**Supplementary Tables**

**Table S1 Lengths of six contigs from the draft genome assembly for *P. paneum* OM1**

|  |  |  |
| --- | --- | --- |
| **Contig number** | **Length (bp)** | **Coverage (x)** |
| Contig\_8 | 7,558,500 | 117 |
| Contig\_6 | 7,466,314 | 118 |
| Contig\_9 | 7,407,378 | 120 |
| Contig\_10 | 4,666,820 | 119 |
| Contig\_11 | 33,219 | 57 |
| Contig\_14 | 27,875 | 854 |

**Table S2 Genome assembly data for *P. paneum* OM1**

|  |  |
| --- | --- |
| **Item** | **Number** |
| Contigs | 6 |
| Total bases (bp) | 27,160,106 |
| rRNA | 49 |
| 5S/5.8S rRNA | 41 |
| 18S rRNA | 4 |
| 28S rRNA | 4 |
| tRNA  Gene | 187  10,679 |
| mRNA | 10,679 |
| Exon | 33,118 |
| CDS | 10,679 |
| Functionally annotated gene | 7,136 |

**Notes.**

CDS, Coding sequence.

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of** ***P. paneum* OM1**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0034354 | 5 | gene\_00551.t1,gene\_02644.t1,gene\_05407.t1,gene\_04082.t1,gene\_07394.t1 | | de novo' NAD biosynthetic process from tryptophan | biological\_process |
| GO:0034356 | 1 | gene\_10020.t1 | | NAD biosynthesis via nicotinamide riboside salvage pathway | biological\_process |
| GO:0046348 | 2 | gene\_08150.t1,gene\_03440.t1 | | amino sugar catabolic process | biological\_process |
| GO:0034198 | 1 | gene\_05367.t1 | | cellular response to amino acid starvation | biological\_process |
| GO:0034194 | 1 | gene\_03435.t1 | | D-galactonate catabolic process | biological\_process |
| GO:0006284 | 3 | gene\_08282.t1,gene\_07283.t1,gene\_10200.t1 | | base-excision repair | biological\_process |
| GO:0006285 | 5 | gene\_06972.t1,gene\_10562.t1,gene\_00314.t1,gene\_09479.t1,gene\_04239.t1 | | base-excision repair, AP site formation | biological\_process |
| GO:0006283 | 1 | gene\_02748.t1 | | transcription-coupled nucleotide-excision repair | biological\_process |
| GO:0006281 | 73 | gene\_08299.t1,gene\_06740.t1,gene\_01043.t1,gene\_06694.t1,gene\_04254.t1,gene\_03935.t1,gene\_02387.t1,gene\_10444.t1,gene\_00391.t1,gene\_00982.t1,gene\_06073.t1,gene\_04443.t1,gene\_10167.t1,gene\_07183.t1,gene\_03774.t1,gene\_10279.t1,gene\_08500.t1,gene\_03702.t1,gene\_06517.t1,gene\_07352.t1,gene\_00682.t1,gene\_01057.t1,gene\_06102.t1,gene\_08063.t1,gene\_09184.t1,gene\_07270.t1,gene\_04166.t1,gene\_05945.t1,gene\_10093.t1,gene\_08530.t1,gene\_04631.t1,gene\_08341.t1,gene\_05141.t1,gene\_01223.t1,gene\_09572.t1,gene\_03358.t1,gene\_07377.t1,gene\_05747.t1,gene\_02787.t1,gene\_09591.t1,gene\_08474.t1,gene\_10065.t1,gene\_06255.t1,gene\_02270.t1,gene\_00455.t1,gene\_10008.t1,gene\_05805.t1,gene\_05518.t1,gene\_09891.t1,gene\_01715.t1,gene\_09781.t1,gene\_06486.t1,gene\_08475.t1,gene\_08889.t1,gene\_00415.t1,gene\_07620.t1,gene\_00274.t1,gene\_00573.t1,gene\_05677.t1,gene\_08025.t1,gene\_04352.t1,gene\_08214.t1,gene\_09206.t1,gene\_03581.t1,gene\_10557.t1,gene\_00652.t1,gene\_04176.t1,gene\_07889.t1,gene\_01877.t1,gene\_08300.t1,gene\_08999.t1,gene\_03200.t1,gene\_09044.t1 | | DNA repair | biological\_process |
| GO:0045859 | 1 | gene\_09602.t1 | | regulation of protein kinase activity | biological\_process |
| GO:0006289 | 15 | gene\_06477.t1,gene\_07736.t1,gene\_02617.t1,gene\_04239.t1,gene\_02228.t1,gene\_09428.t1,gene\_09214.t1,gene\_07906.t1,gene\_09119.t1,gene\_01306.t1,gene\_05871.t1,gene\_04147.t1,gene\_03712.t1,gene\_10227.t1,gene\_01504.t1 | | nucleotide-excision repair | biological\_process |
| GO:0006570 | 1 | gene\_03809.t1 | | tyrosine metabolic process | biological\_process |
| GO:0006571 | 2 | gene\_00560.t1,gene\_05716.t1 | | tyrosine biosynthetic process | biological\_process |
| GO:0006572 | 3 | gene\_03807.t1,gene\_10000.t1,gene\_03810.t1 | | tyrosine catabolic process | biological\_process |
| GO:0006370 | 2 | gene\_09829.t1,gene\_01488.t1 | | 7-methylguanosine mRNA capping | biological\_process |
| GO:0006376 | 1 | gene\_03867.t1 | | mRNA splice site selection | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0006378 | 3 | gene\_07762.t1,gene\_03216.t1,gene\_04188.t1 | | mRNA polyadenylation | biological\_process |
| GO:0006379 | 6 | gene\_03216.t1,gene\_04188.t1,gene\_01093.t1,gene\_08067.t1,gene\_05314.t1,gene\_09823.t1 | | mRNA cleavage | biological\_process |
| GO:0060261 | 1 | gene\_01212.t1 | | positive regulation of transcription initiation from RNA polymerase II promoter | biological\_process |
| GO:0006596 | 3 | gene\_01399.t1,gene\_08118.t1,gene\_08820.t1 | | polyamine biosynthetic process | biological\_process |
| GO:0006597 | 1 | gene\_08168.t1 | | spermine biosynthetic process | biological\_process |
| GO:0030497 | 1 | gene\_06564.t1 | | fatty acid elongation | biological\_process |
| GO:0061640 | 1 | gene\_08241.t1 | | cytoskeleton-dependent cytokinesis | biological\_process |
| GO:0035556 | 11 | gene\_06053.t1,gene\_08522.t1,gene\_08790.t1,gene\_08231.t1,gene\_09815.t1,gene\_03592.t1,gene\_09378.t1,gene\_07148.t1,gene\_05820.t1,gene\_07012.t1,gene\_10560.t1 | | intracellular signal transduction | biological\_process |
| GO:0046654 | 4 | gene\_00474.t1,gene\_07926.t1,gene\_09639.t1,gene\_01051.t1 | | tetrahydrofolate biosynthetic process | biological\_process |
| GO:0035552 | 2 | gene\_09114.t1,gene\_01975.t1 | | oxidative single-stranded DNA demethylation | biological\_process |
| GO:0046656 | 4 | gene\_08648.t1,gene\_00474.t1,gene\_07926.t1,gene\_09639.t1 | | folic acid biosynthetic process | biological\_process |
| GO:0006116 | 3 | gene\_09821.t1,gene\_03273.t1,gene\_02144.t1 | | NADH oxidation | biological\_process |
| GO:0006113 | 1 | gene\_03560.t1 | | fermentation | biological\_process |
| GO:0006119 | 2 | gene\_07269.t1,gene\_09108.t1 | | oxidative phosphorylation | biological\_process |
| GO:0006629 | 35 | gene\_04078.t1,gene\_06565.t1,gene\_09304.t1,gene\_04334.t1,gene\_00377.t1,gene\_10584.t1,gene\_10630.t1,gene\_05337.t1,gene\_08888.t1,gene\_08667.t1,gene\_10013.t1,gene\_06453.t1,gene\_00933.t1,gene\_06246.t1,gene\_01039.t1,gene\_02383.t1,gene\_08056.t1,gene\_03460.t1,gene\_10194.t1,gene\_07175.t1,gene\_00238.t1,gene\_05550.t1,gene\_08491.t1,gene\_02316.t1,gene\_08969.t1,gene\_00174.t1,gene\_04437.t1,gene\_06451.t1,gene\_08627.t1,gene\_08886.t1,gene\_03250.t1,gene\_00884.t1,gene\_00957.t1,gene\_00620.t1,gene\_00969.t1 | | lipid metabolic process | biological\_process |
| GO:0006625 | 2 | gene\_00514.t1,gene\_06332.t1 | | protein targeting to peroxisome | biological\_process |
| GO:0006626 | 1 | gene\_08866.t1 | | protein targeting to mitochondrion | biological\_process |
| GO:0006627 | 1 | gene\_09050.t1 | | protein processing involved in protein targeting to mitochondrion | biological\_process |
| GO:0006621 | 2 | gene\_04156.t1,gene\_02784.t1 | | protein retention in ER lumen | biological\_process |
| GO:0006623 | 3 | gene\_03697.t1,gene\_05682.t1,gene\_01033.t1 | | protein targeting to vacuole | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0009263 | 1 | gene\_05781.t1 | | deoxyribonucleotide biosynthetic process | biological\_process |
| GO:0070897 | 2 | gene\_03056.t1,gene\_03014.t1 | | transcription preinitiation complex assembly | biological\_process |
| GO:0019856 | 1 | gene\_01874.t1 | | pyrimidine nucleobase biosynthetic process | biological\_process |
| GO:0006750 | 2 | gene\_09056.t1,gene\_09033.t1 | | glutathione biosynthetic process | biological\_process |
| GO:0006751 | 3 | gene\_03622.t1,gene\_06808.t1,gene\_08476.t1 | | glutathione catabolic process | biological\_process |
| GO:0006021 | 3 | gene\_05585.t1,gene\_02349.t1,gene\_00961.t1 | | inositol biosynthetic process | biological\_process |
| GO:0051125 | 1 | gene\_05327.t1 | | regulation of actin nucleation | biological\_process |
| GO:0051123 | 1 | gene\_08167.t1 | | RNA polymerase II preinitiation complex assembly | biological\_process |
| GO:0051128 | 1 | gene\_09833.t1 | | regulation of cellular component organization | biological\_process |
| GO:0009395 | 2 | gene\_02894.t1,gene\_07645.t1 | | phospholipid catabolic process | biological\_process |
| GO:0000288 | 1 | gene\_03716.t1 | | nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay | biological\_process |
| GO:0000289 | 4 | gene\_03654.t1,gene\_06697.t1,gene\_02175.t1,gene\_07005.t1 | | nuclear-transcribed mRNA poly(A) tail shortening | biological\_process |
| GO:0000280 | 1 | gene\_04251.t1 | | nuclear division | biological\_process |
| GO:0030705 | 1 | gene\_04190.t1 | | cytoskeleton-dependent intracellular transport | biological\_process |
| GO:0009094 | 2 | gene\_09255.t1,gene\_05716.t1 | | L-phenylalanine biosynthetic process | biological\_process |
| GO:0051012 | 1 | gene\_10487.t1 | | microtubule sliding | biological\_process |
| GO:0051017 | 1 | gene\_01209.t1 | | actin filament bundle assembly | biological\_process |
| GO:0051014 | 1 | gene\_02045.t1 | | actin filament severing | biological\_process |
| GO:0006974 | 6 | gene\_07640.t1,gene\_01226.t1,gene\_07321.t1,gene\_10306.t1,gene\_10392.t1,gene\_04435.t1 | | cellular response to DNA damage stimulus | biological\_process |
| GO:0048034 | 1 | gene\_01447.t1 | | heme O biosynthetic process | biological\_process |
| GO:0006979 | 10 | gene\_03391.t1,gene\_03751.t1,gene\_02272.t1,gene\_10014.t1,gene\_05483.t1,gene\_05839.t1,gene\_03126.t1,gene\_00621.t1,gene\_00545.t1,gene\_01284.t1 | | response to oxidative stress | biological\_process |
| GO:0000750 | 1 | gene\_01701.t1 | | pheromone-dependent signal transduction involved in conjugation with cellular fusion | biological\_process |
| GO:0008608 | 7 | gene\_10529.t1,gene\_05877.t1,gene\_03377.t1,gene\_00873.t1,gene\_08869.t1,gene\_07276.t1,gene\_03170.t1 | | attachment of spindle microtubules to kinetochore | biological\_process |
| GO:0043631 | 1 | gene\_01933.t1 | | RNA polyadenylation | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0051301 | 48 | gene\_08710.t1,gene\_07793.t1,gene\_03094.t1,gene\_08597.t1,gene\_07231.t1,gene\_07822.t1,gene\_05168.t1,gene\_06720.t1,gene\_09038.t1,gene\_08798.t1,gene\_05877.t1,gene\_04228.t1,gene\_02001.t1,gene\_05995.t1,gene\_06343.t1,gene\_04724.t1,gene\_10487.t1,gene\_05155.t1,gene\_09686.t1,gene\_06154.t1,gene\_07311.t1,gene\_01875.t1,gene\_08632.t1,gene\_05897.t1,gene\_02065.t1,gene\_10291.t1,gene\_05740.t1,gene\_00422.t1,gene\_03476.t1,gene\_10063.t1,gene\_08869.t1,gene\_02992.t1,gene\_07276.t1,gene\_06879.t1,gene\_09556.t1,gene\_07202.t1,gene\_03377.t1,gene\_06062.t1,gene\_05154.t1,gene\_01007.t1,gene\_02100.t1,gene\_09773.t1,gene\_09061.t1,gene\_04201.t1,gene\_07003.t1,gene\_09833.t1,gene\_09737.t1,gene\_09787.t1 | | cell division | biological\_process |
| GO:0019563 | 2 | gene\_03977.t1,gene\_10097.t1 | | glycerol catabolic process | biological\_process |
| GO:0009439 | 1 | gene\_06302.t1 | | cyanate metabolic process | biological\_process |
| GO:0019551 | 1 | gene\_09887.t1 | | glutamate catabolic process to 2-oxoglutarate | biological\_process |
| GO:0070084 | 4 | gene\_05363.t1,gene\_00326.t1,gene\_05364.t1,gene\_02643.t1 | | protein initiator methionine removal | biological\_process |
| GO:0070407 | 1 | gene\_09415.t1 | | oxidation-dependent protein catabolic process | biological\_process |
| GO:0030837 | 1 | gene\_06364.t1 | | negative regulation of actin filament polymerization | biological\_process |
| GO:0007163 | 1 | gene\_09833.t1 | | establishment or maintenance of cell polarity | biological\_process |
| GO:0007165 | 19 | gene\_06374.t1,gene\_01703.t1,gene\_05579.t1,gene\_09602.t1,gene\_08179.t1,gene\_07846.t1,gene\_00965.t1,gene\_10307.t1,gene\_03243.t1,gene\_00029.t1,gene\_01175.t1,gene\_05794.t1,gene\_02689.t1,gene\_09274.t1,gene\_08510.t1,gene\_05709.t1,gene\_07449.t1,gene\_02369.t1,gene\_07240.t1 | | signal transduction | biological\_process |
| GO:0007166 | 2 | gene\_00670.t1,gene\_04229.t1 | | cell surface receptor signaling pathway | biological\_process |
| GO:0035835 | 1 | gene\_02597.t1 | | indole alkaloid biosynthetic process | biological\_process |
| GO:0071596 | 2 | gene\_03997.t1,gene\_03983.t1 | | ubiquitin-dependent protein catabolic process via the N-end rule pathway | biological\_process |
| GO:0019988 | 1 | gene\_04600.t1 | | charged-tRNA amino acid modification | biological\_process |
| GO:0019985 | 1 | gene\_06856.t1 | | translesion synthesis | biological\_process |
| GO:0016567 | 6 | gene\_06204.t1,gene\_09212.t1,gene\_02629.t1,gene\_09472.t1,gene\_03286.t1,gene\_07422.t1 | | protein ubiquitination | biological\_process |
| GO:0016560 | 3 | gene\_07529.t1,gene\_03938.t1,gene\_08631.t1 | | protein import into peroxisome matrix, docking | biological\_process |
| GO:1990456 | 1 | gene\_06112.t1 | | mitochondrion-endoplasmic reticulum membrane tethering | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0006298 | 11 | gene\_00724.t1,gene\_00723.t1,gene\_03576.t1,gene\_08513.t1,gene\_01436.t1,gene\_03237.t1,gene\_07403.t1,gene\_05849.t1,gene\_09396.t1,gene\_05619.t1,gene\_00205.t1 | | mismatch repair | biological\_process |
| GO:0046081 | 1 | gene\_01001.t1 | | dUTP catabolic process | biological\_process |
| GO:0006564 | 2 | gene\_06831.t1,gene\_09692.t1 | | L-serine biosynthetic process | biological\_process |
| GO:0006562 | 3 | gene\_03827.t1,gene\_06401.t1,gene\_02585.t1 | | proline catabolic process | biological\_process |
| GO:0006561 | 3 | gene\_01196.t1,gene\_00851.t1,gene\_01582.t1 | | proline biosynthetic process | biological\_process |
| GO:0006569 | 4 | gene\_00551.t1,gene\_02644.t1,gene\_04082.t1,gene\_07394.t1 | | tryptophan catabolic process | biological\_process |
| GO:0006360 | 2 | gene\_02749.t1,gene\_03180.t1 | | transcription by RNA polymerase I | biological\_process |
| GO:0006364 | 59 | gene\_09001.t1,gene\_09857.t1,gene\_04149.t1,gene\_00407.t1,gene\_06495.t1,gene\_00676.t1,gene\_09245.t1,gene\_07034.t1,gene\_02121.t1,gene\_05674.t1,gene\_00411.t1,gene\_06516.t1,gene\_09850.t1,gene\_05954.t1,gene\_03717.t1,gene\_05136.t1,gene\_07250.t1,gene\_01651.t1,gene\_02684.t1,gene\_02479.t1,gene\_07630.t1,gene\_01602.t1,gene\_10484.t1,gene\_07171.t1,gene\_09265.t1,gene\_00904.t1,gene\_06998.t1,gene\_07039.t1,gene\_06245.t1,gene\_07935.t1,gene\_03203.t1,gene\_05450.t1,gene\_06989.t1,gene\_02353.t1,gene\_00829.t1,gene\_08812.t1,gene\_04403.t1,gene\_06280.t1,gene\_10370.t1,gene\_04396.t1,gene\_02572.t1,gene\_06557.t1,gene\_10328.t1,gene\_09290.t1,gene\_02354.t1,gene\_07329.t1,gene\_09012.t1,gene\_07075.t1,gene\_02697.t1,gene\_09567.t1,gene\_07120.t1,gene\_08535.t1,gene\_10571.t1,gene\_05225.t1,gene\_00702.t1,gene\_02183.t1,gene\_08921.t1,gene\_01055.t1,gene\_09818.t1 | | rRNA processing | biological\_process |
| GO:0006367 | 10 | gene\_02334.t1,gene\_00246.t1,gene\_00093.t1,gene\_00098.t1,gene\_08169.t1,gene\_09119.t1,gene\_02099.t1,gene\_10467.t1,gene\_07906.t1,gene\_01112.t1 | | transcription initiation from RNA polymerase II promoter | biological\_process |
| GO:0006366 | 5 | gene\_02207.t1,gene\_07296.t1,gene\_07314.t1,gene\_02110.t1,gene\_05228.t1 | | transcription by RNA polymerase II | biological\_process |
| GO:0006369 | 1 | gene\_04188.t1 | | termination of RNA polymerase II transcription | biological\_process |
| GO:0006368 | 4 | gene\_05205.t1,gene\_01140.t1,gene\_07013.t1,gene\_00642.t1 | | transcription elongation from RNA polymerase II promoter | biological\_process |
| GO:0007186 | 4 | gene\_03006.t1,gene\_01701.t1,gene\_08745.t1,gene\_06747.t1 | | G protein-coupled receptor signaling pathway | biological\_process |
| GO:1904983 | 1 | gene\_10133.t1 | | glycine import into mitochondrion | biological\_process |
| GO:0006582 | 1 | gene\_07943.t1 | | melanin metabolic process | biological\_process |
| GO:0006913 | 2 | gene\_05468.t1,gene\_10558.t1 | | nucleocytoplasmic transport | biological\_process |
| GO:0061077 | 1 | gene\_02711.t1 | | chaperone-mediated protein folding | biological\_process |
| GO:0042545 | 2 | gene\_09474.t1,gene\_06941.t1 | | cell wall modification | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0009113 | 2 | gene\_09629.t1,gene\_09478.t1 | | purine nucleobase biosynthetic process | biological\_process |
| GO:0042546 | 2 | gene\_01195.t1,gene\_09246.t1 | | cell wall biogenesis | biological\_process |
| GO:0006106 | 1 | gene\_00860.t1 | | fumarate metabolic process | biological\_process |
| GO:0006101 | 1 | gene\_04195.t1 | | citrate metabolic process | biological\_process |
| GO:0006102 | 1 | gene\_06798.t1 | | isocitrate metabolic process | biological\_process |
| GO:0035494 | 1 | gene\_08575.t1 | | SNARE complex disassembly | biological\_process |
| GO:0006108 | 1 | gene\_09160.t1 | | malate metabolic process | biological\_process |
| GO:0006633 | 24 | gene\_07489.t1,gene\_02332.t1,gene\_07895.t1,gene\_02649.t1,gene\_01127.t1,gene\_06013.t1,gene\_00004.t1,gene\_00239.t1,gene\_09894.t1,gene\_09503.t1,gene\_01074.t1,gene\_09831.t1,gene\_02860.t1,gene\_08158.t1,gene\_01270.t1,gene\_05606.t1,gene\_01892.t1,gene\_05500.t1,gene\_10275.t1,gene\_04035.t1,gene\_05302.t1,gene\_00854.t1,gene\_01824.t1,gene\_00779.t1 | | fatty acid biosynthetic process | biological\_process |
| GO:0006631 | 10 | gene\_05973.t1,gene\_01335.t1,gene\_08900.t1,gene\_06021.t1,gene\_04772.t1,gene\_08580.t1,gene\_07063.t1,gene\_09792.t1,gene\_08826.t1,gene\_04430.t1 | | fatty acid metabolic process | biological\_process |
| GO:0006637 | 2 | gene\_03283.t1,gene\_01926.t1 | | acyl-CoA metabolic process | biological\_process |
| GO:0006636 | 2 | gene\_08991.t1,gene\_09188.t1 | | unsaturated fatty acid biosynthetic process | biological\_process |
| GO:0006635 | 1 | gene\_01253.t1 | | fatty acid beta-oxidation | biological\_process |
| GO:0006075 | 1 | gene\_10302.t1 | | (1->3)-beta-D-glucan biosynthetic process | biological\_process |
| GO:0009254 | 1 | gene\_03840.t1 | | peptidoglycan turnover | biological\_process |
| GO:0006450 | 2 | gene\_03924.t1,gene\_03313.t1 | | regulation of translational fidelity | biological\_process |
| GO:0070887 | 3 | gene\_03006.t1,gene\_08745.t1,gene\_06747.t1 | | cellular response to chemical stimulus | biological\_process |
| GO:0009253 | 2 | gene\_07692.t1,gene\_01789.t1 | | peptidoglycan catabolic process | biological\_process |
| GO:0006457 | 33 | gene\_02559.t1,gene\_04223.t1,gene\_02160.t1,gene\_09414.t1,gene\_10136.t1,gene\_08085.t1,gene\_08963.t1,gene\_10207.t1,gene\_03193.t1,gene\_03801.t1,gene\_02695.t1,gene\_00827.t1,gene\_00425.t1,gene\_09741.t1,gene\_05558.t1,gene\_09247.t1,gene\_07139.t1,gene\_03178.t1,gene\_00502.t1,gene\_01682.t1,gene\_03945.t1,gene\_01128.t1,gene\_06426.t1,gene\_06699.t1,gene\_06458.t1,gene\_01533.t1,gene\_10423.t1,gene\_03204.t1,gene\_00737.t1,gene\_00738.t1,gene\_01918.t1,gene\_04092.t1,gene\_06242.t1 | | protein folding | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0006749 | 25 | gene\_10218.t1,gene\_03811.t1,gene\_06593.t1,gene\_05410.t1,gene\_04766.t1,gene\_04103.t1,gene\_04630.t1,gene\_05731.t1,gene\_06205.t1,gene\_04798.t1,gene\_07147.t1,gene\_00802.t1,gene\_08416.t1,gene\_06600.t1,gene\_04207.t1,gene\_08466.t1,gene\_08465.t1,gene\_02054.t1,gene\_03343.t1,gene\_06575.t1,gene\_06670.t1,gene\_04292.t1,gene\_03029.t1,gene\_03077.t1,gene\_09595.t1 | | glutathione metabolic process | biological\_process |
| GO:0006031 | 5 | gene\_10650.t1,gene\_09106.t1,gene\_00810.t1,gene\_01290.t1,gene\_07068.t1 | | chitin biosynthetic process | biological\_process |
| GO:0006744 | 8 | gene\_04044.t1,gene\_10312.t1,gene\_07066.t1,gene\_03847.t1,gene\_10412.t1,gene\_07253.t1,gene\_02653.t1,gene\_09298.t1 | | ubiquinone biosynthetic process | biological\_process |
| GO:0006458 | 1 | gene\_09196.t1 | | 'de novo' protein folding | biological\_process |
| GO:0008033 | 26 | gene\_03682.t1,gene\_08067.t1,gene\_09407.t1,gene\_05152.t1,gene\_02357.t1,gene\_04329.t1,gene\_01368.t1,gene\_04011.t1,gene\_09006.t1,gene\_09193.t1,gene\_07641.t1,gene\_06444.t1,gene\_06051.t1,gene\_06778.t1,gene\_04234.t1,gene\_08528.t1,gene\_08685.t1,gene\_06070.t1,gene\_05831.t1,gene\_02587.t1,gene\_09703.t1,gene\_09034.t1,gene\_07483.t1,gene\_06158.t1,gene\_07407.t1,gene\_01719.t1 | | tRNA processing | biological\_process |
| GO:0098703 | 1 | gene\_09233.t1 | | calcium ion import across plasma membrane | biological\_process |
| GO:0018342 | 2 | gene\_01380.t1,gene\_09347.t1 | | protein prenylation | biological\_process |
| GO:0000290 | 4 | gene\_04547.t1,gene\_09855.t1,gene\_08394.t1,gene\_05772.t1 | | deadenylation-dependent decapping of nuclear-transcribed mRNA | biological\_process |
| GO:0043936 | 1 | gene\_04192.t1 | | asexual sporulation resulting in formation of a cellular spore | biological\_process |
| GO:0009100 | 3 | gene\_10012.t1,gene\_00090.t1,gene\_08478.t1 | | glycoprotein metabolic process | biological\_process |
| GO:0000742 | 1 | gene\_03884.t1 | | karyogamy involved in conjugation with cellular fusion | biological\_process |
| GO:0030071 | 5 | gene\_07822.t1,gene\_09747.t1,gene\_02850.t1,gene\_02001.t1,gene\_04135.t1 | | regulation of mitotic metaphase/anaphase transition | biological\_process |
| GO:0001732 | 13 | gene\_00144.t1,gene\_01700.t1,gene\_00555.t1,gene\_01354.t1,gene\_06008.t1,gene\_02418.t1,gene\_05226.t1,gene\_05697.t1,gene\_00493.t1,gene\_05408.t1,gene\_03188.t1,gene\_06800.t1,gene\_00720.t1 | | formation of cytoplasmic translation initiation complex | biological\_process |
| GO:0008299 | 6 | gene\_02693.t1,gene\_07274.t1,gene\_08799.t1,gene\_09133.t1,gene\_06520.t1,gene\_07555.t1 | | isoprenoid biosynthetic process | biological\_process |
| GO:0008295 | 1 | gene\_08168.t1 | | spermidine biosynthetic process | biological\_process |
| GO:0019222 | 1 | gene\_08032.t1 | | regulation of metabolic process | biological\_process |
| GO:0016998 | 2 | gene\_07692.t1,gene\_01789.t1 | | cell wall macromolecule catabolic process | biological\_process |
| GO:0019427 | 1 | gene\_10043.t1 | | acetyl-CoA biosynthetic process from acetate | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0000162 | 3 | gene\_10196.t1,gene\_08809.t1,gene\_10271.t1 | | tryptophan biosynthetic process | biological\_process |
| GO:0072659 | 1 | gene\_09077.t1 | | protein localization to plasma membrane | biological\_process |
| GO:1904382 | 1 | gene\_08332.t1 | | mannose trimming involved in glycoprotein ERAD pathway | biological\_process |
| GO:0016197 | 4 | gene\_10315.t1,gene\_03887.t1,gene\_02853.t1,gene\_02540.t1 | | endosomal transport | biological\_process |
| GO:1901564 | 2 | gene\_02953.t1,gene\_08690.t1 | | organonitrogen compound metabolic process | biological\_process |
| GO:0016192 | 43 | gene\_02180.t1,gene\_10007.t1,gene\_03697.t1,gene\_06397.t1,gene\_03526.t1,gene\_03667.t1,gene\_09677.t1,gene\_03375.t1,gene\_02436.t1,gene\_08919.t1,gene\_04030.t1,gene\_10348.t1,gene\_06937.t1,gene\_08390.t1,gene\_05895.t1,gene\_00582.t1,gene\_02646.t1,gene\_09165.t1,gene\_01549.t1,gene\_06756.t1,gene\_06536.t1,gene\_05682.t1,gene\_01668.t1,gene\_07017.t1,gene\_03659.t1,gene\_03142.t1,gene\_00619.t1,gene\_07361.t1,gene\_03925.t1,gene\_04059.t1,gene\_03371.t1,gene\_09159.t1,gene\_01372.t1,gene\_08040.t1,gene\_09042.t1,gene\_00350.t1,gene\_02725.t1,gene\_00554.t1,gene\_10130.t1,gene\_06752.t1,gene\_04061.t1,gene\_04715.t1,gene\_05343.t1 | | vesicle-mediated transport | biological\_process |
| GO:1901566 | 4 | gene\_01185.t1,gene\_09470.t1,gene\_04024.t1,gene\_03022.t1 | | organonitrogen compound biosynthetic process | biological\_process |
| GO:0008277 | 1 | gene\_05795.t1 | | regulation of G protein-coupled receptor signaling pathway | biological\_process |
| GO:0045490 | 5 | gene\_00523.t1,gene\_09475.t1,gene\_09474.t1,gene\_00787.t1,gene\_06941.t1 | | pectin catabolic process | biological\_process |
| GO:0033674 | 1 | gene\_01161.t1 | | positive regulation of kinase activity | biological\_process |
| GO:0043547 | 2 | gene\_09563.t1,gene\_01246.t1 | | positive regulation of GTPase activity | biological\_process |
| GO:0062197 | 1 | gene\_03326.t1 | | cellular response to chemical stress | biological\_process |
| GO:0016575 | 3 | gene\_07896.t1,gene\_05188.t1,gene\_07577.t1 | | histone deacetylation | biological\_process |
| GO:0016570 | 5 | gene\_05205.t1,gene\_10407.t1,gene\_07013.t1,gene\_00642.t1,gene\_09239.t1 | | histone modification | biological\_process |
| GO:0016573 | 4 | gene\_07183.t1,gene\_07837.t1,gene\_05665.t1,gene\_07471.t1 | | histone acetylation | biological\_process |
| GO:0016572 | 1 | gene\_08500.t1 | | histone phosphorylation | biological\_process |
| GO:0045727 | 2 | gene\_05458.t1,gene\_09037.t1 | | positive regulation of translation | biological\_process |
| GO:0016579 | 17 | gene\_03666.t1,gene\_06133.t1,gene\_03039.t1,gene\_00409.t1,gene\_10416.t1,gene\_08038.t1,gene\_01114.t1,gene\_03470.t1,gene\_07313.t1,gene\_07732.t1,gene\_08301.t1,gene\_04184.t1,gene\_07916.t1,gene\_02020.t1,gene\_00843.t1,gene\_10317.t1,gene\_04108.t1 | | protein deubiquitination | biological\_process |
| GO:1990116 | 1 | gene\_02227.t1 | | ribosome-associated ubiquitin-dependent protein catabolic process | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0006355 | 38 | gene\_09775.t1,gene\_04084.t1,gene\_03744.t1,gene\_01942.t1,gene\_07005.t1,gene\_02804.t1,gene\_09239.t1,gene\_09220.t1,gene\_05796.t1,gene\_10047.t1,gene\_02910.t1,gene\_08023.t1,gene\_07331.t1,gene\_02393.t1,gene\_08721.t1,gene\_03205.t1,gene\_07759.t1,gene\_09848.t1,gene\_10003.t1,gene\_05373.t1,gene\_10140.t1,gene\_05871.t1,gene\_01792.t1,gene\_04049.t1,gene\_02373.t1,gene\_10443.t1,gene\_01316.t1,gene\_03901.t1,gene\_02703.t1,gene\_00833.t1,gene\_10024.t1,gene\_09322.t1,gene\_09052.t1,gene\_06697.t1,gene\_01526.t1,gene\_09828.t1,gene\_03799.t1,gene\_00599.t1 | | regulation of transcription, DNA-templated | biological\_process |
| GO:0006357 | 31 | gene\_01481.t1,gene\_09638.t1,gene\_02427.t1,gene\_03418.t1,gene\_04102.t1,gene\_03195.t1,gene\_04586.t1,gene\_08286.t1,gene\_10618.t1,gene\_06207.t1,gene\_07235.t1,gene\_09400.t1,gene\_04459.t1,gene\_08654.t1,gene\_01050.t1,gene\_00109.t1,gene\_03579.t1,gene\_10253.t1,gene\_03677.t1,gene\_09599.t1,gene\_02513.t1,gene\_02542.t1,gene\_04057.t1,gene\_00906.t1,gene\_01449.t1,gene\_05943.t1,gene\_00985.t1,gene\_07678.t1,gene\_04147.t1,gene\_09082.t1,gene\_00580.t1 | | regulation of transcription by RNA polymerase II | biological\_process |
| GO:0006351 | 216 | gene\_10517.t1,gene\_02526.t1,gene\_09809.t1,gene\_00286.t1,gene\_05810.t1,gene\_06585.t1,gene\_05301.t1,gene\_09897.t1,gene\_04650.t1,gene\_07166.t1,gene\_04378.t1,gene\_01987.t1,gene\_10227.t1,gene\_07583.t1,gene\_08694.t1,gene\_07085.t1,gene\_05373.t1,gene\_09036.t1,gene\_08824.t1,gene\_09192.t1,gene\_02977.t1,gene\_06059.t1,gene\_05808.t1,gene\_05311.t1,gene\_07128.t1,gene\_06936.t1,gene\_00556.t1,gene\_07284.t1,gene\_02170.t1,gene\_10058.t1,gene\_06732.t1,gene\_03295.t1,gene\_06020.t1,gene\_08281.t1,gene\_06963.t1,gene\_04045.t1,gene\_04445.t1,gene\_01145.t1,gene\_06978.t1,gene\_02915.t1,gene\_03544.t1,gene\_06394.t1,gene\_02194.t1,gene\_09814.t1,gene\_09944.t1,gene\_05588.t1,gene\_02808.t1,gene\_05121.t1,gene\_04669.t1,gene\_03050.t1,gene\_09460.t1,gene\_02847.t1,gene\_06532.t1,gene\_02034.t1,gene\_03831.t1,gene\_07827.t1,gene\_01153.t1,gene\_04481.t1,gene\_07168.t1,gene\_09590.t1,gene\_01809.t1,gene\_08041.t1,gene\_10237.t1,gene\_06852.t1,gene\_02605.t1,gene\_05540.t1,gene\_04524.t1,gene\_10056.t1,gene\_03366.t1,gene\_07677.t1,gene\_00564.t1,gene\_06949.t1,gene\_05277.t1,gene\_04081.t1,gene\_00677.t1,gene\_04356.t1,gene\_06614.t1,gene\_06402.t1,gene\_03132.t1,gene\_03951.t1,gene\_07693.t1,gene\_10254.t1,gene\_01612.t1,gene\_06171.t1,gene\_02809.t1,gene\_10553.t1,gene\_05992.t1,gene\_01922.t1,gene\_05736.t1,gene\_04208.t1,gene\_01937.t1,gene\_01345.t1,gene\_06266.t1,gene\_04028.t1,gene\_10663.t1,gene\_04473.t1,gene\_08441.t1,gene\_07955.t1,gene\_06230.t1,gene\_09646.t1,gene\_08638.t1,gene\_10051.t1,gene\_07992.t1,gene\_07948.t1,gene\_00689.t1, | | transcription, DNA-templated | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0006351 | 216 | gene\_01535.t1,gene\_01135.t1,gene\_07382.t1,gene\_00395.t1,gene\_03770.t1,gene\_09652.t1,gene\_02580.t1,gene\_09375.t1,gene\_02652.t1,gene\_05080.t1,gene\_08254.t1,gene\_04515.t1,gene\_02916.t1,gene\_10255.t1,gene\_04594.t1,gene\_08833.t1,gene\_04621.t1,gene\_08947.t1,gene\_04732.t1,gene\_02874.t1,gene\_06934.t1,gene\_02607.t1,gene\_01756.t1,gene\_01742.t1,gene\_06249.t1,gene\_08569.t1,gene\_03655.t1,gene\_01093.t1,gene\_02050.t1,gene\_10083.t1,gene\_08139.t1,gene\_05314.t1,gene\_10374.t1,gene\_06023.t1,gene\_09656.t1,gene\_01498.t1,gene\_07548.t1,gene\_02512.t1,gene\_01262.t1,gene\_02608.t1,gene\_08304.t1,gene\_04352.t1,gene\_01529.t1,gene\_00747.t1,gene\_04647.t1,gene\_06377.t1,gene\_01359.t1,gene\_07785.t1,gene\_03869.t1,gene\_01613.t1,gene\_10197.t1,gene\_04147.t1,gene\_00228.t1,gene\_08148.t1,gene\_09823.t1,gene\_09813.t1,gene\_04304.t1,gene\_09330.t1,gene\_01857.t1,gene\_08034.t1,gene\_10666.t1,gene\_08280.t1,gene\_06823.t1,gene\_05070.t1,gene\_02068.t1,gene\_02086.t1,gene\_01606.t1,gene\_01134.t1,gene\_05477.t1,gene\_01708.t1,gene\_06766.t1,gene\_04651.t1,gene\_08479.t1,gene\_07726.t1,gene\_00654.t1,gene\_05087.t1,gene\_10172.t1,gene\_05814.t1,gene\_05721.t1,gene\_00770.t1,gene\_03408.t1,gene\_09612.t1,gene\_10205.t1,gene\_03870.t1,gene\_03107.t1,gene\_02230.t1,gene\_08062.t1,gene\_04209.t1,gene\_02677.t1,gene\_09748.t1,gene\_03842.t1,gene\_09126.t1,gene\_03748.t1,gene\_04643.t1,gene\_04307.t1,gene\_04203.t1,gene\_10649.t1,gene\_07241.t1,gene\_06172.t1,gene\_03596.t1,gene\_01530.t1,gene\_05972.t1,gene\_03866.t1,gene\_01696.t1,gene\_00634.t1,gene\_00018.t1,gene\_01954.t1,gene\_02730.t1,gene\_09697.t1,gene\_00968.t1,gene\_07525.t1 | | transcription, DNA-templated | biological\_process |
| GO:0006352 | 8 | gene\_06623.t1,gene\_07165.t1,gene\_08353.t1,gene\_02242.t1,gene\_02119.t1,gene\_05884.t1,gene\_05962.t1,gene\_08645.t1 | | DNA-templated transcription, initiation | biological\_process |
| GO:0006353 | 1 | gene\_02253.t1 | | DNA-templated transcription, termination | biological\_process |
| GO:0046417 | 2 | gene\_08154.t1,gene\_05716.t1 | | chorismate metabolic process | biological\_process |
| GO:0046416 | 6 | gene\_07698.t1,gene\_06144.t1,gene\_05946.t1,gene\_10150.t1,gene\_05244.t1,gene\_02986.t1 | | D-amino acid metabolic process | biological\_process |
| GO:0009264 | 2 | gene\_10518.t1,gene\_06835.t1 | | deoxyribonucleotide catabolic process | biological\_process |
| GO:0035023 | 1 | gene\_00958.t1 | | regulation of Rho protein signal transduction | biological\_process |
| GO:0002100 | 1 | gene\_02973.t1 | | tRNA wobble adenosine to inosine editing | biological\_process |
| GO:0043161 | 8 | gene\_08488.t1,gene\_00399.t1,gene\_09250.t1,gene\_06474.t1,gene\_01630.t1,gene\_09214.t1,gene\_07038.t1,gene\_00843.t1 | | proteasome-mediated ubiquitin-dependent protein catabolic process | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0030091 | 1 | gene\_03751.t1 | | protein repair | biological\_process |
| GO:0016233 | 1 | gene\_02492.t1 | | telomere capping | biological\_process |
| GO:0006646 | 4 | gene\_09062.t1,gene\_10329.t1,gene\_02006.t1,gene\_09295.t1 | | phosphatidylethanolamine biosynthetic process | biological\_process |
| GO:0006644 | 5 | gene\_03496.t1,gene\_02872.t1,gene\_00809.t1,gene\_07679.t1,gene\_05347.t1 | | phospholipid metabolic process | biological\_process |
| GO:0006641 | 3 | gene\_05193.t1,gene\_01671.t1,gene\_01468.t1 | | triglyceride metabolic process | biological\_process |
| GO:0000350 | 1 | gene\_08218.t1 | | generation of catalytic spliceosome for second transesterification step | biological\_process |
| GO:0030490 | 1 | gene\_06649.t1 | | maturation of SSU-rRNA | biological\_process |
| GO:0006006 | 2 | gene\_07758.t1,gene\_06816.t1 | | glucose metabolic process | biological\_process |
| GO:0006007 | 1 | gene\_03194.t1 | | glucose catabolic process | biological\_process |
| GO:0006000 | 3 | gene\_09166.t1,gene\_09708.t1,gene\_04120.t1 | | fructose metabolic process | biological\_process |
| GO:0006002 | 1 | gene\_03414.t1 | | fructose 6-phosphate metabolic process | biological\_process |
| GO:0006003 | 3 | gene\_09166.t1,gene\_09708.t1,gene\_04120.t1 | | fructose 2,6-bisphosphate metabolic process | biological\_process |
| GO:0106035 | 1 | gene\_09749.t1 | | protein maturation by [4Fe-4S] cluster transfer | biological\_process |
| GO:0018293 | 1 | gene\_10389.t1 | | protein-FAD linkage | biological\_process |
| GO:0006914 | 18 | gene\_00063.t1,gene\_08294.t1,gene\_03474.t1,gene\_03697.t1,gene\_10308.t1,gene\_07531.t1,gene\_02759.t1,gene\_02838.t1,gene\_03179.t1,gene\_04192.t1,gene\_07354.t1,gene\_00981.t1,gene\_03468.t1,gene\_08284.t1,gene\_08177.t1,gene\_03031.t1,gene\_09511.t1,gene\_07033.t1 | | autophagy | biological\_process |
| GO:0006915 | 5 | gene\_10601.t1,gene\_09087.t1,gene\_10559.t1,gene\_05140.t1,gene\_02560.t1 | | apoptotic process | biological\_process |
| GO:0018298 | 3 | gene\_03901.t1,gene\_01792.t1,gene\_00746.t1 | | protein-chromophore linkage | biological\_process |
| GO:0009117 | 5 | gene\_09266.t1,gene\_03413.t1,gene\_01718.t1,gene\_09581.t1,gene\_07475.t1 | | nucleotide metabolic process | biological\_process |
| GO:0009116 | 22 | gene\_04965.t1,gene\_00772.t1,gene\_10016.t1,gene\_09819.t1,gene\_09719.t1,gene\_02018.t1,gene\_07520.t1,gene\_00164.t1,gene\_09276.t1,gene\_04495.t1,gene\_08132.t1,gene\_00083.t1,gene\_01248.t1,gene\_07023.t1,gene\_09154.t1,gene\_05063.t1,gene\_06265.t1,gene\_08377.t1,gene\_04964.t1,gene\_09009.t1,gene\_04496.t1,gene\_09478.t1 | | nucleoside metabolic process | biological\_process |
| GO:0018343 | 1 | gene\_04040.t1 | | protein farnesylation | biological\_process |
| GO:0018344 | 2 | gene\_09996.t1,gene\_08511.t1 | | protein geranylgeranylation | biological\_process |
| GO:0018345 | 1 | gene\_00203.t1 | | protein palmitoylation | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0045122 | 1 | gene\_02151.t1 | | aflatoxin biosynthetic process | biological\_process |
| GO:0000467 | 1 | gene\_03242.t1 | | exonucleolytic trimming to generate mature 3'-end of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | biological\_process |
| GO:0006821 | 3 | gene\_07629.t1,gene\_08410.t1,gene\_01052.t1 | | chloride transport | biological\_process |
| GO:0006826 | 7 | gene\_10564.t1,gene\_00830.t1,gene\_07511.t1,gene\_00797.t1,gene\_07124.t1,gene\_01257.t1,gene\_03078.t1 | | iron ion transport | biological\_process |
| GO:0019509 | 4 | gene\_02356.t1,gene\_10424.t1,gene\_09578.t1,gene\_03822.t1 | | L-methionine salvage from methylthioadenosine | biological\_process |
| GO:0070647 | 21 | gene\_05613.t1,gene\_09181.t1,gene\_10462.t1,gene\_01082.t1,gene\_07267.t1,gene\_04412.t1,gene\_06971.t1,gene\_00028.t1,gene\_03888.t1,gene\_00857.t1,gene\_08586.t1,gene\_07985.t1,gene\_09107.t1,gene\_01241.t1,gene\_03532.t1,gene\_03042.t1,gene\_00616.t1,gene\_01971.t1,gene\_06292.t1,gene\_10182.t1,gene\_07286.t1 | | protein modification by small protein conjugation or removal | biological\_process |
| GO:0019500 | 1 | gene\_02921.t1 | | cyanide catabolic process | biological\_process |
| GO:0061982 | 6 | gene\_08889.t1,gene\_00205.t1,gene\_10607.t1,gene\_03576.t1,gene\_09184.t1,gene\_05849.t1 | | meiosis I cell cycle process | biological\_process |
| GO:0032933 | 1 | gene\_07125.t1 | | SREBP signaling pathway | biological\_process |
| GO:0019722 | 2 | gene\_03950.t1,gene\_04058.t1 | | calcium-mediated signaling | biological\_process |
| GO:0019346 | 5 | gene\_07328.t1,gene\_01259.t1,gene\_04701.t1,gene\_04197.t1,gene\_05961.t1 | | transsulfuration | biological\_process |
| GO:0019432 | 2 | gene\_01120.t1,gene\_07365.t1 | | triglyceride biosynthetic process | biological\_process |
| GO:0019343 | 1 | gene\_01192.t1 | | cysteine biosynthetic process via cystathionine | biological\_process |
| GO:0019439 | 4 | gene\_02569.t1,gene\_09653.t1,gene\_06959.t1,gene\_02177.t1 | | aromatic compound catabolic process | biological\_process |
| GO:0019348 | 2 | gene\_00979.t1,gene\_02943.t1 | | dolichol metabolic process | biological\_process |
| GO:0043420 | 4 | gene\_00551.t1,gene\_02644.t1,gene\_04082.t1,gene\_07394.t1 | | anthranilate metabolic process | biological\_process |
| GO:1901576 | 3 | gene\_07849.t1,gene\_05257.t1,gene\_04763.t1 | | organic substance biosynthetic process | biological\_process |
| GO:0019430 | 1 | gene\_10408.t1 | | removal of superoxide radicals | biological\_process |
| GO:0019344 | 1 | gene\_07261.t1 | | cysteine biosynthetic process | biological\_process |
| GO:0019236 | 2 | gene\_09242.t1,gene\_03660.t1 | | response to pheromone | biological\_process |
| GO:0033609 | 3 | gene\_00147.t1,gene\_06408.t1,gene\_00074.t1 | | oxalate metabolic process | biological\_process |
| GO:0042147 | 7 | gene\_07863.t1,gene\_06774.t1,gene\_03468.t1,gene\_08974.t1,gene\_06399.t1,gene\_08108.t1,gene\_08590.t1 | | retrograde transport, endosome to Golgi | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0042149 | 1 | gene\_02850.t1 | | cellular response to glucose starvation | biological\_process |
| GO:0016540 | 2 | gene\_09062.t1,gene\_02006.t1 | | protein autoprocessing | biological\_process |
| GO:0033567 | 1 | gene\_10167.t1 | | DNA replication, Okazaki fragment processing | biological\_process |
| GO:0140053 | 1 | gene\_06331.t1 | | mitochondrial gene expression | biological\_process |
| GO:0030261 | 1 | gene\_07003.t1 | | chromosome condensation | biological\_process |
| GO:0043087 | 4 | gene\_02689.t1,gene\_03243.t1,gene\_09729.t1,gene\_10307.t1 | | regulation of GTPase activity | biological\_process |
| GO:0043086 | 1 | gene\_09968.t1 | | negative regulation of catalytic activity | biological\_process |
| GO:0043085 | 1 | gene\_04547.t1 | | positive regulation of catalytic activity | biological\_process |
| GO:1901605 | 1 | gene\_09263.t1 | | alpha-amino acid metabolic process | biological\_process |
| GO:0030004 | 1 | gene\_06398.t1 | | cellular monovalent inorganic cation homeostasis | biological\_process |
| GO:0030007 | 2 | gene\_06654.t1,gene\_07810.t1 | | cellular potassium ion homeostasis | biological\_process |
| GO:0001100 | 1 | gene\_04154.t1 | | negative regulation of exit from mitosis | biological\_process |
| GO:0006123 | 4 | gene\_00354.t1,gene\_08418.t1,gene\_02781.t1,gene\_08159.t1 | | mitochondrial electron transport, cytochrome c to oxygen | biological\_process |
| GO:0006122 | 4 | gene\_10111.t1,gene\_00585.t1,gene\_08819.t1,gene\_03982.t1 | | mitochondrial electron transport, ubiquinol to cytochrome c | biological\_process |
| GO:0006121 | 1 | gene\_10389.t1 | | mitochondrial electron transport, succinate to ubiquinone | biological\_process |
| GO:0043170 | 3 | gene\_05779.t1,gene\_05468.t1,gene\_10246.t1 | | macromolecule metabolic process | biological\_process |
| GO:0006556 | 2 | gene\_05535.t1,gene\_07806.t1 | | S-adenosylmethionine biosynthetic process | biological\_process |
| GO:0006557 | 1 | gene\_08168.t1 | | S-adenosylmethioninamine biosynthetic process | biological\_process |
| GO:0006654 | 1 | gene\_09152.t1 | | phosphatidic acid biosynthetic process | biological\_process |
| GO:0000184 | 6 | gene\_04284.t1,gene\_08813.t1,gene\_05772.t1,gene\_07933.t1,gene\_01856.t1,gene\_07305.t1 | | nuclear-transcribed mRNA catabolic process, nonsense-mediated decay | biological\_process |
| GO:0046386 | 2 | gene\_10518.t1,gene\_06835.t1 | | deoxyribose phosphate catabolic process | biological\_process |
| GO:0006659 | 1 | gene\_10329.t1 | | phosphatidylserine biosynthetic process | biological\_process |
| GO:0009231 | 6 | gene\_01228.t1,gene\_00125.t1,gene\_08770.t1,gene\_02362.t1,gene\_10466.t1,gene\_07127.t1 | | riboflavin biosynthetic process | biological\_process |
| GO:0006499 | 1 | gene\_01408.t1 | | N-terminal protein myristoylation | biological\_process |
| GO:0030488 | 3 | gene\_02659.t1,gene\_01679.t1,gene\_07742.t1 | | tRNA methylation | biological\_process |
| GO:0046281 | 2 | gene\_10373.t1,gene\_00631.t1 | | cinnamic acid catabolic process | biological\_process |
| GO:0006013 | 3 | gene\_07184.t1,gene\_09875.t1,gene\_00838.t1 | | mannose metabolic process | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0006012 | 2 | gene\_08393.t1,gene\_08593.t1 | | galactose metabolic process | biological\_process |
| GO:0006011 | 1 | gene\_04652.t1 | | UDP-glucose metabolic process | biological\_process |
| GO:0006015 | 2 | gene\_10016.t1,gene\_09154.t1 | | 5-phosphoribose 1-diphosphate biosynthetic process | biological\_process |
| GO:0009584 | 2 | gene\_03901.t1,gene\_01792.t1 | | detection of visible light | biological\_process |
| GO:0048193 | 4 | gene\_07961.t1,gene\_08532.t1,gene\_08887.t1,gene\_09729.t1 | | Golgi vesicle transport | biological\_process |
| GO:0051016 | 1 | gene\_07685.t1 | | barbed-end actin filament capping | biological\_process |
| GO:0042773 | 1 | gene\_04152.t1 | | ATP synthesis coupled electron transport | biological\_process |
| GO:0045002 | 1 | gene\_00330.t1 | | double-strand break repair via single-strand annealing | biological\_process |
| GO:0048280 | 1 | gene\_02252.t1 | | vesicle fusion with Golgi apparatus | biological\_process |
| GO:0048288 | 1 | gene\_03884.t1 | | nuclear membrane fusion involved in karyogamy | biological\_process |
| GO:0006904 | 2 | gene\_09722.t1,gene\_04572.t1 | | vesicle docking involved in exocytosis | biological\_process |
| GO:0009166 | 2 | gene\_02326.t1,gene\_10644.t1 | | nucleotide catabolic process | biological\_process |
| GO:0048268 | 1 | gene\_02601.t1 | | clathrin coat assembly | biological\_process |
| GO:0009165 | 3 | gene\_10016.t1,gene\_09009.t1,gene\_09154.t1 | | nucleotide biosynthetic process | biological\_process |
| GO:0044281 | 11 | gene\_00061.t1,gene\_08935.t1,gene\_00062.t1,gene\_09604.t1,gene\_03860.t1,gene\_07145.t1,gene\_10050.t1,gene\_00212.t1,gene\_08940.t1,gene\_09405.t1,gene\_00522.t1 | | small molecule metabolic process | biological\_process |
| GO:0044283 | 2 | gene\_04620.t1,gene\_07600.t1 | | small molecule biosynthetic process | biological\_process |
| GO:0000244 | 1 | gene\_05450.t1 | | spliceosomal tri-snRNP complex assembly | biological\_process |
| GO:0044255 | 8 | gene\_09714.t1,gene\_06616.t1,gene\_05956.t1,gene\_07976.t1,gene\_09463.t1,gene\_05622.t1,gene\_01218.t1,gene\_04514.t1 | | cellular lipid metabolic process | biological\_process |
| GO:0009168 | 1 | gene\_01718.t1 | | purine ribonucleoside monophosphate biosynthetic process | biological\_process |
| GO:0000160 | 5 | gene\_00398.t1,gene\_04615.t1,gene\_07882.t1,gene\_00017.t1,gene\_04034.t1 | | phosphorelay signal transduction system | biological\_process |
| GO:0045132 | 2 | gene\_07290.t1,gene\_05154.t1 | | meiotic chromosome segregation | biological\_process |
| GO:0006839 | 1 | gene\_03943.t1 | | mitochondrial transport | biological\_process |
| GO:0070940 | 2 | gene\_05704.t1,gene\_00538.t1 | | dephosphorylation of RNA polymerase II C-terminal domain | biological\_process |
| GO:0070987 | 4 | gene\_03610.t1,gene\_10061.t1,gene\_08006.t1,gene\_04737.t1 | | error-free translesion synthesis | biological\_process |
| GO:0051225 | 2 | gene\_09991.t1,gene\_10291.t1 | | spindle assembly | biological\_process |
| GO:0016973 | 5 | gene\_01628.t1,gene\_10642.t1,gene\_10643.t1,gene\_05611.t1,gene\_07129.t1 | | poly(A)+ mRNA export from nucleus | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0035999 | 5 | gene\_01168.t1,gene\_07024.t1,gene\_06799.t1,gene\_07886.t1,gene\_03196.t1 | | tetrahydrofolate interconversion | biological\_process |
| GO:0007232 | 1 | gene\_01278.t1 | | osmosensory signaling pathway via Sho1 osmosensor | biological\_process |
| GO:0001682 | 6 | gene\_06449.t1,gene\_00840.t1,gene\_10169.t1,gene\_03157.t1,gene\_01748.t1,gene\_05910.t1 | | tRNA 5'-leader removal | biological\_process |
| GO:0046856 | 5 | gene\_07363.t1,gene\_04510.t1,gene\_06333.t1,gene\_07789.t1,gene\_04548.t1 | | phosphatidylinositol dephosphorylation | biological\_process |
| GO:0046855 | 4 | gene\_01292.t1,gene\_05585.t1,gene\_02349.t1,gene\_03882.t1 | | inositol phosphate dephosphorylation | biological\_process |
| GO:0046854 | 4 | gene\_05585.t1,gene\_02349.t1,gene\_03882.t1,gene\_07371.t1 | | phosphatidylinositol phosphate biosynthetic process | biological\_process |
| GO:0042823 | 2 | gene\_04580.t1,gene\_01088.t1 | | pyridoxal phosphate biosynthetic process | biological\_process |
| GO:0032259 | 64 | gene\_09715.t1,gene\_07369.t1,gene\_03543.t1,gene\_04324.t1,gene\_05187.t1,gene\_09600.t1,gene\_03686.t1,gene\_00786.t1,gene\_02875.t1,gene\_05570.t1,gene\_06238.t1,gene\_00044.t1,gene\_01127.t1,gene\_06694.t1,gene\_02208.t1,gene\_10340.t1,gene\_01301.t1,gene\_03669.t1,gene\_00239.t1,gene\_05279.t1,gene\_05786.t1,gene\_01676.t1,gene\_06837.t1,gene\_05115.t1,gene\_08025.t1,gene\_03477.t1,gene\_01784.t1,gene\_09477.t1,gene\_04497.t1,gene\_02225.t1,gene\_07039.t1,gene\_00382.t1,gene\_03090.t1,gene\_01168.t1,gene\_02625.t1,gene\_01715.t1,gene\_10027.t1,gene\_04278.t1,gene\_02161.t1,gene\_07850.t1,gene\_03196.t1,gene\_01783.t1,gene\_06497.t1,gene\_07963.t1,gene\_03847.t1,gene\_00180.t1,gene\_00612.t1,gene\_00334.t1,gene\_05606.t1,gene\_03441.t1,gene\_06478.t1,gene\_05302.t1,gene\_03893.t1,gene\_04453.t1,gene\_00854.t1,gene\_04044.t1,gene\_01287.t1,gene\_01824.t1,gene\_10674.t1,gene\_02183.t1,gene\_00606.t1,gene\_03309.t1,gene\_03168.t1,gene\_10501.t1 | | methylation | biological\_process |
| GO:0019408 | 2 | gene\_05126.t1,gene\_10116.t1 | | dolichol biosynthetic process | biological\_process |
| GO:0043410 | 1 | gene\_03887.t1 | | positive regulation of MAPK cascade | biological\_process |
| GO:0043414 | 1 | gene\_09851.t1 | | macromolecule methylation | biological\_process |
| GO:0043419 | 1 | gene\_01624.t1 | | urea catabolic process | biological\_process |
| GO:0006783 | 2 | gene\_04538.t1,gene\_09989.t1 | | heme biosynthetic process | biological\_process |
| GO:0071586 | 2 | gene\_09674.t1,gene\_00418.t1 | | CAAX-box protein processing | biological\_process |
| GO:0019243 | 1 | gene\_08534.t1 | | methylglyoxal catabolic process to D-lactate via S-lactoyl-glutathione | biological\_process |
| GO:0033615 | 1 | gene\_01561.t1 | | mitochondrial proton-transporting ATP synthase complex assembly | biological\_process |
| GO:0033617 | 5 | gene\_00454.t1,gene\_09558.t1,gene\_05977.t1,gene\_03201.t1,gene\_09301.t1 | | mitochondrial cytochrome c oxidase assembly | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0072583 | 1 | gene\_01313.t1 | | clathrin-dependent endocytosis | biological\_process |
| GO:0042176 | 3 | gene\_07275.t1,gene\_05847.t1,gene\_01479.t1 | | regulation of protein catabolic process | biological\_process |
| GO:0016559 | 3 | gene\_06344.t1,gene\_03732.t1,gene\_07686.t1 | | peroxisome fission | biological\_process |
| GO:0016558 | 2 | gene\_01977.t1,gene\_05844.t1 | | protein import into peroxisome matrix | biological\_process |
| GO:0034553 | 1 | gene\_03687.t1 | | mitochondrial respiratory chain complex II assembly | biological\_process |
| GO:0071765 | 1 | gene\_02440.t1 | | nuclear inner membrane organization | biological\_process |
| GO:0046279 | 1 | gene\_05589.t1 | | 3,4-dihydroxybenzoate biosynthetic process | biological\_process |
| GO:0030259 | 5 | gene\_03179.t1,gene\_00199.t1,gene\_03481.t1,gene\_07845.t1,gene\_07540.t1 | | lipid glycosylation | biological\_process |
| GO:0006338 | 20 | gene\_09453.t1,gene\_10296.t1,gene\_07303.t1,gene\_08700.t1,gene\_04352.t1,gene\_09736.t1,gene\_00643.t1,gene\_06866.t1,gene\_03376.t1,gene\_08699.t1,gene\_06320.t1,gene\_08995.t1,gene\_08351.t1,gene\_09322.t1,gene\_03937.t1,gene\_07314.t1,gene\_05457.t1,gene\_01333.t1,gene\_00391.t1,gene\_03800.t1 | | chromatin remodeling | biological\_process |
| GO:0006336 | 1 | gene\_03047.t1 | | DNA replication-independent chromatin assembly | biological\_process |
| GO:0006334 | 6 | gene\_02242.t1,gene\_07282.t1,gene\_05665.t1,gene\_07960.t1,gene\_09268.t1,gene\_03509.t1 | | nucleosome assembly | biological\_process |
| GO:0006335 | 1 | gene\_02594.t1 | | DNA replication-dependent chromatin assembly | biological\_process |
| GO:0006078 | 2 | gene\_01195.t1,gene\_06043.t1 | | (1->6)-beta-D-glucan biosynthetic process | biological\_process |
| GO:0006172 | 2 | gene\_04186.t1,gene\_01019.t1 | | ADP biosynthetic process | biological\_process |
| GO:0046475 | 2 | gene\_05869.t1,gene\_05485.t1 | | glycerophospholipid catabolic process | biological\_process |
| GO:0046470 | 1 | gene\_03380.t1 | | phosphatidylcholine metabolic process | biological\_process |
| GO:0006879 | 1 | gene\_09989.t1 | | cellular iron ion homeostasis | biological\_process |
| GO:0030036 | 5 | gene\_10315.t1,gene\_06638.t1,gene\_02045.t1,gene\_10032.t1,gene\_09686.t1 | | actin cytoskeleton organization | biological\_process |
| GO:0002128 | 1 | gene\_03856.t1 | | tRNA nucleoside ribose methylation | biological\_process |
| GO:0006480 | 1 | gene\_06086.t1 | | N-terminal protein amino acid methylation | biological\_process |
| GO:0051304 | 1 | gene\_07172.t1 | | chromosome separation | biological\_process |
| GO:0006486 | 25 | gene\_05724.t1,gene\_04055.t1,gene\_09608.t1,gene\_10310.t1,gene\_08604.t1,gene\_08160.t1,gene\_05800.t1,gene\_01531.t1,gene\_03572.t1,gene\_02233.t1,gene\_08332.t1,gene\_09861.t1,gene\_02462.t1,gene\_05978.t1,gene\_05746.t1,gene\_02421.t1,gene\_03162.t1,gene\_08395.t1,gene\_01247.t1,gene\_02817.t1,gene\_00979.t1,gene\_05126.t1,gene\_05817.t1,gene\_02125.t1,gene\_06325.t1 | | protein glycosylation | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0009820 | 5 | gene\_05483.t1,gene\_07849.t1,gene\_05257.t1,gene\_00621.t1,gene\_04763.t1 | | alkaloid metabolic process | biological\_process |
| GO:0006488 | 7 | gene\_07018.t1,gene\_02943.t1,gene\_02439.t1,gene\_06952.t1,gene\_07000.t1,gene\_08298.t1,gene\_10419.t1 | | dolichol-linked oligosaccharide biosynthetic process | biological\_process |
| GO:0006241 | 1 | gene\_07884.t1 | | CTP biosynthetic process | biological\_process |
| GO:0009229 | 3 | gene\_04276.t1,gene\_07868.t1,gene\_01046.t1 | | thiamine diphosphate biosynthetic process | biological\_process |
| GO:0009228 | 4 | gene\_09923.t1,gene\_00596.t1,gene\_07868.t1,gene\_01046.t1 | | thiamine biosynthetic process | biological\_process |
| GO:0006464 | 7 | gene\_09008.t1,gene\_09100.t1,gene\_03839.t1,gene\_08628.t1,gene\_00453.t1,gene\_10270.t1,gene\_09204.t1 | | cellular protein modification process | biological\_process |
| GO:0006465 | 6 | gene\_08545.t1,gene\_09230.t1,gene\_09050.t1,gene\_03043.t1,gene\_07920.t1,gene\_00277.t1 | | signal peptide processing | biological\_process |
| GO:0000379 | 2 | gene\_05909.t1,gene\_02939.t1 | | tRNA-type intron splice site recognition and cleavage | biological\_process |
| GO:0000028 | 1 | gene\_09004.t1 | | ribosomal small subunit assembly | biological\_process |
| GO:0006796 | 1 | gene\_07215.t1 | | phosphate-containing compound metabolic process | biological\_process |
| GO:0006790 | 1 | gene\_03882.t1 | | sulfur compound metabolic process | biological\_process |
| GO:0006069 | 1 | gene\_00963.t1 | | ethanol oxidation | biological\_process |
| GO:0000083 | 1 | gene\_09058.t1 | | regulation of transcription involved in G1/S transition of mitotic cell cycle | biological\_process |
| GO:0045039 | 1 | gene\_01635.t1 | | protein insertion into mitochondrial inner membrane | biological\_process |
| GO:0045033 | 1 | gene\_06702.t1 | | peroxisome inheritance | biological\_process |
| GO:0006661 | 1 | gene\_10495.t1 | | phosphatidylinositol biosynthetic process | biological\_process |
| GO:0006662 | 1 | gene\_01940.t1 | | glycerol ether metabolic process | biological\_process |
| GO:0031297 | 1 | gene\_03935.t1 | | replication fork processing | biological\_process |
| GO:0006665 | 5 | gene\_06715.t1,gene\_04370.t1,gene\_04434.t1,gene\_09922.t1,gene\_05878.t1 | | sphingolipid metabolic process | biological\_process |
| GO:0051056 | 1 | gene\_09563.t1 | | regulation of small GTPase mediated signal transduction | biological\_process |
| GO:0043967 | 1 | gene\_00391.t1 | | histone H4 acetylation | biological\_process |
| GO:0043968 | 1 | gene\_00391.t1 | | histone H2A acetylation | biological\_process |
| GO:0010133 | 3 | gene\_03825.t1,gene\_02582.t1,gene\_06400.t1 | | proline catabolic process to glutamate | biological\_process |
| GO:1904263 | 2 | gene\_09312.t1,gene\_07017.t1 | | positive regulation of TORC1 signaling | biological\_process |
| GO:0031507 | 1 | gene\_07352.t1 | | heterochromatin assembly | biological\_process |
| GO:0031505 | 3 | gene\_10016.t1,gene\_09154.t1,gene\_01169.t1 | | fungal-type cell wall organization | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0000154 | 1 | gene\_01030.t1 | | rRNA modification | biological\_process |
| GO:0006807 | 18 | gene\_05779.t1,gene\_07811.t1,gene\_10541.t1,gene\_01471.t1,gene\_07891.t1,gene\_10246.t1,gene\_09112.t1,gene\_01256.t1,gene\_06247.t1,gene\_03928.t1,gene\_10165.t1,gene\_09586.t1,gene\_10580.t1,gene\_10011.t1,gene\_07533.t1,gene\_08759.t1,gene\_10588.t1,gene\_04568.t1 | | nitrogen compound metabolic process | biological\_process |
| GO:0006801 | 1 | gene\_00487.t1 | | superoxide metabolic process | biological\_process |
| GO:0006809 | 1 | gene\_08723.t1 | | nitric oxide biosynthetic process | biological\_process |
| GO:0046916 | 7 | gene\_01285.t1,gene\_03300.t1,gene\_10251.t1,gene\_00177.t1,gene\_07729.t1,gene\_10631.t1,gene\_02153.t1 | | cellular transition metal ion homeostasis | biological\_process |
| GO:0070197 | 1 | gene\_05891.t1 | | meiotic attachment of telomere to nuclear envelope | biological\_process |
| GO:0007229 | 1 | gene\_10062.t1 | | integrin-mediated signaling pathway | biological\_process |
| GO:0019674 | 3 | gene\_08533.t1,gene\_09241.t1,gene\_07119.t1 | | NAD metabolic process | biological\_process |
| GO:0019679 | 2 | gene\_00257.t1,gene\_09476.t1 | | propionate metabolic process, methylcitrate cycle | biological\_process |
| GO:0032065 | 2 | gene\_04533.t1,gene\_01180.t1 | | maintenance of protein location in cell cortex | biological\_process |
| GO:0072666 | 2 | gene\_05346.t1,gene\_09100.t1 | | establishment of protein localization to vacuole | biological\_process |
| GO:0002949 | 2 | gene\_04246.t1,gene\_09601.t1 | | tRNA threonylcarbamoyladenosine modification | biological\_process |
| GO:0002084 | 1 | gene\_09078.t1 | | protein depalmitoylation | biological\_process |
| GO:0016126 | 12 | gene\_01364.t1,gene\_04746.t1,gene\_03020.t1,gene\_08853.t1,gene\_10502.t1,gene\_07280.t1,gene\_00352.t1,gene\_01577.t1,gene\_02975.t1,gene\_04541.t1,gene\_03309.t1,gene\_04110.t1 | | sterol biosynthetic process | biological\_process |
| GO:0016125 | 3 | gene\_03504.t1,gene\_01909.t1,gene\_06509.t1 | | sterol metabolic process | biological\_process |
| GO:0016578 | 1 | gene\_10530.t1 | | histone deubiquitination | biological\_process |
| GO:0097720 | 1 | gene\_08141.t1 | | calcineurin-mediated signaling | biological\_process |
| GO:0051276 | 3 | gene\_06720.t1,gene\_03476.t1,gene\_08023.t1 | | chromosome organization | biological\_process |
| GO:0007033 | 1 | gene\_06125.t1 | | vacuole organization | biological\_process |
| GO:0007030 | 2 | gene\_07871.t1,gene\_06774.t1 | | Golgi organization | biological\_process |
| GO:0007031 | 5 | gene\_04177.t1,gene\_07101.t1,gene\_06038.t1,gene\_08176.t1,gene\_03246.t1 | | peroxisome organization | biological\_process |
| GO:0007034 | 13 | gene\_03881.t1,gene\_03659.t1,gene\_09100.t1,gene\_10035.t1,gene\_10321.t1,gene\_03667.t1,gene\_02491.t1,gene\_06105.t1,gene\_06338.t1,gene\_02853.t1,gene\_05209.t1,gene\_05346.t1,gene\_06141.t1 | | vacuolar transport | biological\_process |
| GO:1904380 | 1 | gene\_08332.t1 | | endoplasmic reticulum mannose trimming | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:1901136 | 1 | gene\_06777.t1 | | carbohydrate derivative catabolic process | biological\_process |
| GO:1901135 | 9 | gene\_00152.t1,gene\_00659.t1,gene\_08226.t1,gene\_09623.t1,gene\_06634.t1,gene\_00389.t1,gene\_03848.t1,gene\_04359.t1,gene\_03632.t1 | | carbohydrate derivative metabolic process | biological\_process |
| GO:0071025 | 1 | gene\_02565.t1 | | RNA surveillance | biological\_process |
| GO:0030245 | 6 | gene\_03630.t1,gene\_02981.t1,gene\_08104.t1,gene\_05405.t1,gene\_01844.t1,gene\_02670.t1 | | cellulose catabolic process | biological\_process |
| GO:0046041 | 1 | gene\_01019.t1 | | ITP metabolic process | biological\_process |
| GO:0019878 | 4 | gene\_05493.t1,gene\_10072.t1,gene\_03038.t1,gene\_03989.t1 | | lysine biosynthetic process via aminoadipic acid | biological\_process |
| GO:0006325 | 32 | gene\_00705.t1,gene\_04231.t1,gene\_03101.t1,gene\_02360.t1,gene\_02703.t1,gene\_09874.t1,gene\_07183.t1,gene\_02668.t1,gene\_00682.t1,gene\_02804.t1,gene\_09220.t1,gene\_08500.t1,gene\_01223.t1,gene\_10177.t1,gene\_09828.t1,gene\_10281.t1,gene\_07759.t1,gene\_05805.t1,gene\_05523.t1,gene\_10003.t1,gene\_10008.t1,gene\_05373.t1,gene\_04656.t1,gene\_00415.t1,gene\_07837.t1,gene\_10229.t1,gene\_09585.t1,gene\_07640.t1,gene\_10407.t1,gene\_00548.t1,gene\_00832.t1,gene\_03898.t1 | | chromatin organization | biological\_process |
| GO:0001731 | 1 | gene\_08881.t1 | | formation of translation preinitiation complex | biological\_process |
| GO:0044571 | 1 | gene\_09097.t1 | | [2Fe-2S] cluster assembly | biological\_process |
| GO:0033621 | 1 | gene\_05249.t1 | | nuclear-transcribed mRNA catabolic process, meiosis-specific transcripts | biological\_process |
| GO:0032456 | 1 | gene\_06774.t1 | | endocytic recycling | biological\_process |
| GO:0030026 | 3 | gene\_10247.t1,gene\_00807.t1,gene\_03253.t1 | | cellular manganese ion homeostasis | biological\_process |
| GO:0015940 | 6 | gene\_03893.t1,gene\_03436.t1,gene\_05955.t1,gene\_01676.t1,gene\_01574.t1,gene\_07251.t1 | | pantothenate biosynthetic process | biological\_process |
| GO:0071816 | 1 | gene\_09348.t1 | | tail-anchored membrane protein insertion into ER membrane | biological\_process |
| GO:0006491 | 1 | gene\_06032.t1 | | N-glycan processing | biological\_process |
| GO:0006490 | 1 | gene\_06325.t1 | | oligosaccharide-lipid intermediate biosynthetic process | biological\_process |
| GO:0097054 | 1 | gene\_04134.t1 | | L-glutamate biosynthetic process | biological\_process |
| GO:0097056 | 2 | gene\_09273.t1,gene\_05654.t1 | | selenocysteinyl-tRNA(Sec) biosynthetic process | biological\_process |
| GO:0097502 | 3 | gene\_03572.t1,gene\_09608.t1,gene\_05724.t1 | | mannosylation | biological\_process |
| GO:0097053 | 2 | gene\_00551.t1,gene\_04082.t1 | | L-kynurenine catabolic process | biological\_process |
| GO:0006259 | 2 | gene\_04413.t1,gene\_05741.t1 | | DNA metabolic process | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0030001 | 1 | gene\_10321.t1 | | metal ion transport | biological\_process |
| GO:0045893 | 1 | gene\_08663.t1 | | positive regulation of transcription, DNA-templated | biological\_process |
| GO:0006471 | 1 | gene\_00229.t1 | | protein ADP-ribosylation | biological\_process |
| GO:0010390 | 1 | gene\_09585.t1 | | histone monoubiquitination | biological\_process |
| GO:0006474 | 1 | gene\_05336.t1 | | N-terminal protein amino acid acetylation | biological\_process |
| GO:0046294 | 2 | gene\_04252.t1,gene\_07706.t1 | | formaldehyde catabolic process | biological\_process |
| GO:0009968 | 1 | gene\_07012.t1 | | negative regulation of signal transduction | biological\_process |
| GO:0009966 | 3 | gene\_08172.t1,gene\_05842.t1,gene\_03512.t1 | | regulation of signal transduction | biological\_process |
| GO:0006782 | 7 | gene\_05843.t1,gene\_01680.t1,gene\_04193.t1,gene\_04355.t1,gene\_10525.t1,gene\_05150.t1,gene\_03980.t1 | | protoporphyrinogen IX biosynthetic process | biological\_process |
| GO:0006780 | 1 | gene\_10525.t1 | | uroporphyrinogen III biosynthetic process | biological\_process |
| GO:0006784 | 1 | gene\_03787.t1 | | heme A biosynthetic process | biological\_process |
| GO:0022900 | 3 | gene\_04447.t1,gene\_07137.t1,gene\_09825.t1 | | electron transport chain | biological\_process |
| GO:0006071 | 1 | gene\_07365.t1 | | glycerol metabolic process | biological\_process |
| GO:0022904 | 1 | gene\_00583.t1 | | respiratory electron transport chain | biological\_process |
| GO:0006673 | 1 | gene\_06167.t1 | | inositol phosphoceramide metabolic process | biological\_process |
| GO:0006672 | 2 | gene\_06499.t1,gene\_10132.t1 | | ceramide metabolic process | biological\_process |
| GO:0006120 | 2 | gene\_07351.t1,gene\_08864.t1 | | mitochondrial electron transport, NADH to ubiquinone | biological\_process |
| GO:0045116 | 2 | gene\_03524.t1,gene\_06445.t1 | | protein neddylation | biological\_process |
| GO:0031571 | 1 | gene\_02629.t1 | | mitotic G1 DNA damage checkpoint signaling | biological\_process |
| GO:0006536 | 3 | gene\_05088.t1,gene\_09066.t1,gene\_10583.t1 | | glutamate metabolic process | biological\_process |
| GO:0006813 | 1 | gene\_08146.t1 | | potassium ion transport | biological\_process |
| GO:0006530 | 1 | gene\_07801.t1 | | asparagine catabolic process | biological\_process |
| GO:0006811 | 7 | gene\_07939.t1,gene\_05352.t1,gene\_04031.t1,gene\_05744.t1,gene\_02961.t1,gene\_09989.t1,gene\_05827.t1 | | ion transport | biological\_process |
| GO:0006817 | 3 | gene\_07427.t1,gene\_06183.t1,gene\_07824.t1 | | phosphate ion transport | biological\_process |
| GO:0006816 | 1 | gene\_09583.t1 | | calcium ion transport | biological\_process |
| GO:1902531 | 2 | gene\_05645.t1,gene\_01792.t1 | | regulation of intracellular signal transduction | biological\_process |
| GO:0070966 | 1 | gene\_02565.t1 | | nuclear-transcribed mRNA catabolic process, no-go decay | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0046907 | 9 | gene\_05796.t1,gene\_10035.t1,gene\_02491.t1,gene\_06105.t1,gene\_10545.t1,gene\_06338.t1,gene\_05209.t1,gene\_06141.t1,gene\_00603.t1 | | intracellular transport | biological\_process |
| GO:0006171 | 1 | gene\_03592.t1 | | cAMP biosynthetic process | biological\_process |
| GO:0006656 | 2 | gene\_06238.t1,gene\_05187.t1 | | phosphatidylcholine biosynthetic process | biological\_process |
| GO:0048015 | 2 | gene\_08215.t1,gene\_07371.t1 | | phosphatidylinositol-mediated signaling | biological\_process |
| GO:0019464 | 1 | gene\_03285.t1 | | glycine decarboxylation via glycine cleavage system | biological\_process |
| GO:0051083 | 1 | gene\_03313.t1 | | 'de novo' cotranslational protein folding | biological\_process |
| GO:0070143 | 2 | gene\_00660.t1,gene\_09742.t1 | | mitochondrial alanyl-tRNA aminoacylation | biological\_process |
| GO:0016485 | 1 | gene\_05844.t1 | | protein processing | biological\_process |
| GO:0016480 | 1 | gene\_07105.t1 | | negative regulation of transcription by RNA polymerase III | biological\_process |
| GO:0016482 | 2 | gene\_02853.t1,gene\_02540.t1 | | cytosolic transport | biological\_process |
| GO:0000422 | 1 | gene\_05641.t1 | | autophagy of mitochondrion | biological\_process |
