

Supplementary Table S1. Best protein hits when using *Amoeboaphelidium protococcarum* KAI3631655.1 as a query. BLASTP search on NCBI protein database.

| Protein | Species | Max Score | Total Score | Query Cover | E value | Per. Ident | Length | Accession |
|--|--------------------------------|-----------|-------------|-------------|---------|------------|--------|----------------|
| hypothetical protein MIR68_010128 | Amoeboaphelidium protococcarum | 354 | 354 | 100% | 1e-122 | 100.00% | 190 | KAI3631655.1 |
| hypothetical protein MP228_004238 | Amoeboaphelidium protococcarum | 346 | 346 | 100% | 2e-119 | 96.84% | 190 | KAI3650757.1 |
| hypothetical protein MP228_003631 | Amoeboaphelidium protococcarum | 343 | 343 | 100% | 4e-118 | 96.32% | 190 | KAI3652328.1 |
| hypothetical protein MIR68_002315 | Amoeboaphelidium protococcarum | 340 | 340 | 100% | 6e-117 | 96.32% | 190 | KAI3639621.1 |
| hypothetical protein CXG81DRAFT_17821 | Caulochytrium protostelioides | 130 | 130 | 85% | 7e-33 | 43.43% | 319 | RKP02545.1 |
| PREDICTED: tubulin polymerization-promoting protein family member 2 | Sorex araneus | 128 | 128 | 87% | 2e-33 | 44.44% | 171 | XP_004609762.1 |
| tubulin polymerization-promoting protein family member 2 | Suncus etruscus | 125 | 125 | 86% | 2e-32 | 43.20% | 171 | XP_049624639.1 |
| tubulin polymerization-promoting protein family member 2 | Jaculus jaculus | 124 | 124 | 82% | 3e-32 | 45.34% | 170 | XP_004672419.1 |
| p25-alpha-domain-containing protein | Obelidium mucronatum | 124 | 124 | 81% | 3e-31 | 42.42% | 238 | KAI9342285.1 |
| p25-alpha-domain-containing protein | Polychytrium aggrega | 121 | 121 | 84% | 1e-30 | 42.70% | 327 | KAI9199861.1 |
| TPPP2 protein | Amazona guildingii | 120 | 120 | 73% | 1e-30 | 46.53% | 173 | NXK77861.1 |
| Tubulin polymerization-promoting protein family member 2 | Colius striatus | 120 | 120 | 83% | 2e-30 | 44.17% | 170 | KFP31923.1 |
| PREDICTED: tubulin polymerization-promoting protein family member 2-like | Colius striatus | 120 | 120 | 83% | 2e-30 | 44.17% | 168 | XP_010200717.1 |
| tubulin polymerization-promoting protein family member 2 | Ochotona princeps | 119 | 119 | 82% | 2e-30 | 43.48% | 169 | XP_004584952.1 |
| tubulin polymerization-promoting protein family member 2 | Acomys russatus | 119 | 119 | 86% | 3e-30 | 42.94% | 170 | XP_050998982.1 |
| tubulin polymerization-promoting protein family member 2 | Mus pahari | 119 | 119 | 82% | 3e-30 | 44.72% | 170 | XP_021059760.1 |
| tubulin polymerization-promoting protein family member 2 | Phodopus roborovskii | 119 | 119 | 82% | 3e-30 | 44.44% | 170 | XP_051032834.1 |
| tubulin polymerization-promoting protein family member 2-like protein | Amazona aestiva | 119 | 119 | 73% | 5e-30 | 46.53% | 168 | KQK78373.1 |
| p25-alpha-domain-containing protein | Chytriomyces cf. hyalinus | 118 | 118 | 82% | 3e-30 | 39.53% | 237 | KAI8842263.1 |
| tubulin polymerization-promoting protein family member 2 isoform X2 | Phocoena sinus | 118 | 118 | 72% | 7e-30 | 46.48% | 171 | XP_032478726.1 |
| tubulin polymerization-promoting protein family member 2 isoform X3 | Delphinapterus leucas | 118 | 118 | 72% | 7e-30 | 45.77% | 165 | XP_030618809.1 |
| tubulin polymerization-promoting protein family member 2 isoform X1 | Myodes glareolus | 118 | 118 | 82% | 8e-30 | 45.06% | 170 | XP_048291596.1 |
| tubulin polymerization-promoting protein family member 2 isoform X3 | Zalophus californianus | 118 | 118 | 85% | 8e-30 | 43.45% | 171 | XP_027426320.1 |
| tubulin polymerization-promoting protein family member 2 isoform X4 [| Delphinapterus leucas | 118 | 118 | 72% | 8e-30 | 45.77% | 164 | XP_030618812.1 |
| tubulin polymerization-promoting protein family member 2 | Neogale vison | 118 | 118 | 85% | 9e-30 | 43.45% | 171 | XP_044086477.1 |
| PREDICTED: tubulin polymerization-promoting protein family member 2 | Condylura cristata | 118 | 118 | 85% | 1e-29 | 42.86% | 171 | XP_004694739.1 |
| tubulin polymerization-promoting protein family member 2 | Eumetopias jubatus | 118 | 118 | 85% | 1e-29 | 43.45% | 171 | XP_027950984.1 |
| tubulin polymerization-promoting protein family member 2 isoform X1 | Phocoena sinus | 118 | 118 | 72% | 1e-29 | 46.48% | 180 | XP_032478725.1 |
| tubulin polymerization-promoting protein family member 2 | Marmota flaviventris | 118 | 118 | 72% | 1e-29 | 46.85% | 169 | XP_027778204.1 |
| tubulin polymerization-promoting protein family member 2 isoform X2 | Ailuropoda melanoleuca | 118 | 118 | 85% | 1e-29 | 43.45% | 171 | XP_011233827.1 |
| tubulin polymerization-promoting protein family member 2 isoform X2 | Delphinapterus leucas | 118 | 118 | 72% | 1e-29 | 45.77% | 180 | XP_030618808.1 |

