Supplemental File S4

Acanthamoeba castellani* Mitochondrial Proteins Identified *in silico

Key:

Sequence lacking confirming RNA data is shown in **bold blue**.

Cleavable N-terminal peptide sequence predicted by MitoProt is shown in **bold underline**.

Entries marked with an asterisk (i.e., Bxxx*) are inferred from the *A. castellanii* mtDNA sequence.

PCD = putative conserved domain

>B001_pyruvate_dehydrogenase_kinase
MMNRMRTTVASTSSHVHIPSSISSSAASSSSPVSWQRTMDDMIHRYANLKQTPVSVKNMIVFGKDANMNTLLRSHAF
LRYELPIRLAHIAKEITALPEELLEVEPVQKVLNWYRLSFSEVIESPVPNVADMELKTEDEQCASLHQFQDMLDHIK
DRHSGVVTTMAEGVLELKNRLGREMIDTSVQFFLDRLYMNRISIRMLITQHLELFKQAQTNNNLCAITSGASGRKVT
PNKKNRWVGIIDPQCNVKEIAEDAVDDARYLCSNNYSVCPSVQIIVPPKLGTETSAGAPTLPYVPSHLYHMLFETIK
NSLRAVVEVHGANAQSEDDLPPVRVVLVKGTEDLTIKISDMGGGIPHADVPKLFTYFYTTAAPPTKDTLDSLNEGAA
PMAGLGYGLPISRLYARYFGGDLKVIPMEGYGTDAYIHLKAAGETREVLPEYSPSTYLGSQANLREWLNVDNCAFQL

>B003_fumarase,_class_II
MKRTFCLRPSPTPTTAAAAIFRHSSASSNASFSRGCSTRTTTTHRQSITTLRQLHPIRNVRSISSPFYGKMLSSEVT
NEMPASPATSLWRRALMTTAAAVAQDNHPLYRTERDTFGEIKVPADKYWGAQTQRSLQNFKIGGVPDRMPLPVVHAM
GIVKAAAAKVNLECHGLDPKLGKVMVQAAEEVISGKLDDHFPLVVWQTGSGTQTNMNVNEVISNRAIELLGGQLGSK
TPVHPNDHVNMSQSSNDTFPTAMHVAAAMQVHNLLLPNLATLRDALTDKATEFAHVIKIGRTHLQDATPLTLGNEFS
AYAHQIHKGIVRVKDALVNVYELAQGGTAVGTGLNTPKGFAERIANEIAEATGLPFVTAPNKFEALATHDAMVELHG
ALNTVAVSLMKIANDIRLLGSGPRCGLGELLLPENEPGSSIMPGKVNPTQCEAVTMVCAQVMGNQTAVSIAGASGNF
ELNVFKPVIIRNVLHSIRLIADASLSFTEHCVVGIQANEKRIGQLLNESLMLVTALNPHIGYDNSAKAAKKAHKEGT
TLKEACLSLGLLTSEEFDKWVRPEHMLGPE

>B004*_NADH:ubiquinone_oxidoreductase_(Complex_I),_subunit_2_(Nad2)
MNVINFIYSIFDKKLFKCGTISSRGLFYNDLNFFHFEIYFLLALITFLIFFVILSNKKNYRSYYYLNVGGIFSNLLP
FVVILLLIILNTNTNDSYYLFAGFYYNDAAVVFFKNIILIGFLIFTFAIKQYLSYFKYYDFEFILVLFISLFSSLLI
LNSNDLISLFFIIELQSLTFYILVASKQTSSFSTESGLKYFILGCFSSGIILFGISLIYGFTGLLSYTDLTLFLSEV
YVTNFILDSSFFSFSGFLIGFLLLTVGFLFKLGSAPFHMWMPDVYEGSPLLITAYLSTLPKISLIFVIFKLYYYVFF
EVFLFSQGLFTLTALFSILLGSIAAIYQVKLKRMLTYSMITNTGYLLLGLSFGDISGIYITIFYLISYIFIMIGLFF
CFLSLRDRSSGLLVKRINLFSNLLEVNPSLSFSIFILLFSIAGIPPLLGFYSKFFLFLFSLKYKMYWMTILFVIFSV
VSVFYYIRLVKLMYFNRTTGWIFLYDIPFLNSLIISFITIINCLFFFNPNLLFKLIYNFSFYLYI

>B005*_NADH:ubiquinone_oxidoreductase_(Complex_I),_subunit_4L_(Nad4L)
MTSFNIFFLLFFSFVIFFLGILGIFITRKNIIIILVSIELMLLAVNFNFAIFSVLLEDMFGQVFILYTLTLAGAEAA
IGLAILIIFYRIRGIISVNFVTSLKG

>B006_NADH:ubiquinone_oxidoreductase_(Complex_I),_subunit_AGGG/NIGM/NDUFB2
MGGDHHAPYKGLDVKLPYGGFHPPPVNRVHKNAALFIGTTMWFWVFWRLKHDWRHLFTSHRPYEITHEGEDEHH

>B007_NADH:ubiquinone_oxidoreductase_(Complex_I),_subunit_MLRQ/NUML/NDUFA4
MQAIRRTYNENTKAVWLTLFPVVGGGCLWAAYIGFRTFATHNDVVLKARGNEPYLMRDSPKLLSRDAAITLADKWSN
EMGGDDQFQKPK

>B008_Complex_I_assembly_protein_MidA
MKRITAATRRVVLRGDAALVRCTTSASLCRRGSNNHQIEGLRCNSTNGKPTDGSAQATEEMTSRAISIDTSGLYKHK
PHGPAGNKSADTPLLSHLRANIQLRGPISVATYMKEALTNPMHGYYMNKDAFGQKGDFITSPEISQMFGEALGVWCS
DLWEKLGRPAMWNLVELGPGRGSLMHDMLRVLKKTPELFGQMTIHMVEVSPYLRQKQAATLGCDPTLLSGDAAKETS
STEREGSKILKAGAANFAADTRDTKPTAGREETGHWSSPVLTGADGVRVQWHRHFRDVPPGPFLVVAHELFDALPVY
HFEYTEKGWLERLVDVDQGEGPHHLRYVLSPGPTYATMALLRQAGVSTEPKPKLKQKAPTASFSYRGGEDDDDDNDD
DNRPTDGPKVGDRIEVCAEGMALASQISEKIAREQGRGAALVIDYGQDRTREDTLRAIKNHKIQDVLCEPGLADITA
DVDFSSLRRTAQQTPSITTYGPKPQGQFLQELGIDARLATLLRSAGDDSAQAKDLIAAYERLVDDEQMGLTYKAMTI
CSLHNVKQPPVGFSL

>B009_Complex_I_assembly_protein_NDUFAF1/CIA30
MVFPSQNTQRKMLGRSRAGVGSSVKNLVREALAGPPLLREGAFGGPQARERMLYSFGAGADPAAWEAVTDADFGGRS
RAKLEPTEQGTWVFSGALDLSTEGTEMKQAGYAGLQPRQRKTIKSLDGFDALEVRAKTDGRVYIANIKTDSMVKHHL
FQAFFTTRKDEWTNVVLPFDRFTLTFQGQVEGESLPIDPRQFQAVSFLMAERKDGEFRMELEWVKAINTRLRKGARY
TGLVHDQD

>B010_Complex_I_assembly_protein_NDUFAF3
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AIRPRVSILILGCGQRIKMINPQLRDFFRQKGISIEALDTWNAVATWNILNQEDRAVAAALMPFDYE

>B011_Complex_I_assembly_protein_Foxred1
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PQQPQHPARCANEEAAAAADGGGTGVDVQFRENGYLFLASPQGRPVLESNHQLQRDLGSDIRFLGSPSEIKAQFPYL
HTDDLSAGCFGASGEGWFDPATLLHGFKRKAAALGVNFVHGEVVGTELEADGPRQRVSGVQVTTADGVAHKLSCSHL
VNAMGPQAARLSQMMGLTLPVVPRKRCVFVLRCRDEEVNQAKMPLVIDPSGVYWRPEGCGFIAGVSPLVDPDAHGDF
EVDHDLFEEVIWPVLAHRLPAFEAVKVVGHWAGHYDYNTFDQNAILGTHPSVGNYYHANGFSGHGLQQSPAVGRAVA
ELLLEGAYKTLDLSMFHFERVLENRPIIELNVV

>B012_Complex_I_assembly_protein_B17.2L
MSFFKRLLNRMERRTVVGMDKVGNTYVIEPDPLNPARPFKRMIEAKDTIYDPSSVPALWRSWLNFRREEPPTEKELE
AYEAKQRNLAQKVAELEEEDAKLALQEQAARQAGVRNAGPQGATPKGMLDTLVLQLAAGEIDQRGQKSAEGKEMDVE
DDDLPFPEFPSEAKEWDSPRRPRSTDDTYSRPSCRAASFSAPPDSFADDEDEADQEWKPPSNNK

>B013_succinate:ubiquinone_oxidoreductase_(Complex_II)_subunit_Sdh2-2 (SdhB-
2)
MLPMRQRIASSAVCTARSCVTRSPLKIAPTLTTSRTLHIPGLTKLDKTVPQDGIVDVQVYRWSGKEGEKPYTQNYKV
DVTECSPMVLDALLKIKNEQDPTLSFRRSCREGICGSCSMNIDGQTTLACTKPIKESITNGKIKIYPLPHMEVIRDL
VTDLTHFFEQHREIRPYLMKNDDAALKQSKVEQHQSREDRRRLDGLYECILCACCSTSCPSYWWEGAQDDKFLGPAA
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LAIRKRMHHMPPVAGV

>B014_cytochrome_c:O_2_oxidoreductase_(Complex_IV)_subunit_Cox7c-2
MNFLRRTPLSGVRSFALRGHGPSHGPDGFQLGQAVGTTLPFSTAQTAKPFRVGLSTWGYFVAGIGLPTWAVWYSANK
EAK

>B015_Complex_IV_assembly_protein_Cox10
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TLAMYSELGKIKLGSMVVITTMAGYYMAPFSSFDLKRFALTSLGTGLAVISANTFNHIIEAKLDLRMVRTSTRPLPS
GRMSSTHATMFGVITGIVGPALLMARVDNTAAALALANIVLYAGVYTPLKQMHPINTWVGSVVGAIPPMIGWVAVTK
GKLDLGAWALGGLLFLWQIPHFLSLSFPLKEDYARAGYKMLSVTNVDAVMSLSYVFSAMLLPLGFVSSYAGMTSWVY
AIDSTLCNGYLLWMAHKFYTRRDTTSARKLFFASLIYLPLQMSLMMLHKSNHPVSAAAVATPSLSL

>B016_Complex_IV_assembly_protein_Pet191_[0.0420]
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QAPAQPPAAGGRS

>B017_[Fe-Fe]-hydrogenase
MKKHMTMRRLPWNAVARSLRCTTTSRCAAGLRVRGTATTSSGTGSAASAADRLKQLTQLKADFDPLGKEVEKKLVNV
TINGTPRQVAEGLSIVEACRLFKVEVPTLCYHPMLTIVGQCRLCLVQLANRQGKLVAGCATHVEEGMDIITESETLT
QNVLSNLQLLRCRHPNACMTCEADGHCEFQNLVYKFKVEELLPQYHRDRSHTRDASSHSVVRDMNKCVLCTRCIRAC
SQVQGMHILGMIGRGAEEEVSTINFLPLNQTACISCGQCTAVCPVGALVEKTHSHEVESGLRHKAKEGKIYVAHTAP
AVRVAISEEFNMAPGTVSTGKLVSALKELGFDYVFDTNFAADVTIMEEGYEFIRRLQSNDNLPMFTSCCPGWVNLVE
KSYPELMPHLSTCKSPQGMMGTLVKTYFAQKLGVNPDRIVTVSIMPCVAKKDEIARPQLSMEIEDSKGEKRRVQDTD
YVLTTRELGHLIQRHRIPFVSLGDKEFDTPLGLTTGAGALFGATGGVMEAALRTTYEVMTGKPLPKVELTAVRGYSA
VRKASVMIGDREVRVAVVHGTKKVREVVEAVLSGDKSFDLIEVMACPGGCVGGGGEPKTSAVDPDVIRKRIDAIYSI
DERKQLRRSHENPAVQELYKTFLRGEPNSAEAHHLLHTHYTDRTSEVKSRSDEAFGRVPPALELKPADHPHH

>B018_[Fe-Fe]-hydrogenase_maturation_protein_HydE
MKKTLAPLVQRDVYRVMLLRRGLHDAAPVSGGSPTDLHKLLYSPLLTPDAPAAEDPVAARNALQAALSRGGKKRPVN
RLHLPLEEKIAPLASLVGRALTPGEPLTLEKEQIVHILQTADEGLENALYDYADTVTQRYFGKKIYFRGIVEFSNVC
TKDCYYCGIRKHIQVKRYSMSKEEIVNCAIFAYESGYGSLMLQSGELPTDKRLAFLVDTIKEVKRVTIEKDKERNGV
KEGVENKSLGVAISLGELTKDMFRSLREAGAHRYLLRIESSNPDLYAKLHPADHSWHRRVECLRELNELGFQVGTGV
MIGLPGQTLGDLAQDLLFFKSMDIDMIGMGPYICQKDTPLGKLWQEENSNLDTKRYNEKLFRLSTKMVALARIICGD
VNIAATTALQAINPQGREVALNQGANMLMPILTPRKYREDYQLYEGKPCIDEGAEECRSCLKNRVQWAGKELTLHDW
GDPQHFFSRQSIPSPTSQ

>B019_[Fe-Fe]-hydrogenase_maturation_protein_HydG
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ILAKAKQRALLQDIKGPVGSEYVQGLNLRETATLLNLDAHSKEPENQKLMQELFDTALAIKQNIYGNRIVLFAPLYL
ANYCVNSCTYCAFRGANTHIARSALTKEELIQEVQVLEKQGHRRLLILTGEHPKYTFDQFLDALHTVKNVKTDPCGD
IRRINVEIPALSVSDFRRLKATDCVGTYTLFQETYHRESFRRFHPSGPKSDYEHRLQTMDRAQIAGIDDVGIGALFG
LHDYRFEVMGLLMHAQHLESTFGAGPHTISIPRMRPADHAPDAIRPPAPVDDEDFKKLVAILRCAVPYTGMILSTRE
SAEMRRELLNLGVSQMSAGSKTEVGSYHKGDVGAEAKIKQQFEAEDQKEKKEKKESGQFELADERSTEDVVKDLMQM
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>B020_NADH-cytochrome_b5_reductase_form_2
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TSKVGSEVVATHDEATAVEKKDLHEKKKKKKDDDGVYLPFKIAAAVPISPDTKLFRFQVPADQAQLLRTLPSPVSH
IALRATLPPLPHDPTTSELLKRRPYTILRRFPAPGQQQTTPEDEEDQHVEVMIKRYDTFGLSAHLHSLKEGDTVELQ
LVGKDKHAKMNFPEIHLRHKHIGIVTAGTALAPMISIMRSVLYNAEANDTRVTLLYANRHEEDILLRKELEELWEAY
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>B021_RecQ_family_ATP-dependent_DNA_helicase
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SASEDAAGTVAPAGGVVKATHDLEEELKKHFGFTSFTAGQEAIITSILSGRDTLAVLPTGGGKSLCYQLPSLLHTSG
VAIVVSPLIALMKDQCDSLLRKGIKAATINSFQSKAEQVQVIDEMVSGAYKLVYVSPERFKDDTFLAALEKTTVSLF
AVDEAHCISQWGHDFRPDYARLGTFVDRLVSARGGRPVVAAFTATAGVQVRKDIASRLQMRNPFELVQGFARPNLSL
HITETQETSRRRAYRETLNEIKVLRMKEIVHEMKKGIIYVSTRKRVDQVLELLRDWGVEKCEGYHAGMSDVKRDSAQ
ERYMSGECDVMVATNAFGMGIDRADVRFVLHFAMPASVEAYYQEVGRAGRDGAPARCELLFDREDIQLQEYFITSGN
PSRAAIEEAWRTLRGVHRTQLEERDRERALGLWDEPDASVEGEEKPLPFHHTVPMGDDDEDKGIDKQRVLVKRRRTE
LGDDDLVISLVDLAEFTRQVDAAGLSRCVSILESHGYLERFQVVGERVRGTRLLRPWVSERELELDLTDVNENRARQ
QKKLNAMLQFIRTERICRQQWIMEYFGEANARPCGRCDVCAAFPVESRSVADRTVMAHALEAVRETTEKVTQFYKWG
GGDAVGIVGATKDQIIKLLAGSRAKEMADLGLDRLASYGKLRPRNTSKSKSERAGGGGNKKVAANNNAEAMRNVFLT
LEKEGYVESRGDEEDQHVRHPRVVFLTPKGRQWLQERGLLRQQR

>B022_Pif1_DNA_helicase

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GVGLGEQSQEVLVTKVLSTKRSRDRWVSTKVLIIDEVSMLEGTLFDKLEYVARKVRNYDAPFGGIQLILSGDFLQLP
PVQTKFFCFESAAWKKVVREVIVLTHVFRQSDNAFVALLNDLRVGKVTEEGRSMLARCMIPYHDRARSIHRGDDRIQ
ATLLYPHRRDVDGENTKRLAELAGTSRVYRAVDSGVEPYRSMLARNCSAPDVLELKLNAQVILLKNLDSALELVNGA
RGVVVDFKKPVKQDNKEESYDESKEYPEVLFTSGVRRLITPEEWNIGVAGEPQAWRVQCPLALAWALSIHKAQGMSI
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>B023_DNA_ligase,_NAD-dependent
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FTADRPSPTQQVGYRPLTEESGLLEHATPMLSLANTYDPQELAQFDTRVRKLISAAPASPDVQKPIEYVAELKYDGV
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EYSNPRNLVAGVLNRKQDTDLGLRKKPFNLICYTLMSLSDEGEAGLPPSHQARLEWLDRRGFTIDSRATLCGDLASM
VKFVGEWDNTELRDAFPYLIDGVVVKVNAIAQQQALGANNRAPKWAVAYKFGASKAVTQLLDIVYQVGRSGKVTPVA
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LVREDIDLHCREPSCPEVAVAKIVHFASKQAMDIEGLGEGLVRDLFRQGLLRSAVDIYSLLDDDDNDAGDVSKRAAL
GERKGWGEKKIANLLRSVEQSRHSRDLSSFLFALGIPHLGKHTAQLLADHFKSFESLMAATEEDLRGMHGVGDIISS
SVAHFLHDPKNREDLQRLYAICKPKENMERSRARAARANGEEKPPTCSVSFTGTLSGMARHEASAAAVSALGAVVKP
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AVLRECGYVPALYKIFDEILVNAADNKQRDPNMTTIKVWIDAEQGSIRILNDGQGIPVHVHKQEGLYLPELLFGHLL
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TKETLTTRPRNFGSDCQLSTQLLDNILERTRIVDTVSRWMYMKQSSDLARKAASGRSGTRIYGIPKLDDANLAGSAN
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DAEQSGEVASDGLRYGKVMLMTDQDHDGSHIKGLFINFLHRFWPSLLEKGYVEEFITPIVKATKKGAGNKKEEKVFF
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MAFYEEQKQRVADHNYDVPLYSEDLFKKDEEARMISYSDFINKELVLFSNADNIRSIPSVIDGLKPGQRKVLYACFK
RKLHSEMKVAQLAGYVSEQTAYHHGEASLHSTIVHMAQNFPGSNNVPLLYPAGQFGTRLQGGKDAASARYIFTRLDP
AARLLFREEDDHLLNYLDEDGEQVQPQYFVPVLPTILLNGCEGLGTGWSTQIPSYNPLQIIENLRRKIEGKEMEKIA
PWYRGLQGPILRKKGSPSYVSIGLVEKINPTTIRISDLPAKRWTATYKEFLDQMAKPPRRGRRALIKGFKEHHTENS
VDFHVYMTKEQMELAESVGLVEHFKLYSQISLNNMHLFDKDGKIRRFECPLEIIDEFFPLRMEHYAKRKEWQLKTMS
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CEVLAEDAEPKVQRYQTLVALMLSSQTKDQQTAAAIRRLQKHGLTVGNILDTPENELDELISNVGFHRNKAKFIKRT
SEILREEYDDDIPPDYEGLLKLPGVGPKMAHLTMQCAWHKTEGIGVDVHVHRISNRLGWVHKTKNPEATRKELEEWL
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GPFAHGRASMTLMFQLEVGKRIEARSGTSEYGRLSVMTQQSCTAQTCFNVPASVFVPPPKVTGTMVRIEPRVTPLAP
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QPPPRIEASNKYPSAIVLLPNKELCEQVLSVCKKVVPPILTVKAINGTELPAKRPDILLTTPNGLAKSLNDDMLHWV
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VPFHREMPQGEADRNLRDFLAGKVDVMVSTNLASRGIDFVDVEHVVQFHFAQSLVDHIHRVGRTGRGGRSGEVTCFY
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MGVRVNMGQYEKHLKYRLTCVRGNMFSYEREFYDICRAAMLKYWYQVRIGKMHGIFVCYHNTREVFGFEYMKQEEME
RILFGNSEFADVAFQAPMRLWQNILNEITSRAPPGKTLRVVLNAEKLTKTLDVFVEPVEFDSGWLEPTTSLTSGDMG
MISARTSGYGYLSSTIQRSSMLDPTNPPNPELELERYEWLKTGKLQPSLNHYKLHLATFLNGRPTLDHPISHRVGDR
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RDAEPPTIIPFAKAGGKCDPVDSQIFTFLLSFLRHHRLSTDIRLGGGWLRDRLMFPNARLKSHGMDFVLSDMQGSVF
GQLLSDYARKRKQQKTGQSTQEGVKIVARGDKWTMWFLGRELRFEKRMADTWGDEARWRRDFTINSLFYHLQDQTVE
DYTHQGLDDVANRLLRTTIPAESSLWYDPVRILRAIRFSRSHQLNFDSELEYAMENHEIQSRFATHVQPARVEAELK
KMLIHKNSVWMYKSLARYNLHPVLFKFPASLCANDSDASPARSPPSALSTFSSLPPLAAEISLPVNSWDRLTTTKAL
SSTAYLRKLLQRPKQKEDLKESMALLLAFVSPSLLANWSGHNPFSVQLARVAVREVKSALALPDVWAKELRELLSAT
VNLLHIAHEFIPTIHAFHLMEDEDSSEIESGYRTLVHRRKHDLLHWLRHYPDYWRLATLLGHTMLIHGSPRYYFDWE
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K

>B030_S-adenosylmethionine-dependent_tRNA_m^{1}A_methyltransferase,_putative
MRRTTSAASSCRWTTGPCPSFHTGARPPSAFLSTPLFSPFASAGAIGIVTSRRNLRLGTRLSTVLSMLDLRHPGTIA
DIGYDNGYLLAELDELGHTDLVGVEKNPTLASKVMYTSRHKWRSRPRWITGNGLSCFRPGQVQQAVMAGFGENQIVD
ILQRDQEQALACHRLVFCPAISTGILRPYLNFSKNWRIVDEEIVKEFDRFYSVLCVERGEETNVKDNLDLFIGPFNM
SRPHPMLIDYLEDCRGRIEVDEWKHVAKKKKLYCSFLRSVDKALEQKEQLLERMRQQQQPANATTTAELAIESAVGS
ESDVSSSSHNERVGGDARNDLGASIQDEQRITAPNSQERRPDEPEGRSALLQ

>B031_S-adenosylmethionine-dependent_tRNA_m^{7}G_methyltransferase
MRRTRCVGLQPSSGGSLLSLKTTEMHRHPPSSPLFNRCPQINIQAACLATRLRPTPNPLARHCQKQLEAYPDWRSLY
ADPRLPFHLDLGCGKGHLVYHLACEHPEMNFLGLELQEERVKPFPALPNLAYVCCNVNVSLEPLLKSYASQLADHHH
QQQHDSAVATATAMTVKRVSILYPDPWFKKRHAKRRMVTPELVRTIHGFLDDGPDSEVYLETDFGEGFFEAKDIFLR
DSFVLETDEKHFPPCRFGMSEFAMWVREDPSIRIFTATFRKVPRNATQCEEATTPPPHPNSVPPA

>B032_tRNA(Ile)_lysidine_synthetase,_putative
**MKRCSARAPQMWLNGARAGGLVVPRPRLLRSLPPQGAALATSSVATDAGPLCSPLRAAAFQLHPSSSPITSPAPQSR
RFSTSGPAA**PAKAPQHISSDEFSRLMMQAELDKVPAGSSIAIAVSGGPDSMALCLLTHHWAKKRGIKVLALTVDHGL
RPESGEEAKRGIRHEILHRPWDKPAQPGHIQEAARKHRYMLLYEKCRSEGIHNLLTAHQLEDQVETFIMRLAHFSGV
DGLAGIQKRHAQFFPPVPPGSGSAKAAMTSTRLAPPLFPPLSNQTLNTPSSDSYPSPLYIVRPLLEVSKDRLMATCA
HFGQEAVDDPTNQNMTFHRNRIRQALPLLWETIGKEDLSRTIYHFQKARNEMQAEVNAIMRTHSRFSTRPFPARFSP
FGAEPSLPSPQFLGHVYLPVSLFGGSRDSLSLPLSMRVLQAALVSVGGLRAERLSLKLPMLREITERMQKTAAYAAG
GITATLGRGLTPILPDHLKATFTACGCLIQLLSSPHQSMFVICPERRMTSEKEPIRPGETLLWENRLAISFTVGGRQ
PQRRASTASQPPPTTDDRFFVRRLTTKDYKVSHVIGTAVREVPSDIRVTTPVIVDERDRLVALPTLRFLQNRPDLVF
TTAPVFPLTSEPSPCAPPAQPDELSAKQKFDMLLAQLDEFDRIADQLDDGADDSHDSRDKPPQTR

>B033_S-adenosylmethionine-dependent_methyltransferase_MraW_(small_subunit_rRNA_methylase,_putative)
MATRRAGPRLVATTYGVWHHPGRSPHKASASFAFIRHKSHTISASDAGGTDGATAPTQQTRAHVSVMLEEVMQGLGV
SSAASTRKTPISHLAPKSAKSNENRSRVFVDGTFGRGGHTRALLERDRACRVIAIDCDKAAFEGEEQRRLIAEHQDR

LIPVQGRFGDLANLVAQANVSEKKQVDGILLDLGVSSPQLDTADRGFSFRYDLNGPLDMRMDQSPNSLTAAYVVNNV
AEEEIARIIWMYGEERQSRQIAKAICRYRRERRIDTTTQLADIVRRCLDAPPSSGGGRRSGGSKRGDKSIDPATRTF
QALRIFVNDEIKQLQQALAGAEAVLAPGGRLAVISFHSLEDREVKNFMQHCAGRKKAVLEPQHAGWERDHVDEDDD**G**
DEEEDEKRNRDDDGEEGDESDDEADELFLPSFRVVGKGGKFVAPSDAEVRSNPRARSAKLRVAERTRFPPLRPFG

>B034_rRNA_(cytidine-2'-O-)-
methyltransferase_RsmI_(small_subunit_rRNA_methyltranferase_I)
MLRRRAHRLCAAPYSWNSSRGVPASLQAGATALVAHRSTHGLISIFHSIHARSDSYEASARGEDKDNEGVNHEEEEE
EEKDEEDSSIIEARLLKNREADSTQRSAAAKGSGQLRPGLYVVATPIGNLSDITLRALHVLKSSSLICCEDTRTTRM
MLKRYKIVGEERDRREGRVELMSYHQHSSPSKVNTIIQILKTGAHIVSLVSDAGTPSISDPGVPLITEAHRQNVPVI
PVPGACAVVAALSGSGFPSERFIFEGFLPHERSKRKKLLALLAKQERTVAFYESPHRIVHTLADCVEVWGPEQEAYL
ARELTKLHEQTMRGSLSKLLETITQQGGRGEFTVLIGPRPTTAGDKRRGSRARRPQDFSDMALDDDDVDD

>B035_large_subunit_rRNA_(uracil-5-)-methyltransferase_RumA
MKRFGHLASTKQFLTRPSSSPLALLANATRHRFAAYSANAGDASQFSDDGGPVTTLHPHTTPLAPIKKGGKKDKEIV
FVAKAVVDRLDELDPSQGVVHHEGVKIEVFGALPGEEISFTRPVKKRNATLVEVMKASEHRALPRCGVYGRCGGCSL
MHMTHEKQLEVKHQLALDVLRQEGVEPAEVLPPLHAQQYGYRHSARPNVRHLEDREDRVGGKVLVGFRHKWVMGSQP
VDRCAVLAEPINSFFQDAADVINRMSVRDKVPTVEVMMGDTEKALLLRHLSPLSSQDKRLLTEFARAQGFHLYTQAE
GIDSIKLFYSPTGFVVPKSAPSPPSRSHSSSSSSSS

>B036_large_subunit_rRNA_methyltransferase,_putative
MKMARSATGQLCGTPLHRPATALVGRIRHFSESGPLRSTSLNPSSSSPSSSLDGGEDESPVLAGSGKREGTTPSACR
AEYGGKKNLVGLTKDELKTELLEALAIEPYRLKQLWHWMYFRGARSFDEMGNISKGIRAELAERYVLDWGAIVRDRM
SADGTRKWLLDFGGQQVETVFIPEESRGTVCLSSQVGCTLSCAFCHTGTQKVVRNLKASEIVGQFLNTRKQLFDLPP
QSIRKRTVSNIVFMGQGEPFYNYRNLSKALQVLMDPEGCEMSKRRITVSTSGVVPMIKRLGEDFPGIRLAISLHAPT
DSLRDELVPINRQFKIAELMEACRQFPGLSWTHKITWEYVMLKGVNDSPADARELLRLIKDIPSLVNLIPFNSWPGT
RFEVSSDDTILAFQKILHEANIDAPIRWPRGRDIMAACGQ

>B037_tRNA/rRNA_methyltransferase_(SpoU)_family_protein
MRGSSARCKWAAARVQVGLLSWGCGPVRGFASFRSNEGFSRGWRSKEGGNKHRTHRFRPEGASATQGGEYVYGLQSV
EAALARYRTKDVLRSSSSDVNTEGCTDDGANGSTTARRVHRLFLQMPGRDGESQGGGHNDGEARQGVNGKRSAGAES
IQEMAKELDLPVDYLPRRELTTLVGPNNVHQGVVLHCSALRPALANYMERTEPQQREGRAPLWVALDEVWDPHNFGA
IVRSAMFFGARGIILSERNSCPPSPHVSKASAGALEFARLYRARHLPQFLHESSRRGWNIVGTALEADACPSHKLSL
SAPTILVLGNEGYGLRPSVRNECTMTTKIEHSEASGECAHGSYKLDSLNVSVAAGILIHQLSTSLHGVPQPPS

>B038_pseudouridine_synthase
MRCALFTRPQMRRGAGGVRPFSHFPPRADHGSHEPEPYITDGCRMVRPYWFQYRARAKGHWVGQPLIRILTSHFHRH
PPAYYLEAVETGRVKVNQQRAAPDQLFAATDLLHHDMHIHEPAVTSEPVQIIHSSDELVVVNKPAGLPCHEVSLYKY
NTLSAILRLEMNVNAQSCVNRLDGPVSGVILFPRTFPEARKLHMAIMTGQVGKFYIARVRGKFPIDRVECAVPLVQA
ETGVSLVDYEKGRTAHTIFEHAGYDSATDTSLVKCNPTTGRRHQIRAHLNHLGFPIANDLLYGQGPLVRSRAEFLKL
QQGSAEDWSQMSPEELTAFKESQPERFVKEDLRAQDLDMDCWNCRKGLLHSFRPKQIWLHAHQYRGDGWHFTAPLPS
WAQA

>B039_pseudouridine_synthase_Rsu,_putative
MRAMRARVQPSPSSPLATLLLGRPSASNVLVSRQIAWPLKMNCAPLFPLRSSSARRYNTSSSGTASRSRPTHAEEAR
PKDHRHGGQDVKKSSSVQRTGRNKAVEPKAEAKEVVSATENGTTRNVLPADGPYRLVERLAKRIARSGLCSRREAER
LIEEGLVSVDGAIVKTPAINVTPASVVMINNKKLEKTPPPQVWLHYKKRGVLVTHHDPQGREALFPHLRNMGLPHLV
SVGRLDYTSEGLLLLTNNGRLAQYLEHPSNEYERKYKVRIRGKVEQKVIDRLAKGITVGGVEYGPIKVTPIEKRRSE
EETSTNEWVYVSLTEGKNREIRRVFEHFKLVVTRLIRVQYGPYTLDKKLEPGDVVETRLRLDLVKKADRYWWLWDGD
QESSTVPFPESYFRIDPRKIITSLPTPASSAKPPSVPALDSPPSSTSQE

>B040_pseudouridine_synthase
MRGRCRVLRLLAPLPSCRLMPSRCTAAPGATSRFSTRPHLSKSPPVRQRLLHPDEDWENHRPEIEIRNGLRWVRPYE
TTMLAHVKAAWSGRPLLDVLSSNYDRFPPEYWREAVQDGRITLNGAKADQDTVVPASGHICHRLHMHESPIAADPID
ILHASDHLVVVNKPAGVPMHPVAMYRHNTLEWILAREHQIRPVFMVSRLDMPTSGLVVIPRTPEMARTLRDQLTAHR
VTKKYYARVVGRFPTEAQECSVPLQYEGKRRTTQTSASGEGKSAQTRFVGLSYDSTTDTSLVQCEPMTGRSHQIRAH

LRHLGHPIANDLLYGGSPTLFEHTCLSDDASSPHTTYTHTHTHTQVSWCHDCRQGGVRARKVPRVWLHAIAYTGPDW
HFECPPPPWAQ

>B041_Thg1-like_protein_2_(TLP2)
MKGSRAVRLRLVAGAGGSAGRCSPSAAALLSTVRRSLSSGAQWDGQDRTSSRSDASDVAIRMKSYEQEYSLILDSLR
PYCLRIDGHRFSKFTKPFRKPYDPRISVAMERTALDLMEYFKARAAYTFSDEITLALLPTLTNPPPFRGKIAKLISI
ASGYASARFNHHISSQEYHPHEEAGDKAHRGIAHFDARAFSLPSDEECLENLLWRSADCMRNSVNNLGRAYYSARQL
DRKSNGAVLRLLRHEHNVEWNDYPDHFKHGTLIKKRLAERQGINPQTKESVLVVRGEYVKASVTVLREAPGDESGVA
KFLMAKYANQIDTPVEHPAAVQDPAQSAELSELAERLTQRFTPFDYEPVKAYS

>B042_pentatricopeptide_repeat_(PPR)_protein_AcPPR14
MRGRLGGHRAASSLLTSRASAPQFRSLALSTTVNQHRTFTSHDHAPQPGRGLMRGIEAKQRLEWVQRALYVRPGPLA
QLISFAQRSGDPAFLSQSLAALPKVRMGNTIGYASLVSTLSATNNLDEMFFVYARMKEERVPLNIFSAGALINASLR
HNKLERAFEVLHDMKLYNLRIDNGLVNSFVTYFLEKRDVDRLLSVLDALGDRSDLSIDRVSILDELWQRLSSPHEDS
SLAYRFIERLSAAVPPASDGTTQSTASGQSQQLHQRQQGETKEGENEGGQGEEGDGRPQESEADKWARVGAYWHGRM
DQLLNQLVTRGQLARAHDLTELMVSRWRLQPHKRIITVFIRACITREAAINARGGVISGDDQRRPVQLLDEVGRMVE
EGRLEADLITFTALIDANARLRRKATALRFFELMQQRGIKADTTTYRVLLIMCSVLRDKKEGLRLLDQAEREGVGLE
MALFTDVVRTIRALPDGATP

>B043_pentatricopeptide_repeat_(PPR)_protein_AcPPR15
**MMRATPRSGRAWAPTVAVHRVGSSSGGRCSQLLSSMAPSSSSALLTSRSVSTGFSRRGTSICLVHPSSSSTSIFSTS
NRAFVTHTLDR**SASVDAQFLHHTKNIAAKTPGESWRAFLVYLASLRRLDLAFALLDDLEHHDQATPSVYLSFLSACA
QVVHQEADMRAQEIISRMQARGLKPSASHYTALLSAATSPTRITAALQAMTDAGVEPTPVTYIAYFKACSRFAKVHG
HGPTLHGYHQFKQRFGTSTLEKRTAMHLFGAVVTSLVQFISPTTEQEVMNVLRDMGKMGLKLNSHFMNSLIYMYLHN
DQQEKAYELLNRTKAGTDIEPNEFIYTTFLRYHHDRREYDHCKKLLARMRHDRIPPTHAAMSTFKLLAEQLQDPTIW
AAAKELNNATKPRR

>B044_pentatricopeptide_repeat_(PPR)_protein_AcPPR16
**MPRAGLRCWSAPGGAAGRTSARWTPSACSRLPSTLITTTPAPALLRFPPDALLARTTRRGLTASAATSEVSRPAHRP
PRP**SAATSEVSRPAHRPPRPAWTGSVEDLVAEVRALDNAQPSMPAVASILRRMQSLHDQGKDVGVALDALKEELSRA
GQCHPFICSALIALLGKLQRTDAALDLVTRMTQQGYVPDVFVLTALVSALGRAGEVGKAQYFFNEIQRLGMTPTLHS
YNSMIMAFARAGRIDKVRDMLEVMKHKGIEPDVRTYTEIINNSCKAGRVAEAYQTFIEMQDVGVQPDLKVYSALIAG
FSHVGDHLKAQQLKEEMEALGLEASMITYSGMLSGLARNRQLTEMERVIEAMKKRNMVPNARALGDLINRMSDTMPM
DQAFNMAQALVQKKVEANADVWHALLRVCAKADDVEKGIRILDVMRSHSPELVSASSYCVLIDTFAKAGRVSRGATL
LAHMRKHKIKPDVSIYNVFIEGAMRETGYSKALQVFELMKAEGVRPSHTTFSILIDAAGHAGRPESILIDAAGHAGR
PEEAEAHFAAMGTSPRPDTNNYNSLIEALARNGQLDKAERVLDSLLRHTHTTDNRGSTDDHVGLARPTAKSFSSLLG
FCLERKDVVRARRLAEKMRRASVAPDAIAQRQLDQIPAEQHHHHHQHQPQRQPNTADINSKRPSPRPQHTHPPRRYT
NPKNESK