| GO:0000423 | 1 | gene\_08030.t1 | | mitophagy | biological\_process |
| GO:0000956 | 2 | gene\_09407.t1,gene\_07641.t1 | | nuclear-transcribed mRNA catabolic process | biological\_process |
| GO:0071562 | 1 | gene\_06131.t1 | | nucleus-vacuole junction assembly | biological\_process |
| GO:0019264 | 2 | gene\_01168.t1,gene\_03196.t1 | | glycine biosynthetic process from serine | biological\_process |
| GO:0000959 | 1 | gene\_09628.t1 | | mitochondrial RNA metabolic process | biological\_process |
| GO:0000737 | 1 | gene\_03054.t1 | | DNA catabolic process, endonucleolytic | biological\_process |
| GO:0000731 | 1 | gene\_06439.t1 | | DNA synthesis involved in DNA repair | biological\_process |
| GO:0000349 | 1 | gene\_07836.t1 | | generation of catalytic spliceosome for first transesterification step | biological\_process |
| GO:0019287 | 4 | gene\_00352.t1,gene\_01364.t1,gene\_08132.t1,gene\_08399.t1 | | isopentenyl diphosphate biosynthetic process, mevalonate pathway | biological\_process |
| GO:0019284 | 2 | gene\_02356.t1,gene\_10424.t1 | | L-methionine salvage from S-adenosylmethionine | biological\_process |
| GO:0019285 | 3 | gene\_04677.t1,gene\_01810.t1,gene\_06957.t1 | | glycine betaine biosynthetic process from choline | biological\_process |
| GO:0007021 | 2 | gene\_01139.t1,gene\_05824.t1 | | tubulin complex assembly | biological\_process |
| GO:0007020 | 5 | gene\_06203.t1,gene\_08722.t1,gene\_05691.t1,gene\_08161.t1,gene\_07037.t1 | | microtubule nucleation | biological\_process |
| GO:0007023 | 3 | gene\_06759.t1,gene\_01139.t1,gene\_05824.t1 | | post-chaperonin tubulin folding pathway | biological\_process |
| GO:0030833 | 4 | gene\_06990.t1,gene\_07743.t1,gene\_02382.t1,gene\_03091.t1 | | regulation of actin filament polymerization | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0032981 | 4 | gene\_02773.t1,gene\_02255.t1,gene\_08052.t1,gene\_10382.t1 | | mitochondrial respiratory chain complex I assembly | biological\_process |
| GO:0007029 | 1 | gene\_03296.t1 | | endoplasmic reticulum organization | biological\_process |
| GO:0071705 | 1 | gene\_05468.t1 | | nitrogen compound transport | biological\_process |
| GO:0071704 | 1 | gene\_00701.t1 | | organic substance metabolic process | biological\_process |
| GO:0071702 | 2 | gene\_05468.t1,gene\_09187.t1 | | organic substance transport | biological\_process |
| GO:0009411 | 1 | gene\_06477.t1 | | response to UV | biological\_process |
| GO:0016226 | 12 | gene\_06236.t1,gene\_02122.t1,gene\_07825.t1,gene\_08094.t1,gene\_00550.t1,gene\_09989.t1,gene\_07666.t1,gene\_10005.t1,gene\_00274.t1,gene\_05175.t1,gene\_01557.t1,gene\_00305.t1 | | iron-sulfur cluster assembly | biological\_process |
| GO:0042026 | 1 | gene\_01751.t1 | | protein refolding | biological\_process |
| GO:0034227 | 2 | gene\_01562.t1,gene\_05774.t1 | | tRNA thio-modification | biological\_process |
| GO:0034599 | 13 | gene\_05939.t1,gene\_09415.t1,gene\_05276.t1,gene\_02994.t1,gene\_07238.t1,gene\_06296.t1,gene\_02909.t1,gene\_04070.t1,gene\_02830.t1,gene\_09292.t1,gene\_03631.t1,gene\_07930.t1,gene\_10593.t1 | | cellular response to oxidative stress | biological\_process |
| GO:0006310 | 24 | gene\_01043.t1,gene\_07889.t1,gene\_03702.t1,gene\_06517.t1,gene\_06102.t1,gene\_08299.t1,gene\_03054.t1,gene\_08530.t1,gene\_09591.t1,gene\_05747.t1,gene\_02787.t1,gene\_05811.t1,gene\_02991.t1,gene\_00363.t1,gene\_09891.t1,gene\_05677.t1,gene\_08889.t1,gene\_08214.t1,gene\_04537.t1,gene\_07821.t1,gene\_06740.t1,gene\_09184.t1,gene\_08300.t1,gene\_02270.t1 | | DNA recombination | biological\_process |
| GO:0006313 | 3 | gene\_02212.t1,gene\_01274.t1,gene\_10675.t1 | | transposition, DNA-mediated | biological\_process |
| GO:0051726 | 1 | gene\_01330.t1 | | regulation of cell cycle | biological\_process |
| GO:0071630 | 1 | gene\_00356.t1 | | nuclear protein quality control by the ubiquitin-proteasome system | biological\_process |
| GO:0045905 | 1 | gene\_01551.t1 | | positive regulation of translational termination | biological\_process |
| GO:0045901 | 2 | gene\_01551.t1,gene\_08192.t1 | | positive regulation of translational elongation | biological\_process |
| GO:0015976 | 2 | gene\_10073.t1,gene\_04635.t1 | | carbon utilization | biological\_process |
| GO:0002143 | 1 | gene\_08455.t1 | | tRNA wobble position uridine thiolation | biological\_process |
| GO:0006409 | 1 | gene\_07129.t1 | | tRNA export from nucleus | biological\_process |
| GO:0006265 | 3 | gene\_10607.t1,gene\_01025.t1,gene\_02674.t1 | | DNA topological change | biological\_process |
| GO:0017196 | 2 | gene\_03249.t1,gene\_01755.t1 | | N-terminal peptidyl-methionine acetylation | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0006260 | 32 | gene\_01043.t1,gene\_04551.t1,gene\_04254.t1,gene\_06309.t1,gene\_03702.t1,gene\_06517.t1,gene\_10241.t1,gene\_08299.t1,gene\_01660.t1,gene\_04166.t1,gene\_06076.t1,gene\_08530.t1,gene\_06439.t1,gene\_02787.t1,gene\_04582.t1,gene\_08269.t1,gene\_06219.t1,gene\_05811.t1,gene\_06856.t1,gene\_07010.t1,gene\_05556.t1,gene\_00675.t1,gene\_08300.t1,gene\_06427.t1,gene\_05677.t1,gene\_07821.t1,gene\_06340.t1,gene\_10155.t1,gene\_00595.t1,gene\_07001.t1,gene\_03200.t1,gene\_00297.t1 | | DNA replication | biological\_process |
| GO:0006261 | 4 | gene\_01390.t1,gene\_05741.t1,gene\_09767.t1,gene\_08287.t1 | | DNA-dependent DNA replication | biological\_process |
| GO:0006268 | 1 | gene\_09071.t1 | | DNA unwinding involved in DNA replication | biological\_process |
| GO:0006269 | 1 | gene\_01018.t1 | | DNA replication, synthesis of RNA primer | biological\_process |
| GO:0043328 | 3 | gene\_07913.t1,gene\_06652.t1,gene\_01280.t1 | | protein transport to vacuole involved in ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway | biological\_process |
| GO:0009204 | 1 | gene\_09266.t1 | | deoxyribonucleoside triphosphate catabolic process | biological\_process |
| GO:0006446 | 1 | gene\_03188.t1 | | regulation of translational initiation | biological\_process |
| GO:0006401 | 5 | gene\_06776.t1,gene\_00504.t1,gene\_09856.t1,gene\_00829.t1,gene\_00355.t1 | | RNA catabolic process | biological\_process |
| GO:0006048 | 4 | gene\_02481.t1,gene\_00859.t1,gene\_02361.t1,gene\_06597.t1 | | UDP-N-acetylglucosamine biosynthetic process | biological\_process |
| GO:0006040 | 1 | gene\_03840.t1 | | amino sugar metabolic process | biological\_process |
| GO:0036503 | 1 | gene\_04068.t1 | | ERAD pathway | biological\_process |
| GO:0042744 | 6 | gene\_03391.t1,gene\_02272.t1,gene\_05483.t1,gene\_00621.t1,gene\_00545.t1,gene\_01284.t1 | | hydrogen peroxide catabolic process | biological\_process |
| GO:0000226 | 1 | gene\_06271.t1 | | microtubule cytoskeleton organization | biological\_process |
| GO:0042742 | 1 | gene\_01789.t1 | | defense response to bacterium | biological\_process |
| GO:0065003 | 1 | gene\_08486.t1 | | protein-containing complex assembly | biological\_process |
| GO:0048478 | 1 | gene\_01226.t1 | | replication fork protection | biological\_process |
| GO:0006685 | 2 | gene\_00291.t1,gene\_07110.t1 | | sphingomyelin catabolic process | biological\_process |
| GO:0009156 | 2 | gene\_10016.t1,gene\_09154.t1 | | ribonucleoside monophosphate biosynthetic process | biological\_process |
| GO:0008156 | 1 | gene\_01336.t1 | | negative regulation of DNA replication | biological\_process |
| GO:0008152 | 9 | gene\_09801.t1,gene\_08786.t1,gene\_08783.t1,gene\_08784.t1,gene\_08787.t1,gene\_07780.t1,gene\_08782.t1,gene\_01601.t1,gene\_08780.t1 | | metabolic process | biological\_process |
| GO:0051321 | 5 | gene\_06548.t1,gene\_07611.t1,gene\_01336.t1,gene\_03054.t1,gene\_05747.t1 | | meiotic cell cycle | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0000132 | 1 | gene\_10487.t1 | | establishment of mitotic spindle orientation | biological\_process |
| GO:0140021 | 1 | gene\_02936.t1 | | mitochondrial ADP transmembrane transport | biological\_process |
| GO:0070814 | 2 | gene\_05577.t1,gene\_07261.t1 | | hydrogen sulfide biosynthetic process | biological\_process |
| GO:0006869 | 9 | gene\_07300.t1,gene\_04067.t1,gene\_10059.t1,gene\_06774.t1,gene\_08315.t1,gene\_09579.t1,gene\_02094.t1,gene\_04653.t1,gene\_07273.t1 | | lipid transport | biological\_process |
| GO:0006865 | 25 | gene\_04673.t1,gene\_06496.t1,gene\_08121.t1,gene\_04752.t1,gene\_01817.t1,gene\_02530.t1,gene\_04754.t1,gene\_06626.t1,gene\_08978.t1,gene\_04205.t1,gene\_03345.t1,gene\_06052.t1,gene\_02886.t1,gene\_07016.t1,gene\_09286.t1,gene\_10190.t1,gene\_03370.t1,gene\_01062.t1,gene\_04498.t1,gene\_09371.t1,gene\_03323.t1,gene\_03215.t1,gene\_07033.t1,gene\_07155.t1,gene\_05297.t1 | | amino acid transport | biological\_process |
| GO:0043618 | 1 | gene\_04435.t1 | | regulation of transcription from RNA polymerase II promoter in response to stress | biological\_process |
| GO:0070973 | 1 | gene\_02093.t1 | | protein localization to endoplasmic reticulum exit site | biological\_process |
| GO:0000041 | 2 | gene\_02172.t1,gene\_06588.t1 | | transition metal ion transport | biological\_process |
| GO:0000045 | 4 | gene\_03894.t1,gene\_06906.t1,gene\_05641.t1,gene\_03673.t1 | | autophagosome assembly | biological\_process |
| GO:0055088 | 2 | gene\_03348.t1,gene\_02329.t1 | | lipid homeostasis | biological\_process |
| GO:0016925 | 2 | gene\_06429.t1,gene\_09728.t1 | | protein sumoylation | biological\_process |
| GO:0055085 | 51 | gene\_00014.t1,gene\_07817.t1,gene\_03370.t1,gene\_09335.t1,gene\_05994.t1,gene\_07016.t1,gene\_08121.t1,gene\_03782.t1,gene\_09286.t1,gene\_01215.t1,gene\_02504.t1,gene\_05068.t1,gene\_05476.t1,gene\_02940.t1,gene\_03843.t1,gene\_00016.t1,gene\_10638.t1,gene\_01178.t1,gene\_03826.t1,gene\_08448.t1,gene\_06206.t1,gene\_08978.t1,gene\_04249.t1,gene\_00215.t1,gene\_09363.t1,gene\_02008.t1,gene\_06496.t1,gene\_00456.t1,gene\_00316.t1,gene\_09124.t1,gene\_00749.t1,gene\_05952.t1,gene\_07097.t1,gene\_06363.t1,gene\_07345.t1,gene\_04752.t1,gene\_05326.t1,gene\_10190.t1,gene\_05492.t1,gene\_10493.t1,gene\_01062.t1,gene\_09356.t1,gene\_00951.t1,gene\_03345.t1,gene\_01021.t1,gene\_05144.t1,gene\_08932.t1,gene\_06328.t1,gene\_04498.t1,gene\_07584.t1,gene\_05297.t1 | | transmembrane transport | biological\_process |
| GO:0007249 | 1 | gene\_07623.t1 | | I-kappaB kinase/NF-kappaB signaling | biological\_process |
| GO:0032264 | 1 | gene\_05147.t1 | | IMP salvage | biological\_process |
| GO:0032515 | 1 | gene\_05153.t1 | | negative regulation of phosphoprotein phosphatase activity | biological\_process |
| GO:0032049 | 2 | gene\_08051.t1,gene\_02201.t1 | | cardiolipin biosynthetic process | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0071555 | 18 | gene\_10650.t1,gene\_01725.t1,gene\_02291.t1,gene\_06586.t1,gene\_00810.t1,gene\_04734.t1,gene\_08927.t1,gene\_09106.t1,gene\_02770.t1,gene\_09475.t1,gene\_03591.t1,gene\_06645.t1,gene\_00523.t1,gene\_01063.t1,gene\_02551.t1,gene\_00787.t1,gene\_07068.t1,gene\_05091.t1 | | cell wall organization | biological\_process |
| GO:0010467 | 1 | gene\_09453.t1 | | gene expression | biological\_process |
| GO:0032469 | 1 | gene\_04068.t1 | | endoplasmic reticulum calcium ion homeostasis | biological\_process |
| GO:0010468 | 1 | gene\_09822.t1 | | regulation of gene expression | biological\_process |
| GO:0051403 | 2 | gene\_08916.t1,gene\_08746.t1 | | stress-activated MAPK cascade | biological\_process |
| GO:0042759 | 1 | gene\_02333.t1 | | long-chain fatty acid biosynthetic process | biological\_process |
| GO:0051409 | 1 | gene\_03326.t1 | | response to nitrosative stress | biological\_process |
| GO:0007015 | 5 | gene\_02165.t1,gene\_00869.t1,gene\_03881.t1,gene\_08752.t1,gene\_08716.t1 | | actin filament organization | biological\_process |
| GO:0007017 | 5 | gene\_00668.t1,gene\_01652.t1,gene\_00015.t1,gene\_08913.t1,gene\_10420.t1 | | microtubule-based process | biological\_process |
| GO:0007018 | 12 | gene\_05738.t1,gene\_03046.t1,gene\_07366.t1,gene\_03452.t1,gene\_05745.t1,gene\_05840.t1,gene\_04724.t1,gene\_08235.t1,gene\_10636.t1,gene\_10520.t1,gene\_02766.t1,gene\_00134.t1 | | microtubule-based movement | biological\_process |
| GO:0015031 | 88 | gene\_07871.t1,gene\_01552.t1,gene\_10159.t1,gene\_10290.t1,gene\_05611.t1,gene\_07863.t1,gene\_05127.t1,gene\_09312.t1,gene\_00461.t1,gene\_05641.t1,gene\_02838.t1,gene\_07625.t1,gene\_04317.t1,gene\_06638.t1,gene\_09511.t1,gene\_08590.t1,gene\_00974.t1,gene\_09873.t1,gene\_07007.t1,gene\_01090.t1,gene\_08803.t1,gene\_03696.t1,gene\_05629.t1,gene\_05717.t1,gene\_05131.t1,gene\_02335.t1,gene\_04156.t1,gene\_02706.t1,gene\_03179.t1,gene\_10183.t1,gene\_01023.t1,gene\_07646.t1,gene\_02807.t1,gene\_06774.t1,gene\_10558.t1,gene\_09945.t1,gene\_01728.t1,gene\_07017.t1,gene\_05520.t1,gene\_06906.t1,gene\_09159.t1,gene\_08775.t1,gene\_10308.t1,gene\_02784.t1,gene\_04584.t1,gene\_07961.t1,gene\_09555.t1,gene\_00356.t1,gene\_10042.t1,gene\_07570.t1,gene\_00349.t1,gene\_09260.t1,gene\_09487.t1,gene\_09485.t1,gene\_08367.t1,gene\_10418.t1,gene\_03259.t1,gene\_02033.t1,gene\_09123.t1,gene\_02521.t1,gene\_10095.t1,gene\_04136.t1,gene\_01250.t1,gene\_06461.t1,gene\_00051.t1,gene\_05628.t1,gene\_04308.t1,gene\_05929.t1,gene\_00964.t1,gene\_06590.t1,gene\_06330.t1,gene\_07354.t1,gene\_08108.t1,gene\_09156.t1,gene\_08719.t1,gene\_02217.t1,gene\_07362.t1,gene\_03894.t1,gene\_08575.t1,gene\_07697.t1,gene\_08294.t1,gene\_10294.t1,gene\_05343.t1,gene\_06399.t1,gene\_03764.t1,gene\_06544.t1,gene\_08808.t1,gene\_08974.t1 | | protein transport | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:1990961 | 3 | gene\_05823.t1,gene\_06518.t1,gene\_09522.t1 | | xenobiotic detoxification by transmembrane export across the plasma membrane | biological\_process |
| GO:0038203 | 1 | gene\_10315.t1 | | TORC2 signaling | biological\_process |
| GO:0006307 | 3 | gene\_03350.t1,gene\_09114.t1,gene\_01975.t1 | | DNA dealkylation involved in DNA repair | biological\_process |
| GO:0051716 | 2 | gene\_00548.t1,gene\_00746.t1 | | cellular response to stimulus | biological\_process |
| GO:0006303 | 2 | gene\_04537.t1,gene\_02991.t1 | | double-strand break repair via nonhomologous end joining | biological\_process |
| GO:0006302 | 7 | gene\_03054.t1,gene\_06548.t1,gene\_03583.t1,gene\_04738.t1,gene\_09338.t1,gene\_02776.t1,gene\_00867.t1 | | double-strand break repair | biological\_process |
| GO:0006301 | 1 | gene\_06339.t1 | | postreplication repair | biological\_process |
| GO:0044550 | 28 | gene\_02085.t1,gene\_01621.t1,gene\_01962.t1,gene\_08534.t1,gene\_05410.t1,gene\_08962.t1,gene\_01127.t1,gene\_04763.t1,gene\_07849.t1,gene\_08465.t1,gene\_06013.t1,gene\_04361.t1,gene\_01661.t1,gene\_00239.t1,gene\_06622.t1,gene\_07769.t1,gene\_09894.t1,gene\_09503.t1,gene\_00854.t1,gene\_03216.t1,gene\_05606.t1,gene\_05257.t1,gene\_05500.t1,gene\_05440.t1,gene\_10582.t1,gene\_05302.t1,gene\_10490.t1,gene\_01824.t1 | | secondary metabolite biosynthetic process | biological\_process |
| GO:0006308 | 1 | gene\_04293.t1 | | DNA catabolic process | biological\_process |
| GO:0016104 | 1 | gene\_04414.t1 | | triterpenoid biosynthetic process | biological\_process |
| GO:0061780 | 1 | gene\_09822.t1 | | mitotic cohesin loading | biological\_process |
| GO:0046486 | 5 | gene\_01166.t1,gene\_04813.t1,gene\_04991.t1,gene\_00240.t1,gene\_05011.t1 | | glycerolipid metabolic process | biological\_process |
| GO:0017183 | 5 | gene\_02208.t1,gene\_02666.t1,gene\_07601.t1,gene\_02831.t1,gene\_09990.t1 | | peptidyl-diphthamide biosynthetic process from peptidyl-histidine | biological\_process |
| GO:0006271 | 6 | gene\_09699.t1,gene\_07212.t1,gene\_10065.t1,gene\_07744.t1,gene\_07620.t1,gene\_07617.t1 | | DNA strand elongation involved in DNA replication | biological\_process |
| GO:0006270 | 11 | gene\_01982.t1,gene\_00515.t1,gene\_01710.t1,gene\_01540.t1,gene\_05534.t1,gene\_08245.t1,gene\_06062.t1,gene\_07862.t1,gene\_08595.t1,gene\_09071.t1,gene\_06735.t1 | | DNA replication initiation | biological\_process |
| GO:0006275 | 1 | gene\_01660.t1 | | regulation of DNA replication | biological\_process |
| GO:0006426 | 1 | gene\_09244.t1 | | glycyl-tRNA aminoacylation | biological\_process |
| GO:0033512 | 1 | gene\_07350.t1 | | L-lysine catabolic process to acetyl-CoA via saccharopine | biological\_process |
| GO:0008535 | 1 | gene\_06931.t1 | | respiratory chain complex IV assembly | biological\_process |
| GO:0042255 | 1 | gene\_06349.t1 | | ribosome assembly | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0042254 | 18 | gene\_08509.t1,gene\_01985.t1,gene\_02480.t1,gene\_03926.t1,gene\_00268.t1,gene\_05788.t1,gene\_01678.t1,gene\_06350.t1,gene\_03475.t1,gene\_03548.t1,gene\_02232.t1,gene\_08840.t1,gene\_01599.t1,gene\_08271.t1,gene\_06571.t1,gene\_09251.t1,gene\_07733.t1,gene\_07393.t1 | | ribosome biogenesis | biological\_process |
| GO:0042256 | 2 | gene\_09219.t1,gene\_10589.t1 | | mature ribosome assembly | biological\_process |
| GO:0009308 | 7 | gene\_06041.t1,gene\_09373.t1,gene\_04449.t1,gene\_01764.t1,gene\_10189.t1,gene\_07681.t1,gene\_09128.t1 | | amine metabolic process | biological\_process |
| GO:0048315 | 15 | gene\_09058.t1,gene\_10650.t1,gene\_03571.t1,gene\_00810.t1,gene\_10384.t1,gene\_05891.t1,gene\_04321.t1,gene\_06057.t1,gene\_01163.t1,gene\_01650.t1,gene\_00224.t1,gene\_01290.t1,gene\_03570.t1,gene\_09106.t1,gene\_08876.t1 | | conidium formation | biological\_process |
| GO:0009306 | 2 | gene\_04192.t1,gene\_04140.t1 | | protein secretion | biological\_process |
| GO:0031087 | 1 | gene\_04114.t1 | | deadenylation-independent decapping of nuclear-transcribed mRNA | biological\_process |
| GO:0010265 | 2 | gene\_06416.t1,gene\_06381.t1 | | SCF complex assembly | biological\_process |
| GO:0006695 | 1 | gene\_08132.t1 | | cholesterol biosynthetic process | biological\_process |
| GO:0006694 | 5 | gene\_02639.t1,gene\_07798.t1,gene\_00026.t1,gene\_08399.t1,gene\_02494.t1 | | steroid biosynthetic process | biological\_process |
| GO:2001256 | 1 | gene\_09583.t1 | | regulation of store-operated calcium entry | biological\_process |
| GO:0002191 | 1 | gene\_00144.t1 | | cap-dependent translational initiation | biological\_process |
| GO:0006436 | 2 | gene\_09717.t1,gene\_07095.t1 | | tryptophanyl-tRNA aminoacylation | biological\_process |
| GO:1902600 | 2 | gene\_03967.t1,gene\_08358.t1 | | proton transmembrane transport | biological\_process |
| GO:0031222 | 7 | gene\_03467.t1,gene\_05400.t1,gene\_03663.t1,gene\_01362.t1,gene\_06731.t1,gene\_00037.t1,gene\_09125.t1 | | arabinan catabolic process | biological\_process |
| GO:0000122 | 1 | gene\_07352.t1 | | negative regulation of transcription by RNA polymerase II | biological\_process |
| GO:0009098 | 4 | gene\_07021.t1,gene\_02066.t1,gene\_06642.t1,gene\_10595.t1 | | leucine biosynthetic process | biological\_process |
| GO:0009099 | 3 | gene\_00361.t1,gene\_08592.t1,gene\_09113.t1 | | valine biosynthetic process | biological\_process |
| GO:0009097 | 5 | gene\_00361.t1,gene\_01418.t1,gene\_08592.t1,gene\_09113.t1,gene\_05635.t1 | | isoleucine biosynthetic process | biological\_process |
| GO:1905775 | 1 | gene\_09071.t1 | | negative regulation of DNA helicase activity | biological\_process |
| GO:0051391 | 1 | gene\_01030.t1 | | tRNA acetylation | biological\_process |
| GO:0006878 | 6 | gene\_02696.t1,gene\_07182.t1,gene\_00796.t1,gene\_00624.t1,gene\_06931.t1,gene\_05351.t1 | | cellular copper ion homeostasis | biological\_process |
| GO:0006874 | 1 | gene\_07909.t1 | | cellular calcium ion homeostasis | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0015986 | 8 | gene\_03015.t1,gene\_06355.t1,gene\_00267.t1,gene\_09826.t1,gene\_09484.t1,gene\_03171.t1,gene\_05980.t1,gene\_06648.t1 | | ATP synthesis coupled proton transport | biological\_process |
| GO:0000050 | 1 | gene\_05706.t1 | | urea cycle | biological\_process |
| GO:0000055 | 2 | gene\_06638.t1,gene\_01090.t1 | | ribosomal large subunit export from nucleus | biological\_process |
| GO:0000054 | 2 | gene\_05458.t1,gene\_09219.t1 | | ribosomal subunit export from nucleus | biological\_process |
| GO:0000056 | 1 | gene\_01090.t1 | | ribosomal small subunit export from nucleus | biological\_process |
| GO:0042790 | 1 | gene\_04314.t1 | | nucleolar large rRNA transcription by RNA polymerase I | biological\_process |
| GO:0019594 | 1 | gene\_00578.t1 | | mannitol metabolic process | biological\_process |
| GO:0019441 | 11 | gene\_05407.t1,gene\_03462.t1,gene\_08361.t1,gene\_08894.t1,gene\_04083.t1,gene\_03297.t1,gene\_10549.t1,gene\_03134.t1,gene\_04519.t1,gene\_10649.t1,gene\_09095.t1 | | tryptophan catabolic process to kynurenine | biological\_process |
| GO:0070125 | 1 | gene\_01416.t1 | | mitochondrial translational elongation | biological\_process |
| GO:0090522 | 2 | gene\_09722.t1,gene\_04572.t1 | | vesicle tethering involved in exocytosis | biological\_process |
| GO:0032324 | 1 | gene\_06163.t1 | | molybdopterin cofactor biosynthetic process | biological\_process |
| GO:0033494 | 2 | gene\_10373.t1,gene\_00631.t1 | | ferulate metabolic process | biological\_process |
| GO:0042138 | 1 | gene\_04413.t1 | | meiotic DNA double-strand break formation | biological\_process |
| GO:0033499 | 1 | gene\_06566.t1 | | galactose catabolic process via UDP-galactose | biological\_process |
| GO:0019915 | 2 | gene\_04546.t1,gene\_02505.t1 | | lipid storage | biological\_process |
| GO:0007005 | 3 | gene\_03755.t1,gene\_06104.t1,gene\_03080.t1 | | mitochondrion organization | biological\_process |
| GO:0016024 | 2 | gene\_04100.t1,gene\_02201.t1 | | CDP-diacylglycerol biosynthetic process | biological\_process |
| GO:0019628 | 1 | gene\_00591.t1 | | urate catabolic process | biological\_process |
| GO:0033036 | 1 | gene\_05468.t1 | | macromolecule localization | biological\_process |
| GO:0046039 | 1 | gene\_01019.t1 | | GTP metabolic process | biological\_process |
| GO:0046034 | 2 | gene\_04186.t1,gene\_03967.t1 | | ATP metabolic process | biological\_process |
| GO:0046033 | 2 | gene\_04186.t1,gene\_01019.t1 | | AMP metabolic process | biological\_process |
| GO:0030968 | 3 | gene\_00740.t1,gene\_07380.t1,gene\_00030.t1 | | endoplasmic reticulum unfolded protein response | biological\_process |
| GO:0016114 | 14 | gene\_00780.t1,gene\_00781.t1,gene\_07526.t1,gene\_00784.t1,gene\_00785.t1,gene\_04206.t1,gene\_00786.t1,gene\_00777.t1,gene\_00783.t1,gene\_00779.t1,gene\_07522.t1,gene\_04266.t1,gene\_09298.t1,gene\_00782.t1 | | terpenoid biosynthetic process | biological\_process |
| GO:0015914 | 4 | gene\_04010.t1,gene\_01056.t1,gene\_00896.t1,gene\_09510.t1 | | phospholipid transport | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0042407 | 2 | gene\_05236.t1,gene\_03603.t1 | | cristae formation | biological\_process |
| GO:1903259 | 1 | gene\_03981.t1 | | exon-exon junction complex disassembly | biological\_process |
| GO:0046496 | 1 | gene\_00517.t1 | | nicotinamide nucleotide metabolic process | biological\_process |
| GO:0006198 | 1 | gene\_02073.t1 | | cAMP catabolic process | biological\_process |
| GO:0006190 | 1 | gene\_03413.t1 | | inosine salvage | biological\_process |
| GO:0006207 | 5 | gene\_06009.t1,gene\_01122.t1,gene\_08081.t1,gene\_06540.t1,gene\_00647.t1 | | 'de novo' pyrimidine nucleobase biosynthetic process | biological\_process |
| GO:0008615 | 1 | gene\_08405.t1 | | pyridoxine biosynthetic process | biological\_process |
| GO:1990426 | 1 | gene\_05469.t1 | | mitotic recombination-dependent replication fork processing | biological\_process |
| GO:0030148 | 1 | gene\_00327.t1 | | sphingolipid biosynthetic process | biological\_process |
| GO:0006427 | 1 | gene\_10413.t1 | | histidyl-tRNA aminoacylation | biological\_process |
| GO:0006424 | 2 | gene\_07873.t1,gene\_06273.t1 | | glutamyl-tRNA aminoacylation | biological\_process |
| GO:0006425 | 1 | gene\_02487.t1 | | glutaminyl-tRNA aminoacylation | biological\_process |
| GO:0006422 | 2 | gene\_03141.t1,gene\_00665.t1 | | aspartyl-tRNA aminoacylation | biological\_process |
| GO:0006423 | 1 | gene\_04419.t1 | | cysteinyl-tRNA aminoacylation | biological\_process |
| GO:0006420 | 1 | gene\_03487.t1 | | arginyl-tRNA aminoacylation | biological\_process |
| GO:0006421 | 2 | gene\_09843.t1,gene\_03207.t1 | | asparaginyl-tRNA aminoacylation | biological\_process |
| GO:0000338 | 2 | gene\_07432.t1,gene\_08097.t1 | | protein deneddylation | biological\_process |
| GO:0006428 | 2 | gene\_02254.t1,gene\_04722.t1 | | isoleucyl-tRNA aminoacylation | biological\_process |
| GO:0006429 | 2 | gene\_09679.t1,gene\_10446.t1 | | leucyl-tRNA aminoacylation | biological\_process |
| GO:0120029 | 5 | gene\_07874.t1,gene\_00003.t1,gene\_06942.t1,gene\_00673.t1,gene\_01833.t1 | | proton export across plasma membrane | biological\_process |
| GO:0097428 | 3 | gene\_00274.t1,gene\_07388.t1,gene\_10267.t1 | | protein maturation by iron-sulfur cluster transfer | biological\_process |
| GO:0050896 | 1 | gene\_04415.t1 | | response to stimulus | biological\_process |
| GO:0006513 | 1 | gene\_06339.t1 | | protein monoubiquitination | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0006511 | 33 | gene\_09212.t1,gene\_09182.t1,gene\_06133.t1,gene\_05133.t1,gene\_09472.t1,gene\_04184.t1,gene\_07422.t1,gene\_07916.t1,gene\_10416.t1,gene\_07791.t1,gene\_01114.t1,gene\_03863.t1,gene\_08525.t1,gene\_09635.t1,gene\_01238.t1,gene\_08748.t1,gene\_09768.t1,gene\_00974.t1,gene\_03039.t1,gene\_08301.t1,gene\_03470.t1,gene\_09853.t1,gene\_00680.t1,gene\_03286.t1,gene\_05248.t1,gene\_07309.t1,gene\_10317.t1,gene\_04108.t1,gene\_05689.t1,gene\_00032.t1,gene\_06431.t1,gene\_02020.t1,gene\_09787.t1 | | ubiquitin-dependent protein catabolic process | biological\_process |
| GO:0006515 | 2 | gene\_05844.t1,gene\_09415.t1 | | protein quality control for misfolded or incompletely synthesized proteins | biological\_process |
| GO:0006730 | 7 | gene\_01051.t1,gene\_00302.t1,gene\_01843.t1,gene\_05535.t1,gene\_01409.t1,gene\_05443.t1,gene\_00279.t1 | | one-carbon metabolic process | biological\_process |
| GO:0009311 | 2 | gene\_07604.t1,gene\_09534.t1 | | oligosaccharide metabolic process | biological\_process |
| GO:0009310 | 1 | gene\_00962.t1 | | amine catabolic process | biological\_process |
| GO:0000209 | 2 | gene\_01605.t1,gene\_01604.t1 | | protein polyubiquitination | biological\_process |
| GO:0002181 | 1 | gene\_03856.t1 | | cytoplasmic translation | biological\_process |
| GO:0002182 | 1 | gene\_00519.t1 | | cytoplasmic translational elongation | biological\_process |
| GO:0061817 | 2 | gene\_10059.t1,gene\_04653.t1 | | endoplasmic reticulum-plasma membrane tethering | biological\_process |
| GO:0009408 | 2 | gene\_01682.t1,gene\_09414.t1 | | response to heat | biological\_process |
| GO:0006032 | 22 | gene\_01798.t1,gene\_07912.t1,gene\_07875.t1,gene\_05687.t1,gene\_10573.t1,gene\_03424.t1,gene\_01799.t1,gene\_01037.t1,gene\_06552.t1,gene\_01797.t1,gene\_03719.t1,gene\_02142.t1,gene\_04380.t1,gene\_04222.t1,gene\_06768.t1,gene\_10353.t1,gene\_01801.t1,gene\_01647.t1,gene\_05417.t1,gene\_00971.t1,gene\_01800.t1,gene\_06897.t1 | | chitin catabolic process | biological\_process |
| GO:0030242 | 1 | gene\_10456.t1 | | autophagy of peroxisome | biological\_process |
| GO:0009088 | 4 | gene\_06750.t1,gene\_09231.t1,gene\_03797.t1,gene\_05635.t1 | | threonine biosynthetic process | biological\_process |
| GO:0061587 | 1 | gene\_07352.t1 | | transfer RNA gene-mediated silencing | biological\_process |
| GO:0009086 | 5 | gene\_07261.t1,gene\_00382.t1,gene\_05635.t1,gene\_03115.t1,gene\_02061.t1 | | methionine biosynthetic process | biological\_process |
| GO:0009082 | 3 | gene\_09326.t1,gene\_00766.t1,gene\_00557.t1 | | branched-chain amino acid biosynthetic process | biological\_process |
| GO:0051382 | 4 | gene\_04179.t1,gene\_05640.t1,gene\_09382.t1,gene\_01877.t1 | | kinetochore assembly | biological\_process |
| GO:0046952 | 2 | gene\_02317.t1,gene\_10319.t1 | | ketone body catabolic process | biological\_process |
| GO:0018279 | 1 | gene\_08010.t1 | | protein N-linked glycosylation via asparagine | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0019588 | 2 | gene\_08527.t1,gene\_10503.t1 | | anaerobic glycerol catabolic process | biological\_process |
| GO:0007264 | 15 | gene\_07243.t1,gene\_09005.t1,gene\_00826.t1,gene\_07007.t1,gene\_09833.t1,gene\_03010.t1,gene\_01559.t1,gene\_06269.t1,gene\_09341.t1,gene\_06153.t1,gene\_09397.t1,gene\_01592.t1,gene\_08588.t1,gene\_02435.t1,gene\_03755.t1 | | small GTPase mediated signal transduction | biological\_process |
| GO:0070481 | 1 | gene\_02565.t1 | | nuclear-transcribed mRNA catabolic process, non-stop decay | biological\_process |
| GO:0046514 | 1 | gene\_02496.t1 | | ceramide catabolic process | biological\_process |
| GO:0006996 | 1 | gene\_01675.t1 | | organelle organization | biological\_process |
| GO:0044238 | 3 | gene\_05779.t1,gene\_10246.t1,gene\_07001.t1 | | primary metabolic process | biological\_process |
| GO:0006998 | 1 | gene\_03348.t1 | | nuclear envelope organization | biological\_process |
| GO:0035998 | 1 | gene\_07926.t1 | | 7,8-dihydroneopterin 3'-triphosphate biosynthetic process | biological\_process |
| GO:0051568 | 1 | gene\_02323.t1 | | histone H3-K4 methylation | biological\_process |
| GO:0000455 | 1 | gene\_02854.t1 | | enzyme-directed rRNA pseudouridine synthesis | biological\_process |
| GO:0071840 | 2 | gene\_09807.t1,gene\_05084.t1 | | cellular component organization or biogenesis | biological\_process |
| GO:0035065 | 1 | gene\_00580.t1 | | regulation of histone acetylation | biological\_process |
| GO:0032447 | 2 | gene\_01562.t1,gene\_05774.t1 | | protein urmylation | biological\_process |
| GO:0001680 | 1 | gene\_06335.t1 | | tRNA 3'-terminal CCA addition | biological\_process |
| GO:0034470 | 2 | gene\_00876.t1,gene\_10176.t1 | | ncRNA processing | biological\_process |
| GO:0042128 | 4 | gene\_08724.t1,gene\_08725.t1,gene\_00906.t1,gene\_08723.t1 | | nitrate assimilation | biological\_process |
| GO:0007076 | 3 | gene\_05995.t1,gene\_07311.t1,gene\_07793.t1 | | mitotic chromosome condensation | biological\_process |
| GO:0016052 | 12 | gene\_06443.t1,gene\_05243.t1,gene\_00477.t1,gene\_06442.t1,gene\_04296.t1,gene\_03422.t1,gene\_04047.t1,gene\_08370.t1,gene\_01644.t1,gene\_05379.t1,gene\_00739.t1,gene\_03426.t1 | | carbohydrate catabolic process | biological\_process |
| GO:0019630 | 1 | gene\_05589.t1 | | quinate metabolic process | biological\_process |
| GO:0071266 | 1 | gene\_01259.t1 | | 'de novo' L-methionine biosynthetic process | biological\_process |
| GO:0034765 | 2 | gene\_08146.t1,gene\_05625.t1 | | regulation of ion transmembrane transport | biological\_process |
| GO:0140042 | 1 | gene\_08627.t1 | | lipid droplet formation | biological\_process |
| GO:0019835 | 1 | gene\_01789.t1 | | cytolysis | biological\_process |
| GO:0019836 | 1 | gene\_03264.t1 | | hemolysis by symbiont of host erythrocytes | biological\_process |
| GO:0006189 | 9 | gene\_07647.t1,gene\_09629.t1,gene\_10263.t1,gene\_01843.t1,gene\_08162.t1,gene\_07232.t1,gene\_09478.t1,gene\_00429.t1,gene\_00615.t1 | | 'de novo' IMP biosynthetic process | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0006183 | 1 | gene\_07884.t1 | | GTP biosynthetic process | biological\_process |
| GO:0051603 | 11 | gene\_00408.t1,gene\_02486.t1,gene\_01236.t1,gene\_02375.t1,gene\_07138.t1,gene\_02420.t1,gene\_04461.t1,gene\_09929.t1,gene\_05700.t1,gene\_02372.t1,gene\_03707.t1 | | proteolysis involved in cellular protein catabolic process | biological\_process |
| GO:0051607 | 3 | gene\_03396.t1,gene\_06315.t1,gene\_05841.t1 | | defense response to virus | biological\_process |
| GO:0006545 | 1 | gene\_01051.t1 | | glycine biosynthetic process | biological\_process |
| GO:0009083 | 2 | gene\_03837.t1,gene\_03836.t1 | | branched-chain amino acid catabolic process | biological\_process |
| GO:0006435 | 2 | gene\_06643.t1,gene\_10327.t1 | | threonyl-tRNA aminoacylation | biological\_process |
| GO:0006434 | 2 | gene\_09273.t1,gene\_05654.t1 | | seryl-tRNA aminoacylation | biological\_process |
| GO:0006437 | 2 | gene\_07590.t1,gene\_01435.t1 | | tyrosyl-tRNA aminoacylation | biological\_process |
| GO:0006430 | 3 | gene\_01636.t1,gene\_03790.t1,gene\_00005.t1 | | lysyl-tRNA aminoacylation | biological\_process |
| GO:0006433 | 2 | gene\_05564.t1,gene\_06241.t1 | | prolyl-tRNA aminoacylation | biological\_process |
| GO:0006432 | 3 | gene\_03944.t1,gene\_02682.t1,gene\_02959.t1 | | phenylalanyl-tRNA aminoacylation | biological\_process |
| GO:0006438 | 1 | gene\_07409.t1 | | valyl-tRNA aminoacylation | biological\_process |
| GO:0030150 | 4 | gene\_06037.t1,gene\_00476.t1,gene\_09709.t1,gene\_00730.t1 | | protein import into mitochondrial matrix | biological\_process |
| GO:0032958 | 2 | gene\_05749.t1,gene\_05886.t1 | | inositol phosphate biosynthetic process | biological\_process |
| GO:0042273 | 4 | gene\_05458.t1,gene\_06638.t1,gene\_09219.t1,gene\_09614.t1 | | ribosomal large subunit biogenesis | biological\_process |
| GO:0042276 | 1 | gene\_03610.t1 | | error-prone translesion synthesis | biological\_process |
| GO:0042274 | 3 | gene\_04402.t1,gene\_01030.t1,gene\_08049.t1 | | ribosomal small subunit biogenesis | biological\_process |
| GO:0005980 | 1 | gene\_00709.t1 | | glycogen catabolic process | biological\_process |
| GO:0043001 | 1 | gene\_02470.t1 | | Golgi to plasma membrane protein transport | biological\_process |
| GO:0006506 | 21 | gene\_09564.t1,gene\_06610.t1,gene\_00178.t1,gene\_08086.t1,gene\_09007.t1,gene\_02846.t1,gene\_08128.t1,gene\_01263.t1,gene\_00114.t1,gene\_02076.t1,gene\_02802.t1,gene\_09726.t1,gene\_00966.t1,gene\_02482.t1,gene\_06898.t1,gene\_04734.t1,gene\_00571.t1,gene\_06068.t1,gene\_02828.t1,gene\_03239.t1,gene\_10092.t1 | | GPI anchor biosynthetic process | biological\_process |
| GO:0006508 | 1 | gene\_06760.t1 | | proteolysis | biological\_process |
| GO:0006729 | 1 | gene\_07572.t1 | | tetrahydrobiopterin biosynthetic process | biological\_process |
| GO:0006725 | 2 | gene\_05541.t1,gene\_00790.t1 | | cellular aromatic compound metabolic process | biological\_process |
| GO:0098813 | 1 | gene\_04251.t1 | | nuclear chromosome segregation | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0048208 | 1 | gene\_09511.t1 | | COPII vesicle coating | biological\_process |
| GO:0009435 | 5 | gene\_07903.t1,gene\_03849.t1,gene\_04641.t1,gene\_07335.t1,gene\_00373.t1 | | NAD biosynthetic process | biological\_process |
| GO:0031204 | 2 | gene\_02041.t1,gene\_08267.t1 | | posttranslational protein targeting to membrane, translocation | biological\_process |
| GO:0000105 | 7 | gene\_09625.t1,gene\_02123.t1,gene\_08292.t1,gene\_02197.t1,gene\_01269.t1,gene\_08515.t1,gene\_04327.t1 | | histidine biosynthetic process | biological\_process |
| GO:0000103 | 3 | gene\_05577.t1,gene\_06837.t1,gene\_07261.t1 | | sulfate assimilation | biological\_process |
| GO:2001295 | 1 | gene\_01074.t1 | | malonyl-CoA biosynthetic process | biological\_process |
| GO:0001522 | 8 | gene\_10328.t1,gene\_05787.t1,gene\_09006.t1,gene\_01896.t1,gene\_02232.t1,gene\_09251.t1,gene\_04403.t1,gene\_06280.t1 | | pseudouridine synthesis | biological\_process |
| GO:1902979 | 1 | gene\_06031.t1 | | mitotic DNA replication termination | biological\_process |
| GO:0009102 | 2 | gene\_09469.t1,gene\_09462.t1 | | biotin biosynthetic process | biological\_process |
| GO:1902751 | 1 | gene\_09773.t1 | | positive regulation of cell cycle G2/M phase transition | biological\_process |
| GO:0006857 | 5 | gene\_05098.t1,gene\_02896.t1,gene\_02897.t1,gene\_02895.t1,gene\_03872.t1 | | oligopeptide transport | biological\_process |
| GO:0006850 | 2 | gene\_01367.t1,gene\_00788.t1 | | mitochondrial pyruvate transmembrane transport | biological\_process |
| GO:0009058 | 23 | gene\_08666.t1,gene\_08222.t1,gene\_00462.t1,gene\_04762.t1,gene\_10447.t1,gene\_02648.t1,gene\_03559.t1,gene\_05306.t1,gene\_10105.t1,gene\_05313.t1,gene\_01337.t1,gene\_01491.t1,gene\_00862.t1,gene\_00460.t1,gene\_08102.t1,gene\_06074.t1,gene\_02149.t1,gene\_03736.t1,gene\_03995.t1,gene\_10303.t1,gene\_10066.t1,gene\_01932.t1,gene\_06828.t1 | | biosynthetic process | biological\_process |
| GO:0009052 | 1 | gene\_06446.t1 | | pentose-phosphate shunt, non-oxidative branch | biological\_process |
| GO:0000070 | 3 | gene\_07290.t1,gene\_03245.t1,gene\_10602.t1 | | mitotic sister chromatid segregation | biological\_process |
| GO:0000077 | 6 | gene\_05805.t1,gene\_00573.t1,gene\_08500.t1,gene\_09512.t1,gene\_08078.t1,gene\_10279.t1 | | DNA damage checkpoint signaling | biological\_process |
| GO:0000076 | 1 | gene\_01226.t1 | | DNA replication checkpoint signaling | biological\_process |
| GO:0000079 | 6 | gene\_03270.t1,gene\_08489.t1,gene\_01190.t1,gene\_04106.t1,gene\_00900.t1,gene\_03261.t1 | | regulation of cyclin-dependent protein serine/threonine kinase activity | biological\_process |
| GO:0055070 | 1 | gene\_01837.t1 | | copper ion homeostasis | biological\_process |
| GO:0055072 | 4 | gene\_03446.t1,gene\_04745.t1,gene\_08986.t1,gene\_02448.t1 | | iron ion homeostasis | biological\_process |
| GO:0006986 | 1 | gene\_02005.t1 | | response to unfolded protein | biological\_process |
| GO:0044208 | 2 | gene\_07647.t1,gene\_01989.t1 | | 'de novo' AMP biosynthetic process | biological\_process |
| GO:0044209 | 2 | gene\_08031.t1,gene\_08329.t1 | | AMP salvage | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0044205 | 5 | gene\_06540.t1,gene\_01122.t1,gene\_07023.t1,gene\_01874.t1,gene\_00647.t1 | | 'de novo' UMP biosynthetic process | biological\_process |
| GO:0044206 | 1 | gene\_09819.t1 | | UMP salvage | biological\_process |
| GO:0042843 | 1 | gene\_01649.t1 | | D-xylose catabolic process | biological\_process |
| GO:0032780 | 1 | gene\_02794.t1 | | negative regulation of ATP-dependent activity | biological\_process |
| GO:0032784 | 1 | gene\_01481.t1 | | regulation of DNA-templated transcription, elongation | biological\_process |
| GO:0032786 | 1 | gene\_08074.t1 | | positive regulation of DNA-templated transcription, elongation | biological\_process |
| GO:0000462 | 2 | gene\_03219.t1,gene\_00707.t1 | | maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | biological\_process |
| GO:0000463 | 4 | gene\_01431.t1,gene\_00423.t1,gene\_05521.t1,gene\_05207.t1 | | maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | biological\_process |
| GO:0000466 | 3 | gene\_01431.t1,gene\_00423.t1,gene\_05207.t1 | | maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | biological\_process |
| GO:0000469 | 1 | gene\_04402.t1 | | cleavage involved in rRNA processing | biological\_process |
| GO:0071852 | 2 | gene\_09807.t1,gene\_05084.t1 | | fungal-type cell wall organization or biogenesis | biological\_process |
| GO:0071528 | 1 | gene\_04234.t1 | | tRNA re-export from nucleus | biological\_process |
| GO:0006044 | 2 | gene\_09759.t1,gene\_09762.t1 | | N-acetylglucosamine metabolic process | biological\_process |
| GO:0007064 | 5 | gene\_09618.t1,gene\_07202.t1,gene\_10001.t1,gene\_06314.t1,gene\_06219.t1 | | mitotic sister chromatid cohesion | biological\_process |
| GO:0007062 | 4 | gene\_07290.t1,gene\_00882.t1,gene\_09867.t1,gene\_00812.t1 | | sister chromatid cohesion | biological\_process |
| GO:0016043 | 5 | gene\_04603.t1,gene\_03094.t1,gene\_02689.t1,gene\_05856.t1,gene\_10381.t1 | | cellular component organization | biological\_process |
| GO:0016042 | 23 | gene\_03380.t1,gene\_09152.t1,gene\_04813.t1,gene\_01468.t1,gene\_07148.t1,gene\_03672.t1,gene\_05011.t1,gene\_06777.t1,gene\_02350.t1,gene\_07324.t1,gene\_07763.t1,gene\_01166.t1,gene\_01671.t1,gene\_04991.t1,gene\_06298.t1,gene\_01773.t1,gene\_00240.t1,gene\_05193.t1,gene\_05857.t1,gene\_02999.t1,gene\_08790.t1,gene\_09933.t1,gene\_05096.t1 | | lipid catabolic process | biological\_process |
| GO:0033540 | 1 | gene\_09140.t1 | | fatty acid beta-oxidation using acyl-CoA oxidase | biological\_process |
| GO:0071985 | 2 | gene\_01250.t1,gene\_10159.t1 | | multivesicular body sorting pathway | biological\_process |
| GO:0032012 | 4 | gene\_07337.t1,gene\_05829.t1,gene\_09156.t1,gene\_01064.t1 | | regulation of ARF protein signal transduction | biological\_process |
| GO:0032543 | 9 | gene\_08587.t1,gene\_06115.t1,gene\_08109.t1,gene\_10426.t1,gene\_10358.t1,gene\_03497.t1,gene\_05707.t1,gene\_04425.t1,gene\_02324.t1 | | mitochondrial translation | biological\_process |
| GO:0019805 | 4 | gene\_00551.t1,gene\_02644.t1,gene\_04082.t1,gene\_07394.t1 | | quinolinate biosynthetic process | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0006168 | 1 | gene\_08329.t1 | | adenine salvage | biological\_process |
| GO:0015936 | 1 | gene\_02693.t1 | | coenzyme A metabolic process | biological\_process |
| GO:0015937 | 3 | gene\_06901.t1,gene\_07765.t1,gene\_06905.t1 | | coenzyme A biosynthetic process | biological\_process |
| GO:0016310 | 1 | gene\_00398.t1 | | phosphorylation | biological\_process |
| GO:0034314 | 5 | gene\_06990.t1,gene\_05874.t1,gene\_07743.t1,gene\_02382.t1,gene\_03091.t1 | | Arp2/3 complex-mediated actin nucleation | biological\_process |
| GO:0034316 | 1 | gene\_05913.t1 | | negative regulation of Arp2/3 complex-mediated actin nucleation | biological\_process |
| GO:0006221 | 1 | gene\_06009.t1 | | pyrimidine nucleotide biosynthetic process | biological\_process |
| GO:0006226 | 1 | gene\_01001.t1 | | dUMP biosynthetic process | biological\_process |
| GO:0006228 | 1 | gene\_07884.t1 | | UTP biosynthetic process | biological\_process |
| GO:0008612 | 2 | gene\_09824.t1,gene\_07731.t1 | | peptidyl-lysine modification to peptidyl-hypusine | biological\_process |
| GO:0046785 | 1 | gene\_10486.t1 | | microtubule polymerization | biological\_process |
| GO:0008610 | 8 | gene\_09714.t1,gene\_06616.t1,gene\_01745.t1,gene\_07976.t1,gene\_09463.t1,gene\_05622.t1,gene\_01218.t1,gene\_04514.t1 | | lipid biosynthetic process | biological\_process |
| GO:0034551 | 1 | gene\_10320.t1 | | mitochondrial respiratory chain complex III assembly | biological\_process |
| GO:0046168 | 1 | gene\_00708.t1 | | glycerol-3-phosphate catabolic process | biological\_process |
| GO:0031929 | 4 | gene\_00561.t1,gene\_05323.t1,gene\_03147.t1,gene\_04143.t1 | | TOR signaling | biological\_process |
| GO:0031146 | 2 | gene\_01746.t1,gene\_02629.t1 | | SCF-dependent proteasomal ubiquitin-dependent protein catabolic process | biological\_process |
| GO:0031145 | 4 | gene\_09747.t1,gene\_02065.t1,gene\_02001.t1,gene\_04135.t1 | | anaphase-promoting complex-dependent catabolic process | biological\_process |
| GO:0031144 | 1 | gene\_00356.t1 | | proteasome localization | biological\_process |
| GO:0045892 | 7 | gene\_10177.t1,gene\_05523.t1,gene\_03104.t1,gene\_04231.t1,gene\_09874.t1,gene\_10405.t1,gene\_08663.t1 | | negative regulation of transcription, DNA-templated | biological\_process |
| GO:0010833 | 1 | gene\_03799.t1 | | telomere maintenance via telomere lengthening | biological\_process |
| GO:0045493 | 4 | gene\_05825.t1,gene\_10598.t1,gene\_08100.t1,gene\_00132.t1 | | xylan catabolic process | biological\_process |
| GO:0006084 | 1 | gene\_03020.t1 | | acetyl-CoA metabolic process | biological\_process |
| GO:0006085 | 1 | gene\_03086.t1 | | acetyl-CoA biosynthetic process | biological\_process |
| GO:0006086 | 2 | gene\_02327.t1,gene\_04096.t1 | | acetyl-CoA biosynthetic process from pyruvate | biological\_process |
| GO:0006081 | 2 | gene\_10347.t1,gene\_00823.t1 | | cellular aldehyde metabolic process | biological\_process |
| GO:0006082 | 5 | gene\_02510.t1,gene\_03086.t1,gene\_01843.t1,gene\_09272.t1,gene\_04129.t1 | | organic acid metabolic process | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0006083 | 1 | gene\_00257.t1 | | acetate metabolic process | biological\_process |
| GO:0005993 | 1 | gene\_10343.t1 | | trehalose catabolic process | biological\_process |
| GO:0005992 | 7 | gene\_07341.t1,gene\_10489.t1,gene\_06003.t1,gene\_02593.t1,gene\_03347.t1,gene\_07446.t1,gene\_07447.t1 | | trehalose biosynthetic process | biological\_process |
| GO:0006535 | 2 | gene\_07794.t1,gene\_01192.t1 | | cysteine biosynthetic process from serine | biological\_process |
| GO:0045944 | 16 | gene\_07125.t1,gene\_06826.t1,gene\_09262.t1,gene\_04840.t1,gene\_10396.t1,gene\_02321.t1,gene\_04922.t1,gene\_05064.t1,gene\_03104.t1,gene\_05048.t1,gene\_04902.t1,gene\_04970.t1,gene\_02778.t1,gene\_04914.t1,gene\_04974.t1,gene\_00891.t1 | | positive regulation of transcription by RNA polymerase II | biological\_process |
| GO:0000266 | 1 | gene\_03586.t1 | | mitochondrial fission | biological\_process |
| GO:0090304 | 1 | gene\_09851.t1 | | nucleic acid metabolic process | biological\_process |
| GO:0052837 | 1 | gene\_09923.t1 | | thiazole biosynthetic process | biological\_process |
| GO:0006400 | 3 | gene\_05668.t1,gene\_09687.t1,gene\_02115.t1 | | tRNA modification | biological\_process |
| GO:0043103 | 1 | gene\_01718.t1 | | hypoxanthine salvage | biological\_process |
| GO:0006402 | 2 | gene\_04448.t1,gene\_10141.t1 | | mRNA catabolic process | biological\_process |
| GO:0006406 | 5 | gene\_08105.t1,gene\_08779.t1,gene\_05183.t1,gene\_10171.t1,gene\_08906.t1 | | mRNA export from nucleus | biological\_process |
| GO:0009423 | 3 | gene\_02444.t1,gene\_02892.t1,gene\_02251.t1 | | chorismate biosynthetic process | biological\_process |
| GO:0000002 | 8 | gene\_00455.t1,gene\_06102.t1,gene\_06097.t1,gene\_04131.t1,gene\_04067.t1,gene\_06112.t1,gene\_02094.t1,gene\_09579.t1 | | mitochondrial genome maintenance | biological\_process |
| GO:0000001 | 1 | gene\_02370.t1 | | mitochondrion inheritance | biological\_process |
| GO:1902412 | 1 | gene\_10602.t1 | | regulation of mitotic cytokinesis | biological\_process |
| GO:0044211 | 1 | gene\_09819.t1 | | CTP salvage | biological\_process |
| GO:0044210 | 2 | gene\_09562.t1,gene\_01363.t1 | | 'de novo' CTP biosynthetic process | biological\_process |
| GO:0032220 | 2 | gene\_10068.t1,gene\_06790.t1 | | plasma membrane fusion involved in cytogamy | biological\_process |
| GO:0006337 | 1 | gene\_05665.t1 | | nucleosome disassembly | biological\_process |
| GO:0018142 | 1 | gene\_10392.t1 | | protein-DNA covalent cross-linking | biological\_process |
| GO:0032790 | 2 | gene\_05458.t1,gene\_08109.t1 | | ribosome disassembly | biological\_process |
| GO:0000470 | 1 | gene\_07417.t1 | | maturation of LSU-rRNA | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0006888 | 11 | gene\_03939.t1,gene\_09282.t1,gene\_09487.t1,gene\_01071.t1,gene\_05520.t1,gene\_02093.t1,gene\_09223.t1,gene\_00033.t1,gene\_03214.t1,gene\_02368.t1,gene\_10522.t1 | | endoplasmic reticulum to Golgi vesicle-mediated transport | biological\_process |
| GO:0000902 | 4 | gene\_06759.t1,gene\_01282.t1,gene\_08716.t1,gene\_06490.t1 | | cell morphogenesis | biological\_process |
| GO:0006885 | 1 | gene\_04349.t1 | | regulation of pH | biological\_process |
| GO:0006886 | 48 | gene\_07093.t1,gene\_02540.t1,gene\_10007.t1,gene\_02093.t1,gene\_05346.t1,gene\_05393.t1,gene\_03667.t1,gene\_09193.t1,gene\_06397.t1,gene\_03214.t1,gene\_08919.t1,gene\_05895.t1,gene\_10348.t1,gene\_00505.t1,gene\_00582.t1,gene\_06223.t1,gene\_10522.t1,gene\_05672.t1,gene\_01017.t1,gene\_06756.t1,gene\_02252.t1,gene\_02853.t1,gene\_01668.t1,gene\_03881.t1,gene\_03659.t1,gene\_01313.t1,gene\_05391.t1,gene\_09722.t1,gene\_03142.t1,gene\_07361.t1,gene\_03925.t1,gene\_04059.t1,gene\_04556.t1,gene\_01372.t1,gene\_08040.t1,gene\_09165.t1,gene\_00350.t1,gene\_09100.t1,gene\_00554.t1,gene\_04579.t1,gene\_10480.t1,gene\_07106.t1,gene\_06125.t1,gene\_06752.t1,gene\_04061.t1,gene\_10184.t1,gene\_09561.t1,gene\_08669.t1 | | intracellular protein transport | biological\_process |
| GO:0006887 | 7 | gene\_05127.t1,gene\_08719.t1,gene\_07646.t1,gene\_03986.t1,gene\_06544.t1,gene\_01590.t1,gene\_00718.t1 | | exocytosis | biological\_process |
| GO:0008643 | 11 | gene\_02940.t1,gene\_05144.t1,gene\_02541.t1,gene\_08773.t1,gene\_09248.t1,gene\_05223.t1,gene\_05802.t1,gene\_06570.t1,gene\_00179.t1,gene\_03306.t1,gene\_04756.t1 | | carbohydrate transport | biological\_process |
| GO:0000453 | 1 | gene\_05806.t1 | | enzyme-directed rRNA 2'-O-methylation | biological\_process |
| GO:0051560 | 1 | gene\_04031.t1 | | mitochondrial calcium ion homeostasis | biological\_process |
| GO:0007051 | 1 | gene\_10486.t1 | | spindle organization | biological\_process |
| GO:0007052 | 2 | gene\_06154.t1,gene\_08279.t1 | | mitotic spindle organization | biological\_process |
| GO:0007059 | 10 | gene\_07001.t1,gene\_07003.t1,gene\_08597.t1,gene\_05155.t1,gene\_03476.t1,gene\_06154.t1,gene\_09061.t1,gene\_05168.t1,gene\_06720.t1,gene\_09382.t1 | | chromosome segregation | biological\_process |
| GO:0016070 | 3 | gene\_09702.t1,gene\_06034.t1,gene\_02995.t1 | | RNA metabolic process | biological\_process |
| GO:0016075 | 2 | gene\_04160.t1,gene\_08713.t1 | | rRNA catabolic process | biological\_process |
| GO:0015074 | 9 | gene\_02212.t1,gene\_08700.t1,gene\_01274.t1,gene\_06867.t1,gene\_06866.t1,gene\_08699.t1,gene\_01958.t1,gene\_10675.t1,gene\_02023.t1 | | DNA integration | biological\_process |
| GO:0071467 | 1 | gene\_00092.t1 | | cellular response to pH | biological\_process |
| GO:0032008 | 2 | gene\_03887.t1,gene\_02775.t1 | | positive regulation of TOR signaling | biological\_process |
| GO:0032007 | 1 | gene\_05367.t1 | | negative regulation of TOR signaling | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0016095 | 1 | gene\_02943.t1 | | polyprenol catabolic process | biological\_process |
| GO:0043248 | 4 | gene\_02386.t1,gene\_01921.t1,gene\_09570.t1,gene\_08397.t1 | | proteasome assembly | biological\_process |
| GO:0042632 | 1 | gene\_03887.t1 | | cholesterol homeostasis | biological\_process |
| GO:0030951 | 1 | gene\_10486.t1 | | establishment or maintenance of microtubule cytoskeleton polarity | biological\_process |
| GO:0043488 | 2 | gene\_01674.t1,gene\_03979.t1 | | regulation of mRNA stability | biological\_process |
| GO:0043486 | 3 | gene\_09848.t1,gene\_03694.t1,gene\_01406.t1 | | histone exchange | biological\_process |
| GO:0019354 | 2 | gene\_06837.t1,gene\_09155.t1 | | siroheme biosynthetic process | biological\_process |
| GO:0000493 | 1 | gene\_02232.t1 | | box H/ACA snoRNP assembly | biological\_process |
| GO:0000492 | 1 | gene\_03290.t1 | | box C/D snoRNP assembly | biological\_process |
| GO:0045048 | 3 | gene\_07236.t1,gene\_05695.t1,gene\_09701.t1 | | protein insertion into ER membrane | biological\_process |
| GO:0046373 | 3 | gene\_01362.t1,gene\_00037.t1,gene\_05400.t1 | | L-arabinose metabolic process | biological\_process |
| GO:0006235 | 1 | gene\_01301.t1 | | dTTP biosynthetic process | biological\_process |
| GO:0006233 | 1 | gene\_07888.t1 | | dTDP biosynthetic process | biological\_process |
| GO:0006231 | 1 | gene\_01301.t1 | | dTMP biosynthetic process | biological\_process |
| GO:0016255 | 4 | gene\_03868.t1,gene\_01979.t1,gene\_01432.t1,gene\_02656.t1 | | attachment of GPI anchor to protein | biological\_process |
| GO:0070816 | 1 | gene\_09119.t1 | | phosphorylation of RNA polymerase II C-terminal domain | biological\_process |
| GO:0006099 | 17 | gene\_10230.t1,gene\_06798.t1,gene\_08720.t1,gene\_09160.t1,gene\_08431.t1,gene\_00860.t1,gene\_07453.t1,gene\_02452.t1,gene\_09730.t1,gene\_07137.t1,gene\_04330.t1,gene\_02366.t1,gene\_09444.t1,gene\_01319.t1,gene\_10491.t1,gene\_04426.t1,gene\_07350.t1 | | tricarboxylic acid cycle | biological\_process |
| GO:0006098 | 7 | gene\_03675.t1,gene\_00043.t1,gene\_04418.t1,gene\_03823.t1,gene\_00992.t1,gene\_07980.t1,gene\_06816.t1 | | pentose-phosphate shunt | biological\_process |
| GO:0045047 | 1 | gene\_07756.t1 | | protein targeting to ER | biological\_process |
| GO:0006090 | 3 | gene\_06471.t1,gene\_01374.t1,gene\_09157.t1 | | pyruvate metabolic process | biological\_process |
| GO:0006097 | 1 | gene\_09444.t1 | | glyoxylate cycle | biological\_process |
| GO:0006096 | 15 | gene\_05462.t1,gene\_06196.t1,gene\_07758.t1,gene\_00648.t1,gene\_00838.t1,gene\_00479.t1,gene\_03040.t1,gene\_02419.t1,gene\_09875.t1,gene\_06480.t1,gene\_06014.t1,gene\_00524.t1,gene\_06111.t1,gene\_09513.t1,gene\_03194.t1 | | glycolytic process | biological\_process |
| GO:0006094 | 7 | gene\_03687.t1,gene\_00648.t1,gene\_01374.t1,gene\_06111.t1,gene\_00479.t1,gene\_06471.t1,gene\_03779.t1 | | gluconeogenesis | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0006529 | 2 | gene\_00321.t1,gene\_10129.t1 | | asparagine biosynthetic process | biological\_process |
| GO:0006520 | 13 | gene\_05315.t1,gene\_00359.t1,gene\_03995.t1,gene\_00460.t1,gene\_00088.t1,gene\_02277.t1,gene\_10080.t1,gene\_09401.t1,gene\_00510.t1,gene\_05313.t1,gene\_05306.t1,gene\_00862.t1,gene\_01381.t1 | | cellular amino acid metabolic process | biological\_process |
| GO:0006526 | 5 | gene\_00813.t1,gene\_03625.t1,gene\_04583.t1,gene\_06573.t1,gene\_07598.t1 | | arginine biosynthetic process | biological\_process |
| GO:0006525 | 1 | gene\_05706.t1 | | arginine metabolic process | biological\_process |
| GO:1990544 | 1 | gene\_02936.t1 | | mitochondrial ATP transmembrane transport | biological\_process |
| GO:1990547 | 4 | gene\_07220.t1,gene\_06091.t1,gene\_01931.t1,gene\_07633.t1 | | mitochondrial phosphate ion transmembrane transport | biological\_process |
| GO:0000278 | 7 | gene\_07003.t1,gene\_08597.t1,gene\_06720.t1,gene\_05155.t1,gene\_03476.t1,gene\_00422.t1,gene\_01875.t1 | | mitotic cell cycle | biological\_process |
| GO:0000272 | 45 | gene\_00945.t1,gene\_01578.t1,gene\_08437.t1,gene\_07912.t1,gene\_07875.t1,gene\_06552.t1,gene\_00176.t1,gene\_04755.t1,gene\_05687.t1,gene\_06586.t1,gene\_01798.t1,gene\_10573.t1,gene\_03424.t1,gene\_02291.t1,gene\_03030.t1,gene\_01799.t1,gene\_01845.t1,gene\_06777.t1,gene\_01037.t1,gene\_09452.t1,gene\_03902.t1,gene\_07226.t1,gene\_09758.t1,gene\_03906.t1,gene\_03719.t1,gene\_05104.t1,gene\_01797.t1,gene\_00439.t1,gene\_05417.t1,gene\_02142.t1,gene\_01759.t1,gene\_04380.t1,gene\_02620.t1,gene\_04222.t1,gene\_02922.t1,gene\_04464.t1,gene\_06768.t1,gene\_06897.t1,gene\_10353.t1,gene\_01647.t1,gene\_04322.t1,gene\_07460.t1,gene\_00971.t1,gene\_01800.t1,gene\_01801.t1 | | polysaccharide catabolic process | biological\_process |
| GO:0031047 | 10 | gene\_05887.t1,gene\_03396.t1,gene\_07978.t1,gene\_06315.t1,gene\_05659.t1,gene\_05841.t1,gene\_06857.t1,gene\_10383.t1,gene\_08120.t1,gene\_00284.t1 | | gene silencing by RNA | biological\_process |
| GO:0072344 | 2 | gene\_00722.t1,gene\_02227.t1 | | rescue of stalled ribosome | biological\_process |
| GO:0006487 | 7 | gene\_04999.t1,gene\_01969.t1,gene\_10658.t1,gene\_02904.t1,gene\_04805.t1,gene\_09530.t1,gene\_05113.t1 | | protein N-linked glycosylation | biological\_process |
| GO:0006417 | 7 | gene\_03653.t1,gene\_01161.t1,gene\_08626.t1,gene\_05791.t1,gene\_01605.t1,gene\_07953.t1,gene\_07305.t1 | | regulation of translation | biological\_process |
| GO:0006415 | 2 | gene\_05458.t1,gene\_07129.t1 | | translational termination | biological\_process |
| GO:0006414 | 1 | gene\_02457.t1 | | translational elongation | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0006412 | 103 | gene\_01069.t1,gene\_09911.t1,gene\_09037.t1,gene\_06615.t1,gene\_06639.t1,gene\_01143.t1,gene\_03172.t1,gene\_10488.t1,gene\_00424.t1,gene\_02603.t1,gene\_05698.t1,gene\_04610.t1,gene\_09278.t1,gene\_03284.t1,gene\_05166.t1,gene\_05235.t1,gene\_01386.t1,gene\_03883.t1,gene\_05845.t1,gene\_02997.t1,gene\_06369.t1,gene\_09718.t1,gene\_05192.t1,gene\_02965.t1,gene\_01678.t1,gene\_10173.t1,gene\_04441.t1,gene\_02931.t1,gene\_05390.t1,gene\_01327.t1,gene\_02684.t1,gene\_03088.t1,gene\_06815.t1,gene\_08346.t1,gene\_03269.t1,gene\_02469.t1,gene\_07654.t1,gene\_00559.t1,gene\_08396.t1,gene\_07950.t1,gene\_02779.t1,gene\_09004.t1,gene\_06282.t1,gene\_04091.t1,gene\_07081.t1,gene\_03168.t1,gene\_01160.t1,gene\_03653.t1,gene\_08037.t1,gene\_08736.t1,gene\_01369.t1,gene\_05521.t1,gene\_00402.t1,gene\_06842.t1,gene\_07006.t1,gene\_01094.t1,gene\_04098.t1,gene\_05623.t1,gene\_02536.t1,gene\_05838.t1,gene\_02167.t1,gene\_01594.t1,gene\_00401.t1,gene\_06873.t1,gene\_04240.t1,gene\_07619.t1,gene\_06874.t1,gene\_02637.t1,gene\_01723.t1,gene\_01417.t1,gene\_05876.t1,gene\_04719.t1,gene\_09259.t1,gene\_09745.t1,gene\_08514.t1,gene\_10591.t1,gene\_10017.t1,gene\_00539.t1,gene\_00520.t1,gene\_08028.t1,gene\_09731.t1,gene\_02556.t1,gene\_01627.t1,gene\_01599.t1,gene\_03987.t1,gene\_09486.t1,gene\_04409.t1,gene\_08547.t1,gene\_09596.t1,gene\_09003.t1,gene\_09302.t1,gene\_10540.t1,gene\_05686.t1,gene\_05885.t1,gene\_00481.t1,gene\_00592.t1,gene\_06861.t1,gene\_02434.t1,gene\_01550.t1,gene\_10532.t1,gene\_06717.t1,gene\_01010.t1,gene\_02865.t1 | | translation | biological\_process |
| GO:0006147 | 1 | gene\_07694.t1 | | guanine catabolic process | biological\_process |
| GO:0006146 | 1 | gene\_01718.t1 | | adenine catabolic process | biological\_process |
| GO:0009298 | 16 | gene\_10287.t1,gene\_03793.t1,gene\_10100.t1,gene\_01115.t1,gene\_04976.t1,gene\_03725.t1,gene\_00023.t1,gene\_05151.t1,gene\_10469.t1,gene\_01861.t1,gene\_04903.t1,gene\_10286.t1,gene\_01454.t1,gene\_02395.t1,gene\_03919.t1,gene\_08772.t1 | | GDP-mannose biosynthetic process | biological\_process |
| GO:0001510 | 1 | gene\_10176.t1 | | RNA methylation | biological\_process |
| GO:0009072 | 2 | gene\_05731.t1,gene\_03811.t1 | | aromatic amino acid family metabolic process | biological\_process |
| GO:0009073 | 5 | gene\_00714.t1,gene\_06027.t1,gene\_02444.t1,gene\_02892.t1,gene\_02251.t1 | | aromatic amino acid family biosynthetic process | biological\_process |
| GO:0006741 | 3 | gene\_08533.t1,gene\_09241.t1,gene\_07119.t1 | | NADP biosynthetic process | biological\_process |
| GO:0018027 | 1 | gene\_09083.t1 | | peptidyl-lysine dimethylation | biological\_process |
| GO:0045324 | 1 | gene\_10095.t1 | | late endosome to vacuole transport | biological\_process |
| GO:0045329 | 1 | gene\_02485.t1 | | carnitine biosynthetic process | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0051028 | 13 | gene\_00974.t1,gene\_09312.t1,gene\_06461.t1,gene\_01090.t1,gene\_10042.t1,gene\_09614.t1,gene\_01688.t1,gene\_09711.t1,gene\_01605.t1,gene\_08367.t1,gene\_07305.t1,gene\_00349.t1,gene\_07017.t1 | | mRNA transport | biological\_process |
| GO:0090173 | 1 | gene\_07611.t1 | | regulation of synaptonemal complex assembly | biological\_process |
| GO:0010142 | 1 | gene\_03020.t1 | | farnesyl diphosphate biosynthetic process, mevalonate pathway | biological\_process |
| GO:0006419 | 1 | gene\_07680.t1 | | alanyl-tRNA aminoacylation | biological\_process |
| GO:0019310 | 2 | gene\_01340.t1,gene\_00527.t1 | | inositol catabolic process | biological\_process |
| GO:0001919 | 1 | gene\_03887.t1 | | regulation of receptor recycling | biological\_process |
| GO:0006893 | 3 | gene\_04572.t1,gene\_03048.t1,gene\_08719.t1 | | Golgi to plasma membrane transport | biological\_process |
| GO:0008652 | 10 | gene\_06860.t1,gene\_06027.t1,gene\_09326.t1,gene\_02444.t1,gene\_09263.t1,gene\_02892.t1,gene\_00714.t1,gene\_00766.t1,gene\_02251.t1,gene\_00557.t1 | | cellular amino acid biosynthetic process | biological\_process |
| GO:0006891 | 5 | gene\_03232.t1,gene\_10290.t1,gene\_05460.t1,gene\_09555.t1,gene\_02181.t1 | | intra-Golgi vesicle-mediated transport | biological\_process |
| GO:0006890 | 7 | gene\_08775.t1,gene\_02033.t1,gene\_05676.t1,gene\_07213.t1,gene\_01728.t1,gene\_02521.t1,gene\_10278.t1 | | retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum | biological\_process |
| GO:0006897 | 9 | gene\_03881.t1,gene\_10269.t1,gene\_05990.t1,gene\_00669.t1,gene\_02165.t1,gene\_07272.t1,gene\_07381.t1,gene\_04556.t1,gene\_08752.t1 | | endocytosis | biological\_process |
| GO:0043666 | 3 | gene\_01199.t1,gene\_10037.t1,gene\_08172.t1 | | regulation of phosphoprotein phosphatase activity | biological\_process |
| GO:0006895 | 1 | gene\_03696.t1 | | Golgi to endosome transport | biological\_process |
| GO:0008654 | 8 | gene\_07485.t1,gene\_00961.t1,gene\_02039.t1,gene\_06843.t1,gene\_04684.t1,gene\_07205.t1,gene\_09574.t1,gene\_01086.t1 | | phospholipid biosynthetic process | biological\_process |
| GO:0032366 | 2 | gene\_07028.t1,gene\_07044.t1 | | intracellular sterol transport | biological\_process |
| GO:0007040 | 1 | gene\_03887.t1 | | lysosome organization | biological\_process |
| GO:0055129 | 3 | gene\_01216.t1,gene\_02827.t1,gene\_03398.t1 | | L-proline biosynthetic process | biological\_process |
| GO:0032968 | 2 | gene\_02334.t1,gene\_07299.t1 | | positive regulation of transcription elongation from RNA polymerase II promoter | biological\_process |
| GO:0007049 | 28 | gene\_08710.t1,gene\_05897.t1,gene\_03094.t1,gene\_07231.t1,gene\_07822.t1,gene\_05168.t1,gene\_06735.t1,gene\_04228.t1,gene\_02001.t1,gene\_02882.t1,gene\_01226.t1,gene\_04724.t1,gene\_00515.t1,gene\_02065.t1,gene\_07862.t1,gene\_05740.t1,gene\_05883.t1,gene\_02992.t1,gene\_10449.t1,gene\_01982.t1,gene\_09071.t1,gene\_08245.t1,gene\_01007.t1,gene\_07321.t1,gene\_09773.t1,gene\_09737.t1,gene\_03236.t1,gene\_09787.t1 | | cell cycle | biological\_process |
| GO:0010564 | 2 | gene\_00089.t1,gene\_07370.t1 | | regulation of cell cycle process | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0033566 | 1 | gene\_05213.t1 | | gamma-tubulin complex localization | biological\_process |
| GO:0070475 | 1 | gene\_07288.t1 | | rRNA base methylation | biological\_process |
| GO:0070476 | 1 | gene\_02367.t1 | | rRNA (guanine-N7)-methylation | biological\_process |
| GO:0007131 | 5 | gene\_06455.t1,gene\_05469.t1,gene\_02751.t1,gene\_08341.t1,gene\_07316.t1 | | reciprocal meiotic recombination | biological\_process |
| GO:0006413 | 1 | gene\_05458.t1 | | translational initiation | biological\_process |
| GO:0006479 | 6 | gene\_08347.t1,gene\_00499.t1,gene\_05960.t1,gene\_06651.t1,gene\_01397.t1,gene\_02726.t1 | | protein methylation | biological\_process |
| GO:0034404 | 1 | gene\_09266.t1 | | nucleobase-containing small molecule biosynthetic process | biological\_process |
| GO:0071897 | 3 | gene\_05677.t1,gene\_01043.t1,gene\_05811.t1 | | DNA biosynthetic process | biological\_process |
| GO:0050992 | 1 | gene\_06520.t1 | | dimethylallyl diphosphate biosynthetic process | biological\_process |
| GO:0043386 | 8 | gene\_05437.t1,gene\_00185.t1,gene\_09659.t1,gene\_09661.t1,gene\_09172.t1,gene\_00195.t1,gene\_06116.t1,gene\_00183.t1 | | mycotoxin biosynthetic process | biological\_process |
| GO:0030328 | 1 | gene\_03186.t1 | | prenylcysteine catabolic process | biological\_process |
| GO:0016539 | 1 | gene\_02780.t1 | | intein-mediated protein splicing | biological\_process |
