

Data S1

A

Rhizaria_Ammoniaseq_71ATG7
Rhizaria_Globobuliminalseq_74ATG7
Rhizaria_Eucyrtidiumseq_73ATG7
Rhizaria_Bigelowiellalseq_72ATG7
Rhizaria_Paulinellalseq_76ATG7
Rhizaria_Paulinellalseq_75ATG7
Alveolata_Toxoplasma[CEJ.74723.1]ATG7
Alveolata_Plasmodium[ETW30632.1]ATG7
Alveolata_Vitellina[CEJ.92350.1]ATG7
Alveolata_Chromera[A0A0G4F387]ATG7
Alveolata_Oxyrhiza[A0A673QY57]ATG7
Alveolata_Karenia[A0A674UE81]ATG7
Alveolata_Tetrahymenalseq_01ATG7
Stramenopiles_Phytophthora[seq_79]ATG7
Stramenopiles_Peronosporalseq_78ATG7
Stramenopiles_Aureococcus[A0A6S9EG39]ATG7
Stramenopiles_Aurantiochytrium[seq_77]ATG7
Telonemia_SRR7371266[seq_80]ATG7
Telonemia_SRR7371266[seq_81]ATG7
Centrohelidia_Raineriochytriseq_17ATG7
Centrohelidia_Raphidophryse[seq_18]ATG7
Centrohelidia_Choanocystis[seq_15]ATG7
Centrohelidia_Choanocystis[seq_16]ATG7
Centrohelidia_Acanthocystis[seq_13]ATG7
Centrohelidia_Acanthocystis[seq_14]ATG7
Haptophyta_Calcidiscalseq_45ATG7
Haptophyta_Scyphosphaera[seq_49]ATG7
Haptophyta_Scyphosphaera[seq_48]ATG7
Haptophyta_Isochrysis[A0A670R228]ATG7
Haptophyta_Emiliana[XP_005789984.1]ATG7
Haptophyta_Pymnesium[A0A6S9VW10]ATG7
Haptophyta_Pavloval[seq_46]ATG7
Cryptista_Guillardia[XP_005834743.1]ATG7
Cryptista_Rhodomonadalseq_29ATG7
Cryptista_Goniomonas[A0A672DUH3]ATG7
Cryptista_Palpitomonas[seq_28]ATG7
Glaucophyta_Gloeocharaeata[A0A671G744]ATG7
Glaucophyta_Gloeocharaeata[A0A670VLP9]ATG7
Chlorophyta_Ostreococcus[seq_27]ATG7
Chlorophyta_Micromonas[seq_26]ATG7
Chlorophyta_Lobosphaera[seq_23]ATG7
Chlorophyta_Lobosphaera[seq_24]ATG7
Chlorophyta_Lobosphaera[seq_21]ATG7
Chlorophyta_Lobosphaera[seq_24]ATG7
Chlorophyta_Lobosphaera[seq_20]ATG7
Chlorophyta_Chlamydomonas[XP_001703365.1]ATG7
Chlorophyta_Chlamydomonas[PNNW84948.1]ATG7
Chlorophyta_Arabidopsis[seq_19]ATG7
Chlorophyta_Oryza[XP_015615773.1]ATG7
Sisirophyta_Marchantia[seq_25]ATG7
Chlorophyta_Marchantia[A0A631696.1]ATG7
Ancoracysta_Ancoracysta[seq_31]ATG7
Hemimastigophora_Spironemal[seq_50]ATG7
Ancyromonadida_Nutomonas[seq_41]ATG7
Malawimonadida_Malawimonas[seq_65]ATG7
Metamonada_Trichomonas[OH596604.1]ATG7
Metamonada_Trichomonas[DS113646-3-36765-38645]ATG7
Metamonada_Monoceromonoides[seq_66]ATG7
Discoba_Rhyacozoa[seq_31]ATG7
Discoba_Diplomonad[seq_31]ATG7
Discoba_Trypanosoma[T9297_10_v5.1-6-2739506-2737149]ATG7
Discoba_Euglenal[seq_32]ATG7
Discoba_Naegleriaseq_33ATG7
Discoba_Percomonas[A0A6U1FMM3]ATG7
Discoba_Andalucia[seq_30]ATG7
Breviata_Pygus[seq_61]ATG7
Breviata_Pygus[seq_61]ATG7
Breviata_Pygus[seq_61]ATG7
Breviata_Pygus[seq_61]ATG7
Fungi_Saccharomycetes[ED721648.1]ATG7
Fungi_Komagatellalseq_42ATG7
Fungi_Schizosaccharomycetes[seq_44]ATG7
Fungi_Claridoeomul[seq_37]ATG7
Fungi_Claridoeomul[seq_38]ATG7
Fungi_Gigasporal[seq_40]ATG7
Fungi_Catenariaseq_36ATG7
Fungi_Catenaria[QR240662.1]ATG7
Fungi_Pirromycetalseq_43ATG7
Fungi_Gonapodyal[seq_41]ATG7
Fungi_Batrachochytrium[seq_35]ATG7
Fungi_Batrachochytrium[QAJ39464.1]ATG7
Fungi_Fonticulalseq_39ATG7
Metazoa_Homo[Q95352]ATG7
Metazoa_Xenopus[KA661279.1]ATG7
Metazoa_Danio[A0A0ZKPR3]ATG7
Metazoa_Drosophilalseq_70ATG7
Metazoa_Daphnia[EFX82614.1]ATG7
Metazoa_Caenorhabditis[seq_67]ATG7
Metazoa_Dicymal[seq_69]ATG7
Metazoa_Corticium[seq_68]ATG7
Holozoa_Helgocael[seq_58]ATG7
Holozoa_Stephanocael[seq_64]ATG7
Holozoa_Salpiginet[seq_62]ATG7
Holozoa_Capsasporal[KEJ9298.1]ATG7
Holozoa_Ichthyophon[seq_59]ATG7
Holozoa_Ichthyophon[seq_60]ATG7
Holozoa_Ichthyophon[seq_61]ATG7
Holozoa_Creolimax[seq_54]ATG7
Holozoa_Creolimax[seq_56]ATG7
Holozoa_Creolimax[seq_57]ATG7
Holozoa_Creolimax[seq_52]ATG7
Holozoa_Creolimax[seq_55]ATG7
Holozoa_Creolimax[seq_53]ATG7
Holozoa_Sphaerostecum[seq_63]ATG7
Holozoa_Coralochytrium[seq_51]ATG7
Amoebozoa_Entamoeba[DS571196-6-71419-69677]ATG7
Amoebozoa_Dictyostelium[seq_11]ATG7
Amoebozoa_Vermamoeba[seq_2]ATG7
Amoebozoa_Acanthamoeba[XP_004349643.1]ATG7
CruMts_Mantamonas[seq_10]ATG7
CruMts_Mantamonas[seq_55]ATG7
CruMts_Mantamonas[seq_9]ATG7
CruMts_Rigifal[seq_12]ATG7

1 DDLLKFDALLSNTDSTFWOELGRKLNELKLSSEEAIPFIFFTFTGGIAATLPPTVFNNDSENLSTELRPOYHFOGPCELLNTIKITETFKKLDKKQLREHAMRIVADNOSGAELSNPALLLYRF 122
1 EVVLLKEDKLLSSSDSTFWOELGHHKIDDEFKLSSEDAIPFIFFTFTGGISVTLTPPKIFFNHNEEDLDTSLKFFHKYGPCELLNTIKITSEKEMOKQKLLHNHSMKLVDDILNQNYISNALLLYRF 122
1 -----MG-----V 3
1 CSPSLKFCPLSSAVDVSFWTOLSKKLNELKLNSSALSISAFTTTHSHSTVPLARLOVSSASLDDSPDFGPEFAVAIGOLHNOITLDFKNLDPGLAAEAANKIWHISILSGAALKNPBELLTDF 122
1 RRVLKFCPTLSDISFWOKLEEKLRERWLOTWVLAVSRREKAVSSLSALRLDRTAFD-S-SCFTGDVPLGLFLYKNSLEOFKAROISOVLQAASAFITASPSSEELHAPSEMSYSF 121
1 SYVLKHNNEFKIDISFWOKLEEKLRERWLOTWVLAVSRREKAVSSLSALRLDRTAFD-S-SCFTGDVPLGLFLYKNSLEOFKAROISOVLQAASAFITASPSSEELHAPSEMSYSF 122
1 ARLKHSFPRVVVDISFWOELAAQODRMKLTTRFPIVAPHSASRTSGLRLTRSSFT-HTSSSLHHEWRTGLINVTLEEFKRSFKQLLDTVAALANSGAEBAESDDRAAL 121
1 QQAVHFAFNVSDISFWOELSHRLDVLKISTTIEIVTGVFIAGADKTPGVRDLRLSELKTSKDEKVLVYGRVINFUTLDFKKFRLGAAGQVAAEEVAAEAESVSRBTALTRF 122
1 GEHLFEFGVQSEVGVEFWORVQKNLEHORDVSRKLLWVFSSSSDQKVGAAVRFTDRSFE---DTCGCGCFHCPFWLVNITIEFAAFDQKGMVEKCLDAWAKAVASKEFMODPALLRLV 118
1 SAPLRFTLSLSPADVFVWELTROLDIQRLDSSRLQOQAYFVAPKADVAEKFLRLREAFDLSCKFEAGSTRLRGKLNFIIMEEFKDSRAERSEVARSRLNDIVSGAALSDPELLRRF 122
1 DKKFEIIPFSRMDIIGFVSLTAKKLEEWKLNSDAQIDIVKFKISNFTSKKAFNLVDVYSFOQELGQFVEIVIQTLKKNYNTIEEFKQHFYKDLTKQ-----OISADNLFCKDEAFIMK 117
1 AQVLFKOPVNSAPDVSFWOTLTKLQVWLNDDQCGIIGYFTGRSNNVVARFTTIDESAFAAGQARREYEWAPGQLYNTITLFAFKKLDKSKLLRDAQRLDLDIL-NEEDTSIDHNSF 121
1 AQVLFKOPVNSAPDVSFWOTLTKLQVWLNDDQCGIIGYFTGRSNNVVARFTTIDESAFAAGQARREYEWAPGQLYNTITLFAFKKLDKSKLLRDAQRLDLDIL-NEEDTSIDHNSF 121
1 FETLRFAFSSARKVAFVQAVDARLDRMDVDRGARAIDGAWPGSSSGGARELASSVGGAGGEGALAAPGRLLTVNITVEAFRSDMKALLRDAADALADAMSGAMERFEVLGAG 122
1 TSEVFEAFRSMVQGLVGVFSKALEQIMLSEAFVNLNVAWGLGAAIGALIRVLTGDDLLWSTSEDFNANFRATALLNITVAFKRLKKLLRDAADALADAMSGAMERFEVLGAG 122
1 -----MTALKSHOFPQVLSYAL-----DFVTFBSHNDKVSVPSSFDAD-----V 46
1 -----QLAHKLLHQYKLDTOAVALSEFFQCGNT-----RVALMDASDEDSVPPANRRISGSLIMMLTADFGSGDFQKLSSEDAQVQVWDAIRSGAALDDPELLRFR 98
1 KELVKFCPTSTVDSAFWTLTKLTHQFKLDESERQIRARTTTTTSVPSRLCDHNAVDVDAGGIRFDVHGTIKLYNTIAFKNNKKLIFKLHAQKMDKCKGLSDHPHVMCRF 122
1 --MLQFOPFVTTIDVSFWORLSEKKIKELKLSAALRIQGHFTCGLGQPPSRCLVEGAADFVDELQASKRHYVDGTLIHTITLLEEFKALDKRDIMQSGTMLWDAIRSGEAFSNPQLCRF 120
1 --MLKFCPLVSSLELFWITELTRRVEVFMRLTDRVLTGFLLLPGCGGVENKFLGLDAFKDHVGRSHCARAPGQGLVNTIAEVEGLDKAALLKAAAEALHEAVRSGAAMTDPSLLG 118
1 -----
1 -----ALQ----- 3
1 EATLRFRPLCGALDVSFLTELARRLHEFRLSDEPVEIRSSFLRASHQVAAPLCVGADAFSSGVEVPPTVCVVPGTLVNIANTLEDFKDWKQALLRTARTIWEVDHSGRALVEHRLSRF 94
1 ADTLRFLPLSSAIDVSFLTELARRLHEFRLSDEPVEIRGTABSNHHEVASPLCVSADAFSSGVEVPPSLCVVPGTLVNIANTLEDFKDWKQALLRTARTIWEVDHSGRALVEHRLSRF 122
1 DVLKFCPTTAAIDVFLTELARRLHEFRLSDEPVEIRHSSYARAERHEIRPFCVGADAFSSGVEVPPTMCVVPGTLVNIANTLEDFKDWKQALLRTARTIWEVDHSGRALVEHRLSRF 122
1 -----
1 --MLRIRPPASSLSDASFLSRLIASLHLHLRLSLRLPFTAFCLRHVQSSGOERLVAAADALDLDASAKRAVLITGEVITFMTIESFKELDKKQFLHNIATEMGROITGEEVENPSLVRG 120
1 -----
1 QEPLRYCLTFTSIEAARWKAFFSEKISRLKLSSEEDV-----RFLCDRASFDRES-LQAQAVGLGCEHLVDSIDDFKALDKKALLDQARRLOEKISSEKAEKDACLSV 69
1 --KIAFO-----WRREGDMVAFVKKKGE-----DIGASLFLQKSNR-VGVSIKSHDVEGVIRNFSIDSFKSADKAGALQEEGKLRQYIASGEWVENARKLV 109
1 --MOFVPIISFVDSFWTDLAKKLEEKYLNERRKLAGFYAVGSSREVAGRLCVKSSLDADVAPPAFNIITPGSLLNFTITIEFKADKNDILOOTAAQEIWNVLSGRAEANTSLNRF 119
1 ARALAFAPASADGGFWARWAKMSSETMLRESSI-----SCACRVRAEISGAALDHESDGLNADGGGWWARGDARLLNRREGVITTFDREAFLREIGELIRDIESGAERDPSRLMR 118
1 DVLKFCPTVQSAVDITFWAELARRLNDKGLREDVPIIDGLFACSMHAEVSSVALDKRSFETWTSLATQOARPGTLRRVNTFERFKVEYRQAMLDSEADAWRAVVSQDAARDPHLNOF 122
1 MVLQFCPTVQSAVDITFWAELARRLNDKGLREDVPIIDGLFACSMHAEVSSVALDKRSFETWTSLATQOARPGTLRRVNTFERFKVEYRQAMLDSEADAWRAVVSQDAARDPHLNOF 121
1 -----
1 -----RHGLPDA 7
1 -----
1 -----GTA----- 3
1 SDLCNAALQSVLDSFLAELTDLNLVLKLSSEEVVVGVYFSFNRYDSVPLRLTLDVSSLTAAASSRLDCHAAPGRVLVNTIEGFRSADKALMRRVAAEWIADISGAASEPRLTRF 121
1 MGVIKFAQLQSVLDSFLAELTDLNLVLKLSSEEVVVGVYFSFNRYDSVPLRLTLDVSSLTAAASSRLDCHAAPGRVLVNTIEGFRSADKALMRRVAAEWIADISGAASEPRLTRF 122
1 AIILOAFQSNSSVDEBFWHSSSLLDKLQDDSPISITBFGYPCGCGOVSNHLLTISESLDQECGNRNKCPVPGILNITVIESFNKLDKSLKAEANKIWDISGKALEDPVSLTRF 122
1 BFLMCAAAICVCAETBFDALRRLDLVLQDDSPISITBFGYPCGCGOVSNHLLTISESLDQECGNRNKCPVPGILNITVIESFNKLDKSLKAEANKIWDISGKALEDPVSLTRF 122
1 SSTRLMFAQVQSAVDITFWAELARRLNDKGLREDVPIIDGLFACSMHAEVSSVALDKRSFETWTSLATQOARPGTLRRVNTFERFKVEYRQAMLDSEADAWRAVVSQDAARDPHLNOF 122
1 SSTLMFAQVQSAVDITFWAELARRLNDKGLREDVPIIDGLFACSMHAEVSSVALDKRSFETWTSLATQOARPGTLRRVNTFERFKVEYRQAMLDSEADAWRAVVSQDAARDPHLNOF 122
1 CACVQAPTESAVEVTRWHELAKRLLEVMDLETDVVDHGTFTQITTSSETVRPSVLVHQADDAATLGLSKAPVTRGWMVNTVEEFKKVDKTLAQEQAAQLQAQCHDARN-LVLNKF 120
1 KHELFKVPVSTIHSDFVLELERRIDLEYKLDNRDIAQGLVLSNNGOIPPLRLNRFSTFDOMLARSELPMWHTGLTCOPSLDAFKQADKNAALRESGKIWDAIRSGALDPSLLNRF 122
1 GEVVKFVPVQSAVDITFWAELARRLNDKGLREDVPIIDGLFACSMHAEVSSVALDKRSFETWTSLATQOARPGTLRRVNTFERFKVEYRQAMLDSEADAWRAVVSQDAARDPHLNOF 117
1 MDMRFPQTQSSVPELWELADRRDQDFMLSDAPITGLSCNTQIGIPPSLIAPGSAPFS-SERFNINMFAPVGAHHKQITMEGFKQADKSSLEECAKIMWDIRSGAVERDAPLQRF 119
1 --MATFQOASIIAIEPSFHWALSKOKLNDMLDERPESFVAYQFCQGRSGISSFLFNEESESQTOQYLNATYKALITGLTLVTKNNFSLDRAGILKSLSDSIFQAEITRSWLEQSSLLK 120
1 --MSFONISSLIESFWALNKLNDKMLDETFRDIIISYQFAGRSAGVKAFAPINEDSPKKEFLNVLGTFTFIPTYLNTIKSPFKKLRDKNLSKAEINKNINSEWNNPISLLK 119
1 SKDLKFCPTSSPILFWKVLSEKLDVLKSDDAVIGVFCSCGTEERASHFLFDENAFEGASKREHHYAVPGLSILNITWDAKLLNFKQGLLEDAKGLIKLAKLELHELEHSELR 121
1 CMARFEKSHAKVEFWFKHMSKLELTKLSDDAVIGVFCSCGTEERASHFLFDENAFEGASKREHHYAVPGLSILNITWDAKLLNFKQGLLEDAKGLIKLAKLELHELEHSELR 122
1 NTNADQEKSIITKCYFMSLSLDDKWLKDAEISAILVMSLSLDDKSLSEKQVPSIYEAVIPGTUKCHNITETAEAVDRKSILHSECDKLDQIRSEFLKNQONLH 122
1 MERLKLMDRFRIISFWYELKRLHEWLESEPIIVWFSYRSLVSSLSASRNVTNRLRLD-ETSLRCVHTLHOGIFONTAKQYOLPRRSALWDILKKCKNREESSAEELAVNFSI 121
1 STLLOFELACRVEFWFELEKRLHKEYGVDFEIVGVSAGHGVSSPVAVAEEGAAPD-ATGVFGRIGOLLTNTLEELKRSQGLIAAAGAEWAAQEGAWLORGLNRF 122
1 -----YHANTIEEFNNYDKKSLRNVGLIEYNKIVNQGWLKNPNEITHF 44
1 KMKIKKAKIRLLDQEWTFATQKEITHKKLDLDTIKTYGTIAAGNEMNRVQOTRIGESLRERKIGRDMGSIAGKYKKNQKEEFAIKIKDFVRE-----FEKVFDDSEQEIISILNOF 118
1 KRNVLVFPKPIVDVQVFWLEHRRKLEEWKLDERRPSSASFATSSYSSFSVPFNKESDV-----STQDPRMKGTLLINIVGSDHAKRKSILAE-----EWSHIFSDKTRMFLV 114
1 -----MDVCSFAPKQOL-----SPHIEDGLLALVDYSSFAFLGQPSRWVWFSEFRAADKVAK-----GLDL 64
1 -----
1 -----EARS----- 4
1 MNTLOELPLSSSGVGVFVSLVGGKLEEWKNDVAFQSLQGYTYSVPS-----LSSKFFDELADEFKFS-STFKVKVPGKILIFNLDFKAFNKKKDLHTLQKISASVESEGLDPELLR 119
1 ERLVNLAPFKSFLDSTFFQELSRLLDLNVLKLDSTQVNLDLHNIKASQADVPLFNTRSFENNKNRINEVPLQSGIFRVLDFEKNLQKQLFHORALEOVEDGIKINKCVS-----F 117
1 SMDIPYSQISFVSSNDSFQKLLDNKLYRLDDTDKAIQVDFDKIVG-NORTSLVDSESHNNINTYTHAQFVKGILIKKLLVDFFRKVDVQFLQSGKLVQDQKLSKLT 121
1 GKALOFQSHSSIDATFWHOLSNYVEKOKLDAHLITHKFNTRYR-----GNISIVFGEABSN-SNIDKDLAETGLLNATPOEFTNVKREEGEV-----LNSIKGVSVSRNLLRF 112
1 SBLVOVAFSSAVEATFTSTRKLDLYKDDTSHLDLYFTGHTIISMRAPCLNSGADDDATLPPFSYPSIGKIKNTITVDFKALDKTALFEITEQIWDIKSGEAVKNVYLLTRF 122
1 SNLVOFVSSAVEATFWHTLSTRKLDLYKDDTPOSILBYSVYSYLITMPLRYLIGTAFOATLPPFISYSGAKNTITIEFKNLDKNAFPRETAEGWKDILISGAARKDPVYLTRF 122
1 --MDPFCOSVSGVFWHLKATLETLKLDSDAPICARAIITQSIALBASISLSBTLDFTFAPRISTVYPTKNTITIEFKNLDKNAFPRETAEGWKDILISGAARKDPVYLTRF 119
1 RRALVLAQSHHOARNAQARRLAHLFTTHARRHHPAIRVAFDLGNS-RTARLVAALHLARAHAPRISTVYPTKNTITIEFKNLDKNAFPRETAEGWKDILISGAARKDPVYLTRF 122
1 KTVLVOFSSLSVDEFTWYSLTGNEIKIKSDVLTGIEYYSYNSIKVPSLNDVNSLTNEI-IPSFSPKGLKNTITIEFKNLDKNAFPRETAEGWKDILISGAARKDPVYLTRF 120
1 MSPLOFQSFQTCVASTFWHLRDLDAFRLDDQKRIWASYSLSHTNSPFIISLGYEATDLAVFSSAIPVPGITINTLDEFKSLDKROALADAQGLWDDISGAALACDPLLRF 122
1 SKILOVFPQSAVDITFWHTLSGNINLYKLDASVIGQFYSSGADALSRLCVSSTSFSKIQRPDSRSCIPVGLVKNITITIEFKSVQKNSLKTYSVLEIWDILSAAVADPLTLNK 122
1 DKLLFAPFVRIRIEHGFWDALVKNHDAVARLSDAPITAFYSPLHRASVELDLMVFNHESLSTSSRGASVACRGTLVYVLFSPQNADRNALIKAEAAELWADIVASGKPGATVAQR 122
1 LSKLOFAPSSALDVBFWHELTKQKLENYRDEAPKIKBYYNNDQSAELPRLTLEFSAFDMAPTARCCPAGITLYNTITIEFSKTAADKLLLEQAANEIWESGKSTALENVLNKF 122
1 DAKLOFPTLSALDVBFWHELTKQKLENYRDEAPKIKBYYNNDQSAELPRLTLEFSAFDMAPTARCCPAGITLYNTITIEFSKTAADKLLLEQAANEIWESGKSTALENVLNKF 122
1 SKILOFAPSSALDVBFWHELTKQKLENYRDEAPKIKBYYNNDQSAELPRLTLEFSAFDMAPTARCCPAGITLYNTITIEFSKTAADKLLLEQAANEIWESGKSTALENVLNKF 122
1 EIILOFAPVSSVSTFWHLKLAELDHDRLSDSKRSITHTYTNRNA-SCQLLEVDTYANRMKPKFHSIAISTYIKNTIEFKALDKQLLDAKELLDADMCGGALRDPSSLTRF 120
1 EKILQFLPSSVLSFSSFWHLKLTQMDVYALNDVEITHTYTNQNSISRLAEALNDYSSFENRQVGTNIGICOLLQNTITIEFAKDINKOTAINKCEQWINDILSAAALSNPSSLTRF 122
1 --MATFVPTCLDITFWNEVKNKLNDKMLDETFCISQSLSLHQTEEFKCHLSLYDSLSL-ESTTGLSMGTLTYNTIESFKMDKSLIRSEAKIWESITRKLWNPLRSLRF 118
1 --MKFVPTNTIDTEFWKLSTRLENLRLSEKRVIMGHYSTKIG-ETNNSLIGGESLDEIE-PSFVEVIRGELIYMKSNKSFRE-AQKIVEEKSOFTWTLDPQLFERPQIMOF 115
1 -----IESVSGRAVNDPSLLVDF 18
1 -----MEFKSAVINAAVQT-----IVASITSGALKDSSLLVKF 35
1 -----
1 -----FTITQT----- 7
1 AKLMOFPTSSADASFWHTLQKLESEFKLDESALHEWMAKSSGLDFVARLSLTATAFQPLDSQOONAAIRGVLHNANSNSFKAFEMTSAPRTASALGASIRDSVSKNSYLTDF 122
1 MRLQFAPSSADASFWHTLQKLESEFKLDESALHEWMAKSSGLDFVARLSLTATAFQPLDSQOONAAIRGVLHNANSNSFKAFEMTSAPRTASALGASIRDSVSKNSYLTDF 122
1 -----V----- 2
1 -----
1 -----DG----- 58
1 MSLLFLPLASSAEVAFVYYSROLENIRLSEEL-----LSDAVENVGTGPHLVLDLDFKNIDKQALLLETASKLWDDITSGRALSDPGLNLRV 36
1 ----- 1
1 -----
1 ENILOAFBESAVDAGFWHLTORLDIYKLSDSPOSIHAYYACGEGVPPRCIGSOAFSCYSEVSIRNFVAPGTFLNLTAEFKNLDKKALLEKFSQLQWDRISGAAVSNPSLLSRF 122
1 -----MIRPOFFRALSQLLEVRLDEETEREIFSTVQLGLDPTTLARVRLDNLAEEDKSDPRNVVHGTVLNLTIEFKRLNAQITIDSGAVLWDDLLKQWDDPSRLGRF 111
1 TMTLOKFLDLQIDVTFWHEFTKRLLEVFLSEKAIPIYS-----EASGNIILRTHAFSE-----ROESCELELLNYLTISFKESKALKIYTE-----FSERCKLNEENSIWAK 104
1 INTAKKESSFNIVITKYEFSNKLDELKLSSEISILNGHYTFSSQSDGLFLCFLFNARLNNVPLPRSYLSHGLYVNLVWDDQKSPKIKLENDASKRIVNNNDIKDSTLSLRF 122
1 -----
1 GQLLOFEGVESRSSSSSPRPRVLAHYPIGHHQO-----TTTTTAARVLPRLLEASADAPPHTRKYHFVPGCELLNTITIEFAHALDKKQOLDVAAKWTDIESGEALREPRRLCRF 118
1 KSNLOFEPVLSQVGTWHELSRMDELKLDSSIEIFHYGTITTSISAAKLKLDACGEQON-TEAYHYPIGTLVNTITIEGKKFED-SLLKEAGSIWESIVSGDALTTSSLLNRF 119
1 -----
1 ARPLQFQVSSHCDARWHTLADRLINVLRLHGTILRIFSTYFVAHTHSLAPVFDOLSFQNTSASCMFPIGTIHLVDSLEAFKAVDKARLEHDAKPAWEALISGAALENPSLVNI 122

