Supplemental File S2

Nuclear-Genome Encoded Proteins Identified by Tandem Mass Spectrometry (MS/MS) in Purified *Acanthamoeba castellanii* Mitochondria

Key:

Entries are sorted in order of decreasing protein ion score [see Supplemental Table S1(B)].

Peptides identified via MS/MS are shown in **bold red**.

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

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

>N001_Complex_V_(ATP_synthase)_beta_subunit_(Atp2)
MLRNFSKRALPRTALSRGLATRTAAGLRQGANTTLATSSAPSKYAMWGSRTLATQPEPKTASK**AEAESQAVDTDGKI**
VQIIGAVVDVKFPEDALPPILSALEIQDHNIKLILEVAQHLGRGVCR**TIAMDATEGLQR**GQRVK**DLKGPITVPVGAA**
TLGRIINVIGDPIDEKGPIYSNKRNPIHAAPPTLTEQGASDQILVTGIKVVDLLAPYAKGGK**IGLFGGAGVGKTVLI**
MELINNIAKAHGGFSVFAGVGERTREGNDLYHEMITSEVIKLKDPK**TLKEGDHIGEGSKAALVYGQMNEPPGAR**ARV
ALTGLAVAEYFRDEEGQDVLLFIDNIFRFTQAGSEVSALLGRIPSAVGYQPTLATDMGQLQERITTTMKGSITSVQA
IYVPADDLTDPAPATTFAHLDATTVLSR**QIAELGIYPAVDPLDSTSRMMDAEIVGKEHYDVAR**AVQKTLQDYK**SLQD**
IIAILGMDELSEEDKATVYRARKIQKFLSQPFQVAQVFTGFEGKFVSLKDTISGFK**SILEGKYDHLPEPAFYMVGDI**
EEVVQKAQK**LAADLGGGSAAK**KDGKDASGAKVSGKR**ELTLDAFNDPSYPELKEGDFELNEKSFRVFAEYTK**NVAIPY
AR**DHELKEFPEDAAK**IK**AKYDNILSKIDGETDELVKELHDASQKHDAER**KR**KEQEAALK**AQKAAAPQAAAH

>N002_voltage-dependent_ion_channel_(VDAC)
MSYAPAKPVSVPVVVVPTVVRPAAPLYSNLGKGAKDLLSK**GFPSTYKVEVTTSAENGVQFVSSAEKKQANKTDVVVG**
TFQPKYKLASR**GLELTGTFDTDNQIKAELALDNLFVPGVK**GTFK**AQTGASHDLEAAFEYKHEVGTFTSTFVHNPTTA**
KTLLSATATVSRQSVTAGVESKYSLAPAQPGTLTTVTGALNYKAATHDLTAFVKSDAGSVTDGGDAPRLYSLGAHLH
YTPSKESSFASSLDYDLQKNTIKVTIGGSQKLDARTETKAKFSSDGR**LGLGVAQQLTPAVKATLGTELNTFDLAGST**
PKFGVHFEVRA

>N003_Hsp60
MLRTAAPHARVAVRGSSRSASSLRLYASVAGKEIKFGSEARSLMLR**GVDSLTDAVQTTLGPK**GR**NVVLEQSFGAPKI**
TKDGVTVAKHIEFK**DKYMNMGAQLVR**GVASK**ANDVAGDGTTTATVLAR**AIFSEGTK**VVAAGMNPMDVK**R**GVDQAVSI**
VVGELKKLAK**KVTTTEEIRQVATLSANSDDSIGSLIATAMEKVGSQGVITVTDGKTLENEVEVIEGMKFDQGYISR**Y
FVTDPKTQK**CEYEDALFLLTDGKISSIHSLLPCLEEVSR**EHKKLVIISDNVEGEALATLIINKMRGLPVVAVK**APGF**
GDNRKNNLQDIAVLTGATVVSEEMGLKLENFERSWLGSSK**KVIISSDDTIIMDGGGNSENIK**ER**CEQITEALQRTTS**
SYEQEKLRERLAKLSSGVAVLK**VGGATEVEVSER**K**DRITDALSATRAAVEEGIVPGGGVALLHASKALEGVTGANAD**
QTSGIQLVARAIRIPARTIATNAGKEGGVIVEK**ILQSTDAHWGYNAQTDEYGDMFK**AGIIDPVKVVR**TAIDAAASVS**
SLMTTTEAIVVELPKESSMPAAPGMGGMGGMGGDMF

>N004_phosphoenolpyruvate_carboxykinase,_GTP
MLRSGFRQGGAATAWGLRTSSRVASTSPAMLYPQAVRRWLASSSSSIEASTSNK**KLIEWLK**TQQK**LLQPSAVHICDG**
SVEEDERLKSELVKSGTLIKLNEAK**RPNSYLAR**SDPGDVARVEGR**TYICSTNKADAGPTNNWVDPK**EMRATLNGKFA
GAMKGR**TMYVVPFSMGPVGSPLSKIGVEITDSPYVVANMR**IMTRMGK**QVFDALGSDGDFVPCVHSVGAPLQPGQKDV**
PWPCNPDKYIVHYPETREIWSYGSGYGGNALLGKKCFALR**IASVQARDEGWLAEHMLILGITNPEGK**KK**YIAAAFPS**
ACGKTNLAMMNPTLPGWKIETVGDDIAWMRFGKDGRLYAINPENGFFGVAPGTSMSSNPNAMATTVKNALFTNCALT

DDNDVWWESMTDKLPAHLISWKGKDWTPESKEPAAHPNARFTTPADQCPVLDSKWEDPQGVPISAILFGGRRRTVVP
LVYQAFDWEHGTYIGSSIGSEVTAAAEGKRGEMRHDPFAMLPFCGYNMADYMQHWLNVGSRSAADKLPKIFFVNWFR
RGADGSFLWPGYGENSRVLKWIFDQTDNKSGNAKETPIGYIPKEGALDTSGLDVSPEAIKQLFEVNPSDWKEEVQEM
RRYTEQFGDRLPAGLKKQMDALEKRLA

>N005_malate_dehydrogenase,_bacterial_type
MRRGLSTVSRSATVFGKQACLASSTLRVDRRAYATSPEDAALEAQIEKVLDLVKKQGNLGSEKLTVRKLTELRQTVP
EIDRALSSVGDSAVKYMAELEKPGAGPLSAVPPVRVTVTGAAGAIGYAMLFRIASGEMLGKHQPVILQLLELEPAMK
ALEGVIMELKDCAFPLLHGVTASSDVNKAFEGADFAMLVGAKPRTKGMERGDLLKENANIFSVQGKALNKVANRDTL
RVCVVGNPANTNALIASANAPNIHPRRFTAMTRLDHNRGIAQLADKLKCKVTDIERFAIWGNHSATQYPDISHTQIN
GKWAKDLVDEKWVKDTFIPDVQQRGAAIIAARGSSSAASAANAAIEHMRDWVKGTNGQWTSMGVWTGNGKVGDYGTS
PDIYYSFPVVCADGEYTIVQNVPVDKFSAERMQKTNDELVSEKNGVGELAKRTTDPAALLKEQYKGGKQ

>N006_mitochondrial_carrier_AcMC1_(ADP/ATP_translocator)
MGDLNKKNDLTSFLIDFLMGGVSAAVSKTAAAPIERVKLLIQNQDEMLKTGRLAEPYKGIGDCFKKVIAEEGFGSLW
RGNLANVLRYFPTQALNFAFKDQFKRMFGYNKDRDGYWKWFAGNLASGGAAGASSLLFVYSLDYARTRLANDNKSAK
KGGERQFNGLFDVYKKTLKSDGIVGLYRGFNISCVGIIVYRGLYFGLYDSLKPVLLTGSLSDSFFASFLLGWGITIG
AGLASYPLDTVRRRMMMTSGEAVKYRSSAHAFSEIVKKEGVKSLFKGAGANILRAVAGAGVLAGYDKLQVLVFGKTY
GAGGG

>N007_putative_Complex_V_(ATP_synthase)_d_subunit_(Atp7)
MRRISRVVASSARGTALNKSSRTAAVFSRGYAAPETPQTDFKVTDAGIRVYAHGVVHDMNFLGDLPADAQEVLSGKE
WVPQSVSDFTARWEKDAPELANQARQLESLITKFEKDPVQFGKSEAYLRDIAIHTTLERAAARDVSPVEIALTHFWT
AYSEVPSGGKLRESAPTQLERVKAFLQSKKDPELSAQNSRARKTAAIVKFVQASSAEDKAAAAALLLGSEKGQALKA
ALKGVNDAAKKEQIVKQHLQWDEATQAAAELTQRHPEFTELKEVLAHFPPLVHHIGEPSAVQYRFKHATDKAYKKWQ
QNYSLTSSDEVTEKDPLLKNLRELLYSGKPANTVADAKKAQALQRSFPGLLFSRDVESFSNFVRKDEEVKSQLSTIY
EDSLKEYPNDPALAVPKDLDQRVKLWSKHTQELADVQQQWLDAKIAFIDAKIQEGMVQMDKFVNGTVDDILADHPEW
EKEIEDDIANHRWDPEMEKKEYDNALHHYYEHHTVHA

>N008_aconitase_(aconitate_hydratase)_form_1
MQSLKRATIVTPCTRALPSSVRSALGERNYAALSRLEPSTTLPYEKMKSKLSDVRKRLDRPLTLAEKILYSHLDDTK
QEVVRGKTYLKLRPDRVAMQDATAQMAVLQFMTAGLPKVAVPTTIHCDHLIEAHVGGAQDLKNAKDINREVYDFLAS
SSNKYGIGFWKPGSGIIHQIVLENYAFPGGLMIGTDSHTPNAGGLGMVAIGVGGADAVDVMADIPWELKAPKILGVK
LTGALSGWTAPKDVILKLAGILTVKGGTGYIVEYFGPGLDSISCTGMATICNMGAEIGATTSLFPFNHRMSAYLKAT
SRADIASAAESFKDHLVADPGCEDLQNKLYDEVIEINLSELEPHVNGPFTPDLATPLSKFAEAVKKNNWPEKLAQGL
IGSCTNSSYEDMSRSASIVQQAIDHGVKAKSGFIITPGSEQIRATIARDGIINTFEKVGGTVLANACGPCIGQWKRD
DIKKGDKNSIITSYNRNFTGRNDANPQTHAFVSSPELVTAMSIAGDLTFNPLTDSLTGADGKQFKLKSPYGDELPAR
GFDAGEDTYQPPAADGSKVTVVVDPSSQRLQLLPKFDEWNGSDAIENMPVLIKAKGKCTTDHISMAGPWLKYRGHID
NISNNMFIGAINAENNKANCVQNQLTGEFGAVPDVARAYKKAGVPWIVIGDENYGEGSSREHAAIEPRYLGGKAVVV
RSFARIHETNLKKQGILPLTFANPADYDRISGNDRITIVGLKDLAPGKPVTLRVTPKEGKPFDVVANQTLNEGQIAW
WKAGSALNLMGKQRASAQ

>N009_Complex_III_matrix_processing_peptidase_beta_subunit_(Core1/Qcr1/Mas1)
MSSIRSRAPSMLLPTKLGTSGRLGAAARRLSSGQPQAARDVEKRLRLPEYLLNVPPTQVTALPNKFRVASEHKHGET
ATVGVWIDAGSVWETAENNGVAHFLEHLAFKGTKNRTKEQIEVEIENMGGQLNAYTSREQTVYHAHVFKKDVPKAVE
IISDIIQNSNLKEDDVERERGVILREMEEVESQTEEVIFDHLHSIAFQNTSLGYTILGPEKNIKKIKREDLVSYVGK
HYTAPRMVLSAAGAVDHDELVKLAEKHFSGLSSETNVDYSNREKLFDFTGSMVQVRDTSIPLVHTTVAAKSVGWSDP
DYFTFLVLQQLVGSWDRSLGGAKNLSSNLAETFATEELAHSLMSFNTCYHETGLFGAYFVGEMERTSDAIFEVLREW
VRIGSGVSEVEVERAKNKLKSTYLMQLDGTQAVAEDIGRQLLTLGRRMPAAEAFMRIDAIDAKKVREVAYTYLNDVD
VAVAAVGSVDSGLFPDYNVLRGWTYWNRL

>N010_2-oxoglutarate_dehydrogenase,_E1_form_1
MLSSRARAGLLSRGPLAFTGMGRAGFAGSRVASSSLTGGASSRWYSLTTASRQAAASPTSSSAVPLSRLSETFADGT
SGAYVEDMYQAWKRDANSVHASWASYFRSVDAGRAPGEAFTAPPTLRGATAAVPPAGGVSEEDLSRRVSDSMRLLLL
VRAYQVRGHTLAKLDPLTGGPLSSFVPPELLPSTYGFTDADMDRPIHLGGESVISGFLSHGSATVTLREILVRLKQT
YCSTIGVEYMHIPDRHECNWIRERVETPEPFSFSPEQKFHLLDRLTWATLFERFLAMKYQNTKRFGLDGCETLIPGM
KTMIDTAADLGVESVVIGMPHRGRLNVLANVVRKPLDALLHEFDLEGNKDHSDDLGLGTGDVKYHLGTSYDRPTASG

KKVHLSLVANPSHLEAVNPVVEGKARAKQQYMGDTERTRVMPVLLHGDAAFASQGVVYETLDLGIWKNFTTGGTIHI
VVNNQVGFTTALRGSRTNTASSYPTDVAKTVNAPIFHVNGDDPEAVVHTLKLAAEYRQAFKKDVVIDIICYRRAGHN
EGDEPRYTQPQMYRMIEKHQSTLDLYRAKLKAEGVVDDARIKQMEDFVNEEHNKAFQASSTHVPNKADWFSSYWKGF
KSAHQYSSIRPTAIPDAVISKIGATVSSLPEGMKLHPNLEKLIKRKKLMFESGKNIDWGTAEQLALGSLALEGNLIR
LTGQDVERGTFSHRHAVLHDRETGETYQPLRHIDPAQAPVFVHNSSLSEYAVLGYELGFSLENPNSLVLWEAQFGDF
ANGAQVIVDQFISSGEQKWQRQSGLVMLLPHGYDGQGPEHSSARLERFLQLSDSDPFVIPEMDPTERRQIQQANIQV
VNVTTPANYFHALRRQVHRDFRKPLIVMSPKRLLRHPRCVSSLEEFSDKGTQPRFRRVINDTAENPVSDDRIRKVLF
CSGNVYYDLAERREKAAINDVAIVRVEQLAPFPFDRVAEQALRYRNATTGWVQEEPMNMGAWTFVSPHMRTALAKAA
HAHAEPAYFGRAVSASTATGSAKAHKRQLTQLLDAAFS

>N011_Hsp70_form_1_(chaperone_protein_DnaK)
MLRRVAATRRAPVSAASFLRSSWNAPAAARLYSAKSGDHIIGIDLGTTNSCVAIMEGSTPRVIENSEGERTTPSVVA
FVKDDHGTNRLVGATAKRQAVTNPTNTFFAVKRLIGRDFNDPMTQKDLKMVPYKIVRHSNGDAWLEDSWGKKYSPSE
ISAFTLTKMKETAEGYLGTQVKKAVITVPAYFNDSQRQATKDAGKIAGLQVERIINEPTAAALAYGLTNKGGETVAV
YDLGGGTFDISILEISKEGVFEVKATNGDTFLGGEDFDNTLMQHLVGEFKKAEGIDLSKDKLALQRLKEAAEKAKCE
LSSTVSTEINLPFITATAEGPKHLHIKLTRAQFESLVDPLVQRTIDPCKSCLKDAGLDKSDINNVLLVGGMTRMPKV
QEVVKQFYGKQPSKGVNPDEAVAVGAAIQAGVLKGDVKQLLLLDVTPLSLGIETLGGVCTKLITRNTTIPTKKSQVF
STAADGQTEVEIKVLQGERHMANDNKTLGSFILSGIPPAPKGVPQVEVTFDIDANGIVNVSARDKATGKEQAIRIQS
SGGLSESEIDRMVKDAETHEEEDRKRKDQTEARNHAESVIYDIEKNLNEFKEHVDQTEAERLREQITELRKTLESAD
DHQAIKSGADSLQRESLKAFESAYKQKASSNDSGSSSSTENKEDDTPDADIKK

>N012_succinyl-CoA_synthetase_beta_subunit_form_1_(GDP)
MRKTCRIGTAARATSGRVAATSARSFSSRTLSCGASGFLQSRTSVASSKLIRRAAPINSTQVRFLNLQEFSSKGLMD
QYGVRTQKWKLATTPEEALAAAKELKKNPECKELVVKAQILAGGRGKGVFDNGFKGGVHLCNTPEEAAQLTKQMLGH
KLTTKQTGPEGTLVSKVMIAQSIDLKRETYFAILMDRAFSGPVMVASPQGGMDIEQVAEETPDLIFKEAIDINQGIK
PEQTRRLAIAMGFDDEKKIADAQKQMAGLYELFLKTDATQVEINPFAETPEGEVYCVDAKINFDDNASFRQKAVFDM
GDDSETDQREVEAAKYGLNYIGMDGNIGCMVNGAGLAMATMDIIKLYKGSPANFLDVGGGANEQQVTQAFKILTDDH
QVKAILVNIFGGIMKCDVIAQGIINAAKEVKLNIPLVVRLEGTNVTIGKDLLEKSGLPIITANDLDEAAQKAVASIG
HH

>N013_Complex_III_matrix_processing_peptidase_alpha_subunit_(Core2/Qcr2/Mas2)
MKPQHAARLSLAKGVTRASSPSASVLGSKSYSSWTATSSLKQAHSSVPQTWEATPQTLDNVQTTTLDSGLKVTTVSS
ELPLAAVGLHVKAGARFETGESRGAAHFLRHLAFSRTSSRSPLTVTREMEVATAAFDVSASRENISYSGQLMPDYLE
DYVWMLRDLMHPLAWEYIVRDAAPQVAAEVHEAETNPATALVEAIHREAYRDEGLGNSIYCPNYRVGAVTREAIIRY
HHERYQASNVALVGYGIKHEQLVAQANKYFPADAFAEDKAPWTTLEAADRKPGAVYTAASSYTGGELRLPGPGNSRV
ALAFEGASLADPDVFAVRTLSSLLGGAARFTRDGPGVGLRSRLARNVLAKGDYVLASSALNASYSDSGLFGVFVEAL
PGHGADAARLLSAELNSLAGSFSVDDAELTRAKNQAKASFFREVESRTGLVDYLARHTLAGTAPLAPAQYAARFDAV
TRDDLARVARRVFSSPLTLVSTGDIHGVPTKEELRPKLKA

>N014_citrate_synthase_form_1
MRRATVIATKSAASPAAVAVQARALAQSQRLYATASLKDKFSEIVPKEQARVKKLKTEHGDLPLGQVTLSMAYGGMR
GIKGLVTETSLLDPEEGIRFRGYSIPECQAKLPKAKDGKQPLPEALLWLLLTSEIPTEEQTQNLVHEISERSKKFPA
HVSHILKNLPTTMHPMTQFTIGVNALQTESQFAKAYLEGVNKAKYWEYAYEDMLNLISFLPRTAAEIYRNVYHGGKL
IPSDPKLDMGADYAHQLGFENKEFVDLMRLYLVLHSDHEGGNVSAHTTHLVGSALSDPYLSFSAGLNGLAGPLHGLA
NQEVLRFILKLREKFGGREVTDEELKKALWDLLNSGQVIPGFGHAVLRKTDPRFTAQAEFASEYLPNDPLVKLVKQL
YAVVPPVLTEQGKTKNPWPNVDAHSGVLLQYYGLKEENYYTVLFGVSRALGVLPSLVLDRALGLPIERPKSVTTEWL
EKEAKKHAAAAPKH

>N015_succinate_dehydrogenase_subunit_1_(Sdh1;_SdhA)
MRLSRFSRSSALKSSFAGSAGIRTAPSSGLFRRNYAVVSNATPQAGESQGTLTSSYDVVDHTYDCVVVGAGGAGLRA
ALGLTEKGYKTACISKLFPTRSHTVAAQGGINAALGNADNDDWRWHAYDTVKGSDWLGDQDAIHYMCREAPASVIEL
EHYGMPFSRTEEGKIYQRAFGGQSYNFGKGGQAHRCCAVADRTGHALLHTLYGQAVRHNCTFFIEYFALDLIMENGE
CRGVVALCLEDGKIHRFRSHQTVLATGGYGRTYLSATSAHTCTGDGNGMAVRAGLPCQDLEFVQFHPTGIYGAGCLI
TEGSRGEGGILRNSDGERFMERYAPTAKDLASRDVVSRSITLEIRAGRGVGKHKDHVLLDLSHIPADILAERLPGIS
ETAKIFAGVDVTKEPIPILPTVHYNMGGVPTNYHGEVVTKKGDNPDCVVPGLMAAGEAACVSVHGANRLGANSLLDI
VVFGRAVANRVEETLKKDTPHKPLPKNAGLEAIHNLDKLRFANGKYRTAEVRDKMQRVMQNNAAVFRTGETLQEGVK

LIDEVYDMFKEVKTVDRSLVWNTDLVETLELQNLLSQAVLTMHSAEARKESRGAHAREDFPDRDDANWTKHTLSWMD
MESGKVKLDYRPVHDKPLNDEMPYVPPVKRVY

>N016_aspartate_aminotransferase
MRSCPQRRLLTLGFPSVSRTLGGRSSAVLVQRGYASSVWSHVPKGPEDPILGVTLAFNKDTSPKKMNLGVGAYRDDN
NKPYILPTVRQATSDLQKRLDEGKEDHEYLGIVGDPSFNKAAIKLALGENSQHITDKKVVTVQALSGTGALRIAGDF
LNRFYTHNKQIFVPTPTWANHIPLFTDAGLEVKYYRYYDKAANGLDWKGLIDDINSAPNKSIILLHACAHNPTGQDP
KLDQWKELEKHIKTKEHLVVFDSAYQGFASGDPEKDAAAVRYFVEQGHNIVLCQSFAKNFGLYGQRIGAVSFLTSTP
EEAINVESQLKILVRPMYSNPPKQGAKIVSAILNNSELATEWRKEVKGMADRIITMRDRLVHGLKEAGSTRDWTHIT
DQIGMFCFSGLSPEQVDRLANEFHIYMTKNGRISMAGVTSHNVDYLAKAIHEVTKQ

>N017_nucleoside_diphosphate_kinase
MRRATSISARTATVARPAARSASRLQLSQVATRTFVSGTAQATSSSARTGAMLIGAAAFAGASYYSFASVKADDKVP
HTGLPGTRFERTFIAIKPDGVQRGIVGEIIQRFEKKGYKLVGLKVVKPTKQFAEQHYADLSKKPFFPSLVNYFSSGP
VVAMVFEGRNAIVNGRKIVGATNPADAEAGSVRGDLCIDIGRNIIHGSDGPESAKDEISLWFKEGELANWESENAKW
VYEKL

>N018_Complex_V_(ATP_synthase)_OSCP_subunit_(Atp5)
MYASRSSGMACRSRLASRVAPRMGNAARLVSARGFSQTLVTQQKKGEATTAAPVFKIDEEFDDYKDVTASNEQVEKN
YREPPVQVTSGKHGEFASTLYATASVLNAVEDVERDLKWLVDASQTIPMFQQFLSSGLPDKKVMRKLLQGVLKGADF
HRLTQKFLVTELLEAGELKLVPDIAAVYAQIMKAHRKEVPVVFTFASLPDKDFLTRQIERVKKYRLEADATPMWEFK
INPALIGGFTVEVGSNYKGNFALSSQFDLMRQQLKQAEDKWERVRPKELHINSFDTSSLFAPLSGVKITAADLDKTL
ADVLGSKKEAFQAADLDRTLKQALEDAQRDAGFSGDYEKNVLEQTRNLDFEKLKTVKQLDLAQHEKHLMQKHNIADN
DAEGKRKVKAKIEELKRFKELDTSFIGEVLKKHQPETYKKYQSVFQ

>N019_mitochondrial_translation_elongation_factor_Tu_(EF-Tu)
MASRSFSRLGFSSQITAPARLTLPLRSRADFSRTLPCAYAGAQSYSTYRAKPHFNICTIGHVDHGKTTLTAAITKVL
ADTGLAKFRDYQSIDKAPEEIRRGITINASHVEYETDKRHYGHVDNPGHAEFIKNMITGTSLTDGAILVVDCSTGPM
PQTREHILLARQVGVKNIVVWLNKCDLIPDKELQDMVAMEIREELTRYEYNGDSTPIIHGSALEAIELKDTEYGIQA
IRKLLATVDELPQPERQTDKPFLMAIEALYTISGRGTVATGVVEQGKVKIGDEVEVLGMQEDAKKIKGVVTGIETFH
KQMEEGFAGDSIGLLLRGPNRDDLKRGQVVGKPGTLSAHKKFEANVYVLTKEEGGRHTPFGAGYAPQMFFRTANVTG
KVMMEGDKVAVPGETMNVGFETIWPMPLSEGLKFSCREGGMTVAAGVITKVFPMEEEGKKKKGK

>N020_aspartate_aminotransferase
MFKRAATRTTSGSVSSAAVQQRLFASSSSARAASSLWAHLDVAPLDSNHATNAAFEADQSPLKVNLGRGVYKDDNGK
NWVLPSVRMAEEKIFAEKAGHDYLPFKGWDVFCKRTSEFAFGETNPLLKDKRVATVQAISGTGALRVGAEFLSRFLP
PTHKGVSVYVADPTYVNHLPIFKLNGFEIKRYRYYDPNTNGLDLKGFVEDLQNAPEGSVILLHACAHNPTGVDPSFE
QWKLVSDACKERRHVVFFDCAYQGFASGDIDRDGAAFRYFAQEGHQVLVAQSYAKNMGLYGQRVGALNIVTSDAKET
EAVMSQLNQVIRPMYSNPPAYGARIVGTILSDPTLRAQWQKDVKTMADRIIGSRQALVDNLEGLGSKKSWKHITNQI
GMFAYSGLTPPQVQTLRTLHVYMNLDGRMSVSGVNSHNVEYLAQAMHKATSQ

>N021_dihydrolipoamide_dehydrogenase_(PDH_E3)
MRRGLIQASRSAVPTSASGVFASRAFPRTFIASRGFATAAEQDDVIVIGGGPGGYVAAIKAGQLGLKVTCVEKRGKL
GGTCLNVGCIPSKALLHASHIYEDTKKYFPDHGIVFDNVKLDLGAMMKSKEKAVNGLTSGIEFLFKKNNVKYVKGFG
KVSGANEVTVDLAEGGEKKLSAKNIIVATGSDVIGLPFLPIDEQRVVSSTGALALKEVPKKMVVIGGGIIGLEMGSV
WRRLGTEVTVVEFTDNLCGGAADGEVAKEFKRILAKQGMKFKMGTKVTGAKVEPSSITLITEPRDGGKTEEVACDVV
LCSVGRRPYLDGLGLENVGVKLDNRGRVAVDDHFRSNVPSIYAIGDCIPGPMLAHKAEEDGIAAVEIIAGGHGHVDY
NVVPSVVYTHPEVAWVGQTEEQLKAQGIQYKVGKFPFKANSRARTNDDDEGFVKYLADAKTDKVLGVHMIGAMVGEM
IAEPTLLMAYGGSSEDVARTCHAHPTLSEAVKEAAMATYDKAIHF

>N022_L-alpha-aminoadipic_semialdehyde_dehydrogenase
MKRLSCASKQFVVPSRASLHLQGRRGLATGGSQYAKHARFLQSLGIEEGVNDGVCIDGKWSKGSGEVVDSVNPAYNE
TITRVATAGLKDYERAIEATKSVEKMWAEVPAPKRGEIVRQIGDELRKHLEDLGALVSLEVGKITQEGIGEVQEFVD
VCDYAVGLSRSFSGQIFPSERPNHYMLEQWNPIGTTGIITAFNFPVAVMGWNAALALVCGNPLIWKGAPSTNLCTLA
TQRIIQRVLERNGMPGSICVALTGGAEIGEAISKDPRVPLVSFTGSTQVGKIVATQVASRMGRSLLELGGNNAITVL
DDADLTLAVRSILFAAVGTAGQRCTTARRLFLHEKIHDEFLGSLKAAYEQLGQKMGDPLEKNTLLGPLHRPSSVDLY
KNAVAKAQEQGGKIITGGKVKTDRPGNFVEPTIVSIKHDAPIALHETFAPILYVSKVPDLDTAIRYNNEVAQGLSSS

LFTTNQQNVFKWIGPSGSDCGIVNVNIPTNGAEIGGAFGGNKETGGGRESGSDSWKQYMRRSTCTINYGKELPLAQG
IKFD

>N023_methylmalonate-semialdehyde_dehydrogenase
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SAKKAYAQWSETPISARARVMFKLQALISENMEEIARCITKENGKTLVDARGDVFRGLEVVEHACSTGTVLMGETAE
NVGKNIDTYSYRQPLGVCAGITPFNFPAMIPLWMFPLAVTCGNTFLLKPSEKDPGASMIIARLAREAGLPPGVLNVI
HGAHDSVNFICDDPAIRSISFVGGDAAGRHIHSRGTSNGKRVQSNMAAKNHAAIMPDANKEATLNSLVGAAFGAAGQ
RCMALSTAVFIGESKEWIPELVERARKLKLSSGFTPGADLGPLITKESKDRVIRLIQSGVDQGAAIPLDGRNVSVPE
FPKGNFVGPTVLTGVRPDMTCYKEEIFGPVLLCLTADTLEDAIQLINNNPYGNGTAIFTRSGAAARKYQHEIDVGQV
GINIPIPVPLPFFSFTGSRGSFVGASHFYGKAGVHFYTQTKTITSLWKEEDLSQFGTNMPILSKH

>N024_putative_novel_Complex_V_(ATP_synthase)_subunit_AcAtpN2
MMKRGLRQVPRSVILGQRQSAQAMRLFASAAPSPNVDEIQFQVIGDTATAEYPTRPFTSKSKAQLEEGVQRKANQTR
GQFEAKFSADTPEGALFKDVVQIKPYDEQLLKAELEHVTNPTIQPTVDTAVNTKNHNFLTEFMASRTAGYLEDPTLY
FSYGENPSATLNPNWSTQLSGNLDALVKRELVDALAALSAEVKEIDALDQQAKKAHEELLQKLQADIDILTNKELFA
KSLESSGMSPLHVAQMTDIVTTDPLAVQALPLAQKQAAELAQFRQQSATFQQYSQLVADSRELVKQLQASGLQFDAS
KVSF

>N025_isocitrate_dehydrogenase,_NAD+_alpha_subunit
MRRTSAVALSRTSTSAACNARTLSVGSQRMLATSTGTEAPPASLSTGVRRGLALGSEIPVTLIPGDGIGKEIADSVV
GVFGALRVPIKWEVFERVGDITQNFDLLTSLARNQLCLKGQLKTDYEDSEHFKNNNLVLRKSLNLYANIVPIKSLPG
ITTRHSGIDMVVFRENTEAEYSGFEQEVTSGVVQSLKVVTRAACIRIAEAAFGYAAAAGRKRVHAIHKANIQKMSDG
LFLESVREVAKKYPTVEFKEMIIDNTCMQLVQNPKQFDVLVTPNLYGNLIINVGSGLVGGPGLVAGANYGLHGEAVF
EPGARHVAADIQGANVANPTGMLLSGVMLLRHVGLNEQAGRLEKAIHDILLRGKVLTKDVGGFATTKEFTKAVINHL

>N026_Complex_V_(ATP_synthase)_gamma_subunit_(Atp6)
MRRVSSVGLRTSAFELRTSAVQTARTFERNELGPVGVRHYPGNLKELRLRLVAIKNIKKITSTMKMIAAAKLNKAQA
VLFKTRPYSESSQRFIQEFFPSPQEGEPNPAEEASAGKHLIVAVTSDRGLCGGVNSSIIKASAAVLRNHPENTQLFL
VGEKSKAALQREYANAIVYAVSEVGANKKTSFTEVAQVAELIARQPADNVTLLYNHFNSVLSFTTTRKVFPSPKTFV
EAERKFSAYEFEGSHEEILADYWQFSVASQLYSAITESQTAEVATRMTSMDNATKNASEVLNKLTIKYNRTRQAAIT
TELTEIVSGAAAIEEASS

>N027_phosphoenolpyruvate_phosphomutase
MLARRSSSVAATSAVRLTSSTVTASGLVRPAASATAVISSRNASTKSKAQQLRDMLTSNQLEYIMEAHNGLSAKIVE
EAGFKGIWGSGLSISAQLGVRDSNEASYTQVLEVLEFMSDNTSIPILLDGDTGYGNFNNARRLIRKLEQRGVAGVCI
EDKLFPKTNSLLEGVSQPLADIDEFCGKIQACKDAQKDDAFSVVARCESFIAGWGLDHMMQRAEAYSKAGADAILCH
SKRSDSSEIQAFMKAWKERGNKTPVVIVPTKYYTTPSKDFQDWGVSLVIWANHNLRASVAAMQQTCKQIYADQSLIN
VEGKIAPVNEVFRLQNNAELKEAEKKYLPKKDKKN

>N028_ornithine_aminotransaminase
MQRSRITGATRLFGAPTRAALGARTFAASTQAKELPQTLKTSEDYIAVEDRYGAHNYHPVPVVLSRGEGVHVWDVEG
RRYLDFLSAYSAVNQGHCHPKIINALNEQAKKITLTSRAFHNDVLAPYTRFITSYFGYDRVLPMNTGVEAGETAIKL
TRKWAYLKKKVPKNQAKVIFAANNFWGRTIAAASSSTDPSCYEDFGPFTPGFEIIPYNDLNALREAVKDPNTAGFYI
EPIQGEAGVVVPDEGYLREAKRICKEANVLFIADEIQTGLGRTGKMLACDHEGVRPDILVLGKALSGGVLPRLCRSD
R

>N029_2-oxoglutarate_dehydrogenase_E2_subunit
MMKRTASMGRRPLFSACLVVQSNRGAAATLSGLRGVCSSSSHNGTGRIVASLTSHSRSGLNVLPKRFYATAEVKTQA
VPPMGDSITEGELKNWSKGVGEHVAVDDLVAVIETDKVAVEIRAKEAGVIKEHFAEEGSTVSVGAPLFAYEAGAEAP
KKAEVPKEEPAKKTEQAPKPEAAAPKAEAPKTAAAPAAATEGKAAPKAEASKAPAPKTASPVAGGERKVKVTRMRER
IAQRLKDAQNTYAMLTTFQEADMFNLINMREDFKEEFQKKHGVKLGFMSAFVKASAAALKEIPAVNAVYDGSNREII
YRDYVDISVAVATPRGLVVPVLRDCDHLSFADVEKRLSELSVKARKDEITLEEMAGGTFTISNGGVYGSLMGTPIIN
PPQSAILGMHAINKRPVVVNDQVVIRPIMYLALTYDHRLIDGKEAVTFLRHIKHSIEDPRRLLLEL

>N030_isocitrate_dehydrogenase_NADP+

MRRQAINVAKRSTPTTWALAQRHLGATAVALTHSQVRLAHKKIDVKNPVVELDGDEMTRIIWKRIKEELILPFLNID
LKYYDLGIEYRDQTNDKVTIEAAEAIKQYNVGIKCATITPDENRVAEFKLKKMWKSPNGTIRNILGGTVFREPIICK
NVPRLVPGWSQSIVIGRHAHGDQYKATDLVVPKAGTYDLVFTPADGSPKEVHQVYDFKTPGVIMGMYNTDESIEGFA
HSCFQYALAKNWPLYLSTKNTILKQYDGRFKDIFQAIYDKDYKSQFEANKQWYEHRLIDDMVAFALKTSGGFVWACK
NYDGDVQSDIVAQGFGSLGLMTSLLMCPDGKTVETEAAHGTVTRHYRMWQKGQPTSTNPIASIFAWTKGLEHRAKLD
NNTALAKFATALEEACVETVESGKMTKDLALCVHGSKMTNKDWLTTDDFLAAIRDTFQSKVEKF

>N031_trans-2-enoyl-CoA_reductase_(NADPH)
MKRTFTITGVAPRTLTRSLQANPVVLSARLFATLPSEAKVIKYHATGQPEKVLKLETEKLPQVGDNDVLVGFLAAPI
NPADLNMVEGVYPIGPKAPAVGGNEGVAEVLAVGSKVKGIAVDDWVIPAKPGFGTWRTHAVAPESSLLKVKKDIKPE
YAAAIAVNPCTAYRLLNDFADLKPGDVIIQNGANSAVGQAVIQLAAQREVKTINIIRDRPDLGDTVERMKSYGAYMV
VTEDKLGTPAFHRLISDLPKPKLGLNCVGGTSATEIARVLEKDSTLVTYGGMSRKPVQVPTSLLIFRNIQLRGFWLS
RWVEEHSAEERLAMINTCWDLVKSKRLRMWAERYPLEDFAAALNRTTQAQRNRKAILVMKP

>N032_pyruvate_dehydrogenase_E1_beta
MRRALSSVSRVASTSSAPLLGSAALRSRAVAALATAVEPKKISVREALREAIDEEMERDSRVVMLGEEVAQYQGAYK
VSKGLMEKFGRERVVDTPITEAGFAGIGVGAAMSGLVPIVEFMTMNFSLQAIDHIVNSAAKLRYMSGGMYNVPIVFR
GPNGPPRAVGAQHSQCFGAWYSSVPGLKVVAPWNCNDAKGLLKAAIRDPNPVVFLESEIGYNETYELSPEAQSKDYV
LDIGKAHIEKEGSDITVLTFSRMVGVALEAAQKAAEKGISVEVVNLRSLRPLDLNTIVNSIKKTNRFVTVEEGWPQC
GIGSEIIALANEHCFDFLDAPPERITGADVPMPYTWPLEDEAMVQTQNIVNAIERVCYRNTTNQ

>N033_fatty_acid-CoA_ligase
MLQRSSSLLRSAPASRAASLVSGAQCYATKAGEAAPLLNKTVGELLSDQKAKYEHKDVLVVSHQDIKWTHVELDKYV
RGWGNGLPEARVTRKPAPATPDRVLSFLANDAENIVTQLGTATAGRIVVPASPETTASPAEVDAALKTLQARMVIVP
ARFEDRNNIDALNALDEEIPTWPLGVALNLKKYPNLKHVVNTGEQFYRGHTMWRDLMVYNPTPSNLPAAGSVSPSEA
VLGYLSGGQTAMFSHSAVVNSGALFGSVVGLTSSDRICVASPLHTGHGLQAIVAAIAHGAVAVVPSLVFEADQVLAS
LARDVCTVLQVSPQQLKAVLDSPVLAKHDLAALQKLVIVGSAHESSAEVAQLVERATSALKVKEVVVAHTAPNVAGV
LFAGSATQNASSPAAGRLLPHVEAKLVDGGKAVKPGASGKLYVRGFNVTQGYWGAEKAAVDKEGWLDTGLQASASAD
GLYTIKH

>N034_succinyl-CoA_synthetase_alpha_subunit
MRSNRASLLRTCATTSAPSFATRRLYAAASKPRVLINKDTKVICQGFTGKQGTFHSKQAIEYGTKMVGGVSPGKGGS
KHLDLPVFNSVKEAKENTGADATVIYVPPPFAAAAIIEAIDAEIPLAVCITEGIPQQDMVRVKKRLMAPGCKTRLIG
PNCPGIIKPGECKIGIMPGHIHTPGKIGIVSRSGTLTYEAVGQTTAVGLGQSTCVGIGGDPFNGTNFVDVLKLFAED
PQTEGIILIGEIGGSDEEAAAQWIKDNALVSKKPVVSFIAGLTAPPGRRMGHAGAIISGGKGTATSKIQALQDAGVT
ISESPAKLGSTMLAAMRAAGKA

>N035_propionyl-CoA_carboxylase_alpha_subunit
MLRRAARCSTSASHVELLPKMGVRAFHRSLAPRQAEKLFDKVLVANRGEIACRVMRTCKRLGIKTVAVYSEPDAQAT
HVRMADEAICVGPAASAQSYLRVDRILEAVKSTGAQAVHPGYGFLSENEVFAKALEENGVQFVGPPSSAIRAMGDKI
ESKKLAKAARVNTIPGFLGEVNSDEEVLKIAGEIGYPVMIKASAGGGGKGMRIAWNDEEALSGFRLSKAEAKAAFGD
DRMLIEKFIDNPRHIEIQILADTHGNVLYLNERECSIQRRNQKVIEEAPSPLLDPATRRAMGEQAVALSRAVGYASA
GTVEFLSDQHKNFYFLEMNTRLQVEHPITEKITGVDIVEEMLRVAAGHKLKLRQEEVPLNGWAMECRVYAEDPYRNF
LPSIGRLRTYKEPHAADGSIRVDAGVYEGGEVSVFYDPLISKLVTWGPTRDECIKSMSYALDTYQIEGVNHNVPFLR
SVMENQRFQSGKLSTNFIPEEYPEGFKGHPVTPADIDELIASAAAIHLSRSRRDATISQQLHARPFTSENMDLVVTV
EGKNYPITLVQEPTASPAAGASTHPAIPSLEETDECEVVIKQDDGQERRVKVNYQWQLDSPIFSAIVDGKDVTMQLA
QALPVGYRLVHLGTKFDVLVRTPRQAELAVLMPKPVVQDFSSTVRSPMPGLVISMRVKKGDKVTVGQEVAVVEAMKM
QNVLRAERDGEIEDVMVTPGANVGVDEVLITFKKADAAKEESKKQ

>N036_coproporphyrinogen_III_oxidase
MSETWKQPLSYLGVAALSAGAAVAGYRYLTGYRYTTVVPPPAAAAAVVPAVVDESTNADEIELAFKAVQNHICQFLE
DESGQRYKEDTWSYDKGSGGGISRVWEALSDDERHLLLEKGGVNFSGIHGAAMPDSAATQFKIPPNTAFRATGVSLV
IHPRTPHVPTIHANIRYFECGPRWWFGGGVDVTPYYVNRERVVEFHKLLRALCEEWGYSYEAFKKQCDAYFLNTHRK
EARGVGGLFFDHLTTSDALPKSKKEICDFLVALGMLFPQLYGPFIHEGKDKEVTPEQREFQLYRRSRYVEFNLLHDR
GTKFGLQSEGRVESILMSMPPLARWKYNWHPEEGTPEAELYDIITPKDWASM

>N037_dihydrolipoamide_acetyltransferase_(PDH_E2)_form_1

MKRGVSRSSRVARGVKGTSATAQCLRATAVAQRSASTLSSTSRRSASPLFSGPVARSTATVQQFGVRSYATLPAHEV
LGLPALSPTMTQGNLAKWLKKEGDK**IQPGDLIASIETDKATVDWEATEAGYLAK**ILIPEGSK**DVTVGKPAVVTVEEE**
EDVAKFK**DFSPEGGDAAAPAAPK**EEAPAAPK**AAPAAPEQPK**AAAPAAPKAAPAPQAAPAGGRVFASPLAR**KVAQEQG**
VDVAAVHGTGSNNRVIR**ADVLDYAAKGPAFVPAATSVPTPAPGGLFTDIPNTQIR**KVIAARLTESK**QTVPHYYLSIE**
CRMDKLLK**VRQELNAK**GEGAYK**LSVNDFIIK**AAALALQKKPTCNSAWFGDYIRR**YHNVDINVAVSTDEGLFTPIVQD**
ADKK**GLATIANTVK**DLANKAKEKK**LQPHEFQGGTFTISNLGMFGVK**QFAAVINPPQSCILAVGGTEKKVVPNEDKET
SAAQPYATAHVMTVTLSCDHR**VVDGAVGAEWLKTFKELVEDPVKMLL**

>N038_universal_stress_protein_family_member
MSNPKETTQQR**AHVVALDGSEDADKAFVWALR**NLPKNDKLVLVHGIHTQPLENPHMDWMDQATTLSREERARLAKER
HK**ALFSHYEK**RCK**EADRVCTFETIK**FR**SNGELANNICQVAEEDRASTVIAGSRGLGLYDRVMLGSVSTALLNR**CRCS
VLIARDSS

>N039_short_chain_dehydrogenase/reductase_family_member
MRRTIATHCNLAALPMRRGFASAVPAARRLEGKVAIITGAANGIGREASLIFAR**Q**GAK**IVAVDLGDAR**ETVEGVK**AE**
GGEAVYVKADVSK**AGDCENMVQVAEK**TFGK**VNILFNNAGIMHGDDNGATDTEEKIWDLTMNVNAK**GVFFGCKYGIPA
LRR**AGGGSIINTASFVAILGAATSQIAYTASK**GAVLSMSR**ELAVIHARENIRVNALCPGPLKTELLMSFLNTDEKK**Q
RRLVHVPMGRFGEAQEIAQSALFLASDESSYITGSTFLVDGGITAAYVTPQ

>N040_uncharacterized
MQQDPSVPTTASSAVSSSVSNNRLLVGLGVGALAIAGAVGLAFWLGGQPKIKRKRAAAKKAGAAAGAKGAAKAKVGP
GGKKPMVRADDAKITLEKAAKMTIEEIQDGLEQAEREGDKASQINILFLLASSLLQQEQLEKQHIEAAVQYYNIALQ
FAEEINSEMLGPILLELAVLSFNFKNYPQAMALFEQGLRNFIETPEEEVEATNTKHILSLFVMLTECYFNTKQHQRG
IEFLLDYLKRTEGRKEHAELFPSLMLSVGEFTYALKDYPACIDYLEQGLARAEGTDLPPDLAMLYNYYLAWGNVKAE
RNEQAVKYLERYLDAAKVAKAPVESTLESIMSLVICYK**EQGQLDAAVK**TVDRALQALKQIDEAEHPLLCLKQFYFLG
LYCLNKLEQLDRARDLLERAYQLAKSNSTLSK**EMPWGTIAIDLAEAYHK**LKMRQEALK**MIETGLTALR**ERDTSLVPP
ALIRQAKIYSEMGDKATAVR**ALEEALQVAEELK**KK**ESATVGDAELGSGWLCR**FLRFQLGK**MYTLMGQLSK**ADALLTE
AFNSFVGTTDLEIR**TVVLATIASNLVQAGQK**EAGLK**KIQEVLDVLATPTTQK**LNQGDIR**TELGECYLFLGDYAKAKQ**
ELESALEQFAKEKNEK**SELLVLVRLAAIHDWLGEVDRALECLALAEK**AKER**DSSVIHLGSVGAGYALHHLTVGDIAK**
AQAQADQAAAYVDPACCGATPLNVLAFNGLLAETNFWSNR**MEASIQHFQRCLQHIATFPYARENIVSILNVQTRLAA**
LSLYTENRDQDANALAMLGQLLPLARTRGSLHHVAQLLALTGLAKAR**ALDNAEAEAAALFAEALSVAEETADRR**TLA
FVSRLAGAFYTRHAAADKADEGRK**HLDQALALARQLGDQLLEAVVLRDLAIVAVNEQTGSDEDK**GRTWK**EATADALA**
IAERTGNAYLANLLAHLPGQAPAAASLPLEPLVVEQQTTTETAPAAPVEAVEEAKPEEK**LPEVVAELTPTQTEEEDT**
KSSAEVVQEANEEEAKAEAEEKEEAKQQEEQEQESRTEEESDTK**TNAEVLQEANEEEANAEVEEKEEEATPAQTEEE**
SETKSFAEVVAEAEEKVTIEDVAEEEHDE

>N041_hybrid_cluster_protein_(hydroxylamine_reductase,_putative)
MKRLQHSTARASAVLRTSSSAAAGVSSRRLVASGAQSLTTSTRATALTSRALPRIAGTRALHASAGLRAAAAANAAG
APDMFCFQCEQTRDNK**GCMTVGVCGKTPEVASLQDLLIHATK**GVSIYAKGARDLGGLSDR**EVDNFVLRALFSTVTNV**
NFDSARFNAFLKEAYDMKTRAKALYEKAKASASPAALAK**AQAEEQQEDQWHPTAFKFHSGMSLEELEAEGHR**VGVLQ
R**REVYGPDLSGLQEMAMYGLK**GMAAYAEHAFVLGQESDEVFAFCHEALARLSRKNEQTLEGLLQLCLDVGKVNVEVM
R**LLDLGATTR**YGHPKPTPVRTTAVKGK**CALISGHDLR**DLEELLKQTEGKGINIYTHGEMLPAHGYPGLKEK**YPHLVG**
NYGGAWQQQKIEFSSFPGPILMTTNCIIEPRKSYKNRIYTRSVVGWPGVTHIPDYDFSALVEQALAMDGFEEDEPEK
NTTMTGFARNTVLSVADKVVDLVKSGAIK**HFFLIGGCDGAEGER**NYFKEMALNTPQDTMVLTLACGKYRFNK**FFDQF**
GTIGGLPRMLDIGQCNDAYSAIQIASGLQQAFGLKDINQLPLSFVISWFEQK**AVAVFLTLLHLGIK**NVYLGPQLPAF
ATPAMLDILVKSYGVK**QINNVQADMK**AMLARP

>N042_glycine_cleavage_system_P_protein
MKQSIRLAPSSARTVGRVAPLMRSRFLAAQGSRAVLYRSSSSK**VFPPLDTFPRRHIGVTDASVQEMLSELQLKSIDE**
LVHKTVPANILREPLNFKETGPR**GESELLQEFR**SNLQQKNKLLR**SFIGMGYYGTITPAVIQRNMLENPGWYTPYTPY**
QAEIAQGRLESLLNYQTMVTDLTGMDIANASLLDEATAAAEAMAMCFAGTKKK**GAQAGSFFISDDCHPQTIAVVK**TR
ATALGVNLIVGKPDTFDFKANEVVGAIVQYPTTDGRVVDYGDFVKRAHEHGVAVACGTDLLALSLLKPPGEFGVDIA
FGSAQRFGVPMGYGGPHAAFLATADKYKRNMPGRIIGVSK**DVTGEVALR**MSLQTREQHIRREKATSNICTAQALLAN
MAAMYAVYHGPEGLKQIAQRVHTMTRVLAQGISQAGYQLQGNEFFDTLTVHAGEGGADAVVQAALEKGINIRKLDGS
R**VGVSLDETVSDK**DLVDLLQAFTKAK**TGKEGSVSLEQLLAAVQSGGSRALGDLSAHQRASGYLAHPIFNSYHTEHEL**
LRYLFRLQSK**DLGLNTSMIPLGSCTMK**LNATSEMFPITWPEVSQLHPFVPLDQAQGSIEMHKELESLLSNITGFDAV
SLQPNAGAQGEYAGLLCIKKYHETRGENQR**DVCIIPTSAHGTNPATAVMAGMKVVIVPCDKDGNIDVAELR**KKAEEH

KDKLAALMVTYPSTHGVFEESIVDICNVIHANGGLVYMDGANMNAQVGLTSPGNIGADVCHLNLHK**TFCIPHGGGGP**
GVGAIGVAKHLTPHLPNSPLVPVGGPKSIGAISAAPYGSSAILPIPYVYIKLMGAQGLR**KATEVAILNANYMAAKLK**
DHYPIVYMGKQGMVAHEFILDIRPFKAATGVEAEDVAKRLMDYGFHAPTLSFPIAGTLMIEPTESESKEELDRFVTA
LIKIREEIK**EIEEGKLPRDNNPLHHAPHTQK**VVCGETWERPYTRER**AAFPAPWTK**VHKHWPAVSR**IDNAYGDRNLIC**
TCPSPEAYAEHQ

>N043_NADPH_cytochrome_P450_reductase
MQRACRLSFRTHGGLPHSTHILPSTHSASGRLCQRHLHPSPKALAEVKSMK**VLWGSQTGTATGFADDLARELSAQGI**
TATSMDLRKYNSKK**LATEKEPLALVLACYGQGEPTDNAK**QFYDFVMAKERKQGSLKDVR**YTVFGLGQSKAYPACYQA**
VGRSVDKR**LEELGAQR**IFAR**GEGDDSDDVEADFTAWK**DK**LLQSLTGAGGDGESADAANTTAAAAPAAAAPAAQPPK**A
EPEKPSVQIRVLDR**SAAPASTYQRNPAEPISIVNPVEARIVENEELQSAASDR**STRHLEIELSNTGITYQTGDYLGV
FPVNDEQMVNDLLQSLNIDPDQVIALK**SAADGAGEFSTPR**TIKQHFLENVDLTGRPRKSLFAR**LSAFAGDEATR**AR**L**
SSDDYAEFCVREKRGLYHILKDNPSLR**LGLDSLLSLAPPLLPRYYSIASSPK**FKEGR**MQLTVALAKTKAESGADHYG**
VCSRYICALKPGQTARLFVKTSLFRLPKSPEVPIIMVAAGCGIAPFHGFMQERK**LQCDQASLPYEK**SK**NVLYFGVYS**
KSKDFLYESELTGYERDGLLKLR**MAFSEDHAPNQPPTFAQHR**MMEDMPMLWQLIEKEQANTYVCGHTLLFDGVKEAL
QRTMTEVGRVPANEANDRIAQLQNSGRLQVDVY

>N044_homoisocitrate_dehydrogenase_(Lys12)
MNRCGARASLGLCRQRLASSPTAAARLYSSATVKIEKTGEPVK**VALIPSDGVGKEVVPEAR**RVLEAVEPHLPFAFSW
VPLHAGWETFQQQGVSLPKETIEGLK**GCDGALFGAVSSPSHKVEGYSSPIIGMRKALDLYANLRPVISAPIKTSRPD**
IDMLIVRENTECLYVKKER**MENGPQGRVAIADRVISEYASTRIAQMAFSQAER**RAAVRAGSKRPARVTVVHK**SNVLS**
VTDGLFRECALEVAKKYPHIEVEEQLVDSMVYKMILDPQRYDVVVAPNLYGDILSDAAAALVGGLGLAPSANVSDSF
ALCEPVHGSAPDIAGK**GIVNPLATIR**AAALLLRHLR**GPHADAAAQMGDVIEEAVNRALAAGPLTPDMGGKASTTQVT**
DAVIEHLKSLLLNKH

>N045_FAD-dependent_pyridine_nucleotide-disulphide_oxidoreductase
MKTTQRSQLRLAARAPQGRVSGLRSASVLRRSVHSKAAHGSSPSVVQHDVVVVGGGAAGLSVSHQLRRAMK**GLDVAI**
VEPSSKHYYQPGWTMVGGGVINKRETERNEADLIPAGAKWIK**SAVDQFVPEENAVVTSDGQTVHYKYLVVCPGIQIN**
WDNVKGLRDALGK**KGVSSNYSYEYADK**TWDHIK**HFNGGNAIFTHPATPIK**CGGAPQK**IMYLAEENWR**KR**GVHADVSF**
YTGGPAIFASPYYGKVLTRICQERGIHTHFKHDLVEVR**GANQEAVFK**DLNTQELVTVPYDFMHVTPPMGPPSFVK**SS**
PLADAGGWVDVDKHTLRHK**KYANVFGLGDASNLPTSKTAAAVSSQAAVATANLLATIRDPNAALPESYTGYTSCPLV**
TGYGKLVLAEFDYSLQPCETFPVDQSKERRSMYHLK**KDVMPPMYWHGLIK**GHWKGPRHHATTRLLK**DLVNKPQQQQQ**
S

>N046_NAD+-dependent_aldehyde_dehydrogenase
MLRTVPLASSRVAGTTAHGLSAARALATLPKIKHTKLFIDNEWVSSSSGSTFQTVNPTNEEVLADIHEAGEADVERA
VASARHAFDKGPWSKATCYDRSNLLNR**LADLVELHR**DELAALESADNGKPVHIANAADVGLTIQCLR**YYAGWADK**IS
GK**TIPTASNDYFTYTR**KEPIGVAAQIIPWNFPLLMAAWK**LAPVLATGCVSILKPAEQTPLTALR**LAELIR**EAGYPAG**
VVNVLPGQGNAGALLAKHNLVDK**VAFTGSTEVGHKILAASAASNLKRVTLELGGKSPNIVLPDADLKEAIAGAHFGL**
FFNHGQVCTAGSRVFVHK**KQYDEFVEK**STELAKKRR**VGNPLHAETEQGPQVSQEQMERILHFINIGQKEGASMTAGG**
ARVGDK**GYFVAPTVFADVSDNMTIAREEIFGPVMSIMK**YSELDEVIECANDSVYGLAAGVWTRDVGKAHYVASKLR**A**
GTVWVNCFNVYDSAQPFGGFKRSGMGR**ELGEEALANYLEHK**SVTTKLF

>N047_prohibitin_2_(Phb2)
MSKSPFQGLVKANLPGMGGKGLKTAMSLAVVGVGASAVAYNSLFTVEGGQK**AIIFSRFSGVLPK**VYNEGLHFRMPWL
HIPHVFNVRTRPTSIPSLTGSKDLQMVNITLRVLTKPKWEK**LPEIYK**KLGTDYDQRVLPSIVNEVLK**GVVAR**FNAAQ
LITQRELVSGMIQDRLRER**AADFFIDLDDVSITHLSFGREYTAAIEAKQVAQQEAER**AKFIVEKALQDKRSIVIR**AE**
GDAESARMISEAVQSNPYYLELKTIEAAR**DIAGSLANSQNK**VYLSSDMLMFNLLSSISGSNTASSLVGSVLSAKDAT
IARQ

>N048_enoyl-CoA_hydratase_(crotonase)
MRRSTKIVTSAMRGSAMPARMQVMGASMRLYTTESAAPQYTNILVEK**KEGGVGLITLNRPKALNALCDELIHELNDA**
ARRFELDNEVGAIVLTGSKKAFAAGADIKEMSTKTYMDTYKNNMFSAWDNLTKIR**KPIIAAVNGFALGGGCELAMMC**
DIILAGDKARFGQPEIK**LGTIPGVGGTQR**LTRAVGKSK**AMELILTGDFMNAEEAK**QSGLVSR**VVPEDELLTVALDMA**
KKVASYSQPIVSMAKECVNQAYESTLHEGVHFERRVFHSTFATNDQKEGMKAFIEKAQPAWTHS

>N049_Hsp70_form_2_(chaperone_protein_DnaK)

MRATGRLNPMQGKMAFASLGGCRATAASSSASALFNRSAAMRSTFAGPVFSRRYTSTSDPLVMGIDLGTTNSCVAVI
ENGKPRVIDNVDTGYNTTPSMVAFTKDK**ATGQQTMLVGDPAK**RQCVLNPRGTVYGVKRLIGR**RFDSEEVAK**IKK**HVP**
YEIVKAANNTGDAWVSVGGKSYSPSQIGAFILQKCKESAEKHVGQTISK**AVITVPAYFNDSQR**QATK**DAGAIAGLDV**
LRIINEPTAASLAYGFSEENSKERQRLAVFDLGGGTFDISILEIGDGMCQVVSTNGDTFLGGEDFDETVLQYLMNEF
KKK**EGVDLSKDVFAIQR**LREGAEKAKK**ALDHMPNYEINLPFITRDKNFSYSLTKEKFNELIKPLVDR**TIKPCQSALK
DAGLDKVDNVILVGGMTRTPAVIEK**VKEVFGLNPSKGVNPDEVVAMGAAIQGGVLSGK**VNSLILLDVTPLSLGVSVK
GDLFSRIIKRNSSIPCSNTQTYTTAADGQR**QVVFDLLQGEREIASANHLLGQVTLPVMPAPK**GIAKIDVTFNIDVNG
IVHVTAKDPVLNK**VATVQIQANSGLSQR**DIDRMLKEAELQKERDQQIK**ELAEVKNEAETLIRSAETDYLHNDVVPEE**
DKETIRQAVSQLQTAMDGNSDELK**TIYASLKDTILNVGAK**LYQQGGASSSSSNDGHNHDNNNQETKQ