| GO:1904668 | 3 | gene\_09995.t1,gene\_02100.t1,gene\_07199.t1 | | positive regulation of ubiquitin protein ligase activity | biological\_process |
| GO:1904669 | 1 | gene\_07913.t1 | | ATP export | biological\_process |
| GO:0031124 | 2 | gene\_05890.t1,gene\_01714.t1 | | mRNA 3'-end processing | biological\_process |
| GO:0006418 | 1 | gene\_01446.t1 | | tRNA aminoacylation for protein translation | biological\_process |
| GO:0031123 | 1 | gene\_01933.t1 | | RNA 3'-end processing | biological\_process |
| GO:0030435 | 13 | gene\_00512.t1,gene\_09058.t1,gene\_03685.t1,gene\_00960.t1,gene\_10384.t1,gene\_05891.t1,gene\_04321.t1,gene\_01163.t1,gene\_01650.t1,gene\_00762.t1,gene\_07116.t1,gene\_02974.t1,gene\_05793.t1 | | sporulation resulting in formation of a cellular spore | biological\_process |
| GO:0030433 | 8 | gene\_02817.t1,gene\_00376.t1,gene\_07380.t1,gene\_10310.t1,gene\_07313.t1,gene\_04055.t1,gene\_02421.t1,gene\_02125.t1 | | ubiquitin-dependent ERAD pathway | biological\_process |
| GO:0002098 | 10 | gene\_00353.t1,gene\_05774.t1,gene\_05907.t1,gene\_04181.t1,gene\_01562.t1,gene\_06853.t1,gene\_09540.t1,gene\_09706.t1,gene\_09577.t1,gene\_09082.t1 | | tRNA wobble uridine modification | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0005975 | 125 | gene\_00936.t1,gene\_04418.t1,gene\_00119.t1,gene\_02770.t1,gene\_09759.t1,gene\_09962.t1,gene\_02156.t1,gene\_00100.t1,gene\_09138.t1,gene\_00708.t1,gene\_05575.t1,gene\_03025.t1,gene\_01032.t1,gene\_06929.t1,gene\_03085.t1,gene\_08997.t1,gene\_00043.t1,gene\_03230.t1,gene\_00199.t1,gene\_07809.t1,gene\_00394.t1,gene\_04069.t1,gene\_07788.t1,gene\_02817.t1,gene\_08223.t1,gene\_05651.t1,gene\_06380.t1,gene\_03481.t1,gene\_04526.t1,gene\_08993.t1,gene\_02791.t1,gene\_01454.t1,gene\_02125.t1,gene\_08927.t1,gene\_06645.t1,gene\_08468.t1,gene\_03179.t1,gene\_02551.t1,gene\_01435.t1,gene\_06681.t1,gene\_07770.t1,gene\_00082.t1,gene\_04391.t1,gene\_06881.t1,gene\_08980.t1,gene\_07991.t1,gene\_02243.t1,gene\_03444.t1,gene\_08332.t1,gene\_02102.t1,gene\_09942.t1,gene\_01013.t1,gene\_07334.t1,gene\_02421.t1,gene\_02271.t1,gene\_05091.t1,gene\_09730.t1,gene\_07652.t1,gene\_09695.t1,gene\_08467.t1,gene\_10122.t1,gene\_09762.t1,gene\_03569.t1,gene\_07845.t1,gene\_08633.t1,gene\_05720.t1,gene\_02403.t1,gene\_07399.t1,gene\_08469.t1,gene\_02920.t1,gene\_05610.t1,gene\_01725.t1,gene\_04297.t1,gene\_06714.t1,gene\_10310.t1,gene\_09160.t1,gene\_02284.t1,gene\_01835.t1,gene\_07682.t1,gene\_02885.t1,gene\_00636.t1,gene\_07980.t1,gene\_00649.t1,gene\_06470.t1,gene\_10612.t1,gene\_08772.t1,gene\_05571.t1,gene\_07881.t1,gene\_00950.t1,gene\_08481.t1,gene\_07562.t1,gene\_09669.t1,gene\_08634.t1,gene\_08898.t1,gene\_07032.t1,gene\_06341.t1,gene\_05380.t1,gene\_09961.t1,gene\_07022.t1,gene\_04055.t1,gene\_03420.t1,gene\_02188.t1,gene\_02549.t1,gene\_07540.t1,gene\_04731.t1,gene\_03404.t1,gene\_02548.t1,gene\_02481.t1,gene\_09319.t1,gene\_06903.t1,gene\_03591.t1,gene\_05650.t1,gene\_09816.t1,gene\_09941.t1,gene\_05378.t1,gene\_07473.t1,gene\_05573.t1,gene\_09960.t1,gene\_06726.t1,gene\_04664.t1,gene\_09783.t1,gene\_00992.t1,gene\_01234.t1,gene\_09538.t1,gene\_04675.t1 | | carbohydrate metabolic process | biological\_process |
| GO:0006559 | 4 | gene\_03809.t1,gene\_03807.t1,gene\_10000.t1,gene\_03810.t1 | | L-phenylalanine catabolic process | biological\_process |
| GO:0005978 | 3 | gene\_08420.t1,gene\_07867.t1,gene\_00709.t1 | | glycogen biosynthetic process | biological\_process |
| GO:0006555 | 2 | gene\_07024.t1,gene\_07886.t1 | | methionine metabolic process | biological\_process |
| GO:0006144 | 4 | gene\_05694.t1,gene\_07404.t1,gene\_05784.t1,gene\_00591.t1 | | purine nucleobase metabolic process | biological\_process |
| GO:1900364 | 1 | gene\_03979.t1 | | negative regulation of mRNA polyadenylation | biological\_process |
| GO:0006396 | 21 | gene\_04160.t1,gene\_06123.t1,gene\_06315.t1,gene\_03396.t1,gene\_05421.t1,gene\_07393.t1,gene\_00878.t1,gene\_07733.t1,gene\_09251.t1,gene\_05841.t1,gene\_04512.t1,gene\_10354.t1,gene\_05787.t1,gene\_08713.t1,gene\_00897.t1,gene\_08623.t1,gene\_03181.t1,gene\_04425.t1,gene\_02790.t1,gene\_10512.t1,gene\_08877.t1 | | RNA processing | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0006397 | 40 | gene\_09879.t1,gene\_06622.t1,gene\_00740.t1,gene\_03219.t1,gene\_08291.t1,gene\_05664.t1,gene\_01933.t1,gene\_08924.t1,gene\_01605.t1,gene\_03454.t1,gene\_03654.t1,gene\_09407.t1,gene\_08105.t1,gene\_04131.t1,gene\_02842.t1,gene\_02699.t1,gene\_00549.t1,gene\_04238.t1,gene\_00478.t1,gene\_06051.t1,gene\_09750.t1,gene\_05976.t1,gene\_07173.t1,gene\_10208.t1,gene\_08388.t1,gene\_06365.t1,gene\_06245.t1,gene\_09859.t1,gene\_02253.t1,gene\_07082.t1,gene\_08528.t1,gene\_09536.t1,gene\_07305.t1,gene\_03541.t1,gene\_02495.t1,gene\_06417.t1,gene\_06603.t1,gene\_04534.t1,gene\_01138.t1,gene\_02175.t1 | | mRNA processing | biological\_process |
| GO:0006777 | 6 | gene\_06163.t1,gene\_08455.t1,gene\_02844.t1,gene\_06655.t1,gene\_04702.t1,gene\_06930.t1 | | Mo-molybdopterin cofactor biosynthetic process | biological\_process |
| GO:0006772 | 1 | gene\_03103.t1 | | thiamine metabolic process | biological\_process |
| GO:0000245 | 2 | gene\_03530.t1,gene\_00409.t1 | | spliceosomal complex assembly | biological\_process |
| GO:0060249 | 1 | gene\_03799.t1 | | anatomical structure homeostasis | biological\_process |
| GO:0010960 | 1 | gene\_03636.t1 | | magnesium ion homeostasis | biological\_process |
| GO:0006177 | 2 | gene\_04266.t1,gene\_02686.t1 | | GMP biosynthetic process | biological\_process |
| GO:0009448 | 1 | gene\_08073.t1 | | gamma-aminobutyric acid metabolic process | biological\_process |
| GO:0009446 | 2 | gene\_00589.t1,gene\_08117.t1 | | putrescine biosynthetic process | biological\_process |
| GO:0006606 | 8 | gene\_02554.t1,gene\_10468.t1,gene\_06251.t1,gene\_07673.t1,gene\_02029.t1,gene\_09841.t1,gene\_02002.t1,gene\_08906.t1 | | protein import into nucleus | biological\_process |
| GO:0009443 | 1 | gene\_01000.t1 | | pyridoxal 5'-phosphate salvage | biological\_process |
| GO:0006605 | 2 | gene\_06869.t1,gene\_06545.t1 | | protein targeting | biological\_process |
| GO:0009450 | 1 | gene\_01425.t1 | | gamma-aminobutyric acid catabolic process | biological\_process |
| GO:0042450 | 1 | gene\_07135.t1 | | arginine biosynthetic process via ornithine | biological\_process |
| GO:0000398 | 25 | gene\_02231.t1,gene\_02996.t1,gene\_07820.t1,gene\_08914.t1,gene\_02357.t1,gene\_05449.t1,gene\_05828.t1,gene\_04086.t1,gene\_07641.t1,gene\_10212.t1,gene\_02268.t1,gene\_01054.t1,gene\_03994.t1,gene\_07996.t1,gene\_09915.t1,gene\_08685.t1,gene\_06070.t1,gene\_03076.t1,gene\_02780.t1,gene\_06855.t1,gene\_07946.t1,gene\_02972.t1,gene\_06366.t1,gene\_02203.t1,gene\_08257.t1 | | mRNA splicing, via spliceosome | biological\_process |
| GO:0045721 | 3 | gene\_09250.t1,gene\_08349.t1,gene\_09820.t1 | | negative regulation of gluconeogenesis | biological\_process |
| GO:0045292 | 8 | gene\_08079.t1,gene\_07256.t1,gene\_01308.t1,gene\_08612.t1,gene\_09711.t1,gene\_03864.t1,gene\_05459.t1,gene\_00318.t1 | | mRNA cis splicing, via spliceosome | biological\_process |
| GO:0051103 | 2 | gene\_07821.t1,gene\_05811.t1 | | DNA ligation involved in DNA repair | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0009063 | 2 | gene\_00477.t1,gene\_03435.t1 | | cellular amino acid catabolic process | biological\_process |
| GO:0009062 | 1 | gene\_04485.t1 | | fatty acid catabolic process | biological\_process |
| GO:0009066 | 1 | gene\_07958.t1 | | aspartate family amino acid metabolic process | biological\_process |
| GO:0000027 | 4 | gene\_09858.t1,gene\_07417.t1,gene\_06113.t1,gene\_07628.t1 | | ribosomal large subunit assembly | biological\_process |
| GO:0045053 | 2 | gene\_07913.t1,gene\_10095.t1 | | protein retention in Golgi apparatus | biological\_process |
| GO:0006950 | 3 | gene\_09620.t1,gene\_09252.t1,gene\_00746.t1 | | response to stress | biological\_process |
| GO:0045333 | 1 | gene\_02653.t1 | | cellular respiration | biological\_process |
| GO:0045332 | 1 | gene\_04164.t1 | | phospholipid translocation | biological\_process |
| GO:0001678 | 6 | gene\_06196.t1,gene\_09513.t1,gene\_00838.t1,gene\_09875.t1,gene\_06480.t1,gene\_06014.t1 | | cellular glucose homeostasis | biological\_process |
| GO:0048017 | 1 | gene\_09152.t1 | | inositol lipid-mediated signaling | biological\_process |
| GO:0000730 | 1 | gene\_00330.t1 | | DNA recombinase assembly | biological\_process |
| GO:0036297 | 1 | gene\_04241.t1 | | interstrand cross-link repair | biological\_process |
| GO:0032511 | 1 | gene\_01023.t1 | | late endosome to vacuole transport via multivesicular body sorting pathway | biological\_process |
| GO:0018160 | 1 | gene\_05843.t1 | | peptidyl-pyrromethane cofactor linkage | biological\_process |
| GO:0009712 | 4 | gene\_02569.t1,gene\_09653.t1,gene\_06959.t1,gene\_02177.t1 | | catechol-containing compound metabolic process | biological\_process |
| GO:0018013 | 1 | gene\_09083.t1 | | N-terminal peptidyl-glycine methylation | biological\_process |
| GO:0070682 | 2 | gene\_05203.t1,gene\_10559.t1 | | proteasome regulatory particle assembly | biological\_process |
| GO:0070681 | 2 | gene\_02324.t1,gene\_05707.t1 | | glutaminyl-tRNAGln biosynthesis via transamidation | biological\_process |
| GO:0032979 | 1 | gene\_07239.t1 | | protein insertion into mitochondrial inner membrane from matrix | biological\_process |
| GO:2000601 | 1 | gene\_00869.t1 | | positive regulation of Arp2/3 complex-mediated actin nucleation | biological\_process |
| GO:0032974 | 3 | gene\_03031.t1,gene\_00063.t1,gene\_08284.t1 | | amino acid transmembrane export from vacuole | biological\_process |
| GO:0051259 | 1 | gene\_07388.t1 | | protein complex oligomerization | biological\_process |
| GO:0019303 | 1 | gene\_07851.t1 | | D-ribose catabolic process | biological\_process |
| GO:0034501 | 1 | gene\_06875.t1 | | protein localization to kinetochore | biological\_process |
| GO:0034508 | 2 | gene\_06909.t1,gene\_09546.t1 | | centromere complex assembly | biological\_process |
| GO:0051052 | 1 | gene\_02882.t1 | | regulation of DNA metabolic process | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0043461 | 1 | gene\_08317.t1 | | proton-transporting ATP synthase complex assembly | biological\_process |
| GO:0015693 | 7 | gene\_06075.t1,gene\_04003.t1,gene\_02147.t1,gene\_09812.t1,gene\_00870.t1,gene\_01748.t1,gene\_05086.t1 | | magnesium ion transport | biological\_process |
| GO:0034613 | 2 | gene\_08575.t1,gene\_06343.t1 | | cellular protein localization | biological\_process |
| GO:0051641 | 1 | gene\_03575.t1 | | cellular localization | biological\_process |
| GO:0042183 | 1 | gene\_09683.t1 | | formate catabolic process | biological\_process |
| GO:0007094 | 3 | gene\_09780.t1,gene\_09038.t1,gene\_08841.t1 | | mitotic spindle assembly checkpoint signaling | biological\_process |
| GO:0007095 | 1 | gene\_04738.t1 | | mitotic G2 DNA damage checkpoint signaling | biological\_process |
| GO:0007096 | 1 | gene\_02992.t1 | | regulation of exit from mitosis | biological\_process |
| GO:0046513 | 3 | gene\_09343.t1,gene\_09360.t1,gene\_06384.t1 | | ceramide biosynthetic process | biological\_process |
| GO:0050688 | 3 | gene\_03396.t1,gene\_06315.t1,gene\_05841.t1 | | regulation of defense response to virus | biological\_process |
| GO:0031116 | 1 | gene\_02046.t1 | | positive regulation of microtubule polymerization | biological\_process |
| GO:0035103 | 1 | gene\_07195.t1 | | sterol regulatory element binding protein cleavage | biological\_process |
| GO:0031119 | 1 | gene\_01113.t1 | | tRNA pseudouridine synthesis | biological\_process |
| GO:0006431 | 2 | gene\_05182.t1,gene\_01382.t1 | | methionyl-tRNA aminoacylation | biological\_process |
| GO:0006546 | 2 | gene\_05570.t1,gene\_02293.t1 | | glycine catabolic process | biological\_process |
| GO:0006541 | 14 | gene\_06540.t1,gene\_02361.t1,gene\_08081.t1,gene\_08292.t1,gene\_08809.t1,gene\_05948.t1,gene\_08162.t1,gene\_04134.t1,gene\_09562.t1,gene\_01088.t1,gene\_01363.t1,gene\_00321.t1,gene\_03275.t1,gene\_09668.t1 | | glutamine metabolic process | biological\_process |
| GO:0006542 | 3 | gene\_09443.t1,gene\_10398.t1,gene\_03301.t1 | | glutamine biosynthetic process | biological\_process |
| GO:0006696 | 1 | gene\_06489.t1 | | ergosterol biosynthetic process | biological\_process |
| GO:0006388 | 2 | gene\_04404.t1,gene\_05344.t1 | | tRNA splicing, via endonucleolytic cleavage and ligation | biological\_process |
| GO:0006384 | 4 | gene\_09013.t1,gene\_10633.t1,gene\_06291.t1,gene\_07840.t1 | | transcription initiation from RNA polymerase III promoter | biological\_process |
| GO:0006383 | 4 | gene\_01673.t1,gene\_06259.t1,gene\_04655.t1,gene\_08095.t1 | | transcription by RNA polymerase III | biological\_process |
| GO:0000256 | 3 | gene\_03176.t1,gene\_07404.t1,gene\_05646.t1 | | allantoin catabolic process | biological\_process |
| GO:0060255 | 1 | gene\_09728.t1 | | regulation of macromolecule metabolic process | biological\_process |
| GO:0030041 | 1 | gene\_06990.t1 | | actin filament polymerization | biological\_process |
| GO:0030042 | 3 | gene\_08417.t1,gene\_03932.t1,gene\_00367.t1 | | actin filament depolymerization | biological\_process |
| GO:0043137 | 1 | gene\_07283.t1 | | DNA replication, removal of RNA primer | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0006166 | 3 | gene\_08031.t1,gene\_08329.t1,gene\_03822.t1 | | purine ribonucleoside salvage | biological\_process |
| GO:1903373 | 1 | gene\_03397.t1 | | positive regulation of endoplasmic reticulum tubular network organization | biological\_process |
| GO:0036265 | 1 | gene\_01679.t1 | | RNA (guanine-N7)-methylation | biological\_process |
| GO:0000395 | 1 | gene\_10367.t1 | | mRNA 5'-splice site recognition | biological\_process |
| GO:0006611 | 2 | gene\_06778.t1,gene\_05152.t1 | | protein export from nucleus | biological\_process |
| GO:0006612 | 1 | gene\_04572.t1 | | protein targeting to membrane | biological\_process |
| GO:0006614 | 7 | gene\_09488.t1,gene\_04006.t1,gene\_07051.t1,gene\_05782.t1,gene\_01542.t1,gene\_06620.t1,gene\_04397.t1 | | SRP-dependent cotranslational protein targeting to membrane | biological\_process |
| GO:0009272 | 2 | gene\_05820.t1,gene\_06043.t1 | | fungal-type cell wall biogenesis | biological\_process |
| GO:0000387 | 6 | gene\_03682.t1,gene\_08079.t1,gene\_10367.t1,gene\_04011.t1,gene\_07483.t1,gene\_06158.t1 | | spliceosomal snRNP assembly | biological\_process |
| GO:0051131 | 1 | gene\_09415.t1 | | chaperone-mediated protein complex assembly | biological\_process |
| GO:0006139 | 11 | gene\_03964.t1,gene\_08690.t1,gene\_09473.t1,gene\_09136.t1,gene\_04107.t1,gene\_02953.t1,gene\_01224.t1,gene\_01681.t1,gene\_08293.t1,gene\_00746.t1,gene\_07299.t1 | | nucleobase-containing compound metabolic process | biological\_process |
| GO:0042732 | 1 | gene\_04233.t1 | | D-xylose metabolic process | biological\_process |
| GO:0090114 | 2 | gene\_09312.t1,gene\_01017.t1 | | COPII-coated vesicle budding | biological\_process |
| GO:0045041 | 1 | gene\_04277.t1 | | protein import into mitochondrial intermembrane space | biological\_process |
| GO:0045040 | 4 | gene\_09579.t1,gene\_02094.t1,gene\_06805.t1,gene\_06112.t1 | | protein insertion into mitochondrial outer membrane | biological\_process |
| GO:0044249 | 5 | gene\_07849.t1,gene\_01185.t1,gene\_05257.t1,gene\_04763.t1,gene\_03022.t1 | | cellular biosynthetic process | biological\_process |
| GO:0019290 | 3 | gene\_00532.t1,gene\_01580.t1,gene\_05504.t1 | | siderophore biosynthetic process | biological\_process |
| GO:0000723 | 9 | gene\_02991.t1,gene\_04537.t1,gene\_06252.t1,gene\_08500.t1,gene\_07898.t1,gene\_06102.t1,gene\_09591.t1,gene\_10444.t1,gene\_09891.t1 | | telomere maintenance | biological\_process |
| GO:0000724 | 5 | gene\_09111.t1,gene\_00882.t1,gene\_05469.t1,gene\_03784.t1,gene\_07343.t1 | | double-strand break repair via homologous recombination | biological\_process |
| GO:0008380 | 17 | gene\_10208.t1,gene\_09750.t1,gene\_08388.t1,gene\_06365.t1,gene\_04534.t1,gene\_06603.t1,gene\_05855.t1,gene\_02495.t1,gene\_00549.t1,gene\_04238.t1,gene\_09536.t1,gene\_06051.t1,gene\_08918.t1,gene\_08576.t1,gene\_09859.t1,gene\_07305.t1,gene\_08528.t1 | | RNA splicing | biological\_process |
| GO:0018958 | 2 | gene\_05109.t1,gene\_06641.t1 | | phenol-containing compound metabolic process | biological\_process |
| GO:0045454 | 3 | gene\_04708.t1,gene\_06691.t1,gene\_02054.t1 | | cell redox homeostasis | biological\_process |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0051315 | 1 | gene\_08632.t1 | | attachment of mitotic spindle microtubules to kinetochore | biological\_process |
| GO:0043604 | 1 | gene\_04024.t1 | | amide biosynthetic process | biological\_process |
| GO:0070072 | 4 | gene\_07218.t1,gene\_03177.t1,gene\_09786.t1,gene\_07263.t1 | | vacuolar proton-transporting V-type ATPase complex assembly | biological\_process |
| GO:0046177 | 1 | gene\_10185.t1 | | D-gluconate catabolic process | biological\_process |
| GO:0070676 | 1 | gene\_07913.t1 | | intralumenal vesicle formation | biological\_process |
| GO:0034975 | 1 | gene\_07528.t1 | | protein folding in endoplasmic reticulum | biological\_process |
| GO:0060628 | 1 | gene\_05676.t1 | | regulation of ER to Golgi vesicle-mediated transport | biological\_process |
| GO:0070096 | 2 | gene\_06805.t1,gene\_06112.t1 | | mitochondrial outer membrane translocase complex assembly | biological\_process |
| GO:0009249 | 3 | gene\_06832.t1,gene\_06846.t1,gene\_02443.t1 | | protein lipoylation | biological\_process |
| GO:0019752 | 9 | gene\_06470.t1,gene\_06682.t1,gene\_00805.t1,gene\_03700.t1,gene\_09730.t1,gene\_03988.t1,gene\_10345.t1,gene\_02156.t1,gene\_05675.t1 | | carboxylic acid metabolic process | biological\_process |
| GO:0071788 | 1 | gene\_03397.t1 | | endoplasmic reticulum tubular network maintenance | biological\_process |
| GO:0051260 | 1 | gene\_06595.t1 | | protein homooligomerization | biological\_process |
| GO:0019379 | 1 | gene\_06830.t1 | | sulfate assimilation, phosphoadenylyl sulfate reduction by phosphoadenylyl-sulfate reductase (thioredoxin) | biological\_process |
| GO:0071230 | 1 | gene\_03887.t1 | | cellular response to amino acid stimulus | biological\_process |
| GO:0101030 | 2 | gene\_01300.t1,gene\_07887.t1 | | tRNA-guanine transglycosylation | biological\_process |
| GO:0019521 | 2 | gene\_03823.t1,gene\_03675.t1 | | D-gluconate metabolic process | biological\_process |
| GO:0006072 | 3 | gene\_03977.t1,gene\_10097.t1,gene\_05158.t1 | | glycerol-3-phosphate metabolic process | biological\_process |
| GO:0005838 | 3 | gene\_06760.t1,gene\_06839.t1,gene\_04185.t1 | | proteasome regulatory particle | cellular\_component |
| GO:0005839 | 5 | gene\_00408.t1,gene\_09929.t1,gene\_02375.t1,gene\_02372.t1,gene\_03707.t1 | | proteasome core complex | cellular\_component |
| GO:0005834 | 2 | gene\_03006.t1,gene\_08745.t1 | | heterotrimeric G-protein complex | cellular\_component |
| GO:0005835 | 2 | gene\_02333.t1,gene\_02332.t1 | | fatty acid synthase complex | cellular\_component |
| GO:0005832 | 8 | gene\_02559.t1,gene\_07139.t1,gene\_08963.t1,gene\_03204.t1,gene\_00738.t1,gene\_03801.t1,gene\_04092.t1,gene\_06242.t1 | | chaperonin-containing T-complex | cellular\_component |
| GO:1990131 | 2 | gene\_06662.t1,gene\_04423.t1 | | Gtr1-Gtr2 GTPase complex | cellular\_component |
| GO:0005956 | 2 | gene\_09329.t1,gene\_05406.t1 | | protein kinase CK2 complex | cellular\_component |
| GO:0140602 | 1 | gene\_05249.t1 | | nucleolar ring | cellular\_component |
| GO:0035550 | 1 | gene\_01624.t1 | | urease complex | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0042555 | 6 | gene\_00515.t1,gene\_01710.t1,gene\_01540.t1,gene\_07862.t1,gene\_08245.t1,gene\_09071.t1 | | MCM complex | cellular\_component |
| GO:0031251 | 2 | gene\_03654.t1,gene\_02175.t1 | | PAN complex | cellular\_component |
| GO:0030677 | 3 | gene\_06449.t1,gene\_05910.t1,gene\_10169.t1 | | ribonuclease P complex | cellular\_component |
| GO:0010008 | 12 | gene\_03659.t1,gene\_05990.t1,gene\_08752.t1,gene\_00669.t1,gene\_09062.t1,gene\_03667.t1,gene\_02072.t1,gene\_03468.t1,gene\_08349.t1,gene\_07381.t1,gene\_01023.t1,gene\_07435.t1 | | endosome membrane | cellular\_component |
| GO:0042720 | 2 | gene\_09050.t1,gene\_09110.t1 | | mitochondrial inner membrane peptidase complex | cellular\_component |
| GO:0042729 | 9 | gene\_10529.t1,gene\_05877.t1,gene\_03377.t1,gene\_08597.t1,gene\_05155.t1,gene\_06154.t1,gene\_08869.t1,gene\_07276.t1,gene\_03170.t1 | | DASH complex | cellular\_component |
| GO:0031207 | 1 | gene\_08267.t1 | | Sec62/Sec63 complex | cellular\_component |
| GO:0045281 | 1 | gene\_04426.t1 | | succinate dehydrogenase complex | cellular\_component |
| GO:0070823 | 1 | gene\_07896.t1 | | HDA1 complex | cellular\_component |
| GO:0071339 | 1 | gene\_00109.t1 | | MLL1 complex | cellular\_component |
| GO:0005829 | 31 | gene\_01674.t1,gene\_02540.t1,gene\_09731.t1,gene\_04186.t1,gene\_01627.t1,gene\_00352.t1,gene\_08108.t1,gene\_06873.t1,gene\_07863.t1,gene\_06930.t1,gene\_06774.t1,gene\_09214.t1,gene\_09903.t1,gene\_06815.t1,gene\_02853.t1,gene\_04702.t1,gene\_08590.t1,gene\_08455.t1,gene\_08132.t1,gene\_02536.t1,gene\_04240.t1,gene\_06717.t1,gene\_06399.t1,gene\_03696.t1,gene\_08346.t1,gene\_01386.t1,gene\_04719.t1,gene\_09923.t1,gene\_03468.t1,gene\_02227.t1,gene\_08974.t1 | | cytosol | cellular\_component |
| GO:0005853 | 1 | gene\_05617.t1 | | eukaryotic translation elongation factor 1 complex | cellular\_component |
| GO:0030289 | 1 | gene\_10264.t1 | | protein phosphatase 4 complex | cellular\_component |
| GO:0016363 | 3 | gene\_08417.t1,gene\_03932.t1,gene\_00367.t1 | | nuclear matrix | cellular\_component |
| GO:0030663 | 1 | gene\_00582.t1 | | COPI-coated vesicle membrane | cellular\_component |
| GO:0031390 | 2 | gene\_10001.t1,gene\_06219.t1 | | Ctf18 RFC-like complex | cellular\_component |
| GO:0031391 | 3 | gene\_09699.t1,gene\_07744.t1,gene\_07212.t1 | | Elg1 RFC-like complex | cellular\_component |
| GO:0000811 | 2 | gene\_10241.t1,gene\_10155.t1 | | GINS complex | cellular\_component |
| GO:0042719 | 1 | gene\_01635.t1 | | mitochondrial intermembrane space protein transporter complex | cellular\_component |
| GO:0000172 | 5 | gene\_00840.t1,gene\_01748.t1,gene\_05910.t1,gene\_03157.t1,gene\_08067.t1 | | ribonuclease MRP complex | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0031533 | 2 | gene\_09829.t1,gene\_01488.t1 | | mRNA cap methyltransferase complex | cellular\_component |
| GO:0045271 | 1 | gene\_10039.t1 | | respiratory chain complex I | cellular\_component |
| GO:0045277 | 1 | gene\_03222.t1 | | respiratory chain complex IV | cellular\_component |
| GO:0070652 | 2 | gene\_09991.t1,gene\_10291.t1 | | HAUS complex | cellular\_component |
| GO:0008290 | 1 | gene\_07685.t1 | | F-actin capping protein complex | cellular\_component |
| GO:0005868 | 1 | gene\_08235.t1 | | cytoplasmic dynein complex | cellular\_component |
| GO:0005654 | 6 | gene\_09858.t1,gene\_00423.t1,gene\_01431.t1,gene\_09214.t1,gene\_07283.t1,gene\_05207.t1 | | nucleoplasm | cellular\_component |
| GO:0071439 | 1 | gene\_01372.t1 | | clathrin complex | cellular\_component |
| GO:0005856 | 8 | gene\_08998.t1,gene\_03046.t1,gene\_00134.t1,gene\_06364.t1,gene\_07381.t1,gene\_10520.t1,gene\_02766.t1,gene\_02352.t1 | | cytoskeleton | cellular\_component |
| GO:0055087 | 1 | gene\_06776.t1 | | Ski complex | cellular\_component |
| GO:0005852 | 12 | gene\_00144.t1,gene\_01700.t1,gene\_00555.t1,gene\_01354.t1,gene\_06800.t1,gene\_02418.t1,gene\_05226.t1,gene\_05458.t1,gene\_00493.t1,gene\_05408.t1,gene\_03188.t1,gene\_00720.t1 | | eukaryotic translation initiation factor 3 complex | cellular\_component |
| GO:0016282 | 13 | gene\_00144.t1,gene\_01700.t1,gene\_00555.t1,gene\_01354.t1,gene\_06008.t1,gene\_02418.t1,gene\_05226.t1,gene\_05697.t1,gene\_00493.t1,gene\_05408.t1,gene\_03188.t1,gene\_06800.t1,gene\_00720.t1 | | eukaryotic 43S preinitiation complex | cellular\_component |
| GO:0033255 | 1 | gene\_07471.t1 | | SAS acetyltransferase complex | cellular\_component |
| GO:1904423 | 1 | gene\_05126.t1 | | dehydrodolichyl diphosphate synthase complex | cellular\_component |
| GO:1990112 | 1 | gene\_02227.t1 | | RQC complex | cellular\_component |
| GO:0030479 | 6 | gene\_05990.t1,gene\_02382.t1,gene\_00669.t1,gene\_08684.t1,gene\_00218.t1,gene\_08752.t1 | | actin cortical patch | cellular\_component |
| GO:0005938 | 6 | gene\_04255.t1,gene\_07936.t1,gene\_08232.t1,gene\_04533.t1,gene\_01180.t1,gene\_05165.t1 | | cell cortex | cellular\_component |
| GO:0012507 | 3 | gene\_07218.t1,gene\_03939.t1,gene\_01668.t1 | | ER to Golgi transport vesicle membrane | cellular\_component |
| GO:0005935 | 1 | gene\_07646.t1 | | cellular bud neck | cellular\_component |
| GO:0005934 | 1 | gene\_07129.t1 | | cellular bud tip | cellular\_component |
| GO:0031011 | 9 | gene\_00682.t1,gene\_07303.t1,gene\_04352.t1,gene\_00643.t1,gene\_03376.t1,gene\_10008.t1,gene\_08351.t1,gene\_03937.t1,gene\_00427.t1 | | Ino80 complex | cellular\_component |
| GO:0030014 | 3 | gene\_03834.t1,gene\_04448.t1,gene\_10141.t1 | | CCR4-NOT complex | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0030015 | 3 | gene\_06697.t1,gene\_07005.t1,gene\_08626.t1 | | CCR4-NOT core complex | cellular\_component |
| GO:0005737 | 316 | gene\_01652.t1,gene\_09324.t1,gene\_06251.t1,gene\_02375.t1,gene\_09601.t1,gene\_07933.t1,gene\_10408.t1,gene\_05645.t1,gene\_08597.t1,gene\_08161.t1,gene\_09759.t1,gene\_00005.t1,gene\_09911.t1,gene\_08589.t1,gene\_07261.t1,gene\_00718.t1,gene\_06113.t1,gene\_03284.t1,gene\_02002.t1,gene\_02156.t1,gene\_00517.t1,gene\_04559.t1,gene\_07409.t1,gene\_03977.t1,gene\_05877.t1,gene\_05731.t1,gene\_01236.t1,gene\_04192.t1,gene\_08515.t1,gene\_01562.t1,gene\_01446.t1,gene\_01524.t1,gene\_04082.t1,gene\_07305.t1,gene\_06835.t1,gene\_08036.t1,gene\_10469.t1,gene\_05155.t1,gene\_10242.t1,gene\_02054.t1,gene\_03283.t1,gene\_01340.t1,gene\_01712.t1,gene\_00353.t1,gene\_00665.t1,gene\_08097.t1,gene\_07982.t1,gene\_09602.t1,gene\_01196.t1,gene\_09250.t1,gene\_06123.t1,gene\_06154.t1,gene\_07673.t1,gene\_04190.t1,gene\_01792.t1,gene\_00551.t1,gene\_04327.t1,gene\_03453.t1,gene\_07276.t1,gene\_06913.t1,gene\_07272.t1,gene\_02666.t1,gene\_07640.t1,gene\_01364.t1,gene\_04610.t1,gene\_10424.t1,gene\_03377.t1,gene\_01433.t1,gene\_06232.t1,gene\_09833.t1,gene\_05249.t1,gene\_04062.t1,gene\_05845.t1,gene\_02997.t1,gene\_09706.t1,gene\_00647.t1,gene\_06697.t1,gene\_10009.t1,gene\_01055.t1,gene\_00817.t1,gene\_01718.t1,gene\_02251.t1,gene\_09718.t1,gene\_04109.t1,gene\_07453.t1,gene\_08710.t1,gene\_04234.t1,gene\_02965.t1,gene\_07903.t1,gene\_09256.t1,gene\_02029.t1,gene\_00371.t1,gene\_05892.t1,gene\_02486.t1,gene\_08765.t1,gene\_09289.t1,gene\_06848.t1,gene\_10097.t1,gene\_02368.t1,gene\_09486.t1,gene\_05564.t1,gene\_09596.t1,gene\_05364.t1,gene\_09282.t1,gene\_00361.t1,gene\_03856.t1,gene\_02850.t1,gene\_07825.t1,gene\_05995.t1,gene\_01071.t1,gene\_01503.t1,gene\_02854.t1,gene\_02684.t1,gene\_04608.t1,gene\_07170.t1,gene\_06979.t1,gene\_02356.t1,gene\_07336.t1,gene\_09265.t1,gene\_03080.t1,gene\_10446.t1,gene\_08024.t1,gene\_02643.t1,gene\_03313.t1,gene\_08746.t1,gene\_05907.t1,gene\_00559.t1,gene\_07215.t1,gene\_05374.t1,gene\_06759.t1,gene\_10327.t1,gene\_00527.t1,gene\_07394.t1,gene\_05140.t1,gene\_07980.t1,gene\_06203.t1,gene\_03191.t1,gene\_01073.t1,gene\_01501.t1,gene\_08998.t1,gene\_04722.t1,gene\_01557.t1,gene\_06451.t1,gene\_05840.t1,gene\_01139.t1,gene\_09578.t1,gene\_06125.t1,gene\_02254.t1,gene\_08687.t1,gene\_06132.t1,gene\_00631.t1,gene\_03487.t1,gene\_05624.t1,gene\_02395.t1,gene\_10017.t1,gene\_07067.t1,gene\_04547.t1,gene\_10343.t1,gene\_03170.t1,gene\_08037.t1,gene\_01374.t1,gene\_07355.t1,gene\_01369.t1,gene\_07892.t1,gene\_03094.t1,gene\_09083.t1,gene\_00356.t1,gene\_06698.t1,gene\_07138.t1,gene\_08869.t1,gene\_00624.t1,gene\_09048.t1,gene\_10321.t1,gene\_10420.t1,gene\_04461.t1, | | cytoplasm | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0005737 | 316 | gene\_03811.t1,gene\_10529.t1,gene\_02682.t1,gene\_09266.t1,gene\_10291.t1,gene\_01094.t1,gene\_04098.t1,gene\_10518.t1,gene\_03863.t1,gene\_03474.t1,gene\_05913.t1,gene\_09635.t1,gene\_04105.t1,gene\_01989.t1,gene\_06241.t1,gene\_05689.t1,gene\_03981.t1,gene\_06009.t1,gene\_01192.t1,gene\_09182.t1,gene\_04252.t1,gene\_01636.t1,gene\_03790.t1,gene\_08577.t1,gene\_00709.t1,gene\_09824.t1,gene\_07979.t1,gene\_07313.t1,gene\_02586.t1,gene\_01630.t1,gene\_03187.t1,gene\_07619.t1,gene\_00422.t1,gene\_02830.t1,gene\_04316.t1,gene\_02386.t1,gene\_07038.t1,gene\_04233.t1,gene\_00134.t1,gene\_02554.t1,gene\_09453.t1,gene\_03638.t1,gene\_05182.t1,gene\_02725.t1,gene\_04224.t1,gene\_09703.t1,gene\_05363.t1,gene\_05876.t1,gene\_08722.t1,gene\_07732.t1,gene\_02420.t1,gene\_09259.t1,gene\_03141.t1,gene\_07302.t1,gene\_02892.t1,gene\_05138.t1,gene\_03613.t1,gene\_07670.t1,gene\_09679.t1,gene\_10202.t1,gene\_07432.t1,gene\_01719.t1,gene\_05691.t1,gene\_01300.t1,gene\_09003.t1,gene\_00326.t1,gene\_00399.t1,gene\_03414.t1,gene\_03475.t1,gene\_06330.t1,gene\_07354.t1,gene\_08626.t1,gene\_10373.t1,gene\_03822.t1,gene\_09683.t1,gene\_02352.t1,gene\_03194.t1,gene\_00408.t1,gene\_04717.t1,gene\_06664.t1,gene\_07743.t1,gene\_02565.t1,gene\_03091.t1,gene\_05700.t1,gene\_07791.t1,gene\_07953.t1,gene\_04409.t1,gene\_08329.t1,gene\_08547.t1,gene\_02959.t1,gene\_05375.t1,gene\_08394.t1,gene\_10487.t1,gene\_08575.t1,gene\_00563.t1,gene\_07851.t1,gene\_06358.t1,gene\_07873.t1,gene\_01201.t1,gene\_02790.t1,gene\_05910.t1,gene\_08813.t1,gene\_05772.t1,gene\_05869.t1,gene\_03391.t1,gene\_05774.t1,gene\_07887.t1,gene\_08235.t1,gene\_06236.t1,gene\_09098.t1,gene\_08593.t1,gene\_08916.t1,gene\_06643.t1,gene\_01592.t1,gene\_07395.t1,gene\_07590.t1,gene\_07923.t1,gene\_10216.t1,gene\_02686.t1,gene\_01550.t1,gene\_04284.t1,gene\_07037.t1,gene\_10433.t1,gene\_04096.t1,gene\_08488.t1,gene\_05839.t1,gene\_04266.t1,gene\_10602.t1,gene\_02367.t1,gene\_06990.t1,gene\_04529.t1,gene\_10354.t1,gene\_01010.t1,gene\_06637.t1,gene\_02487.t1,gene\_01234.t1,gene\_05485.t1,gene\_09244.t1,gene\_00871.t1,gene\_09540.t1,gene\_09219.t1 | | cytoplasm | cellular\_component |
| GO:0005732 | 2 | gene\_02232.t1,gene\_09290.t1 | | sno(s)RNA-containing ribonucleoprotein complex | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0005730 | 76 | gene\_08509.t1,gene\_10328.t1,gene\_06349.t1,gene\_04149.t1,gene\_05788.t1,gene\_00423.t1,gene\_06495.t1,gene\_00676.t1,gene\_01431.t1,gene\_08840.t1,gene\_01554.t1,gene\_07034.t1,gene\_06113.t1,gene\_03678.t1,gene\_03181.t1,gene\_02121.t1,gene\_05674.t1,gene\_00411.t1,gene\_09818.t1,gene\_05207.t1,gene\_09850.t1,gene\_05249.t1,gene\_05954.t1,gene\_05136.t1,gene\_04356.t1,gene\_09509.t1,gene\_03927.t1,gene\_01589.t1,gene\_06516.t1,gene\_01602.t1,gene\_06638.t1,gene\_07171.t1,gene\_07393.t1,gene\_07039.t1,gene\_09775.t1,gene\_09258.t1,gene\_07100.t1,gene\_05225.t1,gene\_09001.t1,gene\_03926.t1,gene\_01093.t1,gene\_06329.t1,gene\_06245.t1,gene\_07935.t1,gene\_03203.t1,gene\_05314.t1,gene\_06989.t1,gene\_06649.t1,gene\_00707.t1,gene\_09219.t1,gene\_09512.t1,gene\_02474.t1,gene\_08271.t1,gene\_10370.t1,gene\_01030.t1,gene\_01550.t1,gene\_06557.t1,gene\_02354.t1,gene\_07329.t1,gene\_07733.t1,gene\_06571.t1,gene\_06044.t1,gene\_07075.t1,gene\_09567.t1,gene\_06350.t1,gene\_03548.t1,gene\_09858.t1,gene\_07417.t1,gene\_10571.t1,gene\_09012.t1,gene\_01509.t1,gene\_07283.t1,gene\_00725.t1,gene\_04402.t1,gene\_09823.t1,gene\_05806.t1 | | nucleolus | cellular\_component |
| GO:0005739 | 103 | gene\_05959.t1,gene\_03293.t1,gene\_07146.t1,gene\_07978.t1,gene\_06805.t1,gene\_01900.t1,gene\_03583.t1,gene\_06359.t1,gene\_05570.t1,gene\_08389.t1,gene\_10305.t1,gene\_06102.t1,gene\_09113.t1,gene\_06030.t1,gene\_07608.t1,gene\_01271.t1,gene\_01319.t1,gene\_00632.t1,gene\_09750.t1,gene\_06101.t1,gene\_07642.t1,gene\_00798.t1,gene\_05698.t1,gene\_01561.t1,gene\_07283.t1,gene\_09687.t1,gene\_05707.t1,gene\_01416.t1,gene\_03222.t1,gene\_00660.t1,gene\_07567.t1,gene\_02293.t1,gene\_03540.t1,gene\_08486.t1,gene\_08359.t1,gene\_06069.t1,gene\_09742.t1,gene\_02317.t1,gene\_06832.t1,gene\_09989.t1,gene\_09197.t1,gene\_02503.t1,gene\_08317.t1,gene\_06655.t1,gene\_08587.t1,gene\_00600.t1,gene\_07631.t1,gene\_06972.t1,gene\_08109.t1,gene\_10516.t1,gene\_09462.t1,gene\_03168.t1,gene\_04330.t1,gene\_05493.t1,gene\_00813.t1,gene\_09558.t1,gene\_01219.t1,gene\_03996.t1,gene\_10375.t1,gene\_06573.t1,gene\_08508.t1,gene\_09552.t1,gene\_06121.t1,gene\_03643.t1,gene\_10320.t1,gene\_08282.t1,gene\_10312.t1,gene\_02366.t1,gene\_01545.t1,gene\_04609.t1,gene\_08720.t1,gene\_07214.t1,gene\_07534.t1,gene\_10445.t1,gene\_02794.t1,gene\_08325.t1,gene\_05230.t1,gene\_02452.t1,gene\_10358.t1,gene\_02324.t1,gene\_10319.t1,gene\_00483.t1,gene\_04246.t1,gene\_08094.t1,gene\_03285.t1,gene\_01106.t1,gene\_04329.t1,gene\_02255.t1,gene\_01541.t1,gene\_02394.t1,gene\_08051.t1,gene\_05683.t1,gene\_01020.t1,gene\_00364.t1,gene\_06115.t1,gene\_06601.t1,gene\_05771.t1,gene\_10491.t1,gene\_09301.t1,gene\_09628.t1, | | mitochondrion | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0005739 | 103 | gene\_07368.t1,gene\_02428.t1,gene\_08404.t1 | | mitochondrion | cellular\_component |
| GO:0030659 | 3 | gene\_01917.t1,gene\_09248.t1,gene\_10308.t1 | | cytoplasmic vesicle membrane | cellular\_component |
| GO:0030122 | 1 | gene\_01313.t1 | | AP-2 adaptor complex | cellular\_component |
| GO:0030123 | 2 | gene\_05895.t1,gene\_07361.t1 | | AP-3 adaptor complex | cellular\_component |
| GO:0030121 | 2 | gene\_02540.t1,gene\_07106.t1 | | AP-1 adaptor complex | cellular\_component |
| GO:0030126 | 5 | gene\_02033.t1,gene\_06756.t1,gene\_03142.t1,gene\_01728.t1,gene\_08919.t1 | | COPI vesicle coat | cellular\_component |
| GO:0030127 | 4 | gene\_03214.t1,gene\_09312.t1,gene\_10522.t1,gene\_01017.t1 | | COPII vesicle coat | cellular\_component |
| GO:0000775 | 5 | gene\_07613.t1,gene\_05154.t1,gene\_09025.t1,gene\_09619.t1,gene\_08074.t1 | | chromosome, centromeric region | cellular\_component |
| GO:0000776 | 9 | gene\_05640.t1,gene\_09546.t1,gene\_06909.t1,gene\_04179.t1,gene\_00422.t1,gene\_03245.t1,gene\_10002.t1,gene\_09780.t1,gene\_01875.t1 | | kinetochore | cellular\_component |
| GO:0000178 | 4 | gene\_03164.t1,gene\_07302.t1,gene\_06123.t1,gene\_10164.t1 | | exosome (RNase complex) | cellular\_component |
| GO:0000176 | 6 | gene\_03242.t1,gene\_06239.t1,gene\_02697.t1,gene\_03959.t1,gene\_00829.t1,gene\_01055.t1 | | nuclear exosome (RNase complex) | cellular\_component |
| GO:0090730 | 1 | gene\_08535.t1 | | Las1 complex | cellular\_component |
| GO:0045261 | 4 | gene\_01026.t1,gene\_00280.t1,gene\_08419.t1,gene\_01009.t1 | | proton-transporting ATP synthase complex, catalytic core F(1) | cellular\_component |
| GO:0045263 | 2 | gene\_03171.t1,gene\_06355.t1 | | proton-transporting ATP synthase complex, coupling factor F(o) | cellular\_component |
| GO:0000502 | 9 | gene\_08397.t1,gene\_10539.t1,gene\_05624.t1,gene\_06474.t1,gene\_00356.t1,gene\_02805.t1,gene\_02473.t1,gene\_07275.t1,gene\_03734.t1 | | proteasome complex | cellular\_component |
| GO:0000500 | 1 | gene\_04314.t1 | | RNA polymerase I upstream activating factor complex | cellular\_component |
| GO:0000506 | 2 | gene\_06610.t1,gene\_09007.t1 | | glycosylphosphatidylinositol-N-acetylglucosaminyltransferase (GPI-GnT) complex | cellular\_component |
| GO:0033063 | 1 | gene\_09111.t1 | | Rad51B-Rad51C-Rad51D-XRCC2 complex | cellular\_component |
| GO:0005844 | 2 | gene\_05249.t1,gene\_07129.t1 | | polysome | cellular\_component |
| GO:0005847 | 1 | gene\_03216.t1 | | mRNA cleavage and polyadenylation specificity factor complex | cellular\_component |
| GO:0005846 | 1 | gene\_09711.t1 | | nuclear cap binding complex | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0005840 | 108 | gene\_07146.t1,gene\_01069.t1,gene\_09911.t1,gene\_10009.t1,gene\_06359.t1,gene\_01143.t1,gene\_03172.t1,gene\_04288.t1,gene\_04612.t1,gene\_10488.t1,gene\_08577.t1,gene\_00424.t1,gene\_02603.t1,gene\_05698.t1,gene\_09731.t1,gene\_04610.t1,gene\_07237.t1,gene\_03284.t1,gene\_05235.t1,gene\_01386.t1,gene\_03883.t1,gene\_05845.t1,gene\_02997.t1,gene\_06369.t1,gene\_06113.t1,gene\_05192.t1,gene\_05623.t1,gene\_07214.t1,gene\_10173.t1,gene\_01215.t1,gene\_09486.t1,gene\_02931.t1,gene\_05390.t1,gene\_01327.t1,gene\_02684.t1,gene\_03088.t1,gene\_06815.t1,gene\_08346.t1,gene\_08587.t1,gene\_02469.t1,gene\_07654.t1,gene\_00559.t1,gene\_07950.t1,gene\_02779.t1,gene\_07326.t1,gene\_06557.t1,gene\_05138.t1,gene\_06282.t1,gene\_04091.t1,gene\_06030.t1,gene\_03168.t1,gene\_08037.t1,gene\_08736.t1,gene\_01369.t1,gene\_02457.t1,gene\_00402.t1,gene\_06842.t1,gene\_08508.t1,gene\_06319.t1,gene\_06873.t1,gene\_05838.t1,gene\_01594.t1,gene\_00401.t1,gene\_08682.t1,gene\_04240.t1,gene\_07619.t1,gene\_02637.t1,gene\_01723.t1,gene\_01417.t1,gene\_01678.t1,gene\_04441.t1,gene\_10445.t1,gene\_09259.t1,gene\_07170.t1,gene\_05876.t1,gene\_08514.t1,gene\_08881.t1,gene\_10591.t1,gene\_10017.t1,gene\_00539.t1,gene\_08028.t1,gene\_06239.t1,gene\_02556.t1,gene\_01627.t1,gene\_01599.t1,gene\_10358.t1,gene\_07872.t1,gene\_06664.t1,gene\_04409.t1,gene\_08547.t1,gene\_09596.t1,gene\_09003.t1,gene\_09302.t1,gene\_10540.t1,gene\_05686.t1,gene\_09718.t1,gene\_05885.t1,gene\_00829.t1,gene\_00481.t1,gene\_00592.t1,gene\_06861.t1,gene\_02434.t1,gene\_01550.t1,gene\_06115.t1,gene\_02697.t1,gene\_03959.t1,gene\_01010.t1,gene\_02428.t1 | | ribosome | cellular\_component |
| GO:0005849 | 3 | gene\_05890.t1,gene\_07762.t1,gene\_04188.t1 | | mRNA cleavage factor complex | cellular\_component |
| GO:0030864 | 1 | gene\_08600.t1 | | cortical actin cytoskeleton | cellular\_component |
| GO:0033263 | 1 | gene\_06397.t1 | | CORVET complex | cellular\_component |
| GO:0035145 | 2 | gene\_08918.t1,gene\_07305.t1 | | exon-exon junction complex | cellular\_component |
| GO:0033116 | 1 | gene\_07218.t1 | | endoplasmic reticulum-Golgi intermediate compartment membrane | cellular\_component |
| GO:0071004 | 1 | gene\_10367.t1 | | U2-type prespliceosome | cellular\_component |
| GO:0005905 | 1 | gene\_04556.t1 | | clathrin-coated pit | cellular\_component |
| GO:0061695 | 1 | gene\_09009.t1 | | transferase complex, transferring phosphorus-containing groups | cellular\_component |
| GO:1904949 | 3 | gene\_09699.t1,gene\_07744.t1,gene\_07212.t1 | | ATPase complex | cellular\_component |
| GO:0030008 | 3 | gene\_09223.t1,gene\_08532.t1,gene\_00033.t1 | | TRAPP complex | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0000347 | 1 | gene\_08105.t1 | | THO complex | cellular\_component |
| GO:0030131 | 2 | gene\_04556.t1,gene\_10348.t1 | | clathrin adaptor complex | cellular\_component |
| GO:0030130 | 2 | gene\_01372.t1,gene\_04061.t1 | | clathrin coat of trans-Golgi network vesicle | cellular\_component |
| GO:0030133 | 1 | gene\_06544.t1 | | transport vesicle | cellular\_component |
| GO:0030136 | 1 | gene\_02601.t1 | | clathrin-coated vesicle | cellular\_component |
| GO:0005694 | 13 | gene\_09220.t1,gene\_04254.t1,gene\_07003.t1,gene\_07246.t1,gene\_05627.t1,gene\_04413.t1,gene\_02360.t1,gene\_01025.t1,gene\_03476.t1,gene\_07311.t1,gene\_10167.t1,gene\_06720.t1,gene\_07260.t1 | | chromosome | cellular\_component |
| GO:0000813 | 2 | gene\_05346.t1,gene\_06652.t1 | | ESCRT I complex | cellular\_component |
| GO:0009349 | 1 | gene\_02362.t1 | | riboflavin synthase complex | cellular\_component |
| GO:0008180 | 6 | gene\_08097.t1,gene\_07432.t1,gene\_06270.t1,gene\_00249.t1,gene\_06848.t1,gene\_01217.t1 | | COP9 signalosome | cellular\_component |
| GO:0031510 | 1 | gene\_06429.t1 | | SUMO activating enzyme complex | cellular\_component |
| GO:1990862 | 1 | gene\_05891.t1 | | nuclear membrane complex Bqt3-Bqt4 | cellular\_component |
| GO:0045254 | 1 | gene\_09157.t1 | | pyruvate dehydrogenase complex | cellular\_component |
| GO:0045252 | 1 | gene\_07350.t1 | | oxoglutarate dehydrogenase complex | cellular\_component |
| GO:0070985 | 1 | gene\_07367.t1 | | transcription factor TFIIK complex | cellular\_component |
| GO:0030897 | 1 | gene\_06397.t1 | | HOPS complex | cellular\_component |
| GO:0016602 | 1 | gene\_02408.t1 | | CCAAT-binding factor complex | cellular\_component |
| GO:0005871 | 4 | gene\_05053.t1,gene\_04962.t1,gene\_00076.t1,gene\_04964.t1 | | kinesin complex | cellular\_component |
| GO:0005874 | 33 | gene\_01652.t1,gene\_08710.t1,gene\_03094.t1,gene\_08597.t1,gene\_08722.t1,gene\_05053.t1,gene\_00668.t1,gene\_05877.t1,gene\_03452.t1,gene\_10487.t1,gene\_05155.t1,gene\_06154.t1,gene\_10636.t1,gene\_05738.t1,gene\_08235.t1,gene\_10207.t1,gene\_04180.t1,gene\_00015.t1,gene\_08161.t1,gene\_07395.t1,gene\_08869.t1,gene\_03563.t1,gene\_06203.t1,gene\_01073.t1,gene\_07366.t1,gene\_03377.t1,gene\_08913.t1,gene\_05840.t1,gene\_01139.t1,gene\_07037.t1,gene\_04962.t1,gene\_05691.t1,gene\_10291.t1 | | microtubule | cellular\_component |
| GO:0005876 | 2 | gene\_07276.t1,gene\_03170.t1 | | spindle microtubule | cellular\_component |
| GO:0043564 | 2 | gene\_04537.t1,gene\_02991.t1 | | Ku70:Ku80 complex | cellular\_component |
| GO:0044614 | 1 | gene\_07129.t1 | | nuclear pore cytoplasmic filaments | cellular\_component |
| GO:0071011 | 1 | gene\_07996.t1 | | precatalytic spliceosome | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0005675 | 3 | gene\_09119.t1,gene\_04147.t1,gene\_01504.t1 | | transcription factor TFIIH holo complex | cellular\_component |
| GO:0033290 | 13 | gene\_00144.t1,gene\_01700.t1,gene\_00555.t1,gene\_01354.t1,gene\_06008.t1,gene\_02418.t1,gene\_05226.t1,gene\_05697.t1,gene\_00493.t1,gene\_05408.t1,gene\_03188.t1,gene\_06800.t1,gene\_00720.t1 | | eukaryotic 48S preinitiation complex | cellular\_component |
| GO:0019867 | 2 | gene\_01240.t1,gene\_02864.t1 | | outer membrane | cellular\_component |
| GO:1902494 | 1 | gene\_00876.t1 | | catalytic complex | cellular\_component |
| GO:0031080 | 2 | gene\_08367.t1,gene\_08906.t1 | | nuclear pore outer ring | cellular\_component |
| GO:0042597 | 1 | gene\_07638.t1 | | periplasmic space | cellular\_component |
| GO:0043189 | 1 | gene\_08721.t1 | | H4/H2A histone acetyltransferase complex | cellular\_component |
| GO:1990316 | 1 | gene\_03673.t1 | | Atg1/ULK1 kinase complex | cellular\_component |
| GO:0005688 | 2 | gene\_08685.t1,gene\_06070.t1 | | U6 snRNP | cellular\_component |
| GO:0005685 | 2 | gene\_03867.t1,gene\_10367.t1 | | U1 snRNP | cellular\_component |
| GO:0005684 | 1 | gene\_01308.t1 | | U2-type spliceosomal complex | cellular\_component |
| GO:0005682 | 2 | gene\_00681.t1,gene\_02996.t1 | | U5 snRNP | cellular\_component |
| GO:0005681 | 29 | gene\_08576.t1,gene\_03530.t1,gene\_07820.t1,gene\_02357.t1,gene\_08079.t1,gene\_07256.t1,gene\_04011.t1,gene\_04086.t1,gene\_07641.t1,gene\_00549.t1,gene\_06051.t1,gene\_09750.t1,gene\_01054.t1,gene\_00409.t1,gene\_09859.t1,gene\_08685.t1,gene\_06070.t1,gene\_10208.t1,gene\_03076.t1,gene\_02780.t1,gene\_06855.t1,gene\_07946.t1,gene\_04534.t1,gene\_06603.t1,gene\_07483.t1,gene\_06158.t1,gene\_02203.t1,gene\_05450.t1,gene\_03349.t1 | | spliceosomal complex | cellular\_component |
| GO:0042765 | 5 | gene\_03868.t1,gene\_01979.t1,gene\_01432.t1,gene\_10537.t1,gene\_02656.t1 | | GPI-anchor transamidase complex | cellular\_component |
| GO:0031298 | 1 | gene\_07352.t1 | | replication fork protection complex | cellular\_component |
| GO:0071006 | 1 | gene\_07836.t1 | | U2-type catalytic step 1 spliceosome | cellular\_component |
| GO:0000792 | 1 | gene\_03800.t1 | | heterochromatin | cellular\_component |
| GO:0000793 | 1 | gene\_05154.t1 | | condensed chromosome | cellular\_component |
| GO:0000159 | 2 | gene\_07846.t1,gene\_00255.t1 | | protein phosphatase type 2A complex | cellular\_component |
| GO:0000151 | 1 | gene\_00376.t1 | | ubiquitin ligase complex | cellular\_component |
| GO:0048188 | 6 | gene\_05779.t1,gene\_03112.t1,gene\_04242.t1,gene\_02360.t1,gene\_02111.t1,gene\_02323.t1 | | Set1C/COMPASS complex | cellular\_component |
| GO:0000938 | 3 | gene\_07863.t1,gene\_08974.t1,gene\_06774.t1 | | GARP complex | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0005869 | 4 | gene\_03089.t1,gene\_10469.t1,gene\_08241.t1,gene\_10420.t1 | | dynactin complex | cellular\_component |
| GO:0033620 | 1 | gene\_05249.t1 | | Mei2 nuclear dot complex | cellular\_component |
| GO:1990251 | 1 | gene\_05249.t1 | | nuclear exosome focus | cellular\_component |
| GO:0005786 | 5 | gene\_01542.t1,gene\_06620.t1,gene\_04006.t1,gene\_04397.t1,gene\_07051.t1 | | signal recognition particle, endoplasmic reticulum targeting | cellular\_component |
| GO:0005787 | 3 | gene\_09230.t1,gene\_00277.t1,gene\_07920.t1 | | signal peptidase complex | cellular\_component |
| GO:0005785 | 1 | gene\_09488.t1 | | signal recognition particle receptor complex | cellular\_component |
| GO:0005782 | 2 | gene\_05844.t1,gene\_04206.t1 | | peroxisomal matrix | cellular\_component |
| GO:0005783 | 23 | gene\_05695.t1,gene\_02046.t1,gene\_08604.t1,gene\_07756.t1,gene\_00033.t1,gene\_09223.t1,gene\_09312.t1,gene\_10329.t1,gene\_06474.t1,gene\_10359.t1,gene\_02041.t1,gene\_05802.t1,gene\_06068.t1,gene\_09945.t1,gene\_03652.t1,gene\_02521.t1,gene\_05790.t1,gene\_08680.t1,gene\_05223.t1,gene\_10423.t1,gene\_03121.t1,gene\_05126.t1,gene\_08532.t1 | | endoplasmic reticulum | cellular\_component |
| GO:0005780 | 1 | gene\_06702.t1 | | extrinsic component of intraperoxisomal membrane | cellular\_component |
| GO:0005788 | 3 | gene\_03162.t1,gene\_08283.t1,gene\_10419.t1 | | endoplasmic reticulum lumen | cellular\_component |
| GO:0005789 | 101 | gene\_06489.t1,gene\_06128.t1,gene\_00461.t1,gene\_10522.t1,gene\_04317.t1,gene\_09511.t1,gene\_01668.t1,gene\_00974.t1,gene\_09050.t1,gene\_05746.t1,gene\_08803.t1,gene\_04035.t1,gene\_06564.t1,gene\_10092.t1,gene\_07257.t1,gene\_05187.t1,gene\_04156.t1,gene\_00428.t1,gene\_00203.t1,gene\_03214.t1,gene\_02094.t1,gene\_02828.t1,gene\_02505.t1,gene\_07365.t1,gene\_02439.t1,gene\_01263.t1,gene\_01577.t1,gene\_04541.t1,gene\_02539.t1,gene\_06238.t1,gene\_05987.t1,gene\_00016.t1,gene\_01017.t1,gene\_09200.t1,gene\_07238.t1,gene\_02784.t1,gene\_10605.t1,gene\_01909.t1,gene\_08545.t1,gene\_07380.t1,gene\_09248.t1,gene\_06952.t1,gene\_10456.t1,gene\_09487.t1,gene\_07000.t1,gene\_01120.t1,gene\_04553.t1,gene\_09252.t1,gene\_00418.t1,gene\_02233.t1,gene\_09620.t1,gene\_03939.t1,gene\_09559.t1,gene\_04068.t1,gene\_02462.t1,gene\_03380.t1,gene\_09123.t1,gene\_08298.t1,gene\_10419.t1,gene\_01247.t1,gene\_09196.t1,gene\_03504.t1,gene\_00328.t1,gene\_09348.t1,gene\_08010.t1,gene\_07044.t1,gene\_10308.t1,gene\_06325.t1,gene\_07218.t1,gene\_01084.t1,gene\_06565.t1,gene\_03177.t1,gene\_07018.t1,gene\_02093.t1,gene\_02076.t1,gene\_08297.t1,gene\_01208.t1,gene\_09213.t1,gene\_03043.t1,gene\_07528.t1,gene\_04734.t1,gene\_06254.t1,gene\_09564.t1,gene\_06869.t1,gene\_02943.t1,gene\_10378.t1,gene\_02693.t1,gene\_03296.t1,gene\_09902.t1,gene\_01116.t1,gene\_00553.t1,gene\_08170.t1,gene\_06533.t1,gene\_06043.t1,gene\_04168.t1,gene\_08627.t1,gene\_06509.t1,gene\_00966.t1,gene\_08086.t1,gene\_05817.t1, | | endoplasmic reticulum membrane | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0005789 | 101 | gene\_07362.t1 | | endoplasmic reticulum membrane | cellular\_component |
| GO:0030117 | 3 | gene\_06752.t1,gene\_00582.t1,gene\_00554.t1 | | membrane coat | cellular\_component |
| GO:1990879 | 1 | gene\_02492.t1 | | CST complex | cellular\_component |
| GO:0005672 | 1 | gene\_02099.t1 | | transcription factor TFIIA complex | cellular\_component |
| GO:0005673 | 1 | gene\_10467.t1 | | transcription factor TFIIE complex | cellular\_component |
| GO:0005674 | 1 | gene\_00246.t1 | | transcription factor TFIIF complex | cellular\_component |
| GO:0000781 | 16 | gene\_02991.t1,gene\_02882.t1,gene\_04537.t1,gene\_09034.t1,gene\_06252.t1,gene\_05244.t1,gene\_04388.t1,gene\_08521.t1,gene\_06106.t1,gene\_04642.t1,gene\_07898.t1,gene\_02155.t1,gene\_10369.t1,gene\_00801.t1,gene\_03799.t1,gene\_08500.t1 | | chromosome, telomeric region | cellular\_component |
| GO:0000785 | 3 | gene\_05249.t1,gene\_05457.t1,gene\_02910.t1 | | chromatin | cellular\_component |
| GO:0000786 | 8 | gene\_07352.t1,gene\_07353.t1,gene\_07755.t1,gene\_09619.t1,gene\_02242.t1,gene\_07282.t1,gene\_02241.t1,gene\_03509.t1 | | nucleosome | cellular\_component |
| GO:0000145 | 8 | gene\_05127.t1,gene\_08719.t1,gene\_07646.t1,gene\_09722.t1,gene\_03986.t1,gene\_06544.t1,gene\_01590.t1,gene\_04572.t1 | | exocyst | cellular\_component |
| GO:0000148 | 1 | gene\_10302.t1 | | 1,3-beta-D-glucan synthase complex | cellular\_component |
| GO:0045239 | 1 | gene\_00860.t1 | | tricarboxylic acid cycle enzyme complex | cellular\_component |
| GO:0008540 | 9 | gene\_02486.t1,gene\_05847.t1,gene\_01236.t1,gene\_07138.t1,gene\_02420.t1,gene\_04461.t1,gene\_00032.t1,gene\_05700.t1,gene\_01479.t1 | | proteasome regulatory particle, base subcomplex | cellular\_component |
| GO:0030870 | 3 | gene\_06548.t1,gene\_04738.t1,gene\_10444.t1 | | Mre11 complex | cellular\_component |
| GO:0033588 | 5 | gene\_09706.t1,gene\_00353.t1,gene\_09540.t1,gene\_06853.t1,gene\_05907.t1 | | elongator holoenzyme complex | cellular\_component |
| GO:0000421 | 1 | gene\_04192.t1 | | autophagosome membrane | cellular\_component |
| GO:0015629 | 3 | gene\_08417.t1,gene\_03932.t1,gene\_00367.t1 | | actin cytoskeleton | cellular\_component |
| GO:0005891 | 1 | gene\_05625.t1 | | voltage-gated calcium channel complex | cellular\_component |
| GO:0030904 | 1 | gene\_08108.t1 | | retromer complex | cellular\_component |
| GO:0030906 | 1 | gene\_08590.t1 | | retromer, cargo-selective complex | cellular\_component |
| GO:0030907 | 1 | gene\_09058.t1 | | MBF transcription complex | cellular\_component |
| GO:0034045 | 7 | gene\_10456.t1,gene\_10308.t1,gene\_05641.t1,gene\_02759.t1,gene\_02838.t1,gene\_03179.t1,gene\_03894.t1 | | phagophore assembly site membrane | cellular\_component |
| GO:0034044 | 1 | gene\_03048.t1 | | exomer complex | cellular\_component |
| GO:0035267 | 5 | gene\_00682.t1,gene\_07183.t1,gene\_10008.t1,gene\_00415.t1,gene\_00391.t1 | | NuA4 histone acetyltransferase complex | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0031981 | 4 | gene\_03378.t1,gene\_10468.t1,gene\_07001.t1,gene\_08530.t1 | | nuclear lumen | cellular\_component |
| GO:0072546 | 3 | gene\_07975.t1,gene\_07360.t1,gene\_01675.t1 | | EMC complex | cellular\_component |
| GO:0000796 | 2 | gene\_05995.t1,gene\_07793.t1 | | condensin complex | cellular\_component |
| GO:0005795 | 1 | gene\_09062.t1 | | Golgi stack | cellular\_component |
| GO:0005794 | 20 | gene\_03601.t1,gene\_07871.t1,gene\_02859.t1,gene\_01552.t1,gene\_08258.t1,gene\_09487.t1,gene\_08532.t1,gene\_05829.t1,gene\_05545.t1,gene\_09156.t1,gene\_09641.t1,gene\_05131.t1,gene\_07361.t1,gene\_10095.t1,gene\_00033.t1,gene\_09223.t1,gene\_10183.t1,gene\_02853.t1,gene\_03291.t1,gene\_01549.t1 | | Golgi apparatus | cellular\_component |
| GO:0031965 | 5 | gene\_00974.t1,gene\_02439.t1,gene\_08367.t1,gene\_03348.t1,gene\_08906.t1 | | nuclear membrane | cellular\_component |
| GO:0031966 | 5 | gene\_06626.t1,gene\_03943.t1,gene\_01447.t1,gene\_02044.t1,gene\_05187.t1 | | mitochondrial membrane | cellular\_component |
| GO:0030132 | 2 | gene\_01372.t1,gene\_04061.t1 | | clathrin coat of coated pit | cellular\_component |
| GO:0005663 | 1 | gene\_07620.t1 | | DNA replication factor C complex | cellular\_component |
| GO:0005665 | 3 | gene\_01696.t1,gene\_01093.t1,gene\_05990.t1 | | RNA polymerase II, core complex | cellular\_component |
| GO:0005664 | 2 | gene\_08269.t1,gene\_06427.t1 | | nuclear origin of replication recognition complex | cellular\_component |
| GO:0005666 | 5 | gene\_09013.t1,gene\_06259.t1,gene\_04655.t1,gene\_08095.t1,gene\_04203.t1 | | RNA polymerase III complex | cellular\_component |
| GO:0005669 | 7 | gene\_06623.t1,gene\_00093.t1,gene\_08167.t1,gene\_00098.t1,gene\_08169.t1,gene\_07484.t1,gene\_09109.t1 | | transcription factor TFIID complex | cellular\_component |
| GO:0000795 | 1 | gene\_06455.t1 | | synaptonemal complex | cellular\_component |
| GO:0000220 | 1 | gene\_10123.t1 | | vacuolar proton-transporting V-type ATPase, V0 domain | cellular\_component |
| GO:0048471 | 1 | gene\_00974.t1 | | perinuclear region of cytoplasm | cellular\_component |
| GO:0048476 | 1 | gene\_05747.t1 | | Holliday junction resolvase complex | cellular\_component |
| GO:0016442 | 1 | gene\_07978.t1 | | RISC complex | cellular\_component |
| GO:0001401 | 1 | gene\_02706.t1 | | SAM complex | cellular\_component |
| GO:0001405 | 1 | gene\_00730.t1 | | PAM complex, Tim23 associated import motor | cellular\_component |
| GO:0000139 | 35 | gene\_01969.t1,gene\_01917.t1,gene\_04805.t1,gene\_10406.t1,gene\_10290.t1,gene\_03375.t1,gene\_00571.t1,gene\_03214.t1,gene\_08919.t1,gene\_00582.t1,gene\_02541.t1,gene\_10522.t1,gene\_06756.t1,gene\_05229.t1,gene\_01728.t1,gene\_02252.t1,gene\_05113.t1,gene\_01668.t1,gene\_09248.t1,gene\_06865.t1,gene\_10658.t1,gene\_08128.t1,gene\_03142.t1,gene\_05520.t1,gene\_02033.t1,gene\_09062.t1,gene\_10475.t1,gene\_05343.t1,gene\_09159.t1,gene\_01017.t1,gene\_04999.t1,gene\_10403.t1,gene\_08775.t1,gene\_10308.t1,gene\_08583.t1 | | Golgi membrane | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0046930 | 2 | gene\_00322.t1,gene\_09709.t1 | | pore complex | cellular\_component |
| GO:0031410 | 6 | gene\_08775.t1,gene\_08680.t1,gene\_04192.t1,gene\_02046.t1,gene\_03121.t1,gene\_09945.t1 | | cytoplasmic vesicle | cellular\_component |
| GO:0031415 | 1 | gene\_05336.t1 | | NatA complex | cellular\_component |
| GO:0031417 | 2 | gene\_02587.t1,gene\_01755.t1 | | NatC complex | cellular\_component |
| GO:0070772 | 1 | gene\_10495.t1 | | PAS complex | cellular\_component |
| GO:0031931 | 3 | gene\_04143.t1,gene\_03147.t1,gene\_05323.t1 | | TORC1 complex | cellular\_component |
| GO:0032040 | 9 | gene\_02354.t1,gene\_09012.t1,gene\_08271.t1,gene\_03203.t1,gene\_02353.t1,gene\_02121.t1,gene\_01602.t1,gene\_00411.t1,gene\_06996.t1 | | small-subunit processome | cellular\_component |
| GO:0000439 | 5 | gene\_09119.t1,gene\_01306.t1,gene\_05871.t1,gene\_04147.t1,gene\_10227.t1 | | transcription factor TFIIH core complex | cellular\_component |
| GO:0032865 | 4 | gene\_04067.t1,gene\_02094.t1,gene\_09579.t1,gene\_06112.t1 | | ERMES complex | cellular\_component |
| GO:0030286 | 3 | gene\_01652.t1,gene\_03563.t1,gene\_05840.t1 | | dynein complex | cellular\_component |
| GO:0071821 | 1 | gene\_06486.t1 | | FANCM-MHF complex | cellular\_component |
| GO:0005576 | 57 | gene\_08100.t1,gene\_00945.t1,gene\_03388.t1,gene\_02259.t1,gene\_08104.t1,gene\_10598.t1,gene\_01852.t1,gene\_04755.t1,gene\_01766.t1,gene\_10045.t1,gene\_02551.t1,gene\_09366.t1,gene\_02422.t1,gene\_03424.t1,gene\_01725.t1,gene\_02291.t1,gene\_06586.t1,gene\_03160.t1,gene\_00132.t1,gene\_02150.t1,gene\_09474.t1,gene\_03906.t1,gene\_01041.t1,gene\_07566.t1,gene\_01844.t1,gene\_00439.t1,gene\_05825.t1,gene\_06941.t1,gene\_03404.t1,gene\_04530.t1,gene\_00719.t1,gene\_00145.t1,gene\_06587.t1,gene\_08114.t1,gene\_08437.t1,gene\_06882.t1,gene\_01845.t1,gene\_03622.t1,gene\_00787.t1,gene\_04429.t1,gene\_10546.t1,gene\_05091.t1,gene\_02705.t1,gene\_07429.t1,gene\_07325.t1,gene\_05722.t1,gene\_03161.t1,gene\_05702.t1,gene\_10451.t1,gene\_01388.t1,gene\_08882.t1,gene\_09475.t1,gene\_01036.t1,gene\_00384.t1,gene\_03332.t1,gene\_00523.t1,gene\_08899.t1 | | extracellular region | cellular\_component |
| GO:0034457 | 1 | gene\_09290.t1 | | Mpp10 complex | cellular\_component |
| GO:0005885 | 5 | gene\_06990.t1,gene\_05874.t1,gene\_07743.t1,gene\_02382.t1,gene\_03091.t1 | | Arp2/3 protein complex | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0005886 | 157 | gene\_02770.t1,gene\_04199.t1,gene\_00930.t1,gene\_01794.t1,gene\_06275.t1,gene\_00100.t1,gene\_08915.t1,gene\_05561.t1,gene\_07874.t1,gene\_06057.t1,gene\_06507.t1,gene\_08829.t1,gene\_01032.t1,gene\_00393.t1,gene\_09785.t1,gene\_07381.t1,gene\_01906.t1,gene\_00665.t1,gene\_08725.t1,gene\_05084.t1,gene\_00025.t1,gene\_09807.t1,gene\_02760.t1,gene\_00577.t1,gene\_09573.t1,gene\_00179.t1,gene\_06693.t1,gene\_08982.t1,gene\_03108.t1,gene\_05719.t1,gene\_08449.t1,gene\_03571.t1,gene\_09176.t1,gene\_06546.t1,gene\_09951.t1,gene\_06645.t1,gene\_08993.t1,gene\_09142.t1,gene\_03354.t1,gene\_06925.t1,gene\_10068.t1,gene\_09507.t1,gene\_04167.t1,gene\_05990.t1,gene\_08927.t1,gene\_00622.t1,gene\_05338.t1,gene\_00743.t1,gene\_07318.t1,gene\_02051.t1,gene\_00068.t1,gene\_09106.t1,gene\_06386.t1,gene\_07562.t1,gene\_06504.t1,gene\_00926.t1,gene\_03023.t1,gene\_03306.t1,gene\_09539.t1,gene\_07809.t1,gene\_08848.t1,gene\_03411.t1,gene\_03444.t1,gene\_09430.t1,gene\_02173.t1,gene\_03407.t1,gene\_01781.t1,gene\_04469.t1,gene\_05432.t1,gene\_09310.t1,gene\_01721.t1,gene\_07559.t1,gene\_09468.t1,gene\_08773.t1,gene\_03841.t1,gene\_06574.t1,gene\_09833.t1,gene\_10401.t1,gene\_01611.t1,gene\_09187.t1,gene\_10650.t1,gene\_06264.t1,gene\_00065.t1,gene\_02409.t1,gene\_09948.t1,gene\_03776.t1,gene\_05583.t1,gene\_09940.t1,gene\_03570.t1,gene\_07449.t1,gene\_10193.t1,gene\_00810.t1,gene\_10249.t1,gene\_06398.t1,gene\_00197.t1,gene\_05216.t1,gene\_00224.t1,gene\_10623.t1,gene\_03580.t1,gene\_06570.t1,gene\_03166.t1,gene\_00293.t1,gene\_00034.t1,gene\_08242.t1,gene\_02441.t1,gene\_09975.t1,gene\_07372.t1,gene\_03028.t1,gene\_06942.t1,gene\_06851.t1,gene\_01795.t1,gene\_09019.t1,gene\_06437.t1,gene\_06385.t1,gene\_08302.t1,gene\_10671.t1,gene\_09398.t1,gene\_04521.t1,gene\_09901.t1,gene\_08752.t1,gene\_01833.t1,gene\_04304.t1,gene\_03133.t1,gene\_09943.t1,gene\_09085.t1,gene\_09872.t1,gene\_08671.t1,gene\_05401.t1,gene\_06748.t1,gene\_09274.t1,gene\_07652.t1,gene\_10250.t1,gene\_09063.t1,gene\_07436.t1,gene\_01290.t1,gene\_08876.t1,gene\_08179.t1,gene\_02621.t1,gene\_03591.t1,gene\_07068.t1,gene\_08259.t1,gene\_00669.t1,gene\_00003.t1,gene\_00673.t1,gene\_06968.t1,gene\_04756.t1,gene\_06375.t1,gene\_06726.t1,gene\_05111.t1,gene\_01175.t1,gene\_10147.t1,gene\_02584.t1,gene\_01144.t1,gene\_02782.t1,gene\_04431.t1,gene\_09716.t1,gene\_06489.t1 | | plasma membrane | cellular\_component |
| GO:0016586 | 2 | gene\_09736.t1,gene\_07314.t1 | | RSC-type complex | cellular\_component |
| GO:0032991 | 3 | gene\_04321.t1,gene\_07735.t1,gene\_00548.t1 | | protein-containing complex | cellular\_component |
| GO:0016035 | 1 | gene\_06856.t1 | | zeta DNA polymerase complex | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0030915 | 5 | gene\_08214.t1,gene\_00882.t1,gene\_07343.t1,gene\_03784.t1,gene\_02270.t1 | | Smc5-Smc6 complex | cellular\_component |
| GO:0016459 | 5 | gene\_03570.t1,gene\_08209.t1,gene\_00218.t1,gene\_03571.t1,gene\_09267.t1 | | myosin complex | cellular\_component |
| GO:0044284 | 1 | gene\_05236.t1 | | mitochondrial crista junction | cellular\_component |
| GO:0043332 | 1 | gene\_10068.t1 | | mating projection tip | cellular\_component |
| GO:0030688 | 2 | gene\_08921.t1,gene\_00707.t1 | | preribosome, small subunit precursor | cellular\_component |
| GO:0030687 | 4 | gene\_01431.t1,gene\_00423.t1,gene\_05207.t1,gene\_05806.t1 | | preribosome, large subunit precursor | cellular\_component |
| GO:0030686 | 1 | gene\_00707.t1 | | 90S preribosome | cellular\_component |
| GO:0030176 | 9 | gene\_00979.t1,gene\_09674.t1,gene\_09583.t1,gene\_09726.t1,gene\_07236.t1,gene\_09530.t1,gene\_03397.t1,gene\_07570.t1,gene\_09579.t1 | | integral component of endoplasmic reticulum membrane | cellular\_component |
| GO:0030173 | 4 | gene\_03764.t1,gene\_07961.t1,gene\_04136.t1,gene\_02181.t1 | | integral component of Golgi membrane | cellular\_component |
| GO:0005655 | 4 | gene\_00840.t1,gene\_01748.t1,gene\_03157.t1,gene\_08067.t1 | | nucleolar ribonuclease P complex | cellular\_component |
| GO:0005656 | 6 | gene\_00515.t1,gene\_01710.t1,gene\_01540.t1,gene\_07862.t1,gene\_08245.t1,gene\_09071.t1 | | nuclear pre-replicative complex | cellular\_component |
| GO:0005657 | 1 | gene\_09111.t1 | | replication fork | cellular\_component |
| GO:0031314 | 5 | gene\_04044.t1,gene\_07253.t1,gene\_07066.t1,gene\_03847.t1,gene\_10412.t1 | | extrinsic component of mitochondrial inner membrane | cellular\_component |
| GO:0031083 | 2 | gene\_03575.t1,gene\_00877.t1 | | BLOC-1 complex | cellular\_component |
| GO:0031515 | 3 | gene\_07742.t1,gene\_10437.t1,gene\_04420.t1 | | tRNA (m1A) methyltransferase complex | cellular\_component |
| GO:0031511 | 1 | gene\_08738.t1 | | Mis6-Sim4 complex | cellular\_component |
| GO:0010494 | 1 | gene\_07129.t1 | | cytoplasmic stress granule | cellular\_component |
| GO:0031227 | 1 | gene\_02482.t1 | | intrinsic component of endoplasmic reticulum membrane | cellular\_component |
| GO:0031225 | 26 | gene\_08927.t1,gene\_02770.t1,gene\_02409.t1,gene\_06645.t1,gene\_00100.t1,gene\_01032.t1,gene\_03591.t1,gene\_08982.t1,gene\_03444.t1,gene\_05084.t1,gene\_07809.t1,gene\_09807.t1,gene\_06968.t1,gene\_10623.t1,gene\_06546.t1,gene\_09951.t1,gene\_06726.t1,gene\_06437.t1,gene\_01721.t1,gene\_07652.t1,gene\_09468.t1,gene\_07562.t1,gene\_08993.t1,gene\_10671.t1,gene\_04431.t1,gene\_09716.t1 | | anchored component of membrane | cellular\_component |
| GO:0000124 | 5 | gene\_08771.t1,gene\_01863.t1,gene\_09830.t1,gene\_05658.t1,gene\_08169.t1 | | SAGA complex | cellular\_component |
| GO:0000127 | 3 | gene\_10633.t1,gene\_06291.t1,gene\_07840.t1 | | transcription factor TFIIIC complex | cellular\_component |
| GO:0000126 | 1 | gene\_03056.t1 | | transcription factor TFIIIB complex | cellular\_component |
| GO:0000123 | 1 | gene\_07837.t1 | | histone acetyltransferase complex | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0031428 | 2 | gene\_03203.t1,gene\_09012.t1 | | box C/D RNP complex | cellular\_component |
| GO:0031422 | 1 | gene\_06775.t1 | | RecQ family helicase-topoisomerase III complex | cellular\_component |
| GO:0000221 | 1 | gene\_05546.t1 | | vacuolar proton-transporting V-type ATPase, V1 domain | cellular\_component |
| GO:0000444 | 1 | gene\_09061.t1 | | MIS12/MIND type complex | cellular\_component |
| GO:0000445 | 1 | gene\_01138.t1 | | THO complex part of transcription export complex | cellular\_component |
| GO:0071541 | 1 | gene\_06008.t1 | | eukaryotic translation initiation factor 3 complex, eIF3m | cellular\_component |
| GO:0071540 | 1 | gene\_05697.t1 | | eukaryotic translation initiation factor 3 complex, eIF3e | cellular\_component |
| GO:0000932 | 3 | gene\_01674.t1,gene\_09407.t1,gene\_06101.t1 | | P-body | cellular\_component |