E-value is the measure of likeliness that sequence similarity is not by random chance. An E-value smaller than 1e-50 includes database matches of very high quality. Blast hits with E-value smaller than 0.01 can still be considered as good hit for homology matches. Yellow and green background indicate *Amoeboaphelidium* and other Fungi species, respectively. All other data applies to animal (vertebrate) species.

Supplementary Table S2.

Best protein hits when using *Paraphelidium tribonemae* TPPP (TRINITY_DN24782_c0_g1_i2|m.37417) as a query. BLASTP search on NCBI protein database.

| Protein | Species | <u>Max Score</u> | <u>Total Score</u> | <u>Query Cover</u> | <u>E value</u> | <u>Per. Ident</u> | <u>Length</u> | <u>Accession</u> |
|---|---------------------------------------|------------------|--------------------|--------------------|----------------|-------------------|---------------|------------------|
| p25-alpha-domain-containing protein | <i>Zopfochytrium polystomum</i> | 201 | 250 | 98% | 3e-60 | 41.96% | 304 | KAI9357369.1 |
| p25-alpha-domain-containing protein | <i>Polychytrium aggregatum</i> | 190 | 247 | 98% | 8e-56 | 40.40% | 327 | XP_052963844.1 |
| hypothetical protein HDV00_008104 | <i>Rhizophlyctis rosea</i> | 188 | 244 | 98% | 4e-55 | 41.08% | 319 | KAJ3031848.1 |
| hypothetical protein CXG81DRAFT_17821 | <i>Caulochytrium protostelioides</i> | 187 | 241 | 98% | 6e-55 | 39.07% | 319 | RKP02545.1 |
| p25-alpha-domain-containing protein | <i>Paraphysoderma sedebokerense</i> | 183 | 183 | 98% | 4e-53 | 39.80% | 330 | KAI9140125.1 |
| hypothetical protein MIR68_002315 | <i>Amoeboaphelidium protococcarum</i> | 168 | 212 | 74% | 4e-52 | 47.15% | 190 | KAI3639621.1 |
| Tubulin polymerization-promoting protein member 3 | <i>Clydaea vesicula</i> | 178 | 178 | 98% | 2e-51 | 38.98% | 314 | KAJ3223392.1 |
| p25-alpha-domain-containing protein | <i>Gaertneriomyces semiglobifer</i> | 176 | 231 | 98% | 2e-50 | 39.73% | 312 | KAI9004733.1 |
| hypothetical protein HDU86_003085 | <i>Geranomyces michiganensis</i> | 175 | 233 | 98% | 2e-50 | 39.72% | 314 | KAJ3158133.1 |
| hypothetical protein MP228_003631 | <i>Amoeboaphelidium protococcarum</i> | 164 | 208 | 74% | 2e-50 | 45.83% | 190 | KAI3652328.1 |
| hypothetical protein HDU96_003259 | <i>Phlyctochytrium bullatum</i> | 175 | 175 | 98% | 3e-50 | 39.86% | 318 | KAJ3113561.1 |
| hypothetical protein MP228_004238 | <i>Amoeboaphelidium protococcarum</i> | 164 | 207 | 74% | 3e-50 | 45.83% | 190 | KAI3650757.1 |
| hypothetical protein HDU85_000879 | <i>Gaertneriomyces sp.</i> | 174 | 229 | 98% | 5e-50 | 38.85% | 301 | KAJ3185965.1 |
| hypothetical protein HDU87_003629 | <i>Geranomyces variabilis</i> | 174 | 231 | 98% | 5e-50 | 39.16% | 314 | KAJ3178317.1 |
