

Name	Accession (aa length)	Protein sequence	Domains (Interpro, HMMPanther, Prosite, Pfam)	KOG database	TM Predictions	2D predictions	3D predictions
OUTER MEMBRANE							
TOM complex							
Tom70a	Esi0007_0019 (952)	MCSVFFEVVEPLDHATFLSVCDEVLRDSSLVLAPFGLPRHLREALGSEKEFIRLYGPRFRFILEAVS DVTYKERGVTESQVAVTLHKLTEEEQNPEAMAYLARMGDSLREIYSPARILELPTRAPTSTADLAT IGSSLLGAGAVYTPGPQQAGRRGGRGGGAPLCDGTPRQPQSRAGHAGRCSSSPAGDGDSSCAGEN NKCSTAGRAEGGGGGGGGDSRADKGETDHDKVQRRERVASCLSRGCRELEVFSDELEQAH QALTEAFAGRYSGAAPPGDSAGGSSSSSQELKSRSDVAALDEFAAVPFLDHELFMLVRAIEEERL GEEKGAGKEKESASGGGSSSSATGACSEPTAADGDGDTSLCERPAACLEFLLTSQAVVRRADES MERGLDKEAAASLKEANILMEAFLEEGQRLPRPSRHLAELRAGLAKCEMRGGDLAAIAHAEAAI AEHPACGEAFLIRGQCRRELCDNGGALRDLVNAFVLQGNALNAGDGSQAIEDVSRESCRAR AGEEFSQRAAPNALPADWVVRSFLTSYDTKGLYEEHDVFRLHGEDPVAAAAAEGDEGGQAA AVTEFWQGLSLVREGKYAESIAKFSSSVSAFSSAPVAVLGEGTGAGDTTRIQSALALEYCGSFLYL MGDMNTALEHLRLAGEVDETNAKSWVKRGSVLSDLGRREEAFECFDAAAIAIPRDSDLFLHRGQ GHLLANDFRKATADLRSSVELCPTMPISRAAWGVALFKLATAELPSPSSLSKCVQVLEESRELPF ENPEVLFFFAEVLISMGDFKKGLEFLQTAAASLDPECPVPYVNAARAYLGMNDTKAARRQVVAVV QQGYDFFLDGHAVCPATGCCASENLSVIGRRMRFILRSLMPMCVLLGTVKSLFLHFSFVGICSRF SLAATTWCMVQLFWDIRPIVRGRCLCLWSNRLLRFRDFVCDR	IPR011990 (Interpro), Tetratricopeptide-like helical IPR013026 (Interpro), Tetratricopeptide region PTHR23083 (HMMPanther), TETRATRICOPEPTIDE REPEAT PROTEIN, TPR PF07719 (Pfam), Tetratricopeptide repeat, 0.0011	KOG0547, Translocase of outer mitochondrial membrane complex, subunit TOM70/TOM72	DAS: 4 Transmembrane segments, cutoff 2.2 TMPred: 4 Transmembrane segments	PHYRE: multi α -helical structure	PHYRE: 100% Tetratricopeptide repeat (TPR), 2e-40 100% crystal structure of the yeast tom70, 1.2e-37
Tom70b	Esi0232_0002 (739)	MGQGIKVCSSGPSIPLPARRVQKHHLRTPGPRREGRRWRMDQSKLAVLGTVGLVATAAVCC AIVFSGRSFAGSSTGKPFASSPGTTADAQGVAAASNKVIDDEDDKDKLTGGVSTEGTKGKGDGG GDGSRAPGSGGASVPAEAAAARGVAVGQGAEDGEALIVFRNRANSKAKKLTGQRYALAA EQGIALELCDELPHNDNKRTLHNNRGAAYEKDGGYALALADCSMCLSRREVGHKFARVRSR VLEAMGKHEEALSEVCAHLLLERDRVQAKAALNPSELTTPPAPPANLEGLLQKVASKRADAILLE REQTAEKQEA AAAAGAGTGTEKLKPLVKQVVMELLRSFGSFAQLERRYKGMETAITRELKDAE KAGKEGDGSASATTTTASRVSSLLDRGLLRMVKRNYDGAREDIFEAAELLSTLEADPSEAGADE VPPHYKASVVWEWQGTFLQLSGKLDEAMEAYRRCEEMEAEGEYPADVLIKMAWVCMKDKE DMAKDLFARAGEAHPEYGSFAHRARLDSEKDGAEQVRSFLRKAIELNSEDFAFWEQLCRIHVQA GDIPKATSTIEEGLEFVPNSDALLTLKAEKYSMAMKAGDASSCAILEVFDAAIRANPSSPVLYLN KASCLLQMMSDVGGAMELLEKGVSDPTSVNALVQLANLKIMVAREMAEAEAATALLDKAVAL CTTKEELMETLSVRVATEGRIKALLGRITTLG	IPR011990 (Interpro), Tetratricopeptide-like helical IPR013026 (Interpro), Tetratricopeptide region PTHR23083 (HMMPanther), TETRATRICOPEPTIDE REPEAT PROTEIN, TPR PF00515 (Pfam), Tetratricopeptide repeat, 0.00022	KOG4234, TPR repeat-containing protein	DAS: 51-68, cutoff 2.2 TMPred: 50-69 (in-out) score=2175 48-69 (out-in) score=2252	PHYRE: multi α -helical structure	PHYRE: 100% crystal structure of the yeast tom70
