301111171|ref|XP_002904665.1|con
served hypothetical protein [Phytophthora infestans T30-4] ,
GO:0005509,"XP_002904665.1,EEY54034.1"
Stramenopiles-
Phytophthora_sojae_jgi141282,1218,2054.64,0,gi|301113802|ref|XP_002998671.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,
GO:0005509,"XP_002998671.1,EEY70024.1"
Stramenopiles-
Phytophthora_ramorum_jgi79519,1241,2032.68,0,gi|301113802|ref|XP_002998671.1|con
served hypothetical protein [Phytophthora infestans T30-4] ,
GO:0005509,"XP_002998671.1,EEY70024.1"
Stramenopiles-
Phytophthora_capsici_jgi10385,1107,1929.45,0,gi|301113802|ref|XP_002998671.1|con
served hypothetical protein [Phytophthora infestans T30-4] ,
GO:0005509,"XP_002998671.1,EEY70024.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219129954,312,640.958,0,gi|219129954|ref
|XP_002185141.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0005488,GO:0016021,GO:0016020,GO:0055085,GO:0005743,GO:0006810,GO:0005215","X
P_002185141.1,EEC43273.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224007861,311,639.032,0,gi|224007861|ref|XP_
002292890.1|oxoglutarate/malate translocator [Thalassiosira pseudonana CCMP1335]
,"
GO:0005488,GO:0016021,GO:0016020,GO:0055085,GO:0005743,GO:0006810,GO:0005215","X
P_002292890.1,EED90086.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi180618,307,447.203,9.55E-
124,gi|219129954|ref|XP_002185141.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0005488,GO:0016021,GO:0016020,GO:0055085,GO:0005743,GO:0006810,GO:0005215","X
P_002185141.1,EEC43273.1"
Stramenopiles-Aureococcus_anophagefferens_jgi31501,314,347.051,1.64E-
93,gi|299115887|emb|CBN75896.1|oxoglutarate/malate translocator [Ectocarpus
siliculosus],"
GO:0005488,GO:0016021,GO:0016020,GO:0055085,GO:0006810",CBN75896.1
Stramenopiles-Phytophthora_ramorum_jgi71378,306,597.816,5.06E-
169,"gi|301093843|ref|XP_002997766.1|mitochondrial 2-oxoglutarate/malate carrier
protein, putative [Phytophthora infestans T30-4] ","
GO:0005488,GO:0016021,GO:0016020,GO:0055085,GO:0005743,GO:0006810","XP_002997766
.1,EEY67904.1"
```

```
Stramenopiles-Phytophthora_brassicae_esContig117_3,244,443.351,9.13E-
123,"gi|301093843|ref|XP_002997766.1|mitochondrial 2-oxoglutarate/malate carrier
protein, putative [Phytophthora infestans T30-4] ","
GO:0005488,GO:0016021,GO:0016020,GO:0055085,GO:0005743,GO:0006810","XP_002997766
.1,EEY67904.1"
Stramenopiles-Phytophthora_capsici_jgi95872,306,603.979,6.71E-
171,"gi|301093843|ref|XP_002997766.1|mitochondrial 2-oxoglutarate/malate carrier
protein, putative [Phytophthora infestans T30-4] ","
GO:0005488,GO:0016021,GO:0016020,GO:0055085,GO:0005743,GO:0006810","XP_002997766
.1,EEY67904.1"
Stramenopiles-Phytophthora_sojae_jgi108637,307,609.372,1.41E-
172,"gi|301093843|ref|XP_002997766.1|mitochondrial 2-oxoglutarate/malate carrier
protein, putative [Phytophthora infestans T30-4] ","
GO:0005488,GO:0016021,GO:0016020,GO:0055085,GO:0005743,GO:0006810","XP_002997766
.1,EEY67904.1"
Stramenopiles-Blastocystis_hominis_tbBHL00000953_2,218,369.007,1.86E-
100,gi|300176902|emb|CBK25471.2|unnamed protein product [Blastocystis hominis],"
GO:0005488,GO:0016021,GO:0016020,GO:0055085,GO:0005743,GO:0006810,GO:0005215",CB
K25471.2
Stramenopiles-Blastocystis_hominis_tbBHL00001260_2,216,370.933,5.47E-
101,gi|300120793|emb|CBK21035.2|unnamed protein product [Blastocystis hominis],"
GO:0005488,GO:0016021,GO:0016020,GO:0055085,GO:0005743,GO:0006810",CBK21035.2
Stramenopiles-Aureococcus_anophagefferens_jgi66601,895,130.568,1.01E-
27,gi|291238785|ref|XP_002739306.1|PREDICTED: hypothetical protein [Saccoglossus
kowalevskii],,XP_002739306.1
Stramenopiles-
Phytophthora_ramorum_jgi76758,2206,851.662,0,gi|301100916|ref|XP_002899547.1|con
served hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002899547.1,EEY61907.1"
Stramenopiles-
Phytophthora_sojae_jgi156107,1866,925.235,0,gi|301100916|ref|XP_002899547.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002899547.1,EEY61907.1"
Stramenopiles-Phytophthora_ramorum_jgi85957,216,381.719,2.47E-
104,"gi|301110612|ref|XP_002904386.1|vacuolar protein sorting-associated
protein, putative [Phytophthora infestans T30-4] ","
GO:0008104,GO:0005515","XP_002904386.1,EEY54564.1"
Stramenopiles-
Phytophthora_sojae_jgi136943,3858,2766.1,0,"gi|301110612|ref|XP_002904386.1|vacu
olar protein sorting-associated protein, putative [Phytophthora infestans T30-4]
"," GO:0008104,GO:0005515","XP_002904386.1,EEY54564.1"
Stramenopiles-Phytophthora_capsici_jgi25279,215,380.178,7.86E-
104,"gi|301110612|ref|XP_002904386.1|vacuolar protein sorting-associated
protein, putative [Phytophthora infestans T30-4] ","
GO:0008104,GO:0005515","XP_002904386.1,EEY54564.1"
Stramenopiles-
Phytophthora_ramorum_jgi95794,562,874.389,0,gi|301107866|ref|XP_002903015.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002903015.1,EEY56185.1"
Stramenopiles-
Phytophthora_sojae_jgi156418,1341,1185.24,0,gi|301098165|ref|XP_002898176.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002898176.1,EEY63589.1"
```

```
Stramenopiles-Phytophthora_capsici_jgi3218,489,622.083,4.81E-
176,gi|301098165|ref|XP_002898176.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002898176.1,EEY63589.1"
Stramenopiles-Phytophthora_ramorum_jgi74131,509,598.971,4.11E-
169,gi|301098165|ref|XP_002898176.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002898176.1,EEY63589.1"
Stramenopiles-Aureococcus_anophagefferens_jgi64837,302,112.849,4.04E-
23,gi|38683706|gb|AAR26882.1|FirrV-1-B7 [Feldmannia irregularis virus
a],,AAR26882.1
Stramenopiles-
Phytophthora_capsici_jgi101937,546,775.007,0,gi|301095294|ref|XP_002896748.1|Ca2
:Cation Antiporter (CaCA) Family [Phytophthora infestans T30-4] ,"
GO:0016021,GO:0016020,GO:0055085","XP_002896748.1,EEY66861.1"
Stramenopiles-
Phytophthora_sojae_jgi128640,558,778.089,0,gi|301095294|ref|XP_002896748.1|Ca2
:Cation Antiporter (CaCA) Family [Phytophthora infestans T30-4] ,"
GO:0016021,GO:0016020,GO:0055085","XP_002896748.1,EEY66861.1"
Stramenopiles-
Phytophthora_ramorum_jgi81519,562,765.763,0,gi|301095294|ref|XP_002896748.1|Ca2
:Cation Antiporter (CaCA) Family [Phytophthora infestans T30-4] ,"
GO:0016021,GO:0016020,GO:0055085","XP_002896748.1,EEY66861.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224001622,632,1311.59,0,gi|224001622|ref|XP_
002290483.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0016021,GO:0016020,GO:0055085","XP_002290483.1,EED92235.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219114274,651,1342.02,0,gi|219114274|ref
|XP_002176308.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0016021,GO:0016020,GO:0055085","XP_002176308.1,EEC42700.1"
Stramenopiles-Aureococcus_anophagefferens_jgi30006,198,191.045,5.44E-
47,gi|312374778|gb|EFR22262.1|hypothetical protein AND_15528 [Anopheles
darlingi],,EFR22262.1
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224015509,627,1287.71,0,gi|224015509|ref|XP_
002297406.1|sodium/potassium/calcium exchange protein [Thalassiosira pseudonana
CCMP1335] ," GO:0016021,GO:0016020,GO:0055085","XP_002297406.1,EED86276.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219110569,517,1046.96,0,gi|219110569|ref
|XP_002177036.1|2-phosphoglycolate phosphatase [Phaeodactylum tricornutum CCAP
1055/1] ,"
GO:0005509,GO:0016021,GO:0016020,GO:0055085","XP_002177036.1,EEC51499.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi206099,494,505.753,4.50E-
141,gi|219110569|ref|XP_002177036.1|2-phosphoglycolate phosphatase
[Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0005509,GO:0016021,GO:0016020,GO:0055085","XP_002177036.1,EEC51499.1"
Stramenopiles-Aureococcus_anophagefferens_jgi955,498,309.686,4.86E-
82,"gi|157105620|ref|XP_001648950.1|potassium-dependent sodium-calcium
exchanger, putative [Aedes aegypti] ","
GO:0016021,GO:0016020,GO:0055085","XP_001648950.1,EAT33209.1"
Stramenopiles-Aureococcus_anophagefferens_jgi63519,365,126.716,3.67E-
27,gi|298710240|emb|CBJ26315.1|conserved unknown protein [Ectocarpus
siliculosus], GO:0005515,CBJ26315.1
Stramenopiles-Phytophthora_sojae_jgi129929,378,620.542,8.55E-
176,gi|301114931|ref|XP_002999235.1|conserved hypothetical protein [Phytophthora
infestans T30-4] , GO:0005515,"XP_002999235.1,EEY69381.1"
```

```
Stramenopiles-Phytophthora_ramorum_jgi73114,367,629.017,2.54E-
178,gi|301114931|ref|XP_002999235.1|conserved hypothetical protein [Phytophthora
infestans T30-4] , GO:0005515,"XP_002999235.1,EEY69381.1"
Stramenopiles-Phytophthora_capsici_jgi116114,316,512.686,2.06E-
143,gi|301114931|ref|XP_002999235.1|conserved hypothetical protein [Phytophthora
infestans T30-4] , GO:0005515,"XP_002999235.1,EEY69381.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223993367,1224,2543.07,0,gi|223993367|ref|XP
_002286367.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0046872,GO:0006259,GO:0009055,GO:0008270,GO:0005515,GO:0004518,GO:0005622,GO:
0003677","XP_002286367.1,EED96008.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219128584,1813,3730.26,0,gi|219128584|re
f|XP_002184489.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,
GO:0005488,"XP_002184489.1,EEC43888.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224012930,1994,4108.91,0,gi|224012930|ref|XP
_002295117.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,
GO:0005488,"XP_002295117.1,EED87421.1"
Stramenopiles-
Phytophthora_ramorum_jgi84478,1752,2897.46,0,gi|301109096|ref|XP_002903629.1|con
served hypothetical protein [Phytophthora infestans T30-4] ,
GO:0005488,"XP_002903629.1,EEY55405.1"
Stramenopiles-
Phytophthora_sojae_jgi141204,1751,2933.67,0,gi|301109096|ref|XP_002903629.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,
GO:0005488,"XP_002903629.1,EEY55405.1"
Stramenopiles-
Phytophthora_capsici_jgi112252,1682,2765.72,0,gi|301109096|ref|XP_002903629.1|co
nserved hypothetical protein [Phytophthora infestans T30-4] ,
GO:0005488,"XP_002903629.1,EEY55405.1"
Stramenopiles-
Phytophthora_sojae_jgi137085,1305,2364.73,0,gi|301101758|ref|XP_002899967.1|myos
in-like protein [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0000166,GO:0016459,GO:0003774","XP_002899967.1,EEY60594.1"
Stramenopiles-
Phytophthora_capsici_jgi35759,1307,2405.94,0,gi|301101758|ref|XP_002899967.1|myo
sin-like protein [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0000166,GO:0016459,GO:0003774","XP_002899967.1,EEY60594.1"
Stramenopiles-
Phytophthora_ramorum_jgi83913,1294,2319.27,0,gi|301101758|ref|XP_002899967.1|myo
sin-like protein [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0000166,GO:0016459,GO:0003774","XP_002899967.1,EEY60594.1"
Stramenopiles-
Phytophthora_capsici_jgi104104,614,1152.89,0,gi|301120532|ref|XP_002907993.1|myo
sin-like protein [Phytophthora infestans T30-4] ,"
GO:0035091,GO:0005524,GO:0000166,GO:0007154,GO:0016459,GO:0005515,GO:0003774","X
P_002907993.1,EEY61076.1"
Stramenopiles-
Phytophthora_sojae_jgi108186,778,1485.32,0,gi|301121048|ref|XP_002908251.1|myosi
n-like protein [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0000166,GO:0016459,GO:0005515,GO:0003774","XP_002908251.1,EEY61334
.1"
Stramenopiles-
Phytophthora_ramorum_jgi94417,1935,2356.25,0,gi|301117270|ref|XP_002906363.1|myo
```

```
sin-like protein [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0000166,GO:0016459,GO:0003774","XP_002906363.1,EEY65764.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223998562,828,1724.14,0,gi|223998562|ref|XP_
002288954.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0005524,GO:0000166,GO:0016459,GO:0003774","XP_002288954.1,EED94390.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223998754,741,1536.93,0,gi|223998754|ref|XP_
002289050.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0005524,GO:0000166,GO:0016459,GO:0003774","XP_002289050.1,EED94486.1"
Stramenopiles-Phytophthora_sojae_jgi143662,2404,59.6918,5.44E-
06,gi|145351776|ref|XP_001420239.1|predicted protein [Ostreococcus lucimarinus
CCE9901] ,,"XP_001420239.1,ABO98532.1"
Stramenopiles-Phytophthora_ramorum_jgi82553,2143,166.007,5.13E-
38,"gi|294899268|ref|XP_002776563.1|glutamic acid-rich protein precursor,
putative [Perkinsus marinus ATCC 50983] ",
GO:0005515,"XP_002776563.1,EER08379.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223999695,1151,2377.44,0,gi|223999695|ref|XP
_002289520.1|ABC transporter [Thalassiosira pseudonana CCMP1335] ,"
GO:0016887,GO:0005524,GO:0016021,GO:0000166,GO:0042626,GO:0055085,GO:0017111,GO:
0006810","XP_002289520.1,EED93057.1"
Stramenopiles-
Phytophthora_ramorum_jgi71110,569,1106.28,0,"gi|301118669|ref|XP_002907062.1|ele
ctron transfer flavoprotein-ubiquinone oxidoreductase, putative [Phytophthora
infestans T30-4] "," GO:0055114,GO:0004174","XP_002907062.1,EEY63626.1"
Stramenopiles-
Phytophthora_sojae_jgi125082,565,1093.95,0,"gi|301118669|ref|XP_002907062.1|elec
tron transfer flavoprotein-ubiquinone oxidoreductase, putative [Phytophthora
infestans T30-4] "," GO:0055114,GO:0004174","XP_002907062.1,EEY63626.1"
Stramenopiles-
Phytophthora_capsici_jgi123360,573,1104.74,0,"gi|301118669|ref|XP_002907062.1|el
ectron transfer flavoprotein-ubiquinone oxidoreductase, putative [Phytophthora
infestans T30-4] "," GO:0055114,GO:0004174","XP_002907062.1,EEY63626.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi38810,557,655.21,0,gi|298712252|emb|CBJ26703.1|MG
C81928 protein [Ectocarpus siliculosus],"
GO:0055114,GO:0016491,GO:0004174",CBJ26703.1
Stramenopiles-
Aureococcus_anophagefferens_jgi71690,593,664.84,0,gi|298712252|emb|CBJ26703.1|MG
C81928 protein [Ectocarpus siliculosus],"
GO:0055114,GO:0016491,GO:0004174",CBJ26703.1
Stramenopiles-Fragilariopsis_cylindrus_jgi241815,397,213.001,5.47E-
53,gi|219114789|ref|XP_002178190.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0016051,GO:0016021,GO:0008146","XP_002178190.1,EEC49855.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219114789,482,1013.45,0,gi|219114789|ref
|XP_002178190.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0016051,GO:0016021,GO:0008146","XP_002178190.1,EEC49855.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi208801,416,215.698,7.93E-
54,gi|219114789|ref|XP_002178190.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0016051,GO:0016021,GO:0008146","XP_002178190.1,EEC49855.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219124118,324,682.559,0,gi|219124118|ref
```

```
|XP_002182358.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0016051,GO:0016021,GO:0008146","XP_002182358.1,EEC46259.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi270430,369,228.794,6.92E-
58,gi|219124116|ref|XP_002182357.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0016051,GO:0016021,GO:0008146","XP_002182357.1,EEC46258.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219124116,396,831.247,0,gi|219124116|ref
|XP_002182357.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0016051,GO:0016021,GO:0008146","XP_002182357.1,EEC46258.1"
Stramenopiles-
Phytophthora_parasitica_esContig1189_3,839,915.605,0,gi|301090549|ref|XP_0028954
85.1|ATP-binding Cassette (ABC) superfamily [Phytophthora infestans T30-4] ,"
GO:0016887,GO:0005524,GO:0000166,GO:0017111","XP_002895485.1,EEY56287.1"
Stramenopiles-
Phytophthora_sojae_jgi128576,1885,2941.37,0,gi|301091448|ref|XP_002895909.1|ATP-
binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0016887,GO:0005524,GO:0000166,GO:0017111","XP_002895909.1,EEY54149.1"
Stramenopiles-
Phytophthora_sojae_jgi128572,1952,3091.98,0,gi|301091448|ref|XP_002895909.1|ATP-
binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0016887,GO:0005524,GO:0000166,GO:0017111","XP_002895909.1,EEY54149.1"
Stramenopiles-
Phytophthora_ramorum_jgi82977,1636,2754.55,0,gi|301091448|ref|XP_002895909.1|ATP
-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0016887,GO:0005524,GO:0000166,GO:0017111","XP_002895909.1,EEY54149.1"
Stramenopiles-
Phytophthora_sojae_jgi128568,1950,3450.6,0,gi|301091448|ref|XP_002895909.1|ATP-
binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0016887,GO:0005524,GO:0000166,GO:0017111","XP_002895909.1,EEY54149.1"
Stramenopiles-
Phytophthora_ramorum_jgi76582,1951,3449.83,0,gi|301103213|ref|XP_002900693.1|ATP
-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0016887,GO:0005524,GO:0000166,GO:0017111","XP_002900693.1,EEY60008.1"
Stramenopiles-
Phytophthora_ramorum_jgi82974,1406,2236.84,0,gi|301091448|ref|XP_002895909.1|ATP
-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0016887,GO:0005524,GO:0000166,GO:0017111","XP_002895909.1,EEY54149.1"
Stramenopiles-
Phytophthora_capsici_jgi121856,1931,2958.32,0,gi|301091448|ref|XP_002895909.1|AT
P-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0016887,GO:0005524,GO:0000166,GO:0017111","XP_002895909.1,EEY54149.1"
Stramenopiles-
Phytophthora_capsici_jgi121858,1907,2939.83,0,gi|301091448|ref|XP_002895909.1|AT
P-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0016887,GO:0005524,GO:0000166,GO:0017111","XP_002895909.1,EEY54149.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi186926,499,389.037,6.12E-
106,gi|219122046|ref|XP_002181365.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002181365.1,EEC47288.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219122046,434,896.73,0,gi|219122046|ref|
XP_002181365.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002181365.1,EEC47288.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224002805,999,2087.38,0,gi|224002805|ref|XP_
002291074.1|DNA polymerase [Thalassiosira pseudonana CCMP1335] ,"
```

```
GO:0006260,GO:0006139,GO:0003676,GO:0016779,GO:0016740,GO:0003887,GO:0000166,GO:
0003677","XP_002291074.1,EED91181.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219121567,1087,2257.64,0,gi|219121567|re
f|XP_002181135.1|DNA polymerase delta [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0006260,GO:0006139,GO:0003676,GO:0016779,GO:0016740,GO:0003887,GO:0000166,GO:
0003677","XP_002181135.1,EEC47058.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi135771,996,1240.33,0,gi|224015515|ref|XP_002297409.1
|hypothetical protein THAPSDRAFT_bd439 [Thalassiosira pseudonana CCMP1335] ,"
GO:0016740,GO:0001882,GO:0003677,GO:0005634,GO:0006260,GO:0003676,GO:0000166,GO:
0003887,GO:0016779,GO:0006139","XP_002297409.1,EED86279.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224015515,1141,2373.59,0,gi|224015515|ref|XP
_002297409.1|hypothetical protein THAPSDRAFT_bd439 [Thalassiosira pseudonana
CCMP1335] ,"
GO:0016740,GO:0001882,GO:0003677,GO:0005634,GO:0006260,GO:0003676,GO:0000166,GO:
0003887,GO:0016779,GO:0006139","XP_002297409.1,EED86279.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219114300,1147,2386.68,0,gi|219114300|re
f|XP_002176321.1|catalytic subunit p180 [Phaeodactylum tricornutum CCAP 1055/1]
,"
GO:0016740,GO:0001882,GO:0003677,GO:0005634,GO:0006260,GO:0003676,GO:0000166,GO:
0003887,GO:0016779,GO:0006139","XP_002176321.1,EEC42713.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi30667,1118,921.383,0,gi|224015515|ref|XP_00229740
9.1|hypothetical protein THAPSDRAFT_bd439 [Thalassiosira pseudonana CCMP1335] ,"
GO:0016740,GO:0001882,GO:0003677,GO:0005634,GO:0006260,GO:0003676,GO:0000166,GO:
0003887,GO:0016779,GO:0006139","XP_002297409.1,EED86279.1"
Stramenopiles-Blastocystis_hominis_tbBHL00001784_3,254,424.861,4.14E-
117,gi|300121650|emb|CBK22168.2|unnamed protein product [Blastocystis hominis],"
GO:0005488,GO:0004512,GO:0008654,GO:0008152,GO:0003824,GO:0006021",CBK22168.2
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219116747,530,1103.58,0,gi|219116747|ref
|XP_002179168.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0005488,GO:0004512,GO:0008654,GO:0008152,GO:0003824,GO:0006021","XP_002179168
.1,EEC48991.1"
Stramenopiles-
Phytophthora_parasitica_esContig1425_2,561,1062.75,0,"gi|301121186|ref|XP_002908
320.1|inositol-3-phosphate synthase, putative [Phytophthora infestans T30-4] ","
GO:0005488,GO:0004512,GO:0008654,GO:0008152,GO:0003824,GO:0006021","XP_002908320
.1,EEY61403.1"
Stramenopiles-
Phytophthora_sojae_jgi108192,518,1036.17,0,"gi|301121186|ref|XP_002908320.1|inos
itol-3-phosphate synthase, putative [Phytophthora infestans T30-4] ","
GO:0005488,GO:0004512,GO:0008654,GO:0008152,GO:0003824,GO:0006021","XP_002908320
.1,EEY61403.1"
Stramenopiles-
Phytophthora_ramorum_jgi71157,518,1024.23,0,"gi|301121186|ref|XP_002908320.1|ino
sitol-3-phosphate synthase, putative [Phytophthora infestans T30-4] ","
GO:0005488,GO:0004512,GO:0008654,GO:0008152,GO:0003824,GO:0006021","XP_002908320
.1,EEY61403.1"
Stramenopiles-
Phytophthora_capsici_jgi83448,587,1043.88,0,"gi|301121186|ref|XP_002908320.1|ino
sitol-3-phosphate synthase, putative [Phytophthora infestans T30-4] ","
```

```
GO:0005488,GO:0004512,GO:0008654,GO:0008152,GO:0003824,GO:0006021","XP_002908320
.1,EEY61403.1"
Stramenopiles-Phytophthora_brassicae_esContig670_2,265,437.187,8.91E-
121,"gi|301121186|ref|XP_002908320.1|inositol-3-phosphate synthase, putative
[Phytophthora infestans T30-4] ","
GO:0005488,GO:0004512,GO:0008654,GO:0008152,GO:0003824,GO:0006021","XP_002908320
.1,EEY61403.1"
Stramenopiles-
Phytophthora_capsici_jgi71065,427,673.7,0,gi|301119363|ref|XP_002907409.1|conser
ved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0003676,GO:0008270","XP_002907409.1,EEY63973.1"
Stramenopiles-
Phytophthora_ramorum_jgi77605,440,648.277,0,gi|301119363|ref|XP_002907409.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0003676,GO:0008270","XP_002907409.1,EEY63973.1"
Stramenopiles-
Phytophthora_sojae_jgi128277,438,672.929,0,gi|301119363|ref|XP_002907409.1|conse
rved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0003676,GO:0008270","XP_002907409.1,EEY63973.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi197267,416,266.544,3.73E-
69,gi|224012230|ref|XP_002294768.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,,"XP_002294768.1,EED88128.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223997740,543,1125.15,0,gi|223997740|ref|XP_
002288543.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002288543.1,EED93979.1"
Stramenopiles-
Phytophthora_sojae_jgi119319,446,928.702,0,"gi|301110230|ref|XP_002904195.1|alph
a-tubulin, putative [Phytophthora infestans T30-4] ","
GO:0007018,GO:0007017,GO:0051258,GO:0005874,GO:0000166,GO:0005525,GO:0043234,GO:
0003924,GO:0005198","XP_002904195.1,EEY54373.1"
Stramenopiles-
Phytophthora_brassicae_esContig1698_1,404,712.22,0,"gi|301110230|ref|XP_00290419
5.1|alpha-tubulin, putative [Phytophthora infestans T30-4] ","
GO:0007018,GO:0007017,GO:0051258,GO:0005874,GO:0000166,GO:0005525,GO:0043234,GO:
0003924,GO:0005198","XP_002904195.1,EEY54373.1"
Stramenopiles-
Phytophthora_capsici_jgi7261,355,734.561,0,"gi|301110230|ref|XP_002904195.1|alph
a-tubulin, putative [Phytophthora infestans T30-4] ","
GO:0007018,GO:0007017,GO:0051258,GO:0005874,GO:0000166,GO:0005525,GO:0043234,GO:
0003924,GO:0005198","XP_002904195.1,EEY54373.1"
Stramenopiles-
Phytophthora_capsici_jgi33835,355,677.167,0,"gi|301110230|ref|XP_002904195.1|alp
ha-tubulin, putative [Phytophthora infestans T30-4] ","
GO:0007018,GO:0007017,GO:0051258,GO:0005874,GO:0000166,GO:0005525,GO:0043234,GO:
0003924,GO:0005198","XP_002904195.1,EEY54373.1"
Stramenopiles-
Phytophthora_ramorum_jgi51154,446,930.628,0,"gi|301110230|ref|XP_002904195.1|alp
ha-tubulin, putative [Phytophthora infestans T30-4] ","
GO:0007018,GO:0007017,GO:0051258,GO:0005874,GO:0000166,GO:0005525,GO:0043234,GO:
0003924,GO:0005198","XP_002904195.1,EEY54373.1"
Stramenopiles-
Phytophthora_ramorum_jgi71894,454,943.725,0,"gi|301110230|ref|XP_002904195.1|alp
ha-tubulin, putative [Phytophthora infestans T30-4] ","
```

```
GO:0007018,GO:0007017,GO:0051258,GO:0005874,GO:0000166,GO:0005525,GO:0043234,GO:
0003924,GO:0005198","XP_002904195.1,EEY54373.1"
Stramenopiles-Phytophthora_sojae_jgi138185,252,506.908,7.12E-
142,"gi|301110150|ref|XP_002904155.1|alpha-tubulin, putative [Phytophthora
infestans T30-4] ","
GO:0007018,GO:0007017,GO:0051258,GO:0005874,GO:0000166,GO:0005525,GO:0043234,GO:
0003924,GO:0005198","XP_002904155.1,EEY54333.1"
Stramenopiles-Sargassum_binderi_esgi120455164_6,285,496.123,1.67E-
138,gi|298715658|emb|CBJ28184.1|alpha tubulin [Ectocarpus siliculosus],"
GO:0007018,GO:0007017,GO:0051258,GO:0005874,GO:0000166,GO:0005525,GO:0043234,GO:
0003924,GO:0005198",CBJ28184.1
Stramenopiles-
Sargassum_binderi_esContig89_1,514,951.429,0,gi|299472972|emb|CBN77373.1|alpha
tubulin [Ectocarpus siliculosus] ,"
GO:0007018,GO:0007017,GO:0051258,GO:0005874,GO:0000166,GO:0005525,GO:0043234,GO:
0003924,GO:0005198","CBN77373.1,CBN77378.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224006554,452,945.266,0,gi|224006554|ref|XP_
002292237.1|tubulin alpha [Thalassiosira pseudonana CCMP1335] ,"
GO:0007018,GO:0007017,GO:0051258,GO:0005874,GO:0000166,GO:0005525,GO:0043234,GO:
0003924,GO:0005198","XP_002292237.1,EED90212.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219120255,1317,2713.33,0,gi|219120255|re
f|XP_002180870.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0016887,GO:0005524,GO:0016021,GO:0000166,GO:0042626,GO:0055085,GO:0017111,GO:
0006810","XP_002180870.1,EEC47522.1"
Stramenopiles-
Phytophthora_ramorum_jgi79384,4997,9012.89,0,gi|301097330|ref|XP_002897760.1|dyn
ein heavy chain [Phytophthora infestans T30-4] ,"
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018","X
P_002897760.1,EEY64833.1"
Stramenopiles-
Phytophthora_sojae_jgi129649,4827,6767.94,0,gi|301097330|ref|XP_002897760.1|dyne
in heavy chain [Phytophthora infestans T30-4] ,"
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018","X
P_002897760.1,EEY64833.1"
Stramenopiles-
Phytophthora_capsici_jgi37548,4881,8870.75,0,gi|301097330|ref|XP_002897760.1|dyn
ein heavy chain [Phytophthora infestans T30-4] ,"
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018","X
P_002897760.1,EEY64833.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi70918,4666,4634.71,0,gi|301102724|ref|XP_00290044
9.1|sporangia induced dynein heavy chain [Phytophthora infestans T30-4] ,"
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018","X
P_002900449.1,EEY60242.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223999601,4410,9169.66,0,gi|223999601|ref|XP
_002289473.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018","X
P_002289473.1,EED93010.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi62356,5664,5760.65,0,gi|298711487|emb|CBJ26575.1|
dynein heavy chain [Ectocarpus siliculosus],"
```

```
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018",CB
J26575.1
Stramenopiles-Phytophthora_sojae_jgi142495,313,127.487,2.08E-
27,gi|301102724|ref|XP_002900449.1|sporangia induced dynein heavy chain
[Phytophthora infestans T30-4] ,"
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018","X
P_002900449.1,EEY60242.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi229943,373,325.865,4.63E-
87,gi|224012114|ref|XP_002294710.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,,"XP_002294710.1,EED88070.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224012114,339,698.738,0,gi|224012114|ref|XP_
002294710.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002294710.1,EED88070.1"
Stramenopiles-Aureococcus_anophagefferens_jgi62479,345,148.288,1.14E-
33,gi|308804207|ref|XP_003079416.1|unnamed protein product [Ostreococcus tauri]
,,"XP_003079416.1,CAL54074.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219130807,432,899.427,0,gi|219130807|ref
|XP_002185547.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002185547.1,EEC42912.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi235699,581,166.007,1.18E-
38,gi|224014600|ref|XP_002296962.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,,"XP_002296962.1,EED86690.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224014600,596,1238.02,0,gi|224014600|ref|XP_
002296962.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002296962.1,EED86690.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219126087,304,628.632,2.73E-
178,gi|219126087|ref|XP_002183296.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002183296.1,EEC44996.1"
Stramenopiles-
Phytophthora_ramorum_jgi75442,466,863.988,0,"gi|301115406|ref|XP_002905432.1|arg
inine biosynthesis bifunctional protein argJ, putative [Phytophthora infestans
T30-4] ","
GO:0005739,GO:0004358,GO:0016740,GO:0008415,GO:0005759,GO:0003824,GO:0008652,GO:
0006526","XP_002905432.1,D0N1U4.1,EEY68273.1"
Stramenopiles-
Phytophthora_capsici_jgi99397,466,887.1,0,"gi|301115406|ref|XP_002905432.1|argin
ine biosynthesis bifunctional protein argJ, putative [Phytophthora infestans
T30-4] ","
GO:0005739,GO:0004358,GO:0016740,GO:0008415,GO:0005759,GO:0003824,GO:0008652,GO:
0006526","XP_002905432.1,D0N1U4.1,EEY68273.1"
Stramenopiles-Aureococcus_anophagefferens_jgi27083,326,198.364,8.23E-
49,gi|298709852|emb|CBJ26192.1|similar to sideroflexin 5 [Ectocarpus
siliculosus]," GO:0008324,GO:0016020,GO:0055085,GO:0006812",CBJ26192.1
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224002935,334,693.345,0,gi|224002935|ref|XP_
002291139.1|sideroflexin 5 [Thalassiosira pseudonana CCMP1335] ,"
GO:0008324,GO:0016020,GO:0055085,GO:0006812","XP_002291139.1,EED91246.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219120671,325,667.922,0,gi|219120671|ref
|XP_002181069.1|iron carrier [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0008324,GO:0016020,GO:0055085,GO:0006812","XP_002181069.1,EEC47721.1"
```