>B045_pentatricopeptide_repeat_(PPR)_protein_AcPPR17_(C-terminal_DYW_deaminase_domain-containing)
**MKRCRVSDVQHAFVITPFVATQSRLQSRRLLWSASGGTSALNLTTNAASRARSARQSPAALAPVASQGTNAGSRRVV
ALCKQNRIRE**AASIFDQHPTPFSASALISACGRRRDLKQALGVYAKFIASGHQPNAVLIGSLVSACRRCGEPGRALR
LLDDLDRFDIAIDESSFHMLAAASAEAGDAAAAKRLLVRLQEGRLPFKANSVDCGQLIKGLVTGVDPDSAGASSRIA
DALALLELMEEQAIAQNSCHFTPVLAACAATGEAAIGRQLHTRIVGSQSQAVVNDYTTAALISMYAKCGFVDEAAGV
FADMRRLQQDGRCELRVGSWSAMIQALGQHGRGKEALALFDEMVTDRHATPDGVAVNTVLSACSHAGLVEEALRVYS
GLVAGRYGAIAPDIQHQTCVVDALGRAGRLDEAEQFIDTISRPSEVTWRTLLGACRIHGDVARAERAVARLRKLAPR
DAPTRVLMANVYAAAGHWEERDLERKNMDKAGVRKRPGKSWLVVDGTRHVFTVEDKRHPRIEEIRAELAVLWQRMKN
AGFVPNTSVVLRSMADEEAKECHLCHHSEKLAITFGLMSTPPGTTIRVFKNLRVCPDCHEATKFIAHLTGRDIVVRD
ANRFHHFHGSGQHCSCGDYW

>B046_pentatricopeptide_repeat_(PPR)_protein_AcPPR18
MRARTGGADHLRRWVTSSSSAPRLGGSPSLSCRTCFLSSSSSPPQFSSSFSSSARLSTNAASGSRFASSTHNLEESS
THKARHAGQARPAAVLRRQRYPGLDQWAARFRKLTEREKTLPILLEMLANAPPGPTGAKYEMLIEQCFEEKRPDLAT
QLYDHLRAETTTTQAAAPVPLAVFDVLLQGYGRAGDRQRLAQVQRDMREVGVRPGMSTYTILIDAWGKAGDLRRMWQ
AWEDMREQGLRPNVVVYTSVIATLGKLGDVAAMERTFAEMQRSSGDGVEPNRTTYNAMVHSYGQQQMMDKMEALVER
MRADPGLGLDNFTHSAVVAAWSRAGRVDKALEAFDSIAATGGQPSLHAWTAILHMLGTAGRSDEMLRTLDKMKRLGV

KPSTAVYNTIINAFGKARNIHSMMDTFKAMRRDGVAADVKTYNTLIDTWAKTGKAVEAEKFYVLMKREGLQPTMYTI
ASLMDAYTRADQFEKVLRLISRMKKEGRAPDNVVFNLLIDTYGRMGKPEEAEKVLCGAMKEYGIALETNNFTSVIEA
WARNGNLDKAEEWLHRMNTDYATKPDIKTLTTLLSFCIPAADVKRGRRVIHMIEQHKLQKDKQARETIRQFHAATKR
PDQEKKNQPTSPSTTSPDRS

>B047_pentatricopeptide_repeat_(PPR)_protein_AcPPR19
MRSCQMRRAAVRQLPSGSPFPSTPPTTTATRAIRPPAASAGCPTAQLSTTTSTRLPLSSRQRSSNVVMCVTTRPLQR
FGALGAVRWSSHSTTTDESKVKRRAILASGLPFARYAEELTALEQLPSVPANSLSTIISEYAAAGKHEMILARLRPL
VPRLRGGAGAFGLIIKALQDVRGSVEVAFAVMHQAATRPARSKTDKATAPDARAYHCLIGVCARQGDYTDALRVGQL
MDDNRVAFTSGTYDCLINACARSLTDKLDSALVGVDSVAGANNVDTGARRHPGLDAAFALLDDMRQQRGLEPDRRIY
CSLMRVCLSYGDVARMRRTFDDMRQRAGIAPDIYAFNFLMQGCAVERDLGAAMRVLADMKLARVAPVTITYNMILNL
CAETAAAAASESADSVDSAGTQSVDSLAAAEQVLARMEQSRLAPPDQVTFNTLLKACANAAASRSAAGAAAVGGFVE
ALDKATAYVAAMKARDIDPDVYTYNTLLQVCSHCPRPWKRTTVDDADTGDDAAAAEHGQAAAAARVDKVVEEVMREM
NERGVRPDGATVTLLISHFGAREDPARAFAVLSDMKRANIKPYLPSFTALITACRHYSDPAMAEQMALTALDELKTA
GLTPTAAVMNAFMAVTPQRAPKVLAMMRDHNIEPTESTWNQLIYSVAWRLKSESDKNESGNENETSWRGRELELLEE
AFASADRLQQSSGSGPASVAYGYLLEACLYAAQRISARRESTTGTGVDADEDVSGGQAVLSADDRAELQRVAQLADR
CWRDMLAHQPTAITREACAVRMRLCLRSASRLDPADAAEARAGLQGAIEAYGEMRRRGFLPSPLTYGALARTCARHG
AFERVTQLVEDMRAQGVQPSTATLGATAQALTSSRSAGAAAALAALRDLVLPKSTAAPTST

>B048_pentatricopeptide_repeat_(PPR)_protein_AcPPR20
MRRMTMPARLQRIGGAASVSSSYSSLVLPSGRCCRFALGQQRGLRQPFALFSTTARPPAKPAARPRVTRPPPPPSAP
PAAHRHPPTQRENRGRPSTERTTATTAASPQRKPSTQDVQQTAQRIKHAGAIGEVDELVATIKRTHQLHPSAVSAVL
PLLARTRQWETAVELVELMPRHGHTPNLFVISGLLKVLGQARQPDNAHYLAEIERRGLTPDSHCFSALITALGGAGR
ADEAERYFARMTQLGLAPNLHCFSALINALGNAGRVDDAERCFDAMDQLGVVPDAHCFSTLIAALGTAGRVAEAERH
FAKMEKLGVVPDLHCFSTLMSALTKAGKVDAAQHVFHQIASRGLKPDLVCFNALISGFADAGRADEAEHWFAKITTT
GRLKPDRISYSALIQANEVVARPDRALALLQEMTHKGVRPDVVSYTTVISCLAKARGRHHMDQAQEVFNEMVKQGVR
PNATTFGALIHGHALMGDLETARSRLKQMSTEFNLAPAAEIHNILMDAEKRVATDPVEAYHQVLRAVDHMKQEGVRP
DHATFSIVIDAAGFAGLPHEAEHQFHAMTSLHGLHPNANNFTSLIEALARNGQLDKAEAVLDSLAARQATSALEHDR
LTAKSFNTLLGFCIGAGDAARGQRVAAKMHQAGVEPDDIGQAKLRDLAKLCERRAAPPTPK

>B049_pentatricopeptide_repeat_(PPR)_protein_AcPPR21
MRRSPARLVVASPLSSPLVAHGNAGGVPLGYYARRLQVTSCLLPPRSPALQLVLPKVLLGAGTRTLRQRGGLRPSGA
RRSYASTSGAAAAGRTGEEEATTTPTRKRSGGGGKGQREAEKVITDITPHLAELDAEKRQKGGVDPKHVAAVLRMVW
EGREHVSEKGREGERLLRHLKWLRAGGDDGEGGVEGYTDLISALAKFGLVDDCFAVFDRMKGSGVQPNEWTYTALIS
ACVPQRDRTRAMRVFEEMREQREDLKPDAVTYTLLLKANEGRTVVEVKEAMQLLTKLKKSGVVPNVRLFDALINVIS
GNNFLEGKVGLNQEKKEMEEGRSKYSKYKRRDSMHDQARAQKEMREMGKAQRLELVLDVLERMKEFEKLTREVTGAE
PLRANIYLFNSLFRAYKLNGENQSDFEEAFVVFEELMKPRPNVETYTTLLEIACRMRYRDHGERLIRKMKKAKSVIN
SKATESERAELERLKARVKKLPLSPEAVLQLQLAPEEPVEADLDDDDATIIDSTTA

>B050_pentatricopeptide_repeat_(PPR)_protein_AcPPR22
MRRRLGAGRPGWLVGDGCALTKPRAAPLPAAQAGLHIRTTALPASSALARSGSPRPPACALLVRPEGCHSRWQSRPS
ARTSTAADSTYTTTSPAQSCTAEELITRVNQLQGQRHVTAKEVIKVLLSCDEKELVARLTAHPELRIHLLSLVRRIP
KVCVGEANALLAKLRDIPSSMAAAQHIFELLQRTEAPNIRTLTHYANVARNNHKPEIALAMRDLAHKLGLQVDLLFY
SALIRACGVSKETKKQEALELLAEMKQQGLEPDMSIYLALIRTCARHGDVSAALKVMAMVEADGLPYTLPLLTTLAN
VCSTQPFFAKKGFAVLNLMQQHGIAPDLAAFNALLKCCAIVDDIAGMQQIFQLMKEQDLSSDEFTMLSLIVGQLAND
NLQAARDIVSSFRILGVTPSVKTYHKLFSVCKRTHDLDAALNLWDQMREEQVEPDLPIFNALMDIYAHRGDLEQVHQ
LLDAMKAQGLEPTPTEVACLLAVMYHRDGRVTEAGYQLVEDMRREGKVAPHLATFSPFIDILLKADKIDEAWDVRRN
MMARWDIQPDKVLNRTFLFALAAKRDVDKIDELFRHMEAHPREFFPHCDSIVLLLEHWLARDPRSPRVAEVLETLQR
LNVAHKLSRQVFVEPALQVIDGLIDQNSFDRARKLLRYLDPNKLETYTRLFATCRRPEHWPMLEEFWDMLMEPRRRI
QPDGTVALAYLEALCRLGRTHDAVHFLHNMVHKQSFPDLEHYNLVLRHASSNDKWNFVRKVLKLMRYDRVTGDNVTA
AIRERLHEVDGSLEEESAE

>B051_pentatricopeptide_repeat_(PPR)_protein_AcPPR23
MSLSFPKGKKRNEKRKFLARSIGGAMRAAWQLRPVRPSAVTQFGASCTRSACSLSGRCSFIFPRSLPILATHSSPTA
VHSRHSLRPPVRPFGTTTAAGVANSETMSAQAELQKLNKLNAVSYQRFVRAFKMVQAAQDKSCETDLIMLMNKVDTN
NLLEYNHLMHILTKVRYKPVLVNTAGINLLDRMRKRGIYPDTVTYTSFINLLKKDRNADKAWLVFRRMREEKVQPNE
WTYSTMAHICALKRNPKAAEELLGLMEEDRVVPNFIVMAGFVDAFLAAGQVERTWELIDSMRKQHRVRPNRFTLDYI

MKSTLRENKEWDAWVEQHGEASATVATTPPAESDTESGATSSVSEREAGHASDAVSKKLERVKLVLRFLRREHGLTP
STKTFNALIAWCTKGKRTEIELAWRLKRLMKAYRLRPDNVTYVPLLNYYVKQLKARSTDSDIDYAEPQPRQGDEDGE
DEGEGEECDDGSRYEGGSSADAGEPGVEEPYDGIQRTLQDMQAEGVESDPATTFTLIIDAHAASGDAERCFGAYADM
RRDQVMPTVATYATLLRFCEKHGNVEKACALWEDIKADQIRLPWNVICFLLRATLTNNKTDTAFRLAEELSQLYKPQ
FVYSQLLTICDQLADVWQAERVWRVMRAKKIPVYARTKQLLADFGLNPDEPHHT

>B052_pentatricopeptide_repeat_(PPR)_protein_AcPPR24
MHTQSPMMRCGIQRTQATAVPRARAVGGLAQSLLPSSISAQSILASTALSTSRSVASAISKISTFQTAQARSPFLLI
AGCTRGYRAMQDRLNANVSPRQVSAWYDLVRRKINFGTASEALQVWRDMREEGILPNVSLYHSALVHFKKTNHAKEF
FMLFEEMRNSGQVPDVPIFNMAIHIAAKSAQIEKAFDMSKEMDRLGLPKEAQTYGSLLYACSRVKDFDRALSVVADM
VKAGHSPNEHIFTELVNSCASKQDLEQVAGVLDYVEKQQAAEGQLNMLSPYNCFMGKCLEMGATEMGMEWFKRLNES
KMAPNSRTYFSLIRGSVFSSEPQYDLAMRLFGEMKARRIVPDPAIYEFLLQQAQEPQRLAASFAVLEDMLAQGLKPP
APVWSLLFSAACVKNDPELVSFVWDKMKEQKVPLHLHTLRQFKQFCKRSMPQRYEEARLTMLHWRPDPQTHHTPATP
PHSRNYA

>B053_mitochondrial_translation_initiation_factor_IF2
MRRALAWGNTRPLSAASFHIPLQAASAGSSSAPMHLRRGISSSTFCSSERPFHHRTASSTRSMVSTSTGVGLAYTPR
GSALCVVVALPSSSSALTSSSILTSMEAGGTRRLYATASEMEKSKMVRKRLAATRKRKLEELKERKAKPKEISIPSR
ATPKNLSAVTGLSTIDILKVAIKCGHEPRTVDDVLPPELVDILCEELYFVPRRSDLNEGTGMKLTRTIDEADMVPRP
PIVAVMGHVNHGKTSLLDALRKTSVVDVEEGRITQRLSASMVQLSSGQKITFMDTPGHNAFAAMRQRGAAMTDMVIL
VVAADEGVMQQTEEAIEVTREANVPLLVAINKIEKEGANPSKVKRQLLQHGVILEEFGGDVQCVELSASTGKNLDEL
TDAILLQAEMLDLRADPNGPAESVVIESKIDKGRGVVGTVLVRQGQLKLNNFFVAGGTWGRVRGLTDWLGRSTTKAD
PSTPVEVIGFKTKILPDPGDDLVVVLGEEQAKQILDYRKERLHAKEALTDVVQASDPAARAAAAKQEMEKALNVVIK
ADIGGTLQAVESTISQFPQDEVKLRIIKSAVGDISTTDIGLAKDTGAVVFGFNVPPMNSVLELARVEKVDINNYSII
YQLADDIKKRLESMLAPREVEEEVGRGDVLSVFSVTMPNREQHNVAGLRVVRGALDSRLRVRLLRRNKDVNADEEYA
ALYDGPIESLKKFKDDVTLAKKGDECGLALPKWNDLRPGDIISCYRMKQVPRKFGDPK

>B054_GTP-binding_protein_GUF1/LepA/EF4
MLGRRGLLASRGPAAAVSTSSRFVGLRSTPLASPSPAWSFTPISGNLRIGTSAPILSRLPLPKTLGPLPLGRTLSGL
YPRRCYAQKLTPAEVAAEEAAARGAPDLSKFPPSKIRNFCIISHIDHGKTTMSTRIMEKAGTISLDKEGLYLDKLQV
EKERGITVRAHTTSLVYKHSDGESYLLNLIDTPGHVDFTYEVSRSLKACQGAVLLVDCTQGIQAQTVANYFLAWEAN
LKIIPVMNKIDLPTSDPARVIKELANMGFEESEVLKASGKTGEGVEGILKAVIERLPAPSGDPAKPLKALLFENWYD
QFRGVVCLVNILDGALKKGDRIVAASSNKVYELENVGILYPERAPTGALYTGQVGYIIGGMRSTKEARVGDTLYLEG
APVEPLPGFKSAKPMVFAGLYPADGESLDRLTDAFEKLTLNDASVTYTKERSDALGMGFRCGFLGLLHMDVFLQRLE
QEYGTDVIATAPTVPYIVTTKEGQEIVVNNPSLFPEQHDILTCTEPVAEARIIAPKEYLSPLLRLCLERRGVQQELS
YIDEARLHLRYRIPLSELITDFNDSLKALTSGFATFDYEEAGYEESELVKVDVLINGKPVEALSAIAHQSKGVNYGK
DLVQKLRKVVKRQLFQVAIQASVDGRIVARETLQALRKDVTAKCYGGDITRKRKLLEKQKEGKKRMKTIGNVQLSQD
AFYSILKKGDE

>B055_GTP-binding_protein_YchF
MKVATRRSTTWWGSSSRSATSTFVGGRSVLWPPSSSCLTSGSGVLGVRRQWFAAKAGKQQQTQQAAGGQASALSYFV
ARTASNGCGIVGMPNVGKSTLFNALTSSQRARAENFPFCTIEPNSGMVWVPDPRLDTLAALANSKRILPCQMEFVDI
AGLVAGASKGEGLGNKFLAHIRNVSMILQVVRCFEGADGTEQVTHVEGSVDPARDMEIINTELLLADLESLTTARAK
LEKRTKLDAEAQKRLDLMHRTIAVLDEGQPARSVLISAEEWPTFHAFQLLTSKPVVYCCNVKEEEAATGNAMVEQVK
QAVLKEEPGVDPNERVLVVSAKLESELANMESVEDRKSFLELYGLSEADAGLPKVIRATRQLLQQHQFFTVGETEAR
AWNIPKGTTAVDAAATIHTDFAKGFVKAETIAFADFVAAGGEKRAKELGKVRFEGTSYVVQDGDIILFHHRK

>B056_ribosome_biogenesis_GTPase_EngA/Der
MSCPIASARGLATSRGAGGSRGGGGSGRDRAQQTTRPHSQKSSSSSSSSATRGAGGKGGGGKSNAARGPGAAAATKK
RAPSGEASKARPAAEEEALGGVESDTERYTMRRDPVLALVGLPNCGKSTLFNRLVRMNKSLVTSEPGTTRDRVYAYC
DIGGRSVMVVDTGGMVGTGDFFSPLIHEQALVAINEADIILFLFDFREGVTKKDVEVARVLRKHVHDKDIVLVANKC
DNPDLVLELDERNKAGPTGKPDDYWLLGLGPAIPVSAIHGAGAGELLDKVYDIVQTKFPAEDQSEGDAEAEAELARK
RISISIVGRPNVGKSSFLNQVLGRERVIVTNVAGTTHDAVDHSIMWRGKKPRKRKRRAAKATMGLEEEAATTTTTTE
GKQQDAEVVHAAEDDEVDEQEDDLDDDEHETKVRAKKANNTKLKEPAANPDADGVPIRIVDTAGINRRATHVKGLER
SSVLWAIKSINRSDIVLQLIDATQGITDQDLRIAEHILNSKATTIVVVNKWDMSKESKQKWEKYVQETLKFMKYVPI
MFCSAKTGVNVKETIDLAIRITRERAHFIKTSTLMKLLESAHTRHRPPSKNGRQLKIRYATQAKVKVPSFTFFVNDV
ELVHFTYQRFLENAIREFHPYTGSPMRLIFKDKEKTIV

>B057_GTP-binding_protein_EngB/YsxC_form_1
MRAGRSLLAISSVPSSSRFCVPYLRPAFLATSGPLRPYRLSLIGSSGLQRCTASTFERKGDDWSSKSKQKTDGEGEE
GGQLSKRARALLAWEREQWHKRQKEKEPNAELSKNKIFRMTPVDSKILDYIDRLKLGRRKDEPPPVTDGRRKEQLAK
VRTETDKLWERKVTFLGGATARESFLPEDLPEIAFIGRSNVGKSSLINALTAQGKVRVSDTPGETQQINWYRVGKHL
TLIDLPGYGFAFAAEEKVKAWTELMCEFLTSRKSLKRICVLIDARHGFKPADLDFIDMLEKAKRKYQIVMTKADLVT
PPDLARRYHLVQQAMKRRRHGLERILMVSSWNATGLSAMRTELTNLMVGAREAPPATKPEHQPTSLLPDYEAYEPSE
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>B058_GTP-binding_protein_EngB/YsxC_form_2
MKRVRMPMLRCCPRSSSWSAGLSCTSSSSWRCITATNLRFARSTSSITSSNPAQPPAPPKASSSAANRKGKKLASVF
QYFAAHDPSSSTALPVPPATVDFVRSITDEERKAAHAFFTKNAAFLASSVAAPNLPAEDQPEFAFVGRSNVGKSSLL
NALLSKPLARTSNTPGRTQTINYYQAGSVKLVDLPGYGYAKAPVRIVREWQQFVNTFLTTRKSLYNTSVLVDSRRGI
TDKDAEVIQMLNTHGLPHQVVLTKADKLSRREIFVVLAETKERIKRSPFCSPIIYITSKDGLGVDELRIGLMRAAKS
NQI

>B059_GTP-binding_proten_HflX
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ASSHPEDEDDDDAAFALASAAKSQSSRRKEEEGDSGRQALDAMQPGRFWSATRPPRVCVVHPYMRNTVYADKRKRRL
SLLAEREEEEQVCRGQDHPDLRLKEAVALVEALEWPVEDSMYLTVNTVNPSHFLGKGKIAELRQACQAKRADVVVMD
TNSLTPAQGQKLAKMLGTRVMDRYRLILEIFAQRAQSEESRLQVELAGLAYKSVHLKSAMESKHLAQQRGGGAFLSG
AGETNLEIERRHLVVREKKIKARLEVLQKTRKLHRESRKKQDIPTIAILGYTNAGKSALLNRLCGTSLVSQNQLFAS
LHTFMRKIELPSGCCALAADTVGFISNLPHGLVAPFHSTLEEIGSADVLLHVRDITNAETEMQKANVHKVMKEIGLD
TDPDTQHLEVWNKIDLMDDARLDSLVTTQRVLGKRIFPISARTGAGCDDLLQAIDQRLQALYPERKRVYELLLGENE
QERLEFLTSHGGRVRTVQPDYQVAGRTRLSVEMRPDVYERYRVRYGELPRPQQHL

>B060_ribosome_biogenesis_GTPase_YqeH
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PSSAPSGARGVASSSGSGNGRRGVKGFDETKYPPMAPSPKATPPQPSQQTAREPNPLAALDGPDVIHLLPDEDEARH
KSRKIKAAPAGMEGGLIIQADQLLQEDEEIMASKKQKDHKCPGCGATLQSDDPHSIGYKPPQVLKQEERGLAPVCQR
CHSLRHHGIVTPLKVPYEEVKEHLKLISDQSCLVVKIVDIFDFSGSFINDFRGITGNNPVVLVGNKLDLLPVGAKPE
RIQIWLKRLATEMGLKNVRSVHLISAKSGEGVHSLSRKIEQLRKERDVYVVGCTNVGKSTLINRLISINTKGPKKRN
LITTSIVPGTTLNLISFPLGGKKAFKMGKRAFLYDTPGVINKHQMANLLNMEELSITLPKRRIQPVTYRLVPGKALF
FGGLGRLDYVDGPGPLYLTLFLSKELKVHPTSIAKADDVMSKHAGTLLVPPLGEERAKQLPEFIAKDIHIEADEERG
GLKKSFADIVFSGLGWTSLVTPTFDRDIHLRSLSPEGVGIFLREPLMPFEIEKRKQTPGGIKKHGKVPKPGTQPRTR
DDFGEQAEEEMRRTAGSGRPTPTKTEEEDYDDDDDFEDAFADGDDDEDDSIDEVHGVTDAQGAQKTTKGGQQQQQQQ
QGEKKKRMSERRKRRQAFLARNRNPAWRSAIRLRKGKGKDKGAQPLGGPDSPLQPLS

>B061_GTPase_YlgF
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HKADLTNHNLLPRITKALHERLNGQPVICTSATGAGKAGKAIQSLIPTALEHYKQHRQRLLGEGADDPSTSCPGYPD
KPLTLMIMGLPNVGKSTIINSLRQHCLSDSDKKKRGSQFAKTGPLPGVTRDLTGFKVSSKPLAYLVDTPGVMIPNVE
NADVGLRLALTGAVKESIVGKQAIADYLLYSLNRLNAWEGYVKAWGLDGPTDDIEHLLRRIAQKTGAKQVEGTDDLE
VAAHHFLKRFHAGGFGSLTLDDVP

>B062_peptide_release_factor_Rf1
MKRAARAPVSLCWPILHGRHNLHMPQGRFLLNMSPHGCQTALGVYASSPATPLRRFSLPGTQEDGLSMHTTMNKSIQ
KRLDHMKHQFDDLSATLQTNEALSPEERGMLTKQLHALDPVMGMVRRIEQQREELRELHQLMEESKQTQDKELGALA
EEDYKRILGELMDLEKELENEIMLELLGKDEADEKSAILEVRAAAGGQESQLFTMELFNMYSAYAEMKDWEWETLAV
SDSEVGGYRESSACITGRGVFGRLKFETGVHRVQRVPETETQGRTHTSTVTVAVLPVAQEADIQILPKDIRVDTFRA
SGPGGQHVNKTDSAVRVTHVPTGITVSIQDERSQHKNKDRAMKILRSRLYEIERERLASSRADQRRKQVGTGARHER
IRTYNFPQSRITDHRCGLTVHDIESMMQGHHLDTFIDALVAHHSAEALNSIDLDSF

>B063_ribosome-releasing_factor_2_(EF-G2)
MQLRRATLRVGPAVTTAPRSGGRQWWCQARHSGSSSNSPAAWPPQQQRGSSLVLSSSSSRLIRPSFFLTWVHRRQQH
SEAEVVVERVRNIGVVAHVDAGKTTTCERMLHYSGVTRRIGDVDSGNTVLDFMKLEQERGITIKAAAITFNWEGHKI
NLIDTPGHVDFMFEVERSVRVLDGAVAIFDGVAGVQAQSETVWRQARKYGVPVIAYINKLDREGASLERAADSMRVR

LGARPLLLQLPLPTTLGVLEGVIDVVDMRVIRWTDPSGKAMQVVDLTPEEHPGLYAKALQARETLLEQLADADEAIM
RAVLEEGASAETVAGELLHGALRRVTLAGEGVPVVCGSSLRNRGVQPLLAAICRYLPSPLDRPPVRAVDMETGQHIA
ITPDGPDLCALAFKVVHDVQRGLMVYLRVYSGELTPATEVYNSTRQVKERVSRLLNIQADDMTEVGRVGAGNIVAAL
GLKDTCTGDTLLVPAKGNKKAHKGQHAKGGRLLLEGIDPPPPVFFCSIEPESLSAQKALDDALGLLRKEDPSFSVSL
DPETGQTLLSAMGELHLEILKDRILNHYRVGARVGNVRVSYRATVGRALSHTLAREYEIGGVKQHVELTLDIEPTAR
AHGNEYQNLAVSEALKGAGAKESQALEQALAEGVANGCRSGLF

>B064_mitochondrial_phenylalanyl-tRNA_synthetase_(PheRS)
MRRGLCVTARRLVASRTNALWHPPQRAPLLRRSLTTSPGATLPVAHRVSTLLGAGTGSGAQGSSGGGEQDGQLQVAS
HRLMLQAGIMRQAGSGIYSLLPMGVRAVEKLTALVDREMGGIGGQKLQMPLLLSAAIWKQTGRWESSGPELFRLKDR
RGADFCLAPTHEELITQLFANEAVSYRQLPLLLYQIGLKYRDEVRPRFGLMRGREFIMKDMYSFDITRDDALRTYQH
VVGAYKRILAQLELDYVIAAADSGNIGGDHSHEFHVMANIGEDTILRCNSCTYAANTEKARGRLLHHHEHHRRLDHR
TLDWPALQAGLADPESLPYSVHVVRVATEAPAASAEGGAAREWAVVAPKGRQVNELKVKAHLLRHALAPSGEIVDIT
VRPAAAADAGARPVVLVDESLAAEAVDAAKAVGDFTLTEERDGCAEAGCEGELVGSRGIEVGHVFYLGTKYSAKLDA
RVATPSGTNYAEMGCFGLGVTRLLASIVETSHDERGIVWPVAVAPYKAVVVAMTPKDADVQAHARNLYADLQRSPYF
ANDVALDDSADSPGAKLHRAQLLGFPWMVLVGKAMKNEGRVEFENRKTKEKQFVPYDQMVAHLEQLARDHARTIGAP
LPVGL

>B065_mitochondrial_tryptophanyl-tRNA_synthetase_(TrpRS)
MLRQSCGRRGSGLALAPYRGLPVRRTLKCRSASCLYSTAATPSAISSDSACTAEAGRIFSGIQPKGHLHLGNYLGAV
VNWLQLQEQRKGDRDGVVFCVVNMHSYTTDVTPEDLRDSTREMAIALLACGIDPEKCILYAQSEVAEHAELAWILGC
RTTMGALNRMTQYKEKKASQGAMFGLFAYPVLMAADILLYRASQIPVGDDQLQHLELAREIAEAFNRRYNRTLFPLP
QPILGQATRVMSLRDGTAKMSKSDPNDRSRINLTDSKDEILFKLQKAKTDPLPGIVYDPENRPELANLLSIFSALTN
RSVESLCHEYADAKMPDFKNALAPHLVDTVGPIGERIRELRDKPQWVEDVLQQGASRARTIARRNLQEVKQVIGML

>B066*_mitochondrial_small_subunit_ribosomal_protein_S12
MPTYHQILKNPRRKKMHTNNVKALEGCPQKKGVCVKLRIVKPKKPNSAQRKVAKLRLSTRRMIIAYIPGQGHNLQEY
SSVLVSGGRAPDLPGVRYTLIKGKYDFSWKESFERKKKLSKYGYSTKKKF

>B067_mitochondrial_small_subunit_ribosomal_protein_S27
MAVYLRSLRPAFEASAKIFGQRIGNGEHSGFKYLQALRKGEAMMKWYQEDLDQMKFPGWVSERRERKIIRTASRAER
GKAPRPKKGFGKIALRREKEEKRLAAKAAKGGGKKKA

>B068_mitochondrial_small_subunit_ribosomal_protein_Rsm22
MEELAEDELDGSTDREDEDDDFVEPAAGRSEEEGERREGSGADDEHTGALGDAIEGSAEAHDWLDSRRMRTQHDHLK
PMKLGMVVLPDALKKRIGATLKKVGRTGLRRTAGLLSERLRERTRLVPGQPKSVMPDPVVYRREEAMAYAAHRLPGV
YACTFRVMNEIKLRRPEWTPKSLMDFGSGPGTAVWSATEVWPELDNILAVEPSEAMIDVANELCKGKPVKWKRLLPT
DPNERYDVVIASYVLSELPSEEERLAKINALWKHTRRGGIMILVEPGTPVGFHNIKLARSTVLGDLSHGLPNVLAPC
PHAEVCPMGEDSWCHFTQRMQRIPVQTQSKQNTSINWEDEKFSYVVLTKGNLLVDKNEAFDRLLISPQKRGRHVIMK
TCGQDGEITTRIIAKSDGAIYKEARKAAWGDGFGFPDETSKRDLAGKFRPKAFKYRSLSKVGSVAPATRGRRPPKPA
ADADAKEDSQVM

>B069*_mitochondrial_large_subunit_ribosomal_protein_L6
MELLKVIKSQDKITLKTEKVNKNVFFYFKNKKKILLKITFSGELFLKERTLITLNNLNYSNYSNYIKFMAKNLETFF
YDQYNYFSKLHMIGLGFKNFILRKHLYILVGDCNYIIFRIPDSLKIFCKKNQVFILGESNVEIFNFMSNIKRVKKSN
FYKGKGVLQFKNFKFTKLKVGKKQRFM

>B070_mitochondrial_large_subunit_ribosomal_protein_L17
MRHLVAYRKLSRSPAHRQALLRNLVNAVVKHGRIRTTVPKAKELRRLAEKAVTLAKRGDANARRSAHGMLYEKPVLD
KLFREMPTRMADRNGGYTRIVRLGRRLGDNAEMCYVGFVDVLPSRHDIEQRALEEKQRNTPPTDGKEQAIDDLFLLS
SPTQ

>B071_mitochondrial_large_subunit_ribosomal_protein_L21
MKSLRSVAGASGVPRPTLPLLPFALQTRNATAGSSLLRTMSAAHFTSSTQFASRPLSIFSKRQLHSSGPVSQESASQ
SAEVPAPTPSYIVPESFAVVYVGGRQYKVSKGDTIITERLLVDVGETIHLKKVLMVGSQNFTAIGQPLLTEAVVEAV
VEEQTRAAKVVVFKFKRRKNHRRTRGHRQDITVLRISNVKLGYEQAAPDATTGLSTVFGPTVPASAVLPPRASDDLK
ESILS

>B072_mitochondrial_large_subunit_ribosomal_protein_L30
MATAAGKAAVELGVRQRVRVVGVTLLRSGWHQRPEVRSTLRALGLTKINRTIYHKNIQPIRGQLLKVKHLIAVHPLK
EPESIV

>B073_mitochondrial_large_subunit_ribosomal_protein_L32
MQRFTSLGRLTAPRLPVGNLPAAVGSSFGRAVGDVFLPSPGAIGGVGDAGGLITCAVPKKKVSISRSRKRRHAPGKE
RRNISHIEDCRACGQPKLRQHVCLNCAGWKVS

>B074_mitochondrial_large_subunit_ribosomal_protein_L34
MQRRVLLGSRGAVAFRPACGPSSSSRFLFTSSANVESAFNSEAFALPTLSTSSPLPVSRRPVAAFNDVSPRMAMVPL
DRTLEIAPTPRDSVLDMVLPTLPLPLPLDAPLYPTTEGNAPMEAVKRTYQPSTVKRHHTHGFLVRMRSKNGRRTIAR
KKEKGRHKLGI

>B075_mitochondrial_large_subunit_ribosomal_protein_L36
MKYRAALRRLCIHCRFVLRERRLFVVCSANQRHKQGQIKAKKSSD

>B076_mitochondrial_large_subunit_ribosomal_protein_L41
MGVFGSLTRRTGLGARTTVGTTGFTRGKVSANQGKGRLTPKMTPRGWYKGVGCRSLGFHTKKGGYRVVPAKVPVYVI
PDLTDCPLKPYVSWSTKRVVVQPLRLPSDKELAQLE

>B077_mitochondrial_large_subunit_ribosomal_protein_L53/L44
MSTARWQWRLAQKRAHYELHFLKSLNFSFCPANNHPTVAEFLRRVSNDRARASNPDCEVTVEVLEDIKARPSIKAVY
ENGMEEVLDHEQRVEHLVDDFWKRRERLQFFSELQFSMKNEEEENPFLNAAAQEDEARKKQQQAKGGAKGKK

>B078_glutamyl-tRNA_(Gln)_amidotransferase,_C_subunit_(GatC)
MRRACLTRPFRRGYAAVTMPREPSWSVEKFFQQSSDTQIDAATLQQLAKRAQLTIAPEKEESLCREVGQILSCVHII
QEVNTEGVEPLVSPLDARQAQLRLRADEVTDGDIAEDLMRNAPARDGSFFVVPKVKGQSGGEGGEGADA

>B079_translation_inhibitor_protein_(endoribonuclease)
MKRTLHVARTSVLPISSRGASCGAKMLATRATAPAEKKPRAKRTSASLPKQAAGHHQVVSTALAPAAIGPYSQAVVA
TGPFLFVSGCIGLHPQTMDFTGADVSTQTEQVMQNMGAILEAGGSSFAEVVKCTILLTDMQHFATVNDIYAKYFPRD
PPARATFATNGLPKGALVEIECIASLAQKTTRTRKAGTTSGRGKAKQEP

>B080_ribosome-binding_factor_A_(RBPA)_domain-containing_protein
**MQKTLRGRVARSGHLPPAFPTASRATHFLRFSSHNSLGSAAAAATGIRSRLSSSSSSPLVRSCFPVAPAATYHTSAS
RALPRHDRGGGATKAPPSSSAAAAAAAEKKKAPSTSSSASPSSRS**SSSSSAKKGKPMLDQLLAEYQDLDLTGDRPPRA
KAGRAQKQDKPAATAVDGDDDGDEHSASPKAQQRGPRPGDFTLDDLLAEYDGPAGVGGPVKAQAQAKATTDPLAGRE
GDFTLDDLLADYDDVSGPAAEGEDKGDARRLVQGVLAGKQQADPRLAQLQGDFTLDDLLSAYDHDPRRRPRQRRPGG
GDEWREDMARFGGAPDEREASLEDLVKTYQPPPAEDQSPAPAQGASSKARVREELRHFVQSMVADDLGLTSGGEADE
REAMEPLRATRARARRHPPQATATTQHDDGVRAADVVVDDDDADYDDAEEAEDVLRHEAVDDVDIDEQKDDDDELDD
DEEKALDKMMAEAEAEEDQDMELLTRELEAGRTNLPPRRTREEWERLGGDDVEPAFVGTCIERSESELEGVEVTKRF
DAVNDNETDEQYMERMIQMEEEAEMRRAEGELTGKKQGTPVRLTKKEKAEAKLATVDPAKAKNARTKLKRKERRRQE
HEQHMEKVKRHHKEGGVKLDGSQMFAHGANVPPELMHWFSDPEGLKTKRDAMLAKKCNKLQRMAELRKTREKRIDMP
SDPTTAEVEELLGMTRRQKRMASKIQSHLEDVFVEDLGADSALGQLDININEVVMSRDMRIARVYWKGSGNEDAAER
LLHARTSMLRGMLAQRAGVRFSPELVFYRESAESMYHEVSRYMDQLQKQEGWDEATIKAELKRIRKEREAAAAGGRT
KT

>B081_assembly_of_ribosomal_large_subunit_protein_(C7orf30/IOJAP homolog)
MKRFSMNSSLGTMPRSCPATLRFPLPSALPRSSSMLLPRPTDWQIRGTQRLWSTGGKRSDFDAAAQKKVHILEARDR
VLARLRDKKRDAAEAAKFKKKEKKTGKGGAEGKATKPKDSKKSKSTSTDERSTAAVAAGGVEVVGDGAPAERKRRVR
QAAVVATMEPVEHEEEDEAQELPPPMTLDDVVQVLREEKGLNPMVIDVSQKCNFTHYMIIIEGRSGRHLRAMAERIM
DEMQARQKHPQANVGLEVDRGNDDWIVVDTGDILVQLFSPGARRYYDLEGLWTLQKRMSERDGQNEVVDVEDLEPLP
DLDDVPNAWNPWDQDVQKA