Tom40	Esi0055_0058 (442)	MATRLPRCFAAAAAASATSSASSGSNSSRATPPAAASSKHQSARGDGGKEPWRREAASTPADAA GCTKLASGGCRRGAVGGTAAAAGAASVRPSIEALEASLQGLLSVPLVRIAHADGAAAVAVEAA GAEGEDGAAAAVSELEDGDKPEYIQRADQAAQMRQQLRRPAQFADQFLEVSQLTQVHSFEGRF LDMSKAVTPTFTSHNVFFGNPQFSPGHYQGLTVVGESETMVRASMDADCNVSMDAHAPLGM PGLAGKLTVHGKNDVIGQTLALYHGDTCSSQISLGTGPTISYNQAVTPHLSMGGQGGFSSAQQA VGLLYGFKYNTPSWAVLGRLLGGGANVVTAYQLRRVVPGRVTLGAEYQAQLGAGSQMMVGA EFLKQKSKMSASVDSNGKVDSTLELKCGETFTPTLPVTLTISSSLDHGEDKQTFGLALTCGQ	IPR001925 (Interpro), Porin, eukaryotic type PTHR10802 (HMMPanther), MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 PF01459 (Pfam), Eukaryotic porin, e-value=2.4e-25	KOG3296, Translocase of outer mitochondrial membrane complex, subunit TOM40	DAS: 11-17, cutoff 1.7 TMPred: 5-23 (in-out) score=778, 5-23 (out-in) score=565 TMHMM: 0	PHYRE: N-terminal α -helix following by at least 16 β -strands	PHYRE: 25% Transmembrane beta-barrels, porins superfamily
Tom22	Esi0246_0018 (112)	MAKKLTFNDEKRDNGPGVLQTLVVTGRSLGVAGFGWAQWAAKKTGRGTGVLLTTAVVTLVPL VFEITREAQLIEQEKIHINALLAEGKTRQEIAQMGLYSALDPNVMGPEAS	PF04281 (Pfam), Mitochondrial import receptor subunit Tom22, 1.3e-05	NI	DAS: 50-63, cutoff 2.2 TMPred: 47-64 (in-out) score=1332, 48-64 (out-in) score=1678 TMHMM: 0	PHYRE: 3 or 4 α -helices	PHYRE: 0% TraM-like
Tom7	Esi0179_0016 (57)	MGEKIMRRRRPRKRSAPLLPKVLAVAKPIMRWGIMPAVLLMGMRSEPNLTLEVLPL	PF08038 (Pfam), TOM7 family, 1.2e-06	NI	DAS: 32-40, cutoff 1.7 TMPred: 23-42 (in-out) score=329, 24-44 (out-in) score=156 TMHMM: 0	PHYRE: Protein with a single central α -helix	PHYRE: 15% doa4-independent degradation protein 4
Tom6	NI						
Tom5	NI						
SAM/TOB complex							
Mim1	NI						
Sam50	Esi0503_0006 (451)	MVIPLDELPLRVRTVKIVGNRNTKPYVVEDQLQDAYEATTVGDDVYVGLVEGAQRDLGLGFESV QVSMDAVDDGSLDQTDVTVTVKEKNWYLLQSGATTGTAKGNLDASEFSNLRYSVAGALRNPL GHGEMLDVGYNSPIKQGEHITSAXLHLPHLFTPTVSGTLEAIMDTVVFEDENTRQEHWTLTVE RHASSDVETRAQKRITAIRALTASTCYDQTXXXXXXXXXXXXXXXXXXXSPVPGDHTHF GMRIGLMGDTSFAGKMLEMQRHLPFGVELGPETYSPVTLSLCASGGAIRPGSPSKRTTFFSDFRNL GGPMTLRGFFPYGAGPRSPKEEGCGEGDALGGDIRYTASASLGFPPVPAMATAGWRGYLFTNL GNLTTWDTPLKQYGRDTRVSVGVAAAWNFLGVGRLEINYAHVLRSPRDLHRRPLQFGFGVSE	IPR000184 (Interpro), Bacterial surface antigen (D15) IPR010827 (Interpro), Surface antigen variable number PF01103 (Pfam), Bac_surface_Ag, 3.3e-24	KOG2602, Predicted cell surface protein homologous to bacterial outer membrane proteins	DAS: 0 Transmembrane segments TMPred: 2 Transmembrane segments	PHYRE: N-terminal α -helix following by at least 16 β -strands	PHYRE: 100% structure of the membrane protein flac: a member of the2 omp85/tpsb transporter family