| GO:0000931 | 1 | gene\_05213.t1 | | gamma-tubulin large complex | cellular\_component |
| GO:0016593 | 3 | gene\_05205.t1,gene\_07013.t1,gene\_00642.t1 | | Cdc73/Paf1 complex | cellular\_component |
| GO:0016592 | 23 | gene\_09638.t1,gene\_02427.t1,gene\_05522.t1,gene\_09075.t1,gene\_03195.t1,gene\_10396.t1,gene\_08286.t1,gene\_10618.t1,gene\_06207.t1,gene\_07235.t1,gene\_09400.t1,gene\_01050.t1,gene\_03418.t1,gene\_10253.t1,gene\_03677.t1,gene\_01348.t1,gene\_02513.t1,gene\_02542.t1,gene\_03582.t1,gene\_04057.t1,gene\_01449.t1,gene\_00985.t1,gene\_07678.t1 | | mediator complex | cellular\_component |
| GO:0016021 | 1940 | gene\_04214.t1,gene\_07014.t1,gene\_04689.t1,gene\_01489.t1,gene\_04805.t1,gene\_09951.t1,gene\_00930.t1,gene\_02649.t1,gene\_07664.t1,gene\_08774.t1,gene\_09685.t1,gene\_07182.t1,gene\_04164.t1,gene\_07225.t1,gene\_00469.t1,gene\_10062.t1,gene\_09837.t1,gene\_09632.t1,gene\_02069.t1,gene\_05751.t1,gene\_06986.t1,gene\_03620.t1,gene\_02482.t1,gene\_02975.t1,gene\_00471.t1,gene\_00261.t1,gene\_06678.t1,gene\_06954.t1,gene\_03319.t1,gene\_03478.t1,gene\_08625.t1,gene\_00174.t1,gene\_05949.t1,gene\_10092.t1,gene\_08850.t1,gene\_04787.t1,gene\_08571.t1,gene\_05754.t1,gene\_10659.t1,gene\_04065.t1,gene\_07786.t1,gene\_01350.t1,gene\_01244.t1,gene\_00784.t1,gene\_03044.t1,gene\_06206.t1,gene\_03749.t1,gene\_08370.t1,gene\_06201.t1,gene\_03306.t1,gene\_06543.t1,gene\_02213.t1,gene\_06182.t1,gene\_03976.t1,gene\_02533.t1,gene\_05255.t1,gene\_07338.t1,gene\_05352.t1,gene\_06230.t1,gene\_00823.t1,gene\_01892.t1,gene\_03841.t1,gene\_06984.t1,gene\_01067.t1,gene\_10605.t1,gene\_09187.t1,gene\_01749.t1,gene\_02555.t1,gene\_07553.t1,gene\_04283.t1,gene\_05994.t1,gene\_10228.t1,gene\_08673.t1,gene\_09288.t1,gene\_10349.t1,gene\_00349.t1,gene\_03055.t1,gene\_01170.t1,gene\_03843.t1,gene\_03879.t1,gene\_07591.t1,gene\_07220.t1,gene\_07072.t1,gene\_06479.t1,gene\_09252.t1,gene\_02008.t1,gene\_00354.t1,gene\_07151.t1,gene\_04123.t1,gene\_08902.t1, | | integral component of membrane | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0016021 | 1940 | gene\_07372.t1,gene\_02999.t1,gene\_01150.t1,gene\_05333.t1,gene\_07516.t1,gene\_09150.t1,gene\_05628.t1,gene\_08446.t1,gene\_06180.t1,gene\_06541.t1,gene\_03053.t1,gene\_01711.t1,gene\_08583.t1,gene\_08493.t1,gene\_07022.t1,gene\_00383.t1,gene\_04472.t1,gene\_08098.t1,gene\_00071.t1,gene\_05295.t1,gene\_06286.t1,gene\_06133.t1,gene\_05234.t1,gene\_00820.t1,gene\_02871.t1,gene\_07551.t1,gene\_07002.t1,gene\_04451.t1,gene\_00770.t1,gene\_05649.t1,gene\_01895.t1,gene\_00003.t1,gene\_05343.t1,gene\_03371.t1,gene\_05326.t1,gene\_00825.t1,gene\_06601.t1,gene\_03482.t1,gene\_02400.t1,gene\_07107.t1,gene\_04268.t1,gene\_01056.t1,gene\_03992.t1,gene\_09620.t1,gene\_00796.t1,gene\_07140.t1,gene\_06363.t1,gene\_07915.t1,gene\_00135.t1,gene\_01779.t1,gene\_06275.t1,gene\_00100.t1,gene\_08915.t1,gene\_08958.t1,gene\_07568.t1,gene\_04468.t1,gene\_10321.t1,gene\_09029.t1,gene\_01654.t1,gene\_08751.t1,gene\_00733.t1,gene\_05983.t1,gene\_03699.t1,gene\_03251.t1,gene\_08156.t1,gene\_03571.t1,gene\_04506.t1,gene\_09108.t1,gene\_04350.t1,gene\_02598.t1,gene\_06170.t1,gene\_09309.t1,gene\_07093.t1,gene\_00744.t1,gene\_06925.t1,gene\_02398.t1,gene\_08406.t1,gene\_10515.t1,gene\_07257.t1,gene\_03156.t1,gene\_10077.t1,gene\_08121.t1,gene\_07318.t1,gene\_04813.t1,gene\_07593.t1,gene\_02189.t1,gene\_07486.t1,gene\_09919.t1,gene\_06927.t1,gene\_05642.t1,gene\_04754.t1,gene\_09452.t1,gene\_09188.t1,gene\_03023.t1,gene\_03411.t1,gene\_09352.t1,gene\_08435.t1,gene\_07345.t1,gene\_04653.t1,gene\_00530.t1,gene\_07559.t1,gene\_09468.t1,gene\_04201.t1,gene\_06887.t1,gene\_09306.t1,gene\_06797.t1,gene\_04581.t1,gene\_06093.t1,gene\_02889.t1,gene\_10406.t1,gene\_04334.t1,gene\_10048.t1,gene\_06684.t1,gene\_01254.t1,gene\_05608.t1,gene\_05176.t1,gene\_04151.t1,gene\_05566.t1,gene\_07108.t1,gene\_03154.t1,gene\_07000.t1,gene\_03733.t1,gene\_02494.t1,gene\_09422.t1,gene\_00710.t1,gene\_00276.t1,gene\_04210.t1,gene\_07227.t1,gene\_07765.t1,gene\_00828.t1,gene\_05903.t1,gene\_04499.t1,gene\_08236.t1,gene\_00250.t1,gene\_03007.t1,gene\_07729.t1,gene\_08312.t1,gene\_02904.t1,gene\_05038.t1,gene\_03798.t1,gene\_02936.t1,gene\_05761.t1,gene\_00069.t1,gene\_05780.t1,gene\_00835.t1,gene\_04318.t1,gene\_03547.t1,gene\_07398.t1,gene\_00153.t1,gene\_07416.t1,gene\_07995.t1,gene\_02316.t1,gene\_06375.t1,gene\_09659.t1,gene\_05098.t1,gene\_06039.t1,gene\_09926.t1,gene\_09643.t1,gene\_00057.t1,gene\_05935.t1,gene\_00941.t1,gene\_03083.t1,gene\_08000.t1,gene\_03018.t1,gene\_06689.t1,gene\_02414.t1,gene\_09714.t1,gene\_08935.t1,gene\_04908.t1,gene\_07491.t1,gene\_09785.t1,gene\_01671.t1,gene\_09522.t1,gene\_02886.t1,gene\_02440.t1,gene\_01595.t1,gene\_01450.t1,gene\_07616.t1,gene\_03409.t1,gene\_01640.t1, | | integral component of membrane | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0016021 | 1940 | gene\_00525.t1,gene\_00480.t1,gene\_05117.t1,gene\_00647.t1,gene\_03323.t1,gene\_07201.t1,gene\_07033.t1,gene\_10041.t1,gene\_09487.t1,gene\_06888.t1,gene\_08171.t1,gene\_04434.t1,gene\_09147.t1,gene\_08039.t1,gene\_08250.t1,gene\_02696.t1,gene\_05548.t1,gene\_07369.t1,gene\_07737.t1,gene\_01577.t1,gene\_04541.t1,gene\_09383.t1,gene\_08056.t1,gene\_02173.t1,gene\_00175.t1,gene\_00073.t1,gene\_01781.t1,gene\_10399.t1,gene\_05952.t1,gene\_00331.t1,gene\_03502.t1,gene\_05882.t1,gene\_05245.t1,gene\_05465.t1,gene\_07238.t1,gene\_08549.t1,gene\_03958.t1,gene\_06116.t1,gene\_06091.t1,gene\_01909.t1,gene\_09060.t1,gene\_07919.t1,gene\_09970.t1,gene\_05467.t1,gene\_03287.t1,gene\_10640.t1,gene\_07083.t1,gene\_00641.t1,gene\_01318.t1,gene\_01331.t1,gene\_09232.t1,gene\_10206.t1,gene\_10193.t1,gene\_09047.t1,gene\_09331.t1,gene\_08140.t1,gene\_00215.t1,gene\_06362.t1,gene\_10504.t1,gene\_06107.t1,gene\_03560.t1,gene\_04493.t1,gene\_05310.t1,gene\_10046.t1,gene\_01906.t1,gene\_07414.t1,gene\_02738.t1,gene\_05126.t1,gene\_02820.t1,gene\_00177.t1,gene\_05929.t1,gene\_08553.t1,gene\_05380.t1,gene\_06496.t1,gene\_01919.t1,gene\_04005.t1,gene\_05569.t1,gene\_00602.t1,gene\_05303.t1,gene\_08883.t1,gene\_00896.t1,gene\_05102.t1,gene\_05657.t1,gene\_10368.t1,gene\_06588.t1,gene\_07025.t1,gene\_01410.t1,gene\_02753.t1,gene\_06533.t1,gene\_04756.t1,gene\_06285.t1,gene\_03368.t1,gene\_06790.t1,gene\_07552.t1,gene\_10147.t1,gene\_02031.t1,gene\_07131.t1,gene\_00755.t1,gene\_09812.t1,gene\_03153.t1,gene\_04348.t1,gene\_08068.t1,gene\_06128.t1,gene\_02647.t1,gene\_09176.t1,gene\_06049.t1,gene\_09103.t1,gene\_04122.t1,gene\_10472.t1,gene\_06301.t1,gene\_09101.t1,gene\_00333.t1,gene\_06175.t1,gene\_01086.t1,gene\_05719.t1,gene\_01709.t1,gene\_02471.t1,gene\_08013.t1,gene\_04881.t1,gene\_05542.t1,gene\_08275.t1,gene\_01241.t1,gene\_01412.t1,gene\_05090.t1,gene\_10068.t1,gene\_08669.t1,gene\_08227.t1,gene\_07569.t1,gene\_05187.t1,gene\_02884.t1,gene\_09868.t1,gene\_09069.t1,gene\_06904.t1,gene\_04746.t1,gene\_06965.t1,gene\_05092.t1,gene\_03436.t1,gene\_02058.t1,gene\_05667.t1,gene\_00555.t1,gene\_09185.t1,gene\_00317.t1,gene\_10331.t1,gene\_06924.t1,gene\_07136.t1,gene\_03058.t1,gene\_01525.t1,gene\_05432.t1,gene\_09662.t1,gene\_06508.t1,gene\_04758.t1,gene\_09133.t1,gene\_10163.t1,gene\_06574.t1,gene\_02515.t1,gene\_06926.t1,gene\_04249.t1,gene\_05290.t1,gene\_07725.t1,gene\_06519.t1,gene\_09189.t1,gene\_02508.t1,gene\_02561.t1,gene\_03628.t1,gene\_01685.t1,gene\_04191.t1,gene\_01531.t1,gene\_02275.t1,gene\_04170.t1,gene\_09205.t1,gene\_07967.t1,gene\_08128.t1,gene\_04025.t1,gene\_04068.t1,gene\_09286.t1,gene\_00118.t1,gene\_09671.t1,gene\_03877.t1,gene\_00200.t1,gene\_03882.t1, | | integral component of membrane | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0016021 | 1940 | gene\_07967.t1,gene\_08128.t1,gene\_04025.t1,gene\_04068.t1,gene\_09286.t1,gene\_00118.t1,gene\_09671.t1,gene\_03877.t1,gene\_00200.t1,gene\_03882.t1,gene\_00567.t1,gene\_00764.t1,gene\_08352.t1,gene\_08414.t1,gene\_08459.t1,gene\_03215.t1,gene\_09085.t1,gene\_07018.t1,gene\_02076.t1,gene\_03039.t1,gene\_01807.t1,gene\_04138.t1,gene\_08950.t1,gene\_02675.t1,gene\_05089.t1,gene\_03425.t1,gene\_07672.t1,gene\_04995.t1,gene\_03389.t1,gene\_01379.t1,gene\_06453.t1,gene\_03329.t1,gene\_05991.t1,gene\_02677.t1,gene\_02539.t1,gene\_06177.t1,gene\_07745.t1,gene\_00036.t1,gene\_05285.t1,gene\_10459.t1,gene\_00666.t1,gene\_01136.t1,gene\_04168.t1,gene\_01121.t1,gene\_09207.t1,gene\_03277.t1,gene\_05817.t1,gene\_02439.t1,gene\_04809.t1,gene\_02039.t1,gene\_05357.t1,gene\_08888.t1,gene\_01123.t1,gene\_01814.t1,gene\_03910.t1,gene\_05537.t1,gene\_10651.t1,gene\_06507.t1,gene\_00807.t1,gene\_05878.t1,gene\_06432.t1,gene\_10096.t1,gene\_06510.t1,gene\_01448.t1,gene\_01913.t1,gene\_00025.t1,gene\_00926.t1,gene\_03002.t1,gene\_03403.t1,gene\_08284.t1,gene\_09740.t1,gene\_02772.t1,gene\_09972.t1,gene\_05576.t1,gene\_04035.t1,gene\_02837.t1,gene\_08886.t1,gene\_02847.t1,gene\_05758.t1,gene\_00739.t1,gene\_04440.t1,gene\_00743.t1,gene\_01215.t1,gene\_05406.t1,gene\_06386.t1,gene\_05275.t1,gene\_10217.t1,gene\_07637.t1,gene\_05114.t1,gene\_04457.t1,gene\_09018.t1,gene\_10519.t1,gene\_00038.t1,gene\_02710.t1,gene\_05116.t1,gene\_09000.t1,gene\_07273.t1,gene\_03082.t1,gene\_03075.t1,gene\_04716.t1,gene\_03019.t1,gene\_08714.t1,gene\_06863.t1,gene\_06850.t1,gene\_03526.t1,gene\_04256.t1,gene\_07920.t1,gene\_03439.t1,gene\_01083.t1,gene\_09854.t1,gene\_06818.t1,gene\_05179.t1,gene\_10534.t1,gene\_00224.t1,gene\_03787.t1,gene\_07117.t1,gene\_00914.t1,gene\_09559.t1,gene\_09804.t1,gene\_03045.t1,gene\_07824.t1,gene\_10536.t1,gene\_08453.t1,gene\_07968.t1,gene\_10419.t1,gene\_00086.t1,gene\_05748.t1,gene\_08116.t1,gene\_09269.t1,gene\_07775.t1,gene\_00152.t1,gene\_10142.t1,gene\_07218.t1,gene\_01084.t1,gene\_03457.t1,gene\_08451.t1,gene\_09872.t1,gene\_07451.t1,gene\_09139.t1,gene\_10604.t1,gene\_03043.t1,gene\_10514.t1,gene\_04394.t1,gene\_00379.t1,gene\_00736.t1,gene\_06254.t1,gene\_09168.t1,gene\_09218.t1,gene\_05766.t1,gene\_00240.t1,gene\_08267.t1,gene\_02547.t1,gene\_00114.t1,gene\_06726.t1,gene\_10251.t1,gene\_09889.t1,gene\_06328.t1,gene\_00590.t1,gene\_07809.t1,gene\_06724.t1,gene\_02072.t1,gene\_05773.t1,gene\_01507.t1,gene\_04514.t1,gene\_01211.t1,gene\_00716.t1,gene\_05349.t1,gene\_04668.t1,gene\_06347.t1,gene\_06293.t1,gene\_00467.t1,gene\_03684.t1,gene\_01461.t1,gene\_02872.t1,gene\_05926.t1,gene\_03238.t1,gene\_02621.t1,gene\_04840.t1,gene\_06931.t1,gene\_00070.t1, | | integral component of membrane | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0016021 | 1940 | gene\_10079.t1,gene\_01239.t1,gene\_05634.t1,gene\_01862.t1,gene\_01724.t1,gene\_09142.t1,gene\_01324.t1,gene\_03078.t1,gene\_08991.t1,gene\_06084.t1,gene\_03370.t1,gene\_06246.t1,gene\_05202.t1,gene\_10473.t1,gene\_02401.t1,gene\_07365.t1,gene\_10329.t1,gene\_00948.t1,gene\_01657.t1,gene\_02394.t1,gene\_03695.t1,gene\_08807.t1,gene\_10553.t1,gene\_08061.t1,gene\_00734.t1,gene\_04393.t1,gene\_00389.t1,gene\_01413.t1,gene\_06384.t1,gene\_04469.t1,gene\_03291.t1,gene\_01476.t1,gene\_04141.t1,gene\_03032.t1,gene\_05458.t1,gene\_03305.t1,gene\_07382.t1,gene\_00296.t1,gene\_01944.t1,gene\_02245.t1,gene\_09386.t1,gene\_00081.t1,gene\_10428.t1,gene\_03383.t1,gene\_02839.t1,gene\_00810.t1,gene\_09890.t1,gene\_09456.t1,gene\_00890.t1,gene\_06910.t1,gene\_08480.t1,gene\_06772.t1,gene\_04990.t1,gene\_00021.t1,gene\_06052.t1,gene\_01816.t1,gene\_06610.t1,gene\_08242.t1,gene\_09681.t1,gene\_09975.t1,gene\_05433.t1,gene\_00927.t1,gene\_06294.t1,gene\_00392.t1,gene\_01697.t1,gene\_04204.t1,gene\_10094.t1,gene\_00489.t1,gene\_01968.t1,gene\_09453.t1,gene\_09460.t1,gene\_08972.t1,gene\_09565.t1,gene\_08302.t1,gene\_08010.t1,gene\_03318.t1,gene\_06368.t1,gene\_08462.t1,gene\_04527.t1,gene\_05401.t1,gene\_08627.t1,gene\_05633.t1,gene\_00571.t1,gene\_08165.t1,gene\_02930.t1,gene\_10110.t1,gene\_04488.t1,gene\_09752.t1,gene\_07697.t1,gene\_00586.t1,gene\_08978.t1,gene\_00533.t1,gene\_02493.t1,gene\_00898.t1,gene\_02693.t1,gene\_09902.t1,gene\_06933.t1,gene\_00006.t1,gene\_00047.t1,gene\_10278.t1,gene\_03426.t1,gene\_08621.t1,gene\_06167.t1,gene\_09826.t1,gene\_05108.t1,gene\_06263.t1,gene\_08932.t1,gene\_10031.t1,gene\_02237.t1,gene\_04325.t1,gene\_04199.t1,gene\_08166.t1,gene\_03902.t1,gene\_10302.t1,gene\_03171.t1,gene\_05325.t1,gene\_03004.t1,gene\_02283.t1,gene\_06004.t1,gene\_09345.t1,gene\_06499.t1,gene\_10621.t1,gene\_09099.t1,gene\_04211.t1,gene\_02294.t1,gene\_04525.t1,gene\_07969.t1,gene\_03897.t1,gene\_04054.t1,gene\_04328.t1,gene\_04961.t1,gene\_05544.t1,gene\_02731.t1,gene\_10493.t1,gene\_01474.t1,gene\_09634.t1,gene\_10025.t1,gene\_07281.t1,gene\_04156.t1,gene\_00622.t1,gene\_02204.t1,gene\_03381.t1,gene\_07422.t1,gene\_02262.t1,gene\_01571.t1,gene\_06038.t1,gene\_02026.t1,gene\_10521.t1,gene\_09603.t1,gene\_08851.t1,gene\_09739.t1,gene\_02315.t1,gene\_09782.t1,gene\_02209.t1,gene\_08133.t1,gene\_07880.t1,gene\_07581.t1,gene\_04644.t1,gene\_05934.t1,gene\_07340.t1,gene\_06545.t1,gene\_05356.t1,gene\_09335.t1,gene\_09510.t1,gene\_10401.t1,gene\_00834.t1,gene\_10284.t1,gene\_02887.t1,gene\_03464.t1,gene\_08925.t1,gene\_07990.t1,gene\_03996.t1,gene\_00836.t1,gene\_01225.t1,gene\_01912.t1,gene\_10403.t1,gene\_08868.t1,gene\_07269.t1,gene\_01166.t1,gene\_00584.t1, | | integral component of membrane | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0016021 | 1940 | gene\_08912.t1,gene\_07579.t1,gene\_06026.t1,gene\_03488.t1,gene\_03166.t1,gene\_01929.t1,gene\_08677.t1,gene\_05565.t1,gene\_03337.t1,gene\_05495.t1,gene\_01994.t1,gene\_03028.t1,gene\_02295.t1,gene\_06942.t1,gene\_07230.t1,gene\_04595.t1,gene\_09776.t1,gene\_01052.t1,gene\_08003.t1,gene\_01385.t1,gene\_07141.t1,gene\_00130.t1,gene\_00183.t1,gene\_00072.t1,gene\_03335.t1,gene\_09243.t1,gene\_03361.t1,gene\_08413.t1,gene\_01208.t1,gene\_06469.t1,gene\_04476.t1,gene\_09063.t1,gene\_04539.t1,gene\_00123.t1,gene\_02901.t1,gene\_06889.t1,gene\_06619.t1,gene\_02059.t1,gene\_00933.t1,gene\_08968.t1,gene\_02709.t1,gene\_03296.t1,gene\_03286.t1,gene\_05412.t1,gene\_02308.t1,gene\_07573.t1,gene\_08127.t1,gene\_09305.t1,gene\_06414.t1,gene\_05048.t1,gene\_00954.t1,gene\_03490.t1,gene\_07155.t1,gene\_03561.t1,gene\_05298.t1,gene\_09106.t1,gene\_02140.t1,gene\_06489.t1,gene\_04562.t1,gene\_08408.t1,gene\_08970.t1,gene\_04666.t1,gene\_06155.t1,gene\_05127.t1,gene\_00915.t1,gene\_02938.t1,gene\_09558.t1,gene\_01245.t1,gene\_01583.t1,gene\_03363.t1,gene\_06894.t1,gene\_10033.t1,gene\_00665.t1,gene\_03485.t1,gene\_09344.t1,gene\_05470.t1,gene\_06693.t1,gene\_01440.t1,gene\_07529.t1,gene\_09360.t1,gene\_04130.t1,gene\_08582.t1,gene\_09507.t1,gene\_01105.t1,gene\_00203.t1,gene\_01832.t1,gene\_01453.t1,gene\_02505.t1,gene\_01460.t1,gene\_06504.t1,gene\_05386.t1,gene\_01219.t1,gene\_06536.t1,gene\_01522.t1,gene\_05113.t1,gene\_05381.t1,gene\_09430.t1,gene\_04063.t1,gene\_09821.t1,gene\_04305.t1,gene\_00120.t1,gene\_01384.t1,gene\_00782.t1,gene\_04053.t1,gene\_03941.t1,gene\_06300.t1,gene\_09521.t1,gene\_03201.t1,gene\_00065.t1,gene\_03003.t1,gene\_03943.t1,gene\_03776.t1,gene\_04113.t1,gene\_07279.t1,gene\_06127.t1,gene\_02824.t1,gene\_02305.t1,gene\_09104.t1,gene\_01303.t1,gene\_00281.t1,gene\_09676.t1,gene\_04926.t1,gene\_01917.t1,gene\_00418.t1,gene\_07526.t1,gene\_04316.t1,gene\_04357.t1,gene\_01031.t1,gene\_09866.t1,gene\_08254.t1,gene\_00350.t1,gene\_06085.t1,gene\_09183.t1,gene\_08971.t1,gene\_04080.t1,gene\_02895.t1,gene\_02310.t1,gene\_02500.t1,gene\_04194.t1,gene\_06746.t1,gene\_05068.t1,gene\_04452.t1,gene\_08448.t1,gene\_10552.t1,gene\_01317.t1,gene\_02789.t1,gene\_01741.t1,gene\_04757.t1,gene\_03665.t1,gene\_04275.t1,gene\_05781.t1,gene\_05223.t1,gene\_07558.t1,gene\_07124.t1,gene\_00966.t1,gene\_01502.t1,gene\_04932.t1,gene\_06047.t1,gene\_01255.t1,gene\_07657.t1,gene\_01500.t1,gene\_08298.t1,gene\_01817.t1,gene\_01108.t1,gene\_06616.t1,gene\_03826.t1,gene\_08243.t1,gene\_03352.t1,gene\_01041.t1,gene\_00393.t1,gene\_09691.t1,gene\_02640.t1,gene\_05120.t1,gene\_06583.t1,gene\_01806.t1,gene\_07213.t1,gene\_01891.t1,gene\_02826.t1,gene\_01235.t1,gene\_02576.t1, | | integral component of membrane | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0016021 | 1940 | gene\_02642.t1,gene\_09134.t1,gene\_05347.t1,gene\_09054.t1,gene\_10133.t1,gene\_04526.t1,gene\_01021.t1,gene\_07026.t1,gene\_01905.t1,gene\_04498.t1,gene\_08936.t1,gene\_05464.t1,gene\_03246.t1,gene\_09732.t1,gene\_04970.t1,gene\_04426.t1,gene\_06422.t1,gene\_10123.t1,gene\_02782.t1,gene\_02041.t1,gene\_03407.t1,gene\_08687.t1,gene\_06992.t1,gene\_07097.t1,gene\_00016.t1,gene\_08198.t1,gene\_06178.t1,gene\_03379.t1,gene\_09181.t1,gene\_00220.t1,gene\_09121.t1,gene\_01611.t1,gene\_09472.t1,gene\_02105.t1,gene\_01777.t1,gene\_04377.t1,gene\_10115.t1,gene\_05338.t1,gene\_00552.t1,gene\_08823.t1,gene\_01677.t1,gene\_10656.t1,gene\_04212.t1,gene\_06570.t1,gene\_00293.t1,gene\_00034.t1,gene\_08158.t1,gene\_02441.t1,gene\_04229.t1,gene\_01247.t1,gene\_10400.t1,gene\_01795.t1,gene\_06871.t1,gene\_00051.t1,gene\_10672.t1,gene\_07434.t1,gene\_04715.t1,gene\_06325.t1,gene\_09766.t1,gene\_02116.t1,gene\_02762.t1,gene\_06565.t1,gene\_09934.t1,gene\_08960.t1,gene\_03782.t1,gene\_08909.t1,gene\_07578.t1,gene\_06762.t1,gene\_00178.t1,gene\_04825.t1,gene\_07436.t1,gene\_01290.t1,gene\_00888.t1,gene\_02153.t1,gene\_01405.t1,gene\_05505.t1,gene\_08683.t1,gene\_10118.t1,gene\_03253.t1,gene\_03255.t1,gene\_01787.t1,gene\_01593.t1,gene\_08671.t1,gene\_00749.t1,gene\_10166.t1,gene\_02897.t1,gene\_01549.t1,gene\_00131.t1,gene\_04733.t1,gene\_05085.t1,gene\_09696.t1,gene\_08954.t1,gene\_08853.t1,gene\_08086.t1,gene\_06701.t1,gene\_07101.t1,gene\_01632.t1,gene\_01194.t1,gene\_00133.t1,gene\_06980.t1,gene\_08597.t1,gene\_09694.t1,gene\_07103.t1,gene\_01275.t1,gene\_02460.t1,gene\_04999.t1,gene\_00022.t1,gene\_04466.t1,gene\_01366.t1,gene\_05940.t1,gene\_09763.t1,gene\_04692.t1,gene\_08725.t1,gene\_04984.t1,gene\_04059.t1,gene\_01257.t1,gene\_04010.t1,gene\_05094.t1,gene\_07740.t1,gene\_03108.t1,gene\_06594.t1,gene\_09432.t1,gene\_07427.t1,gene\_03345.t1,gene\_01523.t1,gene\_04167.t1,gene\_04718.t1,gene\_00428.t1,gene\_02990.t1,gene\_03458.t1,gene\_06388.t1,gene\_02051.t1,gene\_07224.t1,gene\_00068.t1,gene\_03106.t1,gene\_09363.t1,gene\_07425.t1,gene\_05379.t1,gene\_01539.t1,gene\_07069.t1,gene\_04495.t1,gene\_05987.t1,gene\_04401.t1,gene\_08607.t1,gene\_09016.t1,gene\_07186.t1,gene\_07648.t1,gene\_01258.t1,gene\_07652.t1,gene\_07702.t1,gene\_01421.t1,gene\_08487.t1,gene\_04574.t1,gene\_03578.t1,gene\_00852.t1,gene\_02760.t1,gene\_08814.t1,gene\_06164.t1,gene\_05848.t1,gene\_08360.t1,gene\_07834.t1,gene\_00172.t1,gene\_08766.t1,gene\_04576.t1,gene\_01419.t1,gene\_04463.t1,gene\_03484.t1,gene\_10102.t1,gene\_05800.t1,gene\_00659.t1,gene\_00425.t1,gene\_02010.t1,gene\_08392.t1,gene\_09657.t1,gene\_03131.t1,gene\_01924.t1,gene\_10646.t1,gene\_05692.t1,gene\_09675.t1,gene\_06354.t1, | | integral component of membrane | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0016021 | 1940 | gene\_00425.t1,gene\_02010.t1,gene\_08392.t1,gene\_09657.t1,gene\_03131.t1,gene\_01924.t1,gene\_10646.t1,gene\_05692.t1,gene\_09675.t1,gene\_06354.t1,gene\_01833.t1,gene\_03133.t1,gene\_05309.t1,gene\_04029.t1,gene\_10152.t1,gene\_08297.t1,gene\_01442.t1,gene\_10298.t1,gene\_10250.t1,gene\_05533.t1,gene\_09213.t1,gene\_02475.t1,gene\_04389.t1,gene\_02370.t1,gene\_05131.t1,gene\_07258.t1,gene\_02807.t1,gene\_00841.t1,gene\_07597.t1,gene\_01485.t1,gene\_04710.t1,gene\_01285.t1,gene\_00456.t1,gene\_00673.t1,gene\_00934.t1,gene\_00611.t1,gene\_05473.t1,gene\_02949.t1,gene\_03386.t1,gene\_01062.t1,gene\_08939.t1,gene\_05111.t1,gene\_05129.t1,gene\_08757.t1,gene\_09007.t1,gene\_01867.t1,gene\_00014.t1,gene\_04205.t1,gene\_07976.t1,gene\_06803.t1,gene\_00688.t1,gene\_06836.t1,gene\_02544.t1,gene\_00211.t1,gene\_01660.t1,gene\_10638.t1,gene\_05011.t1,gene\_06057.t1,gene\_10511.t1,gene\_04317.t1,gene\_06936.t1,gene\_10247.t1,gene\_07262.t1,gene\_08164.t1,gene\_03149.t1,gene\_03364.t1,gene\_05447.t1,gene\_10034.t1,gene\_05434.t1,gene\_07584.t1,gene\_01686.t1,gene\_01690.t1,gene\_09964.t1,gene\_09356.t1,gene\_04602.t1,gene\_05629.t1,gene\_10571.t1,gene\_09467.t1,gene\_03872.t1,gene\_02963.t1,gene\_08458.t1,gene\_03300.t1,gene\_02335.t1,gene\_10237.t1,gene\_08112.t1,gene\_09354.t1,gene\_03936.t1,gene\_03375.t1,gene\_09028.t1,gene\_03612.t1,gene\_06173.t1,gene\_08829.t1,gene\_04027.t1,gene\_01263.t1,gene\_04896.t1,gene\_08200.t1,gene\_05802.t1,gene\_02742.t1,gene\_04592.t1,gene\_08848.t1,gene\_05194.t1,gene\_03348.t1,gene\_02676.t1,gene\_09852.t1,gene\_03229.t1,gene\_07631.t1,gene\_09955.t1,gene\_10671.t1,gene\_05488.t1,gene\_08163.t1,gene\_08773.t1,gene\_06064.t1,gene\_09574.t1,gene\_10007.t1,gene\_09300.t1,gene\_01950.t1,gene\_05775.t1,gene\_04697.t1,gene\_06952.t1,gene\_08278.t1,gene\_01475.t1,gene\_00788.t1,gene\_03586.t1,gene\_10627.t1,gene\_00809.t1,gene\_06753.t1,gene\_09552.t1,gene\_10235.t1,gene\_05863.t1,gene\_00740.t1,gene\_08230.t1,gene\_06472.t1,gene\_08892.t1,gene\_07517.t1,gene\_08440.t1,gene\_02462.t1,gene\_09144.t1,gene\_06470.t1,gene\_07330.t1,gene\_02736.t1,gene\_04055.t1,gene\_06233.t1,gene\_09230.t1,gene\_04003.t1,gene\_07615.t1,gene\_03092.t1,gene\_07455.t1,gene\_08928.t1,gene\_08860.t1,gene\_07280.t1,gene\_07918.t1,gene\_09650.t1,gene\_01165.t1,gene\_08457.t1,gene\_09564.t1,gene\_02943.t1,gene\_07144.t1,gene\_03596.t1,gene\_08383.t1,gene\_00110.t1,gene\_07515.t1,gene\_02584.t1,gene\_05351.t1,gene\_01644.t1,gene\_10012.t1,gene\_07362.t1,gene\_09493.t1,gene\_08666.t1,gene\_04673.t1,gene\_08072.t1,gene\_03336.t1,gene\_08911.t1,gene\_00374.t1,gene\_06281.t1,gene\_09393.t1,gene\_01404.t1,gene\_05086.t1,gene\_02802.t1,gene\_06075.t1,gene\_07501.t1, | | integral component of membrane | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0016021 | 1940 | gene\_07988.t1,gene\_03623.t1,gene\_04500.t1,gene\_05487.t1,gene\_06197.t1,gene\_05229.t1,gene\_03316.t1,gene\_02879.t1,gene\_07391.t1,gene\_09441.t1,gene\_08412.t1,gene\_06279.t1,gene\_00090.t1,gene\_09132.t1,gene\_07175.t1,gene\_00278.t1,gene\_03065.t1,gene\_05492.t1,gene\_00790.t1,gene\_09566.t1,gene\_06564.t1,gene\_10085.t1,gene\_03498.t1,gene\_04265.t1,gene\_01153.t1,gene\_08702.t1,gene\_07492.t1,gene\_04703.t1,gene\_00792.t1,gene\_05941.t1,gene\_00385.t1,gene\_09465.t1,gene\_09340.t1,gene\_06822.t1,gene\_05476.t1,gene\_07679.t1,gene\_09550.t1,gene\_02530.t1,gene\_10439.t1,gene\_02961.t1,gene\_03334.t1,gene\_07197.t1,gene\_02234.t1,gene\_02005.t1,gene\_06218.t1,gene\_10388.t1,gene\_09755.t1,gene\_04901.t1,gene\_05520.t1,gene\_05474.t1,gene\_08750.t1,gene\_03218.t1,gene\_05730.t1,gene\_07195.t1,gene\_05243.t1,gene\_09310.t1,gene\_10308.t1,gene\_07624.t1,gene\_01007.t1,gene\_09615.t1,gene\_09658.t1,gene\_05054.t1,gene\_08410.t1,gene\_00476.t1,gene\_04639.t1,gene\_05297.t1,gene\_08178.t1,gene\_05316.t1,gene\_05268.t1,gene\_06264.t1,gene\_01969.t1,gene\_10157.t1,gene\_01638.t1,gene\_06692.t1,gene\_01075.t1,gene\_00892.t1,gene\_09940.t1,gene\_08478.t1,gene\_10055.t1,gene\_06404.t1,gene\_04683.t1,gene\_06152.t1,gene\_06342.t1,gene\_07490.t1,gene\_08689.t1,gene\_05501.t1,gene\_07205.t1,gene\_05616.t1,gene\_03239.t1,gene\_01855.t1,gene\_07187.t1,gene\_08561.t1,gene\_04215.t1,gene\_05448.t1,gene\_02410.t1,gene\_09836.t1,gene\_03031.t1,gene\_06290.t1,gene\_04575.t1,gene\_07756.t1,gene\_09778.t1,gene\_03504.t1,gene\_08258.t1,gene\_04721.t1,gene\_05622.t1,gene\_03794.t1,gene\_03884.t1,gene\_08642.t1,gene\_04304.t1,gene\_09834.t1,gene\_04577.t1,gene\_03223.t1,gene\_09922.t1,gene\_04478.t1,gene\_03506.t1,gene\_01370.t1,gene\_03993.t1,gene\_10423.t1,gene\_02246.t1,gene\_02527.t1,gene\_10101.t1,gene\_02828.t1,gene\_02319.t1,gene\_09984.t1,gene\_09623.t1,gene\_08259.t1,gene\_01082.t1,gene\_09861.t1,gene\_01299.t1,gene\_09105.t1,gene\_04064.t1,gene\_01230.t1,gene\_02147.t1,gene\_04634.t1,gene\_04679.t1,gene\_09431.t1,gene\_01945.t1,gene\_06487.t1,gene\_02130.t1,gene\_09471.t1,gene\_06183.t1,gene\_05143.t1,gene\_02532.t1,gene\_05744.t1,gene\_04887.t1,gene\_06813.t1,gene\_06010.t1,gene\_06424.t1,gene\_08859.t1,gene\_09240.t1,gene\_09800.t1,gene\_07674.t1,gene\_10434.t1,gene\_10081.t1,gene\_04991.t1,gene\_01925.t1,gene\_07594.t1,gene\_08598.t1,gene\_00243.t1,gene\_02081.t1,gene\_05746.t1,gene\_01986.t1,gene\_08449.t1,gene\_08223.t1,gene\_08263.t1,gene\_02343.t1,gene\_08216.t1,gene\_06238.t1,gene\_08839.t1,gene\_07629.t1,gene\_10288.t1,gene\_08359.t1,gene\_04584.t1,gene\_05670.t1,gene\_01494.t1,gene\_10563.t1,gene\_01689.t1,gene\_08876.t1,gene\_06937.t1,gene\_07966.t1, | | integral component of membrane | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0016021 | 1940 | gene\_07125.t1,gene\_07223.t1,gene\_02876.t1,gene\_01178.t1,gene\_10274.t1,gene\_00670.t1,gene\_00127.t1,gene\_06272.t1,gene\_01496.t1,gene\_09798.t1,gene\_04073.t1,gene\_03816.t1,gene\_09369.t1,gene\_02407.t1,gene\_04473.t1,gene\_00316.t1,gene\_02680.t1,gene\_02236.t1,gene\_10650.t1,gene\_08741.t1,gene\_01304.t1,gene\_06190.t1,gene\_03545.t1,gene\_03570.t1,gene\_06048.t1,gene\_06538.t1,gene\_09159.t1,gene\_06421.t1,gene\_00197.t1,gene\_00570.t1,gene\_00777.t1,gene\_03430.t1,gene\_10052.t1,gene\_03572.t1,gene\_05939.t1,gene\_07485.t1,gene\_01584.t1,gene\_02070.t1,gene\_06680.t1,gene\_00195.t1,gene\_05461.t1,gene\_06671.t1,gene\_04968.t1,gene\_02397.t1,gene\_01447.t1,gene\_04552.t1,gene\_04521.t1,gene\_09901.t1,gene\_09786.t1,gene\_03177.t1,gene\_09811.t1,gene\_05982.t1,gene\_02093.t1,gene\_03333.t1,gene\_02024.t1,gene\_06748.t1,gene\_05296.t1,gene\_02191.t1,gene\_07727.t1,gene\_04274.t1,gene\_01445.t1,gene\_02663.t1,gene\_04550.t1,gene\_09455.t1,gene\_09129.t1,gene\_08219.t1,gene\_01747.t1,gene\_08065.t1,gene\_04734.t1,gene\_03796.t1,gene\_09257.t1,gene\_02193.t1,gene\_00290.t1,gene\_06968.t1,gene\_01116.t1,gene\_00553.t1,gene\_06305.t1,gene\_06715.t1,gene\_03648.t1,gene\_08498.t1,gene\_07556.t1,gene\_03412.t1,gene\_10006.t1,gene\_06509.t1,gene\_02848.t1,gene\_06525.t1,gene\_00459.t1,gene\_05727.t1,gene\_02458.t1,gene\_01794.t1,gene\_00679.t1,gene\_09651.t1,gene\_01468.t1,gene\_07099.t1,gene\_02624.t1,gene\_05561.t1,gene\_09545.t1,gene\_04126.t1,gene\_00461.t1,gene\_07874.t1,gene\_02299.t1,gene\_00575.t1,gene\_07463.t1,gene\_07423.t1,gene\_06485.t1,gene\_03783.t1,gene\_03470.t1,gene\_00797.t1,gene\_00577.t1,gene\_02248.t1,gene\_04100.t1,gene\_05419.t1,gene\_06017.t1,gene\_02979.t1,gene\_07832.t1,gene\_07019.t1,gene\_06898.t1,gene\_10258.t1,gene\_10004.t1,gene\_08143.t1,gene\_03093.t1,gene\_05836.t1,gene\_07691.t1,gene\_02896.t1,gene\_00662.t1,gene\_02368.t1,gene\_00277.t1,gene\_01101.t1,gene\_03282.t1,gene\_00063.t1,gene\_05191.t1,gene\_02812.t1,gene\_03211.t1,gene\_06655.t1,gene\_09913.t1,gene\_05437.t1,gene\_10658.t1,gene\_02745.t1,gene\_00262.t1,gene\_02421.t1,gene\_09026.t1,gene\_02461.t1,gene\_08558.t1,gene\_05158.t1,gene\_05186.t1,gene\_07955.t1,gene\_02774.t1,gene\_01367.t1,gene\_04672.t1,gene\_05705.t1,gene\_09371.t1,gene\_10624.t1,gene\_09330.t1,gene\_10018.t1,gene\_02313.t1,gene\_06626.t1,gene\_01186.t1,gene\_10121.t1,gene\_01365.t1,gene\_09948.t1,gene\_03947.t1,gene\_04752.t1,gene\_01260.t1,gene\_05216.t1,gene\_09124.t1,gene\_01120.t1,gene\_05833.t1,gene\_09089.t1,gene\_00360.t1,gene\_02976.t1,gene\_05549.t1,gene\_08472.t1,gene\_03691.t1,gene\_04372.t1,gene\_05300.t1,gene\_10665.t1,gene\_10578.t1,gene\_07176.t1,gene\_00830.t1,gene\_00328.t1, | | integral component of membrane | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0016021 | 1940 | gene\_07206.t1,gene\_06385.t1,gene\_06042.t1,gene\_09398.t1,gene\_07044.t1,gene\_05137.t1,gene\_08252.t1,gene\_04773.t1,gene\_02504.t1,gene\_04280.t1,gene\_05387.t1,gene\_09661.t1,gene\_04456.t1,gene\_01672.t1,gene\_02641.t1,gene\_03263.t1,gene\_10643.t1,gene\_10282.t1,gene\_05271.t1,gene\_01572.t1,gene\_00717.t1,gene\_06987.t1,gene\_03693.t1,gene\_04494.t1,gene\_06357.t1,gene\_07440.t1,gene\_09216.t1,gene\_07817.t1,gene\_00629.t1,gene\_03298.t1,gene\_05509.t1,gene\_03577.t1,gene\_05596.t1,gene\_03422.t1,gene\_02172.t1,gene\_03437.t1,gene\_01748.t1,gene\_06355.t1,gene\_00886.t1,gene\_05135.t1,gene\_00870.t1,gene\_10418.t1,gene\_04017.t1,gene\_07720.t1,gene\_08151.t1,gene\_02214.t1,gene\_08880.t1,gene\_04544.t1,gene\_01818.t1,gene\_06410.t1,gene\_08803.t1,gene\_03948.t1,gene\_03820.t1,gene\_07413.t1,gene\_07259.t1,gene\_09458.t1,gene\_10641.t1,gene\_02392.t1,gene\_04814.t1,gene\_08206.t1,gene\_00672.t1,gene\_08729.t1,gene\_07633.t1,gene\_02196.t1,gene\_07675.t1,gene\_02296.t1,gene\_10435.t1,gene\_10190.t1,gene\_08425.t1,gene\_10661.t1,gene\_04622.t1,gene\_04112.t1,gene\_06578.t1,gene\_07511.t1,gene\_05294.t1,gene\_10673.t1,gene\_05997.t1,gene\_01103.t1,gene\_04031.t1,gene\_02131.t1,gene\_01693.t1,gene\_05553.t1,gene\_06502.t1,gene\_08847.t1,gene\_03365.t1,gene\_01823.t1,gene\_03593.t1,gene\_09248.t1,gene\_09808.t1,gene\_02658.t1,gene\_10249.t1,gene\_10059.t1,gene\_04222.t1,gene\_03923.t1,gene\_00327.t1,gene\_06398.t1,gene\_05604.t1,gene\_02907.t1,gene\_08866.t1,gene\_02221.t1,gene\_09967.t1,gene\_06851.t1,gene\_04349.t1,gene\_09482.t1,gene\_10362.t1,gene\_05032.t1,gene\_10132.t1,gene\_09348.t1,gene\_03636.t1,gene\_06199.t1,gene\_09943.t1,gene\_08615.t1,gene\_06539.t1,gene\_00730.t1,gene\_06590.t1,gene\_07858.t1,gene\_08461.t1,gene\_00745.t1,gene\_02928.t1,gene\_09772.t1,gene\_04922.t1,gene\_02646.t1,gene\_03725.t1,gene\_01708.t1,gene\_00607.t1,gene\_00758.t1,gene\_08681.t1,gene\_06843.t1,gene\_04628.t1,gene\_00778.t1,gene\_04115.t1,gene\_05193.t1,gene\_09172.t1,gene\_09343.t1,gene\_03250.t1,gene\_08189.t1,gene\_05653.t1,gene\_05494.t1,gene\_05823.t1,gene\_01144.t1,gene\_02543.t1,gene\_09403.t1,gene\_10497.t1,gene\_10615.t1,gene\_08496.t1,gene\_07089.t1,gene\_05144.t1,gene\_00179.t1,gene\_02541.t1,gene\_01191.t1,gene\_06352.t1,gene\_01159.t1,gene\_05978.t1,gene\_09573.t1,gene\_06518.t1,gene\_04768.t1,gene\_10475.t1,gene\_00975.t1,gene\_10554.t1,gene\_07043.t1,gene\_00285.t1,gene\_03354.t1,gene\_00188.t1,gene\_06324.t1,gene\_02025.t1,gene\_07504.t1,gene\_10021.t1,gene\_10442.t1,gene\_00637.t1,gene\_08129.t1,gene\_00377.t1,gene\_04273.t1,gene\_10631.t1,gene\_10564.t1,gene\_02655.t1,gene\_00292.t1,gene\_03669.t1,gene\_09670.t1,gene\_01291.t1,gene\_10013.t1, | | integral component of membrane | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0016021 | 1940 | gene\_10461.t1,gene\_07384.t1,gene\_07470.t1,gene\_04379.t1,gene\_09539.t1,gene\_00783.t1,gene\_09010.t1,gene\_05486.t1,gene\_00769.t1,gene\_10410.t1,gene\_09200.t1,gene\_05491.t1,gene\_02784.t1,gene\_10339.t1,gene\_07390.t1,gene\_07247.t1,gene\_08415.t1,gene\_02385.t1,gene\_04369.t1,gene\_09880.t1,gene\_08791.t1,gene\_05583.t1,gene\_00624.t1,gene\_05543.t1,gene\_06176.t1,gene\_02940.t1,gene\_04297.t1,gene\_01470.t1,gene\_04447.t1,gene\_01569.t1,gene\_04417.t1,gene\_07877.t1,gene\_02233.t1,gene\_08211.t1,gene\_07954.t1,gene\_06852.t1,gene\_02673.t1,gene\_00437.t1,gene\_05603.t1,gene\_07196.t1,gene\_07562.t1,gene\_04308.t1,gene\_08325.t1,gene\_08832.t1,gene\_00185.t1,gene\_03380.t1,gene\_03135.t1,gene\_07268.t1,gene\_00756.t1,gene\_03516.t1,gene\_01118.t1,gene\_01006.t1,gene\_03918.t1,gene\_04144.t1,gene\_02415.t1,gene\_04385.t1,gene\_07068.t1,gene\_01931.t1,gene\_09904.t1,gene\_06869.t1,gene\_10378.t1,gene\_02109.t1,gene\_07016.t1,gene\_04110.t1,gene\_06043.t1,gene\_00167.t1,gene\_04711.t1,gene\_09463.t1,gene\_05009.t1,gene\_10391.t1 | | integral component of membrane | cellular\_component |
| GO:0016020 | 60 | gene\_02601.t1,gene\_02859.t1,gene\_00268.t1,gene\_02046.t1,gene\_05393.t1,gene\_07871.t1,gene\_04060.t1,gene\_03232.t1,gene\_05369.t1,gene\_10310.t1,gene\_08045.t1,gene\_08623.t1,gene\_03601.t1,gene\_08395.t1,gene\_10269.t1,gene\_10480.t1,gene\_03932.t1,gene\_10098.t1,gene\_04188.t1,gene\_04152.t1,gene\_05672.t1,gene\_01271.t1,gene\_05913.t1,gene\_06068.t1,gene\_08160.t1,gene\_02853.t1,gene\_02045.t1,gene\_09945.t1,gene\_03881.t1,gene\_00375.t1,gene\_08417.t1,gene\_08332.t1,gene\_03259.t1,gene\_04196.t1,gene\_07978.t1,gene\_06526.t1,gene\_00367.t1,gene\_02690.t1,gene\_01020.t1,gene\_06399.t1,gene\_07909.t1,gene\_07605.t1,gene\_08040.t1,gene\_02165.t1,gene\_02817.t1,gene\_08680.t1,gene\_02861.t1,gene\_08398.t1,gene\_07477.t1,gene\_03192.t1,gene\_06333.t1,gene\_07456.t1,gene\_03121.t1,gene\_09873.t1,gene\_05146.t1,gene\_09555.t1,gene\_07272.t1,gene\_06364.t1,gene\_02125.t1,gene\_03925.t1 | | membrane | cellular\_component |
| GO:1990071 | 2 | gene\_05460.t1,gene\_08887.t1 | | TRAPPII protein complex | cellular\_component |
| GO:0043231 | 5 | gene\_00624.t1,gene\_06125.t1,gene\_00873.t1,gene\_10607.t1,gene\_04096.t1 | | intracellular membrane-bounded organelle | cellular\_component |
| GO:0034066 | 1 | gene\_05393.t1 | | Ric1-Rgp1 guanyl-nucleotide exchange factor complex | cellular\_component |
| GO:0005643 | 15 | gene\_01652.t1,gene\_05468.t1,gene\_01229.t1,gene\_06461.t1,gene\_09280.t1,gene\_01090.t1,gene\_10042.t1,gene\_08865.t1,gene\_08499.t1,gene\_09312.t1,gene\_08808.t1,gene\_09198.t1,gene\_05611.t1,gene\_00349.t1,gene\_07017.t1 | | nuclear pore | cellular\_component |
| GO:0009316 | 1 | gene\_07021.t1 | | 3-isopropylmalate dehydratase complex | cellular\_component |
| GO:0031305 | 4 | gene\_05977.t1,gene\_04131.t1,gene\_02006.t1,gene\_09298.t1 | | integral component of mitochondrial inner membrane | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0031307 | 3 | gene\_04067.t1,gene\_03755.t1,gene\_06112.t1 | | integral component of mitochondrial outer membrane | cellular\_component |
| GO:0002189 | 2 | gene\_10016.t1,gene\_09154.t1 | | ribose phosphate diphosphokinase complex | cellular\_component |
| GO:0098826 | 1 | gene\_03397.t1 | | endoplasmic reticulum tubular network membrane | cellular\_component |
| GO:0089701 | 1 | gene\_02268.t1 | | U2AF complex | cellular\_component |
| GO:0000922 | 6 | gene\_06203.t1,gene\_08722.t1,gene\_07037.t1,gene\_10487.t1,gene\_05691.t1,gene\_08161.t1 | | spindle pole | cellular\_component |
| GO:0032153 | 1 | gene\_09686.t1 | | cell division site | cellular\_component |
| GO:0033551 | 1 | gene\_01264.t1 | | monopolin complex | cellular\_component |
| GO:0033557 | 2 | gene\_07889.t1,gene\_02787.t1 | | Slx1-Slx4 complex | cellular\_component |
| GO:0016272 | 6 | gene\_10136.t1,gene\_05558.t1,gene\_01918.t1,gene\_01533.t1,gene\_03193.t1,gene\_03178.t1 | | prefoldin complex | cellular\_component |
| GO:0043229 | 7 | gene\_03892.t1,gene\_04224.t1,gene\_04547.t1,gene\_09728.t1,gene\_07602.t1,gene\_09992.t1,gene\_02322.t1 | | intracellular organelle | cellular\_component |
| GO:0043227 | 1 | gene\_09833.t1 | | membrane-bounded organelle | cellular\_component |
| GO:0043226 | 1 | gene\_05146.t1 | | organelle | cellular\_component |
| GO:0016471 | 1 | gene\_08358.t1 | | vacuolar proton-transporting V-type ATPase complex | cellular\_component |
| GO:0110165 | 27 | gene\_05853.t1,gene\_05964.t1,gene\_06273.t1,gene\_02888.t1,gene\_05327.t1,gene\_02917.t1,gene\_02613.t1,gene\_03186.t1,gene\_09239.t1,gene\_07801.t1,gene\_04294.t1,gene\_07324.t1,gene\_10617.t1,gene\_00303.t1,gene\_09928.t1,gene\_00269.t1,gene\_03757.t1,gene\_03071.t1,gene\_08053.t1,gene\_05377.t1,gene\_05666.t1,gene\_08075.t1,gene\_02694.t1,gene\_06024.t1,gene\_08363.t1,gene\_05956.t1,gene\_07387.t1 | | cellular anatomical entity | cellular\_component |
| GO:0097255 | 2 | gene\_00682.t1,gene\_10008.t1 | | R2TP complex | cellular\_component |
| GO:0033178 | 1 | gene\_00893.t1 | | proton-transporting two-sector ATPase complex, catalytic domain | cellular\_component |
| GO:0035658 | 1 | gene\_02436.t1 | | Mon1-Ccz1 complex | cellular\_component |
| GO:0031932 | 5 | gene\_07621.t1,gene\_10315.t1,gene\_00561.t1,gene\_04143.t1,gene\_05323.t1 | | TORC2 complex | cellular\_component |
| GO:0005637 | 2 | gene\_03593.t1,gene\_02440.t1 | | nuclear inner membrane | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0005634 | 837 | gene\_09759.t1,gene\_06503.t1,gene\_07620.t1,gene\_05739.t1,gene\_09809.t1,gene\_10558.t1,gene\_08174.t1,gene\_07038.t1,gene\_02699.t1,gene\_02002.t1,gene\_06706.t1,gene\_08500.t1,gene\_07165.t1,gene\_08595.t1,gene\_10265.t1,gene\_09457.t1,gene\_04873.t1,gene\_02977.t1,gene\_01958.t1,gene\_03228.t1,gene\_06172.t1,gene\_02023.t1,gene\_05976.t1,gene\_01625.t1,gene\_10492.t1,gene\_00353.t1,gene\_01065.t1,gene\_02178.t1,gene\_10022.t1,gene\_05425.t1,gene\_09939.t1,gene\_04045.t1,gene\_07960.t1,gene\_07736.t1,gene\_03544.t1,gene\_06913.t1,gene\_06394.t1,gene\_05277.t1,gene\_07673.t1,gene\_04251.t1,gene\_07105.t1,gene\_10319.t1,gene\_00562.t1,gene\_02847.t1,gene\_02232.t1,gene\_08694.t1,gene\_06819.t1,gene\_09930.t1,gene\_08746.t1,gene\_05717.t1,gene\_00595.t1,gene\_06909.t1,gene\_09549.t1,gene\_08063.t1,gene\_04594.t1,gene\_06856.t1,gene\_07003.t1,gene\_06252.t1,gene\_03740.t1,gene\_07166.t1,gene\_00052.t1,gene\_03342.t1,gene\_04524.t1,gene\_04970.t1,gene\_05168.t1,gene\_07316.t1,gene\_01394.t1,gene\_06864.t1,gene\_10351.t1,gene\_09767.t1,gene\_04933.t1,gene\_09164.t1,gene\_10494.t1,gene\_01025.t1,gene\_05527.t1,gene\_09993.t1,gene\_01864.t1,gene\_06392.t1,gene\_09338.t1,gene\_09546.t1,gene\_04014.t1,gene\_01922.t1,gene\_03104.t1,gene\_06866.t1,gene\_06327.t1,gene\_04656.t1,gene\_02107.t1,gene\_00675.t1,gene\_05883.t1,gene\_01856.t1,gene\_02187.t1,gene\_08645.t1,gene\_02334.t1,gene\_04473.t1,gene\_05445.t1,gene\_06230.t1,gene\_09277.t1,gene\_05786.t1,gene\_00614.t1,gene\_06132.t1,gene\_00689.t1,gene\_09720.t1,gene\_05962.t1,gene\_02788.t1,gene\_08006.t1,gene\_00822.t1,gene\_00412.t1,gene\_04263.t1,gene\_02773.t1,gene\_06488.t1,gene\_02151.t1,gene\_05971.t1,gene\_04676.t1,gene\_07356.t1,gene\_05704.t1,gene\_01695.t1,gene\_07343.t1,gene\_03054.t1,gene\_02882.t1,gene\_05624.t1,gene\_05428.t1,gene\_04732.t1,gene\_05913.t1,gene\_03237.t1,gene\_08560.t1,gene\_08795.t1,gene\_00904.t1,gene\_09428.t1,gene\_05383.t1,gene\_10333.t1,gene\_10083.t1,gene\_01688.t1,gene\_00422.t1,gene\_07064.t1,gene\_05810.t1,gene\_03509.t1,gene\_03984.t1,gene\_04445.t1,gene\_00906.t1,gene\_10576.t1,gene\_00882.t1,gene\_04579.t1,gene\_08288.t1,gene\_00652.t1,gene\_09646.t1,gene\_09578.t1,gene\_05862.t1,gene\_08594.t1,gene\_03105.t1,gene\_01857.t1,gene\_08034.t1,gene\_00268.t1,gene\_08703.t1,gene\_04693.t1,gene\_05639.t1,gene\_03599.t1,gene\_03822.t1,gene\_04826.t1,gene\_07229.t1,gene\_06735.t1,gene\_02068.t1,gene\_05458.t1,gene\_07612.t1,gene\_02027.t1,gene\_02321.t1,gene\_05064.t1,gene\_06606.t1,gene\_08479.t1,gene\_09361.t1,gene\_06675.t1,gene\_05087.t1,gene\_02790.t1,gene\_05910.t1,gene\_07299.t1,gene\_04448.t1,gene\_02661.t1,gene\_00770.t1,gene\_06449.t1,gene\_03304.t1,gene\_00362.t1, | | nucleus | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0005634 | 837 | gene\_02253.t1,gene\_03842.t1,gene\_04795.t1,gene\_06456.t1,gene\_09944.t1,gene\_00274.t1,gene\_07840.t1,gene\_07250.t1,gene\_01333.t1,gene\_07241.t1,gene\_03981.t1,gene\_00059.t1,gene\_05907.t1,gene\_07382.t1,gene\_06223.t1,gene\_07333.t1,gene\_04695.t1,gene\_09703.t1,gene\_02367.t1,gene\_06637.t1,gene\_09406.t1,gene\_03210.t1,gene\_00656.t1,gene\_00580.t1,gene\_10104.t1,gene\_10164.t1,gene\_03694.t1,gene\_03101.t1,gene\_00286.t1,gene\_06585.t1,gene\_05455.t1,gene\_01336.t1,gene\_00496.t1,gene\_00883.t1,gene\_01987.t1,gene\_03707.t1,gene\_05373.t1,gene\_09375.t1,gene\_08824.t1,gene\_08608.t1,gene\_02781.t1,gene\_08521.t1,gene\_09585.t1,gene\_02297.t1,gene\_05808.t1,gene\_07377.t1,gene\_07128.t1,gene\_09536.t1,gene\_00556.t1,gene\_04582.t1,gene\_01305.t1,gene\_04840.t1,gene\_06020.t1,gene\_01948.t1,gene\_03579.t1,gene\_05556.t1,gene\_06963.t1,gene\_07290.t1,gene\_07613.t1,gene\_01145.t1,gene\_06978.t1,gene\_05459.t1,gene\_05273.t1,gene\_10281.t1,gene\_01005.t1,gene\_02451.t1,gene\_08218.t1,gene\_06934.t1,gene\_00982.t1,gene\_05814.t1,gene\_10407.t1,gene\_09590.t1,gene\_04918.t1,gene\_02034.t1,gene\_02652.t1,gene\_04182.t1,gene\_09706.t1,gene\_01212.t1,gene\_10663.t1,gene\_01774.t1,gene\_00817.t1,gene\_01718.t1,gene\_04937.t1,gene\_01433.t1,gene\_10557.t1,gene\_05897.t1,gene\_08282.t1,gene\_00587.t1,gene\_06852.t1,gene\_02605.t1,gene\_07932.t1,gene\_09813.t1,gene\_01352.t1,gene\_01887.t1,gene\_05636.t1,gene\_02617.t1,gene\_04013.t1,gene\_06732.t1,gene\_06524.t1,gene\_05627.t1,gene\_01650.t1,gene\_08214.t1,gene\_08477.t1,gene\_04238.t1,gene\_09265.t1,gene\_06584.t1,gene\_02809.t1,gene\_06795.t1,gene\_10553.t1,gene\_05992.t1,gene\_07321.t1,gene\_04208.t1,gene\_09878.t1,gene\_01937.t1,gene\_02318.t1,gene\_01345.t1,gene\_04028.t1,gene\_05141.t1,gene\_09748.t1,gene\_08833.t1,gene\_07955.t1,gene\_01705.t1,gene\_05517.t1,gene\_07742.t1,gene\_04179.t1,gene\_00138.t1,gene\_04158.t1,gene\_03595.t1,gene\_09756.t1,gene\_03799.t1,gene\_05348.t1,gene\_10151.t1,gene\_10666.t1,gene\_06114.t1,gene\_08071.t1,gene\_08324.t1,gene\_00356.t1,gene\_03831.t1,gene\_06309.t1,gene\_02776.t1,gene\_04398.t1,gene\_00986.t1,gene\_05568.t1,gene\_03650.t1,gene\_09824.t1,gene\_07353.t1,gene\_04621.t1,gene\_00046.t1,gene\_06622.t1,gene\_10279.t1,gene\_00048.t1,gene\_04105.t1,gene\_02607.t1,gene\_07537.t1,gene\_01756.t1,gene\_05595.t1,gene\_02835.t1,gene\_08591.t1,gene\_09572.t1,gene\_09182.t1,gene\_08569.t1,gene\_07164.t1,gene\_02050.t1,gene\_05469.t1,gene\_08699.t1,gene\_09540.t1,gene\_09923.t1,gene\_09339.t1,gene\_04137.t1,gene\_02512.t1,gene\_00803.t1,gene\_03638.t1,gene\_07403.t1,gene\_01529.t1,gene\_06740.t1,gene\_08366.t1,gene\_06031.t1,gene\_09561.t1,gene\_03785.t1,gene\_09879.t1, | | nucleus | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0005634 | 837 | gene\_01621.t1,gene\_09330.t1,gene\_00399.t1,gene\_07320.t1,gene\_07785.t1,gene\_02242.t1,gene\_05559.t1,gene\_05725.t1,gene\_10229.t1,gene\_06009.t1,gene\_09757.t1,gene\_05457.t1,gene\_09025.t1,gene\_06823.t1,gene\_08877.t1,gene\_03642.t1,gene\_00408.t1,gene\_09563.t1,gene\_04307.t1,gene\_06040.t1,gene\_07791.t1,gene\_10355.t1,gene\_09822.t1,gene\_09299.t1,gene\_01014.t1,gene\_08155.t1,gene\_07311.t1,gene\_10172.t1,gene\_05721.t1,gene\_01618.t1,gene\_02119.t1,gene\_07759.t1,gene\_03870.t1,gene\_03107.t1,gene\_02995.t1,gene\_05066.t1,gene\_04902.t1,gene\_03748.t1,gene\_10570.t1,gene\_08299.t1,gene\_09979.t1,gene\_04435.t1,gene\_07707.t1,gene\_05151.t1,gene\_00018.t1,gene\_01954.t1,gene\_06679.t1,gene\_10649.t1,gene\_06339.t1,gene\_03900.t1,gene\_02220.t1,gene\_05741.t1,gene\_09601.t1,gene\_02526.t1,gene\_04241.t1,gene\_09568.t1,gene\_03130.t1,gene\_04257.t1,gene\_02703.t1,gene\_05301.t1,gene\_03864.t1,gene\_03018.t1,gene\_02544.t1,gene\_02328.t1,gene\_05153.t1,gene\_07260.t1,gene\_07085.t1,gene\_02778.t1,gene\_01660.t1,gene\_00330.t1,gene\_03062.t1,gene\_09192.t1,gene\_06059.t1,gene\_10019.t1,gene\_01692.t1,gene\_05311.t1,gene\_09733.t1,gene\_06936.t1,gene\_04976.t1,gene\_01712.t1,gene\_09542.t1,gene\_02170.t1,gene\_10058.t1,gene\_03295.t1,gene\_07730.t1,gene\_09848.t1,gene\_08074.t1,gene\_10254.t1,gene\_08254.t1,gene\_07525.t1,gene\_01390.t1,gene\_09126.t1,gene\_03047.t1,gene\_05121.t1,gene\_08388.t1,gene\_09460.t1,gene\_05664.t1,gene\_07677.t1,gene\_03610.t1,gene\_04176.t1,gene\_05796.t1,gene\_04979.t1,gene\_08753.t1,gene\_07168.t1,gene\_10543.t1,gene\_03606.t1,gene\_02486.t1,gene\_00257.t1,gene\_00959.t1,gene\_03712.t1,gene\_00308.t1,gene\_02317.t1,gene\_00564.t1,gene\_07726.t1,gene\_03800.t1,gene\_06709.t1,gene\_00505.t1,gene\_09865.t1,gene\_01527.t1,gene\_02375.t1,gene\_08484.t1,gene\_05950.t1,gene\_01223.t1,gene\_03132.t1,gene\_10047.t1,gene\_07693.t1,gene\_02356.t1,gene\_00911.t1,gene\_09702.t1,gene\_06255.t1,gene\_07827.t1,gene\_06171.t1,gene\_05685.t1,gene\_01715.t1,gene\_00538.t1,gene\_05884.t1,gene\_00363.t1,gene\_03427.t1,gene\_06102.t1,gene\_09867.t1,gene\_02992.t1,gene\_08135.t1,gene\_04004.t1,gene\_07628.t1,gene\_01982.t1,gene\_04627.t1,gene\_05640.t1,gene\_10205.t1,gene\_07635.t1,gene\_08083.t1,gene\_02523.t1,gene\_05154.t1,gene\_08626.t1,gene\_07992.t1,gene\_07948.t1,gene\_06089.t1,gene\_08550.t1,gene\_04830.t1,gene\_01535.t1,gene\_03812.t1,gene\_04854.t1,gene\_01135.t1,gene\_00640.t1,gene\_07583.t1,gene\_08663.t1,gene\_02387.t1,gene\_01819.t1,gene\_09814.t1,gene\_04669.t1,gene\_09957.t1,gene\_01911.t1,gene\_02668.t1,gene\_06517.t1,gene\_02916.t1,gene\_04048.t1,gene\_10137.t1,gene\_09235.t1,gene\_08947.t1,gene\_09656.t1,gene\_04128.t1, | | nucleus | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0005634 | 837 | gene\_04459.t1,gene\_09635.t1,gene\_02529.t1,gene\_05747.t1,gene\_09485.t1,gene\_10188.t1,gene\_09370.t1,gene\_06885.t1,gene\_01742.t1,gene\_06249.t1,gene\_00256.t1,gene\_02757.t1,gene\_05547.t1,gene\_03994.t1,gene\_03655.t1,gene\_04313.t1,gene\_07010.t1,gene\_08483.t1,gene\_03979.t1,gene\_10374.t1,gene\_06258.t1,gene\_00732.t1,gene\_09036.t1,gene\_06291.t1,gene\_02554.t1,gene\_06417.t1,gene\_01262.t1,gene\_08890.t1,gene\_02946.t1,gene\_00747.t1,gene\_01321.t1,gene\_09131.t1,gene\_06377.t1,gene\_01359.t1,gene\_07284.t1,gene\_00847.t1,gene\_03869.t1,gene\_05152.t1,gene\_06457.t1,gene\_09266.t1,gene\_07670.t1,gene\_05811.t1,gene\_03248.t1,gene\_03741.t1,gene\_01095.t1,gene\_06330.t1,gene\_04645.t1,gene\_01156.t1,gene\_06095.t1,gene\_08280.t1,gene\_03747.t1,gene\_05070.t1,gene\_01310.t1,gene\_01377.t1,gene\_04922.t1,gene\_01134.t1,gene\_01226.t1,gene\_01708.t1,gene\_04946.t1,gene\_06766.t1,gene\_06073.t1,gene\_05932.t1,gene\_07851.t1,gene\_05015.t1,gene\_02110.t1,gene\_10003.t1,gene\_03163.t1,gene\_08488.t1,gene\_10056.t1,gene\_06870.t1,gene\_06365.t1,gene\_03123.t1,gene\_03786.t1,gene\_09915.t1,gene\_03450.t1,gene\_08300.t1,gene\_09935.t1,gene\_04049.t1,gene\_07890.t1,gene\_06145.t1,gene\_03596.t1,gene\_08513.t1,gene\_03581.t1,gene\_05048.t1,gene\_09412.t1,gene\_01714.t1,gene\_00968.t1,gene\_03118.t1,gene\_09261.t1,gene\_08966.t1,gene\_09195.t1,gene\_07755.t1,gene\_00727.t1,gene\_01651.t1,gene\_03682.t1,gene\_01942.t1,gene\_10237.t1,gene\_09038.t1,gene\_04378.t1,gene\_06720.t1,gene\_07623.t1,gene\_07271.t1,gene\_04651.t1,gene\_01679.t1,gene\_04706.t1,gene\_00182.t1,gene\_01524.t1,gene\_06395.t1,gene\_09652.t1,gene\_08345.t1,gene\_02241.t1,gene\_09268.t1,gene\_02228.t1,gene\_00867.t1,gene\_03513.t1,gene\_07282.t1,gene\_04650.t1,gene\_00908.t1,gene\_08055.t1,gene\_09697.t1,gene\_10433.t1,gene\_03447.t1,gene\_02098.t1,gene\_06719.t1,gene\_09584.t1,gene\_05689.t1,gene\_07640.t1,gene\_08029.t1,gene\_02808.t1,gene\_07040.t1,gene\_03050.t1,gene\_09712.t1,gene\_05943.t1,gene\_06532.t1,gene\_02751.t1,gene\_07667.t1,gene\_02657.t1,gene\_01153.t1,gene\_08441.t1,gene\_03784.t1,gene\_01809.t1,gene\_08041.t1,gene\_06446.t1,gene\_03234.t1,gene\_02029.t1,gene\_08291.t1,gene\_06088.t1,gene\_05540.t1,gene\_03408.t1,gene\_08985.t1,gene\_03366.t1,gene\_05998.t1,gene\_05206.t1,gene\_06949.t1,gene\_07683.t1,gene\_04022.t1,gene\_09220.t1,gene\_04081.t1,gene\_02948.t1,gene\_06614.t1,gene\_08341.t1,gene\_02854.t1,gene\_06402.t1,gene\_07750.t1,gene\_05849.t1,gene\_03455.t1,gene\_10255.t1,gene\_01612.t1,gene\_10167.t1,gene\_07639.t1,gene\_01003.t1,gene\_08841.t1,gene\_05736.t1,gene\_05474.t1,gene\_09537.t1,gene\_06697.t1,gene\_07088.t1,gene\_06266.t1,gene\_07355.t1,gene\_04914.t1, | | nucleus | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0005634 | 837 | gene\_02372.t1,gene\_06696.t1,gene\_06972.t1,gene\_05228.t1,gene\_06826.t1,gene\_04481.t1,gene\_05239.t1,gene\_07217.t1,gene\_07474.t1,gene\_10051.t1,gene\_02862.t1,gene\_10211.t1,gene\_04983.t1,gene\_07532.t1,gene\_04730.t1,gene\_02385.t1,gene\_01481.t1,gene\_00395.t1,gene\_04084.t1,gene\_03770.t1,gene\_05402.t1,gene\_02580.t1,gene\_10509.t1,gene\_05970.t1,gene\_01933.t1,gene\_01512.t1,gene\_02786.t1,gene\_08148.t1,gene\_01222.t1,gene\_03761.t1,gene\_10449.t1,gene\_04515.t1,gene\_02282.t1,gene\_03463.t1,gene\_08700.t1,gene\_03863.t1,gene\_02874.t1,gene\_09193.t1,gene\_05299.t1,gene\_07506.t1,gene\_10629.t1,gene\_02910.t1,gene\_03763.t1,gene\_00921.t1,gene\_09262.t1,gene\_10160.t1,gene\_08139.t1,gene\_02042.t1,gene\_06023.t1,gene\_03476.t1,gene\_06515.t1,gene\_01498.t1,gene\_07548.t1,gene\_06225.t1,gene\_07202.t1,gene\_02608.t1,gene\_05588.t1,gene\_02502.t1,gene\_05665.t1,gene\_01436.t1,gene\_04631.t1,gene\_01613.t1,gene\_10614.t1,gene\_04903.t1,gene\_04347.t1,gene\_03884.t1,gene\_09897.t1,gene\_09526.t1,gene\_07352.t1,gene\_04254.t1,gene\_03935.t1,gene\_02207.t1,gene\_09969.t1,gene\_07354.t1,gene\_08867.t1,gene\_03311.t1,gene\_09035.t1,gene\_08344.t1,gene\_02086.t1,gene\_01730.t1,gene\_05898.t1,gene\_07246.t1,gene\_02698.t1,gene\_06672.t1,gene\_03607.t1,gene\_07054.t1,gene\_10498.t1,gene\_08262.t1,gene\_01875.t1,gene\_02270.t1,gene\_04234.t1,gene\_04041.t1,gene\_05805.t1,gene\_06653.t1,gene\_02230.t1,gene\_08062.t1,gene\_03529.t1,gene\_02677.t1,gene\_01998.t1,gene\_02495.t1,gene\_05080.t1,gene\_10216.t1,gene\_00891.t1,gene\_00229.t1,gene\_01530.t1,gene\_05972.t1,gene\_00833.t1,gene\_10602.t1,gene\_00634.t1,gene\_05082.t1,gene\_00992.t1,gene\_09619.t1,gene\_02730.t1,gene\_02783.t1,gene\_04974.t1,gene\_08638.t1,gene\_00812.t1 | | nucleus | cellular\_component |
| GO:0005635 | 1 | gene\_10468.t1 | | nuclear envelope | cellular\_component |
| GO:0009326 | 1 | gene\_09683.t1 | | formate dehydrogenase complex | cellular\_component |
| GO:0000214 | 3 | gene\_04404.t1,gene\_05909.t1,gene\_02939.t1 | | tRNA-intron endonuclease complex | cellular\_component |
| GO:0061617 | 3 | gene\_08793.t1,gene\_05236.t1,gene\_03603.t1 | | MICOS complex | cellular\_component |
| GO:0000407 | 4 | gene\_04192.t1,gene\_06906.t1,gene\_08294.t1,gene\_03673.t1 | | phagophore assembly site | cellular\_component |
| GO:0005742 | 1 | gene\_06545.t1 | | mitochondrial outer membrane translocase complex | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0005743 | 99 | gene\_00014.t1,gene\_06335.t1,gene\_09037.t1,gene\_08646.t1,gene\_00351.t1,gene\_00789.t1,gene\_05086.t1,gene\_00316.t1,gene\_01994.t1,gene\_07616.t1,gene\_07137.t1,gene\_07625.t1,gene\_08864.t1,gene\_04249.t1,gene\_00583.t1,gene\_08412.t1,gene\_06363.t1,gene\_06931.t1,gene\_09108.t1,gene\_09293.t1,gene\_10493.t1,gene\_09356.t1,gene\_10203.t1,gene\_10133.t1,gene\_01021.t1,gene\_01412.t1,gene\_10025.t1,gene\_04538.t1,gene\_00792.t1,gene\_09825.t1,gene\_06034.t1,gene\_01215.t1,gene\_05476.t1,gene\_01057.t1,gene\_01243.t1,gene\_06206.t1,gene\_00870.t1,gene\_07342.t1,gene\_00964.t1,gene\_08196.t1,gene\_05518.t1,gene\_06997.t1,gene\_09821.t1,gene\_07097.t1,gene\_07113.t1,gene\_07345.t1,gene\_04031.t1,gene\_01367.t1,gene\_07247.t1,gene\_06331.t1,gene\_07351.t1,gene\_09613.t1,gene\_03201.t1,gene\_10039.t1,gene\_08818.t1,gene\_02773.t1,gene\_01933.t1,gene\_00788.t1,gene\_04447.t1,gene\_09143.t1,gene\_09260.t1,gene\_02967.t1,gene\_08431.t1,gene\_04542.t1,gene\_03691.t1,gene\_07499.t1,gene\_01713.t1,gene\_00118.t1,gene\_08052.t1,gene\_07330.t1,gene\_08217.t1,gene\_07206.t1,gene\_01409.t1,gene\_03980.t1,gene\_08413.t1,gene\_04080.t1,gene\_01230.t1,gene\_03782.t1,gene\_07239.t1,gene\_01197.t1,gene\_02504.t1,gene\_05068.t1,gene\_02370.t1,gene\_02936.t1,gene\_04277.t1,gene\_10382.t1,gene\_00609.t1,gene\_01931.t1,gene\_05391.t1,gene\_01635.t1,gene\_02201.t1,gene\_00749.t1,gene\_05326.t1,gene\_08961.t1,gene\_00717.t1,gene\_09057.t1,gene\_00091.t1,gene\_06328.t1,gene\_02120.t1 | | mitochondrial inner membrane | cellular\_component |
| GO:0005741 | 10 | gene\_08164.t1,gene\_07093.t1,gene\_06489.t1,gene\_08866.t1,gene\_06104.t1,gene\_00322.t1,gene\_09709.t1,gene\_02644.t1,gene\_03586.t1,gene\_08669.t1 | | mitochondrial outer membrane | cellular\_component |
| GO:0005747 | 2 | gene\_09270.t1,gene\_06779.t1 | | mitochondrial respiratory chain complex I | cellular\_component |
| GO:0005744 | 3 | gene\_06037.t1,gene\_00476.t1,gene\_02807.t1 | | TIM23 mitochondrial import inner membrane translocase complex | cellular\_component |
| GO:0000408 | 1 | gene\_09601.t1 | | EKC/KEOPS complex | cellular\_component |
| GO:0031201 | 1 | gene\_04059.t1 | | SNARE complex | cellular\_component |
| GO:0070824 | 1 | gene\_01639.t1 | | SHREC complex | cellular\_component |
| GO:0033573 | 1 | gene\_05743.t1 | | high-affinity iron permease complex | cellular\_component |
| GO:1990334 | 1 | gene\_04154.t1 | | Bfa1-Bub2 complex | cellular\_component |
| GO:0008278 | 3 | gene\_07202.t1,gene\_09867.t1,gene\_00812.t1 | | cohesin complex | cellular\_component |
| GO:0032300 | 5 | gene\_09396.t1,gene\_03237.t1,gene\_00205.t1,gene\_05849.t1,gene\_03576.t1 | | mismatch repair complex | cellular\_component |
| GO:0071986 | 1 | gene\_03887.t1 | | Ragulator complex | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0030896 | 2 | gene\_09512.t1,gene\_00573.t1 | | checkpoint clamp complex | cellular\_component |
| GO:0046540 | 5 | gene\_05450.t1,gene\_08685.t1,gene\_02231.t1,gene\_06070.t1,gene\_02996.t1 | | U4/U6 x U5 tri-snRNP complex | cellular\_component |
| GO:0048500 | 1 | gene\_05782.t1 | | signal recognition particle | cellular\_component |
| GO:0015934 | 7 | gene\_01094.t1,gene\_07081.t1,gene\_02167.t1,gene\_02536.t1,gene\_03987.t1,gene\_03269.t1,gene\_05166.t1 | | large ribosomal subunit | cellular\_component |
| GO:0015935 | 10 | gene\_06639.t1,gene\_00520.t1,gene\_02965.t1,gene\_04098.t1,gene\_04719.t1,gene\_08396.t1,gene\_06717.t1,gene\_10532.t1,gene\_06874.t1,gene\_02865.t1 | | small ribosomal subunit | cellular\_component |
| GO:0043625 | 1 | gene\_06340.t1 | | delta DNA polymerase complex | cellular\_component |
| GO:0033167 | 1 | gene\_05887.t1 | | ARC complex | cellular\_component |
| GO:0009331 | 2 | gene\_00708.t1,gene\_05158.t1 | | glycerol-3-phosphate dehydrogenase complex | cellular\_component |
| GO:0000262 | 1 | gene\_00455.t1 | | mitochondrial chromosome | cellular\_component |
| GO:0000228 | 2 | gene\_06320.t1,gene\_09322.t1 | | nuclear chromosome | cellular\_component |
| GO:0005751 | 5 | gene\_00354.t1,gene\_07269.t1,gene\_02781.t1,gene\_08159.t1,gene\_08418.t1 | | mitochondrial respiratory chain complex IV | cellular\_component |
| GO:0005750 | 4 | gene\_10111.t1,gene\_00585.t1,gene\_08819.t1,gene\_03982.t1 | | mitochondrial respiratory chain complex III | cellular\_component |
| GO:0031213 | 1 | gene\_10140.t1 | | RSF complex | cellular\_component |
| GO:0022627 | 2 | gene\_09278.t1,gene\_09004.t1 | | cytosolic small ribosomal subunit | cellular\_component |
| GO:0022625 | 5 | gene\_01160.t1,gene\_10484.t1,gene\_05521.t1,gene\_08101.t1,gene\_00519.t1 | | cytosolic large ribosomal subunit | cellular\_component |
| GO:0070939 | 1 | gene\_05676.t1 | | Dsl1/NZR complex | cellular\_component |
| GO:0044322 | 1 | gene\_08332.t1 | | endoplasmic reticulum quality control compartment | cellular\_component |
| GO:0043529 | 1 | gene\_09348.t1 | | GET complex | cellular\_component |
| GO:0070449 | 1 | gene\_01140.t1 | | elongin complex | cellular\_component |
| GO:0030880 | 1 | gene\_07165.t1 | | RNA polymerase complex | cellular\_component |
| GO:0030956 | 2 | gene\_02324.t1,gene\_05707.t1 | | glutamyl-tRNA(Gln) amidotransferase complex | cellular\_component |
| GO:0044666 | 1 | gene\_04242.t1 | | MLL3/4 complex | cellular\_component |
| GO:0005615 | 3 | gene\_03322.t1,gene\_00430.t1,gene\_07700.t1 | | extracellular space | cellular\_component |
| GO:0005965 | 1 | gene\_04040.t1 | | protein farnesyltransferase complex | cellular\_component |
| GO:0005968 | 2 | gene\_09996.t1,gene\_08511.t1 | | Rab-protein geranylgeranyltransferase complex | cellular\_component |
| GO:0000275 | 1 | gene\_01754.t1 | | mitochondrial proton-transporting ATP synthase complex, catalytic sector F(1) | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0000276 | 6 | gene\_03015.t1,gene\_00267.t1,gene\_09826.t1,gene\_09484.t1,gene\_05980.t1,gene\_06648.t1 | | mitochondrial proton-transporting ATP synthase complex, coupling factor F(o) | cellular\_component |
| GO:0005960 | 1 | gene\_03285.t1 | | glycine cleavage complex | cellular\_component |
| GO:0032156 | 4 | gene\_04255.t1,gene\_07936.t1,gene\_08232.t1,gene\_05165.t1 | | septin cytoskeleton | cellular\_component |
| GO:0030532 | 1 | gene\_08528.t1 | | small nuclear ribonucleoprotein complex | cellular\_component |
| GO:0097344 | 1 | gene\_00904.t1 | | Rix1 complex | cellular\_component |
| GO:0005760 | 1 | gene\_06076.t1 | | gamma DNA polymerase complex | cellular\_component |
| GO:0005761 | 1 | gene\_07006.t1 | | mitochondrial ribosome | cellular\_component |
| GO:0005762 | 4 | gene\_04425.t1,gene\_02843.t1,gene\_10426.t1,gene\_03497.t1 | | mitochondrial large ribosomal subunit | cellular\_component |
| GO:0005763 | 1 | gene\_00365.t1 | | mitochondrial small ribosomal subunit | cellular\_component |
| GO:0005768 | 3 | gene\_08574.t1,gene\_03580.t1,gene\_09100.t1 | | endosome | cellular\_component |
| GO:0031262 | 3 | gene\_05897.t1,gene\_05168.t1,gene\_08632.t1 | | Ndc80 complex | cellular\_component |
| GO:0031261 | 6 | gene\_00515.t1,gene\_01710.t1,gene\_01540.t1,gene\_07862.t1,gene\_08245.t1,gene\_09071.t1 | | DNA replication preinitiation complex | cellular\_component |
| GO:0031461 | 2 | gene\_08525.t1,gene\_09768.t1 | | cullin-RING ubiquitin ligase complex | cellular\_component |
| GO:0000015 | 2 | gene\_00524.t1,gene\_02419.t1 | | phosphopyruvate hydratase complex | cellular\_component |
| GO:0008250 | 3 | gene\_02904.t1,gene\_01531.t1,gene\_09861.t1 | | oligosaccharyltransferase complex | cellular\_component |
| GO:0070971 | 1 | gene\_09511.t1 | | endoplasmic reticulum exit site | cellular\_component |
| GO:0070603 | 3 | gene\_06320.t1,gene\_09322.t1,gene\_08023.t1 | | SWI/SNF superfamily-type complex | cellular\_component |
| GO:0019005 | 2 | gene\_01746.t1,gene\_02629.t1 | | SCF ubiquitin ligase complex | cellular\_component |
| GO:0019008 | 3 | gene\_06655.t1,gene\_04702.t1,gene\_06930.t1 | | molybdopterin synthase complex | cellular\_component |
| GO:0019773 | 6 | gene\_05689.t1,gene\_09182.t1,gene\_07791.t1,gene\_03863.t1,gene\_09635.t1,gene\_07038.t1 | | proteasome core complex, alpha-subunit complex | cellular\_component |
| GO:0019774 | 2 | gene\_08488.t1,gene\_00399.t1 | | proteasome core complex, beta-subunit complex | cellular\_component |
| GO:0044695 | 1 | gene\_07195.t1 | | Dsc E3 ubiquitin ligase complex | cellular\_component |
| GO:0000808 | 3 | gene\_04582.t1,gene\_07010.t1,gene\_00675.t1 | | origin recognition complex | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0005759 | 29 | gene\_08093.t1,gene\_04289.t1,gene\_04583.t1,gene\_09157.t1,gene\_06742.t1,gene\_09037.t1,gene\_09189.t1,gene\_01424.t1,gene\_07265.t1,gene\_00305.t1,gene\_03687.t1,gene\_03551.t1,gene\_07918.t1,gene\_07649.t1,gene\_07650.t1,gene\_07164.t1,gene\_10181.t1,gene\_09415.t1,gene\_02377.t1,gene\_04355.t1,gene\_03945.t1,gene\_03604.t1,gene\_07917.t1,gene\_07598.t1,gene\_03944.t1,gene\_10389.t1,gene\_01409.t1,gene\_01019.t1,gene\_07351.t1 | | mitochondrial matrix | cellular\_component |
| GO:0032585 | 1 | gene\_03697.t1 | | multivesicular body membrane | cellular\_component |
| GO:0005758 | 11 | gene\_02122.t1,gene\_09260.t1,gene\_04186.t1,gene\_03957.t1,gene\_00454.t1,gene\_07625.t1,gene\_09057.t1,gene\_07113.t1,gene\_10201.t1,gene\_06951.t1,gene\_09293.t1 | | mitochondrial intermembrane space | cellular\_component |
| GO:0005819 | 4 | gene\_10602.t1,gene\_10291.t1,gene\_08710.t1,gene\_01198.t1 | | spindle | cellular\_component |
| GO:0005811 | 3 | gene\_04192.t1,gene\_04414.t1,gene\_04546.t1 | | lipid droplet | cellular\_component |
| GO:0005816 | 6 | gene\_06203.t1,gene\_05213.t1,gene\_08722.t1,gene\_07037.t1,gene\_05691.t1,gene\_08161.t1 | | spindle pole body | cellular\_component |
| GO:0005815 | 3 | gene\_03191.t1,gene\_10242.t1,gene\_07336.t1 | | microtubule organizing center | cellular\_component |
| GO:0033180 | 4 | gene\_07027.t1,gene\_05578.t1,gene\_03967.t1,gene\_07813.t1 | | proton-transporting V-type ATPase, V1 domain | cellular\_component |
| GO:0017119 | 4 | gene\_03232.t1,gene\_10290.t1,gene\_09555.t1,gene\_03259.t1 | | Golgi transport complex | cellular\_component |
| GO:0005854 | 2 | gene\_09485.t1,gene\_10387.t1 | | nascent polypeptide-associated complex | cellular\_component |
| GO:0030430 | 1 | gene\_01789.t1 | | host cell cytoplasm | cellular\_component |
| GO:0046695 | 2 | gene\_05658.t1,gene\_08169.t1 | | SLIK (SAGA-like) complex | cellular\_component |
| GO:0005680 | 8 | gene\_02065.t1,gene\_02001.t1,gene\_05740.t1,gene\_07231.t1,gene\_07822.t1,gene\_07294.t1,gene\_04135.t1,gene\_09747.t1 | | anaphase-promoting complex | cellular\_component |
| GO:0000243 | 1 | gene\_10367.t1 | | commitment complex | cellular\_component |
| GO:0120114 | 3 | gene\_04011.t1,gene\_03682.t1,gene\_07641.t1 | | Sm-like protein family complex | cellular\_component |
| GO:0005779 | 5 | gene\_06344.t1,gene\_03732.t1,gene\_07686.t1,gene\_08176.t1,gene\_06332.t1 | | integral component of peroxisomal membrane | cellular\_component |
| GO:0005778 | 8 | gene\_04177.t1,gene\_03938.t1,gene\_08631.t1,gene\_06038.t1,gene\_03246.t1,gene\_00514.t1,gene\_07529.t1,gene\_07101.t1 | | peroxisomal membrane | cellular\_component |
| GO:0005773 | 4 | gene\_06164.t1,gene\_10590.t1,gene\_01063.t1,gene\_01006.t1 | | vacuole | cellular\_component |
| GO:0005777 | 17 | gene\_10647.t1,gene\_08069.t1,gene\_09140.t1,gene\_10070.t1,gene\_00591.t1,gene\_00341.t1,gene\_10669.t1,gene\_01977.t1,gene\_01253.t1,gene\_03008.t1,gene\_09821.t1,gene\_03068.t1,gene\_08822.t1,gene\_00443.t1,gene\_04430.t1,gene\_06049.t1,gene\_00885.t1 | | peroxisome | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0005776 | 1 | gene\_04192.t1 | | autophagosome | cellular\_component |
| GO:0005775 | 1 | gene\_09898.t1 | | vacuolar lumen | cellular\_component |
| GO:0005774 | 31 | gene\_02072.t1,gene\_01969.t1,gene\_03697.t1,gene\_04805.t1,gene\_01105.t1,gene\_06519.t1,gene\_03004.t1,gene\_06176.t1,gene\_00063.t1,gene\_04999.t1,gene\_01191.t1,gene\_05641.t1,gene\_04122.t1,gene\_03580.t1,gene\_05603.t1,gene\_07597.t1,gene\_08230.t1,gene\_05113.t1,gene\_10658.t1,gene\_01593.t1,gene\_06177.t1,gene\_08284.t1,gene\_03031.t1,gene\_06178.t1,gene\_08766.t1,gene\_01709.t1,gene\_00200.t1,gene\_05271.t1,gene\_08349.t1,gene\_09815.t1,gene\_07033.t1 | | vacuolar membrane | cellular\_component |
| GO:0031902 | 1 | gene\_01280.t1 | | late endosome membrane | cellular\_component |
| GO:0031901 | 1 | gene\_01186.t1 | | early endosome membrane | cellular\_component |
| GO:0031588 | 1 | gene\_09602.t1 | | nucleotide-activated protein kinase complex | cellular\_component |
| GO:0005875 | 1 | gene\_10487.t1 | | microtubule associated complex | cellular\_component |
| GO:0055029 | 4 | gene\_02194.t1,gene\_09612.t1,gene\_03951.t1,gene\_03523.t1 | | nuclear DNA-directed RNA polymerase complex | cellular\_component |
| GO:0012505 | 1 | gene\_06125.t1 | | endomembrane system | cellular\_component |
| GO:0032777 | 1 | gene\_09599.t1 | | Piccolo NuA4 histone acetyltransferase complex | cellular\_component |
| GO:0090575 | 1 | gene\_00109.t1 | | RNA polymerase II transcription regulator complex | cellular\_component |
| GO:0008622 | 2 | gene\_03200.t1,gene\_08287.t1 | | epsilon DNA polymerase complex | cellular\_component |
| GO:0000818 | 2 | gene\_04228.t1,gene\_01007.t1 | | nuclear MIS12/MIND complex | cellular\_component |