[illegible]

Rhizaria, *Ammoniumia*[seq_71]ATG7
Rhizaria, *Globobulimina*[seq_74]ATG7
Rhizaria, *Eucyrtidium*[seq_73]ATG7
Rhizaria, *Bigelowella*[seq_72]ATG7
Rhizaria, *Paulinella*[seq_76]ATG7
Rhizaria, *Paulinella*[seq_75]ATG7
Alveolata, *Toxoplasma*[CEL74723].1ATG7
Alveolata, *Plasmodium*[CEL74723].1ATG7
Alveolata, *Vitrella*[CEL92350].1ATG7
Alveolata, *Chromera*[AOA004F387].3ATG7
Alveolata, *Oxyrhiza*[OA06V3QY5T].1ATG7
Alveolata, *Karenia*[OA06T4U8BE].1ATG7
Alveolata, *Tetrahymena*[seq_Q1]ATG7
Stramenopiles, *Phytophthora*[seq_79]AT7
Stramenopiles, *Peronospora*[seq_78]AT7
Stramenopiles, *Aureococcus*[OA06S9EG39].ATG7
Stramenopiles, *Phaeodactylum*[seq_77]ATG7
Telonomia, *SRR371266*[seq_80]ATG7
Telonomia, *SRR371266*[seq_81]ATG7
Centrohelida, *Rainieriphyllus*[seq_71]ATG7
Centrohelida, *Raphidocystis*[seq_18]ATG7
Centrohelida, *Choanocystis*[seq_19]ATG7
Centrohelida, *Choanocystis*[seq_18]ATG7
Centrohelida, *Acanthocyrtis*[seq_13]ATG7
Centrohelida, *Acanthocyrtis*[seq_14]ATG7
Haptophyta, *Caldicetus*[seq_48]AT7
Haptophyta, *Scyphosphaera*[seq_49]ATG7
Haptophyta, *Scyphosphaera*[seq_48]ATG7
Haptophyta, *Isocyrtis*[OA06TOR22B].ATG7
Haptophyta, *Isocyrtis*[OA06TOS3V2].ATG7
Haptophyta, *Emiliania*[XP_005789984.1]ATG7
Haptophyta, *Pyrrenomonas*[OA06S9VWL0].ATG7
Haptophyta, *Favosites*[seq_46]ATG7
Cryptista, *Gullardia*[XP_005834743.1]ATG7
Cryptista, *Rhodomonas*[seq_29]ATG7
Cryptista, *Comamonas*[OA06T2DUH3].ATG7
Cryptista, *Palpitomona*[seq_28]ATG7
Glaucochyta, *Gloeochaete*[OA06TGVL944].ATG7
Glaucochyta, *Gloeochaete*[OA06TGYL7P].ATG7
Chlorophyta, *Ostreococcus*[seq_27]ATG7
Chlorophyta, *Micromonas*[seq_26]ATG7
Chlorophyta, *Lobosphaera*[seq_21]ATG7
Chlorophyta, *Lobosphaera*[seq_22]ATG7
Chlorophyta, *Lobosphaera*[seq_21]ATG7
Chlorophyta, *Lobosphaera*[seq_20]ATG7
Chlorophyta, *Chlamydomonas*[XP_00703365.1]ATG7
Chlorophyta, *Chlamydomonas*[PNW84948.1]ATG7
Chlorophyta, *Arabidopsis*[seq_19]ATG7
Chlorophyta, *Oryzax*[XP_0587173.1]ATG7
Chlorophyta, *Oryzax*[XP_0587173.1]ATG7
Chlorophyta, *Marchantia*[OAE31696.1]ATG7
Anacorcyta, *Anacorcyta*[seq_31]ATG7
Hemistastogophora, *Spironema*[seq_50]ATG7
Anycronomadina, *Nutomonas*[seq_41]ATG7
Malawinomadina, *Malawinomonas*[seq_65]ATG7
Metamonada, *Trichomonads*[OH596604.1]ATG7
Metamonada, *Trichomonads*[D13946-3-36765-36645]ATG7
Metamonada, *Trichomonads*[seq_66]ATG7
Discoba, *Rhynchopus*[seq_34]ATG7
Discoba, *Diplonema*[seq_31]ATG7
Discoba, *Trypanosoma*[TB927_10_v5-1e-2-373506-2737149]ATG7
Discoba, *Euglenales*[seq_32]ATG7
Discoba, *Naegleriales*[seq_33]ATG7
Discoba, *Percomonads*[OA06U1FMH3].ATG7
Discoba, *Andalucia*[seq_30]ATG7
Breviates, *Pysyllae*[seq_61]ATG7
Breviates, *Pysyllae*[seq_61]ATG7
Breviates, *Pysyllae*[seq_61]ATG7
Breviates, *Pysyllae*[seq_71]ATG7
Fungi, *Saccharomyces*[EDJ271648.1]ATG7
Fungi, *Komagataella*[seq_42]ATG7
Fungi, *Schizosaccharomyces*[seq_44]ATG7
Fungi, *Claroideoglommus*[seq_38]ATG7
Fungi, *Gigasporales*[seq_40]ATG7
Fungi, *Catenaria*[seq_39]ATG7
Fungi, *Catenaria*[ORZ40662.1]ATG7
Fungi, *Pirionymys*[seq_43]ATG7
Fungi, *Gonapodytes*[seq_41]ATG7
Fungi, *Batrachochytrium*[seq_35]ATG7
Fungi, *Batrachochytrium*[OA39464.1]ATG7
Fungi, *Funticulales*[seq_39]ATG7
Metazoa, *Homo*[95532]ATG7
Metazoa, *Xenopus*[KA686729].1ATG7
Metazoa, *Danio*[RER1013].ATG7
Metazoa, *Drosophila*[seq_70]ATG7
Metazoa, *Cephalopoda*[EFX82614.1]ATG7
Metazoa, *Daphnia*[seq_61]ATG7
Metazoa, *Corymbeles*[seq_69]ATG7
Metazoa, *Dicelyme*[seq_68]ATG7
Holozoa, *Heliocelis*[seq_58]ATG7
Holozoa, *Staphenoceles*[seq_64]ATG7
Holozoa, *Salpingoeca*[VF17].ATG7
Holozoa, *Capasaporis*[KEJ92398.1]ATG7
Holozoa, *Ichthyophonius*[seq_59]ATG7
Holozoa, *Ichthyophonius*[seq_60]ATG7
Holozoa, *Ichthyophonius*[seq_61]ATG7
Holozoa, *Creolimax*[seq_54]ATG7
Holozoa, *Creolimax*[seq_54]ATG7
Holozoa, *Creolimax*[seq_57]ATG7
Holozoa, *Creolimax*[seq_52]ATG7
Holozoa, *Creolimax*[seq_55]ATG7
Holozoa, *Creolimax*[seq_53]ATG7
Holozoa, *Sphaerothericum*[seq_63]ATG7
Holozoa, *Corallorchythium*[seq_51]ATG7
Amoebozoa, *Entamoeba*[DS571196-6-71419-69677]ATG7
Amoebozoa, *Dictyostelium*[seq_1]ATG7
Amoebozoa, *Vermamoeba*[seq_2]ATG7
Amoebozoa, *Acanthamoeba*[XP_00439643.1]ATG7
Crums, *Mentomonas*[seq_10]ATG7
Crums, *Mentomonas*[seq_9]ATG7
Crums, *Riofilices*.12ATG7
242 **Crums**, *Riofilices*.12ATG7

Rhizaria, *Glabronella*seq_71ATG7
Rhizaria, *Ambloimulina*seq_74ATG7
Rhizaria, *Eucyrtidium*seq_73ATG7
Rhizaria, *Bigelowella*seq_72ATG7
Rhizaria, *Paulinella*seq_76ATG7
Rhizaria, *Paulinella*seq_75ATG7
Alveolata, *Toxoplasma*CEL74723.1ATG7
Alveolata, *Pfiesteria*seq_70ATG7
Alveolata, *Vitrella*(CJ92350.1)ATG7
Alveolata, *Chromera*AOA004F387ATG7
Alveolata, *Oxyrhiza*AOA6V3OY5TATG7
Alveolata, *Karenia*AOA6U4UEBIATG7
Alveolata, *Tritonympha*seq_01ATG7
Stramenopiles, *Phytophthora*seq_79ATG7
Stramenopiles, *Peronospora*seq_78ATG7
Stramenopiles, *Aureococcus*AOA6S9EG39ATG7
Stramenopiles, *Phaeodactylum*seq_77ATG7
Telomelia, *SRR731266*seq_80ATG7
Telomelia, *SRR731266*seq_81ATG7
Centrohelida, *Raineriophrys*seq_17ATG7
Centrohelida, *Raphidochrysis*seq_18ATG7
Centrohelida, *Choanocystis*seq_15ATG7
Centrohelida, *Choanocystis*seq_16ATG7
Centrohelida, *Acanthocystis*seq_13ATG7
Centrohelida, *Acanthocystis*seq_14ATG7
Haptophyta, *Caldicladius*seq_47ATG7
Haptophyta, *Scyphosphaera*seq_49ATG7
Haptophyta, *Scyphosphaera*seq_48ATG7
Haptophyta, *Isochrysis*(AOA6TOR228)ATG7
Haptophyta, *Isochrysis*(AOA6TOS3V2)ATG7
Haptophyta, *Emiliania*XP_005789984.1ATG7
Haptophyta, *Pyrenium*AOA6S9VWL01ATG7
Haptophyta, *Pavlova*seq_46ATG7
Haptophyta, *Pavlova*seq_47ATG7
Cryptista, *Gulldonia*seq_005834743.1ATG7
Cryptista, *Rhodomonas*seq_29ATG7
Cryptista, *Goniomonas*(AOA6T2DUH3)ATG7
Cryptista, *Palpitomonas*seq_28ATG7
Glaucophyta, *Gloeochaete*(AOA6TG197)ATG7
Glaucophyta, *Gloeochaete*(AOA6T0DYL6)ATG7
Chlorophyta, *Ostreococcus*seq_27ATG7
Chlorophyta, *Micromonas*seq_26ATG7
Chlorophyta, *Lobosphaera*seq_23ATG7
Chlorophyta, *Lobosphaera*seq_22ATG7
Chlorophyta, *Lobosphaera*seq_21ATG7
Chlorophyta, *Lobosphaera*seq_24ATG7
Chlorophyta, *Chlamydomonas*XP_001073365.1ATG7
Chlorophyta, *Chlamydomonas*PNW84948.1ATG7
Chlorophyta, *Arabidopsis*seq_19ATG7
Chlorophyta, *Oryza*seq_21ATG7
Chlorophyta, *Marchantia*seq_23ATG7
Chlorophyta, *Marchantia*(OAEC31696.1)ATG7
Anacorcyta, *Anacorcyta*seq_31ATG7
Hemistastogophora, *Spironema*seq_50ATG7
Ancyromonadida, *Nutomonas*seq_41ATG7
Malawimonadida, *Malawimonas*seq_65ATG7
Metamonada, *Trichomonas*(OH596604.1)ATG7
Metamonada, *Trichomonas*D313946-3-36765-36645ATG7
Metamonada, *Trichomonas*seq_66ATG7
Discoba, *Rhychnops*seq_34ATG7
Discoba, *Diplonema*seq_31ATG7
Discoba, *Trypanosoma*(TB927_10_v5-1-6-273956-2737149)ATG7
Discoba, *Euglenales*seq_32ATG7
Discoba, *Naegleriales*seq_33ATG7
Discoba, *Percomonas*(AOA6U1FMN3)ATG7
Discoba, *Andalucia*seq_30ATG7
Breviata, *Pysyllus*seq_61ATG7
Breviata, *Pysyllus*seq_61ATG7
Breviata, *Pysyllus*seq_61ATG7
Breviata, *Pysyllus*seq_71ATG7
Fungi, *Saccharomyces*EDJ271648.1ATG7
Fungi, *Komagataella*seq_42ATG7
Fungi, *Schizosaccharomyces*seq_44ATG7
Fungi, *Claroideoglomeris*seq_37ATG7
Fungi, *Claroideoglomeris*seq_38ATG7
Fungi, *Gigasporaceae*seq_39ATG7
Fungi, *Catenarial*seq_36ATG7
Fungi, *Catenarial*seq_36ATG7
Fungi, *Catenarial*(ORZ40662.1)ATG7
Fungi, *Pirionymys*seq_43ATG7
Fungi, *Gonapodytes*seq_41ATG7
Fungi, *Batrachochytrium*seq_31ATG7
Fungi, *Batrachochytrium*(QA39464.1)ATG7
Fungi, *Fonticulites*seq_39ATG7
Metazoa, *Homo*(O935352)ATG7
Metazoa, *Xenopus*(XEN000000.1)ATG7
Metazoa, *Drosophila*AOA002KPR3ATG7
Metazoa, *Drosophila*seq_70ATG7
Metazoa, *Caenorhabditis*EFX82614.1ATG7
Metazoa, *Daphnia*seq_67ATG7
Metazoa, *Corymella*seq_69ATG7
Metazoa, *Dicelyme*seq_68ATG7
Holozoa, *Helgocelis*seq_58ATG7
Holozoa, *Stephanocalyx*seq_64ATG7
Holozoa, *Salpingoeca*seq_63ATG7
Holozoa, *Capsasporum*KJE92398.1ATG7
Holozoa, *Ichthyophonius*seq_59ATG7
Holozoa, *Ichthyophonius*seq_60ATG7
Holozoa, *Ichthyophonius*seq_61ATG7
Holozoa, *Creolimax*seq_54ATG7
Holozoa, *Creolimax*seq_56ATG7
Holozoa, *Creolimax*seq_57ATG7
Holozoa, *Creolimax*seq_52ATG7
Holozoa, *Creolimax*seq_55ATG7
Holozoa, *Creolimax*seq_53ATG7
Holozoa, *Sphaerothecum*seq_63ATG7
Holozoa, *Corallorhynchus*seq_62ATG7
Amoebozoa, *Entamoeba*(DS571196-6-71419-69677)ATG7
Amoebozoa, *Dicystostellium*seq_1ATG7
Amoebozoa, *Vermamoeba*seq_2ATG7
Amoebozoa, *Acanthamoeba*XP_00439643.1ATG7
CrUMs, *Montanina*seq_11ATG7
CrUMs, *Montanina*seq_11ATG7
CrUMs, *Montanina*seq_9ATG7
CrUMs, *Rafflesia*seq_12ATG7