```
Stramenopiles-Fragilariopsis_cylindrus_jgi226433,348,441.425,7.29E-
122,gi|219120671|ref|XP_002181069.1|iron carrier [Phaeodactylum tricornutum CCAP
1055/1] ,"
GO:0008324,GO:0016020,GO:0055085,GO:0006812","XP_002181069.1,EEC47721.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi140510,367,258.84,7.44E-
67,"gi|294881894|ref|XP_002769525.1|Sideroflexin-5, putative [Perkinsus marinus
ATCC 50983] ","
GO:0008324,GO:0016020,GO:0055085,GO:0006812","XP_002769525.1,EER02243.1"
Stramenopiles-Phytophthora_capsici_jgi119189,301,550.436,8.62E-
155,gi|301122845|ref|XP_002909149.1|Mitochondrial Tricarboxylate Carrier (MTC)
Family [Phytophthora infestans T30-4] ,"
GO:0008324,GO:0016020,GO:0055085,GO:0006812","XP_002909149.1,EEY57963.1"
Stramenopiles-Phytophthora_capsici_jgi36205,210,420.624,4.50E-
116,gi|301122845|ref|XP_002909149.1|Mitochondrial Tricarboxylate Carrier (MTC)
Family [Phytophthora infestans T30-4] ,"
GO:0008324,GO:0016020,GO:0055085,GO:0006812","XP_002909149.1,EEY57963.1"
Stramenopiles-Phytophthora_sojae_jgi142591,323,573.933,7.39E-
162,gi|301122845|ref|XP_002909149.1|Mitochondrial Tricarboxylate Carrier (MTC)
Family [Phytophthora infestans T30-4] ,"
GO:0008324,GO:0016020,GO:0055085,GO:0006812","XP_002909149.1,EEY57963.1"
Stramenopiles-Blastocystis_hominis_tbBHL00002097_1,177,310.071,5.53E-
83,gi|300123880|emb|CBK25151.2|unnamed protein product [Blastocystis hominis],"
GO:0008324,GO:0016020,GO:0055085,GO:0006812",CBK25151.2
Stramenopiles-Blastocystis_hominis_tbBHL00001846_5,112,189.889,6.67E-
47,gi|300175531|emb|CBK20842.2|unnamed protein product [Blastocystis hominis],"
GO:0003676,GO:0008270,GO:0005622",CBK20842.2
Stramenopiles-Blastocystis_hominis_tbBHL00000526_3,139,158.303,2.72E-
37,gi|300120166|emb|CBK19720.2|unnamed protein product [Blastocystis hominis],"
GO:0003676,GO:0008270,GO:0005622",CBK19720.2
Stramenopiles-Blastocystis_hominis_tbBHL00001039_3,191,139.043,2.50E-
31,gi|300122251|emb|CBK22824.2|unnamed protein product [Blastocystis hominis],"
GO:0003676,GO:0008270,GO:0005622",CBK22824.2
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224008280,374,766.148,0,gi|224008280|ref|XP_
002293099.1|hypothetical protein THAPSDRAFT_263946 [Thalassiosira pseudonana
CCMP1335] ,"
GO:0016301,GO:0016740,GO:0003824,GO:0016772","XP_002293099.1,EED89560.1"
Stramenopiles-Aureococcus_anophagefferens_jgi19213,409,396.741,2.64E-
108,gi|298709435|emb|CBJ31341.1|conserved unknown protein [Ectocarpus
siliculosus], GO:0005488,CBJ31341.1
Stramenopiles-Aureococcus_anophagefferens_jgi63286,2893,551.977,3.87E-
154,gi|299137414|ref|ZP_07030596.1|protein of unknown function DUF323
[Acidobacterium sp. MP5ACTX8] , GO:0005488,"ZP_07030596.1,EFI56975.1"
Stramenopiles-
Phytophthora_sojae_jgi118482,453,851.277,0,"gi|301121458|ref|XP_002908456.1|mann
osyl-oligosaccharide alpha-1,2-mannosidase, putative [Phytophthora infestans
T30-4] "," GO:0005509,GO:0016020,GO:0004571","XP_002908456.1,EEY61539.1"
Stramenopiles-
Phytophthora_capsici_jgi70245,457,900.197,0,"gi|301121458|ref|XP_002908456.1|man
nosyl-oligosaccharide alpha-1,2-mannosidase, putative [Phytophthora infestans
T30-4] "," GO:0005509,GO:0016020,GO:0004571","XP_002908456.1,EEY61539.1"
Stramenopiles-
Phytophthora_ramorum_jgi50011,455,886.715,0,"gi|301121458|ref|XP_002908456.1|man
nosyl-oligosaccharide alpha-1,2-mannosidase, putative [Phytophthora infestans
T30-4] "," GO:0005509,GO:0016020,GO:0004571","XP_002908456.1,EEY61539.1"
```

```
Stramenopiles-
Phytophthora_sojae_jgi117121,449,831.632,0,"gi|301104020|ref|XP_002901095.1|mann
osyl-oligosaccharide alpha-1,2-mannosidase, putative [Phytophthora infestans
T30-4] "," GO:0005509,GO:0016020,GO:0004571","XP_002901095.1,EEY59081.1"
Stramenopiles-
Phytophthora_capsici_jgi122394,449,835.099,0,"gi|301104020|ref|XP_002901095.1|ma
nnosyl-oligosaccharide alpha-1,2-mannosidase, putative [Phytophthora infestans
T30-4] "," GO:0005509,GO:0016020,GO:0004571","XP_002901095.1,EEY59081.1"
Stramenopiles-
Phytophthora_ramorum_jgi53914,452,847.04,0,"gi|301104020|ref|XP_002901095.1|mann
osyl-oligosaccharide alpha-1,2-mannosidase, putative [Phytophthora infestans
T30-4] "," GO:0005509,GO:0016020,GO:0004571","XP_002901095.1,EEY59081.1"
Stramenopiles-Aureococcus_anophagefferens_jgi16190,102,119.398,1.31E-
25,gi|170085899|ref|XP_001874173.1|glycoside hydrolase family 47 protein
[Laccaria bicolor S238N-H82] ,"
GO:0005509,GO:0016787,GO:0016020,GO:0004571","XP_001874173.1,EDR15965.1"
Stramenopiles-Phytophthora_capsici_jgi36604,905,392.889,8.71E-
107,gi|301099853|ref|XP_002899017.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002899017.1,EEY62381.1"
Stramenopiles-Phytophthora_sojae_jgi131264,915,357.836,3.17E-
96,gi|301099853|ref|XP_002899017.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002899017.1,EEY62381.1"
Stramenopiles-Phytophthora_sojae_jgi131261,562,311.997,1.33E-
82,gi|159485272|ref|XP_001700670.1|ubiquinol:cytochrome c oxidoreductase
biogenesis factor [Chlamydomonas reinhardtii] ,"
GO:0005524,GO:0000166,GO:0017111","XP_001700670.1,EDO97908.1"
Stramenopiles-Phytophthora_ramorum_jgi73260,563,314.694,1.76E-
83,gi|159485272|ref|XP_001700670.1|ubiquinol:cytochrome c oxidoreductase
biogenesis factor [Chlamydomonas reinhardtii] ,"
GO:0005524,GO:0000166,GO:0017111","XP_001700670.1,EDO97908.1"
Stramenopiles-Phytophthora_ramorum_jgi73263,563,315.849,8.52E-
84,gi|159485272|ref|XP_001700670.1|ubiquinol:cytochrome c oxidoreductase
biogenesis factor [Chlamydomonas reinhardtii] ,"
GO:0005524,GO:0000166,GO:0017111","XP_001700670.1,EDO97908.1"
Stramenopiles-Phytophthora_capsici_jgi36603,547,306.605,4.46E-
81,gi|159485272|ref|XP_001700670.1|ubiquinol:cytochrome c oxidoreductase
biogenesis factor [Chlamydomonas reinhardtii] ,"
GO:0005524,GO:0000166,GO:0017111","XP_001700670.1,EDO97908.1"
Stramenopiles-Phytophthora_ramorum_jgi73251,564,298.13,1.78E-
78,gi|159485272|ref|XP_001700670.1|ubiquinol:cytochrome c oxidoreductase
biogenesis factor [Chlamydomonas reinhardtii] ,"
GO:0005524,GO:0000166,GO:0017111","XP_001700670.1,EDO97908.1"
Stramenopiles-Phytophthora_capsici_jgi36607,554,293.508,4.66E-
77,gi|159485272|ref|XP_001700670.1|ubiquinol:cytochrome c oxidoreductase
biogenesis factor [Chlamydomonas reinhardtii] ,"
GO:0005524,GO:0000166,GO:0017111","XP_001700670.1,EDO97908.1"
Stramenopiles-Phytophthora_sojae_jgi137958,565,301.982,1.16E-
79,gi|159485272|ref|XP_001700670.1|ubiquinol:cytochrome c oxidoreductase
biogenesis factor [Chlamydomonas reinhardtii] ,"
GO:0005524,GO:0000166,GO:0017111","XP_001700670.1,EDO97908.1"
Stramenopiles-Aureococcus_anophagefferens_jgi67965,759,223.016,1.10E-
55,gi|71420767|ref|XP_811604.1|hypothetical protein [Trypanosoma cruzi strain CL
Brener] ," GO:0005524,GO:0000166,GO:0017111","XP_811604.1,EAN89753.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219111769,284,587.03,6.93E-
```

```
166,gi|219111769|ref|XP_002177636.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0055114,GO:0016671,GO:0019538","XP_002177636.1,EEC50450.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224008935,298,616.69,8.34E-
175,gi|224008935|ref|XP_002293426.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ," GO:0055114,GO:0016671,GO:0019538","XP_002293426.1,EED89162.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi188492,223,280.026,1.30E-
73,gi|224008935|ref|XP_002293426.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ," GO:0055114,GO:0016671,GO:0019538","XP_002293426.1,EED89162.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219130263,269,556.214,1.20E-
156,gi|219130263|ref|XP_002185288.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0055114,GO:0016671,GO:0019538","XP_002185288.1,EEC43157.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi270824,297,273.092,2.42E-
71,gi|219130263|ref|XP_002185288.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0055114,GO:0016671,GO:0019538","XP_002185288.1,EEC43157.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224005126,759,1566.59,0,gi|224005126|ref|XP_
002296214.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0055114,GO:0016671,GO:0019538","XP_002296214.1,ACI64931.1"
Stramenopiles-Aureococcus_anophagefferens_jgi65690,593,174.096,4.71E-
41,gi|313225993|emb|CBY21136.1|unnamed protein product [Oikopleura
dioica],,CBY21136.1
Stramenopiles-
Phytophthora_capsici_jgi33555,1077,1748.02,0,gi|301105279|ref|XP_002901723.1|con
served hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0046872,GO:0005524,GO:0008270,GO:0005515","XP_002901723.1,EEY57113.1"
Stramenopiles-
Phytophthora_sojae_jgi140065,1210,1823.52,0,gi|301105279|ref|XP_002901723.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0046872,GO:0005524,GO:0008270,GO:0005515","XP_002901723.1,EEY57113.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi67157,4617,986.867,0,gi|302794218|ref|XP_00297887
3.1|hypothetical protein SELMODRAFT_152901 [Selaginella moellendorffii] ,"
GO:0046872,GO:0005524,GO:0008270,GO:0005515","XP_002978873.1,EFJ19830.1"
Stramenopiles-Aureococcus_anophagefferens_jgi68452,765,65.0846,3.62E-
08,gi|159489398|ref|XP_001702684.1|predicted protein [Chlamydomonas reinhardtii]
,,"XP_001702684.1,EDP06463.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi259463,188,357.066,5.07E-
97,gi|219126122|ref|XP_002183313.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0005525,GO:0007264,GO:0000166,GO:0015031","XP_002183313.1,EEC45013.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224001286,201,419.083,1.18E-
115,gi|224001286|ref|XP_002290315.1|ypt1-like rab-type small G protein
[Thalassiosira pseudonana CCMP1335] ,"
GO:0005525,GO:0007264,GO:0000166,GO:0015031","XP_002290315.1,EED92067.1"
Stramenopiles-Sargassum_binderi_esContig14_2,550,409.453,5.86E-
112,"gi|298707797|emb|CBJ30228.1|Rab1B, RAB family GTPase [Ectocarpus
siliculosus]"," GO:0005525,GO:0007264,GO:0000166,GO:0015031",CBJ30228.1
Stramenopiles-Phytophthora_parasitica_esContig893_2,360,350.903,1.47E-
94,gi|301117468|ref|XP_002906462.1|Rab1 family GTPase (PiYpt1) [Phytophthora
infestans T30-4] ,"
GO:0005525,GO:0007264,GO:0000166,GO:0016020,GO:0006810,GO:0005886,GO:0015031","X
P_002906462.1,Q01890.1,AAB40355.1,EEY65863.1"
Stramenopiles-Phytophthora_parasitica_esContig1416_2,228,421.394,3.63E-
116,gi|301117468|ref|XP_002906462.1|Rab1 family GTPase (PiYpt1) [Phytophthora
```

```
infestans T30-4] ,"
GO:0005525,GO:0007264,GO:0000166,GO:0016020,GO:0006810,GO:0005886,GO:0015031","X
P_002906462.1,Q01890.1,AAB40355.1,EEY65863.1"
Stramenopiles-Phytophthora_capsici_jgi98059,202,420.624,5.07E-
116,gi|301117468|ref|XP_002906462.1|Rab1 family GTPase (PiYpt1) [Phytophthora
infestans T30-4] ,"
GO:0005525,GO:0007264,GO:0000166,GO:0016020,GO:0006810,GO:0005886,GO:0015031","X
P_002906462.1,Q01890.1,AAB40355.1,EEY65863.1"
Stramenopiles-Phytophthora_sojae_jgi108764,202,420.624,5.07E-
116,gi|301117468|ref|XP_002906462.1|Rab1 family GTPase (PiYpt1) [Phytophthora
infestans T30-4] ,"
GO:0005525,GO:0007264,GO:0000166,GO:0016020,GO:0006810,GO:0005886,GO:0015031","X
P_002906462.1,Q01890.1,AAB40355.1,EEY65863.1"
Stramenopiles-Phytophthora_ramorum_jgi71391,202,420.624,5.07E-
116,gi|301117468|ref|XP_002906462.1|Rab1 family GTPase (PiYpt1) [Phytophthora
infestans T30-4] ,"
GO:0005525,GO:0007264,GO:0000166,GO:0016020,GO:0006810,GO:0005886,GO:0015031","X
P_002906462.1,Q01890.1,AAB40355.1,EEY65863.1"
Stramenopiles-Phytophthora_brassicae_esContig570_1,424,421.394,1.12E-
115,gi|301117468|ref|XP_002906462.1|Rab1 family GTPase (PiYpt1) [Phytophthora
infestans T30-4] ,"
GO:0005525,GO:0007264,GO:0000166,GO:0016020,GO:0006810,GO:0005886,GO:0015031","X
P_002906462.1,Q01890.1,AAB40355.1,EEY65863.1"
Stramenopiles-Blastocystis_hominis_tbBHL00001506_2,226,410.609,6.42E-
113,gi|300175138|emb|CBK20449.2|unnamed protein product [Blastocystis hominis],"
GO:0005525,GO:0007264,GO:0000166,GO:0015031",CBK20449.2
Stramenopiles-Phytophthora_sojae_jgi135623,1523,573.933,6.28E-
161,gi|56547681|gb|AAV92918.1|pol protein [Phytophthora infestans],"
GO:0000785,GO:0003682,GO:0003677,GO:0005634,GO:0003676,GO:0006333,GO:0003964,GO:
0003723,GO:0015074,GO:0006278",AAV92918.1
Stramenopiles-Phytophthora_sojae_jgi131720,1420,598.201,2.33E-
168,gi|56547681|gb|AAV92918.1|pol protein [Phytophthora infestans],"
GO:0000785,GO:0003682,GO:0003677,GO:0005634,GO:0003676,GO:0006333,GO:0003964,GO:
0003723,GO:0015074,GO:0006278",AAV92918.1
Stramenopiles-Phytophthora_sojae_jgi139928,1447,483.026,1.17E-
133,"gi|77555398|gb|ABA98194.1|retrotransposon protein, putative, Ty3-gypsy
subclass [Oryza sativa Japonica Group]",,ABA98194.1
Stramenopiles-
Phytophthora_ramorum_jgi79115,704,981.474,0,gi|56547681|gb|AAV92918.1|pol
protein [Phytophthora infestans],"
GO:0000785,GO:0003682,GO:0003677,GO:0005634,GO:0003676,GO:0006333,GO:0003964,GO:
0003723,GO:0015074,GO:0006278",AAV92918.1
Stramenopiles-
Phytophthora_ramorum_jgi79617,1241,1063.14,0,gi|56547681|gb|AAV92918.1|pol
protein [Phytophthora infestans],"
GO:0000785,GO:0003682,GO:0003677,GO:0005634,GO:0003676,GO:0006333,GO:0003964,GO:
0003723,GO:0015074,GO:0006278",AAV92918.1
Stramenopiles-
Phytophthora_ramorum_jgi84637,1731,1130.93,0,gi|62147612|emb|CAI72306.1|putative
polyprotein [Phytophthora infestans],"
GO:0003723,GO:0006508,GO:0006278,GO:0004190,GO:0003964",CAI72306.1
Stramenopiles-
Phytophthora_capsici_jgi599,664,1200.65,0,gi|301098081|ref|XP_002898134.1|ATP-
binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4] ,"
```

```
GO:0016887,GO:0005524,GO:0016021,GO:0000166,GO:0042626,GO:0055085,GO:0017111,GO:
0006810","XP_002898134.1,EEY63547.1"
Stramenopiles-Phytophthora_parasitica_esgi222399594_2,232,426.017,1.62E-
117,gi|301098081|ref|XP_002898134.1|ATP-binding Cassette (ABC) Superfamily
[Phytophthora infestans T30-4] ,"
GO:0016887,GO:0005524,GO:0016021,GO:0000166,GO:0042626,GO:0055085,GO:0017111,GO:
0006810","XP_002898134.1,EEY63547.1"
Stramenopiles-
Phytophthora_ramorum_jgi71174,1243,2309.64,0,gi|301098081|ref|XP_002898134.1|ATP
-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0016887,GO:0005524,GO:0016021,GO:0000166,GO:0042626,GO:0055085,GO:0017111,GO:
0006810","XP_002898134.1,EEY63547.1"
Stramenopiles-
Phytophthora_sojae_jgi109245,1293,2346.62,0,gi|301098081|ref|XP_002898134.1|ATP-
binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0016887,GO:0005524,GO:0016021,GO:0000166,GO:0042626,GO:0055085,GO:0017111,GO:
0006810","XP_002898134.1,EEY63547.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi188281,1369,1026.16,0,gi|224008366|ref|XP_002293142.
1|ABC transporter multi-drug efflux transporter-like protein [Thalassiosira
pseudonana CCMP1335] ,"
GO:0016887,GO:0005524,GO:0016021,GO:0000166,GO:0042626,GO:0055085,GO:0017111,GO:
0006810","XP_002293142.1,EED89603.1"
Stramenopiles-Aureococcus_anophagefferens_jgi1068,484,271.166,1.86E-
70,gi|260836917|ref|XP_002613452.1|hypothetical protein BRAFLDRAFT_84588
[Branchiostoma floridae] ,"
GO:0016887,GO:0005524,GO:0016021,GO:0000166,GO:0042626,GO:0055085,GO:0017111,GO:
0006810","XP_002613452.1,EEN69461.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219114296,587,1197.19,0,gi|219114296|ref
|XP_002176319.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0016887,GO:0005524,GO:0016021,GO:0000166,GO:0042626,GO:0055085,GO:0017111,GO:
0006810","XP_002176319.1,EEC42711.1"
Stramenopiles-
Phytophthora_sojae_jgi132363,1281,2212.19,0,gi|301114249|ref|XP_002998894.1|ATP-
binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0016887,GO:0005524,GO:0016021,GO:0000166,GO:0042626,GO:0055085,GO:0017111,GO:
0006810","XP_002998894.1,EEY69040.1"
Stramenopiles-
Phytophthora_sojae_jgi114447,1129,1954.87,0,gi|301114249|ref|XP_002998894.1|ATP-
binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0016887,GO:0005524,GO:0016021,GO:0000166,GO:0042626,GO:0055085,GO:0017111,GO:
0006810","XP_002998894.1,EEY69040.1"
Stramenopiles-
Phytophthora_capsici_jgi503,1225,2126.29,0,gi|301114249|ref|XP_002998894.1|ATP-
binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0016887,GO:0005524,GO:0016021,GO:0000166,GO:0042626,GO:0055085,GO:0017111,GO:
0006810","XP_002998894.1,EEY69040.1"
Stramenopiles-Aureococcus_anophagefferens_jgi62507,426,53.9138,4.73E-
05,gi|308808880|ref|XP_003081750.1|unnamed protein product [Ostreococcus tauri]
," GO:0008270,GO:0005622","XP_003081750.1,CAL56275.1"
Stramenopiles-Aureococcus_anophagefferens_jgi619,704,551.977,9.47E-
155,"gi|102189|pir||A23662myosin I, high molecular weight - Acanthamoeba
sp",,"A23662myosin I, high molecular weight - Acanthamoeba sp"
```

```
Stramenopiles-Aureococcus_anophagefferens_jgi19042,838,547.354,2.64E-
153,gi|281201334|gb|EFA75546.1|class VII unconventional myosin [Polysphondylium
pallidum PN500],"
GO:0005524,GO:0005488,GO:0005856,GO:0007165,GO:0016459,GO:0003774",EFA75546.1
Stramenopiles-
Fragilariopsis_cylindrus_jgi195126,993,1233.01,0,gi|239925803|gb|ACS35536.1|myos
in 29 [Phaeodactylum tricornutum],"
GO:0005524,GO:0008152,GO:0000166,GO:0003824,GO:0016459,GO:0003774",ACS35536.1
Stramenopiles-
Phytophthora_sojae_jgi155779,1319,1497.26,0,gi|301103374|ref|XP_002900773.1|myos
in-like protein [Phytophthora infestans T30-4] ,"
GO:0046872,GO:0005524,GO:0000166,GO:0008270,GO:0016459,GO:0003774","XP_002900773
.1,EEY59580.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi209709,857,853.973,0,gi|219129131|ref|XP_002184750.1
|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0005524,GO:0000166,GO:0016459,GO:0003774","XP_002184750.1,EEC43809.1"
Stramenopiles-
Phytophthora_capsici_jgi114970,1409,2661.33,0,gi|301095493|ref|XP_002896847.1|my
osin-like protein [Phytophthora infestans T30-4] ,"
GO:0046872,GO:0005524,GO:0008270,GO:0016459,GO:0003774","XP_002896847.1,EEY66782
.1"
Stramenopiles-
Phytophthora_sojae_jgi143645,1411,2597.39,0,gi|301095493|ref|XP_002896847.1|myos
in-like protein [Phytophthora infestans T30-4] ,"
GO:0046872,GO:0005524,GO:0008270,GO:0016459,GO:0003774","XP_002896847.1,EEY66782
.1"
Stramenopiles-
Phytophthora_sojae_jgi141887,1383,2617.03,0,gi|301121907|ref|XP_002908680.1|myos
in-like protein [Phytophthora infestans T30-4] ,"
GO:0046872,GO:0005524,GO:0000166,GO:0008270,GO:0016459,GO:0003774","XP_002908680
.1,EEY57494.1"
Stramenopiles-
Phytophthora_ramorum_jgi73512,1382,2606.63,0,gi|301121907|ref|XP_002908680.1|myo
sin-like protein [Phytophthora infestans T30-4] ,"
GO:0046872,GO:0005524,GO:0000166,GO:0008270,GO:0016459,GO:0003774","XP_002908680
.1,EEY57494.1"
Stramenopiles-
Phytophthora_sojae_jgi137533,1314,1979.14,0,"gi|301123145|ref|XP_002909299.1|N-
acetylglucosamine-1-phosphotransferase subunits alpha/beta, putative
[Phytophthora infestans T30-4] ","
GO:0030154,GO:0016740,GO:0016020","XP_002909299.1,EEY58113.1"
Stramenopiles-
Phytophthora_ramorum_jgi84134,1344,1040.02,0,"gi|301123145|ref|XP_002909299.1|N-
acetylglucosamine-1-phosphotransferase subunits alpha/beta, putative
[Phytophthora infestans T30-4] ","
GO:0030154,GO:0016740,GO:0016020","XP_002909299.1,EEY58113.1"
Stramenopiles-
Phytophthora_capsici_jgi34379,1261,2063.5,0,"gi|301123145|ref|XP_002909299.1|N-
acetylglucosamine-1-phosphotransferase subunits alpha/beta, putative
[Phytophthora infestans T30-4] ","
GO:0030154,GO:0016740,GO:0016020","XP_002909299.1,EEY58113.1"
Stramenopiles-
Phytophthora_capsici_jgi117391,806,769.229,0,gi|301116932|ref|XP_002906194.1|con
served hypothetical protein [Phytophthora infestans T30-4] ,"
```

```
GO:0016740,GO:0006526,GO:0051287,GO:0003942,GO:0006520,GO:0005737,GO:0016620,GO:
0003991,GO:0003824,GO:0008152,GO:0008652,GO:0005488","XP_002906194.1,EEY65595.1"
Stramenopiles-Phytophthora_capsici_jgi83954,323,234.958,9.30E-
60,gi|301116932|ref|XP_002906194.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,"
GO:0016740,GO:0006526,GO:0051287,GO:0003942,GO:0006520,GO:0005737,GO:0016620,GO:
0003991,GO:0003824,GO:0008152,GO:0008652,GO:0005488","XP_002906194.1,EEY65595.1"
Stramenopiles-
Phytophthora_sojae_jgi139358,707,1310.43,0,gi|301116932|ref|XP_002906194.1|conse
rved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0016740,GO:0006526,GO:0051287,GO:0003942,GO:0006520,GO:0005737,GO:0016620,GO:
0003991,GO:0003824,GO:0008152,GO:0008652,GO:0005488","XP_002906194.1,EEY65595.1"
Stramenopiles-
Phytophthora_ramorum_jgi78196,720,1296.18,0,gi|301116932|ref|XP_002906194.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0016740,GO:0006526,GO:0051287,GO:0003942,GO:0006520,GO:0005737,GO:0016620,GO:
0003991,GO:0003824,GO:0008152,GO:0008652,GO:0005488","XP_002906194.1,EEY65595.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219111533,330,662.914,0,gi|219111533|ref
|XP_002177518.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0004349,GO:0005737,GO:0016740,GO:0008652,GO:0006526,GO:0003991,GO:0006561","X
P_002177518.1,EEC51981.1"
Stramenopiles-
Phytophthora_capsici_jgi34970,615,648.277,0,gi|190575178|ref|YP_001973023.1|N-
acetyl-gamma-glutamyl-phosphate reductase [Stenotrophomonas maltophilia K279a]
,"
GO:0006526,GO:0051287,GO:0003942,GO:0006520,GO:0005737,GO:0055114,GO:0016620,GO:
0016491,GO:0003824,GO:0008152,GO:0008652,GO:0005488","YP_001973023.1,B2FMD7.1,CA
Q46732.1"
Stramenopiles-
Phytophthora_sojae_jgi139264,538,861.677,0,gi|301096496|ref|XP_002897345.1|conse
rved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002897345.1,EEY65281.1"
Stramenopiles-Aureococcus_anophagefferens_jgi64842,436,204.527,1.79E-
50,gi|167524719|ref|XP_001746695.1|hypothetical protein [Monosiga brevicollis
MX1] , GO:0005509,"XP_001746695.1,EDQ88591.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219119139,149,309.686,5.86E-
83,gi|219119139|ref|XP_002180336.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] , GO:0005509,"XP_002180336.1,EEC48527.1"
Stramenopiles-Aureococcus_anophagefferens_jgi27914,150,127.487,4.70E-
28,gi|167526844|ref|XP_001747755.1|hypothetical protein [Monosiga brevicollis
MX1] , GO:0005509,"XP_001747755.1,EDQ87495.1"
Stramenopiles-Aureococcus_anophagefferens_jgi65953,1145,294.664,4.34E-
77,gi|298712152|emb|CBJ33028.1|Hypothetical Protein RRSL_02205 [Ectocarpus
siliculosus]," GO:0016491,GO:0008152",CBJ33028.1
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224015584,360,742.651,0,gi|224015584|ref|XP_
002297443.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0005524,GO:0000166,GO:0003777,GO:0007018,GO:0003774,GO:0005874","XP_002297443
.1,EED86260.1"
Stramenopiles-Aureococcus_anophagefferens_jgi1821,419,405.601,6.35E-
111,gi|224015584|ref|XP_002297443.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,"
```

```
GO:0005524,GO:0000166,GO:0003777,GO:0007018,GO:0003774,GO:0005874","XP_002297443
.1,EED86260.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219126116,377,783.097,0,gi|219126116|ref
|XP_002183310.1|kinesin family-like protein [Phaeodactylum tricornutum CCAP
1055/1] ,"
GO:0005524,GO:0000166,GO:0003777,GO:0007018,GO:0003774,GO:0005874","XP_002183310
.1,EEC45010.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi225115,377,603.208,1.66E-
170,gi|219126116|ref|XP_002183310.1|kinesin family-like protein [Phaeodactylum
tricornutum CCAP 1055/1] ,"
GO:0005524,GO:0000166,GO:0003777,GO:0007018,GO:0003774,GO:0005874","XP_002183310
.1,EEC45010.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224004298,375,772.311,0,gi|224004298|ref|XP_
002295800.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0005524,GO:0000166,GO:0003777,GO:0007018,GO:0003774,GO:0005874","XP_002295800
.1,ACI64517.1"
Stramenopiles-Phytophthora_capsici_jgi93339,623,598.971,5.63E-
169,gi|301106422|ref|XP_002902294.1|kinesin-like protein [Phytophthora infestans
T30-4] ," GO:0005524,GO:0003777,GO:0007018","XP_002902294.1,EEY56966.1"
Stramenopiles-Phytophthora_ramorum_jgi48862,363,396.356,3.13E-
108,gi|301092936|ref|XP_002997318.1|kinesin-like protein [Phytophthora infestans
T30-4] ,"
GO:0005524,GO:0000166,GO:0003777,GO:0007018,GO:0003774,GO:0005874","XP_002997318
.1,EEY68890.1"
Stramenopiles-Aureococcus_anophagefferens_jgi59386,352,339.347,3.95E-
91,gi|299116432|emb|CBN74697.1|kinesin motor protein-related [Ectocarpus
siliculosus],"
GO:0005524,GO:0000166,GO:0003777,GO:0007018,GO:0003774,GO:0005874",CBN74697.1
Stramenopiles-Aureococcus_anophagefferens_jgi59470,352,338.961,4.51E-
91,gi|299116432|emb|CBN74697.1|kinesin motor protein-related [Ectocarpus
siliculosus],"
GO:0005524,GO:0000166,GO:0003777,GO:0007018,GO:0003774,GO:0005874",CBN74697.1
Stramenopiles-
Phytophthora_capsici_jgi10562,1081,1011.91,0,gi|301123033|ref|XP_002909243.1|kin
esin-like protein [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0000166,GO:0003777,GO:0007018,GO:0003774,GO:0005874","XP_002909243
.1,EEY58057.1"
Stramenopiles-Aureococcus_anophagefferens_jgi2359,367,251.521,1.24E-
64,gi|167524284|ref|XP_001746478.1|hypothetical protein [Monosiga brevicollis
MX1] ," GO:0008152,GO:0003824,GO:0008484","XP_001746478.1,EDQ88865.1"
Stramenopiles-Aureococcus_anophagefferens_jgi61551,2087,232.646,4.41E-
58,gi|241668860|ref|ZP_04756438.1|glycosy hydrolase family protein [Francisella
philomiragia subsp. philomiragia ATCC 25015],,ZP_04756438.1
Stramenopiles-Aureococcus_anophagefferens_jgi64682,290,62.3882,6.16E-
08,gi|255081488|ref|XP_002507966.1|predicted protein [Micromonas sp. RCC299] ,"
GO:0008825,GO:0008610","XP_002507966.1,ACO69224.1"
Stramenopiles-
Phytophthora_sojae_jgi141959,613,768.074,0,gi|301123363|ref|XP_002909408.1|kines
in-like protein [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0000166,GO:0003777,GO:0007018,GO:0003774,GO:0005874","XP_002909408
.1,EEY58222.1"
Stramenopiles-
Phytophthora_sojae_jgi129093,908,1657.5,0,gi|301091307|ref|XP_002895841.1|conser
```