>B082_mitochondrial_fission_protein_1_(Fis1)_[0.0107]
MEDDREYDKQTTEEIKEDIRQQMKSEESIDFRLDLERLEREYKEECRQHGSAGAKKFPYAVLLIRSNNRQQVEFGVR
LLHEELREEIEDGGRANLYYLALGYFRLGDYVAARKSAEALLQLEPHNRQARAMKALLDEQITKDGLVGMGLVGGAT
LLAAGALTAGVFLIRALAKK

>B083_mitochondrial_distribution_and_morphology_protein_31_(Mdm31)
MWRRAHNAPLAPGLCGARSGTTTFPSLHTYNRFPLRARHSSQSLKISLSPATIEPISTHPRHHLSSSTLHVPSITST
STAAAKSRLQSTSIRSSLSPRWPSAARLVPTLRSGPSRFLTASQLSRGGSTGSCRLYTEQLQNRTEKIERIVGEQQP
KRRFKLTTDLKIALFSYFVMGTTTWLLVGTTTLVSVILWAANTLQFQGYIAKTLSDTLTRETGIQITFESAIVPRWK
NGHIRLNKVRVVREEEEALRKNYASMDLTIQQIDVKLSLWWFLEGNGLLKEMILKGVRGHVDRRRLVWTVEPAGEQA
AEAKKKEGSEDEDTMTNETVKPHSPNEAFVPQSVGAFCFSKLTISDLYITLYNANPKRPLPVSIYSYKSAHLVRSTW
LLHDLLYAEYVHGSFDDCLFTLNKPHLHNHPYRRLMINEDMDEDRDADEKWKFVECKLQGLNIDHLAENTTGPLNWI
TSGFIDINVHLLLPPFANTLPPAPNPSNPNARAEPRLLSQLPGINMDFKLVLTNLSASVPLSTPHMSYVNSALIQPI
VLYLNTNYTELPLTFRSVIPQGRFWNAWYPGDCGFWDALSEGAGAAIEKAVSEQTTTPNIWKLIGLLNDGVRRGLLY
YWRFHVLVFLGFSPE

>B084_dynamin_family_protein
MSMDQLIPVINKLQDVFNALGTDAIDLPQIVVVGSQSSGKSSVLENIVGRDFLPRGQGIVTRRPLVLQLINLPTDPK
KKKNVDDDDDSALKEWGEFLHKPNEIFYDFNQIREEIVRETDRMSGKNKGISHMPINLKIYSPHVLNLTLVDLPGIT
KVPVGDQPADIEIQIRTMVLQYIERPNAVILAVTAANTDLSNSDALQIAAVADPDGQRTIGVLTKIDLMDAGTDAMD
MLLNRVIPLRLGYIGVINRSQQDIIKKKPIRAALKAEAEYFTTHPLYRSVASRCGTPFLSKTLNKILMNHIKECLPE
LKAKINKMAGEAQAELLTYGDPLYDGKSSQGALLLQVITKFSTDYKNAVEGKSTDLSLSELCGGARINYIFNDIFAR
CLGRINPNDDMTMNDIRTAIRNATGPRAALFVPEAAFELLVRRQIQRLEDPSLQCVDLVYDELQRIIAQLESKELLR
FANLRERVVEVVNGLLQKCRSPTKAMISNMIAVELAYINTNHPDFVGGGGAITQVFERMAVTHAQEQQMMMQQQQAM
LAQQQQQQMQGQPGQPSQPVPQPQPVPQSQSKATRTPAPMMPQGQGDINGQPGSNGFFNMFFGGQAPPGGQAQGAQA
PRSAAPPSTPMPATPGAPAPRMAPPSASASRSGSGMSRTTSVDKKVKKTTASGGKSEKLDQVPATIRAISAPTDKEK
FETELIQSLLVSYFDIVRKNIQDLVPKSIMHFLVNQAKDSIQNELVANLYKEDYFDNLLEESSAVASRRTAAKGMLD
VLTKAQLILNEVRESSI

>B085_dynamin_family_protein
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VELLKQTREQLEELFLLVVVGEFNAGKSAFLNAMLGKKYLKEGVIPTTSKITSIRHGETASSVLPTEEPDREVIYLP
VDWLKDLNLVDTPGTNAILKYHQQITEHFVPRSDMVLFVTSSDRALSESEHQFLNRIRQWKKKVLVVLQKVDLLEDE
AQLEELRSFVAKGMSQLLGIQPKIFPVSARLALKAKQLMAKENASAEEKAEAAALWEKSRWAELETYILKSLDAGER
SKLKLKNPLGIAHNLLNKYKDVTESRLQVLAKDITSIEHIEEQLEEYRKEMKRDYEFQQNRIDNVLLELANRGDAFF
DEHLSLSNIFALARSEKLRGEFERTVVAETAIQIERSVSDLIDWTVDKNSKQWRRVVDYALERAAHHAQSEGLIGKV
ESEFDYNRAKLLDTMGAGVRNVVASYDKTEEARQLANEVQTAIYSTAAIEVTALGVGSLVVASLLDFTGVLGAGALA
ISGLCVLPYKRAQVKRIFNEKIAGLRVNMRGVMHAHFDRELADNIRKIQGSVSPYTLYVKTEKEKLTKTKTRIEDTM
KRVSNSIHSIDLAFQGESAEAPEEDLQ

>B086_ERMES_component_mitochondrial_distribution_and_morphology_12_(Mdm12)_ho
molog
MSFKIYWDRMGEEQAAKAMDYLNAFFSSAPKPEFIGDIAITALTLGDKAPEVRLIDVSDPPAHFSSLPTVNDAPSSL
DSPATTARSVPAPPAVGSSTGATGTSSSSSSSSSSSSSSTTTEEPEVKATDMDMMIKVFLEYSGTAKLTMRCLISL
VNWPRPRTVCLPVTFTLSDFHFEGVVCAIHHANKVHFCFDKREGDDVGPLKSLKIEAQIGDSTQQVLKNLEKVENFI
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>B087_Tiny_Tim_homolog_Tim9_form_3
MGNRQFGMGYGMGAGQSRAGSASDEERMMQVMMASMQMQDYLTMYNSTTEKCFKKCVFNLRTPQLVEKEEVCLNRCI
EKMSHYNLRFQQKVGAESAALREQQQKEAEQKQQPPTEAAQADKEAPSSK

>B088_Tiny_Tim_homolog_Tim10_form_2
MNGQPMPSGMSEQEREDVLAASEFITIQMDLYNRVLGRCWDKCIAHYWDKDLTVGEGSCVDRCVVKYMTVQRTVAKR
VLGIRAWTKREEERQKVIQKLRDNQMFGV

>B089_Tim22_homolog
MEGRDAASQGEPETARRQESQSPFPQAPPGTWQQKLDAFVEPFVIKYLWDPRFAENCAFRGVQTFVVGGAMGFVMGI
FFSSLGGPSSMGMPDVEMKGGWKKQTAEHFKHMGRSGVSMMKAFAYVGALYATTECVVEKYRGKSDLMNPLIAGCIS
GGLLASRAGFTATAMGCGGFAAFSVGIDWLMMENH

>B090_TIM23_complex_homolog_Pam18
MQRTTAQAAKTSQPKMGPGTIFLALGVGGAGLALAPRLVSSAAKHFSKGGSSGKGFATMGSMWKRSGGGASTGFKNF
YKGGFESEMTRAEAALILGIRQSAPKEKIRLAHRRIMLLNHPDNGGSDYMASKINEAKDVLVKDLN

>B091_core_peptidase_Imp1
MESGGGSRLGAVLRTTIMVGAYYGVAYTFCNTVLKPSTTAGPSMHPTFNAAGDSVWVYRRIDPATDLRVGDIVHART
PTYCRLEGKQPGVLKRIKGLPGDTIKVTFYSPSKVGRTEAEEEADEVTIKVPAGHVWVEGDNPGQSTDSRMWGPLPL
ALIEGKVVSRLNPFSLQTLDAPGHIKRKWERQARDIADSRATGKRSGEEALRAIDRLIKSGSEASDNTLLVSDRHDA
DVNDTALAPPQDTVQGHERVVA

>B092_core_peptidase_Imp2
MESKPSRLLRLGVQYGLGVGVGYCFGYMLADTFPYGAYRVEGESMYPTLEKNDWVLTSSRRNGLHRGDVVVLRSVKE
PKERMIKRVTGLPDDLIHTDDAKLVRVPRGYCWIEGDNASVSLDSNVFGAVPVGLVESRALYRLDRGWRLHKLESVP
RERLQRTKKEREVR

>B093_mitochondrial_carrier_AcMC30
MMHMQGAGKGGKDGKGGASWRHSVYGAISGATARTCVAPFERLKILLELQGMEKARGQATTTAGRPKYSVLRGLGVI
LREEGWRGFYRGHLTNLLHVAPAAAARFYSFEAYRSWLVRDGKPLPPLKRMLCGALAGITSTTLTYPLDLVRTRLAA
QTPDTPMQYRYKGIGDCLVQIVKQEGPLAFWKGLSVSLVGIAPFVAINFTTFETLRQEVTERHGGQMPLLWGPVCGA
ASGTFAMTCTYPFDLLRRRMMLQGRGGEERFYSSIWDACRKIHQFEGVGGFFKGMIPTYLKVVPSVAISFGTYELCK
RVGGE

>B094_mitochondrial_carrier_AcMC31_(similar_to_solute_carrier_family_25)
MAHTQHNAPAAATTTNVVRETDKKWLRGMLGGTSNAFAIILVSPLDVLKIRFQTQNALTKAGAPKTYDGILKGAVTI
VSNEGVRGLFKGLSVSMLRELTFSSARMGLYEPIRNYLVGPGQKEIALGQKILAGLMSGAIAAAVFNPTDVLKVRFQ
ADPARTSELRRYKSVVSAVVEIVRTEGLIAGLYKGVGTTVIRASLLTSAQMASYDESKHFLIDSLAFSDNFLTHFCA
SMFSGFMTSLVTNPVDVVRTRIMTEYASPGQPRTYSNPFTSLVRIFRAEGVLGLYKGFVPSYLRLGSASVVVFMLYE
QLRRLAGIPTL

>B095_mitochondrial_carrier_AcMC32
MSSRQPGDRPKREEGPPHHALPPPSLTVTMLASATASMLSRIPCHPLDTVKAKLQVGAQGGLRGVLRHTLRTEGLRG
LYRGFGAAFVGSGPAGCLYFTTYELAKKGLLSVGLVGQSPFLAHFGAGLLAELVSCALWVPIDVVKERMQVQSTLAA
GKPSYAYTGDLHAAATILRTEGLRGLYRGYGATVLSFGPFSALYFVYYEQLKGLAEAFSASNDSSTSASTRRPPPEV
STTTPLSFGAVLACSATAASLAALCTNVLDMAKLRMQVERAGGERTFGYTNVFHGVARIVSDEGWRGIFRGAGARIA
FQAPTTAIALAAFERLKVGYGRLAERVPAGRENK

>B096_mitochondrial_carrier_AcMC33_(similar_to_Graves_disease_carrier_protein
)
MPEGRRQTKMERRGVRLASIREERKIESWSQLWRTLLCGGIAGCVAKTTTAPLERVKILFQVATIHYPFKGVVPTLR
RIVEREGFRGLYKGNVSSLVRIFPYAATQFAAFDIFKAALTPKDAGISGLANFLAGAGAGATAVAFTYPLDVTRARL
AVQVEKRHYTGLVHAIQNMWRHEGGLKALYRGLQPTMFGILPYAGINFFTYDTLKWYYSKKLRIAANGDPPPPIPTT
LRLAFGAVAGALGQTLTYPLDVVRRRMQIDGLMLEQTYSYKYLSTWHGLQTIAQKEGWRTLFRGLHINYIKVVPLVS
VSFTINDLMRRWMGLKTEGGVER

>B097_mitochondrial_carrier_AcMC34
MSHSDEKSFSVARTLFTGTVSGIVCKFVEQPFDTIKVRVQAGTKVMSPSGAMVPEFNGPWDCFVKTLRREGFTALYK
GLPSPMIGSAMEVASMFVVYNAAKEALMDPETHHVSLPRVCLAGSIAGVATATFLTPVELIKCRLQVQTGGEAGHAA
AGAAARGATPPAASAMSAAAAGGAQQQLRYRGTMHCIMHTLKTEGIPGLWRGWWSTFFRELVGTALWFGTYETVCRT
LAADAGDASDAPPLIQLLAGGCAGCIYWGVPYPMDTVKSRIQIKQATEQTSIFKMFVEVLKEEGVRGLYRGIGPTMM
RAIPGSAVALFTYERSSRFLDWLKEEKPHLCPSFF

>B098_mitochondrial_carrier_AcMC35
MVQSSLSSHIDRNEHQRPIDESGWETTLRVVASLGSMASGWAVHGLGVLGYQWSVTPRPIVGQWLPATTFSAYWNLR
KEAATHPALRYGAFSAAGLWAGAVKAISHMFLQEYVFAPLLHIATSDEELDESFEAYDPIAPIKQGDMYQRGGWTGP
VCAMASAAGAILLSLPFLKAKFLLRTQSRRPDGSFKYTGLFQSIGVIWREQRWGLITNNLSAFISFGILYDVVGFLT
DRYKLSTLIMKIKTREGVLHNLKHALALAIDDIIEAAIIVAFTMPVNVVLRRLEAQAGGVAPFSADGVVYAGVLDCV
QQIFVREGLNGFYKGAMPELLERLLPRVFVDAAVDLGLNSFFGVPATYDNTEEHSHAD

>B099_mitochondrial_carrier_AcMC36
MMHMQGAGKGGKDGKGGASWRHSVYGAISGATARTCVAPFERLKILLELQGMEKARGQATTTAGRPKYSVLRGLGVI
LREEGWRGFYRGHLTNLLHVAPAAAARFYSFEAYRSWLVRDGKPLPPLKRMLCGALAGITSTTLTYPLDLVRTRLAA
QTPDTPMQYRYKGIGDCLVQIVKQEGPLAFWKGLSVSLVGIAPFVAINFTTFETLRQEVTERHGGQMPLLWGPVCGA
ASGTFAMTCTYPFDLLRRRMMLQGRGGEERFYSSIWDACRKIHQFEGVGGFFKGMIPTYLKVVPSVAISFGTYELCK
RVGGE

>B100_mitochondrial_carrier_AcMC37
MSSRQPGDRPKREEGPPHHALPPPSLTVTMLASATASMLSRIPCHPLDTVKAKLQVGAQGGLRGVLRHTLRTEGLRG
LYRGFGAAFVGSGPAGCLYFTTYELAKKGLLSVGLVGQSPFLAHFGAGLLAELVSCALWVPIDVVKERMQVQSTLAA
GKPSYAYTGDLHAAATILRTEGLRGLYRGYGATVLSFGPFSALYFVYYEQLKGLAEAFSASNDSSTSASTRRPPPEV
STTTPLSFGAVLACSATAASLAALCTNVLDMAKLRMQVERAGGERTFGYTNVFHGVARIVSDEGWRGIFRG

>B101_mitochondrial_carrier_AcMC38
MASSSSSSSTSATTTTTTAAAAAAAAGGSASPSLLRAVVDVVGNQKWLIYGAISGGISRTATAPLERLKVLNQVQH
MDKSGPRYQGVLPALRKIWAEEGFRAYWKGNGTNVIRIMPSDAARFYSYDTFKKLISTPGEPITPMIRIMAGGLAGM
VSTIATYPLDLVRTRLSVQTLPGRGAIYAARYRGMWHCLGSIFREEGFFALYKGMGVSILGVAPYVAINFASYETLK
QLVKTDGSETHALEGLVMGGLSGTAAVTLTYPSDVLRRRMMMQGIGGASNMYNGLWDACVKIGREEGVAGFYRGLIP
CYLKVVPAAAIGWACIETLQKVERDFLSSTN

>B102_mitochondrial_carrier_AcMC39_(ADP/ATP_translocator)
MTLASPIQRVKLLLQTQAEMVAAGRLLRPYAGVRDCFRRVVAEEGLLSLWRGNVAHLLRIVSANALGFVLKDRFKNV
LHVDKERDGYWKWMAANVASGSAAGLVTVLCTFSLDYARTRLASDVLRVAHPGAGGERQFSGLMDVYSQVQRREGTA
GLYRGFTSSCIGVILYRGLYFGLYDSLKPVVLRGDLKDSVVASFVLGWGITLGAGLAAYPFDTICRRMMTTTSEHRG
GLMHTLTEIVEREGLAALWKGAAANVAYALIGAGLLVAYDRAVARAAAPKRTKDNN

>B103_mitochondrial_carrier_AcMC40_(similar_to_solute_carrier_family_25,_memb
er 44)
MESEINSAEGSVFVGDDIDWQSLDKSKFYVWSFAFFMGVRTLVYPPILIKTRLQVQQGRSQYRGTFDAFRKIFKLEG
FRGFYKGFLTTSVGIIPGQFMYITVYEFVRHRIKSFFPTDSLRYDALRNFIGGGTASLASSLVSVPLDVISQLLMIQ
DGTVNKRKYSGGINAFCEILKTEGVRGLYRGYTASMMVYVPSSGIWWGTYASVKGKAAAFINEQGGLLRQLDVLVFG
LCGILAGSTAVVVTNPMDVVKTRLQVLAYTNPSSPATSAEAAPPPPQQQTTTSSQRPPIASSTRSYQKISIWATAKQ
LLREEGWRALKKGITARMMSMAPVSFLMTITYEQAKRLSVKQ

>B104_mitochondrial_carrier_AcMC41
MSTHKQSGQKAPFLAQTKAGEEGQASSRQATLPGERQKKVPLGAKLVVGGIAGMVGMTSVFPIDLVKTRLQNRWCES
VSECVRRIRAEEGWRGFYRGLGACLCGVAPEKAVKLAVNEKLREHLAARDHDQITLAHEILAGAGAGMCQATVSNPA
EIVKIRLQVQGSEPANGTKSAVGIVRELGFRGLYKGLPATLLRDVPFSFLFFPIYSNIRQAWLHQRGDAKGEVGLLP
TLAAGAAAGAVAAAAVTPADVVKTRYQVEHSPYTSLHQCARAVWREGGPRTFFKGAVERMAIQAPLYGVALLAFELQ
KKWYLAHHQQQD

>B105_mitochondrial_carrier_AcMC42_(similar_to_solute_carrier_family_25)
MLVSIEESRSTFSDVGARADDEHEDHQETLEIEQCRHDVSACRCAKVVCWISFLLKPKKRVGDVAGTEPPQQNRTPT
AKAAAWTMTSSAAEGEVWHKFLLGMVSCAAPLPVVNPIEVIKTRLQLQGELQEEKAKSGLSRIYGKERKYKGFMHGG
VQILRDEGIAGLYKGIVPAALRECSYAAIRLALYDPIKTLLGENRADGVKDGGLPFWKKLVAGATAGSIGAAIATPT
DVLKVRMQAEGARDKPRYKNTLEGFVTIARTEGIRGLYKGVVPTTQRACILSAAMMSSYDHSKHFILQKGWIKHDNL
YAHICAGMMAGFSMAVVSTPIDVVKTRIMNRSAGGPAPYRGMFDCLVKTAQAEGVLGLYKGFVPTFLRLGPHTILAF
TIYEELRKWAGIRPV

>B106_mitochondrial_carrier_AcMC43_(calcium-binding_carrier_protein)

MPTAPPPSTASRPASSSSPTGAPGSAGAPPSAAPPSASASSIGAAVAALPSAPAQLKASLPAIAREEANVERYRRVF
EELDLDSSGSLDEHEIQAGLQRMGLPSSDKQVHEMMVMVDADKDGSISYGEFASFAQEREKDLRELFDEIDLNGNGL
IEANEIRIALEKIGMSTEVSDGDIIQLIDRMGVDHTKGIDFQVFKRILMLFPSRNISISNVFDYWFRHIIDTGDEVI
IPDIIDHPMKRLIAGGIAGAVSRTTTAPFDRLKMLLQAQNSSAMLAGVATKQLAGGKPAAARPGVIRPAPDAAARAA
AAPEYRGIWNSLKKIYFESGWKGFYRGNGTNIIKIAPESAVKFWAYESIKRMLCRDSSAPAIKEKLIAGSAAGAISQ
TAIYPLEITKTRLAVSAPGEYRGIMHCISSIVRTDGVSALFRGLLPSVVGVIPYAGVDFAVYSTLRDVYTRRYPNTH
PGVLTVFVCGAISSTCGQVVAYPLQLVRTRLQTQGMAGRPMLYNGMSDAFFKIWKCDGLLGFYSGILPNFMKAIPAV
SISYIVYEQVSRGMGISSGL

>B107_mitochondrial_carrier_AcMC44_(carnitine-acylcarnitine transporter)
MSDGGNGQDSGQASRERVRHFLAGTLAGAAGVFVGHPFDTVKVRLQTLPGAFKGPLQCFVQTLRREGVRGLYKGLSS
PITGDSLTNCLVFGVYGLTRRAQLETDQTEEHFPLLSLTQIGLAGGAAGLIGGLIQSPVELIKIKLQVQTGTGAARL
YSGPIDCIKKIVRADGLKGLTRGLGATWWRDIPGFGAYFVVYEGLRRQWADDPLRPDDVSPVKQLVAGGLGGIAAWG
ISYPIDVIKSRLQTNPEYKGMWDCAVKSYRADGHRVFFTGLGTTVVRSFPVNAVIFLVYEVLIKTIPA

>B108_mitochondrial_carrier_AcMC45_(calcium-binding_carrier_protein)
MLLCKLAGPLHEKSRRLPVLWCVTRAIAISFTFLFFSFACIGTFGVVVDATRATLCSSGGRVEFEVPTKVRRLARRL
NSRFPTVLREKMSTTATASIPVPVEQSPATLDKIKGNIANEIARREIQQRPSLMNAAVSFSIGAAASAISATAVYPI
DLVKTRLQNQRTLVGQRGMSMWGCLTSVVRHEGPFGLYKGLIPQLVGQVPEKAIRLFIVDRIRSLSATDGVNYSIEL
LAGLAAGANQVLITNPAEIVKVRMQVQGQEYAKKKADAAATTAKPKGAMSILRELGIKGMYKGASACFLRDVPFSGI
YFGSYAWLKEQLRTGNEPLHSIELFFCASLAGVAAASLTTPADVLKTRMQVEAKKGEGYANLRDCYRRVTTTEGYKA
LWKGVVPRVLRSSPQYGVMLFSYELLQRLFNNDVQSSISMDVLEDKKWVKMLLLEDKMGILLENSWEPPTSFTRFKG
GFKHISVGGSTSVWAISRGDEIYRWKENQWEKTTGAKLKQLSAAEDGAVWGVNNNGEVYRWDGDKQTWQSIPSPFSV
LHVAVGSDREVWAVIDDEKEPTSALKQSNIATWDGKAWIRIPGSEQMKLVSCGADGTLWAINSERFTFRLDRESLKW
EQMPGSFKQVSVGSKKHVWGVDSKDCIYKWKKGTWQRVTMADVPQHISVASDGSIVAMDKDTNGVVNMKKLVLPVED
KEGEVH

>B109_mitochondrial_carrier_AcMC46
MSVTSTSATPTSTSTSSTSSTPSTPVAQVKMPAAHHHPPAWAHFVAGGTGAMVGGVLTSPLEVVKTRLQGTYNKEGL
ANTQHRFGTRTVRALTHLHAEGGVRALYRGMVPHLVGVVPARALYFGTFSWSKRELGKQLELDPHGMLLNWLGGVAA
GVVTITLTSPVWVVKTRLQLQVGNGKGSVAPGTGVRQYRSAWHCVTSMMRHEGPRAFFAGMSASYVGISESSIQFML
YEKFKSLIKQRRVRQCEEAWQLELQRRRRAHTAAAPFDHDADPELVQLRELARSAAASSIGAWETLGISSTAKLVAS
VLTYPHEVARTRLREERAKELYGGFVNCVRVVWRNEGLAGLYGGLAPHLLRVVPNAAIMFLTYEAVLSLFDPSSSAT
R

>B110_mitochondrial_carrier_AcMC47
MAAAREERQVVFGEGEGEEEAVQRRQQIRALFDEFDRDKRGRLTLSQFEQGLKREGLWHRIRDDAHLRRVVWNATRLD
PSDEAGMDFGEFYNIMVEHYQILPHAHLVEVFEDWLSFGEKLSNLPAEAVAGKSRNPWRYLVYGAVSGAVSRTVTAP
LERLKILNQVQYLSKGAGPQYGGVWSALVAMGRNEGWRGYFKGNGVNILRIMPSSAARYYAYEALKRALHPENGQPT
AGVRMLSGALAGIFATGSTYPLDLVRTRLAAQTASAKYKGLMDATRTIVKEEGVAGLYKGLWTSCLGVAPFVAINFT
SYEMLRQWAIDARQGEKPSLFMNLSIGALAGTIAMSITYPSELLRRRMMLQGIGGAEREYKGITDAVVKIARNEGVA
GFYRGIVPCYLKVVPSQAVSWGMLELCKKLAGE

>B111_LETM1_and_EF-hand_domain-
containing_protein_form_1_("Mdm38/LetM_homolog")
**MRRLTRTTSAAAAVDGVVMRQCGRSGLGAARRLVLAPSPVSSSFSSSFALLSSPTGVLATPFRPLPPLLARRFSATT
TTS**TSSSSPSPSSPSPSSSSSSLSAVASSESWAERAKAGAKAMWAQYWGGTRQLWVDAGAARALRRRVRESMASGGV
AADGSVALSRRETRFVRRVADDVRALVPFLAFFMLPFSAYALPVIVRFFPGFLPSTYHSSSYRVAQMQKRQKVKVEA
ARQLRDALSERLLATEGPSARERDLLLDFIHRAAAGEAIPLTQLRPLDRYFATHLKLLDLEPRRSSGASLGSWLGST
LWLCPAELRALCTFYGLSALPLPTFDHCANQLILHASRIQHDDKLLVQEGDRWPTELTDEELLEACDERGLPTDVTE
RDRLVAQINQWLAFRRPPPPVSAELTLFAPALATNTRAK

>B112_LETM1_and_EF-hand_domain-containing_protein_form_2_("Mdm38")
MRKCPTTTTTTALGLRFARRSPSSGLLTARRLFPSSGAYRSQLRPAAVAGWRGMSTTGHGPAAPDTKDEQQPLGATT
TPPPAIAPEAEAAPAAVAAAPKWQTLMAKAKELARGIKDGTVELYRNVKHTRRLRAVVRERGIDALTRREIRLMNRT
REDLKALVPFLILEIVLPEATPFVVMLFPGILPSPYQRLIPQQKRKERERKRTVEALEQMRSELHALGGQRPINFTD

SSLDDLVASLQRDESGLREKLEVASLPDGMVEAMTRYTSVWSRFRTQNGLRSSLQRKLDALRKDDELIAKEGGIDSL
SEEEKEEAYYERRIGLAATSPASPAATVEPSSAVGPTDPDRERHLREWLHLSAAIRDCREQHRATVPDTSLLLLALR
H

>B113_transmembrane_amino_acid_transporter_protein_(possible_sodium-coupled_neutral_amino_acid_transporter)
MRLSSSPAPSSTSSSPLLPPPPRFSSSHIPQTRASYSNGAYHEFSAGRQPPNYDTFSGAAPHDELAGGAGRAQAAMT
SPYYITQRPRVKKKAKAAKLSSSMTSLPLVDMSGSIAPSAGQTLQPPKMTSSSSSSDLISDYMMTIPESGMAESPKP
GRTRSSSASSSSIAYPGAEKPSQAHIDIDLEKKGSDPSGGQLPYDDEASSKKGGEDTAVLVYPSWAYNPVGRIVYAG
WQFVKEHFGEGSVGSSIFVLLSATLGAGTLAFPFAFKECGWALAIFLMAVCGLAAFYSIYLLVLCSIITGRNSYEEL
AHSVFGRATEIVVDISIIIFTWGSTVAYMVIIGDTLPPLMELFGAGDTIMAERWFLLVFSTIFIIFPLTLLSRINSL
RHTSLLGFAATAYLLVAVIADTSRRIADHGLDSDRVSAANFSSRIFVGLPIIFYGFSSHVNIFSIYRELKTPTLAKA
TQVIAGNIIIAFLVYGTLGLFGYLAFLEKTDGNILENYAPENIAIQLGALAMTISVVFYIPLNTHPCRITIDWMITS
LSKELAKVDITVRYVVETIIMDALALLIAIAVPNVVVVFGLLGATATSLCCYVMPGLLYVKAANLPWASKEAFLPLC
LVTGGTLCGIISTVVIIFDMFEDPGQLE

>B114_iron-sulfur_cluster_assembly_protein_Isd11_form_2
MASRPQALRVYRQLMRNGRQYNDYNMREYIQRRVRDEFKANKTMSDAEQIDKCLDKARHELEVVKRQAIISRLYNHG
KLIIEV

>B115_iron-sulfur_cluster_assembly_protein_Isu1/Isu2
MLRTRTRAVFGSATLASHNGGSRMAGGAQRLYHERVIDHYENPRNVGSLDKNATDVGTGLVGAPACGDVMKLQIEVK
DGKIVNAVFKTFGCGSAIASSSLATEWVKGKSLDEAKVIKNSQIAKHLALPPVKLHCSMLAEDAIKSAISDYEKKQK
AKQEAQQ

>B116_iron-sulfur_cluster_assembly_protein_Isa1_(Isca1)
MSVAGTVRVVRKPLTSRFAAKAPITLTPAAVSRLHSLMGGSKDKYEGIRLDVKSRGCGGNSFTLDYAEKKERTDEVV
EADAGVKVFVGSKALLHVIGTEMDYVEDDLQSGFVFNNPQAKSTCGCGESFTL

>B117_Arh1_(ferredoxin_reductase)
MKVWRRGIRTSMALREVGGMGGVPTSRHLKVCVVGSGPGGFYAVEALQRMAEEAKAKGQAPEMALDVDIYERQAVPY
GLVRFGVAPDHPEVKAVQHRYDAFMADPRLRFVGNVSIGSTNSISQSSSSGAAALSVEELLGAYDGVVLAAGAQRDR
PLGIEGEDLPGVYSAREFVAWYNGDPAMRSRQFELSSSREAVVIGQGNVALDVARVLLHEPGQLASTDMPEYAVDAL
RRSQIDTVHIVGRRGPAQASFTNKEVREILNLPGVQCHFLPSGVLALNEASKAETAKERGKKRMIDLFAATEKKAGE
TKGEPKKNLYFHFLLSPLRFLANEKGHVSGIELARNELQGEAGNQKAVPTHEKETLECDVVFKSIGYKSEPLEGVPF
DHHRGVVPNEHGRVVRPDGSTVPGLYVSGWMKRGPSGVIGTNRMDAEETVASMWADLAATRPGEKPGWRAIQDKLRE
RQVAYVDWKQWKAIEDEEHRRGQVLGKEREKFTSVPEMLDVAFKQ

>B118_iron-sulfur_cluster_iron_import_protein_mitoferrin
MEFLVDEALEEELQQSSDPRVHLIAGACAGLMEHCGMFPIDTVKTHQQLAGSRTSIAATIRTIVAKNGVTGLFRGLP
VVVAGSAPVHGVAFSIYEFCKRLLGADQPGHHLLASSMSGVVATLAHDACLAPVDTLKQRLQFSARPYRGVWDCFGH
ILKSEGVSGFYRGYTTAAVMNLPHASIYYGAYESIKKLLKRATGKEYESNDPVTHMLAGAAGGCLAGGLTNPLDVGK
TRLQVGTDAGKSYRGMVSTLRTIYREDGWAGFTKGIRPRMVFHSMSAAISWTTYEYIKHTLEPSFSSHSPPSSNKSG
PS

>B119_ubiquinone_biosynthesis_protein_Coq1_(hexaprenyl_pyrophosphate_synthetase)
MRKMASRSTMRRLGGRATATCATQCTVSGAARPSSLLYASPLPSMARRDLATATPAQTPVEGLEKFVSKYQRQTFDL
DAPHHDGSASSVVEGLLRRALPTALAGGAEAREDPMKVALRLVEKEVKSLNGSIQQQIEAVTERPLLAKVASYFFKL
QGKRIRPVLVLLTAKAIAVHLNPALGAGLTPENADVPVSDRQFSLAEIMEMIHTASLMHDDIIDQAETRRGMPAAHK
VWDSKKAVLAGDFLLARASVKIARLREHEVTELLSTMIADLVEGEFFQMRTNVEKEGKEMTQFDYYMRKTYLKTASL
LEKCCSCAAILGEADRATINIAKAYGAHLGYAFQLVDDMLDFTGTSSDLGKPAAVDLSLGLATAPVLFAMEEFGELR
ALVERGFKEEGDVEKAFSLVQRSQGIARTHALAQEHCAKAVETIGQLAPSPYRDALARLTEKVLSRSS

>B120_ubiquinone_biosynthesis_protein_Coq2_(para-hydroxybenzoate_polyprenyl_transferase)

MKRAAGRSCASLMRPTTTTTMRAGNSLQRWRMRESCAEARNARVATVTTTTAVTAMPRPTCGHLLTTQRAVLLRRRQ
LSSSTTSRSFFPPSSSSPRSRTILPPPAAFSSPSSSSSLSLSSFLSPPAALRARCPPLCRELGTSSAGTPTTPPPTS
LASTFSAAADSEEEPSSSTTTGWAALKQRLTPYGALARVEKPAGTWLLLWPGWWAIGMAAPPMWEHLALLGTFGVGA
FLMRGAGCTINDILDRDFDARVERTKSRPIASGALTRKQAVAFLGLQLTAALGCLVTLNPLSIGVGAASLVLVGTYP
LMKRITYWPQAFLGLTFNYGALLGWTAATGGFDPTVVLPLYASGICWTLVYDTIYAHQDKKDDIMVGVKSTALLFGD
KTKRWLSGFAAGSASGLALAGYGAGMGLPYFASVAAAGAHLAWQVGTVNIHDPADCGRKFAASKWLGAVVFAGIELS
NFLAVM

>B121_ubiquinone_biosynthesis_protein_Coq4
MCCRLCPRATALATSTSLRFASSSSSFSSNSASTAATPQRTAAPPPIIDASCNLYANHRPTSLFQKGLLAAGSALAA
IINPERADMVATLGETTGPSALRALHARMAAHPVGLEILQTKPRITEDTLAFDRLLAMPEDTLGGAYARWMRGHEFT
PDERPAVRFVDDAELAYVMQRYREVHDFWHVLTGVPTTVLGEIALKWFEMYQTGLPMTALSSVVGPLRLPVSEMRVL
YSEYIPWAKRSATNATFLMNFYYERRLGDNLAAIRDELRLEPWHGQCETFFHHYMVLPFLG

>B122_ubiquinone_biosynthesis_protein_Coq7_(demethoxyubiquinone_monooxygenase
)
MQSRIVLRPQRLVSPGGIGRSPFFVGNLVSSSHTPATLPRGTAAISARWQSAQTSPSSEEAEAPGAPTADSDAAASH
DAAAGSDGQERLRQRLYDQIIRVNQAGELGAQQIYAGQLFVMRGTTDEPILQHMADQEKEHLQKFDELMERYRVRPT
VLTPLWRVAGFALGAGTALMGREAAMACTVAVETTVGEHYNDQLRTLHGHNMNSPKDQELRQTIRKFRDEELEHLDI
GLKNDAEKAPLYGLLTKGIELGSKAAIWLSTRI

>B123_ubiquinone_biosynthesis_protein_Coq8
MKRAAGTLSGSAPTHLGDFLRVTQGAYLVADQFAAQAAVNNRASMLGRAIFRSPPPAMRTTSADAATATAPQTGASA
AEIATTQDVAASSSVLAPPVVVPIPPVAPAPTTATALPPHAVHSPVPPSAPAPSALAESTPAPQAAKLSGAGAKVEA
QAPPLEEPLTKTAPPPRPTFDRIKYLQEQQQRIKENSKQRKVPSSQVGRLWHFGGLGVRMGMGTLGEAAMRTVGLGS
SASAHPAVTPANAQRLTNTLGRMRGAALKLGQMLSIQDSALIPPELAEILDRVRYAADRMPDQQLEDVMNHELGHDW
RSRVKEFDPVPIAAASIGQVHRGVLADGREVAIKVQYPGVADSISSDLNNLGSLLKMLGILPKGMYLENTLRVAQDE
LLWETDYHREAEATMKMKELLSDEEIFVVPTVIPEMSSKKVLTTELLDGQPIEHVVKDDQKTRDMVAESMLRLCLRE
IFEFRYMQTDPNWSNFLYNPETRKIGLLDFGACRDFNKSFTDEYMRVIYFAAKQDREGIIDASRKLKFLTGEEPPIM
NEAHCSAVMILGEPFAKPGPFNFGAQNVTQRIHELIPTMLKYRLTPPPTETYSLHRKLSGAFLLCAKLQAQFACQPM
FMDLYRKCGPQ

>B124_ubiquinone_biosynthesis_protein_Coq10
MHARGKVRTVGRATTRVPALRPSGVTGNAIAAQPLYPTSATRHFFNLGWPFSENASAADAGRAIEYKDERVLPYSAD
EVYDVVSDVAKYQDFLPWCTHSRVLFKTPTRMDAELGIGFKMLPGQSYVSQITMERPRSLKVVVTPDSSLFNHLINN
WAFQDLSKDGKKSCRTFFDISFEFRSQLHKSMADAYFQEVAQNMIQVFNDRCAHVYRWGKQ