Rhizaria_Amonia[seq_71]ATG7	593 LKVLNDTKYLEKVSGLQKLEIIDLVDMDVDDIDEED	630
Rhizaria_Globobulimina[seq_74]ATG7	594 IKTLNEPKYIEIVSGLNKLKDDIDLIDMDVDDDDGML	631
Rhizaria_Eucyrtidium[seq_73]ATG7	354 LEVLRSPAYLEDVTGKELMSKIDDFDCAWDEEDSAEE	391
Rhizaria_Bigelowiella[seq_72]ATG7	-----	-----
Rhizaria_Paulinella[seq_78]ATG7	518 -----KQKQKEKV-----	523
Rhizaria_Paulinella[seq_75]ATG7	107 MSRLNCOILEDCGTLQKKEADQLQMDMEIEDD	143
Alveolata_Toxoplasma[CEL74723.1]ATG7	606 QEVIASSSVLEKVSGLDMQRIEARBEDADVIGLSDE	643
Alveolata_Plasmodium[ETW30632.1]ATG7	604 LVVGENPEFKELCDIEEGDDHNEEANDEVEEKSDEN	641
Alveolata_Vitrella[CEL92350.1]ATG7	596 TVQVHDPCHLESVSGRVFMKMSRVEEDVIQIDDEEL	633
Alveolata_Chromera[AAOAG4F3B7]ATG7	608 LRVLRDRVLELERSVGLSEFKEREARATQKGGVGGV	645
Alveolata_Oxyrhiza[AAO6V3QY57]ATG7	588 QRVTANSSITLERMSGLEEMKQRLQSFMDLDDFEPL	624
Alveolata_Karenia[AOAGT4UBE1]ATG7	597 MRVADSSLEELISGLAAMKAHNAFDEFDDFDDGAPD	634
Alveolata_Tetrahymena[seq_0]ATG7	601 QRVINDDVYLQVTKLSELLRDLDTDAFTEVDD----	634
Stramenopiles_Phytophthora[seq_79]ATG7	606 EMAGNSSAYLEELTGUNLTKAADALVIDLESDDEGE	643
Stramenopiles_Personospora[seq_78]ATG7	-----	-----
Stramenopiles_Aureococcus[AOAGS9EG39]ATG7	592 AAVAADPAHLAVSGLTKKADVDG-----YEDDDDDF	625
Stramenopiles_Aurantiochytrium[seq_77]ATG7	609 LQAFNKPDFLEDLTGLDTRLNSASLDDDLDDFDDD	646
Telonemia_SFR7371266[seq_80]ATG7	514 IKCMNDRHMDVTVGLRAEKEAMEAKYANWEDDDLD	561
Telonemia_SFR7371266[seq_81]ATG7	583 IQAFNNRTYLEDLTGITALKACEDSDSDFDWSDEEQ	620
Centrohelida_Raineriophrys[seq_17]ATG7	-----	-----
Centrohelida_Raphidiophrys[seq_13]ATG7	611 FSAFDDPLFLERFTGLDDVKRKAESMDVWDGDDLL	648
Centrohelida_Choanocystis[seq_15]ATG7	607 FRAFNEPSFLEDLAGVSQMLAAEQSQANWEDDDL	644
Centrohelida_Choanocystis[seq_16]ATG7	605 LRAFGEPSFLEDLVAGLITAMKAADAMSGFDDADG	642
Centrohelida_Acanthocystis[seq_13]ATG7	-----	-----
Centrohelida_Acanthocystis[seq_14]ATG7	170 MNCFNDRFTFTITGLAEKKATEIVSYESEEEEEEE	207
Haptophyta_Calcidiscus[seq_45]ATG7	318 RDALNHGSLYLEDLTGLSAMQKQAEASFDEADDEDL	355
Haptophyta_Scyphosphaera[seq_49]ATG7	143 LEAFNRGSLYLEDLTGLSKMHHEAEAFFDEPSEVD	180
Haptophyta_Scyphosphaera[seq_48]ATG7	-----	-----
Haptophyta_Isochrysis[AOAGT0R228]ATG7	580 MEAFNGGTFFLEELTGLQAMHREAEAALEVDL	617
Haptophyta_Isochrysis[AOAGT0S3V2]ATG7	608 LEAFNGGAFLEELTGLQAMHREAEADLFDDVEE	645
Haptophyta_Emiliania[XP_005789984.1]ATG7	607 LQAFNGGVLEELTGLQAMHREAEAALEDVFFDEDED	644
Haptophyta_Pymnesium[AOAGS9VWLQ]ATG7	611 MSAFNSSSYLEDLTGLTEMHRETEAAGLASECD	648
Haptophyta_Pavlova[seq_46]ATG7	-----	-----
Haptophyta_Pavlova[seq_47]ATG7	-----	-----
Cryptista_Guillardia[XP_005834743.1]ATG7	138 LRAFNEPDFLEIFSGURELHKQAAEIAEVL	175
Cryptista_Rhodomonas[seq_29]ATG7	607 LRAFNEPNFLEEASGLTMDLREGEALMEDWDEVEEL	644
Cryptista_Goniomonas[AOAGT0DUH3]ATG7	467 LQAFNEPDFLEELSGUKEFLKAADDMDWDEDE	504
Cryptista_Palpitomonas[seq_28]ATG7	548 LRVFNENFLEDLTGITEMRALADKEDIWSDDEEDDM	584
Glaucophyta_Gloeochaete[AOAGT1G744]ATG7	580 ARVVSGRGELQISGLAAFNASITAEVEEVVD	617
Glaucophyta_Gloeochaete[AOAGT0VLP9]ATG7	458 LRCONDSAVIEEVCGLAEDRLDVDVIEFELO	489
Glaucophyta_Ostreococcus[seq_27]ATG7	605 MDAFGKPHYLEELTGLSAMMAAAAEVIAWDDDD	638
Chlorophyta_Micrononas[seq_26]ATG7	604 ISVFDDPKLLEDAITGLTELLAVDADDAEVLDDDDF	640
Chlorophyta_Lobosphaera[seq_23]ATG7	611 LAAFAADTLEEDKLGITKVMHDAADA--VEV	646
Chlorophyta_Lobosphaera[seq_22]ATG7	-----	-----
Chlorophyta_Lobosphaera[seq_21]ATG7	58 LEALODKKKLEDLTGUTALHSETAAMFDG	95
Chlorophyta_Lobosphaera[seq_24]ATG7	-----	-----
Chlorophyta_Lobosphaera[seq_20]ATG7	-----	-----
Chlorophyta_Chlamydomonas[XP_001703365.1]ATG7	-----	-----
Chlorophyta_Chlamydomonas[PNW84948.1]ATG7	611 AEALASPARLALTGLEELHAAAADEESEEE	648
Chlorophyta_Arabidopsis[seq_19]ATG7	610 LEAINHRTYLEDLTGLTELLKKAANSFNLWD	647
Chlorophyta_Crysa[XP_01615773.1]ATG7	607 MWLINERTYLEDLTGLTLKSAASVQVEWIDEVDD	644
Chlorophyta_Marchantia[seq_25]ATG7	609 LEVLNRPNYLEDLTGLTEMLAATCGLTLDWDEDD	645
Chlorophyta_Marchantia[OE31696.1]ATG7	544 LEVLNRPNYLEDLTGLTEMLAATCGLTLDWDEDD	580
Ancoracysta_Ancoracysta[seq_3]ATG7	600 AQVFSNPNYLEDITGLSQLOQACDQVWVDDDD	637
Hemimastigophora_Spironema[seq_50]ATG7	592 LQVLKNPAMLDEITGLTSMKKATETMTLDWDE	629
Ancyromonadida_Nutomonas[seq_4]ATG7	605 LQVMNSPTVLEDMTGLTAMNKEAEELDFONDDDD	642
Malawimonadida_Malawimonas[seq_65]ATG7	604 MDVLRTPKLLEDISGVTEMTTDADERGEMIVL	641
Metamonada_Tritrichomonas[OH9S9604.1]ATG7	562 MRAVNEPNFLEDSVSGITEMKATMVDEDC	595
Metamonada_Metamonas[DS113646-3-36765-38645]ATG7	563 LRAITVEGLSEVSGINAKMAEMADVDC	599
Metamonada_Monocercomonoides[seq_66]ATG7	606 LQAFNDPEVLERLVGSGMNDNDVDDDEDSV	643
Discoba_Rhynchopus[seq_34]ATG7	602 EKVLNDRSLELTERAGIDAMLKVADDLDM	639
Discoba_Diplonema[seq_31]ATG7	592 LEVLNDRPTOLSKIISGLHAFLEKVKEDFAL	629
Discoba_Trypanosoma[Tb927_10_v5.1-6-2739506-2737149]ATG7	601 LRCINDPMYIEEVSGVKAFKESCALSDCD	638
Discoba_Euglenia[seq_32]ATG7	605 ETVLNNRVELEDMTGLKQVKKEVDAEEEA	642
Discoba_Naegleria[seq_33]ATG7	529 ERCFNDSKYLEELTGLKQHQETLKDYSE	566
Discoba_Percolomonas[AOAGU1FMM3]ATG7	591 YOALLHPEALEELTGLSTLKKQ-----DEK	625
Discoba_Andaliucia[seq_30]ATG7	588 RNVGNDRSILEELISGLQDVDDGSEILEMT	625
Breviata_Pygusial[seq_6]ATG7	-----	-----
Breviata_Pygusial[seq_5]ATG7	93 ETVGNDRTHLE-----	103
Breviata_Pygusial[seq_8]ATG7	-----	-----
Breviata_Pygusial[seq_7]ATG7	-----	-----
Fungi_Saccharomyces[EDZ71648.1]ATG7	578 KKALEHRLYLEEISGLSVTKQEVERLNDV	615
Fungi_Komagataella[seq_42]ATG7	593 KDALNENNYLEDLTGLTKVQKESEIQEFN	630
Fungi_Schizosaccharomyces[seq_44]ATG7	596 LRAINEPDVVEELGSLREVOALGEITMEV	633
Fungi_Claridoeglomus[seq_37]ATG7	-----	-----
Fungi_Claridoeglomus[seq_38]ATG7	280 KRVFDSRTLEELTGLSKLHOSEVDFW	316
Fungi_Gigasporia[seq_40]ATG7	609 NRVFDSRACLLEDLTGLSKLHOSEVDFW	645
Fungi_Catenaria[seq_36]ATG7	592 REVGNAPGVLEKMTGLDENKRAEEALK	629
Fungi_Catenaria[ORZ40662.1]ATG7	578 REVGNAPGVLEKMTGLDENKRAEEALK	645
Fungi_Piromyces[seq_43]ATG7	606 QKIVSTPDVLEQLTGLDNLHKEGLLNCV	643
Fungi_Gonapodyales[seq_41]ATG7	598 ERVLNDRPSYLERVSGLOAMKDKLES	635
Fungi_Batrachochytrium[seq_35]ATG7	607 LKGLASPEVLEEVSGLKDLKHEH--VD	642
Fungi_Batrachochytrium[OAJ39464.1]ATG7	511 LKGLASPEVLEEVSGLKDLKHEH--VD	546
Fungi_Forticula[seq_39]ATG7	608 QRVLREBILLEDLTGISEIKNAADND	642
Metazoa_Homo[Q93532]ATG7	611 AKVFNSSSFLEDLTGLTLHQETQA--AE	647
Metazoa_Xenopus[KA8612791.1]ATG7	611 AKAFNSSSFLEDLTGLTLHQETQA--AE	647
Metazoa_Danio[AOAG2KPR3]ATG7	604 AKVFNSSSFLEDLTGLTLHQETQAAE	639
Metazoa_Drosophila[seq_70]ATG7	603 FKIFETAKFLEDLTGISEFKRLNSEI	640
Metazoa_Daphnia[EPX82614.1]ATG7	608 AEVFNDSVLEQVSGUADLHKDIATIED	644
Metazoa_Caenorhabditis[seq_67]ATG7	595 RDVMNSPGRLEEVTLGDELQNSVNAI	630
Metazoa_Dicymela[seq_69]ATG7	601 LSCQNDSTFIRSLVKLGEDHSNVDFLED	637
Metazoa_Corticium[seq_68]ATG7	507 LQVFNSTPFLFEEVTGSLQHAAEAVE--	542
Holozoa_Helgocaul[seq_58]ATG7	523 IGAGNIPNVLEDLSGLALHDVADE--LE	558
Holozoa_Stephanocaul[seq_64]ATG7	377 TVNGNTSTFLEDLTGLSAMQAAVED	414
Holozoa_Salpingocaul[seq_62]ATG7	596 ----P-----	597
Holozoa_Capsaspora[KJ92398.1]ATG7	608 QKAFNSRTFLEELTGKKLHEETEAALAD	645
Holozoa_Ichthyophonus[seq_59]ATG7	-----	-----
Holozoa_Ichthyophonus[seq_60]ATG7	69 LKALNS-----	75
Holozoa_Ichthyophonus[seq_61]ATG7	-----	-----
Holozoa_Creolimax[seq_54]ATG7	-----	-----
Holozoa_Creolimax[seq_56]ATG7	76 -----RDAFDK-----	82
Holozoa_Creolimax[seq_57]ATG7	-----	-----
Holozoa_Creolimax[seq_52]ATG7	-----	-----
Holozoa_Creolimax[seq_55]ATG7	79 LCA-----	81
Holozoa_Creolimax[seq_53]ATG7	-----	-----
Holozoa_Sphaerothecum[seq_63]ATG7	611 FKVFNLPSYLEDITGLSELHRETDELS	648
Holozoa_Coralochytrium[seq_51]ATG7	591 IEVLADSSYLELSGISTLHASA--ADL	626
Amoebozoa_Entamoeba[DS571196-6-71419-69677]ATG7	546 LDAINDPKILNIVGIDQVE-----ND	578
Amoebozoa_Dictyostelium[seq_1]ATG7	611 INWMDSSCLTKICGIDDLKNTENVID	648
Amoebozoa_Vermamoeba[seq_2]ATG7	400 MEAFNSPKLEDLTGITKMKESANLDV	437
Amoebozoa_Acanthamoeba[XP_004349643.1]ATG7	558 QYVGNNTHTLEDITGLTLQKATVDFS	595
CRuMs_Mantamonas[seq_10]ATG7	-----	-----
CRuMs_Mantamonas[seq_11]ATG7	44 KEAFNNPDVLEVSGLTAMKAMEDMD	80
CRuMs_Mantamonas[seq_9]ATG7	-----	-----
CRuMs_Rigifilia[seq_12]ATG7	603 MRVLSNPSHLEDVTGLTALKESMEVE	640

65 LKRY IVNVEYVYVPLVYMDAYRQGVMDVADLTGRGKAWFLTGLEPGLGRPLCALHPORIALIMAPIMOTSAFSSSSSSSSSSSSSSSSSSSSSSSSSSKARSAPSK
66 LRKGLSVYVAKFPLVYFHYIMDXYKQKATLEIKELGASAKLEIIDLIVPLGFSYFVIOQRNVEKTEYF-FSPITSLMILKLFENLYLKE
65 LLEFHIVYHTIYVQVPLVYFRVQAVDGTVNSNIVYRDLQSGNRFTVAMEEVLPGKPFSLHPCEIATAMQLLAQLQARSTEVQPLVSWLSVQPLVLESLDYB--
65 LLEFHIVYHTIYVQVPLVYFRVQAVDGTVNSNIVYRDLQSGNRFTVAMEEVLPGKPFSLHPCEIATAMQLLAQLQARSTEVQPLVSWLSVQPLVLESLDYB--
65 LLEFHIVYHTIYVQVPLVYFRASAVDGRPLVLEHIVASNDMSIAMEEVLPGKPFSLHPCEIATAMQLLAQLQARSTEVQPLVSWLSVQPLVLESLDYB--
110EWFHVLFTVYSGPELRRLRADWAGAPLSLAEVRRGL--DFDGVSVREAVYGEAFVLVGCACAEKVDAL--AARCCALDGFALPLHLAAGACALISLPGQPIVDA
77 VAEHLVHVLQOVNFVPMVFNLYODDQVMRGCLLERTMTASSWANLTGAEHIVPLGFFLHPCEIOMFNTLIVYHNSNTRTBLFLNFMILSOVNTPTPTPKPKN
92 LLEHLVHNESFQPOLLVTA--TENRYSLELWDOCFKLLEHSLTETMIPR--MGCFHPORIAEWMSVLAKHT-ADTELSTLIVMAAFVSSFLPISKESVWLYPOH
116 LLEHLVHNESFQPOLLVTA--TENRYSLELWDOCFKLLEHSLTETMIPR--MGCFHPORIAEWMSVLAKHT-ADTELSTLIVMAAFVSSFLPISKESVWLYPOH
92 LLEHLVHNESFQPOLLVTA--TENRYSLELWDOCFKLLEHSLTETMIPR--MGCFHPORIAEWMSVLAKHT-ADTELSTLIVMAAFVSSFLPISKESVWLYPOH
82 LLEHLVYNGVRLQVOLLCA--TQOYMSHTOLWEKLSLSSGFSSFMIPILHVFFLHPGOSAEWISML-LAKHTDHNTRFSS--ALLVWAVVTVLPLRLBSAQISOLQ
94 QFELNVYNTAHMQLLHAINENKYLKSHKEWCELEKPEMTLITLFEHPLLR--VFLGHPOSSEWNNILMSVKNINNNND--YLLTWYFVLSLHPLEKFO-QIELEN
86 QFELNVYNTAHMQLLHAINENKYLKSHKEWCELEKPEMTLITLFEHPLLR--VFLGHPOSSEWNNILMSVKNINNNNDYLLTWYFVLSLHPLEKFO-QIELEN
21-----HAH-----SAADFVYTGAEHVLGVPCLMALHPCLASHLMRAMADGAE-----VLDYLVAMGVHAPLVGVADHGLMLVVGQ
100 RVEHLVYEDTVGPMMLFNAYAPGSSPKK-----
81 LRLHICRGATVQVQLLLGLSGDGRVDVDEARAYLOOPLDOMLTPAEHPLGFLPCVALHACHAELLSLMDSDAASREGQRPDLGAWSLVAPLELRQVNTVT--
90 RLEHLVYGATVQVQLLLGLSGAGELWTVSRSHMAIAADSVQVLEHAPLGVFFALHPORAEWMAJLORRESADGQPLVSLASVLAQVADARAMLSSA--
68 RVHVIYVLOVTCOPLVLLLRHOGDGLSALDEIWAHLSADHMAFVFTVEVPLGTGFCFALHPORINELMALMSRARSAPSGGSLVSWMSVITIV-RLV-IRPTVH--
81 MRVHYVVEAFCOPLVFLKGLIBGRLLDLEYIWRHDSQSGWCLPTTEHPVGEFFHFVHPORKOFMDAIOAFLEPCTOSNFKWLSVQVIAV-GRLLPLHSGN-
113 VHYVVEAFCOPLVFLRGGTAAGA--SLPEAWAKQASRSALAEITDDEHGEFFLGLHPORREFMDMMAMRKQDQKDFEACWLVSFGVQV-GRVPLALFQASG-
72 VGHVIAYSAAVPLLLFRGQDQKPLKLEIWAHLSAKWSLSQCEHPVGFVFLAVHPORAEWLSQVLTSTVSTQKDFEACWLVSFGVQV-GRVPLALFQASG-
83 VREHYVYSAFVPCVLCVARDATTAAMTVSRLSTLRNDNDVLYPSNHPRGQWACVPAAGARML-LAADAATS--KLEAWLRQVAREVSD--
93 VLYHIVYSSSFGVCLMLFRAHHOGSGMAEAVDAPLSTSRWTFITLHEHPLH--PAPORIALMELMLRSGSVGLVAVVAVVAPVRLP-SPJIA--
105 LLDVHCYSASVQVPMHFRYSGDGLPLADVAVALFPEQLGVFLGCEHPLGFWALHPCEIADWALVAGAMAGSSGAGEGQVRAWLAVHGVHVLGRAG-
97 YDHYHCYSASVQVPLVFRSCTSGEPLADVAKKVPLESKWTFITGEEHPLNRPWFKLHPCEIGVAILKQSSSSSSSSGQVLYVSSVVGQV-GR--PLEMLN-
90 YDHYHVVSFSYKVPVLFQCGHAGSGLLTDEIKEDIPESKWTFITREEHPFSRWFVTLHPGOSDOCKMLLEVE-NKDQHVQVPAWLSVVGQV-GLKIPLELYMOSS-
88 YDHYHVVSFSYKVPVLFQCGHAGSGLLTDEIKEDIPESKWTFITREEHPFSRWFVTLHPGOSDOCKMLLEVE-NKDQHVQVPAWLSVVGQV-GLKIPLELYASG-
70 YDHYHVVSFSYKVPVLFQCGHSGGLLTDEIKEDIPESRWTFITREEHPFSRWFVTLHPGOSDOCKMLLEMOQKQDQ--VLPWALTIVVGQV-GLKIPGLGHGNS-
92 YDHYHVVSFSYKVPVLFQCGHSGGLLTDEIKEDIPESRWTFITREEHPFSRWFVTLHPGOSDOCKMLLEMOQKQDQ--VLPWALTIVVGQV-GLKIPGLGHGNS-
80 RCTHIVHVSFNVPLVFRHSHSGSPLNWLDAVLDPONRVTFGLTEHPLRWFMLHPGOSLSMSLMLTRIKKQSRGQDQWLLVLSVGAACVRLVPLDGLFSLKN-
72 DDLHIVHVSFNVPLVFRV--ARAFAGMLTEHPVLTACAMLHPCEIOTMIMHALKSSDN--YLVMLVGAACVLA-EISIDAEALLAAR
68 RSHVHLSAAFAAPMLFSFARDGLHCLHADAISPLTQVMDLPLHLOEENIATMOTL--QHTTBEVYQWTVNLVPMPSID--IAEFSRR
8 FANYIYSDOVFTVPLSATFENRCHOLTESELSIAPLEKLDGVSREHDLQKPVFFIHPOQEEFY--DPLKIAS--VILWNLVRVLP--FR-RLP-
43 FVTIYIDVEVQOAPVLSAYTESGHRITDELKIMEKLDMSVSRHITGILPFLFIHPKIEITVL--EHH--GIDEMNFWGLPFL--RLPI-
60 VLNHIVYFDVSVYVYFRATHESEFVNLQLSHT--SDKNITOGIHPYRPFYMHPOQINIL-KLGOTLQSEKMDSDLLFWISLFLRLVDVPLIQCKF
8--DLEVOQHIVYRPLAFASAYTAKGTVYSARIFDLIRNHPSSVLSAASHVITA--CNVHPGEANLKV--NATDTPAYDALISFAGAILVQSSQOLRAECA--
80 KADINLEVOQHIVYRPLAFASAYTAKGTVIRADKLLSNPCNDQDVALSAGLITY--LILNHPGEANLKV--NVS-ASSG--IYTSFSLHGNFIQVSEMOCPVPPR
107 SEFHVHVVSFVSFVPLVFLWYSEDGRSLSLDLYSGVSGTRGAFITGLEHILEKPFYCIHPORIAELLRTWATGPNQKQSGSLLEWISLWGLV-GLHDTMAAAGS
80 SIRHYVNIQIFKCPILVFNLYNNNNLLTQMLEIFONFNRTGAFITGLEHILEKPFYCIHPORIAELLRTWATGPNQKQSGSLLEWISLWGLV-GLHDTMAAAGS
66 FLSHLILVQDVLHPLVFFFRFAGSGCOLLEIRDLKSSISSRPLKFSQPLVSSQPFFFLHPORQDVLSHL--SLSSFLVLSWFLS-
68 FLLHVLVQDVLHPLVFFFRFAGSGCOLLEIRDLKSSISSRPLKFSQPLVSSQPFFFLHPORQDVLSHL--SLSSFLVLSWFLS-
77 HILVLYKSVNPLLLRLWIEIDIMTK-LMLDLEL-TILNLE--BSWYSFHPDSCIV-DOAE--FASTLRWVSF-IFS-WLYDEY-
85 TMHVARDSFSEVPOFFQVANGSDPILKTEQILEQNLAYDALIGOCR--GTWAVIHPORRDEMELE--QIKEDKILSLWLYIHOVLSPLIIRKAVDA
97 TVDHYIYASVQVPLVFNAYRKGTGHPNLEVSLVLDLIGKGSISQDHPILIPFYHHPCEIATLKSIVDKSGSSNNNNNIRASWLSVGVV-GLK-VGSYFL-
95 PMWHIYASVQVPLVFNAYRKGTGHPNLEVSLVLDLIGKGSISQDHPILIPFYHHPCEIATLKSIVDKSGSSNNNNNIRASWLSVGVV-GLK-VGSYFL-
74 WHEHVIYFHVQVPLVFRASDGLPLPPEVIAHLGQDYTNLSLSQDHPFLGTFWFVHPCTALRKLKSGQSKNVSSSSASFLSVGVV-GLK-VGLEFGM-
90 ECKDFVLYASVQVPLVFSIVDDTGMVLSLSEIVMLQDSHRFATISMODVSYPOVILHPCNHAKSEQHSDAT--FLOYLLHINNRLLSINIDIEIVQOEK
117 WYHVLVQVQVPLVFRASDGLGRPLTLK--IGWYSASPILSVTHVYLRPPFMVHPORCROMADLDDATA--GPEYMSAFLVAAGAAGLGOALATLHSLAG-
89 KYEHVLYCSYQVPLVFRASDGLGRPLTLK--IGWYHVGQMDVITQGEHPLGPPFFLHPCEINEFMTLVKNSQKINKN--NEFMSLVGVV-GLNYAKALSDER
97 HYEHLVLYCSYQVPLVFRASDGLGRPLTLK--IGWYHVGQMDVITQGEHPLGPPFFLHPCEINEFMTLVKNSQKINKN--NEFMSLVGVV-GLNYAKALSDER
98 HYEHLVLYCSYQVPLVFRASDGLGRPLTLK--IGWYHVGQMDVITQGEHPLGPPFFLHPCEINEFMTLVKNSQKINKN--NEFMSLVGVV-GLNYAKALSDER
97 HYEHLVLYCSYQVPLVFRASDGLGRPLTLK--IGWYHVGQMDVITQGEHPLGPPFFLHPCEINEFMTLVKNSQKINKN--NEFMSLVGVV-GLNYAKALSDER
47 TDETLNLSNIVYPIIFWNFENFSSPLFTVDIRNISEARSRSHYEPFMGLVLYNHPONSNINKELE-----NTRDS--MLMSVYVGOOL-GLK--DORVL-
39 FKVEIYNSVYPIIFWNFENFSSPLFTVDIRNISEARSRSHYEPFMGLVLYNHPONSNINKELE-----NTRDS--MLMSVYVGOOL-GLK--DORVL-
38 TCDHYIYSSVSEVPIIFWNFENFSSPLFTVDIRNISEARSRSHYEPFMGLVLYNHPONSNINKELE-----NTRDS--MLMSVYVGOOL-GLK--DORVL-
106 VHYVYVQAVPLVFSVLELDTGPISEGAWRHLPQCREQATVYSDADPALORPFYFHPORIAEML--AATVADTPAEALNVSLITREV-GLNVPLAEOLP-
96 QFHYIAYNNAYAPVLFYFVLELDTGPISEGAWRHLPQCREQATVYSDADPALORPFYFHPORIAEML--AATVADTPAEALNVSLITREV-GLNVPLAEOLP-
85 SIPLHWDVATGAPCLMFOAKFTQDQVITSDLPGLTQADVAHEGLSKDHLPGPPFFHHPORIANLDENVRSQDQSGASVDLEFLSVGVSIGIR--VHLHVR-
107 VHYVYVQAVPLVFNENATLEKRSQDQVNDMHQVSRSSFLGAEHVLGKPPFFHHPORIANLDENVRSQDQSGASVDLEFLSVGVSIGIR--VHLHVR-
-----LDQWQVIL--BSRL-----INDVR--SVITQIDHPDQVYFQVHPORIANLRAIDTAN-----ETNPLIIVISLVGLVGLTYLMTNDCI-
90 EAEHIVYSTRVPLVITGRMRGRLRLRLSILNSLTALTGVEEPLGLIFMLVHPORIEELMTLVNSCVRSESKQNVITWALVAPFV-GLYTNIMKET-
101 EAEHIVYSTRVPLVITGRMRGRLRLRLSILNSLTALTGVEEPLGLIFMLVHPORIEELMTLVNSCVRSESKQNVITWALVAPFV-GLYTNIMKET-
90 EAEHIVYSTRVPLVITGRMRGRLRLRLSILNSLTALTGVEEPLGLIFMLVHPORIEELMTLVNSCVRSESKQNVITWALVAPFV-GLYTNIMKET-
91 EODDILYKSVQVPLNLSGSSFFSDPSLNMNWNPLDOSTIBYITVEHPLGNCPCOLHPORIQNLMOQ-KTMH-GENDKRPLVHLVSLFAPLA-GLKPLFKMKN-
66 VYVYVYVYSTRVPLVYFOASHLDRMLTEWADVPEMDRWNVITQGEHPLGVPCHYIHPCEIKALMTSLTADASTSSN