Sam37/ Metaxin1	Esi0338_0018 (407)	MASEEHGDAPVVRTSWNPLRALRSWGRIEEQPDLEQPGPVITHGSALDVMVVTQFRPAWEIQAH LRFVRLPYRVENSSYMGSAATGLYPALTDGQFVLRSEDAAGHIASRRSDVDVGLTEAEKVEAQL AMLVREGLPQLLRVMRYMGDEGEVRQTVHPPMKKALSWPLSWWSPAEGRRSKRESAVRGLD RLSKAELIGRAKEMYAALDLRLGNSKEAFFGSRPTSVDAVVFGHLAEAWTIAVLLDLLPAFDNL SRLFRHYVCNDNYFRPGSPFPSSGEGVEAESKKSGSEDLRLDAMLRADYVNSHNAFNLQAGCALCS EVPYIEDPPYPRPIANAGIPPVLAGDLPGVGAQGTAAAGSTTAAAAAAEAAGKATAANESLPV KYTVISIAAFMVL SNILSRG	PTHR12289 (HMMPanther), METAXIN RELATED PF00043 (Pfam), Glutathione S-transferase, C-terminal domain, 0,022	KOG3027, Mitochondrial outer membrane protein Metaxin 2, Metaxin 1-binding protein KOG3028, Translocase of outer mitochondrial membrane complex, subunit TOM37/Metaxin 1	DAS: 2 Transmembrane segments TMPred: 2 Transmembrane segments	PHYRE: α -helix structure	PHYRE: 100% structure of glutathione s-transferase iii in apo form
Sam35/ Metaxin2	NI						
MDM complex							
Mdm10	NI						
Mdm12	NI						
Mmm1	NI						
INTERMEMBRANE SPACE							
M1A/ERV complex							
Mia40	NI						
Erv1	Esi0202_0015 (194)	MPSSRRSKDPADCEDPACADMA D L L R K G R A L A A K N K Q K A A S N T A T D G K A A G S Q A P S S S A A E T D E H A A S S R N D G C P L D K G E L G A A T W G L I H T T A A H Y P E K P S K E T Q D Q A R A L V T G L A G Y P C T Y C R K D F R E E V R K L P P D V S S R V A L S W A C Q Q H N L V N E K I G K P T G C T L P A L D E R W K K G K P S C W E G G A E G V	PTHR12645 (HMMPanther), ALR/ERV IPR017905 (Interpro), ERV/ALR sulphhydryl oxidase IPR006863 (Interpro), Erv1/Alr (Pfam) Erv1 / Alr family, 7e-25 PF04777	KOG3355, Mitochondrial sulphydryl oxidase involved in the biogenesis of cytosolic Fe/S proteins	DAS: 1 Transmembrane segment, cutoff 2.2 TMPred: 0 Transmembrane segments	PHYRE: Four-helical up- and-down bundle	PHYRE: 100% FAD- dependent thiol oxidase
Hot13	Esi0046_0129 (101)	MLVPGQVSIQFPCCRWYECPECHDERENHPQRISTKNVAFACKTCRKIFVKDLSYGTEDSACPH CETVFVLPAVTPAEKVAQLAL SILAAEVSAEVSKE	IPR008913 (Interpro), Zinc finger, CHY-type (Pfam), CHY zinc finger, 8.1e-13 PF05495	KOG1940, Zn-finger protein	DAS: 1 Transmembrane segment, cutoff 2.2 TMPred: 0 Transmembrane segments	PHYRE: 2 or 3 α -helix structure	PHYRE: 95% ring finger and chy zinc finger domain
TIM8/13 Complex							
Tim8	Esi0109_0044 (125)	MSWFRGKKEPESTPEPTFSDDTSAFEGSTNFASGPPSRGGGGAGTSAGMGDLQAAMQIEQKKAQ MQAIVSRLTDLAFTKCIQKPSSSLSSSEQSCINATVLKYFDTSFVLGRLMKSQQGGGDI	IPR004217 (Interpro), Mitochondrial inner membrane translocase complex, Tim8/9/10/13-zinc finger-like PTHR21535 (HMMPanther), MAGNESIUM AND COBAL T TRANSPORT PROTEIN/MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM8 PF02953 (Pfam), Tim10/DDP family zinc finger, 6.4e-15	KOG3489, Mitochondrial import inner membrane translocase, subunit TIM8 KOG1733, Mitochondrial import inner membrane translocase, subunit TIM13	DAS: 0 Transmembrane segments, cutoff 1.7 TMPred: 0 Transmembrane segments	PHYRE: 2 α -helix structure	PHYRE: 100% tim8-tim13 complex
Tim13	Esi0243_0012 (82)	MDGQASAEQQAIQQLQEQQVAKALQELMTQMTDQCFNRCAKTS S G D R I N S S E Q G G L A M C M D RYMDTMGLV NKAMVAKANR	IPR004217 (Interpro), Mitochondrial inner membrane translocase complex, Tim8/9/10/13-zinc finger-like PTHR19338 (HMMPanther), TRANSLOCASE OF INNER MITOCHONDRIAL MEMBRANE 13 HOMOLOG PF02953 (Pfam), Tim10/DDP family zinc finger, 1.6e-16	KOG1733, Mitochondrial import inner membrane translocase, subunit TIM13 KOG3489, Mitochondrial import inner membrane translocase, subunit TIM8	DAS: 0 Transmembrane segments, cutoff 1.7 TMPred: 0 Transmembrane segments	PHYRE: 2 α -helix structure	PHYRE: 100% Tim10-like, 100% tim8-tim13 complex