>N050_Complex_I_(NADH_dehydrogenase)_gamma_carbonic_anhydrase_subunit_(AcCA2)
MLKRFSYVLGNTVRETAYALDRVGCR**LQGNYAFTEELSR**HRR**RVMGLYDK**QPAISQDVFIAPNASVIGSVSLGEGANV
WYGSVLR**GDVNDISVGKK**SSIGNR**SVVHASGGLTTLAPTKIGDNVVVGDGVVLHGCTLEDECRVDDGAVLNDNVVVE**
KHAIVGPGAVVTSGKRVPSGQVWAGNPAKYVR**DVSEEEKEFAGWAEK**RYTQAKAHLAQTIK**LAEEKEVDLLTEDILR**
EMRPGTRFAD

>N051_Complex_V_ATPase_inhibitor_protein_Inh1
MMRRAATRSALCRPSFAPTAARGYSSVLEAGGRLGEREKAVEDRAIR**GHDLELLKKLRDTLGIQENQPIPETVVSQV**
SSSSSSLNPFAQRAQSQQPSSSSHNDEPLTRGEFLEFRREIVQR**LRNLEDDIMDLQTR**RK

>N052_methylmalonyl-CoA_mutase
MLSLRRSARASTLVRTPAPLLALRSTGAPSTARHFSMSSRVLASTAENEAEWKKRATKELKGSPK**HEGKDPLESLSF**
ETPEGIRMKPLYTPTDVAGLDLTTNPYPGLFPYTRGPYATMYTNRAWTVR**QYAGFSTAEESNK**FYK**QNLAAGQTGLS**
VAFDLATHRGYDSNHPRVKGDVGMAGVAIDTVEDMKVLFKDIPLDKVSVSMTMNGAVLPVLAMYIVAAEEQGVK**QAL**
LSGTIQNDILKEFMVRNTFIYPPKPSMR**VVGEIMAYTSK**NMPKYNSISISGYHIQEAGADASLELAYTIADGLEYVR
TGMAQGLSVDNLAPRFSFFFGIGMNFYMEIAKLRAAR**KVWSQLIK**EKFSPKDERSLLVR**THCQTSGWSLTEQDPYNN**
IIRTTVEAMAAVLGGTQSLHTNAYDEAVGLPTVTSARVARNTQLILRDESGIPK**VIDPWGGSYMMEKLTDDLANTAL**
DIINEVESMGGMSSAVEKGFPK**LRIEQVAAK**R**QAAIDSGEQVIVGVNK**FRLAKEEKMDVR**QIDNTIVR**EAQIK**QLEQ**
IFAGRDK**AKAEQCLANLTKAAAGELSGNLLELAVEAAR**AR**CSVGEISDALEK**VFGRFQLNDSLVSGVYAASHPQQDL
IHR**IQGLSEQFLKDEGR**RPRILVAKMGQDGHDRGAKVIATGFADLGWDVDVGPLFQTPAEVARQAIDADVHAVGISS
QAAGHK**TLVPDLVAELK**KQGAEDVVVVVGGVIPPDDYDFLYK**SGVSCIFGPGTRIPDAAEQVISSIK**KKHLKSAVTA
Q

>N053_uncharacterized
MADERRQALTRIIGER**LSNCFGLGNAADQCVAVKGENDEECLQLESLRLHCFAELLCPQQAQRAVTCLQTRRNPSLC**
QDDIKALR**ACTGPAFDHFVDRYPQHSLVDR**TEKACAGPSDK**LTSCIEANKGDASK**CQVELK**EVDLCVGSVICPAEGR**
TLGECLR**NGTEDSCASQRQAFSACVAEGR**LK**FWEELGIPVNEFAAK**Q

>N054_isocitrate_dehydrogenase_NAD+_beta_subunit
MRAASHLRLRSLPARLGSPLSHASSAPLVSRRLYADKPVENK**TVTLIPGDGIGEEISEAVVQIFAAAKVPVSWETVK**
VSTTTAK**EGSLSSLLGGDVLESVK**TTRLALKGPLATPIGKGHMSLNLALRKQFNLYANVRPARSIPGVK**TPYDNVNI**
VVIRENTEGEYSGIEHQVVPGVCQSIKLITREASR**RVAQYAFQYAETHKK**DKVTAVHK**ASIMNLSDGLFLK**SCREVA
CAYPFVEYEEISVDK**VCMQLVMAPEK**FQVLVLPNLYGDIASDLCAGLVGGLGLTPSGNIGADSAIFESVHGTAPDIA
GQNK**ANPTALLLSAVMMLRHMGLYTHANR**IERAAYDVLREGK**VLTGDLGGSATTTQFTDAICKR**VANDHEA

>N055_malate_dehydrogenase_(decarboxylating)_[NAD-malic_enzyme]
MRRFATRAGGMSSCRLAATSAFARPAQWARTLTNGPHKHLDYRKKSFIEPLLVEK**KGVDLIHDPIYNK**GTAYPYSER
DRLNIRGLVPPR**CTTIEEQAK**RVK**TRFDHITDDLQKYSYISNLRDRNETLFYRMVMDNIDEMAPIIYTPTVGKACIE**
FGSQFRRARGMYFSSADMGQMSAMIYNWPEK**HVDVIVVTDGSRILGLGDLGAHGMGIPIGKLSLYVAAGGIHPARTL**
PVTLDVGTNNEKLLDDPFYLGRQHRR**LTGEDYYNVVEEFMSAVKLRWPSCLVQFEDFSNANASNLLEK**YRDRHLCFN
DDIQGTGSVALAGILTALRAQGKAAKEITKQRIVCLGGGSAGLGVINSLIDGMVEEGLPREVANK**NVWVVDADGLIA**
QGRSTISDAQKPFVRTDLPNGLKLKDTVDK**VKPTILLGLSGAGRTFTEDVVR**SMAANTERPIIFPLSNPTDHAECTA
EEAFTWTDGR**AIVASGSPFDPVQYK**GKTYYPSQGNNMYIYPGIGLGVVCCRAKKVTNAMFYAAAK**KLASIVPEEDVQ**
AGRVYPDIAKIREVSKQIAIEVCKEAFASNLATIHPPNNERELEYLVENAMYIPEYAPLVHAPNIFSHAADPNPYD

>N056_succinyl-CoA_ligase_beta_subunit_form_2_(ADP)
MWRRGARSVGMAGGMGRSLPARSALLQSNTATTLTSTSAQTGAARRWLNIHEYQSQELMRKEGIRVPK**GQVAASPEE**

AYKIAQQMQQGGDADVIVKAQVLAGGRGVGHFDSGLKGGVHTCTSPEEVKDVASKMLGHHIFTKQTGPEGKPCNVVY
LAERLFIRRETYFAILMDRAYNGPVIIGSSKGGSDIETLSAEHPDAIFKIPIDIAEGVTPEKLELVADKLGFQSTKV
KEQTKELVSKLYDLFIKKDCTLAEINPLVEDHQGQIVALDAKLRFDDNAEFRQKEIFALRDESQEDPREVAASKFDL
NYIQLNGNIGCLVNGAGLAMATMDIIKLKGGNPANFLDVGGGATEKQVTEAFRIFSSDKSVKAVMVNIFGGIMRCDI
IAMGILNAVKVLNIKVPLVVRLLGTNMKEAKDLLENSGARIIFASDLDEAAEKAVKVARIVDMAQEAQLNVSFELPL

>N057_pyruvate_carboxylase
MLRFARRSGGQHAVGQLATASLPSTIIAHASPALACGSSLVQTTWGRRHYASASSPTKPTKSKLPYRPIHKLLVANR
GEIAIRVMRAGTELGIRTVGIYSHQDEKSLHRQKADESYEVGKGMSPVEAYLSIPEMVRVAKEVEADAIHPGYGFLS
ESGDFAQACLDNNIRFIGPAPEVVRSMGDKVFARQMAIASGVQVVPGTDAPVSTVEEAELFCNKFGFPVILKAAFGG
GGRGMRVVHAREELHDAFERATSEAKSAFGNGSMFIERFVQNPRHIEVQVLGDRTGQVVHLHERDCSVQRRHQKVVE
VAPAPFLADDIRQKLFSDAVKLATYAGYENAGTVEFLVDEQGRHYFIEVNARLQVEHTVTEEITGVDLVQSQIRIAE
GLTLQDLNLTQDKIHVNGAAIQCRVTTEDPYHNFRPDVGRIDVFRTGEGMGIRLDGGNSYSGATISPYYDSLLVKVT
GKARNHEEAAKKLQRALNEFRIRGVKNNIPFLQNVLSHPKFLAGGVNTSFIDTIPELFQFHETQNRASKILNFLANV
HVNGSLTPLGTSNKPANITPQAPDVPHTDPPQGWRSIFLEKGPNEFAKAVRAHKTLLLTDTTMRDAHQSLLATRVRT
KDLLTIAPATAHLMAPLYSLEMWGGATFDVALRFLRECPWERLQRLREAVPNIPFQMLLRGANAVGYTNYPDNVVHR
FCREAKTNGIDVFRVFDSLNYFPNMELGIDAVGNAGGIVEAAICYTGDVTRGLTEKDYKYNLDYYVDFAEKLVKRHI
HVLCIKDMAGLLTPQAARLLIGTLREKFPEVPIHVHTHDTSGAGVAAMVACAEAGADVVDAAIDSMSGMTSQPSMGA
LVASLKGTPHDTGLKMDQLYPINNYWEQARTLYAPFECTTTMKAGSSDVYEHEIPGGQYTNLHFQAYSLGLAHQWPS
IKKAYAQANRLLGDIVKVTPSSKVVGDLAQFMVQNNLDEESLLEKAEELNFPSSVVEYFEGLIGQPPGGFPEPLRTK
VLKGRPSTNGRAGESLPPLDFHKLKRELIEKHGKYHISELDVLSAAQYPKVFDEYMDFKRLYGNVSSLPTRNYLTGP
EVGEEIKADIEPGKSLHIMLKAVGAPNADHKREMFFELNGQPRSVFVEDKKATAKEGAGHAGSSKSRERADPSNKKL
VGAPMPGSIVGVKVKDGQEVKKGQPLLVLSAMKMETVVAAPADGKVKRIIAKQGDSMTAGDLLVEME

>N058_adenylate_kinase
MQSSKPLRFVFLGPPGSGKGTQADLLKKQHTVCHLSTGDMLRAAVAEGNEIGRQAKEVMAAGKLVSDEIMVNLIKDN
LTKPECKDGFILDGFPRTVVQAEKLDEMLEKSNSKLTAALEFEIDDEIVLDRLGGRYVHPASGRSYHVKYAPPKVAG
KDDITGEPLIQRSDDNPETIKRRLASFHKDTVPVAAYYKKQGILEKLDAKRKPQEVHARVQKIIETRL

>N059_pyruvate_dehydrogenase_E1_alpha
MRRTCAALRPASRFGAEGRAARVLVISRRGYAEEASAFSGAKAEDLGNGKYRFQVETPYAAHKCDGPEQVCETTKDE
LLAMFKQMVRIRRTETEADKLYKQKEIRGFLHLYNGQEAVLVGMEAALTLEDHIITAYRDHGHLLTRGGTPKQVLAE
LMGRADGCSKGKGGSMHMYSKEGNFYGGNGIVGAQVPLGAGIAFSQKYLKTGRVSVSMFGDGAANQGQLFEAYNMAA
LWKLPAIFMCENNKYGMGTSIERSSASTEYYKRGDYLPGIKIDGMDALAVKQGMLYAADWARNKGPIMVEAETYRYG
GHSMSDPGTSYRTREEINRMRSTRDPIEKIRYKMLDNNIATKEEIKAVEAEVKAEVDEALKEALQAPFLPIEATYQH
VLLGEEALGAVRAVELSKSYVHKH

>N060_beta-lactamase_protein
MRRVLSAAATSTTTCRSATHNSLLRLHLRPNLLRAGMATTTSNESHLLLELNGGEACKTYLIADRQRRKAALLDPLK
QNIPKYLGVLAYHQLQLEYIFDSHSHADHFTAGFELAMLTEGKLAMHENAPAPKVKVHVRDGDVLRVGDIEVKVMHT
PGHTPDSIALYLPRLGHLYSGDTLMIGGTGRTDFAGGDPGQSYDSIQRMFALPEDTVLWPGHDYRGNVSSTIGHEKR
TNPRAGGGKTRDEYIHIMNNLGLPLPQKIMEALQCNVSASNDTAMKFPTIAELNEIRQLEPKLVRQLLAESDDKRPV
VVDVRQPDEVDGELGHIPGSITLPLSELTKRYQELEQYKGRNIICVCRAGVRSTTAAALLTGLGFPNIHNMRGGMLA
WNQKESATA

>N061_Zn-dependent_alcohol_dehydrogenase
MRRTVTSQHAVMSRAAGATGQVASRSLKCAMPALQQQPQRYLATSTSRPSIPTTMRAAVVEKFGAPLVIKNVPVPTP
GKDEVLIKVHACGVCHTDLHAADGDWPVKPILPLIPGHEGVGEVVAVGSGVERLKVGDRVGVPWLHSACGYCEHCLG
GWETLCHSQQNTGYSVHGAYAEYTVAPANYVGVLPDALSYVEAAPILCAGVTTYKGLKETGTRPGQWCVVFGAGGLG
HVGLQYAKAMGFNTIAIDISDQALALAKELGADMTINAAKQDPGQVVWKEVGGAHGCLVTAVAPKAFQQAVSTVRRG
GTVALVGLPPSTFPLDIFNVVLNRITVRGSIVGTRLDLQECLDIAARGKIRARIETQPLDNINAIFEKMKKGKLEGR
VVLSPL

>N062_hydroxymethylglutaryl-CoA_synthase
MRRQSTLATLATATRRSATIAGVLRSVNATTTTTACGRGGIATMLATSPTTSARRGVATDFSHYPRDVGIVALDVYF
PSTYVSQADLETHDGVAAGKYTVGLGQTSMAFTGDREDINSICLTAVQSLLEKYNIDPKDVGRVEVGTETIVDKSKS
VKSTLMDLFQKAGNTDIEGVDTTNACYGGTNALFNAINWVESSYWDGRYAVVVAGDIAVYEAGPARPTGGAAAVAML

IGKGAPIVFERGIRSTFMENAWDFYKPVMGSEYPLVDGALSNTCYLRALDQCFYTYAERFEKAHGKKLSLDADVDYA
LFHSPYTKLVQKSWARMNYLEAVKNEAHALHESLKSQNKLQPETTYEDNNLMKEAIKYSDATYKSKVGPSLTLPKEL
GNSYCGSLYTGLLSLVASHADAAATSEAEKRALMFSYGSGLAASLFSVKLKSGLKKIADTSNFQARLAQRKKVAPAD
FVEALKRRETATSDDVPKPFVPSDKVEDLFPGTFYLEQVDEKFRRTYARNQQ

>N063_isovaleryl-CoA_dehydrogenase
MRRTVQLSSRVLGSRTCTTSAASGAQLLRTASVARSYSVSANLRDTVAEGLFDDTQKELKETVHQFAQREIAPLAAE
LDRKNEFPMHLWRKLGEQSLLGITADPEYGGMGMGYTEHCIVMEELSRASGSVALSYGAHSNLCVNQISRNGNEAQK
KKYLPKLITGEHVGALAMSEPGSGSDVVSMKLKAEKKGNKWVLNGNKFWITNGPDADVLVVYAKTDMAAGPKGITAF
LVEKGFAGFSTAQKLDKLGMRGSNTCELIFENCEVPEENVLGQVGKGVYVLMSGLDYERLVLGAGPLGLMQASLDVV
LPYVHDRTQFGQPIGTFQLMQGKLADMYTTTSACRSYVYTVARACDKGQADAKECAGVILYAAEKATQVALDAIQAL
GGNGYINDYPTGRLLRDAKLYEIGAGTSEIRRMLIGRDLNKLYGVERK

>N064_prohibitin_1_(Phb1)
MMQKLQALGPALNKVAIGAVSVGAVGYALNESMYTVDGGERAIIFDRLRNGTRDFIVKPGTHFLIPFLQFPIIYDTR
TTPFNIKTETGSKDLQRVNITLRVLYRPDKKKLPYIYQRLGVDYSANVFNSVGNEVLKAVVAQYDATELISRRETIS
NQIRQRLVKRAGTFGLKLEDVSITHLTFSPEYVRAIEHKQVAQQLAEQAKFVVAKNEQEKLAKIIVAEGEAEAAALI
SKAMSGPGYIALRRIEASRDIAEELSRSRNIVYLPSGTNVLMNLPQVGQQ

>N065_serine_hydroxymethyltransferase
MRSVLARRGGVSAARGAVSATSVGHTARRLVSSSTARPLSEVDPEVHSLIHEEYERQKYGIELIASENFTSRAVLEA
LGSVMTNKYSEGYPGARYYGGNEVIDKNERLCIQRALDAFHLDSAKWGVNVQPYSGSPANFAAYTALLNPHDRIMGL
DLPHGGHLTHGYMSPKKRISATSIYFESMPYRLNESTGYVDYDELRRSALLFRPKIIIAGASAYPRNFDYARMRQIC
DEVGAYLMGDMAHISGLVAAQQVPSPFDHCDVVTSTTHKTLRGPRSGVIFFRRGVKSVDPKTSKETLYDLEERINFA
VFPSLQGGPHNNTIAALAVSLKEAMSPEFVEYQVQVKKNCARLASSLQSKGYTLVSGGTDNHLLLLDLRPQGVDGSR
TETVMEACNITVNKNTVPGDTRPMVPGGVRIGTPAMTTRGLKEAEFEVVSDFLHRSVQITQSLAKQGGGNLKAFKEQ
VEKEKSGGEIARLRKEVIDFSGSFPLPS

>N066_Rieske_Fe-S_protein_(ISP)
MKRTAISAAATLRASTAVSGSASATLTRMAPVLSSGSSKREVHEINVPDWGHYKREAQEGGESGGRAFSYMVLGTAG
VGYAAAAKHTVIKFLDSMNPAANVRAMANVEVDVSNIAEGTIMTVKWRGKPLFIRHRTAEEIADAESAPLTDMRDPC
PDAARRKADKPEWLIVLGVCTHLGCVPLGGQGEYGGWFCPCHGSHYDTAGRIRKGPAPLNLEVPPYVFKDDSKVLVG
VDSV

>N067_putative_Complex_V_(ATP_synthase)_g_subunit_(Atp20)
MNRLCGSLAKGAQKFQALEQSTTSCACNKQLYGYLGTQFGCWSNRWQAFPADAKALWRRVITGQITVGEVGRGVRAS
TPILLAALAGNFLGRGEFLYSPIVGASYTYPEY

>N068_3-hydroxyisobutyryl-CoA_hydrolase_domain_protein
MQRGAQGGRFAFVGGRGALGKTIGGGATHPALALRNMNNKTATAAYSSGSGSKEDRDWFDWSKYRTTSSKYDPFYQH
ITTDARFGMSDVWTQGMDPPQPIFPVDVKGRSKAYLPEVLSRKHYYTKYAMLNRPQQLHALNLATIRHLTPVLKKWQ
AHKETTRAIVLTSSTPEHLSSGTDFVDLLQAVRSGNQEFPKTYFKELYQLIYYINSLDKPFLPIMNGVTMGSGASLG
YSSNSFKITTEQTVFALPEVGMGFFPDAGASYLLPRLADHVGTFLALTGKRIRGWDVLWSGIATHLVPSDRIHIMYD
QLDQLRDKFHSFDQIIHCVHSSAADKIEHPYLLKEKGYLDIIKRCFSQPTVPEIMKALSHEKHPWAKQVLQRLQEQC
PLSLAVTLRSLQEGATKDMGAALRREYRIALRFMLSRDFAEGVTARIVEKRQPNWTHKSVEDVHPDEVQAFFESLRE
DELDIRSLDEERAEDSAIQQLLDKQRRFKKMMRRPWVQNEAKQYLAQELKSVQKELEARQSQTAGQLAAETEKQREE
YQKKIEEGRARKGEALSFLQQLEDELVRRRNVEKEAVTKTTVDKLEWKRWEEDIKNVREAKGILTLDVNTEYDEQLP
TAALQTVLVDGIAEALSGTEDLAKQVSLVAASLDTAGKSALELKEHLFRRTPEGVAEAEAEYERQYVEALQQDELRR
TLREQMADIDIDAIRQAMNEDLGLLQPDERDQLDTLLSSTEIVSHARQLHKQKQREQQQQQQQRPEAEAGATVEPAL
TLDDIAKLVLGGDHNDDAARVAETRAKIESGELAVSEETYAAAVQLMRERSLAAAEPSERATVEATFDTMHDEIVNV
VKAKVAGQSREQMVNALVGGEQGKSKLAQLMTQTAANLPHDSRVALTDPENQALILAEFQDFAKNLDSNASEGKVPL
WKLEDKIANALARRDTEAAWPAEKRQELSRQIAQDRQLRDLHAFPGLRGDDDDGADALQQATGQPGSSSSSEDLDLG
KLVDDAAYELEHGRPAPIPVKLMTEQQKDEFERNQSDMGLANYGKQFVYEKYADRIGHFKRIKERQDEFMSQVPDPI
SEPEQYRDWLVAVRLADLAMPALEDALGNWIDQQAKAGYNVKPIPEALRDDSVDGFVGTGSDDLEEVPTPTPAIFKL
WKMATSPSAESDETDAPVPPVRRTDDASSQELLRSIKKSATASKSSSSPSSGSPSSSSSSTTPQ

>N069_acetate-succinate_CoA_transferase_1B_(ASCT1B)

MKRLQQMSARTTVVSAASAGRASAFGRRSYQGRPQMLSADDAVKVIKTGDR**VFVHSVAAAPQALIHAMTR**RAPELR**D**
VEVCHMHIEGDASYADKKYEGSFK**NNNFFVGK**NVRKGVQEGR**LDYTPVFLSEIPLLFRR**GILPLDVALITVSPPDQH**
GFCSLGTSVDASLAAVQCAKTVIAQVNPHMPRTHGDGFVHESAISFMVDGPAPLIEHKRGKVTETIGK**IGKNVAQLV
EDGATLQMGIGVIPDAVLAELTHHKK**LGIHTEMFSDGIIDLVER**GVITGENKVIAPR**TITVGFCLGTKRLYDFVHEN**
PAVQFRAIEWVNNPILIKENPKMTAINSAVEVDLSGQICADSIGSK**LYSGVGGQMDFMRGAALSHGGKPIIALPSTT**
SRGESKIVPRLK**RGAGVVTTR**AHVHWVVTEWGAVNLFGKPVKERMKALISIAHPLHRPWLEKEVER**GFWFDVDENSP**
KIPESAHVDE

>N070_uncharacterized
MSR**DPAVAAASFGFVNHR**CAKDVKAFQEQKGSSEAVKACFAKETKTLTSTCGKEVHAFAECLADPESGSCSRPEWDL
RVCVR**SNFGFDSALEQKK**QAARLSK**STVPTELADSEKLETAASR**WK

>N071_putative_Complex_V_(ATP_synthase)_i_subunit_(Atp18)
MSARNFGLTEGEIQELKKRPYPR**FAPAPMQR**LISQAKVIWPFAVGWAVTLFLYSR**IPISDDDRAKSHYQYQLDVLDG**
KIKPEDHPIHGHHGH

>N072_acetyl-CoA_carboxylase
MRRALQCTTSTMTMTAAAGWRGGAAARMLHSSGARAALAASAEQRVETK**RAEALVGGGLPR**IAAQHKKGKLTARER**L**
ELLLDPSSFREESMFVEHRSTDPAIVNQKYPGDGVVTGRGTINGR**LVYVFSQDFTVFGGSLSETHAEK**ICKVMDQAM
K**VGAPVIGLNDSGGARIQEGVASLGGYAEVFQR**NVLASGVVPQISLIMGPCAGGAVYSPAITDFTFMVKDTSYMFVT
GPEVVK**TVTHEDITHEGLGGAR**THTSK**SGVAHGSFTNDVEALSMLRQFVDFLPLSNK**HEVPVRYTEDTRERCEESLD
VLVPPDPNHPYDMHEVIDK**IVDDANFFEIMPDYAR**NLIVGFARFEGRTVGVVGNNPVELAGCLDINASTKGARFVRF
CDAFNIPIVTLVDVPGFLPGTAQEYGGIIRHGAK**LLYAYAEATVPK**ITFITRK**AYGGAYDVMSSK**HLRGDANYAWPR
AEIAVMGSKGAVEVLYRGKAGVDMVKLEAEYR**DKFANPLAAASRGFIDDVVSPR**LTRR**IICEDLEVLR**NKQLDNPWK
KHGNIPL

>N073_Complex_I_(NADH_dehydrogenase)_51-kDa_subunit_(NUBM/NDUFV1/NuoF)
MLRRVAVRSGLAPVTENVAAPAAMALASRRDYTTERSYGNLKDSDR**IFTNLYGEHDIFIK**GALARGDWYKTKELLR**K**
GEDWIIKEIKNSGLRGRGGAGFPSGLKWSFMPK**VSDGRPSYLVINADEGEPGTCK**DREIMRHDPHKLVEGCLLAGFS
MKAKAAYIYVR**GEFVYEINNLQRAIDEAYEAGFLGKNACGSGFDFDVYVHRGAGAYICGEETSLIESIEGKPGKPRL**
KPPFPANVGVFGCPTTVTNVETVAVAPTILRR**GAEWFASFGRPK**NSGTKLFCISGHVNNPITVEEEMSIPLKELIER
HAGGVRGGWDNLK**AIIPGGSSVPLLPKSICDNVLMDFDALRDVTSGLGTAAVIVMDKSTDVIAAIAR**LSKFYRNESC
GQCTPCR**EGSPWLWNVMER**MVTGDAKIDEIDMLYELSTQIEGHTICALGDAAAWPVQGVIRHFRGEMEQRIHDYNSK
HGQAIGSATVDEYASRQLHLAKQAPLTFVQ

>N074_Complex_V_(ATP_synthase)_epsilon_subunit_(Atp15)
MSSWRSAGFSYLR**YSNTCAILTR**RALKEPFRAKAAER**DSVNMKVEQWILGK**GQDKVDVK**RANEIAGSAGH**

>N075_2-oxoglutarate_dehydrogenase_E1_form_2
MLRVGARGTRTQGSSFLSSSRFGVTTAAAARFCPAARSQTLGLVGRYSSSTTTTAVEGGK**LTQEEVDNQNK**HANVLR
LVNAYR**TYGHFDAALDPLGR**RQR**GAPEGVLDAARYGLGNEEVQLR**GLFFGLDKEK**ASVSEIVDALK**KTYCSSVGVEF
THVENPEEQTWLAR**RFEAAMGRTATGATAQNALPAEDK**KR**ILNLLQTSEEFDHFLHTK**FRAVKRYGLEGCESMMACM
DTIFSK**AAESSFDEAVIAMPHRGRLNFLTGILR**YPASKIFAKVSGFNDFPTVEGAVRPGTGDVLSHIAQSVDLEYQG
K**NLHVSLIHNPSHLEAANPVAQGK**VRAKQDLGKGRKQALCIVVHGDAAMSAQGVVPETLTLSQLPEYAVGGSMHVVV
NNQIGFTTECHKGR**SSWYCTDVLRSVHAPAIHVNADDPEAVVIATRLAMDYLTTFR**K**DIIVDLHGYR**R**HGHNELDEP**
SFTQPLMYDSIRVRPTIAKLYGEKLIKEQVVTEEEAKAIKDQARQVLDKEFAESQKAQPTVDTMGGKWQK**MTAPQDM**
TKPVDTGYAEEELVKVGVASINPQGKTVHSRLQNFFCKPRQAKLESKTGLDWATAESLAIGSLLLEKYNVRLSGQDV
GRGTFSHR**HVALTDQK**TNER**VIPLNLMSSDQGK**LHVADSPLSEMAVMGFEYGYSMEDPSTLVLWEAQFGDFHNGAQI
IIDQFLNSGEDKWWRQSALTLLLPHGYDGAGPEHSSCRIER**FLQLCDGDR**LNPGDISNLVPNMQVINPTTPANYFHA
LRRQMKRSFR**KPMVVVGPK**TLLR**HPQAVSDLAEMAPGTSFQPVIADTTVSPAQVK**RVVMCSGKVYYDLVKHRETK**KI**
DDVAIIRVEELSPFPYRALADELDKYRNADSYRWAQEEPQNAGMWDYVAPRFSRLSAPVK**LVSRPASAAPAVGLGSI**
HAQQQKAILDGAFA

>N076_succinyl-CoA_3-oxoacid-CoA_transferase_(SCOT)
MRQSTMRGIVLTRGSRGFHTTSLLR**SKIVGSAEEAVK**DVKDGSK**LLVGGFGLCGIPEK**LIGALRTTGVKDLTVVSNN
CGVDDFGLGLLLQTRQIKR**MISSYVGENAIFEK**QYLSGELELELIPQGTLAERCRAGGAGIPAFYTPTGVGTFLEEG
GFPIK**YNTDGSVAIASKPR**EVREFNGRKFIMEEAITGDFSLIKGWKADTRGNIVFRYTAR**NFNPPVATAGK**ICIAEV

EEIVEAGSLHPDEIHLPGIYVNRLIKGTGYEKRIEKLTLDKGQPAKGDAPKNEAAITREKIARRAALEFQDGMYCNL
GIGIPTLASNYIRSGIHIELQSENGLLGMGPFPKPGNQDPDLINAGKETVTTLPGSSIFSSDQSFAMIRGAHVNLTI
LGGMQVSSNGDLANWVIPGKMVKGPGGAMDLTCSGSRVVVTMEHKDKSGKPKILNRCNLPLTAQGCVNRIITEMAVF
DVDRSGLTLIEVAEGVTVDDVKKYTEPEFKVSPNLKKIAYA

>N077_peroxiredoxin_(PRX)_family_protein,_PRX-like_subfamily
MNRTASVSRTAFTVAARQTTVRGSQALFARSYAVGQNLLEGQANLKAVDGKDLSLTDLFKGKKVVVFGLPGAFTPVC
TSRHVPGYVDSADKFKAKGVDNVVCVSVNDPFVMKAWGESLKANNITLVADWDSSFTKLVDKELDLSAAGLGKRCRR
YSLIVDNGKIVKENIENAPNDLQVTSAEAVLAQL

>N078_uncharacterized
MRRASAQTWLASARSQPPLSQISTRIGARSAAILTGAAGSSSRSASLLSTVATATRPNLHTPFTTAASATLRRLGLN
GLAQPLRAGLRSKLPGGRRSYSTEVPAAAETAKVAETPASLDALRAEFYEFQKRTLNWNIGGVSVPKAVLWLVFFQF
LGLAPYSFALERNESVVFVREYMEKVQSMAESSGLPLGDDHNQHMPSFTRGLTGWERTALHSVASVATLSVIAFLWA
RRRTRRSFNSFILSRALGEPTGTYPITMENVVRKGDALKIKGEGLKSVRSDVVRLAGLKAVQASVGLLLASTASSYA
FTTWVDGKVRDGVIRFRRSDVLQGETALSLVLLFNFLVSWAVLVYQPYTIFPFVISNVLMSYLRFTDSTYKHVTLPS
KETPVVTEHKAVEEVDGGKEYITLTEKKSGSGCTRTETRVFVPDAAEAGGNAQRTLDITTKTEGDADTQRSLDTTTK
TDA

>N079_DNA-binding_protein_HU
MSKGPLIEAVFKQHSLANKTGKTISKAAIGRIVDSVFEQVGKQIVGKGYFRYPGFGSFLIKDRSARTMYKALPRTKG
QTMDRSEANKITVPARGVVGFKPAPPLKESVKDLKRVKRAKASKKEQEIV

>N080_acetyl-CoA_acetyltransferase_(ACAT)
MRASRVVNASGIRSAVVVSAVRTPVGSFGGVLSTVSGPRLAAACITAALQRTQGGQVDAAEVTEAIMGNVISANVGQ
APARQAAILAGLKESTVCTTVNKVCASGMKAIMYGAQSIMLGHHEVVITGGFESMSNVPYYLEKARTGYRYGHGQLI
DGVLKDGLTDAYDGQHMGMCAEKCAKDHGFTREHQDEYAVTAYRRAAEAWKQGWFNDEVVPVSVPGGRGKETVVAED
EEYKKVNFDKISSLKPAFHNEGTVTAANASSLNDGASAMLLMSEEKAKALGLKPLARILGFADAEQAPIDFATSPSL
AIPKALKHAGVEAKDVDYWEINEAFSVVALANAKLLGISLDRLNVHGGGVSLGHPIGSSGARIAVSLTHILRQKGGR
IGVASICNGGGGASAIVIEKL

>N081_Complex_III_subunit_Qcr9
MNALKSSGASNWVYQNLFKRNSSYFALILVGAVVVESGVSRTVDFWWNSVNKGRTWNDFKRTQLPKIQAKKAAAAEE
EESDE

>N082_NAD+-dependent_aldehyde_dehydrogenase
MKTTLASLRARSLPTGALSVRHFSASAASASRKLVMVNPATEQQETFAHEADTRESIQSKFNAALQAQKEWGRPENL
EKRVATLKKFLELINDDANVQEGARRLTQDMGKPISHAAGEVKATRARVQFFLDNIHSVLQHEVVNQKDALVEKISR
EPLGVIANIAPWNYPWFVSCNVYAPALLTGNAILYKPSEFALRTGEFQMELLHKAGVPKEVIAPVYGAGDVGAELLR
LPVNGVFFTGSVATGRKINEAVASRMIKVGLELGGKDATYVCEDANVKNAAASLADGAMFNAGQSCCSVERIYVQKE
VYDEFVEEYVKTVKSFKVGDPMDSATYLGPLTRGSQLSFLEEQVKDAVAKGGKLLLGGKRASVAKGYFFEPTVIVDA
NHSMSLMKDESFGPIIGIQKVSSEKEAIELVNDSDLGLTGGVYTKDAERAKRVLGQYNTGTAYWNCCDRVAPALPWS
GRNFSGLGATLGVEGIRTFTIPKAWHLVSPQ

>N083_Complex_III_subunit_Qcr10
MSIHKLDKTHATVNLEEAATRTGTIRSVPYHETIAYQRFYANVFTKATVFGKRLIPLTKNYAPTAFRWGALAGLAAA
YVIEPSFLTKYFTKSESK

>N084_pyruvate-ferredoxin_oxidoreductase_(PFO)
MNRLFARHTRPIVAQRTFPLSSAGTLRALSTPRWTAGPLRRLHGAVPMDGNTAAAHVAYGLSDIHAIYPITPSSQMG
ELADKWSAEGRLNAFGNTPRVIEMQSEMGAAGTLHGAAVGGALVSTFTASQGLLLMIPNLYRVAGELMPAVFHVTAR
AISGQGLSIYGDHSDVMAVKQTGVAMLASASPQEAMDLALVAHLSSIRSSVPFVHFFDGFRTSHEINTVEPIKYEDM
RKLLDEEALEQFRRRGMNPETPNLRGLIDGPEHYFQQVEAANTILDGVLPVVEGYLDEVHKLTGRKYGLFDYHGHPE
PRHVIVACGSSVSTVEEAVNHRNAQGERVGLIKVRLWRPFSIKHLVDALPKSVEKVAVIDRVRDYLASGGPLFQEVC
TSLMMGGRRDVQLVNGRYGLGSKDFTPGMALAIFDNLKQDQPLHNFVVGIKDDVTHKSLTVTEEPDTLPAGTKQSIF
WGIGGDGTVGANEEAIKLIVENSNMYGQGYFAYSAHKSGGVTVSHLRFGEKPINSTYQVQNADLIAVHTTPYLKKFP
SLLGPLKEGGTVILNSPWNDVAHLDRMLPDFVKRRIARRKARLINVDATAIAHEAGLRGRINMVMQAAFFKASEVLP

LDVARAELRRVIDAQYARKGRDVLERNYAALDQGLARTVEVAYPDAWAECRDDVADYIVPDPADAPEQLRKVLRPTQ
RQRMEGDSLPVSAFDPRGAMPSGTSKYEKRGIAPAVAQWTNPDTCTQCNLCSALCPHAAIRPFLFTQEEAGSAPEGW
EGRKAVGKAGKSYQYRVQVSPYDCTGCDVCVKACPTQSLAQVPFVDALDRGQARLWDFAAERLPIRSEVYPKESLKG
SQFAKPCLEFSGACAGCGETPVVKLLTQLFGDELYIANATGCSIVWGGMFPWSAYTTNERGHGPAWGHSLFEDAAEY
GFGIRHAVRYRREALRRCAVQRDLTAGAYAAEHPVLAELLRRWDAAYDDRTQSPSLAAKVREYLERLPAPAAAARGP
LRELHAERHMLARKTQWIIGGDGWAYDIGFGGLDHVLASGEKVNVLVLDNEVYANTGGQASKATPRASQVKFANAGK
TTAKKDLGAMMMQYGNVYVASICLEANPDHAVQALAEAEAFDGPSLVIAYAPCIAHGIKAGISTEVEEAKRAIKAGY
HILYRYNPSLVEQGMNPLSLDSSPPDDQLLQFLRGENRYEALRQQHPELTDEKQRLLVRDVADRYRHYALLKEQLEP
KDDGEEEEEKADEAKEEATA

>N085_NAD+-dependent_aldehyde_dehydrogenase
MLKRQATVGRAFPIFVGGKPVTTATTLKVFDKYTKQVGYEVSLAGPQEIENALQLAHQAAPAMRELPNYKRKEILLY
CAAEIQRRQDELLHSLCVEAGKPLKDARAELGRAYDTFTIAAEEAIRQYGEFLPLDVSVRNPGFTGLVRRFPVGLIS
MITPFNFPINLVAHKVAPAIAAGCPFVLKPNDVTPVGALLVGDILSKAGLPDGAFSVLPCKLEDAKKLSTDPRIQVL
SFTGSEQVGFALQRGAGRSKVLLELGGDAACVVDEGSDVDHVVSRIGFGAFYYAGQSCISVQRVYAHESIYEELKQK
LVAHVKTLKKGDPFDEDTFVGPLISEDSAKRLESWVQEAKEKGGKVLAGGSRDGSVFDPTILEDVPDSAKLACEEAF
GPICVLHKFSDFKEAIEQVNNSRFGLQAGVFTNEWKKAWYAYDKLEVGGVVINDIPSVRVDAQPYGGIKSSGVGREG
LRYTIEEFTEPKILLTKDLGKL

>N086_Complex_I_(NADH_dehydrogenase)_39-kDa_subunit_(NUEM/NDUFA9)
MKRVAAQASFAGPRSIATSLSWEGAAGVRGLHVNLQGGRSSVSGVVATVFGCTGFLGRFVVNRLGKIGSQVIVPYRG
EESAFRHLKVMGDLGQIAPVWFDLRDKETVRRAVQYSNVVINLLGKRWETRNFSFDDVHPEATRTIAEAAKEAGVER
FIQVSAAGADVNSPSAFARSKGESEKVLREIFPDATILRPTVLYGARDNFLVKWGMIARYWPAFVRTLKDTKFQPLY
VADMATALMNALADPETAGKTYELGGPKVYTLEEITELVTRLTFLEPSVVDVPFPALRAFAQVTQPFLRKPRFTVEE
LDYWKSGDVVVPENAPLTINNLNFSTEDLTVLEKEAVNFLRLYRKPATMNLILEDQLDVKSPRARASR

>N087_BadF/BadG/BcrA/BcrD_ATPase_family_member_(putative_N-
acetylglucosamine_kinase)
MRRTSLIRSSVSRAVSCQAVGARTTATALRAHSAPLASTNSSCARRALGTAARSGGQRTGFAGSSSSFLVGAAAAVG
VALGAILYYDEQNQVVYAVQKDGTVKRYFLGVDGGGSKTNVTCIDEEKKVVGEGTSGCTNFNSVGQEKASQHLREAI
LSALKAAGVPEDQVAGICLSMSGVDRPADKQLMRSWITPILPKARIDVHNDAVAALVSGTDGNLFGLVVISGTGTIT
YGVNKEGETTRAAGWGPMLGDRGSGYQIGYEILTAVVRALDGRGPATSLVEAVLTKLNLSKGEELIPWAYSSVAWER
YAQLAPLAAIAARNGDKVAEQILEGQAQDLVVSIQAVAKRLHIENQPFPLVLAGGNFTHEGSYLTALLKKKVNQQLP
QVTVLLPTLKPEYAAALLARNNATAKH

>N088_phosphoenolpyruvate_carboxykinase,_ATP
MMLRSSVRGGRAVASGACVKATEVMGSSLVSARTLATAAAPAAAATAPSTQPRSSALFDYRRLKNRKGWKKVVPDED
LDFVVFPRERLGKTYELNWTICKYAVIPNKDGEAFHNLHSRGLQMLSNAAADKNKALHVTVPEEEYAFSHYFVLPSP
PPAPAEGQAAPVDLMFVPENASVVNDGVAKNVSKEVRRFLSEGRYLFVHDGAVGSHSAAEEKVRFIVSSATTALLLK
HLIPKQPTVNIQDFEESITVFVAPELKATAEALGVSSDRFTLVNFKTNQVFVAGTNAPEAVQQAVSSLATYLLGKKG
ALPLQCDSALTKDGKSVLFFGPGLLQQKPRNDLFGAHGHFWTNEGVSRMYDGASVANPDASLALNRGDLVFHATKGG
KTTKTSLSVPLSLQGHQAPHPSAIVFVSPNSAAGLTKISAEEAAKHYLASFQYPVAVKPELLKQRFAYLLSNKNVTA
YQVGAKSGKVNVDEINAQLHTALKQ

>N089_alpha-ketoadipate_glutamate_aminotransferase_(Aro8)
MQRALASSGASRITDYEPFLSVTSKRRQPSPIRSLQPLLELPGMISLGGGMPNTSFFPIKGVDVHLTDGTTLPIQGV
DMNAALQYSSSYGVTEFVEWLKDYQTREHHPPYASRKDWHVCVTNGSSDANAKAFEMLIDPDDYVLVENPTYSGSLA
GLRPLGCRLVGVETDHSGLSPTHLRSLLDSWPVDRPKPKVLYVIPTGQNPSGATLPEERRREIYGIAQQHNLIILED
DPYFHLQLDKQQDDEPLKSFLSMDVDGRVVRFDSFSKIISSGFRIGWATGPAPLIERIQLHQQASTLHVSGLSQVVL
LTLLKNWGEEGFKRHIAMVQEGYRQRRDLFCKLAEKHLTGLAEWHPPSAGMFVWFKALGVRSTEKMIKERALAQKVL
LVPGVAFTPNGEESSFVRASFSTASPDDMDEALRRFAALLHEERNAHHQ

>N090_mitochondrial_carrier_AcMC2_(phosphate_transporter)
MSQQQTAIPAPVVAHHAPVFDLMYYVKAAVAGGLCCSVTHGAVCPIDVVKTRMQLDPQKYNKGMISAFRQVVSTEGA
GALATGLGATAAGYFVQGWFKFGGVEFFKVNIAHAVGERAAWENRTGIYLASSAMAEFIADLFLCPLEAIRIRSVSD
STFPKGLGAGAARMFSTDGLLGFYAGLGPILFKQIPYTMAKFAVQGKAAELIYKSANTSPDKATKGTNLSISLLSGV
IAGVVAAIVSHPADTLLSKINKKGAGGSGSTTSRLFTIAREMGFAKLCLTGLPARCIMIGTLTAGQFGIFDSVMAAI

GAQKFHFHNPDEKH

>N091_iron/manganese_superoxide_dismutase
MRRTAATRAVQTTTSFTRTAAGARSLFTLNDPPYLKTGLTPAISANTLNFHFNGHHKAYLNKTNDLIKGTPLENKSL
EDVILVAKTTNNAALFNNSAQLWNHSFYWDCMAPVGETGEISAELEQLIKESFGSVAEFKNKFTDSAVANFGSGWTW
LVNINGKLEIQNTSNAESPVTLRVKPLLTLDVWEHAYYLDHQNRRPEYINKWWDVVNWNFVNKQLKQ

>N092_Complex_I_(NADH_dehydrogenase)_subunit_SDAP_(ACPM/NDUFAB1)_acyl_carrier
_protein
MNRIARPALLRASARAPAFAPVASSLRFSSISSSSAALSTTFARRSDAITTFDYQRRHYGAAAGLSEADARERVIKVV
KNFHKVDPNAVNEKSHFINDLGLDSLDTVELVLGLEDEFCIEIPEEQADKIQTIEDAVSYLVTNPAAK

>N093_Hsp10
MSKRLFPLSDRVLIRKAKPVERIGGIVLPESAQKRLNHGTVLAVGPGARNREGALIPTTLKEGDNVVLSEYGGTEVE
IDGEELHLFREDDILGILKK

>N094_3-hydroxybutyryl-CoA_dehydrogenase
MLRNTSRLARASPVACSAPSLRTSAGSARRLYTTDNSTHGVKTLGVVGAGQMGGGIAQVASQVAGVRVVLVDSQQAQ
LERALQTMDHFLAKNIAKGKITEQAAQETKSRIAISTDVAKLQEADFIVEAASENVLIKEKIFKELARVAKPEAILA
SNTSSISITKIGAFTPRPEKVVGMHFMNPVPIMQLVEIIPGLATSEHTLSTTLALAKAMGKTTAQSDDRPGFIANRL
LCPYLNEAINALQDGLGSREDIDTTLKLGCNMPMGPLTLADFIGLDTVLAIMRVLHSELGEDKFRPSPLLIKYVDAG
WLGVKSGKGFYDYAKKQK

>N095_Complex_III_subunit_Qcr7
MAARKGSSGFLSRISSSFKPVSGYQAYGLRLEDFYNAENPEIQEVLRRLPNKTKEERDLRIRRGHELHLKGTTLPES
SWTTPEEDGQTYMEPYMSEVVQEIEERKDFRADFLLPVEKRHKRK

>N096_cytochrome_c
MSFTPPAGMDKACIPGDVDNGEKLFKARCTQCHTINKGGGNKQGPNLYGLIGRKSGMVPDYKYSPANKNAGVTWTND
TLYNYLENPKKYIPKTKMAFAGFKAPQDRADVTAYIVKAAQE

>N097_Complex_IV_subunit_Cox4
MASRAAARVTKNRFALPLDHRATRPGFQAPWGSIDPAQEVRQSSVLMGVLGGIFVSWGLFALTRRDNVRKLPESVKN
KEWATVSEERLAKNRGA

>N098_Complex_IV_subunit_Cox6b
MSSTRIYSVVEDHEDKKAEEVEEEAPVEEEVQEEEAQEEEEEAGERTLGSILKPGVTTVEQFLQFLHPHTPAYNPHF
PNTNQTKHCWSSYINYTQCTKLKGEGDAECRRFYVSARSLCPDEWLDSWAEAKEEDKFASPYDVTSEKSAH

>N099_Complex_IV_subunit_Cox5b
MSRILRRGALSNTSATLNATAFAARRSFAASALRLASLKEPATSLDVESQDDTDARHTGMERLEKVPWTKLYEGDAI
LTGKFGTLEEPTIVHSWFPSRIVGCQGSADHPHDILWHEVRRGRDTVCLECGQVFRLRPNLFHQLSEVEADLFPPTE
AKESAAH

>N100_succinate_dehydrogenase_subunit_2_form_1_(Sdh2-1;_SdhB-1)
MRRITARSVTTPLFTSKTASLAGSARPLFGIVSAADKVVPKDGLVTVEVYRWSADEKEKPYIQSYKLDVNNCAPMVL
DALLKIKNEQDPTLSFRRSCREGICGSCAMNIDGTNTLACLKPVAESVTNGKIKIYPLPHLPVVRDLVPDLSNFYEQ
HKSIQPYLQVDDHAALGSSKTEQLQTREDRKKLDGLYECILCACCSTSCPSYWWAGNENKYLGPAILLQAYRWIADS
RDQHTNQRLRALAKEDMKVYACHTIMNCTKVCPKGLNPALAVAKVKKATLELDVQQKKQALAH

>N101_4-aminobutyrate_transaminase
MSRYESSKKLLSPVWGHLSESIVERASGSFIYTTCGKKLLDFSTGIGVVNTGHCHPRVVAAAQEQVGKLIHGQLNIV
YHKPVLELVEELKPVVPEGLDTFFFSNSGAEAVEASIKLARHATKKQNIITFVNSFHGRTVGTMSLGNSKIVYKNQY
GPLMPGVHVAPYAYCHRCPCKQQRKSAEDCCNQPLLAVEMLLRQQTGPADTAAILLEPVQGEGGYVQPPKSFMQGLR
KICDKHGILLIYDEVQTGFGRTGKYFAAELSGVKPDILVFAKAIASGFPLSGLVASKETHKHWQQGSHGGTYGANAV
ACAAAVATQRVIKEEKLVENAAARGEQLTKLLLQLKDKYPQISDVRGPGLMIGVEFYDERDNAYPFPGHDSKHTVKY
GFTGALTKKCLDHGMLILNTGAHETLRFIPPLTVSAEEIELGVELFEKGLKDTLKELAN

>N102_mitochondrial_carrier_AcMC3_(phosphate_transporter)
MATQQKPIKLYSLEYFAACGLGGILSCGLTHTAVTPIDLVKCNAQANPEHFKNTVQGFRAIYSGSLTSIGFGSGVSG
LLKGWGPTLWGYSLQGLFKFGLYEVFKHYFAEAVGPENAFKYRDLVYMGASASAEFFADIALCPFEAIKVRIQTSPS
FARGIIDGLPKFIKAEGFGNLYAGLGPLWARQIPYTIIKFVAFERICEAIYAMLPKKKEDMSKTEQMGVIFAAGYTA
GIICGAVSHPADTMVSKINKIKSSGSLGEKMKLIYSGTPEAPGIGFAGLWKGFGPRVVMIGTLTGLQWFIYGAFKAY
VGLPTPGASAPAGDKKH

>N103_uncharacterized
MSLPTIEELEDLTSQCLARTFSDQQVQAIISHSRQLASFGVTDYVDREDLRKIFKDEKDKKDKKKDKKKDKKDKKKK
KGKKDKKKDKKKKKSKKDKKKSKKDKKKDKKHKKKDKKDKKKYKEGYKEQPWRPAEWSLSKEASAEGKEYDFDEDET
RYVRTRLQEVREKLLHRREASVSNFAPCMLLYTEGSEPDVKETKLDAQCTLLRKASTHALKSEQCWSQYLAKMDECL
HHRTGEYCLRAFRPLERQCAQSGWRSVNDLRKLTRLRSKEEVDLQ

>N104_uncharacterized
MATNDERFDFEAVLSTQAKDWACASDLQNLTRCFNNRNLAACQGFMDAFDRCTAQAPFPRKPAAADDGDDDDDDEEM
AGGPVSKVAIALAPQVFIGDAPRRKTWLSTTLERLMPKIFTEGGDDDDDDGDDGKGKDKDDKNDD

>N105_ribonuclease_III
MKRTTSSSLRLLASSSSFGARSAPLVLPRTSFAGLISSSSRSTGVHRTRLLATAAKASSSTSSSPSSSKPAPRNADP
EVLHEQLDAFAARIGFKWNNKKLLLQAFTHPSFSHDKEVSNQRLEYFGDRTLNFLVCEHLVNKYPNLPARALAHATH
LFTSNETLTTAGKRLGVQDFVRWTPHEEEDRGEDIIVANTMEALVSSLYFDQGLKAAREFVVKHILPQDENLDLIPF
LRQRLPRHTLSDLLTRRGSGAPYYVVLQESARYSSKSTFVVGVYSDSQLLGQGSGQSIGKAETAAAQEALNKMWGAK
AYTTLPPNDY

>N106_alanine-glyoxylate_transaminase
MMRASVRRCQPQRVASLTATSAQLSARGLNVSAQAALTTKANRLEMPPTDFKPMPYTGPSFDEVKALRAQHMPSAIF
AFYKNPIMLVEGKMQYMWDEKGRRYLDLFGGIVTVSVGHCHPRVTEAGVAQLKKLQHSTTIYYNPEVALFAKELADR
LPSQLSVVYFVNSGSEANDLAMLMARAATGNFDFVALRNGYHGMSMNTMGLTALHTWKYNQPQGFGIHHAVCPNTYR
GPYGPDEPDVAQKYASDVADIIRSSTSGRVAGWISETIQGVGGTVVLPDGYLKEVYKTVRGAGGVCIADEVQTGFAR
LGSHYWGFQTQNVIPDIVTMAKGIGNGAPLAAVATTPEIAETLKQRVHFNTYGGNPVSCAMGRAVLKVVDEEGIQHK
ALSHGAYFTRGLNELKRRYPIIGEVRGKGLMLGVELVKDQTTKEPATAETADIFERAKDMGLLIGKGGLYGNVFRIK
PPMCITKHDIDFSLEVLDQAFKDSAKAM

>N107_2-oxoisovalerate_dehydrogenase_beta_subunit
MKKRISASIGSSATAHRLVGGSVSGASPARSLLQPSARAFHVSPAHAAATAHGGSSSTHQQQPQGEGEVARMNFFTA
VNNALDIALGADPKAVIFGEDVAFGGVFRCTINLREKYGNSRVFNTPLSEQGIAGFAIGMAAVGATPIAEMQFADYI
FPAFDQLVNEAAKYRYRSGGQFDVAGLTVRTPCGAVGHGGHYHSQSPEAYFCHTPGLKVVMPSTPKEAKGLLLSSIR
DPNPVIFLEPKILYRSAVEDVPLGDYELPLGKARIVKEGSDVTVVGWGSQLHVLTDACGLAEKEGISCELIDLRTLA
PWDVDTVEASVKKTGRLVVSHEAPKTGGFAGEICSTIQERCFLHLESPIRRICGYDTPFPLVFEKFYVPDKLKNLEA
IRSTVHF

>N108_Complex_III_subunit_Qcr8
MGVRWTTYTLSPFRQKMFPGFWTGLIPRQIKRWKYNFPRVAPPILAGIAIYTWGNWKHDQIARSHWY

>N109_betaine_aldehyde_dehydrogenase
MATMLRTSTSSSTSTSASRVLGIRSFATKSDRAAAPLALAQRLSGKHFIGGLRPAKSGAVFDVHNPATGETIGHAAL
GDEADINDAVTLASRAQKEWREQSVRARGALVAKCGEVLRAHVEELAQLTSLETGKAIRTESRVEAGLISDTFSFFG
GLAPEIKGQTIPFNPSVLTYTSREPVGVVGAIIPWNAPLLLFALKLAPALVAGNAVVLKSAEAAPFGVLRVTELLNQ
VLPSGLVSTVSGYGKQAGTPLVRHPLVKKVTFTGSVDTGREIYKQAAEKLIPVTLELGGKSPMIVLEDANFEKAVNG
AILSMRFTRQGQSCTAASRIYVHEAIHDKFVAALTEKINALKMGDPLDEATDIGTVISKPQLDKIQRYIALGKGEQG
ATAHECSALPTDASLSKGLYVRPVVFTGISNQSRVAREEIFGPVTCVFKFNDFDAVLDEANSTEYGLSASVWTNDLQ
KALHATRKLEAGVVQVNQNAVVQPNLPVGGWKVSGLGREGSLETMLEHFTHSKTVAINFA

>N110_tetratricopeptide_repeat_(TPR)_domain-containing_protein
MSEPSPVAQTASGEIDWKKILGIGAAVVVGGAVLFYFLGGSDRRSNLKEAEQKFDEAAAKKEEEDWETAEKLYHEAL
TILRRHLDKNDENIAEVYRELATCALNKMELDKAEQYSRDCLRIKEHNHGHDSALICDSLVNLAGILAALKAADALE

YAEKALRIYELPAEDERDYAGLSHALRTKAAIMMSNKKLPEAQEAAIRALECFEKVSSKGDAHSHYRDAMEGHLLLA
KIYMKQDNREAAEGVYKGLVQRAKDTLGPVDTFVAYSLRNLGDFYEERNDVEQAEAAYKEALEVVREKHGEDDSNVF
AFLNYLAHFYWDHNRDSDAQDVFTKLRTMKCLPSPTNSRCLVTRLFAFTFTRARNDPHAIEPVYVGELLPTPKLPER
AFLEVIYENPEDPSNPIRQERELTEDDRETIVLLSPTVKGVKPQMYEIAIHVYKDRSKTEKVGEHHQMCQSVFDTDR
IKTEEDLMLQIPKDRLI

>N111_inosine-5'-monophosphate_dehydrogenase
MKRATSTVVGRTAATLNGRRAPYATIREGSIRLGLTYDDVLLVPKRSPVRSRKAVSVKTKLSRNITLNNPLVSSNMD
TVTEAEMAIAMARNGGIGIIHRYLSVDEQAKEVEKVKRAEGYVIDHPYCIDPSATYKDLDEKMEEAGVSSILVVQEG
KLMGVVTRRDVALIDDPNEPVSKIMTPRKELIVGRPGIGFEEARDIVQANRIKILPLVDEENRLKGLVTSKDILNQM
RRPFASLDKRGQLLVGAAVGVKEGFLQRAERLIKSGANALVIDIAHGHSDLAIDALVALKKHFPTMDVIAGNVATAE
GTRDLIDAGADGIKVGVGPGSICITRIVTGCGVPQLTAVMECAAVGREMGVPIIADGGVKTSGDITKAIAGGASTVM
LGSSLAGTDESPGQTLIKGGKKVKIIRGMAGYGANLSNKERQQLKDDVFEIVPEGVEGVVPYRGAVSGIIRQLVGGL
CSGVSYCGAHDIEGMQANAEFIRITPAGRKESGSHDISEI

>N112_xanthine_dehydrogenase
MMLRHGRRLPSSSSRAALLARNHVASSSTSLQRNGASSVMTRRSNASNTPSKPTQMSAAAAEEMLKTARVPTSAPSS
APSGLPSASQSALKETRHEVVFYINGKRHAPKSVEPDLTLIDYLRDQGLTGTKLACGEGGCGACTVTVAHWDQERGE
VVHRALNSCLVPVCFVDGMEVTTVEGLGSTRSGKLHPVQDKMANLFGSQCGFCTPGFVMSIHSALQKFPAPSLHQLE
KSIDGNLCRCTGYRPIVDALRSLEKEYKGKQSETLKKLHHFPQELIERSTHPLAITGTRAAWFRPTTLEHLLELKAT
HHHAKIVVGNTEIGIEQRFGRKHYPILISAAHIPELNQVAFLDGGVEVGSAVPLTTLWESLEHTNTYLTKNDQGKDA
FKSRSLAAITEQLQWFSGTSIRNGACLGGNIVTASPISDLNPVFVALNAQFRLKSMERGERVVNASDFFQPGYRKVD
LHHDEVLTSVVIPYSHENQYVEAYKQARRREDDIAIVNAGFNVALDDSGRVTSARLAFGGLAPFTLQAKETQAFLVG
KQWNQDTFEKAVDVLRKEVTLKEGTPGGMEKYRTTLALSFFFKYYLAVAQKMKNGPVIPPSYLSALWPLTAESPKGK
QVFAGSDQPVVGQSIVHASAERQVTGEAVYIDDMPRLQGELNGSLVVSQRPHAKLRKVDASKALQVPGVIGFFSHKD
IPGEKIIGDIVHDEEVFASEVVETVGQPIGIVAEDEVTAKHAAHLVEVEYEDLEPIFSIEEAVAKQSFFPLEKKIEK
GNVAKGLAESKNVVEGRVRIGGQEHFYFEPQITIAQPLDTEMVLYASTQNANKTQKHAAAVLDMPENKVSCSLRRIG
GGFGGKESSNIIYSCCAAVAAHHLNRPVRLLLGRDEDMEWTGKRHPFEGTYKAGYDNEGNITAVDVQLYNNGGYSHD
LSWPVLERALFHSDNVYNVPHFRVKGRVCKTNLPSNTAFRGFGGPQGMIVTEAWVEHIAHQLKMEPEDVRKKNMYLY
EDKTHFGQPINLKLHELWDQCEAQSDLRQRKKAIAEFNRENRFRKRGISMIPTKFGISFTFTPLNQGSSLVNVYTDG
TVLITHGGVEMGQGLHTKVMQVAANALGVGMKDVHVSETATDKIPNASATAASQGTDLYCMATFNACEILNERLAPF
REKMPGASFKELVQAAWFDRVNLSAQAFYKVPVSGFNFETGEGKPFCYFTSGVAATEVQIDTLTGDYRPLRTDIVMD
VGKSINPAIDVGQIEGAFVQGAGWLTMEELVWGDKDHPWVRPGRLRTNGPGAYKIPSCDDIPREFNITLMKDSSNPS
AIHSSRAIGEPPLFLGSSALFAIRNAIGAARKDEGLDNWLP