[illegible]

Rhizaria_Ammonia seq_205 ATG12	115 - G K E L - V L H Y S L V P A W A - - - - -	129
Rhizaria_Globobulimina seq_217 ATG12	104 - G E L I L V - - Y S L V P A W A - - - - -	117
Rhizaria_Eucyrtidium seq_210 ATG12	97 - G E L I C V - - Y S T V L A W G - - - - -	110
Rhizaria_Bigelowiella seq_208 ATG12	98 - N N E L - E V S Y C T I N O W G - - - - -	112
Rhizaria_Paulinella seq_222 ATG12	116 - N G E L - V V N Y C L V E A W G - - - - -	130
Alveolata_Toxoplasma ESS29570.1 ATG12	293 - G G S L - M V S Y C Y T P A Y - - - - -	306
Alveolata_Plasmodium ETW54366.1 ATG12	71 - S G S L - N I S Y S F T P A Y - - - - -	84
Alveolata_Plasmodium EUR62061.1 ATG12	98 - S G S L - N I S Y S F T P A Y - - - - -	111
Alveolata_Vitrella A0A6U4JFV6 ATG12	101 - G E Q L - N I G S L I P A F H - - - - -	115
Alveolata_Chromera A0A0G4GWD9 ATG12	108 - E B M A - V O Y G S D N R L S V Q Y N I V S L R S	131
Alveolata_Oxyrrhis A0A6V4NV07 ATG12	108 - G Q Q L - A I T T S L E P A F A - - - - -	122
Alveolata_Oxyrrhis A0A6V4J2U9 ATG12	106 - Q G E L - I L N Y S I V G A W G - - - - -	120
Alveolata_Karenia A0A6T5NH78 ATG12	113 - G N Q L - Q I S Y S E A A F S - - - - -	127
Stramenopiles_Phytophthora seq_234 ATG12	101 - G D - V L - V L N Y S L T O A W G - - - - -	115
Stramenopiles_Peronosporales seq_231 ATG12	93 - G D - V L - V L N Y S L T O A W G - - - - -	107
Stramenopiles_Peronosporales seq_232 ATG12	88 - D G K L - V V N Y A C S M A W G - - - - -	102
Stramenopiles_Aureococcus seq_228 ATG12	122 - G G E L - V V N Y A T I G A Y G - - - - -	136
Stramenopiles_Aurantiochytrium seq_224 ATG12	75 - N G T L - R I T I G Q A V F G - - - - -	89
Telonomia_SRR7371266 seq_241 ATG12	83 - D G R L - H L Y A T N A W G - - - - -	97
Centrohelida_Raineriophrys seq_46 ATG12	123 - K G R L - V V N Y C L T P A W G - - - - -	137
Centrohelida_Raphidiophrys seq_48 ATG12	114 - E G C L - V V N Y C L I A W G - - - - -	128
Centrohelida_Choanocystis seq_41 ATG12	105 - G G S L - S L G Y C E E V A F G - - - - -	119
Centrohelida_Choanocystis seq_38 ATG12	98 - D G C L - V V N Y C P T E A W G - - - - -	112
Centrohelida_Acanthocystis seq_36 ATG12	116 - D K C L - V I N Y C L T A A W G - - - - -	130
Haptophyta_Calcidiscus seq_121 ATG12	106 - D G V L - I L N Y C T T P A W G - - - - -	120
Haptophyta_Isochrysis A0A6T1JSG5 ATG12	87 - - A L S L W C L S S C P T T O P P H L S	106
Haptophyta_Isochrysis A0A6T0XET5 ATG12	106 - G S A L - V L H Y C T T P A W G - - - - -	120
Haptophyta_Emiliana seq_242 ATG12	89 - G S T L - V L H Y C T T E A W G - - - - -	103
Haptophyta_Emiliana seq_123 ATG12	89 - H S - - - H T A R F R K R E H T R T I R R A B T - -	109
Haptophyta_Prymnesium A0A6S9YC33 ATG12	110 - D G V L - I L N Y C O T P A W G - - - - -	124
Haptophyta_Prymnesium A0A6S9YNG5 ATG12	108 - S S T A - - S S W T R - - G W A T S E S A S T S - -	127
Haptophyta_Pavlova seq_127 ATG12	63 - D G V L - S L H Y C T T P A W G - - - - -	77
Haptophyta_Pavlova seq_129 ATG12	82 - D G V L - S L H Y C T T P A W G - - - - -	96
Cryptista_Guillardia A0A6U6D6A0 ATG12	116 - N G K L - V I D Y A L K E A W G - - - - -	130
Cryptista_Rhodomonas seq_73 ATG12	109 - D G K L - Q I D Y A L M E A W G - - - - -	123
Cryptista_Goniomonas seq_67 ATG12	98 - K G C L - V V N N A L E A W G - - - - -	112
Cryptista_Palpatomonas seq_71 ATG12	78 - G S K L - S F N S L T P A W G - - - - -	92
Glaucophyta_Gloeocharaete seq_117 ATG12	83 - D G V L - V L N Y A T T V A W G - - - - -	97
Chlorophyta_Ostreococcus OUS48613.1 ATG12	275 - E G G K - V V F Y S T T P A W G - - - - -	290
Chlorophyta_Micromonas seq_60 ATG12	107 - E G K L - V V Y Y A T T P A W G - - - - -	121
Chlorophyta_Lobosphaerales seq_54 ATG12	77 - D G R L - L V N Y A C T P A W G - - - - -	91
Chlorophyta_Chlamydomonas seq_52 ATG12	77 - E G K L - H V S Y A L T P A W G - - - - -	91
Chlorophyta_Arabidopsis NP_001326256.1 ATG12	60 - - - Y L - - L C L S L V - - - - -	67
Chlorophyta_Arabidopsis seq_50 ATG12	82 - D B K L - V V N Y A C S M A W G - - - - -	96
Chlorophyta_Oryza EA036194.1 ATG12	101 - D G C L - V V N Y A S S M A W G - - - - -	115
Chlorophyta_Oryza EAZ00079.1 ATG12	89 - D G Q L - V V N Y A S S M A W G - - - - -	103
Chlorophyta_Marchantia seq_56 ATG12	89 - D G K L - V V N Y A C S M A W G - - - - -	103
Ancoracysta_Ancoracysta seq_22 ATG12	125 - D G K L - I V N Y C S T P A W G - - - - -	139
Ancyromonadida_Nutomonas seq_26 ATG12	109 - - - G K M L M I N Y A T Q E - - - - -	120
Malawimonadida_Malawimonadida seq_163 ATG12	96 - G G L L - N I S Y C T T A A W G - - - - -	110
Metamonada_Tritrichomonas seq_173 ATG12	74 - V E - E I - D I N Y S I S P O F G - - - - -	88
Metamonada_Trichomonas DS113793-6-20469-20053 ATG12	76 - Q T T L - D I Y Y S S G O V F G - - - - -	90
Discoba_Rhynchopus seq_91 ATG12	77 - S K K L - T V F Y S L K O A W G - - - - -	91
Discoba_Diplonemoides seq_78 ATG12	108 - N T K L - S I T A F K E I A W G - - - - -	122
Discoba_Trypanosoma Tb927_11_v5.1-1-3040801-3041157 ATG12	96 - S S D Q R - H L S F A S L I F H G - - - - -	112
Discoba_Euglenas seq_83 ATG12	102 - Q B T L - V V N Y S R O A W G - - - - -	116
Discoba_Neodieria seq_85 ATG12	114 - N G M L - V I N Y S L K I A W G - - - - -	128
Discoba_Percolomonas seq_89 ATG12	110 - D K K L - C I Y N D I S P C F G - - - - -	124
Discoba_Percolomonas A0A6UOKS69 ATG12	96 - E S H L - I V S Y C T Q S W A W G - - - - -	110
Discoba_Percolomonas A0A6UOKD5 ATG12	83 - E S H L - I V S Y C T Q S W A W G - - - - -	97
Discoba_Andalucia seq_77 ATG12	109 - D B K L - V V H Y C L T P A W G - - - - -	123
Breviata_Pygsuia seq_28 ATG12	85 - D G C L - I V N Y C L T O A W G - - - - -	99
Fungi_Saccharomyces seq_114 ATG12	108 - N D - E L - I V S Y C A S V A F G - - - - -	122
Fungi_Komagataella seq_107 ATG12	108 - N G E L - V V S Y S R V A F S - - - - -	122
Fungi_Schizosaccharomyces seq_116 ATG12	118 - D S H L - L I N Y C I N V A F G - - - - -	132
Fungi_Claroideoglomus seq_98 ATG12	114 - D G H L - I I N Y C T S A A W G - - - - -	128
Fungi_Gigasporales seq_103 ATG12	120 - D G H L - I I N Y C T S A A W G - - - - -	134
Fungi_Gigasporales RIB01942.1 ATG12	70 - D G H L - I I N Y C T S A A W G - - - - -	84
Fungi_Catenaria seq_96 ATG12	79 - T D G H L - V V S Y S M T P A W S - - - - -	94
Fungi_Piromyces seq_109 ATG12	72 - G G E L - Q V N Y A N M P A Y G - - - - -	86
Fungi_Gonapodytes seq_104 ATG12	79 - H G - - - A V A D N G - - - - -	87
Fungi_Gonapodytes seq_105 ATG12	92 - A G D L - V I N Y A T T A A W G - - - - -	106
Fungi_Batrachochytrium seq_92 ATG12	108 - D G K L - I V N Y S I T P A W G - - - - -	122
Metazoa_Homo O94817 ATG12	116 - D G K L - V L H Y C K S O A W G - - - - -	130
Metazoa_Xenopus seq_201 ATG12	114 - D G K L - V L H Y C K S O A W G - - - - -	128
Metazoa_Danio seq_186 ATG12	105 - D G K L - V L H Y C K S O A W G - - - - -	119
Metazoa_Drosophila seq_198 ATG12	97 - N G K L - V L Y Y C K N O A W G - - - - -	111
Metazoa_Daphnia EFX89332.1 ATG12	111 - D G K L - I L A Y C R T O A W G - - - - -	125
Metazoa_Caenorhabditis seq_175 ATG12	99 - D K E I L - E L O V S I T P A Y G - - - - -	114
Metazoa_Dicymela seq_194 ATG12	87 - G B T L - F L S Y C K K V A W G - - - - -	101
Metazoa_Corticium seq_182 ATG12	90 - D G K L - V F H Y C K S O A W G - - - - -	104
Holozoa_Helgocaela seq_148 ATG12	99 - E G I L - E L T Y T V I P S A W G - - - - -	113
Holozoa_Stephanocaela seq_158 ATG12	108 - K - A L I L D V T Y G I N E A W G - - - - -	123
Holozoa_Salpingoecia seq_152 ATG12	119 - K G T S L - I L R Y S L T P A Y G - - - - -	134
Holozoa_Capsasporales seq_138 ATG12	128 - K G O L - D I O V A T T P A W G - - - - -	142
Holozoa_Ichthyophonus seq_150 ATG12	101 - D N A L - D I Y Y C T I E A W G - - - - -	115
Holozoa_Creolimax seq_142 ATG12	98 - D S K L - D I Y Y C T T P A W G - - - - -	112
Holozoa_Sphaerodiscum seq_154 ATG12	115 - D B K L - D I H Y S T T P A W G - - - - -	129
Holozoa_Coralichytrium seq_139 ATG12	84 - S N E L - N I Q V A L V E A Y G - - - - -	99
Amoebozoa_Entamoeba XP_653661.2 ATG12	104 - Q B E I - E L T F S R D N V F G - - - - -	118
Amoebozoa_Dictyostelium seq_17 ATG12	103 - N D - Q L - I I N Y S L O M A W G - - - - -	117
Amoebozoa_Vermamoeba seq_21 ATG12	109 - N G K L - V I N Y A N T A A W G - - - - -	123
Amoebozoa_Acanthamoeba seq_15 ATG12	105 - S G O L - V I N Y C T T A A W G - - - - -	119
CRuMs_Mantamonas seq_30 ATG12	112 - N N K L - A I S Y C E T V A W G - - - - -	126
CRuMs_Rigifilia seq_34 ATG12	143 - N D - I L - I V N Y C I T P A W G - - - - -	157

[illegible]

Rhizaria_Amonialesseq_59/ATG5
Rhizaria_Globobulimina)seq_62/ATG5
Rhizaria_Eucyrtidom)seq_61/ATG5
Rhizaria_Bigelowiell)seq_60/ATG5
Rhizaria_Paulinell)seq_63/ATG5
Alveolata_Toxoplasma)AAQM03000026-2-330440-33361/ATG5
Alveolata_Plasmodium)ETW28760.1/ATG5
Alveolata_Plasmodium)ETW39978.1/ATG5
Alveolata_Plasmodium)KOB58748.1/ATG5
Alveolata_Plasmodium)KOB58177.1/ATG5
Alveolata_Vittellia)A06U4C230/ATG5
Alveolata_Chromera)A06U4V62/ATG5
Alveolata_Karenia)A06A76A5D3/ATG5
Alveolata_Tetrahymena)seq_0/ATG5
Stramenopiles_Phytophthora)seq_67/ATG5
Stramenopiles_Peronosporales)seq_65/ATG5
Stramenopiles_Parvosporales)seq_66/ATG5
Stramenopiles_Aureococcus)A04A6S9GGB0/ATG5
Stramenopiles_Aurantiochytrium)seq_64/ATG5
Telonemia_SRR731266)seq_68/ATG5
Centrohelida_Raineriophrys)seq_10/ATG5
Centrohelida_Raineriophrys)seq_11/ATG5
Centrohelida_Raphidiophrys)seq_12/ATG5
Centrohelida_Chanoocyts)seq_9/ATG5
Centrohelida_Acanthocyts)seq_8/ATG5
Haptophyta_Calcidiscus)seq_37/ATG5
Haptophyta_Isochrysis)A06T1HWB5/ATG5
Haptophyta_Isochrysis)A06T1JHNB4/ATG5
Haptophyta_Emiliana)A046U8L241/ATG5
Haptophyta_Pyrnesium)A06GT08TB7/ATG5
Haptophyta_Pavlovales)seq_38/ATG5
Cryptista_Guillardia)XP_00583979.1/ATG5
Cryptista_Rhodomonas)A06U4PNF5/ATG5
Cryptista_Goniomonas)seq_18/ATG5
Cryptista_Goniomonas)A06T1JQ56/ATG5
Cryptista_Palpitomonas)seq_19/ATG5
Glaucophyta_Glaucocystes)A06T1G970/ATG5
Glaucophyta_Glaucocystes)seq_36/ATG5
Chlorophyta_Ostreococcus)OUS45109.1/ATG5
Chlorophyta_Micromonas)seq_16/ATG5
Chlorophyta_Lobosphaera)seq_14/ATG5
Chlorophyta_Lobosphaera)seq_15/ATG5
Chlorophyta_Chlamydomonas)PNW73408.1/ATG5
Chlorophyta_Chlamydomonas)XP_001692662.1/ATG5
Chlorophyta_Arabidopsis)seq_13/ATG5
Chlorophyta_Oryza)seq_17/ATG5
Chlorophyta_Marchantia)P44619.1/ATG5
Ancoracysta_Ancoracysta)seq_4/ATG5
Hemistaplophora_Spironema)seq_39/ATG5
Ancyromonadida_Nutomonas)seq_5/ATG5
Malawimonadida_Malawimonas)seq_47/ATG5
Metamonada_Trichomonas)A0077224.1/ATG5
Metamonada_Trichomonas)DS113397-4-91101-90688/ATG5
Metamonada_Trichomonas)XP_001292688.1/ATG5
Metamonada_Monoceromonoides)seq_49/ATG5
Metamonada_Monoceromonoides)seq_50/ATG5
Metamonada_Monoceromonoides)seq_48/ATG5
Metamonada_Monoceromonoides)seq_51/ATG5
Discoba_Rhynchopus)seq_25/ATG5
Discoba_Diplanema)seq_22/ATG5
Discoba_Diplanema)seq_21/ATG5
Discoba_Trypanosoma)XP_011774026.1/ATG5
Discoba_Euglenoides)seq_23/ATG5
Discoba_Nautilia)XP_00268039.1/ATG5
Discoba_Percolonas)seq_24/ATG5
Discoba_Percolonas)A06U4VJ83/ATG5
Discoba_Andaliu)seq_20/ATG5
Fungi_Saccharomyces)seq_34/ATG5
Fungi_Komagataella)seq_32/ATG5
Fungi_Schizosaccharomyces)seq_35/ATG5
Fungi_Gigasporales)seq_28/ATG5
Fungi_Catenariales)seq_27/ATG5
Fungi_Pirromyces)seq_33/ATG5
Fungi_Gonapodyales)seq_31/ATG5
Fungi_Batrachochytrium)seq_26/ATG5
Fungi_Funiculariales)seq_29/ATG5
Metazoa_Homo)O9H1Y0/ATG5
Metazoa_Xenopus)seq_58/ATG5
Metazoa_Danio)seq_54/ATG5
Metazoa_Drosophila)seq_57/ATG5
Metazoa_Daphnia)seq_55/ATG5
Metazoa_Caenorhabditis)seq_52/ATG5
Metazoa_Dicorymbes)seq_56/ATG5
Metazoa_Corticium)seq_53/ATG5
Holozoa_Stephanocelis)seq_43/ATG5
Holozoa_Helgomonas)seq_46/ATG5
Holozoa_Salpincgocelis)seq_44/ATG5
Holozoa_Capsaspora)XP_00434817.1/ATG5
Holozoa_Ichthyophonus)seq_43/ATG5
Holozoa_Creolimax)seq_41/ATG5
Holozoa_Serialia)seq_45/ATG5
Holozoa_Corallochytrium)seq_40/ATG5
Amoebozoa_Entamoeba)DS571153-6-30394-29480/ATG5
Amoebozoa_Dictyostelium)seq_3/ATG5
Amoebozoa_Vermamoeba)seq_3/ATG5
Amoebozoa_Acanthamoeba)seq_1/ATG5
CruRs_Mantamonas)seq_6/ATG5
CruRs_Rigillia)seq_7/ATG5