```
ved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002895841.1,EEY54604.1"
Stramenopiles-Phytophthora_ramorum_jgi86730,503,348.206,1.33E-
93,gi|301091307|ref|XP_002895841.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002895841.1,EEY54604.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224014996,968,2009.57,0,gi|224014996|ref|XP_
002297159.1|signal peptidase [Thalassiosira pseudonana CCMP1335]
,,"XP_002297159.1,EED86484.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219109751,1238,2563.87,0,gi|219109751|re
f|XP_002176629.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002176629.1,EEC51092.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi181482,1023,744.577,0,gi|224014996|ref|XP_002297159.
1|signal peptidase [Thalassiosira pseudonana CCMP1335]
,,"XP_002297159.1,EED86484.1"
Stramenopiles-
Phytophthora_ramorum_jgi44351,963,1466.06,0,gi|301106825|ref|XP_002902495.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002902495.1,EEY56421.1"
Stramenopiles-
Phytophthora_sojae_jgi131857,1120,1344.33,0,gi|301106825|ref|XP_002902495.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002902495.1,EEY56421.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi269635,426,152.91,7.54E-
35,gi|83944028|ref|ZP_00956485.1|hypothetical protein EE36_10295 [Sulfitobacter
sp. EE-36] ,,"ZP_00956485.1,EAP83155.1"
Stramenopiles-Aureococcus_anophagefferens_jgi72297,835,295.049,2.56E-
77,gi|260821866|ref|XP_002606324.1|hypothetical protein BRAFLDRAFT_67566
[Branchiostoma floridae] ,,"XP_002606324.1,EEN62334.1"
Stramenopiles-Aureococcus_anophagefferens_jgi4382,193,179.874,1.31E-
43,gi|260821866|ref|XP_002606324.1|hypothetical protein BRAFLDRAFT_67566
[Branchiostoma floridae] ,,"XP_002606324.1,EEN62334.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219124569,1007,2089.69,0,gi|219124569|re
f|XP_002182573.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002182573.1,EEC45860.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi262424,1031,665.996,0,gi|224008466|ref|XP_002293192.
1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002293192.1,EED89653.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224008466,926,1909.42,0,gi|224008466|ref|XP_
002293192.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002293192.1,EED89653.1"
Stramenopiles-Aureococcus_anophagefferens_jgi62913,1857,238.039,9.53E-
60,gi|300123459|emb|CBK24732.2|unnamed protein product [Blastocystis
hominis],,CBK24732.2
Stramenopiles-Aureococcus_anophagefferens_jgi64391,1319,141.739,6.39E-
31,gi|294084042|ref|YP_003550800.1|Sterol desaturase [Candidatus
Puniceispirillum marinum IMCC1322] ,"
GO:0055114,GO:0016491,GO:0005783,GO:0005506,GO:0006633","YP_003550800.1,ADE38716
.1"
```

```
Stramenopiles-
Phytophthora_sojae_jgi119111,444,669.078,0,"gi|301099961|ref|XP_002899071.1|hist
one arginine demethylase, putative [Phytophthora infestans T30-4] ",
GO:0008168,"XP_002899071.1,EEY62435.1"
Stramenopiles-Phytophthora_ramorum_jgi41695,344,581.637,3.88E-
164,"gi|301099961|ref|XP_002899071.1|histone arginine demethylase, putative
[Phytophthora infestans T30-4] ", GO:0008168,"XP_002899071.1,EEY62435.1"
Stramenopiles-
Phytophthora_capsici_jgi35963,440,680.248,0,"gi|301099961|ref|XP_002899071.1|his
tone arginine demethylase, putative [Phytophthora infestans T30-4] ",
GO:0008168,"XP_002899071.1,EEY62435.1"
Stramenopiles-Aureococcus_anophagefferens_jgi3043,290,274.633,8.88E-
72,gi|298713548|emb|CBJ27076.1|JMJD6 protein [Ectocarpus
siliculosus],,CBJ27076.1
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219122056,294,613.609,7.93E-
174,gi|219122056|ref|XP_002181370.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002181370.1,EEC47293.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi271391,423,400.593,1.65E-
109,gi|219122056|ref|XP_002181370.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002181370.1,EEC47293.1"
Stramenopiles-
Phytophthora_capsici_jgi28471,526,783.867,0,"gi|301110176|ref|XP_002904168.1|his
tone arginine demethylase, putative [Phytophthora infestans T30-4] ",
GO:0008168,"XP_002904168.1,EEY54346.1"
Stramenopiles-
Phytophthora_ramorum_jgi82996,1029,1624.37,0,"gi|301092139|ref|XP_002996930.1|hi
stone arginine demethylase, putative [Phytophthora infestans T30-4] ",
GO:0008168,"XP_002996930.1,EEY70308.1"
Stramenopiles-
Phytophthora_sojae_jgi128547,1038,1675.99,0,"gi|301092139|ref|XP_002996930.1|his
tone arginine demethylase, putative [Phytophthora infestans T30-4] ",
GO:0008168,"XP_002996930.1,EEY70308.1"
Stramenopiles-Phytophthora_capsici_jgi20651,294,513.842,8.21E-
144,gi|301117896|ref|XP_002906676.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002906676.1,EEY66077.1"
Stramenopiles-Phytophthora_sojae_jgi134857,294,511.146,5.78E-
143,gi|301117896|ref|XP_002906676.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002906676.1,EEY66077.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi223998624,142,296.59,5.39E-
79,gi|223998624|ref|XP_002288985.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,,"XP_002288985.1,EED94421.1"
Stramenopiles-
Phytophthora_ramorum_jgi77069,352,655.21,0,gi|301112134|ref|XP_002905146.1|conse
rved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002905146.1,EEY53528.1"
Stramenopiles-
Phytophthora_sojae_jgi143839,352,649.432,0,gi|301112134|ref|XP_002905146.1|conse
rved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002905146.1,EEY53528.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi170146,482,893.264,0,gi|219112013|ref|XP_002177758.1
|adenosylhomocysteinase [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0004013,GO:0005488,GO:0016787,GO:0008152,GO:0003824,GO:0006730","XP_002177758
.1,EEC50572.1"
```

```
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219112013,481,993.416,0,gi|219112013|ref
|XP_002177758.1|adenosylhomocysteinase [Phaeodactylum tricornutum CCAP 1055/1]
,"
GO:0004013,GO:0005488,GO:0016787,GO:0008152,GO:0003824,GO:0006730","XP_002177758
.1,EEC50572.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224003341,481,993.03,0,gi|224002559|ref|XP_0
02290951.1|hypothetical protein THAPSDRAFT_28496 [Thalassiosira pseudonana
CCMP1335] ,"
GO:0004013,GO:0005488,GO:0016787,GO:0008152,GO:0003824,GO:0006730","XP_002290951
.1,XP_002291342.1,EED91058.1,EED91449.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224002559,481,993.03,0,gi|224002559|ref|XP_0
02290951.1|hypothetical protein THAPSDRAFT_28496 [Thalassiosira pseudonana
CCMP1335] ,"
GO:0004013,GO:0005488,GO:0016787,GO:0008152,GO:0003824,GO:0006730","XP_002290951
.1,XP_002291342.1,EED91058.1,EED91449.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi69644,481,793.882,0,gi|224002559|ref|XP_002290951
.1|hypothetical protein THAPSDRAFT_28496 [Thalassiosira pseudonana CCMP1335] ,"
GO:0004013,GO:0005488,GO:0016787,GO:0008152,GO:0003824,GO:0006730","XP_002290951
.1,XP_002291342.1,EED91058.1,EED91449.1"
Stramenopiles-
Phytophthora_brassicae_esContig628_2,446,758.829,0,gi|301107277|ref|XP_002902721
.1|adenosylhomocysteinase [Phytophthora infestans T30-4] ,"
GO:0004013,GO:0005488,GO:0016787,GO:0008152,GO:0003824,GO:0006730","XP_002902721
.1,EEY56647.1"
Stramenopiles-
Phytophthora_ramorum_jgi71346,482,952.97,0,gi|301107277|ref|XP_002902721.1|adeno
sylhomocysteinase [Phytophthora infestans T30-4] ,"
GO:0004013,GO:0005488,GO:0016787,GO:0008152,GO:0003824,GO:0006730","XP_002902721
.1,EEY56647.1"
Stramenopiles-
Phytophthora_capsici_jgi100785,482,976.467,0,gi|301107277|ref|XP_002902721.1|ade
nosylhomocysteinase [Phytophthora infestans T30-4] ,"
GO:0004013,GO:0005488,GO:0016787,GO:0008152,GO:0003824,GO:0006730","XP_002902721
.1,EEY56647.1"
Stramenopiles-
Phytophthora_parasitica_esContig636_2,592,739.184,0,gi|301107277|ref|XP_00290272
1.1|adenosylhomocysteinase [Phytophthora infestans T30-4] ,"
GO:0004013,GO:0005488,GO:0016787,GO:0008152,GO:0003824,GO:0006730","XP_002902721
.1,EEY56647.1"
Stramenopiles-
Phytophthora_sojae_jgi109095,482,965.296,0,gi|301107277|ref|XP_002902721.1|adeno
sylhomocysteinase [Phytophthora infestans T30-4] ,"
GO:0004013,GO:0005488,GO:0016787,GO:0008152,GO:0003824,GO:0006730","XP_002902721
.1,EEY56647.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi72791,2824,2806.55,0,gi|299116617|emb|CBN76243.1|
dynein heavy chain dynein heavy chain [Ectocarpus siliculosus],"
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018",CB
N76243.1
Stramenopiles-
Phytophthora_capsici_jgi16,1081,2116.66,0,gi|301101074|ref|XP_002899626.1|dynein
```

```
heavy chain [Phytophthora infestans T30-4] ,"
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018","X
P_002899626.1,EEY61986.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224015082,393,821.231,0,gi|224015082|ref|XP_
002297202.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0009058,GO:0003824,GO:0030170,GO:0016769","XP_002297202.1,EED86527.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi205591,391,503.056,2.10E-
140,gi|224015082|ref|XP_002297202.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,"
GO:0009058,GO:0003824,GO:0030170,GO:0016769","XP_002297202.1,EED86527.1"
Stramenopiles-
Phytophthora_capsici_jgi84133,7661,2520.73,0,gi|190572215|ref|YP_001970060.1|ind
olepyruvate ferredoxin oxidoreductase [Stenotrophomonas maltophilia K279a] ,"
GO:0055114,GO:0016491,GO:0030976,GO:0008152,GO:0003824,GO:0016903","YP_001970060
.1,CAQ43745.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219124797,1321,2726.04,0,gi|219124797|re
f|XP_002182682.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0004386,GO:0003676,GO:0005524,GO:0016787,GO:0006310,GO:0008026","XP_002182682
.1,EEC45969.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi180755,1134,965.296,0,gi|219124797|ref|XP_002182682.
1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0004386,GO:0003676,GO:0005524,GO:0016787,GO:0006310,GO:0008026","XP_002182682
.1,EEC45969.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223997592,1287,2662.1,0,gi|223997592|ref|XP_
002288469.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0004386,GO:0003676,GO:0005524,GO:0016787,GO:0008026","XP_002288469.1,EED93905
.1"
Stramenopiles-
Phytophthora_sojae_jgi157121,854,937.176,0,"gi|301119977|ref|XP_002907716.1|DEAD
/DEAH box RNA helicase, putative [Phytophthora infestans T30-4] ","
GO:0004386,GO:0003676,GO:0005524,GO:0016787,GO:0008026","XP_002907716.1,EEY64280
.1"
Stramenopiles-
Phytophthora_capsici_jgi10908,856,735.332,0,"gi|301119977|ref|XP_002907716.1|DEA
D/DEAH box RNA helicase, putative [Phytophthora infestans T30-4] ","
GO:0004386,GO:0003676,GO:0005524,GO:0016787,GO:0008026","XP_002907716.1,EEY64280
.1"
Stramenopiles-Aureococcus_anophagefferens_jgi7435,126,85.5001,1.89E-
15,gi|224141165|ref|XP_002323945.1|predicted protein [Populus trichocarpa] ,"
GO:0005739,GO:0005488,GO:0016021,GO:0006839,GO:0016020,GO:0055085,GO:0006810","X
P_002323945.1,EEF04078.1"
Stramenopiles-Phytophthora_sojae_jgi122975,299,548.125,4.37E-
154,gi|301122859|ref|XP_002909156.1|phosphatidyl inositol kinase (PIK-B)
[Phytophthora infestans T30-4] ,"
GO:0048015,GO:0016301,GO:0005488,GO:0016740,GO:0004428,GO:0046854,GO:0016773","X
P_002909156.1,EEY57970.1"
Stramenopiles-Phytophthora_capsici_jgi122175,304,553.518,9.22E-
156,gi|301122859|ref|XP_002909156.1|phosphatidyl inositol kinase (PIK-B)
[Phytophthora infestans T30-4] ,"
GO:0048015,GO:0016301,GO:0005488,GO:0016740,GO:0004428,GO:0046854,GO:0016773","X
P_002909156.1,EEY57970.1"
```

```
Stramenopiles-Phytophthora_ramorum_jgi38706,257,326.25,1.92E-
87,gi|301122859|ref|XP_002909156.1|phosphatidyl inositol kinase (PIK-B)
[Phytophthora infestans T30-4] ,"
GO:0048015,GO:0016301,GO:0005488,GO:0016740,GO:0004428,GO:0046854,GO:0016773","X
P_002909156.1,EEY57970.1"
Stramenopiles-
Phytophthora_capsici_jgi424,1257,2285.37,0,gi|301112286|ref|XP_002905222.1|phosp
hatidylinositol kinase [Phytophthora infestans T30-4] ,"
GO:0016740,GO:0004428,GO:0016303,GO:0046854,GO:0016301,GO:0048015,GO:0005942,GO:
0016773,GO:0005488","XP_002905222.1,EEY53604.1"
Stramenopiles-
Phytophthora_sojae_jgi129234,1293,2316.58,0,gi|301112286|ref|XP_002905222.1|phos
phatidylinositol kinase [Phytophthora infestans T30-4] ,"
GO:0016740,GO:0004428,GO:0016303,GO:0046854,GO:0016301,GO:0048015,GO:0005942,GO:
0016773,GO:0005488","XP_002905222.1,EEY53604.1"
Stramenopiles-
Phytophthora_ramorum_jgi77134,1268,2241.85,0,gi|301112286|ref|XP_002905222.1|pho
sphatidylinositol kinase [Phytophthora infestans T30-4] ,"
GO:0016740,GO:0004428,GO:0016303,GO:0046854,GO:0016301,GO:0048015,GO:0005942,GO:
0016773,GO:0005488","XP_002905222.1,EEY53604.1"
Stramenopiles-
Phytophthora_sojae_jgi155701,1300,2450.24,0,gi|301112280|ref|XP_002905219.1|phos
phatidylinositol kinase [Phytophthora infestans T30-4] ,"
GO:0016740,GO:0004428,GO:0016303,GO:0046854,GO:0016301,GO:0048015,GO:0005942,GO:
0016773,GO:0005488","XP_002905219.1,EEY53601.1"
Stramenopiles-Phytophthora_capsici_jgi104814,219,462.611,1.20E-
128,gi|301112280|ref|XP_002905219.1|phosphatidylinositol kinase [Phytophthora
infestans T30-4] ,"
GO:0016740,GO:0004428,GO:0016303,GO:0046854,GO:0016301,GO:0048015,GO:0005942,GO:
0016773,GO:0005488","XP_002905219.1,EEY53601.1"
Stramenopiles-
Phytophthora_ramorum_jgi77130,1374,2617.03,0,gi|301112280|ref|XP_002905219.1|pho
sphatidylinositol kinase [Phytophthora infestans T30-4] ,"
GO:0016740,GO:0004428,GO:0016303,GO:0046854,GO:0016301,GO:0048015,GO:0005942,GO:
0016773,GO:0005488","XP_002905219.1,EEY53601.1"
Stramenopiles-
Phytophthora_capsici_jgi28123,680,923.309,0,gi|301119275|ref|XP_002907365.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002907365.1,EEY63929.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi210020,438,639.032,0,gi|219126933|ref|XP_002183701.1
|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0016301,GO:0005737,GO:0016740,GO:0004618,GO:0006096","XP_002183701.1,EEC44883
.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219126933,448,910.212,0,gi|219126933|ref
|XP_002183701.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0016301,GO:0005737,GO:0016740,GO:0004618,GO:0006096","XP_002183701.1,EEC44883
.1"
Stramenopiles-Aureococcus_anophagefferens_jgi71305,979,579.326,7.90E-
163,gi|299115459|emb|CBN75623.1|phosphoglycerate kinase [Ectocarpus
siliculosus],"
GO:0016301,GO:0005737,GO:0016740,GO:0004618,GO:0006096",CBN75623.1
Stramenopiles-Phytophthora_parasitica_esgi222401461_1,188,217.624,4.27E-
55,gi|301115920|ref|XP_002905689.1|U1 small nuclear ribonucleoprotein A
```

```
[Phytophthora infestans T30-4] ,"
GO:0003676,GO:0000166,GO:0030529","XP_002905689.1,EEY68530.1"
Stramenopiles-Phytophthora_capsici_jgi22685,233,372.474,2.12E-
101,gi|301115920|ref|XP_002905689.1|U1 small nuclear ribonucleoprotein A
[Phytophthora infestans T30-4] ,"
GO:0003676,GO:0000166,GO:0030529","XP_002905689.1,EEY68530.1"
Stramenopiles-Phytophthora_sojae_jgi136102,237,392.889,1.36E-
107,gi|301115920|ref|XP_002905689.1|U1 small nuclear ribonucleoprotein A
[Phytophthora infestans T30-4] ,"
GO:0003676,GO:0000166,GO:0030529","XP_002905689.1,EEY68530.1"
Stramenopiles-Phytophthora_ramorum_jgi93644,230,377.867,4.54E-
103,gi|301115920|ref|XP_002905689.1|U1 small nuclear ribonucleoprotein A
[Phytophthora infestans T30-4] ,"
GO:0003676,GO:0000166,GO:0030529","XP_002905689.1,EEY68530.1"
Stramenopiles-Aureococcus_anophagefferens_jgi28680,215,246.899,9.72E-
64,gi|116781538|gb|ABK22144.1|unknown [Picea sitchensis],"
GO:0003676,GO:0000166",ABK22144.1
Stramenopiles-
Fragilariopsis_cylindrus_jgi227489,717,1006.9,0,gi|219128000|ref|XP_002184212.1|
predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,
GO:0005488,"XP_002184212.1,EEC44390.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219128000,710,1454.11,0,gi|219128000|ref
|XP_002184212.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,
GO:0005488,"XP_002184212.1,EEC44390.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223994285,644,1314.29,0,gi|223994285|ref|XP_
002286826.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,
GO:0005488,"XP_002286826.1,EED96467.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi38752,694,915.22,0,gi|299470767|emb|CBN79813.1|co
nserved unknown protein [Ectocarpus siliculosus], GO:0005488,CBN79813.1
Stramenopiles-Aureococcus_anophagefferens_jgi12738,443,522.702,3.59E-
146,gi|299470767|emb|CBN79813.1|conserved unknown protein [Ectocarpus
siliculosus], GO:0005488,CBN79813.1
Stramenopiles-Aureococcus_anophagefferens_jgi66238,277,454.907,3.82E-
126,gi|299470767|emb|CBN79813.1|conserved unknown protein [Ectocarpus
siliculosus], GO:0005488,CBN79813.1
Stramenopiles-
Phytophthora_sojae_jgi132845,796,1481.85,0,gi|301107612|ref|XP_002902888.1|VAC14
family protein [Phytophthora infestans T30-4] ,
GO:0005488,"XP_002902888.1,EEY56058.1"
Stramenopiles-
Phytophthora_ramorum_jgi95460,769,1441.4,0,gi|301107612|ref|XP_002902888.1|VAC14
family protein [Phytophthora infestans T30-4] ,
GO:0005488,"XP_002902888.1,EEY56058.1"
Stramenopiles-
Phytophthora_capsici_jgi55552,617,1194.49,0,gi|301107612|ref|XP_002902888.1|VAC1
4 family protein [Phytophthora infestans T30-4] ,
GO:0005488,"XP_002902888.1,EEY56058.1"
Stramenopiles-Aureococcus_anophagefferens_jgi67082,1199,232.261,2.86E-
58,gi|167517467|ref|XP_001743074.1|hypothetical protein [Monosiga brevicollis
MX1] ,,"XP_001743074.1,EDQ91788.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219112637,572,1175.61,0,gi|219112637|ref
```

```
|XP_002178070.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,
GO:0055085,"XP_002178070.1,EEC50884.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224001012,504,1030.01,0,gi|224001012|ref|XP_
002290178.1|transporter belonging to the MFS superfamily [Thalassiosira
pseudonana CCMP1335] , GO:0055085,"XP_002290178.1,EED91930.1"
Stramenopiles-Phytophthora_brassicae_esContig1621_3,372,548.895,3.49E-
154,gi|301122213|ref|XP_002908833.1|Major Facilitator Superfamily (MFS)
[Phytophthora infestans T30-4] , GO:0055085,"XP_002908833.1,EEY57647.1"
Stramenopiles-
Phytophthora_ramorum_jgi72570,535,903.279,0,gi|301122213|ref|XP_002908833.1|Majo
r Facilitator Superfamily (MFS) [Phytophthora infestans T30-4] ,
GO:0055085,"XP_002908833.1,EEY57647.1"
Stramenopiles-
Phytophthora_sojae_jgi130057,477,670.618,0,gi|301122213|ref|XP_002908833.1|Major
Facilitator Superfamily (MFS) [Phytophthora infestans T30-4] ,
GO:0055085,"XP_002908833.1,EEY57647.1"
Stramenopiles-Phytophthora_parasitica_esgi68418455_2,267,428.713,2.70E-
118,gi|301122213|ref|XP_002908833.1|Major Facilitator Superfamily (MFS)
[Phytophthora infestans T30-4] , GO:0055085,"XP_002908833.1,EEY57647.1"
Stramenopiles-
Phytophthora_capsici_jgi122099,525,853.588,0,gi|301122213|ref|XP_002908833.1|Maj
or Facilitator Superfamily (MFS) [Phytophthora infestans T30-4] ,
GO:0055085,"XP_002908833.1,EEY57647.1"
Stramenopiles-Aureococcus_anophagefferens_jgi60526,815,197.208,7.93E-
48,gi|120437766|ref|YP_863452.1|cysteine desulfurase-like protein [Gramella
forsetii KT0803] ," GO:0008152,GO:0003824,GO:0030170","YP_863452.1,CAL68385.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219110076,766,1590.47,0,gi|219110076|ref
|XP_002176790.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0004835,GO:0008152,GO:0003824,GO:0030170,GO:0006464","XP_002176790.1,EEC51253
.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi239209,1118,545.428,1.59E-
152,gi|224011465|ref|XP_002295507.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,"
GO:0004835,GO:0008152,GO:0003824,GO:0030170,GO:0006464","XP_002295507.1,ACI64224
.1"
Stramenopiles-Phytophthora_capsici_jgi116031,338,439.113,3.33E-
121,"gi|301114201|ref|XP_002998870.1|Ufm1-specific protease, putative
[Phytophthora infestans T30-4] ", GO:0008233,"XP_002998870.1,EEY69016.1"
Stramenopiles-
Phytophthora_ramorum_jgi83661,665,920.613,0,"gi|301114201|ref|XP_002998870.1|Ufm
1-specific protease, putative [Phytophthora infestans T30-4] ",
GO:0008233,"XP_002998870.1,EEY69016.1"
Stramenopiles-
Phytophthora_sojae_jgi132341,659,934.48,0,"gi|301114201|ref|XP_002998870.1|Ufm1-
specific protease, putative [Phytophthora infestans T30-4] ",
GO:0008233,"XP_002998870.1,EEY69016.1"
Stramenopiles-Blastocystis_hominis_tbBHL00001025_6,275,271.937,4.48E-
71,gi|300121681|emb|CBK22256.2|unnamed protein product [Blastocystis
hominis],,CBK22256.2
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223997602,408,861.677,0,gi|223997602|ref|XP_
002288474.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0003913,GO:0006281","XP_002288474.1,EED93910.1"
```

```
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219119456,515,1082.4,0,gi|219119456|ref|
XP_002180488.1|cyclobutane pyrimidine dimer 1 [Phaeodactylum tricornutum CCAP
1055/1] ," GO:0003913,GO:0006281","XP_002180488.1,EEC47896.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219120881,282,586.26,1.39E-
165,gi|219120881|ref|XP_002185672.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002185672.1,ACI65142.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219114445,998,2065.43,0,gi|219114445|ref
|XP_002176393.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002176393.1,EEC42629.1"
Stramenopiles-Blastocystis_hominis_tbBHL00000230_3,408,261.151,1.84E-
67,gi|300176176|emb|CBK23487.2|unnamed protein product [Blastocystis hominis],"
GO:0005509,GO:0016021,GO:0016020,GO:0055085,GO:0016462,GO:0006810,GO:0005215",CB
K23487.2
Stramenopiles-
Phytophthora_sojae_jgi109723,367,675.626,0,"gi|301107902|ref|XP_002903033.1|glyc
oside hydrolase, putative [Phytophthora infestans T30-4] ","
GO:0055114,GO:0005488,GO:0016491,GO:0016787,GO:0008152,GO:0003824,GO:0008270,GO:
0005622","XP_002903033.1,EEY56203.1"
Stramenopiles-
Phytophthora_capsici_jgi108661,689,1080.86,0,"gi|301107902|ref|XP_002903033.1|gl
ycoside hydrolase, putative [Phytophthora infestans T30-4] ","
GO:0055114,GO:0005488,GO:0016491,GO:0016787,GO:0008152,GO:0003824,GO:0008270,GO:
0005622","XP_002903033.1,EEY56203.1"
Stramenopiles-Phytophthora_ramorum_jgi41436,342,634.795,3.76E-
180,"gi|301107902|ref|XP_002903033.1|glycoside hydrolase, putative [Phytophthora
infestans T30-4] ","
GO:0055114,GO:0005488,GO:0016491,GO:0016787,GO:0008152,GO:0003824,GO:0008270,GO:
0005622","XP_002903033.1,EEY56203.1"
Stramenopiles-
Phytophthora_ramorum_jgi50225,366,662.529,0,"gi|301107902|ref|XP_002903033.1|gly
coside hydrolase, putative [Phytophthora infestans T30-4] ","
GO:0055114,GO:0005488,GO:0016491,GO:0016787,GO:0008152,GO:0003824,GO:0008270,GO:
0005622","XP_002903033.1,EEY56203.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223993651,344,706.442,0,gi|223993651|ref|XP_
002286509.1|alcohol dehydrogenase [Thalassiosira pseudonana CCMP1335] ,"
GO:0055114,GO:0005488,GO:0016491,GO:0004022,GO:0008152,GO:0003824,GO:0008270","X
P_002286509.1,EED96150.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi208777,367,383.259,2.37E-
104,gi|223993651|ref|XP_002286509.1|alcohol dehydrogenase [Thalassiosira
pseudonana CCMP1335] ,"
GO:0055114,GO:0005488,GO:0016491,GO:0004022,GO:0008152,GO:0003824,GO:0008270","X
P_002286509.1,EED96150.1"
Stramenopiles-Phytophthora_capsici_jgi28300,324,567.385,7.13E-
160,"gi|301107500|ref|XP_002902832.1|protein phosphatase 2C, putative
[Phytophthora infestans T30-4] ","
GO:0046872,GO:0008287,GO:0016787,GO:0006470,GO:0003824,GO:0004722,GO:0004721","X
P_002902832.1,EEY56002.1"
Stramenopiles-Phytophthora_ramorum_jgi79659,311,565.844,1.87E-
159,"gi|301107500|ref|XP_002902832.1|protein phosphatase 2C, putative
[Phytophthora infestans T30-4] ","
```

```
GO:0046872,GO:0008287,GO:0016787,GO:0006470,GO:0003824,GO:0004722,GO:0004721","X
P_002902832.1,EEY56002.1"
Stramenopiles-Phytophthora_sojae_jgi132776,314,572.392,2.48E-
161,"gi|301107500|ref|XP_002902832.1|protein phosphatase 2C, putative
[Phytophthora infestans T30-4] ","
GO:0046872,GO:0008287,GO:0016787,GO:0006470,GO:0003824,GO:0004722,GO:0004721","X
P_002902832.1,EEY56002.1"
Stramenopiles-Phytophthora_parasitica_esgi68419426_1,239,357.836,5.89E-
97,"gi|301107500|ref|XP_002902832.1|protein phosphatase 2C, putative
[Phytophthora infestans T30-4] ","
GO:0046872,GO:0008287,GO:0016787,GO:0006470,GO:0003824,GO:0004722,GO:0004721","X
P_002902832.1,EEY56002.1"
Stramenopiles-Aureococcus_anophagefferens_jgi19509,263,131.724,6.93E-
29,gi|307103433|gb|EFN51693.1|hypothetical protein CHLNCDRAFT_139942 [Chlorella
variabilis],,EFN51693.1
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224000471,519,1068.53,0,gi|224000471|ref|XP_
002289908.1|hypothetical protein THAPSDRAFT_262261 [Thalassiosira pseudonana
CCMP1335] ,"
GO:0046872,GO:0008287,GO:0016787,GO:0006470,GO:0003824,GO:0004722,GO:0004721","X
P_002289908.1,EED93445.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219116885,646,1335.47,0,gi|219116885|ref
|XP_002179237.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0046872,GO:0008287,GO:0016787,GO:0006470,GO:0003824,GO:0004722,GO:0004721","X
P_002179237.1,EEC49060.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi204950,256,440.269,8.32E-
122,gi|219116885|ref|XP_002179237.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0046872,GO:0008287,GO:0016787,GO:0006470,GO:0003824,GO:0004722,GO:0004721","X
P_002179237.1,EEC49060.1"
Stramenopiles-
Phytophthora_ramorum_jgi86329,676,935.25,0,gi|301116507|ref|XP_002905982.1|conse
rved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0046872,GO:0008287,GO:0016787,GO:0006470,GO:0003824,GO:0004722,GO:0004721","X
P_002905982.1,EEY67334.1"
Stramenopiles-
Phytophthora_sojae_jgi133867,665,941.799,0,gi|301116507|ref|XP_002905982.1|conse
rved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0046872,GO:0008287,GO:0016787,GO:0006470,GO:0003824,GO:0004722,GO:0004721","X
P_002905982.1,EEY67334.1"
Stramenopiles-
Phytophthora_ramorum_jgi77120,487,967.222,0,"gi|301112262|ref|XP_002905210.1|exo
polysaccharide phosphotransferase, putative [Phytophthora infestans T30-4] ",
GO:0016740,"XP_002905210.1,EEY53592.1"
Stramenopiles-
Phytophthora_capsici_jgi109685,479,963.755,0,"gi|301112262|ref|XP_002905210.1|ex
opolysaccharide phosphotransferase, putative [Phytophthora infestans T30-4] ",
GO:0016740,"XP_002905210.1,EEY53592.1"
Stramenopiles-
Phytophthora_sojae_jgi129214,477,911.753,0,"gi|301112260|ref|XP_002905209.1|exop
olysaccharide phosphotransferase, putative [Phytophthora infestans T30-4] ",
GO:0016740,"XP_002905209.1,EEY53591.1"
Stramenopiles-
Phytophthora_ramorum_jgi77119,477,918.687,0,"gi|301112260|ref|XP_002905209.1|exo
```