>B125_5,10-methylenetetrahydrofolate_dehydrogenase/cyclohydrolase_(FolD)
MKRSAACTSAPGAQARLLLQRRQQWSVHRALACTSSIHVGPNPATFSAWNAATLRTRRYTTASSVSDVARIIDGRKL
ADEILDEIRAEMKQSPPKRPPHLVMVCVAPNHAIKSYMKMKQQACQAVGFTSSVVELEAETSQDALSRKINQHTTDA
SVDGVIVQLPLPEHINPQMAIGAIGAAKDVDGLHPTNVGASVLGFKGGFLPCTPAGVLQALQRSRISLEGQHVVVVG
RSKLVGLPLANMLIGGRDSAKGGRKGPTVTVVHSGTVDIHVHTRMADIVIVAAGHAGLITADSVKQGVVLVDVGINN
VPDSSRKSGYRLVGDCTDEAYRKASRYTPVPGGIGPMTVAMLMRNTWEAAKRHEGLARPSPL

>B126_phytanoyl-CoA_dioxygenase_(PhyH)_superfamily_protein
MRRTTAALSLQGHRRGLGSCRAGGFVRRLATSLSPSSAFFTPEQKAQFQDDGFLVVDRLIDPSLAEAIKNRFPLLFR
GEFDTGVYPDEWHWREGMGRDDVTREIVNSWKSDYTIASAVLSERLGRLAAELAGWMGTRVGQDDIWWKPPGTKAVS
FHQDAPYFDFLNPRRELITCWIALDDTSRTAGTLEYVRGSHKWPQESKMLQNAFFTAQDYRASLDHTAKHLGLPRPE
VVPVEVPAGGAAFHSGPTWHGSGPNTDKTRVRRSLAIHFLPSHATFQPTGVGYIYGRYKKWGSVEMEETFFPITYRH
DGYRSPFLASYCSTTL

>B127_ferroxidase
MLAPLARCGAACARFPLFRPFVRFYKDHTAQVRFVVLTALMVVFVLALLAVVITITNLDPKGKTTSRSGTVRTYYIA
AEEVMWDYAPSGINQITGEPFDSVAQIYTASGPQRIGTVYKKAIYREYTDGSFDTPKPIAPQHAHVGILGPIIYAES
TDEIRVVFKNNASIPLSILAEGVTYITDIYMPTGNASVTSASSVLPGDQHTYVWRARSGPTSDSDPSSSIWSYYSQA
DPNNPFAGLVGAIVITFPGNLVQKVDAKTGITYNALNDMDQEIFALFATFDENLSPYNASNFEQFLGPDSGVDPSNA

AFLESNRKYSINGYLWGNLPVNVSVTINAKTRWYLIALNGRSDTHRPFWPGRMGDLTFSEASSIFTLDAITLFPGEE
KILDMRATATGRTVLMCQVAQNVRAGMNMAYTIVP

>B128_thioredoxin-like_superfamily_member_(putative_glutaredoxin:arsenate
oxidoreductase_(arsenate_reductase))
MLRPVISRKACAAWPSTLQLGGRIAPASSLSARSSSNLRLITRPSAFSASSSVIGATARRFKSSSSTPKRPSPSTSS
SSSSASGSKTTNHAKSSSTRNKMGPAAAAASKSSTRFATPPSATSASFDEMPLFPPNLAAGGAPTRKMGRPTIYHYP
RSKSSYGAIRLLEACSLKPIIIDITVDPLLPRDVERFMAELGIDDPRDFMRTSDPLYAELNLHDPALGRDALIQAII
DHPRLMRRPIVELPFREQGQRRRALVIAQPPQKLFGVIFNESEEEALGLATPRPLEETEADRW

>B129_N-acetyltransferase_superfamily_member
MRSSTWSKSATRHTLPTFLLASQSRQSTLLVSRSARAFSPAAPTAFISCASTSATPLSLLRSRPAQLRGFHSTHVQS
RRPLGPAATRLIYTELSTSKTFSALTTMLRRSSGNKADSPTKGQLQQFWERWIAERPQHPRWSTAWWWDMFIIFTVF
GITGSSTMFFVRPFITKFLKLEGSMKEGPWSYRLISVAIIMPMYSLILMCIATIFGRHAYFKKVVMRMWGRFLPSRW
MKTIEGKKENLGNATTFALPAAAIRPVELPGDLAAVRSLFREYAEGLGIDLGFQDFEAELAALPGKYEVPAGRL**LLA**
WRGGEAVGCVALRPLSGSDAGACCEMKRLYVRPHVRGEQLGRRLAERICQEAREAGYSHIRLDTLPTMTTAVKLYTA
LGFTPTAPYVFNPIPGAMFLEREL

>B130_homoserine_O-acetyltransferase
MRRRLVVGAASTWAAGLPQGAAATFRAARVRPFTRCLATKVEKATIFATSKGRKVRRIQRPFTLELGGTLPELEIVY
EEWGNAHNPVVLLFPSLSVGSHARSSVDDPTAGWWEAMLGPSKGISTEKFRVICPAGLGSPFGSTSPLSINPATGKA
YNGTFPQITPRDMARAHMALLESLSVHKAHALVGASLGGCVALSFASEYPDFVDNLCVISCTGKSTPGSVALRHIQR
QAVLRDPNYCNGNYREQGVNPSNGMAVARQLGMVTYRTREEFNQRFSWDAAGPYHLGDAINFEVESYLQNKAGSFVD
NYDPNSYLLLSKCTDLMDLGRGHKNFSEGLLRINSKVMIMGVDSDFLIPPSEQQYMHHLLQAHGKDVRLRTCGSIYG
HDAFLLDMGWFLPHIRDFLEHDHQRHHHHSHPAFVHPN

>B131_homoserine_kinase
MCSTWRASWRRARRRASAPLSPSPFDRRSLPPIFMMVTIDQQTSNLCCFSRGSFTRLQAEQKDKLATKMEDAPVYTL
LTREQVEELIHTHYDLGRVVEYKKLSGGLANSNYRVDTTTGSYLLKICDEKDRQSLQVQVAALNAVRAVHFPTCLPH
PLKGAEGYVLCQNNDQLRAIVYDFLRGGPGTIEGVTERMMAQLGTAVATLHTLSPVDNLPPFPMGVAAIDPFLEEVK
GTPFEHHEFVRYLREQLNAFRGVIADPTLPQGMMHGDIFPDNVMFDGEELVGIVDFEEVCHGPLLVDVGMTILGCCY
PRDNKLDEGLMQAFVTAYDAKRPMSVQEKAQLPQFIQYAALTIAFWRFRQFNVRTQDELRKDRHQEMVQRIAHITHT
FLAAPPLLPAPTHLS

>B132_lipoyl_synthase
MQSSRARLLAGARHISTRASPIGAAGARTLECGGHFGRRSVATTREQLRDELQSQANASEATLDHFVKLASTPAKPS
TASSSSSAASFPFPLSSSAPPSSSSSCSSSAPAEEKPTKKREGKLPPWLKTKIAGSGDGRYYALKEQLKGLKLATVC
QEAKCPNIGECWGGGKDHTATATIMIMGDTCTRGCRFCAVHTSRTPPALDPTEPLNTAEAVAKWGVGYIVITTVDRD
DLKDFGVNHFAETVQLVKEKTPSILVECLTGDFRGDLSLVEIMANSGLDVFAHNIETVESMQRWVRDYRAGYKQSLS
VLEHAKKARPSLYTKSSIMLGFGEKDDEIRQAMRDLRSAGVDFLTLGQYLQPTRKHMKVHEYVTPEKFDQWREEGEG
LGFKYVASGPLVRSSYKAGEYFIKNLLNQQRTQQHSQPQEQQR

>B133_acyl-CoA_thioesterase
MKRAARRLQGLRVTGIADGTRWTTTKSRSLFHSSAVAREAAEEPLLNRFTTHSTRTRVTSQLWERRMKAEEEQLKRF
EVATDVSVHGLEGTERPSFLIDKTPCDSAIEVVLPFSTDLALREQYINFYGNLRMGKILEDLDACAGNVAHAHADDS
NPKTRPLTIVTASVDRIDLLDKLLPDRDMRMTGFVTYVGRSSMEIRVEVESKDPATDRFYPLIIATFTMVATFEGKA
APVNRLVPQTEREKQLFDLGEKNKLVRKELAKASLFTQPPTPDEQKLLHTLFMDRIAGKQVSGTPMCASRIQSVLLC
QPQERNRHNKIFGGFLMQKAHELAWTNAHTFTGVRPWFLALDQVSFHKPVNIGSIIFFNSEVVYTQSKAVGVRVIAE
VLNPVERTRDKTNSFHFTFTCPEGHGDAPLPAVIP

>B134_acyl-CoA_thioester_hydrolase
MRRNLSMNAAPLKLLRPRLCSSSSSLSLVARPRGVSYMSTTTTSTAKAKRPRDSLVERDLRFSTDPRLQEAFVNSSG
KIRLGMVLEELDTLAARVGYAHALGTPRVAQLEERRKEGLEVPTIVTAACDRIMLLNPISIDRDLKLRGMTTWVGKS
SSEVRVEVSSVRKDPQGNDEATPHLVAYFVMVARRNGVNEAYPIPPLEPVSPAEKRHYDQGASNAARRKEAAATSLL
IQPPKLDEIKIVHDMFARQMHQGQAQQDASEVPMASACHSSTQWTHPQNRNIHGNIFGGFLMRQAFELAHVTCGLFT
GVMPTFLSMDDVSFLRPVHIGSVLALESQVVYTSTSTLDYESDQDRDQQSATGGAKQQQQGFPLVQVRVQANVGNFG
TAFEPSNVFHFNFKAGANQRKVVPNAYSEAMAYLDGRRRMIREKTLRQDIASYLEGFGTAHVE

>B135_molybdenum_cofactor_biosynthesis_protein_A_(cyclic_pyranopterin_phosphate_synthase)
MRRTVVSTLFAPRRLSAVGGARRLLNATGAAVDDLEQRQLESFRIFNDHSGKFRVAVVNRCNMDCFFCHNEGMDNPR
RSAAPLGAADPLSGGGG**HQPAA**AVNGAAAKKRDPLKRKGPSVLSTEQLLGIMNAFTRLGGKQINVTGGEPLAHPEIN
AILRGIDKRNTRVVLNSNVLLAQRLLKEPKIDNVDAIYASLHTTSPQDFREKLGTAASAARSVMDNMVLLKRHGYRV
QINYSLGDYNKAEFARVLDFAVAQGIDLKAIALIRPNDDPQFYGGEWINPQWVERVVDEQHGL

>B136_PLPDE_III_YBL036c_euk_domain-containing_protein_(possible_alanine_racemase)
MRRPISTCRVGSTVCLFPSAARPSPASSSALRLQFQSRSLGTSSPLEMENPEFNIEPTAEECAEVVRRLNGIQQEVT
EVSQRLGLKQEPRLVAVSKTKPAALVRACFEAGHIHFGENYVQELVTKSKQLPEGIKWRFIGHLQSNKCKQVLSVPN
LDCVETVDSVKLATALDKAAAAVGRTTPLSILVQINTSGEESKSGADPEKVVDVVKEIREKCSRLHFAGLMTIGRFD
EHPEPDFRKLVECRKKVCDELGLPVEQVELSMGMSHDFKIAIEEGSTNVRVGSSIFGARVYHK

>B137_phosphoglycerate_mutase_family_protein
MLRHSWRSSHASLSLPFLSSFPSSSSSSLQSLPHLRHYINPHRRWTASFRATIKLVRHGESMANTGHLSHLEVGDFL
IPLTARGRKQARQAGTRVGPAFIDDCLIFCSPYRRAQQTLEEILRGGGVQEDYLQQGAGAQDDVDDLDSSNDEEDGS
SSEEDEERAGDNPPRPYRIREDPRLREVDHGYEDLQAQEAKRERHGWFYYRFNGGESPADCYDRTSIFMESLIRQVE
RKAERENKPVKVLIVSHGLTIRCFVMRYLHLKVADFDTIANPHNCDVITLGLKDDLTKEFGKDSWLFSTGRWAVHGL
KKRDD

>B138_TTL_(tubulin_tyrosine_ligase)_superfamily_member_(putative_alpha-tubulin:L-tyrosine_ligase_(ADP-forming))
M**KKLAGCTKPNLANRLRLHLGLRANVGSGCASTARKRM**ESTNPTSQELGEGSGTGSAGLQLQRAVFINEPSTYVHQR
LMLAFQKRKDWRIVESAADEALDVQWDVYENVDWDRVLKGRLMANFYCFRKGLTRKAQLAFYLKKYCSKRPSSPLVP
CVPKTVILDINPEQVDWCLVDAREAFEEEKERTGKTGLWILKPSLGDKAAGIIILNNLKKLKETVMKDKDLVEWVLQ
KYVEKPLLVNKKKFHLRVHVLAVGRLKVYVHEDVIALIAMDDYIIPEKPKEPDAPVAEPTESVQEEEPKEGASGLSK
KAQKNARKRANRKKNQRERRKADEEDMPELSLYGHITNSCLQRDHPGFDEDATVRLLSELVKELGEEAVKTIWERVK
VNVKETFAAFRGEFSAFMPLPNCFELFGFDFLVDENLNPIILEVNCGPDMKNTGSRLDHAVVSFLDDTLAAAVDPYF
DPELAKQREATEKEMESQIGRLHLVYADATSFPAWGMPNMSFKDY

>B139_dihydrofolate:folylpolyglutamate_synthetase_(bifunctional_protein_FolC_subfamily_protein)
MRRSCLGWGRPRQAASPALHLYDAFRFGHRGYRQLLTDRSFDGAVTALGSLVSNAQAMEAWARERRTNREVDLRHEM
LTLLRRLELDVDRLSCVHVAGTKGKGSTCAFAESILRRGYGLRTGLFTSPHLVDVRERIRLDGKPLERDVFARYFWD
TWDRLHATTQGNETPEMPAYFRFLTLMSLNVFIREEVDVALVEVGVGGRTDATNVVQPDACGISSLGYDHQKVLGDT
LTEIAYEKAGIFKTGVSAYTVPQTDEAMQSLVKQAAIKKVDLSVVPPIEAWGKHCTLGLLGEFQKNNASLAVALCRQ
WLRNNAERLPPHIDRQELAPFLRSTGPSSELPA**QLLRLPTGPGDAEENSHNRGEDELWLHLDGAHTEESMEACARWF
IDSSSRDQDDADSSS**

>B140_carbamoylphosphate_synthetase_1
MSIRS**FGVGKGRLAARTAAAAAGRSSTLAPSSLLREVGRVPLRALSTRREDV**EREDAYLVLSDGTFFRGKSFGARAP
VAGEIVFNTGMVGYPESMTDPSYRGQILTCTYPLIGNYGVPNPATRDELGLAKFFESEHIQVAGLVVQEVSSTYSHW
NAHFSLQEWLRGEGIPAIEGIDTRAVTKKIRSEGAVPAKIVFDRDIPLQNIYERNLVAEVSIKEPKVYGNGPLKIIA
VDCGMKHNIIRSLVGKGTTVKVVPWNYDYTKELQEEYHGLFISNGPGDPSKLTATIEHLRQAMDVGKPIFGICLGNQ
LLAHAAGGRTYKLPFGNRGQNQPVVDQITDLAYITPQNHGFAVDPTSLPHNWKPYFTNATDGSNEGILCTNKPFSSV
QFHPEAKGGPYDTAFLFDKFLGQVKDFADNKTVSLSANLRASHPIKKVVVLGSGGLQIGQAGEFDYSGSQAIKAFKE
EGVKTVLINPNIATVQTAKGLADSVYFLPVTPYFVEQVIKKESPDGIALSFGGQTALNCGVHLYHTKVLEKYGVKVM
GTPVKSIIDTEDRELFAQRLNEINIPSAPSVACDTLGQAHAAANNIGFPVIVRSAYSLGGLGSGFANNPAELESIVV
KALGSSPQVLVEKSMKGWKEVEYEVVRDSKGNAITVCNMENFDPMGIHTGESIVVAPSQTMSNEEYHKLRSAAIKVV
SHLGIVGECNIQYSLDPKSENYAVIEVNARLSRSSALASKATGYPLAYIAAKLALGAELPDLKNAVTKETTACFEPS
LDYLVVKMPRWDLSKFSRVDWRIGSSMKSVGEVMSIARCFEEGLQKAIRMVDVGNKGFEAKKWVTASDEALHQELTE
PTSQRIFALSAALRRGFTVQQLHDLTKIDHWFLDKLNRLHNTEKTVRAYKKDTLPVELLRDAKEQGFSDVQLGEFLG
CGHMEVRELRKANGVVPAVKQIDTLAAEFPAKTNYLYTTYNGTHSDTQQEGGAVMVLGSGVYRIGSSVEFDYGAVEC
IRELRRLGKKTIMVNYNPETVSTDYDESDKLYFEELTLERVLDIYDREKPAGVVVSVGGQQPQNIALALHKAGVKIL
GTSPLSIDAAEDRSQFSALLDRIHVKQPEWNQLSSFAEAKAFARKVGYPCLVRPSYVLSGAAMKIVNNDQQMEEFLA

AAVDVSPDYPVVISKFVTGAREVECDAVANKGTLVNWAISEHIEDAGVHSGDATSVLPAISIPDNIQAQIKSISEKI
TRELQVSGPVNIQYLVKGDEVLVIECNLRASRSFPFVSKVLGIDFLRTATRIFMGEDVPVDPRCHNKVPHYGVKAPM
FSFQRLLGADPILGVEMASTGEVACFGKTPEEAFLKAVLSSNFKWPERKTALFANITPEFALQAKDLHRAGYTFLAT
PESADLLAREGVPVTTVPLQGDSGSAMAHVQNKDVDFVVTFPNHTDDEFYPLRRKTVDFGVSLVTDPKVAGMVARSL
AQIHDLAGLTPAAHETYLRNTL

>B141_DnaJ_domain-containing_protein
MKRAQRPVRAWSMQHSRIPARQPSSPLLAGRVRLTAEARVEGGGSASTFTATLVLKRGYKPLNPYAVDFRLSPTDAL
NAFDKFHKQSWLSPLMTTLKTSSDVRPVFLPFWVFEASVKGTVSGEVGHRVLRPEYNIRTKRMEMRASMQWQPTNRH
KMPLIKFHNNQPEMQVLASYAHKQEYAEAIKGQYIDAAKRMTSAMMEGPQGEKREVEPFEMFPSVARERLITDLKSY
ILHDGSEYLRILYSADDVRSVTIDFDFIGDIKPFPVYLPSYVVEYSYMGHNFRALVNGVNGQVGGEHHYSSFKVGGL
TALGAIAGAAALGLDFLNIPSFISIGLASVVAGVAARYYPFYAAWRKEQRRVAEEALQKRQAHFSWESDSFWRDYGE
HQRQQRDKEREEELRWQKSRQQQQHQRQQYQRTSYDREPPRTRPQSVDPKGYYRLLELSGKEGTATEEEVKTAFRRL
AMKYHPDMQKTEQEKKKNSEIFKRVVTAYQVLRDKTKRSNYDRYGTE

>B142_AAA_family_ATPase
MKANARGLAQRVCGSSHTRLVSTGGQALRSAARSKADKPLRPKFDVLTSHKSVFEYTLGCTLGLAGGYIIWGQELKK
KADAIRELKEALKPEIVEVDPLQRLDQSHSDSQVYTVVLTGGPCGGKSTALATLTKHLRAQGYEVYSVPEIPTLVFT
AGVPTISSMNEEQLLAFEKQILTTQIQLEESMKKIASAMDKPTVILLDRAALDISAYLPYSFWKKLLQDLDITEKQL
RERYTAVVHLVTAANGAESYYTTANNAARTEGIEQARELDDKVKHAWIAHTRTFVADNTTDFPGKMQRVCSFLDDVL
TSQHKAAPTKETPEVK

>B143_AAA_family_ATPase
MLRCSLRVPCRGTWQERATLPFSCGRSLPAPARVRLCPPLRTSHPFSSTPRPHHLLIFTRRLHGLDEASVGQRPSRV
TIGDVSLPLPSGGPRTPAFVPLLPSSLGWMMETQEVLQVLRWMMQKDQLAQDMLLLGPPGELRRRIALRFCEVAQRE
YEFISLSRDTTEADLKQRREIVGNSVRFVDQAAVRAAIEGRVLILEGIEKAERNILPLLNNLLENREMALEDGRFLM
NAKRYDKLLETHTEAEMHRLGLIRVDPNFRVISLSLPVPRYAGNPLDPPLRSRFQAYSVPPLSLSSRIDTLSREAPS
LSADTVKLLASAAEAFRHADTESFSELLAKPIEFTEEGLVSAARLLERFPHTATQDVLRRVYPSRWVAKDAAQADAI
ESAFKKLGVDMKSERAKGYAIASVRHEAPRHKLVTLTRESGREEAKVRVPSGPLPSVAPDSGAFVVTSHGGVLLQHM
LEDHAIGRDMCIIGPKGSGKSTLVKQFAAMLGYETEHMMLFRDMSTRDLLQRRATKKIDRAKQAEALSQSSSARHRE
GLGLVASATDELVREESRIMGNNDALAESLREGEDSESMWELSPLIRAAVNGRIAILDNIDRLPVGALSVLQSLIHE
RQVSLHDGTRLVSSETYGRLLSEHGLTQAELTANRVYAIHPAFRIIATGDLPSASHAYITQEVMSLFHFHHLPSLDN
PVELERFLDRVALRRDGVDSVDNASSPARLDRAREQLAGLVRFNEALKQNKHLQIALSTRQLIRAGRRIANAERPAT
ALDTRDVVHGLLLFDFLPAATKATVTKLLFKSLGGREPFSSHHAKEYAQECEKGNYDYLFSVGTFHDEARNAKALEG
QSPSPSPFSPTGASSLAVEAPAAKAHPVHLIPDIDFFAIPSHVSLLQEMYKDYALGEHLLLIGPQGVGKNKLTDKFL
QTLHLPRQYIQLHRDTTVSSLTLQPSLERGKIVWTDSPLVKAVKEGHVLVVDEADKAPPEVVVVLKSLVDGEMTLAD
GRRIVQSAHIAQQGSSSAPNEAEAVVAMHPNFRLIVLANKPGWPFLGNDFFRECGDLFSCHAIDNPDVASEMALLRA
YAPS**VPTETLSRLTRAFSHLRQLVDEGHLSYPYSSREAIAIARHLERFPGEPFEEALRNVFAFDVW**SDSTVRESIVA
AFKRSGFRVSNTFMQPPVELFEASQAGAGAGATAASGRRRPLRLNYEYDNDRQATKPKHGKVDPANSPHVGGNTWAG
GSGGADTAGLGGKGGPYRLDSGHPVHQISDEEKRKVSKEVLEAAKAMAQEALQKKLQEIEMSEEDAVLYEDYAYAVK
GQVSQLRTMLQGLQSKSKERQWLRRQTHGGELDEAQLVEAMAGEGAIFKRRGEELPPLGFSAGLKPKRIHFVMDVSG
SMYRFNGFDGRLDRMLEAAVLVMESFTGFENRFKYSIGGHSGDSPNIPLVDTVKQPQNRRQRLAVLRRMAAHSQFCS
SGDYTLTATELAIRELEKEEADEHFVIVVSDANLRRYGISPRTLGKILMREPKVQAHCIFIASLADEAERIAEEIPP
GLAYVCLDSKGLPLALNKILTSKIIT

>B144_Xaa-Pro_dipeptidase
MRRCGTSATPLARPVLWLWPRASALSGRAVTLYNLTRGTALGSGCFTSAPAARKPHLLASRNKTRNYSTMQKGTSYS
LGLETHPVPMAMFRENRERLIARFEKSAEGTPEGSVVLLRGGKAKMRHETDHEHLFRQESFFHWTFGVADPDCFGAI
DLKRRRAILFIPRLPAEYAVWMGKIASCEDYTARYEVEETYYVDEIDAVLSKLNTKIIYTLHGLNSDSGNYAKPATF
PGIEKYRVDNGRLWPEMVECRVIKTPMELDVLRYVCRVSSEAHVAVMKQCKPGMMEYQLEALFQHEVYSRGGCRHVA
YTCICGSGHHGSILHYGHAGAPNDKQLADGDLMLLDMGGEYQCYGADITCSYPANGRFTEKQKVVYNTVLAAQQAVF
AAMKPGVAWMDMHALAYRTTLQELARHGLVKGDVDAMMDADLGAVFMPHGLGHFLGIDTHDVGGYSTGAERSTRPGF
RSLRANRSLEAGMVLTVEPGVYFIDPLLDKAIADDKQKQFINVDKVNEFRGIGGVRLEDDVIVTADGIENMTKCPRT
VEEIEAIMAEGRKSH

>B145_rhomboid_family_protease

MRRIGSLRTSPFCAPCLASRALPLRSTLLSRPAFGPKEISSGLPPRCTPKAAPQPRVSAIVAARSFSWTAHPLHGRP
QTNSGLQSLSNTTSSSASSKASGRTSWLTCQPRTPTTPLSSHNNSASTSMWARRYQVWSRDQYEYRGVDVINVLLGI
NALVFGGWWLAPPRFMRENFVSTLRNLREGRVWTLITPAFSHQSPMHLLFNSMAMWVLGKEVMFVLGPSRTLLLYLA
AGVVSCVCHLAYVNEIKPRIMASTPRQYQLYKMVGAEQGALGMSGSVMGISILYAAFFPSAILLLYGVVPVRAPILV
GGFIAADLLFAFSAPESSISHAGHLGGALYGLLYALYLRRRFGRR

>B146_presenilins-associated_rhomboid-like protein
MKRFVRHSTGCAPVRWCLRGDSIPTRSLASANRFTSPLYPAFPITNSASTLSIFKRGFTQTTETVPPLKAGWRARWS
GIGGKGAYALATGLTCAALLTRRDEEDGPKLSRKELAPGDIPSRIEDDEVWGLDRLKRHWANLKLSDAQKTLVPLIA
LNTMVFLAWRIPSPRVQLFMMKHFTCSPTNMMARRYHTVLTSAFSHSGLMHFFFNMTALWTIAPDVVEILGKEKFAL
VYLNGAVVASLASAAWQRRRGTSLPSLGASGALMAVLWVFVSAFPDSELALIFLPFVPFKAINMAFAIAAFDVMGAL
RGWKALDHAAHLGGAVVGAAYFYGLRAMDALEKWDNYGSTILPGGHIYEGQFRGGKMHGKGKVTFAKQGSRSVVYMG
EFRNGQFDGYGVLADERSVIYDGHFKHGKFHGKGLLHANDGSVYRGDWVAGKREGQGVCWLEGKEDGLIYKGHYKND
RYFGSGILQRGPNIIFVGEFEDNGDGRWRATGTLYPPGGQRPTKVVWLENESPVEAA

>B147_Oma1_zinc_metallopeptidase_homolog
MHRLKCAQRAAVGPTLGLGHRHSSSTATLALRPLVSSLLRGCITSNAPPPATATMSQQSITKRFILATTRRTLPALP
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LLLAIPLGGYGYWQYYQDIVPHSGRRRMMDVSREEEQRMGLASFHLLKQQYKDQILPENHELVLAVKRIGRRIIEQT
DLQGLHWEFLVIQSDEMNAFVLPGGKVCVFTGILSVTQDEYGLATVLGHEVGHVVARHGAEKWSKMRWERALGWLTA
ILIAREEPGWLINQFLTLFLALPFSRKFEHEADFIGLMLMAEAGYDPTNAVDLWIRFSAASPSMLKYLSTHPPNADR
IVLLKRWMPQALDQYHKHTRPQATAVIV

>B148_putative_dual_specificity_protein_kinase
MLSRNARQRSTSSASTSPSPSPFSSAPSSPATRARGKTTDSIPSTTSSTSALIPRAAVYVSEKEVVGDDSLGDAWKA
NVKGLPEVVAQRLVIHDTQEDAFYEELQQSVSELAHPGLLPVVGASKELANDEDGTIDYLLVSKKYDITADQLLKQK
REESPSLEVRIGWALSIAQALRFLYDKTEDYFHGQVNLRHVHLDLKTQEAFLACWAFRSYRSVRRGRPPTLSDYHWK
APEVLVKEKRRGSLSNDEGDEDDDTSAMDAQAADVYSFGILLWELCSLKQAFTDYKSLGALIEGVSIRQHRPAIAEE
WPESLGSLAQGCWDSNVEARPKFSDLACRLQGILLETSISDPLAREFWGTCFSGKNEVELEVFQQSFYEFLGLPEPN
KKNDVKCSCLLAILKELHEQNKEIVTIKTFSDMTHWFGPLEKGWRVIDRINELCAKPWFFGRISGKEAEEAVCKADK
GAFLFRFSTSKPGSYAITVHSRRGGAKHFRVYHEPGLNYLIGKTECKSLDEIIFKFKADLNLLGPCPGSPFLELFKQ
DNFLKNRYDSWETEDDDQEGDLW

>B149_SIR2_superfamily_member_(putative_sirtuin)
MKMMRKATGGTGLSHHLLKPSRTARTLGTSLMREAAAVGLLPRSRALHTPATDEREAEEALLHFVASRRNLLVITGA
GISTESGLPDYRGPQGSYAKGHKPTLYRDFVTSPSVRQRYWARNMLGWESFSRVQPNPAHLALARMQREGVFQHLVT
QNVDRLHQRAGSHGVVELHGHNWAVRYDPSHVDEKGGGWWWLVLHPLPPTVKARNGCLGCGHEEDRAHFQARLLAAN
PDWLPEAKAAASSPVVAGTPAPVAPSSVPVSAAFFASSSVSAEEAGGIRPDGDANVPFHDHSQFCVPSCTACHVGVV
VETRGRLLRRERSKGSCGRGHEPHPVL

>B150_tetratricopeptide_repeat_(TPR)_domain-containing_protein
MRRTRIVVAGTTLRRPQVTSLAAVRASASTRLLLRSSTATPTRFYLRTWSRVQAPEKGEQGGNHRTGQVANNAIAEL
QRIEGELARIKESDQADKVAGEATQIVTRLETLGKELKITVIEDEGQQIELPENEDEKKLFTKLKAEGLYLCGDALL
CLGRHQEALSYLDRVIEMRPNHIDALLARGEVYMDLGDDKSAMRDFNEVRFWDPNNPDALFYAASLLRKTMKKIAGD
KQDLDNYFPPATPGGGDEATQSSQPEHKEQDSDLATK

>B151_StaR_like_domain-
containing_protein_(tetratricopeptide_repeat_protein_38-like)
MRLTRATARGWSAPVPRLSLSRSGWSVGLKTWAAASSSRGSPQARHLLDSSIVEHFGIFGNPLLSAEQSVQAEPALV
LGHVMRAGLALFSTGLPYTSPHVQDPLSAARKAVNRLGASEVEKAHVEALDKWVAKESMHEAVGVWEDILSRHPRDE
LAVKFAHDAYFFLGKAPEMKQSLDRVLGEWERSANNEHMFGYLLGMSAFSLEENLCYEQAERRAKAALAINPRDTWS
IHALAHVHEMQGKQEEGINFLTEEMANWKWCTGLACHLWWHMTLHYVEKGKHQQALQIFDHHIAPLMKSSGAMLDLV
DAASLLQRIEFDGGSVGDRWKQVAELFAPHQNDHVLAYNDVHHAVALLGAGDKEGYARLMSSLNGFAQGGNEQQAKI
GNRKMTAEVAEPLCKAFAAYRDKDYEKATSLLLPLVADPEATPLVHSFVGIGGSNAQRDLFAQLFLWSLGQSNPQGD
RKHLLDVLAYHRSEAKGGSSPLTQRMIHRLLIAPFTDDDDITSLSRVRG

>B152_uncharacterized_conserved_protein,_C-terminal_pleckstrin_homology_(PH)_domain
MFKRSATATPSSPLPATPTSPRGSSATPSFREVATVQAAAPLIPYDSSFQNENEKANLLLKRTLVWDKLIDAVYPWV
KQMQKVEANSAKSYAKLTPLIQFQDEVAAGTGDLAKSLDSLREFSTSVMSYHEQFSKYLKEQTLPKLDALQSEIKKH
GKQMNKKIEKAGIKLKKCEEEAVAAMLAHQKICQEMKTTPNLTTVDPWLTEYRVKGKLAVLVAEHNEYKQRMLEVTE
KIVGMDEQVARTIQDAFLQLAKWRAKQLTSLKADVDELGVAMARIMPEADFQQYSNKTGLARHIEHWKQPGGVQAID
YPFRDTELAKVVRAGTLQRQGKVMKSRWHSAQCLLTHSAFLHCFDNYEAAQKDTENPLFSIDLKQCTIQLTSDEQAS
ANCFEITSGNKDRWFIKASDEETMVDWMIAMRKVKADMQALANPPFSPEIVQQFSPVLASAAPPLPAKPSSSTYDAT
PAPPTPASPPLTGEEEEDFYNSALSSSAGGDVYQGGYLHESGDYYAQEDYHGGGDDDHQNYGGGGDGNNDQAW

>B153_polyglutamate_biosynthesis_protein_(MPP_CapA_specific_hit)
MRSAWRNLVSRLATLRLSRIAAAGLHRGHSSPALLPGSSQRTVSREMSDTATATTATTDRAADNELQFTLVGDTMLG
RLVDQFFPTHIETASEDSLHASFWKQRHADIAEKYQSMGHKFVWGNTLDFFLNSDVNIINLETSITTNTEKDPKEFN
YQMHPDNVKALLEARVHYCSLANNHTLDFKVKGMFDTMKHLTDAGLAWAGVGKNRDEAYRPALLRIKDTNIACYSFS
DHYQRWAAGPNRPGINYLDPEQCTDADIQKLKDNIDALRADIQRKGEDLDVVVLSYHWGSNYSWRPPKEFQRLAHRV
IDECGVTLIHGHSAHHVQGIEVYHGIPIIYGCGDFVDDYAVDSAYRNNLGFVYRLRWDKLNKQWTDFRLHPTKIAFF
SVSTRMWPSERQWLVDKVTVLSQEMGTQVSLIPPSEPEADESEAFLRVALPT

>B154_ATP-binding_cassette_(ABC)_family_protein
MSRLLKARGGASLPALHYSAALPSLWRGVPRVGRAAPSLCSRRLTTTNSGAASHSSVAGSKGTPWKFVLFSDLHVSA
ATIDRCIATLGLIRDLSREERAPVVFLGDFWHHRHSLQVRHVDRLLQEFQQWSDEGVRATLIPGNHDQVSVDGLVHG
ISMFGLFPNISIATRPIYDASNRLAFLPWREDSAEQQRQFVHVSELEPLVDSSSSEQTPGWTIFAHAEVGGAVANGG
HIASGRISRAQIEQVARACYVGHYHKRQLIGDRIWYVGSPFEQNFGEMNEPHGVAVVSSESIVPRFVNFEQMPKHWK
FSFPADFQFNAAENGAVEQPTSAMRPFELVRPHDIVEVSSSHEGMRTEAFERAMAELTEKEVLLRRIVKRKTDGGGV
DRAAHTVPASDSTTTPNVAAEGYSSQMLDHFVQEYIDITKKEVDHPDRSALVDFARTALSEVAHQPNTIRPIGKVVS
FKSLSVEDFCAIKGRADLDFTTTGMALLRGPMGVGKTSLGDALTWCLYGNTTPRKPGTAAASLRGDEVIHDDAKEVS
VTLHLEVDGKPLSVSRSKRKGAGAKVKIEGIEEPEGVRDQQMLVNNIVGLDFDMWRMCVYLGQGAVSNFVTDADKRR
KELLSRTLNLGACTLAQKTAKDQKKKLEMEMEKTKIELAKAMAAHETWTKIDYDEQARAWVEENRKAVESAEAKATE
LQQQLDNVKTMEGKEEKEWMDKKQSVQVAINQMNKVINDVAAKHQTTISLLSKRLGQLQAEQLASAKEKKKMEDEIH
RRHPHSSPAQNQETTTAAVDTCNTCGQPISSEIKDRLVADLRQKVAERESLVARLAEELKAVDAEMAAEKRDYAERR
QAGEKDLDQLHRQSTECAEKLTIAANMRNNRKNVERALSEAAAQMKKLNTARNPFEEQKAEKDTKVRTLLQSMAHIK
STMDSTDQQLRVAEFWDTGFGPKGIPVTALSAVLHELEDYANHFLSILLQGKINCTLSMEGDDLQIDFHEFDQVSGK
LRSRSFTQLSGGQRRCAELAFSPFALSEMVFNRSGVRIPFLIVDEMTTHLDPATKPLVCEVLRRLGKETVLVIDHDP
SVQGEFDRILDLARDPHTGRLLIAPESADAGTDAAVAAVAL

>B155_selenoprotein_O
MRGGGQRLLASTTPSTARTYAARFTHQHRPSPALRRVGQCVLQLRGRSMEPMESSPAMRRQGTATSAAGASHQSTAS
DGPKRTLETLQFDNLALRTLPIDPVLENFPRKVPNACFSRVMPTPVKDPFTVAASLPALALIDLDPAETERPEFAQY
LSGNKVLPGAEPAAHCYCGHQFGYFSGQLGDGATMYLGEVVNSKGERWEIQFKGAGKTPYSRTADGRKVLRSSLREF
LCSEAMHYLGVPTTRAGSVVSSDTHVVRDIFYNGNPKKERATIILRIAPSFLRFGSFEIFKPRDPETQREGPSVKNV
KLLFKLLDYTVETFYPDIWRSTTDPEVRYLSFYQEVVRRTARLVAEWQSVGFCHGVLNTDNMSILGLTIDYGPYGFL
DFYDPDFICNGSDDGGRYSYKNQPEMCHWNCKKLAEALAMAIPLTDSERELERIYWPEYNKHYNQKMRNKLGLLQKE
EEGDEQLVKSFFDAMHESGADFTNSFRGLARVALPSPSETIAEKDEAEDEALAYLLQQVCSAAFMSKRDGPSIPMET
LQMMISVAQQNPMMLQMFGMTPQKLIREINKLKKQEERGSGAGNVDSAKRENDTLIWKAWLKKYRERLQREVSGASD
DEIRELNERRVQTMNRNNPKFALRNYIAQNAIEKAENGDFSETERLLTRALYHPYDEQNDTELSEKFAYDAIPPQWA
AELCVT