| GO:0000815 | 1 | gene\_07913.t1 | | ESCRT III complex | cellular\_component |
| GO:0000814 | 3 | gene\_01250.t1,gene\_10159.t1,gene\_01280.t1 | | ESCRT II complex | cellular\_component |
| GO:1990904 | 6 | gene\_06557.t1,gene\_03682.t1,gene\_00876.t1,gene\_08840.t1,gene\_05876.t1,gene\_08877.t1 | | ribonucleoprotein complex | cellular\_component |
| GO:0000812 | 1 | gene\_01406.t1 | | Swr1 complex | cellular\_component |
| GO:0070461 | 2 | gene\_09914.t1,gene\_00832.t1 | | SAGA-type complex | cellular\_component |
| GO:0070469 | 14 | gene\_09613.t1,gene\_04447.t1,gene\_08412.t1,gene\_03957.t1,gene\_10025.t1,gene\_03691.t1,gene\_09825.t1,gene\_08864.t1,gene\_00091.t1,gene\_09057.t1,gene\_07351.t1,gene\_08052.t1,gene\_10382.t1,gene\_00789.t1 | | respirasome | cellular\_component |
| GO:0032592 | 1 | gene\_02329.t1 | | integral component of mitochondrial membrane | cellular\_component |
| GO:0072686 | 7 | gene\_10529.t1,gene\_05877.t1,gene\_03377.t1,gene\_08597.t1,gene\_05155.t1,gene\_06154.t1,gene\_08869.t1 | | mitotic spindle | cellular\_component |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0033179 | 5 | gene\_06164.t1,gene\_08230.t1,gene\_03004.t1,gene\_09011.t1,gene\_07043.t1 | | proton-transporting V-type ATPase, V0 domain | cellular\_component |
| GO:0005801 | 2 | gene\_05520.t1,gene\_05672.t1 | | cis-Golgi network | cellular\_component |
| GO:0043596 | 6 | gene\_00515.t1,gene\_01710.t1,gene\_01540.t1,gene\_07862.t1,gene\_08245.t1,gene\_09071.t1 | | nuclear replication fork | cellular\_component |
| GO:0035101 | 1 | gene\_04166.t1 | | FACT complex | cellular\_component |
| GO:0000324 | 1 | gene\_04192.t1 | | fungal-type vacuole | cellular\_component |
| GO:0031617 | 1 | gene\_06875.t1 | | NMS complex | cellular\_component |
| GO:0000329 | 1 | gene\_06397.t1 | | fungal-type vacuole membrane | cellular\_component |
| GO:1990234 | 2 | gene\_04084.t1,gene\_05796.t1 | | transferase complex | cellular\_component |
| GO:0097361 | 2 | gene\_00274.t1,gene\_05175.t1 | | CIA complex | cellular\_component |
| GO:0009277 | 5 | gene\_06587.t1,gene\_00145.t1,gene\_04429.t1,gene\_08114.t1,gene\_06764.t1 | | fungal-type cell wall | cellular\_component |
| GO:0005639 | 1 | gene\_05713.t1 | | integral component of nuclear inner membrane | cellular\_component |
| GO:0005887 | 5 | gene\_01278.t1,gene\_06654.t1,gene\_07810.t1,gene\_03819.t1,gene\_01059.t1 | | integral component of plasma membrane | cellular\_component |
| GO:0032299 | 2 | gene\_08594.t1,gene\_09856.t1 | | ribonuclease H2 complex | cellular\_component |
| GO:0003918 | 2 | gene\_04413.t1,gene\_10607.t1 | | DNA topoisomerase type II (double strand cut, ATP-hydrolyzing) activity | molecular\_function |
| GO:0051499 | 1 | gene\_06698.t1 | | D-aminoacyl-tRNA deacylase activity | molecular\_function |
| GO:0004814 | 1 | gene\_03487.t1 | | arginine-tRNA ligase activity | molecular\_function |
| GO:0045703 | 1 | gene\_06564.t1 | | ketoreductase activity | molecular\_function |
| GO:0034511 | 2 | gene\_00407.t1,gene\_05225.t1 | | U3 snoRNA binding | molecular\_function |
| GO:0004140 | 1 | gene\_07765.t1 | | dephospho-CoA kinase activity | molecular\_function |
| GO:0017176 | 3 | gene\_06610.t1,gene\_09007.t1,gene\_03239.t1 | | phosphatidylinositol N-acetylglucosaminyltransferase activity | molecular\_function |
| GO:0017172 | 2 | gene\_02958.t1,gene\_06019.t1 | | cysteine dioxygenase activity | molecular\_function |
| GO:0017178 | 1 | gene\_02836.t1 | | diphthine-ammonia ligase activity | molecular\_function |
| GO:0004630 | 3 | gene\_09152.t1,gene\_07324.t1,gene\_06298.t1 | | phospholipase D activity | molecular\_function |
| GO:0004514 | 2 | gene\_04641.t1,gene\_07335.t1 | | nicotinate-nucleotide diphosphorylase (carboxylating) activity | molecular\_function |
| GO:0042030 | 1 | gene\_02794.t1 | | ATPase inhibitor activity | molecular\_function |
| GO:0004143 | 1 | gene\_09000.t1 | | diacylglycerol kinase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0004637 | 1 | gene\_09629.t1 | | phosphoribosylamine-glycine ligase activity | molecular\_function |
| GO:0031072 | 1 | gene\_09414.t1 | | heat shock protein binding | molecular\_function |
| GO:0031071 | 1 | gene\_09097.t1 | | cysteine desulfurase activity | molecular\_function |
| GO:0005484 | 4 | gene\_09159.t1,gene\_00350.t1,gene\_07213.t1,gene\_04059.t1 | | SNAP receptor activity | molecular\_function |
| GO:0052878 | 1 | gene\_10014.t1 | | linoleate 8R-lipoxygenase activity | molecular\_function |
| GO:0051879 | 2 | gene\_10118.t1,gene\_10596.t1 | | Hsp90 protein binding | molecular\_function |
| GO:0004848 | 1 | gene\_07404.t1 | | ureidoglycolate hydrolase activity | molecular\_function |
| GO:0004849 | 1 | gene\_09819.t1 | | uridine kinase activity | molecular\_function |
| GO:0004846 | 1 | gene\_00591.t1 | | urate oxidase activity | molecular\_function |
| GO:0004844 | 1 | gene\_08282.t1 | | uracil DNA N-glycosylase activity | molecular\_function |
| GO:0004842 | 12 | gene\_03850.t1,gene\_10015.t1,gene\_03639.t1,gene\_03834.t1,gene\_08874.t1,gene\_09531.t1,gene\_01334.t1,gene\_03617.t1,gene\_06100.t1,gene\_01616.t1,gene\_09585.t1,gene\_03784.t1 | | ubiquitin-protein transferase activity | molecular\_function |
| GO:0004843 | 23 | gene\_01114.t1,gene\_05133.t1,gene\_04184.t1,gene\_07916.t1,gene\_10416.t1,gene\_10530.t1,gene\_06133.t1,gene\_03666.t1,gene\_03039.t1,gene\_00409.t1,gene\_08301.t1,gene\_03470.t1,gene\_09853.t1,gene\_07309.t1,gene\_10317.t1,gene\_04108.t1,gene\_07313.t1,gene\_07741.t1,gene\_07732.t1,gene\_06849.t1,gene\_02020.t1,gene\_00843.t1,gene\_08038.t1 | | thiol-dependent deubiquitinase | molecular\_function |
| GO:0030674 | 1 | gene\_07381.t1 | | protein-macromolecule adaptor activity | molecular\_function |
| GO:0004534 | 2 | gene\_02253.t1,gene\_07933.t1 | | 5'-3' exoribonuclease activity | molecular\_function |
| GO:0004535 | 3 | gene\_03654.t1,gene\_04448.t1,gene\_10433.t1 | | poly(A)-specific ribonuclease activity | molecular\_function |
| GO:0005227 | 5 | gene\_05633.t1,gene\_07740.t1,gene\_00710.t1,gene\_01711.t1,gene\_08243.t1 | | calcium activated cation channel activity | molecular\_function |
| GO:0031491 | 1 | gene\_10351.t1 | | nucleosome binding | molecular\_function |
| GO:0031493 | 1 | gene\_05805.t1 | | obsolete nucleosomal histone binding | molecular\_function |
| GO:0043743 | 1 | gene\_06078.t1 | | LPPG:FO 2-phospho-L-lactate transferase activity | molecular\_function |
| GO:0000285 | 1 | gene\_02623.t1 | | 1-phosphatidylinositol-3-phosphate 5-kinase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0000287 | 42 | gene\_02627.t1,gene\_09469.t1,gene\_09154.t1,gene\_08592.t1,gene\_08070.t1,gene\_10016.t1,gene\_00524.t1,gene\_03413.t1,gene\_07215.t1,gene\_01087.t1,gene\_10595.t1,gene\_08515.t1,gene\_03025.t1,gene\_00896.t1,gene\_02959.t1,gene\_02481.t1,gene\_01989.t1,gene\_06798.t1,gene\_02115.t1,gene\_02333.t1,gene\_00653.t1,gene\_02634.t1,gene\_08855.t1,gene\_01270.t1,gene\_03558.t1,gene\_07283.t1,gene\_03899.t1,gene\_02366.t1,gene\_04010.t1,gene\_02066.t1,gene\_03017.t1,gene\_05669.t1,gene\_02158.t1,gene\_09009.t1,gene\_08720.t1,gene\_01056.t1,gene\_09510.t1,gene\_02419.t1,gene\_01001.t1,gene\_03086.t1,gene\_01319.t1,gene\_06714.t1 | | magnesium ion binding | molecular\_function |
| GO:0004449 | 2 | gene\_08720.t1,gene\_02366.t1 | | isocitrate dehydrogenase (NAD+) activity | molecular\_function |
| GO:0103045 | 2 | gene\_04583.t1,gene\_06573.t1 | | methione N-acyltransferase activity | molecular\_function |
| GO:0008176 | 1 | gene\_10160.t1 | | tRNA (guanine-N7-)-methyltransferase activity | molecular\_function |
| GO:0051010 | 1 | gene\_10486.t1 | | microtubule plus-end binding | molecular\_function |
| GO:0008289 | 15 | gene\_02702.t1,gene\_07300.t1,gene\_04067.t1,gene\_10059.t1,gene\_06355.t1,gene\_03033.t1,gene\_07310.t1,gene\_10269.t1,gene\_10312.t1,gene\_01129.t1,gene\_09579.t1,gene\_08315.t1,gene\_02094.t1,gene\_04653.t1,gene\_07273.t1 | | lipid binding | molecular\_function |
| GO:0051015 | 4 | gene\_01209.t1,gene\_07456.t1,gene\_02045.t1,gene\_08209.t1 | | actin filament binding | molecular\_function |
| GO:0008650 | 1 | gene\_05806.t1 | | rRNA (uridine-2'-O-)-methyltransferase activity | molecular\_function |
| GO:0048039 | 1 | gene\_02653.t1 | | ubiquinone binding | molecular\_function |
| GO:0048038 | 10 | gene\_06041.t1,gene\_01764.t1,gene\_04449.t1,gene\_03522.t1,gene\_10189.t1,gene\_01707.t1,gene\_07681.t1,gene\_09283.t1,gene\_09128.t1,gene\_09373.t1 | | quinone binding | molecular\_function |
| GO:0140575 | 1 | gene\_05653.t1 | | transmembrane monodehydroascorbate reductase activity | molecular\_function |
| GO:0004664 | 1 | gene\_09255.t1 | | prephenate dehydratase activity | molecular\_function |
| GO:0004665 | 1 | gene\_00560.t1 | | prephenate dehydrogenase (NADP+) activity | molecular\_function |
| GO:0004190 | 13 | gene\_09201.t1,gene\_04924.t1,gene\_09716.t1,gene\_05472.t1,gene\_00340.t1,gene\_06211.t1,gene\_04744.t1,gene\_10352.t1,gene\_01851.t1,gene\_07487.t1,gene\_00828.t1,gene\_06094.t1,gene\_05703.t1 | | aspartic-type endopeptidase activity | molecular\_function |
| GO:0004663 | 2 | gene\_09996.t1,gene\_08511.t1 | | Rab geranylgeranyltransferase activity | molecular\_function |
| GO:0004660 | 1 | gene\_04040.t1 | | protein farnesyltransferase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0003899 | 24 | gene\_06259.t1,gene\_00677.t1,gene\_08353.t1,gene\_04356.t1,gene\_03180.t1,gene\_03951.t1,gene\_10197.t1,gene\_02110.t1,gene\_09612.t1,gene\_06171.t1,gene\_01093.t1,gene\_02230.t1,gene\_04203.t1,gene\_05314.t1,gene\_09944.t1,gene\_09036.t1,gene\_02194.t1,gene\_08304.t1,gene\_04647.t1,gene\_01696.t1,gene\_08095.t1,gene\_04655.t1,gene\_05962.t1,gene\_09823.t1 | | DNA-directed 5'-3' RNA polymerase activity | molecular\_function |
| GO:0004198 | 2 | gene\_01022.t1,gene\_03772.t1 | | calcium-dependent cysteine-type endopeptidase activity | molecular\_function |
| GO:0004668 | 2 | gene\_00589.t1,gene\_08117.t1 | | protein-arginine deiminase activity | molecular\_function |
| GO:0000107 | 1 | gene\_08292.t1 | | imidazoleglycerol-phosphate synthase activity | molecular\_function |
| GO:0003878 | 2 | gene\_06452.t1,gene\_06451.t1 | | ATP citrate synthase activity | molecular\_function |
| GO:0003879 | 1 | gene\_08515.t1 | | ATP phosphoribosyltransferase activity | molecular\_function |
| GO:0003872 | 1 | gene\_03414.t1 | | 6-phosphofructokinase activity | molecular\_function |
| GO:0003870 | 1 | gene\_04355.t1 | | 5-aminolevulinate synthase activity | molecular\_function |
| GO:0003871 | 3 | gene\_00382.t1,gene\_03115.t1,gene\_02061.t1 | | 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity | molecular\_function |
| GO:0003876 | 1 | gene\_05147.t1 | | AMP deaminase activity | molecular\_function |
| GO:0003877 | 2 | gene\_09581.t1,gene\_07475.t1 | | ATP adenylyltransferase activity | molecular\_function |
| GO:0050313 | 2 | gene\_08465.t1,gene\_05410.t1 | | sulfur dioxygenase activity | molecular\_function |
| GO:0004069 | 5 | gene\_05313.t1,gene\_00862.t1,gene\_03995.t1,gene\_00460.t1,gene\_05306.t1 | | L-aspartate:2-oxoglutarate aminotransferase activity | molecular\_function |
| GO:0004060 | 1 | gene\_10026.t1 | | arylamine N-acetyltransferase activity | molecular\_function |
| GO:0004061 | 8 | gene\_05407.t1,gene\_03462.t1,gene\_03134.t1,gene\_03297.t1,gene\_10549.t1,gene\_08894.t1,gene\_04519.t1,gene\_10649.t1 | | arylformamidase activity | molecular\_function |
| GO:0004065 | 2 | gene\_05109.t1,gene\_06641.t1 | | arylsulfatase activity | molecular\_function |
| GO:0004066 | 2 | gene\_00321.t1,gene\_10129.t1 | | asparagine synthase (glutamine-hydrolyzing) activity | molecular\_function |
| GO:0004067 | 2 | gene\_07958.t1,gene\_07801.t1 | | asparaginase activity | molecular\_function |
| GO:0019211 | 2 | gene\_08765.t1,gene\_03613.t1 | | phosphatase activator activity | molecular\_function |
| GO:0102344 | 1 | gene\_04035.t1 | | 3-hydroxy-behenoyl-CoA dehydratase activity | molecular\_function |
| GO:0018580 | 5 | gene\_02947.t1,gene\_00465.t1,gene\_01391.t1,gene\_04117.t1,gene\_04427.t1 | | nitronate monooxygenase activity | molecular\_function |
| GO:0004348 | 1 | gene\_04370.t1 | | glucosylceramidase activity | molecular\_function |
| GO:0071933 | 1 | gene\_05913.t1 | | Arp2/3 complex binding | molecular\_function |
| GO:0000832 | 1 | gene\_02352.t1 | | inositol hexakisphosphate 5-kinase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0016631 | 1 | gene\_02332.t1 | | enoyl-[acyl-carrier-protein] reductase activity | molecular\_function |
| GO:0004345 | 1 | gene\_06816.t1 | | glucose-6-phosphate dehydrogenase activity | molecular\_function |
| GO:0070403 | 12 | gene\_05973.t1,gene\_09874.t1,gene\_10177.t1,gene\_01335.t1,gene\_05523.t1,gene\_04231.t1,gene\_06021.t1,gene\_03898.t1,gene\_08580.t1,gene\_07063.t1,gene\_09792.t1,gene\_08826.t1 | | NAD+ binding | molecular\_function |
| GO:1990380 | 1 | gene\_07741.t1 | | Lys48-specific deubiquitinase activity | molecular\_function |
| GO:0070330 | 1 | gene\_06727.t1 | | aromatase activity | molecular\_function |
| GO:0047750 | 3 | gene\_03504.t1,gene\_01909.t1,gene\_06509.t1 | | cholestenol delta-isomerase activity | molecular\_function |
| GO:0052654 | 2 | gene\_09326.t1,gene\_00557.t1 | | L-leucine transaminase activity | molecular\_function |
| GO:0052655 | 2 | gene\_09326.t1,gene\_00557.t1 | | L-valine transaminase activity | molecular\_function |
| GO:0052656 | 2 | gene\_09326.t1,gene\_00557.t1 | | L-isoleucine transaminase activity | molecular\_function |
| GO:0047710 | 1 | gene\_09419.t1 | | bis(5'-adenosyl)-triphosphatase activity | molecular\_function |
| GO:0061799 | 1 | gene\_06655.t1 | | cyclic pyranopterin monophosphate synthase activity | molecular\_function |
| GO:0016742 | 1 | gene\_01843.t1 | | hydroxymethyl-, formyl- and related transferase activity | molecular\_function |
| GO:0016743 | 1 | gene\_00359.t1 | | carboxyl- or carbamoyltransferase activity | molecular\_function |
| GO:0016740 | 102 | gene\_08666.t1,gene\_09450.t1,gene\_04178.t1,gene\_04412.t1,gene\_06128.t1,gene\_03590.t1,gene\_00671.t1,gene\_10105.t1,gene\_07645.t1,gene\_04626.t1,gene\_08706.t1,gene\_07932.t1,gene\_03347.t1,gene\_03275.t1,gene\_10177.t1,gene\_02149.t1,gene\_05459.t1,gene\_05707.t1,gene\_06546.t1,gene\_04142.t1,gene\_08678.t1,gene\_06776.t1,gene\_01755.t1,gene\_03864.t1,gene\_10080.t1,gene\_04432.t1,gene\_04231.t1,gene\_00857.t1,gene\_09966.t1,gene\_09874.t1,gene\_01092.t1,gene\_05993.t1,gene\_10462.t1,gene\_07852.t1,gene\_10548.t1,gene\_02439.t1,gene\_02854.t1,gene\_09197.t1,gene\_02593.t1,gene\_01088.t1,gene\_04371.t1,gene\_03340.t1,gene\_00114.t1,gene\_06074.t1,gene\_07183.t1,gene\_07446.t1,gene\_07447.t1,gene\_08820.t1,gene\_08799.t1,gene\_05652.t1,gene\_09468.t1,gene\_09133.t1,gene\_03924.t1,gene\_06003.t1,gene\_07853.t1,gene\_02477.t1,gene\_08810.t1,gene\_01254.t1,gene\_10202.t1,gene\_05081.t1,gene\_10547.t1,gene\_01166.t1,gene\_09281.t1,gene\_08982.t1,gene\_01531.t1,gene\_09559.t1,gene\_10565.t1,gene\_04508.t1,gene\_05756.t1,gene\_03029.t1,gene\_00695.t1,gene\_07196.t1,gene\_05948.t1,gene\_03888.t1,gene\_08010.t1,gene\_07141.t1,gene\_05392.t1,gene\_04038.t1,gene\_06397.t1,gene\_02324.t1,gene\_01560.t1,gene\_09505.t1,gene\_09470.t1,gene\_02384.t1,gene\_09623.t1,gene\_02270.t1,gene\_01618.t1,gene\_06022.t1,gene\_05523.t1,gene\_06968.t1, | | transferase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0016740 | 102 | gene\_05193.t1,gene\_06099.t1,gene\_06533.t1,gene\_04292.t1,gene\_05771.t1,gene\_07274.t1,gene\_10303.t1,gene\_09107.t1,gene\_00403.t1,gene\_03898.t1,gene\_07286.t1,gene\_07655.t1 | | transferase activity | molecular\_function |
| GO:0016746 | 30 | gene\_08900.t1,gene\_03496.t1,gene\_01580.t1,gene\_02076.t1,gene\_00532.t1,gene\_08782.t1,gene\_05504.t1,gene\_06977.t1,gene\_10186.t1,gene\_07200.t1,gene\_08786.t1,gene\_06220.t1,gene\_08783.t1,gene\_09758.t1,gene\_09240.t1,gene\_07438.t1,gene\_07205.t1,gene\_01784.t1,gene\_10115.t1,gene\_07134.t1,gene\_02048.t1,gene\_05902.t1,gene\_09676.t1,gene\_08784.t1,gene\_09801.t1,gene\_08780.t1,gene\_07576.t1,gene\_06478.t1,gene\_08787.t1,gene\_05009.t1 | | acyltransferase activity | molecular\_function |
| GO:0016747 | 19 | gene\_05384.t1,gene\_08954.t1,gene\_01953.t1,gene\_06421.t1,gene\_07539.t1,gene\_01462.t1,gene\_08222.t1,gene\_08102.t1,gene\_00785.t1,gene\_01103.t1,gene\_09355.t1,gene\_08872.t1,gene\_01171.t1,gene\_08166.t1,gene\_01932.t1,gene\_02819.t1,gene\_10660.t1,gene\_09751.t1,gene\_01489.t1 | | acyltransferase activity, transferring groups other than amino-acyl groups | molecular\_function |
| GO:0016671 | 1 | gene\_06197.t1 | | oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor | molecular\_function |
| GO:0016162 | 2 | gene\_05405.t1,gene\_01844.t1 | | cellulose 1,4-beta-cellobiosidase activity | molecular\_function |
| GO:0016296 | 1 | gene\_02332.t1 | | palmitoyl-[acyl-carrier-protein] hydrolase activity | molecular\_function |
| GO:0016298 | 1 | gene\_04546.t1 | | lipase activity | molecular\_function |
| GO:0000334 | 1 | gene\_07394.t1 | | 3-hydroxyanthranilate 3,4-dioxygenase activity | molecular\_function |
| GO:0020037 | 115 | gene\_03326.t1,gene\_05483.t1,gene\_09837.t1,gene\_02919.t1,gene\_08439.t1,gene\_00050.t1,gene\_07089.t1,gene\_10673.t1,gene\_10252.t1,gene\_03957.t1,gene\_01732.t1,gene\_02074.t1,gene\_07674.t1,gene\_01461.t1,gene\_10670.t1,gene\_06181.t1,gene\_08016.t1,gene\_08361.t1,gene\_08018.t1,gene\_01818.t1,gene\_05434.t1,gene\_02731.t1,gene\_05974.t1,gene\_05157.t1,gene\_01463.t1,gene\_04764.t1,gene\_08723.t1,gene\_07431.t1,gene\_04130.t1,gene\_01658.t1,gene\_09909.t1,gene\_00545.t1,gene\_07281.t1,gene\_07691.t1,gene\_02013.t1,gene\_04065.t1,gene\_07786.t1,gene\_02311.t1,gene\_06676.t1,gene\_01284.t1,gene\_01460.t1,gene\_03391.t1,gene\_00338.t1,gene\_09504.t1,gene\_09095.t1,gene\_03669.t1,gene\_07369.t1,gene\_01111.t1,gene\_09188.t1,gene\_01903.t1,gene\_07549.t1,gene\_07833.t1,gene\_02026.t1,gene\_09177.t1,gene\_03816.t1,gene\_00994.t1,gene\_00758.t1,gene\_03517.t1,gene\_00220.t1,gene\_01181.t1,gene\_00834.t1,gene\_01324.t1,gene\_01587.t1,gene\_03353.t1,gene\_07934.t1,gene\_06475.t1,gene\_07956.t1,gene\_04361.t1,gene\_01476.t1,gene\_04083.t1,gene\_07490.t1,gene\_00621.t1,gene\_06727.t1,gene\_00777.t1,gene\_07117.t1,gene\_07848.t1,gene\_07526.t1,gene\_03126.t1,gene\_02830.t1,gene\_06168.t1, | | heme binding | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0020037 | 115 | gene\_10593.t1,gene\_00717.t1,gene\_02312.t1,gene\_09778.t1,gene\_02258.t1,gene\_04118.t1,gene\_10672.t1,gene\_08446.t1,gene\_09353.t1,gene\_09980.t1,gene\_08724.t1,gene\_09389.t1,gene\_09970.t1,gene\_03369.t1,gene\_04527.t1,gene\_08017.t1,gene\_07727.t1,gene\_01543.t1,gene\_02248.t1,gene\_05975.t1,gene\_09896.t1,gene\_03978.t1,gene\_00285.t1,gene\_10014.t1,gene\_09981.t1,gene\_08991.t1,gene\_06715.t1,gene\_07507.t1,gene\_07556.t1,gene\_02272.t1,gene\_00543.t1,gene\_02285.t1,gene\_08430.t1,gene\_03226.t1,gene\_09394.t1 | | heme binding | molecular\_function |
| GO:0030060 | 2 | gene\_09160.t1,gene\_09730.t1 | | L-malate dehydrogenase activity | molecular\_function |
| GO:0052862 | 1 | gene\_01601.t1 | | glucan endo-1,4-beta-glucanase activity, C-3 substituted reducing group | molecular\_function |
| GO:0052861 | 1 | gene\_01601.t1 | | glucan endo-1,3-beta-glucanase activity, C-3 substituted reducing group | molecular\_function |
| GO:0033862 | 1 | gene\_06009.t1 | | UMP kinase activity | molecular\_function |
| GO:0034386 | 1 | gene\_08073.t1 | | 4-aminobutyrate:2-oxoglutarate transaminase activity | molecular\_function |
| GO:0008420 | 2 | gene\_05704.t1,gene\_00538.t1 | | RNA polymerase II CTD heptapeptide repeat phosphatase activity | molecular\_function |
| GO:0004855 | 1 | gene\_10070.t1 | | xanthine oxidase activity | molecular\_function |
| GO:0004856 | 1 | gene\_04233.t1 | | xylulokinase activity | molecular\_function |
| GO:0004851 | 1 | gene\_06837.t1 | | uroporphyrin-III C-methyltransferase activity | molecular\_function |
| GO:0004853 | 1 | gene\_01680.t1 | | uroporphyrinogen decarboxylase activity | molecular\_function |
| GO:0004852 | 1 | gene\_10525.t1 | | uroporphyrinogen-III synthase activity | molecular\_function |
| GO:0000773 | 1 | gene\_05187.t1 | | phosphatidyl-N-methylethanolamine N-methyltransferase activity | molecular\_function |
| GO:0004528 | 1 | gene\_04241.t1 | | phosphodiesterase I activity | molecular\_function |
| GO:0004525 | 8 | gene\_03396.t1,gene\_06315.t1,gene\_04160.t1,gene\_05421.t1,gene\_05841.t1,gene\_08713.t1,gene\_04425.t1,gene\_10512.t1 | | ribonuclease III activity | molecular\_function |
| GO:0000774 | 1 | gene\_03945.t1 | | adenyl-nucleotide exchange factor activity | molecular\_function |
| GO:0004527 | 11 | gene\_04510.t1,gene\_02998.t1,gene\_10164.t1,gene\_09922.t1,gene\_07789.t1,gene\_07321.t1,gene\_03737.t1,gene\_06309.t1,gene\_04548.t1,gene\_09684.t1,gene\_04971.t1 | | exonuclease activity | molecular\_function |
| GO:0004526 | 2 | gene\_06449.t1,gene\_03157.t1 | | ribonuclease P activity | molecular\_function |
| GO:0004521 | 5 | gene\_00740.t1,gene\_04402.t1,gene\_04328.t1,gene\_03344.t1,gene\_00030.t1 | | endoribonuclease activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0004520 | 2 | gene\_06548.t1,gene\_00867.t1 | | endodeoxyribonuclease activity | molecular\_function |
| GO:0004523 | 11 | gene\_04909.t1,gene\_06028.t1,gene\_04178.t1,gene\_05388.t1,gene\_04075.t1,gene\_05004.t1,gene\_07853.t1,gene\_04505.t1,gene\_07852.t1,gene\_04116.t1,gene\_04971.t1 | | RNA-DNA hybrid ribonuclease activity | molecular\_function |
| GO:0009922 | 2 | gene\_01892.t1,gene\_08158.t1 | | fatty acid elongase activity | molecular\_function |
| GO:0009039 | 1 | gene\_01624.t1 | | urease activity | molecular\_function |
| GO:0015165 | 2 | gene\_10475.t1,gene\_02541.t1 | | pyrimidine nucleotide-sugar transmembrane transporter activity | molecular\_function |
| GO:0005216 | 3 | gene\_10604.t1,gene\_04721.t1,gene\_09028.t1 | | ion channel activity | molecular\_function |
| GO:0050567 | 2 | gene\_02324.t1,gene\_05707.t1 | | glutaminyl-tRNA synthase (glutamine-hydrolyzing) activity | molecular\_function |
| GO:0000293 | 9 | gene\_10564.t1,gene\_07511.t1,gene\_00830.t1,gene\_00797.t1,gene\_07124.t1,gene\_02172.t1,gene\_06588.t1,gene\_01257.t1,gene\_03078.t1 | | ferric-chelate reductase activity | molecular\_function |
| GO:0000298 | 1 | gene\_05603.t1 | | endopolyphosphatase activity | molecular\_function |
| GO:0004298 | 10 | gene\_00408.t1,gene\_08488.t1,gene\_00399.t1,gene\_07791.t1,gene\_02375.t1,gene\_03863.t1,gene\_05873.t1,gene\_09929.t1,gene\_02372.t1,gene\_03707.t1 | | threonine-type endopeptidase activity | molecular\_function |
| GO:0004451 | 2 | gene\_10345.t1,gene\_00805.t1 | | isocitrate lyase activity | molecular\_function |
| GO:0005458 | 1 | gene\_09248.t1 | | GDP-mannose transmembrane transporter activity | molecular\_function |
| GO:0004452 | 1 | gene\_06520.t1 | | isopentenyl-diphosphate delta-isomerase activity | molecular\_function |
| GO:0004455 | 1 | gene\_09113.t1 | | ketol-acid reductoisomerase activity | molecular\_function |
| GO:0004459 | 1 | gene\_02156.t1 | | L-lactate dehydrogenase activity | molecular\_function |
| GO:0030170 | 56 | gene\_01418.t1,gene\_08884.t1,gene\_08666.t1,gene\_04197.t1,gene\_09469.t1,gene\_03196.t1,gene\_10500.t1,gene\_02197.t1,gene\_06682.t1,gene\_09470.t1,gene\_07598.t1,gene\_01259.t1,gene\_04762.t1,gene\_10447.t1,gene\_05313.t1,gene\_03559.t1,gene\_05306.t1,gene\_10105.t1,gene\_06621.t1,gene\_03700.t1,gene\_09097.t1,gene\_04082.t1,gene\_09066.t1,gene\_02648.t1,gene\_04383.t1,gene\_04701.t1,gene\_02844.t1,gene\_09776.t1,gene\_05675.t1,gene\_00862.t1,gene\_00962.t1,gene\_07328.t1,gene\_10583.t1,gene\_00460.t1,gene\_09185.t1,gene\_01168.t1,gene\_02277.t1,gene\_05315.t1,gene\_05088.t1,gene\_02149.t1,gene\_04355.t1,gene\_03736.t1,gene\_00551.t1,gene\_08073.t1,gene\_02827.t1,gene\_01381.t1,gene\_01167.t1,gene\_05961.t1,gene\_04015.t1,gene\_03995.t1,gene\_06750.t1,gene\_10303.t1,gene\_01314.t1,gene\_03988.t1,gene\_10066.t1,gene\_06828.t1 | | pyridoxal phosphate binding | molecular\_function |
| GO:0102500 | 1 | gene\_00709.t1 | | beta-maltose 4-alpha-glucanotransferase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0004644 | 1 | gene\_00615.t1 | | phosphoribosylglycinamide formyltransferase activity | molecular\_function |
| GO:0046899 | 1 | gene\_01019.t1 | | nucleoside triphosphate adenylate kinase activity | molecular\_function |
| GO:0004181 | 3 | gene\_01063.t1,gene\_06882.t1,gene\_07429.t1 | | metallocarboxypeptidase activity | molecular\_function |
| GO:0004180 | 2 | gene\_05177.t1,gene\_00384.t1 | | carboxypeptidase activity | molecular\_function |
| GO:0004185 | 9 | gene\_05176.t1,gene\_05858.t1,gene\_00369.t1,gene\_09764.t1,gene\_10590.t1,gene\_07464.t1,gene\_08088.t1,gene\_02737.t1,gene\_00605.t1 | | serine-type carboxypeptidase activity | molecular\_function |
| GO:0003887 | 8 | gene\_01057.t1,gene\_05518.t1,gene\_06076.t1,gene\_04737.t1,gene\_06309.t1,gene\_00595.t1,gene\_06856.t1,gene\_03200.t1 | | DNA-directed DNA polymerase activity | molecular\_function |
| GO:0004674 | 50 | gene\_00799.t1,gene\_01198.t1,gene\_10210.t1,gene\_00740.t1,gene\_04066.t1,gene\_03475.t1,gene\_03660.t1,gene\_07626.t1,gene\_02520.t1,gene\_10213.t1,gene\_02088.t1,gene\_07408.t1,gene\_00581.t1,gene\_03903.t1,gene\_08500.t1,gene\_03061.t1,gene\_10369.t1,gene\_00017.t1,gene\_08610.t1,gene\_02432.t1,gene\_02838.t1,gene\_06106.t1,gene\_01223.t1,gene\_03314.t1,gene\_08229.t1,gene\_09242.t1,gene\_00801.t1,gene\_00030.t1,gene\_04388.t1,gene\_09710.t1,gene\_05628.t1,gene\_00848.t1,gene\_07837.t1,gene\_08650.t1,gene\_00208.t1,gene\_02155.t1,gene\_07396.t1,gene\_06526.t1,gene\_08612.t1,gene\_03199.t1,gene\_00548.t1,gene\_07078.t1,gene\_03598.t1,gene\_05629.t1,gene\_04642.t1,gene\_07102.t1,gene\_05244.t1,gene\_03773.t1,gene\_05846.t1,gene\_09034.t1 | | protein serine/threonine kinase activity | molecular\_function |
| GO:0003885 | 1 | gene\_02044.t1 | | D-arabinono-1,4-lactone oxidase activity | molecular\_function |
| GO:0003884 | 6 | gene\_07698.t1,gene\_06144.t1,gene\_05946.t1,gene\_10150.t1,gene\_05244.t1,gene\_02986.t1 | | D-amino-acid oxidase activity | molecular\_function |
| GO:0004671 | 1 | gene\_01116.t1 | | protein C-terminal S-isoprenylcysteine carboxyl O-methyltransferase activity | molecular\_function |
| GO:0003882 | 1 | gene\_10329.t1 | | CDP-diacylglycerol-serine O-phosphatidyltransferase activity | molecular\_function |
| GO:0004672 | 101 | gene\_03602.t1,gene\_05928.t1,gene\_01507.t1,gene\_06412.t1,gene\_07899.t1,gene\_04520.t1,gene\_09211.t1,gene\_08036.t1,gene\_00303.t1,gene\_08804.t1,gene\_07649.t1,gene\_07918.t1,gene\_07650.t1,gene\_09416.t1,gene\_06711.t1,gene\_07804.t1,gene\_01183.t1,gene\_05442.t1,gene\_07924.t1,gene\_08845.t1,gene\_01341.t1,gene\_09046.t1,gene\_02514.t1,gene\_02449.t1,gene\_04923.t1,gene\_03538.t1,gene\_09871.t1,gene\_07312.t1,gene\_09780.t1,gene\_05105.t1,gene\_04467.t1,gene\_03818.t1,gene\_03645.t1,gene\_04566.t1,gene\_07503.t1,gene\_04358.t1,gene\_01564.t1,gene\_00879.t1,gene\_10464.t1,gene\_07298.t1,gene\_04219.t1,gene\_00486.t1,gene\_03627.t1,gene\_03759.t1,gene\_04554.t1, | | protein kinase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0004672 | 101 | gene\_07842.t1,gene\_03351.t1,gene\_03896.t1,gene\_06310.t1,gene\_07695.t1,gene\_04663.t1,gene\_02062.t1,gene\_10372.t1,gene\_07797.t1,gene\_02577.t1,gene\_07370.t1,gene\_06413.t1,gene\_03338.t1,gene\_05866.t1,gene\_03551.t1,gene\_05879.t1,gene\_09271.t1,gene\_09224.t1,gene\_03637.t1,gene\_06792.t1,gene\_03535.t1,gene\_01081.t1,gene\_08044.t1,gene\_09645.t1,gene\_03268.t1,gene\_09582.t1,gene\_02250.t1,gene\_09222.t1,gene\_01353.t1,gene\_07160.t1,gene\_09064.t1,gene\_01556.t1,gene\_05330.t1,gene\_05671.t1,gene\_06117.t1,gene\_09735.t1,gene\_05142.t1,gene\_03960.t1,gene\_06624.t1,gene\_01173.t1,gene\_04302.t1,gene\_03461.t1,gene\_02412.t1,gene\_09870.t1,gene\_02304.t1,gene\_02734.t1,gene\_09325.t1,gene\_05305.t1,gene\_07917.t1,gene\_05837.t1,gene\_08460.t1,gene\_00089.t1,gene\_04567.t1,gene\_08981.t1,gene\_02175.t1,gene\_00625.t1 | | protein kinase activity | molecular\_function |
| GO:0003868 | 2 | gene\_03807.t1,gene\_10000.t1 | | 4-hydroxyphenylpyruvate dioxygenase activity | molecular\_function |
| GO:0003861 | 1 | gene\_07021.t1 | | 3-isopropylmalate dehydratase activity | molecular\_function |
| GO:0003863 | 2 | gene\_03837.t1,gene\_03836.t1 | | 3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring) activity | molecular\_function |
| GO:0003862 | 2 | gene\_02066.t1,gene\_10595.t1 | | 3-isopropylmalate dehydrogenase activity | molecular\_function |
| GO:0003865 | 1 | gene\_02943.t1 | | 3-oxo-5-alpha-steroid 4-dehydrogenase activity | molecular\_function |
| GO:0003864 | 2 | gene\_01676.t1,gene\_03893.t1 | | 3-methyl-2-oxobutanoate hydroxymethyltransferase activity | molecular\_function |
| GO:0001735 | 1 | gene\_03186.t1 | | prenylcysteine oxidase activity | molecular\_function |
| GO:0003866 | 1 | gene\_02251.t1 | | 3-phosphoshikimate 1-carboxyvinyltransferase activity | molecular\_function |
| GO:0018576 | 4 | gene\_02569.t1,gene\_09653.t1,gene\_06959.t1,gene\_02177.t1 | | catechol 1,2-dioxygenase activity | molecular\_function |
| GO:0004077 | 1 | gene\_00453.t1 | | biotin-[acetyl-CoA-carboxylase] ligase activity | molecular\_function |
| GO:0004076 | 1 | gene\_09462.t1 | | biotin synthase activity | molecular\_function |
| GO:0004075 | 1 | gene\_01074.t1 | | biotin carboxylase activity | molecular\_function |
| GO:0004072 | 2 | gene\_09263.t1,gene\_05635.t1 | | aspartate kinase activity | molecular\_function |
| GO:0004070 | 1 | gene\_06540.t1 | | aspartate carbamoyltransferase activity | molecular\_function |
| GO:1901363 | 2 | gene\_03800.t1,gene\_00746.t1 | | heterocyclic compound binding | molecular\_function |
| GO:0016628 | 8 | gene\_04364.t1,gene\_08853.t1,gene\_01993.t1,gene\_06783.t1,gene\_07280.t1,gene\_02975.t1,gene\_08518.t1,gene\_04110.t1 | | oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0016627 | 12 | gene\_08047.t1,gene\_07523.t1,gene\_00970.t1,gene\_03858.t1,gene\_00765.t1,gene\_01480.t1,gene\_10013.t1,gene\_06311.t1,gene\_00377.t1,gene\_01249.t1,gene\_07285.t1,gene\_08764.t1 | | oxidoreductase activity, acting on the CH-CH group of donors | molecular\_function |
| GO:0016620 | 26 | gene\_02911.t1,gene\_09372.t1,gene\_05395.t1,gene\_00449.t1,gene\_10347.t1,gene\_05735.t1,gene\_03825.t1,gene\_06860.t1,gene\_00823.t1,gene\_02341.t1,gene\_00942.t1,gene\_09760.t1,gene\_06893.t1,gene\_02582.t1,gene\_06187.t1,gene\_02926.t1,gene\_03302.t1,gene\_03400.t1,gene\_02918.t1,gene\_01888.t1,gene\_06400.t1,gene\_00251.t1,gene\_04522.t1,gene\_06674.t1,gene\_00976.t1,gene\_09480.t1 | | oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor | molecular\_function |
| GO:0050072 | 1 | gene\_05772.t1 | | m7G(5')pppN diphosphatase activity | molecular\_function |
| GO:0046873 | 15 | gene\_06075.t1,gene\_05542.t1,gene\_04003.t1,gene\_02147.t1,gene\_07637.t1,gene\_09812.t1,gene\_00870.t1,gene\_10034.t1,gene\_02742.t1,gene\_01067.t1,gene\_01748.t1,gene\_07099.t1,gene\_09752.t1,gene\_03612.t1,gene\_05086.t1 | | metal ion transmembrane transporter activity | molecular\_function |
| GO:0046872 | 397 | gene\_02667.t1,gene\_03667.t1,gene\_08646.t1,gene\_00568.t1,gene\_00351.t1,gene\_09113.t1,gene\_00421.t1,gene\_00958.t1,gene\_06101.t1,gene\_04991.t1,gene\_06118.t1,gene\_09188.t1,gene\_01065.t1,gene\_01682.t1,gene\_10229.t1,gene\_09585.t1,gene\_05974.t1,gene\_00180.t1,gene\_09283.t1,gene\_04534.t1,gene\_07456.t1,gene\_07700.t1,gene\_00545.t1,gene\_00595.t1,gene\_05911.t1,gene\_04371.t1,gene\_09044.t1,gene\_00201.t1,gene\_04426.t1,gene\_00722.t1,gene\_09095.t1,gene\_00677.t1,gene\_04402.t1,gene\_10466.t1,gene\_10373.t1,gene\_02349.t1,gene\_07792.t1,gene\_08676.t1,gene\_10065.t1,gene\_00010.t1,gene\_10140.t1,gene\_04656.t1,gene\_02533.t1,gene\_00960.t1,gene\_10405.t1,gene\_03541.t1,gene\_08858.t1,gene\_10245.t1,gene\_06928.t1,gene\_09277.t1,gene\_03019.t1,gene\_02831.t1,gene\_07890.t1,gene\_01292.t1,gene\_06988.t1,gene\_07021.t1,gene\_03769.t1,gene\_09762.t1,gene\_02623.t1,gene\_00291.t1,gene\_04573.t1,gene\_08079.t1,gene\_00762.t1,gene\_01294.t1,gene\_09523.t1,gene\_01630.t1,gene\_02720.t1,gene\_10593.t1,gene\_02091.t1,gene\_06408.t1,gene\_00487.t1,gene\_07453.t1,gene\_09041.t1,gene\_10024.t1,gene\_01300.t1,gene\_04337.t1,gene\_00326.t1,gene\_08354.t1,gene\_05695.t1,gene\_10404.t1,gene\_08483.t1,gene\_08668.t1,gene\_04419.t1,gene\_07761.t1,gene\_05963.t1,gene\_07836.t1,gene\_07066.t1,gene\_04497.t1,gene\_00766.t1,gene\_04246.t1,gene\_10122.t1,gene\_06715.t1,gene\_09296.t1,gene\_04293.t1,gene\_01550.t1,gene\_05579.t1,gene\_07110.t1,gene\_04266.t1,gene\_00805.t1,gene\_01334.t1,gene\_07116.t1,gene\_07887.t1,gene\_04769.t1,gene\_08991.t1,gene\_06339.t1,gene\_00245.t1,gene\_09797.t1,gene\_04696.t1,gene\_03101.t1,gene\_02552.t1,gene\_09120.t1,gene\_02654.t1,gene\_06540.t1,gene\_06831.t1,gene\_09148.t1, | | metal ion binding | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0046872 | 397 | gene\_08521.t1,gene\_06270.t1,gene\_07377.t1,gene\_01441.t1,gene\_03979.t1,gene\_08289.t1,gene\_04093.t1,gene\_00043.t1,gene\_00012.t1,gene\_07115.t1,gene\_01946.t1,gene\_03397.t1,gene\_06429.t1,gene\_01558.t1,gene\_07477.t1,gene\_02185.t1,gene\_02251.t1,gene\_06098.t1,gene\_08162.t1,gene\_04813.t1,gene\_00147.t1,gene\_03391.t1,gene\_06236.t1,gene\_02617.t1,gene\_01210.t1,gene\_06832.t1,gene\_08595.t1,gene\_01254.t1,gene\_01074.t1,gene\_07184.t1,gene\_06655.t1,gene\_01874.t1,gene\_06856.t1,gene\_09531.t1,gene\_09862.t1,gene\_08874.t1,gene\_01504.t1,gene\_08040.t1,gene\_06743.t1,gene\_01705.t1,gene\_01521.t1,gene\_05348.t1,gene\_06162.t1,gene\_09952.t1,gene\_09071.t1,gene\_06309.t1,gene\_01523.t1,gene\_02685.t1,gene\_09528.t1,gene\_04667.t1,gene\_05593.t1,gene\_02122.t1,gene\_05218.t1,gene\_07892.t1,gene\_09324.t1,gene\_10607.t1,gene\_06433.t1,gene\_03322.t1,gene\_09824.t1,gene\_03691.t1,gene\_05535.t1,gene\_06882.t1,gene\_06168.t1,gene\_01473.t1,gene\_04609.t1,gene\_01808.t1,gene\_01280.t1,gene\_06740.t1,gene\_07315.t1,gene\_09478.t1,gene\_08724.t1,gene\_00631.t1,gene\_08511.t1,gene\_04624.t1,gene\_03475.t1,gene\_09832.t1,gene\_01852.t1,gene\_07386.t1,gene\_01197.t1,gene\_05365.t1,gene\_03751.t1,gene\_02565.t1,gene\_10355.t1,gene\_10479.t1,gene\_10000.t1,gene\_09666.t1,gene\_00074.t1,gene\_08170.t1,gene\_08015.t1,gene\_02686.t1,gene\_00717.t1,gene\_03866.t1,gene\_02974.t1,gene\_08185.t1,gene\_09601.t1,gene\_05150.t1,gene\_00029.t1,gene\_10613.t1,gene\_02703.t1,gene\_09414.t1,gene\_00055.t1,gene\_05011.t1,gene\_05483.t1,gene\_02136.t1,gene\_09542.t1,gene\_06370.t1,gene\_08827.t1,gene\_00406.t1,gene\_06718.t1,gene\_07325.t1,gene\_01707.t1,gene\_08568.t1,gene\_08464.t1,gene\_01716.t1,gene\_06995.t1,gene\_10161.t1,gene\_01343.t1,gene\_06323.t1,gene\_10345.t1,gene\_01703.t1,gene\_00338.t1,gene\_08299.t1,gene\_01409.t1,gene\_06471.t1,gene\_03449.t1,gene\_09702.t1,gene\_00944.t1,gene\_01839.t1,gene\_06255.t1,gene\_09629.t1,gene\_03112.t1,gene\_02643.t1,gene\_06455.t1,gene\_05765.t1,gene\_01715.t1,gene\_00538.t1,gene\_03227.t1,gene\_03604.t1,gene\_00512.t1,gene\_03746.t1,gene\_02038.t1,gene\_07429.t1,gene\_00302.t1,gene\_00832.t1,gene\_09990.t1,gene\_01181.t1,gene\_08300.t1,gene\_01284.t1,gene\_10039.t1,gene\_08534.t1,gene\_02387.t1,gene\_00510.t1,gene\_01393.t1,gene\_03810.t1,gene\_08559.t1,gene\_04083.t1,gene\_06475.t1,gene\_07773.t1,gene\_10263.t1,gene\_00430.t1,gene\_07979.t1,gene\_02586.t1,gene\_01066.t1,gene\_03685.t1,gene\_01128.t1,gene\_07015.t1,gene\_08910.t1,gene\_07736.t1,gene\_04647.t1,gene\_06143.t1,gene\_09266.t1,gene\_04109.t1,gene\_06940.t1,gene\_03414.t1,gene\_04173.t1,gene\_03617.t1,gene\_05217.t1,gene\_04329.t1,gene\_03807.t1,gene\_03750.t1, | | metal ion binding | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0046872 | 397 | gene\_03809.t1,gene\_07851.t1,gene\_02110.t1,gene\_09250.t1,gene\_02268.t1,gene\_08076.t1,gene\_00013.t1,gene\_00949.t1,gene\_03406.t1,gene\_04244.t1,gene\_05585.t1,gene\_02476.t1,gene\_06598.t1,gene\_07290.t1,gene\_05846.t1,gene\_04202.t1,gene\_10491.t1,gene\_06077.t1,gene\_02175.t1,gene\_05978.t1,gene\_04241.t1,gene\_07978.t1,gene\_09195.t1,gene\_03326.t1,gene\_04178.t1,gene\_02331.t1,gene\_06049.t1,gene\_08159.t1,gene\_01374.t1,gene\_03957.t1,gene\_09462.t1,gene\_07625.t1,gene\_02123.t1,gene\_08361.t1,gene\_08412.t1,gene\_05871.t1,gene\_10433.t1,gene\_02713.t1,gene\_01513.t1,gene\_08193.t1,gene\_05793.t1,gene\_03008.t1,gene\_08152.t1,gene\_04509.t1,gene\_05364.t1,gene\_03654.t1,gene\_08191.t1,gene\_01243.t1,gene\_06163.t1,gene\_01018.t1,gene\_02503.t1,gene\_01840.t1,gene\_10167.t1,gene\_08455.t1,gene\_04413.t1,gene\_01472.t1,gene\_03353.t1,gene\_07889.t1,gene\_09269.t1,gene\_01933.t1,gene\_05493.t1,gene\_09189.t1,gene\_06842.t1,gene\_02927.t1,gene\_01046.t1,gene\_09097.t1,gene\_09260.t1,gene\_00621.t1,gene\_03643.t1,gene\_08431.t1,gene\_00418.t1,gene\_01855.t1,gene\_10287.t1,gene\_05170.t1,gene\_02272.t1,gene\_02312.t1,gene\_04118.t1,gene\_05363.t1,gene\_07522.t1,gene\_03882.t1,gene\_06771.t1,gene\_06709.t1,gene\_00972.t1,gene\_08058.t1,gene\_02452.t1,gene\_06827.t1,gene\_06397.t1,gene\_04236.t1,gene\_05706.t1,gene\_01131.t1,gene\_05792.t1,gene\_01838.t1,gene\_02270.t1,gene\_05686.t1,gene\_06253.t1,gene\_08107.t1,gene\_01020.t1,gene\_03394.t1,gene\_07825.t1,gene\_04634.t1,gene\_06627.t1,gene\_02830.t1 | | metal ion binding | molecular\_function |
| GO:0004013 | 1 | gene\_05443.t1 | | adenosylhomocysteinase activity | molecular\_function |
| GO:0004014 | 1 | gene\_08168.t1 | | adenosylmethionine decarboxylase activity | molecular\_function |
| GO:0003916 | 1 | gene\_00205.t1 | | DNA topoisomerase activity | molecular\_function |
| GO:0016757 | 45 | gene\_08315.t1,gene\_07807.t1,gene\_05801.t1,gene\_06425.t1,gene\_03767.t1,gene\_05724.t1,gene\_01691.t1,gene\_04005.t1,gene\_00571.t1,gene\_08478.t1,gene\_06904.t1,gene\_07300.t1,gene\_09608.t1,gene\_02938.t1,gene\_09213.t1,gene\_08132.t1,gene\_10106.t1,gene\_01064.t1,gene\_10315.t1,gene\_06898.t1,gene\_09242.t1,gene\_05221.t1,gene\_10127.t1,gene\_03572.t1,gene\_07018.t1,gene\_08128.t1,gene\_02758.t1,gene\_00661.t1,gene\_01248.t1,gene\_09836.t1,gene\_00090.t1,gene\_04474.t1,gene\_04493.t1,gene\_00134.t1,gene\_05140.t1,gene\_07375.t1,gene\_01098.t1,gene\_06265.t1,gene\_05692.t1,gene\_02369.t1,gene\_04094.t1,gene\_02964.t1,gene\_06281.t1,gene\_10012.t1,gene\_03124.t1 | | glycosyltransferase activity | molecular\_function |
| GO:0016758 | 4 | gene\_00199.t1,gene\_03481.t1,gene\_07845.t1,gene\_07540.t1 | | hexosyltransferase activity | molecular\_function |
| GO:0000993 | 1 | gene\_04188.t1 | | RNA polymerase II complex binding | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0000995 | 1 | gene\_03056.t1 | | RNA polymerase III general transcription initiation factor activity | molecular\_function |
| GO:0003910 | 4 | gene\_05677.t1,gene\_07821.t1,gene\_01043.t1,gene\_05811.t1 | | DNA ligase (ATP) activity | molecular\_function |
| GO:0033897 | 2 | gene\_05684.t1,gene\_01869.t1 | | ribonuclease T2 activity | molecular\_function |
| GO:0042393 | 3 | gene\_07532.t1,gene\_05665.t1,gene\_08023.t1 | | histone binding | molecular\_function |
| GO:0061711 | 2 | gene\_04246.t1,gene\_09601.t1 | | N(6)-L-threonylcarbamoyladenine synthase activity | molecular\_function |
| GO:0106364 | 1 | gene\_10412.t1 | | 4-hydroxy-3-all-trans-hexaprenylbenzoate oxygenase activity | molecular\_function |
| GO:0003854 | 4 | gene\_02639.t1,gene\_07798.t1,gene\_00026.t1,gene\_02494.t1 | | 3-beta-hydroxy-delta5-steroid dehydrogenase activity | molecular\_function |
| GO:0047389 | 2 | gene\_05869.t1,gene\_05485.t1 | | glycerophosphocholine phosphodiesterase activity | molecular\_function |
| GO:0003676 | 136 | gene\_04241.t1,gene\_06318.t1,gene\_03242.t1,gene\_00613.t1,gene\_10474.t1,gene\_00005.t1,gene\_03583.t1,gene\_07444.t1,gene\_10377.t1,gene\_10402.t1,gene\_02841.t1,gene\_04777.t1,gene\_06202.t1,gene\_03074.t1,gene\_01097.t1,gene\_05819.t1,gene\_00318.t1,gene\_10492.t1,gene\_03372.t1,gene\_10212.t1,gene\_06245.t1,gene\_03026.t1,gene\_05035.t1,gene\_05055.t1,gene\_02360.t1,gene\_06902.t1,gene\_04955.t1,gene\_10383.t1,gene\_07715.t1,gene\_02203.t1,gene\_04895.t1,gene\_03834.t1,gene\_09756.t1,gene\_06028.t1,gene\_02480.t1,gene\_08063.t1,gene\_00897.t1,gene\_03790.t1,gene\_08291.t1,gene\_05233.t1,gene\_00875.t1,gene\_00166.t1,gene\_03702.t1,gene\_03855.t1,gene\_03654.t1,gene\_02998.t1,gene\_07852.t1,gene\_08484.t1,gene\_03494.t1,gene\_00284.t1,gene\_01990.t1,gene\_08388.t1,gene\_06329.t1,gene\_00845.t1,gene\_00363.t1,gene\_06649.t1,gene\_01826.t1,gene\_07355.t1,gene\_05004.t1,gene\_00597.t1,gene\_04116.t1,gene\_05002.t1,gene\_04909.t1,gene\_09857.t1,gene\_00412.t1,gene\_06488.t1,gene\_07853.t1,gene\_04978.t1,gene\_04788.t1,gene\_03950.t1,gene\_07356.t1,gene\_06050.t1,gene\_01532.t1,gene\_10176.t1,gene\_08342.t1,gene\_02077.t1,gene\_05909.t1,gene\_04921.t1,gene\_04505.t1,gene\_06611.t1,gene\_04404.t1,gene\_07500.t1,gene\_08273.t1,gene\_01636.t1,gene\_01295.t1,gene\_01093.t1,gene\_05314.t1,gene\_01066.t1,gene\_10208.t1,gene\_03638.t1,gene\_09569.t1,gene\_09843.t1,gene\_06360.t1,gene\_10246.t1,gene\_01706.t1,gene\_07129.t1,gene\_09715.t1,gene\_04776.t1,gene\_06256.t1,gene\_04960.t1,gene\_09823.t1,gene\_04971.t1,gene\_03892.t1,gene\_00001.t1,gene\_07364.t1,gene\_03686.t1,gene\_10576.t1,gene\_08924.t1,gene\_09851.t1,gene\_04884.t1,  gene\_01162.t1,gene\_05855.t1,gene\_06073.t1,gene\_00768.t1,gene\_01828.t1,  gene\_02049.t1,gene\_04448.t1,gene\_04174.t1,gene\_07402.t1,gene\_08391.t1, | | nucleic acid binding | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0003676 | 136 | gene\_07819.t1,gene\_04075.t1,gene\_07680.t1,gene\_00011.t1,gene\_02253.t1,gene\_03157.t1,gene\_04293.t1,gene\_05659.t1,gene\_08276.t1,gene\_07716.t1,gene\_01182.t1,gene\_05388.t1,gene\_00977.t1,gene\_05426.t1,gene\_07659.t1,gene\_01762.t1 | | nucleic acid binding | molecular\_function |
| GO:0008375 | 5 | gene\_10658.t1,gene\_05113.t1,gene\_04805.t1,gene\_04999.t1,gene\_01969.t1 | | acetylglucosaminyltransferase activity | molecular\_function |
| GO:0003678 | 15 | gene\_00515.t1,gene\_02991.t1,gene\_01710.t1,gene\_01540.t1,gene\_07862.t1,gene\_04537.t1,gene\_02228.t1,gene\_02715.t1,gene\_00363.t1,gene\_07321.t1,gene\_09071.t1,gene\_09891.t1,gene\_09591.t1,gene\_07906.t1,gene\_08245.t1 | | DNA helicase activity | molecular\_function |
| GO:0046523 | 1 | gene\_02356.t1 | | S-methyl-5-thioribose-1-phosphate isomerase activity | molecular\_function |
| GO:0030272 | 1 | gene\_09195.t1 | | 5-formyltetrahydrofolate cyclo-ligase activity | molecular\_function |
| GO:0047657 | 4 | gene\_04297.t1,gene\_07022.t1,gene\_05380.t1,gene\_04526.t1 | | alpha-1,3-glucan synthase activity | molecular\_function |
| GO:0030276 | 4 | gene\_07272.t1,gene\_02601.t1,gene\_06752.t1,gene\_00554.t1 | | clathrin binding | molecular\_function |
| GO:0097159 | 2 | gene\_03800.t1,gene\_00746.t1 | | organic cyclic compound binding | molecular\_function |
| GO:0052909 | 1 | gene\_09916.t1 | | 18S rRNA (adenine(1779)-N(6)/adenine(1780)-N(6))-dimethyltransferase activity | molecular\_function |
| GO:0017025 | 3 | gene\_03056.t1,gene\_02523.t1,gene\_03014.t1 | | TBP-class protein binding | molecular\_function |
| GO:0017022 | 1 | gene\_01660.t1 | | myosin binding | molecular\_function |
| GO:0042577 | 4 | gene\_02872.t1,gene\_00809.t1,gene\_07679.t1,gene\_05347.t1 | | lipid phosphatase activity | molecular\_function |
| GO:0097027 | 3 | gene\_09995.t1,gene\_02100.t1,gene\_07199.t1 | | ubiquitin-protein transferase activator activity | molecular\_function |
| GO:0097020 | 1 | gene\_02368.t1 | | COPII receptor activity | molecular\_function |
| GO:0003690 | 3 | gene\_08595.t1,gene\_05469.t1,gene\_02751.t1 | | double-stranded DNA binding | molecular\_function |
| GO:0003697 | 11 | gene\_00455.t1,gene\_02617.t1,gene\_04551.t1,gene\_06097.t1,gene\_05469.t1,gene\_02995.t1,gene\_08595.t1,gene\_06339.t1,gene\_10392.t1,gene\_04203.t1,gene\_00867.t1 | | single-stranded DNA binding | molecular\_function |
| GO:0061981 | 2 | gene\_00551.t1,gene\_04082.t1 | | 3-hydroxykynureninase activity | molecular\_function |
| GO:0004864 | 1 | gene\_08172.t1 | | protein phosphatase inhibitor activity | molecular\_function |
| GO:0004865 | 1 | gene\_05153.t1 | | protein serine/threonine phosphatase inhibitor activity | molecular\_function |
| GO:0004866 | 1 | gene\_06474.t1 | | endopeptidase inhibitor activity | molecular\_function |
| GO:0047938 | 1 | gene\_02885.t1 | | glucose-6-phosphate 1-epimerase activity | molecular\_function |
| GO:0004512 | 1 | gene\_00961.t1 | | inositol-3-phosphate synthase activity | molecular\_function |
| GO:0103025 | 3 | gene\_04296.t1,gene\_05379.t1,gene\_04047.t1 | | alpha-amylase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0106322 | 1 | gene\_00963.t1 | | S-(hydroxymethyl)glutathione dehydrogenase NAD activity | molecular\_function |
| GO:0004515 | 1 | gene\_03849.t1 | | nicotinate-nucleotide adenylyltransferase activity | molecular\_function |
| GO:0004516 | 1 | gene\_04641.t1 | | nicotinate phosphoribosyltransferase activity | molecular\_function |
| GO:0106321 | 1 | gene\_00963.t1 | | S-(hydroxymethyl)glutathione dehydrogenase NADP activity | molecular\_function |
| GO:0004518 | 5 | gene\_09781.t1,gene\_05791.t1,gene\_09338.t1,gene\_05747.t1,gene\_09702.t1 | | nuclease activity | molecular\_function |
| GO:0004519 | 21 | gene\_06477.t1,gene\_04510.t1,gene\_07978.t1,gene\_02617.t1,gene\_02939.t1,gene\_07270.t1,gene\_09922.t1,gene\_04548.t1,gene\_09684.t1,gene\_07789.t1,gene\_08535.t1,gene\_03737.t1,gene\_03583.t1,gene\_04176.t1,gene\_01066.t1,gene\_06444.t1,gene\_01020.t1,gene\_09105.t1,gene\_02565.t1,gene\_05910.t1,gene\_04293.t1 | | endonuclease activity | molecular\_function |
| GO:0001228 | 3 | gene\_09058.t1,gene\_02408.t1,gene\_10265.t1 | | DNA-binding transcription activator activity, RNA polymerase II-specific | molecular\_function |
| GO:0036381 | 1 | gene\_04580.t1 | | pyridoxal 5'-phosphate synthase (glutamine hydrolysing) activity | molecular\_function |
| GO:0005200 | 3 | gene\_00668.t1,gene\_00015.t1,gene\_08913.t1 | | structural constituent of cytoskeleton | molecular\_function |
| GO:0004640 | 1 | gene\_08809.t1 | | phosphoribosylanthranilate isomerase activity | molecular\_function |
| GO:0030729 | 3 | gene\_08667.t1,gene\_10584.t1,gene\_00969.t1 | | acetoacetate-CoA ligase activity | molecular\_function |
| GO:0102265 | 3 | gene\_02091.t1,gene\_06558.t1,gene\_07216.t1 | | tRNA-dihydrouridine47 synthase activity | molecular\_function |
| GO:0004467 | 1 | gene\_02649.t1 | | long-chain fatty acid-CoA ligase activity | molecular\_function |
| GO:0004462 | 1 | gene\_03769.t1 | | lactoylglutathione lyase activity | molecular\_function |
| GO:0008972 | 1 | gene\_00596.t1 | | phosphomethylpyrimidine kinase activity | molecular\_function |
| GO:0008757 | 2 | gene\_07733.t1,gene\_10340.t1 | | S-adenosylmethionine-dependent methyltransferase activity | molecular\_function |
| GO:0008977 | 1 | gene\_00560.t1 | | prephenate dehydrogenase (NAD+) activity | molecular\_function |
| GO:0008198 | 3 | gene\_05541.t1,gene\_00790.t1,gene\_07394.t1 | | ferrous iron binding | molecular\_function |
| GO:0008199 | 5 | gene\_02569.t1,gene\_09653.t1,gene\_06959.t1,gene\_09989.t1,gene\_02177.t1 | | ferric iron binding | molecular\_function |
| GO:0102867 | 1 | gene\_02844.t1 | | molybdenum cofactor sulfurtransferase activity | molecular\_function |
| GO:0008193 | 1 | gene\_02115.t1 | | tRNA guanylyltransferase activity | molecular\_function |
| GO:0008194 | 6 | gene\_00199.t1,gene\_07177.t1,gene\_03481.t1,gene\_07845.t1,gene\_07540.t1,gene\_09691.t1 | | UDP-glycosyltransferase activity | molecular\_function |
| GO:0004648 | 1 | gene\_09692.t1 | | O-phospho-L-serine:2-oxoglutarate aminotransferase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0004649 | 1 | gene\_02243.t1 | | poly(ADP-ribose) glycohydrolase activity | molecular\_function |
| GO:0004641 | 1 | gene\_09629.t1 | | phosphoribosylformylglycinamidine cyclo-ligase activity | molecular\_function |
| GO:0004642 | 1 | gene\_08162.t1 | | phosphoribosylformylglycinamidine synthase activity | molecular\_function |
| GO:0004643 | 1 | gene\_00429.t1 | | phosphoribosylaminoimidazolecarboxamide formyltransferase activity | molecular\_function |
| GO:0045127 | 2 | gene\_08150.t1,gene\_03440.t1 | | N-acetylglucosamine kinase activity | molecular\_function |
| GO:0102193 | 2 | gene\_07564.t1,gene\_04104.t1 | | protein-ribulosamine 3-kinase activity | molecular\_function |
| GO:0000175 | 2 | gene\_03242.t1,gene\_03026.t1 | | 3'-5'-exoribonuclease activity | molecular\_function |
| GO:0004888 | 2 | gene\_00670.t1,gene\_04229.t1 | | transmembrane signaling receptor activity | molecular\_function |
| GO:0008479 | 2 | gene\_01300.t1,gene\_07887.t1 | | queuine tRNA-ribosyltransferase activity | molecular\_function |
| GO:0008022 | 1 | gene\_06332.t1 | | protein C-terminus binding | molecular\_function |
| GO:0008379 | 2 | gene\_03631.t1,gene\_02909.t1 | | thioredoxin peroxidase activity | molecular\_function |
| GO:0008374 | 8 | gene\_08056.t1,gene\_03250.t1,gene\_05956.t1,gene\_08886.t1,gene\_02539.t1,gene\_01208.t1,gene\_07175.t1,gene\_06453.t1 | | O-acyltransferase activity | molecular\_function |
| GO:0003855 | 5 | gene\_09377.t1,gene\_05125.t1,gene\_05587.t1,gene\_02251.t1,gene\_05589.t1 | | 3-dehydroquinate dehydratase activity | molecular\_function |
| GO:0003856 | 1 | gene\_02251.t1 | | 3-dehydroquinate synthase activity | molecular\_function |
| GO:0003852 | 1 | gene\_06642.t1 | | 2-isopropylmalate synthase activity | molecular\_function |
| GO:0016538 | 6 | gene\_04586.t1,gene\_06207.t1,gene\_04459.t1,gene\_09737.t1,gene\_04102.t1,gene\_08654.t1 | | cyclin-dependent protein serine/threonine kinase regulator activity | molecular\_function |
| GO:0036361 | 1 | gene\_08759.t1 | | racemase activity, acting on amino acids and derivatives | molecular\_function |
| GO:0008143 | 2 | gene\_03979.t1,gene\_05249.t1 | | poly(A) binding | molecular\_function |
| GO:0003988 | 4 | gene\_07030.t1,gene\_10028.t1,gene\_10634.t1,gene\_06029.t1 | | acetyl-CoA C-acyltransferase activity | molecular\_function |
| GO:0003989 | 1 | gene\_01074.t1 | | acetyl-CoA carboxylase activity | molecular\_function |
| GO:0003986 | 1 | gene\_00257.t1 | | acetyl-CoA hydrolase activity | molecular\_function |
| GO:0003987 | 1 | gene\_10043.t1 | | acetate-CoA ligase activity | molecular\_function |
| GO:0004088 | 2 | gene\_06540.t1,gene\_08081.t1 | | carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity | molecular\_function |
| GO:0004089 | 3 | gene\_10073.t1,gene\_03587.t1,gene\_04635.t1 | | carbonate dehydratase activity | molecular\_function |
| GO:0003983 | 1 | gene\_04652.t1 | | UTP:glucose-1-phosphate uridylyltransferase activity | molecular\_function |
| GO:0003980 | 1 | gene\_03162.t1 | | UDP-glucose:glycoprotein glucosyltransferase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0016531 | 2 | gene\_06931.t1,gene\_06951.t1 | | copper chaperone activity | molecular\_function |
| GO:0015099 | 1 | gene\_01059.t1 | | nickel cation transmembrane transporter activity | molecular\_function |
| GO:0015098 | 1 | gene\_07072.t1 | | molybdate ion transmembrane transporter activity | molecular\_function |
| GO:0015095 | 6 | gene\_04463.t1,gene\_03336.t1,gene\_09232.t1,gene\_00892.t1,gene\_01165.t1,gene\_02031.t1 | | magnesium ion transmembrane transporter activity | molecular\_function |
| GO:0016614 | 20 | gene\_03385.t1,gene\_09799.t1,gene\_09802.t1,gene\_00472.t1,gene\_07061.t1,gene\_09761.t1,gene\_08251.t1,gene\_05272.t1,gene\_05482.t1,gene\_01077.t1,gene\_10298.t1,gene\_10471.t1,gene\_09950.t1,gene\_04408.t1,gene\_01974.t1,gene\_03728.t1,gene\_09906.t1,gene\_09805.t1,gene\_04382.t1,gene\_00546.t1 | | oxidoreductase activity, acting on CH-OH group of donors | molecular\_function |
| GO:0051213 | 53 | gene\_07074.t1,gene\_05732.t1,gene\_00763.t1,gene\_04074.t1,gene\_05911.t1,gene\_00181.t1,gene\_06957.t1,gene\_08152.t1,gene\_07543.t1,gene\_09114.t1,gene\_00457.t1,gene\_04443.t1,gene\_01975.t1,gene\_03774.t1,gene\_03106.t1,gene\_04373.t1,gene\_06877.t1,gene\_08672.t1,gene\_00013.t1,gene\_07708.t1,gene\_09095.t1,gene\_09120.t1,gene\_09148.t1,gene\_04751.t1,gene\_04677.t1,gene\_04083.t1,gene\_06521.t1,gene\_09199.t1,gene\_03358.t1,gene\_07830.t1,gene\_05792.t1,gene\_09788.t1,gene\_01499.t1,gene\_06460.t1,gene\_05541.t1,gene\_07152.t1,gene\_08361.t1,gene\_05931.t1,gene\_01495.t1,gene\_03126.t1,gene\_06967.t1,gene\_07228.t1,gene\_09493.t1,gene\_07319.t1,gene\_05864.t1,gene\_00790.t1,gene\_01808.t1,gene\_09494.t1,gene\_08658.t1,gene\_05930.t1,gene\_02942.t1,gene\_01810.t1,gene\_02845.t1 | | dioxygenase activity | molecular\_function |
| GO:0016616 | 19 | gene\_05973.t1,gene\_06470.t1,gene\_09792.t1,gene\_02634.t1,gene\_07479.t1,gene\_01335.t1,gene\_02157.t1,gene\_08580.t1,gene\_10214.t1,gene\_06021.t1,gene\_10236.t1,gene\_01609.t1,gene\_07689.t1,gene\_06137.t1,gene\_07063.t1,gene\_09683.t1,gene\_06599.t1,gene\_08826.t1,gene\_02167.t1 | | oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor | molecular\_function |
| GO:0008408 | 3 | gene\_09857.t1,gene\_06318.t1,gene\_06050.t1 | | 3'-5' exonuclease activity | molecular\_function |
| GO:0008409 | 1 | gene\_07283.t1 | | 5'-3' exonuclease activity | molecular\_function |
| GO:0016765 | 5 | gene\_10116.t1,gene\_02343.t1,gene\_04197.t1,gene\_05126.t1,gene\_00782.t1 | | transferase activity, transferring alkyl or aryl (other than methyl) groups | molecular\_function |
| GO:0019239 | 6 | gene\_08778.t1,gene\_09473.t1,gene\_01224.t1,gene\_10457.t1,gene\_08641.t1,gene\_08293.t1 | | deaminase activity | molecular\_function |
| GO:0106222 | 1 | gene\_05249.t1 | | lncRNA binding | molecular\_function |
| GO:0000987 | 1 | gene\_00891.t1 | | cis-regulatory region sequence-specific DNA binding | molecular\_function |
| GO:0015140 | 3 | gene\_01317.t1,gene\_07390.t1,gene\_07391.t1 | | malate transmembrane transporter activity | molecular\_function |
| GO:0050113 | 2 | gene\_01340.t1,gene\_00527.t1 | | inositol oxygenase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0004694 | 1 | gene\_08078.t1 | | eukaryotic translation initiation factor 2alpha kinase activity | molecular\_function |
| GO:0019237 | 1 | gene\_04179.t1 | | centromeric DNA binding | molecular\_function |
| GO:0000981 | 340 | gene\_03118.t1,gene\_02220.t1,gene\_02526.t1,gene\_07639.t1,gene\_06503.t1,gene\_04976.t1,gene\_03130.t1,gene\_10151.t1,gene\_04257.t1,gene\_00286.t1,gene\_00732.t1,gene\_06585.t1,gene\_05301.t1,gene\_09549.t1,gene\_03018.t1,gene\_03606.t1,gene\_07166.t1,gene\_06706.t1,gene\_04378.t1,gene\_01987.t1,gene\_04263.t1,gene\_08694.t1,gene\_04651.t1,gene\_04014.t1,gene\_04706.t1,gene\_10237.t1,gene\_00182.t1,gene\_08824.t1,gene\_03062.t1,gene\_09457.t1,gene\_04873.t1,gene\_02977.t1,gene\_02297.t1,gene\_05808.t1,gene\_08345.t1,gene\_01692.t1,gene\_05311.t1,gene\_07128.t1,gene\_03228.t1,gene\_00556.t1,gene\_06258.t1,gene\_01305.t1,gene\_07284.t1,gene\_05527.t1,gene\_03248.t1,gene\_02170.t1,gene\_07241.t1,gene\_03295.t1,gene\_06020.t1,gene\_09813.t1,gene\_01948.t1,gene\_00908.t1,gene\_08441.t1,gene\_06225.t1,gene\_04045.t1,gene\_09339.t1,gene\_08254.t1,gene\_01145.t1,gene\_06978.t1,gene\_05273.t1,gene\_03447.t1,gene\_09375.t1,gene\_06395.t1,gene\_03513.t1,gene\_09814.t1,gene\_05277.t1,gene\_06934.t1,gene\_02808.t1,gene\_05121.t1,gene\_03050.t1,gene\_00562.t1,gene\_04918.t1,gene\_02847.t1,gene\_06532.t1,gene\_02034.t1,gene\_03831.t1,gene\_09930.t1,gene\_04979.t1,gene\_07827.t1,gene\_08560.t1,gene\_01153.t1,gene\_04481.t1,gene\_09656.t1,gene\_04937.t1,gene\_07168.t1,gene\_02946.t1,gene\_09957.t1,gene\_01809.t1,gene\_05721.t1,gene\_02948.t1,gene\_10543.t1,gene\_04650.t1,gene\_06088.t1,gene\_02605.t1,gene\_05540.t1,gene\_00052.t1,gene\_03342.t1,gene\_00959.t1,gene\_00308.t1,gene\_03366.t1,gene\_07677.t1,gene\_01887.t1,gene\_00564.t1,gene\_04041.t1,gene\_02809.t1,gene\_06852.t1,gene\_09809.t1,gene\_04022.t1,gene\_04081.t1,gene\_08155.t1,gene\_01527.t1,gene\_06732.t1,gene\_06614.t1,gene\_05950.t1,gene\_06402.t1,gene\_03132.t1,gene\_08477.t1,gene\_02916.t1,gene\_10058.t1,gene\_10254.t1,gene\_01612.t1,gene\_06584.t1,gene\_01394.t1,gene\_06795.t1,gene\_10553.t1,gene\_07693.t1,gene\_01922.t1,gene\_05736.t1,gene\_04208.t1,gene\_09537.t1,gene\_07635.t1,gene\_09878.t1,gene\_07088.t1,gene\_01937.t1,gene\_05474.t1,gene\_02318.t1,gene\_01345.t1,gene\_09126.t1,gene\_04048.t1,gene\_04028.t1,gene\_05383.t1,gene\_07085.t1,gene\_10666.t1,gene\_09370.t1,gene\_04695.t1,gene\_04627.t1,gene\_04473.t1,gene\_04676.t1,gene\_07382.t1,gene\_07955.t1,gene\_06230.t1,gene\_05517.t1,gene\_08083.t1,gene\_08638.t1,gene\_10051.t1,gene\_10211.t1,gene\_07948.t1,gene\_06089.t1,gene\_06606.t1,gene\_00614.t1,gene\_01535.t1,gene\_03812.t1,gene\_02107.t1,gene\_01135.t1,gene\_02385.t1,gene\_08947.t1,gene\_00822.t1,gene\_00640.t1,gene\_00395.t1,gene\_07583.t1, | | DNA-binding transcription factor activity, RNA polymerase II-specific | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0000981 | 340 | gene\_03770.t1,gene\_09652.t1,gene\_02580.t1,gene\_01819.t1,gene\_02151.t1,gene\_06679.t1,gene\_01512.t1,gene\_02652.t1,gene\_02786.t1,gene\_09590.t1,gene\_05080.t1,gene\_03761.t1,gene\_04013.t1,gene\_04515.t1,gene\_02282.t1,gene\_10255.t1,gene\_03463.t1,gene\_06059.t1,gene\_05932.t1,gene\_08135.t1,gene\_03650.t1,gene\_04594.t1,gene\_08833.t1,gene\_04621.t1,gene\_10663.t1,gene\_00046.t1,gene\_08041.t1,gene\_04732.t1,gene\_02874.t1,gene\_05299.t1,gene\_02529.t1,gene\_02607.t1,gene\_07537.t1,gene\_01756.t1,gene\_10629.t1,gene\_05595.t1,gene\_06672.t1,gene\_07683.t1,gene\_08569.t1,gene\_01742.t1,gene\_06249.t1,gene\_03763.t1,gene\_00921.t1,gene\_02757.t1,gene\_08608.t1,gene\_03655.t1,gene\_08550.t1,gene\_02050.t1,gene\_10083.t1,gene\_05725.t1,gene\_09939.t1,gene\_06172.t1,gene\_10374.t1,gene\_05082.t1,gene\_02042.t1,gene\_06023.t1,gene\_06515.t1,gene\_01498.t1,gene\_09646.t1,gene\_07548.t1,gene\_02512.t1,gene\_00803.t1,gene\_01262.t1,gene\_02608.t1,gene\_05588.t1,gene\_01529.t1,gene\_00747.t1,gene\_01321.t1,gene\_02502.t1,gene\_09131.t1,gene\_06377.t1,gene\_01359.t1,gene\_07785.t1,gene\_00847.t1,gene\_03869.t1,gene\_06766.t1,gene\_04903.t1,gene\_08366.t1,gene\_03427.t1,gene\_08148.t1,gene\_09897.t1,gene\_04524.t1,gene\_09526.t1,gene\_09330.t1,gene\_05547.t1,gene\_07320.t1,gene\_01857.t1,gene\_05559.t1,gene\_03741.t1,gene\_09969.t1,gene\_08703.t1,gene\_04693.t1,gene\_01156.t1,gene\_06095.t1,gene\_09035.t1,gene\_08280.t1,gene\_03747.t1,gene\_07229.t1,gene\_06823.t1,gene\_05070.t1,gene\_03642.t1,gene\_02068.t1,gene\_10614.t1,gene\_01377.t1,gene\_02086.t1,gene\_02027.t1,gene\_02321.t1,gene\_01730.t1,gene\_01134.t1,gene\_10509.t1,gene\_01708.t1,gene\_04946.t1,gene\_05206.t1,gene\_03607.t1,gene\_06936.t1,gene\_09361.t1,gene\_04830.t1,gene\_06675.t1,gene\_07726.t1,gene\_10498.t1,gene\_05087.t1,gene\_10172.t1,gene\_09865.t1,gene\_05814.t1,gene\_02178.t1,gene\_01774.t1,gene\_02661.t1,gene\_00770.t1,gene\_03408.t1,gene\_10056.t1,gene\_10205.t1,gene\_08479.t1,gene\_03870.t1,gene\_03107.t1,gene\_03304.t1,gene\_07612.t1,gene\_02677.t1,gene\_01998.t1,gene\_09748.t1,gene\_03842.t1,gene\_09460.t1,gene\_04795.t1,gene\_06963.t1,gene\_03748.t1,gene\_04854.t1,gene\_09935.t1,gene\_04307.t1,gene\_09979.t1,gene\_08139.t1,gene\_03595.t1,gene\_00891.t1,gene\_05810.t1,gene\_00059.t1,gene\_03596.t1,gene\_06040.t1,gene\_10649.t1,gene\_07040.t1,gene\_01530.t1,gene\_05972.t1,gene\_07333.t1,gene\_00656.t1,gene\_05151.t1,gene\_00634.t1,gene\_00018.t1,gene\_01954.t1,gene\_02730.t1,gene\_09697.t1,gene\_03210.t1,gene\_00968.t1,gene\_07525.t1 | | DNA-binding transcription factor activity, RNA polymerase II-specific | molecular\_function |
| GO:0004329 | 1 | gene\_06799.t1 | | formate-tetrahydrofolate ligase activity | molecular\_function |
| GO:0043399 | 1 | gene\_04600.t1 | | tRNA A64-2'-O-ribosylphosphate transferase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0015075 | 1 | gene\_06626.t1 | | ion transmembrane transporter activity | molecular\_function |
| GO:0051998 | 1 | gene\_08076.t1 | | protein carboxyl O-methyltransferase activity | molecular\_function |
| GO:0051996 | 2 | gene\_04746.t1,gene\_10502.t1 | | squalene synthase activity | molecular\_function |
| GO:0035529 | 1 | gene\_09266.t1 | | NADH pyrophosphatase activity | molecular\_function |
| GO:0043175 | 1 | gene\_00538.t1 | | RNA polymerase core enzyme binding | molecular\_function |
| GO:0003689 | 1 | gene\_07620.t1 | | DNA clamp loader activity | molecular\_function |
| GO:0003682 | 5 | gene\_03593.t1,gene\_07314.t1,gene\_05556.t1,gene\_09822.t1,gene\_01705.t1 | | chromatin binding | molecular\_function |
| GO:0003684 | 13 | gene\_09338.t1,gene\_02991.t1,gene\_10061.t1,gene\_04537.t1,gene\_09428.t1,gene\_04737.t1,gene\_03610.t1,gene\_09214.t1,gene\_07736.t1,gene\_04239.t1,gene\_10200.t1,gene\_03712.t1,gene\_08006.t1 | | damaged DNA binding | molecular\_function |
| GO:0036424 | 1 | gene\_06831.t1 | | L-phosphoserine phosphatase activity | molecular\_function |
| GO:0000340 | 1 | gene\_01012.t1 | | RNA 7-methylguanosine cap binding | molecular\_function |
| GO:0051920 | 3 | gene\_01515.t1,gene\_02994.t1,gene\_01846.t1 | | peroxiredoxin activity | molecular\_function |
| GO:0001216 | 1 | gene\_08925.t1 | | DNA-binding transcription activator activity | molecular\_function |
| GO:0050661 | 38 | gene\_03675.t1,gene\_10513.t1,gene\_06728.t1,gene\_08137.t1,gene\_08705.t1,gene\_08768.t1,gene\_06489.t1,gene\_08570.t1,gene\_05095.t1,gene\_08426.t1,gene\_05358.t1,gene\_06860.t1,gene\_01733.t1,gene\_03823.t1,gene\_08980.t1,gene\_09331.t1,gene\_02054.t1,gene\_09021.t1,gene\_09500.t1,gene\_00932.t1,gene\_06569.t1,gene\_06816.t1,gene\_08094.t1,gene\_07722.t1,gene\_02611.t1,gene\_05553.t1,gene\_05635.t1,gene\_01216.t1,gene\_06522.t1,gene\_01430.t1,gene\_01051.t1,gene\_06491.t1,gene\_07999.t1,gene\_07897.t1,gene\_10641.t1,gene\_09431.t1,gene\_07758.t1,gene\_08675.t1 | | NADP binding | molecular\_function |
| GO:0050660 | 68 | gene\_08137.t1,gene\_08181.t1,gene\_04289.t1,gene\_07897.t1,gene\_08251.t1,gene\_08705.t1,gene\_06489.t1,gene\_09802.t1,gene\_00765.t1,gene\_10298.t1,gene\_02079.t1,gene\_05095.t1,gene\_09906.t1,gene\_06475.t1,gene\_08570.t1,gene\_10513.t1,gene\_09805.t1,gene\_05482.t1,gene\_01249.t1,gene\_00546.t1,gene\_08094.t1,gene\_07523.t1,gene\_06728.t1,gene\_05272.t1,gene\_04623.t1,gene\_01733.t1,gene\_04382.t1,gene\_04134.t1,gene\_01480.t1,gene\_07137.t1,gene\_09331.t1,gene\_02054.t1,gene\_03728.t1,gene\_06311.t1,gene\_07216.t1,gene\_09021.t1,gene\_09577.t1,gene\_09500.t1,gene\_00932.t1,gene\_03385.t1,gene\_08354.t1,gene\_09950.t1,gene\_00970.t1,gene\_07061.t1,gene\_09761.t1,gene\_06558.t1,gene\_09799.t1,gene\_04541.t1,gene\_05553.t1,gene\_10471.t1,gene\_06522.t1,gene\_02091.t1,gene\_08592.t1,gene\_00472.t1,gene\_08047.t1, | | flavin adenine dinucleotide binding | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0050660 | 68 | gene\_06594.t1,gene\_04708.t1,gene\_03858.t1,gene\_07285.t1,gene\_07999.t1,gene\_01077.t1,gene\_10641.t1,gene\_04408.t1,gene\_01974.t1,gene\_09431.t1,gene\_06691.t1,gene\_08675.t1,gene\_08764.t1 | | flavin adenine dinucleotide binding | molecular\_function |