TIM9/10 Complex							
Tim10	Esi0041_0146 (107)	MSWFGNSEPEPPSGPSPMDLAKQEVDYMSDLFTKMSGLCFKKCVVMHGESDLNVGEMSCVDR CVSKYMEAQEKVGVILKRAEESLAQQGGVGGPAAGGVGPVGR	IPR004217 (Interpro), Mitochondrial inner membrane translocase complex, Tim8/9/10/13-zinc finger-like PTHR11038 (HMMPanther), MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM10 PF02953 (Pfam), Tim10/DDP family zinc finger, 2.8e-16	KOG3480, Mitochondrial import inner membrane translocase, subunits TIM10/TIM12	DAS: 0 Transmembrane segments, cutoff 1.7 TMPred: 0 Transmembrane segments	PHYRE: 2 α -helix structure	PHYRE: 100% crystal structure of the tim9 tim10 hexameric complex
Tim9	Esi0075_0052 (88)	MTPVQQQDFLQHLESQQRKDSLAMYNNLVFRCFDECSKSRKRLDDGETKCINVCAEFIKLTS RVALRFQDIQQKAKDEAAGVQR	IPR004217 (Interpro), Mitochondrial inner membrane translocase complex, Tim8/9/10/13-zinc finger-like PTHR10898 (HMMPanther), MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM9 PF02953 (Pfam), Tim10/DDP family zinc finger, 1.9e-14	KOG3479, Mitochondrial import inner membrane translocase, subunit TIM9	DAS: 0 Transmembrane segments, cutoff 1.7 TMPred: 0 Transmembrane segments	PHYRE: 2 α -helix structure	PHYRE: 100% Tim10-like, 100% crystal structure of the tim9 tim10 hexameric complex
INNER MEMBRANE							
TIM23 complex							
Tim50	Esi0000_0471 (547)	MLLGRVGTLLPSCSGRVATRRLAKKAAGGGGGKKKSGTPKKGPAAIKARGAMPVSKAGKQG SKTGKTGGAAAREAAATTTSTAKAAAAEAAASVKPPVGGGGGFTKSEMLAARKARKASVTAKT AAAAATAKAAAPAGAGAGRTGGAGAAASAAGAGGAKGQKGWGWGTKLVAGTSSVGLAALGI AWQLKPDEMRLKLLDDSPIDHFFTWFMGKWALYSSPVKDKLLDCPLPGALPPPTLVLDLEGTL GTIYTRKKGWRVAKRPLDAFLKEMSQLYEIVFTDSMGGLADEWITQMDPQGTISQRYVRDGT RYIDGKYVKDLSALNRPLEQTLIIDDNADCISMQPENAIKVKAFSLEDGSDPTADTALYDLAPFLR ALATQGVADFDRVLRPHVGEDSNNAVADFERSKVNNAVQRKEDAEKSKGLGGLVRQIAPVVGAGG PAAGMGGM L T S K D I V G D A P E T L S P G M A A A A A T A G G K G G G K G G G S K P L A E K Q K G L W K S L Q EGNKEREEDFMRRNEAFQRVMEKRMAREKAKRDEQAQQQ	PTHR12210 (HMMPanther), NUCLEAR LIM INTERACTOR- INTERACTING FACTOR-RELATED IPR004274 (Interpro), NLI interacting factor (Pfam), NLI interacting factor-like phosphatase, 4e-37 PF03031	KOG2832, TFIIH-interacting CTD phosphatase, including NLI-interacting factor (involved in RNA polymerase II regulation)	DAS: 1 Transmembrane segments, cutoff 2.2 TMPred: 3-4 Transmembrane segments	PHYRE: multi α -helical structure	PHYRE: 100% HAD-like, NLI interacting factor-like phosphatase