```
polysaccharide phosphotransferase, putative [Phytophthora infestans T30-4] ",
GO:0016740,"XP_002905209.1,EEY53591.1"
Stramenopiles-
Phytophthora_capsici_jgi118003,478,938.332,0,"gi|301112260|ref|XP_002905209.1|ex
opolysaccharide phosphotransferase, putative [Phytophthora infestans T30-4] ",
GO:0016740,"XP_002905209.1,EEY53591.1"
Stramenopiles-
Phytophthora_sojae_jgi129215,487,976.852,0,"gi|301112262|ref|XP_002905210.1|exop
olysaccharide phosphotransferase, putative [Phytophthora infestans T30-4] ",
GO:0016740,"XP_002905210.1,EEY53592.1"
Stramenopiles-Aureococcus_anophagefferens_jgi69098,335,302.753,3.38E-
80,gi|303278410|ref|XP_003058498.1|MraW methylase/RNA recognition motif protein
[Micromonas pusilla CCMP1545] ,"
GO:0003723,GO:0003676,GO:0008168,GO:0000166,GO:0008270,GO:0005622","XP_003058498
.1,EEH56953.1"
Stramenopiles-
Phytophthora_sojae_jgi156133,1315,1564.28,0,gi|301100762|ref|XP_002899470.1|phos
phatidylinositol kinase (PIK-J) [Phytophthora infestans T30-4] ,"
GO:0048015,GO:0016301,GO:0005488,GO:0016740,GO:0004428,GO:0046854,GO:0016773","X
P_002899470.1,EEY61830.1"
Stramenopiles-
Phytophthora_ramorum_jgi96102,1206,743.036,0,gi|301100762|ref|XP_002899470.1|pho
sphatidylinositol kinase (PIK-J) [Phytophthora infestans T30-4] ,"
GO:0048015,GO:0016301,GO:0005488,GO:0016740,GO:0004428,GO:0046854,GO:0016773","X
P_002899470.1,EEY61830.1"
Stramenopiles-
Phytophthora_sojae_jgi137537,1327,1680.61,0,gi|301123157|ref|XP_002909305.1|phos
phatidylinositol kinase (PIK-K) [Phytophthora infestans T30-4] ,"
GO:0048015,GO:0016301,GO:0005488,GO:0016740,GO:0004428,GO:0046854,GO:0016773","X
P_002909305.1,EEY58119.1"
Stramenopiles-
Phytophthora_ramorum_jgi84131,1343,1710.27,0,gi|301123157|ref|XP_002909305.1|pho
sphatidylinositol kinase (PIK-K) [Phytophthora infestans T30-4] ,"
GO:0048015,GO:0016301,GO:0005488,GO:0016740,GO:0004428,GO:0046854,GO:0016773","X
P_002909305.1,EEY58119.1"
Stramenopiles-
Phytophthora_capsici_jgi119880,675,900.197,0,gi|301123157|ref|XP_002909305.1|pho
sphatidylinositol kinase (PIK-K) [Phytophthora infestans T30-4] ,"
GO:0048015,GO:0016301,GO:0005488,GO:0016740,GO:0004428,GO:0046854,GO:0016773","X
P_002909305.1,EEY58119.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224001960,863,1788.47,0,gi|224001960|ref|XP_
002290652.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0006508,GO:0016020","XP_002290652.1,EED92404.1"
Stramenopiles-
Phytophthora_ramorum_jgi74841,484,863.218,0,"gi|301114335|ref|XP_002998937.1|gua
nine deaminase, putative [Phytophthora infestans T30-4] ","
GO:0016787,GO:0008892,GO:0008270","XP_002998937.1,EEY69083.1"
Stramenopiles-
Phytophthora_sojae_jgi121912,454,829.321,0,"gi|301114335|ref|XP_002998937.1|guan
ine deaminase, putative [Phytophthora infestans T30-4] ","
GO:0016787,GO:0008892,GO:0008270","XP_002998937.1,EEY69083.1"
Stramenopiles-
Phytophthora_capsici_jgi12948,483,865.529,0,"gi|301114335|ref|XP_002998937.1|gua
```

```
nine deaminase, putative [Phytophthora infestans T30-4] ","
GO:0016787,GO:0008892,GO:0008270","XP_002998937.1,EEY69083.1"
Stramenopiles-Aureococcus_anophagefferens_jgi30098,258,174.866,7.09E-
42,gi|299116665|emb|CBN74810.1|conserved unknown protein [Ectocarpus
siliculosus],,CBN74810.1
Stramenopiles-Aureococcus_anophagefferens_jgi25276,625,311.612,1.94E-
82,gi|224002120|ref|XP_002290732.1|cyclic nucleotide and voltage-activated ion
channel [Thalassiosira pseudonana CCMP1335] ,"
GO:0005509,GO:0016021,GO:0016020,GO:0055085,GO:0006811,GO:0005216,GO:0006810","X
P_002290732.1,EED92484.1"
Stramenopiles-Phytophthora_ramorum_jgi95518,384,151.369,1.57E-
34,gi|113478270|ref|YP_724331.1|cyclic nucleotide-binding protein [Trichodesmium
erythraeum IMS101] ,"
GO:0005249,GO:0016021,GO:0016020,GO:0055085,GO:0006813,GO:0006811,GO:0005216,GO:
0006810","YP_724331.1,ABG53858.1"
Stramenopiles-Phytophthora_capsici_jgi20532,410,172.94,5.87E-
41,gi|301095776|ref|XP_002896987.1|hypothetical protein PITG_17082 [Phytophthora
infestans T30-4] ,"
GO:0005249,GO:0016020,GO:0006813","XP_002896987.1,EEY66468.1"
Stramenopiles-
Phytophthora_ramorum_jgi96327,505,930.243,0,gi|301100019|ref|XP_002899100.1|Volt
age-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0005249,GO:0016021,GO:0016020,GO:0055085,GO:0006813,GO:0006811,GO:0005216,GO:
0006810","XP_002899100.1,EEY62464.1"
Stramenopiles-
Phytophthora_sojae_jgi127250,369,681.789,0,gi|301100019|ref|XP_002899100.1|Volta
ge-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0005249,GO:0016021,GO:0016020,GO:0055085,GO:0006813,GO:0006811,GO:0005216,GO:
0006810","XP_002899100.1,EEY62464.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi27794,440,640.573,0,gi|167537422|ref|XP_001750380
.1|hypothetical protein [Monosiga brevicollis MX1] ,"
GO:0008152,GO:0003824","XP_001750380.1,EDQ84879.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi234597,417,650.973,0,gi|223998384|ref|XP_002288865.1
|hypothetical protein THAPSDRAFT_32882 [Thalassiosira pseudonana CCMP1335] ,"
GO:0008152,GO:0003824","XP_002288865.1,EED94301.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223998384,401,835.099,0,gi|223998384|ref|XP_
002288865.1|hypothetical protein THAPSDRAFT_32882 [Thalassiosira pseudonana
CCMP1335] ," GO:0008152,GO:0003824","XP_002288865.1,EED94301.1"
Stramenopiles-Phytophthora_ramorum_jgi86868,917,345.51,1.93E-
92,gi|301103410|ref|XP_002900791.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002900791.1,EEY59598.1"
Stramenopiles-Phytophthora_sojae_jgi118601,310,244.588,1.08E-
62,gi|189531950|ref|XP_001920417.1|PREDICTED: GI11945-like [Danio
rerio],,XP_001920417.1
Stramenopiles-Phytophthora_sojae_jgi143982,2251,387.497,1.19E-
104,gi|291221631|ref|XP_002730823.1|PREDICTED: Gap-Pol polyprotein-like
[Saccoglossus kowalevskii],,XP_002730823.1
Stramenopiles-Phytophthora_sojae_jgi145162,565,486.493,3.79E-
135,"gi|301102191|ref|XP_002900183.1|regulator of nonsense transcripts 2,
putative [Phytophthora infestans T30-4] ","
GO:0005488,GO:0016070,GO:0005515","XP_002900183.1,EEY60387.1"
```

```
Stramenopiles-
Phytophthora_capsici_jgi108983,592,951.044,0,"gi|301110280|ref|XP_002904220.1|be
ta-D-xylosidase, putative [Phytophthora infestans T30-4] ","
GO:0004553,GO:0016787,GO:0008152,GO:0005975,GO:0016798","XP_002904220.1,EEY54398
.1"
Stramenopiles-
Phytophthora_sojae_jgi142411,1419,2451.01,0,"gi|301094310|ref|XP_002896261.1|str
uctural maintenance of chromosomes protein 4, putative [Phytophthora infestans
T30-4] ","
GO:0005694,GO:0005524,GO:0051276,GO:0005515","XP_002896261.1,EEY67708.1"
Stramenopiles-
Phytophthora_ramorum_jgi75570,1331,2374.74,0,"gi|301094310|ref|XP_002896261.1|st
ructural maintenance of chromosomes protein 4, putative [Phytophthora infestans
T30-4] ","
GO:0005694,GO:0005524,GO:0051276,GO:0005515","XP_002896261.1,EEY67708.1"
Stramenopiles-
Phytophthora_capsici_jgi10243,1408,2485.29,0,"gi|301094310|ref|XP_002896261.1|st
ructural maintenance of chromosomes protein 4, putative [Phytophthora infestans
T30-4] ","
GO:0005694,GO:0005524,GO:0051276,GO:0005515","XP_002896261.1,EEY67708.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi212991,1333,1618.59,0,gi|219113225|ref|XP_002186196.
1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0005694,GO:0005524,GO:0051276,GO:0005515","XP_002186196.1,ACI65666.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219113225,1356,2770.34,0,gi|219113225|re
f|XP_002186196.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0005694,GO:0005524,GO:0051276,GO:0005515","XP_002186196.1,ACI65666.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224009910,1268,2586.22,0,gi|224009910|ref|XP
_002293913.1|chromosome condensation protein-like protein [Thalassiosira
pseudonana CCMP1335] ,"
GO:0005694,GO:0005524,GO:0051276,GO:0005515","XP_002293913.1,EED88922.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi72033,2223,934.095,0,gi|219113225|ref|XP_00218619
6.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0005694,GO:0005524,GO:0051276,GO:0005515","XP_002186196.1,ACI65666.1"
Stramenopiles-Phytophthora_sojae_jgi127612,216,325.479,2.45E-
87,gi|301088739|ref|XP_002894782.1|conserved hypothetical protein [Phytophthora
infestans T30-4] , GO:0016021,"XP_002894782.1,EEY66807.1"
Stramenopiles-Aureococcus_anophagefferens_jgi29752,158,181.415,2.87E-
44,gi|147905308|ref|NP_001090480.1|hypothetical protein LOC779393 [Xenopus
laevis] , GO:0016021,"NP_001090480.1,AAI23161.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi164257,130,99.3673,1.14E-
19,gi|307102981|gb|EFN51246.1|hypothetical protein CHLNCDRAFT_59822 [Chlorella
variabilis],,EFN51246.1
Stramenopiles-
Aureococcus_anophagefferens_jgi29439,1034,1155.2,0,gi|145341008|ref|XP_001415608
.1|P-ATPase family transporter: calcium ion [Ostreococcus lucimarinus CCE9901]
,"
GO:0006816,GO:0016021,GO:0016020,GO:0015662,GO:0006812,GO:0016787,GO:0000166,GO:
0005524,GO:0006754,GO:0003824,GO:0005388,GO:0008152,GO:0016820","XP_001415608.1,
ABO93900.1"
Stramenopiles-
Phytophthora_parasitica_esContig1105_3,454,864.759,0,"gi|301108972|ref|XP_002903
```

```
567.1|calcium-transporting ATPase 1, endoplasmic reticulum-type, putative
[Phytophthora infestans T30-4] ","
GO:0006816,GO:0016021,GO:0016020,GO:0015662,GO:0006812,GO:0016787,GO:0000166,GO:
0005524,GO:0006754,GO:0003824,GO:0005388,GO:0008152,GO:0016820","XP_002903567.1,
EEY55343.1"
Stramenopiles-
Phytophthora_ramorum_jgi86978,717,1345.1,0,"gi|301094223|ref|XP_002997955.1|fatt
y acid synthase subunit alpha, putative [Phytophthora infestans T30-4] ","
GO:0016740,GO:0009059,GO:0006633,GO:0005737,GO:0055114,GO:0016491,GO:0003824,GO:
0004312,GO:0005835,GO:0008897,GO:0008152,GO:0000287,GO:0005488","XP_002997955.1,
EEY67793.1"
Stramenopiles-
Phytophthora_ramorum_jgi74442,4124,7542.58,0,"gi|301094223|ref|XP_002997955.1|fa
tty acid synthase subunit alpha, putative [Phytophthora infestans T30-4] ","
GO:0016740,GO:0009059,GO:0006633,GO:0005737,GO:0055114,GO:0016491,GO:0003824,GO:
0004312,GO:0005835,GO:0008897,GO:0008152,GO:0000287,GO:0005488","XP_002997955.1,
EEY67793.1"
Stramenopiles-
Phytophthora_sojae_jgi132304,1003,1228,0,"gi|301105289|ref|XP_002901728.1|fatty
acid synthase subunit alpha, putative [Phytophthora infestans T30-4] ","
GO:0016740,GO:0009059,GO:0006633,GO:0005737,GO:0055114,GO:0016491,GO:0003824,GO:
0018580,GO:0004312,GO:0005835,GO:0008897,GO:0008152,GO:0000287,GO:0005488","XP_0
02901728.1,EEY57118.1"
Stramenopiles-
Phytophthora_sojae_jgi132827,673,1110.13,0,"gi|301094223|ref|XP_002997955.1|fatt
y acid synthase subunit alpha, putative [Phytophthora infestans T30-4] ","
GO:0016740,GO:0009059,GO:0006633,GO:0005737,GO:0055114,GO:0016491,GO:0003824,GO:
0004312,GO:0005835,GO:0008897,GO:0008152,GO:0000287,GO:0005488","XP_002997955.1,
EEY67793.1"
Stramenopiles-
Phytophthora_sojae_jgi140057,3296,5695.93,0,"gi|301094223|ref|XP_002997955.1|fat
ty acid synthase subunit alpha, putative [Phytophthora infestans T30-4] ","
GO:0016740,GO:0009059,GO:0006633,GO:0005737,GO:0055114,GO:0016491,GO:0003824,GO:
0004312,GO:0005835,GO:0008897,GO:0008152,GO:0000287,GO:0005488","XP_002997955.1,
EEY67793.1"
Stramenopiles-Phytophthora_capsici_jgi87093,250,474.937,3.31E-
132,"gi|301094223|ref|XP_002997955.1|fatty acid synthase subunit alpha, putative
[Phytophthora infestans T30-4] ","
GO:0016740,GO:0009059,GO:0006633,GO:0005737,GO:0055114,GO:0016491,GO:0003824,GO:
0004312,GO:0005835,GO:0008897,GO:0008152,GO:0000287,GO:0005488","XP_002997955.1,
EEY67793.1"
Stramenopiles-
Phytophthora_ramorum_jgi85456,2034,3558.07,0,"gi|301094223|ref|XP_002997955.1|fa
tty acid synthase subunit alpha, putative [Phytophthora infestans T30-4] ","
GO:0016740,GO:0009059,GO:0006633,GO:0005737,GO:0055114,GO:0016491,GO:0003824,GO:
0004312,GO:0005835,GO:0008897,GO:0008152,GO:0000287,GO:0005488","XP_002997955.1,
EEY67793.1"
Stramenopiles-
Phytophthora_capsici_jgi10006,3259,4194.42,0,"gi|301094223|ref|XP_002997955.1|fa
tty acid synthase subunit alpha, putative [Phytophthora infestans T30-4] ","
GO:0016740,GO:0009059,GO:0006633,GO:0005737,GO:0055114,GO:0016491,GO:0003824,GO:
0004312,GO:0005835,GO:0008897,GO:0008152,GO:0000287,GO:0005488","XP_002997955.1,
EEY67793.1"
Stramenopiles-
Phytophthora_ramorum_jgi82618,1080,980.319,0,gi|301090425|ref|XP_002895427.1|con
```

```
served hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002895427.1,EEY56709.1"
Stramenopiles-Phytophthora_capsici_jgi19289,330,397.127,1.33E-
108,"gi|301109158|ref|XP_002903660.1|UDP-N-acetylglucosamine transporter,
putative [Phytophthora infestans T30-4] ","
GO:0008643,GO:0016021,GO:0005351,GO:0000139","XP_002903660.1,EEY55436.1"
Stramenopiles-Phytophthora_sojae_jgi142334,361,432.565,3.28E-
119,"gi|301109158|ref|XP_002903660.1|UDP-N-acetylglucosamine transporter,
putative [Phytophthora infestans T30-4] ","
GO:0008643,GO:0016021,GO:0005351,GO:0000139","XP_002903660.1,EEY55436.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224012463,492,1011.13,0,gi|224012463|ref|XP_
002294884.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002294884.1,EED87664.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224015271,737,1522.68,0,gi|224015271|ref|XP_
002297293.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002297293.1,EED86395.1"
Stramenopiles-Aureococcus_anophagefferens_jgi63340,1036,403.29,8.59E-
110,gi|224015271|ref|XP_002297293.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,,"XP_002297293.1,EED86395.1"
Stramenopiles-
Phytophthora_sojae_jgi142893,725,822.387,0,gi|301095335|ref|XP_002896768.1|tRNA
(cytosine-5-)-methyltransferase NSUN2-like protein [Phytophthora infestans T30-
4] ," GO:0003723,GO:0008168,GO:0016740","XP_002896768.1,EEY66703.1"
Stramenopiles-
Phytophthora_ramorum_jgi77667,876,1043.49,0,gi|301095335|ref|XP_002896768.1|tRNA
(cytosine-5-)-methyltransferase NSUN2-like protein [Phytophthora infestans T30-
4] ," GO:0003723,GO:0008168,GO:0016740","XP_002896768.1,EEY66703.1"
Stramenopiles-Phytophthora_capsici_jgi34633,552,596.275,3.66E-
168,gi|301095335|ref|XP_002896768.1|tRNA (cytosine-5-)-methyltransferase NSUN2-
like protein [Phytophthora infestans T30-4] ,"
GO:0003723,GO:0008168,GO:0016740","XP_002896768.1,EEY66703.1"
Stramenopiles-
Phytophthora_sojae_jgi137973,701,1224.92,0,"gi|301095411|ref|XP_002896806.1|tRNA
(cytosine-5-)-methyltransferase, putative [Phytophthora infestans T30-4] ","
GO:0003723,GO:0003676,GO:0008168,GO:0016740,GO:0008270","XP_002896806.1,EEY66741
.1"
Stramenopiles-
Phytophthora_capsici_jgi36436,693,1195.26,0,"gi|301095411|ref|XP_002896806.1|tRN
A (cytosine-5-)-methyltransferase, putative [Phytophthora infestans T30-4] ","
GO:0003723,GO:0003676,GO:0008168,GO:0016740,GO:0008270","XP_002896806.1,EEY66741
.1"
Stramenopiles-
Phytophthora_ramorum_jgi80021,693,1205.28,0,"gi|301095411|ref|XP_002896806.1|tRN
A (cytosine-5-)-methyltransferase, putative [Phytophthora infestans T30-4] ","
GO:0003723,GO:0003676,GO:0008168,GO:0016740,GO:0008270","XP_002896806.1,EEY66741
.1"
Stramenopiles-
Phytophthora_sojae_jgi156076,718,1139.02,0,"gi|301122641|ref|XP_002909047.1|tRNA
(cytosine-5-)-methyltransferase NSUN2, putative [Phytophthora infestans T30-4]
"," GO:0003723,GO:0008168,GO:0016740","XP_002909047.1,EEY57861.1"
Stramenopiles-
Phytophthora_capsici_jgi70434,715,1144.03,0,"gi|301122641|ref|XP_002909047.1|tRN
```

```
A (cytosine-5-)-methyltransferase NSUN2, putative [Phytophthora infestans T30-4]
"," GO:0003723,GO:0008168,GO:0016740","XP_002909047.1,EEY57861.1"
Stramenopiles-
Phytophthora_ramorum_jgi93316,716,1113.21,0,"gi|301122641|ref|XP_002909047.1|tRN
A (cytosine-5-)-methyltransferase NSUN2, putative [Phytophthora infestans T30-4]
"," GO:0003723,GO:0008168,GO:0016740","XP_002909047.1,EEY57861.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi189551,362,375.555,5.07E-
102,gi|223997102|ref|XP_002288224.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ," GO:0003723,GO:0008168","XP_002288224.1,EED93660.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219130185,320,671.389,0,gi|219130185|ref
|XP_002185252.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0003676,GO:0008168,GO:0032259","XP_002185252.1,EEC43384.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi151936,181,197.208,6.36E-
49,gi|219130185|ref|XP_002185252.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0003676,GO:0008168,GO:0032259","XP_002185252.1,EEC43384.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224015927,244,513.457,8.71E-
144,gi|224015927|ref|XP_002297606.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,,"XP_002297606.1,EED86097.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224003919,230,482.641,1.46E-
134,gi|224003919|ref|XP_002291631.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,,"XP_002291631.1,EED91738.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi161387,190,158.303,3.43E-
37,gi|255086063|ref|XP_002508998.1|predicted protein [Micromonas sp. RCC299]
,,"XP_002508998.1,ACO70256.1"
Stramenopiles-Aureococcus_anophagefferens_jgi2314,419,426.402,2.80E-
117,gi|219109923|ref|XP_002176714.1|bifunctional 6-phosphofructo-2-kinase
[Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0016740,GO:0004331,GO:0016787,GO:0005524,GO:0016301,GO:0003824,GO:0008152,GO:
0006003,GO:0003873,GO:0006000","XP_002176714.1,EEC51177.1"
Stramenopiles-Aureococcus_anophagefferens_jgi68696,1080,403.675,6.57E-
110,gi|42569586|ref|NP_180882.2|XID; motor/ protein binding [Arabidopsis
thaliana],,NP_180882.2
Stramenopiles-Aureococcus_anophagefferens_jgi22513,826,622.854,6.00E-
176,gi|300122735|emb|CBK23300.2|unnamed protein product [Blastocystis hominis],"
GO:0005524,GO:0016459,GO:0005515,GO:0003774",CBK23300.2
Stramenopiles-
Phytophthora_ramorum_jgi82014,1256,2373.97,0,gi|301120916|ref|XP_002908185.1|myo
sin-like protein [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0000166,GO:0016459,GO:0005515,GO:0003774","XP_002908185.1,EEY61268
.1"
Stramenopiles-
Phytophthora_capsici_jgi30229,1256,2466.42,0,gi|301120916|ref|XP_002908185.1|myo
sin-like protein [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0000166,GO:0016459,GO:0005515,GO:0003774","XP_002908185.1,EEY61268
.1"
Stramenopiles-
Phytophthora_sojae_jgi127507,1304,2440.61,0,gi|301120916|ref|XP_002908185.1|myos
in-like protein [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0000166,GO:0016459,GO:0005515,GO:0003774","XP_002908185.1,EEY61268
.1"
Stramenopiles-
Phytophthora_ramorum_jgi96407,2085,1887.08,0,gi|301114269|ref|XP_002998904.1|con
served hypothetical protein [Phytophthora infestans T30-4] ,"
```

```
GO:0005524,GO:0000166,GO:0003777,GO:0007018,GO:0003774,GO:0005874","XP_002998904
.1,EEY69050.1"
Stramenopiles-
Phytophthora_sojae_jgi157659,2109,1890.55,0,gi|301114269|ref|XP_002998904.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0000166,GO:0003777,GO:0007018,GO:0003774,GO:0005874","XP_002998904
.1,EEY69050.1"
Stramenopiles-
Phytophthora_capsici_jgi115893,1465,1375.92,0,gi|301114269|ref|XP_002998904.1|co
nserved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0000166,GO:0003777,GO:0007018,GO:0003774,GO:0005874","XP_002998904
.1,EEY69050.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223995915,319,658.677,0,gi|223995915|ref|XP_
002287631.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0006306,GO:0008168,GO:0016740,GO:0003886,GO:0003677","XP_002287631.1,EED95074
.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219122422,495,1021.92,0,gi|219122422|ref
|XP_002181544.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0006306,GO:0008168,GO:0016740,GO:0003886,GO:0003677","XP_002181544.1,EEC46758
.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi148014,464,410.609,1.85E-
112,gi|219122422|ref|XP_002181544.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0006306,GO:0008168,GO:0016740,GO:0003886,GO:0003677","XP_002181544.1,EEC46758
.1"
Stramenopiles-
Phytophthora_sojae_jgi128854,1375,1090.1,0,gi|301120626|ref|XP_002908040.1|ATP-
binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0016887,GO:0005524,GO:0016021,GO:0000166,GO:0042626,GO:0055085,GO:0017111,GO:
0006810","XP_002908040.1,EEY61123.1"
Stramenopiles-
Phytophthora_capsici_jgi112828,1147,1511.89,0,gi|301101152|ref|XP_002899665.1|AT
P-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0016887,GO:0005524,GO:0016021,GO:0000166,GO:0042626,GO:0055085,GO:0017111,GO:
0006810","XP_002899665.1,EEY62025.1"
Stramenopiles-
Phytophthora_ramorum_jgi76830,1337,2386.3,0,gi|301101152|ref|XP_002899665.1|ATP-
binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0016887,GO:0005524,GO:0016021,GO:0000166,GO:0042626,GO:0055085,GO:0017111,GO:
0006810","XP_002899665.1,EEY62025.1"
Stramenopiles-
Phytophthora_sojae_jgi157391,1168,1689.86,0,gi|301101152|ref|XP_002899665.1|ATP-
binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0016887,GO:0005524,GO:0016021,GO:0000166,GO:0042626,GO:0055085,GO:0017111,GO:
0006810","XP_002899665.1,EEY62025.1"
Stramenopiles-
Phytophthora_sojae_jgi139968,1015,1833.92,0,gi|301113204|ref|XP_002998372.1|ATP-
binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0016887,GO:0005524,GO:0016021,GO:0000166,GO:0042626,GO:0055085,GO:0017111,GO:
0006810","XP_002998372.1,EEY69725.1"
Stramenopiles-
Phytophthora_ramorum_jgi77440,502,925.62,0,gi|301113204|ref|XP_002998372.1|ATP-
binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4] ,"
```

```
GO:0016887,GO:0005524,GO:0016021,GO:0000166,GO:0042626,GO:0055085,GO:0017111,GO:
0006810","XP_002998372.1,EEY69725.1"
Stramenopiles-
Phytophthora_ramorum_jgi72881,1356,2119.74,0,"gi|301122975|ref|XP_002909214.1|ry
anodine-inositol 1,4,5-triphosphate receptor Ca2 channel (RIR-CaC) family
protein [Phytophthora infestans T30-4] ", GO:0004872,"XP_002909214.1,EEY58028.1"
Stramenopiles-Phytophthora_ramorum_jgi82645,323,464.151,9.12E-
129,gi|301100226|ref|XP_002899203.1|zinc (Zn2)-Iron (Fe2) Permease (ZIP) family
[Phytophthora infestans T30-4] ,"
GO:0016020,GO:0055085,GO:0030001,GO:0046873","XP_002899203.1,EEY62172.1"
Stramenopiles-Phytophthora_brassicae_esContig1515_3,307,407.912,7.53E-
112,gi|301100226|ref|XP_002899203.1|zinc (Zn2)-Iron (Fe2) Permease (ZIP) family
[Phytophthora infestans T30-4] ,"
GO:0016020,GO:0055085,GO:0030001,GO:0046873","XP_002899203.1,EEY62172.1"
Stramenopiles-Phytophthora_capsici_jgi117284,608,516.153,5.30E-
144,gi|301100226|ref|XP_002899203.1|zinc (Zn2)-Iron (Fe2) Permease (ZIP) family
[Phytophthora infestans T30-4] ,"
GO:0016020,GO:0055085,GO:0030001,GO:0046873","XP_002899203.1,EEY62172.1"
Stramenopiles-Phytophthora_sojae_jgi133759,338,466.077,2.25E-
129,gi|301100226|ref|XP_002899203.1|zinc (Zn2)-Iron (Fe2) Permease (ZIP) family
[Phytophthora infestans T30-4] ,"
GO:0016020,GO:0055085,GO:0030001,GO:0046873","XP_002899203.1,EEY62172.1"
Stramenopiles-
Phytophthora_sojae_jgi143651,1858,1711.43,0,"gi|301095515|ref|XP_002896858.1|cal
cium/calmodulin-dependent protein kinase kinase, putative [Phytophthora
infestans T30-4] ","
GO:0001932,GO:0004674,GO:0004672,GO:0005952,GO:0006468,GO:0000166,GO:0005524,GO:
0016301,GO:0008603,GO:0003824","XP_002896858.1,EEY66793.1"
Stramenopiles-
Phytophthora_ramorum_jgi80068,1848,2843.91,0,"gi|301095515|ref|XP_002896858.1|ca
lcium/calmodulin-dependent protein kinase kinase, putative [Phytophthora
infestans T30-4] ","
GO:0001932,GO:0004674,GO:0004672,GO:0005952,GO:0006468,GO:0000166,GO:0005524,GO:
0016301,GO:0008603,GO:0003824","XP_002896858.1,EEY66793.1"
Stramenopiles-
Phytophthora_capsici_jgi17589,877,1331.62,0,"gi|301109339|ref|XP_002903750.1|pro
tein kinase, putative [Phytophthora infestans T30-4] ","
GO:0004674,GO:0004722,GO:0004721,GO:0004672,GO:0016787,GO:0006470,GO:0006468,GO:
0000166,GO:0005524,GO:0016301,GO:0003824,GO:0008287,GO:0046872","XP_002903750.1,
EEY54805.1"
Stramenopiles-Phytophthora_capsici_jgi108989,415,503.056,2.61E-
140,"gi|301113230|ref|XP_002998385.1|protein kinase, putative [Phytophthora
infestans T30-4] ","
GO:0004674,GO:0004672,GO:0006468,GO:0000166,GO:0005524,GO:0016301,GO:0003824,GO:
0008152,GO:0005488","XP_002998385.1,EEY69738.1"
Stramenopiles-Phytophthora_sojae_jgi130317,459,607.831,8.09E-
172,gi|301122699|ref|XP_002909076.1|ser/thr kinase [Phytophthora infestans T30-
4] ,"
GO:0016301,GO:0005524,GO:0004672,GO:0006468,GO:0004674","XP_002909076.1,EEY57890
.1"
Stramenopiles-Aureococcus_anophagefferens_jgi70153,307,552.747,1.92E-
155,"gi|301093191|ref|XP_002997444.1|ATP-dependent RNA helicase eIF4A, putative
[Phytophthora infestans T30-4] ","
GO:0004386,GO:0003676,GO:0005524,GO:0016787,GO:0000166,GO:0008026","XP_002997444
.1,EEY68752.1"
```

```
Stramenopiles-Phytophthora_parasitica_esContig657_1,559,443.736,2.82E-
122,"gi|301093191|ref|XP_002997444.1|ATP-dependent RNA helicase eIF4A, putative
[Phytophthora infestans T30-4] ","
GO:0004386,GO:0003676,GO:0005524,GO:0016787,GO:0000166,GO:0008026","XP_002997444
.1,EEY68752.1"
Stramenopiles-
Phytophthora_sojae_jgi109443,412,833.943,0,"gi|301093191|ref|XP_002997444.1|ATP-
dependent RNA helicase eIF4A, putative [Phytophthora infestans T30-4] ","
GO:0004386,GO:0003676,GO:0005524,GO:0016787,GO:0000166,GO:0008026","XP_002997444
.1,EEY68752.1"
Stramenopiles-Phytophthora_brassicae_esContig178_1,291,585.874,1.67E-
165,"gi|301093191|ref|XP_002997444.1|ATP-dependent RNA helicase eIF4A, putative
[Phytophthora infestans T30-4] ","
GO:0004386,GO:0003676,GO:0005524,GO:0016787,GO:0000166,GO:0008026","XP_002997444
.1,EEY68752.1"
Stramenopiles-
Phytophthora_ramorum_jgi71460,395,791.956,0,"gi|301093191|ref|XP_002997444.1|ATP
-dependent RNA helicase eIF4A, putative [Phytophthora infestans T30-4] ","
GO:0004386,GO:0003676,GO:0005524,GO:0016787,GO:0000166,GO:0008026","XP_002997444
.1,EEY68752.1"
Stramenopiles-
Phytophthora_capsici_jgi91103,411,830.476,0,"gi|301093191|ref|XP_002997444.1|ATP
-dependent RNA helicase eIF4A, putative [Phytophthora infestans T30-4] ","
GO:0004386,GO:0003676,GO:0005524,GO:0016787,GO:0000166,GO:0008026","XP_002997444
.1,EEY68752.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi267058,417,733.021,0,gi|219113631|ref|XP_002186399.1
|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0004386,GO:0003676,GO:0005524,GO:0016787,GO:0000166,GO:0008026","XP_002186399
.1,ACI65869.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219113631,414,847.81,0,gi|219113631|ref|
XP_002186399.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0004386,GO:0003676,GO:0005524,GO:0016787,GO:0000166,GO:0008026","XP_002186399
.1,ACI65869.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224009464,369,755.747,0,gi|224009464|ref|XP_
002293690.1|eukaryotic translation initiation factor 4A [Thalassiosira
pseudonana CCMP1335] ,"
GO:0004386,GO:0003676,GO:0005524,GO:0003743,GO:0016787,GO:0000166,GO:0008026","X
P_002293690.1,EED88699.1"
Stramenopiles-
Phytophthora_ramorum_jgi71937,407,832.787,0,"gi|301112965|ref|XP_002998253.1|euk
aryotic initiation factor 4A-III, putative [Phytophthora infestans T30-4] ","
GO:0004386,GO:0003676,GO:0005524,GO:0003743,GO:0016787,GO:0000166,GO:0008026","X
P_002998253.1,EEY70599.1"
Stramenopiles-
Phytophthora_ramorum_jgi41525,578,1020.76,0,gi|301108491|ref|XP_002903327.1|phos
phoribosylaminoimidazole carboxylase [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0003824,GO:0004638,GO:0006189","XP_002903327.1,EEY55751.1"
Stramenopiles-
Phytophthora_sojae_jgi116990,550,1039.25,0,gi|301108491|ref|XP_002903327.1|phosp
horibosylaminoimidazole carboxylase [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0003824,GO:0004638,GO:0006189","XP_002903327.1,EEY55751.1"
```