| GO:0004502 | 1 | gene\_02644.t1 | | kynurenine 3-monooxygenase activity | molecular\_function |
| GO:0017136 | 1 | gene\_09874.t1 | | NAD-dependent histone deacetylase activity | molecular\_function |
| GO:0005053 | 1 | gene\_01977.t1 | | peroxisome matrix targeting signal-2 binding | molecular\_function |
| GO:1903425 | 1 | gene\_06264.t1 | | fluoride transmembrane transporter activity | molecular\_function |
| GO:0004108 | 1 | gene\_04195.t1 | | citrate (Si)-synthase activity | molecular\_function |
| GO:0008353 | 1 | gene\_07367.t1 | | RNA polymerase II CTD heptapeptide repeat kinase activity | molecular\_function |
| GO:0008986 | 1 | gene\_06471.t1 | | pyruvate, water dikinase activity | molecular\_function |
| GO:0004479 | 1 | gene\_02437.t1 | | methionyl-tRNA formyltransferase activity | molecular\_function |
| GO:0004478 | 1 | gene\_05535.t1 | | methionine adenosyltransferase activity | molecular\_function |
| GO:0004471 | 2 | gene\_06433.t1,gene\_01131.t1 | | malate dehydrogenase (decarboxylating) (NAD+) activity | molecular\_function |
| GO:0004477 | 1 | gene\_06799.t1 | | methenyltetrahydrofolate cyclohydrolase activity | molecular\_function |
| GO:0004476 | 2 | gene\_01454.t1,gene\_08772.t1 | | mannose-6-phosphate isomerase activity | molecular\_function |
| GO:0102210 | 2 | gene\_02291.t1,gene\_06586.t1 | | rhamnogalacturonan endolyase activity | molecular\_function |
| GO:0004474 | 1 | gene\_09444.t1 | | malate synthase activity | molecular\_function |
| GO:0043295 | 1 | gene\_08070.t1 | | glutathione binding | molecular\_function |
| GO:0005471 | 1 | gene\_02936.t1 | | ATP:ADP antiporter activity | molecular\_function |
| GO:0004252 | 16 | gene\_08545.t1,gene\_05844.t1,gene\_09415.t1,gene\_10410.t1,gene\_06294.t1,gene\_09050.t1,gene\_03043.t1,gene\_00430.t1,gene\_07983.t1,gene\_01516.t1,gene\_05202.t1,gene\_07700.t1,gene\_10601.t1,gene\_03322.t1,gene\_07191.t1,gene\_10536.t1 | | serine-type endopeptidase activity | molecular\_function |
| GO:0008963 | 1 | gene\_07018.t1 | | phospho-N-acetylmuramoyl-pentapeptide-transferase activity | molecular\_function |
| GO:0008962 | 1 | gene\_04012.t1 | | phosphatidylglycerophosphatase activity | molecular\_function |
| GO:0043169 | 1 | gene\_08420.t1 | | cation binding | molecular\_function |
| GO:0061863 | 1 | gene\_10486.t1 | | microtubule plus end polymerase | molecular\_function |
| GO:0004659 | 3 | gene\_07849.t1,gene\_05257.t1,gene\_04763.t1 | | prenyltransferase activity | molecular\_function |
| GO:0004657 | 3 | gene\_03827.t1,gene\_06401.t1,gene\_02585.t1 | | proline dehydrogenase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0004655 | 1 | gene\_05150.t1 | | porphobilinogen synthase activity | molecular\_function |
| GO:0004652 | 3 | gene\_01933.t1,gene\_04542.t1,gene\_06034.t1 | | polynucleotide adenylyltransferase activity | molecular\_function |
| GO:0004651 | 1 | gene\_01488.t1 | | polynucleotide 5'-phosphatase activity | molecular\_function |
| GO:0004650 | 6 | gene\_01725.t1,gene\_09475.t1,gene\_00523.t1,gene\_02551.t1,gene\_00787.t1,gene\_05091.t1 | | polygalacturonase activity | molecular\_function |
| GO:0102148 | 2 | gene\_00936.t1,gene\_07473.t1 | | N-acetyl-beta-D-galactosaminidase activity | molecular\_function |
| GO:0016763 | 1 | gene\_09923.t1 | | pentosyltransferase activity | molecular\_function |
| GO:0003843 | 1 | gene\_10302.t1 | | 1,3-beta-D-glucan synthase activity | molecular\_function |
| GO:0003842 | 3 | gene\_03825.t1,gene\_02582.t1,gene\_06400.t1 | | 1-pyrroline-5-carboxylate dehydrogenase activity | molecular\_function |
| GO:0003841 | 1 | gene\_01086.t1 | | 1-acylglycerol-3-phosphate O-acyltransferase activity | molecular\_function |
| GO:0003847 | 1 | gene\_09933.t1 | | 1-alkyl-2-acetylglycerophosphocholine esterase activity | molecular\_function |
| GO:0003844 | 1 | gene\_08420.t1 | | 1,4-alpha-glucan branching enzyme activity | molecular\_function |
| GO:0003849 | 3 | gene\_00714.t1,gene\_06027.t1,gene\_02892.t1 | | 3-deoxy-7-phosphoheptulonate synthase activity | molecular\_function |
| GO:0003848 | 1 | gene\_00474.t1 | | 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase activity | molecular\_function |
| GO:0016818 | 2 | gene\_06073.t1,gene\_08063.t1 | | hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides | molecular\_function |
| GO:0016813 | 6 | gene\_03227.t1,gene\_09832.t1,gene\_10451.t1,gene\_10044.t1,gene\_09523.t1,gene\_00565.t1 | | hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amidines | molecular\_function |
| GO:0016810 | 18 | gene\_06380.t1,gene\_03401.t1,gene\_04344.t1,gene\_03230.t1,gene\_07682.t1,gene\_02292.t1,gene\_06903.t1,gene\_04069.t1,gene\_04664.t1,gene\_01501.t1,gene\_08253.t1,gene\_00563.t1,gene\_06979.t1,gene\_07991.t1,gene\_06821.t1,gene\_05894.t1,gene\_04675.t1,gene\_07723.t1 | | hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds | molecular\_function |
| GO:0016811 | 5 | gene\_06499.t1,gene\_10192.t1,gene\_10132.t1,gene\_02714.t1,gene\_06700.t1 | | hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides | molecular\_function |
| GO:0016814 | 1 | gene\_08641.t1 | | hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines | molecular\_function |
| GO:0003999 | 1 | gene\_08329.t1 | | adenine phosphoribosyltransferase activity | molecular\_function |
| GO:0003998 | 1 | gene\_03692.t1 | | acylphosphatase activity | molecular\_function |
| GO:0042910 | 3 | gene\_05823.t1,gene\_06518.t1,gene\_09522.t1 | | xenobiotic transmembrane transporter activity | molecular\_function |
| GO:0004096 | 6 | gene\_03391.t1,gene\_02272.t1,gene\_05483.t1,gene\_00621.t1,gene\_00545.t1,gene\_01284.t1 | | catalase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0003995 | 4 | gene\_02079.t1,gene\_08181.t1,gene\_04623.t1,gene\_06475.t1 | | acyl-CoA dehydrogenase activity | molecular\_function |
| GO:0003994 | 2 | gene\_02452.t1,gene\_10491.t1 | | aconitate hydratase activity | molecular\_function |
| GO:0003997 | 2 | gene\_09140.t1,gene\_04430.t1 | | acyl-CoA oxidase activity | molecular\_function |
| GO:0003991 | 1 | gene\_00813.t1 | | acetylglutamate kinase activity | molecular\_function |
| GO:0003993 | 2 | gene\_09797.t1,gene\_07067.t1 | | acid phosphatase activity | molecular\_function |
| GO:0003992 | 1 | gene\_07598.t1 | | N2-acetyl-L-ornithine:2-oxoglutarate 5-aminotransferase activity | molecular\_function |
| GO:0016971 | 2 | gene\_06755.t1,gene\_08482.t1 | | flavin-linked sulfhydryl oxidase activity | molecular\_function |
| GO:0016972 | 1 | gene\_07528.t1 | | thiol oxidase activity | molecular\_function |
| GO:0016603 | 1 | gene\_01441.t1 | | glutaminyl-peptide cyclotransferase activity | molecular\_function |
| GO:0016977 | 1 | gene\_03906.t1 | | chitosanase activity | molecular\_function |
| GO:0008569 | 1 | gene\_05840.t1 | | minus-end-directed microtubule motor activity | molecular\_function |
| GO:0004197 | 3 | gene\_08053.t1,gene\_04251.t1,gene\_10617.t1 | | cysteine-type endopeptidase activity | molecular\_function |
| GO:0003896 | 1 | gene\_06743.t1 | | DNA primase activity | molecular\_function |
| GO:0019887 | 3 | gene\_09329.t1,gene\_05406.t1,gene\_01161.t1 | | protein kinase regulator activity | molecular\_function |
| GO:0019888 | 4 | gene\_07846.t1,gene\_01539.t1,gene\_10264.t1,gene\_00255.t1 | | protein phosphatase regulator activity | molecular\_function |
| GO:0002953 | 2 | gene\_09420.t1,gene\_07843.t1 | | 5'-deoxynucleotidase activity | molecular\_function |
| GO:0008418 | 1 | gene\_04568.t1 | | protein-N-terminal asparagine amidohydrolase activity | molecular\_function |
| GO:0016779 | 5 | gene\_03610.t1,gene\_06335.t1,gene\_01562.t1,gene\_05774.t1,gene\_04173.t1 | | nucleotidyltransferase activity | molecular\_function |
| GO:0051538 | 2 | gene\_04134.t1,gene\_08431.t1 | | 3 iron, 4 sulfur cluster binding | molecular\_function |
| GO:0051539 | 28 | gene\_07021.t1,gene\_02452.t1,gene\_09462.t1,gene\_05493.t1,gene\_06309.t1,gene\_08646.t1,gene\_01018.t1,gene\_04329.t1,gene\_06236.t1,gene\_02122.t1,gene\_07825.t1,gene\_06832.t1,gene\_04152.t1,gene\_06655.t1,gene\_10491.t1,gene\_08431.t1,gene\_00766.t1,gene\_10167.t1,gene\_06856.t1,gene\_10198.t1,gene\_06168.t1,gene\_09283.t1,gene\_02861.t1,gene\_01707.t1,gene\_00595.t1,gene\_08724.t1,gene\_03200.t1,gene\_10039.t1 | | 4 iron, 4 sulfur cluster binding | molecular\_function |
| GO:0016773 | 4 | gene\_01234.t1,gene\_02019.t1,gene\_03840.t1,gene\_00701.t1 | | phosphotransferase activity, alcohol group as acceptor | molecular\_function |
| GO:0016772 | 1 | gene\_00398.t1 | | transferase activity, transferring phosphorus-containing groups | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0051536 | 11 | gene\_00012.t1,gene\_01840.t1,gene\_00550.t1,gene\_09097.t1,gene\_01557.t1,gene\_10005.t1,gene\_07666.t1,gene\_09528.t1,gene\_09296.t1,gene\_01839.t1,gene\_01838.t1 | | iron-sulfur cluster binding | molecular\_function |
| GO:0051537 | 20 | gene\_09462.t1,gene\_04337.t1,gene\_09476.t1,gene\_02122.t1,gene\_08354.t1,gene\_08431.t1,gene\_10267.t1,gene\_08412.t1,gene\_04677.t1,gene\_00010.t1,gene\_06957.t1,gene\_07228.t1,gene\_01716.t1,gene\_09493.t1,gene\_04395.t1,gene\_10070.t1,gene\_09494.t1,gene\_08724.t1,gene\_01810.t1,gene\_00305.t1 | | 2 iron, 2 sulfur cluster binding | molecular\_function |
| GO:0070290 | 4 | gene\_09152.t1,gene\_07324.t1,gene\_06298.t1,gene\_08962.t1 | | N-acylphosphatidylethanolamine-specific phospholipase D activity | molecular\_function |
| GO:0000977 | 1 | gene\_06826.t1 | | RNA polymerase II transcription regulatory region sequence-specific DNA binding | molecular\_function |
| GO:0070569 | 1 | gene\_08343.t1 | | uridylyltransferase activity | molecular\_function |
| GO:0016158 | 1 | gene\_01494.t1 | | 3-phytase activity | molecular\_function |
| GO:0047429 | 1 | gene\_01995.t1 | | nucleoside-triphosphate diphosphatase activity | molecular\_function |
| GO:0047419 | 1 | gene\_09762.t1 | | N-acetylgalactosamine-6-phosphate deacetylase activity | molecular\_function |
| GO:0043565 | 18 | gene\_03579.t1,gene\_08663.t1,gene\_02408.t1,gene\_07750.t1,gene\_02778.t1,gene\_00906.t1,gene\_01321.t1,gene\_09262.t1,gene\_03104.t1,gene\_10443.t1,gene\_02995.t1,gene\_08025.t1,gene\_09052.t1,gene\_10265.t1,gene\_04730.t1,gene\_05943.t1,gene\_09415.t1,gene\_07331.t1 | | sequence-specific DNA binding | molecular\_function |
| GO:0042284 | 1 | gene\_00327.t1 | | sphingolipid delta-4 desaturase activity | molecular\_function |
| GO:0042283 | 1 | gene\_06325.t1 | | dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3-glucosyltransferase activity | molecular\_function |
| GO:0042281 | 1 | gene\_06952.t1 | | dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase activity | molecular\_function |
| GO:0008597 | 1 | gene\_09598.t1 | | calcium-dependent protein serine/threonine phosphatase regulator activity | molecular\_function |
| GO:0019863 | 3 | gene\_01766.t1,gene\_02705.t1,gene\_02259.t1 | | IgE binding | molecular\_function |
| GO:0017040 | 1 | gene\_02496.t1 | | N-acylsphingosine amidohydrolase activity | molecular\_function |
| GO:0003873 | 3 | gene\_09166.t1,gene\_09708.t1,gene\_04120.t1 | | 6-phosphofructo-2-kinase activity | molecular\_function |
| GO:0015187 | 1 | gene\_10133.t1 | | glycine transmembrane transporter activity | molecular\_function |
| GO:0033857 | 1 | gene\_02352.t1 | | diphosphoinositol-pentakisphosphate kinase activity | molecular\_function |
| GO:0010309 | 1 | gene\_09578.t1 | | acireductone dioxygenase [iron(II)-requiring] activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0106306 | 13 | gene\_06995.t1,gene\_06473.t1,gene\_08075.t1,gene\_00538.t1,gene\_05893.t1,gene\_02699.t1,gene\_02586.t1,gene\_08141.t1,gene\_01849.t1,gene\_05815.t1,gene\_07386.t1,gene\_05704.t1,gene\_01669.t1 | | protein serine/threonine phosphatase activity | molecular\_function |
| GO:0106307 | 13 | gene\_06995.t1,gene\_06473.t1,gene\_08075.t1,gene\_00538.t1,gene\_05893.t1,gene\_02699.t1,gene\_02586.t1,gene\_08141.t1,gene\_01849.t1,gene\_05815.t1,gene\_07386.t1,gene\_05704.t1,gene\_01669.t1 | | protein serine/threonine phosphatase activity | molecular\_function |
| GO:0005049 | 2 | gene\_06778.t1,gene\_05152.t1 | | nuclear export signal receptor activity | molecular\_function |
| GO:0005047 | 2 | gene\_01542.t1,gene\_09488.t1 | | signal recognition particle binding | molecular\_function |
| GO:0009916 | 1 | gene\_03691.t1 | | alternative oxidase activity | molecular\_function |
| GO:0005267 | 2 | gene\_05298.t1,gene\_05727.t1 | | potassium channel activity | molecular\_function |
| GO:0005262 | 1 | gene\_09233.t1 | | calcium channel activity | molecular\_function |
| GO:0004798 | 1 | gene\_07888.t1 | | thymidylate kinase activity | molecular\_function |
| GO:0004799 | 1 | gene\_01301.t1 | | thymidylate synthase activity | molecular\_function |
| GO:0004794 | 1 | gene\_01418.t1 | | L-threonine ammonia-lyase activity | molecular\_function |
| GO:0004792 | 2 | gene\_04708.t1,gene\_08455.t1 | | thiosulfate sulfurtransferase activity | molecular\_function |
| GO:0051907 | 1 | gene\_07706.t1 | | S-(hydroxymethyl)glutathione synthase activity | molecular\_function |
| GO:0004791 | 1 | gene\_10408.t1 | | thioredoxin-disulfide reductase activity | molecular\_function |
| GO:0004408 | 2 | gene\_01243.t1,gene\_00351.t1 | | holocytochrome-c synthase activity | molecular\_function |
| GO:0004409 | 1 | gene\_05493.t1 | | homoaconitate hydratase activity | molecular\_function |
| GO:0102205 | 1 | gene\_03179.t1 | | cholesterol alpha-glucosyltransferase activity | molecular\_function |
| GO:0004402 | 7 | gene\_07640.t1,gene\_10281.t1,gene\_03205.t1,gene\_10633.t1,gene\_02668.t1,gene\_10024.t1,gene\_09828.t1 | | histone acetyltransferase activity | molecular\_function |
| GO:0004400 | 1 | gene\_02197.t1 | | histidinol-phosphate transaminase activity | molecular\_function |
| GO:0004401 | 1 | gene\_01269.t1 | | histidinol-phosphatase activity | molecular\_function |
| GO:0005319 | 1 | gene\_07672.t1 | | lipid transporter activity | molecular\_function |
| GO:0004222 | 14 | gene\_00418.t1,gene\_04093.t1,gene\_09674.t1,gene\_02185.t1,gene\_02676.t1,gene\_10098.t1,gene\_03008.t1,gene\_06270.t1,gene\_09189.t1,gene\_01852.t1,gene\_08668.t1,gene\_01197.t1,gene\_03604.t1,gene\_10062.t1 | | metalloendopeptidase activity | molecular\_function |
| GO:0008775 | 1 | gene\_00257.t1 | | acetate CoA-transferase activity | molecular\_function |
| GO:0008776 | 1 | gene\_03086.t1 | | acetate kinase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0005315 | 7 | gene\_07824.t1,gene\_07220.t1,gene\_06183.t1,gene\_07633.t1,gene\_07427.t1,gene\_06091.t1,gene\_01931.t1 | | inorganic phosphate transmembrane transporter activity | molecular\_function |
| GO:0008171 | 14 | gene\_00612.t1,gene\_00334.t1,gene\_03441.t1,gene\_02625.t1,gene\_08992.t1,gene\_04453.t1,gene\_02875.t1,gene\_04278.t1,gene\_05115.t1,gene\_03477.t1,gene\_10674.t1,gene\_06497.t1,gene\_00606.t1,gene\_03543.t1 | | O-methyltransferase activity | molecular\_function |
| GO:0008177 | 2 | gene\_07137.t1,gene\_08431.t1 | | succinate dehydrogenase (ubiquinone) activity | molecular\_function |
| GO:0008175 | 1 | gene\_03856.t1 | | tRNA methyltransferase activity | molecular\_function |
| GO:0004821 | 1 | gene\_10413.t1 | | histidine-tRNA ligase activity | molecular\_function |
| GO:0000155 | 15 | gene\_08922.t1,gene\_05757.t1,gene\_08565.t1,gene\_02390.t1,gene\_03901.t1,gene\_05645.t1,gene\_04216.t1,gene\_06890.t1,gene\_08953.t1,gene\_09971.t1,gene\_02680.t1,gene\_01792.t1,gene\_05278.t1,gene\_07699.t1,gene\_01749.t1 | | phosphorelay sensor kinase activity | molecular\_function |
| GO:0000156 | 1 | gene\_10265.t1 | | phosphorelay response regulator activity | molecular\_function |
| GO:0000150 | 3 | gene\_05469.t1,gene\_08341.t1,gene\_06097.t1 | | DNA strand exchange activity | molecular\_function |
| GO:0004313 | 1 | gene\_02332.t1 | | [acyl-carrier-protein] S-acetyltransferase activity | molecular\_function |
| GO:0004310 | 2 | gene\_04746.t1,gene\_10502.t1 | | farnesyl-diphosphate farnesyltransferase activity | molecular\_function |
| GO:0004316 | 1 | gene\_02333.t1 | | 3-oxoacyl-[acyl-carrier-protein] reductase (NADPH) activity | molecular\_function |
| GO:0004317 | 1 | gene\_02332.t1 | | 3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase activity | molecular\_function |
| GO:0004314 | 1 | gene\_02332.t1 | | [acyl-carrier-protein] S-malonyltransferase activity | molecular\_function |
| GO:0004315 | 17 | gene\_02333.t1,gene\_06013.t1,gene\_09831.t1,gene\_00004.t1,gene\_00239.t1,gene\_09503.t1,gene\_09894.t1,gene\_01127.t1,gene\_05606.t1,gene\_07489.t1,gene\_01824.t1,gene\_07895.t1,gene\_05500.t1,gene\_10275.t1,gene\_00779.t1,gene\_05302.t1,gene\_00854.t1 | | 3-oxoacyl-[acyl-carrier-protein] synthase activity | molecular\_function |
| GO:0102339 | 1 | gene\_06564.t1 | | 3-oxo-arachidoyl-CoA reductase activity | molecular\_function |
| GO:0004318 | 1 | gene\_02332.t1 | | enoyl-[acyl-carrier-protein] reductase (NADH) activity | molecular\_function |
| GO:0102158 | 1 | gene\_04035.t1 | | very-long-chain 3-hydroxyacyl-CoA dehydratase activity | molecular\_function |
| GO:0004139 | 2 | gene\_10518.t1,gene\_06835.t1 | | deoxyribose-phosphate aldolase activity | molecular\_function |
| GO:0050464 | 1 | gene\_08723.t1 | | nitrate reductase (NADPH) activity | molecular\_function |
| GO:0004134 | 1 | gene\_00709.t1 | | 4-alpha-glucanotransferase activity | molecular\_function |
| GO:0004135 | 1 | gene\_00709.t1 | | amylo-alpha-1,6-glucosidase activity | molecular\_function |
| GO:0003860 | 1 | gene\_08548.t1 | | 3-hydroxyisobutyryl-CoA hydrolase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0008312 | 5 | gene\_01542.t1,gene\_06620.t1,gene\_04006.t1,gene\_04397.t1,gene\_07051.t1 | | 7S RNA binding | molecular\_function |
| GO:0008318 | 3 | gene\_01380.t1,gene\_02411.t1,gene\_09347.t1 | | protein prenyltransferase activity | molecular\_function |
| GO:0003839 | 3 | gene\_06808.t1,gene\_08330.t1,gene\_00716.t1 | | gamma-glutamylcyclotransferase activity | molecular\_function |
| GO:0046912 | 2 | gene\_09454.t1,gene\_00056.t1 | | acyltransferase, acyl groups converted into alkyl on transfer | molecular\_function |
| GO:0070628 | 3 | gene\_05404.t1,gene\_10093.t1,gene\_06474.t1 | | proteasome binding | molecular\_function |
| GO:0008080 | 37 | gene\_08938.t1,gene\_05507.t1,gene\_01760.t1,gene\_03319.t1,gene\_03506.t1,gene\_05496.t1,gene\_04016.t1,gene\_03258.t1,gene\_03030.t1,gene\_10040.t1,gene\_02741.t1,gene\_00213.t1,gene\_03185.t1,gene\_01146.t1,gene\_04329.t1,gene\_00190.t1,gene\_03278.t1,gene\_00831.t1,gene\_03688.t1,gene\_05563.t1,gene\_00196.t1,gene\_07690.t1,gene\_02558.t1,gene\_05438.t1,gene\_08854.t1,gene\_01389.t1,gene\_05215.t1,gene\_01030.t1,gene\_03382.t1,gene\_10125.t1,gene\_09022.t1,gene\_01698.t1,gene\_06572.t1,gene\_01288.t1,gene\_02866.t1,gene\_02274.t1,gene\_03507.t1 | | N-acetyltransferase activity | molecular\_function |
| GO:0008081 | 14 | gene\_06246.t1,gene\_05550.t1,gene\_02316.t1,gene\_01039.t1,gene\_04078.t1,gene\_09304.t1,gene\_04437.t1,gene\_05344.t1,gene\_00652.t1,gene\_10194.t1,gene\_08491.t1,gene\_00957.t1,gene\_05337.t1,gene\_09572.t1 | | phosphoric diester hydrolase activity | molecular\_function |
| GO:0070626 | 1 | gene\_07647.t1 | | (S)-2-(5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxamido) succinate lyase (fumarate-forming) activity | molecular\_function |
| GO:0070917 | 1 | gene\_06167.t1 | | inositol phosphoceramide synthase regulator activity | molecular\_function |
| GO:0003949 | 1 | gene\_04327.t1 | | 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase activity | molecular\_function |
| GO:0003942 | 1 | gene\_00813.t1 | | N-acetyl-gamma-glutamyl-phosphate reductase activity | molecular\_function |
| GO:0008553 | 5 | gene\_07874.t1,gene\_00003.t1,gene\_06942.t1,gene\_00673.t1,gene\_01833.t1 | | P-type proton-exporting transporter activity | molecular\_function |
| GO:0050048 | 2 | gene\_09326.t1,gene\_00557.t1 | | L-leucine:2-oxoglutarate aminotransferase activity | molecular\_function |
| GO:0004559 | 1 | gene\_07184.t1 | | alpha-mannosidase activity | molecular\_function |
| GO:0046820 | 1 | gene\_09639.t1 | | 4-amino-4-deoxychorismate synthase activity | molecular\_function |
| GO:0015385 | 2 | gene\_04349.t1,gene\_06398.t1 | | sodium:proton antiporter activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0016491 | 356 | gene\_05287.t1,gene\_05357.t1,gene\_08768.t1,gene\_02287.t1,gene\_08310.t1,gene\_01218.t1,gene\_01991.t1,gene\_06616.t1,gene\_05744.t1,gene\_05878.t1,gene\_04617.t1,gene\_05734.t1,gene\_00798.t1,gene\_06430.t1,gene\_02087.t1,gene\_08780.t1,gene\_00885.t1,gene\_05974.t1,gene\_07121.t1,gene\_06376.t1,gene\_00920.t1,gene\_06568.t1,gene\_01731.t1,gene\_00760.t1,gene\_00209.t1,gene\_04970.t1,gene\_04281.t1,gene\_06528.t1,gene\_09648.t1,gene\_06859.t1,gene\_02721.t1,gene\_02858.t1,gene\_01484.t1,gene\_09898.t1,gene\_05439.t1,gene\_08228.t1,gene\_00490.t1,gene\_05255.t1,gene\_04261.t1,gene\_06895.t1,gene\_05352.t1,gene\_09905.t1,gene\_09502.t1,gene\_09090.t1,gene\_06582.t1,gene\_05888.t1,gene\_09519.t1,gene\_09553.t1,gene\_06403.t1,gene\_07189.t1,gene\_01443.t1,gene\_05331.t1,gene\_03303.t1,gene\_06423.t1,gene\_05606.t1,gene\_09544.t1,gene\_00874.t1,gene\_08354.t1,gene\_03817.t1,gene\_01570.t1,gene\_06673.t1,gene\_05923.t1,gene\_08440.t1,gene\_08186.t1,gene\_09503.t1,gene\_05996.t1,gene\_01464.t1,gene\_06715.t1,gene\_06647.t1,gene\_00066.t1,gene\_06478.t1,gene\_07541.t1,gene\_08378.t1,gene\_02063.t1,gene\_04121.t1,gene\_08153.t1,gene\_09899.t1,gene\_03359.t1,gene\_02552.t1,gene\_02900.t1,gene\_04514.t1,gene\_10504.t1,gene\_01147.t1,gene\_07020.t1,gene\_04790.t1,gene\_00443.t1,gene\_04840.t1,gene\_07861.t1,gene\_01444.t1,gene\_06810.t1,gene\_00752.t1,gene\_06687.t1,gene\_10407.t1,gene\_08519.t1,gene\_05107.t1,gene\_06745.t1,gene\_03129.t1,gene\_05480.t1,gene\_04021.t1,gene\_02163.t1,gene\_05767.t1,gene\_09291.t1,gene\_04052.t1,gene\_03500.t1,gene\_00781.t1,gene\_04629.t1,gene\_03528.t1,gene\_00386.t1,gene\_00633.t1,gene\_04740.t1,gene\_02298.t1,gene\_03973.t1,gene\_03739.t1,gene\_00771.t1,gene\_03321.t1,gene\_10117.t1,gene\_07154.t1,gene\_00917.t1,gene\_02950.t1,gene\_02306.t1,gene\_05093.t1,gene\_04670.t1,gene\_04667.t1,gene\_07086.t1,gene\_08783.t1,gene\_00816.t1,gene\_04162.t1,gene\_02010.t1,gene\_08644.t1,gene\_08930.t1,gene\_08392.t1,gene\_09801.t1,gene\_06168.t1,gene\_02616.t1,gene\_07944.t1,gene\_05258.t1,gene\_04282.t1,gene\_08787.t1,gene\_10551.t1,gene\_07114.t1,gene\_06368.t1,gene\_01936.t1,gene\_07930.t1,gene\_09520.t1,gene\_10086.t1,gene\_07805.t1,gene\_00341.t1,gene\_09655.t1,gene\_02475.t1,gene\_04523.t1,gene\_07445.t1,gene\_05966.t1,gene\_07894.t1,gene\_10101.t1,gene\_03150.t1,gene\_10643.t1,gene\_02597.t1,gene\_04399.t1,gene\_08019.t1,gene\_09589.t1,gene\_07939.t1,gene\_08542.t1,gene\_01253.t1,gene\_01132.t1,gene\_05431.t1,gene\_04675.t1,gene\_02266.t1,gene\_07976.t1,gene\_01966.t1,gene\_07970.t1,gene\_06730.t1,gene\_01127.t1,gene\_01694.t1,gene\_09714.t1,gene\_04565.t1,gene\_06964.t1,gene\_08134.t1,gene\_00239.t1,gene\_08786.t1,gene\_00237.t1, | | oxidoreductase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0016491 | 356 | gene\_10427.t1,gene\_00095.t1,gene\_00854.t1,gene\_05411.t1,gene\_09678.t1,gene\_08784.t1,gene\_04306.t1,gene\_04708.t1,gene\_01716.t1,gene\_09900.t1,gene\_00380.t1,gene\_01343.t1,gene\_08426.t1,gene\_06771.t1,gene\_10435.t1,gene\_01344.t1,gene\_00338.t1,gene\_04262.t1,gene\_04704.t1,gene\_00943.t1,gene\_02267.t1,gene\_08822.t1,gene\_00944.t1,gene\_09383.t1,gene\_05765.t1,gene\_00210.t1,gene\_01821.t1,gene\_05286.t1,gene\_09023.t1,gene\_08445.t1,gene\_09497.t1,gene\_03421.t1,gene\_06411.t1,gene\_03096.t1,gene\_00252.t1,gene\_05499.t1,gene\_00126.t1,gene\_09466.t1,gene\_07962.t1,gene\_08559.t1,gene\_08731.t1,gene\_08912.t1,gene\_10667.t1,gene\_01784.t1,gene\_00956.t1,gene\_05506.t1,gene\_06751.t1,gene\_03119.t1,gene\_05259.t1,gene\_02129.t1,gene\_06969.t1,gene\_02171.t1,gene\_06371.t1,gene\_02169.t1,gene\_06940.t1,gene\_07780.t1,gene\_08782.t1,gene\_10669.t1,gene\_06055.t1,gene\_01100.t1,gene\_04351.t1,gene\_04922.t1,gene\_05076.t1,gene\_04072.t1,gene\_09693.t1,gene\_04743.t1,gene\_07448.t1,gene\_02687.t1,gene\_00042.t1,gene\_07586.t1,gene\_07661.t1,gene\_05048.t1,gene\_09292.t1,gene\_02138.t1,gene\_05500.t1,gene\_03109.t1,gene\_04735.t1,gene\_08057.t1,gene\_00121.t1,gene\_03417.t1,gene\_05382.t1,gene\_02168.t1,gene\_02229.t1,gene\_06435.t1,gene\_02009.t1,gene\_08452.t1,gene\_04868.t1,gene\_02611.t1,gene\_01193.t1,gene\_02581.t1,gene\_09876.t1,gene\_10440.t1,gene\_04008.t1,gene\_10342.t1,gene\_05289.t1,gene\_01729.t1,gene\_03008.t1,gene\_03762.t1,gene\_04368.t1,gene\_08609.t1,gene\_05600.t1,gene\_08945.t1,gene\_09499.t1,gene\_01960.t1,gene\_05350.t1,gene\_02961.t1,gene\_00821.t1,gene\_06659.t1,gene\_00645.t1,gene\_01704.t1,gene\_08069.t1,gene\_03419.t1,gene\_07905.t1,gene\_08022.t1,gene\_08502.t1,gene\_04760.t1,gene\_05360.t1,gene\_02325.t1,gene\_09173.t1,gene\_01907.t1,gene\_01318.t1,gene\_03353.t1,gene\_09806.t1,gene\_08321.t1,gene\_00780.t1,gene\_01434.t1,gene\_06110.t1,gene\_00918.t1,gene\_05430.t1,gene\_05567.t1,gene\_07279.t1,gene\_08364.t1,gene\_07087.t1,gene\_10647.t1,gene\_06569.t1,gene\_01106.t1,gene\_07860.t1,gene\_09068.t1,gene\_05262.t1,gene\_02438.t1,gene\_00751.t1,gene\_09145.t1,gene\_02312.t1,gene\_01615.t1,gene\_04118.t1,gene\_06491.t1,gene\_05622.t1,gene\_01941.t1,gene\_05764.t1,gene\_05304.t1,gene\_09535.t1,gene\_10611.t1,gene\_06200.t1,gene\_03649.t1,gene\_08058.t1,gene\_03459.t1,gene\_02825.t1,gene\_07433.t1,gene\_07560.t1,gene\_06013.t1,gene\_03557.t1,gene\_08309.t1,gene\_06982.t1,gene\_00922.t1,gene\_08132.t1,gene\_10550.t1,gene\_06592.t1,gene\_03394.t1,gene\_03722.t1,gene\_01430.t1,gene\_06695.t1,gene\_05781.t1,gene\_03921.t1,gene\_09463.t1,gene\_01908.t1,gene\_09442.t1 | | oxidoreductase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0016709 | 2 | gene\_10412.t1,gene\_07066.t1 | | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen | molecular\_function |
| GO:0008425 | 1 | gene\_04044.t1 | | 2-polyprenyl-6-methoxy-1,4-benzoquinone methyltransferase activity | molecular\_function |
| GO:0016705 | 91 | gene\_09837.t1,gene\_07431.t1,gene\_08439.t1,gene\_00050.t1,gene\_07089.t1,gene\_10673.t1,gene\_10252.t1,gene\_02074.t1,gene\_07674.t1,gene\_01461.t1,gene\_10670.t1,gene\_06181.t1,gene\_08016.t1,gene\_08658.t1,gene\_08018.t1,gene\_01818.t1,gene\_05434.t1,gene\_02731.t1,gene\_05157.t1,gene\_01463.t1,gene\_04764.t1,gene\_07549.t1,gene\_04130.t1,gene\_01324.t1,gene\_09909.t1,gene\_07281.t1,gene\_07691.t1,gene\_02013.t1,gene\_04065.t1,gene\_07786.t1,gene\_02311.t1,gene\_06676.t1,gene\_01460.t1,gene\_02026.t1,gene\_03669.t1,gene\_07369.t1,gene\_01111.t1,gene\_05398.t1,gene\_07833.t1,gene\_09504.t1,gene\_09177.t1,gene\_03816.t1,gene\_00994.t1,gene\_00758.t1,gene\_03517.t1,gene\_00220.t1,gene\_00834.t1,gene\_01587.t1,gene\_07934.t1,gene\_03106.t1,gene\_09020.t1,gene\_04361.t1,gene\_03360.t1,gene\_01476.t1,gene\_07490.t1,gene\_00777.t1,gene\_07117.t1,gene\_01658.t1,gene\_10569.t1,gene\_07848.t1,gene\_07526.t1,gene\_03126.t1,gene\_02190.t1,gene\_09778.t1,gene\_02258.t1,gene\_10672.t1,gene\_08446.t1,gene\_09353.t1,gene\_03911.t1,gene\_09980.t1,gene\_09970.t1,gene\_03369.t1,gene\_04527.t1,gene\_08017.t1,gene\_07727.t1,gene\_01543.t1,gene\_00601.t1,gene\_07708.t1,gene\_10572.t1,gene\_02248.t1,gene\_05975.t1,gene\_09896.t1,gene\_03978.t1,gene\_00285.t1,gene\_10014.t1,gene\_09981.t1,gene\_07507.t1,gene\_07556.t1,gene\_08430.t1,gene\_03226.t1,gene\_09394.t1 | | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen | molecular\_function |
| GO:0016702 | 3 | gene\_09429.t1,gene\_03746.t1,gene\_01473.t1 | | oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen | molecular\_function |
| GO:0008422 | 5 | gene\_03630.t1,gene\_01601.t1,gene\_06646.t1,gene\_02981.t1,gene\_08104.t1 | | beta-glucosidase activity | molecular\_function |
| GO:0016701 | 2 | gene\_05541.t1,gene\_00790.t1 | | oxidoreductase activity, acting on single donors with incorporation of molecular oxygen | molecular\_function |
| GO:0070577 | 1 | gene\_10093.t1 | | lysine-acetylated histone binding | molecular\_function |
| GO:0050136 | 1 | gene\_09821.t1 | | NADH dehydrogenase (quinone) activity | molecular\_function |
| GO:0070573 | 5 | gene\_04769.t1,gene\_08568.t1,gene\_01855.t1,gene\_07325.t1,gene\_05474.t1 | | metallodipeptidase activity | molecular\_function |
| GO:0019706 | 6 | gene\_08206.t1,gene\_07259.t1,gene\_01186.t1,gene\_06293.t1,gene\_00203.t1,gene\_03798.t1 | | protein-cysteine S-palmitoyltransferase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0042162 | 3 | gene\_04537.t1,gene\_02991.t1,gene\_05883.t1 | | telomeric DNA binding | molecular\_function |
| GO:0047400 | 1 | gene\_02846.t1 | | phosphonoacetate hydrolase activity | molecular\_function |
| GO:0008453 | 1 | gene\_05251.t1 | | alanine-glyoxylate transaminase activity | molecular\_function |
| GO:0052761 | 1 | gene\_03424.t1 | | exo-1,4-beta-D-glucosaminidase activity | molecular\_function |
| GO:0016884 | 1 | gene\_09197.t1 | | carbon-nitrogen ligase activity, with glutamine as amido-N-donor | molecular\_function |
| GO:0030248 | 6 | gene\_03404.t1,gene\_10598.t1,gene\_01844.t1,gene\_01845.t1,gene\_04755.t1,gene\_00439.t1 | | cellulose binding | molecular\_function |
| GO:0016231 | 1 | gene\_03839.t1 | | beta-N-acetylglucosaminidase activity | molecular\_function |
| GO:0030246 | 33 | gene\_08471.t1,gene\_08927.t1,gene\_07380.t1,gene\_07809.t1,gene\_04046.t1,gene\_06645.t1,gene\_06586.t1,gene\_06681.t1,gene\_00082.t1,gene\_00100.t1,gene\_06149.t1,gene\_05679.t1,gene\_01032.t1,gene\_06186.t1,gene\_07184.t1,gene\_09816.t1,gene\_08997.t1,gene\_03444.t1,gene\_06235.t1,gene\_02885.t1,gene\_02291.t1,gene\_01013.t1,gene\_07334.t1,gene\_02271.t1,gene\_06646.t1,gene\_10612.t1,gene\_05571.t1,gene\_06726.t1,gene\_07881.t1,gene\_08481.t1,gene\_07562.t1,gene\_08993.t1,gene\_02323.t1 | | carbohydrate binding | molecular\_function |
| GO:0016987 | 1 | gene\_08925.t1 | | sigma factor activity | molecular\_function |
| GO:0051730 | 1 | gene\_05344.t1 | | GTP-dependent polyribonucleotide 5'-hydroxyl-kinase activity | molecular\_function |
| GO:0051731 | 2 | gene\_05890.t1,gene\_03181.t1 | | polynucleotide 5'-hydroxyl-kinase activity | molecular\_function |
| GO:0017057 | 1 | gene\_00992.t1 | | 6-phosphogluconolactonase activity | molecular\_function |
| GO:0017056 | 10 | gene\_01229.t1,gene\_06461.t1,gene\_07308.t1,gene\_01090.t1,gene\_10042.t1,gene\_09198.t1,gene\_08808.t1,gene\_08367.t1,gene\_08906.t1,gene\_09280.t1 | | structural constituent of nuclear pore | molecular\_function |
| GO:0001164 | 1 | gene\_00617.t1 | | RNA polymerase I core promoter sequence-specific DNA binding | molecular\_function |
| GO:0035299 | 1 | gene\_04076.t1 | | inositol pentakisphosphate 2-kinase activity | molecular\_function |
| GO:0004731 | 1 | gene\_09719.t1 | | purine-nucleoside phosphorylase activity | molecular\_function |
| GO:0035615 | 2 | gene\_01313.t1,gene\_07106.t1 | | clathrin adaptor activity | molecular\_function |
| GO:0106313 | 2 | gene\_07024.t1,gene\_07886.t1 | | methylenetetrahydrofolate reductase NADPH activity | molecular\_function |
| GO:0106312 | 2 | gene\_07024.t1,gene\_07886.t1 | | methylenetetrahydrofolate reductase NADH activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0106310 | 30 | gene\_02155.t1,gene\_01198.t1,gene\_00740.t1,gene\_04066.t1,gene\_03475.t1,gene\_05244.t1,gene\_08500.t1,gene\_03061.t1,gene\_10369.t1,gene\_03660.t1,gene\_02838.t1,gene\_06106.t1,gene\_01223.t1,gene\_03314.t1,gene\_09242.t1,gene\_00801.t1,gene\_04388.t1,gene\_00848.t1,gene\_08078.t1,gene\_05820.t1,gene\_06526.t1,gene\_08612.t1,gene\_09034.t1,gene\_00548.t1,gene\_05628.t1,gene\_05629.t1,gene\_04642.t1,gene\_07102.t1,gene\_08746.t1,gene\_05846.t1 | | protein serine kinase activity | molecular\_function |
| GO:0032132 | 1 | gene\_03350.t1 | | O6-alkylguanine-DNA binding | molecular\_function |
| GO:0005092 | 1 | gene\_00826.t1 | | GDP-dissociation inhibitor activity | molecular\_function |
| GO:0005093 | 1 | gene\_07007.t1 | | Rab GDP-dissociation inhibitor activity | molecular\_function |
| GO:0005096 | 19 | gene\_09563.t1,gene\_05579.t1,gene\_08510.t1,gene\_06053.t1,gene\_03750.t1,gene\_02369.t1,gene\_05824.t1,gene\_00029.t1,gene\_01246.t1,gene\_02829.t1,gene\_07375.t1,gene\_04154.t1,gene\_05709.t1,gene\_10307.t1,gene\_08110.t1,gene\_09815.t1,gene\_00475.t1,gene\_00965.t1,gene\_07240.t1 | | GTPase activator activity | molecular\_function |
| GO:0005094 | 1 | gene\_05892.t1 | | Rho GDP-dissociation inhibitor activity | molecular\_function |
| GO:0004789 | 1 | gene\_01046.t1 | | thiamine-phosphate diphosphorylase activity | molecular\_function |
| GO:0004788 | 1 | gene\_04276.t1 | | thiamine diphosphokinase activity | molecular\_function |
| GO:0004784 | 4 | gene\_07979.t1,gene\_10245.t1,gene\_02136.t1,gene\_02654.t1 | | superoxide dismutase activity | molecular\_function |
| GO:0004781 | 1 | gene\_07261.t1 | | sulfate adenylyltransferase (ATP) activity | molecular\_function |
| GO:0004419 | 2 | gene\_04620.t1,gene\_07600.t1 | | hydroxymethylglutaryl-CoA lyase activity | molecular\_function |
| GO:0004418 | 1 | gene\_05843.t1 | | hydroxymethylbilane synthase activity | molecular\_function |
| GO:0047874 | 1 | gene\_09530.t1 | | dolichyldiphosphatase activity | molecular\_function |
| GO:0004417 | 1 | gene\_01046.t1 | | hydroxyethylthiazole kinase activity | molecular\_function |
| GO:0004416 | 1 | gene\_08534.t1 | | hydroxyacylglutathione hydrolase activity | molecular\_function |
| GO:0004411 | 1 | gene\_03809.t1 | | homogentisate 1,2-dioxygenase activity | molecular\_function |
| GO:0004410 | 1 | gene\_03989.t1 | | homocitrate synthase activity | molecular\_function |
| GO:0004413 | 1 | gene\_09231.t1 | | homoserine kinase activity | molecular\_function |
| GO:0004412 | 1 | gene\_05635.t1 | | homoserine dehydrogenase activity | molecular\_function |
| GO:0047988 | 1 | gene\_03643.t1 | | hydroxyacid-oxoacid transhydrogenase activity | molecular\_function |
| GO:0003688 | 1 | gene\_07862.t1 | | DNA replication origin binding | molecular\_function |
| GO:0008942 | 1 | gene\_08724.t1 | | nitrite reductase [NAD(P)H] activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0008941 | 1 | gene\_03326.t1 | | nitric oxide dioxygenase activity | molecular\_function |
| GO:0005324 | 1 | gene\_02649.t1 | | long-chain fatty acid transporter activity | molecular\_function |
| GO:0008168 | 50 | gene\_09715.t1,gene\_07369.t1,gene\_08347.t1,gene\_07742.t1,gene\_03686.t1,gene\_08400.t1,gene\_00786.t1,gene\_09600.t1,gene\_00044.t1,gene\_01127.t1,gene\_02726.t1,gene\_01679.t1,gene\_10176.t1,gene\_03893.t1,gene\_03669.t1,gene\_00239.t1,gene\_05279.t1,gene\_05786.t1,gene\_01676.t1,gene\_01397.t1,gene\_09477.t1,gene\_04497.t1,gene\_02225.t1,gene\_07039.t1,gene\_04324.t1,gene\_03090.t1,gene\_09851.t1,gene\_01168.t1,gene\_01715.t1,gene\_10027.t1,gene\_01784.t1,gene\_09459.t1,gene\_07850.t1,gene\_03196.t1,gene\_06086.t1,gene\_01783.t1,gene\_07963.t1,gene\_02659.t1,gene\_00180.t1,gene\_05606.t1,gene\_06478.t1,gene\_05302.t1,gene\_10501.t1,gene\_05177.t1,gene\_00854.t1,gene\_08025.t1,gene\_01287.t1,gene\_01824.t1,gene\_02183.t1,gene\_03168.t1 | | methyltransferase activity | molecular\_function |
| GO:0042626 | 5 | gene\_09573.t1,gene\_08358.t1,gene\_05111.t1,gene\_09901.t1,gene\_05827.t1 | | ATPase-coupled transmembrane transporter activity | molecular\_function |
| GO:0140580 | 1 | gene\_08030.t1 | | mitochondrion autophagosome adaptor activity | molecular\_function |
| GO:0008897 | 3 | gene\_01270.t1,gene\_02333.t1,gene\_01087.t1 | | holo-[acyl-carrier-protein] synthase activity | molecular\_function |
| GO:0008892 | 1 | gene\_07694.t1 | | guanine deaminase activity | molecular\_function |
| GO:0004301 | 1 | gene\_01201.t1 | | epoxide hydrolase activity | molecular\_function |
| GO:0004306 | 1 | gene\_09295.t1 | | ethanolamine-phosphate cytidylyltransferase activity | molecular\_function |
| GO:0005254 | 2 | gene\_08068.t1,gene\_06127.t1 | | chloride channel activity | molecular\_function |
| GO:0005524 | 634 | gene\_06204.t1,gene\_08185.t1,gene\_05619.t1,gene\_00005.t1,gene\_05143.t1,gene\_03779.t1,gene\_08963.t1,gene\_03977.t1,gene\_00017.t1,gene\_10098.t1,gene\_09640.t1,gene\_06202.t1,gene\_03074.t1,gene\_03801.t1,gene\_07888.t1,gene\_03372.t1,gene\_04779.t1,gene\_05505.t1,gene\_01682.t1,gene\_05442.t1,gene\_01792.t1,gene\_05707.t1,gene\_02826.t1,gene\_03571.t1,gene\_01352.t1,gene\_09184.t1,gene\_02514.t1,gene\_08746.t1,gene\_08875.t1,gene\_02480.t1,gene\_02627.t1,gene\_09742.t1,gene\_07903.t1,gene\_07003.t1,gene\_03790.t1,gene\_00743.t1,gene\_04210.t1,gene\_05208.t1,gene\_09161.t1,gene\_10355.t1,gene\_00682.t1,gene\_06422.t1,gene\_05954.t1,gene\_03602.t1,gene\_04388.t1,gene\_07409.t1,gene\_01737.t1,gene\_00724.t1,gene\_06516.t1,gene\_03494.t1,gene\_03625.t1,gene\_06272.t1,gene\_10398.t1,gene\_05738.t1,gene\_03046.t1,gene\_07862.t1,gene\_10065.t1,gene\_03407.t1,gene\_00879.t1,gene\_10464.t1,gene\_00321.t1,gene\_10185.t1,gene\_04219.t1,gene\_03627.t1,gene\_10327.t1,gene\_09273.t1,gene\_10020.t1,gene\_07842.t1,gene\_08593.t1,gene\_08741.t1,gene\_00799.t1,gene\_08527.t1,gene\_06310.t1,gene\_04206.t1,gene\_03576.t1, | | ATP binding | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0005524 | 634 | gene\_02623.t1,gene\_06799.t1,gene\_04290.t1,gene\_07797.t1,gene\_03570.t1,gene\_10074.t1,gene\_07343.t1,gene\_02682.t1,gene\_03338.t1,gene\_06611.t1,gene\_03237.t1,gene\_04212.t1,gene\_06241.t1,gene\_00034.t1,gene\_01081.t1,gene\_01556.t1,gene\_09107.t1,gene\_01363.t1,gene\_09829.t1,gene\_00134.t1,gene\_05677.t1,gene\_09554.t1,gene\_04352.t1,gene\_00882.t1,gene\_07453.t1,gene\_05628.t1,gene\_06180.t1,gene\_07102.t1,gene\_04776.t1,gene\_05654.t1,gene\_08245.t1,gene\_09034.t1,gene\_05695.t1,gene\_00514.t1,gene\_00320.t1,gene\_06014.t1,gene\_02024.t1,gene\_07180.t1,gene\_06711.t1,gene\_01445.t1,gene\_04419.t1,gene\_05837.t1,gene\_08909.t1,gene\_03840.t1,gene\_03903.t1,gene\_02959.t1,gene\_09591.t1,gene\_07873.t1,gene\_10351.t1,gene\_02049.t1,gene\_08235.t1,gene\_09704.t1,gene\_00003.t1,gene\_08419.t1,gene\_00030.t1,gene\_09668.t1,gene\_07590.t1,gene\_08078.t1,gene\_08961.t1,gene\_03637.t1,gene\_06901.t1,gene\_07917.t1,gene\_10263.t1,gene\_05211.t1,gene\_08209.t1,gene\_04268.t1,gene\_01056.t1,gene\_00089.t1,gene\_10210.t1,gene\_05928.t1,gene\_03207.t1,gene\_01507.t1,gene\_08389.t1,gene\_00517.t1,gene\_03849.t1,gene\_06412.t1,gene\_07278.t1,gene\_06073.t1,gene\_07874.t1,gene\_02841.t1,gene\_01446.t1,gene\_09211.t1,gene\_06343.t1,gene\_06106.t1,gene\_09029.t1,gene\_08036.t1,gene\_07377.t1,gene\_08023.t1,gene\_05700.t1,gene\_10636.t1,gene\_07649.t1,gene\_07918.t1,gene\_07650.t1,gene\_00515.t1,gene\_09222.t1,gene\_07804.t1,gene\_09396.t1,gene\_05556.t1,gene\_06429.t1,gene\_04010.t1,gene\_04233.t1,gene\_01364.t1,gene\_04663.t1,gene\_00660.t1,gene\_06062.t1,gene\_06902.t1,gene\_03773.t1,gene\_03086.t1,gene\_02251.t1,gene\_10557.t1,gene\_10372.t1,gene\_06495.t1,gene\_08162.t1,gene\_05105.t1,gene\_07906.t1,gene\_03181.t1,gene\_07321.t1,gene\_03855.t1,gene\_03818.t1,gene\_06236.t1,gene\_04460.t1,gene\_07825.t1,gene\_00948.t1,gene\_03211.t1,gene\_01074.t1,gene\_07819.t1,gene\_06655.t1,gene\_09265.t1,gene\_08215.t1,gene\_09717.t1,gene\_07367.t1,gene\_10553.t1,gene\_08388.t1,gene\_08513.t1,gene\_08399.t1,gene\_06526.t1,gene\_07666.t1,gene\_00848.t1,gene\_04469.t1,gene\_03291.t1,gene\_05141.t1,gene\_02774.t1,gene\_04722.t1,gene\_07078.t1,gene\_07559.t1,gene\_00838.t1,gene\_05458.t1,gene\_09562.t1,gene\_03396.t1,gene\_03896.t1,gene\_08071.t1,gene\_07695.t1,gene\_09071.t1,gene\_02155.t1,gene\_07408.t1,gene\_00813.t1,gene\_02766.t1,gene\_10413.t1,gene\_01382.t1,gene\_02077.t1,gene\_05866.t1,gene\_10607.t1,gene\_07899.t1,gene\_09056.t1,gene\_00801.t1,gene\_04139.t1,gene\_02991.t1,gene\_05426.t1,gene\_05469.t1,gene\_04461.t1,gene\_05535.t1,gene\_03524.t1,gene\_05831.t1,gene\_07765.t1,gene\_07403.t1,gene\_09645.t1,gene\_02420.t1,gene\_03204.t1,gene\_08650.t1,gene\_09582.t1, | | ATP binding | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0005524 | 634 | gene\_09875.t1,gene\_07744.t1,gene\_01826.t1,gene\_04092.t1,gene\_00738.t1,gene\_01833.t1,gene\_04624.t1,gene\_01353.t1,gene\_04186.t1,gene\_04315.t1,gene\_05457.t1,gene\_02352.t1,gene\_08813.t1,gene\_03061.t1,gene\_08063.t1,gene\_06315.t1,gene\_05618.t1,gene\_05564.t1,gene\_00218.t1,gene\_09735.t1,gene\_08612.t1,gene\_08575.t1,gene\_08871.t1,gene\_06624.t1,gene\_06458.t1,gene\_00533.t1,gene\_01751.t1,gene\_08070.t1,gene\_00723.t1,gene\_00673.t1,gene\_07680.t1,gene\_01422.t1,gene\_09870.t1,gene\_02734.t1,gene\_09325.t1,gene\_05305.t1,gene\_09891.t1,gene\_08258.t1,gene\_04537.t1,gene\_05111.t1,gene\_03598.t1,gene\_04567.t1,gene\_07212.t1,gene\_07286.t1,gene\_05577.t1,gene\_10520.t1,gene\_00625.t1,gene\_03900.t1,gene\_03476.t1,gene\_00613.t1,gene\_05645.t1,gene\_07503.t1,gene\_02520.t1,gene\_09414.t1,gene\_05374.t1,gene\_07138.t1,gene\_04276.t1,gene\_01236.t1,gene\_04211.t1,gene\_02838.t1,gene\_04724.t1,gene\_10019.t1,gene\_09819.t1,gene\_00303.t1,gene\_08229.t1,gene\_05874.t1,gene\_09416.t1,gene\_09453.t1,gene\_01196.t1,gene\_01183.t1,gene\_01564.t1,gene\_08889.t1,gene\_06480.t1,gene\_08044.t1,gene\_10365.t1,gene\_05890.t1,gene\_09267.t1,gene\_08845.t1,gene\_01710.t1,gene\_01640.t1,gene\_01341.t1,gene\_05629.t1,gene\_04642.t1,gene\_02449.t1,gene\_01319.t1,gene\_08753.t1,gene\_02559.t1,gene\_03538.t1,gene\_10665.t1,gene\_09871.t1,gene\_10097.t1,gene\_05745.t1,gene\_02486.t1,gene\_07312.t1,gene\_09780.t1,gene\_04467.t1,gene\_00875.t1,gene\_06009.t1,gene\_03702.t1,gene\_01435.t1,gene\_03960.t1,gene\_05660.t1,gene\_10462.t1,gene\_08299.t1,gene\_03645.t1,gene\_04566.t1,gene\_05865.t1,gene\_01409.t1,gene\_10515.t1,gene\_06720.t1,gene\_01223.t1,gene\_06471.t1,gene\_03268.t1,gene\_09744.t1,gene\_09629.t1,gene\_09415.t1,gene\_06540.t1,gene\_01715.t1,gene\_02173.t1,gene\_02676.t1,gene\_00363.t1,gene\_01781.t1,gene\_09398.t1,gene\_07298.t1,gene\_07628.t1,gene\_00486.t1,gene\_02523.t1,gene\_00302.t1,gene\_05344.t1,gene\_04173.t1,gene\_08916.t1,gene\_09510.t1,gene\_04520.t1,gene\_07172.t1,gene\_06116.t1,gene\_05846.t1,gene\_10284.t1,gene\_09244.t1,gene\_06196.t1,gene\_04777.t1,gene\_02387.t1,gene\_00510.t1,gene\_10524.t1,gene\_00300.t1,gene\_00426.t1,gene\_02062.t1,gene\_01911.t1,gene\_09708.t1,gene\_06413.t1,gene\_05844.t1,gene\_01532.t1,gene\_08610.t1,gene\_08460.t1,gene\_03551.t1,gene\_03597.t1,gene\_05879.t1,gene\_10043.t1,gene\_00937.t1,gene\_01914.t1,gene\_03580.t1,gene\_01265.t1,gene\_00740.t1,gene\_09224.t1,gene\_03488.t1,gene\_06792.t1,gene\_01636.t1,gene\_09513.t1,gene\_00502.t1,gene\_07157.t1,gene\_07620.t1,gene\_00504.t1,gene\_01030.t1,gene\_06942.t1,gene\_09569.t1,gene\_09703.t1,gene\_10362.t1,gene\_03967.t1,gene\_10324.t1,gene\_03888.t1,gene\_10494.t1, | | ATP binding | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0005524 | 634 | gene\_00474.t1,gene\_08266.t1,gene\_09901.t1,gene\_09679.t1,gene\_01719.t1,gene\_03055.t1,gene\_05462.t1,gene\_04223.t1,gene\_07160.t1,gene\_00643.t1,gene\_04066.t1,gene\_03414.t1,gene\_05840.t1,gene\_01919.t1,gene\_05244.t1,gene\_02324.t1,gene\_03092.t1,gene\_07813.t1,gene\_05330.t1,gene\_03452.t1,gene\_06117.t1,gene\_00896.t1,gene\_10474.t1,gene\_01162.t1,gene\_05142.t1,gene\_07851.t1,gene\_01828.t1,gene\_04302.t1,gene\_00949.t1,gene\_00778.t1,gene\_03123.t1,gene\_06643.t1,gene\_08051.t1,gene\_01019.t1,gene\_09263.t1,gene\_02412.t1,gene\_10370.t1,gene\_03581.t1,gene\_03944.t1,gene\_08981.t1,gene\_02175.t1,gene\_00297.t1,gene\_00280.t1,gene\_09195.t1,gene\_09469.t1,gene\_03153.t1,gene\_06451.t1,gene\_04562.t1,gene\_01790.t1,gene\_09103.t1,gene\_06102.t1,gene\_01374.t1,gene\_07884.t1,gene\_01097.t1,gene\_08804.t1,gene\_02879.t1,gene\_02228.t1,gene\_05811.t1,gene\_00665.t1,gene\_02123.t1,gene\_02715.t1,gene\_07261.t1,gene\_03652.t1,gene\_04120.t1,gene\_04412.t1,gene\_09573.t1,gene\_02647.t1,gene\_07924.t1,gene\_07988.t1,gene\_04959.t1,gene\_07366.t1,gene\_10554.t1,gene\_03199.t1,gene\_09309.t1,gene\_10503.t1,gene\_07715.t1,gene\_09843.t1,gene\_09166.t1,gene\_05820.t1,gene\_06242.t1,gene\_02025.t1,gene\_04923.t1,gene\_10369.t1,gene\_00205.t1,gene\_00355.t1,gene\_08665.t1,gene\_00857.t1,gene\_00581.t1,gene\_07129.t1,gene\_02088.t1,gene\_10016.t1,gene\_09868.t1,gene\_04509.t1,gene\_07095.t1,gene\_02577.t1,gene\_06163.t1,gene\_08324.t1,gene\_03491.t1,gene\_09471.t1,gene\_08341.t1,gene\_08500.t1,gene\_04358.t1,gene\_05849.t1,gene\_09242.t1,gene\_09231.t1,gene\_10167.t1,gene\_10446.t1,gene\_01990.t1,gene\_04457.t1,gene\_04076.t1,gene\_08455.t1,gene\_10008.t1,gene\_04063.t1,gene\_06649.t1,gene\_03351.t1,gene\_09001.t1,gene\_07396.t1,gene\_03759.t1,gene\_07217.t1,gene\_04554.t1,gene\_00548.t1,gene\_05755.t1,gene\_04413.t1,gene\_02254.t1,gene\_00597.t1,gene\_03487.t1,gene\_09082.t1,gene\_09699.t1,gene\_03660.t1,gene\_09269.t1,gene\_00706.t1,gene\_01933.t1,gene\_00982.t1,gene\_03776.t1,gene\_10213.t1,gene\_07370.t1,gene\_05056.t1,gene\_01046.t1,gene\_07416.t1,gene\_09104.t1,gene\_01198.t1,gene\_05164.t1,gene\_09271.t1,gene\_07232.t1,gene\_10289.t1,gene\_03535.t1,gene\_03461.t1,gene\_07716.t1,gene\_04316.t1,gene\_00118.t1,gene\_07202.t1,gene\_05182.t1,gene\_01540.t1,gene\_03192.t1,gene\_01706.t1,gene\_01436.t1,gene\_04631.t1,gene\_03141.t1,gene\_06256.t1,gene\_03165.t1,gene\_02250.t1,gene\_00001.t1,gene\_01043.t1,gene\_04577.t1,gene\_06273.t1,gene\_09046.t1,gene\_09710.t1,gene\_00352.t1,gene\_01283.t1,gene\_09064.t1,gene\_03475.t1,gene\_07475.t1,gene\_05671.t1,gene\_02432.t1,gene\_03931.t1,gene\_02698.t1,gene\_05855.t1,gene\_02415.t1,gene\_07626.t1,gene\_01173.t1, | | ATP binding | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0005524 | 634 | gene\_07402.t1,gene\_07139.t1,gene\_08132.t1,gene\_06405.t1,gene\_05467.t1,gene\_09154.t1,gene\_05285.t1,gene\_02304.t1,gene\_01221.t1,gene\_00208.t1,gene\_09581.t1,gene\_01182.t1,gene\_07821.t1,gene\_05955.t1,gene\_04634.t1,gene\_05841.t1,gene\_09207.t1,gene\_02487.t1,gene\_09111.t1 | | ATP binding | molecular\_function |
| GO:0005525 | 108 | gene\_03293.t1,gene\_03793.t1,gene\_01194.t1,gene\_06785.t1,gene\_04976.t1,gene\_05525.t1,gene\_09037.t1,gene\_05374.t1,gene\_04423.t1,gene\_09005.t1,gene\_03755.t1,gene\_08048.t1,gene\_08956.t1,gene\_10469.t1,gene\_09750.t1,gene\_01668.t1,gene\_02115.t1,gene\_03006.t1,gene\_02465.t1,gene\_03671.t1,gene\_06391.t1,gene\_06104.t1,gene\_09687.t1,gene\_01509.t1,gene\_06165.t1,gene\_03121.t1,gene\_03540.t1,gene\_07127.t1,gene\_10100.t1,gene\_03716.t1,gene\_00023.t1,gene\_05660.t1,gene\_07332.t1,gene\_10558.t1,gene\_01045.t1,gene\_07243.t1,gene\_08232.t1,gene\_02503.t1,gene\_09945.t1,gene\_10286.t1,gene\_01416.t1,gene\_05145.t1,gene\_05536.t1,gene\_04397.t1,gene\_06071.t1,gene\_07812.t1,gene\_10479.t1,gene\_06448.t1,gene\_01115.t1,gene\_04201.t1,gene\_09833.t1,gene\_03919.t1,gene\_08311.t1,gene\_03653.t1,gene\_08109.t1,gene\_04198.t1,gene\_03355.t1,gene\_01861.t1,gene\_08836.t1,gene\_07449.t1,gene\_00668.t1,gene\_00417.t1,gene\_06662.t1,gene\_06121.t1,gene\_01989.t1,gene\_04169.t1,gene\_03274.t1,gene\_07936.t1,gene\_03087.t1,gene\_08027.t1,gene\_10287.t1,gene\_00015.t1,gene\_09829.t1,gene\_01545.t1,gene\_08680.t1,gene\_08080.t1,gene\_08217.t1,gene\_06609.t1,gene\_04903.t1,gene\_08588.t1,gene\_01985.t1,gene\_02046.t1,gene\_09274.t1,gene\_05165.t1,gene\_03548.t1,gene\_03725.t1,gene\_00704.t1,gene\_08179.t1,gene\_03680.t1,gene\_08770.t1,gene\_08745.t1,gene\_09488.t1,gene\_03296.t1,gene\_01019.t1,gene\_03791.t1,gene\_04146.t1,gene\_02435.t1,gene\_06153.t1,gene\_01220.t1,gene\_06879.t1,gene\_04255.t1,gene\_02957.t1,gene\_06571.t1,gene\_08913.t1,gene\_01175.t1,gene\_05151.t1,gene\_10216.t1,gene\_05803.t1 | | GTP binding | molecular\_function |
| GO:0004129 | 2 | gene\_07269.t1,gene\_09108.t1 | | cytochrome-c oxidase activity | molecular\_function |
| GO:0004128 | 2 | gene\_06018.t1,gene\_01626.t1 | | cytochrome-b5 reductase activity, acting on NAD(P)H | molecular\_function |
| GO:0004121 | 1 | gene\_01259.t1 | | cystathionine beta-lyase activity | molecular\_function |
| GO:0004122 | 1 | gene\_01192.t1 | | cystathionine beta-synthase activity | molecular\_function |
| GO:0004127 | 1 | gene\_06009.t1 | | cytidylate kinase activity | molecular\_function |
| GO:0004126 | 1 | gene\_05132.t1 | | cytidine deaminase activity | molecular\_function |
| GO:0003825 | 1 | gene\_10489.t1 | | alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0003824 | 97 | gene\_03878.t1,gene\_08475.t1,gene\_00165.t1,gene\_00462.t1,gene\_08045.t1,gene\_01360.t1,gene\_00579.t1,gene\_01399.t1,gene\_00096.t1,gene\_00541.t1,gene\_03051.t1,gene\_01491.t1,gene\_07520.t1,gene\_04085.t1,gene\_07710.t1,gene\_05713.t1,gene\_04955.t1,gene\_04496.t1,gene\_08901.t1,gene\_07328.t1,gene\_09297.t1,gene\_02511.t1,gene\_03553.t1,gene\_04762.t1,gene\_04483.t1,gene\_08733.t1,gene\_07407.t1,gene\_10066.t1,gene\_07610.t1,gene\_00901.t1,gene\_08444.t1,gene\_00164.t1,gene\_06321.t1,gene\_02065.t1,gene\_04495.t1,gene\_09942.t1,gene\_09136.t1,gene\_03964.t1,gene\_08377.t1,gene\_05456.t1,gene\_10527.t1,gene\_05945.t1,gene\_06828.t1,gene\_03315.t1,gene\_04965.t1,gene\_06983.t1,gene\_05720.t1,gene\_00540.t1,gene\_10175.t1,gene\_02184.t1,gene\_09185.t1,gene\_02832.t1,gene\_04701.t1,gene\_02018.t1,gene\_03430.t1,gene\_08474.t1,gene\_00967.t1,gene\_07341.t1,gene\_01904.t1,gene\_08584.t1,gene\_00128.t1,gene\_09524.t1,gene\_04107.t1,gene\_01024.t1,gene\_09776.t1,gene\_08194.t1,gene\_01154.t1,gene\_01681.t1,gene\_04381.t1,gene\_02276.t1,gene\_06563.t1,gene\_07233.t1,gene\_03350.t1,gene\_00103.t1,gene\_00772.t1,gene\_06493.t1,gene\_00531.t1,gene\_10447.t1,gene\_03626.t1,gene\_04774.t1,gene\_02648.t1,gene\_09557.t1,gene\_01337.t1,gene\_00623.t1,gene\_07393.t1,gene\_08556.t1,gene\_08147.t1,gene\_02036.t1,gene\_05210.t1,gene\_08118.t1,gene\_00687.t1,gene\_05063.t1,gene\_01167.t1,gene\_04964.t1,gene\_02528.t1,gene\_00314.t1,gene\_01923.t1 | | catalytic activity | molecular\_function |
| GO:0008308 | 1 | gene\_00322.t1 | | voltage-gated anion channel activity | molecular\_function |
| GO:0008094 | 4 | gene\_09184.t1,gene\_08889.t1,gene\_05469.t1,gene\_08341.t1 | | ATP-dependent activity, acting on DNA | molecular\_function |
| GO:0008097 | 1 | gene\_08736.t1 | | 5S rRNA binding | molecular\_function |
| GO:0016835 | 2 | gene\_08150.t1,gene\_03440.t1 | | carbon-oxygen lyase activity | molecular\_function |
| GO:0016836 | 3 | gene\_02510.t1,gene\_09528.t1,gene\_04129.t1 | | hydro-lyase activity | molecular\_function |
| GO:0016830 | 4 | gene\_03988.t1,gene\_03700.t1,gene\_05675.t1,gene\_06682.t1 | | carbon-carbon lyase activity | molecular\_function |
| GO:0016831 | 9 | gene\_01575.t1,gene\_09908.t1,gene\_02277.t1,gene\_08350.t1,gene\_05768.t1,gene\_10373.t1,gene\_09179.t1,gene\_08855.t1,gene\_00631.t1 | | carboxy-lyase activity | molecular\_function |
| GO:0016832 | 2 | gene\_09319.t1,gene\_03085.t1 | | aldehyde-lyase activity | molecular\_function |
| GO:0016833 | 1 | gene\_08292.t1 | | oxo-acid-lyase activity | molecular\_function |
| GO:0018738 | 1 | gene\_04252.t1 | | S-formylglutathione hydrolase activity | molecular\_function |
| GO:0102545 | 3 | gene\_02894.t1,gene\_07645.t1,gene\_03380.t1 | | phosphatidyl phospholipase B activity | molecular\_function |
| GO:0015288 | 2 | gene\_00322.t1,gene\_09709.t1 | | porin activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0003959 | 2 | gene\_05358.t1,gene\_07722.t1 | | NADPH dehydrogenase activity | molecular\_function |
| GO:0003958 | 3 | gene\_08094.t1,gene\_06727.t1,gene\_06489.t1 | | NADPH-hemoprotein reductase activity | molecular\_function |
| GO:0003951 | 5 | gene\_02351.t1,gene\_09241.t1,gene\_08920.t1,gene\_07119.t1,gene\_08533.t1 | | NAD+ kinase activity | molecular\_function |
| GO:0003950 | 3 | gene\_07267.t1,gene\_08089.t1,gene\_00229.t1 | | NAD+ ADP-ribosyltransferase activity | molecular\_function |
| GO:0008233 | 21 | gene\_03698.t1,gene\_02486.t1,gene\_03149.t1,gene\_04048.t1,gene\_05702.t1,gene\_10451.t1,gene\_09366.t1,gene\_03050.t1,gene\_00706.t1,gene\_10045.t1,gene\_07138.t1,gene\_02420.t1,gene\_04461.t1,gene\_04246.t1,gene\_03388.t1,gene\_10392.t1,gene\_05700.t1,gene\_03622.t1,gene\_01393.t1,gene\_06138.t1,gene\_02422.t1 | | peptidase activity | molecular\_function |
| GO:0003952 | 1 | gene\_07903.t1 | | NAD+ synthase (glutamine-hydrolyzing) activity | molecular\_function |
| GO:0003955 | 1 | gene\_00973.t1 | | NAD(P)H dehydrogenase (quinone) activity | molecular\_function |
| GO:0003954 | 2 | gene\_03273.t1,gene\_02144.t1 | | NADH dehydrogenase activity | molecular\_function |
| GO:0008237 | 17 | gene\_02780.t1,gene\_08097.t1,gene\_02116.t1,gene\_07761.t1,gene\_04185.t1,gene\_04165.t1,gene\_05226.t1,gene\_02805.t1,gene\_06787.t1,gene\_00863.t1,gene\_04146.t1,gene\_02743.t1,gene\_01201.t1,gene\_02840.t1,gene\_04400.t1,gene\_09936.t1,gene\_05408.t1 | | metallopeptidase activity | molecular\_function |
| GO:0043998 | 1 | gene\_01433.t1 | | H2A histone acetyltransferase activity | molecular\_function |
| GO:0051087 | 5 | gene\_02544.t1,gene\_04415.t1,gene\_07388.t1,gene\_10118.t1,gene\_03945.t1 | | chaperone binding | molecular\_function |
| GO:0051082 | 20 | gene\_10136.t1,gene\_02559.t1,gene\_10423.t1,gene\_03204.t1,gene\_07139.t1,gene\_04223.t1,gene\_01533.t1,gene\_00502.t1,gene\_08085.t1,gene\_08963.t1,gene\_01682.t1,gene\_05558.t1,gene\_03193.t1,gene\_06242.t1,gene\_01918.t1,gene\_03801.t1,gene\_09414.t1,gene\_04092.t1,gene\_01128.t1,gene\_00738.t1 | | unfolded protein binding | molecular\_function |
| GO:0015377 | 1 | gene\_01365.t1 | | cation:chloride symporter activity | molecular\_function |
| GO:0042800 | 1 | gene\_02360.t1 | | histone methyltransferase activity (H3-K4 specific) | molecular\_function |
| GO:0042802 | 1 | gene\_07381.t1 | | identical protein binding | molecular\_function |
| GO:0042803 | 2 | gene\_05883.t1,gene\_03945.t1 | | protein homodimerization activity | molecular\_function |
| GO:0008430 | 1 | gene\_06409.t1 | | selenium binding | molecular\_function |
| GO:0044183 | 1 | gene\_07236.t1 | | protein folding chaperone | molecular\_function |
| GO:0016712 | 2 | gene\_02285.t1,gene\_07956.t1 | | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0015113 | 1 | gene\_08725.t1 | | nitrite transmembrane transporter activity | molecular\_function |
| GO:0110152 | 1 | gene\_09702.t1 | | RNA NAD-cap (NAD-forming) hydrolase activity | molecular\_function |
| GO:0061604 | 1 | gene\_08455.t1 | | molybdopterin-synthase sulfurtransferase activity | molecular\_function |
| GO:0004506 | 1 | gene\_04541.t1 | | squalene monooxygenase activity | molecular\_function |
| GO:0030234 | 5 | gene\_07275.t1,gene\_00979.t1,gene\_05847.t1,gene\_01479.t1,gene\_03734.t1 | | enzyme regulator activity | molecular\_function |
| GO:0004605 | 2 | gene\_04100.t1,gene\_02201.t1 | | phosphatidate cytidylyltransferase activity | molecular\_function |
| GO:0019843 | 11 | gene\_05192.t1,gene\_04098.t1,gene\_07619.t1,gene\_03883.t1,gene\_06874.t1,gene\_07417.t1,gene\_00702.t1,gene\_03284.t1,gene\_07288.t1,gene\_06861.t1,gene\_02479.t1 | | rRNA binding | molecular\_function |
| GO:0030695 | 2 | gene\_10161.t1,gene\_00958.t1 | | GTPase regulator activity | molecular\_function |
| GO:0030697 | 1 | gene\_05875.t1 | | S-adenosylmethionine-dependent tRNA (m5U54) methyltransferase activity | molecular\_function |
| GO:0008239 | 2 | gene\_07140.t1,gene\_09324.t1 | | dipeptidyl-peptidase activity | molecular\_function |
| GO:0017061 | 1 | gene\_03822.t1 | | S-methyl-5-thioadenosine phosphorylase activity | molecular\_function |
| GO:0005085 | 23 | gene\_08231.t1,gene\_06283.t1,gene\_09156.t1,gene\_03189.t1,gene\_08522.t1,gene\_05829.t1,gene\_10106.t1,gene\_01064.t1,gene\_05830.t1,gene\_10286.t1,gene\_07337.t1,gene\_03010.t1,gene\_10287.t1,gene\_09341.t1,gene\_04474.t1,gene\_10560.t1,gene\_07255.t1,gene\_00619.t1,gene\_10130.t1,gene\_01559.t1,gene\_06269.t1,gene\_09397.t1,gene\_01592.t1 | | guanyl-nucleotide exchange factor activity | molecular\_function |
| GO:0009374 | 1 | gene\_01374.t1 | | biotin binding | molecular\_function |
| GO:0000225 | 1 | gene\_06068.t1 | | N-acetylglucosaminylphosphatidylinositol deacetylase activity | molecular\_function |
| GO:0035312 | 1 | gene\_06740.t1 | | 5'-3' exodeoxyribonuclease activity | molecular\_function |
| GO:0031369 | 5 | gene\_10287.t1,gene\_01354.t1,gene\_05226.t1,gene\_10286.t1,gene\_00720.t1 | | translation initiation factor binding | molecular\_function |
| GO:0004420 | 1 | gene\_02693.t1 | | hydroxymethylglutaryl-CoA reductase (NADPH) activity | molecular\_function |
| GO:0004421 | 1 | gene\_03020.t1 | | hydroxymethylglutaryl-CoA synthase activity | molecular\_function |
| GO:0004424 | 1 | gene\_09625.t1 | | imidazoleglycerol-phosphate dehydratase activity | molecular\_function |
| GO:0106073 | 1 | gene\_07000.t1 | | dolichyl pyrophosphate Glc2Man9GlcNAc2 alpha-1,2-glucosyltransferase activity | molecular\_function |
| GO:0016295 | 1 | gene\_02332.t1 | | myristoyl-[acyl-carrier-protein] hydrolase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0008235 | 6 | gene\_01294.t1,gene\_02533.t1,gene\_01523.t1,gene\_08193.t1,gene\_01441.t1,gene\_03019.t1 | | metalloexopeptidase activity | molecular\_function |
| GO:0008234 | 4 | gene\_07354.t1,gene\_09087.t1,gene\_09777.t1,gene\_02560.t1 | | cysteine-type peptidase activity | molecular\_function |
| GO:0008236 | 12 | gene\_02286.t1,gene\_04530.t1,gene\_06378.t1,gene\_07140.t1,gene\_07401.t1,gene\_01041.t1,gene\_01428.t1,gene\_00248.t1,gene\_01916.t1,gene\_00866.t1,gene\_00779.t1,gene\_00247.t1 | | serine-type peptidase activity | molecular\_function |
| GO:0008934 | 2 | gene\_05585.t1,gene\_02349.t1 | | inositol monophosphate 1-phosphatase activity | molecular\_function |
| GO:0005337 | 2 | gene\_04064.t1,gene\_10461.t1 | | nucleoside transmembrane transporter activity | molecular\_function |
| GO:0019784 | 1 | gene\_08524.t1 | | NEDD8-specific protease activity | molecular\_function |
| GO:0036218 | 1 | gene\_09266.t1 | | dTTP diphosphatase activity | molecular\_function |
| GO:0004334 | 1 | gene\_03810.t1 | | fumarylacetoacetase activity | molecular\_function |
| GO:0004335 | 1 | gene\_08593.t1 | | galactokinase activity | molecular\_function |
| GO:0004332 | 1 | gene\_03040.t1 | | fructose-bisphosphate aldolase activity | molecular\_function |
| GO:0004333 | 1 | gene\_00860.t1 | | fumarate hydratase activity | molecular\_function |
| GO:0005247 | 3 | gene\_07629.t1,gene\_08410.t1,gene\_01052.t1 | | voltage-gated chloride channel activity | molecular\_function |
| GO:0005245 | 1 | gene\_05625.t1 | | voltage-gated calcium channel activity | molecular\_function |
| GO:0005244 | 1 | gene\_08146.t1 | | voltage-gated ion channel activity | molecular\_function |
| GO:0036402 | 6 | gene\_02486.t1,gene\_01236.t1,gene\_07138.t1,gene\_02420.t1,gene\_04461.t1,gene\_05700.t1 | | proteasome-activating activity | molecular\_function |
| GO:0004339 | 1 | gene\_05104.t1 | | glucan 1,4-alpha-glucosidase activity | molecular\_function |
| GO:0005536 | 6 | gene\_06196.t1,gene\_09513.t1,gene\_00838.t1,gene\_09875.t1,gene\_06480.t1,gene\_06014.t1 | | glucose binding | molecular\_function |
| GO:0004114 | 1 | gene\_01703.t1 | | 3',5'-cyclic-nucleotide phosphodiesterase activity | molecular\_function |
| GO:0004115 | 1 | gene\_02073.t1 | | 3',5'-cyclic-AMP phosphodiesterase activity | molecular\_function |
| GO:0102483 | 4 | gene\_03630.t1,gene\_06646.t1,gene\_02981.t1,gene\_08104.t1 | | scopolin beta-glucosidase activity | molecular\_function |
| GO:0102953 | 2 | gene\_08476.t1,gene\_10334.t1 | | hypoglycin A gamma-glutamyl transpeptidase activity | molecular\_function |
| GO:0031419 | 2 | gene\_02543.t1,gene\_09755.t1 | | cobalamin binding | molecular\_function |
| GO:0031418 | 4 | gene\_03106.t1,gene\_08658.t1,gene\_07708.t1,gene\_00107.t1 | | L-ascorbic acid binding | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0000049 | 17 | gene\_04329.t1,gene\_04234.t1,gene\_02682.t1,gene\_05774.t1,gene\_02330.t1,gene\_09742.t1,gene\_02254.t1,gene\_00417.t1,gene\_04722.t1,gene\_01562.t1,gene\_06698.t1,gene\_10160.t1,gene\_03944.t1,gene\_00660.t1,gene\_02187.t1,gene\_06273.t1,gene\_06212.t1 | | tRNA binding | molecular\_function |
| GO:0046933 | 7 | gene\_00280.t1,gene\_08419.t1,gene\_01009.t1,gene\_01026.t1,gene\_07605.t1,gene\_07813.t1,gene\_01754.t1 | | proton-transporting ATP synthase activity, rotational mechanism | molecular\_function |
| GO:0016829 | 36 | gene\_04197.t1,gene\_02704.t1,gene\_10404.t1,gene\_00784.t1,gene\_06166.t1,gene\_00088.t1,gene\_07561.t1,gene\_04303.t1,gene\_07984.t1,gene\_07270.t1,gene\_02150.t1,gene\_05909.t1,gene\_10652.t1,gene\_06837.t1,gene\_09527.t1,gene\_02844.t1,gene\_04404.t1,gene\_10011.t1,gene\_01839.t1,gene\_03098.t1,gene\_01840.t1,gene\_00746.t1,gene\_10580.t1,gene\_03552.t1,gene\_09132.t1,gene\_06065.t1,gene\_05961.t1,gene\_07638.t1,gene\_10080.t1,gene\_07522.t1,gene\_07724.t1,gene\_01497.t1,gene\_01036.t1,gene\_01838.t1,gene\_07472.t1,gene\_00939.t1 | | lyase activity | molecular\_function |
| GO:0102555 | 1 | gene\_06846.t1 | | octanoyl transferase activity (acting on glycine-cleavage complex H protein) | molecular\_function |
| GO:0004750 | 1 | gene\_00043.t1 | | D-ribulose-phosphate 3-epimerase activity | molecular\_function |
| GO:0004751 | 1 | gene\_06446.t1 | | ribose-5-phosphate isomerase activity | molecular\_function |
| GO:0004754 | 1 | gene\_03038.t1 | | saccharopine dehydrogenase (NAD+, L-lysine-forming) activity | molecular\_function |
| GO:0102552 | 1 | gene\_06832.t1 | | lipoyl synthase activity (acting on glycine-cleavage complex H protein | molecular\_function |
| GO:0004802 | 1 | gene\_08827.t1 | | transketolase activity | molecular\_function |
| GO:0015297 | 5 | gene\_05596.t1,gene\_05823.t1,gene\_00188.t1,gene\_06518.t1,gene\_09522.t1 | | antiporter activity | molecular\_function |
| GO:0016992 | 1 | gene\_06832.t1 | | lipoate synthase activity | molecular\_function |
| GO:0015293 | 4 | gene\_07427.t1,gene\_02884.t1,gene\_06183.t1,gene\_07824.t1 | | symporter activity | molecular\_function |
| GO:0015299 | 5 | gene\_03485.t1,gene\_01260.t1,gene\_05089.t1,gene\_00744.t1,gene\_04115.t1 | | solute:proton antiporter activity | molecular\_function |