>B156_MORN_repeat-containing_protein_(possible_2-isopropylmalate_synthase)
MKRVAARWQMTSAMRLRPASHGCLLRSTSLTAPGGTLRCSFPASILSSSTRRYSRRGSKEDHMKGVPSLDDLEQRWE
REIQRTGGLPPTEEQQQTAAAQNRPGMRFDMDSSSLTYDDSGTANGLFTSEHITYVGQVDRSGCPHGMGRFTDDEQH
IEYLGEWRAGHWHGWGKLVQANGDVLEGQWDRGVFSGEGRLSQTEGGIYDGQWQYNRPCGEGRYVLPDGTVYSGIWG
RERDFADPFESEKPTSSTAGSPRSAIAGADGSEEMGAPEAEIGIGTIRYPNRAYYDGEWRNLRPHGTGKLRLDDGSE
YKGEFEDGLFHGKGRLRYANKGEYEGEWRNGRKQGQGRMLHPDGKVEIGHWKRDRLVEPAQDKETYVDATQSWLMPD
RHKPASVRGVPDAEVIGPSEPRGKWAGRYSGTGKKPFGDIYADDMD

>B157*_hypothetical_protein_Orf83

MFKFVRDFFENKQSFNIKTFAIWLNSSIKNRAIFVYSMATFSILVRYVYIPFTTIIGYLILLRFTRHFFPTVVLQFA
YSFLVF

>B158*_hypothetical_protein_Orf115
MNGAGNVISESTTGSGLGKKILDKASRVASNSFNYVTDSKNTFTIIRGLVLAGGVIASADYASAEGSHRTTYVTRAF
EVHENGTCSPDPDTRLKAAALRRRGLIYLIVVNQKPAV

>B159*_hypothetical_protein_Orf349
MISPIILISVPVITIISLATAYFFAPDIDPALTLLYPDIPVRRIWPMVFDENRDELSPYELRCFLSNVHRTELGHFT
CNVKYPILAINSFDDVALFTKNYVAACGKSINVNPEGQFSFSWPTTYHNDKNSVHVFSFTGIREILTEGDLTEEDQI
VVDWFNSWAKDNPWWTYLFVSPDDPGNSDGSPSCIKITYFTHQVYTPEPGGVGCDGLVYDTTRLRAQYPEPVMYSTA
DVLNQPPFTVSKEGLFPRLCLIELLKSAIPDYHIGVIHSYSTFYTTLVHPVNNLPPQDFISVHLEGAGSYKDFNPGP
LSSSAGNPADSISSVFPKILIFVACATTLALCTYLGYNYIG

>B160*_rnl_I1-encoded_Orf142_(putative_LAGLIDADG_homing_endonuclease)
MKIDKNWIVGFVDGEGCFYIGINKSVDSKLGYQVLPEFRVVQHKRDIKVLYAIKDFFGHGSVVCNKSNGSEIYEYRV
RKFETLHDVILPFFESNGLLTSKKFNFLAFRDVILIMKRREHLTESGLSKIIDIKSRMNRSSIHY

>B161*_rnl_I3-encoded_Orf164_(putative_LAGLIDADG_homing_endonuclease)
MQKNQFKKLNNEQLAYLAGFVEADGCFLVQIIPGLQYRYKHTIRISIVFYQKKDKHWYFLQLKNLIGLGSIRFRNDG
MLEYSITGLSLVNKFLEMLFPYLILKKNLAVLIFRIIKGLNDVKNEAGFLEVCKLVDEVADHTYSKKRKNTSLTVKN
SLLLPVETEE

>B162*_rnl_I2-encoded_Orf168_(putative_LAGLIDADG_homing_endonuclease)
MKNLDLKQEKALIDPFWISGFVDGEGCFCISFNLKERLTLGIEVRPSFSISQTRDKEGLNLRCLQDFLNFFDCGFIR
FSKRDNTWKYECRDLSDIRSKVLPHFEKFTLRTKKLRDFELFKDVVNSVASKQHLNEVGLKRIIDISYQINMGKRKL
TKDELLSKINLKNL

>B163_Nudix_Hydrolase_domain-containing_protein
MRASNATRAHPRSARGGLRTHATSASQSLKRAATVLVVAPTLRSSATHQDDYRVLMVKRAAKSRFMAGAHVFPGGIL
EDGDSDPRWRDIVPSGKEIDAGELAWRLAGVREVFEECGLLISRPPLSSSPPEAKKWRERSAQDSTHFLRMFTDRES
DDNAGLRHHIPDTEALVPWAHWVTPLEEKWRYDTRFYLSVLPQPYDHAQTDAREVTHLDWFAPTEALRAFDEGTISL
PPPTWFMLKELTNYPSLASLREATTRGRDLTPVQPSLVPTDEGLVIAMSGDRLHWASRGSVAARGFNRMLVPLPSPR
QAEAGPGRQSYALIVDPNPPLSASL

>B164_DUF543_domain-
containing_protein_(likely_mitochondrial_inner_membrane_organizing_system_pro
tein)
MRNRSIARTEFTFKMAEQQVQRSLPRELDAGVKLDRAIERFLIYTPIGATVGLGLSFLFQRRFLKATVFGFSTGTAF
GMAWGDSKWDCAHPSALHGQRLWRATATKQSSPRE

>B165_translational_GTPase_Obg/CgtA
MVMRTSHRWGGVGVQTLLQGTRAQRATVLLMGRSTAEAAKGMGLPRLYASGYPTASTRRGEDPVWLRPDKPTTESKK
KQHDNKNRFIDRIRVRVKAGDGGNGCVAFFRDNRVTEGPPEGGDGGPGGDVIVMATSEERNLGNVGGSVRAESGRPG
GSNMHGKTGELFTIKVPVGTVVKQLPLQRDTGEEVVVLADLEKDGDSITVAKGGKGGKGNRHFKSSTHRSPKFAQDG
EAGEEKMVELELKLLAQIGLVGFPNAGKSTMLNAISRARSKIASYAFTTLFPMLGVVEFDDYTRMTVADLPGIIDGA
HENRGLGLAFLRHIERTKVLCYVLDFSGKGTDQAVEQYEALRFELECYQPGMTSRPSVVAANKMDLPNSQANFDYFQ
AYLKDKGIQTPSFAVSAETGQGLEELLLTLRRQVLSSPLQKPQQQPTSTTTPSISAQ

>B166_peptide_chain_release_factor_C12orf65_homolog
MRRLTRLPGGGAWLRPGVPDYRSTMYHSSTWLPSCSRLGRLGRAWASSSSSSSSGSSPSFSEERER EVDDEGEEDDS
GWFGERGQQREKPQAPAAKPRSLFEKTRQVAESELEEKFIKGGGPGGQKINKTNSCVYLKHLPTGLEVKCQEQRERG
RNRVIARRILHEKLMQLYFPEDSKTFKRQEKIRRRKQRMGRRYGRNETLLPVSTTTTDSDDGDDVAYEPSTDGPRQT
TTSAAAADIAQSSSAGQDGAGEVVVEKKTKRRRTVDPASLPDFVWKQLGIRRSSVVECTEFDPEDFSTDGEEEEEDE
DEDEDEDEDGDEAGDNAQPRPAEKPMTDF**VLEQLGIKPDQGKK**

>B167_mitochondrial_argininyl-tRNA_synthetase_(ArgRS)

MRRWRGVVTGSRWPGALTSPARGHSALITLPLPAAKPLSALPVAAGRQSIFFIASTTITRQRTPQRLAHMRCTFHTT
SDGSTRSLQHIMEASQHTADPFYKFKWAIAEQVASLTDMKPEQALSAVEIPKKEGVADFALCVAKLNRYTKLKGKPQ
DVAVEWAGKFTATPLLTSAKADGPYINYVVDKIPLAEEVLKIVYGSNDQWGNSADGNGRTIVVEYSSPNIAKPFHFG
HLRSTMIGNFLRNLYKALGYNVVGINYLGDWGKQYGLLAVGFSKYGSEEELVKNPIRHLYDVYVQINKEADDNEEVG
KVIHDQARSYFRKMEDGDPDALALWKRFRDLSIDEYKLLYKRLNVEFDVYSGESMFSEGMVEAVNLMQEKGLLQEDN
GALVCDLTKYKLGKIVIKKSDGTTLYITRDIAAAIWRHRTYGFEKMFYVVGSQQNLHFQQLFKILDLMGFDWAKKCN
HINFGMITGMSTRKGTAKFLSDILEAAQEQMLDRMKANEAKMSEITDPEKTADVVGVSAVVVQDFSAKRVKDYGFNL
ERATAAEGDTGPYLQYAHARLSSMERKNDVKISDAINFQLLNDKEALDLMMKLARLPEVVRRTSEENEPCTLVTYLM
DLCHSISAAHRVLWVMGREQDVAEARMLLFWAARKTLENGLKILGLAPLQRM

>B168_mitochondrial_cysteinyl-tRNA_synthetase_(CysRS)
MARRGGASILSSYGWGSRACSQLSTDGPLQALLTSSRRRFSSSLPNSPASSWTRPHGKETGVRIWNSLTSSEVPLIS
TSATNTLSWYTCGPTVYDVSHLGHARTYVTVDIILRALREYFGVHAWHVLNITDVDDKIIKRSNEAGVPALELSQKF
EREFFRDLTALGVEPPSTVLRVSEHIDEVVQFIRKLESDGVAYATPSGVYFDTLRFSGSHSFKMAPAFEDGLEESGD
EVGSRDKRNVRDFALWKAAKEGEPSWASPWGAGRPGWHIECSAMCSSLFGSHLDVHAGGIDLKFPHHCNEVAQCEAF
HGSQQWGNYFIHVGHLHIAGLKMSKSLKNFVSIQDYLKKYTGRQFRIFCLLHGYGKPVDYSEEHMQHSVLPVEKRLD
DFLALTYARMRQAGASRDVNNLKWGEAEKALQQDVLTCEHKVKESLARNIDTEDALTSVLDLVTRGHAYLQASSAPR
TELLASLSRAVSRPLRVFGVLPQAGGEGGDGAAESKEAEILDTLARFRHQVRKTAISSANVKKDVLSLCDQLRDKDL
PAVGFRLEDDPKAGSLWKRAPGGGGVQ

>B169_mitochondrial_glycyl-tRNA_synthetase_(GlyRS)
MRRLSPRSSSPLPLMSFLRHTNRRQTGACILHLSTASTPSLQERVVSLCKRRGFVFPNSEIYGGLTGSFDFGPLGAQ
LKKNIRDLWWRDFVQHRKDCVGIDTPIIINTEVWKAAGHIENFHDLLVECKVCHQRFRADKLVEEHGVEGAGTLSAT
QLEHTIKERDLKPSQCTQKAKPCTYTDVRAFNLMFKTSVGATTVGNDVYLRPETAQGIFVNFQQVYNSMRRRLPFGI
GQFGKSFRNEVSPGNFLFRQREFEQMELEYFCDPAEADQWFGYWVDYCHAWLLKYGIKPENLHLRQHDPKELAHYAK
ATTDIEYRFPFGWGEIWGIANRGDFDLQQHMKHSQKDLRHKDIVTGKVTMPYVIEPAVGLDRILLAFLTDAYDEETN
VPTAKDKAKPGEAEGDTRVVLRLHEDLAPYKFAVLPLMKKEQLASAAKDVYDALVTKAATDYDDTATIGKRYRRQDE
IGTPFCITIDFDTLQDKTVTLRWRDSMKQRRVAIAQLLDRCHDPQWLRQQEQAGEDDETVGAFLR

>B170_mitochondrial_histidyl-tRNA_synthetase_(HisRS)
MKMWRGGRLVCTSGAWSGVAAYAVGWSGCHGGAALAGPLWLQRRYVSSAAAVATGPVGGAPRGTHDIEGGELAAHRF
IVDTARRVASRYAFEEVQTPMFETTQVFQRSLGGDSDVVMKEMYTFDDKGGNSLTLRPEGTAGVVRAFVSKKDFGDL
PRRYFYSGPMFRYERPQKGRLRQFHQVGVENLGPSTPDTVAEVIQAAASFLSSLRLDSSAKLEVNSLGDAESRERYR
TALREYLSTQRTFLSADSVLRLDRGSELRVLDSKDASDQQVVRAAECPVLVDYLSEQSRDHFQQVCGLLTQLDLSFV
VNPRLVRGLDYYGQTVFEFVGQPGPQLGPQQATLLAGGVYDSLVSTFGGPAISGVGWAAGVERLALVLDRTLVPTPP
RPLYVLLVATDDLAPADDTISHLNKPAPAPALVGYAMRVSEQLRRDGFVVVQKVDGSEGSGGKLRKWMKKAVKANAA
AAVFVGADELAANAVTLKLLDTGDQRTVALPQLADALHQHRPSAPTFL

>B171_mitochondrial_lysyl-tRNA_synthetase_(LysRS)
MRMSRTRGLSPMVPMHMWMPSSLGRSASAQLRTTTAHLPQQSVFSASTPLGLLLNRRPALHHQSRHFSAPASVPPQG
GSVATEATGGALYTETRRQALRSAAEVLGTPAYPHYTAARRHTLPEVVARFGGLQPSQSMEEVSVQVTGRLMSKRRS
GQKLVFYDLEGQGGHLQLMALANKHQPTPGGKLSAEEEFRFVHHDLLRRGDLVVVDGYPTRTKSGELSIVPRSVQLA
SPCLHQLPEPNSFTNPESRQRKRHVDLLVNGHVKNTFMLRSKVIKFIRSFLDQRDFLEVETPVLCSMVGGANALPFA
TRSEALDAPLFLRIAPELHLKQLVVGGLERVYEIGKCFRNEGIDATHNPEFTTCEFYMAWANYQDLLTLTETMLYDL
AREVGGSPKVTLDVAGRGEVEIDFTPPFRVISIPDRLREAVHPLPLPDLNSHDSAPALLEICKQLGVDAPAPHTTAR
LVDKLIGHFIEPDLMQPTFLVDHPHIMSPLAKQHPTKEGMTARFELFVAGKEVCNSYTELNDPTEQRARFQAQAEAR
KLGDGEAQMVDEPFCEALEYGLPPTAGWGIGIDRLVMFLSRTHHIRDVQLFSVVKENKVGKKEADDGAATSAVPPSP
ASS

>B172_mitochondrial_methionyl-tRNA_synthetase_(MetRS)
**MRKATSRYAAVLAPSPSSSTGYALRWAAPSSLPLSPSPAITPLSRLNGLIRFRSGARVPSSSSWLRTCEPSRGAVAA
CIHYRSLQTSTSASSNKPVMVTTPIFYVNGSPHIGHLYSALVADALARWHRMLGASTLFV**TGTDEHGLKIQEAAKGK
GKTPAQFCDEVSEEFRSLMVQADISNDQFIRTTEERHKKAVHALWKLLEDRGYIYKGKYEGWYCVSDEAFLTPVQVA
DGVDKQGNPCKVSLESGHVVEWVVEENYKFKLSAFQKPLLRWLENTDQGGSVIPRVRANELFGLLRERELQDLSISR
IGSRIKWGIPVPSDDGHTIYVWLDALTNYLTAAGFPWDGEASAAMSVPPSSAWPADYHIIGKDIIRFHTIYWIAFLM
AAELPLPKKIVAHAHWTVNRHKMSKSLGNVVTPNEIIGKYGLDPVRYFLLRDGGMVDDGDFSHETLVSKLNNDLADT

LGNLFARLTAPSLNPAGLVPACGDLTADDQAFVDRMQRLPDRVSEHYTNVEFGPGISAIFEILYDANKYLQDNEPWK
LRKTDPRRCETVLYVALEAARLSALLLQPIMPRSAAKMLDMLGVAADERSAQALTYGRQPGAKLVKEILFTKVK

>B173_mitochondrial_tyrosyl-tRNA_synthetase_(TyrRS)
MKRLGLCGHARSGALRWRRSSHASNPFSLCNVGSAVQPLASSSCSGRQFHDVVKSLEERGFIYQTTFSSAAPAGASP
TSAAAGEGKGSVYVGFDPTAESLHVGNLLGLLALLHFQRAGHRPIALVGGATGRIGDPSGRATERALLDEATLERNV
RGIESCLRQLDTEGGPAFEIVNNFDWYRGMNVLSFLRDVGKHFRLGTMLAKESVRSRMDRDDNEGMSFTEFSYQVLQ
GYDFLNLYRTEGCRLQLGGSDQWGNITAGCDLIRKVEGVEAHGVTIPLLTTSTGEEVGKSAGNAAVWLCPTRTSHYE
FYQYFRNTRDADLRRFLKLFTLLPLPRIEEIAQAHDLRPEEHAGQKVLAEEVTRLVRGEQGLHTALKATRVMFGDEP
VDSLPPSELLAVLKDVPSVTLPRSSVVGQPLSGLMVACRATASKGEARRLVKGGGVYVNSKRVPNDDYQVGPDDVLG
DALCVLRVGKKSYFLVKLTPQ

>B174_mitochondrial_small_subunit_ribosomal_protein_S23
MVHAGKGGGRMFVNAARINGRKSNFSLLEYIQSEVRAGESPVPPWMPATLISPPPTIPNVPHPGPLTYPEDKLRQVW
FDRHPEARKIKLKTVYVGEHRYWQHPATSFVHRQSKLIKKGYSEQDAYDVVEAEDKKAARYRELERLMAIEQAKELG
FDDLETARDLLAPPDLTQARERMLEELIDVLKAKGVPNVVPELLPKGMKWRDVLAFVHKYPQHAHFFSLGFMATHAI
ETMNPEIADAYNWIYGGEVLLDDDSVPLEEQEELNAFLDEEGFETVEDGDELDQQDLREQERLTSEAVAQYEPVVAG
ASLVEEGLFFDEDEGEDEDESEAAREEEHDEEQRIAMVKKEGEQFKAILKRIEKIYRPEQFPTTADTPWADLVNLLA
LRPQAPDVKLAQDAEQKLRKANQVKRPSGGSSRPQSQQPNKPTKGKEVELQ

>B175_mitochondrial_small_subunit_ribosomal_protein_Ppe1_(YmS2)
MQRELFKGKGAMGPPAPKQASAGTSGSPSQDDAEISSDKWAADLGWDRFFASCQDVAIPNTNDVFRVYFSGPDEGPL
FVLLHGGGHSALSWAATVGALQQTARVLAFDFRGHGHTHTSDDSDLSIETLTSDVITLIRTLYSASPSSPIILVGHS
LGGSVAIHTAISGQIKELSGLIVLDVVEGTAMASLNYMDTYLAKVPSSFPTLEQAIQWTVRSGSVHNLDSARVSVPP
RLVRDESTGHYAWRTNLNLTKHYWEGWYQGLSKKFLSCPAAKVLVLAGTDRLDTELMIGQMQGKFRVVVLADCGHCI
QEDNPDKTAEILLDLKKRYDIIHSKNNTIPRLHE

>B176_putative_SDH_assembly_factor_2_(COG2938,_Sdh5_superfamily)
MRRSSVASAHIISAVRFAPVSRGLILPTSARLLSTSSASSSSSPNFTNQLPTYDDVKYSQLDSRRKRLLFRSKERGM
LETDLILGSFAIQNLEAMNETQLAQFEQILDCIDPDLFLYLTKKVETPAELDNEVMHAIQKHTFNNPLNYDSTANRK
LN

>B177_Complex1_LYR_1_domain-containing_protein
MASMAQRLGTHSVHSVEALRLYREILRTLRRFDDRATRIYYYNYARTHFMQHQEEEDEERVQEIIERGKNDLRWLKA
KYGLDDQEKEEDY

>B178_Complex1_LYR_1_domain-containing_protein
MKRSAAMMGGASSRAAVRDLYKRVVRLGNTWEARNPAQTPKEREYILEEARTLFHQHMYETDPQEVQRLLQEAEGRV
EIAEHYGIPYQRTSNLPPGTSADDYRRGQISFGEAPRYHTPSHPLFDD

>B179_Complex1_LYR_1_domain-containing_protein
MSRVGVSAKAARTEALRLYRDVLRACRLFDTTRNEQGQLMSDVLRTSARKEFEGAREERDPETVARMIITGRDCVMQ
IHDMVAKKQHELMTGEKEPPATQ

>B180_sulfite_oxidase
MRLRTAFRHAASSAAPACSSSSRLSSSILLSSSRRPLLGSRIRPFTSTTATPSTKPSALRRVVTRGGAMAAGVVTGG
IAYYAFMSEDVHASVQKEEEEEEVAAAGELVDGLPEYTKADVKKHNSISTGIWVIYKNGVYDITQFVESHPGGNKIL
LAAGSTIEPFWALYGVHKSNQVYKMLEEHRIGNLAKADREAAANAPVGEGPYAHDPERLPVLIVRSAQPFNGETPGE
LLPASFNTPNNLFYVRNHLPVPVIDSKEYQLEVAIEGTEKKIQLSLDDLKEKFTQYTVTAAIQCTGNRRNEMKSVKD
VKGLDWDKGAIGNATWTGVRLRDVLAYAGLADDGGDLEHVHFEGLDRDMVQTYGVSIPMAKAIDPRGDVILAFEMNG
EPLPRDHGYPVRVVVPGITGARSVKWVGKILASKEESTSHWQQKDYKSFSPSADWDKVDWSSAPAIHDTPVQSAICE
PKEGAILPEGEEEITAKGFAYAGGGRAIIRVDLSADGGKTWHTAKLLQDPKQKQQYNRMWAWTLWEANVPVPVEAKE
SDTVELICKATDSSYNDQPESAAPIWNLRGVLMHSWHRVTLRKEESLDSDAPQQ

>B181_glutamyl-tRNA_(Gln)_amidotransferase,_B_subunit_(GatB/YqeY)
MHRRLLVAAPRGGRAAAAAPNAASAGGGAAPLARHSGASGFPPRRCLATTTASSSRLKHHPAGWEVVVGLELHAQIL
SQSKLFSGARAQFGGASNAQVALFDAAYPGTLPALNEECVRQAVRVGLALGGQVNLRSRFDRKHYFYCDMPSGYQIT

QNTHPIVTGGHLTIFPFDESRRRSIALHRVQLEQDSGKSYHDQHPLNTLVDLNRAGFALLEIISQPDLCSGEEAVEY
LQKMQMLLHCVGASDPRLMDKSSLRCDVNVSVNRVGGPRGTRCEVKNVNSLKQIQRAIEYETERQIELLEGGGVIEQ
ETRYFDPHLDRTVRLRSKEDEVDYRYFPEPDLPPLVIEEGLVEQIRAELPELPDDKCRRLVADYDLPLYDAQVLVDT
YGATHFFEQAVREGRRQGSQSSSSEEPKKREEEEEEEAKGSTKLHRMMASWVTSELFGRLASAGKSVEESPVTPGQV
SSIVGLIHAGTISRATGKQVLDLMALGDSRLAPDIVQAKGWQLTHDASALEQLVLQVVGTYPNDVARYRSGEVKLKR
FFVGEVMKASKGRADPKTINQLLEQHLAADHHPQ

>B182_tRNA_modification_GTPase_TrmE
MRAVRGRAAPSSYCASSLCARDARPKGPHLRLAHRTNLAPLLTSMRACSTSGLVPPRRCGLSPVSLRSLLHFSPSSS
SSLRGSRHYSGGFHYGGQSGESIFALGTSPAGKSGVAVVRISGERAGAAVRQLTRAQELPPPRLASLRKLYHRDELL
DEGLVLWFPGPRSFTGEDMAELHIHGSHAAITAVLNALGKLPGMRSAEPGEFTKRAFQNGKMDLTEAEGLADLIDAE
TEAQRKQALRQMGGALGRLCNEWREELIKCIAHVEAVIDFGEDEHIDHEVAAAVQPRIKRLHDMIALHLSDSHRGER
MRSGASLAIVGPPNAGKSSLLNLLARRKAAIVSSIPGTTRDVIEVSLDLAGYPLTIADTAGIRHSEDEIEKEGVALA
RERFASSDIKICLFDGTTYPSLEPDLLSLVDTSTLVVLNKKDLLTSAPASVRLADGTQRRVITISCKNYEGLEDLTK
ALESQVKSFFESGAAPDGAVVTRARHREHLERSLQHLRTYLDMAEEASASREARMSIDMAAEELRRGLAELGRITGR
VDLDEILDVIFSDFCIGK

>B183_mitochondrial_alanyl-tRNA_editing_protein_Aarsd1
MLPTTARASRRTFFAPFTSTSRRRFATLMTTSASSHVDPLVLACQRDSYTRELQTRVKAHQPTEGGVLVEFEDSILF
PEGGGQPSDAGTVDGVPVGQVFRHADGRVLHALPSVPADPSKVVLSVDWGRRFDHMQQHTAQHLISALAMSRFNADT
ASWSLGKELCTIDFNVPKISQEDLGRLEELVNEEIRQAKPVRCHEVRTDEDKAALPEAVRSRGLPTNLGVIRLIEIS
GVDMNTCCGTHVSNLSELQMIKFVGTEPKKGMVRVSFLAGNRLSRAVSTWSEREKKLNITLQCAATEHVAAATRINN
DIKALTQQKRKLMKDLAVFVGQSAVKEGHKLVDVHRDDVDMSFLQTTAKAAQDAARAAASELVLFLSFSEGEGGQFI
LQGPQALVAETGKQVAELLQGKGGGRGNTFQGRAGSFKRRNEVVELLRAQLRSSS

>B184_SpoU_class_RNA_methyltransferase
MKRTATIALLRPRADRVWASARQTMCGTSKSGWWTTTRSVFTHAPPADEAEGSLEMQRHKPPVPLLRPREVVVACVP
LKSNVNVSAIARTCSCLQVRQLVCCGTAKLLNKVARDAVLLQDSAKDNKSGDAEGSASSGSWFKVVNTLRHPLLRFK
EEGYEVVGLEQTAASTSLYDFRFARKTVLVIGSENKGIPPDILAVCDRVVEIPLNGPPHSLNVASAAAIGLYEYCRQ
HPS

>B185_ribonuclease_T2_superfamily_protein
MKVSLFVLSRVGPRSSASASSTSGPPLSVTPSDSPKPPDCVLFSSPSPHHFHHLHQAPSIRPSYRSFSRRKHTTKKQ
TLGDMKVVGLAVALVAVLVVMSCLAPNSGAEAQSTSWDFLLLVQQWGPGVCATSRGKQCVIPSYVRYWTLHGMWPNN
FDGSYPANCPDSESFNMQRLEPIRKSLTAYWPTLYPSNTLESFWEHEFEKHGTCAASDPTLATELAYFNATLTARAT
FDISVAFSKAGIQPSSNKAYSIDTISKAIQSAYGGVPLVQCSRESSRARGPEALTSIGFCISSSLTIIDCPTNIIHK
EGCHNYDDGVYFLPF

>B186_uracil-DNA_glycosylase_
MRARTLGVTQRTSFGSLPLLSVHCARPTSHLLIARKFISTRAGTSHRLGHLIITPRNSTTGLWHCNMSTPQKKQASL
LAFFGSRGSSSSSPSSDAAPSSSSTTSSASSPAKRKLPSSFSSGELSSPSTAEPPKKQTRPTELQPQVKHLIAGLHE
PAWRRVLANEFTEGYFVQLAKFLEQERQTKTIYPPPEHVFSQLNLCPFDEVKVVILGQDPYHGPGQAHGLAFSVALG
VTPPPSLKNIFKELENDPEVDFTKPDHGNLEKWARQGVLLLNAVLTVEARKPNSHKDKGWERFTDAIIKAVNDKREG
VVFMLWGKYAQDKGKIISKRKHHVLTSAHPSPFAAHNFFGNKHFSTANNLLKQRTLTGESKKPIEWQLDPKDVEREN
QRRWLEEREAEWTHEEQEEEEKGSSDHDQPSPAPQEEDDEKDSGEEEEDEAA

>B187_DNA-3-methyladenine_glycosylase
MKQQAKLTTFLRTAASPLRNKTAACSPNRSLAASTKSTEEDIPWPEIDLTSDPTSTSSTTATTPTSPYAPLKRKPDS
TSSAGTQKIELQLPSPKRAKKETLPLLESKQPDSLEDIEEFEEVPEKMKEPMPDFTDEELIAISEQIERGKSAGAPS
QACTTSSTSSSSSPSPQHPFFARGGRGKRWGKEFYEHDCETLAKMLLGQVLVRVTSDKQRLAGRIVETEAYLGGEDK
GAHSYGGKITNKNKSMFEPPGTAYIYKIYVTNFCFNVSSLGAGAAVLVRALEPVEGLARMRTNRMAGKISGAPMRDA
DLTSGPGKTCQALELNLAEDGLDLVTSEELWIEEGRKIDERNIVAGPRINIDYAEEWKDKPLRFHVKGNPHVSKPAF
SNNKSPFRGGKKV

>B188_S-adenosyl-L-methionine-dependent_methyltransferase_superfamily_protein
MRRAVRGLAPTRSTNLLGLEALQRCTTRGTALRFNKASTTANESAARPGCGVGRSEDMERLRAAQAKMEKVVAEKPQ
GEAWDTLWKDKVTPWEAKKPAPPLVELLETTRHVSDTAKVLVPGCGSAHDVVALAGKARYVVGLDISETAAQIARKN

LEEHGLSEDKAVIRVADFFTFGEGPFDVIYDYTFLAALPPSMRQDWASGTNRLLAKNGKLITLIFPLGEFEGGPPYA
MSYSLVEGLLKPFGFEAIESGPAKVSHAARQGREWVAVWQKKQAAGRL

>B189_TatD-related_DNAse
MRRVRCSPRVHIFLPQRCLSRPTLLNCEYSTKSRFVKKMEPRFLFDTHSHAHDDLAHLDDIPELDVDKVALMGTSQN
DWGVVERLHRAKPDKVLAAFGVHPYFAHRLAEGWLEELREKLVANPRAIVGEIGLDKAAITPDTARNEYDAQTTAFT
AQFDLAVELQRPISFHCVRAFGHVMTLFRQHALRYDQLMRSGEEDKARGTLPPAIIMHSFAGTVGGMESLLSNKGRK
GNIQERLYFSFSKIVNMRAPKTIDVIKAVPEDRLLIESDQHSPAHGEEDLSRVCEIVAEARGWSVEQTARITHANAT
RVFSFIA

>B190_>B190_endoribonuclease_L-PSP-/UK114-
like_protein_(YjgF_YER057c_UK114_family_member)
MKRTLHVARTSVLPISSRGASCGAKMLATRATAPAEKKPRAKRTSASLPKQAAGHHQVVSTALAPAAIGPYSQAVVA
TGPFLFVSGCIGLHPQTMDFTGADVSTQTEQVMQNMGAILEAGGSSFAEVVKCTILLTDMQHFATVNDIYAKYFPRD
PPARATFATNGLPKGALVEIECIASLAQKTTRTRKAGTTSGRGKAKQEP

>B191_pseudouridine_synthase,_RsuA/RluD_family_protein
MRAAVNGRRRLPIAAGTTTYARATGVPHIWQRGFNGAPARQSSVHSIPLFVSLNHLSHRSIATSAPPFTRKGAKPLP
VADDGEEDEDGESAGWRSDDEGEDDHAPLANSLQSADEKRRRLLNSKRRDINKKGVTYQGDIGPVTAGAGVQLNADD
DGEEDLVMVDGQGDHYEDDDGTEGEEALELDAADDEEDDEEEAGDEQGVPTGDRPKPKTRDRRRVVPEGDADMRLDR
WLKLQLPHLPNSLFQKLLRKRKIRVVGAAEQVVDEEGDAPTSSKRTAKLDGKRQLQVGDVITYPAYLDTLKLDAKPR
IKREMNPLSEEDTKLAQSWVIYKDSRLIALNKPPGLPVQGGSDVGDNHLGRFLSALKFDKEEVPRLVHRLDKECSGV
LIMGRSRADAAHFTSLFKNKHVTKQYWAVLAGVPNPRSGRLAVPLKELGQGMGVAANMQDEGAKMAVTRYETRADAT
NEVSFVELWPWTGRKHQLRVHCAEVLKAPILGDDKYGSREAFDRFELMLDNIDNLHLHCRSLEIPHPIKENQRLRIV
AAPPTYFRRTMDTFEFSEHDAPLPPARVTSTAGLKKKAQKEAKKAEREAQNRNKKARSAEAAAAKGKQKKKESKPKK
LHIK

>B192_tRNA_pseudouridine_synthase,_TruB-like
MMRRRAVMARGMRRAASEASFTGGLCAVYKPAGSSSFAIVARVRDILKRAEGLRPRDPADVRPRTRVPQPKVGHGGT
LDPFATGVLVLGVGDGCRLLQQYLVGPKEYVATGQLGVETDTLDTEGKEVLHRPCDHITKEMMEKTIEQFVGNIWQA
PPAYSALRVNGVRAYKLARSGQEVDIPPRQVFVHSLTLVDFSPPFFTIRVKTDGGLYVRTLVKDIGHKLDSCAYTTA
LERTQHGPFTLDMALREHQWTADALHQAIAKWRAANPTPTA

>B193_8-oxoguanine_DNA_glycosylase_family_protein_(HhH-GPD_domain-
containg_protein,_base_excision_DNA_repair_protein)
MTLLLRVSSRVPSRHRLYSTICLSSSSSGVASRASPPLRFFSAAAAPLRSTANQHHRTSLFSSAASTMEGEHVAVKA
EVQEEEQLMPDSQESTSWHRLQLDSPDELRLHLSLPSGQSFRWSTCLVDGREVWAGVIKQTAYFLHQPLDDPALVLF
RYLNSSDADRESGVEVEAKRQELEDYFQLGMRMEDAWNRWTAQREKDPPIVAHFRDACLRFRGLRTLRTDPVECLFS
FICSQNNNIARITQMVNALCTRYGDKIGEAVVQRTSDTKAETRAFYAFPTLETLAG**VPERALRDMSFGYRAKYIPTA
AQQVLDKDDPELGAGR**DWLYGLRERAVSRERAQKELTSLLGVGKKVADCVCLVSLDKLDAIPVDTHVRQIAQRFMPS
LKRKANSSLTDALYGEISSFFKDHFGANCGWAHSLLFAAELPIFRLPKRKAAKKEEDEENENENENESDNESEAAVK
VAKREKKAKREAAAAATVTTTTRRRSSRLSGKRALAVVEEEEEKEVLVVKREKKEGENGETPITSRRKKRRASVE

>B194_tRNA_nucleotidyltransferase,_putative_(polyA_polymerase_domain)
**MLRSGRWRSVPAAWYPGCLPPTLSGRAASLATTANARRWAAAFNERFCLIRRCTPLTCASASPPPSFVMPRRLAYST
TRSSSLPLRL**PGKSIAVSDEERRIFEYLVDVVKASNLNSELRVAGGWVRDKLLAAGGAAPASAPKQQEKVDLDIALN
NMMGQEFARWISRYNKHHNLPTSKIGIVRINPAKSKHLETAVVSIFGHSVDLVNLRTESYRPGSRIPTAVGLGSPKQ
DSSRRDFTINALYYNIREDRIEDYTGHGLADLEAGLLRTPDEPLATLLDDPLRVLRGVRFKAMLAFRFVPELAEAMQ
RPEVHEALRAKVSRQRVGLELNKMLRLDTEKALDALEQIAALDLHDVIFPLPPYLPSSAGQDVDVVGSSPQGQPPQR
RPLQDATGEEVIVGSWSPDLKQTALRCLREHFRLVNEAPKGTELVQALPSVSGGMPVGNGLALASAFLMPALLNNIG
ASDSSMAHATGAGDVDDVEPNGGRGEDELSYLENNRIRGHTEAVFKLGLALSSEQASCVAGVLIATKRLLPLIEKLA
AEVESGSESLPRVLHNNRVELGNWMRSIEQTTGGHAWETAARLAFVARTHLLGLPPSPGIDDGNAFVQAMKDSGLVS
LSGIPPLLSGREIMEILQVKPSPFVGEVKAKLISWQLANLDQSTKDAAIAYVKTLKPSSSS

>B195_SAP_domain-containing_protein_(putative_DNA/RNA_binding_proein)
MYKRSTQSPRAQSLHSRRRRPPLVRPERATRLRFRTQESLEEIHYIVHAPPAYHYSLDGFADEEVEENWEAEELTVP
ELRAALSKRRLLTSGRKMDLVERLSGAL**QRERTER**RQDAGTAKRRKLDDILSAQQDEMEDRLEAYNLAAPPNTTFTS

TTSTTTSTTTTTATTDDDADRDANNDTTTSSSSTTNFSFFFNSLEAESSSPPRPSSSSSSAELSSSSSSANGHGGPS
RKRKMPEEENGEQEEKEKGKEKEKGKEEKEAGEAVVSGSRFTWGAKEETDGGEDGLVSKLTRFLELVPSSSPSRA**AA**
TAQRKPELLPEDLLPAAAACSSPVIIAAAAAAASTPPTAPALPISSPPASPMRRPLKGVLKRREVKAPEDMTAGELKE
HLIAYGVAGAALKQKKAALVALLHKTIQQHSKKASA

>B196_pentatricopeptide_repeat_(PPR)_protein_AcPPR25
MKRTQSLVARLANRGVAASPCCPMLLRSNRIALSSQRAFGQKELTRYITEYVPPTEMLVDLDEEAERYYAPAPPELD
PHGSELQTSLDGGHAAQLAFERSLPPKSKASNSVVFHAQYTEEFVDLDEDLDLPPRLAPNQPVTALQ**VARLLRRFAN**
TQHTRSPAQNEELLGQVVALLDRIVVRAGVPIPPPSRSSTTTTSTTADEPELNERYAEHVVLRSNLPAGNKVINWRQ
LIEALAEVGKVDAALGLFESLEPRFRIIPNITLFLSVWKLCKDYHRTDKTLGYMDYFFSCRARSVGSDDWVSAATFN
YILSAVRDVKVTLRVVDKMKKEKVELDAGSYEQIIFNMIKQGQINTALDYVKLMKSSGLQPTLNIYASLFNGLLHHP
ADPYYTNKGFRMVKGPRSEDDPPSDMSEHHHYSFSLMLKLFDDLKTLHKPNSEIYSQLLRACAQMGEYEKAFELFEE
LKQTCPVHFSHIGSLIAACGTNWQADRALELFWTMRDRHRVDPSPACLNALLVALVRSGRYDLLEPTMDRAYEAYQL
CVWPKTVGYIIRSAVQLEDLEFSRGFLEMVAEKWPRTVDTKKVQGPVAVLEAKLAARHAAKEHHQVA