Tim44	Esi0086_0051 (602)	MLRLGRHGSTLKACSLRQPAAAAYARATRPSSIWRDPPIVPSGPHDNIVRGITTNTFTNTTINTEQQ RSVALSRWIQADRRRGPHVGPAPAAVSTQLQQWRGLASGSSGKKGGEEGGMFDRCLKTFTTEE IDKNPSLKSLSKLKDAEQKLRENPSVKENLAKLKEAEKKFRENPSVQENLSKLKDAEKKWREDA KSKQGEFAEQAEKAREKAQQGGGAFQEKFKQLKQTLKEEKLGVKGESDGKDGEGEKDGAENE FVRASKEKFSGAQKALDENSLSFKLRVKTQAFREAVAGASSELFPSEGQKAESAASVVKKLKQPKKE KSKKKKKKKDKGEKAPVEGEDDEEEEEEEEEKGGMGSLMIVKTAGEAWERLQERLKESPIIQDLL GASRVVASGSLGQGAKSADKTYKDKVEDVQEAWETSQHPLVYKLSSAWDSLTAESDEGIGVREIL RRLDPSFSVEDWKRDQELFLPEFMSAFLRGDVKLLKQWTGEACYNKLASEAKQRKADGMVLDL HVLDIRQGEVLAIKADAGKANPTIALQFMCQQINCVRNKKGEILEGAEDDIRATYIILAFQREFND DEAELRWRVVDMMVVGAFWPY	IPR007379 (InterPro), Mitochondrial inner membrane translocase complex, subunit Tim44-related PTHR10721 (HMMPanther), MITOCHONDRIAL INNER MEMBRANE TRANSLOCASE SUBUNIT TIM44 PF04280 (Pfam), Tim44-like domain, 6.2e-28	KOG2580, Mitochondrial import inner membrane translocase, subunit TIM44	DAS: 0 Transmembrane segments TMpred: 0 Transmembrane segments	PHYRE: multi α -helical structure	PHYRE: 100% TIM44-like
Tim23	Esi0047_0026 (206)	MASEPTEESGGVQDPYSDASAKYGPLKLPELQNVDSLKMYGGAAQKEPEYLDYNIKGRGFWER MPYNAGALYITIGLGGGAAGVREGFAKAPNRRSRVLLNSIMNHAGKKGSFYGNTFAVLATYYTC AETLLDHFEVDQMGPVQAGLGEIHNPLLAGASTGLLYKSSAGPRLALMASVAGLGAVGVAYAV DKTSASVLGGQIIF	PTHR15371 (HMMPanther), TIM23 IPR003397 (InterPro), Mitochondrial inner membrane translocase complex, subunit Tim17/22 PF02466 (Pfam), Tim17/Tim22/Tim23 family, 3.4e-13	KOG3324, Mitochondrial import inner membrane translocase, subunit TIM23	DAS: 4 Transmembrane segments, cutoff 1.7 TMpred: 3 Transmembrane segments	PHYRE: 4 α -helices structure	PHYRE: 25% Mitochondrial carrier
Tim21	Esi0103_0070 (205)	MMSKASRKGDSDKSGEQQQKQKQGEQYEDADYEPEEEKISIVKTAVGCVLGLVVAALSAT ITELWPSHMAPQSIMSHAHDVFQADPTANHFGLPKGYGRDNNHREGRRNFVEVHDHEDPID KSKRTRVRNFVEGPHGGMAYAEVSNKMESEGWVYLCVQDLQTGHVITLHDNRALLMAQAQA GSDEEKNAFRKLMLGQ	PTHR13032 (HMMPanther) FAMILY NOT NAMED IPR013261 (InterPro), Mitochondrial inner membrane translocase complex, subunit Tim21 PF08294 (Pfam), TIM21, 9.8e-12	KOG4836, Uncharacterized conserved protein	DAS: 44-67, cutoff 1.7 TMpred: 51-69 (in-out) score=1978, 47-63 (out-in) score=1876	PHYRE: 2 N- α -helices followed by 4 β -sheets	PHYRE: 100% structure of the ins domain of the mitochondrial import2 protein tim21 from s. cerevisiae
Tim17	Esi0117_0080 (264)	MGDRDPCPHRIVGDVGGAFAFLAGGGIWHSVKGRNPSKPGQTQGALKAVMYRAPVLGGNFA VWGFALFVCDCLSLVAVRHKEDAWNPLSGAATGGILALRAGPRTAAKNVVGALLAVIEGMGI LLSRYMAQVEPPMEAGDGAGGAGGGLGAPQAPRPLGLAPPLPVGAPAGYRPMGDGGEVDSSA TRSHDVTVTSGSFETGSRFEDTLATQDPFASNTGDRYLEGGAAPRGAGDAAAAAEGAESRGWFG RMIGRGGGK	PTHR10485 (HMMPanther), MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM17 IPR003397 (InterPro), Mitochondrial inner membrane translocase complex, subunit Tim17/22 PF02466 (Pfam), Tim17/Tim22/Tim23 family, 4.1e-34	KOG1652, Mitochondrial import inner membrane translocase, subunit TIM17	DAS: 4 Transmembrane segments, cutoff 1.7 TMpred: 4 Transmembrane segments	PHYRE: 4 α -helices structure	PHYRE: 25% ammonium transporter amt-1 from a. fulgidus (ma)
Pam17	NI						