| hypothetical protein HK097_002729 | <i>Rhizophlyctis rosea</i> | 174 | 231 | 98% | 7e-50 | 39.07% | 321 | KAJ3039857.1 |
| uncharacterized protein SPPG_08463 | <i>Spizellomyces punctatus</i> | 174 | 228 | 98% | 1e-49 | 39.38% | 315 | XP_016604112.1 |
| hypothetical protein HDU84_006415 | <i>Entophlyctis sp.</i> | 173 | 229 | 98% | 1e-49 | 38.52% | 310 | KAJ3379779.1 |
| hypothetical protein HDU83_002002 | <i>Entophlyctis luteolus</i> | 173 | 228 | 98% | 2e-49 | 38.52% | 310 | KAJ3356088.1 |
| hypothetical protein HDU82_000297 | <i>Entophlyctis luteolus</i> | 173 | 228 | 98% | 2e-49 | 38.52% | 310 | KAJ3199598.1 |
| hypothetical protein HDU84_006465 | <i>Entophlyctis sp.</i> | 172 | 228 | 98% | 5e-49 | 38.54% | 310 | KAJ3379674.1 |
| hypothetical protein MIR68_010128 | <i>Amoeboaphelidium protococcarum</i> | 159 | 203 | 68% | 1e-48 | 48.48% | 190 | KAI3631655.1 |
| hypothetical protein HDU89_005536 | <i>Geranomyces variabilis</i> | 171 | 227 | 98% | 2e-48 | 38.81% | 314 | KAJ3155973.1 |
| hypothetical protein HDU83_004219 | <i>Entophlyctis luteolus</i> | 170 | 226 | 98% | 2e-48 | 38.19% | 310 | KAJ3345323.1 |
| p25-alpha-domain-containing protein | <i>Geranomyces variabilis</i> | 171 | 227 | 98% | 2e-48 | 38.81% | 314 | KAI8589706.1 |
| hypothetical protein SpCBS45565_g07343 | <i>Spizellomyces sp. 'palustris'</i> | 171 | 219 | 98% | 3e-48 | 37.70% | 336 | TPX61118.1 |
| hypothetical protein HKX48_003590 | <i>Thoreauomyces humboldtii</i> | 167 | 225 | 98% | 3e-47 | 39.66% | 314 | KAJ3017344.1 |
| hypothetical protein HK100_002929 | <i>Physocladia obscura</i> | 167 | 221 | 98% | 3e-47 | 36.33% | 312 | KAJ3142486.1 |
| p25-alpha-domain-containing protein | <i>Powellomyces hirtus</i> | 167 | 221 | 98% | 3e-47 | 39.44% | 303 | KAI8908161.1 |
| hypothetical protein PhCBS80983_g03683 | <i>Powellomyces hirtus</i> | 166 | 219 | 98% | 8e-47 | 39.08% | 303 | TPX57673.1 |
| p25-alpha-domain-containing protein | <i>Fimicolochytrium jonesii</i> | 164 | 217 | 98% | 3e-46 | 41.28% | 304 | XP_052926454.1 |
| hypothetical protein HDU98_010151 | <i>Podochytrium sp.</i> | 164 | 217 | 98% | 7e-46 | 35.57% | 328 | KAJ3066530.1 |
| 45 kDa subunit of RNA polymerase II | <i>Entophlyctis luteolus</i> | 170 | 226 | 98% | 2e-45 | 38.19% | 647 | KAJ3209884.1 |
| p25-alpha-domain-containing protein | <i>Gorgonomyces haynaldii</i> | 162 | 215 | 98% | 3e-45 | 38.54% | 311 | KAI8912588.1 |
| p25-alpha-domain-containing protein | <i>Zopfochytrium polystomum</i> | 161 | 161 | 98% | 5e-45 | 38.65% | 287 | KAI9325442.1 |
| uncharacterized protein BATDEDRAFT_89639 | <i>Batrachochytrium dendrobatidis</i> | 160 | 160 | 95% | 1e-44 | 38.03% | 289 | XP_006680205.1 |
| hypothetical protein BDEG_26054 | <i>Batrachochytrium dendrobatidis</i> | 160 | 160 | 95% | 1e-44 | 38.03% | 299 | OAJ42613.1 |