>B197_pentatricopeptide_repeat_(PPR)_protein_AcPPR26
MMKAANRFSSRLNPLPRLSSPPMVPTSRGLGQFYANRSAIHLKSRFCTSAARHPSLHLTTHTSRHGLHRLTVRRFAD
VWTSPLIEEDFYVPEHERIAVTTMPPATHPTPAALDTPRSPAPQIPVKKSKARLAPSDLTTVEKANYYMKEALKDET
PGEVVHLWKLMKRNNLIPNRDSYKLLVRAFAMEGQADEPLQLINEMDENNIQPDLDIYNGLLNCLAEAKQGSSFGIA
SILLYGVRHGLTPNATSQHLLVLAYVNAGDFRRGWRQVEVMKEKGIQPSAEVFHALLSSSMLRALPRNTIQVVEEMV
RLGIKLRKNDVQQVLDICLRNEQLDDLQNFIKHMEASNTPISEKQLTPILVFAGRRANPEFTLQLKEKYVHAGCTRH
AAHTAYESLIRSQANAIRFPEAFKTLAEMHKEGLRLRSHASRALVEAMSRDCRVIDDVYVHVEQLQSSEDVEVDPDV
MRTYLNLIIEACSQTQQFSKAFDTFAALESFGLKPDVQSFHAVLKGICSVPGHLAAVTQVYDQLAKNDLRPTAETFH
HVISAFLVNNELQNGLELLGVARDLEVNVGYDTCAMIVRKMARVQHTELLERAQQAMESLGYRPDPALESYLSRPRS
MPVDLDTLRQRRPY

>B198_pentatricopeptide_repeat_(PPR)_protein_AcPPR27]
MRNNWKRGPILYAGSQRPGPSGQSSGSLLFALPSTASSSSSPLSCLLPRRLHSPSHLAQNQPHVRSNRPSPSPKPAP
KPSSSSSSSSAAAAPYVHDERPSTNTRRGERNPNHHRRRT**TASAQHAASASVSARSTDSASVEQLKETFNRLRQRLS**
ADAGGSGKQQPWLLWDVVAAIKQLGGAMQRLKVRSGKLGGIELDVDVFPLVWRLEIDQLHRLNGLMSALSTLPGAGR
VMQDIIENLYAQNSPVKPDVRVYGKLIARYARSRQTEQAFAALDLMRAHGLHPNLRVITALLPVCTMATV**EPVFDQI**
RRHDLRPDRVFLVGTLELYARSHATDKLLELLRVMEPEFKVAPDVHIFNVALQGCVNAEDLAAGWRVREMMREFKVA
PDRASVVQLIALCS**QKQLRWDQQRQAWGRAERQRPHPYARPDPQQELMDRWLGDVFADMRRHRIVPDQTIFTALMGF**
NSPDIERAWGLFQIMLDAGVEANEVAYNVLLKRCRDLAECDRGLALWETMRASGVPPSATTFALLLQLCGRMPDAVE
GAARAQRVWDSMVHEHGRQPDHGHLGALLYACGRTGDVDAALALLDDVKLRHGVAPIEDTFTSLLDGLTAHNNNNNS
NDNDDDNEVDGDGESEERDRQYEACLRVMRRAEAEGVTPRMQKVKYTFKMSMRRDRFDEAEWLLGCMRRKGLPDAAH
QSFAASLASAKAAASVGLVTM

>B199_pentatricopeptide_repeat_(PPR)_protein_AcPPR28
MANLCGKIAARDAGRLLPICARSASPLPTCFRSRSVACSSSMRSSSSSAPSAWARPLLPFSRSSASAPYTTVSAAEE
APALSPEATAPAEEADDMVEAMDTETRPRRYPRSPAYVLAVQWEKGKITDAQFADGLTEQLIELEMSTQYRLPFAQV
AMLIQQACRTSDDICKHLLPRCLALLSRMGPAPLINYNRLISFLAKKGDLQATLMVYKRMREHKVVPDRLTLSALLG
ACSKGGNVDAAFRLFKSLIEQGIIPNTTNYNGLIGACSKNKKLDLGLSTYAEMRARGLPPDFHTFNVLIELTTGCDR
AELAARFFEEMVTEHAEMVDNASARLLAHVIRECAKAGKLDDALRVFDLACTRTRLKPDLIALSSLVNACGLAGDLD
RARKVFKDMESVYRVTPNIVTYGGLIRALATQNRLEEAIQIHKDMVGRGIAPNSTTYQCLLTGAAQDGRVDLALATL
QEMEQKGIPFNPTTLPFFINTLVGNNQSARTQAAKEMDKSDMLATTEVPVDRHRLSQALEMADTFDKKYNLWLDRAS
LHTLLRACVQTEQWPQAKQLVARAHQRRVNVDAPLLALIKAH

>B200_pentatricopeptide_repeat_(PPR)_protein_AcPPR29
MWARLRPLQQRRLLFTRSSPGGSTSSAAASAGRLISSLPPPPAAAGGGGSVSRRQGIALVAGGGGGGSRG**GGSRGGG**
GGRGKERQQQQQGKVPTATRSGQLTQQQRQGGGGGGGGGGEWPPAAAAAAGSSSHGLVDAKADADRFFDILMLPSQS
PMVSKKEELKLAEVDEDKLFRRHVRTAKRYNLLIRAQAERMGLAPIERTFENMLRHGIVPNVEIYTSMVVACAKNKD
PHAAERYLARMTEEGLEPNIWTYTALAQAYTRAGQLQDAFQVLERLKEASIRPNVVIYTSLIHGCLLADNVDRAWDT
FDHMRQREAIEPDEVTFTLMITACAQKGQVERARNVMEEMQLLQLSPTEVTYNAQIDACAQRRDYYAEAFLNLERMK
AAGFRPDEVTYSALLHASSRNGDVKMAEIVFKSMNDSGMLVAKPEATRFWNSLLSAYASAQPHADSLTRTTTIATAA
RIIHTMKQIGQQADRYTANTLLSLYAHAHRIRSVEALFDVAFLPPRPLSAASAAPVVVASQGAATAVVDHSAGQSPP
GPVSDSDDMGRRGDGGDLWAFGERFTPDVVTYTCLVQLYADTRRPDKALHAWQLMKESGVEPNMRTYEYMVRCLARS

GYLNSAMKTLREMREKGFVPSHHVVTLLMQRTQAYPELRDEVRRLTGLPVPVKVDEKSILALRLRRAGRSDHNPFAS
PGRRSPPLHYPL

>B201_serine/threonine_phosphoprotein_phosphatase_2C_superfamily_member
MKRVSSWRVGLPRATALGAGRHTTAAPLRMTTLPPRPQFRCGTASRFFASRIESSAPEARASADGAAPSTPPVERLG
LLSGSALHERATFGGRDVALLADTYGAIGVFDAVGGWHGAGGSEFARLLERHVQRSLASIDLVKQEIMTSTTKSEDD
TDDVEEAEQADDDLDDILYKPGSEEERFKEESDAMEEELQGVYSQVQARKSSSTAAARKRLLTRYSVEQLLPSEILM
RARNELLDKNMTGVSTALLLILSEKHEDQDWEKVLQMGSPTWKIEEKGTWLHTATMGDPCFMVIRNGKRFYRSTPSY
AQFNEPNHFSGSVITFAMDPSIKHNSVKLLKGDIIVVGTNGLFDNVWDDEIVEVVNRTIENTKVDEETAAAYPLEGM
IDPEIIAEALVKQATANSTNLEKKSPFAEYAEKEGYIYIGGREDDVTAVVSYVVPQKN

>B202_ABC1_superfamily_member,_aminoglycoside_3'-
phosphotransferase_(APH)_choline_kinase_(ChoK)_family_protein
MRQSCAALRVRPGGPALRTAAGSALRPWSRPTGFPLPPLATRAHNAATVLRQWPRPRRFFTTSATSPPPPATGRTRK
VLVATAGTGLVLGTAALGGLWHVAKGKYPRLEELSWSERGEHLARFMRTAWTGLVVSLDYKTLARYEYGTPEYAAAR
SKIHQRTADRLLWLCRANAGVYVKAGQHLASMNHVLPREYTDTLTVLQDQAPSRPFAVIEKAFIEQLGAPPSHFFSF
LEEQPIAAASLAQVHRGWLADGTQVAVKVQYPDFERLTWGDLFSIEAAAQAIAWFFPDFQFSWVVGEFEKNLEMEMD
FVNEAKNAERIAHNFAHNKQIYVPKIYWNMTRRKVLCMEFIHGAKITDVPKLDQMGINKREVAQLLHELFCEQIFVH
GFIHSDPHPGNILIRHLPSSPTHPQLVLLDHGLYRTLDEQFRLDYCHLWKAIFTGNREAVEKYSRRMGAGEHHEIFS
VILTFRPLDTGKTGPALVKDSEMSVAQVRLIRSQMRERNFQTVLSELLENMDRQLLLVLRTNNLIRSIIKDLEEGGS
VDRFLVMARYAIRGLYHRHDNSLSLPRRLRGVVESTKFEARLQILSLVIHLYQWWTRVVSWFYSFPASPVPVLDS

>B203_ABC1_superfamily_member,_putative_ubiquinone_biosynthesis_protein_UbiB
**MRRAFGAACRRISTTRPLNARGGACYAKGLLGRCKTTTPRSTTTSPATGAGRHAGPPRSCRTSNNGSSGGRDPSAGV
ATTSSAAASSRTTRLLALAGAGL**NGVVDWQQLAGVVDAGPLRPPNPRATCAWPHTAPPLSSTPSLRLCSPALFSDDV
ATSRLGRLLSKLWHGVLLGLRAAELCVRFAPLVVLYPVCVYVLPTWAEDLWYRLLTWSLRHSGPCFIKLGQWLSTRR
DLLPEHLCHRLAGLRSQAPAHAMRHTRRVFRKAFGRDIGQIFSQFPTTPIASGAVAQVYRATLKAPIDGVSEVAVKV
RHPHVREHITRDLALLQGLVCVIEWVWDAPWLQLGANVQNFASRMSAQCNLAVEAGNLVHFKQNFRDARSIRFPTPV
EGFYHPLVLVESFEPGIHVERFTREDIAPDVRKTIASVGMDAFLKMMLVDNFVHADLHPGNILVDDGRDAGSSPQVV
LLDVGLITQLSEKDRDNFLKLFSAVVAGDAALVGHLITDGQDHLTPQVVQQFTEEVGRLMAKVKLTRLDEVPLSEIF
FEMLSIARRNKVILEANFTTLIIGTVVIEGLGRQLDPDLNLLQRAVPLLVKDRAIRDAYIKARLSARLPSLFRPTSV

>B204_XPG_I_2_domain-
containing_protein_(putative_constitutive_coactivator_of_peroxisome
proliferator-activated_receptor_gamma-like_protein)
MGVRGLSAFMRQYGGRASASPTDIRLLALAAIKRSGQARSTVCVDGNSLLYYLYEDAGLNWLLGGQYAEFEQKVEEW
LDAFESCGIGLVFFFDGLVDPLKRATSLERRSRDAKYATSVLHSLQERANTDGPPRVLLPILAAAAFVGTLQRRGVE
MRFSNFEADRDIACYCTTHPECIGAVSQDSDFLIFDMGEACYVPLDSLQIKQASKPGKWTITCQTFRVDLTASMFNF
DKKWMPIFASLVGNDYTREDTRLIKLYRQMNIIAGDNVGQIIRKIAKFLSRFRAEEKELDVYMYLMKYIRKEDRNHL
HQVLKRSVNVYTITSEAPPTDVQVGHGGLAFKHDSGMNEALALEFRQGRLATQHMSVLADGEYWAGVSVVDHTLFDP
GEIYLQLRATMYRALLGHQLEQSKASKKLQPGEQESGQPQSAGASAGSGKAQQQKKQPTKGGGPTLCVSELMQTQRS
YRKRSTVTLKPGDAGCQMPPIADLRSMAESDRLHIFLSSMRADDLLAADLPTGLLLPCAVLRYLLVEQNDSATLDGG
GERLGRAEPLLYEWELNTYLLHLVRLQHKQPTAVKAAAWDWKMQGADRKRFVCLVGLLQTGLLHALL**LHQLCGHPLG
LQLPPPSHYYDGFAFLREY**CHRWDARRAERRLRGGAPSTPRQPRDEEQERERERTEEANKQDDDDAREELKLKEQVV
EKEENDDKESDSTVLKAREAIVAGLRPHPDSAKQNERAGPSLFKPETTKQTNKKRRRKENNGGSGAREKEKEKERRD
QDHGEEEGSDDQDADRLATHNSFALLG

>B205_glutathione_peroxidase
**MRRGAKRVVLRHHQELRFTTTTTPTSSQLFFSSFRTASTCVKLSASRLHLARTATASSPHLHNSSTSALITRPHARR
FSSTSTDM**STAKSLHELTAEDNQGQTFDFSQLKGKVVLIVNVASKCGFTPQYKELQALYEKYKDQGLEIVGFPCNQF
GSQEPGSDAEIQEFCQKNYGVSFPIMKKIHVNGDEVHPVYAFLKSSKSGLLGLSRIKWNFEKFLVDSEGVVEERYSS
LTKPESLESTIEKLLHK

>B206_glutaredoxin
MRRTAQMVRLGCRGTNVATSSTVLRGAASVRTLNSRASSLGARRGFASGVTPKVVEVYTTAWCPFCDRIRALLNSKG
VQYKEIDVTSVAGAKDEMEKRTNGRRTVPQLFIDGEYIGDCDGTHKLDAQGLLDAKLGLKERSTA

>B207_DsbA_family_thioredoxin_domain-containing_protein_
MWHCRSLAVVLSSRTAASCASRSLSSVSTGGGEHQPPPAAAAASSSGGAPPPVEVRFYFDYRSPFAYLAKDLVYGIE
DHYPPDAVHVRWLPFAFPVEEGFGLPGSRSRYHLNKVKYAYVDARQWANERDPPLVIKGPQRVFDSTRANAAGLFAQ
SLGRPVFRAYTDRVYREFFERRLDIEQAEAIRCVLQDAVARHAGDHSQAAAGWESRYAA**FVGDDEQQQEEGG**GGAAR
GQLAEIREAAEEEGVFGVPSFVVGGHLFFGADRFHWVRRRLDALLAARHTPGTTQPTTSSST

>B208_PAS_domain-containing_protein
MAVNCSQVLPRRLSGRLFLIVIRLQPQPPATMGNGVSNEEFERQGKLLGVKSVPGKPSQKFKPLSIKRMKEIQKQII
FEYPYLTNVFESILVTDNELPDCPIVWANDQFERMTLYPKEDIIGRNCRFLQGNYTDPATVGKIRAAVKGGESLDVE
ILNYRRDGTAFWNRFRILPVHKKGKKEGPVSHFIAIQKDVTLLKDFASRETSTWSPPEVAMWLQANVLGQFGRAFVV
QGITGARLLEMEREDLFAKVGMEMTKKEKAQIWQLVSELQQNGQEVVQHTAKKMKEKAGHPDYHAPTHDDVSDEVPD
FWNMEQTQGDYMMPVKCYVEGYEPVIFLIKRLITYKELNKKIERTFGRPMDISFVEDDEENQVKEDDDVEAAILLAE
GGTVCLKVA**RPRKKKSVVSKAKAKMLDALPVAVLLTDAFGEVMFANQSALLMVGESSRAALVKRMTNIKDLVTGEDI
AKIENIHLSSREGEGYSVELARGQKKVTLFATKDDKGRLVFTLLKKRYELFKDRKQE**

>B209_NABD_Rossman_superfamily_member_(NmrA-like family protein)
MRIAVTGATGNTGAAVVRALAQTGRHHVLAITRDPQGKAAQQLAELPGVVPVTLEDAFTEPVDRIYLASAVTRDQFL
VETDVIIAARKAGVEYIVKLSTVDAWMEVYSDIFYARSHLAVECFLERGDIPFTCLRANLFHTSVGIDLDAVPKTNQ
FRTFLHGASVATIDPDDVGRAAAALLSLEDPSRHYSKKYMLTGPEDVNDQSIGEALREVLQADVTFGGTLTVDEFTT
GSPINPKSLLPPITFFRQGKGDRAHTVASPEMLALAPPKGTFKEFITRYYAKN

>B210_acyl-CoA_dehydrogenase_domain-containing_protein
MTSHSSTALLSKRLAVLHGHLAAARTSDARLAVVPTAGAAVAVPPSDFLGFEELLGPEERQWRDKARAFAQNHVAPI
IDKYYEKAEFPFELLPKLKELGIMGGTIKGYGCPGMSFMSAAMVVLELARVNSEFAGFFIIVTYLVMLSIEQCGSEE
QKQKWLPRLASVDAVGSFGLTEPGAGSDASGLQTTAKKVAGGWRLNGQKRWIGNATFADVIIIWARNEETGEVNGFL
VEKGTKGLRTEKIENKMCFRCVQNADIYLEDCVVPESARFPNADSFLKGTAGILSASRIFVGWLPVGLAMGSYDAAL
KHLKERQQFGSPLAAFQLMQEKLVRMLANAQAMYLMSWRLSELFVKHGQVTRGQSSLVKAHNTLKGRECVALAREVL
GGNGIIYDNVVARHFLDMEAAYTYEGTYEVNALVCGREITGIAAFKAPKNK

>B211_phosphatidylethanolamine-binding_(PEBP)_domain-containing_protein
MRRFARPPSSSTSSTTLRLALRPAAAYTTTTSKPLDFGKDPSKSRPMSSSYQDVLSSHPPKKLHVRWPDLPDMMQEG
QELRPDQSARMPTVCWDGDENDFHTLAMVDPDAPSRDDPKFGEWRHWLVTNIPGSQVNKGTVLAPYMGPGPPPGTGH
HRYVFVVFKQKDQIPHETMNNEGKGRANFKIEQWAHKHGMTEPLAASYFIAKHH

>B212_triacylglycerol_lipase
MKTTKQPFARALFRRHQPTRLFIRHRPAVLAGTVSLLSVHRCIHSSIAPCSPREKEIKHAKNLPEGEQPTAGHRNRE
DKEETIPPPPSTGEEQPVDPRYPFLLCHGLLGFDTLKVVPSLIEVDYWRGGIAQTLRRRRRPEEGAQGGVFISRVPS
TGHVHERALCIKKQVAQILDPPLASKVPGAGLDEGDWKRKRPEKVNLVGHSMGGMDCRYAVSMLGIAEGVSSVTTIG
TPHQGSPVANWAKDVLFDKLRLEGLFRFLFNDTAAIHCLTTDYLKDEFNKMVVDQPGVKYYSFGGHRDRAQIPLFWH
FTYDMIRKLEGENDGLVSVKSCAWGEYIETLEADHLEMINWHCRKYTAPFTRTPYKPFNALNFYDRLASFLAQRGH

>B213_triacylglycerol_lipase
MQHFTRWLVPTVSRTSSTGARLLSTTAAGSEPQSGRAHTLVPRLPIVLCPGLIFWNQLDLKGVGRVEYWGGVASHLR
HRGATVVEAVVPGTGHIRERAAELRRHVDAFLAAHPDVKKVNLVAFSMGGLDARSMIHHLQGHEVVESLTTIATPHR
GSSLAKRFIDQGYDRHLARLGIGAEAFR**CLTPQFVQGLNEATPDHPDVRYYSYAGFKPRNAMSGWGRWAYDRVHERE
GANDGFVGVQGAVWGRFLG**TVSAAHLELIDWRLGVRRAHRFRVLPDFYDQVLHNLAQLGH

>B214_acetyltransferase
MTSASVALSCRLRSSCSLSGLTQRKMEERSCAETPTLRPMALRDVQAAWSIQVIAYSDPSLHETADHYERRLAAYPQ
GCWVAELKEDDSAEPVLVGYLVSYPSRLDDPPALSSHEWAVPHPADAYFIHEVTVDPRRQGLGLGRLLSAKATECAR
TSGLGPAAQYVALVSVQGSSPFWHRHGGYLPYDFDVNRLHTSLPSASSSQADGPCLFDETTAHKLKTKLIQSYGPGA
LMMLTAMPQHQ

>B215_acetyltransferase
MRRSSQVLLRATTTGRATSRLLVVPHRTAMSSSSSSAKKQHQVVHLPKEHKFAITFEDGDQALLEYEEREGGKVWDF
VHTFTPPAKRGQGLAAQVVNGAMEHVKREGKVKVVASCWYVRDDFLPRHPEYADCLLADHSAAKM

>B216_N-acyltransferase_superfamily_protein
MPTTAWTASSRVTLQNSKARSASPQAERAPRRTVFSRPSPGETPTVVLPKMEPRRTERRFAVRSYVPADRDRVLQLF
VEGMQENIETSPPDVRLVIEDSERRFIEWSLHDDLADIDAVYMACTTSPRSHFWVLVECIEGSEGEQGKREVIQGMV
GLYRVDDDYAKVRRMSIASAVRRQGLARRLLDHIIDYASKEGFRRVILSTGQYMSAANALYTTYGFIKTKEEPDEVG
TMENHYEYCLVPHA

>B217_GNAT_superfamily_N-acetyltransferase
MLLRKSQSVTCFRFGRHARTSSLMSLVPSAVAAATQVRSNDGGQRQQRSATTSSCSTSAPETAATRHVTIRDARRAD
ARFLSQVMLQASRSHLDKGVYDIYFPTFSDDERLALLADMADCSPDAGSVCCWDGFLVAEVNGTPAAALAGYGSDTK
STQGYLDTMWDALKRRGWTRDQFERMLEKREAIDSVTTKDSRRLWVVDWVTTLPEFRKLGLISKLLHLILQRGKERG
YKLAEVSVFLGNDPAILAYKKKGFEEYQSIASPVWQRVINCPGIMRLVKPLNDNDPGAAPTQPSAESRL

>B218_phospholipase/carboxylesterase_family_protein_(putative_acyl-protein_thioesterase)
MQSPSRGLHLRRKMRRCVAPCARIAPLRWRLHLSGLRMISSTSGRGAPQVSYDPKEGTGIIQPKAGRKHTATVLFMH
GLGDTAMGWMDAMHFLYERLAQEGHPTRFVLPTAKTRRITINGGMKMPGWYDITGLDERAKEDFDGIEQSYDTVSRI
LRSEMEDEGIPPNKIFLGGFSQGAAMSLYSCYFKQEQTLGGVIALSGYLPFAYRAEQLVQKQNKTPLLMCHGLDDGV
VLYPWAKGSFDQLKKCGVEGEFKTYPDLAHSASEAELDDVLTFIRQRLQS

>B219_guanylate_kinase
MLARVRPIVFAGPSGAGKSTLIKKLMTEFPSAFGFSVSHTTRKIRPSEVDGVNYHFVEREAMEKEIAEGKFIENAVY
SGNMYGTSIKAVQDVVDSGKVCLLDIDLQGVLLVKKTDLNPYYVFISPPSMEELERRLRGRGDTEEDAMQQRLETAK
KEMAYRDQEGLWDYVLINESLEDAYAKLRAFITERYPL

>B220_flavin_reductase_domain-containing_protein
MFSRPTFHRNTTARHLVAVPLVLSSAARNTHPPHLLLPRTARGHTTSVSTQKKMSHHPPFKQVEAARPDFEEEPFAY
TKTPAPEWVPGQGSNQLPWPVDAPFKHIDPAHEQPGLVYKLIIGGITPRPIAFVSSQDEHGKQNLAPFSYFAPCGHN
PPMVVFSCSSPGPDKQKDTCNNVKTTKEFVVNIISEAFIEAANYTSIDAPADLSEWDLAGLTREPSQVVKPPRVKES
AFSMECVLEHYYDMKDDEGRVTGTSLFGRVKLFHVREDVLQPNYVIDQAKLQSMSRLGGISYGRTTKGLELARPVWS
PVESQRKEVEQALLPVNNPGSTKADAPPS

>B221_3-dehydroquinate_dehydratase
MRRVGLLRTSLLVHSSAATLAPAPAPTSTRWHRPSSLIQINTNSSKRMATTVTKEEEERQARANKWAQEGTQPEGRS
KRKVLVVHGAGLCMRGKAQIEKFGTLTLADYERHILHYAEQHHLDIEFFQSNSEGSVIDRLYAAHDDGDVDGAIINP
GGFTKGYRALGLACGQVCYPVVEVHISNTAAGGTISEVTPNCKATVQGFGIYGYNMALAGLASFLLPNNTKP

>B222_hypoxanthine_phosphoribosyltransferase
METPFAPTNLHRIVLSISAARPRLIFLSRISLHHKMARARSGSFSEQMMDMEEVLVSEGAIEARVRQLAEQINKEYK
GKSIVVIGILKGSVMFMTDLVKRLHVDAKIEFMAVSSYGSSTVSSGAVKIVMDTRTSIEGQHVVVVEDIVDSGYTMR
YLKNLLLSRKPASLEICVLLEKPSRLKVAPEELGIKYIGFEIPDKWVVGYGMDYDERYRCLPFIGVLKRSVYDSTFV
VEAEATNSQ

>B223_rhodanese_homology_domain_(RHOD)-containing_protein
MRRIGSASVRQSSRGGVVPLAHQQCGTHRRWSSSVPGIISKEELQLKLATNPDGFHLLDVRQAYELESLPAIHPRAR
LIPLQELPGALEMSEDQWEDTYDFPKPQPTEEVVCYCKSGMRSEMACNFLRQKGFTRVANYQGSALDWWSS

>B224_NUDIX_domain-containing_protein_(NTP_pyrophosphohydrolase)
**MRRGGPVLDRFVRPVALRRVSASSSASILRRRSFQARSKHPSMTSPETVLLYYCALRGISTSPPAGHFSTSSAPPPT
PPSPATQPPSSSPQRSPARG**GVPVNPSYLGIHLKEDEERSFKAAGILPIAFFTSPPPGGLVG**PPPKAAKQGEAKPGD
ESEDEDG**GGGGGADEKSSTAPSAAATKGGVPVPYVLLGCETRRKQVKTDEVYINLFGGKREDSDGSAAETAWREFWE
ETGRLLPDQAQPFLDHCRDGADRRRVLWFAPGKYVLFLYHLPYPAPEWTTKLAEQYRQLETREEGSEMDSLHWVSLP
ALLKAVGRRAPADRAVYGADDGRPYPVFRFSADIVVHLSRYFQSVVKGQAHAVPPLDSTTSPARRSPYRAPHGPPHG
SSAGGQSPARSYHTTPPRSTVKHQRSPHTAKPTPATYSAPLSARAKPFYPKSPCPTQFVAVTANPND

>B225_NADPH-dependent_FMN_reductase_domain-containing_protein

MASRKSLKILGISGSLRHGSSNSGLIRSAAASAARLNQSTQDYHINFQIYQRLKDIPLYDGDVEAKAMPESVVHFCQ
AIAEADALLIATPEYNYSVSGVLKNAIDWASRPYRRTPLTGKPVAILGAGGVSGTSRAQYHLRQVLLDVAMPVLPKP
EVMVNFFAPGKFDATTGELLDKQVKGEIERQLRALAVWTATLRGWTPTM

>B226_sulfite_oxidase_(SO)_family_molybdopterin-binding_domain-containing_protein
MPTLRRSPLRATKPGYHQTAIKAFPTQQSSNTPHTQPNAKERTRKMEKAKTVSKEVRKDVKQMTFPYHTDKTDDFTS
EEVNLANRCHGLHLEGLDLALTPAGMHYLLIHFDIPTGPATAESTYRLKLRGLVDRPLELSMADIRRRPRVSIPVTM
ECAGNGRINMKKRYWTHVPWQNEALGTAVWTGTPLKDLLEEAGLQDKAIELLFTGLDKGLQGGEMQYYQRCLTIDDA
TREEVILAYEMNGQPLLPQHGAPLRLIVPGWYGMTNVKWLDSIEAISTPFDGYQMQAYMFTQYPGDPQGKRMRHLKV
RSLMVPPGVPDFFTRVRLVEEGNVKLKGRAWAGPLAVKQVLVSVDGG**VTWAEATL**AAKAVGKFAWIAWSFEWRNARA
GAKHFLMTKAIDELGNVQDNAEEWNYYAMGATVPQSVPVVVVSSPEWRITGKPLPNPPRHPKL

>B227_FAD-dependent_oxidoreductase_domain-containing_protein
MHRRLGTRLAGRGWTTRQVVGSRVAVAHFSTASQVSSQAPDLPERAKTVIIGGGCIGCGIAYSLVKAGEKDVVVLEK
EPALANVTTAQAAGLVGQVRDNLERVKLAMWSVQTFSDLQQDSDYNPNWRQVGSLRVAYTKERQEEFNKMLNVCEKA
GLHVETLSPKAAQKMWPGMNFEKATSILWCPTDGYLQPCDLAFSYQHQSRSMNGAKFVTDAWVEDIELSPEGTHVKA
VKTNRGTIKCDTVINAAGAHAYHIAKLVGLELPIVPVRHEYFITEPTVPPTITPNLPVMRIPDATLYLRPDVNGLLL
GGWEPNGLSLDPRSYPITQKPPAIAEDWPVLSTLGEELAPTYPQVNELGIRAVFSGWPTFTPDGRFIIGPTKKVRGF
IMAGGCNAHGVSGSAGIGHHVVESMFEKDPSPYVRSLSPDRFTDGSWDWDKAEKQARHIYETYYHIRKT

>B228_histidine_phospatase_domain-containing_protein
MSTCTLPARTTSSSGATYGRSMNMADVKVVHFIRHGEAEHNVAARRHGCQEYRNWAYLDAPLTEKGRGQAREAQKVV
LAQMKPQVVLVSPLTRTLQTAEEVFQPLMDSSEGKPRFEVCEGVRERIGHHPCDKRRTVSELKPQFPQFSFDAILDE
DDCLWSEAREPTEDILQRAKAFLEVLRQRSENCIGVVSHSAFLTAMFVVLTTECGLRSDGPDGPPDITSASSPDAVA
NGGPMNGESKPYFANGEVKTVVILPHSS

>B229_NUDIX_hydrolase_superfamily_protein
MRVRALASNTRTRAYAPSLPCRTSHHHLRLQSTTFVTALFNARPMSSTTKQRKSPSLAADIAVMREREGKRELLMIK
RGGRTFHGCLAFPGGFVEYGEEPKHAALRELQEETSLVGTDPQLVGVYGDPARDPRGHTVSTFYYVTVKDFSTMKAG
DDAAHADFYDVEELKGQTDKMAFDHALLLHDLLEFVKKHNIDIPRA

>B230_argininosuccinate_lyase
MRRATASCVRALPRTSAAASGLRMAGARTLHTTQPVEMDMEKKSTKMWGGRFSKDIDSSILAWTESITVDSHLVAED
LWGSMAHVAMLGSQGIIPAN**NAAAILDTLYKLQQDWIEGRWQWIPSQEDVHMNAEKMVIDALGMDVGGRMHTCRSRN
DQVVLDSKLYARRRLLELRSRVVDAVEALLKKAEAHKDDVMVSYTHVQHAQPVSVAYWLTHYAGVLLRDLQRLKAAY
DTTDQNPLGSGAIAG**TSFPIDRQLTTDLMGFQEVHLHGMDATSSRDFMLESLSAATILQVTMSRLAEEFILWSSYEF
RTLTLDDGFAMGSSMMPQKKNPGA**L**ELLRGRGGRAIGYLTAACTMMKGLPSGYNRDFHEDKELLVATMELMNKAVQV
VPPLINSTTINLKRMEELSWGNFANATELANYLVAKHDVPFRRAHDIVGNENFSNTQFCFEHLKKWDIKAPESEVLA
VLNPTHVMKTYTSLGATSPSSVSHIIDTYTAKLGEHRHVLQTDQTRVKRAYDASRSLASEAAKVVHNKDDLVKLIQK
YRPTSH

>B231_molybdenum_cofactor_biosynthesis_protein_1
MNGRRGSGLACINSGKVLRRASERGARRLFSAEAAALRVQKQEPSSVLSATTQPATAPQADSILADNFNRHHNYLRI
SLTERCNLRCVYCMPEEGIDLQPNDKILTKDEIVRVARLFVDAGVDKIRFTGGEPLVRKDLEDIVSEVGALPLRALA
MTTNAITLARKLPKLHKMGLNQLNISLDTLDSEKFTQITRRKGWEKVMEAIDMAVDYGYSPLKINCVVMRGVNDNEI
VDFVKMTRDKPIQVRFIEYMPFDGNRWNDQKFLSYKEMIEIIKRDFGNEFLRLPDPTPNETAKTWSIPGFAGSVGFI
TSMSDHFCGSCNRLRITADGNLKVCLFGSSEVSLRDAMRVGYATDAELSRMINAAVKRKKEHHGAAESSDGGSGLTH
VDAKTNTPTMVDVSAKQVTKRTALARSYVRLPSAVLGALSGNEIASPKGPVFATAIVAGTMGVKKTSELIPFCHPLP
IEGCKFTIKMEEDASPPAKKKKEGEESRRVVIDCEVSLHHKTGVEMEALTGASVAALTIYDMCKALSHDIVIEETRL
ITKTGGKSDYDSVNLAASSSTRSGATNTNSSQPTPKRKARAPTPPKA

>B232_pterin-4-alpha-carbinolamine_dehydratase
MRSSAGVGAFQRKLGLVGASSGAVATKTITLHLRPRSKKMSTTAGLSREKLEGEERERRLREEVPFWQQVMCRDAIQ
RTFTFKDFKEAWRFMNLTAEKAEEMDHHPEWFNVYNRVEVTLATHTCKGVSEYDVVLAKAMDQFALQAAAETLEAEE
QKNKQ

>B233_thiamine_biosynthetic_bifunctional_enzyme_(thiamine_monophosphate_synthase_(TMP synthase)/4-methyl-5-beta-hydroxyethylthiazole_(Thz)_kinase)
MKSLQRACTRCAVHRGGVRRAFSTATTSRRASLNYSLYLITDSGALTRGRPLEELVEQAIRGGVTMVQVREKKASTR
DFIEQASRIKSVTHRHGVPLIINDRLDVALAVGADGIHVGQDDMAATTARALLKQSSSPARKMLLGVTATNEAQARA
AELAGADYLGTSAVFPTDTKKDGGAGYVIGLDAVQRICRATSLPVVAVGGINATNAHQIVAHGAAGVGVVSAIVGAD
CPRTAAAGLAAVVDSALPKYSQELAAKAAEAFERVRERRPLVQNVTNYVVMNDTANATLQAGGSPVMAHENGEMTEH
AQAVVLNMGTLDDHWLRQMKAIGQVANAIGVPIVFDPVGAGATHYRTGAALQLLDELRVSVLRGNPGELAALHVALC
SIERSLASELLVRGVDSPGYLPDSESIIRSLARTKRTIVAMTGKQDLVSDGERLLQVHNNHILLGQLTGTGCMVTSL
IGAFVGALPTTEQTHAVAERRQHVLEATAAALAYFCHAAERAGARTIAEGLGPGSFHTALLDELFLLTPHELEQHAR
IVDMRHAS

>B234_aspartate_carbamoyltransferase
MRSVSSSRIALSSAPLQRLGLRTVSTHSAQLIDMSKTRPLAGGDVISAKQFDKSSIEYVFKVAAGLKKEVERNGGVD
LLKHRVLANVFMEPSTRTASSFHAAMLRLGGAVVPINELTSSAQKGETLEDTVRTMENYADVLVLRHPKVGSAATAA
HYARIPVINAGDGQGEHPTQALLDLFLIHQERGSIDGASITLLGDLKYGRTVHSLSVMLALFPGIKINLVSPPNLAM
PAEVVAEVKAKGITVTETADLDAVLSTTDVLYQTRVQKERFASLEEYEKSKGAYIITPATLSPAKKSLLLLHPFPRV
DEITPDVDQDPRAMYFKQPQYGMYMRMALLASVLGKEGPVL

>B235_malate/L-lactate_dehydrogenase_domain-containing_protein
MRGRLAQGIVRPRAASPGLLLRASSSSIPFAPSSSSRPYSTTKNRDFERVEAHELRAFVDRCMRAVDCTPEHAATVA
DILVAADLRGVHSHGVNRLEMYVGEVRNGEVDPRVRPEVTSETPAIACVDGRNGLGMVVGRYCMELAMEKAQTMGVG
WVVARGSNHYGIAGYYAMMAAERGLVGMSYTNTSPISFPTRSAQHVLGTNPIAVAAPSTDPKDPFVLDMATTTVALG
KVEIRDREERQCPPGWGADKAGRPSTDPKEVLGGGGLLYLGGEEETGGYKGYGLAMMVELFSAILSGADYAAKIPPW
RCGRGRAANLGQCFVALNPALFAGGFNERMGDLMHQMRSLPHVDPALPVLVPGDLEKVMEEKYKKEGIAFHVNLVDA
LQRLAADLRVDPLPLRE

>B236_glycerol-3-phosphate_dehydrogenase
MRRSATGTNSLRVVGLGRCTFPRAPKKTSSSSAVLRFLPLNSSAFIFSPVARFIPSRPTASPAPPSSSTSSSSANPE
RIPDAHLQHHIPHHHSPHQPHPNTPHHPRGSHHHHPHPSSFWHVLKMEGGKEAMEQADIVVFGGGSFATALAYVLSK
NHHTVTLLTRNEAVAQSINEQHRNPKYLSAFTLPPNVRASTRAEDVVPQARYIVHAVPVQASREYLQRLAPLIAPDT
PIISSSKGLHTESLRYMSDIVPEALGRNQPMAFISGPSFAKELMQDVPTAVVVASVDSVTRERVQRLFASPSFRVYT
TDDVVGVEIGGALKNVFAIAAGMSEGLGLGTNTLAALVTRGCSEMTRLAVKMGARPDTVSGLSGIGDLMLTCFGSLS
RNRTVGKRLGSGESLESILATMEEVAEGVATTPAACKLAEQYGLDLPIIKAVAAILRGDLQAREAVLHLMTLPLSDE
KTW