225 GSFNNYLKOCVFLSSNNVAAVSAKSKSDQDTLWSGVKADNLLVFPVYHSIFGKH-----LIRYPPRLILRFNEOVDVPTORPILDCGGRRLRECLQOIIPGVLCQOQSEIGITVOGVRVALNIP 243
226 TFFNNYLKOCVFLSSNNVAAVSAKSKSDQDTLWSGVKADNLLVFPVYHSIFGKH-----LIRYPPRLILRFNEOVDVPTORPILDCGGRRLRECLQOIIPGVLCQOQSEIGITVOGVRVALNIP 246
80 QNFMFLKOCVFLSSNNVAAVSAKSKSDQDTLWSGVKADNLLVFPVYHSIFGKH-----LIRYPPRLILRFNEOVDVPTORPILDCGGRRLRECLQOIIPGVLCQOQSEIGITVOGVRVALNIP 172
119 EFFFHSLKOCVFLSSNNVAAVSAKSKSDQDTLWSGVKADNLLVFPVYHSIFGKH-----LIRYPPRLILRFNEOVDVPTORPILDCGGRRLRECLQOIIPGVLCQOQSEIGITVOGVRVALNIP 235
125 SFFNNALKEFLVYASSOAVMGVSQSDFSALWDSIASDPRDFSGARSKIMSVSVAASGCEPLRVLLVSPGLIIOQPTPLRLTDDSKPOIIRTLFESMLPGVOKPEVEVLVCGIKPPLITP 247
226 SFFNNALKEFLVYASSOAVMGVSQSDFSALWDSIASDPRDFSGARSKIMSVSVAASGCEPLRVLLVSPGLIIOQPTPLRLTDDSKPOIIRTLFESMLPGVOKPEVEVLVCGIKPPLITP 250
126 EYIINQLKANYILNKNRLEILPQRIQKDLVYSKHFHIEKICSLYREYIDYNIQINGEEESPVKITHCYDNEYLDQIQNDSSSDHVHLTIGDFLHEQLPSFLIFSPYMFIIVNGIQIPLNTP 250
126 EYIINQLKANYILNKNRLEILPQRIQKDLVYSKHFHIEKICSLYREYIDYNIQINGEEESPVKITHCYDNEYLDQIQNDSSSDHVHLTIGDFLHEQLPSFLIFSPYMFIIVNGIQIPLNTP 250
126 EYIINQLKANYILNKNRLEILPQRIQKDLVYSKHFHIEKICSLYREYIDYNIQINGEEESPVKITHCYDNEYLDQIQNDSSSDHVHLTIGDFLHEQLPSFLIFSPYMFIIVNGIQIPLNTP 250
126 IRFLNTLKEFLVYASSOAVMGVSQSDFSALWDSIASDPRDFSGARSKIMSVSVAASGCEPLRVLLVSPGLIIOQPTPLRLTDDSKPOIIRTLFESMLPGVOKPEVEVLVCGIKPPLITP 247
125 SFFNNALKEFLVYASSOAVMGVSQSDFSALWDSIASDPRDFSGARSKIMSVSVAASGCEPLRVLLVSPGLIIOQPTPLRLTDDSKPOIIRTLFESMLPGVOKPEVEVLVCGIKPPLITP 243
123 KVMVNOFQALVYONSLAPGKLGKQQQDTLWESIKSSNVEAFKVTQNSDOLLFRNLTCRSLAVRLICAGQVLLHPLAPLREDTISRVDOLFKEAMRV-----VELIMHGIRPLEP 241
125 KIRFALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
119 SFFHSLKOCVFLSSNNVAAVSAKSKSDQDTLWSGVKADNLLVFPVYHSIFGKH-----LIRYPPRLILRFNEOVDVPTORPILDCGGRRLRECLQOIIPGVLCQOQSEIGITVOGVRVALNIP 243
124 WNFINALKEAAYIITGNCKNIMNMSQSDQTELWRSVLNQLAEVLRVSSKLLDITDATSGKIPVRLVY-----RTIEEDVD-----ELEB-----VEVIL-DSWVKVHYINS-----PVE----- 223
126 SFFHSLKOCVFLSSNNVAAVSAKSKSDQDTLWSGVKADNLLVFPVYHSIFGKH-----LIRYPPRLILRFNEOVDVPTORPILDCGGRRLRECLQOIIPGVLCQOQSEIGITVOGVRVALNIP 214
114 KAFVHALKQAVHLRQRTARALQDAALFALADOLSAAFSRFRTRKAALLEHRA-----PRGPPPAWR-LAL-LAFALDQDQRDCLADARRATLS-DOBIVVVEEHHVTMAY----- 224
115 GEFPHLFRGMPFLNRSRLRLREHDDADLWESIAEEDRMVITLORMEYFA-----PKAAPVRILOQVRAI-LSQVPPFLDSSL-----FACELVDDILGL-----DSRKLRCOGILPADAL 227
122 QLFRRARKEATFLSSSVSTIMSLELQOQALWQAY-LDISQRRHISGIGTELSEROGROPIRVRY-LGDO-----TLLRPLA-EEAFVQQLQSL-----DOAEACQWQVQKVEA 235
123 WALVNSLKEATVLRHNSRAVMSKESQOMLDGLVEHNKRKWSVNOGLDSD-----CRYVPILFDLCKG-EVKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
124 WALVNSLKEATVLRHNSRAVMSKESQOMLDGLVEHNKRKWSVNOGLDSDSTG-CRYVPILRILV-FDALFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WNFHSLKOCVFLSSNNVAAVSAKSKSDQDTLWSGVKADNLLVFPVYHSIFGKH-----LIRYPPRLILRFNEOVDVPTORPILDCGGRRLRECLQOIIPGVLCQOQSEIGITVOGVRVALNIP 243
123 WNVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
123 WNVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
24 RLSIGLGA-----EQ-----PRALIPRVY-TAQTWRLPVQSGSAGQCLSHALATLLQOL-TFFPALVOGIRPLITP 94
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
123 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 243
123 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WNFHSLKOCVFLSSNNVAAVSAKSKSDQDTLWSGVKADNLLVFPVYHSIFGKH-----LIRYPPRLILRFNEOVDVPTORPILDCGGRRLRECLQOIIPGVLCQOQSEIGITVOGVRVALNIP 243
123 WNVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
24 RLSIGLGA-----EQ-----PRALIPRVY-TAQTWRLPVQSGSAGQCLSHALATLLQOL-TFFPALVOGIRPLITP 94
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
123 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 243
123 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WNFHSLKOCVFLSSNNVAAVSAKSKSDQDTLWSGVKADNLLVFPVYHSIFGKH-----LIRYPPRLILRFNEOVDVPTORPILDCGGRRLRECLQOIIPGVLCQOQSEIGITVOGVRVALNIP 243
123 WNVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
24 RLSIGLGA-----EQ-----PRALIPRVY-TAQTWRLPVQSGSAGQCLSHALATLLQOL-TFFPALVOGIRPLITP 94
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
123 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 243
123 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WNFHSLKOCVFLSSNNVAAVSAKSKSDQDTLWSGVKADNLLVFPVYHSIFGKH-----LIRYPPRLILRFNEOVDVPTORPILDCGGRRLRECLQOIIPGVLCQOQSEIGITVOGVRVALNIP 243
123 WNVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
24 RLSIGLGA-----EQ-----PRALIPRVY-TAQTWRLPVQSGSAGQCLSHALATLLQOL-TFFPALVOGIRPLITP 94
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
123 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 243
123 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WNFHSLKOCVFLSSNNVAAVSAKSKSDQDTLWSGVKADNLLVFPVYHSIFGKH-----LIRYPPRLILRFNEOVDVPTORPILDCGGRRLRECLQOIIPGVLCQOQSEIGITVOGVRVALNIP 243
123 WNVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
24 RLSIGLGA-----EQ-----PRALIPRVY-TAQTWRLPVQSGSAGQCLSHALATLLQOL-TFFPALVOGIRPLITP 94
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
123 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 243
123 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WNFHSLKOCVFLSSNNVAAVSAKSKSDQDTLWSGVKADNLLVFPVYHSIFGKH-----LIRYPPRLILRFNEOVDVPTORPILDCGGRRLRECLQOIIPGVLCQOQSEIGITVOGVRVALNIP 243
123 WNVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
24 RLSIGLGA-----EQ-----PRALIPRVY-TAQTWRLPVQSGSAGQCLSHALATLLQOL-TFFPALVOGIRPLITP 94
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
123 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 243
123 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WNFHSLKOCVFLSSNNVAAVSAKSKSDQDTLWSGVKADNLLVFPVYHSIFGKH-----LIRYPPRLILRFNEOVDVPTORPILDCGGRRLRECLQOIIPGVLCQOQSEIGITVOGVRVALNIP 243
123 WNVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
24 RLSIGLGA-----EQ-----PRALIPRVY-TAQTWRLPVQSGSAGQCLSHALATLLQOL-TFFPALVOGIRPLITP 94
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
123 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 243
123 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WNFHSLKOCVFLSSNNVAAVSAKSKSDQDTLWSGVKADNLLVFPVYHSIFGKH-----LIRYPPRLILRFNEOVDVPTORPILDCGGRRLRECLQOIIPGVLCQOQSEIGITVOGVRVALNIP 243
123 WNVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
24 RLSIGLGA-----EQ-----PRALIPRVY-TAQTWRLPVQSGSAGQCLSHALATLLQOL-TFFPALVOGIRPLITP 94
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
123 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 243
123 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WNFHSLKOCVFLSSNNVAAVSAKSKSDQDTLWSGVKADNLLVFPVYHSIFGKH-----LIRYPPRLILRFNEOVDVPTORPILDCGGRRLRECLQOIIPGVLCQOQSEIGITVOGVRVALNIP 243
123 WNVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
24 RLSIGLGA-----EQ-----PRALIPRVY-TAQTWRLPVQSGSAGQCLSHALATLLQOL-TFFPALVOGIRPLITP 94
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
123 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 243
123 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WNFHSLKOCVFLSSNNVAAVSAKSKSDQDTLWSGVKADNLLVFPVYHSIFGKH-----LIRYPPRLILRFNEOVDVPTORPILDCGGRRLRECLQOIIPGVLCQOQSEIGITVOGVRVALNIP 243
123 WNVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
24 RLSIGLGA-----EQ-----PRALIPRVY-TAQTWRLPVQSGSAGQCLSHALATLLQOL-TFFPALVOGIRPLITP 94
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
123 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 243
123 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WNFHSLKOCVFLSSNNVAAVSAKSKSDQDTLWSGVKADNLLVFPVYHSIFGKH-----LIRYPPRLILRFNEOVDVPTORPILDCGGRRLRECLQOIIPGVLCQOQSEIGITVOGVRVALNIP 243
123 WNVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
24 RLSIGLGA-----EQ-----PRALIPRVY-TAQTWRLPVQSGSAGQCLSHALATLLQOL-TFFPALVOGIRPLITP 94
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
123 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 243
123 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WNFHSLKOCVFLSSNNVAAVSAKSKSDQDTLWSGVKADNLLVFPVYHSIFGKH-----LIRYPPRLILRFNEOVDVPTORPILDCGGRRLRECLQOIIPGVLCQOQSEIGITVOGVRVALNIP 243
123 WNVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
24 RLSIGLGA-----EQ-----PRALIPRVY-TAQTWRLPVQSGSAGQCLSHALATLLQOL-TFFPALVOGIRPLITP 94
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
123 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 243
123 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WNFHSLKOCVFLSSNNVAAVSAKSKSDQDTLWSGVKADNLLVFPVYHSIFGKH-----LIRYPPRLILRFNEOVDVPTORPILDCGGRRLRECLQOIIPGVLCQOQSEIGITVOGVRVALNIP 243
123 WNVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
24 RLSIGLGA-----EQ-----PRALIPRVY-TAQTWRLPVQSGSAGQCLSHALATLLQOL-TFFPALVOGIRPLITP 94
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
123 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 243
123 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WNFHSLKOCVFLSSNNVAAVSAKSKSDQDTLWSGVKADNLLVFPVYHSIFGKH-----LIRYPPRLILRFNEOVDVPTORPILDCGGRRLRECLQOIIPGVLCQOQSEIGITVOGVRVALNIP 243
123 WNVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
24 RLSIGLGA-----EQ-----PRALIPRVY-TAQTWRLPVQSGSAGQCLSHALATLLQOL-TFFPALVOGIRPLITP 94
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
125 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 244
123 ALVRGALKESLHIFDSQDTILMOAEKQNWESIKNLLNQTFSSILDOIQLKLQNNKAIKLPVRVY-IEEYIQOLSSQID-SENIGDFLTKYFKKINDNKNYKVICNGIVGNLNM 243
123 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WALVNSLKEAMVYHSGAKAMALTKDSQQHFOFKLHNRFRVMSQOQLQVEYDGHGVKQVHIFRFRFLRCQFVQKPIPFDDSGKHTLNTLNMIMRHTLHIFRILASLLQSLQICQOAP 241
122 WNFHSLKOCVFLSSNNVAAVSAKSKSDQDTLWSGV

Rhizaria_Amonia[seq_59]ATG5	244	M I W L V R H A T V A D C F L Y V V I V K K - - -	265
Rhizaria_Globobulimina[seq_62]ATG5	247	I M W L V R H A T V A D C F L Y V V I V K Y - - -	268
Rhizaria_Eucyrtidium[seq_61]ATG5	197	Q V L I R T A R N P D L F L H V I R R K K E E	221
Rhizaria_Bigelowiella[seq_60]ATG5	236	F Y L A E N M C A D O F L Y I C L S L H T T E	260
Rhizaria_Paulinella[seq_63]ATG5	248	L R W L G S Y F V H P D F W L Y V V V I V H S A S	272
Alveolata_Toxoplasma[AAQM03000026-2-330440-333361]ATG5	251	L Y W L W K N A S C M D L F L H V V V L P P T V	275
Alveolata_Plasmodium[ETW28760.1]ATG5	251	L Y W L A A N F S O F D H F L H I T I R I P P Y -	274
Alveolata_Plasmodium[ETW39978.1]ATG5	251	L Y W L A A N F S O F D H F L H I T I R I P P Y -	274
Alveolata_Plasmodium[KOB58748.1]ATG5	251	L Y W L A A N F S O F D H F L H I T I R I P P Y -	274
Alveolata_Plasmodium[KOB85177.1]ATG5	251	L Y W L A A N F S O F D H F L H I T I R I P P Y -	274
Alveolata_Vitrella[AOA6U4C230]ATG5	248	R W L A L Y G L R C C C L H I V V R L P R A L	272
Alveolata_Chromera[AOA6U4V462]ATG5	244	I A G L I S S A L A P D G S V Y I V V R V P C H L	268
Alveolata_Karenia[AOA6T6A5D3]ATG5	242	L Y W L A L N G S Y L D L F V H L V A R V P B H L	266
Alveolata_Tetrahymena[seq_0]ATG5	245	L L F Y K Y F S Y D G F T Y L C I Q K - - - -	265
Stramenopiles_Phytophthora[seq_67]ATG5	241	I V E L R N F A Y A D G F L Y V A L S S K S - -	263
Stramenopiles_Peronospora[seq_65]ATG5	224	V R G E G K S F T L N D S I K A L L P Q L F T K E	248
Stramenopiles_Peronospora[seq_66]ATG5		-----	
Stramenopiles_Aureococcus[AOA6S9GGBQ]ATG5	225	V V D A A P D V A D R R P F S H V V V K L S T A G	249
Stramenopiles_Aurantiochytrium[seq_64]ATG5	228	V D L I E A L A H A D M F L Y I C L Y T D E T -	251
Telonemia_SRR7371266[seq_68]ATG5	232	Q C E L V L R H P P D F L H M S L I T A I M G	256
Centrohelida_Raineriophrys[seq_10]ATG5	242	N H N L S S O C P Q H F L H L R I H I H L T	266
Centrohelida_Raineriophrys[seq_11]ATG5	242	L L W G D N L M S G D G F V Y V K V M T S T Q	266
Centrohelida_Raphidiophrys[seq_12]ATG5	242	T Y P S H H N T N N N N N N N N N N N N N	266
Centrohelida_Choanocystis[seq_9]ATG5	244	L A W L M N N A T S A D D F Y V I T V R M S T A	268
Centrohelida_Acanthocystis[seq_8]ATG5	247	L A V I M D H C C G D F I Y V I I S I S A T A	271
Haptophyta_Calcidiscus[seq_37]ATG5	95	L W L Y R W C C P D G - - - - - - - - - -	107
Haptophyta_Isochrysis[AOA6T1HWS]ATG5		-----	
Haptophyta_Isochrysis[AOA6T1HN54]ATG5	244	I L P S G A V T V G B A L G L L P G T A E G G	268
Haptophyta_Emiliana[AOA6L241]ATG5	246	S W L I E A S S P D G F L Y V V L M P G S G	270
Haptophyta_Prymnesium[AOA6T0B7T7]ATG5	248	L W L I G A C S P D G F L Y Y V Y S C S P S	272
Haptophyta_Pavlova[seq_38]ATG5	245	D W L C A A C A H P D G F L H V V L H A R A T	269
Cryptista_Guillardia[XP_005835979.1]ATG5	249	V L W L G O O L A G A D T F L Y I C V I P K S K D	273
Cryptista_Rhodomonas[AOA6U4PNF5]ATG5	248	V L W L G O O L A A C D G F L Y V S L V P T R A E	272
Cryptista_Goniomonas[seq_18]ATG5	239	I W L A S T I F G - - - - F T C R R G P V A P	259
Cryptista_Goniomonas[AOA6T1QN56]ATG5	246	L W L A D N L A S I D N F L Y F V P S G S G G	270
Cryptista_Palpatomonas[seq_19]ATG5	236	A E W L L Y A C N P D T S L N I A L R K R K - -	258
Glaucophyta_Gleocochaete[AOA6T1G970]ATG5	173	Q W L V E H F C P A D G F V T I A L A A N B K L	197
Glaucophyta_Gleocochaete[seq_36]ATG5	239	Q A M M E M A H P D F L Y V V M I O I - - -	260
Chlorophyta_Ostreococcus[OUS45109.1]ATG5	223	L A K I E A L R H V D G F L Y L V H C G T S S	247
Chlorophyta_Micromonas[seq_16]ATG5	246	E L I H A S L R G P R F S H L V F S R A K - -	268
Chlorophyta_Lobosphaera[seq_14]ATG5	248	V A W L H S R F S Y A D H F L Y V V V I Q H T - -	270
Chlorophyta_Lobosphaera[seq_15]ATG5	198	V T S A D T D C P C P T A M P S G L A A V R	222
Chlorophyta_Chlamydomonas[PNW73408.1]ATG5	248	L G V L H A A M S P D L F L Y V V V R L D E E G	272
Chlorophyta_Chlamydomonas[XP_001692662.1]ATG5	203	L H C T Q L C A C S S W L G L R L L - - - -	222
Chlorophyta_Arabidopsis[seq_13]ATG5	246	F S W V V N N L M N P E F V L H I S V L V K A R Q	270
Chlorophyta_Cryzela[seq_17]ATG5	249	F L V A V A N L N K N P C H L H I C V Y V E R K	270
Chlorophyta_Marchantia[PTQ44619.1]ATG5	247	D W V A R N L C P S M F I H L G I C T W M S R	271
Ancoracysta_Ancoracysta[seq_4]ATG5	236	Q V L C D T L G P D L F L Y I S V A Q R E A F	260
Hemimastigophora_Spironema[seq_39]ATG5	210	L V E L L D C F S C P D H F V V Y T I R E D T T E	234
Ancyromonadida_Nutomonas[seq_5]ATG5	224	V G L W K I A M N V D T W L W M A F D H Q K	248
Malawimonadida_Malawimonas[seq_47]ATG5	240	V A W L W R N O M S A D N F L Y I V V V - - - -	259
Metamonada_Tritrichomonas[OHT07224.1]ATG5	219	L E E V V P I L L G A D G F I Y I V L K - - - -	238
Metamonada_Trichomonas[DS11397-4-91101-90688]ATG5	118	K T L I P T L V P D G F L Y V V V - - - - -	136
Metamonada_Trichomonas[XP_001292688.1]ATG5		-----	
Metamonada_Monocercomonoides[seq_49]ATG5	176	V K D E A G I S A D V S L S S E A K E E E	200
Metamonada_Monocercomonoides[seq_50]ATG5	242	L A S E R N F B E E E E D A N K O D E A E	266
Metamonada_Monocercomonoides[seq_48]ATG5	162	F D W M A K E E E K E E E K E S E E E E E E	186
Metamonada_Monocercomonoides[seq_51]ATG5	247	M L L D L N F C F P E L F L R C A O R S F A R S	271
Discoba_Rhynchopus[seq_25]ATG5	241	L W L T E Y M A H P D G F L H I V V S T A D R D	265
Discoba_Diplonema[seq_22]ATG5	217	M I L Y L H L L Q H T D E L L H I S V L W E S V S	241
Discoba_Diplonema[seq_21]ATG5	242	L W L A E Y M A H P D C F L H I T I E T S S - -	264
Discoba_Trypanosoma[XP_011774026.1]ATG5	239	V K L L E R F T S A D G R L Y V I F T V F - -	260
Discoba_Euglenia[seq_23]ATG5	242	L R F V A K - G S P D L W I Y L V L I R E T D	265
Discoba_Naegleria[XP_002680539.1]ATG5	247	M L V L F E N G A H P D G F L M C K - - - -	266
Discoba_Percolomonas[seq_24]ATG5	232	K S C C E L F M A D C F L Y M I A Y L E E E -	255
Discoba_Percolomonas[AOA6U0JY83]ATG5	248	L F D V E A F S P Q D L L Y I V V V I E A S E	272
Discoba_Andalucia[seq_20]ATG5	236	R F L R D V G A Y P D L L I H C V N R D G C	260
Fungi_Saccharomyces[seq_34]ATG5	233	L Y D L S K L R S F D G F L Y I T L V I K G G	257
Fungi_Komagataella[seq_32]ATG5	248	L I D L S Y F A F S D G F V H I S V V F N O P K	272
Fungi_Schizosaccharomyces[seq_35]ATG5	225	L D E L N R D F C Y I D G F L H I V L M K V - -	246
Fungi_Claroideoglomus[seq_28]ATG5	242	L W A S Q N L C P D N F L H I V V L L E T - -	264
Fungi_Gigaspora[seq_30]ATG5	240	I W A S Q N L C P D N F L H I V V L L S I - -	262
Fungi_Catenaria[seq_27]ATG5	234	L A V V R H L V C V D G M Y L V V E R I L K	258
Fungi_Piromyces[seq_33]ATG5	240	L W L G O Y L S Y P D N W L H I V I K Q I K E -	263
Fungi_Gonapodytes[seq_31]ATG5	246	V W L G M N M T Y A D G F V H V V R G A - - -	267
Fungi_Batrachochytrium[seq_26]ATG5	227	L W L R H A S Y S D G F L H F V F Y T D - -	248
Fungi_Forticula[seq_29]ATG5	238	C L W L M V N M C A D M F V H V L R H I - - -	259
Metazoa_Homo[Q9H1Y0]ATG5	247	Q V L S E H L S Y P D N F L H I S I I P O R T D	271
Metazoa_Xenopus[seq_58]ATG5	247	Q V L S E H L S Y P D N F L H I S I I P O R T D	271
Metazoa_Danio[seq_54]ATG5	248	Q V L S E H L S Y P D N F L H I S I I P A B S D	272
Metazoa_Drosophila[seq_57]ATG5	242	Q V L S E H L S Y P D N F L H S I D Y Q D V -	265
Metazoa_Daphnia[seq_55]ATG5	243	Q V I S E H L S Y P D N F L H L C I R Y S Q T -	266
Metazoa_Caenorhabditis[seq_52]ATG5	238	I F A A K N L S Y P D N F I H V L L L V V G -	261
Metazoa_Dicymela[seq_56]ATG5	227	Q V L M N M S F P D G F I H - - - - - - - -	242
Metazoa_Corticium[seq_53]ATG5	240	L Q F L R E H F S Y P D N F L H I A I V T R - -	261
Holozoa_Helgocela[seq_42]ATG5	239	Q V L C E H F V P D N F L H I T V A T S A Q	263
Holozoa_Stephanocela[seq_46]ATG5	242	Q V L C E H O T Y P D N F L H L T V F S A A V	266
Holozoa_Salpingocela[seq_44]ATG5	237	Q V L A A H L A P D N F C H V V V H K L D Q S	261
Holozoa_Capsaspora[XP_004348117.1]ATG5	243	L W L G E H C C P D N F L H I C I L - S E L	266
Holozoa_Ichthyophonus[seq_43]ATG5	198	Q V L S D N L S Y P D N F L H I V I S F T D	222
Holozoa_Creolimax[seq_41]ATG5	245	Q V L R D C S S Y P D N F L H I V R T C O S S R	269
Holozoa_Sphaerothecum[seq_45]ATG5	243	I W L S E N M S Y P D N F L H I C I L P P R Q I	267
Holozoa_Coralochytrium[seq_40]ATG5	229	L A W L S K A S Y A D N F L Y I F V K - - - -	248
Amoebozoa_Entamoeba[DS571153-6-30394-29480]ATG5	229	L W L A L N L S H S O L F L H V I I R K T D E L	253
Amoebozoa_Dictyostelium[seq_2]ATG5	242	A W L Y E H F G P D N F L Y I V L I D S Q N	266
Amoebozoa_Vermamoeba[seq_3]ATG5	239	V W L A N N L A H P D N F V Y I S L V H O N K	263
Amoebozoa_Acanthamoeba[seq_1]ATG5	242	I L W L G E N A H P D N F L Y V V V K E N - - -	263
CRuMs_Mantamonas[seq_6]ATG5	213	R E R E G K G R T D L V L F F K M N S - - -	234
CRuMs_Rigifilia[seq_7]ATG5	238	V A W L E N L A H P D N F L H I V L R P Q O L E	262

[illegible]

Rhizaria_Amonites1seq_50|ATG16
Rhizaria_Globobulimina1seq_52|ATG16
Rhizaria_Globobulimina1seq_51|ATG16
Rhizaria_Eucyrtidium1seq_61|ATG16
Rhizaria_Bigelowella|A0A6U1DX27|ATG16
Rhizaria_Paulinella1seq_53|ATG16
Rhizaria_Palaeomonas|A0M000005-2|13658-16585|ATG16
Alveolata_Plasmodium|XP_001350893|ATG16
Alveolata_Vitellina|CEM27357|ATG16
Alveolata_Chromera1seq_6|ATG16
Alveolata_Chromera|A0A0G4EZ71|ATG16
Alveolata_Oxyrhiza|A0A6V3VN06|ATG16
Alveolata_Karenia|A0A6T4VB16|ATG16
Alveolata_Tetrahymena1seq_7|ATG16
Stramenopiles_Phytothorales1seq_54|ATG16
Stramenopiles_Phytothorales1seq_1|ATG16
Stramenopiles_Aureococcus|A0A6S9GLY8|ATG16
Stramenopiles_Aurantiochytrium1seq_1|ATG16
Telonemia_SRR7371266|seq_0|ATG16
Telonemia_SRR7371266|seq_60|ATG16
Centrohelidia_Raineriophrys1seq_16|ATG16
Centrohelidia_Raphidiophrys1seq_17|ATG16
Centrohelidia_Choanocystis1seq_15|ATG16
Centrohelidia_Acanthocystis1seq_14|ATG16
Cryptista_Guillardia|A0A6U6DUJ1|ATG16
Cryptista_Rhodomonas_31|ATG16
Cryptista_Rhodomonas|A0A6U4W9|ATG16
Cryptista_Goniomonas1seq_21|ATG16
Cryptista_Palatomonas1seq_22|ATG16
Glaucophyta_Gloeochaete|A0A6T0X249|ATG16
Chlorophyta_Ostreococcus|XP_003082300_2|ATG16
Chlorophyta_Lobomonas1seq_19|ATG16
Chlorophyta_Lobosphaera1seq_18|ATG16
Chlorophyta_Chlamydomonas1seq_PNW83451|ATG16
Chlorophyta_Aradipops1seq|AB09394_1|ATG16
Chlorophyta_Crya1seq_31|ATG16
Chlorophyta_Marchantia|OAE30304_1|ATG16
Ancoracysta_Ancoracysta1seq_10|ATG16
Hemistastophora_Spironemalis1seq_35|ATG16
Ancoromonada1seq_55|ATG16
Malawimonadida_Malawimonas1seq_44|ATG16
Metamonada_Tritrichomonas|A0A1J4JQ14|ATG16
Metamonada_Tritrichomonas|A0A1J4K1G6|ATG16
Metamonada_Tritrichomonas|A0A1J4J3W9|ATG16
Metamonada_Tritrichomonas|OH707110_1|ATG16
Metamonada_Tritrichomonas|XP_011212-1-10691-108462|ATG16
Metamonada_Trichomonas|XP_001318993|ATG16
Metamonada_Monocercomonoides1seq_57|ATG16
Discoba_Rhynchopis1seq_59|ATG16
Discoba_Diplonemal1seq_24|ATG16
Discoba_Trypanosoma|T9297_11_vs_1-5-1961-487-1959754|ATG16
Discoba_Euglenal1seq_25|ATG16
Discoba_Naegleri1seq_26|ATG16
Discoba_Percolonemal1seq_A0A6U0M3Q1|ATG16
Discoba_Andiculis1seq_23|ATG16
Breviata_Pyruis1seq_11|ATG16
Fungi_Saccharomyces1seq_34|ATG16
Fungi_Komagataella1seq_32|ATG16
Fungi_Schizosaccharomyces|ENP.596308.1|ATG16
Fungi_Dactyloleoidem1seq_5|ATG16
Fungi_Gigasporal1seq_30|ATG16
Fungi_Catenari1seq_29|ATG16
Fungi_Piromyces1seq_33|ATG16
Fungi_Gonapodycel1seq_31|ATG16
Fungi_Batrachochytrium1seq_27|ATG16
Fungi_Batrachochytrium1seq_28|ATG16
Fungi_Batrachochytrium|XP_006675434_1|ATG16
Fungi_Fonticula1seq_56|ATG16
Metazoa_Homo|Q67605|ATG16L1
Metazoa_Homo|Q8NA44|ATG16L2
Metazoa_Xenopus|KAE8604610_1|ATG16
Metazoa_Xenopus|A0A6B8QBR3|ATG16
Metazoa_Xenopus|CAJ82169_1|ATG16
Metazoa_Xenopus|XP_004919569|ATG16
Metazoa_Xenopus|XP_004919571_2|ATG16
Metazoa_Xenopus|XP_004919572_1|ATG16
Metazoa_Danio1seq_47|ATG16
Metazoa_Drosophila1seq_48|ATG16
Metazoa_Daphnia|EFX75688_1|ATG16
Metazoa_Caenorhabditis1seq_45|ATG16
Metazoa_Dicymal1seq_58|ATG16
Metazoa_Corticium1seq_46|ATG16
Holozoa_Helgocela1seq_39|ATG16
Holozoa_Stephanocela1seq_42|ATG16
Holozoa_Stephanocela1seq_43|ATG16
Holozoa_Salpingoelma1seq_41|ATG16
Holozoa_Capsasporal1seq_36|ATG16
Holozoa_Ichthyophonus1seq_40|ATG16
Holozoa_Creolimax1seq_38|ATG16
Holozoa_Sphaerothecium1seq_2|ATG16
Holozoa_Coralichthyrium1seq_37|ATG16
Amoebozoa_Entamoeba|A0A5K1UAD5|ATG16
Amoebozoa_Entamoeba|IN43|ATG16
Amoebozoa_Dictyostelium1seq_04|ATG16
Amoebozoa_Vermamoeba1seq_08|ATG16
Amoebozoa_Acanthamoeba|XP_003407936_1|ATG16
CRuMs_Mantamonas1seq_12|ATG16
CRuMs_Rizqiella1seq_13|ATG16