E-value is the measure of likeliness that sequence similarity is not by random chance. An E-value smaller than 1e-50 includes database matches of very high quality. Blast hits with E-value smaller than 0.01 can still be considered as good hit for homology matches. Yellow and green backgrounds indicate Aphelidiomycota and Blastocladiomycota species, respectively. All other data applies to Chytridiomycota species.

Table S3. Accession Numbers of fungal proteins shown in Figure 4.

| Name on Figure 4 | Species | Phylum | NCBI Accession No. |
|------------------|---------------------------------------|--------------------|------------------------------|
| Allomyces | <i>Allomyces macrogynus</i> | Blastocladiomycota | KNE68590 |
| AMOEOAPHELIDIUM | <i>Amoeboaphelidium</i> | Aphelidiomycota | KAI3631655 |
| | <i>protococcarum</i> | | |
| Batrachochytrium | <i>Batrachochytrium dendrobatidis</i> | Chytridiomycota | XP_006680205 |
| CHYTRIOMYCES0 | <i>Chytriomyces confervae</i> | Chytridiomycota | TPX78276 |
| Chytriomyces1 | <i>Chytriomyces confervae</i> 1 | Chytridiomycota | TPX65886 |
| Chytriomyces2 | <i>Chytriomyces confervae</i> 2 | Chytridiomycota | TPX72533 |
| Caulochytrium | <i>Caulochytrium protostelioides</i> | Chytridiomycota | RKP02545 |
| GORGONOMYCES0 | <i>Gorgonomycetes haynaldii</i> | Chytridiomycota | KAI8912823 |
| Gorgonomycetes1 | <i>Gorgonomycetes haynaldii</i> | Chytridiomycota | KAI8912588 |
| OBELDIUM0 | <i>Obelidium mucronatum</i> | Chytridiomycota | KAI9342551 |
| Obelidium1 | <i>Obelidium mucronatum</i> | Chytridiomycota | KAI9351240 |
| Obelidium2 | <i>Obelidium mucronatum</i> | Chytridiomycota | KAI9342285 |
| Olpidium | <i>Olpidium bornovanus</i> | Olpidiomycota | KAG5460860+ |
| | | | KAG5458366 |
| Paraphelidium | <i>Paraphelidium tribonemae</i> | Aphelidiomycota | TRINITY_DN24782 ¹ |
| Paraphysoderma | <i>Paraphysoderma sedebokerense</i> | Blastocladiomycota | KAI9140125 |
| Powellomyces | <i>Powellomyces hirtus</i> | Chytridiomycota | TPX57673 |
| Rhizoclosmatium1 | <i>Rhizoclosmatium globosum</i> | Chytridiomycota | KAJ3297182 |
| Rhizoclosmatium2 | <i>Rhizoclosmatium globosum</i> | Chytridiomycota | ORY45507 |
| Spizellomyces | <i>Spizellomyces punctatus</i> | Chytridiomycota | XP_016604112 |
| MONOSIGA | <i>Monosiga brevicollis</i> | Choanoflagellata | XP_001743131 |
| AMPHIMEDON | <i>Amphimedon queenslandica</i> | Porifera (sponges) | XP_003384590 |
| CAENORHABDITIS | <i>Caenorhabditis elegans</i> | Nematode | NP_491219 |
| DROSOPHILA | <i>Drosophila melanogaster</i> | Arthropoda | NP_648881 |
| HOMO | <i>Homo sapiens</i> | Chordata | NP_776245 |
| Tetrahymena | <i>Tetrahymena</i> | Ciliophora | XP_001023601 |

¹Taken from https://figshare.com/articles/dataset/Commun_Biol_aphelid_datasets/7339469/1