| GO:0004373 | 1 | gene\_07867.t1 | | glycogen (starch) synthase activity | molecular\_function |
| GO:0003968 | 2 | gene\_08120.t1,gene\_06857.t1 | | RNA-directed 5'-3' RNA polymerase activity | molecular\_function |
| GO:0003964 | 2 | gene\_06867.t1,gene\_08777.t1 | | RNA-directed DNA polymerase activity | molecular\_function |
| GO:0004807 | 2 | gene\_00648.t1,gene\_06111.t1 | | triose-phosphate isomerase activity | molecular\_function |
| GO:0070773 | 1 | gene\_04568.t1 | | protein-N-terminal glutamine amidohydrolase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0106141 | 2 | gene\_10375.t1,gene\_00632.t1 | | flavin prenyltransferase activity | molecular\_function |
| GO:0032266 | 3 | gene\_06865.t1,gene\_07435.t1,gene\_01280.t1 | | phosphatidylinositol-3-phosphate binding | molecular\_function |
| GO:0015369 | 5 | gene\_01191.t1,gene\_01593.t1,gene\_06177.t1,gene\_06176.t1,gene\_06178.t1 | | calcium:proton antiporter activity | molecular\_function |
| GO:0032041 | 3 | gene\_02703.t1,gene\_07759.t1,gene\_02804.t1 | | NAD-dependent histone deacetylase activity (H3-K14 specific) | molecular\_function |
| GO:0002161 | 5 | gene\_07409.t1,gene\_02254.t1,gene\_09679.t1,gene\_10446.t1,gene\_04722.t1 | | aminoacyl-tRNA editing activity | molecular\_function |
| GO:0061798 | 1 | gene\_06655.t1 | | GTP 3',8'-cyclase activity | molecular\_function |
| GO:0015450 | 1 | gene\_07093.t1 | | protein-transporting ATPase activity | molecular\_function |
| GO:0004475 | 13 | gene\_10287.t1,gene\_03793.t1,gene\_10100.t1,gene\_04976.t1,gene\_03725.t1,gene\_00023.t1,gene\_05151.t1,gene\_10469.t1,gene\_01861.t1,gene\_04903.t1,gene\_10286.t1,gene\_01115.t1,gene\_03919.t1 | | mannose-1-phosphate guanylyltransferase activity | molecular\_function |
| GO:0008444 | 1 | gene\_08051.t1 | | CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase activity | molecular\_function |
| GO:0008441 | 1 | gene\_03882.t1 | | 3'(2'),5'-bisphosphate nucleotidase activity | molecular\_function |
| GO:0008448 | 1 | gene\_09762.t1 | | N-acetylglucosamine-6-phosphate deacetylase activity | molecular\_function |
| GO:0050155 | 1 | gene\_02827.t1 | | ornithine(lysine) transaminase activity | molecular\_function |
| GO:0015103 | 2 | gene\_05596.t1,gene\_00188.t1 | | inorganic anion transmembrane transporter activity | molecular\_function |
| GO:0015109 | 1 | gene\_10249.t1 | | chromate transmembrane transporter activity | molecular\_function |
| GO:0034450 | 1 | gene\_00376.t1 | | ubiquitin-ubiquitin ligase activity | molecular\_function |
| GO:0019104 | 1 | gene\_10200.t1 | | DNA N-glycosylase activity | molecular\_function |
| GO:0032051 | 1 | gene\_01372.t1 | | clathrin light chain binding | molecular\_function |
| GO:0015039 | 1 | gene\_07567.t1 | | NADPH-adrenodoxin reductase activity | molecular\_function |
| GO:0015035 | 3 | gene\_04277.t1,gene\_01940.t1,gene\_07528.t1 | | protein-disulfide reductase activity | molecular\_function |
| GO:0004427 | 1 | gene\_07215.t1 | | inorganic diphosphatase activity | molecular\_function |
| GO:0003796 | 2 | gene\_07692.t1,gene\_01789.t1 | | lysozyme activity | molecular\_function |
| GO:0030599 | 2 | gene\_09474.t1,gene\_06941.t1 | | pectinesterase activity | molecular\_function |
| GO:0043333 | 1 | gene\_03847.t1 | | 2-octaprenyl-6-methoxy-1,4-benzoquinone methylase activity | molecular\_function |
| GO:0035673 | 13 | gene\_09670.t1,gene\_02335.t1,gene\_06590.t1,gene\_00051.t1,gene\_03628.t1,gene\_05487.t1,gene\_05628.t1,gene\_05629.t1,gene\_04308.t1,gene\_05929.t1,gene\_08851.t1,gene\_04138.t1,gene\_07697.t1 | | oligopeptide transmembrane transporter activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0046975 | 1 | gene\_09220.t1 | | histone methyltransferase activity (H3-K36 specific) | molecular\_function |
| GO:0000309 | 2 | gene\_03849.t1,gene\_00373.t1 | | nicotinamide-nucleotide adenylyltransferase activity | molecular\_function |
| GO:1990610 | 1 | gene\_00361.t1 | | acetolactate synthase regulator activity | molecular\_function |
| GO:0043813 | 1 | gene\_06333.t1 | | phosphatidylinositol-3,5-bisphosphate 5-phosphatase activity | molecular\_function |
| GO:0031176 | 2 | gene\_10598.t1,gene\_00132.t1 | | endo-1,4-beta-xylanase activity | molecular\_function |
| GO:0031177 | 29 | gene\_09801.t1,gene\_07489.t1,gene\_00173.t1,gene\_05503.t1,gene\_07895.t1,gene\_08782.t1,gene\_07415.t1,gene\_01127.t1,gene\_06013.t1,gene\_00004.t1,gene\_00239.t1,gene\_08786.t1,gene\_08783.t1,gene\_09894.t1,gene\_01784.t1,gene\_00854.t1,gene\_04024.t1,gene\_05606.t1,gene\_05500.t1,gene\_01184.t1,gene\_07847.t1,gene\_08780.t1,gene\_00534.t1,gene\_08784.t1,gene\_06478.t1,gene\_05302.t1,gene\_10072.t1,gene\_01824.t1,gene\_08787.t1 | | phosphopantetheine binding | molecular\_function |
| GO:0009881 | 1 | gene\_01792.t1 | | photoreceptor activity | molecular\_function |
| GO:0003779 | 27 | gene\_05990.t1,gene\_03453.t1,gene\_09267.t1,gene\_04603.t1,gene\_02382.t1,gene\_06990.t1,gene\_03932.t1,gene\_08684.t1,gene\_00218.t1,gene\_08716.t1,gene\_05913.t1,gene\_09686.t1,gene\_07381.t1,gene\_05874.t1,gene\_10032.t1,gene\_00669.t1,gene\_08417.t1,gene\_07685.t1,gene\_07743.t1,gene\_03571.t1,gene\_00367.t1,gene\_00869.t1,gene\_05146.t1,gene\_03374.t1,gene\_07272.t1,gene\_06364.t1,gene\_08752.t1 | | actin binding | molecular\_function |
| GO:0043021 | 3 | gene\_01431.t1,gene\_00423.t1,gene\_05207.t1 | | ribonucleoprotein complex binding | molecular\_function |
| GO:0015112 | 1 | gene\_08725.t1 | | nitrate transmembrane transporter activity | molecular\_function |
| GO:0043023 | 4 | gene\_06330.t1,gene\_05374.t1,gene\_09219.t1,gene\_02227.t1 | | ribosomal large subunit binding | molecular\_function |
| GO:0043022 | 11 | gene\_08192.t1,gene\_03313.t1,gene\_01161.t1,gene\_10320.t1,gene\_07330.t1,gene\_07206.t1,gene\_03188.t1,gene\_09037.t1,gene\_09219.t1,gene\_05374.t1,gene\_01551.t1 | | ribosome binding | molecular\_function |
| GO:0003774 | 7 | gene\_03571.t1,gene\_03046.t1,gene\_08209.t1,gene\_00218.t1,gene\_09267.t1,gene\_10520.t1,gene\_03570.t1 | | cytoskeletal motor activity | molecular\_function |
| GO:0003777 | 8 | gene\_05738.t1,gene\_07366.t1,gene\_03452.t1,gene\_04724.t1,gene\_05745.t1,gene\_10636.t1,gene\_02766.t1,gene\_00134.t1 | | microtubule motor activity | molecular\_function |
| GO:0017070 | 2 | gene\_02780.t1,gene\_08079.t1 | | U6 snRNA binding | molecular\_function |
| GO:0050023 | 1 | gene\_00477.t1 | | L-fuconate dehydratase activity | molecular\_function |
| GO:0004435 | 2 | gene\_07148.t1,gene\_08790.t1 | | phosphatidylinositol phospholipase C activity | molecular\_function |
| GO:0004430 | 1 | gene\_03580.t1 | | 1-phosphatidylinositol 4-kinase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0035091 | 18 | gene\_03881.t1,gene\_05186.t1,gene\_10425.t1,gene\_03659.t1,gene\_01211.t1,gene\_02369.t1,gene\_07324.t1,gene\_01282.t1,gene\_02165.t1,gene\_03667.t1,gene\_05389.t1,gene\_03468.t1,gene\_07161.t1,gene\_06399.t1,gene\_02853.t1,gene\_08108.t1,gene\_03137.t1,gene\_10411.t1 | | phosphatidylinositol binding | molecular\_function |
| GO:0030570 | 2 | gene\_00945.t1,gene\_08437.t1 | | pectate lyase activity | molecular\_function |
| GO:0004439 | 1 | gene\_07363.t1 | | phosphatidylinositol-4,5-bisphosphate 5-phosphatase activity | molecular\_function |
| GO:0004438 | 1 | gene\_02966.t1 | | phosphatidylinositol-3-phosphatase activity | molecular\_function |
| GO:0045131 | 1 | gene\_03076.t1 | | pre-mRNA branch point binding | molecular\_function |
| GO:0003963 | 1 | gene\_04512.t1 | | RNA-3'-phosphate cyclase activity | molecular\_function |
| GO:0005344 | 1 | gene\_03326.t1 | | oxygen carrier activity | molecular\_function |
| GO:0008926 | 1 | gene\_00578.t1 | | mannitol-1-phosphate 5-dehydrogenase activity | molecular\_function |
| GO:0102769 | 1 | gene\_04434.t1 | | dihydroceramide glucosyltransferase activity | molecular\_function |
| GO:0004698 | 1 | gene\_05820.t1 | | calcium-dependent protein kinase C activity | molecular\_function |
| GO:2001070 | 1 | gene\_05104.t1 | | starch binding | molecular\_function |
| GO:0000166 | 34 | gene\_09401.t1,gene\_03242.t1,gene\_00526.t1,gene\_06309.t1,gene\_04007.t1,gene\_07165.t1,gene\_08708.t1,gene\_10662.t1,gene\_05582.t1,gene\_03928.t1,gene\_06101.t1,gene\_04702.t1,gene\_03099.t1,gene\_09419.t1,gene\_06856.t1,gene\_01610.t1,gene\_01534.t1,gene\_04330.t1,gene\_03024.t1,gene\_04187.t1,gene\_09702.t1,gene\_02686.t1,gene\_04609.t1,gene\_06775.t1,gene\_06452.t1,gene\_04266.t1,gene\_10644.t1,gene\_03200.t1,gene\_00924.t1,gene\_08901.t1,gene\_09266.t1,gene\_00595.t1,gene\_06282.t1,gene\_04454.t1 | | nucleotide binding | molecular\_function |
| GO:0004322 | 1 | gene\_09989.t1 | | ferroxidase activity | molecular\_function |
| GO:0004321 | 1 | gene\_02333.t1 | | fatty-acyl-CoA synthase activity | molecular\_function |
| GO:0004320 | 1 | gene\_02332.t1 | | oleoyl-[acyl-carrier-protein] hydrolase activity | molecular\_function |
| GO:0004326 | 2 | gene\_01409.t1,gene\_00302.t1 | | tetrahydrofolylpolyglutamate synthase activity | molecular\_function |
| GO:0004325 | 2 | gene\_04538.t1,gene\_09155.t1 | | ferrochelatase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0005509 | 38 | gene\_06880.t1,gene\_05990.t1,gene\_04249.t1,gene\_04055.t1,gene\_09598.t1,gene\_05379.t1,gene\_02641.t1,gene\_00996.t1,gene\_04603.t1,gene\_03755.t1,gene\_06811.t1,gene\_10310.t1,gene\_06206.t1,gene\_05216.t1,gene\_04058.t1,gene\_02126.t1,gene\_08332.t1,gene\_00669.t1,gene\_00456.t1,gene\_04068.t1,gene\_09821.t1,gene\_04296.t1,gene\_05378.t1,gene\_02421.t1,gene\_10063.t1,gene\_00016.t1,gene\_08790.t1,gene\_10343.t1,gene\_02817.t1,gene\_09062.t1,gene\_05853.t1,gene\_10637.t1,gene\_03515.t1,gene\_10423.t1,gene\_04047.t1,gene\_05625.t1,gene\_02125.t1,gene\_08752.t1 | | calcium ion binding | molecular\_function |
| GO:0005506 | 113 | gene\_09837.t1,gene\_07976.t1,gene\_07431.t1,gene\_08439.t1,gene\_00050.t1,gene\_07089.t1,gene\_01218.t1,gene\_09714.t1,gene\_10673.t1,gene\_01476.t1,gene\_06616.t1,gene\_10252.t1,gene\_04677.t1,gene\_04134.t1,gene\_02074.t1,gene\_07674.t1,gene\_01461.t1,gene\_10670.t1,gene\_02485.t1,gene\_06181.t1,gene\_08016.t1,gene\_08658.t1,gene\_08018.t1,gene\_07228.t1,gene\_01818.t1,gene\_09493.t1,gene\_05434.t1,gene\_02731.t1,gene\_05157.t1,gene\_01463.t1,gene\_04764.t1,gene\_09923.t1,gene\_07549.t1,gene\_04130.t1,gene\_01324.t1,gene\_09909.t1,gene\_07281.t1,gene\_07691.t1,gene\_02013.t1,gene\_04065.t1,gene\_07786.t1,gene\_02311.t1,gene\_06676.t1,gene\_06019.t1,gene\_01460.t1,gene\_09504.t1,gene\_03669.t1,gene\_07369.t1,gene\_01111.t1,gene\_09177.t1,gene\_00305.t1,gene\_07833.t1,gene\_02026.t1,gene\_02958.t1,gene\_09429.t1,gene\_04514.t1,gene\_03816.t1,gene\_00994.t1,gene\_00758.t1,gene\_03517.t1,gene\_01557.t1,gene\_00220.t1,gene\_00834.t1,gene\_01587.t1,gene\_07934.t1,gene\_00107.t1,gene\_03106.t1,gene\_07956.t1,gene\_04361.t1,gene\_00527.t1,gene\_07490.t1,gene\_06727.t1,gene\_00777.t1,gene\_10672.t1,gene\_07117.t1,gene\_01658.t1,gene\_10070.t1,gene\_07848.t1,gene\_07526.t1,gene\_03126.t1,gene\_09778.t1,gene\_02258.t1,gene\_09494.t1,gene\_08446.t1,gene\_05622.t1,gene\_09353.t1,gene\_09980.t1,gene\_01810.t1,gene\_09578.t1,gene\_09970.t1,gene\_03369.t1,gene\_04527.t1,gene\_08017.t1,gene\_06957.t1,gene\_07727.t1,gene\_01543.t1,gene\_05458.t1,gene\_07708.t1,gene\_02248.t1,gene\_05975.t1,gene\_01340.t1,gene\_09896.t1,gene\_03978.t1,gene\_00285.t1,gene\_10014.t1,gene\_09981.t1,gene\_07507.t1,gene\_07556.t1,gene\_02285.t1,gene\_09463.t1,gene\_08430.t1,gene\_03226.t1,gene\_09394.t1 | | iron ion binding | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0005507 | 27 | gene\_03055.t1,gene\_03740.t1,gene\_06951.t1,gene\_06041.t1,gene\_06695.t1,gene\_09648.t1,gene\_05744.t1,gene\_01837.t1,gene\_04617.t1,gene\_02010.t1,gene\_07894.t1,gene\_01764.t1,gene\_07681.t1,gene\_06931.t1,gene\_07616.t1,gene\_08795.t1,gene\_07939.t1,gene\_08542.t1,gene\_09373.t1,gene\_04449.t1,gene\_09876.t1,gene\_10189.t1,gene\_01941.t1,gene\_09128.t1,gene\_05304.t1,gene\_07382.t1,gene\_10284.t1 | | copper ion binding | molecular\_function |
| GO:0004100 | 10 | gene\_10650.t1,gene\_03571.t1,gene\_00810.t1,gene\_06057.t1,gene\_01290.t1,gene\_08876.t1,gene\_00224.t1,gene\_03570.t1,gene\_09106.t1,gene\_07068.t1 | | chitin synthase activity | molecular\_function |
| GO:0004107 | 1 | gene\_02444.t1 | | chorismate synthase activity | molecular\_function |
| GO:0004105 | 1 | gene\_05219.t1 | | choline-phosphate cytidylyltransferase activity | molecular\_function |
| GO:0003883 | 2 | gene\_09562.t1,gene\_01363.t1 | | CTP synthase activity | molecular\_function |
| GO:0004109 | 1 | gene\_04193.t1 | | coproporphyrinogen oxidase activity | molecular\_function |
| GO:0008324 | 11 | gene\_10251.t1,gene\_01285.t1,gene\_03300.t1,gene\_09808.t1,gene\_07729.t1,gene\_03337.t1,gene\_02153.t1,gene\_01235.t1,gene\_02275.t1,gene\_10631.t1,gene\_00177.t1 | | cation transmembrane transporter activity | molecular\_function |
| GO:0008320 | 2 | gene\_06869.t1,gene\_09709.t1 | | protein transmembrane transporter activity | molecular\_function |
| GO:0102965 | 2 | gene\_00238.t1,gene\_10630.t1 | | alcohol-forming fatty acyl-CoA reductase activity | molecular\_function |
| GO:0050385 | 1 | gene\_07404.t1 | | ureidoglycolate lyase activity | molecular\_function |
| GO:0046923 | 2 | gene\_04156.t1,gene\_02784.t1 | | ER retention sequence binding | molecular\_function |
| GO:0016857 | 1 | gene\_08726.t1 | | racemase and epimerase activity, acting on carbohydrates and derivatives | molecular\_function |
| GO:0016853 | 19 | gene\_08331.t1,gene\_02408.t1,gene\_08629.t1,gene\_05731.t1,gene\_03811.t1,gene\_09113.t1,gene\_03824.t1,gene\_10014.t1,gene\_08997.t1,gene\_00919.t1,gene\_07334.t1,gene\_03848.t1,gene\_03442.t1,gene\_09116.t1,gene\_00649.t1,gene\_08394.t1,gene\_05581.t1,gene\_00925.t1,gene\_01336.t1 | | isomerase activity | molecular\_function |
| GO:0016851 | 1 | gene\_06126.t1 | | magnesium chelatase activity | molecular\_function |
| GO:0004749 | 3 | gene\_10016.t1,gene\_09009.t1,gene\_09154.t1 | | ribose phosphate diphosphokinase activity | molecular\_function |
| GO:0004748 | 1 | gene\_00297.t1 | | ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor | molecular\_function |
| GO:0042799 | 1 | gene\_01095.t1 | | histone methyltransferase activity (H4-K20 specific) | molecular\_function |
| GO:0004743 | 1 | gene\_02627.t1 | | pyruvate kinase activity | molecular\_function |
| GO:0004742 | 1 | gene\_09157.t1 | | dihydrolipoyllysine-residue acetyltransferase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0004747 | 1 | gene\_07851.t1 | | ribokinase activity | molecular\_function |
| GO:0003972 | 1 | gene\_05344.t1 | | RNA ligase (ATP) activity | molecular\_function |
| GO:0003975 | 1 | gene\_07018.t1 | | UDP-N-acetylglucosamine-dolichyl-phosphate N-acetylglucosaminephosphotransferase activity | molecular\_function |
| GO:0003978 | 1 | gene\_08393.t1 | | UDP-glucose 4-epimerase activity | molecular\_function |
| GO:0071949 | 66 | gene\_02306.t1,gene\_06200.t1,gene\_03326.t1,gene\_10412.t1,gene\_08134.t1,gene\_03459.t1,gene\_00751.t1,gene\_06144.t1,gene\_03949.t1,gene\_05289.t1,gene\_04749.t1,gene\_05255.t1,gene\_10070.t1,gene\_02986.t1,gene\_02644.t1,gene\_03624.t1,gene\_07805.t1,gene\_04772.t1,gene\_09140.t1,gene\_01890.t1,gene\_07502.t1,gene\_06859.t1,gene\_05946.t1,gene\_04704.t1,gene\_00943.t1,gene\_09983.t1,gene\_01443.t1,gene\_06250.t1,gene\_07528.t1,gene\_06300.t1,gene\_04671.t1,gene\_05069.t1,gene\_04536.t1,gene\_00126.t1,gene\_05933.t1,gene\_02044.t1,gene\_08309.t1,gene\_09898.t1,gene\_03390.t1,gene\_08407.t1,gene\_00358.t1,gene\_09466.t1,gene\_08132.t1,gene\_06895.t1,gene\_01444.t1,gene\_06933.t1,gene\_00752.t1,gene\_06160.t1,gene\_02298.t1,gene\_10643.t1,gene\_08828.t1,gene\_04430.t1,gene\_00946.t1,gene\_04662.t1,gene\_10664.t1,gene\_06976.t1,gene\_10150.t1,gene\_07055.t1,gene\_01850.t1,gene\_09499.t1,gene\_08228.t1,gene\_04672.t1,gene\_05244.t1,gene\_00783.t1,gene\_09654.t1,gene\_07698.t1 | | FAD binding | molecular\_function |
| GO:0010181 | 31 | gene\_01936.t1,gene\_00252.t1,gene\_03008.t1,gene\_04670.t1,gene\_06403.t1,gene\_10086.t1,gene\_00973.t1,gene\_00341.t1,gene\_08248.t1,gene\_04134.t1,gene\_06727.t1,gene\_08822.t1,gene\_00443.t1,gene\_10647.t1,gene\_08069.t1,gene\_08405.t1,gene\_10669.t1,gene\_05358.t1,gene\_02597.t1,gene\_00922.t1,gene\_07860.t1,gene\_06489.t1,gene\_10427.t1,gene\_06168.t1,gene\_07086.t1,gene\_07087.t1,gene\_00885.t1,gene\_07722.t1,gene\_01132.t1,gene\_08094.t1,gene\_10039.t1 | | FMN binding | molecular\_function |
| GO:0070122 | 8 | gene\_02780.t1,gene\_08097.t1,gene\_04185.t1,gene\_05226.t1,gene\_02805.t1,gene\_06787.t1,gene\_06270.t1,gene\_05408.t1 | | isopeptidase activity | molecular\_function |
| GO:0103026 | 1 | gene\_08076.t1 | | fructose-1-phosphatase activity | molecular\_function |
| GO:0004020 | 2 | gene\_05577.t1,gene\_07261.t1 | | adenylylsulfate kinase activity | molecular\_function |
| GO:0051377 | 3 | gene\_09564.t1,gene\_09726.t1,gene\_01263.t1 | | mannose-ethanolamine phosphotransferase activity | molecular\_function |
| GO:0032450 | 2 | gene\_06646.t1,gene\_04046.t1 | | maltose alpha-glucosidase activity | molecular\_function |
| GO:0047451 | 1 | gene\_02332.t1 | | 3-hydroxyoctanoyl-[acyl-carrier-protein] dehydratase activity | molecular\_function |
| GO:0042132 | 1 | gene\_10122.t1 | | fructose 1,6-bisphosphate 1-phosphatase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0047453 | 1 | gene\_00517.t1 | | ATP-dependent NAD(P)H-hydrate dehydratase activity | molecular\_function |
| GO:0042134 | 2 | gene\_09245.t1,gene\_08812.t1 | | rRNA primary transcript binding | molecular\_function |
| GO:0019135 | 1 | gene\_09824.t1 | | deoxyhypusine monooxygenase activity | molecular\_function |
| GO:0019133 | 3 | gene\_04677.t1,gene\_01810.t1,gene\_06957.t1 | | choline monooxygenase activity | molecular\_function |
| GO:0016597 | 2 | gene\_06540.t1,gene\_00359.t1 | | amino acid binding | molecular\_function |
| GO:0019783 | 2 | gene\_07922.t1,gene\_06150.t1 | | ubiquitin-like protein-specific protease activity | molecular\_function |
| GO:0016209 | 2 | gene\_09292.t1,gene\_07930.t1 | | antioxidant activity | molecular\_function |
| GO:0016208 | 1 | gene\_10043.t1 | | AMP binding | molecular\_function |
| GO:0019825 | 2 | gene\_02919.t1,gene\_03326.t1 | | oxygen binding | molecular\_function |
| GO:0019829 | 6 | gene\_03055.t1,gene\_09269.t1,gene\_09471.t1,gene\_04634.t1,gene\_09029.t1,gene\_10284.t1 | | ATPase-coupled cation transmembrane transporter activity | molecular\_function |
| GO:0036374 | 2 | gene\_08476.t1,gene\_10334.t1 | | glutathione hydrolase activity | molecular\_function |
| GO:0030366 | 2 | gene\_06930.t1,gene\_04702.t1 | | molybdopterin synthase activity | molecular\_function |
| GO:0035243 | 2 | gene\_00483.t1,gene\_07534.t1 | | protein-arginine omega-N symmetric methyltransferase activity | molecular\_function |
| GO:0000339 | 2 | gene\_09407.t1,gene\_09711.t1 | | RNA cap binding | molecular\_function |
| GO:0030145 | 7 | gene\_06548.t1,gene\_03891.t1,gene\_04742.t1,gene\_05772.t1,gene\_02071.t1,gene\_01205.t1,gene\_03194.t1 | | manganese ion binding | molecular\_function |
| GO:0004150 | 1 | gene\_08648.t1 | | dihydroneopterin aldolase activity | molecular\_function |
| GO:0050897 | 1 | gene\_03176.t1 | | cobalt ion binding | molecular\_function |
| GO:0043014 | 1 | gene\_10207.t1 | | alpha-tubulin binding | molecular\_function |
| GO:0043015 | 5 | gene\_06203.t1,gene\_08722.t1,gene\_05691.t1,gene\_08161.t1,gene\_07037.t1 | | gamma-tubulin binding | molecular\_function |
| GO:0003746 | 13 | gene\_03293.t1,gene\_01481.t1,gene\_08192.t1,gene\_02465.t1,gene\_05617.t1,gene\_03866.t1,gene\_09595.t1,gene\_03540.t1,gene\_04316.t1,gene\_01551.t1,gene\_01416.t1,gene\_06949.t1,gene\_07299.t1 | | translation elongation factor activity | molecular\_function |
| GO:0003747 | 5 | gene\_09256.t1,gene\_09560.t1,gene\_07346.t1,gene\_03716.t1,gene\_03220.t1 | | translation release factor activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0003743 | 48 | gene\_00144.t1,gene\_05739.t1,gene\_08169.t1,gene\_00426.t1,gene\_06773.t1,gene\_10287.t1,gene\_07180.t1,gene\_04717.t1,gene\_00246.t1,gene\_06804.t1,gene\_00417.t1,gene\_01354.t1,gene\_02418.t1,gene\_01045.t1,gene\_05226.t1,gene\_02503.t1,gene\_05408.t1,gene\_10286.t1,gene\_03188.t1,gene\_05697.t1,gene\_01700.t1,gene\_00555.t1,gene\_10467.t1,gene\_00617.t1,gene\_05884.t1,gene\_07923.t1,gene\_05818.t1,gene\_03292.t1,gene\_05169.t1,gene\_09219.t1,gene\_03450.t1,gene\_07237.t1,gene\_01545.t1,gene\_01427.t1,gene\_02334.t1,gene\_05228.t1,gene\_06623.t1,gene\_05239.t1,gene\_05138.t1,gene\_06008.t1,gene\_07293.t1,gene\_05898.t1,gene\_00658.t1,gene\_00493.t1,gene\_01551.t1,gene\_08881.t1,gene\_06800.t1,gene\_00720.t1 | | translation initiation factor activity | molecular\_function |
| GO:0052926 | 1 | gene\_02233.t1 | | dol-P-Man:Man(6)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase activity | molecular\_function |
| GO:0052925 | 1 | gene\_05817.t1 | | dol-P-Man:Man(5)GlcNAc(2)-PP-Dol alpha-1,3-mannosyltransferase activity | molecular\_function |
| GO:0003984 | 1 | gene\_08592.t1 | | acetolactate synthase activity | molecular\_function |
| GO:0047844 | 1 | gene\_05132.t1 | | deoxycytidine deaminase activity | molecular\_function |
| GO:0005034 | 2 | gene\_01278.t1,gene\_08242.t1 | | osmosensor activity | molecular\_function |
| GO:0030544 | 3 | gene\_01682.t1,gene\_01128.t1,gene\_03313.t1 | | Hsp70 protein binding | molecular\_function |
| GO:0008138 | 8 | gene\_02724.t1,gene\_07595.t1,gene\_00345.t1,gene\_08755.t1,gene\_05850.t1,gene\_07644.t1,gene\_02992.t1,gene\_02930.t1 | | protein tyrosine/serine/threonine phosphatase activity | molecular\_function |
| GO:0008139 | 1 | gene\_06461.t1 | | nuclear localization sequence binding | molecular\_function |
| GO:0008137 | 6 | gene\_09283.t1,gene\_06779.t1,gene\_04152.t1,gene\_01707.t1,gene\_03833.t1,gene\_10039.t1 | | NADH dehydrogenase (ubiquinone) activity | molecular\_function |
| GO:0008131 | 7 | gene\_06041.t1,gene\_09373.t1,gene\_04449.t1,gene\_01764.t1,gene\_10189.t1,gene\_07681.t1,gene\_09128.t1 | | primary amine oxidase activity | molecular\_function |
| GO:0031543 | 1 | gene\_00107.t1 | | peptidyl-proline dioxygenase activity | molecular\_function |
| GO:0045145 | 1 | gene\_02235.t1 | | single-stranded DNA 5'-3' exodeoxyribonuclease activity | molecular\_function |
| GO:0004358 | 1 | gene\_04583.t1 | | glutamate N-acetyltransferase activity | molecular\_function |
| GO:0004359 | 3 | gene\_07903.t1,gene\_01088.t1,gene\_08292.t1 | | glutaminase activity | molecular\_function |
| GO:0004356 | 3 | gene\_09443.t1,gene\_10398.t1,gene\_03301.t1 | | glutamate-ammonia ligase activity | molecular\_function |
| GO:0004357 | 1 | gene\_09056.t1 | | glutamate-cysteine ligase activity | molecular\_function |
| GO:0004354 | 1 | gene\_09401.t1 | | glutamate dehydrogenase (NADP+) activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0004352 | 1 | gene\_09887.t1 | | glutamate dehydrogenase (NAD+) activity | molecular\_function |
| GO:0004350 | 1 | gene\_01216.t1 | | glutamate-5-semialdehyde dehydrogenase activity | molecular\_function |
| GO:0004351 | 3 | gene\_05088.t1,gene\_09066.t1,gene\_10583.t1 | | glutamate decarboxylase activity | molecular\_function |
| GO:0004590 | 1 | gene\_01122.t1 | | orotidine-5'-phosphate decarboxylase activity | molecular\_function |
| GO:0004591 | 1 | gene\_10230.t1 | | oxoglutarate dehydrogenase (succinyl-transferring) activity | molecular\_function |
| GO:0005519 | 1 | gene\_05327.t1 | | cytoskeletal regulatory protein binding | molecular\_function |
| GO:0004594 | 1 | gene\_06901.t1 | | pantothenate kinase activity | molecular\_function |
| GO:0004596 | 2 | gene\_05336.t1,gene\_03249.t1 | | peptide alpha-N-acetyltransferase activity | molecular\_function |
| GO:0004176 | 5 | gene\_05844.t1,gene\_10098.t1,gene\_09415.t1,gene\_02676.t1,gene\_07191.t1 | | ATP-dependent peptidase activity | molecular\_function |
| GO:0004177 | 7 | gene\_07140.t1,gene\_01769.t1,gene\_01294.t1,gene\_07031.t1,gene\_02840.t1,gene\_08193.t1,gene\_04400.t1 | | aminopeptidase activity | molecular\_function |
| GO:0008682 | 1 | gene\_07066.t1 | | 3-demethoxyubiquinol 3-hydroxylase activity | molecular\_function |
| GO:0004170 | 1 | gene\_01001.t1 | | dUTP diphosphatase activity | molecular\_function |
| GO:0008864 | 1 | gene\_01843.t1 | | formyltetrahydrofolate deformylase activity | molecular\_function |
| GO:0008689 | 1 | gene\_04044.t1 | | 3-demethylubiquinone-9 3-O-methyltransferase activity | molecular\_function |
| GO:0008863 | 1 | gene\_09683.t1 | | formate dehydrogenase (NAD+) activity | molecular\_function |
| GO:0008047 | 1 | gene\_04547.t1 | | enzyme activator activity | molecular\_function |
| GO:0016846 | 11 | gene\_03449.t1,gene\_04236.t1,gene\_07773.t1,gene\_00055.t1,gene\_07115.t1,gene\_01946.t1,gene\_06827.t1,gene\_08107.t1,gene\_00201.t1,gene\_02331.t1,gene\_05365.t1 | | carbon-sulfur lyase activity | molecular\_function |
| GO:0080101 | 1 | gene\_05187.t1 | | phosphatidyl-N-dimethylethanolamine N-methyltransferase activity | molecular\_function |
| GO:0000062 | 2 | gene\_08860.t1,gene\_00651.t1 | | fatty-acyl-CoA binding | molecular\_function |
| GO:0042781 | 1 | gene\_06657.t1 | | 3'-tRNA processing endoribonuclease activity | molecular\_function |
| GO:0004775 | 2 | gene\_01319.t1,gene\_04330.t1 | | succinate-CoA ligase (ADP-forming) activity | molecular\_function |
| GO:0004777 | 1 | gene\_01425.t1 | | succinate-semialdehyde dehydrogenase (NAD+) activity | molecular\_function |
| GO:0018506 | 1 | gene\_02667.t1 | | maleylacetate reductase activity | molecular\_function |
| GO:0004000 | 1 | gene\_01718.t1 | | adenosine deaminase activity | molecular\_function |
| GO:0004001 | 1 | gene\_08031.t1 | | adenosine kinase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0016504 | 1 | gene\_10093.t1 | | peptidase activator activity | molecular\_function |
| GO:0008265 | 1 | gene\_02844.t1 | | Mo-molybdopterin cofactor sulfurase activity | molecular\_function |
| GO:0008260 | 2 | gene\_02317.t1,gene\_10319.t1 | | 3-oxoacid CoA-transferase activity | molecular\_function |
| GO:0003908 | 1 | gene\_06694.t1 | | methylated-DNA-[protein]-cysteine S-methyltransferase activity | molecular\_function |
| GO:0097023 | 1 | gene\_08076.t1 | | fructose 6-phosphate aldolase activity | molecular\_function |
| GO:0008660 | 1 | gene\_00962.t1 | | 1-aminocyclopropane-1-carboxylate deaminase activity | molecular\_function |
| GO:0070006 | 9 | gene\_00326.t1,gene\_05363.t1,gene\_03891.t1,gene\_09324.t1,gene\_04573.t1,gene\_02071.t1,gene\_01205.t1,gene\_05364.t1,gene\_02643.t1 | | metalloaminopeptidase activity | molecular\_function |
| GO:0019120 | 2 | gene\_01179.t1,gene\_02166.t1 | | hydrolase activity, acting on acid halide bonds, in C-halide compounds | molecular\_function |
| GO:0019901 | 8 | gene\_03270.t1,gene\_01161.t1,gene\_04062.t1,gene\_08489.t1,gene\_01190.t1,gene\_04106.t1,gene\_00900.t1,gene\_03261.t1 | | protein kinase binding | molecular\_function |
| GO:0019903 | 1 | gene\_10037.t1 | | protein phosphatase binding | molecular\_function |
| GO:0031625 | 4 | gene\_08748.t1,gene\_08525.t1,gene\_09768.t1,gene\_09787.t1 | | ubiquitin protein ligase binding | molecular\_function |
| GO:0019905 | 1 | gene\_01392.t1 | | syntaxin binding | molecular\_function |
| GO:0043531 | 7 | gene\_04002.t1,gene\_07516.t1,gene\_06189.t1,gene\_08557.t1,gene\_07515.t1,gene\_07544.t1,gene\_00240.t1 | | ADP binding | molecular\_function |
| GO:0052723 | 1 | gene\_02352.t1 | | inositol hexakisphosphate 1-kinase activity | molecular\_function |
| GO:0052724 | 1 | gene\_02352.t1 | | inositol hexakisphosphate 3-kinase activity | molecular\_function |
| GO:0050291 | 3 | gene\_09343.t1,gene\_09360.t1,gene\_06384.t1 | | sphingosine N-acyltransferase activity | molecular\_function |
| GO:0046553 | 1 | gene\_00653.t1 | | D-malate dehydrogenase (decarboxylating) activity | molecular\_function |
| GO:0016274 | 4 | gene\_08577.t1,gene\_02483.t1,gene\_05856.t1,gene\_01712.t1 | | protein-arginine N-methyltransferase activity | molecular\_function |
| GO:0046558 | 4 | gene\_06731.t1,gene\_03467.t1,gene\_03663.t1,gene\_09125.t1 | | arabinan endo-1,5-alpha-L-arabinosidase activity | molecular\_function |
| GO:0046559 | 1 | gene\_08100.t1 | | alpha-glucuronidase activity | molecular\_function |
| GO:0016279 | 3 | gene\_09083.t1,gene\_09289.t1,gene\_02725.t1 | | protein-lysine N-methyltransferase activity | molecular\_function |
| GO:0004450 | 1 | gene\_06798.t1 | | isocitrate dehydrogenase (NADP+) activity | molecular\_function |
| GO:0030975 | 1 | gene\_04276.t1 | | thiamine binding | molecular\_function |
| GO:0030976 | 8 | gene\_02158.t1,gene\_10230.t1,gene\_08592.t1,gene\_03558.t1,gene\_03899.t1,gene\_08855.t1,gene\_05669.t1,gene\_03017.t1 | | thiamine pyrophosphate binding | molecular\_function |
| GO:0005516 | 1 | gene\_08141.t1 | | calmodulin binding | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0106261 | 1 | gene\_04329.t1 | | tRNA uridine(34) acetyltransferase activity | molecular\_function |
| GO:0016303 | 1 | gene\_08215.t1 | | 1-phosphatidylinositol-3-kinase activity | molecular\_function |
| GO:0016300 | 1 | gene\_04181.t1 | | tRNA (uracil) methyltransferase activity | molecular\_function |
| GO:0016301 | 78 | gene\_02627.t1,gene\_09358.t1,gene\_08657.t1,gene\_02704.t1,gene\_05776.t1,gene\_05886.t1,gene\_01244.t1,gene\_05312.t1,gene\_09602.t1,gene\_00300.t1,gene\_10257.t1,gene\_03606.t1,gene\_10016.t1,gene\_04555.t1,gene\_02211.t1,gene\_00517.t1,gene\_00304.t1,gene\_03779.t1,gene\_04276.t1,gene\_05195.t1,gene\_08551.t1,gene\_08060.t1,gene\_05406.t1,gene\_05124.t1,gene\_06947.t1,gene\_03840.t1,gene\_06669.t1,gene\_05592.t1,gene\_03607.t1,gene\_04829.t1,gene\_07339.t1,gene\_06002.t1,gene\_07371.t1,gene\_04936.t1,gene\_04980.t1,gene\_07663.t1,gene\_08224.t1,gene\_00701.t1,gene\_05667.t1,gene\_02096.t1,gene\_03913.t1,gene\_05355.t1,gene\_08572.t1,gene\_05017.t1,gene\_09330.t1,gene\_07564.t1,gene\_04034.t1,gene\_03265.t1,gene\_06665.t1,gene\_04605.t1,gene\_09154.t1,gene\_10346.t1,gene\_09329.t1,gene\_00113.t1,gene\_04694.t1,gene\_01504.t1,gene\_09015.t1,gene\_07816.t1,gene\_02019.t1,gene\_02426.t1,gene\_02095.t1,gene\_09009.t1,gene\_03555.t1,gene\_06513.t1,gene\_08552.t1,gene\_07882.t1,gene\_04104.t1,gene\_07726.t1,gene\_00474.t1,gene\_09587.t1,gene\_05749.t1,gene\_07518.t1,gene\_01234.t1,gene\_04958.t1,gene\_10299.t1,gene\_08707.t1,gene\_09673.t1,gene\_00939.t1 | | kinase activity | molecular\_function |
| GO:0016307 | 1 | gene\_07278.t1 | | phosphatidylinositol phosphate kinase activity | molecular\_function |
| GO:0005452 | 1 | gene\_03075.t1 | | inorganic anion exchanger activity | molecular\_function |
| GO:0046316 | 1 | gene\_10185.t1 | | gluconokinase activity | molecular\_function |
| GO:0004592 | 1 | gene\_05955.t1 | | pantoate-beta-alanine ligase activity | molecular\_function |
| GO:0042300 | 1 | gene\_04414.t1 | | beta-amyrin synthase activity | molecular\_function |
| GO:0140684 | 1 | gene\_08858.t1 | | histone H3-tri/dimethyl-lysine-9 demethylase activity | molecular\_function |
| GO:0140680 | 1 | gene\_09878.t1 | | histone H3-di/monomethyl-lysine-36 demethylase activity | molecular\_function |
| GO:0003714 | 3 | gene\_08119.t1,gene\_00256.t1,gene\_05789.t1 | | transcription corepressor activity | molecular\_function |
| GO:0003713 | 3 | gene\_01212.t1,gene\_10112.t1,gene\_00580.t1 | | transcription coactivator activity | molecular\_function |
| GO:0004854 | 1 | gene\_10070.t1 | | xanthine dehydrogenase activity | molecular\_function |
| GO:0030151 | 5 | gene\_09776.t1,gene\_01167.t1,gene\_08723.t1,gene\_02844.t1,gene\_09185.t1 | | molybdenum ion binding | molecular\_function |
| GO:0120013 | 1 | gene\_09048.t1 | | lipid transfer activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0031151 | 1 | gene\_05805.t1 | | histone methyltransferase activity (H3-K79 specific) | molecular\_function |
| GO:0008869 | 1 | gene\_03435.t1 | | galactonate dehydratase activity | molecular\_function |
| GO:0003756 | 3 | gene\_01029.t1,gene\_05790.t1,gene\_08283.t1 | | protein disulfide isomerase activity | molecular\_function |
| GO:0003755 | 18 | gene\_01268.t1,gene\_06699.t1,gene\_07747.t1,gene\_02695.t1,gene\_06100.t1,gene\_03609.t1,gene\_02160.t1,gene\_03613.t1,gene\_02711.t1,gene\_08344.t1,gene\_00737.t1,gene\_06426.t1,gene\_08765.t1,gene\_01092.t1,gene\_00827.t1,gene\_00425.t1,gene\_05580.t1,gene\_09741.t1 | | peptidyl-prolyl cis-trans isomerase activity | molecular\_function |
| GO:0010997 | 3 | gene\_09995.t1,gene\_02100.t1,gene\_07199.t1 | | anaphase-promoting complex binding | molecular\_function |
| GO:0000213 | 2 | gene\_04404.t1,gene\_05909.t1 | | tRNA-intron endonuclease activity | molecular\_function |
| GO:0000210 | 1 | gene\_07902.t1 | | NAD+ diphosphatase activity | molecular\_function |
| GO:0009982 | 6 | gene\_05787.t1,gene\_09006.t1,gene\_01896.t1,gene\_09251.t1,gene\_06280.t1,gene\_01113.t1 | | pseudouridine synthase activity | molecular\_function |
| GO:0030798 | 1 | gene\_02161.t1 | | trans-aconitate 2-methyltransferase activity | molecular\_function |
| GO:0047834 | 24 | gene\_02566.t1,gene\_01649.t1,gene\_02883.t1,gene\_05361.t1,gene\_02650.t1,gene\_00528.t1,gene\_10090.t1,gene\_09588.t1,gene\_07751.t1,gene\_00753.t1,gene\_06035.t1,gene\_08507.t1,gene\_05288.t1,gene\_08758.t1,gene\_05454.t1,gene\_09033.t1,gene\_05403.t1,gene\_10223.t1,gene\_04601.t1,gene\_00136.t1,gene\_04172.t1,gene\_08146.t1,gene\_00837.t1,gene\_09032.t1 | | D-threo-aldose 1-dehydrogenase activity | molecular\_function |
| GO:0001181 | 1 | gene\_00617.t1 | | RNA polymerase I general transcription initiation factor activity | molecular\_function |
| GO:0008412 | 1 | gene\_09298.t1 | | 4-hydroxybenzoate octaprenyltransferase activity | molecular\_function |
| GO:0008124 | 1 | gene\_07572.t1 | | 4-alpha-hydroxytetrahydrobiopterin dehydratase activity | molecular\_function |
| GO:0008121 | 1 | gene\_08412.t1 | | ubiquinol-cytochrome-c reductase activity | molecular\_function |
| GO:0008120 | 1 | gene\_04434.t1 | | ceramide glucosyltransferase activity | molecular\_function |
| GO:0000104 | 1 | gene\_04426.t1 | | succinate dehydrogenase activity | molecular\_function |
| GO:0102340 | 1 | gene\_06564.t1 | | 3-oxo-behenoyl-CoA reductase activity | molecular\_function |
| GO:0102341 | 1 | gene\_06564.t1 | | 3-oxo-lignoceroyl-CoA reductase activity | molecular\_function |
| GO:0102342 | 1 | gene\_06564.t1 | | 3-oxo-cerotoyl-CoA reductase activity | molecular\_function |
| GO:0102343 | 1 | gene\_04035.t1 | | 3-hydroxy-arachidoyl-CoA dehydratase activity | molecular\_function |
| GO:0004349 | 1 | gene\_01196.t1 | | glutamate 5-kinase activity | molecular\_function |
| GO:0102345 | 1 | gene\_04035.t1 | | 3-hydroxy-lignoceroyl-CoA dehydratase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0140078 | 3 | gene\_06972.t1,gene\_10200.t1,gene\_04239.t1 | | class I DNA-(apurinic or apyrimidinic site) endonuclease activity | molecular\_function |
| GO:0004347 | 1 | gene\_00479.t1 | | glucose-6-phosphate isomerase activity | molecular\_function |
| GO:0004343 | 2 | gene\_00859.t1,gene\_06597.t1 | | glucosamine 6-phosphate N-acetyltransferase activity | molecular\_function |
| GO:0004342 | 1 | gene\_09759.t1 | | glucosamine-6-phosphate deaminase activity | molecular\_function |
| GO:0004588 | 1 | gene\_07023.t1 | | orotate phosphoribosyltransferase activity | molecular\_function |
| GO:0004587 | 1 | gene\_02827.t1 | | ornithine-oxo-acid transaminase activity | molecular\_function |
| GO:0004582 | 1 | gene\_08604.t1 | | dolichyl-phosphate beta-D-mannosyltransferase activity | molecular\_function |
| GO:0004581 | 1 | gene\_04592.t1 | | dolichyl-phosphate beta-glucosyltransferase activity | molecular\_function |
| GO:0004164 | 1 | gene\_02208.t1 | | diphthine synthase activity | molecular\_function |
| GO:0008693 | 1 | gene\_02332.t1 | | 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase activity | molecular\_function |
| GO:0004160 | 1 | gene\_00766.t1 | | dihydroxy-acid dehydratase activity | molecular\_function |
| GO:0004163 | 1 | gene\_00352.t1 | | diphosphomevalonate decarboxylase activity | molecular\_function |
| GO:0004169 | 3 | gene\_04168.t1,gene\_07257.t1,gene\_05987.t1 | | dolichyl-phosphate-mannose-protein mannosyltransferase activity | molecular\_function |
| GO:0016879 | 1 | gene\_05831.t1 | | ligase activity, forming carbon-nitrogen bonds | molecular\_function |
| GO:0016872 | 1 | gene\_02547.t1 | | intramolecular lyase activity | molecular\_function |
| GO:0016874 | 52 | gene\_08185.t1,gene\_09212.t1,gene\_04624.t1,gene\_03109.t1,gene\_04440.t1,gene\_00173.t1,gene\_07029.t1,gene\_04206.t1,gene\_05466.t1,gene\_00510.t1,gene\_04713.t1,gene\_03443.t1,gene\_07415.t1,gene\_03472.t1,gene\_04509.t1,gene\_02423.t1,gene\_06905.t1,gene\_08807.t1,gene\_08238.t1,gene\_00521.t1,gene\_05385.t1,gene\_05256.t1,gene\_03725.t1,gene\_04444.t1,gene\_06468.t1,gene\_04659.t1,gene\_08180.t1,gene\_05284.t1,gene\_06591.t1,gene\_04619.t1,gene\_02535.t1,gene\_02443.t1,gene\_04024.t1,gene\_04508.t1,gene\_00761.t1,gene\_05760.t1,gene\_00498.t1,gene\_01184.t1,gene\_05503.t1,gene\_07847.t1,gene\_00534.t1,gene\_02534.t1,gene\_07453.t1,gene\_01142.t1,gene\_01174.t1,gene\_04761.t1,gene\_01824.t1,gene\_06640.t1,gene\_07524.t1,gene\_06188.t1,gene\_04618.t1,gene\_06896.t1 | | ligase activity | molecular\_function |
| GO:0009055 | 8 | gene\_08093.t1,gene\_04289.t1,gene\_08431.t1,gene\_03957.t1,gene\_02122.t1,gene\_04395.t1,gene\_04426.t1,gene\_00717.t1 | | electron transfer activity | molecular\_function |
| GO:0004767 | 3 | gene\_09922.t1,gene\_00291.t1,gene\_07110.t1 | | sphingomyelin phosphodiesterase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0004765 | 1 | gene\_02251.t1 | | shikimate kinase activity | molecular\_function |
| GO:0004764 | 5 | gene\_05584.t1,gene\_05125.t1,gene\_00923.t1,gene\_05587.t1,gene\_02251.t1 | | shikimate 3-dehydrogenase (NADP+) activity | molecular\_function |
| GO:0004768 | 2 | gene\_08991.t1,gene\_09188.t1 | | stearoyl-CoA 9-desaturase activity | molecular\_function |
| GO:0004019 | 1 | gene\_01989.t1 | | adenylosuccinate synthase activity | molecular\_function |
| GO:0004018 | 1 | gene\_07647.t1 | | N6-(1,2-dicarboxyethyl)AMP AMP-lyase (fumarate-forming) activity | molecular\_function |
| GO:0051287 | 33 | gene\_08768.t1,gene\_08426.t1,gene\_09374.t1,gene\_07689.t1,gene\_06137.t1,gene\_00813.t1,gene\_09683.t1,gene\_00214.t1,gene\_06860.t1,gene\_00708.t1,gene\_10595.t1,gene\_07479.t1,gene\_10214.t1,gene\_10236.t1,gene\_01131.t1,gene\_02167.t1,gene\_00653.t1,gene\_02634.t1,gene\_06569.t1,gene\_06798.t1,gene\_02123.t1,gene\_06433.t1,gene\_02157.t1,gene\_01609.t1,gene\_02366.t1,gene\_02066.t1,gene\_06599.t1,gene\_08720.t1,gene\_03522.t1,gene\_06491.t1,gene\_07758.t1,gene\_09272.t1,gene\_10039.t1 | | NAD binding | molecular\_function |
| GO:0140326 | 4 | gene\_04010.t1,gene\_01056.t1,gene\_00896.t1,gene\_09510.t1 | | ATPase-coupled intramembrane lipid transporter activity | molecular\_function |
| GO:0016151 | 4 | gene\_09586.t1,gene\_06247.t1,gene\_03928.t1,gene\_01624.t1 | | nickel cation binding | molecular\_function |
| GO:0004017 | 3 | gene\_04186.t1,gene\_01019.t1,gene\_09265.t1 | | adenylate kinase activity | molecular\_function |
| GO:0004016 | 1 | gene\_03592.t1 | | adenylate cyclase activity | molecular\_function |
| GO:0003917 | 2 | gene\_01025.t1,gene\_02674.t1 | | DNA topoisomerase type I (single strand cut, ATP-independent) activity | molecular\_function |
| GO:0008271 | 4 | gene\_10157.t1,gene\_09026.t1,gene\_06354.t1,gene\_01677.t1 | | secondary active sulfate transmembrane transporter activity | molecular\_function |
| GO:0008270 | 501 | gene\_06503.t1,gene\_09809.t1,gene\_07790.t1,gene\_09549.t1,gene\_07166.t1,gene\_06706.t1,gene\_09473.t1,gene\_09457.t1,gene\_04873.t1,gene\_02977.t1,gene\_03228.t1,gene\_06172.t1,gene\_10492.t1,gene\_05734.t1,gene\_02178.t1,gene\_09939.t1,gene\_04045.t1,gene\_03544.t1,gene\_06394.t1,gene\_03076.t1,gene\_00562.t1,gene\_06376.t1,gene\_02847.t1,gene\_08694.t1,gene\_06420.t1,gene\_09930.t1,gene\_01454.t1,gene\_08560.t1,gene\_09897.t1,gene\_08063.t1,gene\_04594.t1,gene\_00209.t1,gene\_00052.t1,gene\_03342.t1,gene\_04524.t1,gene\_07820.t1,gene\_02809.t1,gene\_10073.t1,gene\_02721.t1,gene\_10058.t1,gene\_03997.t1,gene\_04014.t1,gene\_01922.t1,gene\_07635.t1,gene\_02107.t1,gene\_08293.t1,gene\_01017.t1,gene\_09370.t1,gene\_04473.t1,gene\_06230.t1,gene\_09181.t1,gene\_00614.t1,gene\_10377.t1,gene\_00689.t1,gene\_09052.t1,gene\_00822.t1,gene\_04263.t1,gene\_05888.t1,gene\_02151.t1,gene\_03115.t1,gene\_08962.t1,gene\_07356.t1,gene\_05517.t1,gene\_10255.t1,gene\_04732.t1,gene\_08148.t1,gene\_02061.t1,gene\_05314.t1,gene\_05082.t1,gene\_05810.t1, | | zinc ion binding | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0008270 | 501 | gene\_04445.t1,gene\_00906.t1,gene\_09769.t1,gene\_02840.t1,gene\_10402.t1,gene\_01857.t1,gene\_08034.t1,gene\_04693.t1,gene\_10666.t1,gene\_08703.t1,gene\_07229.t1,gene\_06673.t1,gene\_02068.t1,gene\_07612.t1,gene\_02027.t1,gene\_09361.t1,gene\_06675.t1,gene\_05087.t1,gene\_02661.t1,gene\_00770.t1,gene\_03304.t1,gene\_02253.t1,gene\_03842.t1,gene\_04795.t1,gene\_06647.t1,gene\_07241.t1,gene\_00059.t1,gene\_07040.t1,gene\_06478.t1,gene\_07333.t1,gene\_08813.t1,gene\_03210.t1,gene\_00656.t1,gene\_00580.t1,gene\_03983.t1,gene\_04043.t1,gene\_00286.t1,gene\_06585.t1,gene\_08310.t1,gene\_03606.t1,gene\_01987.t1,gene\_04400.t1,gene\_03587.t1,gene\_09375.t1,gene\_08824.t1,gene\_01302.t1,gene\_02297.t1,gene\_05808.t1,gene\_07128.t1,gene\_00556.t1,gene\_06258.t1,gene\_01305.t1,gene\_00382.t1,gene\_00409.t1,gene\_06020.t1,gene\_01948.t1,gene\_03579.t1,gene\_06963.t1,gene\_01145.t1,gene\_06978.t1,gene\_05273.t1,gene\_06395.t1,gene\_03513.t1,gene\_00660.t1,gene\_09590.t1,gene\_06232.t1,gene\_04918.t1,gene\_05107.t1,gene\_06745.t1,gene\_02034.t1,gene\_02652.t1,gene\_08503.t1,gene\_07827.t1,gene\_00616.t1,gene\_10663.t1,gene\_04481.t1,gene\_08761.t1,gene\_01718.t1,gene\_02786.t1,gene\_06852.t1,gene\_02605.t1,gene\_09813.t1,gene\_03214.t1,gene\_10509.t1,gene\_01887.t1,gene\_06732.t1,gene\_05627.t1,gene\_08477.t1,gene\_09131.t1,gene\_10212.t1,gene\_03176.t1,gene\_06584.t1,gene\_01394.t1,gene\_10553.t1,gene\_05992.t1,gene\_04208.t1,gene\_09878.t1,gene\_01937.t1,gene\_02318.t1,gene\_01345.t1,gene\_00963.t1,gene\_04028.t1,gene\_09748.t1,gene\_07955.t1,gene\_10374.t1,gene\_04635.t1,gene\_10614.t1,gene\_06606.t1,gene\_03595.t1,gene\_07382.t1,gene\_00917.t1,gene\_10151.t1,gene\_03831.t1,gene\_06795.t1,gene\_03650.t1,gene\_09742.t1,gene\_08833.t1,gene\_04621.t1,gene\_00046.t1,gene\_05595.t1,gene\_02607.t1,gene\_07537.t1,gene\_01756.t1,gene\_07706.t1,gene\_01063.t1,gene\_08591.t1,gene\_08569.t1,gene\_02050.t1,gene\_09339.t1,gene\_05311.t1,gene\_00803.t1,gene\_03638.t1,gene\_08304.t1,gene\_09126.t1,gene\_01529.t1,gene\_04147.t1,gene\_02227.t1,gene\_00228.t1,gene\_03892.t1,gene\_09330.t1,gene\_05541.t1,gene\_07320.t1,gene\_07785.t1,gene\_05559.t1,gene\_05725.t1,gene\_06823.t1,gene\_03642.t1,gene\_08366.t1,gene\_04307.t1,gene\_06040.t1,gene\_04523.t1,gene\_08155.t1,gene\_10172.t1,gene\_05721.t1,gene\_06088.t1,gene\_04174.t1,gene\_03870.t1,gene\_03107.t1,gene\_08301.t1,gene\_04399.t1,gene\_03748.t1,gene\_04643.t1,gene\_09979.t1,gene\_10200.t1,gene\_05151.t1,gene\_08025.t1,gene\_00018.t1,gene\_01954.t1,gene\_06679.t1,gene\_10649.t1,gene\_03200.t1,gene\_10517.t1,gene\_02220.t1,gene\_02526.t1,gene\_04257.t1,gene\_05301.t1,gene\_03018.t1,gene\_03062.t1,gene\_09192.t1,gene\_06059.t1, | | zinc ion binding | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0008270 | 501 | gene\_01692.t1,gene\_02512.t1,gene\_06936.t1,gene\_00095.t1,gene\_05132.t1,gene\_08772.t1,gene\_02170.t1,gene\_03295.t1,gene\_08479.t1,gene\_08074.t1,gene\_07525.t1,gene\_02915.t1,gene\_10208.t1,gene\_06934.t1,gene\_05121.t1,gene\_09460.t1,gene\_07677.t1,gene\_04979.t1,gene\_07168.t1,gene\_10367.t1,gene\_04650.t1,gene\_00959.t1,gene\_07422.t1,gene\_00308.t1,gene\_00564.t1,gene\_07726.t1,gene\_02641.t1,gene\_09865.t1,gene\_01527.t1,gene\_08484.t1,gene\_05950.t1,gene\_07085.t1,gene\_03132.t1,gene\_10254.t1,gene\_07331.t1,gene\_07693.t1,gene\_02676.t1,gene\_00210.t1,gene\_08135.t1,gene\_04695.t1,gene\_04627.t1,gene\_10543.t1,gene\_08083.t1,gene\_03421.t1,gene\_07992.t1,gene\_07948.t1,gene\_06089.t1,gene\_08550.t1,gene\_05932.t1,gene\_00897.t1,gene\_01535.t1,gene\_03812.t1,gene\_04854.t1,gene\_01135.t1,gene\_03096.t1,gene\_00640.t1,gene\_07583.t1,gene\_09652.t1,gene\_01819.t1,gene\_09814.t1,gene\_10424.t1,gene\_04669.t1,gene\_09957.t1,gene\_09935.t1,gene\_02916.t1,gene\_04048.t1,gene\_08342.t1,gene\_08947.t1,gene\_09656.t1,gene\_07306.t1,gene\_02529.t1,gene\_01742.t1,gene\_06249.t1,gene\_02757.t1,gene\_08608.t1,gene\_05477.t1,gene\_09781.t1,gene\_06751.t1,gene\_00732.t1,gene\_01262.t1,gene\_02946.t1,gene\_00747.t1,gene\_06377.t1,gene\_01359.t1,gene\_00847.t1,gene\_03869.t1,gene\_10197.t1,gene\_05547.t1,gene\_03741.t1,gene\_01156.t1,gene\_06095.t1,gene\_08280.t1,gene\_03747.t1,gene\_05070.t1,gene\_04351.t1,gene\_01377.t1,gene\_01606.t1,gene\_01134.t1,gene\_01708.t1,gene\_04946.t1,gene\_06766.t1,gene\_06073.t1,gene\_05173.t1,gene\_04830.t1,gene\_01201.t1,gene\_05814.t1,gene\_01774.t1,gene\_10056.t1,gene\_10205.t1,gene\_03786.t1,gene\_01224.t1,gene\_03286.t1,gene\_02799.t1,gene\_10443.t1,gene\_03596.t1,gene\_07694.t1,gene\_08586.t1,gene\_00968.t1,gene\_03118.t1,gene\_08966.t1,gene\_03512.t1,gene\_04976.t1,gene\_10237.t1,gene\_04378.t1,gene\_03607.t1,gene\_04706.t1,gene\_00182.t1,gene\_10522.t1,gene\_08345.t1,gene\_02168.t1,gene\_02229.t1,gene\_07284.t1,gene\_06332.t1,gene\_03248.t1,gene\_08281.t1,gene\_00908.t1,gene\_09697.t1,gene\_03806.t1,gene\_03447.t1,gene\_00790.t1,gene\_02808.t1,gene\_03050.t1,gene\_05943.t1,gene\_06532.t1,gene\_02203.t1,gene\_01153.t1,gene\_08441.t1,gene\_03784.t1,gene\_01809.t1,gene\_08041.t1,gene\_08291.t1,gene\_05540.t1,gene\_03408.t1,gene\_06566.t1,gene\_09874.t1,gene\_03366.t1,gene\_08945.t1,gene\_06672.t1,gene\_06949.t1,gene\_07683.t1,gene\_04022.t1,gene\_04081.t1,gene\_01960.t1,gene\_02948.t1,gene\_06614.t1,gene\_06402.t1,gene\_01612.t1,gene\_00645.t1,gene\_07639.t1,gene\_05736.t1,gene\_05474.t1,gene\_09537.t1,gene\_07088.t1,gene\_06266.t1,gene\_05383.t1,gene\_10083.t1,gene\_04676.t1,gene\_09646.t1,gene\_10051.t1,gene\_10211.t1, | | zinc ion binding | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0008270 | 501 | gene\_03040.t1,gene\_09322.t1,gene\_02385.t1,gene\_00395.t1,gene\_08321.t1,gene\_03770.t1,gene\_02580.t1,gene\_04040.t1,gene\_09380.t1,gene\_01512.t1,gene\_04937.t1,gene\_03761.t1,gene\_04515.t1,gene\_02282.t1,gene\_03463.t1,gene\_09065.t1,gene\_08364.t1,gene\_02874.t1,gene\_09728.t1,gene\_05299.t1,gene\_10629.t1,gene\_03763.t1,gene\_00921.t1,gene\_01093.t1,gene\_08139.t1,gene\_02042.t1,gene\_06023.t1,gene\_06515.t1,gene\_01498.t1,gene\_07548.t1,gene\_09145.t1,gene\_06225.t1,gene\_08254.t1,gene\_02608.t1,gene\_05588.t1,gene\_02502.t1,gene\_01613.t1,gene\_05277.t1,gene\_04903.t1,gene\_10532.t1,gene\_03427.t1,gene\_09823.t1,gene\_04304.t1,gene\_09526.t1,gene\_06273.t1,gene\_09472.t1,gene\_09969.t1,gene\_09035.t1,gene\_02086.t1,gene\_01730.t1,gene\_03655.t1,gene\_05206.t1,gene\_04651.t1,gene\_10498.t1,gene\_00654.t1,gene\_04041.t1,gene\_01082.t1,gene\_02230.t1,gene\_08062.t1,gene\_04209.t1,gene\_02677.t1,gene\_01998.t1,gene\_04146.t1,gene\_05080.t1,gene\_03649.t1,gene\_01530.t1,gene\_05972.t1,gene\_00833.t1,gene\_00634.t1,gene\_02730.t1,gene\_08638.t1 | | zinc ion binding | molecular\_function |
| GO:0036002 | 1 | gene\_08079.t1 | | pre-mRNA binding | molecular\_function |
| GO:0102121 | 1 | gene\_02496.t1 | | ceramidase activity | molecular\_function |
| GO:0008478 | 1 | gene\_01000.t1 | | pyridoxal kinase activity | molecular\_function |
| GO:0008474 | 1 | gene\_09078.t1 | | palmitoyl-(protein) hydrolase activity | molecular\_function |
| GO:0008670 | 1 | gene\_04485.t1 | | 2,4-dienoyl-CoA reductase (NADPH) activity | molecular\_function |
| GO:0008677 | 3 | gene\_01574.t1,gene\_03436.t1,gene\_07251.t1 | | 2-dehydropantoate 2-reductase activity | molecular\_function |
| GO:0070037 | 1 | gene\_07288.t1 | | rRNA (pseudouridine) methyltransferase activity | molecular\_function |
| GO:0070039 | 1 | gene\_05806.t1 | | rRNA (guanosine-2'-O-)-methyltransferase activity | molecular\_function |
| GO:0052856 | 2 | gene\_04609.t1,gene\_06101.t1 | | NADHX epimerase activity | molecular\_function |
| GO:0016040 | 1 | gene\_04134.t1 | | glutamate synthase (NADH) activity | molecular\_function |
| GO:0032549 | 3 | gene\_00677.t1,gene\_04647.t1,gene\_09944.t1 | | ribonucleoside binding | molecular\_function |
| GO:0047547 | 1 | gene\_09476.t1 | | 2-methylcitrate dehydratase activity | molecular\_function |
| GO:0030942 | 2 | gene\_01542.t1,gene\_07051.t1 | | endoplasmic reticulum signal peptide binding | molecular\_function |
| GO:0043495 | 1 | gene\_06131.t1 | | protein-membrane adaptor activity | molecular\_function |
| GO:0016462 | 2 | gene\_07892.t1,gene\_09668.t1 | | pyrophosphatase activity | molecular\_function |
| GO:0016903 | 1 | gene\_03857.t1 | | oxidoreductase activity, acting on the aldehyde or oxo group of donors | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0061575 | 1 | gene\_01504.t1 | | cyclin-dependent protein serine/threonine kinase activator activity | molecular\_function |
| GO:0035226 | 1 | gene\_09033.t1 | | glutamate-cysteine ligase catalytic subunit binding | molecular\_function |
| GO:0061578 | 2 | gene\_02805.t1,gene\_06787.t1 | | Lys63-specific deubiquitinase activity | molecular\_function |
| GO:0070840 | 1 | gene\_10487.t1 | | dynein complex binding | molecular\_function |
| GO:0031924 | 1 | gene\_02782.t1 | | vitamin B6 transmembrane transporter activity | molecular\_function |
| GO:0030411 | 1 | gene\_07943.t1 | | scytalone dehydratase activity | molecular\_function |
| GO:0043115 | 2 | gene\_06837.t1,gene\_09155.t1 | | precorrin-2 dehydrogenase activity | molecular\_function |
| GO:0003724 | 30 | gene\_02480.t1,gene\_00355.t1,gene\_06495.t1,gene\_00426.t1,gene\_07129.t1,gene\_00875.t1,gene\_08389.t1,gene\_07180.t1,gene\_03855.t1,gene\_06516.t1,gene\_05954.t1,gene\_08299.t1,gene\_02077.t1,gene\_02841.t1,gene\_05855.t1,gene\_06611.t1,gene\_03074.t1,gene\_01097.t1,gene\_03494.t1,gene\_07819.t1,gene\_02049.t1,gene\_01990.t1,gene\_05426.t1,gene\_06649.t1,gene\_00504.t1,gene\_10370.t1,gene\_09001.t1,gene\_06902.t1,gene\_08813.t1,gene\_00597.t1 | | RNA helicase activity | molecular\_function |
| GO:0003725 | 5 | gene\_08713.t1,gene\_08964.t1,gene\_01854.t1,gene\_01719.t1,gene\_02300.t1 | | double-stranded RNA binding | molecular\_function |
| GO:0003723 | 177 | gene\_04707.t1,gene\_09006.t1,gene\_05674.t1,gene\_10164.t1,gene\_04178.t1,gene\_06335.t1,gene\_06857.t1,gene\_02371.t1,gene\_10370.t1,gene\_09842.t1,gene\_06516.t1,gene\_08623.t1,gene\_02973.t1,gene\_07256.t1,gene\_05668.t1,gene\_09349.t1,gene\_01958.t1,gene\_03940.t1,gene\_09733.t1,gene\_02023.t1,gene\_10484.t1,gene\_01869.t1,gene\_00424.t1,gene\_07792.t1,gene\_01196.t1,gene\_03164.t1,gene\_09486.t1,gene\_08528.t1,gene\_10433.t1,gene\_03568.t1,gene\_07304.t1,gene\_03281.t1,gene\_05368.t1,gene\_05826.t1,gene\_02232.t1,gene\_06492.t1,gene\_00436.t1,gene\_09918.t1,gene\_04149.t1,gene\_00355.t1,gene\_02965.t1,gene\_05515.t1,gene\_08234.t1,gene\_07034.t1,gene\_06596.t1,gene\_10314.t1,gene\_07820.t1,gene\_03664.t1,gene\_01435.t1,gene\_09850.t1,gene\_03875.t1,gene\_01939.t1,gene\_01368.t1,gene\_00993.t1,gene\_04238.t1,gene\_06051.t1,gene\_07302.t1,gene\_09702.t1,gene\_03080.t1,gene\_03206.t1,gene\_08101.t1,gene\_06866.t1,gene\_06867.t1,gene\_06284.t1,gene\_03311.t1,gene\_02722.t1,gene\_01856.t1,gene\_10405.t1,gene\_06070.t1,gene\_09001.t1,gene\_03541.t1,gene\_06557.t1,gene\_07244.t1,gene\_02587.t1,gene\_10591.t1,gene\_06928.t1,gene\_07754.t1,gene\_05612.t1,gene\_05772.t1,gene\_04604.t1,gene\_02183.t1,gene\_08338.t1,gene\_08647.t1,gene\_01160.t1,gene\_03396.t1,gene\_03682.t1,gene\_06639.t1,gene\_00676.t1,gene\_01933.t1,gene\_07374.t1,gene\_01222.t1,gene\_07234.t1,gene\_02357.t1,gene\_10328.t1,gene\_09916.t1, | | RNA binding | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0003723 | 177 | gene\_08700.t1,gene\_04131.t1,gene\_00978.t1,gene\_09723.t1,gene\_07733.t1,gene\_08914.t1,gene\_00478.t1,gene\_08120.t1,gene\_08344.t1,gene\_06349.t1,gene\_06495.t1,gene\_04196.t1,gene\_08699.t1,gene\_01896.t1,gene\_06717.t1,gene\_07933.t1,gene\_03071.t1,gene\_03221.t1,gene\_08685.t1,gene\_00504.t1,gene\_06280.t1,gene\_04376.t1,gene\_04160.t1,gene\_06123.t1,gene\_04224.t1,gene\_07329.t1,gene\_05876.t1,gene\_09567.t1,gene\_07483.t1,gene\_04719.t1,gene\_06158.t1,gene\_09175.t1,gene\_00287.t1,gene\_05450.t1,gene\_09251.t1,gene\_03785.t1,gene\_03344.t1,gene\_06140.t1,gene\_09879.t1,gene\_07052.t1,gene\_05684.t1,gene\_00520.t1,gene\_08840.t1,gene\_08111.t1,gene\_01605.t1,gene\_02381.t1,gene\_05328.t1,gene\_05787.t1,gene\_03676.t1,gene\_06315.t1,gene\_04011.t1,gene\_04611.t1,gene\_01651.t1,gene\_02959.t1,gene\_05375.t1,gene\_07641.t1,gene\_08877.t1,gene\_02268.t1,gene\_06953.t1,gene\_06870.t1,gene\_03216.t1,gene\_00362.t1,gene\_05885.t1,gene\_02995.t1,gene\_07082.t1,gene\_00507.t1,gene\_05954.t1,gene\_07457.t1,gene\_07250.t1,gene\_02434.t1,gene\_01113.t1,gene\_06807.t1,gene\_04284.t1,gene\_03704.t1,gene\_10532.t1,gene\_01214.t1,gene\_05841.t1,gene\_08813.t1,gene\_09337.t1,gene\_10354.t1,gene\_01714.t1,gene\_02175.t1 | | RNA binding | molecular\_function |
| GO:0003721 | 1 | gene\_08521.t1 | | telomerase RNA reverse transcriptase activity | molecular\_function |
| GO:0003729 | 11 | gene\_01674.t1,gene\_01012.t1,gene\_10367.t1,gene\_04188.t1,gene\_03867.t1,gene\_07762.t1,gene\_03530.t1,gene\_05249.t1,gene\_09614.t1,gene\_02790.t1,gene\_07305.t1 | | mRNA binding | molecular\_function |
| GO:0061608 | 1 | gene\_06251.t1 | | nuclear import signal receptor activity | molecular\_function |
| GO:0061605 | 1 | gene\_08455.t1 | | molybdopterin-synthase adenylyltransferase activity | molecular\_function |
| GO:0010945 | 2 | gene\_04123.t1,gene\_07207.t1 | | CoA pyrophosphatase activity | molecular\_function |
| GO:0061599 | 1 | gene\_06163.t1 | | molybdopterin molybdotransferase activity | molecular\_function |
| GO:0061598 | 1 | gene\_06163.t1 | | molybdopterin adenylyltransferase activity | molecular\_function |
| GO:0098808 | 1 | gene\_00144.t1 | | mRNA cap binding | molecular\_function |
| GO:0005199 | 6 | gene\_06587.t1,gene\_00145.t1,gene\_01169.t1,gene\_06764.t1,gene\_08114.t1,gene\_04429.t1 | | structural constituent of cell wall | molecular\_function |
| GO:0005198 | 9 | gene\_08775.t1,gene\_00582.t1,gene\_03142.t1,gene\_06756.t1,gene\_09312.t1,gene\_04061.t1,gene\_08919.t1,gene\_01372.t1,gene\_07017.t1 | | structural molecule activity | molecular\_function |
| GO:0052832 | 2 | gene\_05585.t1,gene\_02349.t1 | | inositol monophosphate 3-phosphatase activity | molecular\_function |
| GO:0052833 | 2 | gene\_05585.t1,gene\_02349.t1 | | inositol monophosphate 4-phosphatase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0004932 | 2 | gene\_09099.t1,gene\_04550.t1 | | mating-type factor pheromone receptor activity | molecular\_function |
| GO:0004484 | 1 | gene\_09829.t1 | | mRNA guanylyltransferase activity | molecular\_function |
| GO:0004482 | 1 | gene\_03785.t1 | | mRNA (guanine-N7-)-methyltransferase activity | molecular\_function |
| GO:0004488 | 2 | gene\_06799.t1,gene\_00279.t1 | | methylenetetrahydrofolate dehydrogenase (NADP+) activity | molecular\_function |
| GO:0000386 | 1 | gene\_06855.t1 | | second spliceosomal transesterification activity | molecular\_function |
| GO:0004425 | 1 | gene\_08809.t1 | | indole-3-glycerol-phosphate synthase activity | molecular\_function |
| GO:0004370 | 2 | gene\_03977.t1,gene\_10097.t1 | | glycerol kinase activity | molecular\_function |
| GO:0004371 | 2 | gene\_08527.t1,gene\_10503.t1 | | glycerone kinase activity | molecular\_function |
| GO:0004372 | 2 | gene\_01168.t1,gene\_03196.t1 | | glycine hydroxymethyltransferase activity | molecular\_function |
| GO:0004801 | 2 | gene\_07980.t1,gene\_04418.t1 | | transaldolase activity | molecular\_function |
| GO:0004806 | 4 | gene\_03672.t1,gene\_05193.t1,gene\_01671.t1,gene\_01468.t1 | | triglyceride lipase activity | molecular\_function |
| GO:0004375 | 1 | gene\_02293.t1 | | glycine dehydrogenase (decarboxylating) activity | molecular\_function |
| GO:0004376 | 3 | gene\_10092.t1,gene\_02828.t1,gene\_04734.t1 | | glycolipid mannosyltransferase activity | molecular\_function |
| GO:0004377 | 1 | gene\_02462.t1 | | GDP-Man:Man3GlcNAc2-PP-Dol alpha-1,2-mannosyltransferase activity | molecular\_function |
| GO:0004378 | 1 | gene\_05746.t1 | | GDP-Man:Man1GlcNAc2-PP-Dol alpha-1,3-mannosyltransferase activity | molecular\_function |
| GO:0004379 | 1 | gene\_01408.t1 | | glycylpeptide N-tetradecanoyltransferase activity | molecular\_function |
| GO:0004809 | 1 | gene\_02330.t1 | | tRNA (guanine-N2-)-methyltransferase activity | molecular\_function |
| GO:0008296 | 1 | gene\_06548.t1 | | 3'-5'-exodeoxyribonuclease activity | molecular\_function |
| GO:0004573 | 2 | gene\_07604.t1,gene\_09534.t1 | | Glc3Man9GlcNAc2 oligosaccharide glucosidase activity | molecular\_function |
| GO:0004571 | 6 | gene\_02817.t1,gene\_08332.t1,gene\_10310.t1,gene\_04055.t1,gene\_02421.t1,gene\_02125.t1 | | mannosyl-oligosaccharide 1,2-alpha-mannosidase activity | molecular\_function |
| GO:0004577 | 1 | gene\_10359.t1 | | N-acetylglucosaminyldiphosphodolichol N-acetylglucosaminyltransferase activity | molecular\_function |
| GO:0004578 | 1 | gene\_10632.t1 | | chitobiosyldiphosphodolichol beta-mannosyltransferase activity | molecular\_function |
| GO:0004579 | 1 | gene\_05978.t1 | | dolichyl-diphosphooligosaccharide-protein glycotransferase activity | molecular\_function |
| GO:0052905 | 1 | gene\_06780.t1 | | tRNA (guanine(9)-N(1))-methyltransferase activity | molecular\_function |
| GO:0052906 | 1 | gene\_07164.t1 | | tRNA (guanine(37)-N(1))-methyltransferase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0004399 | 1 | gene\_02123.t1 | | histidinol dehydrogenase activity | molecular\_function |
| GO:0004396 | 6 | gene\_06196.t1,gene\_09513.t1,gene\_00838.t1,gene\_09875.t1,gene\_06480.t1,gene\_06014.t1 | | hexokinase activity | molecular\_function |
| GO:0004395 | 1 | gene\_04044.t1 | | hexaprenyldihydroxybenzoate methyltransferase activity | molecular\_function |
| GO:0008061 | 28 | gene\_05471.t1,gene\_01798.t1,gene\_07912.t1,gene\_09962.t1,gene\_05687.t1,gene\_10573.t1,gene\_01799.t1,gene\_01037.t1,gene\_06552.t1,gene\_01797.t1,gene\_03719.t1,gene\_10538.t1,gene\_06082.t1,gene\_02142.t1,gene\_08633.t1,gene\_04222.t1,gene\_09960.t1,gene\_06768.t1,gene\_10353.t1,gene\_06380.t1,gene\_01801.t1,gene\_01647.t1,gene\_05417.t1,gene\_09961.t1,gene\_08634.t1,gene\_00971.t1,gene\_01800.t1,gene\_06897.t1 | | chitin binding | molecular\_function |
| GO:0016868 | 2 | gene\_03025.t1,gene\_06714.t1 | | intramolecular transferase activity, phosphotransferases | molecular\_function |
| GO:0033819 | 1 | gene\_06846.t1 | | lipoyl(octanoyl) transferase activity | molecular\_function |
| GO:0000009 | 7 | gene\_00659.t1,gene\_08226.t1,gene\_06634.t1,gene\_00389.t1,gene\_10092.t1,gene\_04359.t1,gene\_03632.t1 | | alpha-1,6-mannosyltransferase activity | molecular\_function |
| GO:0004712 | 36 | gene\_02155.t1,gene\_01198.t1,gene\_00740.t1,gene\_04066.t1,gene\_02838.t1,gene\_05244.t1,gene\_08500.t1,gene\_08916.t1,gene\_03061.t1,gene\_08078.t1,gene\_03660.t1,gene\_04388.t1,gene\_06106.t1,gene\_01223.t1,gene\_03314.t1,gene\_10524.t1,gene\_09242.t1,gene\_00801.t1,gene\_10369.t1,gene\_01422.t1,gene\_00848.t1,gene\_03475.t1,gene\_00208.t1,gene\_05820.t1,gene\_06526.t1,gene\_08612.t1,gene\_09034.t1,gene\_00548.t1,gene\_10324.t1,gene\_05628.t1,gene\_05629.t1,gene\_04642.t1,gene\_07102.t1,gene\_08746.t1,gene\_07172.t1,gene\_05846.t1 | | protein serine/threonine/tyrosine kinase activity | molecular\_function |
| GO:0004713 | 1 | gene\_07102.t1 | | protein tyrosine kinase activity | molecular\_function |
| GO:0102752 | 1 | gene\_08420.t1 | | 1,4-alpha-glucan branching enzyme activity (using a glucosylated glycogenin as primer for glycogen synthesis) | molecular\_function |
| GO:0005375 | 5 | gene\_00624.t1,gene\_05351.t1,gene\_02696.t1,gene\_07182.t1,gene\_00796.t1 | | copper ion transmembrane transporter activity | molecular\_function |
| GO:0102756 | 2 | gene\_01892.t1,gene\_08158.t1 | | very-long-chain 3-ketoacyl-CoA synthase activity | molecular\_function |
| GO:0004719 | 1 | gene\_07348.t1 | | protein-L-isoaspartate (D-aspartate) O-methyltransferase activity | molecular\_function |
| GO:0003922 | 1 | gene\_09668.t1 | | GMP synthase (glutamine-hydrolyzing) activity | molecular\_function |
| GO:0003923 | 1 | gene\_01979.t1 | | GPI-anchor transamidase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0003924 | 71 | gene\_03293.t1,gene\_02046.t1,gene\_08109.t1,gene\_06785.t1,gene\_03716.t1,gene\_03006.t1,gene\_04198.t1,gene\_03355.t1,gene\_09945.t1,gene\_09037.t1,gene\_09274.t1,gene\_06153.t1,gene\_07449.t1,gene\_06747.t1,gene\_04423.t1,gene\_00668.t1,gene\_07243.t1,gene\_09005.t1,gene\_07332.t1,gene\_03755.t1,gene\_08048.t1,gene\_00417.t1,gene\_06165.t1,gene\_10558.t1,gene\_04397.t1,gene\_06662.t1,gene\_00704.t1,gene\_03928.t1,gene\_08179.t1,gene\_02503.t1,gene\_06071.t1,gene\_06121.t1,gene\_01416.t1,gene\_01668.t1,gene\_03274.t1,gene\_08588.t1,gene\_01985.t1,gene\_08027.t1,gene\_09488.t1,gene\_02465.t1,gene\_03680.t1,gene\_03087.t1,gene\_04169.t1,gene\_03671.t1,gene\_03296.t1,gene\_08956.t1,gene\_05145.t1,gene\_00015.t1,gene\_03791.t1,gene\_04146.t1,gene\_09687.t1,gene\_09750.t1,gene\_01545.t1,gene\_03653.t1,gene\_01220.t1,gene\_02435.t1,gene\_02957.t1,gene\_07812.t1,gene\_08680.t1,gene\_06391.t1,gene\_08913.t1,gene\_08080.t1,gene\_01175.t1,gene\_06609.t1,gene\_03121.t1,gene\_08745.t1,gene\_03540.t1,gene\_10216.t1,gene\_08311.t1,gene\_05803.t1,gene\_06104.t1 | | GTPase activity | molecular\_function |
| GO:0003925 | 1 | gene\_09833.t1 | | G protein activity | molecular\_function |
| GO:0004022 | 1 | gene\_03643.t1 | | alcohol dehydrogenase (NAD+) activity | molecular\_function |
| GO:0080019 | 2 | gene\_00238.t1,gene\_10630.t1 | | fatty-acyl-CoA reductase (alcohol-forming) activity | molecular\_function |
| GO:0004622 | 3 | gene\_02894.t1,gene\_07645.t1,gene\_03380.t1 | | lysophospholipase activity | molecular\_function |
| GO:0004151 | 1 | gene\_01874.t1 | | dihydroorotase activity | molecular\_function |