>B237_cobalamin_synthesis_protein_CobW
MRASSGGGRAKGFVPVAVVTGFYGSGKTSLLHRLAAKLVAPSSSPLSIALLLHSLSEESVEAGWVRGRLRNVPRGRL
AVEEVTGCGPDLPQRFIEALSRLARSDLYDYIFVELLGDQNPLHLAHLLTLSDARGTPLSDFLQLDAIVCVVDASRL
ITDAKSRLDVVRAQLAAAQVVVLNKTDLVSSQELRKVETAMRLVAHNSTDELDARVYHAVHADLAPTLLTNTGLFSY
NRVMTLPSWPQQLWVPEQCMNAFVYRAQRPFQPDRLWKVASSSISHLKAVVRAKGLVWLVSRPDRWGYWSQNPQSID
ISGGDAWSISSGKDKRQEILFVGGQDLDKEAISRLLDACLLKDTEATPERMATVHDPFPAWEPLSSSDSASASAS**TP**
THTPAGAPSTRPSSTDSAALPASRQSAPSPQSPSPASMGSGGQPMARRHHANAAMEAKAKAKKAEMKDFAGALRDAA
KQVVADCRALAEFVEHQSTTSLTADEDSETFNEPEEGDGEVEAQVLQLAKNLAMAATTLDQEITSHITAHPQNFGSL
KEKKFLGLLQQVKDAVLSLIKASKHVVSNPRDWMTKQKVTNSLRDVGVSIKELVALADNMHTPQSVAAVVSA

>B238_CaiB_domain-containing_protein_(predicted_acyl-CoA_transferases/carnitine_dehydratase)
MHARAVVSRTLLDRAHVVLSPATRASLTPQHMFIGSGGRRTAHIASPVRGALSHVRVLDLSRVLAGPWATQTLADFG
ADVIKVERPQQGDDTRGWGPPFIKDKEGNNTKQSAYFLSANRGKRAITCDITRPEGQELIRQLAAKCDVVVENFKAG
GLAKYGLDYASLKQVNPSIIYCSITGFGQTGPRKDQAGYDFLLQGMSGLMSITGDPQGHPMKVGVAIVDIMTGLYAT
SSILAALLERDAQSEGKREGQHIDLSLFDVSVAFLANQASNYLVSGKAPQRMGNYHPNIAPYQSFEASDGYFILAVG
NDSQFAKFCATAGKPELAADPRFITNAKRVENRKALESEITELTKRRTQQDWIGALKEVGVPCGQVNDIAQAFSDPQ
LHHRNMFLHLDHPASGADAPVPLMNSPIHMSRTPPECRLPPPALGEHTDEVLRELLSMRDAQIQALRDRSVL

>B239_Nucleotide-Binding_Domain_of_the_sugar_kinase/HSP70/actin_superfamily_homolog

MRRTSLIRSSVSRAVSCQAVGARTTATALRAHSAPLASTNSSCARRALGTAARSGGQRTGFAGSSSSFLVGAAAAVG
VALGAILYYDEQNQVVYAVQKDGTVKRYFLGVDGGGSKTNVTCIDEEKKVVGEGTSGCTNFNSVGQEKASQHLREAI
LSALKAAGVPEDQVAGICLSMSGVDRPADKQLMRSWITPILPKARIDVHNDAVAALVSGTDGNLFGLVVISGTGTIT
YGVNKEGETTRAAGWGPMLGDRGSGYQIGYEILTAVVRALDGRGPATSLVEAVLTKLNLSKGEELIPWAYSSVAWER
YAQLAPLAAIAARNGDKVAEQILEGQAQDLVVSIQAVAKRLHIENQPFPLVLAGGNFTHEGSYLTALLKKKVNQQLP
QVTVLLPTLKPEYAAALLARNNATAKH

>B240_alpha-ketoglutarate-dependent_dioxygenase_alkB_homolog
MRRHCGVRSALALRAHSTKSVARPHYLQSSRLFSGGSNQGGSVLDDSCVEYINDAHQIAGLTVLPGFLAADEQDEMV
RELEAVFKGKRYSFAEHWDQVIIGYRECERALFKFSPKNQHTIERLTDAIGSEVKLFPHVHVLDIHEDGEMKPHVDS
VKFSGGVVAGLSLLSPCVFELHHEKSPARVHLLLEPGTFYIMQGDARYEWAHGIRKGAVSFKGRDITRTRRLSVMLR
DFKEDDILQDHHMATTHNAPPTPPRQY

>B241_putative_Co/Zn/Cd_cation_transporter
MKRLARPQCQAAGMRGRAVGSSPSYLTGNTARSFSLRILAPMGPPSSKSQRFTSLPAPTLSRCSPSSHRSSSLSLRT
PSAPPTSLLPSTQARFHGGVSDGGGGGPPRHHKPDHHGKEGSSAFSLAALWRKISGQEEAEDQKRKEEEEKEVDYRK
EAEDVQEQNKQMRVITWVGLGLNILLGTGKAIAGTMGNSQALVADAVHSFTDGISDIVTLWAIHMMQLPHNAQYPYG
HGKFETMGTFLVAVTLVATGVGIGGHAVDSLMNMSTEVPSNLALYGALGSILFKEALYHATVRIGKRAGSELLIANA
WHHRTDAISSVVALFGVAGAQYGVAWLDPVAGLAVGVMIVKMGVEMGMKSVRELTDASIEHDMLNYMEKLIRNVEGV
VEARKIRARKMGTYSIVDVKIQVDHLLSVSAAHQVAKRVRLTLLDAVPQVNDVMVHVDPEPPQSQTLQTLMRPQSEI
YQDVVAKVDLFPEVYLSYMCCHYYNMRLTVEVDLLFGDETISLKQAQELAKKIQKEVLAIKDVHHADIMVNLTLQSA
NKEREWNNWIKQQRMMRARMEEEGGKGLGDLKLPLSPPSLPSFPAIREAEYPQGRPGHMWK

>B242_putative_Co/Zn/Cd_efflux_system_component
MTMSSTFLRPYRVPRQLHKNPKNAATKTRKSARRRIQLDCVTHILMEDGLSSPKGRGPVSLLTWPALLLVAAKCGRA
LTAHTSYQFVGGAGQVPVVVWTCLLLFAASLFYVLRQPWKDGKKRLRTKLWARIGFNAGLYALELVLWHHCLSLYGP
VRTLLVVDYGDVLLAPLFNPRQGSSSGGGASSGKRGSRMQGSLLVLLAYVLLFAFDAPVSGFAEEWGLVDKLYGAGV
VAAAIAVAFARKRYHRKLAVQVGSAKRLTALSVMMGAAILVPFALYAYAFQATTGQEGEGGSASININSSGGSSEGS
SSGFGLWVAVGLAAALFVVGDSWAEHVVRSRLPSPALATKLGLAGAVACATVAGWLWPPTSLSLVTFAVAALVMFGA
HMRFQGEQETSVQHSMFAAEGADEGLPTEAFSGSHGGGQLWPFFKNTLREILANSESRSIFLFLVINLAFMGVEVAY
GYWTNSLGLISDGFHMLFDCTALFIGLYASVISKWKPNQMFTYGYGRVEVVSGFVNGIFLVFIALFVLLESVERFVE
PPKIETDKLLLVSSLGLLVNLIGVFAFAHGHAHGGHGHSHGGDGGHTKKKKKHKKGKHGHSHGHGDHGHAHGHDDHG
HAHGHHDDHHDDHHDHDDHDDHHDHDDHHGHSHKQKKKKHSFSASKSVLGKLVEPFADFFHRLWHEGLTDNLSGIWL
HVMADTLGSVGVIFSSFCIMNFGWTIADPICSFCIALTILISVIPLLKQCSVTLALRSPAHLQKDIDKAVLKITRLE
GVMGVRDVHVWKLAGDTVVATLHVQVQNHVDEQKIIKAVKGFFADTVENLTVQVEKDRFYDLQTRLQKQPLSLPSSA
LPMAAPAPFTPQPAPVLAPYITNASRSHSVGSLAASASSPPTSSSFFSADPAADEGHRHHHDYHHHDHHHDHPHHDH
HHDQHIDITVDKSL

>B243_putative_permease_(sulfite_exporter_TauE/SafE_superfamily_member)
MKRTTLRLLPQRTQLPGGSRRLGAWGIGAGVHSVRPQRPPRSPTTTLRSGYGALRPTRRFVGTKYSQEGAGAATPQA
PPPTGWQLHRTGGLIGSAMGFFGGLVGQGGGVVGIPLMTSLGRLTQHQAHGTSLVAVASTGLAGALAYWQAGGAEEG
VDTLAALMLAGSASLFAGVGARLSRRVSSPNLKKYMGAFMVAASVSVAVKAYSDYPDHRGSLTSTVASAASATTVAS
PVLSMSDKAALLTPAHIATIGAIGAVTGFASGFLGIGGGLVMVPLLTLCTSMHQSQVLGTSLLAMVIPAAVGSWTHL
RLGNVFVPIVPSMVAGTLVGGYLGGKLSTNLTQTQQRAIVSITIFTLALRMLRK

>B244_CorA-
like_divalent_cation_transporter_superfamily_protein_inner_mitochondrial_memb
rane_Mg2+_transporters_Mfm1p-_and_Mrs2p-like_family_protein)
MWRRVPMCRLLGNTNNGTAAAGHLLAVAQPLVRRVGLPLRGHVPATSRSFASIGASAAWDRPGGQESDQQADETLSV
PQYGGREELDRTNLVRAITVDEAGSFREVSLTKADLSRELRVQKRDLRAVDVSFPNQLACFLVRDGVILINLEAFKA
IVKHNSLILFTTETARGTVLQQFCPFLQYRLTREVGAHVGGGFEFRVVEAVLTVLCDTLYERYGELKARIDHLLFGL
EQATNGQDDYLPFLADLSHHNKTLNSFQKRVHEVRGALHQVLESDEDLAAMYLSVQAATGHRRRTDQHEEAEILIEN
YVAQLDDILSEVAELQSSIDVSEEYFRLTLDSQRNKIMKMNLLLTLGTFSTACAGVVTGVFGMNLQNFLETSESAFL
VTTGGLTISMAASFASIYTYFRLKKML

>B245_DUF1992_domain-containing_protein_(putative_DnaJ-
like_protein_subfamily_C)

MQRARCFHPSASAASMWPCSLRRVSAGAALVDRGYGCSPTTNQSCNHPHLRLYAASPQVERHAQVEEATVVTRAEEG
GQLPANARHVEAKSPALEGEVTTDTPRQPKSAFFSAGLADLAKEMQTLLGDIKKATKYALWFGDRSNSASYLRNARS
MPDDEHKPVFRRTFLNAAVEYLPITRRTPLSVREKEASAMRAMRAREDVNNYKKPMEERLEDIQRPKSLAEWGGFVE
ARIREDMDNFQGSSVNLMELCNQPEYNNPYLDSTTRIMYRIMKKNDFLPYWLQLDKDIKHELNELRRELADLKQQWR
RESMMAGRDTSLLGAGLRFEDSRTWKNDATQARLAKKVKKLNGQILNFNLAAPHMNFQKFFIDLNQEVAALE

>B246_Hsp70_form_3_(chaperone_protein_DnaK)
MRSTRRWNLMQSNMVFPLGRAAAAGSTSTLFAGRLQRPFISHHHHTRSPNVVLGVDMGTTKTCAAVLVNKGKPLWVD
NADVVARLPSMVAFSQDPATGESTVLVGDQAKRQRDSNPRGTIFGFMPLLGGRHDSEEVAKLKQRVPYDIVKAPNGS
GDAWVAIGGQAHSPAQIATFIIEKCKQSAEKHMGHPITEAIFAVPTYLNIDEATTTQIKEAARVAGLNVFRFVHGHV
AALMGTAFWHMNYGKPQRVAVFELGGGACSVSFFEMTDFGLCELTSSSSDAFLGGEDFDATVLQYLMDELKKRKNEA
VDLSLLDVAAIRQLREGAERAKKALDSVPTTEIDLPAAVTGDKHLTARLTRDHFNQLTKPLVDRTATLCELALKAAG
PKKVDQVLLVGGMTRTPAVVEKVKEVFGLNPMEVPNPDEVAAVGVAIQGNVLQC

>B247_tetratricopeptide_repeat_(TPR)_domain-containing_protein
**MLARGGVTQPALQRMRLGVMSGGSSLPRLGTNSVVCGRNASIPLTPANRIHLASTAKQAGRLATVLHATARSCKVPQ
QIIFPIFANRGY**ATSTQDDINQRQRTARFHTFEARMMAEEGKWQQAIEEYNRAIDAVASDPVPLIERAEAHMALQDF
DACIADSQKALKMLRGSNDAEQRATCHVQIGLAYLAMEKYESARDAFQASLKEQKDEEVESLWKRASIMAQMKFVAR
STPAPDTDKEFYAKLTEGHAISVRSSRDPKTEETRGRGVFADKDFQEGEIVFVEEPLVSIADSIHEKLSHCEHCLRP
LVDVEFLADDELSAEIKGRLTPDLMQQITSKLGAELPPIDQTECVKHCGWNYCSTECRDKAWHDHHEDSPLCSTASL
SASNALSEHLDAFPHTQGAKQGGKELTLLMVKLLNKLSLERRHHKVKPDTIFNEDLDRLTYMAYISEAPLVLPEHEK
ERYQLMRTLFPSLGELLTEKNYMRLLSTINLNTMTVELHQLGVKVVGDVIERPHDNHDDHDHEHGPDCGHH

>B248_tetratricopeptide_repeat_(TPR)_domain-containing_protein
**MRRATVNQHLRQLPIKSLHPVRRVLSVAPSAIARSSGNRNATGTLLTSFTRCRALHTTPAQLRASLKYPPVGRGLRR
T**ATAAPDKEAGTASDDDDNDLERELDEFDPEELFEDEDITNRPQQRDTTVGSADAAIMKEISDFNLSGEQYHRLGMW
DEAEQAFRDTLALVDENLGSHHPTAAVVLNNLAMVYRQKGDLEEAERLLHQALNLRRAHFGQSHPRVALILDHLGSI
YRQQKRTEEALEVFRQSLAIIEECDARKRTPDGTVAVLAAKVEGDADSQQDDDGVVVPVAPQEADGEATSGAGGGDD
EDWEDLINLGTAQNNLGLVYYQVEDYAKAEVLFASAVTKAKQRERERERREEMERRGEAGEEQVKAQRIAHPLASTSTVI
QKNLAQCLFKQGKLEQSERELKDVLDHLREEVGLREHDEPVIDVFRHLARVYSAMGKTDESTFYADKVARNEERKKA
AAGAVPQ

>B249_tetratricopeptide_repeat_(TPR)_domain-containing_protein
**MKQMRSMRSLCRLGVTRNQALTSALPLTTRSPCLGRLLTTHSPSSSAPNSSSTSSSASERSSTGDSSTAGGAQPDGA
APELEKAEALLLAGQREEAGGRWAAALQTYDQVAAQHPDLPSAHTARAHLLARAGRPE**EALAAYREVLRCVPGHPHT
CVAVARCLLALGKPDEAMSQLSNVLDAHPRNVAALGERGDLYLRRGQVREAAEDYKAIITMEERSAGAWLGLAKVRT
LKGHMKTARKALDLSLRFATEAWDRIQKQQEQEQEQPQPVQGETAATGAASTAEAGASPQEVDPIKVQQAQRRLRDL
VAAHSFKGVYL**QAAGDMAHALEALDHAIHLAEI**ALPTTTAAELKETDDSPSLDAAMLGEDRALLSDLYCKRAASTFA
AERYDDCLRDCDLALRHSAGGNHLVRLLRGQCYLFGGRFADAIADLQLYLQAEEKARLATGSPGQHPAAEVQRQQVQ
EAIAHCQRALAGKT

>B250_tetratricopeptide_repeat_(TPR)_domain-containing_protein
**MKRLTPRDLPRSCWRNSAAVPLVAAARGQATALRCQLPRASAWDCVRSSSTTCWGVSAGRVASSSAGIRPKNSHQRR
HY**AAGSSAGQPDASQGVADAAPLSPAAKASLENASKLMEKASVKFEAEDYAGALTLYHDVLKLREGALGAAHPDVGE
AYHLVGETLWTLGKYKEAEAALNRSLAIMRNHLGPKHKAVGSILKNIAECRQAYLNDDETKIAPAKRAKVLEQTLPL
MVEATEIAQAHATGAEDDDYLDAVYALGEVYIQLERYAEALPCFEKTLPSFLKNAASDSMDTLLCWRNMSACYRALG
DVKKWEEAEAKVAEIENHWKNETGSEMHDLASMRETMMAMGLEKELSQFDDTYQELLTDEDKAKLKRKPTDKQPAKP
S

>B251_Complex1_LYR_1_domain-containing_protein_(possible_acetate_non-utilizing_homolog_ACN9)
MNSSASLLRSPGHRRGVRGLYRAILRTHRRRLPQNMRDLGDAFVSQEFRLHMDVKDGQVVAAFLARWREYLTTLRSS
DVEQKEGAPLDEDAVAALSDEQRQQLHRLRTTLLEDKEKD

>B252_ankyrin_repeat_protein
**MRLRTATSAGSRFPVNRACSPSSSLSLFLNRTYTSASPNGSLAASIRALHFSNLHHSSTIRAWPSTAAQQRGIAARA
SSMIHRRSFATYQEQT**EQERKQKRKSKPKSKDPWWKQNDNDFNKGQKAFAGDSIEMAVRDQNIKLLEKIMSQNADFA

QRKDSILMVAALYRGKKLMETLLRRGEDPNYKNALFCTPLHYCCSHDFPRGVSLLLSYDADVEAHDEEGLTPLHQAA
LANSVECAKLLVEHGARITSEDKDGDHPIHTAARLGSGDFVTYLLEKGADVNSKNFKGESPLHLAVTSDEAKMAMLL
LEKGASVGSRDSEGLTPLHRAAQSSDDKGCISMLIKAGADINDTLVAGISPLHFTAFSGNLDGMGKLVDAGALMEEK
THEGWNALMISAQEGHLGCLSFLMKSGAQLNNRNDEGLSALHLAVAGGHAACATLLLKKGADVNIKENNRLTPLHLA
AQSEKDDATLAQLLIENGADVSASTPEDGITALHAAIDHENVQIALLLLESGADPNQAEANGTTPLHLALQAELPEV
VEALCQLGADVNAKDASGKTTLELARDIEVGSAEVTKLLKRYGAK

>B253_B-Box-type_zinc_finger_and_WD_domain-containing_protein
MKAFRKALPQRPAAPLPPSPSIGATKPAPPAKTSPKPPVVSAAMTSSSNKCVECEKDQAVKYCQQCDAHLCSGCDRT
VHASRVASAHVRVDVNAGALASSSSSLVAKVQVDKATAAKWAAEAYTRLEEIKSLEADLSSCEQAAKEALDKYFDEL
GRAVTNRKQELVAELVAWKSDRQAAMTELKQKAAQVAEGRQSGPVPPLERGQGIAFIPGSEGGTAIRSSGKWFQGPL
GSGGEMKPPARDYASIQGPKYILGYGRGDAPGHNITPCDIAVHPGTGEIYQVDLGNHRVQVWSSDGDHIRTFGRDEE
SSKSMHFPKAITFDLDGNLAVADGRDRVTVWTTDGELLRRVEGTPAMEKGVETITGLTLQAGTGNYVVVDSRNRRVQ
IWRPDGAFVSSFSGDIKDPRDIAVDPFTGNFLIADFYGHKVTVWSPKGQFIRDFRGTLRGDKEPFKPSSVDVDAAGN
ILVVDQGNHRVQVWSREFELLCAFGTPGYQQPDHLWDPNFVTVAPNGDVIVSVCASNRCLVF

>B254_F-box_domain-containing_protein
MISRLFGRRSSQAPSSSAAVPPPPPPPLGGAQTHEEHQMVRAFGPAPPQPLFPWQFHANAAKLVEVRQRRRDQAEEA
KRKRREEAAKAGQPLPAEEVDVLHPASIPPEDGTCLLDLLPREILLYILQDVGEETLAADCPLVSQQFNDLAHDEQL
WKHRFLVDIGRQPPNFQPPSKYSNAKWHRQPVTSKEEYYHKVWKWYENYGGSIYEMRQVRFPVRVQDWLGASPHANS
RLALLGAIAAFDRRQLRRVRTIDKSAPRLGY

>B255_Ybjq_1_domain-containing_protein_(heavy_metal_binding)
MYTRGRVLAASSSFAYNSSGVRLGTSASSRRLLHICATETVPGRTSAGDLGMVFGHTVRSRNIVGNTWAQVQTIWGG
EIGGDTRLLQEARKEATARMEEAAQELGADAIVRVQYQCMSGHVTEVMCYGSAVRLAPASSKAA

>B256_YCII-related_protein
MYLPRRLLPSFSSVCGRSHLPGAAALVVGAGRLQPTTQYSSSANESTFLLLYEYVEDMTVRRTSYRAAHLALAQFHK
EQGKVVMGGAFADAAGAAYVFKVPRREDVEEFVRADPYFEHGLVSHYSIKEWHLTS

>B257_Cupin_8_domain-containing_protein_(putative_lysine-
specific_demethylase)
MSKVARRLASCVGRSSLVAAHTARPFSSLAQAENGQSAQVPRVENVELERFEMDYMKAEQPVVLTQAIDHWPALRLW
ADLDHLRRRATTDAAEPSDEVVVPIEQGSTYLDPEMEHRHVSFTSYLDNLEKAERGTDTASTGGRSQGAAVGYLAQF
RLFDAIPSLQQDFEIPAFCRLGRGDYYGTHAWLGPQGTVSPLHKDPYHNCLAQVVGSKYIRIYHPRHQACLYPFADF
TRKNSSQVDAENPNLDYYPRFADAPYLECVLGAGQMLYIPKGHWHYVRSLSRSFSISFWWQ

>B258_MORN_repeat-containing_protein
**MKRSRLIFPACGLRPSRLVASSRGTLPVLRSMPPAARWQTSLIDLAGSTGSPFSSTILRTKRVEATVHLALWRQPAS
LPRSHRCY**STTSSSESSSTAWILENYKGDRKDGKPHGQGYVRLPDGTTITGDWVEGELVRGRQVNMHEGGGMLYEGE
YRDGLFHGHGRGCNADHMYVGEWVDGVPHGRGRFVSTTERRTYEGDVSQGKPHGQGRETDEIANTVYEGQFKHGMKH
GVGVMQGPHHRYEGGWVHDRVEGKGTKRWKTSHKPDSNEEQYEGEWRAGLQHGTGTLTVFHRGGRRKTIFEGDWRDG
LMHGQGRELTPRGVVLRSGTWTRGVFVEGQQNEQAPPPPAATIAPSLSTETPKKKAPQRRGRKPAAQKLSQSPTSL

>B259_uDENN_domain-containing_protein
MSHSYSRASSYTFRTSSARSLRTSASIATRNSSAMLREFLWWSTAPEGGQRLELDPEAMTKQERLSRMLHVQKEYTP
LPTSGPLFEHFIVVGLPTPTAQRPEILYSYPPSNPVSIPGLADFCFPSGILSKKLRKTKSNSSLLQVVYSQSYHHEP
ENAYVFLLTTAEREFLYGVCVIKHESVYNKPSFFPRDGQLPPVADGSDVVAPRCYCFVSRFPFFKLHFETIYSILDL
EYMASVSDLQSLPASLGSTRESQSPPALAHSQSMSALVAP

>B260_leucine-rich_repeat_and_filamin/ABP280_repeat_family_protein
MSCAVGAPRLVRTPTLCRLSRALAPISVVVSSALSALDQRSPQPKTQPTKMGGAMTKKAKDQVSLCRQTGGTELNLS
DCEIRKLGSFKSIVRLKLLVRLNLSHNYLQGMPPTVKKLVNLEELDISYNEIHVLPWELYQLTNLRVLITEGNGITA
LPAPAISRLVKLETLSVAGNRLTGLPEDFTGLHSLTSLSLAKNHLVKVFPEVFQLKQLKHLNLSINPGLEVPERFGE
LPNLQVLELTECGIKSLTSAIGNATSLTNLRLDKNELTSLPDELANLSKLQILNVSFNQLTVIDNVTFRNFTALEEI
HGSNNRLDHLPRGLGQCKKLRVIDLSHNQLKSINREVGWLHATIRKLLLGDNKIKTVPGELSFLNPAVDLDLGNNPL
GSPFVQWYTQGIITLMENLAPYLRAYPAHCVAEGDALAGTTAGTPTMFSIRAADYHGNTRLNGGDEFEAVFRGVDKD

NNPIEQKAVIKDNQDGTYTVFFNATVAGKFELHITESGESIGNSPLPYVIEPGRVDVNETIITGVPPSSVPVGNPIQ
LSITARDRFRNATTPDQPFLVTVATPGGQVAKLSCQATSPNVFMCAFTPASAGDHHVSIQYQGVHLPDSPFLVYAV

>B261_TraB_domain-containing_protein
MRRSALAYVGGHARANGAHLPSQIFARRVAATTRASSTSLLQQQRWLATSAGSDSSGGAPVYGHVTEGAEGDTVLYM
RDTGSGREYWLIGTAHISKRSADQVLQIMQRVRPDSVMVELCEGRARRMQEEDGQDPFKQLSAQVSRIFAGPFAGFG
APFLEASLRSFYNVFKLLGFVPGLEFKVAMNEAKKLKIPVVYGDQESSKTFQRLSSVFSLDRLMRINSDAAHNQQMQ
SLFQQIQANSIEEMVEKLKNRKLVRRFVQVMKQAYPEVVNVMLTERDVVMAANLRRCPGKVVV

>B262_tetratricopeptide_repeat_(TPR)_domain-containing_protein_(Sel1-
like_repeat-containing_TPR_subfamily_protein)
MRRCTVGIPCRLPIYGQNATRLQASSRPVLPSVSFSSAASRSSLHRLLPLSPATSPCLSSSTASRWHRPIAGRRVYT
NDATPSTEVGRLTPAAAAELRHQLEARAEAGDAEAQFRLGVLHCFGTGGGGGCSNHKQASSEQDSPVIDKDSLDFLI
GPGYVVPKTDGENTRITNWKQWLKVERRKLKASQDTSDETKQPETAGVGPNYALAAKWFHQSARQGHPLAQHFFAMQ
LMRGMGVEQDVEEAMKWLTMAATSGNSLSHYELGQMYYDGSLVPKDEAKANEYFVQAADLDNPNAQFWMGYCYHQGL
HVEGSVEKGLEYLEKAAGHKHPGALYYLGMMYRSGEGVPKDAEKMLAYLTSSAAEGEAEASFCLGDIYYNGSDAVEV
DYPKALQHYREAARKGHANAMCCEGVMHFHGLGTEQSDEKAFYAYQAAALQNHPHACRNLAYMYHHGRGCAKSEANA
EYFLKLANQLESQQS

>B263_SET_domain-containing_protein_(putative_lysine_methyltransferase)
MRSCARVSCRPSTRPGALVTSSSWQGAVGTHRSSQRLRQTTDHHSTSVVRQLRCFSSSTAPGEGSEFEPEVVDQFKR
AFYDQLAGGPNSPVMIADVEGRGRAIVARHNITKGQLITAEKPFVSYLSERVETHGAAHPPKPTRCDHCMRGLPPAA
AKAAQHNNPAEDERLCGSCGQAYCSHACREEAKAQYHEAICELGKEVREMEIHCSKDKRKFPLLAMRTMARILLNFR
DTGSLDATWVPLQVLGFAKQKPELWTQDYDVFKRCFIHNEDQADFFSYEWYCRMMQIFYINSVSVTMDSTQQNVGAG
LYILSSFYNHSCVPNTRSSYPENNTWHVYASKPIEAGQEIFISYVDHMKSNKTVETRRQHLYNHYGFWCECPRCRLE
LDLARREQGPA

>B264_SET_domain-containing_protein
MTTLSSRTPTPFRWALTHGHGRSKRLWSSLLHPPTIQRSRQRGIVEVSTLTTNASLEEDGRGSDKAEGAQSGESVLQ
WQERMERRYKYEDITRQLYTYFEALHAFHHQRAPDIAAADTNTNRATTTADMMRTQFGFALVKRRSTIPDAGHGLFL
EGAVSEGTCVCIYPGAVYQPGDPLLLPSLRNDYLIRRSDGSSVDGRPRGLSRYFYRSIYEKFGPFAGLCDATWLDIK
EGGTNEHNPFGWGHLINHSDVPNVMYFEYQFPPDTPAHYLSSIPNVFYSSKDPACAVKTIVLMAMRRIRDEELFSNY
NFIGRATPESRRDKIMR

>B265_PH_(pleckstrin_homology)_domain-containing_protein
MRGCLGRVASLRSLLSTSQRNAVHKPLPSSMTEGDHINRVDAAPTTVDGSELHVRRERAGEGGHGAGAAEKETNYNN
CGGGRKTKMDGAKLKRTLSQRSNRSLGRKKYLARGRSNVPSVAPSTRNHPAGAAAYVEVGEGSMVPVVFQWPRSATE
ISVLFRAEGAEQWEEYSMCGDSAKGYRLMALLDPAVYHFKFWADGIYYQHPGCPLPDNFPDDFVVSFNLQFVCKRIR
PEHVKKLMHKYAVKTWVRHAAKRGFGPKRSSDRSGGRHGLKALTQSLKKVPVAEFERQQPHQKKRIISLRRKKSKKK
DERAVAATAAASGAS**PKPRSGS**RVQPRREGPSLCEEEDIDTASSITDDEGDDDENLPRDDLLSSEGVNDAEASPPPQ
QQPLEDLTNDDSPGDNLNQAAKRRTLFAATIEEDDSDNGAEEKFYSDSSYYSSSEDSDATDSGSDSAGSDNEDADEK
SEAEKNEDEADVTVSECDDKDDEGEAASEAETTEYEDDGDEGEEGERPNAGGKADSENKNKEKRRRRGEKALSASER
REKRRTRRRDELEQREEEKEGKRQRMKRGPLVRLHPKTVLPVTFFWPGPAHSVKLIYKSYFHAKWKSKAMQPCSPSS
SRWSVRITLLPGIYQTCYLIDGEHYYASLTRRVVDPQHVLSDCNLYRIDVDTKPWLEATKKRGHLIKQGGRIKTWKH
RYTTLQHHEIHYFRDDKEEEPINVIPLSSVEGEIEASELAGKKRACFHLHTPGRTYVFSSASQEEIEDWVRCINRSA
FMHKNWERVLAHYRPPPATYHNTV

>B266_Cupin-2_domain-containing_protein
MLRQAKRTSTSPVWSVVRPRRCQLQLHTPASIMQTTTTTAASSSSSSDATAPTSGSAFFFRHDVQHGGRAYGLHPPR
TIYPLVKTAHLDFGVEEVEVGSEIPWHHHDDKEEVIFVWRGQGQAYIETDQVAEGVATAGVESSDLQAGVTMYVPPR
HRHRLVNTGAEPLWITWTFAPPGDGFEAALIKQKQSQPQA

>B267_hemolysin_III-related_protein
MLRGVLTAMTSSEKSRASKLHSPSLVKRSPTISRPASHVADDPRSICKHNKCLTYRTVGFDDAPAYQQDNPFIRTGY
RANFAVSTCLVSLFRLHNQTCNVWSHLLGVPIFLALALYTYLFIAPEDNFSGTTLMFFLFLASAIVSMLTSSCYHLF
QCHSEGAWLRLLQVDLSGMSALIAGSCYPSLWIVFGNGCHGQTAVVYITAISFICSVGILGPLWPPFNTPRYRRARV

IIYSGMGLSSLVPLFHIPFVFPAAIAWPILADVGLSLLFFAVGVWFYASKFPEARWPGKFDVWFHSHTNWHICCVLG
SVQTFITACHCYTNRHLYTTCLL

>B268_hemolysin_III-related_protein
MCFFCAKRSLLSAAAAPSSSSFTTNHAGMKNSKGLVGAGSLQLTAPPTFKITEIDEHLKWNPYIWSGYRENYTFGQC
LYSFFTIHNESVNVWSHFAAVLVFAWAMHHTLFDVLLPSTSLLHLVIWATFFLTAIACFAGSAVYHLFFPQSVAAVY
WLGILDFTGIAALVLGSYFPPVFYGFHCFPFWQRLYITSISLLGTVTLVAPWFRFFHSQRYLAIRVSLYAMVAVAGI
VPAVHSYFLLQTIPHNYTDGSFDEVYHRLYIMYGLYTIGVLFYMSKFPESRFPGQFDIWFNSHQWWHLLVVCGTLVH
WSNCLLIYDNYLKLLSFCPADSAAPLPW

>B269_regulator_of_chromosome_condensation_(RCC1)_repeat_domain-
containing_protein
MLAARAASRGGLSTAGAAPAPPEEVARRRSLLLDAAEGETNAVTSGRLYTWGRNDYGRCGLGDTKHRAVPTRVPDLG
RVVKVRGGAGHTLAVTADGTAVAFGKNYLGQLGVGDDDDRYYPHRLQLDDKPAASCSGGGNFSAIVAQSGEVYAMGC
GYFHATGQPTEAHLRLPTLVPFPVGVKVVDVACGELHAIALSAEGVCFAWGRNTKGQCGQGETSRFCPAPVPVKGAL
EGKPVAAIASCFDWNMVIASDVDRGKELRRVWAWGDNGSGQLGPSHCGDSVAERPPYSALPMQIIGGLEAQRIVAIS
CGNDHGVAVDDKGDVWAWGVGELGQLGFGEECGLAVQTPRMVPFFQRRKASVIVVDVAAAKKHTLYLTQNGQVYVSG
DDQFGNERVDAPVNPRQQPHLLDLPFRVSAIGVGGYHSCLVTE

>B270_gamma-glutamyl_cyclotransferase_(GGCT)-like_domain-
containing_protein_(AIG2-like_family_protein)
MRRQASIAHGRRLLFSHCLPIASRTPQGIVHRTMSSATTVVPFPAGHRVFVYGSLRPDINASIHQRFMGKCIPVGPA
YYQGRMYIVDKRTEEEQLLGLKETTDVSVPSEVRKYPAVVPSDDPAERVHGMLFDVPDEHRDEVLRGLDEYEDAVGI
PEGLAEYRRDRVTVRMGQGHVHENVEVESWMYVWAREVHTLARVHDGDYRSVYVLRADAEESASLPQA

>B271_CDGSH-type_iron-binding_zinc_finger_domain-
containing_protein_(possible_glutamate_synthase)
MMLALRSSRATGMRSALGRVSTPVSAKPLWGLSRRFSSSEGAQSPPEVVQPVVVAQNAPYAFQVVKDQRYSWCTCGR
SAKQPLCDGAHKGTGLKPLRMVAEQDETLFLCGCKHTSSPPHCDGTHVKNAGW

>B272_conserved_hypothetical_DUF2383_domain-
containing_protein_(putative_aldehyde_dehydrogenase)
MQRRALSRSVCLVRPRQATISLGVRNLNINTNAASASPVSTLNTLIETTKDSKEGFKTAADHVKDANIKKNFQEYAQ
QREQFSKELQDQVKKLGGTPETSGSTLGAIHRGWVNFVDASKDQSLPQEALGLVQKQHAKVQESLNY**AKDLYNKL**

>B273_conserved_hypothetical_protein_(no_PCD,_bacterial_homologs)
MVRRCVGRTSVLAGLLGAAGHGLAGARVQNLLSHAEGRGRHLDQLVVGDVGDGLLQGENARRREANVLVLEQGAHVG
EGLGLDRVDVHVALLRVLADDHAHVDRGAGSDEHGAALLQALERVGGRGAVRVGEEHALAHVLDDALVRDERVEQVV
QHHGAAAQLVELLPEADQRTRRTHEDEPRLVAVRLHLHQLALAQAESLEDDAAELGGHVDGDLLLGLEELALLLLEE
DLGRGHADLEALTPHVLNQHRQLQLAPALHLERTLSASVTDLESDVALKLSVETLTKKRRCQLGALASGQRRVVHAE
NDRQHGRIDGVGGERMDYRWRTDRVRHGAGAEAGDADDVAALAPLDGGALEAAAAEHLEHLGLLQLLGLARQPVQLV
TRRHASRTHPPDQNSAQVHVVFHGGHQHGEGRIRIRERRRHLLDDGLEELGHVGPGGGAVLDGPSLARRGVEGDVVQ
LLIRRVQRDEQVEELAFDLVRSDGVAVHLVEDDDGLEAVAEGLGEHELGLGHGTLRAVDQHHHAVHHAQHSLHLASE
IAVAGSVNDVDGVVLVLDGRLLGHDRDTTLLLQRVRVHDAFAAAKGRGAALGEELVDEGRLAVVDVGDDGDVPELLV
AHAFAQVLGALGLGRQP

>B274_conserved_hypothetical_DUF167_domain-
containing_protein_(putative_UPF0235_protein_C15orf40_homolog)
MIVTLQNRLSMRRAGLAMSRSSKKKAATATTPQMAGPGVGGTASGLPQCIGTTKEGNVKLTVHVKPNAKISAVTDMS
SEAIGVALAAPPRDGEANAELVDFMAGVLEARKKQVELVSGSKSRDKVLLVTAMTPEQVHEKLRRHLDIADE

>B275_conserved_hypothetical_alpha/beta_hydrolase_family_protein_(Abhydrolase
_5_domain-containing_protein)
MIRRTHTLVRPSGRLLRLTTAQATERLNTTLRHHYYSVQQEKKMADEVKVEAAPGIFLSGNLNIPPGAKGIVVFAHG
SGSGRFSPRNRYVARVMQEGGLGTFLFDLLTPKEEEIDDVTRELRFNIPFLADRMVTVTKWLRGTDATKDLNVGYFG
ASTG**GGAAIVAAARLKGDPQVQAVVSRGGRP**DLAGKSLRDCIVPTLLLVGGWDGPVIDMNKDALDKLAAPVKELRII
PGATHLFEEPGKLEEVARQARDWFKKYLDTPQAPSASEER