[illegible]

Rhizaria_Amonia[seq_50]ATG16
Rhizaria_Globobulimina[seq_52]ATG16
Rhizaria_Globobulimina[seq_51]ATG16
Rhizaria_Eucyrtidium[seq_61]ATG16
Rhizaria_Bigelowiella[A0A6U1DX27]ATG16
Rhizaria_Paulinella[seq_53]ATG16
Alveolata_Tooplasma[AAQ03000005-2-13658-16585]ATG16
Alveolata_Plasmodium[XP_001350993.1]ATG16
Alveolata_Vitrella[CEM27357.1]ATG16
Alveolata_Chromera[seq_61]ATG16
Alveolata_Chromera[A0A0G4EZ71]ATG16
Alveolata_Oxvrrhis[A0A6V3VN06]ATG16
Alveolata_Karenia[A0A6T4VB16]ATG16
Alveolata_Tetrahymena[seq_71]ATG16
Stramenopiles_Phytophthora[seq_54]ATG16
Stramenopiles_Personospora[seq_41]ATG16
Stramenopiles_Aureococcus[A0A6S9GYL8]ATG16
Stramenopiles_Aurantiochytrium[seq_11]ATG16
Telonemia_SRR7371266[seq_0]ATG16
Telonemia_SRR7371266[seq_60]ATG16
Centrohelidia_Rainenophrys[seq_16]ATG16
Centrohelidia_Raphidophrys[seq_17]ATG16
Centrohelidia_Choanocystis[seq_15]ATG16
Centrohelidia_Acanthocystis[seq_14]ATG16
Cryptista_Guillardia[A0A6U6DUJ1]ATG16
Cryptista_Rhodomonas[seq_31]ATG16
Cryptista_Rhodomonas[A0A6U4W919]ATG16
Cryptista_Goniomonas[seq_21]ATG16
Cryptista_Palpitomonas[seq_22]ATG16
Glaucochyta_Gloeocetea[A0A6TX0249]ATG16
Chlorophyta_Ostreococcus[XP_00302300.2]ATG16
Chlorophyta_Micromonas[seq_19]ATG16
Chlorophyta_Lobosphaera[seq_18]ATG16
Chlorophyta_Chlamydomonas[PNNW3451.1]ATG16
Chlorophyta_Arabidopsis[BAB09394.1]ATG16
Chlorophyta_Oryza[seq_20]ATG16
Chlorophyta_Marchantia[OE30304.1]ATG16
Ancoracysta_Ancoracysta[seq_10]ATG16
Hemistagophora_Spironema[seq_35]ATG16
Ancoromonadida_Nutomonas[seq_55]ATG16
Malawimonadida_Malawimonas[seq_44]ATG16
Metamonada_Tritrichomonas[A0A1J4J144]ATG16
Metamonada_Tritrichomonas[A0A1J4K1G6]ATG16
Metamonada_Tritrichomonas[A0A1J4J3W9]ATG16
Metamonada_Tritrichomonas[OH700110.1]ATG16
Metamonada_Trichomonas[DS113312-1-106981-108462]ATG16
Metamonada_Trichomonas[XP_001318993]ATG16
Metamonada_Monoceromonoides[seq_57]ATG16
Discoba_Rhynchopis[seq_21]ATG16
Discoba_Diclenemoides[seq_24]ATG16
Discoba_Trypanosoma[T927_11_v5.1-5-1961487-1959754]ATG16
Discoba_Euglenia[seq_25]ATG16
Discoba_Naegleria[seq_26]ATG16
Discoba_Percollomonas[A0A6U0M3Q1]ATG16
Discoba_Andalucia[seq_23]ATG16
Breviata_Pygusul[seq_11]ATG16
Fungi_Saccharomyces[seq_34]ATG16
Fungi_Komagataella[seq_32]ATG16
Fungi_Schizosaccharomyces[NP_596308.1]ATG16
Fungi_Claridiales[seq_51]ATG16
Fungi_Gigasporae[seq_30]ATG16
Fungi_Catenaria[seq_29]ATG16
Fungi_Piromyces[seq_33]ATG16
Fungi_Gonapodya[seq_31]ATG16
Fungi_Batrachochytrium[seq_27]ATG16
Fungi_Batrachochytrium[seq_28]ATG16
Fungi_Batrachochytrium[XP_006675434.1]ATG16
Fungi_Forticul[seq_56]ATG16
Metazoa_Homo[Q676U5]ATG16L1
Metazoa_Homo[Q8NA4A]ATG16L2
Metazoa_Xenopus[KAE8604610.1]ATG16
Metazoa_Xenopus[CAJ82169.1]ATG16
Metazoa_Xenopus[XP_004919969.2]ATG16
Metazoa_Xenopus[XP_004919971.2]ATG16
Metazoa_Xenopus[seq_49]ATG16
Metazoa_Danio[seq_47]ATG16
Metazoa_Drosophila[seq_48]ATG16
Metazoa_Daphnia[EFX75688.1]ATG16
Metazoa_Caenorhabditis[seq_45]ATG16
Metazoa_Dicymela[seq_58]ATG16
Metazoa_Corticium[seq_46]ATG16
Holozoa_Helgocael[seq_39]ATG16
Holozoa_Stephanocael[seq_43]ATG16
Holozoa_Stephanocael[seq_42]ATG16
Holozoa_Salpingocea[seq_41]ATG16
Holozoa_Capasporea[seq_36]ATG16
Holozoa_Ichthyophonus[seq_40]ATG16
Holozoa_Creolimax[seq_38]ATG16
Holozoa_Sphaerothecum[seq_21]ATG16
Holozoa_Carolinichytrium[seq_37]ATG16
Amoebozoa_Entamoeba[A0A5K1UAD5]ATG16
Amoebozoa_Entamoeba[B1M4G3]ATG16
Amoebozoa_Dictyostelium[seq_81]ATG16
Amoebozoa_Vermamoeba[seq_91]ATG16
Amoebozoa_Acanthamoeba[XP_004340796.1]ATG16
CRuMs_Mantamonas[seq_12]ATG16
CRuMs_Rigifilia[seq_13]ATG16

305NRAPIVDLYGP..... 315
363 L I F S G S H D R T I K L W D L E T A A C K Y T M A H S S I N D L T S P D E Y Y L A T A H D G C I R F W G K D R K E L F K L T E P O M O I N G I O F S P D G I Q I L T S G O K G I I I W D L R K Q O K L N E I F N K E Y K N T N I L T G 483
363 L I F S G S H D R T I K L W D L E T A A C K Y T M A H S S I N D L T S P D E Y Y L A T A H D G C I R F W G K D R K E L F K L T E P O M O I N G I O F S P D G I Q I L T S G O K G I I I W D L R K Q O K L N E I F N K E Y K N T N I L T G 483
191 T V T Y G S Y D R A K I W D L N K E I N T R I V M S S I N C L A I S D M S I V A T A H L S A V R F W S G D E L Y T H K E L S S Q A Q V D F A R D Q T V L V N S I T S G I Q L D L R T F I L K K I S B H T N T C S W A 306
357 Q A Y T G S Y D R T I V I W D M T K R K S H I D G S A V N Y L S W A G N I L G A H L S R V L W S S G D E Y Y T H K I T R O A S I E F G D G H A V N S K O N T Q L I D I T T Y N S I K V F K D I T R S H M N N 477
360 H V Y T G S H D R T V K I W D L S T G C O T K I M A S A O G C L T S I S V G C V L S A H I S H S V R M S M A T E L W R K O K L S Q Q V S V D W A S D G R T I L N S K S I L K L D V T R M A V S G S A B R K R N G N 490
364 S W S C L D E T V L W D A R R S A D V K T S L D A A T M T S A S P D E W L A I S H O N S L V L N V A E K C E R V A L Q L T E A A G A V A D P S G R L A L C G O K Q K V V D I A M K E M T L H I E R Y N I V O A 484
Alveolata_Plasmodium[XP_001350993.1]ATG16
243KELKKLYOEIT..... 254
347 K A Y S A S A D K T I K I W N I H R S V Q V K T A H I S M I T C A S I H P S D C L V T G R D G H I K I W T L R G D D C Q O S M O A H E D E L V G T E Y S P D G E Y I V S C A K N S V H S N D M F R V R K O L G E P G G R S Y R K R 467
257 L L F T A L D D R T Q L W D F N K G S P L H S L S V S K L T S A A V S R D F E T A V T G R N G T V M I L S L R G N K I I E I R D E H T Q E V T G V K I E D M S S F V T Q G E D N T V K W D L A Q R V E L S V P L D E W N F A V G H A 377
327 L L F T A L D D R T Q L W D F N K G S P L H S L S V S K L T S A A V S R D F E T A V T G R N G T V M I L S L R G N K I I E I R D E H T Q E V T G V K I E D M S S F V T Q G E D N T V K W D L A Q R V E L S V P L D E W N F A V G H A 447
327 K G S A G F A O R T I V K I W D L R G R N V R S I S C P Q V L H A S S E D G A F L A T C H O N G H A V M A N S E M G O M L G A V H D P A V G V H F A D G R C I A S F C G R S R V L L S D T M T S L R V M S G S M R P P P V T S 447
279 K A F T A S M K T V R L W D L E K C O L L K S T P I S S P I T G A S V Q A S S C V V T V T G S G S I S V L D P P E R A R M O O P I V H V G O G I V G L R V P P G R S V L G A O E D T L C I L A L D T L R T H T L D S L G O L V S G S 398
360 K V V S G S T D R S L K I W D I N K V S Q I K S I L C G S I M R A I D I F O S E P I V S G H D G S I R L S I D S N N Y N V G V F E N V G V K I N C O N Y I L A S S E G F T K L V V D L R K N V G S I T P N Q O F N N H F N 480
329 E V I T G S S D R S L R W D V L R V R L Q V G V S S O R D I A A S G F V O P A S A P O D G A V R F M T T R C V O E L R L H T E C Q S V S F G S E L L I N S R H T K L V I D P T Y B V L R E L H H K D C O C F P M G 447
209 V L V T A A T D R F V K P V N R A S O T M P A P G C L A D L D P L S D D L V T G H G A L R W B A S P D V A L E I K D A H C A V A S A V A D G R T S O L A S L A K H T R L F V D A T S R L H A L S H D N R C G A A R C 328
169 Y A A G G R K I I W D V S S S N V R V D M S K C L A L D N E Q G T L L V S G H V B K G R L W D M T B E R A G V T A L H T N P L S V S F K L G - D I V T A A M N R L A I L D O R K L B E P R Y L S D R E F R A N Q W C 286
116 H V F S T S T D R T V R W D V A R E Q L T N T I M C L S G C N D V R V N D K V A T G H G O G M R L Y D S R O C K E A G V R - M O K P I T S L R F S Q D G F A L T S K O N T I K V C D V R T L N P L Y E L T H P N L S V S N I Q 233
361 N A V T G S H D R T V K I W D L G T K C L O L T I G A S M I N D V A P P D G M H V S G H Y G S I R F N D P T K E E L A K L E - M A G H V T S V C Y T P C G T K L V S C R D S S L K I D I R M F G E L C T M K D D S Y R T L S N S 480
360 R V V S G S C D R T I K O W L S R G Y C T R I L L C I S S N S V C P D R S G F M V A S G H F K S V K L W D V D R E V K O I E D L H T Q O V H F E P S G R H L I N G R O N V L K I D V R M M O T I N T M T H P E L Y V P L T Y S 470
354 R V V S G S C D R T I K W D L N R G Y C T R I L L C I S S N S V S R D T B A M V A S G H F K T L R W D V D G T E I K V D D A S Q O V A H F A P D G H F I M S C S K S I K I D A Y T E T V O L G H K S H K L O I K W A 474
347 R V V S G S C D R T I K O W L R G Y C T R I L L C I S S N S V A D A A G Y L V A S G H F K S V K L W D V S E K E Y K I E N L A A O I V A F D P S G R H L I L G E S T K L I T A D T Y E T V I G H R D L Q V A V N T 467
Alveolata_Plasmodium[XP_001350993.1]ATG16
355 Y A F S G G Y D M I K W D L H E L L V S K I T A G S S S C N A V T V S S V I V S V L N S I R L W D T I T S E F E H M T I G S Q P I T S I C P S M S D M N S R O S A L S D F K Y S C V R K F O H S T I R N G V M N N 477
149 B L Y S G G Y D M I K W D V S L S E T L H S Y N C S S C D A T M S E G A V L M S V H L B A S L R W D L T R T G A F A H E V A G M T O P V S C H N E A N Q O V L N G R D O C L V D Y R K Y D C V R K H A B X N G V M N N 269
360 Q V I S G S Y D R T I R W E L S K Y G I K T L F T S I S I N D L C S P D S S V L C S V H L D F H L R F W D F S G T V O H E V S - V H S H P I T S V S L Y P A N V Y V T L G R D D V L K L V D V T Y Q A V A R S D S F H H G T Y A 479
359 R I V T A G A D R K M V Y L G K G N C V L L H P S T O N A L A I T T - D N O L I T G H F D G G L R W D L S G E V V M E K H T A A I T O E A S P D M T G V T G T G O D F V T V T D V R M E K K M A S M T S F K N T Y A F T 478
359 R M V S G S Y D R S V K L W I A K G Y O V K M L C I S S N S V D S S I T I S G H V D G L R F D A S S A L E H I S D M T S O I G H L H V D G H V L A L S R O N T K L I D T R T Y A T M T F D E B F R V G T M N 479
340 R A I S A S D R T L K I W D L V R G L A T T M L A T I A S H L S I G A T E R H A F S G H F D G S R W D L I A N Q V E K E N K - V H A G P I S I V A V S E N E V L L N S R O N K L K L V D V M H E V V R N S S K P F R V G T M S 459
364 R A V S A S D R T I K W D L H K F O V A S I M A S A I A S E S S I S I S H F G A C R W D L O K R G S H E V K - E H A C H V S V L V A P K S H F M C A S R O N T K L V O L P E C Q O T K A T A R S S O W A 483
220 R A V S A G N D R L K W D L R G Y C T R I V C A R T O N S R L R C T G D A M F C S G F D G T L R W D M S N P V H V A G L S G O I S V A V M G S G E T L C S R O N T K L V D M F E E R H T R A P F V G V T I W C 340
364 L A V S I S G R V W S P D R K Y G N G - S V L G A A G A A A A G T D D V Y L R L Y A G A R I S D S M A V A N - I V D F A A A D A L W R N P S I A F I A A G N S S A K V L N V A A D T W A Y L R T G V T I G A A A 482
323 H V F S T S T D R T V R W D V A R E Q L T N T I M C L S G C N D V R V N D K V A T G H G O G M R L Y D S R O C K E A G V R - M O K P I T S L R F S Q D G F A L T S K O N T I K V C D V R T L N P L Y E L T H P N L S V S N I Q 233
322 V L A S S N D H I K I W D L S G F O K S I M S G N A N S L A F I - D G V T L C S G H R G H L R W D I S A K C O S I F - A H - L D V S S V S R N R N F L I S G C O N V N I F D P R T M E V G C K F A M G N R V S W S G 438
319 R A V A S Y D R T I K W D L G T G Y G V N T I V C Y S N S V C V T S D G A L I C S G H G O G L R F W D I S G K L A N E V A - A H G L G I S V S L S R T H T V L S G R A N I N F D V S L E I R A T R S R N F R A A T N W C 439
355 H V M T G S S D R T I K W D L M T G Y C L O T V I G C I S C N S V A L S D N Q L M S G H F C T V R L T A S K E E V Q T L S N L T Q O V N V R F S P D G T Y L L A S R S T K L V D I T F O T Y L S H E K K N I M W S 475
346 H V I T G G H D R V K I W D L N K Y G V T N L F T E N C I A C L S I D B L V T S G H M G N L R W D I T E K L L S E V A - G S S A V S S V L R N R N R I L S G G N V N D V F D T T L E I C G T R A S G N R L A S H N S 442
156 T C F T G S D R T L K W D L K D F N K L Y I C M G S Y D L A L S D C G T I M S G H G L R F M S T I R T D - I O E G A P V D O I C R L R S I T R L L V L S R O N K M L I F D T M A S L P M T H S D F S V M C S W S 275
364 R A V S A S D R T I K W D L H K F O V A S I M A S A I A S E S S I S I S H F G A C R W D L O K R G S H E V K - E H A C H V S V L V A P K S H F M C A S R O N T K L V O L P E C Q O T K A T A R S S O W A 483
322 K Y S G S R D L L K L V D Y T K T R I N T F K K A T P R Y V I T L D S L E I T A H A D G H L W D I S N S O I G I - V K R D K V S O V I G I R S M T V S L S I D K T I S V S D Y R V N L G K N I A T T A - G I R S D 439
290 O F I A C S N E R K I K Y D I D R L K L S L K A S T A P L Y T I L N K S Y L A S S A D G R V C L W D S E H T P I Q T I K - E N S S R I Q V L G I - N D S L I V S L M O C N L F I D K S G A K I I E K I L K L A - S V N S E 406
319 R V V S C C R D T V L V D Y N K S T I S S F T S S I R Y S T V L - G S O I V T S H D G K L R W D F T H G A P I I K - V H K S A I Q V I G R O S T L V S L G T D K A I V S D W S G K I I G K V S I L K S - B L R S E 434
299 Q L I S A S D R T V I F D I N K G S M S T I S I I A V A Y S C A T N S T P F A V G C N D G A I L V D T R E K K I A K I E K I S K O I S L I P S T A K R I V L S L G M D C V C E S I D G R V R I Q L S H L V V K N H A 419
267 Q L L S A S D R T V I F D I N K L A C I T I I S S E Y S T P T A N N L V A G C F E K I R F I D P R K I V A N T I D - L K S G A V L S I I P S I T G D V I S L G L G M D C V C E S I D G R V R I Q L S H L V V K N H A 419
314 K F V T C G R N S I L F D I Q R S A P N T I S S T P N S I P L O G E S L V T G H Y G G Y I R G Y L D S S Q H V F I K - B K Q P I Q V C G R O A S K I M S I S C K T I A S I D L K E T S V S W F N H R A - B L R S E 431
298 T V S S T D K R I I W D I N K A E P O V S Y G C G Y A L S A T - H E T I Y S G T E G A I K W D R A S S S I G E I O N C H E S T I V L G S P D R Y L L V A R G S S S V A D F P M L T M C K W F S P M S T Q N T 417
327 L L C S A S D R T I K W D L N K Y G V T N L F T E N C I A C L S I D B L V T S G H M G N L R W D I T E K L L S E V A - G S S A V S S V L R N R N R I L S G G N V N D V F D T T L E I C G T R A S G N R L A S H N S 442
331 T L I C A N R T I R W D L N K Y G V T N L F T E N C I A C L S I D B L V T S G H M G N L R W D I T E K L L S E V A - G S S A V S S V L R N R N R I L S G G N V N D V F D T T L E I C G T R A S G N R L A S H N S 442
331 N A V S A S D R T I R W D L Q S A T I O K L L V F S C C D L C V A - D S H L S A H Y S I C W D S G R N P D E K N V H P C G A C R V R V N - N C L V S L G C A G I S V R D T R M A L F R E R E D I S T S H L A 448
367 V V Y T A A H D R T V W D L S G R C V K T A L C G S C N D L A V H P C S D I M C T A H L S B Q L K W D P T Y V T V V H S I E A D F A R Q V S V L T P S S S V L A S G R G G V L K I F D L T Y E A L H T G K D M V A S I N H Y 478
361 K V Y T A A H D R T I K P V E L Q Y G T O E K I T O C S S N D V S E Y S R O T I A S A H F D S A V R W D M S K F L I S E I A R A O F S V S V S F C G D L L S N G O N L N I Y D L M Q V N T L K H D T K N T I A Y N 480
356 R V V T G S H D R M I W D I S R G A L I K I V O R S T N D L E I S K P S N L I V S A H F N S I R I H O L S K C L V T L E K N H T Q O V S V N I S R D G K Y V L S M G R H S L R W D L N F K Q Y V Y F T N S A F K N Q L N M 476
358 R A V S G S D R T I K W D L N K G F S I R T L C L S C N D V D F V G D N S V S A H F D G S V R F M D A S S E S V Y I E E L L E G P V S V O I S D D G Q L V L S N G R O N V L R L S D V M H S T L O A R T E S Y R N L N N W 478
327 R V V T A S D R T V W 340
.....A..... 52
52A..... 53
361 K V I T G S H D R T I K W D L O K Y G I R T I F F S C N D V R L D E G T I V S G H L N N R F W D V S G K I E L T G I L G O I S V S P D S G S K V L I N S R O N T K L V D L R T Y D V E Q T H A D B Y K T G A N M S 470
363 V L S Y S G A D R T I K W D M A R K Y C A K L M A F A C M D V A I G S A A T L V S A H L O G K V R W D S S G G A G E V V A R B E G C V S K V - L D P S T I V L A R D N A I R I D L S Q T I W N S I H S S F F R I G - N T 480
313 N I S C C O R T I K I W N I S G S C O T S I F H S C N D V L D M S G N V V T A H L D N S L I W D M H N K K L I O E I T I S S P V I S K T P E N E I L S L S R O N S K L I D I R M Y N T L F R D D N L R T F N N S Q 433
359 R I I S G S H D R T I K W D M S G I C T R T A F I F S C N D V L D Q G S M A G L D N N V R I W D M S V N I R E I T G L S D R V T G V T V P O R T H L I T C R O N S L R L I D R T F O L V N S T S D K P R V S W S 479
324 R I V S G S H D R T I K W D L V K G Y I R T L F L S C N D L A L D E G O I I S G H L N N V R I W D A T G N N I R E I T G I S G O V S E V S P N Q H E L T S R H T L O L L D V T Y T I I A T I A D G Y R V G M N N A 394
257N..... 257
360 R I V S G S H D R T I K W D L V K G Y I R T L F L S C N D L A L D E G O I I S G H L N N V R I W D A T G N N I R E I T G I S G O V S E V S P N Q H E L T S R H T L O L L D V T Y T I I A T I A B W A M A 475
297 R A V S A S D R S I R W D M T G Y S Q V V I L A S M N D V L M S A T L I S A C S H S F S D P T S H R N V T I L N V A T O N S G L Y S P Y Q V L V A S R O N T K L I D R T K L A S M A T K A P A R S T S S Y T 417
362 R I V S G S H D R T L K W D L R S K V G I K I V F A G S C N D I V C T - E C C V M S G H F D K K I R F W D I T E C I V R E L E - L - G K I A L D N P E R T Q L L S C R D L K V I D R T N A I K O T S A P O F K C S D W T 478
362 Q A V T G S R D R T V E W D L G R A Y C S R I N V L S Y C N D V C G - D H I I I S G H N Q K I R F W D S G R G H Q V I P V - O G R V I S L N S H Q L L S C R D T K V I D R V S N I R O V F R A D G F K C S D W T 478
362 R I V S G S H D R T L K W D L R S K V G I K I V F A G S C N D I V C T - E C C V M S G H F D K K I R F W D I T E C I V R E L E - L - G R I A L D N P E R T Q L L S C R D L K I I T O R A N A V Q O T F A P G F K C S D W T 478
362 R I V S G S H D R T L K W D L R S K V G I K I V F A G S C N D I V C T - E C C V M S G H F D K K I R F W D I T E C I V R E L E - L - G R I A L D N P E R T Q L L S C R D L K I I T O R A N A V Q O T F A P G F K C S D W T 458
362 R I V S G S H D R T L K W D L R S K V G I K I V F A G S C N D I V C T - E C C V M S G H F D K K I R F W D I T E C I V R E L E - L - G R I A L D N P E R T Q L L S C R D L K I I T O R A N A V Q O T F A P G F K C S D W T 478
348 R A V T C L D R T I R E W D L Q K A A D I R R I V S Y S G S D V S G - D Y M I S G H P K K I R F W D S S E S C F R E V T - L E E K I S L F M D O C G O L L S C R D A L S L F D L S S N V R O V F R A D G F K C S D W T 464
348 R A V T C L D R T I R E W D L Q K A A D I R R I V S Y S G S D V S G - D Y M I S G H P K K I R F W D S S E S C F R E V T - L E E K I S L F M D O C G O L L S C R D A L S L F D L S S N V R O V F R A D G F K C S D W T 464
344 R I V S G S H D R T L K W D L R S K V G I K I V F A G S C N D I V C T - E C C V M S G H F D K K I R F W D I T E C I V R E L E - L - G R I A L D N P E R T Q L L S C R D L K I I T O R A N A V Q O T F A P G F K C S D W T 460
359 R I V S G S Y D R T L K W D L R S K V G I K I V F A G S C N D I V C T - E C C V M S G H F D K K I R F W D I T E C I V R E L E - L - M R V S I D L N H R T E L L S C R D L K I I D R T N A V R O T F A P G F K C S D F T 475
364 K V V T G S H D R T L K W D L R S I A C I E K I V A S G H L V I T D L S G I T I S G Y D K K I R F W D I T E A S Q A D V L L - M A K I S L S D L K C N Y L I C S V D R T K L L D R K N V I S T E N H E K I S C D F A 472
327N..... 327
326 S A V S G S A D R V K I I W D I O N O R C S R S L F A S K V L D V A I N M S P L F A S G H F D K K L R F Y D G S T D P V R T V D - M - G G R I T S L D V I M S G C E L L V S T R O O T I S L I D R T F Q T V H C S A E N V R T S S D L S 444
327 R V V S G - C R I I K L L D V R K S Q N I Y L F A G S T V I D L L A V - D S S V I S T H F D K S V R W D T R E K S A L S D C I L D O E K I T G A D I F S E S H V - I C S L D G R S L V N D R A N V T V M V G S A D D V D F V Y S 443
354 R V V T G S H D R T L K W D L R S K V G I K I V F A G S C N D V S D A B A C I S G H F D K K I R F W D I T S D A S A N E I S - L - G K V I S L D S P O R T L L S S R O O T L K I D R M N Q V I G T R Y 462
355 T V T A S R D R T I K A F D I K R E V I K E N A L A D T O A L C A I A - D A Y O L V A H F B K T I K I R F E D O L G Y S E S S A H I I C A P I S N K V L A A Q H T R L E D L M H S T V O T E M H D D R L G S C 474
359 N M S A S K D H I K W D I K R S K A S A L O D T G T W G V K E F L - R V A S A L A E H E V R - D L V W R H T V I V T L E S C I I A N S F H T Y S 447
363 R V V T G S H D R T I K W D L R S K V G I K I V F A G S C N D I V C T - T A T W L V A H A K T L N R P W D T A D I N K L G I A T E N T T I I M A C S P D D V A L L A S H R N L R V D T L T H R V R G S V S A H A A T T 478
349 R V V S A S O R T I K I W S L S R G V E R I I M I T G F D I V A V - D H R F F I C H F D K R L E F D S A L D R I A L S L P A R Q A L C L V D S H N S L I A T S N E V C V I D R I S L E K V K T W R S - D B V G G C G 467
364 K V I S G S H D R T I K W D L A K G Y C I K I F F S C N D I I G S D T A L V S G H V N H I R F W D S T G D C S I T G I T G O I S L A V T R R V L V S R O N T M K L D V M L Q V N T L F H D S Y R N G V M N S 484
358 T G F S S S D R T L K W D L K R G N I I H T F N P K S C H D V L I D T G I S T I S G Y A D G H L R V S G S K Q C S Q I V N V S T A I S L D L T N R T M I L T S G R O N S K M M D I M S N K V 463
11 K I T A S H D R T L K W D L O K Y C Y T R I M F G A S S N V V F T D S G A I S A S D G C V R F W D V A D C I Y O M K G T S A S V C N I V L T S R T Q L I T S K O N T K L I D R N F F V L S T F C H P N F S C L I T S 231
35 R V V S A S H O R T I R W D L H R G O A S S V F M A T G R D I A I T D D R V I G G Y G K L R L Y D F A D S O M K V - L H M T A I G S D G R N R V E I G O K I L H V V D V N D O K L F E M S H P O T I S H L A 474
312 K I M T G S H D R T L K W D I N K Y G L K T I F F S C N D I V S G H M G N L V L F D G C N T I R F W D I S C D I N K N I T S S V A D I I N V L G R F V S I G O K I L H V V D V N D O K L F E M S H P O T I S S S 431
312 T V T G S T D R L R W D M A H S R O K L S I S V S G S L T M - R N Q A V T I S S I R F M N O K I R F W D V N V F E I A C S V D G A E Y L L N G O N T I M M O F F M R V O K F N D O N I N 428
363 R V V T G S H D R T I K W D L R S K V G I K I V F A G S C N D I V C T - T A T W L V A H A K T L N R P W D T A D I N K L G I A T E N T T I I M A C S P D D V A L L A S H R N L R V D T L T H R V R G S V S A H A A T T 478
363 R V V T A S H O R T L K W D L S K Y C I R T L F O F S A N A V A L S Y D N S I A S H L S H L R I W D M N E P I R M D N L S Q O I S S P A D G R T V L I N S R O N T K L I D R T N E E V V T L K H D S Y R N G V N A 483
331 K I T G S O R T V K W D L G K Y G V S P N A V S E S T R M L C S A H A D R R V R W D L T A D P V A I I D V O S K A S I S W S P A W E L V L T A P D N T A Q L D I T W O K S A H T R G V L S 446
357 R V V S G S H D R T I K W D L S G F O K S I T I A F S S V N D M A L N G P A T A F S G H F N H V R W D L T A D P C H M D E G S A O V S S I T I N T N T L L N C D N V R L D V R M M V N S E F K D Q A F I N S N S I 477