Tim16/Pam16	Esi0237_0006 (155)	MANPFARIIAQLAVASAGIVSRAFVSAYSQAVHNARTGTLESAKMSRTSKLSTLEAMQILNLQK GEMKPDLIKQRYDYQYFGINDPKGGSFYLQSKVFRAKEALDEQLALQAKQASEEAALKAKAAAG KGKGAGGAKARPAAGGARRPSANRRR	IPR005341 (InterPro), Protein Transporter, Pam16 IPR001623 (InterPro), Heat shock protein DnaJ, N-terminal PF03656 (Pfam), Pam16, 2.7e-26	KOG3442, Uncharacterized conserved protein	DAS: 1 Transmembrane segment, cutoff 2.2 TMpred: 1 Transmembrane segment	PHYRE: multi α -helical structure	PHYRE: 100% structure of the tim14-tim16 complex of the mitochondrial2 protein import motor, 1.5e-09
Tim14/Pam18	Esi0159_0032 (209)	MAARPLVRIAGLKPSVSHRCPDLLRLGALTSSNRESGANDRHARAQALVSQARDIHSVRRNESS VLITGAGIIVSAMVARYGLMEYQKYQAAHPITEEADSGAAGDQTAAGETGKASPGQAAKGAGA SAGGFFGAFGKRHYDGGFEEMTRKEAAILGVRESATAQRIKDSHRRLMINHPDKGGSKYMAA KINEAKEILLKGRK	PTHR12763 (HMMPanther), UNCHARACTERIZED IPR001623 (InterPro), Heat shock protein DnaJ, N-terminal PF00226 (Pfam), DnaJ domain, 6.5e-09	KOG0723, Molecular chaperone (DnaJ superfamily)	DAS: 1 Transmembrane segment, cutoff 2.2 TMpred: 1 -2 Transmembrane segments	PHYRE: multi α -helical structure	PHYRE: 100% j-domain of dnj-12 from caenorhabditis elegans, 6.9e-12
mtHsp70	Esi0010_0066 (689)	MLGARLGRSVAKRQLAHIRGGPSSAPSLPLCAAASRRALSSKGPAGDIIGIDLGTNTSCVAIMEGR SARVIENTEGARTTPSVVAFQPDGTRLVGLVAKRQSVTNPESTLYATKRLIGRRFKDKEVQGVQK LVPIYKIVESQDGAAWVEVQGNKMSPSQVGSMLVTMKMETSESFLGRPVGKAVVTVPAYFNDSQ RQATKDAGRIAGLEVMRIINEPTAAALAYGLDKADGKLIADVFLDGGGTFDISILEISGGVFEVNSTN GDTMLGGEDFDEVLLKHLISEFRKESGIDLSDGTLAMQRLREAAEKAKRELDGMPQTDVSLPFIT ADSSGPKHMNVKVTRAEFENLDGLIERAIKPKCDCMRDAGLETDEVHEVLLVGGMTRMPKVQ SKVEAFFGKPPSRGVNPEDEVAMGAAIQGGVLRGVSVDILLDVTPLSLGIETLGGVMTKLINRNT TIPTTKVQVTFSTAADNSQSVQIKALQGEREMATDNKMLGGFDLVGIPPAQRGVPIQEVSFIDADG ILHVGAKDKQTGKEQSIVIQSSGLGEADIEKMVRDAEEHAEADKKRRDLIEAKNSADSAVYGTE KNLLEHKDKIPEDVKADVQKAIDELKAVMESEDAEQIKEKVQALQTAALKIEGAIYGNKGGAAGD DAEGAPEGGDAESDKENIQDAEFEEKKEEGEKKSQ	IPR018181 (InterPro), Heat shock protein 70, conserved site PTHR19375 (HMMPanther), HEAT SHOCK PROTEIN 70 (HSP70) PF00012 (Pfam) Hsp70 protein IPR001023 (InterPro), Heat shock protein Hsp70 IPR013126 (InterPro), Heat shock protein 70 IPR012725 (InterPro), Chaperone DnaK	KOG0102, Molecular chaperones mortalin/PBP74/GRP75, HSP70 superfamily	DAS: 0 Transmembrane segments, cutoff 2.2 TMpred: 0-1 Transmembrane segment	PHYRE: α/β structure	PHYRE: 100% crystal structure analysis of sse1, a yeast hsp110, 1.4e-45 100% crystal structure of the 70-kda heat shock cognate protein2 from rattus norvegicus in post-atp hydrolysis state, 1.8e-41
Mge1	Esi0000_0394 (281)	MVVASLSTAADVKGKQSSLAARAGGQGVVWHPHAFAGRGQRGLCPGGVRSLSNKADEEEDKA KEGGAGGEAEQSNSKGEGEDEDEDQGLAEKLAKEERLMDTKEKALYLAEMENVRSIAKK DAESARLYAVYQKFAKQLLDVADNLERIAISAKEAEGEGGDSHDVLLQGVEMTSNELTKVFRS QGLEYKVEVDKDFPHLHDAMFEFVNPAQEPGLTGVLYKCGYTLHGRVIRAAQVGTGVKAA	IPR000740 (InterPro), GrpE nucleotide exchange factor IPR013805 (InterPro), GrpE nucleotide exchange factor, coiled-coil IPR009012 (InterPro), GrpE nucleotide exchange factor, head PTHR21237 (HMMPanther), GRPE PROTEIN, MITOCHONDRIAL PF01025 (Pfam), GrpE, 8.4e-52	KOG3003, Molecular chaperone of the GrpE family	DAS: 0 Transmembrane segments, cutoff 1.7 TMpred: 0 Transmembrane segments	PHYRE: multi α -helical structure + one β -strand	PHYRE: 100% crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnaK
TIM22 complex							
Tim54	NI						
Tim22	Esi0063_0018 (192)	MPADDDRRHGECCNQQGEPLRSLHPQLGSRLPFFLPWVPRPAAGAADAMPTPPVLTESCGFKLI MGTVGGAGMGFVFLGLGAMGDMQPLQMINGREVPQAPFREQARLAYKYQTADRSLSMGRNFAS FSAIFMGSECVIEKMRGKTDMMNSVYAGCATGAAFGMKGQQAACFCGCVGMATFSALMDKLM GH	PTHR14110 (HMMPanther), MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM22 IPR003397 (InterPro), Mitochondrial inner membrane translocase complex, subunit Tim17/22	KOG3225, Mitochondrial import inner membrane translocase, subunit TIM22	DAS: 3 Transmembrane segments, cutoff 1.7 TMpred: 3 Transmembrane segments	PHYRE: 4 α -helices structure	PHYRE: 70% structure of the multidrug transporter emrd from2 escherichia coli, 1.3
Tim18	NI						
Tim12	NI						
Tim17/22-like proteins							

Tim17/22-A (Tim22-like)	Esi0019_0065 (217)	MAYCRLLLQGLLLSVALGCNALPGWSRNSVGAAVQPHHGLAWTSRTPTTTRLRRQFPVAAAVAS TSHLTTRGTASGVMEQCMEACLTMMQSFIGGTIMGCVIGGVMGGSFGRVPDVGWLKSVMQTKAVE MGGNWGQLSAAFTGFTSISTVIRGRNDKWDQVLGACGAGAFLNRAKGPPQMAQGAATYGLFSL JFAPPSGQDDELVDVDPVDA PKTR	P51257 (Prosite), PROKAR_LIPOPROTEIN IPR003397 (InterPro), Mitochondrial inner membrane translocase complex, subunit Tim17/22 PF02466 (Pfam), Tim17/Tim22/Tim23 family, 5.4e-17	KOG1652, Mitochondrial import inner membrane translocase, subunit TIM17	DAS: 4 Transmembrane segments, cutoff 1.7 TMPred: 4 Transmembrane segments	PHYRE: 4 α -helices structure	PHYRE: 5% ammonium transporter amt-1 from a. fulgidus
Tim17/22-B	Esi0046_0104 (318)	MGWFLGRRRKPADESSPSSLTSDGINMSTGCGQAASESTGRSCTPMAEPVGPAPKTTLNAPAA AMRADACDASPVEEQEQQGEVYADSSPGYAHRLKAFAFLDTVATAKRAPETMEEAMAVIKG ERAVKPDYGRAVGTVSAFAAGGCAHGWWHGAALAAKYPPHQSRIVRVAGARRGLRFATFALI FEGSSAYMEALRRKKDFVGGTVGGALAGMAYGVSGGVAARSGLFYGVWLGGVFGLFRNHVA SLREQARLAEEERLQAQEERDAIGETALRRSIAGIDAQVTRWPTAAADSEDETDTTELASSQRTP	IPR003397 (InterPro), Mitochondrial inner membrane translocase complex, subunit Tim17/22 PF02466 (Pfam), Tim17/Tim22/Tim23 family, 5.8e-07	NI	DAS: 4 Transmembrane segments, cutoff 1.7 TMPred: 3 Transmembrane segments	PHYRE: multi α -helical structure	PHYRE: 65% Phase 1 flagellin, 1.4
OXA complex							
Oxa1a	Esi0028_0040 (412)	MSTAAGTGHSGDVTATTADLGPDAMAGGADAAMAAAGTADQAQAALVAPETFKMALYTPPVQV AMMAVDYVHATTGMPYVWMTIVAITVIRTAILPIGLLAARNGARTAAAMKPEMDELQAAIKGDQQ SSQPRKADRYRQETKALFQKHKASLVMNAAALPIVQLPLFIGFFLGLRRMPDVVPEFATGGVLWFQ DLGAPDPYMIFFVMTGVMMMAAELGGEAGALAGSSVKMKAGMRGMALLVTPLTMYVSTGV FVYWTTSNFYSILQTLAFKSSGIKKFFDFPDLPPNKLKSNTAEKEIGWLDVLGGDHPHPIEYRKMQD QREVAQWVFVEGEGGWTRKAHNAEQGECCNVAREGAPFHAPPSMAGPVS GKAKTPSFASSAAAG TPKVVLRSVRPKPADGRGKTAARGP RKNRG	IPR001708 (InterPro), Membrane insertion protein, OxaA/YidC PTHR12428 (HMMPanther), Oxa1, 3.3e-58 PF02096 (Pfam), 60Kd inner membrane protein, 3.9e-40	KOG1239, Inner membrane protein translocase involved in respiratory chain assembly	DAS: 4 Transmembrane segments, cutoff 2.2 TMPred: 4 Transmembrane segments	PHYRE: multi α -helical structure	PHYRE: 95% membrane protein / hydrolase