>N113a_alternative_oxidase_isoform_1_(AOX-1) [paralog of N113b]
MKQHCSQRIASLRGGGRDAFARLATTTASSLASGNGGVRASTLVQARRHLSLRLAPTTTSRTSSATATTMTTRGRWC
QGGALAWSRANTTSAAMTDGEPKQTQEEKKAAASNPSIAAQQTVERAQQQSGKSTRVAYTLPHPIWQNEYVDAVEIN
HTPPENLTDKLALNTVRLMRFNFDWMSGYSWGKLTEADWLRRIIFLETVAGVPGSVAAILRHLHSLRRLKRDHGWIH
TLLEEAENERMHLLTGLKLKQPGKIFRTAVWVTQGIFFNFFFAAYLVSPRFCHRFVGYLEEEAVRTYTHLLHDLDAG
KLPEWKDTPAPEIARQYWKMGDDAKWRDVVALIRADEAHHREVNHTFANLQLEQDNPFPPGH
>N113b_alternative_oxidase_isoform_2_(AOX-2) [paralog of N113a]
MKQHCSQRIASLRGGGRDAFARLATTTASSLASGNGGVRASTLAQARRHLSLRLAPTTMTSTTSRTSSATSTTMTTR
GRWCQGGALAWSRANTTSAAMTDGEPKQTQEEKKAAASNPSIAAQQTVERAQQQSGKSTRVAYTLPHPIWQNEYVDA
VEINHTPPENLTDKLALNTVRLMRFNFDWMSGYSWGKLTEADWLRRIIFLETVAGVPGSVAAILRHLHSLRRLKRDH
GWIHTLLEEAENERMHLLTGLKLKQPGKIFRTAVWVTQGIFFNFFFAAYLVSPRFCHRFVGYLEEEAVRTYTHLLHD
LDAGKLPEWKDTPAPEIARQYWKMGDDAKWRDVVALIRADEAHHREVNHTFANLQLEQDNPFPPGH

>N114_antibiotic_biosynthesis_monooxygenase
MARPGFVRTNIVRWVKEGSEASFLSQMRDLRRLALNADGFIGSEHLWSVEHKHKHLTTQTWTSLDAWHRFKSHPDRV
HMVKKLQDHLTEEPLEDVYTPYVKERFSIDLEALQSGRHGN

>N115_branched-chain_amino_acid_aminotransferase_form_1
MRRTISVASSSSFLVARSGRLAASASCRSLATSGVPQPKQDVDWEAMGFNLTKTDFMYVANTPKGSDFSRGEIRKYG
PLELEPAATVFSYGQSLFEGLKAFRTANNRIVIFRPTENCKRMNEGAARFLMSPIPEDVFMDGIKETVKANAHYVPP
FGKGALYLRPIVFGSGPALGVAPSPVFTFVIYASPVGNYFKGGIRGINLIASEDVHRAAPKGAGYVKAAGNYAPCFQ

IQQASKKAGYDEVLFLDAKEDKYVEEAGASNFFCVTPDDTIHTPSLRGTILPGVTRKSLIHLAREKGIKVNEGSVSI
DTVCQAKEAFCSGTGASVTPVASVTYKGNKYLFNNGEVGKVT

>N116_1-pyrroline-5-carboxylate_dehydrogenase
MRRIATRSHLVTPQQMASLAPLGARSMHAGGSLNIPKPTNEPNSINNEAQRNATLAKVAELRKGKLDVPLIINGKEV
RTGNTGEIRPPHDHQHLLGVYHKAGEKEVKEAIEGSLAAHKHWRNLAPEHRLGIFMKMASLLATKYRPLLAASTTLG
QGKNLFQTEIDTPCEAIDFLNFNAHYAEQIYNEQPASEYVDPYGRGSVRAWNRVEYRPLEGFTYAVTPFNFTAIALN
LATAPAMLGNTVVWKPSDHAILSNYYLTQLYKEAGVPDGVINFIPGDPQLVTKVVLENPKLSAIHYTGSTDVFRLLW
KGLGDNIDRYANYPRLVGETGGKNFVFVHQSADKDAVVTALLRGAYEFSGQKCSAASRAYVPASMWKELKGKLVEGI
KSFKVGNPEELDTMVGPVIHKASFERCKSFIQTAKSDSNTYTIHAGGVCDDSKGYFVHPTLVETKDPHGVLMEKEIF
GPILTVYVFPDEQIEDTLHMAEKSTYGLTGSIFANDRYFVKKAMDVLEYGCGNLYINDKPTGAVVGQQPFGGSRASG
TNDKAGGKHNLLRFVNVRSIKENFVPDTNPFYPYMSAPKH

>N117_hydroxymethylglutaryl-CoA_reductase
MRSSLRIARASAPSSFGSLRTTRLSLGGSLYTRTSALASARLYADDASKAKKKIDLTDKSDEEIIELVTAGKLHSHK
LEEYLPGNLERAVRIRRLGLEAHVQAKSDHKPDLSKLPYQSYNYDSVYGACCENVVGYVPIPLGMAGPLLVNGKLVH
IPMATTEGCLVASTHRGCKAITESGGATSVVIADGMTRGPAVRLPSAKRASEVIAWVKNTDNFYLLASAFNSTSRFA
RLNSIKTGIAGRTLFLRFKSATGDAMGMNMISKGVEKALDVITDYFPDLEILSLSGNYCTDKKPSAINWLEGRGKSV
VAEAIIEERIVKEVLKTTVQSLVDLNIQKNLVGSAVAGSIGGNNAHASNIVSAMFLATGQDPAQNVESSNCMTLMEV
APNGKDLFISCTMPSIEVGTIGGGTHLGPQSTCLDIMGVKGSNLTNPGANARALAEAICAAVMAGELSLMSALAAGH
LVRSHMAHNRKKDPQVSEPHKLPDFTNTPSENDSPKEEKFGACVVGDKK

>N118_electron_transfer_flavoprotein_alpha_subunit
MLTRQARRCFSSSAVLRKTLVLAEHTNAALVDSTLPAITAAAKLGDVEVLVAGKNCKGVAEQVSKLEGVKKVLVAEN
PAYEHGLAEDLAPLVANFSKKEEYTHILAPASAWGKNLTPRIAGILDITALSDVISIEGQDTFKRPIYAGNAIATVQ
SGEKLKLLTVRTTAFEKAKEGSSSAEVKEISVEGDANTKSTWVEEMQQKSERPDLTSANIVVSGGRALKSKENFKLI
EDLADKLGGAVGASRAAVDAGYAPNEWQVGQTGKVVAPQLYLAVGISGQIQHLAGMKDSKLIVAINNAADAPIFQVS
DYGLVQDLFQAVPELTKELEKAKQ

>N119_3-hydroxyisobutyrate_dehydrogenase
MQQSRRFSSLAALSAVRGTTATTSGRISFALRCYSTGDKKPVGFIGLGNMGGFMAQNILKAGYPLVVFDVNKGAVER
LTSQGAKAAATPREVASQVHQLVTMLPSSPHVQEVYTSENGIFNGIKEGSLLIDASTIEPAVARGVIAKAAEHKVTM
VDAPVSGGVGGAEKGTLTFMVGGSQEEFDRAKPLLSVMGKNIVLCGGAGSGQAVKICNNLVLAISMIGVSEGMNLGV
KLGLEPKILAGIFNTSSARCWSSDTYNPVPGVMEGVPASRGYTGGFGVDLMAKDVSLAINAAHGVKAPIPLGAVALQ
VYNMISTQGGGGKDFSSVFEFFNKGSAPKQ

>N120_methylcrotonoyl-CoA_carboxylase_alpha_subunit
MYAARRTLGGNAAAAAVTCYGATSSRSVLLMLERRAATTGRFAVPLSSRAAYSSRPGLGKDGRMFDKVLIANRGEIA
CRVMRTCKRLGVKTVAVYSEADAKSMHVAMADEAYLIGPPPAKESYLKGDYIIEVAKKAGAQAIHPGYGFLSENSRF
ANLVEQSGLVFIGPPASAINSMGSKSESKKIMSNAAVPIIPGYHGEKQDVDYLMAEAEKIQYPVLIKAVMGGGGKGM
RIVETKEDFVEALLSAKREAMSSFGDENVLVEKYITKPRHIEFQVFADKYGNVVHLFERDCSVQRRHQKIIEEAPAP
GMTEELRARMGEAAVNAAKAVGYVGAGTVEFIMDSTTKGFYFMEMNTRLQVEHPISEMITGQDLVEWQLKVASGQHL
PLTQDQLKINGHAFEARIYAENPRKGFLPGTGKLVHLSTPEPSSQVRIETGVRQGDQVSIFYDPMIAKLVVWDTDRT
SALRRLNASLGHYQVVGLNTNIEFLGKLATHPSFIEGDVETGFIEHHRNELFPAISAPSEKVLALAALSVLSEERAA
NLKEAERNSADAHGAWSLPGWRLNEEQTRELRFVAQVGEEESAEFAVLATYRPDNTVSMKCKKVVAQEKGKKAHHHE
EDSAEFTVTGQVGPTGEIKASVGDETITDGRVVRHKNTLNVFLKGVHHEVNLALPKFLSAGTEGRKGGLTSPMPGKI
VKLFVQPGEEVKKGQPLIVMEAMKMEHTIRSPADGKVKSVGVSVDQFVEQNVALVQVE

>N121_glutaryl-CoA_dehydrogenase
MRRATSVVAPVARRGISARINAIGARTFATGTEKVTFDWADPLNFEAQLTEEERAIRNQVADYCQEKLLPRVTLANR
NEKFDREIFNEMGELGMLGATIDGYGCSGVNYVTYGLIAREVERVDSGYRSALSVQSSLVMYPIYAYGTEEQKQKYL
PDLATGKKVGCFGLTEPNHGSDPGGMETRARKDGDSYVLNGSKTWITNSPIADVFIVWAKDDENVIRGFILEKGMPG
LEAPKIEGKFSLRASETGMIMMENVRVPAANLLPGAAGLKGPFGCLNNARYGISWGTLGAAEFCFHAARDYTMQRKQ
FGKPLAQMQLIQKDLAEMQTEIALALHSCLHLGRMKDAGKATPEMISMMKRNSCMKSIHIARTAREMLGGNGISDEY
HIIRHVMNLEAVNTYEGTNNVHALILGRAITGLQAFSS

>N122_iron-sulfur_cluster_assembly_protein_Grx5_(glutaredoxin)_form_1

MQKATSSLAMRGAVRSTAQRRLFSTALNRSRSVVTSRAALLSLRSVSSPCSYAPIAPRQQRWYTTDDNK**EVGSEVAT**
DSVQDAIKK**VVSEYPCVVFMKGTPDAPQCGFSNATIKALNTVGAHYEAFDVLQSAELR**DGIKKFTDWPTIPQVFIGG
EFVGGCDITLQHLR**SGELTTLLEK**AKALKSQQ

>N123_electron_transfer_flavoprotein_beta_subunit
MKRRVLVGVKR**CIDYNVK**IR**VKPDNTGVLTQNVKFSMNPFDEIAVTEAVK**MKK**EGGFEEIVAVSVGPKECQETIR**RA
LAMGADR**GIHVETDEELQPIAVAR**IFKK**LAEKEQPQVVVLGK**QAIDDDANQTGQMLAGMMDWSQGTHAYRLK**FAPEE**
VECTRETDTGLQTLKLK**LPSVITCDLRLNEPIFAK**LPEIMKAKSKPLQK**FTPQELGVETATPVK**VVKVTEPPKREAG
K**IVESVQELVAALKK**EGAIQ

>N124_glycine-rich_RNA-binding_protein
MNRLCLASRPAASLLIARQGSSAANRMAIRRFTEDINPSRLFIGGLSWGTDENKLKEAFEGFGEVRHVRVVVNRETG
RSR**GFGFVTFQSPEDAAAAAEAMHDK**ELDGR**RLSVSYAR**NTPREGGFRQRPVEGKEEESM

>N125_SAM_complex_protein_Sam50_(Omp85_homolog)
MSYTDEDEPIDLGVRGEDAWRVRRVWVKGNRRTRPDVVAACVKPVLKAR**TFDEVLAR**VAEAAGELKGLGIFK**SVNLV**
LDDLPDDVAAADPSACDLRVELVEHKLTRIEVKTSTTVGENEPDVQATVGLCNAFGRAETVSVSAQVGASNWREHWS
SAFSLAFKRPVLGQGPGPR**HIEADATR**ASHR**LPWCALTQTTHGLALRYSLPSHQVSYEASARHVIPESSAPLALR**SH
AGHSLKSAVK**YVYAHDTRDDPLTPTTGHAFTSSTELAGLGGDVR**FVK**QEMAAQLNLPLGK**TRCSFNVLAKAGYLHAL
DSGSRIVDR**FFLGGPGSIRGFQYNAVGPSHQQR**ALGGGAYWAGSLHLSFPLPLR**DVPDFVSGHLFANAGNLR**QPTPG
R**SVAANVQDLFSADDVRAAVGAGLVLR**TMFGRVELNLSHPIRK**AATDLVQPFQVGLSVR**FL

>N126_Complex_IV_subunit_Cox1-c
MRRCITSSTLRGSFSSRAISSARSLAAPAHAHASAQPDASVYRSKQGGSFEEALDINVVDVEDLFNPASGYWENPAN
WNDMDYVWKLKVER**LQQELNIPAEQAAK**FRKEHDISK**GYLTLEWILPSPPPEHTFEELPILKETEEEPATSFEAR**AA
RLLESAHKAK**TVSAEHTQTFESLAK**EFSFSDREK**TAFKELLNR**YAK**GQTPSFPNEYEEHAHDEHH**

>N127_3-hydroxyisobutyryl-CoA_hydrolase
MKATLRVATSNVRSAGSTRVCSAASSFRSQRRCYSESAETEVLVQPLGK**GQEVVLNRPK**ALNALNLNMVHLLRPHYT
HWEKDPHTAFVLMKGAGGK**AFCAGGDIRAIYDEGIAAR**QAGK**NAGGDPASLGYR**FFHDEYVLDYQIATHPKPQVAFL
NGITMGGGVGLSMHNKYKVATEHTVFAMPETAIGFFCDGGGSHFLPR**LSPGFEVGMYLALTGAR**LKGYDLVRAGVAT
HYVPSSKTQVLEEKLKNAENEDHVR**HTLAELNEHDTANDANSELIK**HADAIHKCFGK**ASVEDIIVALEREGSEWATH**
TRNALSKLSPTALKVVFRQLHHGKQLPLNKCFEMEFRMAQR**FMAGHDFFEGVR**SVLVDKDRNPQWKPARLEQIADSE
VDSYFEPLADPSLELHLHPIEHHLQ

>N128_MAPEG_(membrane-
associated_proteins_in_eicosanoid_and_glutathione_metabolism)_family_protein
MASGFPILRDVVAYPTLAVAASLVVYQWQCVAVGLARHKYGVAAPK**TTGNDDFER**VFRTQQNTLEALVIFVPSVYTF
SYFVHPVGAGVLGGVFAVGR**LIYGLGYAK**QAEKRSAGFALSLLANAVLLGGTVYGVGR**YLLTRPC**

>N129_glycine_cleavage_system_H_protein
MRRTATLLKTRPVSHQRLSTASAGLLKPSSAWAFLASRSYSSNVPTDLKYTKSHEWVRMTNGVATIGITDHAQEALG
EVVFVDLPETGATYGQKESFGAVESVKTVSDIYAPVGGEVVEVNADLK**DKGSVNINSDPYGNGWMVK**LK**VSNQAELN**
DLLDAKAYEEHCASEAH

>N130_galactose_oxidase/kelch_repeat_domain-containing_protein
MRSSTSRAARLTALPSIGTSSASSSAPSATALFLHHQRRTYAAKANARKCGEFKKDMFGHHTIK**VDDGHLLVLPSTR**
TLNPFARPSVYKVDTTKDEWHWEEK**SVSAPFPQTGPRGHLFGQQLIVAGTLTTLGPLK**RKGMVTLDMKDFTTSR**VTM**
LDPASQKATK**TVNMTNFVSEATHNPDKVWFFGENYLNAKNENASCEVMVWNKGNNTLYSATANTLPIVGDGPK**EK**KE**
LAVAAVGKDK**IYVISPDINSTKLETYVLDTER**LEWSLVKTKGDKPVNPR**AGFSITASGDKLVFLGYDMSLSDK**LMEV
YVLDTDTSTWEK**VEVTGDEISPRFGHTTTHLGGNQYAVIGGKGYGYFSTSVK**DFFKLQLDF

>N131_adenylosuccinate_synthetase
MRAFFGSTSPSAARCAVGQGSIRSFSLAANGTWSFAGRTAVLSRNLAARNYSTATSTTTTEEAAPAAAVATPAAEAV
EKPK**VEEPKPATPK**VEKKGNISRVAAEQVIAVMGGQWGDEGKGK**LVDVLGANFDIIARCAGGSNAGHTVIVEGK**KYA
FHLLPSGILHERPVCLIGNGTVVHVPTLLK**ELTSLDEK**GVNYKGRVKLSDR**AHVVFDFHQQIDAFLEDAAK**KGNKDG
SIGTTR**KGIGPAYGAK**IGRVGIRVGDLR**FPDTLPEK**LTK**LVEYYQRSFPLEVNLNHEIEAYK**AFAHKLQPMIVDSVH

YINKAYGEGKRIMVEGANATMLDIDFGTWPYVTSSNASIGGAVTGLGLAPSKIDGVIGIVKAYTTRVGAGPFPTELK
DDLGESIRKIGHEFGTTTGRPRRCGWLDAFAIKYAHMINNFTLLNLTKLDVLSDLDEIKIATSYKYNGEHLASYPSN
LEILDQVEVEYETLPGWKKDVSGVRYFEDLPAEARKYVERVEQLVGCPIGWVGVGPGREAMAIRKPK

>N132_putative_novel_Complex_V_(ATP_synthase)_subunit_AcAtpN3
MATPLQVPCGCRNSLQSFGAAAAFTVAFVWTSQSVQVKRNAYFSNLKSEIDTLKKKNHDLEHEVELLKNPPEPKEAH
TDFAADFESGNIDFEKILEQVASDH

>N133_glycine_cleavage_system_T_protein
MAMASMRRGGVRAAQNSMTTTRRAFLATDAAPLKRTALHADHVALGGRMVPFCGWDMPVQYKESIIDTHTHTRTHAG
LFDVSHMGQLKLHGRDRVEFMESLVVGDIKGLATDNARLSLFTNEQGGIKDDTVITNGADWLYVVVNAGCADKDLAH
IQEHLARFKASGKEVDLEILSPDYSLVALQGPEAAAVVGEHIAGGPESLRGLAFMSGRDTRFDSLPVRITRCGYTGE
DGFEISVPTSDAVTLWRTLLQHTGKVMPVGLAARDSLRLEAGLCLYGNDITEETTPIEAGLAWTIGKRRRAEGGFPG
ADVILKQIKEGVTRKRVGFVLAEGIARAHATVHDEKGELLGEATSGGYGPSLKKAVGMTYLPTALAKNGTPIQVQVR
KKFYPATVAAMPFHPTNYYKPTQ

>N134_hydroxyacylglutathione_hydrolase_(glyoxylase_II)
MSTYRVVPVPVLSDNYAYLLIDERDKVAAAVDPVEPKKVLEAAEKEGVPIKAIYTTHHHWDHAGGNEELLKALPAGT
PVYGADDRIPGLTHKVANAEVLQLGSTGVKVLFTPCHTAGHVLFLAGSDHAPRALFSGDTLFIGGCGRFFEGTAQQM
YHALHDVCAQLPQDTQVWCGHEYTVKNLQFAQSVEKDNQELQAKLKWAEERRSQEPPLPTIPSTIHDELQCNPFMRV
NRESVKRALGLATEADPIEVMAKLRHMKDKW

>N135_fumarase_class_I
MRRLQPLLSSTAIAARSPACFAAAGPGRLIGLRALATAAPAKKSTPPAFEFEPLFQADPFSATPYRKLFGPESGLIR
TEKVAGREILHVEDEAIERLTFEAMRDISHLLRPGHLEQLNSILKDPPEASDNDRFVALELLKNANIASGMILPSCQ
DTGTAIVMAKKGQYVWTSGDDEAAISKGIYQTYTQTNLRYSQMAPIDMYKEVNTGTNLPAQIDIYASEGNAYKFHFI
AKGGGSANKTYLYQQTKALLNPDSLMKFVNENIRSLGTAACPPYHLAIVIGGTSAESTLKTVKLASTKYLDTLPTEG
NKHGRAFRDLELEKKILELAQKTSIGAQFGGKYFCHDVRVIRLPRHGASCPVGIGVSCSADRQAVGKITPEGVFLEK
LETNPAKYLPEITEDKLSDTVVNIDLNKPMSEIQATLSKYPIKTRLSLSGTLVVARDIAHAKLKERLDNGQGLPQYV
KDHIIYYAGPAKTPEGYASGSFGPTTAGRMDSYVDMFMKNGGSLITLAKGNRSKQVTEACKKYGGFYLGSIGGPAAR
LAQDCIRKVEVLEYPELGMEAVWRIEVEDFPAFVIVDDKGEDFFKNLSH

>N136_Complex_V_(ATP_synthase)_delta_subunit_(Atp16)
MRRISASSRVLGMSAAAGGRFGPRTASVLTTTTRRSYATDDAQREAHEKAVKEGKLIFTLACPHETLINAEPVRIAT
VPSATGDMGILAHHVPTIAQLKPGVVKVTKFDESGATRDADYFISGGFVTVYPDSHCNVNVVEAFPLDQLDPEKAKK
GLEDFTKELASASDAEAKTVATIGVEVYKAMCSALKV

>N137_cyclophilin
MWKRLFTTNAAPVTANPRVFFEVTRENKPLGRIVMELYKDKTPKTAENFRALCTGEKGVGSIGKPLHYKGSIFHRVI
PNFMIQGGDFTNFNGTGGESIYGAKFADENFVMKHVEPGTLSMANAGRNTNGSQFFITTVPTPWLDGRHVVFGKVVE
GMDVVQKIEAARRDSNDRPLEIIKISDCGELKQ

>N138_D-lactate_dehydrogenase_(cytochrome)
MRRFGSIGRSQRWAASSAGSTRLLPARGRSRTTATFSSSSSFTGSARRLWFLVPATMSAAALAATAYGFGLPDVQAL
DQAKASEAHHEQEQSKLPQGFIDELSAHLNTAGETRFVIERAERENHSKDASYHAQGMPDAVAFPKTPEEVQHIVTI
CAKYKVPIIPYGSGTSLEGHTLADHGGVALDFTRYMNKVLKVHVEDMDVVVQPGLKREELNDYLKQYNLFFPLDPGP
SASLGGMVGTSCSGTHAVRYGTMKENILSLKVVLPNGKMVKTGQRSKKSSAGYDLTHLFVGSEGTLGVTTEITLRLR
RLPEKTAVAVCQFPTVHDAANTVIQAMQEGVQIGRVELIDELMIKAVNLSAGLNEQEKPTLYFEFSGSPVEVDEQEK
AMRRLSGANNGGVFTFAEGEKSEELWSARKNALWHSLALRPGADMLITDVAVPISRLAECIDQTKEDLAGSYLLAPL
VGHVGDGNFHLMILFDAKNPKEVEEANRLNNRLVQRAITMEGTCTGEHGVGSGKKKWLAVEKGPEAVELMRTIKRSI
DPENILNPGKIV

>N139_D-2-hydroxyglutarate_dehydrogenase
MKALRATTSRSAFTCSGGVVPGTSLLTQRSGKSAATRIAIWSMHRPVAASTTVACSRRSYASMEKPPRDARYAKLEE
RDVQHFRSIVADPQASVVTDPDALAPLNEDWLHKYRGYSKLGLQPRTVEEVARILKYCNERKLAVVPQGGNTGLVGG
SVPVHDEIILSMSKMNKVLSFDPVSGVLTCEAGCVLQTLDEYLEEKGFTMPLDLGAKGSCHIGGNVATNAGGVRFLR
YGSLHGNVLGLQVVLPDGTILDSLNGLRKDNTGYDLKQLFIGSEGSLGVITAVSLLTPARPKSVNVAVLSVPSFEAV

QKAFVEVKQDLGEILSAFEFWDRQSMELEMQQLPHIRDPLSSPSPFYILVETHGSNEAHDTEKLNGFLERAMGEGLV
TDGTVAQDTTQFRALWQIRESFAEAGSKAGFNYKYDLSIPINKMYDLATEVRERLGDKAQTIAYGHVGDSNLHLNMV
TPKYDAEVHGLIEPFVYEWTSKQGGSISAEHGLGLMKRDCLHYSKPEQAIRYMRVIKETFDPQLILNPYKVIPLQ

>N140_putative_RING-H2_finger_protein
MSKKHDDLPDQGGSLDYRGNYVPFYPNPEENLNLWERVMRYPWVALGAFSTAGILGAGLWTLKTGNSALGQKLMRAR
VAAQFTTVVLLLGASGVITLNSLNSDKPKPKAVAAPISSSSSSTSETH

>N141_2-oxoisovalerate_dehydrogenase_alpha_subunit
MMRLTRPTAFAASSSAAASSSLLPRFFASSVASSSRLFSKSAEPVASSACTPLAPPDYTTGIQFIAHRETFPVYRIM
DDEGEVLDAAQLPEVGQELTQKMYKNMVTLNVMDGVLYDAQRQGRISFYMTASGEEATHVGSASVLDPEDVIYAQYR
EAGVLMWRGFTIADFMNQCFSNELDMGKGRQMPVHYGSRRLNFQTISSPLGTQIPQAAGTGYALKLAGRSNVCICYF
GEGAASEGDFHPALNFAATLRSPTIFFCRNNGYAISTPVKEQYAGDGIAGRGPGYGVATVRVDGNDVWAVYNVTKAA
RKIALEESRPVLIEAMTYRVGHHSTSDDSSAYRSKEEVQSWAQNNNPISRLRKFMEKRGWWSQEQEDEIRKAARKEV
LEQLKLAEQRPKPHVDELFTDVYDSVPKHLQEQKAELEAMMRKYPDHYTAASH

>N142_carnitine_O-acetyltransferase
MMKRTALRFAGTTTATARPATVGLRHLQRARGLSSSVTSGEEAWAEHQKGLRRLPVPSLEETVARYAEYVAPLVSEA
EAAHARALAEEFARGEGRALQSELLALDRESPTSWLEGWWDTMYLTIRDPLPVNVNPFFIMQDDPERRSQVARAAGL
ANACAKFQRLVRTGQLKPDMEKTTPLDMSQYTKLFAAARIPRASRDEMVYHPDSRHMAVLSHNHFYTVEIITEDGSV
VPEKDIQRQLQQILNESAPSGTREPGLGVLTADWRDSWASVRSELISSHGDNKHALEKIDSALFVLVLEPEAPAKGD
DIAKVFLHGDMRQRWFDKLQVIVAANGKAGINLEHTPIDGHTGIRLPGEVPGLLQSQEGEANGPISARPQRLKWHLS
PAVIKGLEKAEAVADELVSHTEIRSLEFNHFGKKYITSKKLSPDGFVQMAYQLAYHQLTGKTVSTYESCMTKQFLHG
RTETLRSVTRESAAFTRAFATPGATPKEKEQALRLAVQAHGNRAKEAKEGFGVDRHLFGLKNLAYHKQQRLPGYTIP
ALFQDKAYRVLSASVLSTSNCGSDALTMFGFGPVVGDGLGLGYMIQNEKIPITVSSFQRQALPYARALEKSLLEMRD
VLDASTTSTSA

>N143_ClpB_ATP-dependent_protease
MRRAALGGTRSGSALSGLLSRRAPQQAGAVRRVLSSEPAASSRSSAMRTSAASRWPAALGTSTVLLHPPALVFPLCR
GYANGYTRGGQPIPPPYVNPDAAVPGDALKKYGKDITALAKEGKLDEVIGRDEEIRRTMQVLSRRTKNNPVLIGEPG
VGKTAIVEGLATRIIHGDVPDSLKGKKVIGLDMGTLVAGAKFRGEFEERLKSVLKDVHDLKGEVILFIDEMHTLVGA
GASEGSMDASNMLKPALARGELHCVGATTLNEYRKYIEKDPALARRFQSVFVPEPTVQDTISILRGLKERYEVHHGV
RITDGAIVCAAVYSHRYITDRFLPDKAIDLVDEAASRLRLQQESKPEQIEDLDRQIITLKIELEALRKETDPASAER
RQKVESEIARVEGKSQELTRAWQEERDKLHKIKNLKEQLKRAKLDLQRAERNGDLARAGELAYGIIPTLERQLPKDQ
GAETTMLGEAVTDNDIALVVSRATGIPVHNLLMGEREKLLHMEQVLASRVKGQNDAVGAVSNAVRISRAGLHSHSRP
LGSFLFLGPTGVGKTELCKQLASFLFDSENAMVRIDMSEYMERFSVSRLIGAPPGYVGYEEGGTLTEAVRRRPYQIV
LFDEFEKAHRAIHNILLQILDEGRLTDSQGRKVDFRNTIIIMTSNLGAEILADLPPGHSSSEARDAVMGAVRGAFTP
ELLNRIDEIVLFNRLSHEDMDSIVNIQLKDVSNLLADRRIQVELTPEAREWLAERGYDPVYGARPLRRIIQKHILNP
LSREMLKGDVLDGDLIRISRKAVDPEEVLKNTAATDSWSSALEELDLEVVHTEQSTPEVHNAKPLLKAEFGVEDD

>N144_C-terminal_MRP-S28_domain-containing_protein
MLSSRAKIRHSAARLPHVQHHLQRQQRSAGALVLNARSYAATHEMTQQEESSDSIKHLLKGPVTPLTIFATSPPPEP
HPSTYQVPAAAADGATLDFRLSFAFPTVQKIKEERFKEEMGVFKILYERPFLQEYKNVMQEKKQQKKSERAAAKKAK
KEMKKLGLLPNDRKKTLFELEQDRQRKLFLQTLHYPYQVPDMSVKGEELKKYFNFIATHSEKEIYDRLYPEFFGDTR
EHVENLVPHKHDGYVWNTFFDPENPSDYPNQADAEGDVWETLNMSAEEQLSDLADAMEGEQEKEARLATWEMDPARF
KGKWTPRAWTKEDLELSHIKQRARNLRYLREQLKKHGLLPEEDEATTREALMSVESGGQASAAAESFDIDEIADKID
DNEESVLLLFEDDAQKKPAAVPEQKGTEDEIANLLNAVLPPTEKDQSHAALLDALMPAGQPQEQAQPESGAAASEPT
TTATEQELAEWRAKVDKFQDGLKKRIRDGATEETIEEDVINFITAEGGGAQDEAEEDEIDWESRLQDIPGLDQPGEG
GFKVTGGREEAMQRSRERERAARLHKLQEHVKVLFDESPKKQVFANEPIPGEPAIEFIHSYTMDPDVTMGSLARREFLQ
RKVVLKVHVPSLSLPPPVQQRLADLVGTRYDARSGWLKLVGDKHPNRHLNQKHLTLLMRELLNESFLADSRFTPLTD
LSIEDPSSLRRKYSLPTNLQNIFDGKTGKGGWEYKMFTFSQLDGRFPSAQESTEEAAKLRQRLASALSL

>N145_ATP_citrate_lyase_beta_subunit
MQRARSVVRATGVWSGGAQWGPSSQLWVGTRRLFATSATGHGALRSWLFVPGRQDMLLKVLQKKGDMALPDVLVPDM
EDSVPLAEKASARQAIASLLPQLAQLGAHTKVLPRVNSLDTGLMEDDLQAVIAQGGLIFGVSVGKVGSAEDMRRIDE
IVSALESKNGVRAGKIHIVPWLETAAGVVNAHEICKSSSRIIGVAYGGDDFLTDMGVQGASDQTPSGLVTYARSAIS

VAARAANVLSLETPYVNFRSAEGLRAQATDVKRLGYRGMFAIHPNQVQTINECFSPSAQEIEYAKKVVAAYEEAERQ
GKGSTSVDGKMVDAPVVKRAYALLKTLPQP

>N146_uncharacterized_(possible_novel_CI_subunit)
MADENRDFPEYEAWVKKQSAFARWAIRTRAAIADQDETNNAEYLRHVAKNMIIMKEESYLWSSSAQRPDDYYKGRSP
LTAAYRDHGMFKSPYEIRAKELRGELIRWNHWHSWDLKPSATTSYPKPPAKYDPLNPTRPNIRKQRLEREAAH

>N147_Complex_I_(NADH_dehydrogenase)_PGIV_subunit_(NUPM/NDUFA8)
MASTRKEGEQLYADINAGGRTHLDVETTDFNVLVAGAKYTSYMCAAEELDFLECKAKDENPRACVPENVALTECAHA
ALDKISRQCASEFDEVVDCLESPSVHGELSACRQSERDLRVCVQARFGVDVVVEERKRRMASLQTWASTRRRPQPTI
IRPREQKKVDAAVAKYKKEHDITE

>N148_saccharopine_dehydrogenase_(NADP-dependent,_L-glutamate-forming)_(Lys9)
MFMRRLTRVSTSSAAPTGRTASALRGQVPCRRLLATSPDGDGIGALKAELKAAEDRVATLKEAIVSHKDPAKKSILV
LGAGRSSSFLINYLLQNAARERWAVKVGDEDEHTARRKVQDHPDGTAFRFNINDTRQREEEIRRADVVVSLLPAFMH
PVVAAECVKQGAHMVTASYSAALAPFDEQARRAGVTILMECGLDPGIDHMSAMEVIDAIKRDGGQLTAFRSYTGGLV
APESDDNPWGYKFSWNPRNVVVAGQGVCQYLQQGEYKYVPYHQLFRRTDEIRVPGHGTFEGYPNRDSLSYRTIYGIP
DCPTVLRGTLRKPGYCSAWNVFVQLGMTDDTYTIENADSLTYRDFLNSFLPYRPHDTVELKLAHYLGLDINSPEMQK
IKWLGMFGEQKISLKSATPAQVLQQILEKKWALQEGEKDMIVMYHHFVYTNKNGELKETKSSLVVKGDGTDTGTAMA
KTVGLPLAVATRMVATEQVKGKTGVHVPTTPDLYEPILRELEKDHGIIFSHQHDTVHQA

>N149_iron-sulfur_cluster_assembly_co-chaperone_Mge1_(Grpe)
MRAAVRRLPNVASHSAASRGIFALNVPLRSRTLAIARPFSTEQNGEQKVEGEHPPAQQQAEGENKEQQQEQQDPQAA
KIDELQNKVKDLEEQNKELNGNYLRSLADLDNMARIGKTNVENAKLYSIKSFAEGMLEIADNLSRALESLPEEKRGL
PDVKVLFEGVAMTERVLQQVFARYGIKKFNPLNEKFDPTKSSALFEIQDPTKAPGTVAFVQAPGYTLHDRLLRAAQV
GVVAQPPDEPSSSDQA

>N150_alanine-glyoxylate_transaminase
MKSSRRVGSALALGGRVQRGQRMGATALGSLGASRRSVQTTPGETKGAKPLLMIPGPIEFSEGVLQSISLPTLSHVS
PDFIEQFGQALEQLRSVFLTEKGQPFVLAGSGTLGWDMAACNLLQKGDKALVVNTGYFGDRFGECLTAYGADVTHAR
TDIGNCPSVADVTQLLGQRDSFKMVTLTHVDTSTGVLVDIESFAQAIRKHSPNAIVVVDGVCASGGEELRMDEWDVD
VVLTASQKAIGVPPGLAILMASQRAMSLFKSRTAPVANYFCDWSKWLPIMESYEGRKPAYFATPPVNLIRGLHTSLY
EILSEGEGAMDKRFKAHQTAGKAVREAVKALNLTTVAVSDKLAANTITAVRFPQGVSGPALLPKVKAHGAELAGGLH
QAIKAEYFRIGHMGVSVTDLNRGHLEQTIRAVEQGLVECGYTGFERGAPVKALQRVLTAQ

>N151_mitochondrial_carrier_AcMC4_(putative_ornithine_transporter)
MSAASAQPGLPYYPMPRGGGVGAGGGPIPSGPAGYPQPGVPVATGTPAVEEPQFLSLSSIVTRLVLKVGEYSLVNVP
SRTLYERQIAAAASAARMGGPGRTLDEQVQAKDENVVNTLLNYYKEEGAVRIIGATSLAFTNDLFYGVIASISYVFC
RMVPVLLGMTSGEDVDWQSSSFMSLITSHSIASAVTYPLFLASYQVRHHAWTGFSGLLPSGENFYGKLRDNVVAHLA
EMVTLHTIRPAIVDTLYVLFGEWLLAKADGETLADQAAYHVGIRGVHFMGSLFVGLIHLPVSTIVTKLRAHPDAYDS
LWDCIKKTWKTQGLKGFYGSAFWYLLANNQLIMP

>N154_mitofilin
MLRRGFNGSRARAACRLPASSTHARVPAARQVTSRRLFANAGATPPPSSGGGGVAFGVLVGAAVGASAWTGYRYYTD
PPFRARLNDFWASLSSSTTSSPSQPTAAASPKPSVTHEEQQQQEEAGAPLLAAQVLLAAAEEATALDAQEEAVVALP
DSLVVQQQREHQQQQEHQQQQQQQEEVEVEQMDPAATQSNDGEGEEETEQPAIIAAPAPLVVEVVGPEASHAHVATD
GVAPEEAKAAVPAAVVALVTESFAASDAHQEAVAAVAHDDHHHHHHHDKASPAEEQQQQQQQQQQDAANPAEPAGEQ
RDHEGEQQQQEQQQEQQQQEEQQEQRQEQPAAEGATRLQELQAIKEIIAIQAESCERQVREKVERLRQKYEHKMAAL
RQHMDEVVAEHVDVERQKISDDYQNRLHQQLDTLQHQFVEERQRLYSEMEDVVAGLNARFVELVREEKQLLNEQLEE
STRLHAHTLAYLQTLVDDAQYRIRHLSEEREWWSWTERLASAVRALESAALGPEGHLASFQAELDLVRSLAATRPLY
KAVAHHIEAQASRGVYSVGRLRERFEQVEKHVRVAAQVPEGGGLLRHAVAPLLAATVSLNPYHAPTPQELLLDSARR
HLLDDDLLTALRDLEQLTGLAHELAHDWIEEARKRLVVEQAISVISADVTTLKPPTDL

>N155_armadillo_repeat-containing_kinesin-like_protein
MDTRAVAVPTSVVVSTQASSSSSSSSSWWPLSTKGWLIVGGAVVSGLVLYLLRRRTRAANAWQSPPGEYDDILKSLR
SSEPQQTVALKQLYEYSRYPKKHDSIRQTGVLEILLQILAQHPDNDVLLLHLTRVVANLAINEENRLVLGRASTVSD
LFYLLEHTEDRIKEHILRCLLNLSLEDVIEDVIRETGGLKQLTEMFASPHTSPSVLFQTTRVLINLVHNANNRALTT

QEGLVQQAVQRLTASATVENIDFCLRLLNLVGLFAVDCAPEVLAQIATKETAEAFNNLLSLSQSVDHVSTVLQATLK
ILARKHTQPQEVQPFIDALIEKTGPQPSGLEHVVAFYKNSDGPVLELARHVLADLAENNEKATSAINEIDPALLSLG
SSPSTTDSADERAS

>N156_Hsp90
MRSAAVKNSSRPHRAVLRAPAPAHHVPARPLAEVAGTHNKVVVVGRRSRSCVPSALQVNHTAGAKRAYRSTAIGMRA
AGAREPEEAELVRTAEAAATPESARAGGAVSEAEEGKETLIEETETVSGQAETLPFQSETAKLLRIVAHSLYTDKEV
FVRELISNASDASEKLRHLDVTGKEYDDKYLPLEIHIATDDKNKTITIQDFGIGMKKEELIKNLGTIAHSGTQEYLR
QLEGKDASNIIGQFGVGFYSAFMVGNRVKVYSRSAAPGSKGYCWTSDGTGAYTIAEAEGVSRGTKIIIQLLEGQEHF
AKKQTIDSIIKKYSNFVGFPIKLNGERVNTVRPLWTLPKQSISEEDHKQFYQFLAHSYDLPIYRLHFTSDAPFSIQS
LFYVPEQHQEKYGMGRMDPGVSLFSRKVLVKPKMKALVPDWLRFMKGVVDCEDVSLHLSREHFQDSDLIKRLGNVVT
GRLLKLFQDEAASDPDKYNAKFWKEYGSFIKEGICTDAKWKDELGGLLRCESSATGEGDVTSLEAYAKRMQDQQTAI
YYLCVPSRTFAESSPYYEAFKQRGVEVLFLYTSMDDFVMQNLAEYAGKRILSIESAQLPAELARPASTTTGNNNNND
ASSSPQAHAGELSLDPQEVEELAKWMKTTLLDRVSSVKETKRLVSSPAIIVDHESASFRRMMKFVDPSRAPKLPKQR
LEINAAHPIITRLNSLRRREPSFAKAVAEQVFDNALIAAGLMDDPRSMLARLNSILEAAARNSDTTSTTSTSTA

>N157_BTB/POZ_domain-containing_protein
MAKHSGSRRATLLSLAMSAGWVDIARLLIAEVKRRDKRKLKTFVTQRAADGTQLLHSACYFGSVECVDLLLSLRDDV
TGEPLIDADGPDSDGVPPIFYASLSSAACIARLLEEGAPPTVNSGKTVLHMCANTGNVPAVEMLLQGWKENKWGLRD
KLDLNAEDPNAAGSTPLHAAIFSTSALAHKNVAALLDAGVDPKKRLHNDDGSLLLHAARSGTAKAVEELLLRNFDVE
EADSFGSTPLTAALARQYPTLATSGQQVLLRLLEAGAKVKWGATPLVDVECYINTGSPEENMKSGHTATYYDAGRSA
YQVVVGGHFNGVHPPGIYFLSTHYRAWDATYFDNNVFVNRRGHTCTLVGDTIVLFGGLRYAPLPRTHFNDVYFISAV
NGRVTKPLILGEAPLARESHTATLVGRKIYFMYGCSATAFMDDIVVLDMDSLEWSRPSVTSLKRPSMRFGHTATLVN
DHEIWLYGGINRVVNVAGRTHLVSTDPDWHVFDTHTLQWRTINASVAVPASGKGSPAKLPTPRANHTATLVGEEIYV
FGGDAVRREHLEIVLRFIYTDVIDVDNIPGFPPSGTHCAAPPFVRDLIDAAKLYAAERLGQFVARLLRQSMPFHRDT
ADYEPRSLLAFLNNIEYSDVRLVCEGKIINAHKAILSRCPYFDAMLRMSSSSFFGSESDESEDDVEELVITDTSHDI
LQVILRYLYELADENPVGEGAFVTEETAVEVLITAEKYGLDTLKLWCEKLIVEVMEEQNIPYFLQLGDTYHAPHLRR
YCLSALSAQYDHIDAVLRAAPGSAGGVEEQIESDELRAEVLGIVHERRRKRNALLADYEDVNDKVYFNTVLPTLADS
RQPLGRASAVFGVMVGVAAAWAFLGGI

>N158_putative_novel_Complex_V_(ATP_synthase)_subunit_AcAtpN1
MSKRLITRATLNGRLATAWAPSRSYAEAAVPKLGKDIQPKNYRRPDGTYEPCDEILFLSVIGYGEDLRAVTNAKEGI
TNTLVLSRYNKTASQ

>N159_AAA_family_ATPase
MKKMRTRSSKASWTFGRAWSMWAARRPTSTPPRRTRRTRSPTASRTPSTRAGTSRSRAWTSWTPTTGKRVETVSKVI
IKDATLEGTLQSFDVTLTYDAESSKLAAIFPWLKKPPFCPLEALMMRLPILRNSTYGGAQMEELVKFLEKERPRMVR
KIEAHLKKGLISYSGLWYLFSKGNRFYVDIGKGILVGSSAEYTRYMPAVGLCAPNFYVQGPIIKSDGVKFFRQNRAF
DIPVFKGLMPISGLDVQPMTKQVLRILNKRGRVFQKVALKHHYMQYEKFMLKRGAFSDTWIKADGRVMVDISTFNRM
NPEYTEFGSSAHDTSTQQQLQQLMAAQQRFTGDYTQTTLPVAGQKRISKAMRYQTWPYVAGFSFTAKRWGELLVESL
SDIQFDDKAYDRLVLPEDKKALVKALVEDNKRVQEGRAGVSFSDVISGKGGGVIFLLHGSPGVGKTLTAEAIAEYLH
YPLYSVSVGELGVTADHLESKLNDILELAGTWNAVVLIDEADIFLERRSDIDVLRNAMVGVFLRKLEYHQGVLFLTT
NRVKAFDPAFNSRINVAIRYHDLTKEARGQVWRNLLGHMGDDESSDLDFDQLADIEINGREIRTVIRLALALARCEG
VALNAEHIKRTVAISQQFGKDLNSVEDW

>N160_ATP-dependent_HslUV_protease_ATP-binding_subunit_HslU
MLKRAARLNAAVVGASSSSIPIMQRAAAARALRSSMREEALCLSSTSVHGNGRTEADRLRFYSSENDTTTATVKSEE
AAPPPVEEGKDEEQQEVAAPATPAEVERALLPSEIVNELDKFIIGQAEAKKAVAIALRNRWRRRQLSPELATEIIPK
NILMIGPTGVGKTEIARRLAKLAQAPFIKVEATKFTEVGFHGRDVDMIIRDLVDVAVHDFTMKAREQEKQRVKQEVE
ERLLDILAGAQAQERTKTMFRKMLQNGELEGKRVDFEVPQSTPATQMPFGSEMGAQGVFVQLDKIFGGAKKQKRKMT
IAECRPYLEEQEAEKLINKDAIVKNALEAVQSNGIVFIDEIDKICKDKNSYGADASSEGVQRDLLPLIEGTTISTKY
GNVDTSKILFVASGAFHSCKPSDLLAELQGRLPIRVQLKPLKKGDYYRILTETKFNQIDQAKALLLTEGVELDFTDD
AIHEITKLTAEVNETVENIGARRLHTVMERILEEVSYECTPGKVTIDVAEVRKHLSELLLKTDLSRYVL

>N161_glutamate_dehydrogenase
MRRATAALPYARSAAPMRSSALLACRPYSTTPATAARELMSFLESVLHNFNKAAALTGLSEPQIANIRKCAAVFRVKF
PVRVNLNEKTGEYDTMIVEGFRVQHSHHRLPCKGGIRYSEHVDQEEVMALASLMTYKCAIVDVPFGGAKGGIKINPR

ELGVSQIEAITRRYASELIKRNMLGPGMDVPAPDMGTGPREMAWIKDTYEAFHPQDVNSLACVTGKPISQGGIRGR**T**
EATGLGVFFTVREAVNYEEDMKALGLTTGLKGK**RVVIQGFGNVGSYSAK**FMHEAGAKIIAIGERDGGLYNKDGIDIT
ALWNHIGEK**KPFLSFPGAAVVK**NPESLLEEECDILVPAALENQINATNALRIKAKIIAEAANGPVTATADEMLEKRG
IIVIPDILCNAGGVTVSYFEWVKNLSHVRMGRLERRYDQRSKER**LLEHFSNITGR**KEDVPAGVVSGANEADLVHSGL
EDTMIEGYANVRSVSKLKNCSMR**TAAFVDAIRK**VARSYAELGVFP

>N162_pyruvate_dehyrogenase_phosphatase_regulatory_subunit
MLRLRQLASRSGPARGATSHVLKTTSGGYAFASPWASSPLFSTSAATATDKRVPDKSRVVIIGGGVIGTSVAFHLAK
LGWTDVVLLEQGTLGCGTTWHAAGLIGQLRANETETKLSRYGIQLYADLEKETGQGTGWKQCGGVTVARTQERMTHI
KRTLSRMRAFGIEGHLVSPEEAKKHWPLLSTEGITGALWIPHDGVATSSDITSAFAAGAKSKGVKIIENVRVTGIHK
SDKHAVTGVSTSEGDIKCEYVVNCGGMWAKQVGRLAGVNVPLHTCEHFYISTKPIDGVDSYLPVLR**DPDGYIYFR**EW
SGGIIMGGFEPVAKPCFADGVPNDFQFQLFDEDWDHFSILMNSALER**CPALETAEVR**QLLNGPESFTPDNQYILGEA
PEVR**NFFVAAGFNSSGIASAAGAGK**ALSEWLIQGYPTMDLWSVDIRRFGK**YHANDNFQK**QRSMETLGLHYQIPWPKY
ELQSGRPLRVSPLYERLAARGAQFGSKMGWERPNYFLPSSVSPSSIKYTFDRPAWLPYVGEEHK**ATRDEVALFDQTS**
FAKFVVKGR**HVESFMQRLCANDVAVPVGRVVYTPMLNPRGGYETDCTVTRVSEDSYFVVSSTAQATR**DYDWISRNIQ**
EDEEVSIVDVSPQYSTLSLMGPKSRELLSRVIADRDLSNEAFPFGTSQEVPLGITQVRASRITYVGELGWELYVPIE
STLLVYDLLHAKANEGTRIGLR**DAGYYAIDGLR**LEKGYRAWGSDITPDDTPLEAGLGFAVDLKNETKNFLGKDVLLR
QKKEGLEKR**LAVFVIDNDQEVYPHGGEPIFRDGQVCGYLTSVAYGHTVGR**SVGLGYVRKLANTATKEDRLVTPDWVK
AGR**YEVEVASK**RVPASVSLQPPFDPKNERVRM

>N163_mitochondrial_ribosomal_protein_L12/L7
MRRSTVHVFPRLALRQGQQTSALCLFSNGSRTAVSSETNMASIARNYAAPAKGGK**GAPAAAKPAEDEPAEPLKLETV**
TFPDFGEDKAFTADISDFPAPKDWK**YVSDWKEFEFSPR**VR**KIGEALFQLNQVEMFELVK**LLQLRFDVPDSALMGGGV
VVQAAGAGAPAAAAEPAAEEPKEEKKEK**MIFDVQLTAVAEADKFK**VLKEIRALKPGMKLLESKEMVEKLPSMLKQNV
PKEEAEQMVAK**FKELGGTVELK**

>N164_mitochondrial_leucyl-tRNA_synthetase_(LeuRS)
MLRALSRSPSGAVANAGLRTRLPTTVSGGVAANACGASSRFLRSHNAKTPDFFRFRFFQRAYTAEAPKEAGSWAATY
QHKAVEDKWRKVWTELQHQKQQRQK**LGADEQATAAAAK**DKQYVLSMFPYPSGQLHMGHVR**VYTISDCLSR**YHQMKGK
EVLHPMGWDAFGLPAENAAIERGIAPHTWTHSNIATMKSQMLRLGIQFDWDKEVTTCEPEYYKWTQWIFLQLHKAGL
AYQK**EAAVNWDPIDK**TVLANEQVDADGKSWRSGAKVEQKLMKQWFFK**ITEFADALVEDLAGLK**GWPEQVKLMQQHWI
GKSK**GAYLEFPIKR**ELSASSGAKAEEPLRIFTTRLDTLLGVTYVVLAPQHPLVQEIAKNTEDAKLR**AFVDEFAK**SKR
SLQEDYGKSKKGMK**LPGVTAVHPVTK**ESLPVYIADYVLMDYGEGAVMAVPAHDTRDYEFAKQFDLPIKTVITPDQHT
EEHKEGDPFCGEGR**VVNSGPELDNLTSEEAR**RKLLR**ILGEQGVGGEYTNYR**LRDWLISRQRYWGAPIPMVYCEADCG
VVPVPEK**DLPVVLPVDGLEFSGR**GGSPLGSLEHWLHTDCPKCGGRAKRETDTMDTFVDSSWYFLR**YPDANNTDAPFD**
KAVTNKWMPIDVYIGGIEHAILHLLYSRFITKFLHAQGHLNFSEPFPNLLTQGMVQGRTFKDPHTGAFLKPDTVEKV
GDK**FIHKPTNQEVAISWEK**MSKSKYNGVDPDR**IVDEWGADTAR**LFVLFK**APPHLELEWENAGITGAYR**WIGR**LWNLV**
NTFVQRDPSADTPSPPPSVTERAKEEK**DLLALTHETITSVTK**ALDAAPYSFNTAVADLMKLSNKITTLPADSPQYYL
SLRSLVLLLHPFAPHVSSEMWQALVAHGPAHESAWAGSSAAPELSRQLWPVANEEFMKKDEVVVAVQVKGKTR**GTFV**
MPAAEVGDKAAVERYARESAVGKKALWQRDVKKVVIPPNGKIVNFVC

>N165_4-carboxymuconolactone_decarboxylase_domain_protein
MLRQGSRSVIRGGAVNRGAWGLLSVSSRLPRATAVLSSSSTPAISSPRRQASATTPPAEPPVVVNRSARKRYVR**HPW**
NDSESMLSDDLRILTYLAGNTAAGNLSAVGRDWCYLDPAK**HAAGMDVILQTLVFAGVPKILNALQTVSELGVDNR**QI
LEPTFPEGEEFKEPVSYGEFVERGEAEMHLAFCHKYPRLRERMAELHPALDRWMVDTVWGRLRSRTGLAAKERQLCA
LAALAGNIVWPQFK**SSIIVALNSGCTLEEVRSVLDQTEK**VWGTSAQIMVDALWTDLNKKSLHSWQDGSCESTLHNHG
GSHIPASTPIPTSNHVKYATSGKHPFMYLNRMEDAIPQHLR**VLALLAAHTASGNLTR**VGVDWSYLGEEHHEAGLEII
LQTTIFGGFQK**AINALQVVHNIGVSPTAINYAAEEVPEDR**RANVKRGTELLKLIYQKQYPRLREKMRWMHADVEK**VI**
VEWAYGRVLARPSPVLAPKDRELCALACLSGQIVFPQLHSHILGALNAGARLEEIRAIFDQTEYVWGKDEQIMVDGF
WLDFAQRYSYHKQMAAAKKKDAAAKATARPESGPSSGAAKNDAGSVFTG

>N166_6-phosphogluconate_dehydrogenase
MRRATRSFALRPTARQLWAGADSLTAHRGFVSVAKPETTRVGWVGTGVMGGHMCGHLLSAGYQVTLYSRTAEKAQGL
LGRGAKLAASPK**EVAQQSDVVFTMVGFPHDVR**SVILGSSGVLEGLCSDGVVVDMTTSEPSLALDIYNEAKKK**GVHSI**
DAPVSGGDVGAKEARLSIMVGGDEEAVSAVKPLFDVMGKNIVHLGPASSGQHTKMVNQILIATTMVGMVEGLLYGHK
AGLDLNQVIEAVGKGAAGSWSINNLGPRIVKR**NFDPGFFVEHFIK**DMGIALKEAERMK**LSLPGLGLAHQLYVAVAAQ**
GHGRKGTHALQLALEKLNNMDHDHSSPKSGLPKAL

>N167_Complex_II_subunit_Sdh3_(SdhC)
MLRQATARTAPLFAVRGTVTGLQVLSRSPVALATRTLATLPSDASTEAKPNRPLSPHVSIYRFPLPALTSITNRATG
GALTAGIYTAGALALFGAHDLPVYIDAFKAAVPLLVYPTKLLVSFPFVYHTLAGIRHLYWDYTAKGLTLPEVYTSSY
ALMGATALLTLGLTFYSI

>N168_Complex_I_(NADH_dehydrogenase)_gamma_carbonic_anhydrase_subunit_(AcCA1)
MMRGLLRRLRPSTPAAVLPTRNGADIPDVPLEKFGLTVPVQATAYNDLYNKHTTLVNLPGKRPQISSESFVAPSATL
VGNVEVWDRASVWYDCVINADTKLIRIGAGTNVQDGTVITEADEELTEDHDGSTIVGHWVTIGHRCVLKACTIEDHC
LVGMGSVLGAGSYMESHSILGAGSVLPAWQRIPSGQIWVGNPAKYLRDLTEEEFDFLEKSSAHYTVLSKQHAYEFYL
PGHAYIDAEKKGIQVGYQVEPLSGEESVLLAPNYKEKVSVH

>N169_uncharacterized
MRRAATSAWRRQANPPHGGSGGGGGRMVRYAVGLPIAFKLGLDLGNLVSPLQSHYLEDEKEKKTDVWNAVGSDLVEQ
VKTSTPLQAQLGSEPASRVQVSDVLSLSKSHLKWQFFTHCSPDDSKEESLWDMVTNNRVVMATEELQLQVPLKTRSK
GASDLSLVVDTHNDGRGWKVDNAWVETQGEGAVCVPLTPPRHA

>N170_glycine_cleavage_system_regulatory_protein_(R_protein)
MRRTGRLASSSLRQLGAPRRFLYSTQSEPKQARLVLTAAGPDRVGVTAAITKAVVDAQGDVDSGRLTSLGGDYCIHM
LVSVPETQEQAFRKEAQAAVGKFGDWDLSIRKNTPRAAVGPSLRQRLVALSGEDKPGIMHAVSSFFADKGINILSMN
VYNEPAPFASSRLFKLQALVQVPQGMSDDQLEEGIDAVGENEGVDMWLESSQQPSTPPAALHEAAPQSHRA

>N171_Complex_I_(NADH_dehydrogenase)_B14_subunit_(NB4M/NDUFA6)
MATSGVATTASRSFADAAARNQHLYRSAMRAAPRIIQMYDLPYNVGQVRSRIAEEFRKHQNVRDPVTMDMLWFKGKS
ELDETLLTWKQRPHILHYFAPKKKEESDFLRKFYANEDID

>N172_mitochondrial_ribosomal_protein_S29
MSMLRTAMHRSNGGRWGGRRAAASFQEWLTSSSTSSSTTTSSSSSALLPLRPHFVAGLATASRPVYAKRMKNDGGNQ
SGREVSDLESTENQDDAEGVQDENDDDMRSLEKQVTKELSRIGMADLKDEVLKQGKGEEEAVSESADPFDTVLREIA
DLHAKGLLGDHDTLTKYERYLHKKKSHQGLVRDINASLAAMSPDQQSFLSHFVEFVKPVDVEAEAAAKAAAAALAAK
QSEEAIREKEAIAFAFAPGDATKLTVGKSLLRFSAQDQKQYLPEGVAGQLKNTQFKFGDESVVFRRAAYDLIQELKR
RQESGFLASAGNDSLILNGEGGSGKSTVLSQAVLWARKNDWFVVWIPDGRAWTGGERIVPSTLEHAHYDQIEKAARF
AARLNVTHGDKLKAIKLKGDYEIEDFHRKSDSTLFDLLEFAYKHDKRAVNAVYYFRRELNRITEFPTLIAIDRYNYF
WDNTGYFDPADVNRGNYRHLDAQKLMLTKMFSDHQDHGLVNGTMVCALETTKPATIKPFLRRCGDKHMHEIPAYSLN
EFHEVMKHYKEIEYVNIDDTTKATERFIYQLCNGMPGLVFKYCGLQ