```
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219112303,608,1239.56,0,gi|219112303|ref
|XP_002177903.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0005524,GO:0003824,GO:0004638,GO:0006189","XP_002177903.1,EEC50717.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi277172,642,813.913,0,gi|219112303|ref|XP_002177903.1
|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0005524,GO:0003824,GO:0004638,GO:0006189","XP_002177903.1,EEC50717.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223998128,604,1237.25,0,gi|223998128|ref|XP_
002288737.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0005524,GO:0003824,GO:0004638,GO:0006189","XP_002288737.1,EED94173.1"
Stramenopiles-Aureococcus_anophagefferens_jgi24362,383,335.88,4.87E-
90,gi|300772048|ref|ZP_07081918.1|phosphoribosylaminoimidazole carboxylase
ATPase subunit [Sphingobacterium spiritivorum ATCC 33861] ,"
GO:0005524,GO:0003824,GO:0016829,GO:0004638,GO:0006189","ZP_07081918.1,EFK57177.
1"
Stramenopiles-Aureococcus_anophagefferens_jgi62259,1410,145.976,3.01E-
32,gi|301111810|ref|XP_002904984.1|Voltage-gated Ion Channel (VIC) Superfamily
[Phytophthora infestans T30-4] ,"
GO:0005509,GO:0016021,GO:0016020,GO:0055085,GO:0006811,GO:0005216,GO:0006810","X
P_002904984.1,EEY53366.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219129179,1040,2155.95,0,gi|219129179|re
f|XP_002184773.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002184773.1,EEC43832.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi223993229,262,536.184,1.25E-
150,gi|223993229|ref|XP_002286298.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ," GO:0003755,GO:0006457,GO:0016853","XP_002286298.1,EED95939.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219124753,145,298.516,1.61E-
79,gi|219124753|ref|XP_002182661.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0003755,GO:0006457,GO:0016853","XP_002182661.1,EEC45948.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi226832,161,216.853,5.96E-
55,gi|219124753|ref|XP_002182661.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0003755,GO:0006457,GO:0016853","XP_002182661.1,EEC45948.1"
Stramenopiles-Aureococcus_anophagefferens_jgi15418,147,176.022,9.71E-
43,gi|312896100|ref|ZP_07755570.1|peptidyl-prolyl cis-trans isomerase
cyclophilin type [Planctomyces brasiliensis DSM 5305]
,,"ZP_07755570.1,EFQ18824.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219124429,171,353.984,3.19E-
96,gi|219124429|ref|XP_002182506.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0003755,GO:0006457,GO:0016853","XP_002182506.1,EEC45793.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi264008,307,241.891,7.08E-
62,gi|219124429|ref|XP_002182506.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0003755,GO:0006457,GO:0016853","XP_002182506.1,EEC45793.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223995509,322,669.078,0,gi|223995509|ref|XP_
002287428.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0003755,GO:0006457,GO:0016853","XP_002287428.1,EED94871.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi182355,238,190.66,1.10E-
46,gi|223997172|ref|XP_002288259.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ," GO:0003755,GO:0006457,GO:0016853","XP_002288259.1,EED93695.1"
```

```
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223997172,314,651.358,0,gi|223997172|ref|XP_
002288259.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0003755,GO:0006457,GO:0016853","XP_002288259.1,EED93695.1"
Stramenopiles-Aureococcus_anophagefferens_jgi62264,286,231.491,8.75E-
59,gi|223997172|ref|XP_002288259.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ," GO:0003755,GO:0006457,GO:0016853","XP_002288259.1,EED93695.1"
Stramenopiles-Aureococcus_anophagefferens_jgi1789,374,263.077,3.44E-
68,gi|156362330|ref|XP_001625732.1|predicted protein [Nematostella vectensis] ,"
GO:0008152,GO:0003824,GO:0008484","XP_001625732.1,EDO33632.1"
Stramenopiles-Aureococcus_anophagefferens_jgi70521,914,303.908,6.31E-
80,gi|167524284|ref|XP_001746478.1|hypothetical protein [Monosiga brevicollis
MX1] ," GO:0008152,GO:0003824,GO:0008484","XP_001746478.1,EDQ88865.1"
Stramenopiles-Aureococcus_anophagefferens_jgi1327,498,273.478,4.20E-
71,gi|167524284|ref|XP_001746478.1|hypothetical protein [Monosiga brevicollis
MX1] ," GO:0008152,GO:0003824,GO:0008484","XP_001746478.1,EDQ88865.1"
Stramenopiles-Aureococcus_anophagefferens_jgi28497,314,300.827,1.40E-
79,gi|255077171|ref|XP_002502235.1|predicted protein [Micromonas sp. RCC299] ,"
GO:0055114,GO:0048037,GO:0005488,GO:0016491,GO:0008152,GO:0003824,GO:0016616,GO:
0051287","XP_002502235.1,ACO63493.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219116687,348,724.546,0,gi|219116687|ref
|XP_002179138.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0048037,GO:0005488,GO:0008152,GO:0003824,GO:0016616,GO:0051287","XP_002179138
.1,EEC48961.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi267482,296,331.257,8.30E-
89,gi|219116687|ref|XP_002179138.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0048037,GO:0005488,GO:0008152,GO:0003824,GO:0016616,GO:0051287","XP_002179138
.1,EEC48961.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223995643,340,702.975,0,gi|223995643|ref|XP_
002287495.1|glycerate dehydrogenase and hydroxypyruvate reductase-like protein
[Thalassiosira pseudonana CCMP1335] ,"
GO:0008465,GO:0051287,GO:0055114,GO:0016616,GO:0016491,GO:0003824,GO:0048037,GO:
0008152,GO:0005488","XP_002287495.1,EED94938.1"
Stramenopiles-Aureococcus_anophagefferens_jgi61643,366,213.772,2.87E-
53,"gi|254427042|ref|ZP_05040749.1|D-isomer specific 2-hydroxyacid
dehydrogenase, catalytic domain, putative [Alcanivorax sp. DG881] ","
GO:0055114,GO:0048037,GO:0005488,GO:0016491,GO:0008152,GO:0003824,GO:0016616,GO:
0051287","ZP_05040749.1,EDX88170.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi259260,956,148.288,4.09E-
33,gi|260831236|ref|XP_002610565.1|hypothetical protein BRAFLDRAFT_117849
[Branchiostoma floridae] ," GO:0008152,GO:0003824","XP_002610565.1,EEN66575.1"
Stramenopiles-Aureococcus_anophagefferens_jgi64875,768,162.54,1.77E-
37,gi|260831236|ref|XP_002610565.1|hypothetical protein BRAFLDRAFT_117849
[Branchiostoma floridae] ," GO:0008152,GO:0003824","XP_002610565.1,EEN66575.1"
Stramenopiles-Aureococcus_anophagefferens_jgi27415,491,376.326,4.40E-
102,gi|299473637|emb|CBN78031.1|conserved unknown protein [Ectocarpus
siliculosus],,CBN78031.1
Stramenopiles-
Phytophthora_ramorum_jgi72218,457,796.193,0,gi|301089635|ref|XP_002895098.1|Fola
te-Biopterin Transporter (FBT) Family [Phytophthora infestans T30-4]
,,"XP_002895098.1,EEY60273.1"
```

```
Stramenopiles-
Phytophthora_sojae_jgi109065,527,843.573,0,gi|301089635|ref|XP_002895098.1|Folat
e-Biopterin Transporter (FBT) Family [Phytophthora infestans T30-4]
,,"XP_002895098.1,EEY60273.1"
Stramenopiles-
Phytophthora_capsici_jgi123800,511,854.744,0,gi|301089635|ref|XP_002895098.1|Fol
ate-Biopterin Transporter (FBT) Family [Phytophthora infestans T30-4]
,,"XP_002895098.1,EEY60273.1"
Stramenopiles-
Phytophthora_capsici_jgi18944,547,937.176,0,gi|301123155|ref|XP_002909304.1|Fola
te-Biopterin Transporter (FBT) Family [Phytophthora infestans T30-4]
,,"XP_002909304.1,EEY58118.1"
Stramenopiles-
Phytophthora_sojae_jgi137538,540,913.294,0,gi|301123155|ref|XP_002909304.1|Folat
e-Biopterin Transporter (FBT) Family [Phytophthora infestans T30-4]
,,"XP_002909304.1,EEY58118.1"
Stramenopiles-
Phytophthora_ramorum_jgi84132,568,803.897,0,gi|301123155|ref|XP_002909304.1|Fola
te-Biopterin Transporter (FBT) Family [Phytophthora infestans T30-4]
,,"XP_002909304.1,EEY58118.1"
Stramenopiles-
Phytophthora_ramorum_jgi86845,603,842.417,0,gi|301111478|ref|XP_002904818.1|fola
te-Biopterin Transporter (FBT) family [Phytophthora infestans T30-4]
,,"XP_002904818.1,EEY53200.1"
Stramenopiles-
Phytophthora_capsici_jgi36320,597,887.1,0,gi|301111478|ref|XP_002904818.1|folate
-Biopterin Transporter (FBT) family [Phytophthora infestans T30-4]
,,"XP_002904818.1,EEY53200.1"
Stramenopiles-
Phytophthora_sojae_jgi135717,591,819.305,0,gi|301111478|ref|XP_002904818.1|folat
e-Biopterin Transporter (FBT) family [Phytophthora infestans T30-4]
,,"XP_002904818.1,EEY53200.1"
Stramenopiles-
Phytophthora_ramorum_jgi87756,723,1134.01,0,gi|301119505|ref|XP_002907480.1|exos
ome complex exonuclease RRP6-like protein [Phytophthora infestans T30-4] ,"
GO:0006139,GO:0003676,GO:0004527,GO:0000166,GO:0044237,GO:0003824,GO:0008408,GO:
0005622","XP_002907480.1,EEY64044.1"
Stramenopiles-
Phytophthora_sojae_jgi142047,1490,2190.62,0,gi|301119505|ref|XP_002907480.1|exos
ome complex exonuclease RRP6-like protein [Phytophthora infestans T30-4] ,"
GO:0006139,GO:0003676,GO:0004527,GO:0000166,GO:0044237,GO:0003824,GO:0008408,GO:
0005622","XP_002907480.1,EEY64044.1"
Stramenopiles-Aureococcus_anophagefferens_jgi63530,550,155.992,1.04E-
35,gi|115653109|ref|XP_001198503.1|PREDICTED: similar to exosome component 10
[Strongylocentrotus purpuratus] ,,"XP_001198503.1,XP_001189337.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi178610,204,209.534,1.57E-
52,gi|224003495|ref|XP_002291419.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,"
GO:0006139,GO:0003676,GO:0008408,GO:0005622","XP_002291419.1,EED91526.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224003495,181,372.859,7.59E-
102,gi|224003495|ref|XP_002291419.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,"
GO:0006139,GO:0003676,GO:0008408,GO:0005622","XP_002291419.1,EED91526.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219126108,311,627.861,4.57E-
```

```
178,gi|219126108|ref|XP_002183306.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0006139,GO:0003676,GO:0008408,GO:0005622","XP_002183306.1,EEC45006.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219118959,682,1428.31,0,gi|219118959|ref
|XP_002180246.1|beta-xylosidase [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0004553,GO:0016787,GO:0008152,GO:0005975,GO:0016798","XP_002180246.1,EEC48437
.1"
Stramenopiles-Aureococcus_anophagefferens_jgi28884,308,248.054,8.63E-
64,gi|219118959|ref|XP_002180246.1|beta-xylosidase [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0004553,GO:0016787,GO:0008152,GO:0005975,GO:0016798","XP_002180246.1,EEC48437
.1"
Stramenopiles-
Phytophthora_capsici_jgi24562,809,1082.78,0,"gi|301090543|ref|XP_002895482.1|bet
a-glucosidase, putative [Phytophthora infestans T30-4] ","
GO:0004553,GO:0016787,GO:0008152,GO:0005975,GO:0016798","XP_002895482.1,EEY56284
.1"
Stramenopiles-
Phytophthora_sojae_jgi134112,705,924.85,0,"gi|301090543|ref|XP_002895482.1|beta-
glucosidase, putative [Phytophthora infestans T30-4] ","
GO:0004553,GO:0016787,GO:0008152,GO:0005975,GO:0016798","XP_002895482.1,EEY56284
.1"
Stramenopiles-Phytophthora_capsici_jgi117022,659,572.778,5.26E-
161,"gi|301118693|ref|XP_002907074.1|glycoside hydrolase, putative [Phytophthora
infestans T30-4] ","
GO:0004553,GO:0016787,GO:0008152,GO:0005975,GO:0016798","XP_002907074.1,EEY63638
.1"
Stramenopiles-
Phytophthora_sojae_jgi144049,806,1461.82,0,"gi|301118693|ref|XP_002907074.1|glyc
oside hydrolase, putative [Phytophthora infestans T30-4] ","
GO:0004553,GO:0016787,GO:0008152,GO:0005975,GO:0016798","XP_002907074.1,EEY63638
.1"
Stramenopiles-
Phytophthora_ramorum_jgi73436,808,1441.79,0,"gi|301118693|ref|XP_002907074.1|gly
coside hydrolase, putative [Phytophthora infestans T30-4] ","
GO:0004553,GO:0016787,GO:0008152,GO:0005975,GO:0016798","XP_002907074.1,EEY63638
.1"
Stramenopiles-
Phytophthora_ramorum_jgi81321,791,1206.05,0,"gi|301110280|ref|XP_002904220.1|bet
a-D-xylosidase, putative [Phytophthora infestans T30-4] ","
GO:0004553,GO:0016787,GO:0008152,GO:0005975,GO:0016798","XP_002904220.1,EEY54398
.1"
Stramenopiles-
Phytophthora_sojae_jgi138254,777,1204.89,0,"gi|301110280|ref|XP_002904220.1|beta
-D-xylosidase, putative [Phytophthora infestans T30-4] ","
GO:0004553,GO:0016787,GO:0008152,GO:0005975,GO:0016798","XP_002904220.1,EEY54398
.1"
Stramenopiles-Aureococcus_anophagefferens_jgi72703,745,459.529,6.48E-
127,gi|167525174|ref|XP_001746922.1|hypothetical protein [Monosiga brevicollis
MX1] ,"
GO:0004553,GO:0016787,GO:0008152,GO:0005975,GO:0016798","XP_001746922.1,EDQ88329
.1"
Stramenopiles-
Phytophthora_capsici_jgi123803,586,946.421,0,gi|301090782|ref|XP_002895593.1|con
```

```
served hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002895593.1,EEY55822.1"
Stramenopiles-
Phytophthora_sojae_jgi158906,597,976.082,0,gi|301090782|ref|XP_002895593.1|conse
rved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002895593.1,EEY55822.1"
Stramenopiles-
Phytophthora_ramorum_jgi84332,416,717.613,0,gi|301090782|ref|XP_002895593.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002895593.1,EEY55822.1"
Stramenopiles-Blastocystis_hominis_tbBHL00001124_2,175,224.942,2.77E-
57,gi|300120357|emb|CBK19911.2|unnamed protein product [Blastocystis
hominis],,CBK19911.2
Stramenopiles-Fragilariopsis_cylindrus_jgi234217,671,408.297,1.62E-
111,gi|219116374|ref|XP_002178982.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002178982.1,EEC49680.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219116374,686,1414.05,0,gi|219116374|ref
|XP_002178982.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002178982.1,EEC49680.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224006954,754,1555.81,0,gi|224006954|ref|XP_
002292437.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002292437.1,EED90412.1"
Stramenopiles-Phytophthora_sojae_jgi120543,404,559.681,2.31E-
157,gi|301098051|ref|XP_002898119.1|myotubularin-like protein [Phytophthora
infestans T30-4] ,"
GO:0046872,GO:0016791,GO:0016311,GO:0006470,GO:0004725,GO:0008270","XP_002898119
.1,EEY63532.1"
Stramenopiles-Phytophthora_capsici_jgi13947,219,374.4,4.34E-
102,gi|301098051|ref|XP_002898119.1|myotubularin-like protein [Phytophthora
infestans T30-4] ,"
GO:0046872,GO:0016791,GO:0016311,GO:0006470,GO:0004725,GO:0008270","XP_002898119
.1,EEY63532.1"
Stramenopiles-
Phytophthora_ramorum_jgi51394,404,653.67,0,gi|301098051|ref|XP_002898119.1|myotu
bularin-like protein [Phytophthora infestans T30-4] ,"
GO:0046872,GO:0016791,GO:0016311,GO:0006470,GO:0004725,GO:0008270","XP_002898119
.1,EEY63532.1"
Stramenopiles-
Phytophthora_sojae_jgi130134,1102,1724.52,0,"gi|301122381|ref|XP_002908917.1|alp
ha-1,3-mannosyltransferase, putative [Phytophthora infestans T30-4] ","
GO:0016740,GO:0009058,GO:0016311,GO:0016791,GO:0016757,GO:0005622,GO:0005515,GO:
0005097,GO:0032313","XP_002908917.1,EEY57731.1"
Stramenopiles-
Phytophthora_ramorum_jgi72636,1565,2481.44,0,"gi|301122381|ref|XP_002908917.1|al
pha-1,3-mannosyltransferase, putative [Phytophthora infestans T30-4] ","
GO:0016740,GO:0009058,GO:0016311,GO:0016791,GO:0016757,GO:0005622,GO:0005515,GO:
0005097,GO:0032313","XP_002908917.1,EEY57731.1"
Stramenopiles-
Phytophthora_sojae_jgi135799,1575,1967.2,0,gi|301111654|ref|XP_002904906.1|myotu
bularin-like protein [Phytophthora infestans T30-4] ,"
GO:0016791,GO:0016311,GO:0016787,GO:0004725","XP_002904906.1,EEY53288.1"
Stramenopiles-
Phytophthora_capsici_jgi92445,891,1618.98,0,gi|301111654|ref|XP_002904906.1|myot
```

```
ubularin-like protein [Phytophthora infestans T30-4] ,"
GO:0016791,GO:0016311,GO:0016787,GO:0004725","XP_002904906.1,EEY53288.1"
Stramenopiles-
Phytophthora_ramorum_jgi79916,1149,1982.61,0,gi|301111654|ref|XP_002904906.1|myo
tubularin-like protein [Phytophthora infestans T30-4] ,"
GO:0016791,GO:0016311,GO:0016787,GO:0004725","XP_002904906.1,EEY53288.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi227544,389,635.95,2.11E-
180,gi|219122853|ref|XP_002181752.1|diaminopimelate decarboxylase [Phaeodactylum
tricornutum CCAP 1055/1] ,"
GO:0008836,GO:0009089,GO:0003824","XP_002181752.1,EEC46966.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219122853,481,993.03,0,gi|219122853|ref|
XP_002181752.1|diaminopimelate decarboxylase [Phaeodactylum tricornutum CCAP
1055/1] ," GO:0008836,GO:0009089,GO:0003824","XP_002181752.1,EEC46966.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223993801,484,995.727,0,gi|223993801|ref|XP_
002286584.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0008836,GO:0009089,GO:0003824","XP_002286584.1,EED96225.1"
Stramenopiles-Aureococcus_anophagefferens_jgi39321,464,557.37,1.34E-
156,gi|308813676|ref|XP_003084144.1|diaminopimelate decarboxylase (ISS)
[Ostreococcus tauri] ,"
GO:0008836,GO:0009089,GO:0003824","XP_003084144.1,CAL58560.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224005430,4494,9383.83,0,gi|224005430|ref|XP
_002296366.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,
GO:0005509,"XP_002296366.1,ACI65083.1"
Stramenopiles-
Phytophthora_sojae_jgi127903,1034,1826.99,0,gi|301103201|ref|XP_002900687.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0008270,GO:0005622","XP_002900687.1,EEY60002.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi72156,4237,1122.46,0,gi|224005430|ref|XP_00229636
6.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,
GO:0005509,"XP_002296366.1,ACI65083.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224002727,367,733.791,0,gi|224002727|ref|XP_
002291035.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0016021,GO:0016020,GO:0055085","XP_002291035.1,EED91142.1"
Stramenopiles-Phytophthora_sojae_jgi108485,362,612.838,1.98E-
173,gi|301100672|ref|XP_002899425.1|Ca2 :Cation Antiporter (CaCA) Family
[Phytophthora infestans T30-4] ,"
GO:0008324,GO:0016021,GO:0016020,GO:0055085,GO:0006812","XP_002899425.1,EEY61785
.1"
Stramenopiles-Phytophthora_ramorum_jgi71942,362,620.542,8.61E-
176,gi|301100672|ref|XP_002899425.1|Ca2 :Cation Antiporter (CaCA) Family
[Phytophthora infestans T30-4] ,"
GO:0008324,GO:0016021,GO:0016020,GO:0055085,GO:0006812","XP_002899425.1,EEY61785
.1"
Stramenopiles-
Phytophthora_capsici_jgi110993,437,704.131,0,gi|301100672|ref|XP_002899425.1|Ca2
:Cation Antiporter (CaCA) Family [Phytophthora infestans T30-4] ,"
GO:0008324,GO:0016021,GO:0016020,GO:0055085,GO:0006812","XP_002899425.1,EEY61785
.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224006648,352,692.96,0,"gi|224006648|ref|XP_
```

```
002292284.1|calcium/proton exchanger, calcium antiporter [Thalassiosira
pseudonana CCMP1335] ","
GO:0016021,GO:0016020,GO:0055085","XP_002292284.1,EED90259.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219116302,348,698.738,0,gi|219116302|ref
|XP_002178946.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0016021,GO:0016020,GO:0055085","XP_002178946.1,EEC49644.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi186975,384,461.455,7.59E-
128,gi|219116302|ref|XP_002178946.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0016021,GO:0016020,GO:0055085","XP_002178946.1,EEC49644.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219125724,311,624.394,4.57E-
177,gi|219125724|ref|XP_002183124.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002183124.1,EEC45342.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi226887,233,155.221,4.70E-
36,gi|223994479|ref|XP_002286923.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,,"XP_002286923.1,EED96564.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224014284,419,868.611,0,gi|224014284|ref|XP_
002296805.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002296805.1,EED87006.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224012457,317,656.751,0,gi|224012457|ref|XP_
002294881.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002294881.1,EED87661.1"
Stramenopiles-Aureococcus_anophagefferens_jgi62660,247,80.4925,1.63E-
13,gi|219129927|ref|XP_002185128.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0016021,GO:0016020,GO:0055085,GO:0006811,GO:0005216,GO:0006810","XP_002185128
.1,EEC43260.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219129781,629,1280.39,0,gi|219129781|ref
|XP_002185059.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002185059.1,EEC43506.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi179560,207,239.965,1.19E-
61,gi|224001800|ref|XP_002290572.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,,"XP_002290572.1,EED92324.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224001800,622,1280.39,0,gi|224001800|ref|XP_
002290572.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002290572.1,EED92324.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi206011,1216,1540.4,0,gi|224004696|ref|XP_002295999.1
|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0016021,GO:0016020,GO:0006812,GO:0015662,GO:0016787,GO:0000166,GO:0005524,GO:
0016887,GO:0006754,GO:0003824,GO:0008152,GO:0016820","XP_002295999.1,ACI64716.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219126433,442,917.916,0,gi|219126433|ref
|XP_002183462.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0005524,GO:0006412,GO:0005737,GO:0004812,GO:0006434,GO:0000166,GO:0006418,GO:
0004828","XP_002183462.1,EEC45162.1"
Stramenopiles-
Phytophthora_sojae_jgi144153,497,905.975,0,gi|301108605|ref|XP_002903384.1|seryl
-tRNA synthetase [Phytophthora infestans T30-4] ,"
```

```
GO:0005524,GO:0006412,GO:0005737,GO:0004812,GO:0006434,GO:0000166,GO:0006418,GO:
0004828","XP_002903384.1,EEY55808.1"
Stramenopiles-
Phytophthora_ramorum_jgi75725,504,914.835,0,gi|301108605|ref|XP_002903384.1|sery
l-tRNA synthetase [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0006412,GO:0005737,GO:0004812,GO:0006434,GO:0000166,GO:0006418,GO:
0004828","XP_002903384.1,EEY55808.1"
Stramenopiles-Aureococcus_anophagefferens_jgi26929,203,104.375,7.70E-
21,gi|260786970|ref|XP_002588529.1|hypothetical protein BRAFLDRAFT_79485
[Branchiostoma floridae] , GO:0004872,"XP_002588529.1,EEN44540.1"
Stramenopiles-Aureococcus_anophagefferens_jgi62223,1307,75.485,4.87E-
11,gi|149639273|ref|XP_001507896.1|PREDICTED: hypothetical protein
[Ornithorhynchus anatinus],,XP_001507896.1
Stramenopiles-
Fragilariopsis_cylindrus_jgi185193,573,897.116,0,gi|219119306|ref|XP_002180416.1
|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0016874,GO:0006418,GO:0006420,GO:0000166,GO:0005737,GO:0006412,GO:0005524,GO:
0004814,GO:0004812","XP_002180416.1,EEC47824.1"
Stramenopiles-Phytophthora_capsici_jgi20843,416,526.939,1.68E-
147,gi|301119857|ref|XP_002907656.1|Voltage-gated Ion Channel (VIC) Superfamily
[Phytophthora infestans T30-4] ,"
GO:0016021,GO:0016020,GO:0055085,GO:0006811,GO:0005216,GO:0006810","XP_002907656
.1,EEY64220.1"
Stramenopiles-
Phytophthora_capsici_jgi3197,542,890.182,0,gi|301119857|ref|XP_002907656.1|Volta
ge-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0016021,GO:0016020,GO:0055085,GO:0006811,GO:0005216,GO:0006810","XP_002907656
.1,EEY64220.1"
Stramenopiles-
Phytophthora_sojae_jgi135067,783,991.875,0,gi|301119857|ref|XP_002907656.1|Volta
ge-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0016021,GO:0016020,GO:0055085,GO:0006811,GO:0005216,GO:0006810","XP_002907656
.1,EEY64220.1"
Stramenopiles-
Phytophthora_ramorum_jgi79282,610,856.284,0,gi|301119857|ref|XP_002907656.1|Volt
age-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0016021,GO:0016020,GO:0055085,GO:0006811,GO:0005216,GO:0006810","XP_002907656
.1,EEY64220.1"
Stramenopiles-
Phytophthora_ramorum_jgi74787,618,945.266,0,gi|301111304|ref|XP_002904731.1|Volt
age-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0005249,GO:0016021,GO:0016020,GO:0055085,GO:0006813,GO:0006811,GO:0005216,GO:
0006810","XP_002904731.1,EEY53113.1"
Stramenopiles-Phytophthora_ramorum_jgi85655,359,465.692,3.35E-
129,gi|301111304|ref|XP_002904731.1|Voltage-gated Ion Channel (VIC) Superfamily
[Phytophthora infestans T30-4] ,"
GO:0005249,GO:0016021,GO:0016020,GO:0055085,GO:0006813,GO:0006811,GO:0005216,GO:
0006810","XP_002904731.1,EEY53113.1"
Stramenopiles-
Phytophthora_sojae_jgi140823,641,955.281,0,gi|301111304|ref|XP_002904731.1|Volta
ge-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0005249,GO:0016021,GO:0016020,GO:0055085,GO:0006813,GO:0006811,GO:0005216,GO:
0006810","XP_002904731.1,EEY53113.1"
Stramenopiles-
Phytophthora_capsici_jgi20085,692,969.533,0,gi|301111304|ref|XP_002904731.1|Volt
```

```
age-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0005249,GO:0016021,GO:0016020,GO:0055085,GO:0006813,GO:0006811,GO:0005216,GO:
0006810","XP_002904731.1,EEY53113.1"
Stramenopiles-Aureococcus_anophagefferens_jgi15708,161,110.923,4.72E-
23,gi|47185111|emb|CAF95008.1|unnamed protein product [Tetraodon
nigroviridis],,CAF95008.1
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219129852,870,1786.93,0,gi|219129852|ref
|XP_002185093.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0003723,GO:0009451,GO:0001522,GO:0009982","XP_002185093.1,EEC43540.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219113940,870,1788.08,0,gi|219113940|ref
|XP_002176153.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0003723,GO:0009451,GO:0001522,GO:0009982","XP_002176153.1,EEC42860.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi242240,873,488.804,1.39E-
135,gi|219113940|ref|XP_002176153.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0003723,GO:0009451,GO:0001522,GO:0009982","XP_002176153.1,EEC42860.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223997338,1310,2716.41,0,gi|223997338|ref|XP
_002288342.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0008270,GO:0005622","XP_002288342.1,EED93778.1"
Stramenopiles-Aureococcus_anophagefferens_jgi63253,863,348.977,1.50E-
93,gi|223997338|ref|XP_002288342.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ," GO:0008270,GO:0005622","XP_002288342.1,EED93778.1"
Stramenopiles-Aureococcus_anophagefferens_jgi66742,1794,417.542,7.91E-
114,gi|224000561|ref|XP_002289953.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,,"XP_002289953.1,EED93490.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224002789,798,1657.11,0,gi|224002789|ref|XP_
002291066.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0003723,GO:0009451,GO:0001522,GO:0009982","XP_002291066.1,EED91173.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219109731,798,1675.99,0,gi|219109731|ref
|XP_002176619.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002176619.1,EEC51082.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi236841,920,692.189,0,gi|219109731|ref|XP_002176619.1
|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002176619.1,EEC51082.1"
Stramenopiles-
Phytophthora_ramorum_jgi80031,810,1280.39,0,gi|301095443|ref|XP_002896822.1|spor
angia induced conserved hypothetical protein [Phytophthora infestans T30-4] ,
GO:0005509,"XP_002896822.1,EEY66757.1"
Stramenopiles-
Phytophthora_sojae_jgi137985,843,1266.91,0,gi|301095443|ref|XP_002896822.1|spora
ngia induced conserved hypothetical protein [Phytophthora infestans T30-4] ,
GO:0005509,"XP_002896822.1,EEY66757.1"
Stramenopiles-Aureococcus_anophagefferens_jgi63054,6272,513.072,5.33E-
142,gi|145345747|ref|XP_001417362.1|predicted protein [Ostreococcus lucimarinus
CCE9901] , GO:0005509,"XP_001417362.1,ABO95655.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi234116,4550,5243.32,0,gi|224005430|ref|XP_002296366.
1|predicted protein [Thalassiosira pseudonana CCMP1335] ,
GO:0005509,"XP_002296366.1,ACI65083.1"
```