Oxa1b	Esi0025_0161 (553)	MLTGARLSRQSRRLVGRVHNGASLTAPAIAENRLTHHDGSDNSKRTCRGYLRPPQHLLQAQTL HVPALQQRGHRSSSVTRLGGDGAIGAALGGGRGLDLSAAWRGAAAAGGTVGARRSFWGRSG GDGSQAGSSGSDSGSGSSEDGAGFPETGGAADADGWSAPPDAAWAPDEVPEIPQDASVPGFDVG EGFSVDSAAAAADAVAGAAPDASAVGTAMTATGLSAADLGMYPHHLFMHVEIYVQATAGVPYW EAIVMVSAARIAVLPAVATFLGMSKRLNMIKPEMAVHQGMQDIKNRMEANPEIKEAAMAEM MLVSQEMGNLLKQHRIHPKMMLSMFAQFPVFISFLATRDGMTYFPGYMTGGLDWMMNLNAP DPTWTLPILTSGSMILLMELGSDMPAAHGPDKPNFNPKVMFRVMSVVFPVAFSMPAGVLVYWT TTNVFGMLQRGLFEMRPVQQALGWLPEDMPAPAAPADKKEPAEADFASKEDLERWGGGGGEGA SGEASRAAAEAERAREAVAKASKVRHEELKRQHGERSGEDGPK	IPR001708 (InterPro), Membrane insertion protein, OxaA/YidC PTHR12428 (HMMPanther), Oxa1, 5.3e-41 PF02096 (Pfam), 60Kd inner membrane protein, 4.1e-34	KOG1239, Inner membrane protein translocase involved in respiratory chain assembly	DAS: 4 Transmembrane segments, cutoff 2.2 TMPred: 5-6 Transmembrane segments	PHYRE: multi α -helical structure	PHYRE: 95% membrane protein, transport protein
Oxa1c	Esi0170_0057 (261)	MHVMGGVQSGVQAVHHHTTGLPWWTATIAVATIGVKISLLPVVVYQAGHMDRMRAAWPEIQILRG YLATSLEEIPQERVLERWRKYKVFSGARGVLGLHGTHLRGMFATPLVNLVPVITFVWSIRGMLR DCTVPOLDTGEADTVHSLMLPIIGTLCTYTSLEIVKMKGATGWMKFFQDGMQTHILMLPWVSTF PQGVFMFYWIPSAVFQMGQTYTMKNKNVRELLGLKPLGLPPREAAGATPSLAPAPAPAPIAPKAI GG	IPR001708 (InterPro), Membrane insertion protein, OxaA/YidC PTHR12428 (HMMPanther), Oxa1, 3.8e-32 PF02096 (Pfam), 60Kd inner membrane protein, 2.1e-19	KOG1239, Inner membrane protein translocase involved in respiratory chain assembly	DAS: 4 Transmembrane segments, cutoff 2.2 TMPred: 4 Transmembrane segments	PHYRE: multi α -helical structure	PHYRE: 95% Voltage-gated potassium channels
TAT system							
TatA/B	Esi0067_0034 (171)	MKLACCVLVWACALAAVVAEAFVPALAGRAGIMSAAGRQASMSPAAGRQNAFSHTSYGSPAQ AQSSRWLSGRPPSGASTTTMGLFGLGAPEIAVCIAAALILGPDKMAGFAKDMGKMAGELKDVP KEFQAGVEEGEAKTKQKTIREIESNGLAVEDAEPATKKEEEKA	PF02416 (Pfam), mttA/Hcf106 family	NI	DAS: 2 Transmembrane segments, cutoff 2.2 TMPred: 2 Transmembrane segments	PHYRE: multi α -helical structure	PHYRE: 25% crystal structure of the c-terminal tropomyosin fragment2 with n- and c-terminal extensions of the leucine zipper
TatC	mt genome (254)	MKRLQLSYIIQELNRYLAAYALGTTLIFFTTYTYKQGLIFLLLPKGLSHFVSAGLIEIFFTYIQLCH LSISFGIFLIASQSYVFLRPGMYTYESSFTLKLISAFICYTYIYILVFPALIKVSWELFLTYSQNFTPIN LTFEPLNNYLDHIQQLNKILIFSPCLLLTLNLFKYQYTNKLWVKHKGIAIYIAFFIAAFITPPDIISQI LVGAPLIFFFEIQJILWAFYKEYKKQLLVVRQPIKSHKNTLRNKE	PF00902 (Pfam), Sec-independent protein translocase protein (TatC)	NI	DAS: 7 Transmembrane segments, cutoff 2.2 TMPred: 6 Transmembrane segments	PHYRE: multi α -helical structure	PHYRE: 85% Rhodopsin-like, 0.014