| GO:0004152 | 1 | gene\_00647.t1 | | dihydroorotate dehydrogenase activity | molecular\_function |
| GO:0004156 | 1 | gene\_00474.t1 | | dihydropteroate synthase activity | molecular\_function |
| GO:0008483 | 12 | gene\_08884.t1,gene\_10500.t1,gene\_03559.t1,gene\_04015.t1,gene\_04383.t1,gene\_06621.t1,gene\_09469.t1,gene\_10153.t1,gene\_03736.t1,gene\_05570.t1,gene\_03588.t1,gene\_07094.t1 | | transaminase activity | molecular\_function |
| GO:0008484 | 10 | gene\_09150.t1,gene\_01726.t1,gene\_06414.t1,gene\_01263.t1,gene\_10077.t1,gene\_10579.t1,gene\_06388.t1,gene\_02901.t1,gene\_01379.t1,gene\_08880.t1 | | sulfuric ester hydrolase activity | molecular\_function |
| GO:0000906 | 1 | gene\_02362.t1 | | 6,7-dimethyl-8-ribityllumazine synthase activity | molecular\_function |
| GO:0008641 | 6 | gene\_06204.t1,gene\_08455.t1,gene\_08294.t1,gene\_08220.t1,gene\_09204.t1,gene\_08221.t1 | | ubiquitin-like modifier activating enzyme activity | molecular\_function |
| GO:0050353 | 1 | gene\_02485.t1 | | trimethyllysine dioxygenase activity | molecular\_function |
| GO:0050354 | 2 | gene\_08527.t1,gene\_10503.t1 | | triokinase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0016787 | 208 | gene\_03900.t1,gene\_02220.t1,gene\_02339.t1,gene\_04316.t1,gene\_00613.t1,gene\_10474.t1,gene\_09569.t1,gene\_02226.t1,gene\_02326.t1,gene\_06359.t1,gene\_06011.t1,gene\_07596.t1,gene\_02376.t1,gene\_08774.t1,gene\_04777.t1,gene\_08730.t1,gene\_03352.t1,gene\_06202.t1,gene\_09503.t1,gene\_06929.t1,gene\_01097.t1,gene\_09045.t1,gene\_08023.t1,gene\_04001.t1,gene\_00819.t1,gene\_03372.t1,gene\_04779.t1,gene\_10535.t1,gene\_01773.t1,gene\_08937.t1,gene\_05211.t1,gene\_00684.t1,gene\_03992.t1,gene\_09665.t1,gene\_05094.t1,gene\_06512.t1,gene\_09666.t1,gene\_00174.t1,gene\_02791.t1,gene\_09054.t1,gene\_01053.t1,gene\_01352.t1,gene\_01388.t1,gene\_10644.t1,gene\_07715.t1,gene\_01486.t1,gene\_08753.t1,gene\_07122.t1,gene\_01965.t1,gene\_05574.t1,gene\_09908.t1,gene\_00355.t1,gene\_01267.t1,gene\_06448.t1,gene\_00815.t1,gene\_10620.t1,gene\_08882.t1,gene\_00875.t1,gene\_04526.t1,gene\_10355.t1,gene\_04640.t1,gene\_04365.t1,gene\_02291.t1,gene\_03771.t1,gene\_08324.t1,gene\_04071.t1,gene\_10648.t1,gene\_10439.t1,gene\_03871.t1,gene\_01737.t1,gene\_06216.t1,gene\_03494.t1,gene\_04776.t1,gene\_03140.t1,gene\_00952.t1,gene\_10146.t1,gene\_10055.t1,gene\_08388.t1,gene\_01715.t1,gene\_07964.t1,gene\_02568.t1,gene\_01826.t1,gene\_08050.t1,gene\_05536.t1,gene\_10376.t1,gene\_01213.t1,gene\_01575.t1,gene\_10165.t1,gene\_00953.t1,gene\_07217.t1,gene\_06511.t1,gene\_10557.t1,gene\_06463.t1,gene\_09658.t1,gene\_03952.t1,gene\_04599.t1,gene\_06372.t1,gene\_10018.t1,gene\_06667.t1,gene\_05526.t1,gene\_02090.t1,gene\_02387.t1,gene\_01487.t1,gene\_02219.t1,gene\_01842.t1,gene\_08469.t1,gene\_02685.t1,gene\_01911.t1,gene\_03815.t1,gene\_03778.t1,gene\_10304.t1,gene\_05242.t1,gene\_06467.t1,gene\_04297.t1,gene\_01532.t1,gene\_04576.t1,gene\_10019.t1,gene\_02077.t1,gene\_03000.t1,gene\_08628.t1,gene\_06556.t1,gene\_08949.t1,gene\_01166.t1,gene\_05308.t1,gene\_07377.t1,gene\_09636.t1,gene\_04597.t1,gene\_00793.t1,gene\_05426.t1,gene\_09179.t1,gene\_06840.t1,gene\_07716.t1,gene\_07592.t1,gene\_01096.t1,gene\_10224.t1,gene\_08220.t1,gene\_00504.t1,gene\_03813.t1,gene\_01968.t1,gene\_07704.t1,gene\_08737.t1,gene\_04315.t1,gene\_08272.t1,gene\_05905.t1,gene\_01706.t1,gene\_06907.t1,gene\_04631.t1,gene\_01375.t1,gene\_06256.t1,gene\_01949.t1,gene\_06087.t1,gene\_00001.t1,gene\_01471.t1,gene\_02764.t1,gene\_00910.t1,gene\_07022.t1,gene\_00664.t1,gene\_05768.t1,gene\_03475.t1,gene\_06974.t1,gene\_07179.t1,gene\_05457.t1,gene\_05644.t1,gene\_01785.t1,gene\_08813.t1,gene\_10541.t1,gene\_04386.t1,gene\_00178.t1,gene\_06892.t1,gene\_01332.t1,gene\_06686.t1,gene\_00218.t1,gene\_08350.t1,gene\_02698.t1,gene\_01162.t1,gene\_10659.t1,gene\_01600.t1,gene\_07454.t1,gene\_01828.t1,gene\_10351.t1, | | hydrolase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0016787 | 208 | gene\_02537.t1,gene\_07811.t1,gene\_10056.t1,gene\_07402.t1,gene\_07665.t1,gene\_03123.t1,gene\_01964.t1,gene\_04366.t1,gene\_09321.t1,gene\_09987.t1,gene\_03450.t1,gene\_09538.t1,gene\_08567.t1,gene\_00260.t1,gene\_00381.t1,gene\_09855.t1,gene\_04111.t1,gene\_04575.t1,gene\_10429.t1,gene\_06012.t1,gene\_01182.t1,gene\_00191.t1,gene\_03581.t1,gene\_06169.t1,gene\_02052.t1,gene\_06054.t1,gene\_00861.t1,gene\_00451.t1 | | hydrolase activity | molecular\_function |
| GO:0016783 | 1 | gene\_04727.t1 | | sulfurtransferase activity | molecular\_function |
| GO:0016780 | 4 | gene\_09574.t1,gene\_07485.t1,gene\_02039.t1,gene\_06843.t1 | | phosphotransferase activity, for other substituted phosphate groups | molecular\_function |
| GO:0016788 | 20 | gene\_03294.t1,gene\_08465.t1,gene\_06417.t1,gene\_06482.t1,gene\_05410.t1,gene\_09123.t1,gene\_03254.t1,gene\_01536.t1,gene\_01506.t1,gene\_01148.t1,gene\_02925.t1,gene\_04317.t1,gene\_05484.t1,gene\_02011.t1,gene\_02531.t1,gene\_00337.t1,gene\_06932.t1,gene\_08566.t1,gene\_03308.t1,gene\_01815.t1 | | hydrolase activity, acting on ester bonds | molecular\_function |
| GO:0004174 | 1 | gene\_08646.t1 | | electron-transferring-flavoprotein dehydrogenase activity | molecular\_function |
| GO:0015079 | 3 | gene\_06654.t1,gene\_07810.t1,gene\_03819.t1 | | potassium ion transmembrane transporter activity | molecular\_function |
| GO:0015078 | 13 | gene\_06355.t1,gene\_10123.t1,gene\_00267.t1,gene\_07043.t1,gene\_05578.t1,gene\_06164.t1,gene\_09484.t1,gene\_09011.t1,gene\_03171.t1,gene\_08230.t1,gene\_05980.t1,gene\_03004.t1,gene\_06648.t1 | | proton transmembrane transporter activity | molecular\_function |
| GO:0033971 | 1 | gene\_05694.t1 | | hydroxyisourate hydrolase activity | molecular\_function |
| GO:0046577 | 1 | gene\_06594.t1 | | long-chain-alcohol oxidase activity | molecular\_function |
| GO:0046570 | 1 | gene\_10424.t1 | | methylthioribulose 1-phosphate dehydratase activity | molecular\_function |
| GO:0033204 | 2 | gene\_06449.t1,gene\_05910.t1 | | ribonuclease P RNA binding | molecular\_function |
| GO:0051751 | 1 | gene\_04734.t1 | | alpha-1,4-mannosyltransferase activity | molecular\_function |
| GO:0030955 | 1 | gene\_02627.t1 | | potassium ion binding | molecular\_function |
| GO:0071885 | 1 | gene\_09083.t1 | | N-terminal protein N-methyltransferase activity | molecular\_function |
| GO:0033192 | 1 | gene\_08141.t1 | | calmodulin-dependent protein phosphatase activity | molecular\_function |
| GO:0002083 | 1 | gene\_09298.t1 | | 4-hydroxybenzoate decaprenyltransferase activity | molecular\_function |
| GO:0004726 | 1 | gene\_07067.t1 | | non-membrane spanning protein tyrosine phosphatase activity | molecular\_function |
| GO:0016251 | 1 | gene\_08169.t1 | | RNA polymerase II general transcription initiation factor activity | molecular\_function |
| GO:0017128 | 1 | gene\_04411.t1 | | phospholipid scramblase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0017124 | 1 | gene\_05140.t1 | | SH3 domain binding | molecular\_function |
| GO:0001056 | 1 | gene\_03523.t1 | | RNA polymerase III activity | molecular\_function |
| GO:0001054 | 1 | gene\_03523.t1 | | RNA polymerase I activity | molecular\_function |
| GO:0001055 | 1 | gene\_05990.t1 | | RNA polymerase II activity | molecular\_function |
| GO:0042123 | 2 | gene\_09807.t1,gene\_05084.t1 | | glucanosyltransferase activity | molecular\_function |
| GO:0003735 | 111 | gene\_01069.t1,gene\_09911.t1,gene\_10009.t1,gene\_06359.t1,gene\_08736.t1,gene\_01143.t1,gene\_03172.t1,gene\_10488.t1,gene\_00424.t1,gene\_02603.t1,gene\_05698.t1,gene\_02843.t1,gene\_09278.t1,gene\_03284.t1,gene\_05166.t1,gene\_04610.t1,gene\_01386.t1,gene\_03883.t1,gene\_05845.t1,gene\_02997.t1,gene\_06369.t1,gene\_09718.t1,gene\_05192.t1,gene\_02965.t1,gene\_01678.t1,gene\_10173.t1,gene\_04719.t1,gene\_02931.t1,gene\_05390.t1,gene\_01327.t1,gene\_02684.t1,gene\_03088.t1,gene\_06815.t1,gene\_08346.t1,gene\_03269.t1,gene\_08587.t1,gene\_02469.t1,gene\_07654.t1,gene\_08101.t1,gene\_00559.t1,gene\_08396.t1,gene\_07950.t1,gene\_02779.t1,gene\_09004.t1,gene\_06282.t1,gene\_10426.t1,gene\_03497.t1,gene\_04091.t1,gene\_05235.t1,gene\_07081.t1,gene\_01160.t1,gene\_08037.t1,gene\_06639.t1,gene\_01369.t1,gene\_02457.t1,gene\_05521.t1,gene\_00402.t1,gene\_06842.t1,gene\_00365.t1,gene\_07006.t1,gene\_01094.t1,gene\_04098.t1,gene\_05623.t1,gene\_00519.t1,gene\_02536.t1,gene\_05838.t1,gene\_02167.t1,gene\_00401.t1,gene\_06873.t1,gene\_04240.t1,gene\_06717.t1,gene\_06874.t1,gene\_02637.t1,gene\_01723.t1,gene\_01417.t1,gene\_05876.t1,gene\_04441.t1,gene\_10445.t1,gene\_09259.t1,gene\_08514.t1,gene\_10591.t1,gene\_10017.t1,gene\_00539.t1,gene\_00520.t1,gene\_08028.t1,gene\_09731.t1,gene\_02556.t1,gene\_01627.t1,gene\_01599.t1,gene\_10358.t1,gene\_03987.t1,gene\_09486.t1,gene\_04409.t1,gene\_08547.t1,gene\_09596.t1,gene\_09003.t1,gene\_09302.t1,gene\_10540.t1,gene\_05686.t1,gene\_05885.t1,gene\_00481.t1,gene\_00592.t1,gene\_04425.t1,gene\_06861.t1,gene\_02434.t1,gene\_01550.t1,gene\_06115.t1,gene\_10532.t1,gene\_07619.t1,gene\_01010.t1,gene\_02865.t1 | | structural constituent of ribosome | molecular\_function |
| GO:0031681 | 1 | gene\_01701.t1 | | G-protein beta-subunit binding | molecular\_function |
| GO:0031683 | 3 | gene\_03006.t1,gene\_08745.t1,gene\_06747.t1 | | G-protein beta/gamma-subunit complex binding | molecular\_function |
| GO:0061630 | 16 | gene\_09065.t1,gene\_00722.t1,gene\_01065.t1,gene\_08291.t1,gene\_09250.t1,gene\_05248.t1,gene\_03983.t1,gene\_01630.t1,gene\_03997.t1,gene\_02227.t1,gene\_01605.t1,gene\_03454.t1,gene\_06339.t1,gene\_06455.t1,gene\_09380.t1,gene\_01604.t1 | | ubiquitin protein ligase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0061631 | 1 | gene\_04460.t1 | | ubiquitin conjugating enzyme activity | molecular\_function |
| GO:0022857 | 398 | gene\_05935.t1,gene\_00930.t1,gene\_01123.t1,gene\_01255.t1,gene\_03910.t1,gene\_01500.t1,gene\_07014.t1,gene\_01108.t1,gene\_10651.t1,gene\_06813.t1,gene\_06507.t1,gene\_05310.t1,gene\_07225.t1,gene\_08859.t1,gene\_06510.t1,gene\_00393.t1,gene\_00469.t1,gene\_05120.t1,gene\_06583.t1,gene\_07594.t1,gene\_00025.t1,gene\_02081.t1,gene\_05509.t1,gene\_03403.t1,gene\_03620.t1,gene\_01986.t1,gene\_01891.t1,gene\_08449.t1,gene\_04318.t1,gene\_02642.t1,gene\_09134.t1,gene\_05949.t1,gene\_08571.t1,gene\_05670.t1,gene\_06386.t1,gene\_03044.t1,gene\_07223.t1,gene\_04758.t1,gene\_10519.t1,gene\_03306.t1,gene\_09539.t1,gene\_01496.t1,gene\_06543.t1,gene\_00038.t1,gene\_02710.t1,gene\_05116.t1,gene\_01817.t1,gene\_04716.t1,gene\_03841.t1,gene\_01611.t1,gene\_09187.t1,gene\_02105.t1,gene\_01777.t1,gene\_04377.t1,gene\_09352.t1,gene\_03545.t1,gene\_08673.t1,gene\_03439.t1,gene\_00552.t1,gene\_07591.t1,gene\_00197.t1,gene\_03430.t1,gene\_06479.t1,gene\_09800.t1,gene\_07151.t1,gene\_02441.t1,gene\_04017.t1,gene\_07372.t1,gene\_01795.t1,gene\_05748.t1,gene\_05333.t1,gene\_08116.t1,gene\_06541.t1,gene\_04521.t1,gene\_03457.t1,gene\_08451.t1,gene\_09811.t1,gene\_00383.t1,gene\_04472.t1,gene\_06748.t1,gene\_04027.t1,gene\_09340.t1,gene\_06762.t1,gene\_02889.t1,gene\_09139.t1,gene\_09129.t1,gene\_10514.t1,gene\_00820.t1,gene\_00888.t1,gene\_09866.t1,gene\_05649.t1,gene\_00290.t1,gene\_03032.t1,gene\_02897.t1,gene\_00131.t1,gene\_04372.t1,gene\_09696.t1,gene\_02848.t1,gene\_00590.t1,gene\_06980.t1,gene\_01794.t1,gene\_01779.t1,gene\_09651.t1,gene\_09694.t1,gene\_06275.t1,gene\_08958.t1,gene\_05561.t1,gene\_01275.t1,gene\_00022.t1,gene\_03948.t1,gene\_04468.t1,gene\_00575.t1,gene\_07423.t1,gene\_05940.t1,gene\_09763.t1,gene\_04692.t1,gene\_05983.t1,gene\_03699.t1,gene\_03409.t1,gene\_03783.t1,gene\_02308.t1,gene\_08156.t1,gene\_10615.t1,gene\_00179.t1,gene\_03108.t1,gene\_01724.t1,gene\_08791.t1,gene\_09142.t1,gene\_08143.t1,gene\_04167.t1,gene\_06084.t1,gene\_02896.t1,gene\_07318.t1,gene\_02051.t1,gene\_07224.t1,gene\_00068.t1,gene\_07593.t1,gene\_04754.t1,gene\_03023.t1,gene\_03411.t1,gene\_08061.t1,gene\_00734.t1,gene\_09121.t1,gene\_04283.t1,gene\_00530.t1,gene\_07702.t1,gene\_03305.t1,gene\_01944.t1,gene\_09386.t1,gene\_00852.t1,gene\_02760.t1,gene\_10121.t1,gene\_09948.t1,gene\_06684.t1,gene\_03947.t1,gene\_05566.t1,gene\_09456.t1,gene\_03733.t1,gene\_07573.t1,gene\_06888.t1,gene\_06052.t1,gene\_01816.t1,gene\_00069.t1,gene\_09975.t1,gene\_01697.t1,gene\_05300.t1,gene\_00489.t1,gene\_07176.t1,gene\_10646.t1,gene\_08250.t1,gene\_06385.t1,gene\_08302.t1,gene\_03133.t1,gene\_04029.t1,gene\_09147.t1, | | transmembrane transporter activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0022857 | 398 | gene\_05401.t1,gene\_08252.t1,gene\_04773.t1,gene\_10250.t1,gene\_10110.t1,gene\_09176.t1,gene\_01672.t1,gene\_09144.t1,gene\_00841.t1,gene\_00586.t1,gene\_05275.t1,gene\_01485.t1,gene\_02493.t1,gene\_00898.t1,gene\_07398.t1,gene\_07725.t1,gene\_04683.t1,gene\_06375.t1,gene\_05098.t1,gene\_06039.t1,gene\_01867.t1,gene\_00057.t1,gene\_08829.t1,gene\_02237.t1,gene\_04205.t1,gene\_04325.t1,gene\_04199.t1,gene\_00688.t1,gene\_05325.t1,gene\_00211.t1,gene\_02283.t1,gene\_02414.t1,gene\_00886.t1,gene\_07491.t1,gene\_02294.t1,gene\_10511.t1,gene\_04525.t1,gene\_09785.t1,gene\_06680.t1,gene\_08151.t1,gene\_02886.t1,gene\_04544.t1,gene\_06410.t1,gene\_01595.t1,gene\_04668.t1,gene\_01686.t1,gene\_07413.t1,gene\_01690.t1,gene\_09964.t1,gene\_04602.t1,gene\_03872.t1,gene\_09371.t1,gene\_03323.t1,gene\_08558.t1,gene\_10041.t1,gene\_08480.t1,gene\_00622.t1,gene\_08171.t1,gene\_02296.t1,gene\_02262.t1,gene\_08950.t1,gene\_07440.t1,gene\_00036.t1,gene\_07720.t1,gene\_02209.t1,gene\_08848.t1,gene\_02315.t1,gene\_05194.t1,gene\_09852.t1,gene\_00175.t1,gene\_03229.t1,gene\_04126.t1,gene\_10399.t1,gene\_05245.t1,gene\_07581.t1,gene\_05465.t1,gene\_07340.t1,gene\_09955.t1,gene\_01693.t1,gene\_08461.t1,gene\_06502.t1,gene\_08773.t1,gene\_10401.t1,gene\_09926.t1,gene\_03365.t1,gene\_01823.t1,gene\_01950.t1,gene\_08278.t1,gene\_01475.t1,gene\_00836.t1,gene\_01912.t1,gene\_10206.t1,gene\_10193.t1,gene\_05863.t1,gene\_08140.t1,gene\_02407.t1,gene\_08892.t1,gene\_09967.t1,gene\_10152.t1,gene\_06107.t1,gene\_01929.t1,gene\_05565.t1,gene\_03028.t1,gene\_02295.t1,gene\_06851.t1,gene\_04595.t1,gene\_08850.t1,gene\_02736.t1,gene\_02738.t1,gene\_02820.t1,gene\_00130.t1,gene\_06199.t1,gene\_00072.t1,gene\_09943.t1,gene\_05488.t1,gene\_09972.t1,gene\_06469.t1,gene\_08928.t1,gene\_09063.t1,gene\_04539.t1,gene\_05102.t1,gene\_06746.t1,gene\_06889.t1,gene\_04628.t1,gene\_04756.t1,gene\_03425.t1,gene\_05309.t1,gene\_05494.t1,gene\_10147.t1,gene\_00954.t1,gene\_02584.t1,gene\_01144.t1,gene\_09403.t1,gene\_02949.t1,gene\_10497.t1,gene\_07155.t1,gene\_04673.t1,gene\_08911.t1,gene\_01404.t1,gene\_04666.t1,gene\_00915.t1,gene\_08163.t1,gene\_01906.t1,gene\_09101.t1,gene\_06693.t1,gene\_04768.t1,gene\_05719.t1,gene\_03354.t1,gene\_08582.t1,gene\_08702.t1,gene\_07492.t1,gene\_00637.t1,gene\_00385.t1,gene\_09069.t1,gene\_06822.t1,gene\_05092.t1,gene\_09550.t1,gene\_06504.t1,gene\_02530.t1,gene\_10081.t1,gene\_00926.t1,gene\_05381.t1,gene\_04379.t1,gene\_09430.t1,gene\_04305.t1,gene\_00120.t1,gene\_09010.t1,gene\_04053.t1,gene\_05432.t1,gene\_09310.t1,gene\_10339.t1,gene\_10163.t1,gene\_06574.t1,gene\_09521.t1,gene\_04639.t1,gene\_09507.t1,gene\_05268.t1,gene\_05926.t1,gene\_01572.t1,gene\_04369.t1, | | transmembrane transporter activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0022857 | 398 | gene\_00065.t1,gene\_06692.t1,gene\_05583.t1,gene\_02508.t1,gene\_09940.t1,gene\_02561.t1,gene\_00081.t1,gene\_06342.t1,gene\_02839.t1,gene\_00021.t1,gene\_04170.t1,gene\_07187.t1,gene\_08561.t1,gene\_04215.t1,gene\_04350.t1,gene\_04357.t1,gene\_06570.t1,gene\_03877.t1,gene\_00764.t1,gene\_08642.t1,gene\_03215.t1,gene\_04304.t1,gene\_09834.t1,gene\_09085.t1,gene\_02895.t1,gene\_08671.t1,gene\_01807.t1,gene\_01370.t1,gene\_03516.t1,gene\_05548.t1,gene\_02527.t1,gene\_03918.t1,gene\_05108.t1,gene\_07880.t1,gene\_09904.t1,gene\_05991.t1,gene\_01299.t1,gene\_10459.t1,gene\_04757.t1,gene\_01136.t1,gene\_04679.t1,gene\_01741.t1,gene\_01945.t1 | | transmembrane transporter activity | molecular\_function |
| GO:0004497 | 96 | gene\_09837.t1,gene\_07431.t1,gene\_08439.t1,gene\_00050.t1,gene\_07089.t1,gene\_10673.t1,gene\_10252.t1,gene\_02074.t1,gene\_07674.t1,gene\_01461.t1,gene\_10670.t1,gene\_06181.t1,gene\_08016.t1,gene\_08018.t1,gene\_01818.t1,gene\_05434.t1,gene\_02731.t1,gene\_05157.t1,gene\_01463.t1,gene\_04764.t1,gene\_07549.t1,gene\_04130.t1,gene\_01324.t1,gene\_09909.t1,gene\_00783.t1,gene\_07281.t1,gene\_07691.t1,gene\_02013.t1,gene\_04065.t1,gene\_07786.t1,gene\_02311.t1,gene\_06676.t1,gene\_01460.t1,gene\_02026.t1,gene\_03669.t1,gene\_07369.t1,gene\_01111.t1,gene\_04671.t1,gene\_09020.t1,gene\_07833.t1,gene\_09504.t1,gene\_09177.t1,gene\_03816.t1,gene\_00994.t1,gene\_06160.t1,gene\_00758.t1,gene\_03517.t1,gene\_00220.t1,gene\_09654.t1,gene\_00834.t1,gene\_01587.t1,gene\_07934.t1,gene\_03022.t1,gene\_04361.t1,gene\_03360.t1,gene\_01476.t1,gene\_07490.t1,gene\_00777.t1,gene\_04536.t1,gene\_07117.t1,gene\_01658.t1,gene\_10569.t1,gene\_07848.t1,gene\_07526.t1,gene\_03126.t1,gene\_02190.t1,gene\_08828.t1,gene\_09778.t1,gene\_02258.t1,gene\_01850.t1,gene\_10672.t1,gene\_08446.t1,gene\_10664.t1,gene\_09353.t1,gene\_03911.t1,gene\_09980.t1,gene\_09970.t1,gene\_03369.t1,gene\_04527.t1,gene\_08017.t1,gene\_07727.t1,gene\_01543.t1,gene\_00601.t1,gene\_10572.t1,gene\_02248.t1,gene\_05975.t1,gene\_09896.t1,gene\_03978.t1,gene\_00285.t1,gene\_10014.t1,gene\_09981.t1,gene\_07507.t1,gene\_07556.t1,gene\_08430.t1,gene\_03226.t1,gene\_09394.t1 | | monooxygenase activity | molecular\_function |
| GO:0004496 | 1 | gene\_01364.t1 | | mevalonate kinase activity | molecular\_function |
| GO:0004491 | 3 | gene\_09253.t1,gene\_09642.t1,gene\_10422.t1 | | methylmalonate-semialdehyde dehydrogenase (acylating) activity | molecular\_function |
| GO:0004499 | 18 | gene\_08137.t1,gene\_10513.t1,gene\_06728.t1,gene\_08705.t1,gene\_10641.t1,gene\_01733.t1,gene\_07897.t1,gene\_09500.t1,gene\_09021.t1,gene\_05553.t1,gene\_05095.t1,gene\_09331.t1,gene\_07999.t1,gene\_09431.t1,gene\_08570.t1,gene\_08675.t1,gene\_06522.t1,gene\_00932.t1 | | N,N-dimethylaniline monooxygenase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0036243 | 1 | gene\_01425.t1 | | succinate-semialdehyde dehydrogenase (NADP+) activity | molecular\_function |
| GO:0008108 | 1 | gene\_06566.t1 | | UDP-glucose:hexose-1-phosphate uridylyltransferase activity | molecular\_function |
| GO:0031267 | 14 | gene\_02554.t1,gene\_04234.t1,gene\_04579.t1,gene\_00505.t1,gene\_06223.t1,gene\_02029.t1,gene\_09193.t1,gene\_05152.t1,gene\_07673.t1,gene\_09686.t1,gene\_02002.t1,gene\_09561.t1,gene\_01549.t1,gene\_10032.t1 | | small GTPase binding | molecular\_function |
| GO:0004367 | 1 | gene\_00708.t1 | | glycerol-3-phosphate dehydrogenase [NAD+] activity | molecular\_function |
| GO:0030628 | 1 | gene\_06855.t1 | | pre-mRNA 3'-splice site binding | molecular\_function |
| GO:0004813 | 3 | gene\_00660.t1,gene\_07680.t1,gene\_09742.t1 | | alanine-tRNA ligase activity | molecular\_function |
| GO:0004812 | 2 | gene\_01446.t1,gene\_06212.t1 | | aminoacyl-tRNA ligase activity | molecular\_function |
| GO:0004815 | 2 | gene\_03141.t1,gene\_00665.t1 | | aspartate-tRNA ligase activity | molecular\_function |
| GO:0004362 | 1 | gene\_02054.t1 | | glutathione-disulfide reductase (NADPH) activity | molecular\_function |
| GO:0004817 | 1 | gene\_04419.t1 | | cysteine-tRNA ligase activity | molecular\_function |
| GO:0004816 | 2 | gene\_09843.t1,gene\_03207.t1 | | asparagine-tRNA ligase activity | molecular\_function |
| GO:0004819 | 1 | gene\_02487.t1 | | glutamine-tRNA ligase activity | molecular\_function |
| GO:0004818 | 2 | gene\_07873.t1,gene\_06273.t1 | | glutamate-tRNA ligase activity | molecular\_function |
| GO:0030623 | 1 | gene\_02780.t1 | | U5 snRNA binding | molecular\_function |
| GO:0005543 | 3 | gene\_07272.t1,gene\_04533.t1,gene\_01180.t1 | | phospholipid binding | molecular\_function |
| GO:0005544 | 2 | gene\_03515.t1,gene\_06880.t1 | | calcium-dependent phospholipid binding | molecular\_function |
| GO:0005545 | 1 | gene\_02601.t1 | | 1-phosphatidylinositol binding | molecular\_function |
| GO:0005546 | 1 | gene\_10315.t1 | | phosphatidylinositol-4,5-bisphosphate binding | molecular\_function |
| GO:0004368 | 1 | gene\_05158.t1 | | glycerol-3-phosphate dehydrogenase (quinone) activity | molecular\_function |
| GO:0004560 | 2 | gene\_05650.t1,gene\_00636.t1 | | alpha-L-fucosidase activity | molecular\_function |
| GO:0004563 | 2 | gene\_00936.t1,gene\_07473.t1 | | beta-N-acetylhexosaminidase activity | molecular\_function |
| GO:0004565 | 4 | gene\_02403.t1,gene\_02188.t1,gene\_08468.t1,gene\_08467.t1 | | beta-galactosidase activity | molecular\_function |
| GO:0004567 | 2 | gene\_04731.t1,gene\_03424.t1 | | beta-mannosidase activity | molecular\_function |
| GO:0052918 | 1 | gene\_02233.t1 | | dol-P-Man:Man(8)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase activity | molecular\_function |
| GO:0052917 | 1 | gene\_10419.t1 | | dolichyl-P-Man:Man(7)GlcNAc(2)-PP-dolichol alpha-1,6-mannosyltransferase | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0004568 | 24 | gene\_04391.t1,gene\_01798.t1,gene\_07912.t1,gene\_09962.t1,gene\_07875.t1,gene\_05687.t1,gene\_10573.t1,gene\_01799.t1,gene\_01037.t1,gene\_06552.t1,gene\_01797.t1,gene\_03719.t1,gene\_02142.t1,gene\_04222.t1,gene\_09960.t1,gene\_06768.t1,gene\_10353.t1,gene\_01801.t1,gene\_01647.t1,gene\_05417.t1,gene\_09961.t1,gene\_00971.t1,gene\_01800.t1,gene\_06897.t1 | | chitinase activity | molecular\_function |
| GO:0008841 | 1 | gene\_00302.t1 | | dihydrofolate synthase activity | molecular\_function |
| GO:0008810 | 3 | gene\_01578.t1,gene\_07226.t1,gene\_03404.t1 | | cellulase activity | molecular\_function |
| GO:0051118 | 6 | gene\_03433.t1,gene\_02590.t1,gene\_00288.t1,gene\_09937.t1,gene\_03934.t1,gene\_08861.t1 | | glucan endo-1,3-alpha-glucosidase activity | molecular\_function |
| GO:0008073 | 1 | gene\_08290.t1 | | ornithine decarboxylase inhibitor activity | molecular\_function |
| GO:0004385 | 2 | gene\_05164.t1,gene\_03491.t1 | | guanylate kinase activity | molecular\_function |
| GO:0004386 | 39 | gene\_03396.t1,gene\_03242.t1,gene\_00613.t1,gene\_07993.t1,gene\_04315.t1,gene\_06974.t1,gene\_01706.t1,gene\_05457.t1,gene\_07245.t1,gene\_01532.t1,gene\_06315.t1,gene\_08324.t1,gene\_05421.t1,gene\_10474.t1,gene\_01737.t1,gene\_01162.t1,gene\_06202.t1,gene\_08023.t1,gene\_09554.t1,gene\_08591.t1,gene\_03372.t1,gene\_07402.t1,gene\_08713.t1,gene\_01308.t1,gene\_08388.t1,gene\_05211.t1,gene\_09569.t1,gene\_10512.t1,gene\_07494.t1,gene\_04425.t1,gene\_10365.t1,gene\_04160.t1,gene\_06560.t1,gene\_04352.t1,gene\_01182.t1,gene\_05841.t1,gene\_00897.t1,gene\_06256.t1,gene\_07580.t1 | | helicase activity | molecular\_function |
| GO:0046961 | 5 | gene\_00893.t1,gene\_05546.t1,gene\_08419.t1,gene\_07813.t1,gene\_07027.t1 | | proton-transporting ATPase activity, rotational mechanism | molecular\_function |
| GO:0004707 | 5 | gene\_10324.t1,gene\_01422.t1,gene\_08871.t1,gene\_10524.t1,gene\_08746.t1 | | MAP kinase activity | molecular\_function |
| GO:0005381 | 2 | gene\_05743.t1,gene\_08549.t1 | | iron ion transmembrane transporter activity | molecular\_function |
| GO:0005384 | 3 | gene\_10247.t1,gene\_00807.t1,gene\_03253.t1 | | manganese ion transmembrane transporter activity | molecular\_function |
| GO:0005385 | 2 | gene\_02709.t1,gene\_00243.t1 | | zinc ion transmembrane transporter activity | molecular\_function |
| GO:0005388 | 4 | gene\_02415.t1,gene\_03092.t1,gene\_08909.t1,gene\_06180.t1 | | P-type calcium transporter activity | molecular\_function |
| GO:0004709 | 1 | gene\_08916.t1 | | MAP kinase kinase kinase activity | molecular\_function |
| GO:0018024 | 2 | gene\_05627.t1,gene\_07260.t1 | | histone-lysine N-methyltransferase activity | molecular\_function |
| GO:0004030 | 1 | gene\_02614.t1 | | aldehyde dehydrogenase [NAD(P)+] activity | molecular\_function |
| GO:0004037 | 1 | gene\_05646.t1 | | allantoicase activity | molecular\_function |
| GO:0004035 | 2 | gene\_02772.t1,gene\_10053.t1 | | alkaline phosphatase activity | molecular\_function |
| GO:0003938 | 2 | gene\_04266.t1,gene\_02686.t1 | | IMP dehydrogenase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0003937 | 1 | gene\_00429.t1 | | IMP cyclohydrolase activity | molecular\_function |
| GO:0003935 | 2 | gene\_08770.t1,gene\_07127.t1 | | GTP cyclohydrolase II activity | molecular\_function |
| GO:0004038 | 1 | gene\_03176.t1 | | allantoinase activity | molecular\_function |
| GO:0008252 | 2 | gene\_01513.t1,gene\_03406.t1 | | nucleotidase activity | molecular\_function |
| GO:0008251 | 1 | gene\_02973.t1 | | tRNA-specific adenosine deaminase activity | molecular\_function |
| GO:0000703 | 1 | gene\_06972.t1 | | oxidized pyrimidine nucleobase lesion DNA N-glycosylase activity | molecular\_function |
| GO:0000702 | 1 | gene\_09479.t1 | | oxidized base lesion DNA N-glycosylase activity | molecular\_function |
| GO:0004639 | 1 | gene\_07232.t1 | | phosphoribosylaminoimidazolesuccinocarboxamide synthase activity | molecular\_function |
| GO:0004638 | 1 | gene\_10263.t1 | | phosphoribosylaminoimidazole carboxylase activity | molecular\_function |
| GO:0004149 | 1 | gene\_07350.t1 | | dihydrolipoyllysine-residue succinyltransferase activity | molecular\_function |
| GO:0004148 | 1 | gene\_06691.t1 | | dihydrolipoyl dehydrogenase activity | molecular\_function |
| GO:0004631 | 2 | gene\_08132.t1,gene\_08399.t1 | | phosphomevalonate kinase activity | molecular\_function |
| GO:0004146 | 1 | gene\_01051.t1 | | dihydrofolate reductase activity | molecular\_function |
| GO:0004144 | 2 | gene\_01120.t1,gene\_07365.t1 | | diacylglycerol O-acyltransferase activity | molecular\_function |
| GO:0004635 | 1 | gene\_02123.t1 | | phosphoribosyl-AMP cyclohydrolase activity | molecular\_function |
| GO:0004634 | 2 | gene\_00524.t1,gene\_02419.t1 | | phosphopyruvate hydratase activity | molecular\_function |
| GO:0004141 | 1 | gene\_09469.t1 | | dethiobiotin synthase activity | molecular\_function |
| GO:0004636 | 1 | gene\_02123.t1 | | phosphoribosyl-ATP diphosphatase activity | molecular\_function |
| GO:0090560 | 2 | gene\_02666.t1,gene\_07601.t1 | | 2-(3-amino-3-carboxypropyl)histidine synthase activity | molecular\_function |
| GO:0008495 | 1 | gene\_01447.t1 | | protoheme IX farnesyltransferase activity | molecular\_function |
| GO:0008496 | 6 | gene\_05243.t1,gene\_03422.t1,gene\_08370.t1,gene\_01644.t1,gene\_00739.t1,gene\_03426.t1 | | mannan endo-1,6-alpha-mannosidase activity | molecular\_function |
| GO:0008659 | 1 | gene\_02332.t1 | | (3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase activity | molecular\_function |
| GO:0019001 | 1 | gene\_06747.t1 | | guanyl nucleotide binding | molecular\_function |
| GO:0015267 | 7 | gene\_05316.t1,gene\_03329.t1,gene\_08689.t1,gene\_03976.t1,gene\_10472.t1,gene\_10235.t1,gene\_07578.t1 | | channel activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0046983 | 30 | gene\_05990.t1,gene\_01133.t1,gene\_05048.t1,gene\_04200.t1,gene\_04970.t1,gene\_09612.t1,gene\_07125.t1,gene\_04892.t1,gene\_06860.t1,gene\_04922.t1,gene\_05008.t1,gene\_05064.t1,gene\_07614.t1,gene\_05043.t1,gene\_03951.t1,gene\_04811.t1,gene\_04840.t1,gene\_07428.t1,gene\_05340.t1,gene\_03523.t1,gene\_04902.t1,gene\_03324.t1,gene\_00891.t1,gene\_06826.t1,gene\_04569.t1,gene\_04847.t1,gene\_00863.t1,gene\_08691.t1,gene\_04914.t1,gene\_04974.t1 | | protein dimerization activity | molecular\_function |
| GO:0046982 | 25 | gene\_07352.t1,gene\_07755.t1,gene\_02207.t1,gene\_02242.t1,gene\_08169.t1,gene\_07353.t1,gene\_05524.t1,gene\_07532.t1,gene\_07246.t1,gene\_00099.t1,gene\_05658.t1,gene\_02241.t1,gene\_03455.t1,gene\_08167.t1,gene\_08411.t1,gene\_06486.t1,gene\_02119.t1,gene\_00109.t1,gene\_02359.t1,gene\_03509.t1,gene\_09109.t1,gene\_05228.t1,gene\_02408.t1,gene\_04124.t1,gene\_09619.t1 | | protein heterodimerization activity | molecular\_function |
| GO:0016791 | 12 | gene\_01641.t1,gene\_04510.t1,gene\_07789.t1,gene\_01410.t1,gene\_04748.t1,gene\_03592.t1,gene\_07210.t1,gene\_10438.t1,gene\_04548.t1,gene\_10470.t1,gene\_02030.t1,gene\_05240.t1 | | phosphatase activity | molecular\_function |
| GO:0070273 | 1 | gene\_02859.t1 | | phosphatidylinositol-4-phosphate binding | molecular\_function |
| GO:0016799 | 2 | gene\_02953.t1,gene\_08690.t1 | | hydrolase activity, hydrolyzing N-glycosyl compounds | molecular\_function |
| GO:0016798 | 9 | gene\_07110.t1,gene\_09862.t1,gene\_06024.t1,gene\_08898.t1,gene\_09783.t1,gene\_00291.t1,gene\_05573.t1,gene\_02548.t1,gene\_02549.t1 | | hydrolase activity, acting on glycosyl bonds | molecular\_function |
| GO:0046556 | 3 | gene\_01362.t1,gene\_00037.t1,gene\_05400.t1 | | alpha-L-arabinofuranosidase activity | molecular\_function |
| GO:0061710 | 1 | gene\_01719.t1 | | L-threonylcarbamoyladenylate synthase | molecular\_function |
| GO:0050032 | 1 | gene\_06056.t1 | | L-rhamnonate dehydratase activity | molecular\_function |
| GO:0033743 | 1 | gene\_03751.t1 | | peptide-methionine (R)-S-oxide reductase activity | molecular\_function |
| GO:0033961 | 2 | gene\_06770.t1,gene\_00685.t1 | | cis-stilbene-oxide hydrolase activity | molecular\_function |
| GO:0033699 | 1 | gene\_06255.t1 | | DNA 5'-adenosine monophosphate hydrolase activity | molecular\_function |
| GO:0052381 | 1 | gene\_09703.t1 | | tRNA dimethylallyltransferase activity | molecular\_function |
| GO:0016407 | 6 | gene\_07290.t1,gene\_04976.t1,gene\_00023.t1,gene\_05151.t1,gene\_01115.t1,gene\_04903.t1 | | acetyltransferase activity | molecular\_function |
| GO:0102553 | 1 | gene\_06832.t1 | | lipoyl synthase activity (acting on pyruvate dehydrogenase E2 protein) | molecular\_function |
| GO:0003677 | 565 | gene\_05891.t1,gene\_06503.t1,gene\_09809.t1,gene\_09549.t1,gene\_07166.t1,gene\_06706.t1,gene\_08645.t1,gene\_09457.t1,gene\_04873.t1,gene\_02977.t1,gene\_03228.t1,gene\_06172.t1,gene\_01625.t1,gene\_05425.t1,gene\_09939.t1,gene\_04045.t1,gene\_03544.t1,gene\_06394.t1,gene\_07357.t1,gene\_00562.t1,gene\_04534.t1,gene\_02847.t1,gene\_09184.t1,gene\_08694.t1,gene\_06819.t1, | | DNA binding | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0003677 | 565 | gene\_09930.t1,gene\_00595.t1,gene\_10614.t1,gene\_09897.t1,gene\_05990.t1,gene\_04594.t1,gene\_06856.t1,gene\_03740.t1,gene\_00052.t1,gene\_03342.t1,gene\_04524.t1,gene\_04970.t1,gene\_01394.t1,gene\_06864.t1,gene\_07125.t1,gene\_04892.t1,gene\_00677.t1,gene\_04933.t1,gene\_01025.t1,gene\_05527.t1,gene\_10058.t1,gene\_06302.t1,gene\_04014.t1,gene\_05518.t1,gene\_01922.t1,gene\_07635.t1,gene\_02107.t1,gene\_09370.t1,gene\_02334.t1,gene\_04473.t1,gene\_05445.t1,gene\_06230.t1,gene\_04321.t1,gene\_00614.t1,gene\_00689.t1,gene\_10205.t1,gene\_07890.t1,gene\_00822.t1,gene\_04263.t1,gene\_06259.t1,gene\_02151.t1,gene\_01954.t1,gene\_01695.t1,gene\_10255.t1,gene\_03054.t1,gene\_07532.t1,gene\_05547.t1,gene\_04732.t1,gene\_08560.t1,gene\_08795.t1,gene\_08148.t1,gene\_07428.t1,gene\_05082.t1,gene\_05810.t1,gene\_03509.t1,gene\_05677.t1,gene\_04445.t1,gene\_04352.t1,gene\_01274.t1,gene\_07898.t1,gene\_09646.t1,gene\_07730.t1,gene\_00326.t1,gene\_01857.t1,gene\_08034.t1,gene\_04693.t1,gene\_05639.t1,gene\_05862.t1,gene\_08703.t1,gene\_07229.t1,gene\_02068.t1,gene\_10306.t1,gene\_07612.t1,gene\_02027.t1,gene\_02321.t1,gene\_05064.t1,gene\_09361.t1,gene\_06675.t1,gene\_05087.t1,gene\_01005.t1,gene\_07299.t1,gene\_02661.t1,gene\_00770.t1,gene\_09221.t1,gene\_03304.t1,gene\_03842.t1,gene\_04795.t1,gene\_03248.t1,gene\_07840.t1,gene\_07241.t1,gene\_01550.t1,gene\_00059.t1,gene\_07040.t1,gene\_07382.t1,gene\_07333.t1,gene\_03210.t1,gene\_00656.t1,gene\_04163.t1,gene\_00286.t1,gene\_06585.t1,gene\_05455.t1,gene\_00496.t1,gene\_01987.t1,gene\_06694.t1,gene\_09375.t1,gene\_08824.t1,gene\_09192.t1,gene\_08521.t1,gene\_01133.t1,gene\_10188.t1,gene\_07128.t1,gene\_00556.t1,gene\_06258.t1,gene\_01305.t1,gene\_00515.t1,gene\_04840.t1,gene\_06020.t1,gene\_01948.t1,gene\_05556.t1,gene\_06963.t1,gene\_10351.t1,gene\_01145.t1,gene\_06978.t1,gene\_05273.t1,gene\_06395.t1,gene\_02451.t1,gene\_00982.t1,gene\_02110.t1,gene\_10407.t1,gene\_09590.t1,gene\_04918.t1,gene\_02034.t1,gene\_02652.t1,gene\_04182.t1,gene\_01212.t1,gene\_10663.t1,gene\_04481.t1,gene\_02786.t1,gene\_06852.t1,gene\_02605.t1,gene\_09813.t1,gene\_07906.t1,gene\_10056.t1,gene\_07321.t1,gene\_01057.t1,gene\_06732.t1,gene\_06524.t1,gene\_01163.t1,gene\_08477.t1,gene\_01126.t1,gene\_06584.t1,gene\_04811.t1,gene\_02809.t1,gene\_10553.t1,gene\_05992.t1,gene\_04208.t1,gene\_01937.t1,gene\_02318.t1,gene\_01345.t1,gene\_04028.t1,gene\_08833.t1,gene\_07955.t1,gene\_10374.t1,gene\_01521.t1,gene\_00138.t1,gene\_06606.t1,gene\_03595.t1,gene\_03799.t1,gene\_10151.t1,gene\_09944.t1,gene\_10666.t1,gene\_09071.t1,gene\_03831.t1,gene\_06309.t1,gene\_04013.t1,gene\_06795.t1,gene\_03650.t1,gene\_07353.t1,gene\_04621.t1,gene\_00046.t1, | | DNA binding | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0003677 | 565 | gene\_10607.t1,gene\_08473.t1,gene\_05595.t1,gene\_02607.t1,gene\_07537.t1,gene\_01756.t1,gene\_02835.t1,gene\_08474.t1,gene\_08569.t1,gene\_02050.t1,gene\_09339.t1,gene\_05311.t1,gene\_00803.t1,gene\_08304.t1,gene\_09126.t1,gene\_01529.t1,gene\_06740.t1,gene\_07744.t1,gene\_08366.t1,gene\_00228.t1,gene\_09044.t1,gene\_02212.t1,gene\_07320.t1,gene\_07785.t1,gene\_02242.t1,gene\_05559.t1,gene\_05725.t1,gene\_04315.t1,gene\_09757.t1,gene\_06823.t1,gene\_03642.t1,gene\_04307.t1,gene\_06040.t1,gene\_10509.t1,gene\_01014.t1,gene\_08155.t1,gene\_10172.t1,gene\_02955.t1,gene\_05721.t1,gene\_06088.t1,gene\_03870.t1,gene\_03107.t1,gene\_04902.t1,gene\_03748.t1,gene\_04643.t1,gene\_09979.t1,gene\_10606.t1,gene\_05151.t1,gene\_00018.t1,gene\_07212.t1,gene\_05008.t1,gene\_06679.t1,gene\_10649.t1,gene\_03200.t1,gene\_10517.t1,gene\_02220.t1,gene\_05741.t1,gene\_02526.t1,gene\_03130.t1,gene\_04257.t1,gene\_05301.t1,gene\_03018.t1,gene\_08475.t1,gene\_01660.t1,gene\_03062.t1,gene\_06221.t1,gene\_06059.t1,gene\_10019.t1,gene\_01692.t1,gene\_02512.t1,gene\_06936.t1,gene\_09151.t1,gene\_06215.t1,gene\_02170.t1,gene\_03295.t1,gene\_08479.t1,gene\_08889.t1,gene\_07283.t1,gene\_07525.t1,gene\_02915.t1,gene\_01390.t1,gene\_02194.t1,gene\_01710.t1,gene\_06934.t1,gene\_05121.t1,gene\_09460.t1,gene\_07677.t1,gene\_04979.t1,gene\_07168.t1,gene\_03606.t1,gene\_08287.t1,gene\_00959.t1,gene\_10137.t1,gene\_00308.t1,gene\_00564.t1,gene\_07726.t1,gene\_05277.t1,gene\_08299.t1,gene\_07270.t1,gene\_09865.t1,gene\_01527.t1,gene\_05950.t1,gene\_07085.t1,gene\_03132.t1,gene\_10047.t1,gene\_04646.t1,gene\_10254.t1,gene\_00911.t1,gene\_10065.t1,gene\_06255.t1,gene\_06171.t1,gene\_07693.t1,gene\_05685.t1,gene\_08691.t1,gene\_08135.t1,gene\_04004.t1,gene\_04695.t1,gene\_10543.t1,gene\_08083.t1,gene\_02523.t1,gene\_07992.t1,gene\_07948.t1,gene\_06089.t1,gene\_08550.t1,gene\_05932.t1,gene\_01535.t1,gene\_03812.t1,gene\_04854.t1,gene\_01135.t1,gene\_00599.t1,gene\_01774.t1,gene\_00640.t1,gene\_07583.t1,gene\_09652.t1,gene\_02228.t1,gene\_01819.t1,gene\_09814.t1,gene\_03744.t1,gene\_04669.t1,gene\_09957.t1,gene\_01018.t1,gene\_06517.t1,gene\_02916.t1,gene\_04048.t1,gene\_05808.t1,gene\_08947.t1,gene\_08530.t1,gene\_02529.t1,gene\_05747.t1,gene\_08099.t1,gene\_01742.t1,gene\_06249.t1,gene\_02757.t1,gene\_08608.t1,gene\_05477.t1,gene\_04313.t1,gene\_07010.t1,gene\_09781.t1,gene\_05699.t1,gene\_07620.t1,gene\_00732.t1,gene\_09036.t1,gene\_06427.t1,gene\_06291.t1,gene\_01262.t1,gene\_02946.t1,gene\_00747.t1,gene\_04647.t1,gene\_09131.t1,gene\_06377.t1,gene\_01359.t1,gene\_00847.t1,gene\_03869.t1,gene\_10197.t1,gene\_01877.t1,gene\_05428.t1,gene\_03741.t1,gene\_08483.t1,gene\_01156.t1,gene\_06095.t1, | | DNA binding | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0003677 | 565 | gene\_06801.t1,gene\_08280.t1,gene\_03747.t1,gene\_05070.t1,gene\_01310.t1,gene\_01377.t1,gene\_04651.t1,gene\_01606.t1,gene\_04922.t1,gene\_01134.t1,gene\_01708.t1,gene\_04946.t1,gene\_06766.t1,gene\_04830.t1,gene\_05015.t1,gene\_05814.t1,gene\_03163.t1,gene\_09612.t1,gene\_09748.t1,gene\_03519.t1,gene\_08300.t1,gene\_03324.t1,gene\_04049.t1,gene\_03596.t1,gene\_09330.t1,gene\_05048.t1,gene\_07254.t1,gene\_00968.t1,gene\_06550.t1,gene\_03118.t1,gene\_08966.t1,gene\_07755.t1,gene\_04976.t1,gene\_01942.t1,gene\_04200.t1,gene\_10237.t1,gene\_04378.t1,gene\_07271.t1,gene\_03607.t1,gene\_06102.t1,gene\_00246.t1,gene\_04706.t1,gene\_00182.t1,gene\_08345.t1,gene\_02241.t1,gene\_04660.t1,gene\_01540.t1,gene\_07284.t1,gene\_05811.t1,gene\_03513.t1,gene\_07282.t1,gene\_02674.t1,gene\_04650.t1,gene\_08281.t1,gene\_00908.t1,gene\_02715.t1,gene\_09697.t1,gene\_10675.t1,gene\_03447.t1,gene\_02098.t1,gene\_07617.t1,gene\_08269.t1,gene\_04569.t1,gene\_02808.t1,gene\_03050.t1,gene\_09712.t1,gene\_06532.t1,gene\_01153.t1,gene\_08441.t1,gene\_05368.t1,gene\_04983.t1,gene\_09058.t1,gene\_01809.t1,gene\_08041.t1,gene\_03234.t1,gene\_05540.t1,gene\_03366.t1,gene\_05998.t1,gene\_05206.t1,gene\_07683.t1,gene\_04022.t1,gene\_04081.t1,gene\_02948.t1,gene\_04356.t1,gene\_06076.t1,gene\_06614.t1,gene\_08341.t1,gene\_06402.t1,gene\_10467.t1,gene\_01612.t1,gene\_10167.t1,gene\_07639.t1,gene\_01003.t1,gene\_05736.t1,gene\_05474.t1,gene\_03529.t1,gene\_09537.t1,gene\_07827.t1,gene\_07088.t1,gene\_06266.t1,gene\_04914.t1,gene\_06696.t1,gene\_06972.t1,gene\_05383.t1,gene\_10083.t1,gene\_04676.t1,gene\_08245.t1,gene\_10051.t1,gene\_10211.t1,gene\_04413.t1,gene\_02385.t1,gene\_09699.t1,gene\_00395.t1,gene\_03770.t1,gene\_05043.t1,gene\_02580.t1,gene\_07065.t1,gene\_01512.t1,gene\_04937.t1,gene\_03761.t1,gene\_04515.t1,gene\_02282.t1,gene\_03463.t1,gene\_04314.t1,gene\_02874.t1,gene\_05299.t1,gene\_07506.t1,gene\_10629.t1,gene\_02910.t1,gene\_03763.t1,gene\_00921.t1,gene\_09656.t1,gene\_08139.t1,gene\_02042.t1,gene\_06023.t1,gene\_06515.t1,gene\_01498.t1,gene\_07548.t1,gene\_06225.t1,gene\_08254.t1,gene\_02608.t1,gene\_05588.t1,gene\_02502.t1,gene\_01613.t1,gene\_04903.t1,gene\_03427.t1,gene\_04304.t1,gene\_09526.t1,gene\_01043.t1,gene\_07352.t1,gene\_04254.t1,gene\_09969.t1,gene\_09035.t1,gene\_01696.t1,gene\_02086.t1,gene\_01730.t1,gene\_03655.t1,gene\_06672.t1,gene\_05708.t1,gene\_07054.t1,gene\_10498.t1,gene\_00654.t1,gene\_09775.t1,gene\_03408.t1,gene\_02230.t1,gene\_08062.t1,gene\_04209.t1,gene\_02677.t1,gene\_01998.t1,gene\_05080.t1,gene\_01530.t1,gene\_07821.t1,gene\_05972.t1,gene\_05841.t1,gene\_00634.t1,gene\_04655.t1,gene\_09619.t1,gene\_02730.t1,gene\_04974.t1,gene\_08638.t1 | | DNA binding | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0030983 | 10 | gene\_00724.t1,gene\_00723.t1,gene\_03576.t1,gene\_08513.t1,gene\_01436.t1,gene\_03237.t1,gene\_07403.t1,gene\_05849.t1,gene\_05619.t1,gene\_00205.t1 | | mismatched DNA binding | molecular\_function |
| GO:0004106 | 3 | gene\_08154.t1,gene\_09255.t1,gene\_05716.t1 | | chorismate mutase activity | molecular\_function |
| GO:0017116 | 1 | gene\_10167.t1 | | single-stranded DNA helicase activity | molecular\_function |
| GO:0017110 | 2 | gene\_03291.t1,gene\_08258.t1 | | nucleoside-diphosphatase activity | molecular\_function |
| GO:0043546 | 2 | gene\_10070.t1,gene\_08723.t1 | | molybdopterin cofactor binding | molecular\_function |
| GO:0047617 | 6 | gene\_01307.t1,gene\_01211.t1,gene\_01926.t1,gene\_07008.t1,gene\_07738.t1,gene\_03283.t1 | | acyl-CoA hydrolase activity | molecular\_function |
| GO:0003700 | 39 | gene\_06215.t1,gene\_09262.t1,gene\_03740.t1,gene\_09757.t1,gene\_03384.t1,gene\_00496.t1,gene\_09388.t1,gene\_04217.t1,gene\_04398.t1,gene\_07831.t1,gene\_00138.t1,gene\_01423.t1,gene\_06656.t1,gene\_02778.t1,gene\_07554.t1,gene\_03069.t1,gene\_08484.t1,gene\_01650.t1,gene\_05708.t1,gene\_09151.t1,gene\_08663.t1,gene\_09516.t1,gene\_02612.t1,gene\_03104.t1,gene\_03579.t1,gene\_05693.t1,gene\_00244.t1,gene\_03144.t1,gene\_08795.t1,gene\_07750.t1,gene\_00906.t1,gene\_06299.t1,gene\_05943.t1,gene\_02914.t1,gene\_08025.t1,gene\_10128.t1,gene\_04347.t1,gene\_07670.t1,gene\_09328.t1 | | DNA-binding transcription factor activity | molecular\_function |
| GO:0052857 | 2 | gene\_04609.t1,gene\_06101.t1 | | NADPHX epimerase activity | molecular\_function |
| GO:0052855 | 1 | gene\_00517.t1 | | ADP-dependent NAD(P)H-hydrate dehydratase activity | molecular\_function |
| GO:0097573 | 4 | gene\_09296.t1,gene\_02546.t1,gene\_05191.t1,gene\_00012.t1 | | glutathione oxidoreductase activity | molecular\_function |
| GO:0016906 | 1 | gene\_03179.t1 | | sterol 3-beta-glucosyltransferase activity | molecular\_function |
| GO:0004824 | 3 | gene\_01636.t1,gene\_03790.t1,gene\_00005.t1 | | lysine-tRNA ligase activity | molecular\_function |
| GO:0004825 | 2 | gene\_05182.t1,gene\_01382.t1 | | methionine-tRNA ligase activity | molecular\_function |
| GO:0004826 | 3 | gene\_03944.t1,gene\_02682.t1,gene\_02959.t1 | | phenylalanine-tRNA ligase activity | molecular\_function |
| GO:0004827 | 2 | gene\_05564.t1,gene\_06241.t1 | | proline-tRNA ligase activity | molecular\_function |
| GO:0004820 | 1 | gene\_09244.t1 | | glycine-tRNA ligase activity | molecular\_function |
| GO:0030619 | 2 | gene\_06114.t1,gene\_10367.t1 | | U1 snRNA binding | molecular\_function |
| GO:0004822 | 2 | gene\_02254.t1,gene\_04722.t1 | | isoleucine-tRNA ligase activity | molecular\_function |
| GO:0004823 | 2 | gene\_09679.t1,gene\_10446.t1 | | leucine-tRNA ligase activity | molecular\_function |
| GO:0004828 | 2 | gene\_09273.t1,gene\_05654.t1 | | serine-tRNA ligase activity | molecular\_function |
| GO:0004829 | 2 | gene\_06643.t1,gene\_10327.t1 | | threonine-tRNA ligase activity | molecular\_function |
| GO:0004555 | 2 | gene\_02271.t1,gene\_10343.t1 | | alpha,alpha-trehalase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0004556 | 3 | gene\_04296.t1,gene\_05379.t1,gene\_04047.t1 | | alpha-amylase activity | molecular\_function |
| GO:0004550 | 1 | gene\_07884.t1 | | nucleoside diphosphate kinase activity | molecular\_function |
| GO:0004553 | 54 | gene\_01845.t1,gene\_08927.t1,gene\_03569.t1,gene\_08420.t1,gene\_04755.t1,gene\_02770.t1,gene\_09941.t1,gene\_07399.t1,gene\_07652.t1,gene\_00176.t1,gene\_02920.t1,gene\_03420.t1,gene\_00100.t1,gene\_05610.t1,gene\_06681.t1,gene\_09138.t1,gene\_07562.t1,gene\_03030.t1,gene\_06777.t1,gene\_03902.t1,gene\_01032.t1,gene\_09758.t1,gene\_09452.t1,gene\_02284.t1,gene\_03591.t1,gene\_00119.t1,gene\_01835.t1,gene\_00439.t1,gene\_09816.t1,gene\_09695.t1,gene\_03444.t1,gene\_07770.t1,gene\_07809.t1,gene\_01759.t1,gene\_00394.t1,gene\_01013.t1,gene\_05378.t1,gene\_04380.t1,gene\_02620.t1,gene\_07460.t1,gene\_02670.t1,gene\_02922.t1,gene\_04464.t1,gene\_05722.t1,gene\_08223.t1,gene\_05651.t1,gene\_06726.t1,gene\_07881.t1,gene\_00950.t1,gene\_06645.t1,gene\_08993.t1,gene\_04322.t1,gene\_02102.t1,gene\_07032.t1 | | hydrolase activity, hydrolyzing O-glycosyl compounds | molecular\_function |
| GO:0015205 | 1 | gene\_08462.t1 | | nucleobase transmembrane transporter activity | molecular\_function |
| GO:0031593 | 1 | gene\_09214.t1 | | polyubiquitin modification-dependent protein binding | molecular\_function |
| GO:0044877 | 2 | gene\_07735.t1,gene\_00548.t1 | | protein-containing complex binding | molecular\_function |
| GO:0016887 | 127 | gene\_05374.t1,gene\_08389.t1,gene\_07138.t1,gene\_01790.t1,gene\_06516.t1,gene\_06102.t1,gene\_01236.t1,gene\_02841.t1,gene\_10098.t1,gene\_06343.t1,gene\_03074.t1,gene\_01540.t1,gene\_05700.t1,gene\_09269.t1,gene\_00515.t1,gene\_02715.t1,gene\_03652.t1,gene\_04139.t1,gene\_10365.t1,gene\_01710.t1,gene\_09071.t1,gene\_06062.t1,gene\_06902.t1,gene\_07321.t1,gene\_06242.t1,gene\_08875.t1,gene\_02480.t1,gene\_02559.t1,gene\_00205.t1,gene\_07003.t1,gene\_06495.t1,gene\_02486.t1,gene\_05208.t1,gene\_07129.t1,gene\_07906.t1,gene\_03702.t1,gene\_03855.t1,gene\_00682.t1,gene\_06236.t1,gene\_05954.t1,gene\_08299.t1,gene\_07825.t1,gene\_07862.t1,gene\_06720.t1,gene\_08963.t1,gene\_05849.t1,gene\_09744.t1,gene\_09265.t1,gene\_10167.t1,gene\_10074.t1,gene\_10008.t1,gene\_08266.t1,gene\_01990.t1,gene\_10065.t1,gene\_09415.t1,gene\_02676.t1,gene\_00363.t1,gene\_06649.t1,gene\_07666.t1,gene\_10444.t1,gene\_09001.t1,gene\_07628.t1,gene\_08245.t1,gene\_02523.t1,gene\_00597.t1,gene\_04959.t1,gene\_09699.t1,gene\_02228.t1,gene\_00706.t1,gene\_08071.t1,gene\_03576.t1,gene\_02623.t1,gene\_00982.t1,gene\_04290.t1,gene\_05056.t1,gene\_07343.t1,gene\_05844.t1,gene\_03597.t1,gene\_00937.t1,gene\_06611.t1,gene\_01914.t1,gene\_08961.t1,gene\_01265.t1,gene\_05695.t1,gene\_02991.t1,gene\_10289.t1,gene\_00502.t1,gene\_07157.t1,gene\_03801.t1,gene\_03476.t1,gene\_07620.t1,gene\_00118.t1,gene\_01919.t1,gene\_07202.t1,gene\_04352.t1 | | ATP hydrolysis activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0016887 | 127 | gene\_00882.t1,gene\_03192.t1,gene\_09161.t1,gene\_02420.t1,gene\_03204.t1,gene\_07744.t1,gene\_03165.t1,gene\_04092.t1,gene\_00738.t1,gene\_04223.t1,gene\_00426.t1,gene\_00514.t1,gene\_07180.t1,gene\_05618.t1,gene\_03931.t1,gene\_05855.t1,gene\_08575.t1,gene\_09591.t1,gene\_09396.t1,gene\_02049.t1,gene\_06458.t1,gene\_01751.t1,gene\_07139.t1,gene\_07819.t1,gene\_05556.t1,gene\_06405.t1,gene\_10370.t1,gene\_01221.t1,gene\_09891.t1,gene\_04461.t1,gene\_04537.t1,gene\_07212.t1 | | ATP hydrolysis activity | molecular\_function |
| GO:0061928 | 1 | gene\_06808.t1 | | glutathione specific gamma-glutamylcyclotransferase activity | molecular\_function |
| GO:0000026 | 1 | gene\_02828.t1 | | alpha-1,2-mannosyltransferase activity | molecular\_function |
| GO:0004739 | 2 | gene\_02327.t1,gene\_04096.t1 | | pyruvate dehydrogenase (acetyl-transferring) activity | molecular\_function |
| GO:0004795 | 1 | gene\_06750.t1 | | threonine synthase activity | molecular\_function |
| GO:0004730 | 1 | gene\_09862.t1 | | pseudouridylate synthase activity | molecular\_function |
| GO:0004733 | 1 | gene\_08405.t1 | | pyridoxamine-phosphate oxidase activity | molecular\_function |
| GO:0004735 | 3 | gene\_00851.t1,gene\_01582.t1,gene\_03398.t1 | | pyrroline-5-carboxylate reductase activity | molecular\_function |
| GO:0004736 | 1 | gene\_01374.t1 | | pyruvate carboxylase activity | molecular\_function |
| GO:0004737 | 6 | gene\_02158.t1,gene\_08592.t1,gene\_03558.t1,gene\_03899.t1,gene\_05669.t1,gene\_03017.t1 | | pyruvate decarboxylase activity | molecular\_function |
| GO:0004047 | 1 | gene\_05570.t1 | | aminomethyltransferase activity | molecular\_function |
| GO:0004044 | 1 | gene\_09478.t1 | | amidophosphoribosyltransferase activity | molecular\_function |
| GO:0004045 | 2 | gene\_09226.t1,gene\_03993.t1 | | aminoacyl-tRNA hydrolase activity | molecular\_function |
| GO:0004042 | 2 | gene\_04583.t1,gene\_06573.t1 | | acetyl-CoA:L-glutamate N-acetyltransferase activity | molecular\_function |
| GO:0004043 | 1 | gene\_10072.t1 | | L-aminoadipate-semialdehyde dehydrogenase activity | molecular\_function |
| GO:0004040 | 5 | gene\_01286.t1,gene\_01482.t1,gene\_06796.t1,gene\_02075.t1,gene\_02324.t1 | | amidase activity | molecular\_function |
| GO:0103068 | 2 | gene\_08476.t1,gene\_10334.t1 | | leukotriene C4 gamma-glutamyl transferase activity | molecular\_function |
| GO:0140359 | 47 | gene\_08741.t1,gene\_04577.t1,gene\_10665.t1,gene\_04562.t1,gene\_00743.t1,gene\_05467.t1,gene\_04210.t1,gene\_03153.t1,gene\_03776.t1,gene\_04469.t1,gene\_02024.t1,gene\_09103.t1,gene\_01445.t1,gene\_04211.t1,gene\_07988.t1,gene\_09104.t1,gene\_10515.t1,gene\_00948.t1,gene\_03211.t1,gene\_04212.t1,gene\_06272.t1,gene\_02879.t1,gene\_03488.t1,gene\_00533.t1,gene\_00034.t1,gene\_10553.t1,gene\_05505.t1,gene\_00778.t1,gene\_02173.t1,gene\_06422.t1,gene\_03407.t1,gene\_04063.t1,gene\_01781.t1,gene\_05285.t1,gene\_02647.t1,gene\_07416.t1,gene\_02826.t1,gene\_01640.t1,gene\_02774.t1,gene\_10554.t1, | | ABC-type transporter activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0140359 | 47 | gene\_10362.t1,gene\_07559.t1,gene\_04268.t1,gene\_09207.t1,gene\_09398.t1,gene\_06116.t1,gene\_02025.t1 | | ABC-type transporter activity | molecular\_function |
| GO:0004365 | 1 | gene\_07758.t1 | | glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity | molecular\_function |
| GO:0004048 | 1 | gene\_10196.t1 | | anthranilate phosphoribosyltransferase activity | molecular\_function |
| GO:0004049 | 2 | gene\_08809.t1,gene\_10271.t1 | | anthranilate synthase activity | molecular\_function |
| GO:0008712 | 1 | gene\_08980.t1 | | ADP-glyceromanno-heptose 6-epimerase activity | molecular\_function |
| GO:0004364 | 3 | gene\_04630.t1,gene\_06568.t1,gene\_06205.t1 | | glutathione transferase activity | molecular\_function |
| GO:0045330 | 2 | gene\_09474.t1,gene\_06941.t1 | | aspartyl esterase activity | molecular\_function |
| GO:0004363 | 1 | gene\_08070.t1 | | glutathione synthase activity | molecular\_function |
| GO:0036054 | 1 | gene\_03898.t1 | | protein-malonyllysine demalonylase activity | molecular\_function |
| GO:0036055 | 1 | gene\_03898.t1 | | protein-succinyllysine desuccinylase activity | molecular\_function |
| GO:0001671 | 3 | gene\_01306.t1,gene\_07388.t1,gene\_10118.t1 | | ATPase activator activity | molecular\_function |
| GO:0080030 | 1 | gene\_09903.t1 | | methyl indole-3-acetate esterase activity | molecular\_function |
| GO:0004360 | 1 | gene\_02361.t1 | | glutamine-fructose-6-phosphate transaminase (isomerizing) activity | molecular\_function |
| GO:0004608 | 1 | gene\_06238.t1 | | phosphatidylethanolamine N-methyltransferase activity | molecular\_function |
| GO:0004609 | 3 | gene\_09062.t1,gene\_02006.t1,gene\_04684.t1 | | phosphatidylserine decarboxylase activity | molecular\_function |
| GO:0030620 | 1 | gene\_08257.t1 | | U2 snRNA binding | molecular\_function |
| GO:0004604 | 1 | gene\_06830.t1 | | phosphoadenylyl-sulfate reductase (thioredoxin) activity | molecular\_function |
| GO:0008821 | 2 | gene\_08999.t1,gene\_03054.t1 | | crossover junction endodeoxyribonuclease activity | molecular\_function |
| GO:0008824 | 1 | gene\_06302.t1 | | cyanate hydratase activity | molecular\_function |
| GO:0004601 | 19 | gene\_07679.t1,gene\_00809.t1,gene\_10014.t1,gene\_05347.t1,gene\_00543.t1,gene\_08255.t1,gene\_01732.t1,gene\_09389.t1,gene\_03126.t1,gene\_10266.t1,gene\_02830.t1,gene\_09952.t1,gene\_01472.t1,gene\_00928.t1,gene\_02872.t1,gene\_10593.t1,gene\_06152.t1,gene\_00855.t1,gene\_01903.t1 | | peroxidase activity | molecular\_function |
| GO:0004602 | 1 | gene\_02994.t1 | | glutathione peroxidase activity | molecular\_function |
| GO:0052692 | 6 | gene\_06443.t1,gene\_06442.t1,gene\_07788.t1,gene\_07143.t1,gene\_03912.t1,gene\_01435.t1 | | raffinose alpha-galactosidase activity | molecular\_function |
| GO:0102203 | 1 | gene\_03179.t1 | | brassicasterol glucosyltransferase activity | molecular\_function |
| GO:0102202 | 1 | gene\_03179.t1 | | soladodine glucosyltransferase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0010485 | 1 | gene\_01433.t1 | | H4 histone acetyltransferase activity | molecular\_function |
| GO:0010484 | 1 | gene\_04435.t1 | | H3 histone acetyltransferase activity | molecular\_function |
| GO:0019787 | 2 | gene\_04588.t1,gene\_02380.t1 | | ubiquitin-like protein transferase activity | molecular\_function |
| GO:1990837 | 1 | gene\_00109.t1 | | sequence-specific double-stranded DNA binding | molecular\_function |
| GO:0019781 | 2 | gene\_03524.t1,gene\_06445.t1 | | NEDD8 activating enzyme activity | molecular\_function |
| GO:0019789 | 2 | gene\_00320.t1,gene\_03784.t1 | | SUMO transferase activity | molecular\_function |
| GO:0050334 | 1 | gene\_00596.t1 | | thiaminase activity | molecular\_function |
| GO:0018549 | 1 | gene\_06409.t1 | | methanethiol oxidase activity | molecular\_function |
| GO:0019948 | 1 | gene\_06429.t1 | | SUMO activating enzyme activity | molecular\_function |
| GO:0032977 | 2 | gene\_08165.t1,gene\_02461.t1 | | membrane insertase activity | molecular\_function |
| GO:0043727 | 1 | gene\_10263.t1 | | 5-amino-4-imidazole carboxylate lyase activity | molecular\_function |
| GO:0008534 | 1 | gene\_04239.t1 | | oxidized purine nucleobase lesion DNA N-glycosylase activity | molecular\_function |
| GO:0016657 | 3 | gene\_05939.t1,gene\_05276.t1,gene\_04070.t1 | | oxidoreductase activity, acting on NAD(P)H, nitrogenous group as acceptor | molecular\_function |
| GO:0016651 | 3 | gene\_03522.t1,gene\_09825.t1,gene\_02861.t1 | | oxidoreductase activity, acting on NAD(P)H | molecular\_function |
| GO:0016652 | 1 | gene\_04172.t1 | | oxidoreductase activity, acting on NAD(P)H, NAD(P) as acceptor | molecular\_function |
| GO:0016653 | 1 | gene\_03787.t1 | | oxidoreductase activity, acting on NAD(P)H, heme protein as acceptor | molecular\_function |
| GO:0032866 | 9 | gene\_05403.t1,gene\_02566.t1,gene\_01649.t1,gene\_04601.t1,gene\_00136.t1,gene\_04172.t1,gene\_05361.t1,gene\_09032.t1,gene\_00528.t1 | | D-xylose:NADP reductase activity | molecular\_function |
| GO:0016433 | 1 | gene\_09258.t1 | | rRNA (adenine) methyltransferase activity | molecular\_function |
| GO:0016435 | 1 | gene\_02367.t1 | | rRNA (guanine) methyltransferase activity | molecular\_function |
| GO:0030337 | 1 | gene\_01660.t1 | | DNA polymerase processivity factor activity | molecular\_function |
| GO:0046421 | 2 | gene\_10345.t1,gene\_00805.t1 | | methylisocitrate lyase activity | molecular\_function |
| GO:0030332 | 1 | gene\_02629.t1 | | cyclin binding | molecular\_function |
| GO:0008519 | 3 | gene\_08259.t1,gene\_09872.t1,gene\_08915.t1 | | ammonium transmembrane transporter activity | molecular\_function |
| GO:0008173 | 5 | gene\_07733.t1,gene\_08295.t1,gene\_10354.t1,gene\_08992.t1,gene\_06596.t1 | | RNA methyltransferase activity | molecular\_function |
| GO:0102389 | 1 | gene\_02943.t1 | | polyprenol reductase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0050262 | 1 | gene\_10020.t1 | | ribosylnicotinamide kinase activity | molecular\_function |
| GO:0030429 | 2 | gene\_00551.t1,gene\_04082.t1 | | kynureninase activity | molecular\_function |
| GO:0017108 | 4 | gene\_07889.t1,gene\_07283.t1,gene\_02787.t1,gene\_10167.t1 | | 5'-flap endonuclease activity | molecular\_function |
| GO:0015105 | 1 | gene\_00293.t1 | | arsenite transmembrane transporter activity | molecular\_function |
| GO:0043047 | 2 | gene\_02492.t1,gene\_06252.t1 | | single-stranded telomeric DNA binding | molecular\_function |
| GO:0003712 | 22 | gene\_09638.t1,gene\_02427.t1,gene\_03418.t1,gene\_09075.t1,gene\_03195.t1,gene\_10396.t1,gene\_08286.t1,gene\_07235.t1,gene\_09400.t1,gene\_01050.t1,gene\_01863.t1,gene\_03455.t1,gene\_10253.t1,gene\_03677.t1,gene\_10618.t1,gene\_02513.t1,gene\_02542.t1,gene\_06145.t1,gene\_04057.t1,gene\_01449.t1,gene\_00985.t1,gene\_07678.t1 | | transcription coregulator activity | molecular\_function |
| GO:0050151 | 1 | gene\_04772.t1 | | oleate hydratase activity | molecular\_function |
| GO:0000257 | 3 | gene\_02921.t1,gene\_10011.t1,gene\_10580.t1 | | nitrilase activity | molecular\_function |
| GO:0000250 | 1 | gene\_04414.t1 | | lanosterol synthase activity | molecular\_function |
| GO:0030515 | 5 | gene\_03203.t1,gene\_04403.t1,gene\_09012.t1,gene\_03219.t1,gene\_07630.t1 | | snoRNA binding | molecular\_function |
| GO:0060090 | 1 | gene\_02386.t1 | | molecular adaptor activity | molecular\_function |
| GO:0097367 | 4 | gene\_02361.t1,gene\_03848.t1,gene\_08150.t1,gene\_03440.t1 | | carbohydrate derivative binding | molecular\_function |
| GO:0043130 | 15 | gene\_03034.t1,gene\_03881.t1,gene\_03659.t1,gene\_01280.t1,gene\_10130.t1,gene\_03752.t1,gene\_02165.t1,gene\_03667.t1,gene\_09214.t1,gene\_05212.t1,gene\_01975.t1,gene\_07381.t1,gene\_07002.t1,gene\_02853.t1,gene\_06716.t1 | | ubiquitin binding | molecular\_function |
| GO:0043139 | 3 | gene\_00682.t1,gene\_06102.t1,gene\_10008.t1 | | 5'-3' DNA helicase activity | molecular\_function |
| GO:0043138 | 2 | gene\_00982.t1,gene\_03702.t1 | | 3'-5' DNA helicase activity | molecular\_function |
| GO:0030196 | 1 | gene\_02921.t1 | | cyanide hydratase activity | molecular\_function |
| GO:0016817 | 1 | gene\_10494.t1 | | hydrolase activity, acting on acid anhydrides | molecular\_function |
| GO:0048487 | 2 | gene\_01139.t1,gene\_05824.t1 | | beta-tubulin binding | molecular\_function |
| GO:0004832 | 1 | gene\_07409.t1 | | valine-tRNA ligase activity | molecular\_function |
| GO:0004831 | 2 | gene\_07590.t1,gene\_01435.t1 | | tyrosine-tRNA ligase activity | molecular\_function |
| GO:0004830 | 2 | gene\_09717.t1,gene\_07095.t1 | | tryptophan-tRNA ligase activity | molecular\_function |
| GO:0004834 | 1 | gene\_03969.t1 | | tryptophan synthase activity | molecular\_function |
| GO:0030600 | 3 | gene\_05825.t1,gene\_08015.t1,gene\_08910.t1 | | feruloyl esterase activity | molecular\_function |
| GO:0004540 | 5 | gene\_04376.t1,gene\_04707.t1,gene\_10164.t1,gene\_05612.t1,gene\_02354.t1 | | ribonuclease activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | **GO term** | **Category** |
| GO:0004311 | 1 | gene\_07522.t1 | | farnesyltranstransferase activity | molecular\_function |
| GO:0008681 | 1 | gene\_10412.t1 | | 2-octaprenyl-6-methoxyphenol hydroxylase activity | molecular\_function |
| GO:0043864 | 5 | gene\_01286.t1,gene\_01482.t1,gene\_06796.t1,gene\_02075.t1,gene\_02324.t1 | | indoleacetamide hydrolase activity | molecular\_function |
| GO:0008017 | 14 | gene\_05738.t1,gene\_03046.t1,gene\_07366.t1,gene\_03452.t1,gene\_06271.t1,gene\_03094.t1,gene\_01503.t1,gene\_05745.t1,gene\_04724.t1,gene\_10636.t1,gene\_10520.t1,gene\_02766.t1,gene\_00134.t1,gene\_09514.t1 | | microtubule binding | molecular\_function |
| GO:0000034 | 1 | gene\_01718.t1 | | adenine deaminase activity | molecular\_function |
| GO:0000030 | 4 | gene\_05800.t1,gene\_08395.t1,gene\_08160.t1,gene\_08086.t1 | | mannosyltransferase activity | molecular\_function |
| GO:0102092 | 1 | gene\_02352.t1 | | 5-diphosphoinositol pentakisphosphate 3-kinase activity | molecular\_function |
| GO:0004729 | 1 | gene\_03980.t1 | | oxygen-dependent protoporphyrinogen oxidase activity | molecular\_function |
| GO:0004725 | 14 | gene\_02724.t1,gene\_07595.t1,gene\_05656.t1,gene\_00345.t1,gene\_08755.t1,gene\_05850.t1,gene\_07644.t1,gene\_09773.t1,gene\_01231.t1,gene\_03838.t1,gene\_02966.t1,gene\_02992.t1,gene\_02402.t1,gene\_02930.t1 | | protein tyrosine phosphatase activity | molecular\_function |
| GO:0004722 | 7 | gene\_02460.t1,gene\_02038.t1,gene\_05218.t1,gene\_06098.t1,gene\_05217.t1,gene\_02713.t1,gene\_08599.t1 | | protein serine/threonine phosphatase activity | molecular\_function |
| GO:0004721 | 2 | gene\_01885.t1,gene\_09051.t1 | | phosphoprotein phosphatase activity | molecular\_function |
| GO:0102704 | 1 | gene\_05746.t1 | | GDP-Man:Man2GlcNAc2-PP-dolichol alpha-1,6-mannosyltransferase activity | molecular\_function |
| GO:0047293 | 1 | gene\_09298.t1 | | 4-hydroxybenzoate nonaprenyltransferase activity | molecular\_function |
| GO:0004055 | 1 | gene\_03625.t1 | | argininosuccinate synthase activity | molecular\_function |
| GO:0004057 | 1 | gene\_03953.t1 | | arginyltransferase activity | molecular\_function |
| GO:0004056 | 1 | gene\_07135.t1 | | argininosuccinate lyase activity | molecular\_function |
| GO:0004053 | 1 | gene\_05706.t1 | | arginase activity | molecular\_function |
| GO:0008703 | 2 | gene\_01228.t1,gene\_00125.t1 | | 5-amino-6-(5-phosphoribosylamino)uracil reductase activity | molecular\_function |
| GO:0001664 | 2 | gene\_03006.t1,gene\_08745.t1 | | G protein-coupled receptor binding | molecular\_function |
| GO:0004612 | 1 | gene\_03779.t1 | | phosphoenolpyruvate carboxykinase (ATP) activity | molecular\_function |
| GO:0004610 | 1 | gene\_02481.t1 | | phosphoacetylglucosamine mutase activity | molecular\_function |
| GO:0004617 | 1 | gene\_09272.t1 | | phosphoglycerate dehydrogenase activity | molecular\_function |
| GO:0004616 | 2 | gene\_03823.t1,gene\_03675.t1 | | phosphogluconate dehydrogenase (decarboxylating) activity | molecular\_function |
| GO:0004615 | 1 | gene\_02395.t1 | | phosphomannomutase activity | molecular\_function |

**Table S3 Detailed Gene Ontology (GO) classification of protein families in the genome of *P. paneum* OM1 (*Continued*)**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **GO ID** | **Seq Num** | | **Seq List** | | **GO term** | | **Category** | |
| GO:0004619 | 1 | gene\_03194.t1 | | | phosphoglycerate mutase activity | | molecular\_function | |
| GO:0004618 | 1 | gene\_05462.t1 | | | phosphoglycerate kinase activity | | molecular\_function | |
| GO:0003934 | 1 | gene\_07926.t1 | | | GTP cyclohydrolase I activity | | molecular\_function | |
| GO:0050483 | 1 | gene\_03413.t1 | | | IMP 5'-nucleotidase activity | | molecular\_function | |
| GO:0052689 | 2 | gene\_01102.t1,gene\_04252.t1 | | | carboxylic ester hydrolase activity | | molecular\_function | |
| GO:0008686 | 1 | gene\_10466.t1 | | | 3,4-dihydroxy-2-butanone-4-phosphate synthase activity | | molecular\_function | |
| GO:0045290 | 1 | gene\_06035.t1 | | | D-arabinose 1-dehydrogenase [NAD(P)+] activity | | molecular\_function | |
| GO:0015204 | 4 | gene\_00567.t1,gene\_01654.t1,gene\_02191.t1,gene\_03361.t1 | | | urea transmembrane transporter activity | | molecular\_function | |
| GO:0016428 | 1 | gene\_02187.t1 | | | tRNA (cytosine-5-)-methyltransferase activity | | molecular\_function | |
| GO:0000822 | 1 | gene\_07129.t1 | | | inositol hexakisphosphate binding | | molecular\_function | |
| GO:0000827 | 1 | gene\_02352.t1 | | | inositol-1,3,4,5,6-pentakisphosphate kinase activity | | molecular\_function | |
| GO:0008521 | 1 | gene\_06910.t1 | | | acetyl-CoA transmembrane transporter activity | | molecular\_function | |
| GO:0000829 | 1 | gene\_02352.t1 | | | inositol heptakisphosphate kinase activity | | molecular\_function | |
| GO:0008526 | 1 | gene\_08170.t1 | | | phosphatidylinositol transfer activity | | molecular\_function | |
| GO:0003838 | 1 | gene\_03309.t1 | | | sterol 24-C-methyltransferase activity | | molecular\_function | |
| GO:0000215 | 1 | gene\_02570.t1 | | | tRNA 2'-phosphotransferase activity | | molecular\_function | |
| GO:0016429 | 2 | gene\_10437.t1,gene\_04420.t1 | | | tRNA (adenine-N1-)-methyltransferase activity | | molecular\_function | |
| GO:1904047 | 1 | gene\_02854.t1 | | | S-adenosyl-L-methionine binding | | molecular\_function | |
| GO:0052665 | 1 | gene\_00871.t1 | | | tRNA (uracil-2'-O-)-methyltransferase activity | | molecular\_function | |
| GO:0000700 | 1 | gene\_10562.t1 | | | mismatch base pair DNA N-glycosylase activity | | molecular\_function | |
| Total  GO ID: 2566 | Total  Seq Num: 18804 | | |  | | Successfully annotated 7098 protein sequences  in the GO database | |  |