>N173_Complex_I_(NADH_dehydrogenase)_B8_subunit_(NI8M/NDUFA2)
MSWRARLSTNMQELRFIMCTTSPNSGGVRSFLNSNYAELKKLNPRLPILMRTGEQAPPKVYARYDWGEERGFDLHNA
TEKEVEDRVRELTLMGEKMEKSFESIPKDRDLIDESDVRKFDTY

>N174_acyl-CoA_dehydrogenase_family_member
MKRSAIATATARSASAATVRRSTAVPLVLRSATRSAMVSAPRFSAISGAGQAHPGFAALSSILPRRCGYSTYIPDMS
VGLSDEQREIQQVALDFARKEMLPHAEKWDEEEIFPEDTLRKLAELGFAGIYIKDDIGGSGLSRQDAAIVFEALSTA
CPSTTAYLSIHNMCAWVVDQYGNQEQREKYLPTLLSMEKFASYCLTEPGAGSDAAALKTTAAKDGNDYVLNGEKAFI
SGGGASDVYIVMARTGQSGPKGISCFVVDKNTPGLSFGKKEKKLGWNSQPTRAVIFENVRIPSTNLIGKEGEGFRIA
MKALDGGRINIAACSVGAAQACFELARDHVQVRKAFGAPLSANQTIQFKLADMATSITASRQMIHLAARKIDSGAED
LTAYCAMAKRFATDEGFQVCNDALQLFGGYGYLKDYALNRYLRDVRVHQILEGTNEIMRLIVARQVLKDAPPA

>N175_Complex_I_(NADH_dehydrogenase)_B15_subunit_(NB5M/NDUFB4)
MNSNKFYVPRGPRVEHAIKDPAIEEWAFYRENTHRYFRMNPKIARKALIWAVAVPYITYQLTKMAQIEQDNQNPRSQ
LAVPDRKYL

>N176_mitochondrial_ribosomal_protein_S34
MTTGLPTGYKQFSLVVPKPSSRVKKGKNLFDIAFSFKNFGVGARFTRTGWQYPEPCYWTVTSVKPRKNEPDMKRGKA
WGVLTWRGVTDATPRRIRTTTKKDWSYIKEGEEVPTYSLDEETHSRRYNYFEGGVAEPEPHVTEGAEHVFRATRRGV
TEDIKPRLAPWKVENFTDEEIDKMIANVGKRSKSQATEGENKEKSDLS

>N177_putative_TOM_complex_homolog_Tom22
MVRLNIEELKQPQKKGFFGSIGLPEPVRRVANTWSNGLYAASMYAQQGLGYVSSFAWIFATAAVVIYLPLLRAMDSD
RETIRAIRAEMVQKTAGMVPGAAPRGPDLGNLDISGLDFKIQL

>N178_pitrilysin_presequence_protease_(Mop112_homolog)
MKRLLATTARGRSLSARAAAASAGIVDASRHALPTGAAATRLLRSRLSGSSGATRPQRRGWATQAAAPSTTSQSTSI
DFTGLKRGEERERPALAAGDKLHGFRVLKVVPIPERNFMTYQLVHEKTGARLFHVDCSDTNNVFCVTFKTVPTDSTG
VAHILEHTTLCGSEKYPVRDPFFNMLKRSLNTYMNAYTAPDHTSYPFSTQNVKDYYNLLSVYLDATFFPKLEPFDFM
QEGHRLEFEKIDDPSSALKFKGVVYNEMKGAMSEGDSIFYQALHSNLFSKTTYKNNSGGEPKAIPDLTYDQLIEFHR
SHYHPSNAWFYTYGDLSLEHRLQQINENVLSRFSQIDPGTDLPDEVRLTQPKRVEAVYPPVAGSDPKRQEKFTVAWL
TNKTTDPFENMSMNLLSRLLLNGPNAPMYKVLIDTNIGLDYAPSTGYDSGAREAPFAIGLSGMNEKDVPKVEEGIMS
TLKQVAAEGFPEERIQSVLHQIELSQKHVTTDFGMSVGHAINYTWIHGADPAEVLSVNKKIERLKQELEAGPYFQHK
VKQYFLDNPHMVSLLMKPDEKYLEKLDKEEQARLEKIRASLSQAEIDDIIAKAKFLKERQEQQQNVSILPTLHVSDV
PREAPNKDTRFERKTIPLAHSAHQIPLLSVPQPTNGLTYFRGMASLNSLPSDLVPYVPLFCSAMASMGAGSMDYRQL
AQKIESHTGGIEFSPVCSTHHSDLSKFRAGIYVSSFCLDRNLDHMFELLHTVLSAPRFEDVERLKSIIYGNTSDMQE
SLVESGHSYARSLAASVFSRASALHETWSGISQVTLMQQLAQSEDVSTVIPHLKAIAEHVLDASLMRCSIVGEEGSL
PQAEQKLTHLLGGLKSSSSAQPTAAADYRESEYAPLSRPHRLFVPIPAQVNFVSQILPTVPFTHPDFPKLKALSSLV
SSSYLHPEIREKGGAYGSGAMSGEGLWSFYSFRDPNTTKTLDVFSSLREWMKKDGAFQDKDIDEAKLRLFSSIDHPV
APSRQGALEFTSGITWEMRQKNREGILDATRKDLIEMAEKYLVPATSSTSQDGGRYPSIAILGNTAHNPFTAEETLN
LGLNNSNAGIIEEGDEGSDDDDSDNDEEHGQRA

>N179_pentatricopetide_repeat_(PPR)_protein_AcPPR13
MLMRRSFRQASPRPSALLSSVAAGREGSARLALAATSSQQLWSTRALATMPISATLREAQKKLDGNGLAGIERLTAE
EAYEVLQSRFAEYGTIRAGFVTHLFRKAQTPAHLDRALEAFYFAQSQLVEPNEHMIWEIIHACRRAGEPRRALELFV
NSAKYRVWPLARQFNRLMADFMAAGDHEGAVLTYGALRKRQVVPNAQTFGLLVRAHAAQGNADQALAAADEAKRALQ
TETLPGPVADALMGVHWKAQNFEGLRSLVEQTSDTTRSLDGALYASLAHLQANNVSAAADLVRQAVTATPATTEQFE
KWANTLAEEATSANLAQPAAGLLRALTGVAPADAALEELAAQLDAEAASAAAAAAAPETTEQAADSEPAAAEADGAE
KKEEAQA

>N180_beta_carbonic_anhydrase
MRRGLASSISLRSSAIARGGVSVLPRMAASSPLHSTTSTCLCARCATATTLPQRSISTDDKLKDEMLRMRESYNDLI
NGNKEWVAQQLEKDPDLFKRLSAGQSPQVLWIGCSDSRVPANVITGSDPGSIFVHRNIANTVVHTDMNLLSVLQYAV
DVLQVKHVIVCGHYGCGGVIASMTNNQFGMVDNWLRNLKDEYMLHREELESIPNDADRAKRMTELHVIEGVYNVCRT
SIIKDAWERRKSANVFPHVHGWVYGIHDGFVRDLNVSVRGPDDVPLLVRKPVNPSKC

>N181_Lon_protease
MKTCLGRLTPRPAAAQSHRYASSMLRGNASRLVGLRASAGARRPPLSTSSPLICGSHHGPAYRFGFVRAVHDQAGGN
GRKNGGGGTNNRGVGAAATDKKPSLVLSQADTGAMLRNMATMPTPQTVYILPLTLNPVFGGTSYYALVDRRTLERMQ
DLQAKGDLFLGLFLQKDPNPNVKVADVSQLYQVGQLGCAIGAVQYTSNPDVHLLQITPLSRRIRIKAPVPGAEREND
ATLLAVEIEELIEGEYNRKDPVIRTNHEAIVSAIQQLHEHDPSSHYQKLLDEMDPDNPAEFVDLAAAVMTSEPEMQQ
AVLETTDVKQRQLKCLELLHKKLEMFKKQKDVRTENMEQEAKLEAAQKKLYLERKKKAIEKELKLDVEDSDKLIEDF
KKKLETLQVPEEAMHVINEEMNKLTSLERSSSEYNITRTYLNWLTTLPWGLHSKENLNLSHAISVLNEDHFGLKDIK
ERILEFIAVGNLKGSVQGKILCFVGPPGVGKTSIGQSIARALDREFFRFSVGGMSDVSEIKGHRRTYVGAMPGKIVQ
SMKNLKSANPVILIDEIDKMGNSRQGDPASALLEVLDPEQNKTFLDHYLDVPFDLSKVLFVCTANVSDTIPGPLLDR
MEVIQLSGYILEEKMNIAKKYLVPQIMKDSGLQPGQIAVNDSALHALIQSYAREAGVRELYKHIEKIFRKVAYKVAK
ERKLATDATDATPAGGDGAEKTKKRSRKTKKPSKADEEEGKETKSEGESGDGQTQPVVITASNLTEFVGQPKFTSDR
FYDVTPPGVVMGLAWTAMGGATLYIETVNDRPLYSALKRSQPAELEHAKEGDAEGDKDRGVKTFGGAGGAMRLLTTG
QMGSVMQESTSIAFTFARNFLEDVSPRNEFFDRAALHMHIPEGATPKDGPSAGCTMVTSLLSLATGRPVPPDIAMTG
EITLTGKILTIGGVKEKTIAARRSGVKRLFFPDGNRKDWEELPDYIREGLEARFVKDYRQIYDVIFADPDPAASSTS
TTTTSTTAIDGETTKKPRATRRRKPTDKETELL

>N182_glutamine_synthetase
MRSAVLRRTQSHVIRGSATAHQLGQRGLATARPLQGMLNYDEFKRAVEAEELDTVIVAFTDLTGRQLGKRYDAEYVL
DHYHDFESHACDYLLTIGVDMNPLDGFKAANWQRGYGDFHLVPRMGSLRHAAWLDRTAYLVCDVADRDTHQLLTHAP
RTVLSKQVEQAQKDGFGALCASELEYFIYNDTYETAFKKGYKNLQTAGWYSEDYHILQGTRTEDLQKAVRYYLKKSG
IPVESSKGEFGRGQHELNVAYSDILTMADNHVLYKQCFKEVAEAQGKSVTFMAKPHHDEAGSSCHIHLNLTSAETGK
NAFAGDKDLQGIKCSDTFRHFLGGWIKYTPEIMPFLAPTINSYKRYQTASWAPTSLAWSPDNRTAGFRIVGSGKSLR

IECRIPGADVNPYLAFAGSLAAGLEGVRKGIEPPPMMSGDAYRAPSTTKVPVTLNEAAHALEESKFARQAFGDDVVD
HYAHYYKKEVEAFRKSVTDWEKQRYFEQI

>N183_rhodanese-related_sulfurtransferase/oxidoreductase_family_protein
MQRRLISSSASGAFGSRSLFNRSYASWIRHRPDQAFHATRRGYFPQFVDVREEDEHFKERLTGTLNVPLTKLKAETK
DADTADKLAYLDRSRPVYVHCDGGERAEEGATLFCNLGFTDVKLLEGGVFEISRDSGLIIERE

>N184_amoebozoan-specific_protein_(no_putative_conserved_domains)
MRAALVKRSTSRLHPLTRGPCASSLRWFGTAKKETAKATTAHASTPLEASNLPDPRAFAQEKAFWATQEPLKQKRLQ
AKEKGEPHFVFLEGSGGAGKKDLLWRLNKMGHEVVFHPYLTFLLDSQYPYTPTRDHDILQVRWGNKIINALENIASL
SKTGKAYKSNLVFVHRSPISSYHYARDRNPDEAALYLSLMRQITTAFSSSVVLCKADPLRVQERLGERLMVPPEKEK
ALRRELGESTDLDVIQREIDAYERLLLTPPSTEREHHGIGATVVHTTSSKQATAQILKTYGVEMNWVWEDLKKTSSP
PAH

>N185_malate_dehydrogenase,_cytosolic_type
MSADSNATTRRAVSRMSRIAAHMGVGSQTGFEAAATSASRVVSQQPPVTVLVTGAAGQIAYSLVFLVAQGRLLGEET
PIKLHLLDLPQFVGALQGLAMELEDCAFPLLRGVVCTGDLKEAFKGVDVALLVGSFPRQAGMERNDLLAKNAAIFKE
QGRALDQYASKNVKVCVVGNPANTNALIAQACAPSIPKENFTALTRLDQNRAKGFLAKKLHVSPGQIHNAIIWGNHS
STQFPDVSHGQVSIDGRTVSLKEAVGGTEWVEKEFIPGVQQRGAAVIKARQKSSAASAANAVVGHVHDWLVGTPQGE
WVSMGVYSDGSYGIPPGVIYSFPLTCSRGNWAIVQGLPVDAAARKRMQATYDELHSEKETAFSFLGLDKKH

>N186_Complex_III_subunit_Qcr6_(hinge_protein)
MSENWAGCAIKKSLEEKAHPKCLKKWAEYDACGQRIKGDTTGEAQCSGQYFEYWHCVDALVANDLFKRLK

>N187_methylcrotonyl-CoA_carboxylase_beta_subunit
MLQRGGLVMRRGGCAPTTLRCAATRFGRPTSIGFDGRAALPTVLVGREYHAERDFNVVDGSVEMSQDEWRENGRVML
DLVNKLKHEVATVKAGGGESARNRHVAKGKLLPRDRILRLLDPSSPFLELSQLAGHGLYEDHVPAGGIITGIGRVQG
QECMIVANDATVKGGTYYPITVKKHLRAQEVAQQNRLPCIYLVDSGGANLPRQDEVFPDKEHFGRIFYNQANMSAQG
IPQVAVVLGSCTAGGAYVPAMADECVIVKGNGTIFLGGPPLVKAATGEVVTAEELGGADLHCQTSGVTDHYAHDEEH
ALALARRIVANLNPSHTKQRKASWEPEPVIEPRYPQTDLYNLIPSDARKPFDMRKILARVLDDSRFDEFKALYGPTL
VTGFGRIHGHPVGVVANNGILFSESARKGAHFVELCAQRGVPLLFLQNITGFMVGRSYEAGGIAKDGAKMVTAVACA
QVPKITVVVGGSFGAGNYAMCGRAYNPRFMFMWPNSRISVMGGEQAASVLTQIKREAMVKSKSSHQWSAEEEEAFRQ
TMLAKYDKEGHPYYASARLWDDGIIDPAETRNVLGLTLAACRNAPIPQTQFGVFRM

>N188_rhodanese-related_sulfurtransferase/oxidoreductase_family_protein
MWRRGTGSVLAGALGQRATTATASSWGAQRLMSSHTRTTPWVSVDELRRVLAEPKAHSKERVVLVDTRGAEAYDKGH
LDGAVRIEECFTHLATSDPAGLASLEATFRDLFGRRAGITGAANERVVIYEEGLTSGFAQSCRGYFLLKWLGHPNVS
VLQGGLAAWRNAGGELSQQAPQVTPAQLKTQVDASLMATKDDVLQALKDKSKDAVLLDVRDQDEWIGTSSSPYGKDF
CPRKGRLPGAKWLEWYKLHDRKDGVAYTKPVDEVKATLTDMGIKPEQDVIVYCFKGSRASNTLMQLRHAGFKATNYF
GSWNEWSRDDSLPIESSLLSTPHA

>N189_mitochondrial_carrier_AcMC5_(ADP/ATP_translocator)
MSFWMDFLLGGLSAAVSKLGAGPVNRAKIVHQAQGELLRQGRLGRPYGGLADALARTVRAEGPLSLWRGAMYDVISY
FPTQALNFALKDSFKKLFPFDRRQHGYGLWFFGNIMSGGLAGATSLLIVTPLQLATTVLAADVLAPELGRTTYQYTG
MADVISKTFQHSGPLGLFNGFGVSVAGIVLYRGAYFGLYDTLRPLVPQNNFLASFLVGWGVTIAAGLATYPLDTIRR
RMMIAGATPMAYSSALECTLTIWREEGVAGFFRGALSNIVRAIIGAMILVLYDQLQAALTAPPAPAPAPAPAANGDS
E

>N190_pantothenate_(vitamin_B5)_synthetase
MQRRVKVVREVAEVRALREAWRREGRRVGFVPTMGALHAGHISLISHALPHSDALFCSIFVNPTQFGVGEDFDKYPR
DVAKDVLAIEQGLSAAAAAQGDGGRDVEAVVFAPSVRELYGDRFSTRVDIGLMADTSEAHARPQFFSGVATVVSKLF
NITQPHRAYFGQKDALQCVAVRRLVEDLNFGLEVVVCDTLREADGLAMSSRNVYLSAEERKRAPILYKALCAGRSRY
LDGERSAQEIIKATKEALEKGEHWWAAGPPRPEVQYVSIADAGFGHELDYIDPKGPGAFLSTAVRLGSTRLIDNIVL
PPL

>N191_Lon_protease

MLRSRSWLKHSATPSLLRTGGRGWAPQCRSGLSVAGALPSPRGANLPFSTTPLPALRCSRGPTGTSGSSLSVQTWRD
RQWRNAAAAAPNGARRGFRTTAPAAAAAGDDNDDNENNKKKDEPEYREDSDDDDDDDDFSDGEQDGEDVMPPRDMPL
QVMVK**TVTTPEQVLVVPVIK**TSIMPGTMGR**ATVRDPEFLK**ELQELRQKHPSPYIGLFIVKDAEEAKQKGVQITTLDQ
LHQTGVLGVLTNVVPMRPSQQKDGVVGVIQFLSVHKRIKIDETVSGTKRLVAKVSELQDKPYDPKDPQIR**GFQAELE**
AIVHRIGAKGDVFARDNAAQLLLNFWTFHNPLNAAESADFVAGIITHIALDDAAMQAQQAVIEELDVSERLKKTLAL
TKR**ELSLSDLTQKIKEDINAK**MEERHRQMTLRDELKAIR**TELGLEQPQTETLMAK**FKERIKDKQVPEHAAKVINEEM
EK**FQHLSPSSTEYNVVR**TYLDWLTTLPWDTLTKDNLDMHHAEK**VLEDEHYGLK**DVKERILEFIAVGALKGEVTGKII
CLVGPPGVGKTSIGKSIANALQREFFRFSVGGMTDEAEIKGHRRTYVGAMPGKLLQALKRVKTSNPVVLLDEVDKVG
TSSYKGDPSSALLEVLDPSQNTK**FLDHYLDVSYDLSK**VLFICTANVLHTIPRPLLDRMEVIR**LSGYVEEEKVAIAER**
YLVPK**AVSEAGLSEIK**VNFEREALHKLIHSYAREAGVRNLQQQIDKIMRKVAHQVVVEQEKRQEGAVEGSDGKKGAK
GGVRKGRGKKKSTQER**ADESAQPGSSEALTLEK**DQHGAIVIKPAGLGQFLGKPPFSNDRYYDTTPPGVVMGLAWTSM
GGSTPYIETVVDKHQLLVRKEEKRKRREAKEKEKNKKTNDDVASSESPATASSEDDAEEEGGSGSGRLITTGQMGEV
MQESCSIAYTCAKIFWNKLGQTHKQTATSTATSTTTTTSSSAKRAR**SPQGATQGEDEGFDEGFFR**DVTLHMHLPEGA
TPKDGPSAGIGMVSSLLSLGLGTALR**QDVAMTGEITLTGK**VLPVGGIKEKVIAARRAGVKTLVFPEGNRKDWDELEP
FLREGLDAHFVDYYGDVFQVVFPDAPKEYHQALRRTSA

>N192_Complex_I_(NADH_dehydrogenase)_B17.2_subunit_(N7BM/DAP13)
MAKMLTNLRSEVSRRGVLGTLMAWHRGYLRPGVNSVLVGTDERGNR**YFEATELPFGQDR**WVEYSTSDDWGHDYDASQ
VPPAWHAWLHHVHDKPVPHQAVYSKPHKENK**TGSQEAYHPHNYVYGPR**VK**STTDPNCEEWDPTR**HSPFKENELR

>N193_peroxiredoxin_(PRX)_family_protein,_typical_2-Cys_PRX_subfamily)
MSTHAVIGKPAPDFDEEAVLGQDFTRVKLSDFNGKYLVLFFYPLDFTFVCPTEILAFSDRADEFRK**INTEVVGVSVD**
SKYSHLAWINTPRKQGGLGGALKIPLVADLTKSISR**KYNVLMEEAGHTYR**GLFIINPK**GVLVQATLNDAPVGR**SVDE
TLRLVQAFQYVDEHGEVCPVNWTPGSATMKADPK**ESLAYFEK**VNQ

>N194_mitochondrial_ribosomal_protein_L46
MRKAWSGVRQQLAVPPCAVVGPSTTGMSRQFVRGITHSQHERAYLQRLRQMEAEAAAGKTWR**LVGGIAVQRLPLIIP**
TPDPIEDQYEQFRFDRDNYFSINVERNLELMEEDRRKGSKISKTQKKKKEKK**EGVSDAGPAGGK**QK**GGEQDEADSLY**
QKAEETAYREETLEDVRAKMERLSPR**ITAADLANDRK**SLNRALASR**LYLIVQKPRTEHAWQFPQGGR**ESGETMRQCC
ER**ELREEIGTK**VK**VHFWSNAPAGCYSYPYPDNYSHNDGHHGSK**VFFYHAEYVSGEPHPDNK**EVVDFAWVTRDELQEY**
FDPQLFKFVRDMLPA

>N195_FAD-dependent_monooxygenase
MKMSRHAAVQQRGAALASLIVPRGGGLPAATMPTTSLLLRSYAAAATTTASSR**GSLSSSGSSGTPPAADEGR**AVAHV
RRREGGPLR**VLISGATVGGLTLAHCLR**AR**GIQAEVVEADSNYDR**FVGR**SAVVSGDALR**VLQGLGLRSVLEREGTVLA
KAVTGLYSGKSIHQQNFEPPTQDQGAGAVAIPAFALAELLAESWESRGGR**INTSTAILTMR**EVAGTGVRCSFRDAKM
GSR**DYDLIVLADGVNSGNTPEVLK**EEIYQNPYMTATQVGAYGVWSTYLPRPFTIAPDQAVDVLGLGSR**AGYVPMPED**
LLYFWATHRADMAPFLKGGAREAR**EWPSVGGGFEK**GFSMR**TVVQQVEQSDR**TCWVHYPRDMRIKQWTHRAGRVALLG
SGAYSTAPLPLHEAALPIEDAAVLAHALATHPLPADALAAYAARRKPR**VEAAQDWAWYLHTQATK**TGRWQLALR**NFW**
LTAGPGRLTFARR**SSALARPLSSSSS**

>N196_mitochondrial_carrier_AcMC6_(2-oxodicarboxylate_transporter)
METQRAYSPVGASNLPFHKQVMAGALAGLCEVLCMYPLDVVKTR**FQLQTAAEARYSSVLGTFR**DIIKTEGFSKLYR**G**
IASPIMAEAPKRAMKFSMNEQYKKLFTNASGQLSGPGHVAAGGCAGMTEALVNCPFELVKVRMQARSNAGLYKNTWH
AAR**SVIQTEGALTLYRGFGSMLWRNGVWNGAYFGIIQQVK**R**LLPVWSSER**GQLATNFTAGTISGLIATMLNTPFDVV
KSR**IQNTLPGQPR**R**YTYTLPALATVAR**EEGFAALYKGFVPKVLRLAPGGGIMLVAFDFFARIL

>N197_signal_peptide_peptidase_SppA
MLRGYRAASPLYSGGATSMGLPRYLCSSHVGGSASFLARSGQQLRRLAQTQATPPPPPPPQGEVPPPTAGAQLKRVG
EAGAKVFRVVRGIAILAAVGYGVLLYSAYK**AAEAIPTDVVLK**LNFERPFPDVSQTSQLFPVLTLQEVVDGLDAAAKD
PRVR**GIIATVGSEVMELPMAQVQELR**DALKKFREAHKAAVCHSEGFGGNNTDYYLATAFDQIVMQPSGWLNLTGVAM
SATFLRGLFEKLEIEPRLLQRHEYK**SFANTFNEK**GFTPAHK**ESVDAMATSLHKQLLQDISDAR**GIAPK**KLQALMDQG**
PLLPRDAR**DAGLIDEVAYRDKAYSLITGK**VLDSLK**HEQQGKPTPEVELAK**AVLAVPAKKVKFMSFKKYVKKTKEEKE
LEKLKKKKETATLMAADTANFQALKQVYDKQEHPEQGDPETQKTSRRLARRAERGKTGVPK**VAVIYATGEISSGHHE**
KTGVVASKTFSTILRTVVRDKDVKAIVLR**VNSPGGSAVGSDTIWWETIR**AKEAGLPLVVSMGDYAASGGYYISAAAD
R**IIAQPGTITGSIGVIFGK**MVLGKFLANKLGVTQESVEKGKHANIMSAYYDWKPSELELCNKLADESYKEFVTKVAS

GRGITYEEAHKIAKGRAWTGTEALEIGLVDELGGLSRAVEVAKELAGPLPPGVDYEVTVLPRPKGLRELLLKGSAVS
ESAEDEDEEPDSGSGLGGLMDESMAEWAAAARVVHFLSSIPALKPLMRQLESGMRASAGPQYRMNDVSVGAKESDLV

>N198_i-AAA+_ATPase_(Yme1_homolog)
MSATPSATPNLTSLLKLRSTGGRIGGQYWNVHRKLPLSLYRTITSSSQRSGSPLFSSPHARLPLAAETPHSVERFPA
LNGRRTFFSGAGSKRLEGLERQVESGRASGTIWASYFRELNKMDSPKEVIRQFERLEESAKTQEVVKEYLKALVLTG
RLEGANLGHLLSRGASGGAGGNAGRLTLVADSPIPITVTGGSLTGSAGGSTFSKIANVTGFMVSLAILYYLFTAMFK
GGDSIMGVNTKVKFAQKSNITFEDVLGVDEAKSELQEVVQYLKDPQKYTKLGAKLPKGILLVGPPGTGKTLLAKAIA
GEAGVPFLYCSGSEFDEVFVGVGPRRVRKLFEEAKKNAPAIIFIDELDSVGGSRNRDHHQVYTHTINQLLTEMDGFQ
ENQGVIVLAATNFPDVLDPALTRPGRFDKQVEVPRPDVRGRKMILEHYLKKIVVAPDVNVDMIARGTPGFTGAELAN
LVNIAATKAATKGMEAVTTACMDEARDDVMMGVQRKSMIMSDDEKKLTAYHEGGHALVAIYTEGAKPLHKATILPRG
RALGVTHFLPESDQLSLSRMQIMADVAVAMGGRAAEEVIFGPKMITTGASSDFKHATRLANAMVAQMGMSDKVGPIY
RDERDLERASSETRQKIESEVEALLQGQYAVAKRILTDHQDELHRLAQALLEHETLNKEEIMAVIKGKKLTNLFYQ

>N199_mitochondrial_ribosomal_protein_L45
MHRPRASAAVLGTWRASGATFAPIQAGQMASSRLILRTPIARIFPQTAGGSPMLLSATAVLPSQRRPLFPATCGMTT
RHYAQTSKRVGGMSYKPRIFVASLGQIADPAIPPSGAELLNPKKLWARLMSSMRNYASLWQVRKLLKKEKYPTSAWL
IVGRWTAEAANQYRAFCEARANGNKQALQKLTTDEFFDVVKGSLIDPSSKLKREWQSQDLRVKVLALRMVMLQEPDV
KFVQMLFRFTSQQKLKITDSKGALIAGSDSAVPVTEYYVLERPLQDIHLFDWKFMGKLDPSHKEPLAKPLLEQ

>N200_mitochondrial_carrier_AcMC7_(putative_citrate_transporter)
MSEVKPLTVYSPAPTSKKRHPVKSIISGGLGGAIEICITMPTEYIKTQMQLYPAKYGKEGVMYCVRDTVKNHGVLGL
WRGLGPLVVFAVPKNAVRFFFVEMIRNQLRNDKGAISLSGNFFAGLCGGLMEAVLVVTPQETMKVRLIHDRLSPNPR
FHGTFHGITTLLKEQGISGCYKGLTATMIKQGSNQALRFTTFYQLKTWMLGDPALDFDRSTIKAVFQTIFAGATAGA
VSVFGNTPIDVIKTKMQGLEASKYRNTWDCVQQTWKADGLKGFYKGTVPRLGRVCADVAITMFLFDYITMALDAVWK
TE

>N201_pentatricopetide_repeat_(PPR)_protein_AcPPR6
MQRHLRRHFPRLLVLVLSSSSLRSSCASLPRPLRRTFTAAGSSSSLRTLPSSRTTTTTTATAAAAAGSAKRPLRREV
GVEQAVARLTALRTAGRRAARETSVGVAETPDLVGRTLRPGDLRAGLEAVEAAHALAVRRVREAGVPMGLDHYHLCL
RFHRRSPEHARHLLEDLLRDGVRPTAATFDMVVDIYGVGRPRAHWLSEAVQLFHRFIGMGVEGIANLSAFRRLIQFC
HRAGDINQAFELHEGLRGLGLRADMDTYISLLALAHRCGDAERVKKLWTMITLAGIEPNTRLVNSFIANCNSPERAL
IAFNKMAEADLQPDVHTFAALTTTLARAGHVEDLRRVYHLMRSLGLGSPAIYTTLLWAHVGGSSANVWEAGRMWSDL
VGSGLPITPSALSAMAHVHCSHSGARAALDFLATVRKGEGEGRGMAGSQDLYEELLGASASIEEAREVLHEMRALGY
APSSTTPFRRLAARLPSRLPVSERTQVLDLMQESGVGGDGEVYRWLILHGHPDDGMGLLNRMLHEGLQPDVRVYNAL
LLKTDGDEPKSAASSPPSRKSMHNIWHHGGRARAEALFRSMREGTVSTDRTYAYNPKLNAESFMILLRKCRRHREPD
MAIALFDTLLTECRHIPRESGMYGLLLASLQPSVVSPASEAEAERYREHLGRVVAQMEADGVPLAGPHAASALVDSF
VRHRGPPAAPASQSGTGGGKGSLFAELQERLGPNSRYLKTSLMHVYGTLADLPKLETLFAQMVEEGEVDLAAWSALV
AGYVRNGRVEEALGVLYGMLEQHGQVPPVSLLGQVGRALEQDGRLVQPGALRPLFTGTFADIRRQVFRVARHRRLDR
DAAFRQLAFNRFLYFHLTLLARRRRDGGPPSSPSAAARAPPPSFLPSLLSRIGIAGSGRGSSTATTGGGGGVERERR
QERVDAQRTQLILGRMEDEDVYVSVPLQRLMASFISSSSPLGGPEGRF

>N202_GTP-binding_protein_TypA/BipA
MLRSALSRSSSSSPLAGSASSRSSLVRAFSSSRSTAASSSASSSSSSSGNRLHRCLAAPSTSSSAQPSSSTLISSQR
PLGASLRRTAPWSALRQVGHGWPSLASHHRSGVVGGRALARRWLSTEAEGAEDLGEGVRNEKLRNIAIIAHVDHGKT
SLVDKLLSQSGTTSLRGGERVMDSNALEQERGITIMAKQTSIKYKDYTINIVDTPGHGDFGGEVERVLGMVDGVVML
VDGTEGPMAQTKFVLSKALGYGLKPIVVLNKMDRDTIRPDEVESELFDLFVSLDASDEQLDYVTLYASAREGWAVKN
RTAPRTDMTELFETIIEKVPPPLTYPDAPFSMLVTTMEYDMHLGRILVGRVRSGSVTTGDQLHGLSREAKELEKSKV
LKVLGRRGLERSPIERGECGDIIGIAGFGACSVTDTICAPSVVHALPANPIDPPVLSVVLSVNDSPLAGREGTKLTS
TLLRQRLYRELESNVTLQIGDTGREGALEVKGRGELQLAVLIENMRREGFEISVSPPKVLFKQEEGELLEPQEEVTV
DVPTEFSGVVLERFGLRKGELVEMKTDGDKARLIFMCPSRSLIGFRQELNQLCRGTVVLHHLFHSFIPHKGVIENVR
KGVLLSNTNGTTTTYALESLEQRGTMFVGPGTTVYMGMIIGENSKKGDMDVNPVKAKALTNMRTLLKDENVRLTPPR
ILTLEEAITYIADDELVEVTPSALRMRKEILDTSTRETMARRAKKSG

>N203_acyl-CoA_dehydrogenase_family_member
MRRIGSSLISQRLVTAAITSTRASARAATLRSTHSEASRPAVTTLSEDEEMLRSSVEQFARERIGPKVRSMDEKSEL
EPALVKECFEQGLMGIEIPQQYGGGGMSFMSAILAIEEVAKVDGSVSVFMDVQNTLVNNAVIRWGTEKQKEQWLPRL

AQDTVGSFCLSEWSCGSDAFALKATAKKDGDGYLLNGTKAWITNSKEAGLFLVMATVDPSAGHRGITTFLIDKNTPG
ISIGKKEDKLGIRASSTCEVVLENCRVPASQVLGEVGKGYKIAIETLNEGRIGIGAQMLGVAEGCFDHTMKYINERK
AFNSSIADFQGVQFQYASMYSDILAAKLMVYNAARLKEAGQPFVIDAAIAKLRASEVAEKVASLCINLMGGVGFTKE
FPVEKYFRDCKIGQIYEGTSNIQLQTIAKYIQQQYK

>N204_cysteine_synthase
MKHMTPRSLMPSRRAGSLRHTTSPSFSPATLLSLHRSSSFSRRWSTFNNGLVEGFPGAVGNTPLIKLRGLSEETGCE
ILGKAEFMNPGGSVKDRAALYIVRDAEERGLLTKGGTVVEGTAGNTGIGLAHICKARGYKCKIFMPNTQSQEKIDLL
RSLGAEVIPVPAVAYDNPANYNHQARDFAQATPNCVWTDQFDNVANRYGHFSTTGPEIWFQTQHKVDAFTCSTGTGG
TLAGVGLFLKQKKPSIKIILADPPGSVLYSYVKEGKLEREGSSITEGIGQGRITKNLKDAPIDDAIQIPDEETMSMF
FRLLDEEGLFVGASAALNVVAAVKVAKKLGPGHTVATVLCDGAQRYYSRLLNKKWLDEKKLLHTLPDKYLQFLH

>N205_mitochondrial_translation_elongation_factor_G_(EF-G)
MYSASRRASSNPSASGFMRHSAGLMRPSTSSASTLCLNRAPSAMINLPLLSRFSTDAEGSAPQLQKELHKIRNIGIS
AHIDSGKTTLTERILYYTGRIQKIHEVKGRDNVGAKMDSMELEREKGITIKSAATYARWGENHINIIDTPGHVDFTI
EVERSLRVLDGAILVMCGVSGVQSQTITVDRQMKRYDVPRITFINKLDRMGADPFKALRQMKEKLTHVKSAALQIPV
GLEDHFQGVVDVITREAYVYEGGSGEVLSKVAVPENVRAEMEARREELLETLYEVDDVLAEVVIAEGREPSVEEIKA
AIRRATIALKFTPVLMGSAYKNKGVQNLLDAVVDYLPNPTEVPSVGYDLDNNEAPVNLVPEHDKPFVGLAFKLEENP
FGQLTYMRMYQGVLKKGDTIVNMSTTKRTKVPRIIRMHSDEMEDIQEVGAGEICALFGIECSSGTTFTDGNTRLSMS
SMFVPDPVLSLAIWPKAKGQDKNLSKALNRFQREDPTFRVHTDPESNQIIISGMGELHLEIYMERMRREYNVDLDSS
PPRVAYRETLTGKGAFDFTHKKQTGGQGQYARVAGYVEAIEEEDLEEHEQKALASGKRVLFQNQTIGGSIPPNFIPA
CEKGFFEAATEGPLIGHPIQGVRVTLTDGGWHPVDSSELAFKIACINAFKQGMLKANPQVLEPVMGVEITVPKEFQS
TVVSSIGKRKGVILNSENMTGTDYTRVDAEVPLSNMVGYSTDLRSTTQGKGEFSMEFKKYAIVPRDSMEKLIAKYKE
DKAKEKKD

>N206_mitochondrial_carrier_AcMC8_(calcium-binding_carrier_protein)
MRKGLVVRRSSTVSSRLLGGGRQGGSASLLRLPRRSIITDNQPIRTHAQEEVASSNGSSGVIKRILAIGVGAGLVVT
ALTLPLADEITNREEKPLALLEKLFTKYASAERNGVKFMTRRDFIASMMPPDSELGPALALDTFRELFPTDDTLISF
SEFVLFDALSSSTKKALATSFQVFDTDSDGLLAKDEFRKVVASTGVGPRLMFDLDDPYWERYFGKDGKGKISEAELG
LIFGSLKEGILAQEFSRNSFESDKNAIPMEAFARVLLVNVPSTRIPKRVVDNLKTVSAAFKDASVTFDRFREFNIFI
YRLSEFERALKMAMVANSGNITRDDFRRTARVSTGVELNPSEIELVFHLFEDQNKRGMLDCNAFLDIMEFRRARRLY
DIQQLKVIKHAVNPGRAMVKAMESFAIGGFAGAIGATFVYPIDLVKTRMQNQRRTKGGIVPPGRVIYTSSWDCAAKV
LKYEGFKGFYKGLGPQLIGVAPEKAIKLVVNDYLRSWFGQVQGAKPGEIYFPLEVLAGAGAGASQVIFTNPLEIVKI
RLQVQGETPGAKKSAYQICKELGFTGLYRGASACFLRDIPFSGIYFPAYAKLKQSFRDEEGRLSNTNLLLAGSLAGV
AAASTTTPADVIKTRLQVEARLGEARYNGILDCFVQVLKSEGPTAFFKGVVPRVFRSSPQFGITLLSYEFLQDMFHP
EDIVVSAPTNAPVAQDDIKPAPSVIHLSVAAAAKEEVEVK

>N207_mitochondrial_carrier_AcMC9_(solute_carrier_25_family_protein)
MHLSSAGIPFEKRPQLPAEPTVLAGFSADALTRTLLNGFYVVKTRLQVRRPRYHFCHAFVETQNLWREGIFGFLRGN
AAGCLRAVPYSAAKYATHRAVEPLLKERLPAARAEWVANGLATAVAVAVTYPLNTLQTRIALLPLEQARYAHIINEL
ANSNGGLLDGLYAGILSVIPGQLAYQAGLHLADKLFLAVIGPTDESQHPTRAFVQSCLRATLANVLSYPFDTVCVRM
QAGIFADKSVLHCIKSIYEEQGVGGFYQGVGVTLLKVLPFALFMYFAFHFSNQWFEKHGRDERFSSLHSYLHTYWRA
LSTHLETGSLQWRSHAQKQFHHAE

>N208_glycerol-3-phosphate_dehydrogenase
MWRRLKRVTIYAGVGSAVAAGGLLLYASSPFTGVNASTSLTGPRKTTLIPDFPAPATTVPTRDEQLAKLQEGKEFDL
LVVGGGATGAGIALDAATRGLNIALVEKYDFSSGTSSRSTKLVHGGVRYLEKAIKNLDYEQYKMVREALHERATVLK
VAPHLSYQMPIMLPIYKWWQVPYFWAGSKLYDVFAGSQRLESSYFLSKGKALEKFPMLRSDSLVGAMVYYDGAHNDS
RTNIALALTAATYGATVANHVEVVSLIRAKVTDESGKEKEVVSGAVVRDTLSGKTWEVKAKGVINATGPFTDAVRKM
DEGDKCENLVIPSAGVHIVLPDYYSPRDMGLLDPATSDGRVIFFLPWEGNTISGTTDTPTTLSDQPRPLEEEISFIL
KEVSNYLNQDVTVRRGDVLAAWSGIRPLVKDPTKLGKAGTQGLARNHIITISDSKLLTIAGGKWTTYREMAEEAVDK
AIAEYGLKPRNICVTTDVYLLGARDWTPTMFIKLIQNYGIQREVAQHLASTYGDRAFEVAKVATPTGKRWPVLGRPL
AEGYPYLEEEVRHAVHHEYACTAEDVLARRYTRLAFLNANVALDVLPRVIDIMAEELRWDDARKKHEYENTKKFLRT
MGLEDINSRGVFNNMDILHYRECFDAIDTEHKGHISKQKLKEFVKSEKKDMRDTEIDARLDYIDENKDGVIEFNEFL
ELMAAIDTHEERDKYRRARSMERKIPTHRSAGGL

>N209_peptidyl-tRNA_hydrolase

MKRSLGLWKRPYAGVNHLIVGLGNWYYPLSRESVGLYALERYAQR**YSLVWDFIPNICSDALASKTGIALIKPK**TYQQ
KDMGKAVAMATEAMNLTIDDVTILHYDANLPCGQVRYRTGALDAPNVAVQSIINMFDTERLNR**VSIGIKPVSEDEVF**
VPTIVQAIDKRYLDNFNDIWIRNVLSDTERPLVDKASDKVTDELLHSATNTTDNTFSRLNTL

>N210_ubiquinone_biosynthesis_protein_Coq6_(putative_flavin-dependent_monooxygenase)
MRAARGSVRAALWRRPGAGAAMVLHSAPHAASSPLRFMTTTRDDSDFDVVIIGGGMVGSALACALGSTPATGHLR**VG**
LVETSVVAPLHPLPPTPDLRVVSVNPASARLLQAVGAWDAIVNARVAPFYSMKVWDTSGKASISFRHNEVGMDYLGF
LVENR**VITSALFER**MQQLPSVKLFSPMSVQRIELEENGKGDKHEVDWSSPQPTVGLHLKNGDKLRTK**LLIGADGAQS**
IVRQTFNFGAVGWQYSQRGVVATVTLPPHMANMTTAWQR**FLPTGPVALLPLWDR**YASIVWSTNLPHADHLLGLDEKA
FLEELNHAFHDPPAATTGPLAFIEDKLPFNPFAGADPQPPVLQEVVGKRAAFPLRIAHATDYIRPRVALIGDAAHTI
HPLAGQGVNLGFADVASLTNSVIDAVHTGRDVGDVSVLKQYEEDRR**VANAVMLTAVDGLK**R**VWGTSFLPLAALR**NVG
LKLTDSFSPLKKEMMKFAVGSFDTSAIGAHVPDTTST

>N211_NADH-cytochrome_b5_reductase_form_1
MRRIASTNTRSFARASTFTSTTLSSSSSSAASLSLPLHRRFASSEDNKQQKQDDQQSSGSGFLTTLVVAAAFAAGGY
HWYK**EVVGEPFEER**KK**VAPVAAVAQEGK**K**EAEAAEVKPLPPVSLNKDEFREFELVEVEDLTPNTR**RLRFALPSR**DHV**
LGLPVASCVVTKANIGENGKPVIRPYTPVTNDKSDK**GYFDFVIK**DYPTGVMSSHIYHLKKGEKLQVKGPIPKLAYSK
NMKKHLGMLAGGTGITPMLQVLEEVLSEDDDKTHVSLVFANNTEQDIILKDRLDALAKKHPNRFEVHYVVAQPADAA
SWK**GHTGFINADIIK**KHIPGPAEDVMVYVCGPPPFYKALSGSK**APDYSQGELDGVLK**DLGYIKEQVFKF

>N212_cytochrome_c1
MLRQRTLTSATGMAFRSQTRSFATSAGASAKRLHPNVLGLVIGAGAVGAAAGTLISRARCSDDVLVAPAYPWSHKSE
WK**SYDVASLRR**GHQVYKEVCAACHSLNYIAWRNLIETLYTEEEVIAMAAETEVEDGPNDDGEMFTRPGKPTDYLPRP
YPNEEAAR**SANAGAIPPDLTEMVK**AR**EQGADYIFALLTGYMPAPAGLNVR**EGLYYNPYFPGGAIGMPPPLNDGMLEY
EDGTEASVSQMAK**DVSAFLCWTARPEQDER**RVMGIKVLIYLGALFGCSWYIKRFKWSVLKNRKVQFPGKNWPTV

>N213_uncharacterized
MKSTRGTWGLLRSSRPTPASAAAETLRVPFPRRTYALSTDGRNITSSSSLLRVGSSLRKTYLRAEDAKELEQRYLKW
ITPAGK**DPWEYNR**HLLPSWKGLMGDANVAFSAIKTPERLLTTFLTHMTYPSELGHNPRINTDPSGIFSHKR**LYHWAD**
ENIFGLPPVAVVRLSYRNTLRQREILVAEVHWWRRILRVIKMEKVYLR**DGQDSVDHILGEVSEDDYELR**KEAAEYVI
PPRWLHEFKKLRWPEPPSVEELRFPDLDAEEPPPKTLLPYNTEPFPHPQASMLGRPFR**ADETEAELESLDTRLDPSD**
ETAADLAVGNIFVKVENEEDATAALPRS

>N214_mitochondrial_carrier_AcMC10_(2-oxoglutarate_transporter)
MATGERKAGKGMQFLFGGLSGMLATCVVQPLDLVKTR**MQLSGEGGGAK**AHKTSFHAMANIAR**TEGPSSLYK**GLSAGL
LRQATYTTAR**LGMYSIINDWLVARNNGNAAIPFYQKLVAGMMAGGFGAVIGTPAEVALIR**MTSDGRLPPEQRRGYKN
VFDALLRICREEGVLAMWRGCTPTVAR**AMILNAAQLGTYTQAK**QVLMKNLPLQDNVYTHFLASLASGFLATAVSIPV
DITKTRIQTMKTINGVPEYSGVMDVLSKIVK**TEGVTALWK**GFTPYFLR**LGPHTVLTFIALEQMNAAYNR**FAM

>N215_TOM_complex_homolog_Tom40
MDKLPSPPAAAPSALPSVPVPMPPLPPLAGAGSPSEPIAPAETHKEAPPSFWRRVLDHGPLPYPGKFDDLSKESKGIL
DSR**ENFDGFNFDVSR**TITANFDMTHAIHFGSQTEPPSYNFMTR**YFSPTGMFLDGKLSPGPMLLNGTVQGR**IAFPLKT
WYRTTPGGRSKPVSKLSLRLTGVVGKPSAKPIPPQFNMELDMKGSDYQAQFKWHNPGMYELSYAQSVHPNVALGLHG
LFDSRMGRTELTAAGRVAWNGRKCIATASMASYGHLTSSYTQVMEDGRKSWSTDMQLIHLEDHGVWEAVYSAGYAYN
LLQSRVRGRVDSNWCCSAILEEKVLDTVTLLICGDMNYAKDVYK**VGFGFSFHL**

>N216_cytochrome_b5_family_protein_form_1
MRRSTSLARSFGGAASSRPFLLSSTRSTALYTRRAYADDAHVPTPTAADVKTEPERLRTFTRADVAKHAYEDDCWVI
INNKVYNVSQWADIHPGGSAIIHAHAGGDATDLWVEVGHTPRARALMERYCIGKVAEPK**RYMGASYGAMDLDESGYA**
LPEGTPKEDILEDASSYRYSTR

>N217_nucleoside-diphosphate_kinase
MRTARWLPCQRPTALLSGHALGRATGGPSTAALVFPSAHNSSHQKRHTSIHRVRQGEQLSFALITPK**SLAKSLTGGI**
IARLLATPELQFVGAR**MLRPSAKLT**DEFFLEMQR**AAHEDGVIDPYEDTFLK**AYPTIFGEEELKESGVANHTMLLLFA
GGAQTR**QVLADVVGANVPNPNDFGK**TIRGTYGDYFKDRTGKINLFQPAVVVPPSDESNRRCLEVLAKYLDSDHALRT
INAEERNQPLGWAKQTGLVMIKPDNLERPSSLPGHIIDLFGTTGLQLIGARVFCMSVRRGMEFYGFLENVFVKKLKP

NLEEAMKQRLASAFEYEVTDQDYAKMADVVINRHARCEVAKIIHYMTGVHPDDAKTDELFRKPGPAKCFALLYRGDN
AIEIIRSKLGVTDPKKARAGTIRSDYGHDLMRNGAHASDSPEGALRERRIVGLMGDEPSEEKAVILEWLHASSAPLS
RQ

>N218_malate_synthase/isocitrate_lyase_fusion_protein_(MalS-ICL)
MLTARNSLLRGGGRSILSSSGLTVTSRALGSTLWRTYARKTERDLSHDINRSLQTDGIEILAPVNEERASVLTPAAL
HFVASLSRQFEPTRQELLGSRERVQQELNAGKLPDFLEETRHVRESEWKVAPVPEAIQDRRVEITGPVDRKMIINAL
NSGASCFMADFEDSNSPTWTNNVDGQVNLRDAVNKVIGYTNEQGKSYQEQTATLFVRPRGWHLPERHMLVDGKPVSG
SLFDFGLYFFHNAKTLARQQEGPFFYLPKLEHYHEARLWNDVFNFSQDRMGLSRGSVKATVLIETILAAFQMDEILY
ELRDHSAGLNCGRWDYIFSFIKKFRERPDFVLPDRSEVTMTQPFMKAYVDRLIQTCHRRGAHAMGGMAAQIPIKNDP
QANEEAMKKVREDKEREVKAGHDGTWVAHPGLVPVAKEIFDAHMKAPNQINTPRRDEAKVAAADLLRVPQGNITEKG
LRHNVSVGLQYLELRGQGCVPIFNLMEDAATAEISRMQVWSWLRHQAPVTWSDGKKKELSRDTLSKVLEEELGKVYK
QIGKKAYDESKFKLASKLFIDMCTSSKPPEFLTSYAYPFIIDPSLTRHMVADGQLMNGQEESNFWLEVEDVRRWWQD
ERWADTVRHYSPEDVVRQRGTLQQDYASNQTAKKAWKLFSHLRETKGYSHTFGALDPVQVISMAPYLSTVYVSGWQC
SSTASTSNDPGPDLADYPMDTVPNKVDHLFRAQVFHDRKQRHARFMMSREERNATPPVDYFRPIIADGDTGHGGNTA
IMKLTKLFIERGAAGVHFEDQKPGTKKCGHLAGKVLVSTREHIDRLAAARLQADIMGTDTLVVSRTDAEEAATLLDS
NVDERDHPYILGTPNGALPALNDLLTDAIAKGATKEDIQSLTEKWMEEAQLSTYHEAVANHLQNEKRDAASYLKEWE
KARKLGHSKARELAKDLGVSLPWCWDKPRTREGYYRLQNGIPVSIDRAIAFRPYADLLWMETSVPHLKDAKEFAEGV
KRVYPNAMLAYNLSPSFNWSAHGMTDSDIENYTKQLASYGFVWQFITVAGFHSDGLIATQLARDYAKRGMLAYVERI
QRTEEREQIPTLTHQKWSGTQLIDAAVQTITGGAASTLSMGKGVTEVQFGKEKSE

>N219_mitochondrial_genome_maintenance_protein_MGM101
MQRTMMRGGLNRGASAVIRTSRSSSGASRLTALSVPLSSDSSAVRPLRLGALQQRGYARRRAFPFVDAQMAMNDEGG
AEEDNETEDDEDEDYADDGETTQYSPFFGNAAAAPAAQPRHTENSFDGISTRAFPRKVADRLVAPVDPNIVEIKPDG
TVYLPEIMYRRILNSAFGPGGWALMPRGPATHGDKFLTREWALFCHGRFVAQASGESEMLTSFTGPATALEGVKSQA
LVRCCKDLGVASELWDMAYVTDWKNKYAVAVWCENQKTGQKKTLYRRLDRPPFPYPWKESQLTTSTAASSPSSSSSS
SPAPKTSTSAATSSSSATSAGAAKAAYSTAAEPFDMEALLPRELKKFAGKRWSEVVSTDEGQKYLDYIANNFEGAAR
GLAQRALDSHHASRK

>N220_aconitase_(aconitate_hydratase)_form_2
MRANRACTTFFGPARLPTMTGANRLFGTSRGVLQRPAAMSRWEPDTQLPYQRIDQNLFTVKKLLQRPLTLAEKIVYG
HLEDPATSADIQRGKTYLKLKPDRVAMQDASAQMALLQFISSGLTSTAVPASTHCDHLIEAETGAAQDLESAKVTNK
EVFEFLSSASQKYGIGFWKPGSGIIHQIVLENYAFPGAMMIGTDSHTPNAGGLIAIGVGGADAVDVMAGMAWELEQR
APNVLGVKLTGKLRGWASPKDVILKLAGKLTVRGGTGSIIEYFGPGVETLSCTGMATICNMGAEVGATTSVFPLTES
MLSYLAATGRKDIADTITAAKEIRGHLRADEGCHYDEVIEINLDELEPYINGPFTPDLATPLSQFADAVKKNQWPEK
ISAGLIGSCTNSSYEDMSRAAAIARQASEKGTKAQSVFTVTPGSEQIRATIERDGQMQALRDIGGLVLANACGPCIG
QWKRSDAKGEKNSILTSFNRNFSARNDGNPNTHNFLASPELVTAMSLAGSLTFNPTTDYLTDAQGNKYKLKSPDAVD
GYDQATATLPAAGFDAGRSQDTYLAPPPADQRASLEVAVSPTSDRLQLLEPFAPWPKGEKDIRDAAVLIKVQGKCTT
DHISAAGPWLKYKGHLENIANNTLIGAVNADTGKVNAVVSQLTGKEGTVPDVAREYQKAGVPWVVVAGKNYGEGSAR
EHAALQPRYLGGQAIICQSFARIHETNLKKQGILPLTFADPADYDKITGGDKITIEGVGEIEEGKPLRAKVTRRAAA
GGGQEESFGVTLQHTLNPGQIAWFKAGSALNLIAAMSSNQQQHA

>N221_dihydrolipoamide_acetyltransferase_(PDH_E2)_form_2
MKAANRAIAGFHIRQTAVAGLRGSTFTVGSGLPRLCTRRGISTKPYLEEPYGYEPVLSPAVAMLVANNGIKNAHTVI
KGSGPKGRILKSDVLAFLKGEQPPLAAFAQQIRPAAAAAAPKAAAPKQAQPLVPPKGGKYEDLPNSNVRKIIASRLT
ESKSTIPHHFLSADCKLDNLLHVRKLLNETEGVKLSVNDFIVRAIALALRDVPEANASWAGESIRRYKSVDVSVAVA
TDKGLLTPIIKNAHQKGLATIAKEIRELASRAREGKLKPEEFQGGTVSVSNLGMFGISEFSAVINPPQGAILAVGEG
RQVVLPSGSSSSGPSHFDNADDIVLDEEETLLAPPKLATVVSVTLSCDNRAIEADVAGRLLHTFQSYVENPELMA

>N222_Band_7_stomatin-like_domain-containing_protein
MRRACAQPSHYGALARCATGAIRSTSASSTLATRLRPLETRSLRLYAVGRYSRQRLPTNLGVLFVPQQEGWVVQRFG
KYKEVLEPGLRFLIPFVDRVAYRHSLKMVTLEIPNQVGITKDNVNIEIDGILYYRIVDPYKASYNIDDPEFAIQQLA
MSTMRVEVGKLDLEKIFEEREIMNRAIVNEINKSVDSWGLHCDRYEIRDIKPPVKAMRAMELQMIAERRRRQKVIRS
EAERTAVVNRGEGQRTATILAAEAKKLEKQLYAEGEANAIRARAEATAEGLERVAKALHQSKASDAVSLVIAEQYVK
AFGELAQKGNTLLLPTNAGDVSSMVAQALTIYQNISAAQQKRSGSSTSTNAAGSETGAQTEDNTPPSSDSSSFDLPF
TPKQ

>N223_ATP-dependent_protease_HslVU,_peptidase_subunit
MKSFARRGAITTAGLGARSSIATTGNGSRPLLAPMTNGIITSSAAAAASYHSEGGSGRHPGFWGPDNPAYATTILCV
RKGNSVVMVGDGQVTLGSTVVKPNARKVRQIRPGIVAGFAGATADAFTLFERLEEKIEEHQGQLLRSCVDLAKQWRT
DKYLRRLEALMVVADKNISLTLTGTGDVIEPNDGIIAIGSGGTYALACARGLIDLPDIDAETIALKSMKVAADLCIY
TNHNFVVERISIDADEAKEKGGSNILSAPDQHKEEP

>N224_Complex_I_(NADH_dehydrogenase)_B12_subunit_(NB2M/NDUFB3)
MASNPKVSGPFGGPIESWRTHPMLRITHPRDVLPGFGTALGLFAIVCVGEWMWKSAGAPKLRATGKSAWKDASAAHD
DEKVLKSHSH

>N225_4-aminobutyrate_transaminase
MRRISQQVAGASTVATGQRTASLALRLTAAQHVRLLSSPPSTPMPAFPGEATEPTIKTEVPGPASKAARAAMEQFQD
VRTGHFFADYGKSLGNYVVDADGNVLLDVFSQIASLAVGYNNPVLLKAATSPEWGRFLVNRPALGIMPPADWGNTLH
DTFMSVAPKGLHQVFTAMCGSCANECAYKAVFMNYMHKKRGGRAFNEEELNSSMQNLPPGSPELSILSFQGGFHGRL
FGSLTTTCSKPIHKVDIPAFDWPKAPFPKIKYPLDKYEAENRKEEDRCLEEVRRVIKTHKVPVAGLIVEPIQAEGGD
NWASPYFFQGLRNITKENDVAFIVDEVQTGVCATGKFWAHEHWNLSSPPDIVTFSKKMQAAGYFHNIQYRPSEGYRN
FNTWMGDPVRVLLMKSILGEIRDQHLLENVQITGKYLKEGLLELQDKHAALLSNVRGLGTFLAFDLPTAQSRDQLIH
TLRQKGVESGGSGTASVRLRPQLVFGPRHAHQFLSILDDALKVHPKQ

>N226_acyl-CoA_dehydrogenase_family_member
MQTTVTKRVARIEAHLTPKIVRGLEDAAVEIARCAAALDLPDVSNGPAVMASERSQASFNVRELTHLLDGGERGTQR
KHAAYELVRNEPVFIDPGYYDRSRDEARYRVMQKLKRFAELVQKDPEQNYLLHNIIGIYDPAFYTRYGVHAYLFGGA
IAGQGTDEMVAKYMDDVDNMRIVGVFGMTEMGHGSAIRDFETTATYNKAKDVIVINTPTITATKWWIGGAAHIATHT
VVFGRLLVDGKDYGVHSYVVQVRDINGNLMPGVVIGDCGKKMGRDGIDNGWMQFNNVEVPRTNMLMKWAKLSPEGVY
TKPPKAQLAYGALLKGRVGLIMNSAHNLEKALIIAIRYSVIRRQFASTSKGLETQILDYQTHQIRLLEPLAAAFAWH
FVALRVDKDIRHLSKSLAQGELGNIADIHAALAGVKASCTWYVAEALEQVRQCLGGHGYSSYSGLPSLIADYAVNQT
WEGDNTVMSLQTAQYLIKSLSQVMRGKTLTGSVQYLERTVAILGQAQWRATTEQDLSDASVLAEALERAAVKSVTRV
AERLQREMQGGKSKAEAWDCCLIDLVQAASHHSYVYVLDAFVQSVEKARNKCKDSNVSAILSKLLELFVLNRINKVS
QIFLMDGFMNEKHIDLIEKKIRGLLLEIRKQAVPLTDAFDLPDFLVNSPLGKSDGDIYNAYMQTVKSAPGAMSKAPY
WDELVKPCLRKDLA