>B276_conserved_hypothetical_protein_(no_PCD,_protist_homologs)
MKLNQMAAARSSAGHRWSGFSSRLPAPFVSSQIGTRGATRPYFVSASPHATATDETERGEKAKKPSRRTTRVARPQD
GEEADDSSHLAEGKQHATQNKVWRSAELGLGVVTRERCLLTAERSAEWVLGLDINTNSTGFTVLHAPTGEMAECGVI
ETKAIPDLFDKVTFLRRRLAAIHAAKKGDDKEATTWVVGIEDFLKSFGGAQWRTSDIMKLACLNSLVSYECWHLFFC
HHQEHSPPTLEFGEADDEFALQHLPPENDDEANEDDEASYMTFGTRRPFKVHPSQARTYFGIRKRSAEDKIKDLGFH
RVKNLFPSDHPWIIKKTGRLSEKNYDVVDSFMVAHYTRKMAVESALYSDPHLFAEFEAAWLLKNSAAVETLRPRHTN
NHQPPADVDVVSKRAASAERRKQKGVERRAEKEWKEEVDRRARAAFKKAISA**AAEAALPAPSTLVRV**

>B277_conserved_hypothetical_FIST_domain-
containing_protein_(cyanobacterial_homologs)
MRRWMAPCVGGRASLHMCHLPTRQSLRCPDRWSILPVPLIATASSVAVMLPRIMPTGRAAGYARQRATKQVPKIVKA
KGPAVKTNKDEDQSAAAALKEWKFTGWVSTKRDIKAAVDECVQNIRPKFGDVKPDVCFVFSSHQSDDKLRRIPALVK
NALKPRALFGSSSFGVFGAGGAMPQGQEVANKQALSIVAATMPDVEIYPFHVRTPSLPSFPPDFDWATHTLPKRKNG
GAAEDDEISSALFVITDGFDFREDELLQRLDFAFPSCPKFGGLASSRNVRLFVNDKAYPDGAAGLLVHGKFRLDQIK
AESFRPIGRSYTVSEVTPYSEKEFETFLTSVGAEGAGEGGDDDGERDDTKPSFAYASDDDDDDDEESDDDDEVEDLS
SVIHAISGRTVHDVVQELASDLSSRDKSRFLSGQFLVGVDPRVPSSSETKPRPPSVFVARNVKEMEVDSESNEGGYL
TLYENVPQGKHIQFCLKDRNKGLADLRAQLARLDPPVPAAVAASPAPPAPFCPLTLERTSEVGMLGFSSIGRSLYAK
DAAAQIELAHEGVFPLAGRTPLDSVADQLVADMHANADTSEVQSFIEGELAPSVDRPAATAASGNFAAAPTTAVEGR
HDDDDDWVEQLEETTTTTTPTQQQQKTERKNEDDDDIVSYSQKAKKKPQQPEESASSRQQLEEFFDDEEDSEERRMM
LKKKKVEEEEEEEEEEEDSSATDASVIAERFGSRVTFGGMFCKGEFFTTNTRQEHENEESKNNIDDDERSTLLHGYI
NSIAVIMPPKSYHQLRKEK

>B278_conserved_hypothetical_DUF3429_domain-
containing_protein_(possible_membrane_protein)
MKRASILRPRFVFSNATSRNRLPAQALLYSTTAAPVNAREERLQDRSVPKAPLWLGAAGLIPFVSCAAGVAAGGVDL
TLLSLSVTPDQLVHLQAVYGVNILSFMGGVHWGLAMANYQRPPSAKASVVPTTPSETKEQDMPSSTGGNREEWRYGL
SVVPSLVGFGALGLFPSSPSVQLAALMAGFASVYAGDLTAASHQMVPRWYLKLRTPLTLIVLLSLGVSYAHLPPQQ

>B279_conserved_hypothetical_DUF4396_domain-containing_protein
**MKRVPSALSLPSRAGRPIALLHARSLVTTSTSPPPASSSSSASSSSSSCCAKKSSSPTSSNPPTPPAPAPAPTSLAF
WQSPPHWRRAGVNTLRCLVGCSLGD**LSTLFALTAAFPALPVHVTMPAAMVAGITTSVSLETVLLKRSESALLRDISW
REAFKMATKMSMVSMLAMEATENMVDLYLTGGVMDFSSPLFWASMGVSMAAGFVVPLPYNYFMLRRFGKSCH

>B280_conserved_hypothetical_Oxidored-like_domain-
dontaining_protein_(oxidoreductase-like_protein)
MILRSGRPPVLLAPVAVGPRRTPRGSGLLTSHLRRSLVSLAQEGMAAPPLTPPPRPVEGECCGSGCANCVWVTYWEQ
CEDYERRRKALQRLQQSGSGKLDHHQHHQH

>B281_conserved_hypothetical_protein_(no_PCP)
MRRGLVVQRFGGSSGSTGSLFAASAASSCGRRQLVLTGPALTRSFRTTPCSAAPEDLEDDKDGVEINAEDVEGEEYV
SNSNESQADKKRRSKEARYAAENAELDFLAKALIWDYRGQHAPRPMLAEETKEELYRLHKEDPKRWDLENLSLYFGL
RKDRVQAILTFMGMRDVAVRNGEVLNGGVVELLEQEFGVVGRLADKRVLDEERAGGRPGSGLPLEEDAIDNDARLLD
HARAVRLARAPRGAPLKELPPQPPKAADGSQVPEAKPHVLRRPTPTEPRSFKGTIFMERDSRRPPWGRRRRYNDATR
IMYISEPDGTLRTPTWDERRLLTSADKHIPTTARYAVGENRFFKDDN

>B282a_conserved_hypothetical_protein_(no_PCD;_possible_UPF0598_protein_C8orf
82_homolog) **[paralog_of_B286b]**
MLCFIIISMRVARHCPSPRGIGSQWVGGAVHASRGLRGVHHHHHHGAAGPATTTPSSSSTTAPDRVAVTAAAPPREY
FYWVDLRGHLYCIDKDATTLPRQNDPAFLRDGRFLNFFWRQLQLNTPTSPGRARHGAVYPYVSPCGRELNYVRAADR
PIAFHSLQTLPSGESVLLYAHDLSVPFDPAELCMRDNGRLYHPSPVGLGLLRSALASELSGCIEGDEEEEEE**DRFVF
GWRGRRTPIRRIVDDDHTTIDADHQ**
>B282b_conserved_hypothetical_protein_(no_PCD;_possible_UPF0598_protein_C8orf
82_homolog) **[paralog_of_B286a]**
MRVARHCPSPRGMGSQWAGGAVHASRGLRGVHHHHRHYGAAGPATTTPSRSSTTAPDRVGVTAGAPSREYFYWVDLR
GHLYCIDKDATTLPRQNDPAFLRDGRFLNFFWRQLQLNTPTSPGRARHGAVYPYVSPCGRELNYVRAADRPIAFHSL

QTLPSGESVLLYAHDLSVPFDPAELCMRDNGRLYHPSPVGLGLLRSALASELSGCIEGDE**EGREEDRFVFGWRGRRV**
PIRRIVDDDHTTIDADHQ

>B283_conserved_hypothetical_protein_(no_PCP)
MRAALRLNVSMVPSRATAPALHYAASTTTATRVPPLLLDSSRMQLHSLLQRPSSAATWATSRRTPRLSSHRRGYANV
LAERRKELEKLAALFSEARDEIENARESAGTTYFNEDFAEAKSCATNALDYYNQLLKELQPEEAIKLKEEQNPKMEQ
LKMELSMLEELAAD

>B284_conserved_hypothetical_protein_(no_PCP)
MQRTYPMITAAVQRRTTAALVSSCRTLAPAARHYAEGPQTSTEKDFKEGGEKYDRQARGEPSMISGHAQYVKGAVEQ
TLGSMIGSESLKKAGQEDKEAGVTEMKAAYHGQDDWMSPELEKKLGKVIGCEGMAEIGDEKLRKKHDQ

>B285_weakly_conserved_hypothetical_protein_(no_PCD)
MFRKRSPKWCQARTKFSTRLIHHPRQDKMAALPADYSRNGAPPIYDRYKLAKERPKFRGCWTAAVADPTVRSFVPVA
STAVPKAAPRPAAVPRAAPAPKPEPKLVEVPTSGVRLKILDRCRDLRSFITDDGTCTDKYGRVIGYINFNEWTVGGP
DESFWGSLLEEQILDKDDKQIGEVDFGRAWVRDQVGNTVCEMENTGECKGHDCSFIGQFEGFTFHDLKAVALYLIIV
DPLMYNTVAG

>B286_conserved_hypothetical_protein_(no_PCP)
MYAGRRNMMASGLRGRPTLALAATVGRPQYPMMAMSARTFISHDPPIAEPDDPERSMREAEKQKRINLEGKAVSDVP
DAPGWNDRLASDSEANVKADRSELEDVHEMQEFTIKTIEQREEIEQEVEKEIEMSGLANDAVKAFAQESKEFPAGP

>B287_conserved_hypothetical_DUF3605_domain-containing_protein
MMRRGYATLRASGQANGTLCRRLSWSQVVDIVRERAFDRFGRLPEEQALYHRRMKEMREEFASVGDYVLHHKFKYPF
DIQANLHQGKKFVIPPPADVENDRYVWVLNDFPYALGDEIDHYLLWSLRPFPEPKIESIIRDHVDSRAIDCVYFTNP
PVLRSVPNVSHVHIMTHPLSPPHLEI

>B288_hypothetical_protein_(no_PCD)
MKRAIVASARSGVPTSALRVRSRIQWNRIDLVQMRNGWRTHNCSRRPYSTNPAPAEASPSTSSTSTASTLPPPLPPR
RPRVELKRTDETVEIVFRKKTFYMIVTSVAAFAFLYSTDFTAWLYHALHKDELEAHWAGRLYDESYQLLLKRSKRRL
LEERNFLAASEDRDALSRTDLRVVKVEPKHSFLTWRYSIAKDGSVNHTFKLWKFDVQIDIDYALKVRTAHVGNMRAR
GLLGIEDMHLLAAEVVPRAAQPPPILLTKREKPLSFDLGVTAYPPHLSLPDKWGVAKQ

>B289_hypothetical_protein_(no_PCD)
MQRARAVIAPSKGQAIRSALGASSSHALPARQFAIIATRSSSRLIQRSLLSSPSSSLLPLRFHVSLRHFHASRHIQQ
SAAAPEAVEEKVMDGTDPDQVARAILSHLRDAAPQGDAAKRNARLRSLLRDLKLGEGVGRALLAVSRDLGLRRTGRL
LPLLYSSQEKGSINRLTYLLLTLAHGHIQQGDKEPKDLTKALGLLTNGVVETWEAEDVAKLLRVIPRSSYFSLAEGK
EYQPGSIEWSPRELGGLVGQLKHERAERRDLEFFMDILVKLLTSPEREGGWGREKSVAPAEATSDSPATTTQRKDLP
KSSKPTVAYDLDYVPKVVGPALAPFFDYWGNQDYATVIQCLITAFSQHAVATYGQQTLTKEQYHDFCMEMMAQTAIS
SKPTVGMLHYMINDITSGWEEHDVDALSTRLEARMKPHSFFRRWFRKLFNQPTPN

>B290_hypothetical_protein_(no_PCD)
MKAAVGRSGGVVSMRCTARGSPWTALPLASTAALVGAQVRAKHYISYRLEGEDDPYRHLRRCKSPSKKKQSRQQPQH
DEELLMGEAKEEASSSSLASFLFGPTTQHDEEVNRSPVEAATSQRDA**EVASGLGAGGGVVHRSKGAMPSRRPSVEGG**
VGGQLTGGAAGQGPQPQTPRERGGGGEDRGSAESRAMMADRPRVEGEDHEPVFWVPQAVKETGKKVLERVGGAAASV
GHTAKQLWVGALKRVSAQPDHHHGLVDKAKDVGKGTVHVVDTGYEKTIEKAADKMLEALDASLKSAKARGFPPGLTV
TTIASVMGAQLMMAYTTKEEDVKTESGRKDANITRPKQQSRKTAQPRQRKESEKSKKGSGHLAQEQR

>B291_hypothetical_protein_(no_PCD)
MRRVASTRSLARASCLRRSHSLLPKTCYLSTTGCVLARSALVGVKQQRYSEELHSNHGISVGDQLAGPHQRDPHEYL
KQLSTKWSWPPPSAKLKAPPTATHFLYRAQDRMDSVEALWRGVVQPSWQAYRSGYFDDKKAWSTGFIHGASGVGKTR
FNLEFLALLADYLTSDASKAYRSPDDEVESLHAALKNSKTVVLDIRHNGLALKVDETEWPPEVILGLRLAHNYWWPH
VPYSEVYDAFRWQVREDPTLWGTFSLGRVLFAIRQHKAAPTRDDPSPRIPSMLHIAIDEIQSVFDTMAPYGGGSSVR
SAPEPLSTALNRALQGAISQSQGLYVLGTLSGTAARHATEVLHATDATSTGVLLSPLSAKTVRQIVASFQFRFEPQP
GQPEMVSGQEWLEKGGKPFERLLTTIGGNARALECLERVLKTQGSPSKPLRLNQITTELTKEVRNTFNIESWGRKGS
GQFGLLLALAGIPVTRESVVAFEEPSTPQQPPRPITVAELEKIGVVHLRPPPPSDPGQPDSWVNTWDVQELAVMEVP
FVLAKAALDLAVKSKRHQRHQLHQLLKEASRLLADFYPTAASFEKLALEHRVLRHNVASEWARRQGLTYVDAADLFC

GTICHPSLTELSFVPAATVRHVSEPAGAGVWWRAAKGGGPQASKEVPPTSVILEDGTTVELGSTSPYALLLSGSNAV
DGVLNEQLSHTPPKNVRVYIDTKHTQIGAPADDALSYSDDIKALISKRRYLAEQFPEEEHIMVITSNKRAQQPGGKP
HTAATLLRVPTAGRNETTSVDPRTCIITVTDDSLAWAMSPTLAHFLVLE

>B292_hypothetical_protein_(no_PCD)
MKRAGLLCRPFSAKNALRSTAFASPRWNLSGSPQSGGLLTSSSSFSAPPLPANIFSSSLLPGTAPHRSTCFSRFAST
LRTYSLPAYRRLLSSATSTTAATRLGHGRTTSARLVAATTRRYVTLNELQRGGKLHLVYTGPNPATIRTPAAPRPYR
RVFLRDVLLLCTALIIAPFCSHLVSYASGMDKASFERVMLWWLKYREKGPTPPHTGYTIVDGQELQKVLETKLGRPY
TMEILESRLDDKINALADNMDGVELLIISGKKTFGGWSVPYLTVGIHARIRWTETVKIVGPNGIAHLNVTLRTISNP
EKRDLSTQLLKSKRVLIEKVELAFADNSSYVLSEASFGRQKRFTAAKLNKD

>B293_hypothetical_protein_(no_PCD)
MKKVISLPSSPAALRRFSPSSSHSPSSSTRSSSTHNNKTTSPALRRPSPNSHHHHKPNNKKSANKKKLSLSIKLAAS
SDSEWGRTDDEGDDDDSTTTWGSSDEDEWESSFDPLWVVDADELELHRRWTDQNGITTAGQPAGVIKGKPLRRSPLA
TNSTVSTSLSLPASEHHPTAQHLDV**GAGACADVSTSRPPSPSTTATATGHQISYAQLQSAANAASSAAARHSPSSSP**
RKPVDVPAGSLLPALDLDRVVSSPVSLGSSMSRRNTIATPREARGDASSAAAVVSQWKVGKISPRGDDDVKSEATPA
QKNESEEATVAKWSPRRSELQISFERFEARLALKKQQSAVIGVKTPESNEQPQPQRDQGKTANSKRSGSKRKMKKNV
RSLNKEETDAKRKKKRSEAETRRTYRRSQGSPPMLLRSAAAAVESDSDSSEVAGYLAECGGSETESEEEKRAKASSA
PVSPHSSSSSSMSSLAVIASLALRSGGGFPLNRSRSSEVQAKARRTISKEDKKRDDANNVGAGAISTDHLPAIATAT
PLPPNNNINSSSVNKASSNHTHDSSATDNAELTWKTIWQDPHEGETEGAVTLTSSSSSSTPPLTSSLSANEASTRKA
L**KRGLEGRSASLPPVPSRPPLAPPSSPSLPPHIEPLPFPPFATSPPASLNPLASPPAPAPSSSVASPSLRHRC**RAES
SGAPQQLMLVPPPLLPHVYQKQQQQQLLHHHPHRSLERVRTVVLSPSLATRQPLRLQQQRQAGLSVVSLGCSSRAAA
ESGEINTSSFLRSQSEEISARSFDDDFDNGDDDSGGVDQVDDGLHERRQVTSWRGRSGGEWRNRSRESGFHHQSDDL
ATRRARIERARSFGGAKADADHCDSGDDDDDDLLLFVSDDDDDSVFVDDEVDGGEEEEHLIEAELTSFLKRTRSGSH
KPLRDFSGSLEGRRSPLTVRLVPHHHHHHHHPHASMTPTTRDACGDELTITDGGLESGESHTAGGASRDSGHELPCR
SPWGITIE

>B294_hypothetical_protein_(no_PCD)
MQRVPTASLARSSSMGNLATSSSRAASLLASQQRSSFSTFLGAVNTNTLGFLREKLITHDQPQRDRKRAAGKKSEGV
GLAPVSRDLYRNIFFNSNERSALRHVELTPDYIRLEFSEPNEEYRKHADLLFASEAERRAQGVPNWLVPVELQNNEH
CGGGATILLDKNSVYDSLSHEGARRRSSRHVARH

>B295_hypothetical_protein_(no_PCD)
MLLRSLRRGSTVAYRSASPCGRLASGSRHLHATTSTARGLSRSAKCGWVAAGTVVGAGLGKELLAKARAEEAGDETT
GSVSLDSSASADSPPINPTFPMYRTRGDVLYWVQYYYRHPEADLLKLAVESLLKERMKPEDGWLMAGLVAGIMKNRP
ESLSHFAVHDIYNVLQDFRQALLVGLWLGGSHGKEHLQKLVDEVTDEATKQTINNLLTTPPPDPLLAEMDIVNANMN
LHVLLGVFYATGDTAVVDKMIDLCRDWSVEVLTKGGREGAARFYVAKTVREKLALLCQEHEVARCAESCPRPRADRP
PRECCAASSAARW

>B296_hypothetical_protein_(no_PCD)
MQRRGTMLAAASWGRGGSALPSGRLAFLASSFRRPLTTSTDVSFENVSLHSALLQVAQVKGLTASALESWNRASRLV
LEPAGLNTVGDLLSLPAQDVDEDLLTNNDSAAQRAKHLRELALPKGVLRALVHMRAGHHDEALRGLATALAKRQPPV
SPFAEADETPAETPEDETSPQAAQ

>B297_hypothetical_protein_(no_PCD)
MKRTAAVRTLMVHQLRLGTPNTRLSFSGSRIARDRLLSTSAEEAVVPTPSLVLNRFLERDAAQRQWQVGLLAVPKFS
VAVLAGVAVSGGLAAMQNHTERTRPIVLRGSATAAYGIKNDPFTYLGLWGIGICTAAAVGSLYGFLRMGRRFGKWSQ
QQPNEWLPIMPAARALLAKRTFARTGLGTAGFLAGVFAVDRAMDRVLLSAYTSEAQNNLFTQKNLPPTSTVDAYILS
THVGYLLVATLLLSFTPHIVLPSLIAAAFAAVANFKVYMLASQRNRRLAAAGVVRGGPFPPADATTTTREAATSSQD
TTSSQST

>B298_hypothetical_protein_(RNA_recognition_motif_(RRM)_superfamily)
MRRISSSAQLFSSSPARLAPGSVRHYGVQPMSVKTMGLLPRGQGFLFQKEEGATSCVQQLNRIYILDKELRDLLRTE
ARMKPQEVAQSTQASSAEAAPLSSSTLVSTSPASKKAPRSRSARSAQSNKPIREPRASRKAVGSPSS

>B299_hypothetical_protein_(no_PCD)

MAKWCAQAVFGRKLGPGRTALSQHIGSSRSFLFTLRLPHRPVTSSPSRSFTTTTTMQSSFSLPRLAASRLSTPAATP THRAKTVVPLVGGACLGLGLWTNNSSQPLSLPHLRSAVATSRRQLSGLFLSDDLHQSIGVNILE

>B300_hypothetical_protein_(DUF566_superfamily_protein)
MATTSKARSSGAVPTRRSRRFSWNFARPSPSFDLDPSAYKDSPIFIAPRTPPAEPKVDDSPSASSCSQPTTYQSPRR
VALRRRATVAIGAAELQGRLSDMSLESIAEEEEGEARQEAKREEADDLDQSPPPPPPEKKKDKKLSRMFPLLRRHNT
KG

>B301_hypothetical_protein_(RNase_PH_superfamily_protein)
MRRASFLRSTPSSFIPVGSRRIGAAQQLPSVATGPLRSISSSTSAALPLLTKRSSLPLSRQSARWMATQGDASSADS
SKKEQQQHDNDQQQTKNEQQNEKEKQDDERKEEDQKKEDWEKSRGGGYKQEVNTFQKLLAVGIPVTAIVLGVKVLLD
MQATGAEDDTLQVDMNVIMGHVFQNTVYNVLDSKRLVGLLGDPLLVEPSKAKFSFTKDSAWVCYPLYAPQGHVCTVT
VDLLRIDPKGKDVKTKKPHMWYVAQVEVDLNNGKKVLMSTRMSDGLRQPFNVLTLFAKLYHDLKKQEQEFLQQQAAA
ALNQGPAPQ

>B302_hypothetical_protein_(no_PCD)
MRRATRVMNAGLGGQQAARLLGGCRSASIWRSDKTKDSIVSDPVQDLNPQSTREKRFADEDTRPISTLSQDTAAGVA
PRMDQREGDSSYGKDDIRSTKEKMKNMDGTSFNKETGLDKDIKDERNRQGVSLEQDTPLYKEGAEYSDASATDVRK

>B303_hypothetical_protein_(Tim44_superfamily_protein)
MMRRSCSSSAALRRVALPLPSTLGGMTRPLPMAPARCLITSSCLHNSRPCLVGTAARRSYSSTAPPPSSTPPQDNKP
QNDNNSEAPSSSTAEEAKDQSRPASYTPPTEPGTQQPPPEQPSQQPEPINLFTAAAGVPTGVRVAVLPQRRWRWPLF
TPLKVNFMLNWLEKKDPSFNRDEFLEGAKGAFAGMMEKFPPDRPERFREVLDPALYRAMLDSSEAYQQSPLRIAARL
EKLESAEIVNVHILADAEQEELPEDEEELKQQPETVHIEVKFDCVEQLTTQVEVEGKPAQVISKDVFPRSHEWVFEG
TFRPGSSPLWKLAMI

>B304_hypothetical_protein_(no_PCD)
**MRRVNALGGVQSWSAARSGFAISRGASSPSFLQWPHPNSSMLSSDAFGVGMSVRYASTTVKGRAGAKLRTRKETTTG
VVAKRQ**RVQKANAAATAEEREDYSTTTTSTTTTTASAGRAAGTKKARKSKAKTQPQEDAKQEYDKAQLGEEPSTPPL
VVYPQTLVPSSVLDMISTPQQGKTSNGGPASLQLNAIFIWPKAVRAMLVDQKRIQKQKLLLQARHAEEAKIVQPAAA
LDAAAATATATAASGTHDQSGQEGTNQ

>B305_hypothetical_protein_(no_PCD)
MSSLFRRGVVRGSPLPRSSCFSPARCPSAVALRWTAAPTTTSTFWRSRQPRQLVTPTTSSVRPHFVGAAAGTRRHPH
SASGQPERQQEKKEREDFVRSYLHLLAQEAFFFDDETWQVLGVHHVPGSDRVHVEAIPEDAEYIGFPAFKFVFSFDP
ALGKLRGGNDDQTVPGSDEAKLVKRLRELEAARGLTVTCVGCYAFSKGNNKFFLLSPGLAEEETIEEECEPLFYHGA
AAPAAET

>B306_hypothetical_protein_(no_PCD)
MRSRQRHLKSFAVVTAYQCRSASGLRWYSSAPPQQSPKTRRVLFGLETDASTLLWGGGLLVLGLGSIYGTYYKMQRD
ERREQRRLERKETRDKIVGTVLDKFGNKTTNASAKSQHAAAETAATQEEEEEDDKRRSATPPTEKKEESVEGQHKAK
EGVREKLRSLRHSKRPSSEE

>B307_hypothetical_protein_(no_PCD)
MSYRPSARLMFRASPFRAGGHGHGAHSLHAPPKPRMQLVEAEQVFDRPFLNILGVSAGAAFVFYHLIAIPFFKGSDK
PAAQKLAQNKH

>B308_hypothetical_protein_(no_PCD)
MTIWKTCSPRCSRTAASSARRGALTGSVFDRPKEPSHHESWTSTTTNECDSRCAKRAIRFSISDDRQPRGRCRRRRK
RPTKNVKRTNQRINEAVTAPTLMVAWQSPIRDTHILKPRKEDT**TAKCRPAELRRKEQGKRD**

>B309_protein_kinase_domain-containing_protein
MKRSAPSSSSSASSRTASASSQRPRLPPSPERETVYEGTKYVRAYSASLVKIDGREYSFEEIRAARHAYVEHASIDH
RDAEAIKSREFTRKRWRESELEKQRQSAKMAEERRQLDEQRRSMEEMKREIEETKRRLDEQVKAAAAAEEEA**RRARL
LRPRVLPLFADGADDGAPRDETTSLTAALRGGFLQDAAPSRESLAGVGGGRHAHGDAPPTPTVTMNTRAAMANV**MSM
FSGDFDDDTRALGDATLSSIPIEDRENAAPARSRGASGRSAAAKSAQTPGAVAPARKGLGLAVQPTKKTNREVLQEE
LAAKENRQAAANVPRFEPAHNKRTYGDAVREVIAARNQGEEPDEITSNLSWDDTGLLPAGALAQAPSAGGFQIYEDE

QGSPVPLKQQGAGALRPPKLDFAVFDDGAQEGDGADTTSLLTLPVLQKPQAASFAIFSDFDDNPPASSTAQATGGGK
RQPADERLGQVKQKASVVDPWLLSEEKRLLQLLGDKVTRYPNFFDCRPEKAPGRNILKVPRGRRVSSVAEPQLELPE
VCIEVEERVGEGAFATVFKVDIIECSFIDLEGGETNAALKVLNEPSLWEWYIHHQILERIPRNLHHNFVRFHSIHMY
SDKALTLMQFSDGTLQDAMNCFHKMNKRMDEPLIIYYTLEMLKIIEILHGAGIIHGDIKPDNFLIKNNPGVELDDWG
SGSAGWDGKGLVLIDYGRSIDTRLYPEGTVFNSGNHVEGFKCTEMTEGRPWTYQADLFGICGVVHCLLHGNFIDVIR
DPRTKDLMPKMPFKRYHQADLWRPLFRDFLNITDCNNIPDVSQHRRRFEEHLKKNPPKAKTIKTLLARQNILMFERD
KKQK

>B310_hypothetical_protein_(no_PCD)
MSSVVKRATRSLSFRAMRNKNENKLDRSTSISASDSDNEDTTTTANSNSSSPSSPIPSPSSSSSKTSKHKKTKSKSK
IKSPRSPPSPSSASGAPATSCTTIPSPRSATSARQSVTMMMMVPSPASSPGCLSSSSSTEIVAVNNSAGTRSREHLQ
EESRGRINSIALSPRRAALDVDADDTGSTTIIKSKSAESEAVAEERKRRESECESGEAVSRKKGRGRANSTPAPRPR
IVPGL**TGLHALAHNAPSPSPSPPSTSTSPSP**RSPKVLGSSKSSSAAASQGRKSGGSGGKLKQSKSARVPKSARGEGW
SFTSARATGIASSSPASSSLSSTPSASSSLSSSSSRLGSSSSRRAASESSSPVVEVVFAKSDATAWVRKHHITAEEA
RDHNTLVALMPSSMRRNIPMGDVLGAGDQWTIDGTDVEAADESSAAAASKENESEDKAKSESEDGERMKAYGSGEVH
VFKRPAVAGLAIPS**AREQPASALRTYRDE**KEKEKEKAGGSTIIRRGMAAMASPRTWLGKKDDKDGMLAGSPPSGSPE
SHSPKNGERRKGWWDKKEKEKDKENEKGLEDCKKEGKWRSRSKRLMRKKPDADAVEPSGDKIAAAPRTGLADGGDDD
EGHNKSTATTTAGDESSSAQPVE**DEEQPSEGEDEEDIRGEDDDAVAVIHGVDSATAAPAAAATR**SSDQLDQAVGGEP
NNAAAPAPEAAAAKKKPAAGQERRPSVVATKTVKMAMEEELLSRVKERAPDSGSASALGNGTSGGGADDDDEEEDEL
FFSEANEAVVIQLPQKAE

>B311_hypothetical_protein_(no_PCD)
MRSRQRHLKSFAVVTAYQCRSASGLRWYSSAPPQQSPKTRRVLFGLETDASTLLWGGGLLVLGLGSIYGTYYKMQRD
ERREQRRLERKETRDKIVGTVLDKFGNKTTNASAKSQHAAAETAATQEEEEEDDKRRSATPPTEKKEESVEGQHKAK
EGVREKLRSLRHSKRPSSEE

>B312_hypothetical_protein_(no_PCD)
MSLARRLRQLAGPQAAHNRGAQHKTSLANDQVVVRVQGQSGKITFWIPERSDKKYTLTFDSLCEGNDCVNTFASQQF
AFSTPATVRFHNISAKLVSFDSTLATKKQSGVKLTADLYVFLETGNYTVGDQTFYAVENAFKWSVNISGWVFANAAN
KLELGMGLLHPSYKASWDAANYTLSYPGEDAVIQFAKTATHDGKTEEAVAVTTKVKGSNVDIVMAFSSAESSIWYDP
QVTVATGAASSASSFLFSLGAHLL**SLLS**

>B313_hypothetical_protein_(no_PCD)
MRRTATRAMGMAGGLMPRRVASLGACRSVSNMGTANKDSISRAGSYNDDPQAKLANDIFATDVGNKGLTDDTGTPIG
SLAHDKSGGYDPNLDQREGQQPMGDEVLKRATEKMAKENPMSQGRESAMEKDIRDAPRAGPGVENPNKQNPRDNDVK
SGVQ

>B314_hypothetical_protein_(no_PCD)
MQRASTITIALQRRSTAALLSSVSCRALAPASRRYADLGGQLNKEYENYIRKERALQRELEGSDKHNVQDQAKDGER
LTSPEGAESEKPLNPGGRQFGEPQPPEKVTDPKEHDLPLF

>B315_hypothetical_protein_(no_PCD)
MQRAANITQRQATRALMPAQRTLLARPYAILGGQLNKEYEASQREEKSNQQQQQQQELEGAEGVLPDDAAGPEVIED
WKAMHEPVSGKGRLHPGIVQPEDLVKKDPKMHELPIF

>B316_hypothetical_protein_(no_PCD)
MYRTPTRTLGRVANTSTLAPFHLRALAAAAGTSSAKSSSSHHAQHLGRRGHKEHGRKRPAKDEDDDSDREDEEDINK
LAGADDAKTPDELVVGDLREQMAENVGLDGDHEIGREGGEGRLHALHDAEQDALERRGYGGEEVPYTASATDDPDDR
SEQVDIGRSA

>B317_hypothetical_protein_(no_PCD)
MEKGGSRVRVGHSSMVSRICTLALLQPPRSRMQQISGAQHLQSSLLCHDFLWVGLWWRPSPLVPSPFTLCGTSCGSQ
HPRALRLRYRHRR

>B318_hypothetical_protein_(no_PCD)

MKQLRSTTPLNSPTAARRLVASSSPTSCSLTPLARRDHSAPSFVASSTTRMSSTSATQAVKHESAVVVSALLRGLAA
PRSLDLHRNIFLNPNRESSLKHVELTDDSIRLEFSKATAEYKRHAELMFLTEEEKEERGVEEWLVPLRLKNLTFCGG
GATIELDRRKVIQFLARPRLHEEVAAASHDPSEHLHARASMH

>B319_hypothetical_protein_(no_PCD)
MKRVGARSLPLPATAVAYFPCASRTGSVARLHLLRPLVGHRSGCALPPNGSDACLSSWRGGQWRGEEGGTTQNSSSP
AAPGVGWRNRGRTAAQQCWAVARRYTGPPSSLLLAAAAAPELCLRRSPAVPLLQPVASTPTALLLARRRSLATSTGP
LRRHQQQPAAASNDTLDTDEDEALTSDDEEDDGEDNDDDEAEENEDAHADVEDVYEDLVEEDEDEDEEDLDDEDDEE
EDLDDDEAEWDDEEAAEDEEDDWEDDEDDEEEWEDDDEDDDEEGNEEEWEDEEEEKEDDAENYRREVPPARKGAAGD
RRP

>B320_hypothetical_protein_(no_PCD)
MSRITAARRSKSFAPAHFNAFIKKERPSWTAQYALPTQDEENHSVDDTNKHRKMGNRATDLARLRDESTNLQARIER
FKVVAHEAAAKAQMINSGALTLRARHAPSISAIT**RPPPRHRACWPSSVSYRCTSTSAQRARRQLSPVVAPPAPPTPS**
PHPASLTKTESKHTLSLGDFLATIPGEHRANTLRKRKAAPPASPPARGEEEESVAKEEAEAILSSPVLKRRLQDALL
AQIEADRETTSVTISITISSTSAAGETDSSRPEETASEANEEEGEEEEVVVAAVEEVVVLERNTRAHKSVDKHVDEG
MLKRKDIVVRKKKKADLRDEEEEDDEDEDEAKRKGKKRKTASSFLASIIHPKKKMKKSKRARKERECVADEAKANEK
KVNMAAAIIEQEKHDQRVAYIKRKIEERYGVVRREAKRSGKRVRIQE**PNAAVVAVPQPPSSEGKQTGEAREKVVCNE**
TTSAVEGGGRRRRAVTVEEVTSEMASAIAGARQPLIKQRGVILLDKENLGNVADVGETKKEMVTKNNKTKTDTDTDD
TKKRKTKKATRNISSSSASLTSSSASASSSGSAILVSSAGGRGVDVPRRPLQPRN

>B321_hypothetical_protein_(no_PCD)
MSLAGSSSSVTCLPPLRSALGQGLSPPTAHHLPSFSSSFSGMVKRERMNVESSKILEEDDALPLLMSMAQIQTKAAL
DASRLPTISSILPSLPATFGSSTSTHFSQMAPSTPPIDRTSSSSPVPQSSPPSPSTLSPGLFGSYSLISTSSASSTS
FGHATSSATPVPSATSSHHHQQQAYVSATNSLMELSDIISSSTQKLPVPISPAATSVKPERSDDSESDNGADVDNGE
YVDSDGLATTGSDSPVSSRTRRVTRSQQKQIDRLRSEIELERERARELEQTLQFALRERSDLLAGKQKQQQQLSGPS
FVNVLSAASADGSPQVVFVDLPRTPHSAPPAATSSESSAEAEPRPLSVGRSRSAPMLPPIASIPALSPYLSRKRGSL
PSPFGAAASPLPGSPSTSPLRAPAGAESAYVGARGASSRRRKSVDRDDTDEDYDPASSAATKKIKRTRSMSEAAGRR
LPGVGSTRRRRSESQYQAGSRSAYGGDDDHDHGHVAAAFMAMRAKAIEERYARESRLMDVVEGADQEDDNDDGDDYA
EYRQQQEQKHQQQQPSRVATRRDSVLDFIKDHPHASFWLKARN

>B322_hypothetical_protein_(no_PCD)
MRRTLSSTPSQYAAATVLARTSCAHTCTGGFAASGLVFTRDFSRIRCAGDNGKYQKDRRVKRLKNWTRKQERRQAER
QAAAHRLGTDDIEWYEGEYYPRAELEVFMEERRQALRAATARILPESDSAPATAQ

>B323_hypothetical_protein_(no_PCD)
MRAGGCNRLSSLKGPPALRFLHSTPPLRLKTDMSASADPFLRGRVARFEHAGKAFVLVGTHHGLPRASSIAVERVLE
AERPDTIVAESTYSRFKLPPYDTRACEFAFTSQWALKHNVRLVQGNPVHRSIQGLHRPFHEVRWG**GIPAEEQSGAYV**
RPPPAGHANTDVTSSMSMSTSLWSAGARWLLGASVPLYSAAVVPLLRLGDLASRGTHRLLEWDDRNYFLHHHPLEYK
VYMSSVEREMFFIKALREAPGTKVVGVFGMLHLAGIMAMWEEYGKAPYRLWQTTEHEGKDVT**RALATAYMPAVAAHW**
QAHIQALQKQNKKM

>B324_18-kDa_translocator_protein_TSPO_(cholesterol/porphyrin_import)
MNLALIGSVALPVVVGSVSGFVYSVHREETKSWYNALRKPSFNPPSWLFPPVWTGLYMSMGYAAYLVGKEGGWERQA
VPLALYGTQLALNVAWSPLFFGAKKLGAALVDIGLLDVAVAATAYSFYGVNETAGLLMVPYLAWISFATLLNYQIWD
MNTIKAKPE

>B325_copper_chaperone_for_superoxide_dismutase_(Lys7)
MYHRQQGTPHYSTTFTTTRSARSLRFHRPSRALLLPLRTRTPPPTPQRLFSPARESNQHHRHQQQQDEEMEGTQGSE
KLRTGVKAQLNVEMTCQSCVEGITTALKAVPGVTVLDVDLDRGEVELLTQRVPVEKLLRILRETGRSASLQGLGGEG
EQLGSAVSQLEPADGSKEGPHATVRFAQVALDRCLVEAILDGFPPGEYDLAVHEFGDLSDAERSVGDVFGRHPGYAD
KPAGEIGRIAVGQNGEGTIMADNKQLKVWDIIGRSVVARPASPGGARGVAFGVIARSAGVRENPKKICRCDDPDF