Rhizaria_Ammonia[seq_50]ATG16
Rhizaria_Globobulimina[seq_52]ATG16
Rhizaria_Globobulimina[seq_51]ATG16
Rhizaria_Eucyrtidium[seq_61]ATG16
Rhizaria_Bigelowiella[AOA6U1DX27]ATG16
Rhizaria_Paulinella[seq_53]ATG16
Alveolata_Toxoplasma[AAQM03000005-2-13658-16585]ATG16
Alveolata_Plasmodium[XP_001350893.1]ATG16
Alveolata_Vitrella[CEM27357.1]ATG16
Alveolata_Chromera[seq_61A]TG16
Alveolata_Chromera[AOA0G4EZ71]ATG16
Alveolata_Oxyrrhis[AOA6V3VN06]ATG16
Alveolata_Karenia[AOA6T4VB16]ATG16
Alveolata_Tetrahymena[seq_71A]TG16
Stramenopiles_Phycopithorax[seq_54A]ATG16
Stramenopiles_Personospora[seq_4]ATG16
Stramenopiles_Gleococcyus[AOA6S9GYL8]ATG16
Stramenopiles_Aurantiochytrium[seq_71A]TG16
Telonemia_SRR737126[seq_0]ATG16
Telonemia_SRR737126[seq_60]ATG16
Centrohelida_Rainenophrys[seq_16]ATG16
Centrohelida_Raphidiophrys[seq_17]ATG16
Centrohelida_Choanocystis[seq_13]ATG16
Centrohelida_Acanthocystis[seq_14]ATG16
Cryptista_Guillardia[AOA6U6DUJ1]ATG16
Cryptista_Rhodomonas[seq_22]ATG16
Cryptista_Rhodomonas[AOA6U4W9]ATG16
Cryptista_Goniomonas[seq_21]ATG16
Cryptista_Palptonomonas[seq_22]ATG16
Glaucoophyta_Gleococcyus[AOA6T0X249]ATG16
Chlorophyta_Ostreococcus[XP_00302300.2]ATG16
Chlorophyta_Micromonas[seq_19]ATG16
Chlorophyta_Lobosphaera[seq_18]ATG16
Chlorophyta_Chlamydomonas[PINW83451.1]ATG16
Chlorophyta_Arabidopsis[BAB09394.1]ATG16
Chlorophyta_Oryza[seq_20]ATG16
Chlorophyta_Marchantia[OAE30304.1]ATG16
Ancoracysta_Ancoracysta[seq_10]ATG16
Hemimastigophora_Spironema[seq_35]ATG16
Hemimastigophora_Spironema[seq_35]ATG16
Malawimonadida_Malawimonas[seq_44]ATG16
Metamonada_Tritrichomonas[AOA1J4JQ14]ATG16
Metamonada_Tritrichomonas[AOA1J4JQ14]ATG16
Metamonada_Tritrichomonas[AOA1J4JQ14]ATG16
Metamonada_Tritrichomonas[AOA1J4JQ14]ATG16
Metamonada_Tritrichomonas[OH700110.1]ATG16
Metamonada_Tritrichomonas[D5113312-1-106981-108462]ATG16
Metamonada_Tritrichomonas[XP_001318993]ATG16
Metamonada_Monocercomonoides[seq_57]ATG16
Discoba_Rhynchopus[seq_59]ATG16
Discoba_Diplonemias[seq_44]ATG16
Discoba_Trypanosoma[Tb927_11_v5.1-1961487-1959754]ATG16
Discoba_Euglenas[seq_25]ATG16
Discoba_Naegleria[seq_26]ATG16
Discoba_Percomonas[AOA6U0M3Q1]ATG16
Discoba_Aldicula[seq_23]ATG16
Breviata_Pygus[seq_11]ATG16
Fungi_Saccharomyces[seq_34]ATG16
Fungi_Komagataella[seq_32]ATG16
Fungi_Schizosaccharomyces[MP_596308.1]ATG16
Fungi_Claridoglossum[seq_5]ATG16
Fungi_Gigasporas[seq_30]ATG16
Fungi_Catenaria[seq_29]ATG16
Fungi_Piromyces[seq_33]ATG16
Fungi_Gonapodydse[seq_31]ATG16
Fungi_Batrachochytrium[seq_27]ATG16
Fungi_Batrachochytrium[seq_28]ATG16
Fungi_Batrachochytrium[XP_006675434.1]ATG16
Fungi_Forticulus[seq_56]ATG16
Metazoa_Homo[Q676U5]ATG16L1
Metazoa_Homo[Q8NAA4]ATG16L2
Metazoa_Xenopus[KA8604610.1]ATG16
Metazoa_Xenopus[AOA6I8QBR3]ATG16
Metazoa_Xenopus[CAJ82169.1]ATG16
Metazoa_Xenopus[XP_004919969.2]ATG16
Metazoa_Xenopus[XP_004919971.2]ATG16
Metazoa_Xenopus[seq_49]ATG16
Metazoa_Danio[seq_47]ATG16
Metazoa_Drosophila[seq_48]ATG16
Metazoa_Daphnia[EFX75688.1]ATG16
Metazoa_Caenorhabditis[seq_45]ATG16
Metazoa_Dicymela[seq_58]ATG16
Metazoa_Corticium[seq_46]ATG16
Holozoa_Helgocaela[seq_39]ATG16
Holozoa_Stephanocaela[seq_42]ATG16
Holozoa_Stephanocaela[seq_43]ATG16
Holozoa_Salpinoecaela[seq_41]ATG16
Holozoa_Capsasporas[seq_36]ATG16
Holozoa_Ichthyophonus[seq_40]ATG16
Holozoa_Creolimax[seq_38]ATG16
Holozoa_Sphaerothecum[seq_2]ATG16
Holozoa_Coralochytrium[seq_37]ATG16
Amoebozoa_Entamoeba[AOA5U1UAD5]ATG16
Amoebozoa_Entamoeba[PINW83451.1]ATG16
Amoebozoa_Dictyostelium[seq_5]ATG16
Amoebozoa_Vermamoeba[seq_9]ATG16
Amoebozoa_Acanthamoeba[XP_004340796.1]ATG16
CRuMs_Mantamonas[seq_12]ATG16
CRuMs_Rigifolia[seq_13]ATG16

316-----LNFNITPPOLKSKMWOAHSSDVCALLHFDOTGKKLIS-----G
484KPCYSPDGOVITIGGSSKYSLF IWKTKTSKLOHTLT-EH TSQISKV IWHGRG-GVASSDRSGVMAMWC
484KPCYSPDGOVITIGGSSKYSLF IWKTKTSKLOHTLT-EH TSQISKV IWHGRG-GVASSDRSGVMAMWC
307IAOFADGRVCVAGSTNOE VV IWDCKTGKVEKRFY-EHES I VFWWKE-----MLATSDRKGNK I K VFS
478NATFSDGRKVVVAGSSNSELFWSSVKTEKLEKRLKRLNANITCWKISPNKHWACDNAGYVVLWD
481IAVFPDGRPLVVAAGSASBELFWOTSSKLLTTTIAADAAHILSLDINBNKQI IATQTGMLTFFI
485BVEBBDGAFVAAA-AGPHVYKMTIRKCGDDVLLR-SQMTDVTCLSWQLHR-GLVCGGKDSVMWLA
255-----NKQKKYIL-----FKNNOFYNNLYF
468AVVMSPGSAWIVSPMGDGLVFWNALSGOYATRKVPSEVOVTSLTWRF-G-KLITAHRRSGIVFWT
378CAD IAPDGLLVIPHKEGIL-CYNRLKKKEESSIS-LR-EMPLALEWTFPG--VVS GSKEGRLTFWT
448CAD IAPDGLLVIPHKEGIL-CYNRLKKKEESSIS-LR-EMPLALEWTFPG--VVS GSKEGRLTFWT
448VPVFPSPDAS IAVVC-CGRS IHOWEAISGDAHKPFE--LSTVLALSWSL--ELVAAQDGHV-FWK
399AFAFSSDSAHV IARGAN-SIGOWNASTGACVCLHE-EQOQPI-SVOWDFH--MALSIHODGHAAALWS
481KCCFSPDGV I IAGSSDSS IIMFNFKDGTGKSVLKNKPSV I VANDH I NVGSNLVS GDSRNL I IWN
448IASLSPDGRVALAGASBLF IWSARTKLERQKPGHAAVACWWRPDCGVASCDKNGVVVLWE
256KCMSPDGGVVAAGSADGSQV IWSVANAK I VSTLK-ENTSPVLSCAVSNLKKPLATSDKNGN I C IWS
329KLAYSFGCTVVAAPSSSTGDALVFTDTTGLLAALLABLNTPPVAAVAVSLARTOLATVDKAGALALWD
287KACVSPGALLAAAGSKTGLSLF IWDNGLSLOR IYSEQ-AH AOP ITCVAVSTPSQOLASVDSSGAI VOWR
418LALSPDGK YCS TGS TSCVYVWECNAGRVVSTLN-SHAGHSNVAVVSPQKGLAA ISTDKKLVMF
481KAAVSPNGRVVAAAGHNGSVH IWDLTSLR IAKRLYDAITET I ICSGWSNGQDLAVSDRTGVVCCVS
471KACLSPDANVCA I GNDGNV VVFDSTTAKLE I I I LKGNHNSY I SSCTVGA I GSC IAI I DKNGMVAWV
475KCMSPDGRVVAAGHNDGNVFLNVASGEIE I I LKGNHNSY I TACAVSMVQSTLAI I DKNHGRVVMW
468KACFSPDGNV VVVGQTVGVFVDAHTGHE T V L-KHEFVVSQVSNVSGVVA I I DKNGR I VFW
264-----L
476KATSPDGKFLAAGGSDSGIFWEAEENLVSQIRNVRSVAVAGSWASN-DOLASIEKEHOMV IWE
270KATSPDGKFLVVAAGGCGDSIT I I WNAETTE I VDTLRGHHKSPVVSQWGN-DLFASAEKEHRLM IWE
216-----KG-----GGEEEDVE
480KAT I SPDGOV I IAGSSSGSVH I WEMOSAKEVAVLA-GHKGPVSCSGV I AN-DOLASCDKDRK I I IWE
479GCGFSPNGAV I IACGGANGNVYAFDVKKSSCAVVGQGGKGMVTAALVTDGENVVTS GSKDKS I VFW
479KCMSPDNSVVAAGSTG I V I V IWSA I NGKLKATLRGCTHGVVCGAWSSRG-QLAS I SKDRVALVW
460NFCALPDCG I I IAGGSDGGLF IWRVQDGRMLTTLH-GDAVAVSGVSSSG-MLASADKNBVLCLWE
484NFCVSPGSGSVVAGSADGVFWSVHDSITTLER-ADAAVATEH I GORE-LATADKNB I AVLVA
341TACMSPDERHVAAGSTDGTVFWELEKGVATTLEK I PASG I LAISWSFGTPLVSSDTKLLT I FW
483AAFFPSGMLLASGQOAAVLV IYDYD IATVERVVT-AHSLALLBOWAFSRTRPAPRKRRS-IQVL
443KCLSPDDBVVAAGSADGSVHWSLSKGN I V I LK-EQTS I I LCGSWSG I GKL I ASADKNGYV I WT
440PCCLSPDENS I IAGANDGSV IWSRLKDGVT I LO-GHSSSVVS I SWGGLG-PLATADKH-H I Y IWT
439KCLSPDNENVAVAGSADGAVVWSRKNNEGSVLKGGTYPVLACAVSGVKKPLATADKSGR I C IWE
476KACVSPNGOVI IAGSADG I V I WNTKKGKFEKALTKGKSAV I AGAVSPLGDOFVS GSKDKS I V IWE
477KAAFSPDARVAL I GGLGR I VWDNTNTRHEAV I SRDPSMS I SEVGNPNSSQVVASAHKDKV I FW
270KACVSPDARVAL I IAGGANSTV I WDRSSAKV I KQLG-GR I R I NAWAVSGK V I SADKN I V IWE
474KACVSPDARVALVAGSADGSVH I WDRSSAKV I KQLG-GR I R I NAWAVSGK V I SADKN I V IWE
440KVRMLKNRNLV I GGSN I YG I S I DSKOTDNFN-CBDNY I VALAVK-DONKMI I DKNBVL I WT
477MKMMLKDEMDVL I GGGNGS I FEFSSQTFKQKSELT-SHK I PL I LAAS-SGNSLASGDNQYV I WT
435HQMMLNDSDA I I GSTDGS I YN I DLENFKFNKSG-GR I TPVFCVAVKQNLGTMA I DKSNGN I WT
420KLSASPCGGFVVAAGSDGDTVL I FDMQENK I VYENK-HNKPVLCGS I AFAY-NML I TADTNHTLAWT
476KLSASPCGGFVVAAGSDGDTVL I FDMQENK I VYENK-HNKPVLCGS I AFAY-NML I TADTNHTLAWT
476KLSASPCGGFVVAAGSDGDTVL I FDMQENK I VYENK-HNKPVLCGS I AFAY-NML I TADTNHTLAWT
432 I IOMAMVDDA I I GSTTGD I YE I DLSNFKLRGTSK-A I DHPVYCVAASTQYGLLATGDRDGVV I FW
418TSSVPT I RKFVCCVSGKNGM I GDI I TON I MF I FTR I EGRN I I G I AWSNDR I T I V I-----A
446KLS I SPDCS I V I G I I D I A I V I WDT I L I S I K I L A I S I G I A I D I S I H I V I A I D I R I A I W I
451KACLSPDGRV I VAGSADG I VYVNE I O I YD I T I K I S I R I V I T I-----I S E I V I C I V I A I D I S I G I A I D I S I H I V I A I D I R I A I W I
449 I I A I L S I P S I G R I C I A I V I T I S I R I S I L I V I D I L I D I E R I V I A I E A A I O E H V I S I V A I A I O R I E V I A I T I S I N I D I K I R I V I W I
479KACVSPDGK VVAAGSSSTQCLCWMG-GR I V I A I R I K I E I G I V I T I S I G I A I D I S I H I V I A I D I R I A I W I
481KACFSPCGE I VAGSADG I T I G I K I F I W I S I L T I P I T I K I L V I N I G I S S I I T I G I T I W I I D I S I G I A I D I S I H I V I A I D I R I A I W I
477KAVFSPRGE I V I A I G S S N G I F W I D I L G G L Y Q I H I K A I K D I S I G V S W R D D G S I I A S C D R K I L V I F Q
478KATFSPHSR I VVAAGSSSGLFWNTASGL I E C S W S-GH K K S I S C G A W I H I M K F V I L I S S L D G I V F W
-----M
140-----GK
177-----GR-----GRN
139-----KG-----NA
54-----ELSEKSAAEK I V
482KCFSPDGRVVAAGSLDST I F W I N I O K S I L E K T A K-EH N A L V C G V S I S P G G G V F S A D K D R T V I C I W R
471MTLS I PGGG F V A A G A V D S V F G W D R T K E Q T I-VTGG I Q T V N E V S I N P Y D S O M Y I D K S I G L S I W R
434NACYS I G D G K V A I C G S N G S I Y I F N T F T N K K E V L K-QSPT I I M K I W D P T G K S I Y S E F K N N I I N I W I
480KCLSPDGRV I VAGSADG I V I V W R A D A T I V E V L L R-AH N A V M S I G S P L G G Y M I A D L D K N V A W I
395KCFSPDGS I I S S G A D G T V F F W D I A S K K I M V O S N K-EH K S A V C G V W I H P G G S A S A S D K D K C V W O N
258-----M
476KCFSPDGS I I S S G A D G T V F F W D I A S K K I M V O S N K-EH K S A V C G V W I H P G G S A S A S D K D K C V W O N
418KVLSPDGS KAAAPASAKGVFWVDLSNEN I I S M S S D P L F S I G S P L S Q I I A G S K S G R L H I W A
479KVLSPDGS VVAAGSAGSLY I W S V L T G K V E K V L S K O S S I N A V A V S P S G S H V V S V D K E C K A V I Y
479KAVFSPDRSVALAGSCDGLY I W D V D T G K L E S R L O G P I C A A V N A V A V C Y S G S H M V S V D Q G R V L V W
479KVLSPDGS VVAAGSAGSLY I W S V L T G K V E K V L S K O S S I N A V A V S P S G S H V V S V D K E C K A V I Y
459KVLSPDGS VVAAGSAGSLY I W S V L T G K V E K V L S K O S S I N A V A V S P S G S H V V S V D K E C K A V I Y
479KVLSPDGS VVAAGSAGSLY I W S V L T G K V E K V L S K O S S I N A V A V S P S G S H V V S V D K E C K A V I Y
465KVLSPDGS I TLAGSADG I T I F I W N T R I G L L E R S I N B O R A S V N A I T W S M S G D Y V S V D R K M A V V W
465KVLSPDGS I TLAGSADG I T I F I W N T R I G L L E R S I N B O R A S V N A I T W S M S G D Y V S V D R K M A V V W
461KVLSPDGS VVAAGSAGSLY I W S V L T G K V E K V L S K O S S I N A V A V S P S G S H V V S V D K E C K A V I Y
476KVLSPDGS VVAAGSADG I V L W N I T G K L E K T I D K G S S A I N S V S L S G A F V A S V E K S A V L W M
473KASFNSGLK I A C S A D G A I V I W N V N-GFLEATLK-GSTAVN A V S I S E N N N M L A S V E K N K R C T I Y S
328-----PDE-----IFLR
445KVLSPDGS VVAAGSAGSLY I W N R N S T K L E K O L C S N E N A I F S L S W N P T G Y G L L S S K O K F V I L W K
444KVRVSPCGOFLASGSKDS I Y W D T N T A E L V S K W E P N S S G V S S V M S P V S G L I S T Y L N G D V M W H
463-CV I D D I-----MKGR I D K O I D E-----QTHGOTSNNR
475KCFSPNAAV VVCGSVS I A V V I W A K D G T I E K V L T D G T R D V T A C A W K N S E M L E V S K D K H F V I W
448KCM-----BQLHKAS I A W F S F L H S G R N L A C S I T D V L H F A P Q O D R H I M K R S T A I L L W
479KAVFSPDR I M C-----GSCVWL T M D S V-----GLQV I L A S L I F I S T N S E-SVVC
468KAVFSPCQVVA I G L A S G I L L W H I A K G E V E K R I S P C H S N A V T S L W S H D--H L I S V A K D I R L W A
485KACFSPDGRVVAAGSADG I V L W N I T T G K M E K T F K-EH P N N G N A V A W I A G H Q V I S C D K D K N V V I Y
464-----VASYR-----