>N227_aminopeptidase_N
MLRRRCSTSAQRCSAPLPQFRPVAWQASATLRPRQGFSAPLATTSVSSSAVPRAPLSQQPHYVRGHATTATATATAT
ATATATATATAPAEQQSAELGLTWLADYRPPLYTVDDVHLTFGIEDAHTTVSSILHCRHNPKAGEMAPIVLDGGPPS
DMKLLSVTLDRVPLQAGSDYKVDEASGRLHISKRPAQPAFTLEIATAIEPKKNTALEGFRRITYFFDRPDVLAKYTT
TIVADKVKYPVLLSNGNLVAEGQTEGGKHWAKWEDPYPKPAYLFALVAGQLHYLEETYTTAASKRKVTLRIYTEEEN
VYKVGHAMASLRRAMKWDEDKYGLEYDLANMNIVAVNDFNMGAMENKGLNIFNSKYLVADSRTATDDDFMNVERVIG
HEYFHNYTGNRVTLRDWFQLSLKEGLTVFRENQFMADHHSPAVQRINEVTTLRNSQFREDSGPMAHSVRPASYIDIS
NFYTTTIYEKGAEVVGMLHTLLGDDTFTRGVQTYLRENDGKAATVEDFVRAMETVSGRTLSQFYRWYDQAGTPEVKV
AKESFDERARQYKLTLAQSPASTPGQPAESKRPFLIPVTVGLLGRDGQPIHSQLSDSDPELASHTLELSDVEQSFVF
NNVASKPVLSVLRHFSAPVKLVHQQTKEDRLLLLRHDTDAFNRWESCQHLALDAALALVEQQATSPDVDPSQVDPQF
VEALGSVLKSVLDSPGLNDNAFIARLLSLPSESYIGQQMAVLDVVRVHKARKALKAVIGKEHRKHLERVYDKFHELV
PIDFSDEPGRGKREVKNMALDYLMHGDLHEGRTDATSRCTQQFGDARNMTDKLAALTLLAHMPQTQREAVKALDKSL
QE

>N228_Complex_II_subunit_Sdh4_(SdhD)
MRRATALFSARAAPSAAGASRGAARRLYATSTESSVLDTVLPATGAGKHRLYHYTSIGLVTLIPIALVAPSSVVLPV
DLALGFLLPIHAHIGMAHIVEDYVPKAGRTAAGWGLMLATGIAVAGLLKLNVTGSGLTSSVKTLWRKEPLTTTQKES
STA

>N229_mitochondrial_carrier_AcMC11_(solute_carrier_25_family_protein)
MDNPPVRRNQTGASARNNHGKRLFEMMLPLQPFTGLLSAVTVRFQAHHDRLDNDRAFPLGVWREVWRGNSSPLKRPV
LSRPTALGLMYSPGSLYTILYQFVEHKLGQVLASAVCRRYLEWATLDRADFKHTKEAFEEGDVMSRPGLYAGYLAVK
CAVFAAVHVVSHPFSILRTVVLMRGNVPLLEDGVWANLHYASPWAKTGLYMSSLGAHVVAGTAEVCLTDVALRTLRH
AYRGFLTRQQAASGATRRRGEQLPGTHVDRLRAKLNYATVVSALQVVASFAVHTLLFPLLTVRMRLEAQGGVDDEPV
TALRHLGLVECVRSIWANEGGAGFYRGFGAHVLTFAGNALWIGIIYGLTEAYINLDVDEDD

>N230_mitochondrial_translation_initiation_factor_3_(IF3)
MKTTTRRLSLVTPRLSHGVGLGSAQPFRSYSRPASYCGHERACSSLVAQFNLYRSHQPLVTSSFTAGQRRAYAGGYR
KTRVRALLVDDAITSDVVQLVSLEGRNLGEVALADAKLLAKQKGLRLACVVPLANPPVCRLQRIPVVPEVDELDDRR
PDPEDEIDDFDEDGMPIHRPSSASSSSSSYNEAAGGGVAKDVPDPNGNIKRRPKGEKELRFSDTIAEHDVQNKVNQL
RRFLDKGLRVRVSVYFKSVAQFDPDLARALLDNIVTRADDLGRVEGDINIANRFASLLLVPTSPDAATKDK

>N231_putative_Complex_V_(ATP_synthase)_subunit_f_(Atp17)
MSRSLITRSLPLRSSSHGALGGARPVFSEVPLKEVPSYVRLHVLGNTRRLTKEFVQWYWRTYFHAGKADPIIHGILL
VSGVGYLLHNHWHGSHP

>N232_acetoacetate_decarboxylase
MLRRSHSAARSVLSGAPCVLATSGTRCLASSTLNGGLTREQILALPSMPAISPSYPMGPYRFVNREYFIVTYETDMD
SLRRVIPEPLEPISNQVLYEWIAMPDSSGFGSYQESGTVVPCLYEGKPVNYTVQMFLNDEPPIACGREIWGFPKKYA
EAELRVEKDTLTGILTYGGRRAAMGTMAYKYNRLDKTTATNSLSKLNCNLKIIPGYDFKPQIAQLVAYNLQDIEVME
AWEGPARLHLIPHVNAPAADLPVRKIVGGKHIRANLTLPHGFVLHDYISERKKSEANFYMNGNPLAAAAEKAKATEK
EKAKVAPQDDKAGLTREKVLNLPSMPAICPSYPAAPSQMSNREYMIISYKTDPEAVRRWVPELLQPDDNVHLSWVKT
ESSGYGVYQKMTASVGCKYNGEDCTFPLMAIVNCSSAITAGREVHGQPQKFGFPSLTVDKDTLYGETKYGQQEVATG
SMVYKHHRLDLSQAYKFFEKPEINLKVIPSVTGEAEIAQLISLLPKDVKIKDAWRGPARLNIIPHVNAPLADLPVVE
GTCEGHYIVVEDMVLPEGTLIHDYTLDAGKEDHQQQSEPAEASAAAPQPGTGDASDSASQEERFRRRMERFLQMPTI
VQ

>N233_kynurenine-oxoglutarate_transaminase
MRKCFVARSCLNSPVQGGLLKGGSLEAVSVLAPRLFAPLSSWASSSRQCRSYAVTVPPSEKFARAKRIETFGETVWS
EFTPLAQKYQAVQLGQGFPDFPAPDFVLAAAQTAIHNNLNQYTRMQGHPRLVKALANTYSPLFGRELDPMNDILVTV
GATEGIFAVISALVNPGEEVIMLEPFYDAYPTDTILNEGVPVYVPLRPPKVPKGTITSANDWKLDFDELESKITPKS
KILIFNNPTNIPGKVWTREEMEEVARLAKKHNLIVLSDEVYEWMTYDDATHIRMASLPGMWERTITLGSAGKSFSVT
GWKVGWAIAPPHFTTALGTIHQFDCFTHGTPLQEAIAVAFEQAEEKNYFPDLKQMYWRKRDKLVATLRDCGLAPVVP
KGSYFVMADTSSIPSSVFMGKGKAEPGIGGDGPKEETRDYQFCRWLTRELGVGAIPPSAFFSKENAHIAENFVRFTF
CKRDEVLDAAATKLHKLRDLSAQ

>N234_long_chain_fatty_acyl_CoA_synthetase
MRAIRGAVAYFYWCFRQFLSPEARDRRSAATSSATAQTRTGPVLKWPQKRKMESLHDVWDEYGTAITATGLAVVGAA
AAYHLLGSAKPAPTGPQSVMMPPEKKGESHVYRSIHSPDTLVETFVPETTTLYENFKRGFTLNPEGNCLGWRQGDGP
YQWLSYRQVQDRFLALGAGLLELGFKPKDTVGIYSRNRPEWVITEQAANAFSMVVVPLYDTLGEEAVEHILRETSLK
LVFCTNEKVQQLIRVLDKSDITHIVTFDSFDDEEAKSVLQERNISLHTIDELIELGKKNPAKPIPPSRDDLCTICYT
SGTTGTPKGAMLSHGNFIANVAGVFVLKPDLVTSSDVVISYLPLAHVFERILQAAVFLQGASIGFYRGTVPELFDDI
ATLRPTVFPSVPRLFNRLYDKVMAQRATLTGVKKMLFERAWAAKVQLLKEGKVSSPLWDRLVFSKIAAKLGARVRLI
ISGSAPISADVKDFLRICFSAELLEGYGQTECCAAACATMPGDTTSGHVGAPLPNSELKLVDVPDMKYFATDKPNPR
GEICFRGPAVFSGYYQNPEKTAEVLEDDGWLHSGDIGEMQPNGTLKIIDRKKDIFKLSQGEYIAPDKLESAYVKSPF
VAQIFIYGSSLKASLVAVVVPDPEILLPWAKEKAIDGDLAELCRKDQVKKEIMASLKKAGEAAHLKGFERLADIHLE
PEAFSSDNGLVTPTFKLKRPQLHEHYKEQIDAMLAKLD

>N235_rotenone-insensitive_NAD(P)H_dehydrogenase
MLRSSNKVASTRGMQRACFASRTTISHGSKQLQVPSGGRLYSSTTSTAGSASRQSAFRWPVVAAITAVGVGGGLYLL
QGHVFAAESQPKPKLVILGSGWGALSVVRELDTSKYDVTIVSPRNYFLFTPLLPSVTVGTLEPKAIIEPIRKYCRRS
HADVDYFEAVATDVDPTNKTVSCHVSTPGLDDSARDFTLPYDKLVVAVGAINNTFGTPGVEENCLFLKEIDDAMAIR
NKMLDCLELASLPTTSEEEKKRLLHFVVVGGGPTGVEAAAELRDFVQSNVHKWFPKLEPHVSITLVELMDHILSTYD
AKISTYTTSHFKNTNIDIRTKSRVVAVKPGDVIIQRTDTKETQHIPYGLCIWSTGIGTSPLINKIREKLPQDIQTNR
RALLTDQFLRVKGADGIYALGDCATIAQEAMLGKLNDLFKEADLNKDNHLQIEEFRSLIDKYKKTYPQIDVYGKKAE
EIFQEADVDKTGALSLEQFENLVKKIDSKIKQLPATAQVASQEGQYLGKLLNRVANKSVELDTGFHYKHLGSFCFIG
SEHAVAEFAEGLVLEGFGAWWLWRSVYLSKQYSLRNKLYVGVNWLKTWIFGRDITRA

>N236_pyrroline-5-carboxylate_synthetase
MSARREFQSKKRILIKAGTGVITDESGGVSLGRFGHLVEQVAELKKRGKEVIIVSSGAVAMGKQKLHESAAPPSHNP
RACAAAGQSGLMALYETLFRQKDIWCSQILLTDEDFLNEERRSNFRETVDELIRLGAVPILNENDVISSRKTPYTDS
EKRIFWDNDSLAALVAGETNADLVILLSDVEGLYKEPPSASGKKGELIDTYQHDAKFTIGAGSRTGRGGMQAKIEAA
RYALSRGAFAVVIASGYTLNVITNIVAGARIGTLFVEHPERELATARQMASCSRKAAQALLALGPQRRQALLGAIAT

NLTAAKAQILEANQRDIANARENNLRPALAARLVLDDKKLHTLASGVR**QIAAGEDPIGK**VLKRRELADGLVLEEVRV
PIGVLLVIFEARPDVLPQVAALAIRSGNGLILKGGKEALHTNTVLHGIITRTVEQFGVDPQLVGLVQTYEQIDELLQ
LKEIDLVIPR**GSAELVSHIQHNTR**IPVLGHSEGLCHVYVDQAADLDKATRIAVDSKTDYPAACNAAETLLLHRDLLA
DRRAHAVLDALARANVKLYAAPHAATHFPDLPRAQSLRTEYSDLGMTVEVVDSLEAAIAHVNEYGSGHTDAIITEDK
EAAQK**FSQFVNSACVFHNASTR**FSDGYR**FGLGAEVGISTSR**IHAR**GPVGIEGLLSSK**WVLVSQTGGSVASDFSAGKR
TFTHRDIYPPFAPQPASVFADFQPKL

>N237_Complex_I_(NADH_dehydrogenase)_subunit_8_(Nad8)
MYAGRRAVSINRTSPLRGAFILPRASASSTLVATERSVVLATRGVMAGGSYQDEHKRTKLK**GAHAEPETLYEDLPTA
HLHK**NLTWSGLIEGSAHTFALSEMMRGFMLTLAYMFKPK**VTLNYPFEK**GPISPRFRGEHALR**RYPSGEER**CIACK**LC
EAICPAQAITIEAEPR**ADGSRRTTRYDIDMTKCIYCGFCQEACPVDAIVEGPNFEFSTETHEELLYNKEK**LLANGDQ
WEPELAANLR**ADFLYR

>N238_rotenone-insensitive_NADH_dehydrogenase_form_1
MRSRVTTSTARTSTSTLLAVAYRPAAHTATALPLSGPRFVRALATTTTVDGGKQRKK**LVVLGNGWAGYR**LILDVDIS
KYELSVISPRNYFLFTPLLTSTTVGTLEFRGVIEPVR**TARPGLNYIQAGATSVDTTNKVVTFESVYEERETDEEVPV
HPAASIKYDELVIAVGAAPNTFGVPGVEK**YCYFLKSVADARNIRQR**IIECFERASSPTTTEAER**SRLLHFVIVGGGP
TSVEFSAELHDFLRKDVHKIYPDLEK**QVQITLIEAGKTLLSTFDQRLSDYTMR**TFRKRNIDVRTSVSVKQVKRHEMV
LSDGAVIPFGLGVWSTGLSTRKIPFIKGLPFPKDRSGRLLVDEYLHVKAPDVEGVYAVGDCAAFETNPLPATAQGAE
QEGK**YLAQALNAK**ARGEEPKKFQYHHKGMLAYVGGYR**ALIDSPLIK**RSGFLTWIMWNAAYITKLVSIKNKMMIPMYW
FKSFVFGRDIYPNY

>N239_thioredoxin_(TRX)_family_protein_(possible_protein_disulfide_isomerase)
**MRAALCRSSMRSTARRGATSVATELAGAHRPALPLFAGTVSLPILQSSSQRLGRGVVLARPYASGAVKQTPLAAKSV
WLPLGSVLVASTLGGMALSRRRVLAQEQSAD**SNADNAEKKPQDETNEGPQSNKEDFVHYLLERPILLLLLDREDVDE
K**MDANLEEILADEELKAMHLLDYQFFSEDR**KKFPPNAIGLVYNYNTETK**QVETYVYPADR**ELTAENIKQFLADIKEH
KLDDLRLHPSEPRPAEDKHPQVKDLKVVTKESFQDLVLNSDKDVLVYVHLPSQSVPTDLQVLANAYAGEDDIVITEC
SSFLNELDPTYFGDTPIEGIKLFRKGHKNEPVTYHGK**GDLLDVVAFIEQQR**GTRGDVAYRHLRKADTTRLLRDLEK**T
LGDYYMHTLAYK**EFVPTSDKAKDLFNKLFDMYDQLNTNEDPFKRSVAALKQQLKDELKSLERAGMRNIKIVDKDKYK
EELEEARNKGKVVVFFWRKGCWPCKKLNPMIGQLSQDFPEVTFLK**VDADAEGLNATPAFWVYEAKKADDDTNANEEV
KPSQLSGMKLITQFHPLAR**QRGLPGYAKWLPPAERSKLEEPVTEETQSKHEEKEQKNDDNDGETKKDHEEVR**APTDE
EVTTK**NESEQHEEDAKPSTLL

>N240_5'_nucleotidase_domain-containing_protein
MRRALAGINRPQCIRSITTSRATSAFGGRRFATTTTSVRARTLTSSPSTSSGIFQGAHRCQSVQAPGHQLRTYAVR**S
SEFASSNAGDNGTPLPNGR**LK**TLCDELR**GIRAAAKASKAQGGEGLHPDIVRLLVDFEEMTEMHKRYVK**ELPLANPQD
IFTNGEIR**LDELDILGFDYDYTLASYTDKVSYFIYDKALQYLLR**NHGYPQELK**HK**TFDPTFAIR**GLHYDTKKGYMMK
LDYLNLIQADTVHFGR**TKLTEDRLYSAYPSLFISRQYMAENMRLLIDIFGQPEACLIADIIQYLADRK**TEFDPAYVY
EDVSK**AIQHVHASRLLHTEIMNHLDVYLNANPALGETLWRVKEAGRQLFLATNSPFDFVNAGMEFLLQGHLPNGVKH
WTEMFDLVMTSCRKPSFFLHNRPFRVYDPATGRVTWDRPNPKNYSGQVLVEGSLNQLIALTGWKGDRVLYFGDHIFH
DLKEPSSVAGWKTGVIIR**ELEKEVEIQNSSVYRSVLAELLEVER**LMKKCMFISGEWSQEVVFALRQHRIRLRKDLK**N
CMNPTFGSAFR**THKHASHFAYLLQRYCRVYTSK**LENFLNYPTHYVFYPER**TFLPHEAQIPPASLWKTICPPRGDHPA
GDE

>N241_pentatricopeptide_repeat_(PPR)_protein_AcPPR1
MSRFSAFGRRAPVQLLPSAMRINGNSFWLAGRPSICGNGASCGLQLLCSAASVSRFSSTHSLAQNDVLLESQQLAKQ
GNFSKASELASAFVKEHEALPLESATYTALIDVFARAKRLDKAHSLLRDMEAKGVSPSLAACIGVVR**AANRPDSVGV
ADAVYDK**LVDEGATLDAEFYDAYISSLVGARKFRRAHQIYFHMSKRQK**LPATATTYK**NLITIYGESK**RWDLVQDVLR
KMASR**NVLTEAVHYSAAVLAVAKAEGIDEAFAWVER**LGAEREKYPAPNEKVYNSLIEACCLDADTLDRSWRALRNMK
KAGVRPSTRTYNAILAGHSKFGRSGEISTVLEEMTKDEVPKDSYTYSLLVRAYASAADMRK**AFDLYSDYK**AAGFPPR
HDLCNHLLNGLRQQVAAHTSHGEQGADSACQEGVSEALAHADALFDEMVQADMQINAFSFFNLIQANHLARNNGKAL
ELYDEMKR**RGVQLNAR**LVHLMGAVIATETDRLVLNGQF

>N242_carnitine_O-acyltransferase
MEDKYRREVVPQGSRNVQPYPWLEVTTLPR**LPIPTIEETARRYDEYLQPLLAEASPADLAR**TRRFVADFVK**HDAAGL
QADLHNLAR**VSPTSWLEGWWDTGYLEFR**VPSFINVNPFFVFK**ADPANPAQTAR**AAQIVGSAVR**FYKKVATKGGLTPD
LERKTPLCMTQYGRVFATARIPLPGR**DAVYSWTGVR**HIVVLRKRQFFTLDVLTSAGEAVAESHIHAQLDAVVREADR

PGTHQSFPIGALTAEDRDAWSAARAELVRAHPINVASLEVVDRALFVLVLEDEAPADLDATARLFLHGDVRNRWFDK
LQFLVCANGVAGVNMEHSPIDGHTILRLLTEIHNEVLARNGTILTEGPTAPAPRRLEWIVPASSPVADALEAAKVHA
GELIAKTDTSVLIFKDFGQKRIVERKVSPDGFVQMAYQLAYYKLYKKTASTYESVQMKQYYHGRTECLRSVTNESVH
FTKTFTCPKADNAKKEAALRQAIEAHGRRAKECKEGRGVDRHWLGLKSIARHKEQWYPGFVMPEMFSDPSYSKLFGS
VLSTSNCGTRALDLFGFGPVMDDGFGLGYMIHPEAIHICVSNFHGQAAAFAAALRESLVQMLAILSTSTPAQARL

>N243_branched-chain_amino_acid_aminotransferase_form_2
MRRRGIAHFTSAGIASRTTQIGARSFEGIRRGLYSTSAQLAELDHNKLVIDRTKAPKPKIPNEQLVFGTQFSDHMLT
VEWDKEKGWDKPHIKPYQNLSLDPASSVFHYALECYEGMKAYKEANGKVRLFRPMENMKRFNRSCSRLVLPTIKEEE
LLECIKELVRIDKDWVPQGKGYSLYLRPCMIATQNFLGVAPTGKALCFVILSPVGPYYRSGWKPVRLIADTKFVRAW
PGGTGNSKVGGNYGPTVLSQKEAEKMGYNQILWLYGPDHQVTEVGTMNMFVAFQHKNGEKELVTAPATSEGVVLSGI
TRDSIIQLVKQLPGWRVTERPYTMKEIVDAHDEGRLIEAFGCGTAAVVSPIQAIGYNGKEISFPLGNSGQAGNLTQH
LADTLAAIQYGEVPHDWSIVID

>N244_uncharacterized
MLLNRTSNAAKNRNNFSKMMISMGQRYPTLRGARHLHHQEASFDHHLAISASRSSSSTAAAAPHLVHSTRLRTLATT
VFIRGIATRSGKDSMAQMKAEADPLPLGEFKKEVTKLIDQEVKESSSALDPAAEYLAELNYKLFVSDGVATLKRTQG
KQVVELSFAVEEEDEEGENEEGEEKEEEESEEEDEEETAEGFQAQDINPLMGVQDLYIPTEVKITIVDKMDKEVSSM
SLACSAFESRFFIDTLYSADGKNSVHFEQLSDGLQEKIYDYLESLKLDHRLGTFIFEYTRNYHAHKSAQVLSDLKQF
VSHLRDE

>N245_m-AAA+_ATPase_(Yta12_homolog)
MLNVRRDMMRMGTRAAHGSGYAMPRTLSLLGRTSYSPSALSRLPRHPLLSSTSTQTTLYPPRVLGVRRGLTTPAGGP
PPGGNLPYGWERWRNVAPNGQQTPKQSASGTGGSGAGSRQQSGGGGGGGGPERNEGGGGGGSWGPWANPREKGDKSDK
SGGGGGGGGGGGAKPPLEPWTNSLALAAVGVIALPLLLAGLGAPTPTGSEISFQQLTNELLPEDKIAKLEVVNGNRV
RVYLKDDATRDPRTGELQHTKAAYTITIGSVETFEKQLEEVQRLLEIDPHQFIPVTYTTLPDWGGMLANWLPPLLLV
GFLVWMTRSSLKAAGGPLKGMFDAASNPAKLYNKETGVKLSFSDVAGLEEAKEEIMEFVSFLKFPEQYRALGAKIPK
GALLVGPPGTGKTLLAKATAGEASVPFYSVSGSDFIEMYVGVGPARVRGLFEEARKNAPCIVFIDEIIDAVGRARGK
GKFKGGGNDERENTLNQLLVEMDGFNSQAGIVVLAGTNRPDILDRALLRPGRFDRQIALDKPDVKSREAIFLVHLSK
VSTEKPAPEIAPRLAQLTPGFSGADIANVCNEAALIAARHNKLAVDEQDFEAAIDRVIGGLEKKNKVLNPEEKRTVA
YHEAGHAVAAWFLRHCDPLLKVSIVPRGQAALGYAQYLPKDTYLVTQEELFDRMCMALGGRIAEQLEFQKMSTGASD
DLDKVTRMAYSQVIGYGMNERVGPIAFNPNEESSGRPYSENLAEIVDEEVREMVKKAYATTRALLQDKYEGLKQVAE
LLLQKEKIRGEDLEAVLGPRPFKDTALEDIRHLLPAGYDEMEKAREKLFHDERERIQQREQELREAGGSSTPPSATQ
PQP

>N246_amine_oxidase_family_protein
MQHPVVIVGAGAAGLYAAHVLQKEHNIPVELVEAADYVGGRVKQDWKFSGNGRPIEIGGELVHGENNMLGKMVRELG
LDTADVFSVFQVNTSRPEYEYFYLGRERKLFGLHSDDADLKHLYKLIGELEENPPKGDVSFMQWLVDHGLPYRMLGV
ADALYAKTWGTTVDKLSAVQFAVEQAAANEEEGEGNLQVKQSYAPVIQRLQKDLKIHLNWPVKKIDYTNPDAIKVTN
ARGETVLASQVIITVSLKVLQEGDIQFVPSLPQDKLRGIAGLRMDAGMKIFAKFNKIFWQEKHHLVICADTFVPQFW
TYGKDVPIVTGFVTGDQAAAASALPPRQAADSFIKQLDAVYGTESNPRPATDAFVDFMIQDWTKQPYVRGSYSAPSV
GGNGCREALAKPIGRSIFFGGEATSLSAAATIHGAMATGQRAAEDLLKARQQKVAKL

>N247_pentatricopetide_repeat_(PPR)_protein_AcPPR2
MQRSMSLGSRMWGSQCSAASSPVAFAMRNHLQRTVVRSPAAAPWGRGSSCLELASSSSSSSSSSGLRSSGSHRRGYA
TEAARDLVRREVELLEDAYRAGVPVGRKRVVQAVQLCARTRDTELVKKMADLGVRLLPRDRVVRNSIVGAHANVSGG
TRVGEAMEAMEAVGLAGVKPNRVTWNTLVASYAKAGQRGQALTALDRMQEAGVLPDRVTFNTLIKAHVAVGDIEDAL
ATFELMKARRIAPNERTYATLIDGHLKQGHNDRATQLLQEMEGRRIVPSLPTLTSFIYANCKANALDAAQRILERLG
EEGQQPNRVTYTAIIEGMCRNGLGQQALLVFNEMVDRHGIAPDVLTYTSLLKGTERQPERAWTLYQDMLTRGVIPDA
VFYRDLIRTQRQSADDATLNQLVDKAIEVGARMAPTMNAAGCQRLLRVLSERPASALHAWRAMLQAKLPLDREVFEV
ASQIIGQTGDSQARAELQATARDYFKEE

>N248_mitochondrial_ribosomal_protein_S17
MKRVAVMQPMRFAGVAAARTNAWGLAMPRLSTVAQRRWTSSTPSTEDRAAAVESAPKEGEGEEKMTPNAYKQEAAFR
KDPIQPYIDGRTRDPLYNPVVDDWVDYNNPRWKALKHTFNRPGPFFIGKCVSTKTAKTSMIEVPYWVRSMKYGKHMA
VRRTTRFMAHDEDQICEPGDVVEIRQSKKWSKRKNTVVTRILKKDPGNAFIAEHPEFAIVRSRADLRKRIEQMREDE
LASAGLDVGQGKRKTDSSEGSESGQQHQQQ

>N249_Complex_I_(NADH_dehydrogenase)_subunit_B22_(NI2M/NDUFB9)
MNKGGLSSVANAAVGEAHRRHVCHLYKRALKLQLDWLVKRETWYPEANKTRALFRQHMNETDPRTISRLVKDTENLL
YTYRHPDPYVSPMSEGGTKWQRNVPVPPEVAENGWAEFDYEEFEQPPPKADF

>N250_uncharacterized
MYFPAPDDVPPSPFRTPGFTTHFPRLTSLARNLLSDEGYDLPFHFRLGHANVSSSPAYPLSKTELLMRKRGKNSARL
VFSHTTPTNSRLVFGMNGVGQLEGELFSSFAAGAAEEEEATAAGVDEPASHVEDGRGVRWGYDAGFEAVNNCPAPSY
IDFFWEHSYHISTNNYLRGGFVVGGMLPGSMLPFAFDAGGVDLGATLQAVRGPWALGMDCQVRTMWLDLTGGRCFLN
SVVAYQKPTFALTMNMHGFGERFIASAVANPVGLYRALCKTNTAKDEDLYNCTWLAGVEADTAQRNGVFSTRCLSFA
LTRRNTSPYPFSAPHTTKTTEAEVFKVDEPLLRDGENKIKFDILNLGVGNNAYRLSVHSSSLVRLYRNTHVKLSSSL
QADVLPFDPNTARIGLSLVFVV

>N251_mitochondrial_ribosomal_protein_L15
MRRFSTPFSCSGGVMNLRSTFNLAAASPLRPSSSAWAAALASCNSTSMARAYATRARKGVRSSSPTSYLGGGLPYLT
RKLELEAQRELEPFDPFSIALNKIADNPGAHKKARKVGRGTGSSKGKQCGRGTKGQKARGRGKVSPGFEGGQTPLYK
RVRKHGFTNAMFRSEFVGINLGQLQQWIDAGRLSPEGKITMATLQQSGLSSKLTKSYEKGIKLLAGGSEFFAAKLDL
EVSKVSQAAREAIEKNGGSVQEVYYHPRQLRMALRHPENPLPPPQEYRTRP

>N252_uncharacterized
MEKRNLYSLCEAHFEGFKERCLTYDGDPALKPRECQGTYDFLSECVGVATISCCEKEAADFRTACDAVEAGADGGRP
WENTQPCYENTRRLVRCMTGTYGIKERIDLQNAEDRDLDRRARELEKEAARVEALQRNHNPRS

>N253_histidine_kinase
MRRSSGRLLSGAQTRLGGAVVSAPRQATTAAHVGWRRLASGPAQPLVPPFTEQTARAKVQAAENLWNTKDPSKVALA
YTEDSVWRNRDRFLQGRAAIRAFLEEKWAKEHDYRLRKELFCFAGDRIAVEFNYEYRDDNGRWWRAYGLEHWTFDER
GLMHTRQASINDVPIEEKDRIVQ

>N254_alanine_aminotransferase
MRRAATTPQLPRTAALRMSLPGRAASPSASLLLGTSRRPLSTAPSASAAPSGPIRGRLTTASMNQAVVGAAYAVRGE
LVMKADQYQRVLADPAQRDTLPFKEIIYCNIGNPQQLQQKPITFFRQVLSCMEYPALLDHPAAAQIYPQDVLQRARH
LLANFSGGTGAYSHSKGERIVREHVAGFLQKRDGYAAEPEDIYLSDGASGSVSKALNILIHSRRDGVMIPIPQYPLY
SATIPLLGGTQLNYYLDEENSWGLQVSELESLVEDAHKKNVNPRALVIINPGNPTGQCLAESNMQEVIDFCRRRGIV
LLADEVYQTNAYTKPWLSFKKVLRDMGPKYKDVELISFHSVSKGVIGECGHRGGFMELVGIDEEVKQQFYKLASISL
CPNLPGQVVVDLMVRPPVAGEPSYDLYHQETTGIFESLKRRALRLTEAFNKLEGVTCNEAEGAMYLFPRVRLPAKAV
HEAVKQKKTPDSFYCLALLDQTGICVVPGSGFGQKDGTYHFRTTFLPPEDKIDAVAKSIAKFHHDFMQKYRD

>N255_mitochondrial_ribosomal_protein_S15
MKSGRTMKGARLVLLPQLRQPLSLVRGYSATSASDGGSKATNRFAAQFNALGRTTPSSDDKSSSKPEKSVDPATEKQ
AMENIFSSISLARSTPASSAIKTSREPRFIPKTLEVTKRRLWLTDLKHFKLYPKTIKEWVIDCKTPCGVWWKDGTWR
ASVSLENEEKDETSAETAAQAREREILLGAKVLPADLRDRYRFGVMEEDIAALNLQGPQANKLKEILSFKYAGRAEI
NQFRIAESLKKWSRKPNDTGSSEVQIAVLTEKIRYMTDHLKGHHKDQRTKRALGITIDKRRALLKHLKKQNVSTYYH
LLRDLNLRDMVSI

>N256_mitochondrial_carrier_AcMC29_(carnitine-acylcarnitine_carrier_protein)
MSQSQGVIKDTIAGGFGGACLVLVGHPLDTIKVRMQTMVVQPGVPPPYTSTWDCAMKTMKAEGPLALYKGMVAPLTG
VTPMYSLCFLGYSFGQKIFCKEDTYKNLDLVRIGLAGATSGIFTTPILAPLERVKCLLQIQGKTGQYKGPWDCAVKL
YKEGGIANVNKGYMATMLRDSVASFFYFSTYAILKHAMTPEGQAQPSAWGTLFAGGMAGIFNWLGCIPIDTLKTKLQ
TAPEGKYPNGIRSVFKDVIKNDGWRALYRGIGPILIRAFPANAACFLGVETAMKAMNYVGL

>N257_enoyl-CoA_hydratase/isomerase_family_domain-
containing_protein_(putative_methylglutaconyl-CoA_hydratase)
MRRATLKVVAGRGAVPAGQAVRSCFGRRAFTTAAASTEVKQKYDFINVEDKGEVRWVSLNRPDTHNAFNELVIGEIT
DAFRTIQRDAAQEKFRAVVLTGNGKSFSAGADLNWMKKMASYTQKENELDSHKLFDMFNSIYACPMPVIGRINGNAI
GGGSGLVSACDFAFSVNKAVFGFTEVKLGLIPAVISPFVMMKIGKGNCSRYFLTGERFYATEATRLGLIQGSFETVE
ELDKAVDSVLTEIKANSPAAMRSCKQLINNVYHSLGSPKKGEGLSDVKEQLASEIARIRVSKEGQEGLSAFLEKRKP
SWIVS

>N258_phosphatidylserine_decarboxylase_domain_protein
MWRSGTRLAPSSSRCSLHQGWRPSLCGLPVWATSISATTRAARPLSHRVGGILITRGSLSKPAPSSTPFSFKRHSAN
K**TGNENVEQIPK**EPIRLNTLGKTPEAAAKPLRAAENGGKTKKGTTRRVIKYVLLGSAVGIGVATFAFLNQSEPATPR
QMR**FLTAIPSR**AISALWGK**ANDVELPLWLR**TQLFLLWTWMYDCKLDEMRDPLESYK**NLGEFFTR**HLKEGVRPMGDGM
VSPVDGR**VLIFGEIK**DAQVEQIK**GLTYELESLLGDTK**LHLKVQDKNEAQGRPDKKLYHVVIYLAPGDYHGIHTPVDM
TVTHRR**HFPGHLFPVAPTVVNLIK**GLFALNERVALLGKWEHGFYSLIPVGATNVGSIALTIEEGFRTNLATHKVGR**G**
DGNQNFYERIYAQPIKLAKGDEVAFFKLGSTVVLIFESPEFEWTIQPGQKIKLNETIGRVVSNKKN

>N259_mitochondrial_carrier_AcMC12_(calcium-binding_carrier_protein)
MSATATTNTTATEAATIDNGGVMSKVREVFAKLDANGDGHLTRDELHDGLK**LLKLPATEADVDALLAR**LDIDKDGNV
SLLEFEAFAMAQSKLLRKVFDDLDADK**SGTIDVEEVR**GSLRRLGMKYDDGAVTKLIKRIDVDGNGKIDFNEWQTFLL
LVPSATVDAIFRYWEDAMMAFDSEDGVILPPAHKPKTLMDSVAFLSSGAIAAMTSRTATAPLERIR**TIYQVQSTKPS**
IDAISRQIYAESGVSGFWRGNGANLLKVAPEKAIKFWTYETIKATFGKKDADISPHERFIAGAGAGVFTHTLSFPLE
VIKTR**LAAAPNGTYTGITDVVR**KIVTK**EGPMAFFR**GLTPSLLSTAPHSGIDLTVYEVLKREYTKRNEGKSPGVITLL
GCASASSVAGLLACYPLHVAKTRMIMQSMHGAPQIYSGVWNVFTQTYSK**EGFVGLYR**GLVPSILKSVPSHCITFVTY
EFLKKQFGVEKHSKH

>N260_DDX5_DEAD-box_RNA_helicase
MMQRSLPNVARNGAPARLPGASLRSLLPSSSSSTSSLQIAHLHRRLVSGYSPASSTSSTYRGDDSGSAASGSFFDRI
KNSRFEDLVGSLAKPKWEAKAGKLAHFKK**DFYVEHPDVASMPEAEVAR**ILEEAQIKVVDIKPGATPPPRPIVEFSQA
GLPRAMVDRLSRNGITRPSSIQTQAIPIALSGRDMVGRAQTGSGK**TLAFALPACVHIGAQPPLRSGDGPVGLVLAPT**
RELALQIQAEVAR**YALLPDGSPLR**SACVYGGASKVPQIKDLRRGVHMLIATPGR**LLDLLQMGVTNLERVTYLVMDEA**
DRMLDMGFEQQIRAIVDQIRPDRQTLMWSATWPKEVESLAQDYLNTPTTVTVGSTELSANPDITQIIDYCRPVEKKP
KLLALMDELHKAGHK**TLIFVNTKVSAELLSDELR**AKGMKAAAIHGDKTQVMRENVLYQFKRGHVDFLIATDVAARGL
DVKNIECVVNFDFPGNLEDYVHRIGRTGRAGAKGTAYSFLTNSHDKMIPKLVKILKQAK**QEIDPTLLEMAARASSGQ**
SFHETPSFGQRRAPPGGNTRRYRSSDASSTRDSFRRSDFGRGGERKLKYAINSRGWSADHQ

>N261_uncharacterized
MRRFSSSIVASGRIASSSALVRTAVLGQGRLAATYATKKR**NAETELHSYFEKEVELLDQDEEAKTQDQELQKRLDDW**
AKR**FHFNVNMGATEIVATKKDAALNADVTVK**IDPNIEEADNYGDEEDAEDEEGEEGEDAEEAEKAEGEEGDEEEGDE
EEEEPEADGFGSVHFTVEVKKPEQTMLLYGVVSESAVTVTEVALQAADGTEKSAYDAQR**LDDEGQEKFR**LYLSSLGV
NDSFVPAAYAAAHLHDEHAYHKWVKDVMAFTKQ

>N262_universal_stress_protein_family_member
MATNEPKEEEEEERGVERRRKEEENESSGIIPLTSSHGRPIERPLDRDEEDEDEAERRAAEKHWERTLDRLK**SELVP**
VTHVVAIDGSPNSDRAFSWAVRSLPRHDR**LLLVYGTR**KVPMPGLEVTLLERRSADEQRRKQRRKAR**TLAQHYAHR**CE
DAGRECYFER**LEYWGSGDLAGQICRAADVNGAHTVVAGSR**GLGPMQRWMLGSVSTALLHQCHSTVVIARDAPEPERE
IQPDPSHRL

>N263_pentatricopetide_repeat_(PPR)_protein_AcPPR3
MRRSSELSRTLWQRGPRVLPCATSFSSRATHTPALLFPSSAPRPATGVSLLRRMLATSAQPSAASAK**SIPASTMTDE**
DDDVEDFAKLSQRSLFENR**LQTLEANSNEVAPR**QLATLLRAMVLGKREKLKEFQPRVLALHKRVRGGTKLDGTAVLA
ALSYIGNLEATYAEYERLRAENIKSFELNYGYLIEVSSSQGNLKQAFSVVDLMRRDRDLLVESRPSTFVFNRLIIAC
GRNQSLGRAYRAFELMHEEGLRPTPTTFAAYIDACAR**TGDLQSGLK**VLSQMKRILRLSPEK**YQLDASYYTGLIPACH**
QPQDFDRIVAEMIR**EDIAPAEETLAALIKDCATNGGLSR**ALGMFKELR**LFQEVTQQQQSQK**KDHKQARAELAEERRK
VVHKPSLGSIFF

>N264_amine_oxidase_family_protein
MDAYDCIVVGAGLAGLQAATKLAERGHTVLVLEARDRVGGR**TLNIQVGQDAWDGGAGWIGAQQPLVK**GLCEQLGIAT
YPQYDEGKHILMINGK**VSTYTGNISSLNR**SDLGELEQVVQQWDELMLKVPLDKPYACANALEWDSMNLEVWERQNMK
SEVAINLLNFIIRTVFAVEPSQVSFLFFLFFLRSGFGYNCLSDIRGGAQQER**VVGGTQSISLALAQVLGSK**ILLNAP
VRKIEQWAGGVVVHSDLGVHRSKYVVVAVPPVVAGSIQHSPPLPAMRDQLTQRMPMGCVIKCYALYDRPFWREKGFS
GEVLTTSSPLCLYYDATNYR**GSAALVGFTAGDGAVNWSGR**EAELK**AAIIEQVVSLFGEEGR**RPREVIIKDWMQEQPW
SRGCYVGVMPSGMLSSFGKALREPVGRIHWAGTETAMEWIGYMEGALSSGLRAADEVVARLHTDPVPARL

>N265_N-terminal_homology_to_plant_B12D_(Zea_mays)_protein

MKSMNKKATTSTMSSFVKKFVPPEVYPLLVPVTFACGFGTYIGYRTLVGAPDVHVFGRQPRFESGHHRSDPHFAGIH
SKASRFDPHPELGQAEANFHSSYASSDSNNSY

>N266_short_chain_dehydrogenase/reductase_family_member
MEIDKLFGVKGKVVLVTGGGRGIGFMISQGFVRNGATVYIASRSKKECDKAAEELTAAGPGKCVALSSANISTAEGR
KKVVEELSSLEDHLDILVNNSGCTWGMPIEDFTESAWDKVMDLNVKALFFLTRDLLPLLQKKATAVDPARVINLGSI
DGIRIPTLETYPYSASKAAVHQLTRVLANRLASMNITVNAVAAGPFESKMMAETLRTFGELLKANVPRGRIGEPEDI
AGACIFLGSRAGAFLTGAVIPLEGGILSAARL

>N267_mitochondrial_ribosomal_protein_L3
MMKPSLPLWHPARAGVSAFGASSFVQGPVRAAALVCVRDAERKRIKKKFMRGWRSSVNKDQVEARRTAVDPRTLSDP
STGWDQRKRRTGLVAIKVGMTSEYSEYMEWLPLTVLQVVDCQVVQVKKERHNEYEEEKVGLQVGAVDGKWRRLAKAQ
RGHFFHAGVNPKKVLMEFKISPDAVVPVGTELRAEHFVPGQLLDLTGKTKGKGFQGVMKRWGFSGGPASHGNSASHR
EPGSTGQHSIPSKVWKGKKMPGRMGNKYRTTKNLLLWKIDTKNNLLYVKGPVPGAPGSYIRVRDAKNKLHSLVPPYP
TYMRQPEEVLPEVITANSPEPMWYKKMMARQAAFAEDLSKNTDDNQTAVQVVLAHKEAFPSYDKWKKGLLPPGPNPS
KHHSCLSVGEPMEFPWLADTIADYEDPSTAEEDQLQIHYAES

>N268_CBS-domain-containing_protein
MRRMSRYQYVRDIMAKPVLTTTPDTALNVALGTMLQKRIHRLPVVDSSNPNKVVGIVTERNLRLAADSPFLEESAQE
VLEHLAKHKVGEIMRSSVTTVTEDASIVEAAKMMRVSNVGGVPVLDKQGQLVGIITRTDMIDHLIRVLEPLDEGQRE

>N269_iron-sulfur_cluster_assembly_protein_NifU
MQAALKRAFARTSPRFLPAASLARGRGGSTLWSTTTLTSSARGEGSWRWTAGGARSMFIQTENTPNPDSLKFVPDGN
VVLESGTMDFPDARSSLSSPLAKSLFTVTGVQRVFFGNDFITVTKKPDVEWHEIKAQIFANIMDFYASGESVVSEQQ
DTSNTTILPTDSETVAMIKELLEVRIRPSVQEDGGDIEYKGFDEEAGVVYLKMVGSCSGCPSSSVTLKSGIERMLMH
WIKEVTGVVAVESDDELDRLTKQEFAKLEKKLGEEGKGDDTAKESTVA

>N270_EF-hand_calcium-binding_protein_(putative_MICU1_homolog)
MFVATRQRSASALAGRRLTTRAFSTASSSSRLFASNHSMVLATGAAVGVLASAYYLGSSPLLAVDETKGAPIDKDAN
WKEKWRARYNDKIKNWSTPEKIFNVFATVRKNGESFMTVEDFCDAILPADHRPPSEKGKIKRIPDFIRFADLDGDEL
ISFGEYSFFTTLLSLPEEHLKVAFQMFDLDGSGAISKQEFRKVLRVLRKESPLGSQQTTHKKEVEKSGIYAHFFGLD
GKKELTYTEFENFIKSLHQGVLQLEFDRYDSKGEGKITARAFGMSVIGYVDPKDLPSFLTRVESLDNRKGELSFEDF
VNFNRALKKLPEIGLAVKLYAQGGEINKKDFGRAVKAISGVDLKPVQIDVIYHVLDKDGNGKLDHNELVEVMAKRVE
KGMAHHRDVGVARFVNCLVTCCSRKAL

>N271_rotenone-insensitive_NADH_dehydrogenase_form_2
MRAACTRSLVAPGCAARGRAATTAGSRLFCGGGGWVQQRRALATSSAGGRGGWRGVGTVAGLVVAAGALGAVALEGL
QDDENDSLLSRTPFVSAVRAEEKTTPNAKAPPSIVSQNPPVDRAVQREQQGGADKPMRTKKRVVILGSGWAAVGVLR
ELDNEAYEVVVVSPRNYFLFTPLLPSVTVGTLDSRSVVESIRRTFKRAGASDVQFLNAECTAINHQSNSITCNDVSG
DGAVRSFDLEYDQLIVAVGCDNTTFGTPGVEKYCHFLKELNDARRIRQQITQNFEVAGLPGQPEEEIKRLLHFVVVG
GGPTGVEFAAELHDLLVEDLEKWFPRSLTQHVRITIIQSAAHILNTYDAKISDAEKRFGRDDINVKPLCRVLSVDEK
TLSYNDKQTNKTETLPYGMCVWATGIGPRPLVKKFCSTIKEQTNRRAIVTDSHLRVLGTTNVYAIGDCGTVEQRRLL
SKFVDLFDQADENKDGVVSFDELSALVVKNKDEYPQLLIYAAKMQELFETVDLDKNQVLDREEFKALLTEVDKNLVE
LPATAQVASQEGKYLGQALNALARGQEVEQFHYKPLGSLAYIGARESVLELPGGFSFGGFTTWFAWRSAYLAKQVSW
RNKFMVAMDWMKELLFGRDISKC

>N272_mitochondrial_ribosomal_protein_S5
MRRISLLGPSAESSRIVPPHAASTEGRSLLYRRAGGLSFGSKSLHHPYHSGGGTLVNGSSRRQLATSSSSSKPASSE
QTTAAKKGGLVGDAAAASTIQTHTATWVDEDEALSLDPRDYAFDQDDSQDQWERLAGVSDNPLMGDRSGAPRGHGRA
KERLAKKFPIEYADEDEEDEDEDNLPGLGGGRRQSAAQQQQQGQEGEEEREDLTPLELRHRAKEEEKEKKWTQIINP
LKDDLEAQISAGKHVPLWHPHVDEYDGDGYDDYARTLQGAWEDDSPFHRDYEYNEKEFKNHFAFSVSGNQHILNVGR
HTKTTKAGRVFSYLCHRD

>N273_pentatricopetide_repeat_(PPR)_protein_AcPPR4
MRSARLSQPSVPLCWRGHSFVSRSNSLLVHYRQPLFTAPLPPLVSSARPGLHVGLPVVRRFATRPAKSHPNHGAVKP
PSEPSGARVSLPTKENEQMVKKLTNLLRNKNPVTARQFVGFLRKTSDQREPTILSDKVVSLLPQLTFEDERTRAKER

YEQQAKELKKDSRQGSNAAAKKPAVPKRKESAEEREYKARELLIKEDEDERRKFTIILASLGKMRKIEGMLYVYNML
KSRERQEDERIRQALDEAASRKEKAPVMEDSRWKVDVYMYNLVLDALAKAGYLGKMEEILQDMAQSRVDKDRVTYSV
LYGAYSSRGDDTRADQVWQEMKDRGVEMDLAGYNGLMNTFARRDDVDRVLETYKQMQTAGIQPDQGTFSILLECCAR
DALEFRTRTSAAAAAATETEKAGDEEGEAVKTGEEEDDDGLYAIDEKERVRILQSKRRRMEAVMRAMKKAKVRLDNI
LVNSIIRCYASLGEVEEMFSVVRFLVEEENIKLAEDNYSLMVYCAGREKAIDVGRLTKVLEEMKWSNVQPTAKTINA
AIHSFAFAGPQQLEAFILPPSAPTTNEAGAAAGDDGKNESEAEKAKKRKADGAKEKKEEQQVSLWQLIKKYGVVVTD
DILFDLLKVYATNEAAPVAPAGADVVGIVEGARRQLDRARLAKLLHKMKEEGFGSSLTVFNSLMRFHAAYGENRVRE
VTVLYSQMKKRQVRPNLQTYLVMVDTILSTERKVQPEQRPASSGKASGEEKEREKERAELSYLLFSEMQSEGVQPNL
KLFNGLIELSGFEERRRRASVVDSTTHNVDGDRSAALGEEEFRQKVLSILTEMRRLGIRPNTKTLKCISSACAVAGA
GEALGPAIFDELPRLFA

>N274_putative_Oxa1_complex_homolog_Mdm38_form_1_(LETM1_and_EF-hand_domain-containing_protein)
MQRIRAATKGPVVGRAFAGPSGSLLGAPGAFGSFSTALVVRRSTTGCTASSSSSLRLRRLHSPILPTALPSPPLVHL
RHGGPCNYSLVSSPSSLSRLRCGELQPPGNVRSYTTPTTTTTPTIGSSSPAVAAADTAPPSTPTATTATPQKVGLGQ
KVMDTLRHFWAGSRLLAANVKAASMLLRKKIAGQNLTRRERRLLTQTTVDLFRLVPFLAIVVIPFAELLLPVLLAVF
PNMLPSTFEDKIKKEEARRKAVQLKLEMAKFLEDALYLRSLQISHDTPSAATFAEAMKKVKEGQSLETKEILGLSKL
FEDKFTLEMLDRQQVVAMCKYMGLSRFGTTHYLRNQLRSKLHDIREDDDLIAQEAALDKFTEAEMKQATQVRGMDYK
DFNTAKAQMEQWLLLSAQHVPPSLLILSRAFALTSAYSSLKPLEGQQVVTKKAETGEIALPKAMEEALHKTISALPD
QLVADTKLTSATKTTQDMVSKLEVLQEQIQAIKTEEKEKKEKEREEKAKAPATEAEAKQATKKDAAGAYSAEQMKVV
SEAVSLLFASAPSKIKREREALEQLKERKEERKEEREEELSAASASTDQPQHQPQPPPQDKVVHTLETKLEKMIAKL
DKEMDKIDQRAHTLMSIIDTNQDGQISFEEFQEAVSHLKAKYSPEDITTMWRKLDTNNDGQVSLEQLEQLYSAGADE
HHER

>N275_C-terminal_IGR_domain-containing_protein
MRRAATLHRATPGAAAFSSRISFPSSSVLAATSSARIQLGTSSNAIAPSHPLVIIGARGLRLRKGREDWYNEQEGKP
HPGAEYPWGVRRIYPESWIREPRGSLFPLVPEPRKGETVESFFQKIKLTDHASKFSSWEELFTTKTRAMRAKGIKKS
KDRRLILSWVEKYRQGVDPGTSKYLLYYPKGSW

>N276_single-stranded_DNA-binding_protein
MKRAALQSIALRSEEAALRNPFVAKASRGINKVILLGNAGAEPKMRTYNDGTASVTYFPLATNQIYTNKSGERVNKP
QWHNIVIYNDNLSQVAQKTVKKGSLVYVEGALSTRTYKDATGAEKTICEIILPKYKGDLNVLSKREGQDEEAGHEVD
HHDLVEDKENVTLA

>N277_tetratricopeptide_repeat_(TPR)_domain-containing_protein
MKRTVAACRVNGVAYNLPQSRSLVRLASQPTRSSSLLIAQQPRLLASSAFPASVRFTSRRGYSAQAAPQDFSEEEKE
IAKLRQQGAKSPAAQSSVNQRRIEELFNSANGYVSEEKWTQAEDKLSTILDLQSSAKADDTLLGRVLINLAFVEQNI
GKREKAEKHYEEGIAALKKTLGEDHHEVARGLLNYAEVLAFLSKVEQAEAVSRQAIPIFEKNYGPKSELVGALLSNL
GGYLCAQKKLEEAEPVLKRALEVLDSALGCDNEYTSACLGNYARLLKDLDRNDQLNELKAKYSSNAATFTATEALEK
DVNDPEMKAMVDQFKGLADSRAFNPEGLFKPDAFHKDELKKFITQWESKHKEKLDPALIPAVLEELEAMPREEIDKM
CADALKELAESKRGGPAVDPSRLNAIADEIDDEALAEEEGDEGDDSSSSDSDDEEGEDEDDEIMERLDQGDEDEGDL
WRATEAHEREAAKNIEIDMSHIELTDDKKQQ

>N278_TIM23_complex_homolog_Tim44
MRAARAALGPSRSCYALGPYRGGALLLRPSYSNGIYGSAHVFTTRSEQGCRTRVSWAAVPTREERRTMSFWSEFVKS
FKEQAENSKELNESMAELKKLQESESLKKTKESVEKLKDKSAEGLAQLKNLGEKAAATGGRVTARVSDSVTSTLGDI
TQRVGMDEKLEKTKEGFEKVADSLNKARENIEKVGENIKTSAEESELVKKVKEKVPFGLLDGSDAAAGEGSGGEGAV
AGARSQLVVKTQEVQTAIEKRLQDARDRLRATGAFKKALALREKIVESDNPLIQRVLDLGDGITRTTSKLFSENDHA
KTIKLIHELDPTFSPEKFKQKMASSFVPTLRSALLRGDPAPISALMSKRLAEHELEAYKEWDAHGYRSHSKLLNLDT
VEILNAHTRDDGRPTLLIHFVSQENHCIRDSSGAVVEGAPDNIQDVEQTWAMQINSQGEWEVIEYMVVASRPSW

>N279_uncharacterized
MMRRATLALREQGSGCMLMGISRLPAVSSPFTSGSRSLSTSADDLLHLFKQAASKSAPSAPAAPAQQPRPVSAGRGR
MPTSAATTSSGNWAQQLANQLDDRAIESPASHPAAKPLYQGQDEKKRKFRPARHAFDPSAPRGGSMEDVASPLSRGG
RGRRMRGGVSLGFDDARFQDAAEEGEDDDFDMRMVLREEKDDAKDLVSLSSAMDEGGDDDWEAMAAEINAWGKKLQN
SLRPHIEVLNKHTKTRRMRRQKYRAFLERCLARREAKRGGAPKPAGWPWPKERDLVYNTDLFVPLNLELKGIEEEGE
DLHALLTQQMEDAARAIGHNASWPLEEKRKLMLGLKRFYEQAVRSGPGSYDLFADHRHALDDDDFIGGGGGPSSSE

>N281_short_chain_dehydrogenase/reductase_family_member
MEHNTNALAASRRVTAIARHVEASAPSAAELLDLHRTAATNQGGLLK**GQVAIVTGSGQGIGEATAHLFAAEGAK**VVV
TDLDKAKSDKVAADIKAK**GGEAISVAGDVTDPK**FPEHIIKATIDAFGR**LDILVNNAGYTWDGIAHR**MTDKQWEAMLL
VHNTAPFRLIRAAAPYMR**DAAKQEIETSGK**AAPR**SIINVSSTSGLHGNTGQANYATAK**AGILGLTKTIAK**EWGAFNI
RCNAVAFGWINTR**LTAAK**GQENFIEVEGKKVALGIPGATNSAEAVAKTVPLARPGNVDDAAGSVLLLASPHASYITG
HCLEVTGGAGI

>N282_mitochondrial_phenylalanyl-tRNA_synthetase_(PheRS)
MRTAHRSASTSIHCASRRAGASLTLGSSRGVSLQLRPRVLGTPASGSVLATRCHLLEQAQPLRLSSAAKRFYASSFS
FK**EHGIEPDEVTNVTDR**ILGKIGTNLHKEDKHPLNTIKKRIEQYFVNKYTTEDNKPLFNIYDSFKPVVSVKQNFDDL
LFPVDHVGR**SANDTYYLNK**STLLR**THTSAHQAELMR**SGER**QFLVTGDVYR**RDAIDKTHYPVFHQMEGVRIFTPEQLK
AQNKTPEEFVAADMKDALEGMISAVFGKVQVRWVDAYFPFTHPSWEMEIFFENKWLEVLGCGIVNPQIVRNCGMPIS
EDGGYGAEGNVGWAFGLGLER**LAMVLFDIPDIR**LFWSQDRR**FLDQFASGENVK**FQSYSKFPPCYKDITFWVPDHFHE
NAFFELVGQVAGDLVECVEVVDKFTHPKTNRTSLCFRITYRSMDR**SLTNEEINELQAK**VRDEVPVKLGVELR

>N283_zeta_crystallin_homolog_(putative_quinone_oxidoreductase)
MRSTRTTTLTTLASSCSPYRLPLALHQRSAAQYFTGLHPHINTSYTTLTSNMRAIIVSKQGDPSVLELKHDLPLPTP
APGQVLVEVK**AAGVNPVDTYIR**SGGNGYNVSLPYTPGADGAGVVVDAPAPSAFKPGDRVYFASTLTGSYASHALAKE
SQLHPLPEK**VSFGQGAAVNVPYSTAYR**ALIIKGKARPGQTVLVHGASGGVGIAAVQIAASLGLRIIGTASTK**EGQEL
VLR**EGAHAVFNHRDEDYLQRIKESTRDGAGVDIVIEMLANVNLAKDLDVIKRGGSVVIVGSRGEINFAPRLIMAKEA
IVTAVALAQSTPEELAEHHAFIGAGLANGTLRPVVDK**EFALGDAPK**AHEEVISGTHAGKIVLLP

>N284_Zn-dependent_alcohol_dehydrogenase
MNGDSNTKVLLVKRPGTGMPDASLFK**IVEEPIPEPADGQFVVK**NVYLSLDPAMRGWMNDVKSYIAPVKLGDVMRGQT
VGQVIASKNPKFRVGDLVSGIGGWQKYAVADGKRGGWEKLVPGFAPTLFLGVLGGTGITAYFGLLRVGLPKAGETVL
VSGAAGAVGSVVGQIAKIKGCR**VVGIAGSDEK**CKWLVDELGFDAVVNYKGKSADQLNDEIRQACPKGVDVFFDNVGG
DILDVALKRIRKGARIVICGAISQYNAAQTKGPANYLSLLVHSARMEGFVLFDYIPEYPLAIRELGQWVKEGKLK**YA
EEVVEGLER**APEYLNMLFTGANKGKLIVK**LADEPAQFAQAR**L

>N285_N-terminal_MRP-L20_domain-containing_protein
MQNQARRAVVGSARTTPLLAGPLPLQRLHLRWRHGGGLVSEQPMVVR**TEALSGVQLLGGGAVFAHR**LQAPAHAPPSR
PGLGQLAEAEVAEMRRLRAEDPSRWTQRRLAER**FGVNALLVAR**LAPAPAER**FAQLEEEEQLR**ELRRVFGDRGGASAR
PAHKSYSESDQQRINRAK**FQQQVAEQGGLK**ATLKQHNAVPKRRRQGVRPPFMQVADQEVVVDTAEFQPGVVGPEVDF
AKATRPLTVR**SPTPDEAAAIR**RHLAETAAKAPLDPAAAK**AAADEFER**DLQAVRSEAKAQGIQRKYRRK

>N286_Complex_III_assembly_protein_Cbp3_(chaperone)
**MRIMRKTLYRPHLSAGALTMATPSCRALSITSRCNSSMARHPIVHRSRAGAINGCMPIRGHVPSFLLFGRCSSTLRG
TPEMPASSFGGRAEASATTGPSADPDLTYMSPVIFAR**RTPEERRRDELGVQKILEVAKER**ANQGESEDGLLR**FLGYY
GKKNQSLR**SGSALYANVFYR**SLDEEFYDLLGYEEKGLLPWFLISTLHMWMTSVRLRKDASSRALDTRAYFADSFWMD
VEEK**LNNVGVNYVGMGK**AFKQMPNLYAHATLSLDKALK**STTDDQLGDALFR**HIFFNRLPRQSHMTALIAYVRQELAH
LDTIPNNLLLHGYLPWGSLPR**VDASPVSAASPSPSPQNDTSETGAAR**