```
Stramenopiles-
Phytophthora_capsici_jgi95679,1047,2043.85,0,"gi|301108972|ref|XP_002903567.1|ca
lcium-transporting ATPase 1, endoplasmic reticulum-type, putative [Phytophthora
infestans T30-4] ","
GO:0006816,GO:0016021,GO:0016020,GO:0015662,GO:0006812,GO:0016787,GO:0000166,GO:
0005524,GO:0006754,GO:0003824,GO:0005388,GO:0008152,GO:0016820","XP_002903567.1,
EEY55343.1"
Stramenopiles-
Phytophthora_ramorum_jgi71769,1045,1971.44,0,"gi|301108972|ref|XP_002903567.1|ca
lcium-transporting ATPase 1, endoplasmic reticulum-type, putative [Phytophthora
infestans T30-4] ","
GO:0006816,GO:0016021,GO:0016020,GO:0015662,GO:0006812,GO:0016787,GO:0000166,GO:
0005524,GO:0006754,GO:0003824,GO:0005388,GO:0008152,GO:0016820","XP_002903567.1,
EEY55343.1"
Stramenopiles-
Phytophthora_sojae_jgi109296,1044,1996.48,0,"gi|301108972|ref|XP_002903567.1|cal
cium-transporting ATPase 1, endoplasmic reticulum-type, putative [Phytophthora
infestans T30-4] ","
GO:0006816,GO:0016021,GO:0016020,GO:0015662,GO:0006812,GO:0016787,GO:0000166,GO:
0005524,GO:0006754,GO:0003824,GO:0005388,GO:0008152,GO:0016820","XP_002903567.1,
EEY55343.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223994413,1015,2085.07,0,gi|223994413|ref|XP
_002286890.1|cation transport ATPase [Thalassiosira pseudonana CCMP1335] ,"
GO:0006816,GO:0016021,GO:0016020,GO:0015662,GO:0006812,GO:0016787,GO:0000166,GO:
0005524,GO:0006754,GO:0003824,GO:0005388,GO:0008152,GO:0016820","XP_002286890.1,
EED96531.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi188142,1242,1193.72,0,gi|219125902|ref|XP_002183209.
1|probable serca-type calcium ATPase [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0006816,GO:0016021,GO:0016020,GO:0015662,GO:0006812,GO:0016787,GO:0006811,GO:
0006810,GO:0000166,GO:0005524,GO:0006754,GO:0003824,GO:0005388,GO:0008152,GO:001
6820","XP_002183209.1,EEC45427.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219125902,1028,2097.4,0,gi|219125902|ref
|XP_002183209.1|probable serca-type calcium ATPase [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0006816,GO:0016021,GO:0016020,GO:0015662,GO:0006812,GO:0016787,GO:0006811,GO:
0006810,GO:0000166,GO:0005524,GO:0006754,GO:0003824,GO:0005388,GO:0008152,GO:001
6820","XP_002183209.1,EEC45427.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223997222,966,1981.84,0,gi|223997222|ref|XP_
002288284.1|calcium transporting ATPase [Thalassiosira pseudonana CCMP1335] ,"
GO:0006816,GO:0016021,GO:0016020,GO:0015662,GO:0006812,GO:0016787,GO:0000166,GO:
0005524,GO:0006754,GO:0003824,GO:0005388,GO:0008152,GO:0016820","XP_002288284.1,
EED93720.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224010143,1001,2047.71,0,gi|224010143|ref|XP
_002294029.1|cation transporting ATPase [Thalassiosira pseudonana CCMP1335] ,"
GO:0006816,GO:0016021,GO:0016020,GO:0015662,GO:0006812,GO:0016787,GO:0000166,GO:
0005524,GO:0006754,GO:0003824,GO:0005388,GO:0008152,GO:0016820","XP_002294029.1,
EED88384.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi10071,1030,928.702,0,gi|219125902|ref|XP_00218320
9.1|probable serca-type calcium ATPase [Phaeodactylum tricornutum CCAP 1055/1]
```

```
,"
GO:0006816,GO:0016021,GO:0016020,GO:0015662,GO:0006812,GO:0016787,GO:0006811,GO:
0006810,GO:0000166,GO:0005524,GO:0006754,GO:0003824,GO:0005388,GO:0008152,GO:001
6820","XP_002183209.1,EEC45427.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi210916,1059,1119.38,0,"gi|301108972|ref|XP_002903567
.1|calcium-transporting ATPase 1, endoplasmic reticulum-type, putative
[Phytophthora infestans T30-4] ","
GO:0006816,GO:0016021,GO:0016020,GO:0015662,GO:0006812,GO:0016787,GO:0000166,GO:
0005524,GO:0006754,GO:0003824,GO:0005388,GO:0008152,GO:0016820","XP_002903567.1,
EEY55343.1"
Stramenopiles-Blastocystis_hominis_tbBHL00001738_1,242,372.474,1.98E-
101,gi|300122119|emb|CBK22693.2|unnamed protein product [Blastocystis hominis],"
GO:0004553,GO:0016787,GO:0008152,GO:0005975,GO:0043169,GO:0016798,GO:0003824",CB
K22693.2
Stramenopiles-Aureococcus_anophagefferens_jgi66064,1631,251.521,7.64E-
64,gi|188501582|gb|ACD54708.1|beta-D-galactosidase-like protein [Adineta vaga],"
GO:0004565,GO:0004553,GO:0016787,GO:0008152,GO:0005975,GO:0043169,GO:0016798,GO:
0003824",ACD54708.1
Stramenopiles-
Phytophthora_sojae_jgi155253,1207,820.461,0,"gi|301123859|ref|XP_002909656.1|bet
a-galactosidase, putative [Phytophthora infestans T30-4] ","
GO:0004565,GO:0004553,GO:0016787,GO:0008152,GO:0005975,GO:0043169,GO:0016798,GO:
0003824","XP_002909656.1,EEY58470.1"
Stramenopiles-
Phytophthora_ramorum_jgi96749,1029,768.844,0,"gi|301123859|ref|XP_002909656.1|be
ta-galactosidase, putative [Phytophthora infestans T30-4] ","
GO:0004565,GO:0004553,GO:0016787,GO:0008152,GO:0005975,GO:0043169,GO:0016798,GO:
0003824","XP_002909656.1,EEY58470.1"
Stramenopiles-
Phytophthora_capsici_jgi112967,804,1087.79,0,"gi|301123859|ref|XP_002909656.1|be
ta-galactosidase, putative [Phytophthora infestans T30-4] ","
GO:0004565,GO:0004553,GO:0016787,GO:0008152,GO:0005975,GO:0043169,GO:0016798,GO:
0003824","XP_002909656.1,EEY58470.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219126351,492,1025.77,0,gi|219126351|ref
|XP_002183423.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0006004,GO:0005975,GO:0004560,GO:0043169,GO:0003824","XP_002183423.1,EEC45123
.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219126356,473,985.712,0,gi|219126356|ref
|XP_002183425.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0006004,GO:0005975,GO:0004560,GO:0043169,GO:0003824","XP_002183425.1,EEC45125
.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219126245,500,1036.94,0,gi|219126245|ref
|XP_002183372.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0006004,GO:0005975,GO:0004560,GO:0043169,GO:0003824","XP_002183372.1,EEC45072
.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi138084,417,332.798,4.98E-
89,gi|219126356|ref|XP_002183425.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0006004,GO:0005975,GO:0004560,GO:0043169,GO:0003824","XP_002183425.1,EEC45125
.1"
```

```
Stramenopiles-Aureococcus_anophagefferens_jgi1895,392,153.295,4.84E-
35,gi|183221259|ref|YP_001839255.1|putative cyclic-nucleotide-gated cation
channel [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Paris)'] ,"
GO:0005249,GO:0016021,GO:0016020,GO:0055085,GO:0006813,GO:0006811,GO:0005216,GO:
0006810","YP_001839255.1,YP_001962905.1,ABZ94327.1,ABZ97979.1"
Stramenopiles-Aureococcus_anophagefferens_jgi65551,1788,190.274,1.82E-
45,gi|299469723|emb|CBN76577.1|conserved unknown protein [Ectocarpus
siliculosus],"
GO:0005249,GO:0016021,GO:0016020,GO:0055085,GO:0006813,GO:0006811,GO:0005216,GO:
0006810",CBN76577.1
Stramenopiles-
Phytophthora_sojae_jgi142935,1986,860.136,0,gi|301111924|ref|XP_002905041.1|Volt
age-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0005249,GO:0016021,GO:0016020,GO:0055085,GO:0006813,GO:0006811,GO:0005216,GO:
0006810","XP_002905041.1,EEY53423.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223995263,702,1457.58,0,gi|223995263|ref|XP_
002287315.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0005249,GO:0016021,GO:0016020,GO:0055085,GO:0006813,GO:0006811,GO:0005216,GO:
0006810","XP_002287315.1,EED94758.1"
Stramenopiles-Aureococcus_anophagefferens_jgi61436,1310,275.789,2.59E-
71,gi|223995263|ref|XP_002287315.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,"
GO:0005249,GO:0016021,GO:0016020,GO:0055085,GO:0006813,GO:0006811,GO:0005216,GO:
0006810","XP_002287315.1,EED94758.1"
Stramenopiles-Phytophthora_capsici_jgi10033,1992,639.032,1.97E-
180,gi|301091504|ref|XP_002895936.1|Voltage-gated Ion Channel (VIC) Superfamily
[Phytophthora infestans T30-4] ,"
GO:0016021,GO:0016020,GO:0055085,GO:0006811,GO:0005216,GO:0006810","XP_002895936
.1,EEY54117.1"
Stramenopiles-Phytophthora_sojae_jgi129135,581,167.933,2.92E-
39,gi|113478270|ref|YP_724331.1|cyclic nucleotide-binding protein [Trichodesmium
erythraeum IMS101] ,"
GO:0005249,GO:0016021,GO:0016020,GO:0055085,GO:0006813,GO:0006811,GO:0005216,GO:
0006810","YP_724331.1,ABG53858.1"
Stramenopiles-
Phytophthora_capsici_jgi117481,747,1193.33,0,gi|301100019|ref|XP_002899100.1|Vol
tage-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0005249,GO:0016021,GO:0016020,GO:0055085,GO:0006813,GO:0006811,GO:0005216,GO:
0006810","XP_002899100.1,EEY62464.1"
Stramenopiles-Aureococcus_anophagefferens_jgi8067,142,141.739,2.11E-
32,gi|299117087|emb|CBN73858.1|Putative sodium calcium exchanger [Ectocarpus
siliculosus]," GO:0005509,GO:0016021,GO:0016020,GO:0055085",CBN73858.1
Stramenopiles-Aureococcus_anophagefferens_jgi19015,153,149.828,7.89E-
35,gi|300175109|emb|CBK20420.2|unnamed protein product [Blastocystis hominis],"
GO:0005509,GO:0016021,GO:0016020,GO:0055085",CBK20420.2
Stramenopiles-
Aureococcus_anophagefferens_jgi38329,1234,1708.35,0,gi|301101902|ref|XP_00290003
9.1|DNA-directed RNA polymerase II 135 kDa polypeptide [Phytophthora infestans
T30-4] ,"
GO:0016779,GO:0016740,GO:0003899,GO:0032549,GO:0006350,GO:0003677","XP_002900039
.1,EEY60666.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi185130,1221,1700.26,0,gi|219111265|ref|XP_002177384.
1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
```

```
GO:0016779,GO:0016740,GO:0003899,GO:0032549,GO:0006350,GO:0005634,GO:0003677","X
P_002177384.1,EEC51847.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219111265,1147,2385.91,0,gi|219111265|re
f|XP_002177384.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0016779,GO:0016740,GO:0003899,GO:0032549,GO:0006350,GO:0005634,GO:0003677","X
P_002177384.1,EEC51847.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224008096,1069,2237.22,0,"gi|224008096|ref|X
P_002293007.1|DNA directed RNA polymerase i, second largest subunit
[Thalassiosira pseudonana CCMP1335] ","
GO:0016779,GO:0016740,GO:0003899,GO:0006350,GO:0005634,GO:0003677","XP_002293007
.1,EED89468.1"
Stramenopiles-Phytophthora_brassicae_esgi144599670_2,234,437.573,5.34E-
121,"gi|301119239|ref|XP_002907347.1|DNA-directed RNA polymerase I subunit RPA2,
putative [Phytophthora infestans T30-4] ","
GO:0016779,GO:0016740,GO:0003899,GO:0032549,GO:0006350,GO:0005634,GO:0003677","X
P_002907347.1,EEY63911.1"
Stramenopiles-
Phytophthora_ramorum_jgi42703,1145,2283.06,0,"gi|301119239|ref|XP_002907347.1|DN
A-directed RNA polymerase I subunit RPA2, putative [Phytophthora infestans T30-
4] ","
GO:0016779,GO:0016740,GO:0003899,GO:0032549,GO:0006350,GO:0005634,GO:0003677","X
P_002907347.1,EEY63911.1"
Stramenopiles-
Phytophthora_sojae_jgi108266,1158,2298.09,0,"gi|301119239|ref|XP_002907347.1|DNA
-directed RNA polymerase I subunit RPA2, putative [Phytophthora infestans T30-4]
","
GO:0016779,GO:0016740,GO:0003899,GO:0032549,GO:0006350,GO:0005634,GO:0003677","X
P_002907347.1,EEY63911.1"
Stramenopiles-
Phytophthora_parasitica_esContig432_4,400,779.63,0,"gi|301119239|ref|XP_00290734
7.1|DNA-directed RNA polymerase I subunit RPA2, putative [Phytophthora infestans
T30-4] ","
GO:0016779,GO:0016740,GO:0003899,GO:0032549,GO:0006350,GO:0005634,GO:0003677","X
P_002907347.1,EEY63911.1"
Stramenopiles-
Phytophthora_capsici_jgi124178,1169,2313.11,0,"gi|301119239|ref|XP_002907347.1|D
NA-directed RNA polymerase I subunit RPA2, putative [Phytophthora infestans T30-
4] ","
GO:0016779,GO:0016740,GO:0003899,GO:0032549,GO:0006350,GO:0005634,GO:0003677","X
P_002907347.1,EEY63911.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi55255,1149,920.228,0,"gi|301119239|ref|XP_0029073
47.1|DNA-directed RNA polymerase I subunit RPA2, putative [Phytophthora
infestans T30-4] ","
GO:0016779,GO:0016740,GO:0003899,GO:0032549,GO:0006350,GO:0005634,GO:0003677","X
P_002907347.1,EEY63911.1"
Stramenopiles-Aureococcus_anophagefferens_jgi3378,258,160.614,1.54E-
37,gi|281207787|gb|EFA81967.1|protein kinase [Polysphondylium pallidum PN500],"
GO:0016301,GO:0005524,GO:0004672,GO:0000166,GO:0006468,GO:0004674",EFA81967.1
Stramenopiles-Aureococcus_anophagefferens_jgi3980,247,176.792,1.66E-
42,gi|302813132|ref|XP_002988252.1|hypothetical protein SELMODRAFT_10499
[Selaginella moellendorffii] ,"
```

```
GO:0005524,GO:0004672,GO:0000166,GO:0006468,GO:0004674","XP_002988252.1,EFJ10671
.1"
Stramenopiles-
Phytophthora_capsici_jgi121238,534,835.484,0,"gi|301096480|ref|XP_002897337.1|pr
otein kinase, putative [Phytophthora infestans T30-4] ","
GO:0016301,GO:0005524,GO:0004672,GO:0000166,GO:0006468,GO:0004674","XP_002897337
.1,EEY65273.1"
Stramenopiles-Phytophthora_capsici_jgi108580,194,361.303,2.63E-
98,gi|301102897|ref|XP_002900535.1|serine/threonine protein kinase [Phytophthora
infestans T30-4] ,"
GO:0016301,GO:0005524,GO:0004672,GO:0006468,GO:0004674","XP_002900535.1,EEY59850
.1"
Stramenopiles-Phytophthora_ramorum_jgi84879,303,457.218,9.72E-
127,gi|301102897|ref|XP_002900535.1|serine/threonine protein kinase
[Phytophthora infestans T30-4] ,"
GO:0016301,GO:0005524,GO:0004672,GO:0006468,GO:0004674","XP_002900535.1,EEY59850
.1"
Stramenopiles-Phytophthora_sojae_jgi145351,283,444.506,5.71E-
123,gi|301102897|ref|XP_002900535.1|serine/threonine protein kinase
[Phytophthora infestans T30-4] ,"
GO:0016301,GO:0005524,GO:0004672,GO:0006468,GO:0004674","XP_002900535.1,EEY59850
.1"
Stramenopiles-
Phytophthora_sojae_jgi131471,1989,1634.39,0,gi|301102899|ref|XP_002900536.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0005509,GO:0005515","XP_002900536.1,EEY59851.1"
Stramenopiles-
Phytophthora_capsici_jgi100297,622,1157.51,0,gi|301115766|ref|XP_002905612.1|ser
ine/threonine protein kinase [Phytophthora infestans T30-4] ,"
GO:0016301,GO:0005524,GO:0004672,GO:0000166,GO:0006468,GO:0004674","XP_002905612
.1,EEY68453.1"
Stramenopiles-
Phytophthora_sojae_jgi142455,711,1225.31,0,gi|301115766|ref|XP_002905612.1|serin
e/threonine protein kinase [Phytophthora infestans T30-4] ,"
GO:0016301,GO:0005524,GO:0004672,GO:0000166,GO:0006468,GO:0004674","XP_002905612
.1,EEY68453.1"
Stramenopiles-
Phytophthora_ramorum_jgi75533,687,1137.48,0,gi|301115766|ref|XP_002905612.1|seri
ne/threonine protein kinase [Phytophthora infestans T30-4] ,"
GO:0016301,GO:0005524,GO:0004672,GO:0000166,GO:0006468,GO:0004674","XP_002905612
.1,EEY68453.1"
Stramenopiles-Phytophthora_sojae_jgi109318,264,389.808,1.61E-
106,gi|301111286|ref|XP_002904722.1|Voltage-gated Ion Channel (VIC) Superfamily
[Phytophthora infestans T30-4] ,"
GO:0016021,GO:0016020,GO:0055085,GO:0006811,GO:0005216,GO:0006810","XP_002904722
.1,EEY53104.1"
Stramenopiles-
Phytophthora_ramorum_jgi74792,630,870.537,0,gi|301107526|ref|XP_002902845.1|Volt
age-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0005216,GO:0005245,GO:0005244,GO:0006816,GO:0016021,GO:0016020,GO:0006811,GO:
0006810,GO:0005262,GO:0055085,GO:0005891","XP_002902845.1,EEY56015.1"
Stramenopiles-
Phytophthora_sojae_jgi132791,1641,2760.33,0,gi|301107526|ref|XP_002902845.1|Volt
age-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
```

```
GO:0005216,GO:0005245,GO:0005244,GO:0006816,GO:0016021,GO:0016020,GO:0006811,GO:
0006810,GO:0005262,GO:0055085,GO:0005891","XP_002902845.1,EEY56015.1"
Stramenopiles-
Phytophthora_capsici_jgi36518,1640,2800,0,gi|301107526|ref|XP_002902845.1|Voltag
e-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0005216,GO:0005245,GO:0005244,GO:0006816,GO:0016021,GO:0016020,GO:0006811,GO:
0006810,GO:0005262,GO:0055085,GO:0005891","XP_002902845.1,EEY56015.1"
Stramenopiles-
Phytophthora_ramorum_jgi79674,489,917.531,0,gi|301107526|ref|XP_002902845.1|Volt
age-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0005216,GO:0005245,GO:0005244,GO:0006816,GO:0016021,GO:0016020,GO:0006811,GO:
0006810,GO:0005262,GO:0055085,GO:0005891","XP_002902845.1,EEY56015.1"
Stramenopiles-
Phytophthora_capsici_jgi121273,750,1307.35,0,gi|301118034|ref|XP_002906745.1|Vol
tage-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0005216,GO:0005245,GO:0005244,GO:0006816,GO:0016021,GO:0016020,GO:0006811,GO:
0006810,GO:0005262,GO:0055085,GO:0005891","XP_002906745.1,EEY66146.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223998927,1491,3060.4,0,gi|223998927|ref|XP_
002289136.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0005216,GO:0005245,GO:0005244,GO:0006816,GO:0016021,GO:0016020,GO:0006811,GO:
0006810,GO:0005262,GO:0055085,GO:0005891","XP_002289136.1,EED92673.1"
Stramenopiles-
Phytophthora_capsici_jgi117209,830,1161.36,0,"gi|301114771|ref|XP_002999155.1|gl
utamine-dependent NAD(+) synthetase, putative [Phytophthora infestans T30-4] ","
GO:0006807,GO:0005524,GO:0016810,GO:0009435,GO:0003952","XP_002999155.1,EEY69301
.1"
Stramenopiles-Phytophthora_parasitica_esgi222392215_5,267,414.846,4.00E-
114,gi|301111163|ref|XP_002904661.1|Major Facilitator Superfamily (MFS)
[Phytophthora infestans T30-4] ,"
GO:0022891,GO:0016021,GO:0016020,GO:0055085,GO:0006810,GO:0005215","XP_002904661
.1,EEY54030.1"
Stramenopiles-Phytophthora_brassicae_esContig1628_2,310,453.366,1.53E-
125,"gi|301111137|ref|XP_002904648.1|sugar transporter, putative [Phytophthora
infestans T30-4] ","
GO:0008643,GO:0022891,GO:0016021,GO:0016020,GO:0055085,GO:0006810,GO:0005215","X
P_002904648.1,EEY54017.1"
Stramenopiles-
Phytophthora_ramorum_jgi85416,496,870.152,0,"gi|301111135|ref|XP_002904647.1|sug
ar transporter, putative [Phytophthora infestans T30-4] ","
GO:0008643,GO:0022891,GO:0016021,GO:0016020,GO:0055085,GO:0006810,GO:0005215","X
P_002904647.1,EEY54016.1"
Stramenopiles-
Phytophthora_ramorum_jgi72326,512,888.641,0,"gi|301111135|ref|XP_002904647.1|sug
ar transporter, putative [Phytophthora infestans T30-4] ","
GO:0008643,GO:0022891,GO:0016021,GO:0016020,GO:0055085,GO:0006810,GO:0005215","X
P_002904647.1,EEY54016.1"
Stramenopiles-Phytophthora_sojae_jgi135955,206,329.717,1.03E-
88,"gi|301111135|ref|XP_002904647.1|sugar transporter, putative [Phytophthora
infestans T30-4] ","
GO:0008643,GO:0022891,GO:0016021,GO:0016020,GO:0055085,GO:0006810,GO:0005215","X
P_002904647.1,EEY54016.1"
Stramenopiles-
Phytophthora_capsici_jgi39178,508,874.774,0,"gi|301111135|ref|XP_002904647.1|sug
ar transporter, putative [Phytophthora infestans T30-4] ","
```

```
GO:0008643,GO:0022891,GO:0016021,GO:0016020,GO:0055085,GO:0006810,GO:0005215","X
P_002904647.1,EEY54016.1"
Stramenopiles-Phytophthora_capsici_jgi27709,206,360.147,8.37E-
98,"gi|301111135|ref|XP_002904647.1|sugar transporter, putative [Phytophthora
infestans T30-4] ","
GO:0008643,GO:0022891,GO:0016021,GO:0016020,GO:0055085,GO:0006810,GO:0005215","X
P_002904647.1,EEY54016.1"
Stramenopiles-
Phytophthora_sojae_jgi136061,1602,806.209,0,"gi|301111137|ref|XP_002904648.1|sug
ar transporter, putative [Phytophthora infestans T30-4] ","
GO:0008643,GO:0022891,GO:0016021,GO:0016020,GO:0055085,GO:0006810,GO:0005215","X
P_002904648.1,EEY54017.1"
Stramenopiles-
Phytophthora_ramorum_jgi85260,520,901.353,0,"gi|301111137|ref|XP_002904648.1|sug
ar transporter, putative [Phytophthora infestans T30-4] ","
GO:0008643,GO:0022891,GO:0016021,GO:0016020,GO:0055085,GO:0006810,GO:0005215","X
P_002904648.1,EEY54017.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219112765,258,527.324,6.07E-
148,gi|219112765|ref|XP_002178134.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0055114,GO:0005488,GO:0016491,GO:0008152,GO:0003824","XP_002178134.1,EEC50948
.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi141982,271,287.345,1.04E-
75,gi|219112765|ref|XP_002178134.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0055114,GO:0005488,GO:0016491,GO:0008152,GO:0003824","XP_002178134.1,EEC50948
.1"
Stramenopiles-Aureococcus_anophagefferens_jgi25442,264,247.669,1.05E-
63,gi|219112765|ref|XP_002178134.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0055114,GO:0005488,GO:0016491,GO:0008152,GO:0003824","XP_002178134.1,EEC50948
.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi224159,453,438.343,8.19E-
121,gi|224005116|ref|XP_002296209.1|aldo/keto reductase [Thalassiosira
pseudonana CCMP1335] ," GO:0055114,GO:0016491","XP_002296209.1,ACI64926.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224005116,359,751.125,0,gi|224005116|ref|XP_
002296209.1|aldo/keto reductase [Thalassiosira pseudonana CCMP1335] ,"
GO:0055114,GO:0016491","XP_002296209.1,ACI64926.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi208308,515,400.979,1.91E-
109,gi|219110757|ref|XP_002177130.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0055114,GO:0016491","XP_002177130.1,EEC51593.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219110757,455,957.592,0,gi|219110757|ref
|XP_002177130.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0055114,GO:0016491","XP_002177130.1,EEC51593.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224003433,373,780.4,0,gi|224003433|ref|XP_00
2291388.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0055114,GO:0016491","XP_002291388.1,EED91495.1"
Stramenopiles-Aureococcus_anophagefferens_jgi70538,734,348.591,1.54E-
93,gi|156358643|ref|XP_001624626.1|predicted protein [Nematostella vectensis] ,"
GO:0016788,GO:0016787,GO:0006397","XP_001624626.1,EDO32526.1"
```

```
Stramenopiles-Phytophthora_ramorum_jgi73888,298,555.444,2.54E-
156,"gi|301121318|ref|XP_002908386.1|protein phosphatase 2C, putative
[Phytophthora infestans T30-4] ", GO:0003824,"XP_002908386.1,EEY61469.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224010896,267,551.977,2.40E-
155,gi|224010896|ref|XP_002294405.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,"
GO:0046872,GO:0008287,GO:0016787,GO:0006470,GO:0003824,GO:0004722,GO:0004721","X
P_002294405.1,EED88239.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi213563,394,335.88,4.88E-
90,gi|219111241|ref|XP_002177372.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0046872,GO:0008287,GO:0016787,GO:0006470,GO:0003824,GO:0004722,GO:0004721","X
P_002177372.1,EEC51835.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi223994799,302,628.632,2.21E-
178,gi|223994799|ref|XP_002287083.1|hypothetical protein THAPSDRAFT_31637
[Thalassiosira pseudonana CCMP1335] ,"
GO:0046872,GO:0008287,GO:0016787,GO:0006470,GO:0003824,GO:0004722,GO:0004721","X
P_002287083.1,EED96724.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219126266,320,663.685,0,gi|219126266|ref
|XP_002183382.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0046872,GO:0008287,GO:0016787,GO:0006470,GO:0003824,GO:0004722,GO:0004721","X
P_002183382.1,EEC45082.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi151473,257,273.478,1.40E-
71,gi|219126266|ref|XP_002183382.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0046872,GO:0008287,GO:0016787,GO:0006470,GO:0003824,GO:0004722,GO:0004721","X
P_002183382.1,EEC45082.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224010523,273,567,6.70E-
160,gi|224010523|ref|XP_002294219.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,"
GO:0046872,GO:0008287,GO:0016787,GO:0006470,GO:0003824,GO:0004722,GO:0004721","X
P_002294219.1,EED88574.1"
Stramenopiles-Phytophthora_sojae_jgi140041,347,584.719,5.18E-
165,"gi|301105313|ref|XP_002901740.1|protein phosphatase 2C, putative
[Phytophthora infestans T30-4] ","
GO:0046872,GO:0008287,GO:0016787,GO:0006470,GO:0003824,GO:0004722,GO:0004721","X
P_002901740.1,EEY57130.1"
Stramenopiles-Phytophthora_ramorum_jgi74456,345,609.757,1.44E-
172,"gi|301105313|ref|XP_002901740.1|protein phosphatase 2C, putative
[Phytophthora infestans T30-4] ","
GO:0046872,GO:0008287,GO:0016787,GO:0006470,GO:0003824,GO:0004722,GO:0004721","X
P_002901740.1,EEY57130.1"
Stramenopiles-Phytophthora_capsici_jgi107781,300,555.058,3.02E-
156,"gi|301105313|ref|XP_002901740.1|protein phosphatase 2C, putative
[Phytophthora infestans T30-4] ","
GO:0046872,GO:0008287,GO:0016787,GO:0006470,GO:0003824,GO:0004722,GO:0004721","X
P_002901740.1,EEY57130.1"
Stramenopiles-
Phytophthora_sojae_jgi129945,1842,3495.67,0,gi|301114967|ref|XP_002999253.1|myos
in-like protein [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0000166,GO:0016459,GO:0003774","XP_002999253.1,EEY69399.1"
Stramenopiles-Aureococcus_anophagefferens_jgi26057,717,605.52,7.51E-
171,"gi|298710270|emb|CBJ31893.1|myosin I, high molecular weight-Acanthamoeba sp
```

```
[Ectocarpus siliculosus]","
GO:0005524,GO:0005856,GO:0000166,GO:0016459,GO:0003774",CBJ31893.1
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224015608,1245,2587.76,0,gi|224015608|ref|XP
_002297455.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0003723,GO:0006278,GO:0003964","XP_002297455.1,EED86272.1"
Stramenopiles-Aureococcus_anophagefferens_jgi70767,1641,206.068,2.91E-
50,gi|119486609|ref|ZP_01620659.1|hypothetical protein L8106_12700 [Lyngbya sp.
PCC 8106] ,,"ZP_01620659.1,EAW37358.1"
Stramenopiles-Aureococcus_anophagefferens_jgi67927,1406,184.111,1.01E-
43,gi|298705074|emb|CBJ28533.1|conserved unknown protein [Ectocarpus
siliculosus],,CBJ28533.1
Stramenopiles-Aureococcus_anophagefferens_jgi64385,3255,188.348,1.41E-
44,gi|298709658|emb|CBJ31466.1|conserved unknown protein [Ectocarpus
siliculosus],,CBJ31466.1
Stramenopiles-Phytophthora_capsici_jgi34886,1017,424.091,4.96E-
116,gi|301101421|ref|XP_002899799.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002899799.1,EEY60853.1"
Stramenopiles-Phytophthora_sojae_jgi143184,1135,405.986,1.40E-
110,gi|301101421|ref|XP_002899799.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002899799.1,EEY60853.1"
Stramenopiles-Phytophthora_capsici_jgi80704,271,422.55,2.19E-
116,gi|301116683|ref|XP_002906070.1|sporangia induced hypothetical protein
[Phytophthora infestans T30-4] ,,"XP_002906070.1,EEY67422.1"
Stramenopiles-Phytophthora_ramorum_jgi79127,410,493.041,2.46E-
137,gi|301116683|ref|XP_002906070.1|sporangia induced hypothetical protein
[Phytophthora infestans T30-4] ,,"XP_002906070.1,EEY67422.1"
Stramenopiles-Phytophthora_sojae_jgi137707,400,495.738,4.14E-
138,gi|301116683|ref|XP_002906070.1|sporangia induced hypothetical protein
[Phytophthora infestans T30-4] ,,"XP_002906070.1,EEY67422.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi238225,326,79.7221,5.21E-
13,gi|119945975|ref|YP_943655.1|hypothetical protein Ping_2315 [Psychromonas
ingrahamii 37] ,,"YP_943655.1,ABM04056.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219111439,282,588.571,2.47E-
166,gi|219111439|ref|XP_002177471.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002177471.1,EEC51934.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224012731,283,587.8,4.31E-
166,gi|224012731|ref|XP_002295018.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,"
GO:0055114,GO:0016705,GO:0005506,GO:0031418","XP_002295018.1,EED87798.1"
Stramenopiles-
Phytophthora_capsici_jgi22227,509,715.301,0,gi|301106386|ref|XP_002902276.1|lact
ation elevated protein 1 [Phytophthora infestans T30-4] ,
GO:0005524,"XP_002902276.1,EEY56948.1"
Stramenopiles-
Phytophthora_sojae_jgi141751,511,747.273,0,gi|301106386|ref|XP_002902276.1|lacta
tion elevated protein 1 [Phytophthora infestans T30-4] ,
GO:0005524,"XP_002902276.1,EEY56948.1"
Stramenopiles-
Phytophthora_sojae_jgi114824,382,660.603,0,gi|301107600|ref|XP_002902882.1|conse
rved hypothetical protein [Phytophthora infestans T30-4] ,
GO:0005524,"XP_002902882.1,EEY56052.1"
```