232KSVSCDSKFLAAGSSKDG I F W N L S G G A L L R O L S S L H S P V N S V O S I L K N E I L A C Y D K D T L I W V
475KTFSPDGRFVA I G H D G N I V F N A L N G L D S I I K T P H A G E I M S I K W N D G D T F V L B K K-EH I H W
432KCCSPDGK V I IAGSSNEVFOND I TOSKLE I V L K P P K A G C V A S I N P V O S Q I V S G H A N K I V I W N
429K I S V A B K S I M V S V D G A V V W N L T T S F A C C V Y G G Y G S G C O M P L S S Q L I S G Y-BRNV I W D
484KASVSPDGRV I A S G I D S I C I W D A T N G I K V K L T K V I G S S V C C S S P L A N I F I S A D K D K N I O W E
484KACFSPDGOVVAAGS I D G L V I W E T T T G K L S I L K K G K T T V A V A W I H N G H O I A S C D R N G A V L W E
447KACFSDAGNFVAAGSTTGCVFWNNTHTAALAH I T E G H A G V S S C T V G A R G K P L V T G S D A S L W S
226-----D-----OFLMLL
478KACLSPD I A H V A S G G M D G R I F W N V H S R K V S V L O-SHKCPE-ALRW I GDS--LEKKT K S G S K I A V

352
548
548
369
544
547
548
274
532
439
509
508
460
547
514
321
395
352
299
547
537
540
547
264
541
335
225
544
545
545
524
547
407
547
508
503
505
542
533
541
540
504
471
500
483
470
497
474
514
514
515
544
546
543
544
142
181
143
163
547
536
499
545
258
460
541
484
545
545
545
525
545
531
531
527
542
537
334
511
510
489
541
507
526
532
550
550
298
540
497
494
550
550
513
232
540

Rhizaria_Amonniae|seq_107|ATG3
Rhizaria_Globobulimina|seq_110|ATG3
Rhizaria_Globobulimina|seq_109|ATG3
Rhizaria_Eucyrtid|seq_108|ATG3
Rhizaria_Bigelowiella|AOA677HA05|ATG3
Rhizaria_Paulinella|AOA676VJ01|ATG3
Rhizaria_Toxoplasm|EPPR60315_1|ATG3
Alveolata_Plasmodium|EUR72290_1|ATG3
Alveolata_Plasmodium|ETW36828_1|ATG3
Alveolata_Plasmodium|ETW42986_1|ATG3
Alveolata_Vitrella|seq_3|ATG3
Alveolata_Chromera|AOA604FRI0|ATG3
Alveolata_Oxyrrhis|AOA6V4C0S8|ATG3
Alveolata_Oxyrrhis|AOA6V5V0L1|ATG3
Alveolata_Karmania|AOA6T5FGZ0|ATG3
Alveolata_Tetrahymena|seq_OIATG3
Alveolata_Tetrahymena|seq_1|ATG3
Stramenopiles_Phytophthora|seq_118|ATG3
Stramenopiles_Phytophthora|KAF403916_1|ATG3
Stramenopiles_Perosporas|seq_15|ATG3
Stramenopiles_Perosporas|seq_117|ATG3
Stramenopiles_Aureococcus|seq_14|ATG3
Stramenopiles_Aurantococcus|seq_113|ATG3
Telonemia_SRR371266|seq_129|ATG3
Telonemia_SRR371266|seq_119|ATG3
Centrohelida_Raineriophrys|seq_25|ATG3
Centrohelida_Raineriophrys|seq_26|ATG3
Centrohelida_Raphidiophrys|seq_23|ATG3
Centrohelida_Chaoanocyttis|seq_23|ATG3
Centrohelida_Chaoanocyttis|seq_22|ATG3
Centrohelida_Acanthocystis|seq_41|ATG3
Haptophyta_Calcidiscus|AOA6USNW81|ATG3
Haptophyta_Scythosphaera|seq_74|ATG3
Haptophyta_Isocyrtis|AOA6UQ08B7|ATG3
Haptophyta_Emiliana|AOA6S9UP68|ATG3
Haptophyta_Prymnesium|seq_73|ATG3
Haptophyta_Pavlova|AOA616TAPQ0|ATG3
Cryptista_Guillardia|AOA6UDC0J3|ATG3
Cryptista_Rhodonas|seq_42|ATG3
Cryptista_Comononas|seq_39|ATG3
Cryptista_Palptonomas|seq_41|ATG3
Glaucophyta_Gloeocheete|AOA6702I63|ATG3
Glaucophyta_Gloeocheete|seq_69|ATG3
Chlorophyta_Ostreococcus|XP_022839285_1|ATG3
Chlorophyta_Micromonas|seq_36|ATG3
Chlorophyta_Lobosphaeroides|seq_32|ATG3
Chlorophyta_Chlorella|seq_31|ATG3
Chlorophyta_Arabidopsis|BAB0895_1|ATG3
Chlorophyta_Oryzal|EEC67434_1|ATG3
Chlorophyta_Oryza|XP_025879457_1|ATG3
Chlorophyta_Marchantiales|seq_35|ATG3
Ancoracysta_Ancoracysta|seq_8|ATG3
Ancoracysta_Ancoracysta|seq_10|ATG3
Ancoracysta_Ancoracysta|seq_12|ATG3
Melaiomonadida_Melaiomonas|seq_91|ATG3
Trichomonada_Trichomonas|XP_02992361_1|ATG3
Metamonada_Trichomonas|S113238-4-17545-16739|ATG3
Metamonada_Monoceromonoides|seq_95|ATG3
Metamonada_Monoceromonoides|seq_93|ATG3
Metamonada_Monoceromonoides|seq_94|ATG3
Discoba_Rhynchopus|seq_53|ATG3
Discoba_Rhynchopus|seq_52|ATG3
Discoba_Diplonemal|seq_47|ATG3
Discoba_Diplonemal|seq_46|ATG3
Discoba_Trypanosoma|XP_01177640_1|ATG3
Discoba_Euglenia|seq_48|ATG3
Discoba_Naegleria|XP_002674391_1|ATG3
Discoba_Percolomonas|seq_51|ATG3
Discoba_Percolomonas|AOA6U0UX23|ATG3
Discoba_Andaliacae|seq_43|ATG3
Breviata_Pygusil|seq_13|ATG3
Fungi_Saccharomyces|seq_11|ATG3
Fungi_Komagataella|seq_63|ATG3
Fungi_Schizosaccharomyces|seq_67|ATG3
Fungi_Claroidoelomus|seq_58|ATG3
Fungi_Gigasporae|seq_60|ATG3
Fungi_Catenulales|seq_56|ATG3
Fungi_Pirromyces|seq_65|ATG3
Fungi_Gonapodytes|seq_62|ATG3
Fungi_Gonapodytes|XP_01736114|ATG3
Fungi_Batrachochytrium|seq_55|ATG3
Fungi_Fonticulae|seq_59|ATG3
Metazoa_Homo|Q9N762|ATG3
Metazoa_Xenopus|seq_106|ATG3
Metazoa_Danio|seq_102|ATG3
Metazoa_Drosophila|seq_105|ATG3
Metazoa_Daphnia|seq_103|ATG3
Metazoa_Caenorhabditis|seq_97|ATG3
Metazoa_Dicelymae|seq_104|ATG3
Metazoa_Corticium|seq_100|ATG3
Metazoa_Corticium|seq_101|ATG3
Holozoa_Helgocetes|seq_81|ATG3
Holozoa_Staphanocetes|seq_88|ATG3
Holozoa_Salpingoecetes|seq_85|ATG3
Holozoa_Casparosetes|seq_75|ATG3
Holozoa_Ichthyophonus|seq_78|ATG3
Holozoa_Creolima|seq_79|ATG3
Holozoa_Sphaerothecum|seq_87|ATG3
Holozoa_Coralochytrium|seq_77|ATG3
Amoebozoa_Entamoeba|DS5711-9-30822-31628|ATG3
Amoebozoa_Dictyostelium|seq_41|ATG3
Amoebozoa_Vermamoeba|seq_8D|ATG3
Amoebozoa_Acanthamoeba|AC43782_1|ATG3
CRuMs_Mantamonas|seq_16|ATG3
CRuMs_Riiofilas|seq_18|ATG3

[illegible]

[illegible]

Uncolored

1

2

3

4

5

6

7

8

9

10

11

12

13

14

15

16

17

18

19

20

21

22

23

24

25

26

27

28

29

30

31

32

33

34

35

36

37

38

39

40

41

42

43

44

45

46

47

48

49

50

51

52

53

54

55

56

57

58

59

60

61

62

63

64

65

66

67

68

69

70

71

72

73

74

75

76

77

78

79

80

81

82

83

84

85

86

87

88

89

90

91

92

93

94

95

96

97

98

99

100

101

102

103

104

105

106

107

108

109

110

111

112

113

114

115

116

117

118

119

120

121

122

123

124

125

126

127

128

129

130

131

132

133

134

135

136

137

138

139

140

141

142

143

144

145

146

147

148

149

150

151

152

153

154

155

156

157

158

159

160

161

162

163

164

165

166

167

168

169

170

171

172

173

174

175

176

177

178

179

180

181

182

183

184

185

186

187

188

189

190

191

192

193

194

195

196

197

198

199

200

201

202

203

204

205

206

207

208

209

210

211

212

213

214

215

216

217

218

219

220

221

222

223

224

225

226

227

228

229

230

231

232

233

234

235

236

237

238

239

240

241

242

243

244

245

246

247

248

249

250

251

252

253

254

255

256

257

258

259

260

261

262

263

264

265

266

267

268

269

270

271

272

273

274

275

276

277

278

279

280

281

282

283

284

285

286

287

288

289

290

291

292

293

294

295

296

297

298

299

300

301

302

303

304

305

306

307

308

309

310

311

312

313

314

315

316

317

318

319

320

321

322

323

324

325

326

327

328

329

330

331

332

333

334

335

336

337

338

339

340

341

342

343

344

345

346

347

348

349

350

351

352

353

354

355

356

357

358

359

360

361

362

363

364

365

366

367

368

369

370

371

372

373

374

375

376

377

378

379

380

381

382

383

384

385

386

387

388

389

390

391

392

393

394

395

396

397

398

399

400

401

402

403

404

405

406

407

408

409

410

411

412

413

414

415

416

417

418

419

420

421

422

423

424

425

426

427

428

429

430

431

432

433

434

435

436

437

438

439

440

441

442

443

444

445

446

447

448

449

450

451

452

453

454

455

456

457

458

459

460

461

462

463

464

465

466

467

468

469

470

471

472

473

474

475

476

477

478

479

480

481

482

483

484

485

486

487

488

489

490

491

492

493

494

495

496

497

498

499

500

501

502

503

504

505

506

507

508

509

510

511

512

513

514

515

516

517

518

519

520

521

522

523

524

52

Rhizaria_Amonimnialseq_90ATG4
Rhizaria_Globobuliminialseq_93ATG4
Rhizaria_Eucyrtidialseq_52ATG4
Rhizaria_Bigelowiellalseq_91ATG4
Rhizaria_BigelowiellaOA61T52T90ATG4
Rhizaria_BigelowiellaOA61U1E37TATG4
Rhizaria_Paulinellalseq_95ATG4
Rhizaria_Paulinellalseq_94ATG4
Alveolata_Toxoplasmalesseq_16ATG4
Alveolata_PlasmodiumFUR64051_1ATG4
Alveolata_PlasmodiumXP_00134834.1ATG4
Alveolata_VitrellaCEM25538_1ATG4
Alveolata_OxyrrhisCEM2060_1ATG4
Alveolata_ChromeraOA09G4JMT1ATG4
Alveolata_OxyrrhisOA6V4Q0L0AT4
Alveolata_KarenialOA6ATL4C07ATG4
Alveolata_KarenialOA6T58X9ATG4
Alveolata_Tetrahymenalseq_001026038.2ATG4
Alveolata_Tetrahymenalseq_3ATG4
Alveolata_Tetrahymenalseq_1ATG4
Alveolata_Tetrahymenalseq_0ATG4
Stramenopiles_Phytophthora102005171_1ATG4
Stramenopiles_PhytophthoraAF4153498_1ATG4
Stramenopiles_Percnosporelseq_94ATG4
Stramenopiles_AureococcusXP_009038807.1ATG4
Stramenopiles_Auraculacanthalseq_95ATG4
Telonemia_SRR731266seq_99ATG4
Centrohelida_Raineriophryalseq_20ATG4
Centrohelida_Raineriophryalseq_21ATG4
Centrohelida_Raphidophryalseq_22ATG4
Centrohelida_Chaococystisseq_18ATG4
Centrohelida_Chaococystisseq_19ATG4
Centrohelida_Chaococystisseq_17ATG4
Centrohelida_Chaococystisseq_19ATG4
Centrohelida_Acanthocystisseq_1ATG4
Centrohelida_Acanthocystisseq_15ATG4
Haptophyta_Calcidiscusseq_51ATG4
Haptophyta_Calcidiscusseq_50ATG4
Haptophyta_Scyphosphaeralseq_55ATG4
Haptophyta_Scyphosphaeralseq_54ATG4
Haptophyta_PavlovaXP_0057112ATG4
Haptophyta_IsochrysalOA06T7QWJ3ATG4
Haptophyta_IsochrysalOA06T7QWJ3ATG4
Haptophyta_IsochrysalOA06T1G2W11ATG4
Haptophyta_EmlinalXP_005781094.1ATG4
Haptophyta_Phyllisiamusseq_53ATG4
Haptophyta_Pavlova1seq_52ATG4
Haptophyta_PavlovaOA06T5Y923ATG4
Cryptista_Guillardialseq_28ATG4
Cryptista_Guillardialseq_27ATG4
Cryptista_RhodomonasOA06T719ATG4
Cryptista_RhodomonasOA06J4XJ2ATG4
Cryptista_GoniomonasOA06T2FN80ATG4
Cryptista_GoniomonasOA06T1ZEB6ATG4
Cryptista_Paltoniomonasseq_29ATG4
Cryptista_GloeocystisXP_0046185-534018-33167ATG4
Chlorophyta_OstreococcusOUS48866_1ATG4
Chlorophyta_OstreococcusXP_022838668.1ATG4
Chlorophyta_Micromonasseq_26ATG4
Chlorophyta_Lobosphaeralseq_25ATG4
Chlorophyta_ChlamydomonadXP_001691049.1ATG4
Chlorophyta_ChlamydomonadXP_001691049.1ATG4
Chlorophyta_Arabidopsialseq_23ATG4
Chlorophyta_Arabidopsialseq_24ATG4
Chlorophyta_OryzalAR88722_1ATG4
Chlorophyta_OryzalECC75888_1ATG4
Chlorophyta_OryzalCAJ86292_1ATG4
Chlorophyta_MarchantiaOAE22546_1ATG4
Ancoracysta_Ancoracystalseq_8ATG4
Hemiasysophora_Synalga1seq_58ATG4
Ancyromnadiida_Natomonasseq_9ATG4
Malawimonadida_Malawimonasseq_70ATG4
Malawimonadida_Malawimonasseq_69ATG4
Metamonada_TritrichomonasOHT08429_1ATG4
Metamonada_TritrichomonasOHT08429_1ATG4
Metamonada_TritrichomonasOHT06355_1ATG4
Metamonada_Tritrichomonasseq_75ATG4
Metamonada_Tritrichomonasseq_74ATG4
Metamonada_TrichomonasDS113262-2-111053-111978ATG4
Metamonada_TrichomonasOHT09381ATG4
Metamonada_TrichomonasDS113332-3-111930-112781ATG4
Metamonada_TrichomonasDS114140-5-2886-1912ATG4
Metamonada_TrichomonasDS114357-4-5429-4539ATG4
Metamonada_Noncercomonoidesseq_71ATG4
Metamonada_Noncercomonoidesseq_73ATG4
Metamonada_Noncercomonoidesseq_72ATG4
Discoba_Rhynchopisseq_38ATG4
Discoba_Rhynchopisseq_37ATG4
Discoba_Rhynchopisseq_36ATG4
Discoba_Diplonemalseq_33ATG4
Discoba_Diplonemalseq_32ATG4
Discoba_Diplonemalseq_31ATG4
Discoba_TrypanosomalT9227_11-5-471102-570116ATG4
Discoba_TrypanosomalT9227_11-5-471102-570116ATG4
Discoba_Euglenalseq_35ATG4
Discoba_Naegeliaseq_36ATG4
Discoba_PercolomonasOA04UHB63ATG4
Discoba_PercolomonasOA04UHB63ATG4
Discoba_Andacualiseq_30ATG4
Breviata_Pyruvalseq_11ATG4
Breviata_Pyruvalseq_10ATG4
Fungi_Saccharomycesseq_48ATG4
Fungi_Komagataalseq_47ATG4
Fungi_Schizosaccharomycesseq_49ATG4
Fungi_Claridoeaolomusseq_43ATG4
Fungi_Claridoeaolomusseq_44ATG4
Fungi_GasparalR102035_1ATG4
Fungi_Gasparalseq_45ATG4
Fungi_Catenarialseq_41ATG4
Fungi_Catenarialseq_41ATG4
Fungi_PromycesORX60991_1ATG4
Fungi_GonapodyxKVS18344_1ATG4
Fungi_Batrachochytriumseq_40ATG4
Fungi_Fonticulaeq_45ATG4
Fungi_FonticulaXP_009494799.1ATG4
Metazoa_HomoINP_116241.2ATC4C
Metazoa_HomoXP_008722990.1ATG4
Metazoa_HomoINP_443168.2ATG4A
Metazoa_HomoINP_037457.3ATG4B
Metazoa_Xenopusseq_89ATG4
Metazoa_Xenopusseq_87ATG4
Metazoa_XenopusXP_01282605.1ATG4
Metazoa_Danioseq_82ATG4
Metazoa_DanioXP_01232507.1ATG4
Metazoa_DanioXP_01720992.1ATG4
Metazoa_Danioseq_83ATG4
Metazoa_DanioOA04R4IXG1ATG4
Metazoa_DanioXP_00516990.1ATG4
Metazoa_Drosophilalseq_83ATG4
Metazoa_Drosophilalseq_85AT411ATG4
Metazoa_DaphniaEPFX2987.1ATG4
Metazoa_Caenorhabditisseq_77ATG4
Metazoa_Caenorhabditisseq_76ATG4
Metazoa_Dicelymaleq_84ATG4
Metazoa_Corticuliseq_79ATG4
Metazoa_Corticuliseq_81ATG4
Metazoa_Corticuliseq_80ATG4
Metazoa_Corticuliseq_78ATG4
Crustacea_Helgocarpalseq_63ATG4
Holozoa_Helgocarpalseq_63ATG4
Holozoa_Stephanocarpalseq_68ATG4
Holozoa_Stephanocarpalseq_67ATG4
Holozoa_Salpincarpalseq_65ATG4
Holozoa_Capsasporelseq_58ATG4
Holozoa_Capsasporelseq_57ATG4
Holozoa_Ichthyophonulseq_64ATG4
Holozoa_Cremonalseq_61ATG4
Holozoa_Cremonalseq_60ATG4
Holozoa_Sphaerotherculiseq_66ATG4
Holozoa_Caractochytriumseq_59ATG4
Amoebozoa_EntamoebaDS571181-3-61809-62867ATG4
Amoebozoa_EntamoebaXP_653798.2ATG4
Amoebozoa_EntamoebaXP_653798.2ATG4
Amoebozoa_EntamoebaDS571322-3-5886-6992ATG4
Amoebozoa_EntamoebaDS571161-4-22406-21408ATG4
Amoebozoa_Dicystelluliseq_51ATG4
Amoebozoa_Dicystelluliseq_49ATG4
Amoebozoa_Vermamoebalseq_41ATG4
Amoebozoa_Vermamoebalseq_40ATG4
Amoebozoa_AcanthamoebaXP_004334148.1ATG4
Amoebozoa_AcanthamoebaXP_004334121.1ATG4
Crulle_Martamonas1seq_73ATG4
Crulle_Raffinialseq_13ATG4

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

[illegible]

Data S1. Multiple sequence alignment of ATG7 (**A**), ATG10 (**B**), ATG12 (**C**), ATG5 (**D**), ATG16 (**E**), ATG3 (**F**), ATG8 (**G**), and ATG4 (**H**) homologs identified in this study. Columns with more than 50% gaps are removed. For ATG8 and ATG12, columns with many gaps are removed manually. Sequences with “?” in Figure 2 are included.