>N287_Complex_IV_subunit_Cox6a
MQRTTPFLRSSAPSLLGRTSSRGFASAAGHGAHGNHAYGYYSAAGFGVVIVAHLIIALQAHEHEHRHEYSHMHQMRK
KFPFRDGTTPLFGLVDEEEHR**DLYDTLVGIQTERVPDNYGWLYDPFADKQ**

>N288_mitochondrial_glutamyl-tRNA_synthetase_(GluRS)
MKSSTLVLRSRFVPAGARLGGVLGRLPTTTAGRFPYTPSSTGRLHSTCSAESSSPASGLIDPGRRVRVRYAPSPTGQ
MHLGGLR**TALYNFLFAR**K**HGGDYVLR**LEDTDQSRKVEGASANFDR**ILEWAGIPYDEGPSK**GGNYGPYVQSERLPLYH
KHAHDLIEKGEAYRCFCTEERLDQLKRSSNIRGIPPLYDR**FCLNLTPQEVQHK**LMSGVPHTVRMK**VPSGVTSFTDIV
RGAVSFNNAFVNDQILVK**SDGFPTYHLASVVDDHLMEISHVIRGEEWLASTPKHVMLYNQFGWDVPR**FAHLPLLLNP
DK**SKMSKRQGDASVDHYIEREYLPESVVNFVAFIGWAPEDTQEIFTLEQLIEKFSLERVHKGGAIVNINKLDWFNGQ
HLRAKCTDDIDWVSARVRPVLEQALPSSASFPDAYLHQVIRLNKDR**AQNFTDFVEPSRFFFEEADLASPEAQK**ARST
LWKPGQSETLVRALLDRLEKADVPMEHDPLLALVKEVCKEHGAGSKVLFHALRYLLTGGKEGPGVVDTMATLGRPRT
LHRLRQAFSPAAPPS

>N289_mitochondrial_ribosomal_protein_S9
MRGSSKSTAVLGLPFPSPAGSKAALCTASSSRISSRVLPPARLHSLASSPLLPLSVLSSQRRHYAVKSKNFERKEAR
YDFSEITNRVWPR**HPPPQIDYR**NYVPAEEEDEEDDWKPEEDYPEPTFTADQTSDQYIYPVITPQTVPVKIDSRTGAF
LGTGRRKAAIARAALVSGQGKITINGRSFLDYFPCFFER**GAVLAPFVAIERPNTFDVNVNVSGGGTKGQAEAIQLGI**
ARALQSYNLAFRPALKKAGCLERDPRVVESKKAGRVKARKRPQWSKR

>N290_N-terminal_MRP-25_domain-containing_protein
MVHAGKGGGRMFVNAARINGRK**SNFSLLEYIQSEVR**AGESPVPPWMPATLISPPPTIPNVPHPGPLTYPEDKLRQVW
FDRHPEARKIKLKTVYVGEHRYWQHPATSFVHRQSKLIKKGYSEQDAYDVVEAEDKKAARYRELERLMAIEQAK**ELG**
FDDLETARDLLAPPDLTQARER**MLEELIDVLK**AK**GVPNVVPELLPK**GMKWRDVLAFVHKYPQHAHFFSLGFMATHAI
ETMNPEIADAYNWIYGGEVLLDDDSVPLEEQEELNAFLDEEGFETVEDGDELDQQDLREQERLTSEAVAQYEPVVAG
ASLVEEGLFFDEDEGEDEDESEAAREEEHDEEQRIAMVKKEGEQFKAILKRIEKIYRPEQFPTTADTPWADLVNLLA
LRPQAPDVKLAQDAEQKLRKANQVKRPSGGSSRPQSQQPNKPTKGKEVELQ

>N291_mitochondrial_carrier_AcMC13_(putative_carnitine/acylcarnitine_transpor
ter)
MAAAPQQEKEKAKVDVPPKGALMGAGSGLREGLFGFGCGVLYGMTSPLIGHPFDTVKTK**MQAQEGYR**TGGMMRTFAT
VIKNEGFFALYK**GLLPPLIGSGIFR**SVQFGVYNSSWAMLRDWSFGRK**EIPGTGGLEVRVVAAGVVASTAR**TVIETPL
ELIKVRRQMGQTWKFNELYRGFNVTWIRTCGLMCTFFILVDSGVRHLPNLINAPYVGPFLKGGLCSTISWWIIWPFE
TLK**SQVQGNTPGPK**GIFSR**LAFVAQTGGLAGLFR**GIVPGSTRSLLANGCSMIVFTQCQSLRHHFIGDEQPPEGESLP
HAPLDADGNAIIEPAISPPASSTEK

>N292_pyrroline-5-carboxylate_reductase
MRSCRRAFVLQAQLSPLTATVPYPIYKRPLPEHLIYIGPNNTSSSTHQQPPARSNNKMSEPR**IAFLGAGQMATALAR**
GFIDANVTRPENIIASDAYEPQLPRFQKDTGGSTKTTKSNLEAVENSDVVILSVKPQVMSTLLKEIKDAVASSPHLI
ISIAAGITIDTITKQLGSDTRVVRVMPNTPCLVGK**TAAAFSLGGK**ATPEDGKLVAHLLSSVGLGTEVPERLLDAVTG
LSGSGPAYVYQFIEALSDGGVAAGLPRDVAAK**LAAQTVLGAAQMVVQTGEHPGVLK**DKVASPGGTTIAGIHALENGR
LR**ATVMNAVLAATER**SKELAKSE

>N293_ubiquinone_biosynthesis_protein_Coq3_(dihydroxyhexaprenylbenzoate_O-
methyltransferase)
MKRTLLLAGRCGSTATALPSCTRVCRTTAAAWRVPTRAAFQSVRSTATAHGSPQQQQGAATGGSTVDEEEVQRLSES
ARLRWWDPEGEMKPLHRMNPKRVAYLRTCLTKRLGLPPLAPQPFTGLR**FLDVGCGPGLLTESLARLGGEVLGVDASA**
ANIQTAIKHSSGDSSLSTLAYRHGTAEGLAAEGQQFDVVSSLEVIEHVNNPELFINSLSGLVKPGGSLFLSTINRTM
KSYALAIVGAEYILGWVPPGTHQWNK**FVQPTELGVLLQR**AGMNLEELTGLAYQPWNGSWSFTTDTSVNYLLWATKPL
AQ

>N294_putative_Oxa1_complex_homolog_Mdm38_form_2_(LETM1_and_EF-hand_domain-
containing_protein)
MAARSRYLATTTYMATPSATIVGTPFVRMSQTSMLRLGATSRGISSSAVALALPRGTSGSCAFLLGPHAAASWRRSG
RSSATVLQWPGAGSSAAAGRLRVSEAACARYYATGGSLPDSNQSPKAVSAEDKEAVPKKTLVGRAVHSTKKVVTFIK
EGIHHYWLGSKLLALNVRTAFNIAVRLKNGHTLTRRERQHMIRTTADLFRLVPFAVFVIVPFMEFLLPIALKIFPNM
LPSTFQDTMKKEEDMRKQLLLKLKMASFLQDTLQEMAETGETHADIPKEEFLDFMKRVRGGGEVSGEEVLKFAKLFK
DDFTIMNLSRAQLSSICKFLNLRPYGTDAFMRWQISRRVSKLREDDTMIAQEGVKSLTFEELQQACIARGMPATGLS
KVALREQLEEWLDSSLNEQLPAVILILSRALSLTTASQKVDAALRETISTLPEDVVEEAELEMDLQKGTPSDRQLKL
EVLRNTNEKLREELEEEAETFKEIEALESPGSVIPEEDAEHLRDVAEALSVLASPVSAERKALEQLEAREALLARAK
TLKDQETATVVDAVVKAVKTRSDRSKERLGQQLEDLLDDLREELSETEQKLGDKMVLIDKDRDGVITTEEVALACSL
LKDRPSDAEIRNVLRVLDADEDGVVALEDVQKIRQKLEELHLEEAPAEEKERK

>N295_uncharacterized
MSATGPPSSSMNEGYVPPHMRKGGKQGGGPPPGAGGGARPPVPWRLRPGAKFLTAGLLALGVGWTFFYTMRS**VSQDD**
FADIDDSGNKIRERPRV

>N296_adenosylcobalamin-dependent_ribonucleoside-triphosphate_reductase
MLRCSSAGAPGSVCLPGAASHTPRACFSRFVGGYVHSSRKASLLGGQDRLVMLISSTSPTPSLRAHYSATAAPAVAK
PAAATTKEQEELLEMDIHTFDQRASAPFRLSSKFVSKFKDK**QPPFGFNGLGEFVYR**RTYSRLKKDGSKEEWHETVER
VVNGTYNMQKKWIETHQLGWNPWKAQKSAQEMYTRIYEMKFLPPGR**GLWAMGSNITEER**GLYAALNNCAFVSTEAMR

EDASKPFVFLMDASMLGVGVGFDTKGAGSMVVKGSRRDRTPELVKIPDSREGWVESVRLLLDSYFHGNPCPEFDYSL
IRKAGEPIKGFGGVSSGPESLKELHHTLREVLDKQVGEPISVTTIVDIMNLIGRCVVSGNVRRSAEIAFGDPHLEEY
LDLKNYGVNPQRAAYGWTSNNSVLAHIGMDYDDICKRIAINGEPGIAWLDNMQAFSRMNGVVDNRDSRARGGNPCLE
QTLEPYELCCLVETFPGKHESLEDFKRTLKFAYLYGKTVTLGKTHWPETNRVMLRNRRIGCSMSGIAQFISDRGLEN
LRVWCEEGYNTIRHYDDLYSDWLAIPKSIKVTSIKPSGTVSLLAGATPGMHYPISSQYIRRVRLSSNSDLLPALKEA
GLKVEPAVGSESNTAVVEFPVSVGKGIRKANELSMWEQLALASFLQRHWADNQVSCTVTFDPETEASQLKHALDYYQ
YQLKGISFLPRSTGVYPQMPYEEIDEATYQEMLAHFKQPDFRRSEAPQEAYPEKFCDTDVCTIDEAATPAAAVGAKT
DSQ

>N297_armadillo_repeat-containing_kinesin-like_protein
MSRQAPTHDAMRQLGLLQAMLAMLKPVTAGASSSSGAGSSSGGGGGVGSSKHPLTDYESVMVELTKVVANLAANNGN
RQVMGESGAIRDILRLLQDLPNEEIRENLLRTIMNLSIAAENEDRIREEGGLTLLLEFLQADDTSPALLLQTVRVLV
NLSCNETNKTIMQRAGVVDRVVVLLLGSTDVDTGLAHRLVRLLGTFSVGCDLAVYEKITDRAVAQFLVTSLRKQMEK
VEPDRDDKSFSEILLMAIWKITTERAPKFADALTRFQNLFIEESEADGSCGIDFIFPYLRLTHPDDRTLVLSCLNTL
QHLARGNDQVQAKIRGSGALGALKELYNSREPVIAEKAVELVKSLSMIAALD

>N298_thioredoxin_(TRX)_family_protein
MRRSLSSSARSASVRRAASSCASSQPLRAYTLQRNGRNLISSICARSSSSSPLLPVLAPSAGRRFYATAENGASSDS
APVTAPQPTVSPIISIQTPEEYQKLVLDVSKTRPIIVDCYADWCKPCKDLTPVIEAVIKSREGKVTLAKVDIDKVSE
VAVQLSVSSIPAVFAIYKKETISKFVGLKSKAELEDFVDAVLKKTTQS

>N299_ribosome_recycling_factor_EF-G2
MRRARVAGQSWAICSTSRAGVVRRPLSTATVIASRSCSTPLIASGRINFGSEQLPPTTSLAWIQRASYAKSSKGGKG
KKDDDDGPAVSVSELMAQTKDSLTSQMKRSVDWLTEEFAKLRVGRANTEILNRIKVEGAPLAKKGSVYVKDSFTLAI
TPFEKEQTKKIVEALRDADMDLNPQTDGDNIIVRLPKATDEYRQSLLKQATKMNEEVKNSIRRARQGALTDLKKHKD
AVSKDDMKKLENEVQKITDEYNKKTEQLHKAKEQAITGAGN

>N300_uncharacterized
MATLLRLSPLKPLRHLRNGTPLGAAFDLRATSRLINGPTEFAQVLDDAPHAAEAGHALPSTAPGALPSLQLTSRTSV
GVTRGPRVHVFSRRQFE

>N301_mitochondrial_ribosomal_protein_S36
MASTGVRQLRQHVPLIKFPQRHGAAVQSLQDAALPSRHTGGVESTPLTAPPKTTTMQTSPNLPTPAKFDIKSRGPVT
HHESMDELPARYRRALLSEEAIDLIQMGGAVDH

>N302_pentatricopetide_repeat_(PPR)_protein_AcPPR5
MWRAGGQGPRLACRSHHHHGGGGGARLMCGDVLPAEHRRRGSGGALLRFAATSTRTTPATATATLRRGQWAASLVVR
RAITGRPGAAGVLAEDMEGAVGAVGRLLASPHARDQEAGRTLATDLLARQPLPPGGGAPSALLASARCSPSVLQAIA
TNSPAEALALLKRMERSGQEVSVEAVNGLVRGCLDGGNAVAARQLFEALRQHLLGRGTTPDSATYALGIEAVGRSAK
LPEVRALIDEVLQRSVPLDGKLLASMLTALAHKEAYDDALRLRRQLQTAHPHLASPPHAQDVQRGLISASAVKGDLR
TCLEAAHELQRLMRAPPDLNTLTTILQCYSRSSLFEQEHSMLLRYLASLRSLDPAHQKEKEAHGQLRASGTEASPPT
TITTGGGGGRAEGASWQDVVHRALARGPASKAGAPSSSDPGDGALHLLEEILRSEGSFLGEQLTLRQFNPAIYALVR
LGQVDRALTLVEDIQTHGLQPDIATHNTILKGFALRGDAVGAVRYYNAMLRKGVKPTTKTFEALLRAQSEVVAREVG
SLQPAALVTAQLYNFDESNVLRAASPGHIQDAYSQLLLEMQAHGVKPKAQFLSSLVYGMCLTGLVEAALPLVVSALQ
QGDAEESGRGGGGGGGRGVGGAWLRQERADVKLFNQLLLGISLQPQPSLDMTAQVLEMMEGAGVMPNQHTYTTLINV
YANFTQHTAFPRGPPWLSPRNTPELREAGREALMKALSVYFSMRRQHLREQAASPSSSARGVPTATFNSLVKLVGTE
DLLDVSCHDIDHLHDELLLLAAHHDAPAPPPPPRAKQQRGQQQQQQDEAEAWTRLPLAELQKRYAERPLPLPAYLPA
ERTASQMTPLELLAWRDLAANGASPDRVTYNHLIFHLTASGRLPHAEHYLRFLLLLHHHHHHHHSPPPTHENPSSAA
SSSSSGPAAQAADGGGGRPDFLGRQLNPKYSSYLIKQRNDRRAQFAKLLAKTPPSAAVGTVHHEQQQRQQEEEAQES
TDVFGFDEAPGVEAGAHHHPLFLRTLWRVGEEYLRTHRFDDFVECYRLARQSYPVSATKCFGFLLRAWRTPGSPDLV
PDASAENALRQALRKHAMADPEAASPPSSAPINALFQ

>N303_leucine_aminopeptidase
MQGKAKCLLWGAASFRSSLRAGAASSSAACIFTRSATHRSPLLSHSLSPSGTKLIFVAPSTCGTTKTCYSTAAGDKQ
VDGVVVGIFEGGELTPAGQAIDKSTSGALTRRIKLSKKAAKGEVGSGEVFLDLGEDYPRVAVVGLGKHPRDVKLTSE
QEDYREGQPKPSDAVRQGAARGARLLRDAGSKVIGVESFGQFTDLPSVQLAAEGALLGLHKFDELFSKKDDEPVDVQ
PWGVEADKQEEWNRGKIIATAQNFARVLTDTPANLMTPTIFSQKVEEKFASLPNKADVKIFAHDKAWAEEQGMGCFL

GVTRGSEEPPK**FLEIHYNPLGDEAQDVAPIIFVGK**GVTFDSGGISIKPSEGMGMMRGDMGGAAAVVSTVWALASLQI
KTKAICLTPLCENMPSGTATKPGDVLRAKNGK**TVEVDNTDAEGR**LILADALVYANSFKPAAVIDVATLTGAMVVALG
AGATGVFTTSDKLWREMDEAGWKTDSRVWRMPLFSSYKRQIKSAYADLKNVGGRPAGSSTAALFLKEFVETPAWMHM
DIAGVMHSDDRNAYTPKGMAGEPVRTLVQWVRDKVEKH

>N304_putative_NADH_dehydrogenase_B14.5a
MASSKTPGLWSRIRAALRPNFTLHPVPTAPDYVQYPTNFRVPYSK**TEYSPETIPAK**AHR**DLSTIYYWR**HAAGKRSPP
VPRKPDVLKELEKEGSATGPAR**VGGLTDITELR**ITRPPGEMR**KWNEIPNELYQ**

>N305_Complex_I_(NADH_dehydrogenase)_AQDQ_subunit_(NUYM/NDUFS6)
MKRLTIARRPFTFAGATPLYRSAAPLSSQQRFLK**DIASNSANEAPPNTDAAQVR**LHMAIK**GNADEVSEER**RK**SISAV
MGTPVEHLK**RRVRIYIPARCTMQSGVHSATFWKISYPEEEK**NHWANPLMGWTATKDPVSNLHVK**FDTKEAAVAFCKQ
HGLDYEIEDSTTPYENITPNKDYADNFKFKVERSLEPDIY

>N306_Complex_I_(NADH_dehydrogenase)_PSST_subunit_(Nad10)
MSSGVTQK**LAHFGKPQALTGLSKTEFVISKLDQIVNWIR**KGSIWPMTFGLACCAVEMMHAAASRYDMDRFGIVFRAS
PR**QSDVMIVAGTLTNK**MAPALRK**VYDQMPEPR**YVVSMGSCANGGGYYHYSYAVVRGCDRVVPVDIYVPGCPPTAEAL
LYGLMQLQKKIARER**NLLSWYR**K

>N307_histidine_triad_nucleotide-binding_protein
MRRAIGVGRRLDVLSRQLICPSAAATSSSSTLLLTSSPASSTLAQRQFTSRPPVRMASDGDKHGATAAALKVEPKDT
IFAK**IVDGTIPAK**KVFEDDTTIAFHDIAPQAPTHILIIPK**KPIGGIGDVK**QDEEALVGHLMFVATQVAR**EQGLGDDG
YRLVINEGTNGQQSVR**WLHIHLLGGRKLTWPPG

>N308_Complex_IV_assembly_protein_Cox17
MSSATATSSTSAAPAAAAAPTTNAAGKRICCVCKDTKK**VRDECIFQFGEEK**CQEPIELHKVCLRSEGFDIQ

>N309_Complex_IV_assembly_factor_Cmc1
MAQADASQTKTYR**LSDDPSFLTNQEK**NHIYRVQHKRAYKLCDPVVKPYVDCTKHR**LISLLWACR**DEKAQMADCLHEV
AER**AREEVTEEYLR**QRQAK**RAAEDAALSK**ETAASS

>N310_mitochondrial_carrier_AcMC14
MNTAPAPAVDLRDLSRDNMSHLDNVPTPEFAVAGDEEGQQR**AEEVGDEGEGGGGEATEKSNEAAAVQDIVSEQLAED
ERRLQMQVASGGK**AAPPVGKGRGGMLQQAFEAFLRHHQGNNRIDAGQLQSVLQEAGLEMDTEQAAAILKAANVSATG
ELDFEEFYSIFVGLKIFKHLDQNKTACIQEHDLIR**TLENYGLPTDR**SMAEKMIQMVGEDEEGYVSFPAFFRIYLDVH
HQHHRNIDLLEHAVRYWYSGASKDTILAQNQNLTPLQDFIAGTLAGVAITLVGHPFDTIKVR**LQTQQQAYGSAIQAT
LK**TVREEGIRGLYKGMGSPMATIPLINAIVFAAYGQAKAYLQDPNAPDADLSIPQLALAGAWAGFVNAGVVTPVELI
KIR**LQNQTENTAAQFNLNLK**ERLRSGLRSSLFERRIFYNGPIDCIVKIFKEKGFPGLWKGMSATVYREVPGYMGQFV
VYEYIKQYLISRQGPECTVDDLHPLHLMLAGGMSGIGAWIASYPMDYVKTHIQSASDTEKYRKNKLLLDGGFFDCWR
QMVKERGLASLWRGFGPCVARAFPANAAGFLGYEVIARLFRDQNAASTPTFATPS

>N311_uncharacterized
MRRAACAFRPAPTHSLCTAVLSSPAVGRTLATVTRNARPK**FVFPADGLPLYTANR**RGEFLIQAGVAVISCMAYGTYA
LTQYEAKK**QTGEFVGSSDTVTK**VAIGLGAFCVVTTPLFTWASTRRAVRRLWAVPR**SANTNVASALR**VETHSFFGGPG
K**TTDVQISEIVPVGHINPAER**LVRFQLRDNKLFVMTR**DRGEFHNEEALQRLLNNKPVTFS**

>N312_m-AAA+_ATPase_(Yta12_homolog)
MLRLRSGWSMAGRASCSAGQLGGGSRQLLSRNAALHSSYISTSAPQLASKSSAWRWSCVGQRINTLGGRNTGLPTGG
AKRRFSSRPENEGNNNPGGGGQRGGPEGEPPKVWNSPLFVASAVMGGLTLAMSTLLAFTSDGNEIDFNTFRTEYLEN
GKVR**EIVIVNGER**ARITLENEVRPTLYFNIGDLHNFERKLEEAQR**NMGLDPFDFVSVR**HVREENLAGDLLAVALPTL
LLIGTLIWVSRK**TASSMGGGLFSVGK**HKATLFTKDMKVGTTFNDVAGCDEAKQEIMEFVAFLKNPDKYRQLGAKIPK
GALLVGPPGTGKTLLARATAGEAGVPFFSISGSDFIEMFVGVGPSRVRDLFAAARK**NAPCIIFIDEIDAVGR**ARSKS
GYNDERENTLNQLLVEMDGFNPTLNIVVLAGTNRPDILDDALLRPGRFDRQVSVDLPDVKGRQAIFNVHLKPLK**LAE
ELVGTIGDK**LAVLTPGFSGADIANVCNEAALVAARHRKPAVELIDFEKAIERIIGGLEKKSRILSREERTRVAYHEA
GHAICGWFLEHTDPLLKVSIVPRGVAALGYAQYLPKEQNIYTKEQLLDRMCMMLGGR**AAESLIFGKITTGAQDDLQK**
VTK**LAYSQVSR**YGMSEEVGTISFAFAEGDGERPQVDKPYSQATARLIDDEVRSVIMNAYKRTEQLLREKQSQLESVA
KLLLTKEVLSADDMISLLGQRPYGLPR**KVDPNPEFK**VEL

>N313_hydroxymethylglutaryl-CoA_lyase
MKRTSVMASRRRLVPCLGSTYTTRGMMPAAQGARFLSTSSSSSLEDEPRFSWFGPLPKKVKMYEVGPRDGLQNEKEV
IPTEVKVELIERLSRTGLSVVEATSFVSPKKIPQMADSVEVMTSIKREPGVIYPVLVPNDKGYENAVKTGCSHIAVF
TAASETFAQRNINSTIGDSLARYRELCKKAAKDGLQVRGYLSCVLGCPYEGHISPKKVADVAAELHEMGCYEISLGD
TIGVGTAGSTHRMLDEVLKRVPLEKVAVHYHDTYGQALANILTSLQFGVATIDASVSGLGGCPYAVGATGNVATEDV
VFMLHGMGIETGVDLEGLVDAGDFISKQLRRPSHSRVAVALVQKKKDHMMRRARGLLDELSNGKFSAPTTKTTSTST
STSTTSTSSTACV

>N314_mitochondrial_carrier_AcMC28_(glutamate_transporter
MSKPTEQKAPHKQQRVPLPAKLVVGAIAGVIGTTCIFPIDMVKTRLQNQKVGPSGERLYKGALDCFRQIVSKEGTRG
LYRGLGPNLIGVTPEKALKLAVNERLREALEEEDGSITLPHEIMAGGGAGFCQVIATNPMEIVKIRMQVQGTLPPEN
RKPAAQIVKELGIRGLYKGTPVTLLRDVPFSFIFFPAYANLKAIFSDADGNIGLVRLFLSGAFAGATAAGLVTPADV
VKTRVQVENSRYTSIPQCAATVLREEGIAAFWKGVVPRMAVQAPMFGIALMAFELQKKFILAHQNPQ

>N315_acyl-CoA_synthetase_family_member
MLRRATAITTTTGGASSFRRSSSAAVRRLAAALPPLRGLRALHSSPAALRAAPALLPRLGLVERAVGHRQRTAVVAP
ADAAVDSTANQRERSYGRLLADATALAGHLRQLAGVAPEKDMKEGRVAFLCPADYSYVATQWGIWSAGGVAVPIGVH
HPGPEVEYVISNSEASAVVIHPTFEQLVEPIARRLNVPVLTLAPQLFPARPAELEPSFFDVDLDRGAHIVYTSGTTG
RPKGVYTTHRNVEAQVSALVDAWGWTPDDHILNVLPLHHVHGIIAVLTSALWSGAKCEMMSKFDASAVWRRFTDTTQ
PQLSLFMAVPTVYAKLIEAYDQMTPEQQRHATDACRHFRLMVSGSAALPETIMARWQEISGHLLLERYGMTEFGMAI
SNPLHGQRRPGCVGTPLPGYKVRILPAAAEGQAAASAATTEHGVSGDLQVTGPAVFKEYWKNPEATAKEFTNDGWFK
TGDIAEYVDESGVIRILGRSSVDILKSGGYKISALDVERVLLEHPAIAECAVVGLPDPSFGQTITAVVVLKQGEKEL
ELGALKEWCQDRMSGYKVPRKLLALAQMPRNAMGKVNKKDLVKSIITTTATA

>N316_Complex_I_(NADH_dehydrogenase)_15-kDa_subunit_(NIPM/NDUFS5)
MSTGFGFQGAGRCYPIWRDFALCKNGSANPGECTPFFQDYITCTYGWADPENVELFKRQVALSEEQEKWQKQYGKKM
AAHVRTFETEAAYEEWKESLGAKVVETPATMDELNAFTKEKLNPQ

>N317_dihydrodipicolinate_synthetase
MKLSHRLALTSSVRSCGFAAVRGFGSVTGGQEPLFRGVFPPITTPFVEGTEDVDHAALAHNVQRYARKENGLSGLVV
LGSNGEFPFLTSAERIEVLRTAKLEAAKAEQETGHKLRLIAGTGCVSTRETIELTNAAKDLGYDAVMLVTPYYYTNT
MQNNLQHHYTEVAKNVGGMPIILYNVPPMAGGVAFTVPLIRDLAEIPNIVGIKDTSGNIVQLTEIVQKVKLPLASKG
KSFSVLAGSGSYFFPALTVGADGGVMALANIIPHVLSQLYKDFHAAEAQPHLLHQCQKVQHAVVELNQKITAEFGTP
GMKRALDLSNVYRGGVPRRPLRSLSDERAQVLVSVLERTGKDLGHLGLKL

>N318_C-terminal_mitochondrial_carrier_homology
MSDIEYQAPHSLRAAEAEAAAEQPNLSSSHSDSSGSTSSSSSSPTAPRRQRRASSLSTSAPSGPAASMQASGERRIS
RRERLSGRGFMPPASGGGGGFDEELDDYEDGDVGTTDVLLYLARRIACEFGANLAFNLPLRLVSLRQAARPLGHPQH
SLAHEVKSLISPSSSSADSWKYVLGTSAFIGMSEVVAGLFSGGVSMYFDSGHIPTVDEWHEHEKPTIYGVSRKQLAV
FAGKLLTGVFFYPFFAVAPILLATHRWPGTGQFFRDLAYNRNGFWNALALNVAKYSIIDLAPFLETKLYHYLQLVPE
EDEENEDEWEAENSSLFSAKRFIKYGLSFTSTALACLLYVPLDVLTTQMVVYPTQYSGVVDCARKVWAAEGLKGLYR
GCWANLLSEQELLFI

>N319_TIM23_complex_homolog_Tim17
MDAYRDPCPSRIVTDCGSAFAMGAIGGSLWHGVIMGWPQAPRGMRMSSAITALKTKAPSLGGSFAVWGGLYSSFDCT
FAYLRGKEDFKNSIMSGAATGAVLAARTGWKGSLKSGVVGGGLLALIEGIVFVISRQSPAQQQDFGYAPPPPPLEDV
LDVEEKGGFFSSLTNLFSKKEESKPFEMEEETTMDDFGQETKEDDFGDLFQPPPATSW

>N320_enoyl-CoA_hydratase_(crotonase)
MQRASLRLRHARPSCASALARFYSTAGSSANSEQLVRLEADHLPDGRPSGVYVMTLNRPDKFNALTEAVGEEFRAHV
ADLAAMPPRSLRSLVLTGAGPAFSAGGDLDFLWARTKTPAEDNTEIMLKFYKRFLSIRSLPVPVIAAINGPAVGAGF
CLAMSSDLRIAAKDAKLSANFVKLGLHPGLGATHYMPRSLGPQVANRLLFTGETLTGDEAARLGVVLEAVEKNQVLP
HALNLARTIALNSPSAVRLLVRTLRYDDDVQLERALLREADGQAHSYASADLQEGLTAIKAKRPPTF

>N321_glycerol-3-phosphate_acyltransferase

MADVTEASGGPHGHGEAEEQVQISNEEESTEAQNIEGEKGTAAVPVQEEEMLGQQRLNAAEYSHENLFRQRRIRSEN
FVVRRLVGNFFDLWKAYAGYQHLPGAHEPFPRTENIIKNAILKDERVIRATQKYAIEKKMSEEAAKRHVAEMIGNMI
ASFSSRITRSFEYVMTKILKRLFVSIHVDDQGLRMVKELEEKGVPVVLIPTHKSHIDYIVMSIICFHYNLPLPYIAA
GDNLNIPIVGYLFRRAGAFFIRREFAGDPLYSLLFRCYVEQILNESSVLEFFIEGGRSRSGKVLRPKMGMLSVITNT
VLEGQVDDAMVVPVAISYDKVIEGEAYKKELLGGQKEPETVAGVIRAARLLKFKFGRVDVNIGDAISIKQFIANQYV
RHQLRAETGPDDPAVRRLVSALAYRVLYECNKVTVARPTALVATALLTHTGRGLPITQLRNKVLQLRQMIVERGGFV
ASLKEDKISALRITENALNVLDNLVEKHKQGTHETVYQPKQRLELTFYKNSIIHWFVLEGIVSAALYASIKPHIRVA
QPEDISKFKVNKRDLLNDVRFVSQLLKLEFIYKPSPDIEVNFEQTLNQMQERGILKQEQVARTALPEEEQEDEESPT
MVSIQASEDAQEMFLFLCSLFWPFIDSYWLVINAFKSLLPSIIMEKNSFLERVRVFSMAQYYSGELSFIEALSTEGL
SNALEFFHEQRVIRLDRVSHSKVVTIKLRHQYHQGQGEKLEELIYNIGRFRRATFRGLAFTFKTKKEKKRINFPKSS
AKL

>N322_mitochondrial_carrier_AcMC15_(phosphate_transporter)
MTVAAFVHENYNKRQKQKSTTTIMGEHLVSAVGGALTAALSHVTSFPLDVLKVRAQVGRSWLPLGEGFRHGLAASLV
GWSLHGGAKFLGYNMLREELHDVLPWGPSNTYLFASLTAETVATLLLAPFHTCEVKLVSDPLFAPSLIAALLKIIRL
SGVRGLFAGLPVLLLRQLVAGFCKFHLFEKCARASFNYLEPGYAKDRKIKRYHRVAGVLFSSLVTSAVCAIVSNPFD
VIYTHIAASPSPLSVLDVYAQVGLTGLFAGVGYRVASTTLNNFFIWVYYDLFKELIAM

>N323_uncharacterized
MMKRVGVCGSAAERFGARGGFVAAGAARSLFSNSRGAISSSSRFYTTTTLAEGGSRTPWIPGNPPTLEQASEGAEWT
RETIYQVMYPGHVEVADEIARGVSLRSVVQGLFKKAVREGGLPPRQEERVWSKWHAALERLEHERGVTTLADLAGLN
RVAWWRTRVPHALRTALNTYVYHHRLPAAVLPSSSSSSTASSA

>N324_Complex_V_(ATP_synthase)_assembly_factor_Atp12
MRRSCASVAAGGARWGRCGHQAASRFPTSMLRQAGSDGFRFLRPSLTTMRMLGATRSYAERVKVDYHYGHEKFGKDQ
AEPASEDTTKPKVKGAKLSGVQGGSKTRRWYKQVSVGEREGGWAPLLDGRVILTPMEHPLVVPSQHNALMIAAEWEM
QQPYIKPDTMPITRLATTIMDRLVEGKPEIRHALTLEMLDYIETDTICYRPDDREKEQVLYDKQQAQLRPFLKWFSS
FFNMELMLHFSVIPEAQPEETINGLRLLLHNTTDWELGCLDTLVSRTKSLVLGLALWKGPFSVDQCIAASRIEEDHN
IAEWGECEGAHDLDKVDIYKHVAAATAFLRSLPPEQSSLKQW

>N325_mitochondrial_ribosomal_protein_L28
MIRRSALQETTCRGWTKRSQRGLFAGRTVVFGNQISFSHKLTRRTWKPNVHKKKLFSELLNETFHINVTTAALRTID
KMGGLDNYILYTKDHKLDSLFGLQLKERLKEVYELKHGVKFQAKAAPAVSVKDQWQQIIDNYNRKKEGSSSSSSTA
SATSSPPPVAQREQSEVV

>N326_kynurenine_3-monooxygenase
MDSGTSTGAGENSGNENKSIIVVGAGLAGSLLAVYLAKRGYKVDVYERREDIRTAEIVEGRSINLALSTRGLTALEK
AGMGHIGRQLGTPMYGRIIHAQEEDPKLQFQQYGVDPKQHLMSISRTVLNERLITAAEEYPLVKFHFKHRCLKTDFA
KTSIQFLNEETGETVTATADVILGSDGAYSSVRAALQKTQYFNFSQYFLDHAYKELTLSPAADGSYQLPSNGLHIWP
RENFMLIGLPNLDKSFTITLFMPVKMFESLQTKEDVRRFFSIYFPDALRLMPNVPDQYFANPTGSLVWIKCDPHHKD
HVAILGDAAHAMVPFYGQGMNCCFEDVRVLDELLEKYNDDWDQVLPALTATRTKNTDAICQLSYRNYKEMSSHVSHA
DYLLRKKFDTMMNYFFPASWIPLYSMVTFSNIPYSEVIERSEWQDRVVGKIKTAAPVVALGAASLLALYFPRSRAFV
RQALTNLADRL

>N327_3-hydroxybutyrate_dehydrogenase
MKRTLAMMERSGLAAASTSGSRVTGTRAFATSSTPGLHLSLTGKTALVTGSTQGIGLGIAEELRKGGVALVVTGFGD
AAEVERTRQRLADLIPGDDRVHYVPADLGKAEDVEHLIKESEKKLGGPIDIVVNNAGIQHLSPIEDFPVEKWNQIIE
INLNSVFHTMRLTLPAMKERGYGRIINISSVHGLVGSKHKAAYVAAKHGVVGLTKVAALEYAGSGVTINCINPGWVL
TDLVRKQIEARAESLGVSYDEASRSLLAEKQPSETFATPSQIGQLAVFLSSDAASQITGISLPVDGGWTAQ

>N328_uncharacterized
MRRVASTRSLARASCLRRSHSLLPKTCYLSTTGCVLARLALVGVKQQRYSEELHSNHGISVGDQLAGPHQRDPHEYL
KQLSTKWSWPPPSAKLKAPPTATHFLYRAQDRMDSVEALWRGVVQPSWQAYRSGYFDDKKAWSTGFIHGASGVGKTR
FNLEFLALLADYLTSDASKAYRSPDDEVESLHAALKNSKTVVLDIRHNGLALKVDETEWPPEVILGLRLAHNYWWPH
VPYSEVYDAFRWQVREDPTLWGTFSLGRVLFAIRQHKAAPTRDDPSPRIPSMLHIAIDEIQSVFDTMAPYGGGSSVR
SAPEPLSTALNRALQGAISQSQGLYVLGTLSGTAARHATEVLHATDATSTGVLLSPLSAKTVRQIVASFQFRFEPQP
GQPEMVSGQEWLEKGGKPFERLLTTIGGNARALECLERVLKTQGSPSKPLRLNQITTELTKEVRNTFNIESWGRKGS

GQFGLLLALAGIPVTRESVVAFEEPSTPQQPPRPITVAELEKIGVVHLRPPPPSDPGQPDSWVNTWDVQELAVMEVP
FVLAKAALDLAVKSKRHQRHQLHQLLKEASR**LLADFYPTAASFEK**LALEHRVLR**HNVASEWAR**RQGLTYVDAADLFC
GTICHPSLTELSFVPAATVRHVSEPAGAGVWWRAAKGGGPQASKEVPPTSVILEDGTTVELGSTSPYALLLSGSNAV
DGVLNEQLSHTPPKNVRVYIDTK**HTQIGAPADDALSYSDDIK**ALISKRRYLAEQFPEEEHIMVITSNKRAQQPGGKP
HTAATLLRVPTAGRNETTSVDPRTCIITVTDDSLAWAMSPTLAHFLVLE

>N329_DNA-directed_RNA_polymerase
MSLLRARQPILGRSLTSGPILPRASLPSSTILRHDQLRSSTRLFTSSSASSPSSILFPLSRTGPSSSRSSTTANFAR
AKHSTSTQPKEPVFIASLQSHKESAPVTK**SASQTELEK**QQREWEAKRELENLEYEWETKSVEKAVERYKKISKSLKQ
LGLAFELLQGNQILGHWFEPLCAAIR**AEQNAALLK**TSAADAAASPKKGKKKTQKAEDRELSAYLVTIPPEKLAVITI
HETMCEILKSHHPEGAPFAALVVAVGRAVEYEYNCERLAKEGWKPQLRNRSATPTKQQICSLIRTQSRAQFEDASWG
AALHAK**IGSLLVQQLLGTATIAR**KAEEADVAAAQSSPARLLSGAPRKRPAFVTKEEALLEPAFNHHQAMLRGKLTGF
LGCHEQVLALMEHEEVQRGVMQARYMPMLVEPQPWVAPNQGGYLVARTQVLRAKGSRMQTEVLRSASMDKVYECLNL
LSSTPWRINNRMHEVICEAWDNGGGIADLPSRTNLPELEPPADYYSDLEVKQKFDRERKKAKIANYNLHSLRCDVTY
KLQVAKECQDRTFYYPHNMDFRGRTYPIPPHLNHLGQDLCRGLLTFAEGKPLGESGLRWLKVHLANVFGNDKITFED
RVRFVENNMEHIMDSASNPLGGQRWWLKADKPWQCLAASIELINAYNSGQPETYVSTLPIHQDGSCNGLQHYAALGG
DEMGARQVNLLPSERPQDVYSGVVELVVR**RLEDDAANGVEIAQR**LLGKVDRKVIKQTVMTSVYGVTFIGARQQIENA
LKDKGKVSDDDMFLASR**YLATSTFSSIK**EMFSGAREIMTWLSDCATLIAKQGKPVTWVTPMGLPVVQPYRTKGKQTQ
TVVTALQNVMLVKEENDSLPVNTRKQRTAFPPNYVHSLDSTHMMLTALQCHEAGLTYASVHDSYWTHASSVDTMNHI
LRRTFVDLHSQPLLDDLLAHFKRTYPGIEFPPVPPKGDLDLKEIINSPYFFQ

>N330_porin_3_family_protein
MGAEESRPRYTLVPPVFKRRRPLRFVEAHEREYDEAGKEVRRLLSDLYTTDSSVSGEFFASPEENVDCYAEIHHPYQ
SVGGNTIEGSALFTVR**SEPMTVEGLLFSK**NGGGASITLGYRTKDDSTTSYVAAEHMVNKPGGGSGTDLKAGIFYRYK
YLSCGASVTSPLDLTLNAASQRGGLQALRQRVDGNVWAMFKQGTVALGTACQLVDGRPDALNGVICYR**NQWTRPDEP**
CTELTIRTTQK**IADGQSAPTFHGSYYQR**MVTRRKVQNPFEEANVQFITNYVDLGVETTVAATGTKMAVGAAWQVNKN
TLVKGK**IGNSAFSFLVAAK**SWWDPSATVALTVSKPFDGASRGTRIGLAFSIENWGGIGYHRPSDTYKRYVPMQMDR**V**
SDETEPDTAEALLRRQKTAAN

>N331_L-lysine_6-transaminase
MSSSAPLTREQVK**NLKPNQVHETLGR**KLLVDGFDVVYDLDKSKDLYLHDARTGRDFLDFFSFFASWPISHNHPKMSD
PDFKQRLLK**AALHNPANSDIYTVEMAQFVATFER**VAMPPQFKHLFFIQGGSLAVENAMKAAMDWKVRLNFQNGLKQE
KGKKVLHFKEAFHGR**GGYTVSVTNTADPNK**YK**YFALFDQWPR**ITNPKIKFPLAGENLVQAIKDEEKAIAEIVHHLET
DGDDVCCILLEPIQGEGGDNHFRPEFWQQLRQIANKYDVLLIADEVQSGMGLTGKFWAHQYYDVVPDVIVFGKKSQV
CGFMATDRMDIVKENVFVVPSR**INSTWGGNLVDMVR**SRHFLEIIEEDNLVQNSAQTGAYLLQLLHGLQREFPHLINN
VRGK**GLLCSFDTVTPEVTNK**LKAFAYEK**NMLIISCGTQTVR**FRPVLDSKKEHFDIAARILREALVHIDRENKKAAL

>N332_uncharacterized
MRRASFLRSTPSSFIPVGSRRIGAAQQLPSVATGPLRSISSSTSAALPLLTKRSSLPLSRQSARWMATQGDASSADS
SKKEEQHDNDQQQKEQKEKQDDERKEEDQKKEDWEKSRGGGYKQEVNTFQK**LLAVGIPVTAIVLGVK**VLLDMQATGA
EDDTLQVDMNVIMGHVFQNTVYNVLDSKR**LVGLLGDPLLVEPSK**AKFSFTKDSAWVCYPLYAPQGHVCTVTVDLLRI
DPKGKDVKTKKPHMWYVAQVEVDLNNGKKVLMSTRMSDGLR**QPFNVLTLFAK**LYHDLK**KQEQEFLQQQAAAALNQGP**
APQ

>N333_uncharacterized_conserved_protein_(mitochondrial_K+-H+_exchange-related)
MQAATGKGGPRIRLLVVPVLRDRWVFSVPHHAEALASHDTSSPVSGWGPKGLQRKGAELLGRAKDSFDRLPREGLKG
RLKAGVDALNRRLDPSESMLKCLTAAHR**TVAPAADEAVTTR**GVANDEGNQPEGLTEAER**ELQLEVVYPAK**LSGEQVR
ATLSQLVAARTKRHQNLAYGSTAMLPVSLAMGLLPGPNVFLAWNVYRLYSHVQALRGGK**LFLDLSSR**NR**ISYSPSHE**
LEEIVRTEERHEEPLSQAQIEELSATYGLR**TLLEDVER**LRIVGVAQRQDSGKEPTGK

>N334_adenylate_kinase
MYGRSAVAGRAGSIKIWRANCAQQFRFFTTNGSGSASALR**LIIIGPPGGGK**GTQAER**IERDYGLSQISTGQLLR**AER
DKK**TPLGLVIEEK**LTK**GELVADDLMLDLVNNAVASHTNPK**GWLLDGFPRTTAQAQMLKNLLDQIAKPITGVLYINVD
KNVIAERLKDRYIHPGSGR**TYNLQYNPPKVAGKDDVTGEPLVQR**EDDKPETVLSRLTVYEEKTRPVLDYYAQTGLLH
TIDSPNSDVGYERIKKLMDQLLRQ

>N335_copper/zinc_superoxide_dismutase
MATKTAVCVLRGFGDAAVEGTVRFSQTADDEPTTIDVEIKGLKPGPHGFHVHEFGDNTNGCVSAGGHFNPFGKKHGG
PDDEERHVGDLGNVVADETGVARTTIKDRLVTLGGPHSIIGRTMVVHADEDDFGKGGFEDSLTTGHAGARLACGVIG
LSK

>N336_rhodanese-related_sulfurtransferase/oxidoreductase_family_protein
MRRGASVAIARCSVPVGRTLHSGTVLRSSALHLSAPHRRHIATTEENAGGRPANVVWDSDHSWKKKDARSLPSDQLV
TRAQLKALLANNSSGALLLDLRSVGECKVEPGIPGATNIPSEDLVRSVALDEGKWRARYGFAKPRPDTHLIIYTTPE
QKAKAIETVDTLLQHGYGRVSVYEGGAREWNKFENATC

>N337_inorganic_pyrophosphatase
MLRATCGSRVLGRTAVTRCSVALHGRGPAMTTSVEAREVGTPDTPGYRVFFYNTEGKKISPWHDIALTEPGTRIEQG
VLRYVVEIPKGTDQKMEIATDEPWNPIKQDTRKDGALRYLKHGPVLCNYGAFPQTWEDPSAEAHPQVNLAGDNDPID
VIEIGSRVAQRGEVVKVKVLGAFALVDEGELDWKVLAIDVNDPKAASLNDVSEVEKQMPGTLGAVQEWYRVYKVAEG
KQKNSYAFDDKALDRAFTLSVLQHGHESWRKLFTARSSPKFAFDSTSGAQ

>N338_thioredoxin
MRRVAAISHKGGNGPLLARSIRSSGVPLARRGNASAADSTSQLLRSSRSVVPARAFNQWRGLATQTQPPPTASSFAQ
KKTNSPPQQKSSSAADSNIYEVNEANFLKEAIEASDKRVVLIDCYADWCAPCKQLAPLLEAAVRNSGGRLALAKLNV
DNNPTLSRQMQVTSLPTVMALSGRKVVDSFVGLLKPAELTKFVEGLLQDFAPAAPAEEAETGGNLLEEAEAELAKGD
VNQAAAKFSQALEKDKECTHLVYAGLARCALAENNLQAAQHLVKELKDKYKAKLNDPAVGKAIAAVELRAELADKSG
GSAQDLEAKVTEWRAKLQADANDHQARYDLAHALFSTGQTEEALDQILDLIKRDKHWNDEAARKLMLKIFSALGPNN
ELTTKARKRFASIWFC

>N339_putative_mandelate_racemase/muconate_lactonizing_enzyme_domain-containing_protein
MKRATSVSRTLVGLNKQVTGPRAGTMPLLSSRHFSSTTPVQREKPRVKELRAYVVQKDEAGADYHRQQSGHWIIDTP
ISNPMSVYPPYRKSRVSWGIDVLGTVIVEAELEDGTVGVGTSIGGEPACYLIENHFSRFVEGQDVRNVELMWDQMWR
GSMPYGRKGLAIQALSAVDLALWDCLGKLWQEPIYNLLGGKTKEKLPVYATTSRPDLAKKMGFHAAKFPLPYSHAEG
EEGMRKNIECVRKHRESVGPDFPLMIDCYMSLTVPYAIALAKAVEPYKIKWIEEFLPPDDYDGYSQVKKGKGEASCL
LTTGEHEYTRYGFRELIERRCVDILQPDITWVGGLTEAKKIYSMAAAYDIPVIPHGSSVFSYHLQFAYANSPMAEIL
IMSPKADKVVPVFANLFTNEPLPDDQGYLQLDENKHGWGVDLNKDGLKLQRPYPRHQH

>N340_homoaconitase_(Lys4)
MKRFLGSSAVSICGSVHASASVRGGTRCLASNFHTSAAAWQRPQNLVEKIVQKYAVDAGGREVQSLDFVTIRPRHVM
THDNTSAVIKKFKSIAASVKDREVRVANPRQPVFTLDHNIQDRSDANLNKYKQIQEFADKYGIDAYPAGRGIGHQVM
CEEGYAFPGTMVVASDSHSNMYGGLGCLGTPIVRTDAAAIWATGATWWQIPPVAKVELRGQLPEYATGKDIIITLCG
LFNKDEVLNHAVEFVGEGVGRLTIDDRLTIANMTTEWGALAGVFPIDDHTIGWLRERESYIASARGQRKPIASDVDG
HGQHHPRINSRTIQELEENVLAADRSAFYAKELVLDLSTVRPHVSGPNHVKVMHSVDDMERRGIKVSKAYIVSCTNS
RVQDLSAAANVLRGKKVAEGVELYIAAASSEVESDSAKRGDWQALIDAGAIPLPPGCGPCIGLGAGLLKAGEVGISA
TNRNFKGRMGSREADVYLASPEVVAASALAGIIKAPGGPGANGLTAQGSVKVNSKDTQDSGEGETVAILPGFVEKLE
GELVFCHQDNINTDGIYPGKYTYNEDISPQQQAEVSMENYDPAFTKKARKGDLLVSGYNFGTGSSREQAATCLKHYG
ISLVLAGSFSETYKRNAFNNGYLVIEVPELVDYLKQKAASDKGTNELTQRTGLKAVLDFKSSVLSVDGRKFAFPPVG
AVAQEIVLAGGLEQWVEKKL

>N341_Complex_IV_subunit_Cox7c-1
MNFLRRTPLSGVRTLFVRGHGPTHGPDGRLLGQGIGTTFPFSTAETAKKKYHTGRAVWGYFVVGVVAPCWAVWFSAN
KEAK

>N342_uncharacterized
MRRIVYSASAATRAGSPFHGSTLCRLNFDSHRSLSTSLVLQAAKAGSAVEATKETKVKKAKQEKTNAESTLVTKQKE
KKEKVAKAKETKPKKAKKETNAAVSAIEQAATGEEVARFLHGVEREGHVSAALAHAGMPQEDQMQLKGFVDALEKIG
KTRPADKPWGVFKIQDDGQVEPLGLFRTEQEANVAFGDDQEPATKPKKEKKEKSADGENQKSRKEKRDEKKAKEKVK
KEEKAKKAEDKKLAKVAAKETKADKPKSTKKGSKKAETASGKEEELK

>N343_Tiny_Tim_homolog_Tim13

MAQITDQQRADFYRKQEESVGQQLFQQMVQTTKNRCFKTCVTRPGAALSKDEQKCLINCVDRFFEARAIVMHSYNKV
YQSMMQQEGGSDEF

>N344_putative_Complex_I_(NADH_dehydrogenase)_B14.5b_subunit_(N4BM/NDUFC2)
MATVCVLSGAALGLSSTLYANAIRKTYLLRAPWRHLGGIVGGGLLGYYYHKLDQHEDAKMAALGKKYREMYGALDNP
LLVQPPYLRTSSESKESSSDE

>N345_uncharacterized
MEQPDIKSGEGANDVVSSVLSESLYRGLTASVDPYFGFLASLGAVGWAAVRTGAWRTVQTGGPWAWAWAGSAWLGAV
GATWALTRTVRGIEEAQKLDYFLQSGALVPTAALRDFIDAMRPRPLWNVAVWTSFVASVGSLAVWTYRLPAGCTERS
LVGVSAAFLVFATAHLARFAADQSDAEQWTLFRLPSRRAGSSTAGDN

>N346_DNA_topoisomerase_III
MQRCGGLARYPLLRGVPGSGSLPSAMLVGPRFTNSIIGSHLHFIPRLSFTTRGRPRKSVEEVATPKEPKEPKNKHNV
AGTSDPGPKVKSGAKAKKGAEGQTTEKKTKKEAPATEAKETVPKAKKARAEKAAKPTAKLPKTTLEAVKTAKKAATQ
RAEVEAPDELLNKAEAKAPEKRPKKGKVEPTTQVATATGGAAERTEAVKEEKPARVVEAERGETTKEDAEAALPKWE
HLTQAQLKEECKKRRLKVTGSKKQLVERLQEATRPPPAAAVEPQPQGPVIRIILAEKKSAAENIARALGIKKFKKEG
AKEPGFIGNVELTPNGVQVVPDESGSGGATVVTWASGHLFELQKYAMWKLDKLPMLPSEWTFSCKGPAQKRQFEVIR
RLFESADEIVNACDAGREGELIFREIFEQAKPKAPFKRLWISSLTDEAIKEGFRKLQAGTEYDSLYHSALARTKADW
LIGMNATQVYTLSYRPKVPSFQGKEAVSLGRVQTPVLKMIVDRWKAAHNFKPEPYWELHLRCRPQGSDEHLRLKYFS
PEAASERIASEQEAEDVRHALGPVCTVQQLTHKRRIEKPPKLFDLTALQREANRRYGYTAERTLGALQGLYEHHKLI
SYPRTDSRYLTKDIFNDVNTILDGIGKHSMYAPAIEDVRNSKRLSLSNKAVFDAGKVSDHHAIIPTTNIPSEKTLAH
LSPDERKLYHLIVSRLLSCFMPDCEKQHTELVAVNKSKHFRGRGVELVKPGWRSVYSLSPFAAPQDGSSVDEKEVDD
QSTTGDGGDSIGDGDEEEATTDDGNLCSIASKLKENDTLACVLPAEVKCEHTRPPPLLNEASLLFLMETAAKYVAKK
GAYDAENEADDGAEESLKEFGLGTPATRAQTIERLIAVKYVRREGKKLVPTEKGKILIELLQKTHSSLTSPQMTGQW
EKRLQDIAKGEGSHEAFVEDIKRFTEQVVDEAKVGATRLPDFRKMMRTINQQEEGTPQTSEAAGAEAATQARGGWEE
EEEEVLGDCWKCGKGHVVSRARSNRWTCSTESCDFIIWKTTASREMQREELKELLTEGVTPFLSGFKSRAGKPFEAR
LAINQDGKVVMMFPFTVRRSAGGGSGGGHGRGGLSRRLPGITESSETDE

>N347_glutathione-disulfide_reductase
MKRFNFDLFVIGAGSGGVRASRIAAGQYGARVGICEESRVGGTCVIRGCVPKKLLVYASHYPEEFRDARSYGYSFPG
VDGKEEDTAWAFDWGRMMASKNRELNRLEGVYRNLLTKANVDLMEGRGVLLDPHTVQIGGSGGKTVTAERILVAAGG
WPQLPQIPGIEHTITSNEALELESLPKQVAIIGAGFIACEFAGIFHGSGTDVTIIHRGPVLLSGWDEDVQKTVTSLH
RERGIKLASQSGVAKIEKDPRTGKLRVFTFDSKTKAEGPVVEADVVLSATGRAPKVEGLGLENAGVKVNEKGAVMVD
EWSRTSVPHIYAVGDVTDRVNLTPVALAEGHAFADTVFGKKPRQCDYRHLPWAVFSQPPASAVGLTEQQARKELGDD
GVDVYVSSFSPLKHTITKRTTDRVMMKLVVDRKSDVVLGCHMVGPDAPEIIQGLAVALKCGARKAQFDATIGIHPTS
AEEFVTMRTKRT

>N348_mitochondrial_valyl-tRNA_synthetase_(ValRS)
MLQSLRRKKAGGGLASIHASGALIPRLEIRSSAVLFRSTFVRSSTTSRRTLTSAPRTKPPTQGPLAAAYDPKAIEGA
GWYQWYESQGYFRGKNGVPPGHNFSMVIPPPNVTGTLHIGHTLTVAIQDSIVRWRRMMGDNVLYVPGTDHAGIATQT
VVERRLQKEKKLTRHDLGREAFIDEVWKWKETHGNHINNQLRRLGTSLDWSREVFTMDPQRSKAVTEAFVRLHDEGL
VYRSTRLVNWCCFLQTVISDIEVEYESLSRRTMIALPGKGTKKYEFGVIHHFLYRVEGGGELEVATTRPETILGDSA
LAVHPEDPRYVDFIGRRAIHPFTGQPIPIVADPILVDRELGTGVVKITPGHDFDDFACGVRHNLPRINLLRNDGTLN
QHGLHFQGLDRMEARRKVVEELEKMGLYKDKKDHESRIALCSRSGDVLEPLLKPQWYVACQDMGADAARMVRDGTIE
LIPDFHKHEWYRWMENVEDWCVSRQLWWGHRVPAYKVVAEGEERAAANNKDNDTLPEDWQKERWVIARNQEEALEKA
KALYPDIAAPKLEQDEDVLDTWFSSSLFPISALGWPDNTQDLKEFYPLSVMETGADILFFWVARMAMICSKLSPTQQ
APFKKVYLHGMVRDAHGRKMSKSLGNVIDPLHVIEGIPLEQLLQNLNHNLLDEAERKKATAGIKSDYPAGIPQCGTD
ALRFTLVNYTQQTRNINLDINKVVANRHFCNKMWNATRFVLSYAESTPVAQPEPDDLASKWILSRLSQVVTKCNQGM
SDSEFHVATSSLYDFFLNEFCDVYLEYAKLYISGEPRPRQAQIKNVLNTCLESYFRLLHPFMPYVSEELWQRLPTSH
GQEKEDCLMHAAYPLAANQVAAWRNEETYEKPMEEVLRVLHAVRSLRDGHGATPLKYSVSIHTTDASLYDLLSNEAS
VIRHLARASRIDVQHNAAEPEGCGVRVLDSRTQIFLPLLHLGGGDHQQTTATSAEVSLSPENVANLQKEVEKMNKRK
KKLEKEIEWIEQKVAGPYYLDKVPLDVRNQDKEAKAEAEKQLKDVERSIRSVSDFMHKYQPL

>N349_amine_oxidase_family_protein
MDTAPLEQGSNWDVVIVGSGLSGLTAATRILQENKERKVLIVDAVDWFGGRTRSIELAKYDSKVSIGGTFALFEHND
TLQLAKEINCSPTETLKISDVNFNQFSKALFDPSGLPLFFKLMYKGAKIVKEGKIDWSCKTAKELEKISLEDWISKH

WILNKFNPNFTREFFYLLETFPNLHGVSALVCAIALYVRFRGIPRNGIEIPPKVLRWEGGTGVFTQALVESLSHHEN
FRLKLNSPVEQIIQPAINAGANAGPYPVQVVVNDNHTGSVTVNAQYVVVATSPLAAAPANLGGTINYTPALEPGAAQ
LFSSMEATPTVSRQILVVYKNRWWKKQGGGMFIMPPYATHVNEMGVWGNVVDGSMKDERKAGIVRIFVDSR**RLDGMS**
PKQVEQSTIDFLKHLFPKQHDLVEGYEEIIFHDWNTAKPTIPGVTFTYAPTNNGVLSKFGK**YFTQPYGR**IHWGGSER
SVWGANWMEGAVERGNDVSEELMKMAGWVGPDYNVRKTAATLRVAKRAMPVAAMGAFAVETSAEEDDLEAEPDLEPI
KLLPTPTSPLGLAESLQPDDGDKLDIHELYTRVSQVEKPRLLQENDVWISPQMCLDALRELEKAKLLKKKRAAEAEA
EAEAEDEAEVASSSSSSSSSVPHPATSSSPLLAGVTPRPAHLPEGTTPFSSSSNEKPTVQQLQAVPTLRGEVPAFLL
GLTVGVFVTMAAFRFAKGSSQ