```
Stramenopiles-Phytophthora_ramorum_jgi48733,331,604.364,6.51E-
171,gi|301107600|ref|XP_002902882.1|conserved hypothetical protein [Phytophthora
infestans T30-4] , GO:0005524,"XP_002902882.1,EEY56052.1"
Stramenopiles-
Phytophthora_capsici_jgi31678,461,808.52,0,gi|301107600|ref|XP_002902882.1|conse
rved hypothetical protein [Phytophthora infestans T30-4] ,
GO:0005524,"XP_002902882.1,EEY56052.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219125067,378,778.089,0,gi|219125067|ref
|XP_002182810.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,
GO:0005524,"XP_002182810.1,EEC45546.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi149389,382,395.201,6.04E-
108,gi|219125067|ref|XP_002182810.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] , GO:0005524,"XP_002182810.1,EEC45546.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224000303,352,735.717,0,gi|224000303|ref|XP_
002289824.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,
GO:0005524,"XP_002289824.1,EED93361.1"
Stramenopiles-
Phytophthora_sojae_jgi137569,516,642.499,0,gi|301123229|ref|XP_002909341.1|Major
Facilitator Superfamily (MFS) [Phytophthora infestans T30-4] ,
GO:0055085,"XP_002909341.1,EEY58155.1"
Stramenopiles-
Phytophthora_ramorum_jgi96427,655,651.358,0,gi|301123229|ref|XP_002909341.1|Majo
r Facilitator Superfamily (MFS) [Phytophthora infestans T30-4] ,
GO:0055085,"XP_002909341.1,EEY58155.1"
Stramenopiles-
Phytophthora_sojae_jgi137568,531,664.07,0,gi|301123229|ref|XP_002909341.1|Major
Facilitator Superfamily (MFS) [Phytophthora infestans T30-4] ,
GO:0055085,"XP_002909341.1,EEY58155.1"
Stramenopiles-
Phytophthora_ramorum_jgi82740,518,798.89,0,gi|301123229|ref|XP_002909341.1|Major
Facilitator Superfamily (MFS) [Phytophthora infestans T30-4] ,
GO:0055085,"XP_002909341.1,EEY58155.1"
Stramenopiles-
Phytophthora_sojae_jgi137567,523,816.609,0,gi|301123229|ref|XP_002909341.1|Major
Facilitator Superfamily (MFS) [Phytophthora infestans T30-4] ,
GO:0055085,"XP_002909341.1,EEY58155.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223998945,546,1126.31,0,gi|223998945|ref|XP_
002289145.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002289145.1,EED92682.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219117005,543,1120.15,0,gi|219117005|ref
|XP_002179297.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002179297.1,EEC49120.1"
Stramenopiles-Aureococcus_anophagefferens_jgi65191,591,293.123,6.98E-
77,gi|298714004|emb|CBJ27236.1|conserved unknown protein [Ectocarpus
siliculosus],,CBJ27236.1
Stramenopiles-Phytophthora_ramorum_jgi79554,383,620.928,7.90E-
176,gi|301113894|ref|XP_002998717.1|Drug/Metabolite Transporter (DMT)
Superfamily [Phytophthora infestans T30-4] ,"
GO:0008643,GO:0016021,GO:0005351,GO:0000139","XP_002998717.1,EEY70070.1"
Stramenopiles-Phytophthora_sojae_jgi141239,312,526.168,1.59E-
147,gi|301113894|ref|XP_002998717.1|Drug/Metabolite Transporter (DMT)
```

```
Superfamily [Phytophthora infestans T30-4] ,"
GO:0008643,GO:0016021,GO:0005351,GO:0000139","XP_002998717.1,EEY70070.1"
Stramenopiles-Phytophthora_capsici_jgi105487,385,622.854,2.19E-
176,gi|301113894|ref|XP_002998717.1|Drug/Metabolite Transporter (DMT)
Superfamily [Phytophthora infestans T30-4] ,"
GO:0008643,GO:0016021,GO:0005351,GO:0000139","XP_002998717.1,EEY70070.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi233370,649,155.221,2.55E-
35,gi|284036172|ref|YP_003386102.1|glycoside hydrolase family 28 [Spirosoma
linguale DSM 74] ,"
GO:0016787,GO:0005975,GO:0004650","YP_003386102.1,ADB37303.1"
Stramenopiles-Aureococcus_anophagefferens_jgi65104,916,153.295,1.33E-
34,gi|225464581|ref|XP_002273669.1|PREDICTED: hypothetical protein [Vitis
vinifera],,XP_002273669.1
Stramenopiles-Fragilariopsis_cylindrus_jgi179730,443,199.134,9.48E-
49,gi|297844882|ref|XP_002890322.1|glycoside hydrolase family 28 protein
[Arabidopsis lyrata subsp. lyrata] ,"
GO:0016787,GO:0008152,GO:0007047,GO:0005975,GO:0016798,GO:0004650","XP_002890322
.1,EFH66581.1"
Stramenopiles-
Phytophthora_sojae_jgi135207,1852,3172.87,0,gi|301089940|ref|XP_002895229.1|myof
erlin-like protein [Phytophthora infestans T30-4] ,,"XP_002895229.1,EEY59281.1"
Stramenopiles-
Phytophthora_ramorum_jgi82063,1356,1588.16,0,gi|301106296|ref|XP_002902231.1|con
served hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0006355,GO:0003676,GO:0003677","XP_002902231.1,EEY56903.1"
Stramenopiles-
Phytophthora_sojae_jgi138371,1366,1704.49,0,gi|301106296|ref|XP_002902231.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0006355,GO:0003676,GO:0003677","XP_002902231.1,EEY56903.1"
Stramenopiles-
Phytophthora_capsici_jgi115881,869,1076.23,0,gi|301106296|ref|XP_002902231.1|con
served hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0006355,GO:0003676,GO:0003677","XP_002902231.1,EEY56903.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219119668,1240,2543.84,0,gi|219119668|re
f|XP_002180589.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0006355,GO:0003676,GO:0003677","XP_002180589.1,EEC47997.1"
Stramenopiles-Aureococcus_anophagefferens_jgi70872,3584,553.132,2.25E-
154,gi|193213949|ref|YP_001995148.1|Fibronectin type III domain protein
[Chloroherpeton thalassium ATCC 35110] ,,"YP_001995148.1,ACF12701.1"
Stramenopiles-Aureococcus_anophagefferens_jgi62682,2990,147.517,2.33E-
32,"gi|291237909|ref|XP_002738875.1|PREDICTED: predicted protein-like, partial
[Saccoglossus kowalevskii]",,XP_002738875.1
Stramenopiles-Aureococcus_anophagefferens_jgi71856,2102,142.124,6.79E-
31,gi|298710187|emb|CBJ26262.1|conserved unknown protein [Ectocarpus
siliculosus]," GO:0030154,GO:0016020",CBJ26262.1
Stramenopiles-
Phytophthora_sojae_jgi128893,1082,1765.36,0,gi|301116828|ref|XP_002906142.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0005525,GO:0003924","XP_002906142.1,EEY65543.1"
Stramenopiles-
Phytophthora_ramorum_jgi77912,1056,1697.56,0,gi|301116828|ref|XP_002906142.1|con
served hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0005525,GO:0003924","XP_002906142.1,EEY65543.1"
```

```
Stramenopiles-Aureococcus_anophagefferens_jgi70671,1116,266.929,1.02E-
68,gi|301116828|ref|XP_002906142.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ," GO:0005525,GO:0003924","XP_002906142.1,EEY65543.1"
Stramenopiles-Phytophthora_sojae_jgi156701,279,347.821,8.15E-
94,"gi|301114425|ref|XP_002998982.1|tRNA (guanine-N(7)-)-methyltransferase,
putative [Phytophthora infestans T30-4] ","
GO:0008168,GO:0006400,GO:0016740,GO:0008176","XP_002998982.1,EEY69128.1"
Stramenopiles-Phytophthora_ramorum_jgi95818,279,348.591,4.18E-
94,"gi|301114425|ref|XP_002998982.1|tRNA (guanine-N(7)-)-methyltransferase,
putative [Phytophthora infestans T30-4] ","
GO:0008168,GO:0006400,GO:0016740,GO:0008176","XP_002998982.1,EEY69128.1"
Stramenopiles-Phytophthora_capsici_jgi119087,267,350.903,7.28E-
95,"gi|301114425|ref|XP_002998982.1|tRNA (guanine-N(7)-)-methyltransferase,
putative [Phytophthora infestans T30-4] ","
GO:0008168,GO:0006400,GO:0016740,GO:0008176","XP_002998982.1,EEY69128.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi223999641,253,523.087,1.07E-
146,gi|223999641|ref|XP_002289493.1|methyltransferase [Thalassiosira pseudonana
CCMP1335] ,"
GO:0008168,GO:0006400,GO:0016740,GO:0008176","XP_002289493.1,EED93030.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219122557,245,505.753,1.76E-
141,gi|219122557|ref|XP_002181609.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0006400,GO:0008176","XP_002181609.1,EEC46823.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi151939,234,299.671,1.57E-
79,gi|219122557|ref|XP_002181609.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0006400,GO:0008176","XP_002181609.1,EEC46823.1"
Stramenopiles-
Phytophthora_ramorum_jgi78884,945,1616.67,0,gi|301105773|ref|XP_002901970.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002901970.1,EEY57360.1"
Stramenopiles-
Phytophthora_capsici_jgi33482,958,1638.24,0,gi|301105773|ref|XP_002901970.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002901970.1,EEY57360.1"
Stramenopiles-
Phytophthora_sojae_jgi130424,1892,1584.31,0,gi|301100744|ref|XP_002899461.1|WD
repeat protein 35 [Phytophthora infestans T30-4] ,
GO:0005488,"XP_002899461.1,EEY61821.1"
Stramenopiles-
Phytophthora_ramorum_jgi79800,1118,1644.4,0,gi|301091307|ref|XP_002895841.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002895841.1,EEY54604.1"
Stramenopiles-
Phytophthora_capsici_jgi20545,866,1369.76,0,gi|301091307|ref|XP_002895841.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002895841.1,EEY54604.1"
Stramenopiles-
Phytophthora_sojae_jgi141544,872,1542.71,0,gi|301102506|ref|XP_002900340.1|conse
rved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002900340.1,EEY60133.1"
Stramenopiles-
Phytophthora_ramorum_jgi84999,864,1540.78,0,gi|301102506|ref|XP_002900340.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002900340.1,EEY60133.1"
```

```
Stramenopiles-
Phytophthora_sojae_jgi132856,1035,807.749,0,gi|301107632|ref|XP_002902898.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002902898.1,EEY56068.1"
Stramenopiles-Phytophthora_capsici_jgi832,742,574.318,1.80E-
161,gi|301091307|ref|XP_002895841.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002895841.1,EEY54604.1"
Stramenopiles-
Phytophthora_sojae_jgi142078,1223,1059.67,0,gi|301093131|ref|XP_002997414.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0008270,GO:0005622","XP_002997414.1,EEY68722.1"
Stramenopiles-
Phytophthora_capsici_jgi92769,773,1446.41,0,"gi|301116894|ref|XP_002906175.1|Cul
lin family protein, putative [Phytophthora infestans T30-4] ","
GO:0031461,GO:0031625,GO:0006511","XP_002906175.1,EEY65576.1"
Stramenopiles-
Phytophthora_sojae_jgi109251,759,1387.09,0,"gi|301113194|ref|XP_002998367.1|Cull
in family protein, putative [Phytophthora infestans T30-4] ","
GO:0031461,GO:0006281,GO:0031625,GO:0004518,GO:0006511,GO:0005622","XP_002998367
.1,EEY69720.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi169868,763,1071.23,0,gi|219125259|ref|XP_002182902.1
|CULlin protein 3 [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0031461,GO:0031625,GO:0006511","XP_002182902.1,EEC45638.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219125259,762,1585.85,0,gi|219125259|ref
|XP_002182902.1|CULlin protein 3 [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0031461,GO:0031625,GO:0006511","XP_002182902.1,EEC45638.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224012136,742,1536.16,0,gi|224012136|ref|XP_
002294721.1|cullin family-like protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0031461,GO:0031625,GO:0006511","XP_002294721.1,EED88081.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi70316,751,825.469,0,gi|298709420|emb|CBJ49233.1|c
onserved unknown protein [Ectocarpus siliculosus],"
GO:0031461,GO:0031625,GO:0006511",CBJ49233.1
Stramenopiles-
Phytophthora_ramorum_jgi71375,756,1441.4,0,"gi|301112495|ref|XP_002998018.1|Cull
in family protein, putative [Phytophthora infestans T30-4] ","
GO:0031461,GO:0031625,GO:0006511","XP_002998018.1,EEY70364.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224002625,520,1084.32,0,gi|224002625|ref|XP_
002290984.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002290984.1,EED91091.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi209324,560,544.273,1.51E-
152,gi|219111615|ref|XP_002177559.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002177559.1,EEC50373.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219111615,475,992.645,0,gi|219111615|ref
|XP_002177559.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002177559.1,EEC50373.1"
Stramenopiles-
Phytophthora_sojae_jgi141649,480,860.907,0,gi|301108013|ref|XP_002903088.1|conse
rved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002903088.1,EEY55512.1"
```

```
Stramenopiles-
Phytophthora_ramorum_jgi75207,472,869.381,0,gi|301108013|ref|XP_002903088.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002903088.1,EEY55512.1"
Stramenopiles-
Phytophthora_capsici_jgi35854,470,853.973,0,gi|301108013|ref|XP_002903088.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002903088.1,EEY55512.1"
Stramenopiles-
Phytophthora_sojae_jgi141565,675,929.858,0,gi|301102536|ref|XP_002900355.1|conse
rved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002900355.1,EEY60148.1"
Stramenopiles-
Phytophthora_ramorum_jgi73103,537,805.053,0,gi|301114953|ref|XP_002999246.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002999246.1,EEY69392.1"
Stramenopiles-
Phytophthora_ramorum_jgi80015,459,848.581,0,gi|301095375|ref|XP_002896788.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002896788.1,EEY66723.1"
Stramenopiles-
Phytophthora_ramorum_jgi71107,512,1011.52,0,"gi|301118717|ref|XP_002907086.1|pro
pionyl-CoA carboxylase beta chain, mitochondrial precursor [Phytophthora
infestans T30-4] ","
GO:0016874,GO:0009317,GO:0006633,GO:0003989","XP_002907086.1,EEY63650.1"
Stramenopiles-
Phytophthora_capsici_jgi37913,543,1052.35,0,"gi|301118717|ref|XP_002907086.1|pro
pionyl-CoA carboxylase beta chain, mitochondrial precursor [Phytophthora
infestans T30-4] ","
GO:0016874,GO:0009317,GO:0006633,GO:0003989","XP_002907086.1,EEY63650.1"
Stramenopiles-
Phytophthora_sojae_jgi109606,511,1007.28,0,"gi|301118717|ref|XP_002907086.1|prop
ionyl-CoA carboxylase beta chain, mitochondrial precursor [Phytophthora
infestans T30-4] ","
GO:0016874,GO:0009317,GO:0006633,GO:0003989","XP_002907086.1,EEY63650.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219118993,581,1207.2,0,gi|219118993|ref|
XP_002180263.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,
GO:0016874,"XP_002180263.1,EEC48454.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi167310,576,867.455,0,gi|219118993|ref|XP_002180263.1
|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,
GO:0016874,"XP_002180263.1,EEC48454.1"
Stramenopiles-Blastocystis_hominis_tbBHL00001687_1,382,88.5817,1.37E-
15,gi|301105150|ref|XP_002901659.1|choline transporter-like protein
[Phytophthora infestans T30-4] ,"
GO:0016021,GO:0016020","XP_002901659.1,EEY58715.1"
Stramenopiles-
Phytophthora_ramorum_jgi76250,743,1273.84,0,gi|301105150|ref|XP_002901659.1|chol
ine transporter-like protein [Phytophthora infestans T30-4] ,"
GO:0016021,GO:0016020","XP_002901659.1,EEY58715.1"
Stramenopiles-
Phytophthora_sojae_jgi141480,748,1269.6,0,gi|301105150|ref|XP_002901659.1|cholin
e transporter-like protein [Phytophthora infestans T30-4] ,"
GO:0016021,GO:0016020","XP_002901659.1,EEY58715.1"
```

```
Stramenopiles-
Phytophthora_capsici_jgi20394,501,851.277,0,gi|301105150|ref|XP_002901659.1|chol
ine transporter-like protein [Phytophthora infestans T30-4] ,"
GO:0016021,GO:0016020","XP_002901659.1,EEY58715.1"
Stramenopiles-
Phytophthora_ramorum_jgi80623,792,1201.81,0,gi|301107706|ref|XP_002902935.1|chol
ine transporter-like protein [Phytophthora infestans T30-4] ,"
GO:0016021,GO:0016020","XP_002902935.1,EEY56105.1"
Stramenopiles-
Phytophthora_ramorum_jgi85821,814,1234.55,0,gi|301107706|ref|XP_002902935.1|chol
ine transporter-like protein [Phytophthora infestans T30-4] ,"
GO:0016021,GO:0016020","XP_002902935.1,EEY56105.1"
Stramenopiles-
Phytophthora_capsici_jgi120310,743,971.074,0,gi|301107706|ref|XP_002902935.1|cho
line transporter-like protein [Phytophthora infestans T30-4] ,"
GO:0016021,GO:0016020","XP_002902935.1,EEY56105.1"
Stramenopiles-
Phytophthora_sojae_jgi131651,820,1240.33,0,gi|301107706|ref|XP_002902935.1|choli
ne transporter-like protein [Phytophthora infestans T30-4] ,"
GO:0016021,GO:0016020","XP_002902935.1,EEY56105.1"
Stramenopiles-
Phytophthora_sojae_jgi134863,660,1093.95,0,gi|301117904|ref|XP_002906680.1|conse
rved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0032313,GO:0005622,GO:0005097","XP_002906680.1,EEY66081.1"
Stramenopiles-
Phytophthora_capsici_jgi20617,646,1056.97,0,gi|301117904|ref|XP_002906680.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0032313,GO:0005622,GO:0005097","XP_002906680.1,EEY66081.1"
Stramenopiles-
Phytophthora_ramorum_jgi84807,661,1077,0,gi|301117904|ref|XP_002906680.1|conserv
ed hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0032313,GO:0005622,GO:0005097","XP_002906680.1,EEY66081.1"
Stramenopiles-Phytophthora_sojae_jgi137108,324,508.834,3.22E-
142,gi|301101808|ref|XP_002899992.1|putative RabGAP/TBC domain-containing
protein [Phytophthora infestans T30-4] ,"
GO:0032313,GO:0005622,GO:0005097","XP_002899992.1,EEY60619.1"
Stramenopiles-
Phytophthora_ramorum_jgi96136,397,679.478,0,gi|301112821|ref|XP_002998181.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0032313,GO:0005622,GO:0005097","XP_002998181.1,EEY70527.1"
Stramenopiles-
Phytophthora_sojae_jgi138679,557,821.617,0,gi|301112821|ref|XP_002998181.1|conse
rved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0032313,GO:0005622,GO:0005097","XP_002998181.1,EEY70527.1"
Stramenopiles-Phytophthora_brassicae_esContig876_2,159,219.935,6.89E-
56,"gi|301104156|ref|XP_002901163.1|FKBP-type peptidyl-prolyl cis-trans
isomerase, putative [Phytophthora infestans T30-4] ","
GO:0003755,GO:0006457,GO:0016853","XP_002901163.1,XP_002907146.1,EEY59149.1,EEY6
3710.1"
Stramenopiles-Phytophthora_ramorum_jgi71104,109,215.312,1.66E-
54,"gi|301104156|ref|XP_002901163.1|FKBP-type peptidyl-prolyl cis-trans
isomerase, putative [Phytophthora infestans T30-4] ","
GO:0003755,GO:0006457,GO:0016853","XP_002901163.1,XP_002907146.1,EEY59149.1,EEY6
3710.1"
```

```
Stramenopiles-Phytophthora_sojae_jgi108555,109,217.624,2.95E-
55,"gi|301104156|ref|XP_002901163.1|FKBP-type peptidyl-prolyl cis-trans
isomerase, putative [Phytophthora infestans T30-4] ","
GO:0003755,GO:0006457,GO:0016853","XP_002901163.1,XP_002907146.1,EEY59149.1,EEY6
3710.1"
Stramenopiles-Phytophthora_capsici_jgi93234,109,221.09,2.83E-
56,"gi|301104156|ref|XP_002901163.1|FKBP-type peptidyl-prolyl cis-trans
isomerase, putative [Phytophthora infestans T30-4] ","
GO:0003755,GO:0006457,GO:0016853","XP_002901163.1,XP_002907146.1,EEY59149.1,EEY6
3710.1"
Stramenopiles-Phytophthora_sojae_jgi121523,316,569.696,1.39E-
160,"gi|301118336|ref|XP_002906896.1|peptidyl-prolyl cis-trans isomerase,
putative [Phytophthora infestans T30-4] ","
GO:0005488,GO:0003755,GO:0006457,GO:0016853","XP_002906896.1,EEY66297.1"
Stramenopiles-
Phytophthora_capsici_jgi121867,480,908.672,0,"gi|301118336|ref|XP_002906896.1|pe
ptidyl-prolyl cis-trans isomerase, putative [Phytophthora infestans T30-4] ","
GO:0005488,GO:0003755,GO:0006457,GO:0016853","XP_002906896.1,EEY66297.1"
Stramenopiles-
Phytophthora_brassicae_esContig1667_1,527,880.167,0,"gi|301118336|ref|XP_0029068
96.1|peptidyl-prolyl cis-trans isomerase, putative [Phytophthora infestans T30-
4] "," GO:0005488,GO:0003755,GO:0006457,GO:0016853","XP_002906896.1,EEY66297.1"
Stramenopiles-Phytophthora_ramorum_jgi84236,289,530.02,1.14E-
148,"gi|301118336|ref|XP_002906896.1|peptidyl-prolyl cis-trans isomerase,
putative [Phytophthora infestans T30-4] ","
GO:0005488,GO:0003755,GO:0006457,GO:0016853","XP_002906896.1,EEY66297.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223993147,483,996.112,0,gi|223993147|ref|XP_
002286257.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0005488,GO:0003755,GO:0006457,GO:0016853","XP_002286257.1,EED95898.1"
Stramenopiles-Aureococcus_anophagefferens_jgi36393,428,217.238,2.62E-
54,gi|167521233|ref|XP_001744955.1|hypothetical protein [Monosiga brevicollis
MX1] ," GO:0005488,GO:0006457","XP_001744955.1,EDQ90188.1"
Stramenopiles-
Phytophthora_sojae_jgi128805,880,1519.98,0,gi|301096035|ref|XP_002897116.1|phosp
holipase D; Pi-TM-PLD [Phytophthora infestans T30-4] ,"
GO:0008152,GO:0003824","XP_002897116.1,EEY65487.1"
Stramenopiles-
Phytophthora_ramorum_jgi81941,871,1533.08,0,gi|301096035|ref|XP_002897116.1|phos
pholipase D; Pi-TM-PLD [Phytophthora infestans T30-4] ,"
GO:0008152,GO:0003824","XP_002897116.1,EEY65487.1"
Stramenopiles-Phytophthora_ramorum_jgi83803,512,618.616,5.77E-
175,gi|301102536|ref|XP_002900355.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002900355.1,EEY60148.1"
Stramenopiles-Phytophthora_ramorum_jgi84987,315,393.275,1.89E-
107,gi|301102536|ref|XP_002900355.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002900355.1,EEY60148.1"
Stramenopiles-
Phytophthora_sojae_jgi129939,553,853.203,0,gi|301114953|ref|XP_002999246.1|conse
rved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002999246.1,EEY69392.1"
Stramenopiles-
Phytophthora_capsici_jgi23378,570,905.205,0,gi|301114953|ref|XP_002999246.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002999246.1,EEY69392.1"
```

```
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219128655,560,1139.79,0,gi|219128655|ref
|XP_002184523.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002184523.1,EEC43922.1"
Stramenopiles-Phytophthora_brassicae_esContig1574_3,224,337.035,8.98E-
91,gi|301103137|ref|XP_002900655.1|caltractin [Phytophthora infestans T30-4] ,"
GO:0003676,GO:0005524,GO:0005509,GO:0008026","XP_002900655.1,EEY59970.1"
Stramenopiles-Phytophthora_sojae_jgi108216,173,333.569,4.66E-
90,gi|301103137|ref|XP_002900655.1|caltractin [Phytophthora infestans T30-4] ,"
GO:0003676,GO:0005524,GO:0005509,GO:0008026","XP_002900655.1,EEY59970.1"
Stramenopiles-Phytophthora_parasitica_esContig32_3,378,343.199,2.73E-
92,gi|301103137|ref|XP_002900655.1|caltractin [Phytophthora infestans T30-4] ,"
GO:0003676,GO:0005524,GO:0005509,GO:0008026","XP_002900655.1,EEY59970.1"
Stramenopiles-Aureococcus_anophagefferens_jgi34189,198,96.6709,1.48E-
18,gi|302850021|ref|XP_002956539.1|centrin [Volvox carteri f. nagariensis] ,"
GO:0003676,GO:0005524,GO:0005509,GO:0008026","XP_002956539.1,EFJ42476.1"
Stramenopiles-Aureococcus_anophagefferens_jgi36419,150,295.049,1.63E-
78,gi|189081811|sp|A8CEP3.1|CALM_SACJARecName: Full=Calmodulin; Short=CaM ,
GO:0005509,"A8CEP3.1,BAF80878.1,CBJ33511.1"
Stramenopiles-Aureococcus_anophagefferens_jgi58710,150,295.049,1.63E-
78,gi|189081811|sp|A8CEP3.1|CALM_SACJARecName: Full=Calmodulin; Short=CaM ,
GO:0005509,"A8CEP3.1,BAF80878.1,CBJ33511.1"
Stramenopiles-Sargassum_binderi_esContig81_2,643,308.916,1.10E-
81,gi|189081811|sp|A8CEP3.1|CALM_SACJARecName: Full=Calmodulin; Short=CaM ,
GO:0005509,"A8CEP3.1,BAF80878.1,CBJ33511.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224004208,149,295.434,1.13E-
78,gi|224004208|ref|XP_002295755.1|calmodulin [Thalassiosira pseudonana
CCMP1335] , GO:0005509,"XP_002295755.1,ACI64472.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi166325,150,213.001,8.15E-
54,gi|124809127|ref|XP_001348497.1|calmodulin [Plasmodium falciparum 3D7] ,
GO:0005509,"XP_001348497.1,P24044.4,P62203.2,AAN36936.1,AAA29510.1,AAA29508.1"
Stramenopiles-Phytophthora_capsici_jgi104184,302,556.214,1.42E-
156,gi|301100728|ref|XP_002899453.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,"
GO:0035091,GO:0007154,GO:0005515","XP_002899453.1,EEY61813.1"
Stramenopiles-Aureococcus_anophagefferens_jgi64548,1087,154.836,4.92E-
35,gi|298713385|emb|CBJ33597.1|conserved unknown protein [Ectocarpus
siliculosus],,CBJ33597.1
Stramenopiles-
Fragilariopsis_cylindrus_jgi156478,696,697.967,0,gi|224002190|ref|XP_002290767.1
|structure specific recognition protein 1 [Thalassiosira pseudonana CCMP1335] ,"
GO:0005634,GO:0003677","XP_002290767.1,EED92519.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224002190,765,1568.52,0,gi|224002190|ref|XP_
002290767.1|structure specific recognition protein 1 [Thalassiosira pseudonana
CCMP1335] ," GO:0005634,GO:0003677","XP_002290767.1,EED92519.1"
Stramenopiles-Phytophthora_brassicae_esContig757_3,296,356.295,2.13E-
96,gi|301097589|ref|XP_002897889.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ," GO:0005634,GO:0003677","XP_002897889.1,EEY64689.1"
Stramenopiles-Phytophthora_ramorum_jgi73033,212,358.992,2.02E-
97,gi|301097589|ref|XP_002897889.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ," GO:0005634,GO:0003677","XP_002897889.1,EEY64689.1"
Stramenopiles-Phytophthora_capsici_jgi110007,214,353.984,6.65E-
96,gi|301097589|ref|XP_002897889.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ," GO:0005634,GO:0003677","XP_002897889.1,EEY64689.1"
```

```
Stramenopiles-Phytophthora_parasitica_esContig356_3,269,379.793,1.44E-
103,gi|301097589|ref|XP_002897889.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ," GO:0005634,GO:0003677","XP_002897889.1,EEY64689.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi145199,82,137.502,3.86E-
31,gi|219119941|ref|XP_002180721.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0005634,GO:0003677","XP_002180721.1,EEC48129.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219119941,90,184.882,2.06E-
45,gi|219119941|ref|XP_002180721.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0005634,GO:0003677","XP_002180721.1,EEC48129.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi223994915,85,175.637,1.43E-
42,gi|223994915|ref|XP_002287141.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ," GO:0005634,GO:0003677","XP_002287141.1,EED94584.1"
Stramenopiles-Blastocystis_hominis_tbBHL00002718_3,234,186.808,1.37E-
45,gi|300122950|emb|CBK23957.2|unnamed protein product [Blastocystis hominis],"
GO:0005634,GO:0003677",CBK23957.2
Stramenopiles-
Phytophthora_ramorum_jgi73027,1726,2526.51,0,gi|301097569|ref|XP_002897879.1|Vol
tage-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0005216,GO:0005245,GO:0005244,GO:0006816,GO:0016021,GO:0016020,GO:0006811,GO:
0006810,GO:0005262,GO:0055085,GO:0005891","XP_002897879.1,EEY64679.1"
Stramenopiles-
Phytophthora_capsici_jgi119794,1674,2487.22,0,gi|301097569|ref|XP_002897879.1|Vo
ltage-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0005216,GO:0005245,GO:0005244,GO:0006816,GO:0016021,GO:0016020,GO:0006811,GO:
0006810,GO:0005262,GO:0055085,GO:0005891","XP_002897879.1,EEY64679.1"
Stramenopiles-
Phytophthora_sojae_jgi128674,1914,2756.09,0,gi|301097569|ref|XP_002897879.1|Volt
age-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0005216,GO:0005245,GO:0005244,GO:0006816,GO:0016021,GO:0016020,GO:0006811,GO:
0006810,GO:0005262,GO:0055085,GO:0005891","XP_002897879.1,EEY64679.1"
Stramenopiles-
Phytophthora_capsici_jgi38040,455,669.848,0,gi|301108179|ref|XP_002903171.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002903171.1,EEY55595.1"
Stramenopiles-Phytophthora_ramorum_jgi75839,436,633.254,1.55E-
179,gi|301108179|ref|XP_002903171.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002903171.1,EEY55595.1"
Stramenopiles-
Phytophthora_sojae_jgi141452,905,661.374,0,gi|301108179|ref|XP_002903171.1|conse
rved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002903171.1,EEY55595.1"
Stramenopiles-
Phytophthora_capsici_jgi20194,583,900.582,0,gi|301102536|ref|XP_002900355.1|cons
erved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002900355.1,EEY60148.1"
Stramenopiles-Phytophthora_parasitica_esgi68419650_1,239,78.9518,4.98E-
13,gi|260809656|ref|XP_002599621.1|hypothetical protein BRAFLDRAFT_77720
[Branchiostoma floridae] , GO:0005529,"XP_002599621.1,EEN55633.1"
Stramenopiles-Aureococcus_anophagefferens_jgi62439,2280,211.075,1.50E-
51,gi|260809656|ref|XP_002599621.1|hypothetical protein BRAFLDRAFT_77720
[Branchiostoma floridae] , GO:0005529,"XP_002599621.1,EEN55633.1"
Stramenopiles-Aureococcus_anophagefferens_jgi63985,4513,134.035,4.10E-
28,gi|298709582|emb|CBJ31408.1|expressed unknown protein [Ectocarpus
siliculosus],,CBJ31408.1
```