>N350_methylmalonyl-CoA_epimerase
MRRSSALARGFAPLRSNAPASALFTTRRTLTTSAGASQLAVGVGK**LNHVAIAVPDLEQATSLYR**DVMGAKVSEPLAL
AEHGVTTVFIELGNTK**LELLHPLGENSPIANFLK**TKPSGGIHHICLEVK**DIHAALEVLK**AKGIRAIDQKPKIGAHGK
PVVFCHPK**DLNGVLVELEQV**

>N351_mitochondrial_ribosomal_protein_L13
MTTSFAPCKQPLTNTHMWHVVNGRGLKVGHAASRIARLLIGK**HKPTYNPAFDAGDYVVVTNAEK**LIFTGDKWKQKLY
RWHTGYPGGLKEVKAKDMLYKHPDAIIRTAVSKMLPKNKLRWERLKRLRVFVGEEHPHEGQVSQGYHYQVEPQSR**SA**
VDPALAAFRDQVVADPDAFVRKYGGGK**FSIVPQEQGMAVVATK**IKGTHAHAVRSFGNTRSLRAARLDRLR**KVVEDIQ**
SAQAREAAKRDPL

>N352_Zn-dependent_alcohol_dehydrogenase
MKAATTKLATRSRPVTPMLSPALLTRCSVGPTCTSQSLLARRFSSDVKKTMK**AAVVPQYDLEDSDEVHPASLIVR**SD
WPVPSLHDVESRHDEGDVLVQVAASSVNPIDSMLRRGYGR**ALLEATAQGR**SRLPFIPGFDVAGTVVDVGTGVWNWKK
GDMVWGGAELFRNGAHAEYIAINQHALAPKPANLTMEEAGSLPFVALTSWR**GLVDTAGLSSSTSK**RIFINGGSGGIG
VFSIQLLKSWGHYVVASCGERNVEKLTK**LGCDQVLDYR**SPQFQQFLDTPESVDVVLDTVGGAKSEARGLRVVKPGGH
YLSLRGPLATMTDSGGLVGGLLGAATTIAQKKLAAFTQDRRHVHVDYVIYKPNGDALREVGKLVEMGRIKPDIDR**VF**
DLGDIREAHQYLEGGHARGKVVIKVM

>N353_Complex_I_(NADH_dehydrogenase)_ESSS_subunit_(NESM/NDUFB11)
MRSATRRATLAVPSARSIVSTSSLSSSSRLLATHAAPGVTSAGHDFKADEHHDDHHHDDHHHEDGPTGYLWSRQPGV
KYPRESWEMITYVGIAATLLLGWVAISKSGK**VSVEEFGQMEIAR**RRR**EREQGQPQPEPLQLQVDPTK**FR**KTPQVTEH**
GPQ

>N354_alpha/beta_hydrolase_domain-containing_protein
MQRQMRNRLLRSSVVNFNATPLASHARILSRTLSSAVSEEHPYLHTTAK**APPPEGTVVLHNTAVTSR**APKAFSRPPL
AIAHGLFGAGINWRSVAKKITPACNVNSLLLDLRNHGSSPHHPEHTYDAMIGDLHYLLTQRYGINTFSLMGHSMGGN
MAMRMALKYPDLIDR**LIIVDFAPTSYQSIEK**YKDYIEIMQSIDLTAIKSRGDVDKIMAHTIHEPLLR**AFLVSNLVHE**
ADKSWRWRLNLDALKRFIGPIRSWDIQPQEGLQYK**KPTLFVGGGK**SQFIKPEYHEKIHAFFPNAKIEMIPDADHWVH
FEKPNEFCHAVESFLHRTQQ

>N355_uncharacterized
MRRMARPAPARFLLAGPPLPTRGATSLLSAPSARSLSASLASKWPVRASGTRRFFVSSTIIHRQARDNVVDAEPVQP
NPGQSSPPR**SELPQQQIDEQFDR**VYEKLFNKKRPARGERDSHDAANPFTQDWRERLFDIMFSNAGNLFMMTVVASLF
FQIMREQGEHKEYKRLTTARLDDAQHALRVCQAQVHQAADAR**RQELASALER**TNTAVPPEEVKRLVDQLLTSLVADI
DASLTTDESKATTQTEASSDSALVDTNTPATSSTAVATTAEGHQAGYHKVV

>N356_nicotinamide_nucleotide_transhydrogenase
MKARACLPLGGASSPNLSLFKRIGSYVPGRAYFTTRPSASAVSSASNGGVPYSRLTIGVPKEIHHTERRVAISPANA
RLLTKQGFK**VVIEDNAGFNAK**FLNEEYVANGAEIAANSTETLAAADIVLKVRPPLENKELGRHEVEMLKDRSTLISF
LWPAQNRDLVDRMVAQNKGLNVFAMDAIPRISRAQTFDALSSMANIAGYK**SVVLAANHFGRYFTGQITAAGK**VPPAK
VLVIGAGVAGLSAVATARSMGAIVRAFDTRPAAREQVQSLGAEFLEVLIKEEGEGGGGYAKEMSKEFIEAEMALFAK
QLKEVDIVITTALIPGKPAPRLITKAMVDAMKPGSVLVDLAAETGGNIEVTRPGEIYTYKDITCIGLTDLPSQLPTQ
SSTLYSNNITKFLLSLTPADGTKNAFGINLEDEVVRGSIVLHNGQLVWPAPKPAQPAVAQAMAAAADQAVKELKKEE
LVQDPYKAALKNITMTSAAFTAALALGTFSPPGFDTALTTFALASIVGYQVVWGVTPALHSPLMSVTNAVSGVVGIG
GLHLMGGGYLPDDMPSLLAASAVYMSAVNVFGGFKVTGRMLDMFKREGDPKDYGYLYTIPTGLFIGGALAAQSIYGP
QSLHSLAGLVSAGSCIGALACLSNQKTARLGNTLGQVGVAIGVAATLSHIAPSPEVLAQMALISGLGGATGLAISKK
VAITDLPQLVAGFHSLVGLAAVAVSVAQYMLDYDTFAMDPMGNVEKGAIFLGTFIGGVTFTGSLTAFAK**LQGLLNSK**

PLQLPGRNVLNAGLALSNVGAFAGFMSTADPIAGLGYLAYSTISSFALGAHATASIGGADMPVVITVLNSYSGWALC
AEGFMMGNDLLTIVGALVGSSGAILSYIMCKAMNRPLLSVIFGGYGISTAPQTQLSGTVQECNVDEAVEMLTNAKSV
IITPGYGMAVAKAQYAIAEITKLLRENNVNVRFGIHPVAGRMPGQLNVLLAEASIPYDIVHEMEEINEDFPKTDLAL
VIGANDTVNSAAEEDPNSLIAGMPVLQVWKAKNVIVMKRSLAGGYADVPNPVFYKPNTSMLFGDAKKTCDALLAKIA
LHYNVDRE

>N357_esterase/lipase/thioesterase_family_protein
MRRTPLRGALLFHNKSGSVSSLSSILAPSRILPTPAIHSASSCASSVRLVSQARLLATQANSKNLK**ISNEENQIEK**D
WKQEAKELREELRLLKEAVRLLQREASSTNKPVRAKKSAAAAATHLEDAASPPSTLATELPPLPPATTTKVEVTVTD
ASVKEDRVNRDVKEMVKRALLALR**GPADATVTPDAANSNWQAR**LKKLMR**QDDVAWVDR**LLASNVAK**RLPSETDWDR**L
LEQTKNLSKEVKEVKVKKWLAEHK**AVAWLQTR**LEKLNTVNPK**VEWEQVLTR**LKAIPPGILSLDHVRTLQQQSKTLDG
DAQVNRKQLEWMAKVAARLAKNQAKRK**VNLPEVPAPTKYPIVLAHGLGGDKPFLK**CFMGIPEDLKPLGVPVYTPKVA
RYGTVFARAETLKEQIMQVLEETRAPKVNIIGHSMGGLDARHFISNLGGHEVTASLTTLGTPHRGSSYSDWIIAMTD
AIGLERLFQAQILPFPMEGHHHVTPKFMKDVFNPQTPDHPDVAYFSMGGSKKIARTHPLFICQRILSK**YEGLENDGL
VSVESSK**WGEYLETLDMDHAAMINWSYQYDARELYRRLVNLLRDKGF

>N358_rhodanese-related_sulfurtransferase/oxidoreductase_family_protein
MQRSRLISRSSGSSLFQRRPACEHNVARLVTGGLGRRFLATSPAGDQAPAFGVLQATEAKSHLPDFDLLLDVR**EPDE
WAAGVIGTPK**TITLGRVMR**DVATDELQSLK**GKKLLVYCRSGAR**SALACGVLAKNGFQVTNLAGGFR**GWREANSSSSD
APPNKA

>N359_electron_transfer_flavoprotein-ubiquinone_oxidoreductase
MKRLSARLSPSASAAALGVRVSSRHLHLARTAQVQSSSSLLPR**APITSSLRSFRTSPSLR**QDDDPRKQPRESDNVDV
LIIGAGPAGLSAAIRLKQLANEQGKEIRVVVLEKGAEVGAHTLSGAVIEPR**ALNELIPYWK**DKGAPIYTEATEDHFV
FLGEGFHVRLPTPPQMHNQGNYVVSLGNVVRWLGEQATELGVEIYPATPAAEVLYNEDGSVKGVATVDMGVSKTGEP
KDSFTRGFELHARVTMFGEGCRGSLTKSVDKKLGLWKESMAGFQTYGLGIKELWQVDPKKHKPGKIVHTIGWPMDFS
TYGGSFLYHLENNYVAVGYVVGLDYTNPYLNPYREFQRWKHHPFVKDTFEGGQCISYGAR**ALVEGGIQSVPR**LAFPG
GLLLGDSAGFINLPKIKGSHNAMKSGMVAAETVFEALDQEEHTIDPKAYPDRIKSSWLWEDLHKVRNIRPYMAKGLV
PGLALSAVDTYVFRGNAPWTLNHHKPDHEATKPAKECKPIEYPAPDGK**LSFNLLENVAR**SGTNHGHDQLCHLTLKDS
TVPEKINLPVYAAPESR**YCPAGVYEYVDSK**LVINYQNCVHCKTCDIKDPTQNINWVVPESGGPLYSYM

>N360_dihydrolipoamide_branched-chain_transacylase_E2_subunit
MRRFASASTSRAPASRSIFSRALRTNATRNVPRVECSASLMTGCRGVLAKETIPLSATISTARRGFHATRVASSGQT
IQFNLADVGEGITECEVLKWHVKEGDRIEEFQPIAELQSDKANVEVTSRYTGKITK**IHYAVGDLAK**VHTPLVDILLD
ASESAAPAAAAAAPSPSSSSSSSSQSSPSSSSSSSSGHSGPVLTTPAVRRIAKENSIDLSKVAGTGRDGRVLKEDVL
AYLEGSPLAHQAPPQFALPTAAGAVPPLPPSVTTTTTTEAGGLAHVVARKAVVGADREVEIRGLQRAMVKTMTAANQ
IPHFGYSDEIVVDQMVALRDELKPIAEARGVKLSYMPFILKAISLALK**SYPVLNSSVNADVSK**IIYKASHNLGVAMD
TPQGLIVPNIKDVQVLTIFEIAQELNRLQRLGKEGRLGKEDLTGGTFTLSNIGVIGGTYAKPVLMPPEVTIGALGKI
QKLPRFDER**GNVVPTHIMIASWSADHRVIDGATMANFSNLWK**NYLENPKAMLMDMQ

>N361_universal_stress_protein_family_member
MAEKRAQKTKKDGDGNYEEDLDTYFVDRLRFLNQRDHTTQHLKQRFKERNGR**LEAQEETGDADKATTTQR**QVVDDEG
LAVVCVDGSPAADEALRFTLAQMPHAR**SLVLAHGIR**VSLTSSSSSSSGSTHAPFGEDEETEALHQALERRYLKMCRD
AGRHCMVKHFTYTTRGGFGHAVCYLADKK**DAAAVVIGQR**HPRPLLGASGTAVMK**YCGQRPVILVPESR**ASVATDREK
EKPTAVGHH

>N362_mitochondrial_ribosomal_protein_L9
MRSSVFRVGGVSPLALSSYAPLRAGSLFRTSSILPQHDWTALVSSRGYATKKTAAPAKAKPKSKASGPQKSNKPVKN
KKIK**IVLTSDVPSVGVK**GEDVEVAKGFARNYLFPQK**LAVYCTEENLK**LYEADRANIDYEKRQKLQELAKAKKRLSKV
EVLMKR**QIIQVQPEQILHAPVTADNIVEK**LWLQHKIQLAK**DQLDLEAPISQLGTFSVPVKLEDIDVPLK**VRVQAR

>N363_L-threonine_dehydrogenase
MRRTAVFGVTAQGGLSLGGKSGARSATALFRSSSPIAATSDRRTYSVEKKQPKVLITGALGQIGTELVPLLR**QQYGA
ENVVASDVR**KASGPVGDGGPFAYLDILNMADLERLVVEHKIDWLIHNASILSAAGER**NPQLALEINVK**GLTNALEAA
KRHNLR**IFAPSSIAAFGPSTPR**DATPDLTIMRPTTVYGVSK**LYAELLGDYYHR**RWDVDFRSLRYPGVLSSVAPPGGG
TTDYAVDIFYWALQKGEFKSFLNKDSALPMMYMPDCLK**ATTMLLEAPTEALK**QRTYNVTAISFTPEELAAAIKKRIP
NFRITYEPDFRQAIADSWPASLDDSMARKDWGWKHDFDLEAMVDDMLAKLRIKLGIKQ

>N364_UPF0041_domain-containing_protein_1_(putative_pyruvate_transporter)
MSGSAWTKLEQRFFAKYHGVEGGVLLKGPFWQNLAQKYPVFGKVNNALWAAPAFKWGLAIVPLYGILEGKPAVKDLD
LNQSLALSLTGLVWTYYGFLVVPRADLLIAVNVALLSVNGYNVYRKINYDKQMQAAQAHA

>N365_AAA_family_ATPase-like protein
MKANARGLAQRVCGSSHTRLVSTGGQALRSAARSKADKPLRPKFDVLTSHKSVFEYTLGCTLGLAGGYIIWGQELKK
KADAIRELKEALKPEIVEVDPLQRLDQSHSDSQVYTVVLTGGPCGGKSTALATLTKHLRAQGYEVYSVPEIPTLVFT
AGVPTISSMNEEQLLAFEKQILTTQIQLEESMKKIASAMDKPTVILLDRAALDISAYLPYSFWKKLLQDLDITEKQL
RERYTAVVHLVTAANGAESYYTTANNAARTEGIEQARELDDKVKHAWIAHTRTFVADNTTDFPGKMQRVCSFLDDVL
TSQHKAAPTKETPEVK

>N366_iron-sulfur_cluster_assembly_protein_Nfs1_(IscS)_(cysteine_desulfurase)
MKRNSSSITHRGALLRKGWPRAAPSAAPIRLSSGAARMASSVPSATQGGRSVYLDMQATTPVDPRVLDAMLPVYTEA
YGNPHSRTHHYGWETQDLVEDAREKVARLIGADAKEVVFTSGATESNNAAIKGVARFYGEKRKHIITTVTEHKCVLD
SCRVLEAGEGFEVTYLPVEKNGVLDVAKLEAAMRPDTVLVSVMAVNNEIGVIQPVGEIGQLCRRRGVFFHCDAAQAV
GKIPLDVNAMSIDLLSISGHKLYGPKGVGALYVRRKPRVRLHPIISGGGQERGLRSGTVPTPLVVGLGKACEVALEE
MERDGAWVKHLFHRLYDGIRARVPEVYLNGDLERRYHGNLNISFAYVEGESLLMALKEVALSSGSACTSASLEPSYV
LRALGVSEDMAHTSLRFGIGRFTTEREVDHAIELCAKHVDRLREMSPLWEMVKEGVDISKIQWTQH

>N367_cytochrome_b5_family_protein_form_2
MAAPAKTYTLEELKKHNTTEDIWIAIQGRVYNITPFLEEHPGGDGVLVDNAGLDCTGEFEAVGHSDEARATLEQFYI
GDLVTADGAPVKSEKAPVQPKVSLADTKAPKPKVAAPAPAVWKQAAVPLLIIAVGFVLRYYFSS

>N368_uncharacterized
MSDSVVAVPPSSSSSSSASTQGVQTRLSTSGAVVPIRQLGFISRFTKSIKKYLLQPFVVGFAVALGMSFGYSAYDAI
VHRVATFWKS

>N369_mitochondrial_ribosomal_protein_L4
MKAAGRHCARAPRSNQRLISSAALSLGVPSPSSTAGHLRFIASRTPLISMRYPRMSPILAQMGVHSSVPSSSIFGGV
KEEQKEHNKAAASDEEDEEEDAELDAAEDEAEATAVVQRATGLIDGTQRWAPTLELPVESFLNEEQQGPLGSVTLNP
NIFMVPIRRDILHRVVVWQLAKRRQGTHKSKTKAEVRGGGRKPRPQKGSGRSRQGSIRSPLWVGGGHAHAKKPRNYY
FPLLRKVRKLGLKTALSLKFAQGKLKIVRSTHVDEAKTKNLARVVEGKDWSKALVIDGKSVDDSFRKASNNLPSVKV
LPVGGCNVFDILNHDLLVLSLEAMQHLEELLLEENEPTFYPEPATFQAKEETLA

>N370_DUF607_domain-containing_protein_(putative_calcium_uniporter_MCU)
MHRAATARTAASRLCGLATTSSMACAPSSALLRGFAASGALLRPSAAVRRLPSRRYASIAEVKEPLEDVLRKAQYRQ
VTDALERDGSRVRVSLAEYLDLCKQYNVEEAEARELLKSLHKSGRVLHYENSPELAATVIVRPDALAASFVKLLDVQ
GEYTKGFVQAKQQELDALRQELQELEVTRQGLETKAYQRADNWIRLGLAYIVLQAGLVARLTWWELSWDIMEPVTYM
LTFTTGIGAMAYFTHTGTEYTYEALRRHLAEGRLKKLYRKHNFDINRYQELQRAVVQTEVELAAPEVHLLKFQTLAL
Q

>N371_deoxyuridine_5'-triphosphate_nucleotidohydrolase_family
MSQQLVLRVKRLSPNAVLPFRATVGAAGYDLCSSENCVVPGRGKALVSTDLAMAIPPDHYGRIAPRSSVSWKNHVDV
GAGVIDADYRGHVKVCLFNHADADFTIQQGDKIAQLIVERISLPDVEEVDDIDATVRGEGGFGSTGVSSKH

>N372_acyl-CoA_dehydrogenase_family_member
MEDGGQGFLQDPPRLGNQYIEDTPLREVLQRLLPEDVLQSIEPDLQRFGWRVVEECTLHGKNIKQQPPVLVQYNAWG
RRIDQIRIGEGWKRLNDVSAEEGLIAIGYERKQKEYSRVYQFAKMHLFGPYSAVYTCPLSMTDGATRLCEIMKPRVG
DDSGTPYSIHDLFDHYTSKDPAKFWTSGQWMTEKPGGSDVGNTETIARPVPGDKLMYRLHGIKFFTSATLSETAFAL
ARVIDDKTGPTGVAGSRGLSLFYIQLRDDEGNLKNIKIRRLKEKLGTKSLPTAELELCGTPARLVGQVGRGVATIAT
LFNITRIYSASASVASMRKAIAVARDYAHRRHAFGKAIAELPLHVQTLAQQEVAYRGCLQLLFHTVLLEGKMETGRA
TKGENDLLRVLTTLGKLYTAKLSLATISECIEALGGNGYMEDATDLPELLREQQVNTIWEGTTNVLSMDILRILDRE
PNAFVEYRNHINRVVALPSLSAPLKDCADQVRQAVKALTDIVEAITHDMDTDKRHVFSQSIARDVSYAMAAAFIAAL
LIEHAAWPGGGEAGLTGAEDGVRTFAAQQWCARHLAGHVLALNDALNLAKLNRKKASYEATRKLGLDVDPNGNFRGM
GDLCPVTGKYRASY

>N373_mitofusin_GTPase
MRRTTAATMAQGRVVTTATFSTSAWLRRCGSETTSALMPSTSSLGRSAASRGVASARLHYPRPRTSLFGDAPGSRGA
AAISSSLAFNRHLLPAASSCRRRQATATEVSLQKQGEGKEGLRRVLNADQAALLQQEICLLEDVLAFLQKIGADQED
VELLKQTREQLEELFLLVVVGEFNAGKSAFLNAMLGKKYLKEGVIPTTSKITSIRHGETASSVLPTEEPDREVIYLP
VDWLKDLNLVDTPGTNAILKYHQQITEHFVPRSDMVLFVTSSDRALSESEHQFLNRIRQWKKKVLVVLQKVDLLEDE
AQLEELRSFVAKGMSQLLGIQPKIFPVSARLALKAKQLMAKENASAEEKAEAAALWEKSRWAELETYILKSLDAGER
SKLKLKNPLGIAHNLLNKYKDVTESRLQVLAKDITSIEHIEEQLEEYRKEMKRDYEFQQNRIDNVLLELANRGDAFF
DEHLSLSNIFALARSEKLRGEFERTVVAETAIQIERSVSDLIDWTVDKNSKQWRRVVDYALERAAHHAQSEGLIGKV
ESEFDYNRAKLLDTMGAGVRNVVASYDKTEEARQLANEVQTAIYSTAAIEVTALGVGSLVVASLLDFTGVLGAGALA
ISGLCVLPYKRAQVKRIFNEKIAGLRVNMRGVMHAHFDRELADNIRKIQGSVSPYTLYVKTEKEKLTKTKTRIEDTM
KRVSNSIHSIDLAFQGESAEAPEEDLQ

>N374_putative_Complex_I_(NADH_dehydrogenase)_ASHI_subunit_(NIAM/NDUFB8)
MWKQSSRVAVVARSRAVVPSSSGLRRSAGALLPRRAGAETEPEWKLYEEGDPNLFDNWKGKAPGALAEQVDIDPNDW
HAMTPDYDTSVSIQHALISLGTAFGVLAGFYYFCKAIAPEPALIPRNDWRTVPPSIVNDQPGTPYTPRPQ

>N375_uncharacterized_conserved_protein
MSNVEVGAVAAAAAGGVPVIAQAEAEAVAVEAADEALLEEEEAANSKRVGEDEAGVARTMRRWTASGCGEVHWERSC
GAHFLRSFARNFAVGSGVKTLLNLVGFLLRKRRKGKGVPKRLVPKLVKLVDLRWGFFLGSLAAVWKAVSCLSRRAII
AHAGADPCDLAQVRALQPRFAAADLVAGAATGLSLICVRPEDRRTLAIYSLVRSMEFFFAFLGRQQILPAWLLRFSS
HLDVLLMCATAGQVLYCYAFEQDTLAPSYRNFLNVHGGKDPRVRGFIKHTHFGLPLELDHLKSFSRERKIDPEVARQ
NLLNFNICTVLHPHETCVQHFFTFAWAGFKRALPLYAPLHIVTTLVVLLAKLTSKVKESVKRAGSFSNLSRSFSIDD
FIEATDAQQQTHDGAHAPVPAQPPARKEPLQAALDKAQAFAARMLKVLTKRRILRVTSFTLALVRRVIFNIVRSSVF
LGVYCSAAWLAACFAHNMSGVKGPFWVRLHLMFSGLACLLEAKSRRIELAMYCIPQALNSAVNEAIKYNKLPRWLVN
LRHLDVLFFCLASAVTVFCYKNDPKSIRPSFYFLMKWLWA

>N376_peroxiredoxin_(PRX)_family_protein,_bacterioferritin_comigratory_protei
n_(BCP)_subfamily
MSLGDVAPSFALESDEGQVVHLHDFRGRSVVLFFYPGDFTSVCTKEAEHFRDSIDAFSAKGAVVLGVSKDPVESHRK
FKKEHKLPFTLLSDLTGKVHRKYRVAGSLGGLLKGRKTFVIDKEGIIVHIFESALNWKMHVSEALAHC

>N377_Complex_I_(NADH_dehydrogenase)_B13_subunit_(NUFM/NDUFA5)
MMRRGLTLFASAGVRTVPTSSSRLFLTTSRLASSDAAPSPVPRKNVKASTGIAGLDVVPNAREVLIGLYNKYLAELQ
VIEPTSPYRKLVENMTRERLRIVEENEDIAKIEELIDNGQVEELIQEAMEDIKEVPWWAEHKPWEDSPHKRIPVFER
EF

>N378_mitochondrial_translation_elongation_factor_P_(EF-P)
MRRHLQQSTAGSVRFLHAGGLRASAASSSLFSHPRHVVSLQSSVQLPSSVQHRRNYKAPISDIKRVWVIEHLGKLWE
VTETSQSRKTAQRRAHINMELRDLAAGTKKSERFRVEDRVETIILDVHKCIFSRSEGKKLLFTNAETGEEVSVKKEM
VGPAEAYLKPGTSVARLSVHNGEAVTVKLPGKAVVTVKEADSTQSATAGYKKAVLDNGRTVRVPPYLEAGDVIIVSL
PDEVYVGKSDGSALADDGDEEDDEEDDDDDTDTDDEDEDEDEDEDDEEDEEDAKKK

>N379_DEAD/DEAH-box_RNA_helicase
MLRIGGHVVPRGGGLILPAPSWGGFRGGPTASLLGIPSRLHLAISSPFLTSAKILGRAEAGTHRLRRLGTPTGREKR
QAGEDRVARRRPSQDDDHNPMLNEVRQKREEVQSEIQRLRERARASSQRSSNNNNNNKAAKQRVEEKEVKREHAGAE
DSASGRQKPLLSVSELRVKYAQGKELLKKQKEHREGRKKKSKKRQPKFADLGLIPPLLQAVEAKGWQVPTDIQQRAI
KLILRGHNVVCSSQTGTGKTGAFTLPLLQRVHKRKQDDERVGIVRGNGQPLMLAVTPTRELAEQLVTEARALAQHLS
PPLNILEIYGGAENQFQVKALKTKNVDILVATPGRLLHYLKQGEAGLDKPEQTVFVEDDESWGDEDDVDDDDEGTED
EADDGDYDDDEEEEEDEEIRESDTLVMPTPKGAKVRSKREQLLAQKMRADHMAAQMPGGASGGAQQYQSPVAPGGLL
DLGFVESLVLDECDKMVELGFFPAIKQLYRLLPKPKKILRGGKKKGDMQTCLFSATLSPRIEDVISRFSPKSQLINL
NVDLQPPSQVKHLVFPVSNRRKRALLTYFLKRKGSPFMKDQKALIFCRTKQRAERLAQTLEEDGFKALPIHKGLTVT
QRRNAIQMFRDGEVQLLCSTEVMARGIDIPDLPFVINFDVPPRGEDYVHRTGRTGRAGNAGTAINLVATAPYTLKLG
GRVCEINEQHYLKDIETFLDARSLEIRKVPGPWKDEPIDIAQDPEAQKQKQLREEGVLTLLKRKDLVGKVQDIENNK
RLSLYEKMKLKVSIKSALNEKQKSDRRKAGLVDDEDDEAAEEQKTSPAAGRKMMKKKSASGESLLPSLRNFKEGRYE
DLLVEFDKKKARKAGVAVESPDKTEQKRQQRKKLRKAVRHMEQRGLFDGDHKKAH

>N380_uncharacterized

MWASDVDFEASLLQQGDAATDLVEHMTWRTRRFPGLHLPNRAALAREWAVARGTSTRLLVTTLRDPDFFANTPAQTA
AASGAWVPWLSFVHSQPEAALGVMGDGMR**AQVVGALDVVPGVR**LSTNFGVIPASANDPRGSLLNKGIGLIPKTESEL
ECYAIDGLQLSLTHATASLEGVDYVVNATVSVNPMALARRFAAASKLETPKRAFLERWQLEARITRIKPLNQPALGL
PSLAVQYSHPLGPAPGDGRRVPRLVLTAKAQALNTLRLSVTYDPVDILAALDEGASQGKPAVTGVCASGVLSVSPSA
RAMQCLGTLRYYGDGYRATATAGWAVDPRQPSAAWTGTLSWVQRARNTSVGAFVSGGR**FNDQLVTPR**FGITLTHHI

>N381_short_chain_dehydrogenase_family_member
MNSNKIDLGLKGKTIFITGASRGIGLAIALRAAK**EGANVIVASKTDSPHPALPGTIYSAAK**EIEAAGGKALALKCDI
RNEEDVKKAVEEGAKHFGGIDICINNASAIFPKGTLDVPVKR**YDLMQGVNTR**GTFITSQACLPYLIESAKKGRNPHI
LTLSPPLNIDAKWFKDHTAYTISKFGMSMCVLGMSAEFKDRGVAVNALWPKTGIATAAIRNVLGGDDLMNQCRTPDI
MGDAAYYILTSPATECTGNFFVDEKVLR**AVGQTNFDHYAYVPGTK**EFWPDFFIEEQDGDGVGLRKARL

>N382_alpha/beta_hydrolase_domain-containing_protein
MSSRVVEYFLRFPHRQLARVVVCCEQVSMNKVAGFFVVLLAVVVGLVVLYPGAAQRALVTGLIKADVLLLKHWYNVT
STER**SLESIALEHLLR**FQAYTLDVAATRSNLDAYGR**LLPLGPGVVAER**VNISRHDGTVLPAYWITPPGYNNKTILFY
LHGGAYIAGSFTSHGGSVAELARRAGAK**VLFVEYRLAPEHPFPAPVEDAITAYK**WLVYDQKVAANRTVFVGDSAGGG
LVLLALLALQDEDKGTIPAPAAAVTLSAVTDMSADRPSYLKNAESDTLVKEAFVTWAASQCTKTRPEDRAARKSHK**V
SPIFAAADK**VAKLPPLYMSVGESEILHDDTAHFAGKALQAGGDVKLVAAPFMQHVFPYFYHFVPEADQELTQIANWV
KKQQQKI

>N383_putative_mitochondrial_escape_protein_(RNA12_superfamily_member)
**MFRFSTNRVGCGGAAHHLRLSPLPLSSSSSSLSLSLSGRLLPSSSLFTTSSSVTASTTIRGLPAKRPLVWGTQSPTA
TTASSPFGSRSLLVNYSGCRRH**NSTTPASSSESGATPPTAPPSGAGSSAAEAAARKKAEAILQEYTALFRPGPQAPK
EEFTAR**VLGAPFDVAFR**GTVGVAVAVLLILVTFGVAAK**ISDAWDVYQLAR**KLLDEDLPPSPKDCFGREEDVRKMESR
LGERPEFIYFVGGSPR**SGLSTVVSRVLNDYAGNSYIINLR**ESSPMTGMEDVTHSLNKSLGFLEILPSFQSLKHHFSG
WEIK**GVLIPATEAQR**VEALKSTLEKLTKALKFIRFLSRLKFSRTRENTYPIIAFDHFKEVMNIPESKQTLNVLLKWA
LYITHEAHLAHVILVSSDPKVAYALTNDELLSGRIISVNIDSIAKEPALKYLRKRLARSRYPREITEEEGEKIFSEI
GSAFVDLNRVEAHLSSGPHISVDQALDIMHRTTIAHIVGALGAEGR**SWTPTQLWR**TIKMLAESETGELDYFQLKTTV
FNGNERVLHELFDAGILLYRVFPFKPNGVQMTPVVTAYTPFVMFCCKQLANDLRLNTIMNRQMADEEAAASSLAGRL
SSAMMMVS

>N384_aldo-keto_oxidoreductase_
MRRSCSSSALFPSKACGALLPPYGSARRGYGDVVRAAGLRGHATPEGTAAFHQR**LGSKLPFRLVPRTQWSLAPFGFG
GYRVSART**SSHRSALKKAIRLGCNVVDTSSIYSDGDSELLFGQVVRELVDKEDIKREEVVIITKAGYLSEKAEHNRS
SAPSYSDKDVDHVSPGLDYSLSPRVLEDQISASLERLGMERVDLLMLHNPEQLLEVHPHLGPAFYELVSKAFAHLEK
EVQRGRIQYYGVSSNTLAVPSSSPDHVCVDK**LVQAANSVSEK**NALAAVQYPFNLIESEVLTEGVSAKAKAHGLIRFS
NRPLNAVYEGKLQRIATFPSHDDKDLVQLLKEAFDYAIHLEKNYPGADKASLPPASDYAWAQILAHNQATLGTIDRW
VNALESTILPSYEPAIARLEDHAQLRSWGDKYRVAIARLFERFTWVNEANASKNSEQLTLAADATWPELNERGMATL
SQKALLAARSSDVADCVLVGMRRATYVREVLLNVGPSAAVDTASDPARYAQFAAELQKAKAGP

>N385_SAM_complex_protein_Sam37_(metaxin-like_homolog)
MASSSSSAAPAVLKLHQYGARWELPSFDPFCLSAQAYMRLAGVTFEEVPSNNPDVSPTSNLPLVQLGDDYVAGTNAI
FTYVGNKTGKSLDSALNAEQK**ATAAAFIHLIETKLHPTLLYNWWAEK**QNMGQTLVLPHFNSMVFPLGYVLPRLKQR**N
VQSYLYTLNLTQDEK**VYNDAEECYAALADFLGDKHFFFGDSLSSLDAVAFGHLAIHLVAPQSHKLRSRLLQHKNLEA
FCKRVMTLYFGQDFPAIPAPPPATEDKDQKQEMSQHKKTGMYLLTGAGLLILLHYLTKQHQAAHQ

>N386_mitochondrial_carrier_AcMC16
MVLSPSSMSQQQPPYNQQDLAQGSEGEDATAALMGVGTYFGLFALVIPARVVYDRTAASVGTSHLYRGFLATLR**GGF
SDLVGGYR**QLWREDGLRMFAKWPALGFAIGVGAFAIQEGAQQACHR**LLGVTQEDMEAR**SHKWHLSKAMCLISTGVLL
YPATILWTVHSTNR**MPSWTVYLR**DKVWKGKDYFYSAAPLSSLSFLVFFLSDIIRAKVLHWNKKTFFPELLASPPQTE
DEVYDEEPTQQAALVGGAYRPLLHQITNLSLYTLSSMLSAMLTGPIDAVTARMIANPLLYGPLGILGTVKTIYR**EEG
VWAFFK**GFVPNVVFLLGTYYAGISEEADTGKPPL

>N387_carnitine_O-acetyltransferase
MLRRSARASSQGLVAARGGGSTARTAALIRPHFVRGTSSSAAGKKTWR**TFEYQSQLPSLPVPALEATVAK**YVENAR**L
FLSPQELER**TRQEAER**FLQGPGPVLQQK**LLERADLKKKENKSWLIDWWNSWAYMDYKDSVVINVSYAFNFVEPRLGR
VSQTRRAAQLIHGAVLFEQQLHKYTPPLPDMGKDGPMCMNMYQLMFNTTRIPSAK**TDHWATYHDDPEAR**RKVLVAHK

NRFFIVDVYDQSNQLLSVPELEMQLEKVKSLGSTKEEWAVGVLTSDNRVQWAEARDLLLRDQQNRASLQQIEKTLFG
VCLDEGAKSGLELERNFWHADGKNRFFDKSFQFIVMEDGLAGLNGEHSGVDGSPAWRMTNFVLDWEEEFQRNPEHAA
NKNRNSAALSPVEASFNITDDVKPYITNAEKRLAKAASEVDLQVKYFNKFGKDAIKSWKISPDAFCQMAMQLAVHSL
TGEIYPTYESGQTRKFLWGRTETVRSVSAESVEFVKSMKRTDLKDSDKLELLRKACNRHTQTNQDACDGLGIDRHLL
GLRLIAAEQGVEEPGLYKDPAYSRISTWRLSTSQLTSPHFQVVFGPVAEDGIGCCYGILDNGLHFKASTALKCKTNA
TAFVNAVEDSLVQMAKICATGTTHASKAKL

>N388_4Fe-4S_ferredoxin_iron-sulfur-binding_domain-containing_protein
MSSARFERSFSLKDIGALQYLRHLTQLLATVFANGKLLGLASTGLIVPYLHVTQSPWSTVHGAYESLEYTIARGVFP
LLVLGVIYLTAVTVGRLFCGWACPFGLVQDILSYLPFKKEKLSASTTSQLKDLKWAVLGFSLISVILVAWRRASAMG
HEDPMGVFSDSPFSVISPAGTLFAYLPWLALWNTNVLLSAGLIAWIKLALCVAVLVPSVYIPRFFCRYLCPMGTLLE
PLSSYKVLRIARSSKTPVQDANKVLGDVCPMGVQLEKEDYVSDHPSCIHCGKCVTEAPATFAQTLFEKSN

>N389_uncharacterized
MKLARSQFTVTPRRAGLVLATSGGAAMLGSRFSLPSVHAHEKDVAVDEEQPEAVAVAAEAEESPVVSQQQWEEVWEE
EKGTFLRPYITSVRIAAQETLADACGQWKSFKEKTDFDHKWGTTKHYATRYYWLLTGQKLGPEIAFAATTGVLTLVA
TRKVLRLPFRLALLSGGVATAALLPPYEKTVPYLVHQYETFEWAKVADKFDPVAIKDAAIDELKASLPPFGLGKSTK
KNVEKELLEEKKEQHVDDVAEEAPKKEESHAVVHHQPAADKKACCHDNNGDKQEHKSENHHHHHKSERHHHDEEKEV
LDVEPLSDKEAEDVL

>N390_isochorismatase_domain-containing_protein
MQQVRRLGKLQAHSSVLMVCDVQERFRSVITHMPSVLHVARTMVKAAPLLRVPVLVTEQNPKRLGRTASELGVDETE
GVRVFEKLKFSMLTDEVRQTLERDHPERKDVLLLGIEAHVCVLQTVLDLLEGGYNVHVLADGTSSSRQADRLLALQR
FSQAGAYVTTSESALFQLMQSAEHPSFKAISALVKEERPDSGLSRL

>N391_mitochondrial_carrier_AcMC17
MENTTGETTLKAPSETFLAHLLCGAGAGLISDAIVHPIDTCRTRLQVQRGVGSGLFYKNTADAFTKIVRQEGAKALY
KGFTIVASFTVPAHALYFWGYETAKRTLQPSVPLEEKGALVHFVSGMFADLMGSFIWVPQDVVKQRLQVQKTSLASA
AADTVKYKGSLHCIKTIIKEEGFLALWTGFLPALAVYCPFVGIYFMTYEQAKRVFQKTRGYASVDDLPLPYQLVGAA
SAGAIAAAVTSPLDIIKTRIQVGSDYKGAVDAARRIWTEEGPRAFTKGMGARILWIAPATTITMAAYEQLKHVVPF

>N392_AMP-dependent_synthetase/ligase-like_protein
MASRGGSAAPSSSSVLPEWLRSVTAKQAALAGLGVSAALGYAYLNSMSPDLSKDFGTIMRLARVKRKVDSALKNKQT
VADMFNAVLQAHPNKEAIVFVDKQDHLTRNTKVSNTKVSYTYAEVEAESNKVANWALSIGLKEKDVVALMMDNRPEF
IFMWLGMTKIGVLTSLINTNLRGHVLRHSMAVCKATHYFVGHEHMDVISRELVSDLGGKWYSCGGPAPEGNLFDLDS
LLAVSNNTTAIPRSFRANTSATDKLFYIYTSGTTGAPKAALVSHLKFLTAGLGFVDLMDVGENDRLYTALPLYHSAA
TLIGVSTTWNGMGTLILRRKFSANSFWEDIATHKATVFQYIGELCRYLLSHPPKPSDSQHQLRLAIGNGLRPDIWAE
FQKRFNIPQIGEFYAATEGNVALLNSFNKVGAVGYLSPLIRMVHPGRLVKFDVESEMPVRDPKTGFCLECEQNEIGE
MLGNIKPDDPLRQFLGYTDSSATEKKVLRDVFTKGDMWFRTGDLLRIDREGYVYFVDRIGDTFRWKGENVATTEVAE
VITTGNVGVQECNVYGVKVPHKDGRAGMACIIPVDRATFDMAALYKLVRTELPLYAAPLFVRVTTAAMDVTGTFKHK
KTELVEQGFNPHVITDDELYFRDDLKGAFVPLTKDLYQRITNNTTEAKL

>N393_mitochondrial_ribosomal_protein_S18
MRGAARSNLLLRGGGRRAAVLRPSLPQAAPIRIGGPQSNHIFSSSATASSQRPFHASTRALWAISSAEGENGDNASP
TEEVQTESDAAFEEKERSEAYARWVESVRRELKHIEEMVLKRAPAAADSEEGIEKLEEIFLSNPRMQLTESLFPDEA
RPAPSRIITFDKETRRPTQMPYVMLDPKWYQGTTDEERLQQVLAWRPFTARAVAAEKADHQFREDPFRNKSHAFSGR
VVSDAFRRQRLDKYLNEELANKRKVYSNVKEEEEEDSNVTLDEMKQAFRANLAMVENISGEESTEEIVEPEVTRDDK
YIKPPGFVSATDMLKFSEEKMQSDLDKLMKKAKKCVFCRPSAQRPVLDPMNVSLLTMFLTPTGDIIGRRHNGNCRRH
QRKLATTIKRAKHMGIFSYKYGGFTIYSPFHEPPETYAEDDGEGDEEQYGESDEEGDYSDYDDDEDEGQQNLH

>N394_uncharacterized_conserved_protein
MNRVIASEGLGSVAARATGPNWQRWNIPIALAARPQLINGSWRKPLISRRHLAKLRNEHLENGRPWEEPAANYSVTK
VRNPDKPLYKGHKRLRPETIAKRQKMIETKMKEIPAVEKAQKKIRDEYKQRPLKGLELFYVKPARKEVAKIKAKCRG
GSGGSAQPEAD

>N395_uncharacterized

MQRATNAALRKGVMPLHSRLKIATGRQLWESGLLPPLPTLRPLFLHLPPNVPSGLGWVDENAMEHRFTMFVQTAVGK
MMLDHAPHHCTVHLPAVLPFELPHVKAKVAEKEYATVEEDIAKYKCREVHWK**DFVWPLWQLSR**LHEMAHLDPEAEPL
PLSPLSFRETVCGR**DTHEFLHHVEAAVQAQLLR**LPRDKELTHEKAVHGKTSNHLSPEKMQRGIAAEKAAAKDLWLYP
QLGTDLCPATAEFVIDDTVLNVSATTDPRRHWEKGLTELFAYAALARQQGMAVGEVGLFYPFSRHLVHVPIHDWDHR
PLFDRVLSSPDVEVGPAPDDLYRAVDSR

>N396_sucrase/ferredoxin-like_family_protein,_putative
MDDKTKIVQLTALAGAGAVLLGAYYLGTRHATAPAATSSSAAAETCECGLTVAQGGCAPASSSSASLYNSQLLGTVK
KYEKHFIICSGTEPDEWGAK**IDKDEGSFAQLAK**QAISARKAELTFKFKLTNSDERSK**GSEGTDLIVFPER**IRYLGVT
AETMPFIVEDHLVNGHVSERVKHEPFESELVLVCCHNNRDTRCGAEGPIIVSAFDRLLAARGLGEDKVMVRSSSHLG
GHK**YAGVVVVYPR**GDWFGFITEQQVEK**LLDNYIEHGSMVPEHWR**GRMGIDKQEAKDLADSVTLAVETSS

>N397_glyoxylate_reductase/hydroxypyruvate_reductase
MKTRASSTTRAWWAAARPAGPPQGMPSMARRFYGGAAAATAAKVVVTRALPDSTLEALRAGGCAWEGR**YWSEPETAI
PRSTLLSWLSPDTLGLYCLLTDKVDGEVLDRAPNLRVVSSMSVGVDHIDLAACKARGVHVGHTPGVLTDSTADLAVA
LTFATVR**KIVPGVAAVK**NGEWKTWSPFWMASPFDVSGSTVGVVGLGRIGAAFAKRMAHGFGCKILYSGSRPKPEEAE
PLGATYVPLDELLQR**SDIVSVHCPLTPETR**GLFGKEAFARMR**SSAVFINTSR**GPVVDQEALYDALASNTIAAAGLDV
TDPEPLPTSSPLLGLPNLVVVPHIASATYPTRMKMAMMAADNLVAGVQGKTLPFAVKL

>N398_uncharacterized
MSWTSWLSSGDSSARARNLTGAHIRWAAVTNHPQIAPYFSAAFRKDKATYAAMSCEADLVALAECEYKNPHDDGKCE
PYRLRSLLCMESVVNPAR**AEQFTTCLRTAGNPSAVQAK**CMPIFEDVLKDLEK**ASEDAPLPLTPQEKQVVQECDQPDK
GEEARMEEGMACFIPRVCASPYGSFHSCVEANGGDIDKCVPEGQQVMECWGDFCVRMYR**DQNVETAADH**

>N399_mitochondrial_isoleucyl-tRNA_synthetase_(IleRS)
MLRRVTNKGLGSPLHRGAPPLLPHRLGGNYNLQSLHFANSSARRLHRGFASSPASEANSAAAAPAATANSKAFGHTL
NLPRTTFPLYTTEKAQLQLEGSLLAEVSDNLYAWQAQQQRQKSFVLHDGPPYANGPLHTGHVMNKVLKDIVNRYKLL
RGHAIKYVPGWDCHGLPIELKAVDQAK**SGSTLSPTEIR**AKAHACAEEAIAQQMKGFRSWGVMGEWNNPYATKDPKYE
ASQLGLFLDLYKKGYVYRGLKPVIWSPSSRTALAEAEVEYSDTHVSPSVYVAFSVKHLANKAGELSRFNNLHALIWT
TTPWTIPANMAICVNPNIEYSVVKTTDQHDKHYVIASDRLQAMQELLKQEIEVCARLPGSSLADTIYVHPLDGRELK
VLPGTHVTTESGTGLVHTAPAHGADDYVVCKAHGIPLRSFVDDNGKFTQDLPEFAGK**FVLGPGNELVIQALTDK**GAL
VHQHKYTHKYPYDWRTKKPIIMRATEQWFVDLKDVVAPALDEISRVQMVPATGRTRLESFIRSRQEWCISRQRVWGL
PIPVFYSRQGELLLTEESVGHVQKLVAKHGSDCWWSMPTSELLPPSEKHNADKWEKGRDTMDVWLDSGVSWHSVLHN
RELPFPADMYLEGSDQHRGWFQSSLITSVALTGKAPYRAVLTHGFVLDEHGRKMSKSLGNTIDPVALVNGDEKKAGC
GVDVLRMWVASSDYSRDTLIGPVVINKMKGSLRKLRNTARFLLGNLADYDRRQAIPDDDLTGIDRYMLHKLHEFSHG
VTTDYDDYQFSKVYRGLVNFATVDLSAFYFEVVKDRLYADATDSLRRRSTQTVLRHTLDALTAALAPIAPFTAQDIH
RHDAQAAAVAPNVFHLEWPRAGDQWK**QDGMAQQWDAIR**DVRSQTYKVLEAARAHK**VIGSSLDAR**VR**LYTGSDDNQVA**
RWLAEPTSDELAEILVTSAVDLVPEAPAFEVVDDRPPQADLTSGPTPSFVGGGLVHAVPVGVEVVPASMHAVKCPRC
WRYASAEENTPCPRCAQAMA

>N400_Complex_IV_assembly_protein_Cox11
MRRTAAARGLTSRPLRSWFSSSPSSTTALRLFSTTRPLGSLRSSPSRSGLWSPASLLRSGTCRLPSSSPFLLTIRRA
YATPGGKGGSKQEWQQKNKNMGMILTTLILGGIAISYASVPLYQRFCQVTGYGGTTR**RVEESNMSSPDR**WKKRPERP
LTVKFYSNTNSNIPWVFYPLQNEVK**LVPGESTLAFYR**AENPSPDDIVGIASYNVVPAKAGIYFQKIQCFCFEEQLLP
AKKGVDMPVYFVIDPDFVDDPNMHDVESISLFYTFFRAKDFDDLNAQAYDESQQQKEQQTPHQLAQLQAVVEKKEET
QT

>N401_mitochondrial_ribosomal_protein_L20
MSGMNKKKLLKFVKGFRGRAKNCPSVARERAYK**ALQYAFVGR**KLKKR**LFRETWIQQINAATR**IHDLSYSRFMQGCVL
SDVKLNRKMLSELAIYEPYSFSAVTKLVGERLKKEEVAKEVERRAAAKKNIHPGNR**DLTADQKEWLLAQK**LKEMQIV

>N402_putative_Degp2_serine_endopeptidase
MRQGFISTLARGWAEQGGHLRSSRTVKALGQSYGPLTRRDYSAAASSKMKINNNPAVSSSVRTKEVTKRAPRGLGKR
KAEAEVLAAPQLIGSEMAGDK**TTAASAPVPVATVGQNEALR**SVVRLEVAAAEPDYSLPWQKGDPYYTSGSACVIESP
PGKLR**ILTAAHVVANNTFVR**AQRQDTARFFSATVVAINQDCDLALLEVSNPKFFDGLKPLQFVDTPSLQNTVVVFGY
PEGGESLCATRGVVSR**LELQQYQIVR**SFKDEGLKLLTLQIDAAINPGNSGGPVLDQENKIVGVVFQKMGGMWTESVG
YVIPTEIIRHFLTDVENGRSPQFCSAGFEYQKTDNDSLRKWAKLKKGQTGVMVTKVDELSSAK**SVIQPGDVITR**VEG

VEIGNDGTVSLSESKDKENLRLSFEYFVTKKFVGEKLSLTLVRNGEEHSVKVTAEPRKYLIPPHEEQHGVAVPNYFI
HAGLVFIGLNENYVGHVDAEPIVGRYYYQNTKRFEDEQVVVMTKILQDQVNAGFSQEHAHQLLSLNGCDIRNLR**HLI**
DEVERCAEPFLEFRFDSGERIVLATQPARKATERILRKYGIRSAKSSNFLPVKAKATTKKKTATKAQTSSPRMKKKK
EKKNDSSTEKKEEELS

>N403_mitochondrial_ribosomal_protein_L43/L51
MSRSGIWQLRKLKLQYCDFGGSSRGMREFLETRLPEFQK**KNPQVLVDVVK**RRNR**HPHLSGEYLIGR**EKSVGVGGLEA
DEVEHYIYHLRNQWGLKSRR**LGAGQIVSQR**R**SVQGVWNPFVK**YD

>N404_mitochondrial_ribosomal_protein_L24
MLRAGSRNLRSNQIKNPITSWKIVRGDTVQVMQGADHGKKSVVIKVSRKTNRVVVRGIKLAKRRIK**ATEESQGGFVY**
REQPIHYSNVSLVDPSDGKPCK**ISMSYLADGTK**VRVSKRTGTVIPKPAELTAKRFKNYLDGVK**DTKPEVVTLKTFDE**
TSLVPELDELTIAKVHEKLLLEKEEAEQKRLAREQAR**VAYGFSSSSDEPR**NVGSDSKKEEAEVV

>N405_Complex_I_(NADH_dehydrogenase)_B14.7_subunit_(NUJM/NDUFA11)
MAHEHDHHTAKDSKKDVEIPDLFGIDALDIHGGEPCLVQGAKMAATSFIAGSFFGGVLVYWKDVGVVQKRGR**FAALQ**
GTLKSIGSYGAFFALVGATYGTAFCALQHSR**TKNDPFNTVLASCAAGGVIGAR**VNGTVFGSVLGCAVTGGLAAMGEF
FDWTLSPNSAKLFALREQKHQRLLRTSPGVGSDAASSDSDAQ

>N406_RNA_helicase_SUPV3L1
MWTSRLPYSSLRERGAREAAQTDSSTKKKKQQQQARKHEGWDEGKEKKMKKKTMTKKNGRTGAGGGQQGNAYGAATA
GVPPLRALTTGVGQVERDKDVVALRLEAFVRDASVRREVRARLAAR**ALQADQAPR**GAAAAANDDDHERDDDDDEGDG
YEEAEEQEEGARGRRRVREVKGHRSRGERVMGLLGRERDLEAALALFEARTTSDDHLRRMPPALLSLLADPKRTHHE
CAEPLMEMFVEFVWEHYYYGRPLKSSAGDEGGRGAVLLPPADDLRAETDEEEEEEKNAWRTFRRMATDLRHPHAWYP
LARALPGGRRIVLHVGPTNSGKTHEALTRLAASRSGVYCGPLR**LLAEEVFR**RMNKEGVACSLLTGQRVVTDPTARHL
ACTVEMADVASEVECAVIDEIQMLGDQDRGWAWTRALLGLPAAEVHLCGNESIVPLVQKICQDTGERLHVHHYTRLS
PLVVSDTPLGRKWYKSLRAGDCVVAFSRADIHTLKREIERNTRHRCCVVYGNLPPQTRVEQAELFNDPASEYEVLVA
SDAIGMGLNLNISRVVFSTLHKFDGHKRRLLTDSEIKQIAGRAGRYR**SIFPTGEVTAFDGADLPR**IRRALLRELEPL
PSAGLAPTFEQVSMFSRVYPQSPFYELLDELTLKAAVSSHYFLCGNDDRVSVAK**LIESVPLSLR**ERFKFSIAPVRSD
DSSLMWHLLKFANSHASEGEVEMDLRPERGDSKSGRLAELESFHHVLDLYLWLSYRFDSFTGRDRAIRLKQETEQR**I**
QELLVSQTEASKQSRAQKGSALDHIKGHLQRQQEGQRAAERPPVVLGTTTTAAGGGERRKARRRSSEATGTDAPSPH
EPAQWAQALNAALAASTTRRKGTPAKAQRKRNSREEEDDEDE

>N407_uncharacterized
MNSSSRMTSLAFRTSTRSQLVGARLLPATTAQRTLFQGAGSEQKTEKKPLLDEDWKDLMVVDYGTGATSSVPPTAIE
ETR**HHPAAFESSSELR**IFQHWSSGLVREVEDPLL

>N408_3-methyl-2-oxobutanoate_hydroxymethyltransferase
MKRSMSQTAKASPMRSLLCRVSPATVAHTSSRSLTTTTSTTSISTSSSSVARVQDGSGRRGYSAHPRPTSTKDIGKR
TTVLDLGEKYRKNIPLTMLTAKDFPSAVIIQQVGGIDLILVGDSLGMTTMGYESTIPVTMTDMLHHAKCVHRGNQTS
FLVGDMPFGSYEPSSALAVENAMRLIKEANMNAIKLEGGKRMAARAKAIVEAGIPVMGHIGLTPQSIHSLGGFKVQG
RTSGQATAILEDALALQDAGVFAMVLECIPDR**VATFITQQLR**VPTIGIGSGNGCSGQVLVWDDMVGQSDIQSFQPKF
LKKYANVGEEMRKAVEDYRNDVVARKYPEDGTHTFAIKDDEFDAFTKKAQAQHQTSAEPLTT

>N409_uncharacterized_conserved_protein_(DUF155_superfamily)
MKRAANAATRGPFLTARQGFGRFPSTLTPSPFFRAQRAACSSSLATSQQAGHRHILSSIRCAGRGNGAMAFPSFRRN
WHSSASPLFASTTSSVGDAESQRTPEEEKEERAEEDAEMGREDQHHTPPPRQSMESSNGGTAKRASKKKAARRATST
AIDEEQDPEGARQQQEEEEVRRLQQLRLERAEMGRDQRDEDNRPRAREERKKCLAYCTADAYVLHKLYRALR**ADDVI**
ASEWKISYIRRDRKYIRLRCLDDSEIYIFPFGSFVCWDVDDADFIRVRQLIRACERGERTELYEDFDFVYGSDTAVD
PEDDELILKEDDSTAKWPVSFALAQSIKLDYFEKEVK**DTFQEMQALSHYLAR**NGSIPLGPKKIVQEMGKIMELLVNV
NLGETDFVSDIPDEFWEDTESANTWK**IFNSHLGVK**NRAKVLDSQLKMFNDFYSMLSSEVHVKKSTRLEWAIIFLISI
EVVFGVADHSDWLASFIP

>N410_uncharacterized_conserved_protein_(DUF543_homology)
MGDR**VPSEFLVAK**R**WDYCSEAILR**STGYGALFGSLSLFLFGKRWMRLVGIGASAGAGFGLGVSECRASFNR**ATNYDP**
DRILVVPHGTKVQADGTPRH

>N411_uncharacterized_conserved_protein_(possible_transmembrane_protein)
MEELSSRYPAKYDVQLMALADFFESKFGKASLGPAKLLDEKSFARKLEIPYAYLDDAVAEALQTWLATVPPTVMAEF
TQFLLNEVFSAEKNHKTSGIGLRMLLAAIARGFPDVVRGAVDHASFVQK**YLGDSPATYPKHEPNVLSEDTALLR**ANF
VPVLVWYFGQTIEDHPALAFDLWAEFLLPFLLISAPETIRTLVLDYFHLLFTDVGGKVKRADPVVTARALERLAAYR
ENVSENQLKKGAINPIYLAIENAIVWRNSSSVHNYLNVYLRRAASANKHVRDEAQKKVLRALAVDKESYQTWDSLYP
RYVIQSTQVILFLTDKWDKYVLTQDK**GTIQASDVAETVHNFLYTNEK**LAESHYRLTTRVKKGAKAKKEAKADQADVE
ASTAACRELLRRTGAKVSATASSRPTSRSRAQHAAAASSRASSASSSSGFLGTLVYLLLFVALVAAIAVLYLR**QTQ**
PETYEELLRTGLAYYREGQAHATVLTAQASAKAQDLLAQAYELKAKYMAQAQPLLAQASAKAQELLAQAHELKAKYM
PATASPAAAVAGKA

>N412_putative_sodium/alanine_symporter
MRRTSLRTLAQPLARSSTLSSSALRCGSVSGSFLTSRGFASEPPAATKLKPDQPHPSWNDYSQLLNNFMDKLVHKER
MGYKWWVRPNPSAQTESPSNYHLWFDEDQFPEGKTVVAMASYAPDRLERTLTINWKTWEMTIAQK**DLVDNTLSATR**T
IQIPPDWLLAMKKVRWPLLEQAKKNAQESVPAKLPLIRSKDLYTIAKQK**FKDEEELAYLK**EKLMAAHI

>N413_malonyl_CoA-acyl_carrier_protein_transacylase
MLRTRLGARLRLASWPALQPGGCARCFTSYDQPFIRVSRHTKDDADLQRRDREKHPRVKRAVVFPGQGTQYVGMGAD
LAKEFPEARR**VFEEVDEALGFR**LSQIMWDGAQQELTMTENAQPAILAHSLAVFRVLQKELGLSAPRGYASMLGYSLG
EWSAICASGALPLWDTARLVHYRGR**VMQEAVPLGEGAMVALMPIDVPTASAIAK**KAAEETGGLTCQVANINSPKQIV
LSGAAGAIDKAVEIAKREHKRIKLVQKLNVSAPFHCEMMRPAAQKLQDYMADSTNKVKFADPSVPIVSNVTARPITQ
AGELLDLEVK**QVTDAVQWLDSIRLLAYPATAAASSEDVMR**HAAGRPAWKEIEEEEKLWQWK**GFDDFLELGPGK**TLSG
FVRQIGTELQATNVGTAQEVIDYCKHYRE