```
Stramenopiles-Phytophthora_sojae_jgi131954,466,257.299,2.91E-
66,"gi|157106769|ref|XP_001649474.1|ankyrin 2,3/unc44 [Aedes aegypti]
",,"XP_001649474.1,EAT33004.1"
Stramenopiles-Phytophthora_sojae_jgi131955,379,226.868,2.96E-
57,"gi|157106769|ref|XP_001649474.1|ankyrin 2,3/unc44 [Aedes aegypti]
",,"XP_001649474.1,EAT33004.1"
Stramenopiles-
Phytophthora_sojae_jgi131195,2823,1197.96,0,"gi|115709795|ref|XP_794477.2|PREDIC
TED: similar to ankyrin 2,3/unc44 [Strongylocentrotus purpuratus]
",,"XP_794477.2,XP_001195551.1"
Stramenopiles-Aureococcus_anophagefferens_jgi13311,173,104.76,3.24E-
21,gi|229582572|ref|YP_002840971.1|Ankyrin [Sulfolobus islandicus Y.N.15.51]
,,"YP_002840971.1,ACP49049.1"
Stramenopiles-Aureococcus_anophagefferens_jgi71275,1409,180.259,1.67E-
42,gi|299116665|emb|CBN74810.1|conserved unknown protein [Ectocarpus
siliculosus],,CBN74810.1
Stramenopiles-
Fragilariopsis_cylindrus_jgi206915,452,639.417,0,gi|219114433|ref|XP_002176387.1
|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002176387.1,EEC42623.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219114433,444,913.294,0,gi|219114433|ref
|XP_002176387.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002176387.1,EEC42623.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223994641,399,819.305,0,gi|223994641|ref|XP_
002287004.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002287004.1,EED96645.1"
Stramenopiles-Aureococcus_anophagefferens_jgi70027,479,481.485,9.07E-
134,gi|219114433|ref|XP_002176387.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002176387.1,EEC42623.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224010002,420,871.307,0,gi|224010002|ref|XP_
002293959.1|hypothetical protein THAPSDRAFT_264191 [Thalassiosira pseudonana
CCMP1335] ,,"XP_002293959.1,EED88968.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219119654,363,749.199,0,gi|219119654|ref
|XP_002180582.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002180582.1,EEC47990.1"
Stramenopiles-
Phytophthora_sojae_jgi129188,542,857.825,0,gi|301112192|ref|XP_002905175.1|cell
division cycle protein 20 [Phytophthora infestans T30-4] ,
GO:0051301,"XP_002905175.1,EEY53557.1"
Stramenopiles-
Phytophthora_capsici_jgi35809,537,808.135,0,gi|301112192|ref|XP_002905175.1|cell
division cycle protein 20 [Phytophthora infestans T30-4] ,
GO:0051301,"XP_002905175.1,EEY53557.1"
Stramenopiles-
Phytophthora_ramorum_jgi77091,538,827.395,0,gi|301112192|ref|XP_002905175.1|cell
division cycle protein 20 [Phytophthora infestans T30-4] ,
GO:0051301,"XP_002905175.1,EEY53557.1"
Stramenopiles-
Phytophthora_sojae_jgi108837,500,683.715,0,gi|301119993|ref|XP_002907724.1|WD
repeat-containing protein srw1 [Phytophthora infestans T30-4]
,,"XP_002907724.1,EEY64288.1"
```

```
Stramenopiles-Fragilariopsis_cylindrus_jgi150968,287,213.386,2.44E-
53,gi|219111927|ref|XP_002177715.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0003676,GO:0000166","XP_002177715.1,EEC50529.1"
Stramenopiles-Aureococcus_anophagefferens_jgi7168,131,120.553,5.98E-
26,gi|198424334|ref|XP_002120556.1|PREDICTED: similar to leucine rich repeat
containing 51 isoform 2 [Ciona intestinalis],,XP_002120556.1
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223996579,970,2003.02,0,gi|223996579|ref|XP_
002287963.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0016998,GO:0005634,GO:0003677","XP_002287963.1,EED95406.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219110082,869,1809.27,0,gi|219110082|ref
|XP_002176793.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]
,,"XP_002176793.1,EEC51256.1"
Stramenopiles-
Phytophthora_ramorum_jgi72621,1389,2325.05,0,"gi|301122337|ref|XP_002908895.1|ry
anodine-inositol 1,4,5-triphosphate receptor Ca2 channel (RIR-CaC) family
protein [Phytophthora infestans T30-4] ", GO:0004872,"XP_002908895.1,EEY57709.1"
Stramenopiles-
Phytophthora_sojae_jgi130115,1402,2382.83,0,"gi|301122337|ref|XP_002908895.1|rya
nodine-inositol 1,4,5-triphosphate receptor Ca2 channel (RIR-CaC) family protein
[Phytophthora infestans T30-4] ", GO:0004872,"XP_002908895.1,EEY57709.1"
Stramenopiles-Aureococcus_anophagefferens_jgi21207,236,112.849,3.18E-
23,"gi|24644950|ref|NP_649757.1|CG2767, isoform A [Drosophila melanogaster] ",
GO:0055114,"NP_649757.1,AAF54175.1,AAM50797.1,ACL84508.1,ACL89445.1"
Stramenopiles-Aureococcus_anophagefferens_jgi39075,563,424.476,1.76E-
116,gi|301105663|ref|XP_002901915.1|AP-1 complex subunit gamma-1 [Phytophthora
infestans T30-4] ,"
GO:0015031,GO:0016020,GO:0008565,GO:0030131,GO:0005794,GO:0006886,GO:0005515,GO:
0030117,GO:0016192,GO:0044431,GO:0005488","XP_002901915.1,EEY57305.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi38872,832,764.607,0,gi|301105663|ref|XP_002901915
.1|AP-1 complex subunit gamma-1 [Phytophthora infestans T30-4] ,"
GO:0015031,GO:0016020,GO:0008565,GO:0030131,GO:0005794,GO:0006886,GO:0005515,GO:
0030117,GO:0016192,GO:0044431,GO:0005488","XP_002901915.1,EEY57305.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi225310,925,1145.57,0,gi|219121222|ref|XP_002185839.1
|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0015031,GO:0016020,GO:0008565,GO:0030131,GO:0005794,GO:0006886,GO:0005515,GO:
0030117,GO:0016192,GO:0044431,GO:0005488","XP_002185839.1,ACI65309.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219121222,939,1946.01,0,gi|219121222|ref
|XP_002185839.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0015031,GO:0016020,GO:0008565,GO:0030131,GO:0005794,GO:0006886,GO:0005515,GO:
0030117,GO:0016192,GO:0044431,GO:0005488","XP_002185839.1,ACI65309.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224009504,871,1798.87,0,gi|224009504|ref|XP_
002293710.1|gamma subunit of tetrameric clathrin adaptor complex AP2
[Thalassiosira pseudonana CCMP1335] ,"
GO:0015031,GO:0016020,GO:0008565,GO:0030131,GO:0005794,GO:0006886,GO:0005515,GO:
0030117,GO:0016192,GO:0044431,GO:0005488","XP_002293710.1,EED88719.1"
Stramenopiles-
Phytophthora_ramorum_jgi47796,841,1486.09,0,gi|301105663|ref|XP_002901915.1|AP-1
complex subunit gamma-1 [Phytophthora infestans T30-4] ,"
```

```
GO:0015031,GO:0016020,GO:0008565,GO:0030131,GO:0005794,GO:0006886,GO:0005515,GO:
0030117,GO:0016192,GO:0044431,GO:0005488","XP_002901915.1,EEY57305.1"
Stramenopiles-
Phytophthora_sojae_jgi133449,823,1431.39,0,gi|301105663|ref|XP_002901915.1|AP-1
complex subunit gamma-1 [Phytophthora infestans T30-4] ,"
GO:0015031,GO:0016020,GO:0008565,GO:0030131,GO:0005794,GO:0006886,GO:0005515,GO:
0030117,GO:0016192,GO:0044431,GO:0005488","XP_002901915.1,EEY57305.1"
Stramenopiles-
Phytophthora_capsici_jgi72092,852,1526.92,0,gi|301105663|ref|XP_002901915.1|AP-1
complex subunit gamma-1 [Phytophthora infestans T30-4] ,"
GO:0015031,GO:0016020,GO:0008565,GO:0030131,GO:0005794,GO:0006886,GO:0005515,GO:
0030117,GO:0016192,GO:0044431,GO:0005488","XP_002901915.1,EEY57305.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi223998812,223,456.062,1.37E-
126,gi|223998812|ref|XP_002289079.1|inositol monophosphatase [Thalassiosira
pseudonana CCMP1335] , GO:0004437,"XP_002289079.1,EED94515.1"
Stramenopiles-Aureococcus_anophagefferens_jgi71581,1017,323.168,1.21E-
85,gi|224011679|ref|XP_002295614.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,"
GO:0005488,GO:0016491,GO:0008152,GO:0003824","XP_002295614.1,ACI64331.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi232331,408,399.823,2.93E-
109,gi|219113331|ref|XP_002186249.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0005488,GO:0016491,GO:0008152,GO:0003824","XP_002186249.1,ACI65719.1"
Stramenopiles-Aureococcus_anophagefferens_jgi28648,506,431.024,1.52E-
118,gi|300120331|emb|CBK19885.2|unnamed protein product [Blastocystis hominis],"
GO:0004553,GO:0004563,GO:0005975,GO:0043169,GO:0003824",CBK19885.2
Stramenopiles-
Phytophthora_ramorum_jgi46952,1905,2978.73,0,gi|301117022|ref|XP_002906239.1|con
served hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0016887,GO:0005524,GO:0000166,GO:0017111","XP_002906239.1,EEY65640.1"
Stramenopiles-
Phytophthora_sojae_jgi115586,1830,2916.33,0,gi|301117022|ref|XP_002906239.1|cons
erved hypothetical protein [Phytophthora infestans T30-4] ,"
GO:0016887,GO:0005524,GO:0000166,GO:0017111","XP_002906239.1,EEY65640.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi206499,128,216.853,5.43E-
55,gi|219125612|ref|XP_002183070.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0046872,GO:0008270,GO:0005515","XP_002183070.1,EEC45288.1"
Stramenopiles-Sargassum_binderi_esgi120455146_1,125,112.079,2.20E-
23,gi|298714696|emb|CBJ27621.1|conserved unknown protein [Ectocarpus
siliculosus]," GO:0046872,GO:0008270,GO:0005515",CBJ27621.1
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi224002296,122,255.758,1.06E-
66,gi|224002296|ref|XP_002290820.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ," GO:0046872,GO:0008270,GO:0005515","XP_002290820.1,EED92572.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219125612,134,279.641,6.44E-
74,gi|219125612|ref|XP_002183070.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ," GO:0046872,GO:0008270,GO:0005515","XP_002183070.1,EEC45288.1"
Stramenopiles-
Phytophthora_sojae_jgi108201,697,1359.74,0,gi|301121282|ref|XP_002908368.1|trans
ketolase [Phytophthora infestans T30-4] ,"
GO:0004802,GO:0008152,GO:0003824","XP_002908368.1,EEY61451.1"
Stramenopiles-
Phytophthora_ramorum_jgi71153,696,1314.67,0,gi|301121282|ref|XP_002908368.1|tran
sketolase [Phytophthora infestans T30-4] ,"
GO:0004802,GO:0008152,GO:0003824","XP_002908368.1,EEY61451.1"
```

```
Stramenopiles-Phytophthora_capsici_jgi99199,696,1363.21,0,gi|301121282|ref|XP_002908368.1|transketolase [Phytophthora infestans T30-4] ," GO:0004802,GO:0008152,GO:0003824","XP_002908368.1,EEY61451.1"
Stramenopiles-Phytophthora_parasitica_esContig825_2,786,721.079,0,gi|301121282|ref|XP_002908368.1|transketolase [Phytophthora infestans T30-4] ," GO:0004802,GO:0008152,GO:0003824","XP_002908368.1,EEY61451.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi206407,694,863.603,0,gi|219124318|ref|XP_002182454.1|transketolase [Phaeodactylum tricornutum CCAP 1055/1] ," GO:0004802,GO:0008152,GO:0003824","XP_002182454.1,EEC46355.1"
Stramenopiles-Phaeodactylum_tricornutum_CCAP_1055/1_gi219124318,684,1427.54,0,gi|219124318|ref|XP_002182454.1|transketolase [Phaeodactylum tricornutum CCAP 1055/1] ," GO:0004802,GO:0008152,GO:0003824","XP_002182454.1,EEC46355.1"
Stramenopiles-Thalassiosira_pseudonana_CCMP1335_gi223993045,719,1500.34,0,gi|223993045|ref|XP_002286206.1|transketolase [Thalassiosira pseudonana CCMP1335] ," GO:0004802,GO:0016740,GO:0008152,GO:0003824","XP_002286206.1,EED95847.1"
Stramenopiles-Sargassum_binderi_esContig137_2,298,407.527,9.31E-112,gi|299471379|emb|CBN79333.1|conserved unknown protein [Ectocarpus siliculosus]," GO:0004802,GO:0008152,GO:0003824",CBN79333.1
Stramenopiles-Fragilariopsis_cylindrus_jgi259247,573,687.182,0,gi|301106605|ref|XP_002902385.1|regulator of chromosome condensation (RCC1)-like protein [Phytophthora infestans T30-4] , GO:0005515,"XP_002902385.1,EEY56311.1"
Stramenopiles-Phaeodactylum_tricornutum_CCAP_1055/1_gi219125443,341,693.73,0,gi|219125443|ref|XP_002182991.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,,"XP_002182991.1,EEC45727.1"
Stramenopiles-Phytophthora_capsici_jgi34059,546,1102.43,0,gi|301106605|ref|XP_002902385.1|regulator of chromosome condensation (RCC1)-like protein [Phytophthora infestans T30-4] , GO:0005515,"XP_002902385.1,EEY56311.1"
Stramenopiles-Phytophthora_sojae_jgi127329,546,1097.42,0,gi|301106605|ref|XP_002902385.1|regulator of chromosome condensation (RCC1)-like protein [Phytophthora infestans T30-4] , GO:0005515,"XP_002902385.1,EEY56311.1"
Stramenopiles-Phytophthora_ramorum_jgi84750,546,1091.26,0,gi|301106605|ref|XP_002902385.1|regulator of chromosome condensation (RCC1)-like protein [Phytophthora infestans T30-4] , GO:0005515,"XP_002902385.1,EEY56311.1"
Stramenopiles-Phytophthora_capsici_jgi37534,1098,1031.17,0,gi|301101976|ref|XP_002900076.1|regulator of chromosome condensation (RCC1)-like protein [Phytophthora infestans T30-4] ,,"XP_002900076.1,EEY60703.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi179159,412,464.922,8.46E-129,gi|219129772|ref|XP_002185055.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,,"XP_002185055.1,EEC43502.1"
Stramenopiles-Phytophthora_ramorum_jgi84680,1713,2861.63,0,gi|301109150|ref|XP_002903656.1|myosin-like protein [Phytophthora infestans T30-4] ," GO:0035091,GO:0005524,GO:0000166,GO:0007154,GO:0016459,GO:0005515,GO:0003774","XP_002903656.1,EEY55432.1"
```

```
Stramenopiles-
Phytophthora_capsici_jgi93537,840,1480.31,0,gi|301109150|ref|XP_002903656.1|myos
in-like protein [Phytophthora infestans T30-4] ,"
GO:0035091,GO:0005524,GO:0000166,GO:0007154,GO:0016459,GO:0005515,GO:0003774","X
P_002903656.1,EEY55432.1"
Stramenopiles-
Phytophthora_sojae_jgi108230,4439,8892.32,0,gi|301102724|ref|XP_002900449.1|spor
angia induced dynein heavy chain [Phytophthora infestans T30-4] ,"
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018","X
P_002900449.1,EEY60242.1"
Stramenopiles-
Phytophthora_capsici_jgi8,4282,8490.55,0,gi|301102724|ref|XP_002900449.1|sporang
ia induced dynein heavy chain [Phytophthora infestans T30-4] ,"
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018","X
P_002900449.1,EEY60242.1"
Stramenopiles-
Phytophthora_ramorum_jgi95148,4253,6297.23,0,gi|301102724|ref|XP_002900449.1|spo
rangia induced dynein heavy chain [Phytophthora infestans T30-4] ,"
GO:0030286,GO:0016887,GO:0005524,GO:0000166,GO:0003777,GO:0017111,GO:0007018","X
P_002900449.1,EEY60242.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi267868,330,489.96,1.54E-
136,gi|224014228|ref|XP_002296777.1|metalloprotease [Thalassiosira pseudonana
CCMP1335] ,"
GO:0006508,GO:0008237,GO:0008233,GO:0004222","XP_002296777.1,EED86978.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224014228,654,1366.67,0,gi|224014228|ref|XP_
002296777.1|metalloprotease [Thalassiosira pseudonana CCMP1335] ,"
GO:0006508,GO:0008237,GO:0008233,GO:0004222","XP_002296777.1,EED86978.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219128716,744,1562.36,0,gi|219128716|ref
|XP_002184552.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0006508,GO:0008237,GO:0004222","XP_002184552.1,EEC43951.1"
Stramenopiles-
Phytophthora_capsici_jgi56,2259,2452.94,0,gi|301105359|ref|XP_002901763.1|pre-
mRNA-processing-splicing factor 8 [Phytophthora infestans T30-4] ,"
GO:0005681,GO:0000398","XP_002901763.1,EEY57153.1"
Stramenopiles-
Phytophthora_sojae_jgi109256,2451,4653.2,0,gi|301105359|ref|XP_002901763.1|pre-
mRNA-processing-splicing factor 8 [Phytophthora infestans T30-4] ,"
GO:0005681,GO:0000398","XP_002901763.1,EEY57153.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi168318,2260,4126.63,0,gi|219117712|ref|XP_002179646.
1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0005681,GO:0000398","XP_002179646.1,EEC48632.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219117712,2347,4885.47,0,gi|219117712|re
f|XP_002179646.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0005681,GO:0000398","XP_002179646.1,EEC48632.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223995761,2269,4725.23,0,gi|223995761|ref|XP
_002287554.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0005681,GO:0000398","XP_002287554.1,EED94997.1"
Stramenopiles-
Aureococcus_anophagefferens_jgi54877,2385,4103.9,0,gi|301105359|ref|XP_002901763
```

```
.1|pre-mRNA-processing-splicing factor 8 [Phytophthora infestans T30-4] ,"
GO:0005681,GO:0000398","XP_002901763.1,EEY57153.1"
Stramenopiles-
Phytophthora_ramorum_jgi71209,2339,4639.33,0,gi|301105359|ref|XP_002901763.1|pre
-mRNA-processing-splicing factor 8 [Phytophthora infestans T30-4] ,"
GO:0005681,GO:0000398","XP_002901763.1,EEY57153.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi261278,372,286.189,4.26E-
75,gi|163792415|ref|ZP_02186392.1|hypothetical oxidoreductase yiaK [alpha
proteobacterium BAL199] ,"
GO:0055114,GO:0016491,GO:0005737,GO:0008152","ZP_02186392.1,EDP66629.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi287428,416,287.73,1.51E-
75,gi|163792415|ref|ZP_02186392.1|hypothetical oxidoreductase yiaK [alpha
proteobacterium BAL199] ,"
GO:0055114,GO:0016491,GO:0005737,GO:0008152","ZP_02186392.1,EDP66629.1"
Stramenopiles-
Phytophthora_sojae_jgi143499,363,685.256,0,gi|301111970|ref|XP_002905064.1|conse
rved hypothetical protein [Phytophthora infestans T30-4]
,,"XP_002905064.1,EEY53446.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224015006,2464,5142.4,0,gi|224015006|ref|XP_
002297164.1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002297164.1,EED86489.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi243335,1413,1310.05,0,gi|224015006|ref|XP_002297164.
1|predicted protein [Thalassiosira pseudonana CCMP1335]
,,"XP_002297164.1,EED86489.1"
Stramenopiles-Aureococcus_anophagefferens_jgi26166,705,461.84,1.14E-
127,gi|42569537|ref|NP_180749.2|XIF; motor [Arabidopsis thaliana],,NP_180749.2
Stramenopiles-Aureococcus_anophagefferens_jgi327,644,493.812,2.64E-
137,gi|1346638|sp|P47808.1|MYSH_ACACARecName: Full=High molecular weight form of
myosin-1; AltName: Full=High molecular weight form of myosin I; Short=HMWMI ,"
GO:0005524,GO:0005856,GO:0003779,GO:0000166,GO:0016459,GO:0003774","P47808.1,AAA
27709.1"
Stramenopiles-
Phytophthora_ramorum_jgi80864,3303,5918.19,0,gi|301113386|ref|XP_002998463.1|myo
sin-like protein [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0008152,GO:0000166,GO:0003824,GO:0016459,GO:0003774","XP_002998463
.1,EEY69816.1"
Stramenopiles-
Phytophthora_sojae_jgi140880,3276,5915.11,0,gi|301113386|ref|XP_002998463.1|myos
in-like protein [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0008152,GO:0000166,GO:0003824,GO:0016459,GO:0003774","XP_002998463
.1,EEY69816.1"
Stramenopiles-
Phytophthora_capsici_jgi85864,401,833.943,0,gi|301113386|ref|XP_002998463.1|myos
in-like protein [Phytophthora infestans T30-4] ,"
GO:0005524,GO:0008152,GO:0000166,GO:0003824,GO:0016459,GO:0003774","XP_002998463
.1,EEY69816.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219122035,1027,2136.69,0,gi|219122035|re
f|XP_002181360.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1] ,"
GO:0005524,GO:0000166,GO:0016459,GO:0003774","XP_002181360.1,EEC47283.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi156363,889,977.237,0,gi|239925821|gb|ACS35545.1|myos
```

```
in I [Phaeodactylum tricornutum],"
GO:0046872,GO:0005524,GO:0000166,GO:0008270,GO:0016459,GO:0003774",ACS35545.1
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224010952,810,1695.25,0,gi|224010952|ref|XP_
002294433.1|myosin heavy chain-like protein [Thalassiosira pseudonana CCMP1335]
," GO:0005524,GO:0000166,GO:0016459,GO:0003774","XP_002294433.1,EED88267.1"
Stramenopiles-Aureococcus_anophagefferens_jgi19710,870,516.924,4.81E-
144,gi|299117468|emb|CBN73971.1|myosin II heavy chain [Ectocarpus siliculosus],"
GO:0005524,GO:0000166,GO:0016459,GO:0003774",CBN73971.1
Stramenopiles-
Phytophthora_sojae_jgi142328,1540,2868.18,0,gi|301109150|ref|XP_002903656.1|myos
in-like protein [Phytophthora infestans T30-4] ,"
GO:0035091,GO:0005524,GO:0000166,GO:0007154,GO:0016459,GO:0005515,GO:0003774","X
P_002903656.1,EEY55432.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi271794,304,301.212,9.99E-
80,gi|219127562|ref|XP_002184002.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002184002.1,EEC44671.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219127562,291,610.527,6.48E-
173,gi|219127562|ref|XP_002184002.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002184002.1,EEC44671.1"
Stramenopiles-Aureococcus_anophagefferens_jgi64344,211,142.124,3.40E-
32,gi|219127562|ref|XP_002184002.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002184002.1,EEC44671.1"
Stramenopiles-
Phytophthora_capsici_jgi889,694,1011.91,0,gi|301111810|ref|XP_002904984.1|Voltag
e-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0005509,GO:0016021,GO:0016020,GO:0055085,GO:0006811,GO:0005216,GO:0006810","X
P_002904984.1,EEY53366.1"
Stramenopiles-
Phytophthora_ramorum_jgi79981,984,1335.47,0,gi|301111810|ref|XP_002904984.1|Volt
age-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0005509,GO:0016021,GO:0016020,GO:0055085,GO:0006811,GO:0005216,GO:0006810","X
P_002904984.1,EEY53366.1"
Stramenopiles-
Phytophthora_sojae_jgi138717,997,1258.05,0,gi|301111810|ref|XP_002904984.1|Volta
ge-gated Ion Channel (VIC) Superfamily [Phytophthora infestans T30-4] ,"
GO:0005509,GO:0016021,GO:0016020,GO:0055085,GO:0006811,GO:0005216,GO:0006810","X
P_002904984.1,EEY53366.1"
Stramenopiles-Aureococcus_anophagefferens_jgi64273,1883,147.132,2.25E-
32,gi|301111810|ref|XP_002904984.1|Voltage-gated Ion Channel (VIC) Superfamily
[Phytophthora infestans T30-4] ,"
GO:0005509,GO:0016021,GO:0016020,GO:0055085,GO:0006811,GO:0005216,GO:0006810","X
P_002904984.1,EEY53366.1"
Stramenopiles-Aureococcus_anophagefferens_jgi62252,1086,254.603,4.56E-
65,gi|301111810|ref|XP_002904984.1|Voltage-gated Ion Channel (VIC) Superfamily
[Phytophthora infestans T30-4] ,"
GO:0005509,GO:0016021,GO:0016020,GO:0055085,GO:0006811,GO:0005216,GO:0006810","X
P_002904984.1,EEY53366.1"
Stramenopiles-
Phytophthora_sojae_jgi108780,1178,1511.51,0,gi|219128321|ref|XP_002184364.1|prec
ursor of carboxylase pyruvate carboxylase [Phaeodactylum tricornutum CCAP
1055/1] ,"
GO:0005524,GO:0016874,GO:0005737,GO:0008152,GO:0003824,GO:0009374,GO:0004736,GO:
0006094","XP_002184364.1,EEC44113.1"
```

```
Stramenopiles-
Phytophthora_capsici_jgi117052,1216,1509.58,0,gi|219128321|ref|XP_002184364.1|pr
ecursor of carboxylase pyruvate carboxylase [Phaeodactylum tricornutum CCAP
1055/1] ,"
GO:0005524,GO:0016874,GO:0005737,GO:0008152,GO:0003824,GO:0009374,GO:0004736,GO:
0006094","XP_002184364.1,EEC44113.1"
Stramenopiles-
Phytophthora_ramorum_jgi71512,1177,1511.12,0,gi|219128321|ref|XP_002184364.1|pre
cursor of carboxylase pyruvate carboxylase [Phaeodactylum tricornutum CCAP
1055/1] ,"
GO:0005524,GO:0016874,GO:0005737,GO:0008152,GO:0003824,GO:0009374,GO:0004736,GO:
0006094","XP_002184364.1,EEC44113.1"
Stramenopiles-Phytophthora_brassicae_esgi144596192_3,151,270.011,4.90E-
71,"gi|301113592|ref|XP_002998566.1|pyruvate carboxylase, mitochondrial
precursor [Phytophthora infestans T30-4] ","
GO:0005524,GO:0016874,GO:0008152,GO:0003824,GO:0009374","XP_002998566.1,EEY69919
.1"
Stramenopiles-
Phytophthora_capsici_jgi37362,606,1212.21,0,"gi|301109779|ref|XP_002903970.1|end
omembrane protein 70-like protein, putative [Phytophthora infestans T30-4] ",
GO:0016021,"XP_002903970.1,EEY55025.1"
Stramenopiles-
Phytophthora_sojae_jgi108609,589,1159.44,0,"gi|301109779|ref|XP_002903970.1|endo
membrane protein 70-like protein, putative [Phytophthora infestans T30-4] ",
GO:0016021,"XP_002903970.1,EEY55025.1"
Stramenopiles-
Phytophthora_ramorum_jgi54939,578,1143.64,0,"gi|301109779|ref|XP_002903970.1|end
omembrane protein 70-like protein, putative [Phytophthora infestans T30-4] ",
GO:0016021,"XP_002903970.1,EEY55025.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219115499,203,422.165,1.71E-
116,gi|219115499|ref|XP_002178545.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,"
GO:0003723,GO:0006413,GO:0006412,GO:0005737,GO:0003743","XP_002178545.1,EEC50210
.1"
Stramenopiles-Blastocystis_hominis_tbBHL00000921_2,257,253.062,2.01E-
65,gi|300121246|emb|CBK21627.2|unnamed protein product [Blastocystis hominis],"
GO:0003723,GO:0006413,GO:0006412,GO:0005737,GO:0003743",CBK21627.2
Stramenopiles-Phytophthora_sojae_jgi142035,197,350.517,4.67E-
95,gi|301119537|ref|XP_002907496.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,"
GO:0003723,GO:0006413,GO:0006412,GO:0005737,GO:0003743","XP_002907496.1,EEY64060
.1"
Stramenopiles-Aureococcus_anophagefferens_jgi72235,787,96.6709,1.17E-
17,gi|114619671|ref|XP_001154346.1|PREDICTED: kinesin family member 13B [Pan
troglodytes],,XP_001154346.1
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224003875,376,767.303,0,gi|224003875|ref|XP_
002291609.1|calreticulin-like protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0051082,GO:0005509,GO:0006457,GO:0005783","XP_002291609.1,EED91716.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi171081,422,509.605,2.50E-
142,gi|219129933|ref|XP_002185131.1|calreticulin [Phaeodactylum tricornutum CCAP
1055/1] ,"
GO:0051082,GO:0005509,GO:0006457,GO:0005783","XP_002185131.1,EEC43263.1"
```

```
Stramenopiles-Phytophthora_capsici_jgi117813,169,281.952,1.28E-
74,gi|301107273|ref|XP_002902719.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002902719.1,EEY56645.1"
Stramenopiles-Phytophthora_ramorum_jgi80810,147,268.47,1.71E-
70,gi|301107273|ref|XP_002902719.1|conserved hypothetical protein [Phytophthora
infestans T30-4] ,,"XP_002902719.1,EEY56645.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219123949,136,281.952,1.33E-
74,gi|219123949|ref|XP_002182277.1|predicted protein [Phaeodactylum tricornutum
CCAP 1055/1] ,,"XP_002182277.1,EEC46178.1"
Stramenopiles-Aureococcus_anophagefferens_jgi30428,268,158.303,7.77E-
37,gi|66825415|ref|XP_646062.1|SET domain-containing protein [Dictyostelium
discoideum AX4] ,,"XP_646062.1,EAL72127.1"
Stramenopiles-Aureococcus_anophagefferens_jgi29200,509,385.956,6.40E-
105,gi|195996373|ref|XP_002108055.1|hypothetical protein TRIADDRAFT_36979
[Trichoplax adhaerens] ,"
GO:0006629,GO:0055114,GO:0016717,GO:0020037,GO:0016491,GO:0005506,GO:0006633","X
P_002108055.1,EDV28853.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi224003319,493,1027.31,0,gi|224003319|ref|XP_
002291331.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0006629,GO:0055114,GO:0016717,GO:0020037,GO:0016491,GO:0005506,GO:0006633","X
P_002291331.1,AAX14504.1,EED91438.1"
Stramenopiles-Fragilariopsis_cylindrus_jgi188378,477,369.392,5.20E-
100,gi|156405194|ref|XP_001640617.1|predicted protein [Nematostella vectensis]
,"
GO:0006629,GO:0055114,GO:0016717,GO:0020037,GO:0016491,GO:0005506,GO:0006633","X
P_001640617.1,EDO48554.1"
Stramenopiles-
Thalassiosira_pseudonana_CCMP1335_gi223997060,560,1174.07,0,gi|223997060|ref|XP_
002288203.1|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0055114,GO:0005509,GO:0000287,GO:0016616,GO:0051287","XP_002288203.1,EED93639
.1"
Stramenopiles-
Fragilariopsis_cylindrus_jgi168262,485,753.821,0,gi|223997060|ref|XP_002288203.1
|predicted protein [Thalassiosira pseudonana CCMP1335] ,"
GO:0055114,GO:0005509,GO:0000287,GO:0016616,GO:0051287","XP_002288203.1,EED93639
.1"
Stramenopiles-
Phaeodactylum_tricornutum_CCAP_1055/1_gi219124414,357,746.117,0,gi|219124414|ref
|XP_002182499.1|isocitrate dehydrogenase [Phaeodactylum tricornutum CCAP 1055/1]
,"
GO:0055114,GO:0006102,GO:0000287,GO:0016616,GO:0004450,GO:0051287","XP_002182499
.1,EEC45786.1"
Stramenopiles-Aureococcus_anophagefferens_jgi71458,491,588.186,7.18E-
166,gi|223997060|ref|XP_002288203.1|predicted protein [Thalassiosira pseudonana
CCMP1335] ,"
GO:0055114,GO:0005509,GO:0000287,GO:0016616,GO:0051287","XP_002288203.1,EED93639
.1"
Stramenopiles-Aureococcus_anophagefferens_jgi51995,635,434.491,1.79E-
119,gi|61394184|gb|AAX45785.1|glucose-6-phosphate dehydrogenase isoform B [Ips
typographus],"
GO:0055114,GO:0006006,GO:0005488,GO:0016491,GO:0004345,GO:0008152,GO:0005975,GO:
0003824",AAX45785.1
```

```
Stramenopiles-
Phytophthora_capsici_jgi91110,565,1065.45,0,gi|301119447|ref|XP_002907451.1|Ca2
:Cation Antiporter (CaCA) Family [Phytophthora infestans T30-4] ,"
GO:0005509,GO:0016021,GO:0016020,GO:0055085","XP_002907451.1,EEY64015.1"
Stramenopiles-
Phytophthora_sojae_jgi128229,565,1058.51,0,gi|301119447|ref|XP_002907451.1|Ca2
:Cation Antiporter (CaCA) Family [Phytophthora infestans T30-4] ,"
GO:0005509,GO:0016021,GO:0016020,GO:0055085","XP_002907451.1,EEY64015.1"
```