>N414_NADPH_cytochrome_P450_reductase
MFRSAKRRAHQLLTPPRLANAHSSRHLAPPNLQQQQQQRWYRAVPPAAAPVNLNVMFGSQTGTAMGFAQQLGKMARK
KSIKARVVDLEEFEPADMLGKPSEVYVFVQATFGQGEGTDNAKGFFEWLKANEREDDKSRFSPLR**FAVFGLGMSQTY**
PARYQAAAKWVEKRMLELGAQEIVERGEGDDNGDIETNFEEWVDKLFPKLQELDDTSSASENKDVGAR**TTTAAAVEE**
EKLFSLKVLPRTDVKQLAASRPFDPTRAVDIRNPYPAPLLTKVELHTQTSTRSCKHIELDISNAPNMRYMTGDYLGV
FPRNHPELVTQYAERLGLPLDTVMDFNVKPDTKVTLPFATPCTLGTYLAHYADLSAPLKKAHLSSLLPFVARPAEKE
QLESVIADNEVVKRMVDEEQILLDVMNR**YASIDVPLGGFVELAPPLQPRYYSISSSDR**VHPQHIHLTVGLTQHKTRA
DRLHR**GVCSDYLCNR**VEVGDRVPIFVKNSLFK**LPDSSHPIVMIAAGTGLAPFR**AFVQDRTYLHDHEGKMLGGTVLYF
GCYHQDQDFLYRDELAKEIDRGNLQLVTAFSHAQEERVFVQHKLMQNADRIWHLIHHEDANLYVCGATQMAMGVEDA
LVSIVEKCGKMERPLAEQYIRTLKEKNHYQEDKFG

>N415_homocitrate_synthase_(Lys20)
MNRTTALRNPIFNTCSASRRAASVTSSVARSQQLPSVIATRRDFSKITAKKHVSNVTNFKIIESTLR**EGEQFANAFF**
TTDKKLEIATLLDDFGVEYIELTSPAASAQSLHDCQKVAALPLRKSKTLTHIRCTMEDAKLAIESGVDGIDLVFGTS
SVLREFSHGK**DIEYIIDQATK**VINYVKDAGKEVRFSSEDSFRSDIVDLLKIYSSVNKLKVDRVGIADTVGVASPLQV
MEMVKTIRGVVDCDIEFHAHNDTGCAIANSFVALEHGVTHIDTSILGIGER**NGITPLGGFVAR**MYSVDREYVKNKYN
LKLLRELENLVADCVSVQVPFNNYITGYTAFTHKAGIHAKAILNNPETYEILSPEDFGMQRYVHIAHRLTGWNAVKS
RAQQLNLELTDDEVKEVTRRIKQLADVKNQSMEDVDAVLRSFHSEVTKNEMSHHVGIALANGHTPNFFANP

>N416_dimethylaniline_monooxygenase
MEVSVKERTHPAIAKLLAKGTKPR**VCIVGGGWNGLYALK**WFVEEGLDDVVLFEQTNSIGGVWVYTPDKPGGCFKGTR
TTASKSYLHASDFPMPESFGHFPNHVEVLNFLKDYANHFNLHPYIKLQQTVHKAR**KTEDGAQWK**VVTVPTKEGHNDD
EGNAKKEEHYFDILVCCSGQHQVPRSTHKDHPFNQFTGEMMHSHAYKKPTKAMKGKTVLVVGGGESASDVAAEVCEK
AGRTILAIR**SGTWFQDRTVGANQPADMVFTK**HQRLLGFSDFQSWLVWIGRYTMIEMMWGKGGSGLKEWQPSCAYFHG
FLNKSRDIVDKAALGKVVARRGVERIEGKRVWFTNESKPEDVDLIIFATGYLSNLPFLAPELDFTTQAYKLVFDPQD
PTLCYVGTARPMIGSIPALGELQARWAVKVYTGQVALPSTDAMLTQLAADKIRHKRVFPADDHHLPQLVNHWEYSDE
IASYFGAKPDLVRWFFRNPFKWWTIISAPWSAHIYRVEEPKAR**DEAIANINRTWLPDHYSFNFFNK**AMLAFDLWLVL
NVVAVFCLLYVYLFLM

>N417_Complex_V_(ATP_synthase)_assembly_factor_Atp23_(inner_mitochondrial_membrane_metalloprotease)
MRERQHSQCETTIRDILIKDRVMQHLMAGMEDRGCRVFYKNFFHCKQCTGSDHGGYWDPDEGVVICENNLEQKEMVR
DTMLHEGVHAFDDCRANVDWSNCVHHACSEIRAANLSGDCSFRAEVARGHFNVRAQQKECVRRRATLSVIKNPNCPG
ADADWAVNKAWERCYSDFEPFGQVPN

>N418_uncharacterized_conserved_protein
MRRGLVVQRFGGSSGSTGSLFAASAASSCGRRQLVLTGPALTRSFRTTPCSAAPEDLEDDKDGVEINAEDVEGEEYV
SNSNESQADKKRRSKEAR**YAAENAELDFLAKALIWDYR**GQHAPRPMLAEETKEELYRLHKEDPKRWDLENLSLYFGL
RKDRVQAILTFMGMRDVAVRNGEVLNGGVVELLEQEFGVVGRLADKRVLDEER**AGGRPGSGLPLEEDAIDNDAR**LLD
HARAVRLARAPRGAPLKELPPQPPKAADGSQVPEAKPHVLR**RPTPTEPR**SFKGTIFMERDSRRPPWGRRRRYNDATR
IMYISEPDGTLRTPTWDERRLLTSADKHIPTTARYAVGENRFFKDDN

>N419_ferredoxin
MMKRTTTLVTGGRRFAGLQSPVVPFAWAGRQATSSSASTLRSARLYSADADSKKTVHVTFIDK**DGTEIPLEAPVGKS**
VLELAHDNKIDLEGACEASLACSTCHVILDKEYYDKLPAPVEEEEDMLDLAFGLTETSR**LGCQIIISPELEGIR**LKL
PPATRNMMVDGYKPPHH

>N420_uncharacterized
MKRLARTSTAGAIAPSALHTVGRHSVSPASRHLLLQSHGSSSIGPMGQMTSRGFRATPSTNNDIREALNAAFSFRPT
PQSLEASTLLAKNNEVPAEIDFDLHLPLLKSALSQHKKADVIRLMQDLARANAPARAFILQRVERYTKQMEEQMTQA
QQKAASSSNAAKISANAKNIDVQQPPSDKEAKEGSPAPSDKMSLQEAVLHGQLSARELEGVLRDLHRDITLSPADEQ
QIKDEAR**ALWEAGTAAVLAVDQSLPK**HFTAMVIDAFPWADLLLADEVTK**LVIESPVSK**AAARIRATEVLARQENIKK
NMSWISR**LILPSIAPSK**IKKGQTPHVYDAALDAYIHNDFDKLLSTPSGEKLTEATFRHVVQK**FEDAPENIAR**TIAAT
LHDTFVGHFIARTMASGIDYYSPKSFAKKLLTPMKPLNPYFAQRKRELDSTASASASASASA

>N421_putative_mitochondrial_carrier
MVRTAAPGGAGGSQQRPVTEEETPPIAMFAVPPVYSIVCGVLYCPLMLSYSNAWNAWVRAINRPPTPSASGWDRVVG
SPLKDFKAEAVISNRSWKRFALLVGTDMLELLTALYAGLAVSLTLDAFRAPPGQQPGNMESPSLFSSLWGNVAGTVI
AFPLSILTWQLHTDNWR**GWGSLVPFTSLGR**LHWRALPAK**YFELLALNVLK**VRLADAVTSVTGIGCEPLGWLASDVKN
HQDDPDFYDEREERSTARVIVDRARLWAIGTVGSWLSSLVLVGMQVPAAIVCHRMLAEPGR**FGSVVECVR**HIWASEG
LSGFYRDLPLFSLLIINELM

>N422_SAM_complex_protein_Sam35_(metaxin-like_homolog
MHLSLLEEGSLPCLALLFILGAIGARAVFRFLREEPEPKTSDVIDR**GDSSVTHIK**LHTFKQPASAQTACSLSPFCEK
LELFLRMAALDFK**AIDGNVVTAPK**AKLPMIEHGENLVPDSELAIR**YLINTFGENK**THLGRIRIKLTPEEQARSVLLT
NVTNDSLYQLLLHARWVDLSVWNVVK**GLYFGDLPLPFRLLIVPSIR**RNMVGWLWGHGYSRYSQKDRVWLARREIDAL
ATILGDHPYFNGDEPTPVDAAVFGILDNCIYGIGSVYGIRDHVQTKK**NLVAFVEGIR**QEFF

>N423_FAD-dependent_pyridine_nucleotide-disulfide_oxidoreductase_domain-
containing_protein
MRRVLGSVSREQQVVRSGVVATARSVRSYTTAAAASATVSGRKWDAIVVGGGHNGLVTAAYLAKAGKKVAVLERRHV
VGGAAVTEELLPGYKFSRASYLCSLFRPQIFKDLKLKEKYGVKLYQR**NPSSFTPLLDGR**YLLMGGGTMEETQRAIAQ
FSKADAEAYPEYEAMLDK**LVHFINPLIDEIPPNLGESPFSGSPK**QVLDKLASLSRLGLRTAKLGKDIAPLYEIVTAP
AAQILNKWFESEPLKSTLATDAIIGAMTSPQVPGSGYVLLHHVMGETDGIPGAWSYVEGGMGSISRAIASAAADEGV
TIVTDAAVKSIIVSER**GASGVELADGTK**LESDLVISNATPEVTFHSLLSQESQARLPSSFRQQLK**HYDYTSPVMKIN**
IALNQIPNFTCLPNQAPGVAGPQHRCTIHLGAESMADIETAYQDALQGTPSRKPVIEMTIPSSLDPTLAPEGHHVAS
LFVQYAPYHIRGGTWDEKTKEEYADR**VFSLIDQYAPGFK**QSVIFKDILAPPDLERVFGLTGGNIFHGAMGLNQLFFM
RPSSGFARYQTPIPGLYLCGSGAHPGGGVMGAAGKNCARAILNNA

>N424_mitochondrial_ribosomal_protein_L25
MRKSSVVLTRNPYWRTSILQFKGYNDSWDRVVQSLSVVEHLEAVPRPFLGQKACEKYRKRGLVPGVLK**GLGAGYFDI**
PIALRISDLVSFRERGGFLNREYKLIIENKIKYVKPVDIVLDQTSMAPEHIVLQELR**ELTPPPVLTEEEEK**TKAKLE
RLMTSHFYGAKTYGPKNPIPLWYKEDGGVV

>N425_mitochondrial_carrier_AcMC18_(2-oxoglutarate/malate_transporter)
MASTQAKNPYDTLIQFVGGGVGGCVASICTHPVDLLKVRLQVQGSASGLAAPQLGLWKTTVSVFKEGGMVALYQGLS
ASLLRQATYTTTRFGCYMYLR**DLLADSQGNLPFYQK**VLASMLAGAGGAVVGTPADVTLVRMQADGRLPPEKQRRYKH
AVDGLIRIVREEGFFTMWKGCLPNVYRAMFMTAGQLASYDQAKMLLLATNIFKDDPVTHFTASTIAGLIAAVITSPL
DVVKSRVMNAEKGYYKGSIDCTLRTLR**AEGPLAFYR**GFLPYAIR**LTPHTIITFLAFEQFNK**ACIWLLKKAGKLPTDV
AA

>N426_TIM23_complex_homolog_Tim50
MRRIASGTPRSYAAMSGVWTSGAAAAASFSSQSLFKCATSSAAPLFTRSASLATPSTARLFARTTKPLGLAGRPLQQ
RFASTTAEGVQASGSGRARITAIGVLIAAVGGVTGVVYAAEGGNQGEEAGLFANLKKKFTAQTNKLLNIDENKKILP
DAHPPPYGKPITVVISDDVLLVQEYQPLSGGMLTKKRPGVEFFLAQLSQDYELVIWSLQQVMSFGPVIEKLDPNHHA
AHRVYVDATVVNAEGMNVKDLKFLNRPLDKTIVLDISPDHVVQKENLIVAPKYDGRLEDVYLLEMLNFFRLLAASSK
SQSGVPDVRNWVAAMNKKGPQYFKELYADAVKKAKDRAEEERKKREEQLQMRDVGNTGRKW

>N427_ubiquinone_biosynthesis_protein_Coq5_(2-hexaprenyl-6-methoxy-1,4-
benzoquinone_methyltransferase)
MRKASTTTVPMFAGMGAVNRTVSNASFCLLPSFSFASNGAKSAVIGSLLQRTYSTSPSPAAASLHASPPPANAAPKQ
REEEEEVTHFGFKNVRAKEKASMVGEVFHRVASNYDLMNDVMSAGVHRYWKDRFVTTLNPLPGTRILDVAGGTGDIA
FRCLDRMKSTSTFFSKAPGTGQRASSSVTVCDINPSMLAVGKERGIARGYTESTDPSVAWVVGDAEQLPIDDASMDA
FTIAFGIRNCTHIDKVIKEAYRVLKKGGRFMCLEFSHLENHLMQQVYDTYSFQVIPVMGHVVAGDMDSYQYLVESIR
RFPRQEVFADMIGQAGFRAVTFENLTFGVAAIHSGWKL

>N428_transmembrane_protein_53-like_protein
MRSKARALTLHVASRTTAAGFLRCASSWTSPAWQRDGFSFLPAQAEKVGQKPRPLVLTLGWLGANERHLGKYSSWYS
SQGYDTLSFISPATSILFPQFGRKHAAQLLDYAIDLSEQTKDGKQEKRPILFHVFSNNGLYFYANVLQQVARSSQYE
RVLHSTLGCVFDSTPSHLSVEIFTKGFGGALLGAMGITNDGRPAYDHWLVSPIIRALFSVALAPPFLRNNVSSLLES
YVRFQPKCPQLFLYSKGDELIPYTDIELAIRATNDLGIPATGKCWEDSPHVSHFRMHPEEYREAVAQFVEGATERWH
HHGQHTAIVQQQPAPLSHAGLDKVVEEWKRLIIHF

>N429_uncharacterized
MLRRSIAPVTGAGIQPATSSSCLVARTASAFVSSGSSQGQPILFKRNIQKYWSKEARQFKGKRPVKVMSIKRAARLA
ARRAAEEAEAAHLDSKYGTRCTSAFLAERVRWNEDYEGPVISTPTEEPKKTKREVPIATGAQEEKPSFFARLFGRS

>N430_uncharacterized
MSPASKMNMVKKGVVATPIGEAGQGFSTAQKVLRMSGALRQNWRGVHPLQPERQMQPSRARLLLRQRTNFRIWKTWA
GKTKQLALSPRIYGSVTTVIVPTWTHTAHPVDESYGHDASNETFYPYKSTVKGTRHRDEKTVLGIINDQ

>N431_uncharacterized_conserved_protein
MNRSTASLARCAFSPRGTRSSAVPLLRTVQRGLATDDQGQPLGGGMFDHLQEIEVVGNSLSKSGGIVEVTARGGGTE
VVKAQIDPILAGDAALLSKLLTQAAQDAYDQVQYEVKRKLVEVSMRDRRKQQMKERDQMAIDLEAFKEK

>N432_uncharacterized
MEGGGNQNEACAGLFAHADSVCGTATATTTNDALAPACREATARALSCLRAKSTFMGPRARVVLECVAEHRRDPSPC
NGLREDFERDTTHIREQAKLDEGWQKRMVELCEGPFTRLHKCHALMAAQGGEQRLAEVCEEPLDEMSACIQRVACPA
RLSAVRACLQSSGGREEVCEVEVDRWVGCTLNTAVESLRGLSGSRA

>N433_uncharacterized
MKARSSLLATVRCASGAGGRLPAPRLSATTLGAGHLRSGRTATATLARCSLRPSHQPWQLSSVLLPRRDFTASAAPS
SGQPEGEATSPALIKETSELFYQQLFVAKDEKAAFHLYKILNSLTRNRAFAVEFGQREGGRAIDQLFRLFREAATTH
YSQEKILAVLTNLARHDATQRRAIAVSGAEPLRQALVCKTTLRGVVAQAVQLLNVTLQSKAAELPSSLFEGYVPATMD
LMVDFADKPELQLDLIHLLGLLSTDCAFEDYKKLSPLGAAMLIRNMQAYIFEPQSDSFIARQMTETLQALHRILSRR
PAGGEHSEEESKLAQAFQNTFLEHDSKARYAVLNGLNCVVLLTKSTNPTVSSLATEVVELLGRDNPGVFAEVAKIRS
SQE

>N434_2-amino-3-ketobutyrate_CoA_ligase
MRRVVSKCPVTLGQRAAAQGAIRLYAGKSSGASVYAATLQPRLDQALKEIEEAGLYKRERTIVTPQSSSISVKERSE
PVINFCANNYLGLADSQELIDVAKDHLDKFGLGLASVRFICGTQSIHKDLEKKIAEFHKTDDTILYTSCWDANGGIF
ETVLGEGDAVISDALNHASIIDGIRLCKAKRFRYKHLDMADLEEQLKKADGEGAKVRMIATDGAFSMDGDVAPLDKI
CALADKYNALVMVDESHATGFFGPTGRGVPEYFDVMDRIDVTNSTMGKALGGATGGYTTGRKAIVDLLRQRSRPYLF
SNSLPPALVGATLRTFELLTTSTKLRDQLEANTARFRQGMKKAGFNVLGNDAHPICPVMLGDARLASKMAEEMLAHN
IYVIGFSFPVVPKGEARIRVQLSAIHTPEQIDKAIAAFTAVGKKLNVIA

>N435_mitochondrial_carrier_AcMC19

MTTTEHKGAVPAAVAPRKDPVRTANYLLYGAIAGICSKTATAPLERLRILQMVEHLHGGEGRYQGILRPLLIIAREE
GIRGYWKGNATNVVRIIPTSAARFYTFEIYKTFLRRFVRRDQLNTGEVLLASASAGTTAAVVTFPMDFVRTR**LTVQT**
AGNTYYRGVTNAVLSIYRQEGLLGFYKGVTAAVLNTAPYIAINFTTYEKLKEYTQAGGGSPGTVLSLAMGAIAGTLA
TTISYPADLIRKRIIVQEMGGK**EGTYGGISDAVR**KIMREEGPKGFYRGLTATYLKVVPSTAVTWWVIELCRSLSTNP

>N436_Complex_I_(NADH_dehydrogenase)_PDSW_subunit_(NIDM/NDUFB10)
MSSGR**AVPDFNDTDFDTEDPVAYQK**AIRQR**VVEHIVATEEMAELQTQLSQCYYR**EGVNYRKKCRPLAEEYMKRLEKW
K**AYIPPEGEETDSVVR**MRS

>N437_carnitine_O-acetyltransferase
MRSTRGANLQRLAHKSTTAVTGARALLPAECRATATRTTPPPAPTYAYQDKLPSLPVPPLEETLAKYLRSLQPFEML
GIFSPEEMKRTRALAEEFKAAGGRGQRLQSKLVARSQQKRNWLEEWWLKYAYNIWRCPTPVNVSYYFLFDEKVQGPE
RPDVSQSLVASLCIKGVLDFKAVLDKQGVPAEMMRGTVPLDMSQYSKLFTTARYPQQGEDYIATFEPEPYVLVLSNK
QFYVLDVLDKASNRALTVKELQAQIERILQASQESNDGLGVGILTGEDRDKWAKAR**QELVSISATNAR**NLDVIDKAL
FVLCLDEESPRDVDTAGHLCLVGNGENRWYDKIVQYIVFKNGRGGLNGEHTPIDAPTAGAMTDHMLRYLRRAQESSL
PSEEQSVASDLRAPTK**LQWTLSPSLRTAQEEAVESYGKVGQDVDFR**LLHFRTYGADWIKEKAKLSPDSYVQMALQLA
YYKLYHTGTATYETGQTRQFYHGRTETVRSFCAESVEWTKAMTDASAPKQKRIDLLRKAIEHHSKALMADATNARGV
DRHLLGLKLVAMEDEEEKSLGMPELFKDRAYAESSTFRLSTSNMPGKLYISGFGPVAADGYGVCYGTRNDMLQFTIT
SLRSCPTTDSARMRETLHNTLVEMGALFADAGQAKL

>N438_iron/manganese_superoxide_dismutase
MMKRASATRPLLASTALRFGASSPSSSALVGGAAKWRVLSSSSSMQRRSIHKLPELNWLDQPAALNTCFSEEAFKQH
LKKHHMVHLQATNK**LIEGTDMETLSLEELIVK**ASKNKSKTVLLNHAAEAWNHNFFWQCMSPTPSAPSPTLINSFELH
FGGLEQFKEK**FEQFATVHLGSGWTWLVDR**DGHMEVINTSNSGTVITDPQYTPLLVLDLWEHSYFLDYRESR**KDYLAQ**
WWKVVNWKFVAGQLKEAESKNTWMQSSTSAQALKPYPAS

>N439_mitochondrial_translation_elongation_factor_Ts_(EF-Ts)
MKSAFACRAAFALAAATTGSGRGAAVFAVRSSSSLVSLRTPASGGCSNSRAFADAAAGGGGGGMMGQIKELRARTGA
GVMDCKEALAASAGDPAK**AELWLLDK**ARSRFAKKAERPTTEGTLALALASSEALLLELNSETDFVGRLEGFQK**LALD**
AAAAALARAGQVAADGQGPHHLDSAWLSALPLGDGTPKTVGDGVVGLFMQVGENMKARRAVLLRTAGSEGALGTFIQ
GTGLPHTGTLAALVALQAQPSGGGGAAVGEKLVPLANALAKHIAGINPR**YLSLEDVPETEAK**EVGKEHVVLEQEVTY
GEETGRVRELLEREGAKLGARVSIVHFVRWK**VGDGLEKPTTDFAAEVEK**ELQRSTKH

>N440_terpene_utilization_protein_AtuA,_putative_(DUF1446_multi-domain)
MEGASGKVVRIGGASAFWGDSPTGAWQLVGSEGSNLHYLVADYLAEVTMAILARQNKEGGGFVGEFVQSVWKPLMKQ
ILANKTKVVTNAGGMNPVACKAAIEQAAR**DAGLPVPVVAAVAGDDLMPR**YEELSAK**SAFTTFEEVPGEAEPK**WHERG
KLMSFNAYHGARAIAEALDRGAQIVVTGRCADSALVLGPLVHEFRWTWADHDLLSSGSLAGHIIECGCQATGGNFTD
WELSLAGGVDGVESGRGWDNVGFPVVECR**ADGSFVVTKPK**GTGGVVTTATVGEQMLYEIHNPAAYILPDVVCNWEQV
RMKQVGPNRVLVHGARGLPPTPFLKISATSVDGWK**IGGTLFIGGIDAR**KK**ALAVADAILAR**TRRILSMRGLPDFIRT
HAEVLGAESSYGPHARPEVMATREVMLHITVHHAEPTALGLFAREVAPAATAMAPGISGGGTGRPRPQPLIHHSAVL
VSRKEVPASLFVGDQPETRVPSTFEGPYSTSFPSPYTSTSGGAAAPFAFPTGVEMVEVPLVRLCYGRSGDKGDVANI
GIIARNPAHYPFLRSALTEEVVHRYLAHLVKGTTRRFEVPGISGLNFVLTQALGGGGLASLHMDRQGKAYAQILLSL
PVTVPRQWLAATDSPARL

>N441_mitochondrial_ribosomal_protein_L49
MMRRGTAVLGSCVRPSTTGAYAAAAGWRRTIAGSTSTSATSETVVPLGSLRYPPPHSEEAVTGAGPTGYKPPLGNTD
ALPFRVLRTKSGR**LPIYTDYK**NGRTKKITILRKFSGDRKELREEVWRVLGGPK**NPGLEVVER**AGSLEIKGDYTWQLQ
MWLKRLGF

>N442_glutamyl-tRNA(Gln)_amidotransferase,_A_subunit
MEATRKGGRAVYRLSRGARRCCFRETSDCGSRRLYSGTSGGSADLVRQSLADVGRALAEGRTTSEEVTRACLLQADH
TATLNAFVSR**HSDEHLLSLAALSDK**RRRDGHQVGKLEGIPVAVKDSFNTHDLPTTCASRMLKDHRPPCDAAVVSALR
KEGAIIMGKTNMDEFSMGSGNTQSYFGPVINPWSPSTKPEEAFVAGGSSGGSAAAVASDSCFGALGGDTGGSVRLPG
AYCGVVGFKPSYGRISRWGLVAYGSSLDTPGVLTKTVEDAAIMLGVLAGMDARDSTSVDIEVPDYVKSMNQPRKLRV
GIPKEYLVKELSEDTRKLWEEGAEAMAQQGAEVVEISLPHTQYALPAYYILAPAEASSNLSRYDGLRYGYRGAGDSI
TEMYSSSRSEGFGEEVQRR**ILLGTFTLSR**RLYDSYYRKAQQIRRLVLNDFETAFGQGVDVLLHPTAPTPAFALAEKL
NPVDMYINDIMTIPASMAGLPAVSVPVR**QSAASNLPQGLQLVGR**YMDEGTLLAAAR**LLEQAFPR**AHALRPPLA

>N443_CHCH_domain-containing_protein
MGRRGGSSRSSARPASKPTATAAPAKKAAPPATQQRAQPPATQQHAQTAPAMGGGGQSFLGGVAQMAAGYAVGHVAS
R**AIENVIFGGHNATPEQIQK**AEEQVQQGPCARPYDGFLKCLK**KNEDDATECDWAYDMFK**ECQTTNRANRDFGYGGES
KEQSATY

>N444_mitochondrial_fission_process_protein
MDDPK**ATELDVLR**DTWAR**YLGYANEVGEACR**GVLPLSLVHASYGLVGLYVLADAIHKGRRASHRKHGSVAERRFDIV
DNVADTLLWQTLASLLVPPLLINRTCKLTAFGLGK**YFPPAAYPSLTPR**RRALVQTAVGLAVIPFIVHPIDHGVHFAL
DHTSRVLSGIIRRKYFPVPSSSSPPLQTPQGSDNQQQHE

>N445_putative_Complex_I_(NADH_dehydrogenase)_MWFE_subunit_(NIMM/NDUFA1)
MSKAYGLFYSWELLPALTVMGVFLTTVPMGTYAGFKLILGEPKKIAAK**AIEYESELR**NHNHGVKKRYYGHSKTASSE
TH

>N446_uncharacterized
**MQRQGTKIVAGIAVGRGAARLGRVAATASVLSSRATFHGYAQSTTTRSAGWKLARTAPFSGPAGLLLHRRCLASSAT
PS**RGDNKQKKAEVEEEDTEEEETDDDEDDEEEDEDTEEETDDEEEEDEDEDEEKSK**GAPAPAGVSQAELAK**QRKEA
KDLKRLERKERQQKKKDIRKEQLQRRREQDAKKKEKEELKSREGARKKEKKEAVVSDIDWEEDLEAGTTAAAQAAKK
SNKKTSKKRQKDAAFVPAVNPNLFNPE

>N447_Zn-dependent_alcohol_dehydrogenase
MRGVRLASFGEGDPHSR**LEVRDDLLVPPLNPSTNDVLVRVEATSVNPIDLAMR**KGYARKILFRARAKESPMTLGFDC
VGTVVQTGKSAWSFKVGDRVWGSTSLFRDGCNAEYVLVEEPALAQAPANLTSVEAAALPTAAVAAWK**ALVESGQLGP
VGSPSPLNPSATTDR**QRVFINGDSDGVGVIALQLLKHYGHHASAVCSAPNVPK**FTQLIDAGGGEVIDHTR**EPDWAAR
LAGEGKEYDVLLDTVGTDEAEAQCVKLLKRGGKYLSLRPLVLDLIHEHGPFMGAMKGWWSIVKKQVEMKKEKDVLVN
YVTCGPDGKVLEQVRRLVEEGVIRPDVDRVFDDLAQLPEAHALLERGEARGKVVIK**VQDPLTAAAAAH**

>N448_adenylate_kinase
MRRNLPPFSISSCLSPPLRPPQAVLRRAQGAGSATRSCVGEQQQRFCTTRLTAGPPRAARGTTSWLSLQRPYSSTAT
AAAAGAKTVKDALSAVPSAPDMTGKPSATVTSPKDGKDKSDGEIKNSQLMFDSVWNKLKAKYTEERMVFPK**EIIWLM
GAPGSGKGTNTPFILEARGITASPVVLSDLLDSPEFR**VIKAEGGMISDAQVTETLLETLLQDQYRVGALVDGFPRTE
IQVDHVSLLYDRMLTLKRQNPQLYPRPVFRMSVLFVEERTSIERQLARGKRATIHNAKVKETGIGELAPERPTDMSE
KAAAKRYAIFKQHFATLTTLQQRFPFHLINAQDSIEQV

>N449_mitochondrial_ribosomal_protein_L40
MMKRLVVARPSAVGVAQSSLLSSSFSSTTTMCLRSSSVAGIQISSRSYAGSFTKKKKEKKKSGGGEEGEAAEGKRFD
EELWKLRPQWVTLTR**TPEQLAEEEALIK**SYAKLKMKQLHEESRQLSKMLKLKLEALNELPPDLR**AEALVEEVSNAPR**
ERVLPLWTAPIPGYQDSLPPEKRDEPFDFTKLGSIRKRSS

>N450_uncharacterized
MTLDSIKAGGSALLASLLQGGGESTPTGLLAGLGVTAAALGLGAAYMLVLRQPSYASFQLNASFPTVPPNVLFDFLV
EPANYYDPRINRKGYRPVVVEREAGK**IAYVLEDDALGGLLHFSTPVVR**RFYEHPDGRDSTDGEDKRHSGSR**VLILDC
CALGVFVK**IIWHFVGTNMEGEGGGEGGGEADVGTDVKIK**VSLQGPWWK**LKLMQTGMKKEIGAKLAKLQLLAEQEGGL
N

>N451_hydroxyacid-oxoacid_transhydrogenase,_mitochondrial-like
MKRTCSARRAAVVCRSTAAVAQGSSTRSLHSAQPTQSGHRAIPPHHVHGPTCPCSAAHNPQYFYRGLLGAEGAEARA
SLTRPGVRFARRTQSTPTTHARLSSSAATGGLSRSGPKESEADYAFEMAGSNIRFGVGATREVGLDLVDMGARHVCV
FTDSTLK**DLAPVITVLQSLQDAKVNFVLYDK**VK**VEPTDASFK**HAIEFVTQTARKVTPTGHFDAFVAVGGGSVIDTCK
AANLYATYPPEDFFDYVNPPVGKGKPPPGALKPLIAIPTTAGTGSEATGVAIFDHVERNSKAGIAHRRLKPTLGIVD
PENTKSMPPQVAAASGFDVLCHALESYTAIPYDQRTPRPATPLLRPAYQGSNPIADVWSLKSLEMLAKYFVRSVENR
DDTEARAQMALAATYAGIGFGSAGVHLCHGMSYPVSSLAHHMTYKPKDYNVDSPMIPHGMSVVLHAPAVFRFTASAN
PDRHKQVAALLGAKDIENVRDSDAGPVLADRIIELMKRLDIPNGLQALGFSSNDIDALVEGALPQHRVLKLAPVPTG
QEELAKLFQQSMQIW

>N452_BolA-like_family_protein

MSKGTGVRRLGLAMKQKLESGLLPVK**LNIVDESHLHAGHR**FVKESGITQETHFKVFVVSKAFEGKSLVARHRLCYSL
IDQEIKEGVHAVALTTLTPEEDKEKEVV

>N453_mitochondrial_carrier_AcMC20_(putative_carnitine-
acylcarnitine_transporter)
MSDAVKDFIAGTFGGMALVITGHPFDTLKVRLQTAPPGYFSSFGDCVKQTYTKEGAKGFYKGVGSPLVGVSAINSVL
FWTWGRSQRLFQPDKSIPLTTSQLIGAGAITGLVVAFAEGPVDLIKSKMQVQYGAGGQYKNSFDCAR**QLVSTYGIRG
LYQGIVPTILR**NIPANAAYFAGYEYMRRKFTGDDGGAGEKKLSAGAVLAAGAIGGVGYWVSSFPFDVVKSR**IQTQPT
DLSQR**QYKSTWDAMVQLNKAEGWRGFWRGFTPCMLRACPANAACFFAYETARSLLG

>N454_2-methylisocitrate_lyase
MWLRGVNGLGVEATAGWRLREAVRVGVASKGGAWGGVVPVVGAPNAYAALLAERAGLPLLYLSGSTLSASSFGLPDL
GLTTLDEVVEDARRITRVSKLPLLVDADTGFGGVLNVARTIQELERVGAAGVHIEDQETQHKRCGHRPNKRVVTTGE
MVDRLQAAVAARRDRSFVIMARTDSVASEGLDAALKRAQAYIDAGADMLFPEALTHIDHYKAFTSAFPDTPVLANLT
EFGR**TPLFTLEELSQAKVALALFPVSAFR**AAARATQHVYETVAKDGSQSAAIPLMQTR**EELYDVLGYDEYEK**ALDAL
YPPPATPAAQAPAAAAPAAVASLASSGGIGTEGQSVEEAKAKEEKNEEKEEEEEEGEVLLVEENGEKKEEKVVSETA
APNNEDEKKEKKKEDEESEDEDEDDDTGVVITADSAAAIEEELASGKEIKLKD

>N455_3-ketoacyl-CoA_thiolase
MKKALSRRTFVVGGRTLPFIGKGHPDFVWKKHPLFGKKENPSLEDYITQSVQAALKDTNTPASAIEKAWIGNFAGEL
FSSQGHLGAALAGASPEFRFLPAMRVEGACASGGLAFASAVEAIQAGTDVTLVCGAEVQNTVSAREGGDYLARASHY
RSQR**QLDDFTFPALFAQR**MKHYCKTHNVGPKDFARVSVKAYANANKNPLAHMHAVKMDLDTASTASDKNPNFLANED
LKPHLRTSDCSQVSDGASAMVVVSEEGLRRLGKSPRDAIEVLAVQVAADNLYVDR**DYDKFETTHAAAQR**AFQSTGLT
AKDIGVFEVHDCFSIAEVLMYEALGLADHGKGTHFAADGHTHIDGKFPVNTGGGLIGFGHPVGATGVKQVLEIYRQM
KGQSGAYQIPNHESKLK**LGLAANMGGSDKTAVVSLFANH**

>N456_ras-related_protein_Rab32
MSHGHGGK**AAEGPATEYLYK**ILVVGDIGTGKTAIIRRCVENQFSESYK**TTIGVDFALK**TIQRSNATIHLQLWDIAGQ
ERYGNLTRVYYK**EAVGAFVVFDLTR**NSSFEAVKRWKEDIDNKVRLPNGDPLPVVLLANKCDLVKTPLSEEVMNDYCK
ENGFLAWFATSAKENINIDEAVNFLVENIIVHGSNDAIKGPGPDALKVGGERGGAPDSNACGC

>N457_pentatricopetide_repeat_(PPR)_protein_AcPPR7
MSFLAQSKNGFMPRRLAGLTSTSLPSPPAPTLHLARSFRTLPASAVSSIGCGSATLRWLASSSSRGRAPVVTEDKGN
RMVILGKGMIPLDVLSTQELRNEVDRLERAEHAVIQPRRYCSLLVSCTNPKLRARVLRLADKVTDVSAADSAAHGYA
LIFHTLWKSRVLQRRELDPLVATILSTMRDQEVQVNGQCLNYLLNLYFAYGDVAK**ACDLFDLLR**EGEGRWRAEPNVM
TYTTLVRGLAGRDAGGQLDGSVRPDLPRALRYFEQMVKRDGVRPDRVAFTALLHVCAAEADLPRALQVWDEMKRAGV
APDTFAFNSLLHVCNRALDLDLALKLTDGMQSRQLEPNDVTYSSLIDLCCRVNDFGRAHELLNEMKERGIAPTVITF
TSFISAYGQAGDVERCFDVLALMAQERVRPNQITLAGLVQACLNAGDFRKAVQTLGDMKRRYGLAPSAYVLYHLIHK
AGPKAKTTDLLRLLER**IEATEGVPLETR**TYSELIKLCGTRNELELAFLIHEKAQQQQRGGNADAGQRLVDR**SLFNAC
IQNQNPR**KALEIVDAIMQRESLKERDVAQVDGEEVVLDEEDTRDPVNVTMFNALLRTVDTNTVESVIDRMKRLHVAP
NMATIDLLITHYESSGRLDRMWAVLRDLQDHKVIEREDLIYNSFIKVFLRRDDTDKAYTVFTELLTRNTPLPPATYH
LFLDTRDSRTAAAGNISDNGMDGVDGDEQHAALGAESEEERAVRLRRVGERAALIPSLVKLLYERDPSAPPTALLPF
IRFCVLHYKPAELQPLVDRLERDAGRGAALVERIQEAYIMLHEADRAIELIHTLRQRGLKVDASLYNALVR**LATPES
PGSALR**LRALMRADRIPDEDTQDPFAPLELQPQAARPRYYNRPQQQQQHQPYQRRQRLAPDYRTPAAAERHDMEVEV
DLLDPEGEYGQSATTTTTR**EAVKDAAAER**KRRKKEKRLLNTEKADEEEGVKKEKERAKVEPIKRPKVTGDLLSLSFS
LLGQQAKKRE

>N458_uncharacterized
MR**TGILGDSTSLER**LVGVPKQLQVLRHDGHINWVETAAMAAAEGGHHRHGAVFTSTLLDNNRELLRVASGAASTEEG
DHLDLDLIVFSFAAADRCSLEDRNFK**AAFQWADAYFR**ARNKPAQVGVLLVDYAVNKPAGPARVDDDRIIGLVAGDPY
LEALMRARRIVRWNATTPALDDHDHHDGLPDLSDDLARVLADFCRRPVVSLQAASGSSLRGGSGGARAGGDRFVNGL
LVCSLAVLVALLVLHLSPSLQALAAGALLPESAAELTRLRLENGAQEAMTVGLQKDNELLKEINARQKKHNDELTKD
VTDLKHRNTRLQAQVDQLTAAQLAATQTLTDRTLVISSLCQGCCQGETAVGGSMCRLCSSAPAA

>N459_adenylosuccinate_lyase
MKRAGVVTKCAWPLGSASTMRSGLVGASSASRLLLRQAGGESLLLATARPLATSSHRDVFENPLVSRYASRAMSGNW
SPQKKFSTWRRLWLALAEAQK**ELGLPITEK**QLAEMRAHLDDIDFAAAEKKEKEVRHDVMSHIHAFGTVCPTAMPIIH

LGATSCYVTDNTDLIQLRDGLRIVQQHMLQLMQHLREVSLRYKDLPTLGFTHYQPAQLVTVGKRATLWLQDLLFDYE
QLSERANRLPFLGVKGTTGTQASFLELFNGDHNKVRELDRRVTEMMGFNK**SLGVSGQTYTRKIDYQVLSSLSAVAQS**
LNKMAVDIRLLMNLKEIEEPFESKQIGSSAMAYKRNPMRCERICGLARYVISLTDNAAHTHANQWFERTLDDSANRR
LSLPEAFLATDVILRVACNVVDGLQVWPLVIKKHIDAELPFMATENILMAAVKAGGDRQALHESIREHSMEAGRLVK
EQGLDNDLIERIRNDPHFAAVRHKIDDMLDPAKFVGRAPQQVEEFVRDEVDPVLARDAHLLRDFDHKTAAQLHV

>N460_mitochondrial_ribosomal_protein_S25
MGKRFWRAARQFGLEKGMPKPK**TPEDWNR**LYLK**HQVYLHGIK**SLELQMVKTGAGKTGARHFHYWKVPPIRWWNPDVN
IHEQKLLAGESKLIIEKVDGKKIELVVDGMKDEEIYNALLSHSDAAPVASKEASVQ

>N461_lipoyltransferase_and_lipoate-
protein_ligase/thymidylate_kinase_domain_fusion_protein
MKFGKHLLSSALPAWLASYLDYKALKRAIKVQAQTGDTSLFDTLLSAEIKKADAFYKAREEDLLQLFSALIERPGSK
RPSADEKTPLLTKGFSKSDVGADASGEAWRSMSREEVLQRLDEVEALATNLLKFSALNYTGVSKSLKKSFKKTGISS
EDAWLPRLHQTHFFVSRKCDEVLTKTTLIRRELKEDDRVAAKKKIAQGGNGGSSSSSSAGAADEQAPSLWAFILGTF
IHQIADNANKLVVPLVYLQITSVGVMSILTGVMTLLQTFGTLPAGRWSSMIGPKALIQWITLGRALLTTILAIVFFF
FSTGALPSGLTLFLVTLITSADWFIRGAIDTARNVLPMAYSQNSKKMLDEINIRFFTVFELGALVGPVVQGIILALG
WGLAVTLWVPVVFLVLNLVVNFWIPEADSSKYSFLQSKDKETEGEKKKKKPSLLESYVRGIKECIDPTIGLVFILVI
LLQLNKIRLVIPQIIAVELFNDDSYAAWIFSTYSLGGVIGSGVYALVKNTFTPAMNMVFASTGVLILAVSWWPALAQ
ASIIPFLSHKDEWLLWVLLGAMLFSIVKQSARTSMQSIFQYALKDSKSAADIMALNR**FGVNGLATGLR**FALGIPFIF
LSVTTAFLSISGGLAVIATVMFIGTYLLTKLPINNQNLKKDKDEKKEKDVDDSEDEDKKIKKLKKRKPSKKLNRKLS
DEEIAQLVDIPKDTGVLIVFEGLDGAGKSTQVERLKSFMQGEGYVSLVTTWSKSAHHYDLIRQLKRQTPMRSILLTV
VQAMDFQQMIKQDVIPALRAKKVVLCDRYFYTGIARGVARGLSKTWLRQLFTADVNLEPDLVLYHQCVAAVAVSRVL
SRSNSNTAQLSDDSMTHRVIVTLKSEDGGDKSRDLSAARISVYEAGLDVANPDLDPYDNFVSFQTRVSGEYDAMIPE
YRFKVVDGTQGRDEQESKVRSYVEPMLADLKKEVSRPFKTNLFDKNPKLDSGKKVKEYYLTKDGLHWYFRTMYFPMR
NRLSELIDLSKAPRVFLHGNPHINNFARFPGGSAMIDFDRTCIGPYLWDLVRLMVSTAFKQAGEDEIGGTFLRLGVL
QRLKSGYEWGLLHKDEPSAHPQRNEPFISEEAAPAPPAQPKPFAIPPGVKGNLAPPAPLVRARSASLVFGEGGHADP
SFYLKRLEEMRKNHADLDDSLREMARTYLEVRS

>N462_pyruvate_dehyrogenase_phosphatase_catalytic_subunit
MLRVAGVGCRGARGHCLTNDLHLHHPSSTTASALSRSFVPHSTLPASAPAKKATTQSAPVATAAALPTSSSSTSPSS
TATASPSTLLASHSHSPRAIPTLNSLFVLRNARPIAVSGVGRGPMAFGVAARRRMSASTGPNPNELPQFPHTSTPAT
SSIFKKLSRPLFIGGVGIASFAASYGYFEYQKKKRKYATSASPILDALTPSVSPDLVEQVTRKINANAQAFTVAPGN
CHITEFHTNTIASNSPIEDRHNQLLHDPQIYDGSLFGMYDGHGGWAASEFVKNELFDFVKLELGILKLKQEKFIDSI
VKEKELRDRIVDFLAKDPASPQLYEDLKGIIAKQSQLDEAHREQLLTPLDALFNPERNISQCLQLAFLRADSYFLYE
ALLDPEKLRDGFSGACVLLSYFLNDHIYVANAGDCRAVLGRKRDSSGDPIKGADTRRVWEAIELSHDHGTENLEERK
RLIEAHPNEDDIVLDERVKGSLQPTR**GIGDGLFKDPNFNDALAR**KLENWHPPYTTAMPEVISHKITPADQFVVLATD
GLFDFFTSQEVVDMVGHYLEHMQRDPKDDSHNSVQQPPSSELKLK**LQENASSYLIGK**VLNKAGYGKTPEVRMNFCIT
LPKEAKRGFFDDTTVTVIFLGPHITSGAVQDEHGQEDTEAGTGSGGSEPVLAKPAVMERVEGLIEQKVREDQESGMM
WKAWHQSFAGGRSG

>N463_carbon-nitrogen_hydrolase
MQRTLRVGTAAAVRLGASSGTCARTLHASAAVGQSAASTNPEAVQVALIQFHSASANPDENQAKAEGFVREAAR**NGA**
QFILLPELYRTMLPREQMPQYAESIPDGPTSRRWAGLAKELGVWLLGGSMIEPVEGQPGK**LYNTAVLFSDSGDLAAR**
YRKIHLFDVCVPGVVDFQESALISSGKETTTVASPFGKLGLSVCYDLRFPELFRHLAKQGMDILCLPAAFNYGTGQK
HWLHLLKARAIENQCFVLAPNQVGEAPNKFKSWGHSLILDPWGDIVAEGGDGEEIVYGKLDLSLLGKYREALPSLKH
IRKDIFHV

>N464_ATP-binding_cassette_(ABC)_sub-family_D_member_2-like_protein
MSSTPISVEALTRLLRENVTKRHLVSGLGILASVGAGVYLTRKRVNQMEAEKEHR**AQQDALEEATTGVVVK**AKPQFN
RQQFYKRLGRLLRIVLPSIYSKEAGILGMHTFFLFTRTLLSIYVAYIDGQIVRSIVGRSPFAFMWLLAKWLALSVPA
VYTNSMIKYLEDKLAIAFRTRMSDHLYQKYMESETYYRVGNLDSRLTNADQCLTEDVSKFSSHLASLYSQLSKPMFD
VVLMVVQLWVLITRQAGFMSGLPPLAGGVMCVWLTSKLLRRMSPPFGALVAKQAALEGQLRFVHSR**LITNAEEIAFY**
RGHKIEHGVIARSYYALVKHMNLIFQQRVFYTMLEGFLMKYVWSAIGMNIIAFPTFLADYKQQKIEKATGTVEGLSS
MGDR**TQNYIVAR**K**LLLDSADAVER**IMLAQKQISELDGYVTRVTDMLDVFEDMHDGKFVKTMINNVDDDDDGAKAKRI
KGEPDGEDSDEDDAEEESTTVKEKRIRHHDNGPAEPLDLTKPQGVVQEADYIQFDKVPIVSPNGDVLVESLSFEVTP
GRHLLITGPNGCGKSSLFRILGGLWPVYRGSVVKPSISDMFYIPQRPYLAIGSLRDQVIYPHTVQDMHSANITDKDL

DDIMEWVNLTKVVVREGGWDAVSDWKDVLSGGEKQRVAMARLFYHRPKYAILDECTSAVSVDVEGKMYAHAQDLGIT
LLTVTHRPSLWQYHNYLLQFDGEGGWQFLPLNATARMGLKEEKMRLEAQLQGMPTMHKRLRELCNLLGEDSIALQQE

>N465_uncharacterized_conserved_bacterial_protein
MAARRPPR**GFEELFVRFPFFTPFRVVGWGTLALINAGLAESK**GRSRLFWGGVSLGAGPLATAYIVFTPSHKHDHS

>N466_AAA_family_ATPase
MLRHTKRSQLPAAVARDLFLSWRHTSAAKASFAGGQQSYATTPPTPPESQFAYGDGSFPSVFSQENGMFWVDRTGFI
PLLEALKAKAVVSLRNRRMGKTLWIDTLAHYYDVAHKGRFKELFGHLEIGKAPTQLANTFHVLPLTFAGIKSHNFDD
FRRSLNAALNQAAADFKERYNLSFELNDRDAAVTFQGLVDELKRKNEKLYVLIDEYDVSINK**ALGDLPLVSALQVSE**
KGLLKSMENTYAEFFSRIKTACDRNVARCFVTGVTPLALNEFTSGFNIAEHITRDRRFASLYGFTEADVRNGLARLH
RLQPEVVDRIVDSWRRDHNGYHFHPRQEVALYNPTRVLHGLRQLEQVLSFDPPLSTLRPEEAADFLLNEIQSDPNSM
PAEATLEAIKSSPYASLVVAEALSSDDAELECAGGVANQFRLSHMHELNTGRTPLLSFMFYTGALTYARSPPKLKHS
LRIPNNVARKEFTVELQR**LLDIDEIGVQQLR**GAIVKMVDGRQVEPFCRAVSRFLLRGLDGRDALGGEDPFAQAVYDA
MLLARRPGDCVRKEYKVDPVARHSNTSGPALDVVYIGQQAVAPQKPQHYCFTLKNVKVQGLVLGQGVQSWEKQVEIS
RTIDNMGGDDEAVLDLPLAKGDNFRKPGSTVR**TVLEEAIQEAR**GKYVPALQAEVGEANVHCWALVRVGMTRIVCKKV
LPVEQQQ

>N467_ribonuclease_II
MRRLCRVQRLPSPKARPGQTKPLSCTVGATPASRFLSQFRCISREAGWRGINARLGVSTRQHSTTTLPRHALCTSSS
YSTRAFEPAIGEVPEDEPNLAEEGRVIEYIEDGVPKLGLLLQKLEEHERESKSLWIVGSQDARKFALSQAKFSYVWP
EMPQLGLVDGITAQAVRGNAKQLAALAKEAEDLRATIAPERLQALWEEAQLTGDSPDSPRKTITPVQAAQFLFGSTG
PLETYAAHGLLWETRVYFKPRGKTFVCRDREMAEELKDSLQDRVDSVKHSKLFLIKMRHKLERAVGGDQAPSAFLPD
IADLSKEYQACWKSLNYAEDRASTDVDLVAGGMDSLTEKQHLDFLKKYAAMIISETPSSEPIDVTEHTPLEGLLKEG
ANSVDLFNAMVQLGVFSEKENLDIILHRRPLHFPEEASTWVNEVLAQPPPDSDGGKRLDLRQLPVYTIDPHDAYEID
DGLSIQTDEDGDTWVYVHVADPTRWITPDSPLDLLARDRAQSLYLPNGVSLPLFPPKFTSQAVALRPNTRSCALTFA
AKLDRESGEIKDYKIAPTLVENVHGLTYGQADSLILSGQEKYAKATAQYLPLHLQEEQQLLAVPDADEREERKNDIK
ESLRRLGLNHKLGKKKGEASRKEAPHRTLDLQR**VESADTFSNR**ELARPGVDKEAAMGAVWGLHEMAKLRRRYREQRG
AVIVSLPTTAIRIDDVAQHRGVRVRRLESKVTEEGANLGQEGASEEGEEEEEIEGMQESTGARMMVEELMLLAGEIA
GKFAEARGIPIPFRVQQRPPGDSKYLDYLVRGKEKKAVVKSWKSLVGLPPTKYSSVPGPHFSLALDSYAQVTSPMRR
YADVLAHHQIKAALRGEEPPFLSWHFVPMFQTMIQRKQEFASLVEVISRRWIIQYLKENKDRPFRAVVLEVQEKRAG
GNLIGDSR**ATVLLSELGWR**TIVTVPKSVKQGHALTLRVRTADPWTNYVSFFKLRQ

>N468_uncharacterized_conserved_protein
MGAASSRPHEEAEDWEDHFQHEYEQPTAANWAEDEEEEASVSVHLGPRLVRRLQQRQSGGAAARRPQQQQREKQEQQ
QRFDEAALELDVDEALPPPLSEEELDSIAFSTPLPLLLGDDDVEEEVR**HGAGEASTSVVVPAR**R**AGGVSQADREFAQ**
QEVAEVRQRFRAEQEKISATEVEQLHKLRGLLDAMTRHRRASEDSCEAERSACLECYAKETDDPLACAAKARAFKQC
ATAPVRKGAPV

>N469_DnaJ_protein
MRATKTASHVAAAKSIVHNQGANRSLASSLRSLNGSSSSSIIFTHSSCSNHTHCGIRNHSTVSSFTAGNKTAASSTP
LSFIVSWKQASLRQFHATSSTRKEEDLYETLGVPRTASADEIKRQYYKLAMQYHPDRNKGDKKAEEKLQKINAAYTV
LKDEDKRRQYDQFGSAAFDGSGGGGFEGFDPNDIPVDMR**DIFEGIFSGFGGGGGR**RAKTKGDDVEVPLRINFHEAVN
GCEKDISYMGKLPCPTCHGSGAAAGSKAKKCPRCNGQGIEQIAHGFIPIATQCRQCGGEGTIISDPCGTCKGQGIIS
GNRKIQVK**IPAGVDDGANIR**LVGQGDAGMKGGKPGNLFLRVHVSPDKVFKR**DGVNVHTDIPVTLAQAVLGGTVKVPT**
LSGAEVEIKVPPGTQPEEKRVLR**NQGVSAVGQPGTK**GHHYIHFKVEIPTKLTPKQKELMEEWQKEEEQSGGIADKLK
GYFKS

>N470_NIPSNAP_domain-containing_protein
MRRTSSIALGRGSPLMASASRSFASATPPSQAIWQSLTNARHSIVTSK**KTEATTTPVEDPHVHELRVLTINPGHLKE**
FVQVSEKALAHKTKEGAKLIGYFNVTLGECTNEVMQIWQWESYKHR**EQATENLANNPAWEEYTK**TVKPMLQHQKYSI
ILQFPFWPLNYSQTKGGIYELRTYR**LIPGAVWVWGDYWEQGLK**HRSKYVQPVAAWYTEIGHLNTVHHLWR**YDDMDQR**
RQLREAVWDEPGWSEIVELTHPLIQTMDSR**ILTPTDFSPLQ**

>N471_mitochondrial_aspartyl-tRNA_synthetase_(AspRS)
MKARLGSTGVLRAGRTGRAASSAAVPARHAAGRASAPVREGISSSNSRPGAIISGLRWGRPSSTWLPSSAAPQWPQL
RSFSTSSSPAPKKAGLGSTTPALDRTHHCGRVTAADAGTSVR**LCGWLTASRDFGGVLFLV**VKDHTGPVQVLVDEKRL

TPGLREQVASWRIESVVTVTGKVQLRPASMQNKDMPTGEIEIVCEDIALLNPTSHTSLPFPSWSSPLHGDERDALPP
EELRLRYRFLDIRRPYIQDNLRLRSQLSLAARNYLHGQGFSEIETPTLFRSTPEGAREFIVPTRTRGKFYSLPQSPQ
QYKQLLMVGGIDRYFQFARCYRDEGIRFDRQPEFTQIDMEMAFVGDRDVCNLTEGLVRTMWKTAGHTLPDPFPRMSF
R**HAMETYGSDKPDTR**YDLLLR**DVTDILQQSR**VNVLTAPLTAGASTDAAAHKKGPGRCIKAINVRGMADLSREDSDGI
QKRARDLGGKGVVEIRCGPEGKWRSPIEKHLTDGERRRLGDALEAQEGDLLLLCSGPER**DDVSLILGGIR**SHCAKLM
KRRGKLSIPDDQYNFLWVEEFPLFSFESASPGEAKRIVTTHHPFTAPHPDDIDLLMSSDAEHDLLRVRGLHYDCVVN
GVELGGGSIRVHNEAMQRHIFRVLGMSDNVMTRFQHLLDALGMGCPPHGGLAIGFDRLMAILCHAESLREVIAFPKT
ATGNELMTGAPSEPGLDELKEYHISVAAAPPS

>N472_regulator_of_chromosome_condensation_(RCC1)_repeat_domain-containing_protein
MKRVAHGATGRMLMPGRTATAAKLCTPPASSSMCLVEKRRYSIQPERVPKPGQGVYTCGTGRNAQLGVGDLEDYQLP
VPVQELPVGASYIDAAAGWTQNFLLTTRHELYYWGSSGVYALLPMRRDKRIYYPTLCEPAQSLGIVKIRTGRQHGIA
LSKNGEVYIWGNSEFGQTGLGNKEAQHLPIRMEFFRDKSIVDVSCGLDHSAAVSKDGRVWTWGYGIDGQLGHNGTED
ELKPKELTVIRGEGISRVTCGTDFTGLLNETEGR**LFTFGNGEAGQLGHGERGLCLEPSVVPLDNVK**EVAAGGAHMLA
LTKDGQAWSWGWGEDGRLGHGATEDFLKPEPIPTLGPAVGVVSVSAGGGHSLALTESGQVYGWGFNASGR**LGLGNES
SVMTPTLIK**ALADKRVLRAICGLDHSLFITQA

>N473_uncharacterized
**MMRRSMAAGLPLVAVPWGAHVAWRTTTSAKGALLVGFVAGTAIPAGSAMTRVARVVGGQRRHYAQMGAQFAPGPKSF
SEMRSAAVSIKRRYMRL**AVYLSVGFFFVVFPVSTLAAQAWEQRNWPTLQAK**IVEVVPIEGTNK**RRVTYRYKVLGRVV
EK**TQVNWNVPWWDRINNTQLDFK**VGDFVTIYHHPHNVMLSIFKPGNFAHPNFGR**LKGEVIEDTTKPAR**RTLPQVGPH

>N474_SAM-dependent_methyltransferase
MARRALLKRMNAGPATTVLPALHPTLAARLFPNSDHSSPEQPPRRVWSLPENCVPQLQGSGTTAASRPPPQGFVAVT
NPLTSTSAGPADDR**AVLLVDPTLSPPIR**VVGYGMSAVDEAYVEGALREALTYRRQLAGEGRLELDDARHTSAFR**LVH
ELGDGLTALAIDVYGR**YADVQTYSVHWDRFLPFIRDKLWSPEFLPFLRGITVRRRFRKKRPTARFYYNPAFFNDEQE
DDVGAAAGDADDLDEEDDVEGFDDEELDGGGDDRERAQQQQLRAGDRSAEFR**DVVVEEDGLK**YHVDLRTSALSSGLF
LDQRENRKWMLENVFTRPKMSLLNLFAHTGAWSVSAAVKAKALTTSVDHSAMCLDVAMANFRLNGIPLAFSADKSKS
RGADKKGWQGGRKRGEGHEFVARDAFQELIALRAKSRKFDVVLLDPPALARTSALSGSVWSAKSDYGRLVKLAAPVV
APSGYIVAFNNTRSRSEEAWVREIMEKGLKDESGRWRRVTALGQAADFRWRAGDERVGKYLKGLVLQKV

>N475_mitochondrial_asparaginyl-tRNA_synthetase_(AsnRS)
MRIAGRPILAGRAPFSASSLFSVNAATKILYRRSHTAGLMPWRVSDILSKATPGQDLVIKGWVRTVRQQKQHAFVEL
SDGSHQTPLQIVATPELVKGASTGCSIEVEGKIVESPAGKQKLEMVASRLNIIGACDPEKYPLAKKKHSLEFMREIP
HLRARTNTIGGVLRVRDTAASAIRDFFHENGFIELHTPILTSSDCEGAGEQFTVSALMPASSSEQGPREFFDRTVGL
TVSGQLQAEMAACALSRVYTFGPTFRADNSMTRNHLAEFWMIEPEIAFCDLNLNMRVAEHMVKAVIEAVLAKCDEDM
AFFHKRVDEGLMARLHK**TLAGPFQEVTYTDAVK**LLEKSGKKFEFPVAWGLDLQKEHERYLVEFEFDNRPVFVTHYPK
DIKPFYMKLDEDGRTVQAMDLLVPTIGELIGGSVR**EENLDTLQAR**MKAMNMNVDDYQWYLDLRRFGTVPHAGFGLGF
ERLLQYVTGMDNIRDVIPVPRYRGYCRF

>N476_ERMES_component_mitochondrial_distribution_and_morphology_34_(Mdm34)_homolog
MSFQIEWPTLDEITLEKIKAQITEVMNKGELPDAICDVMRVTDLDLGNIAPTLQFMDIPDVSEDGFEGHFKVAYAGN
GSITLQTKVQVNPFAAKTVPSKRALRHLGGLIAHEPMVVPLRITISQVR**IDGDLVLNIK**KRAKAHDPRSDGSLILEN
TNTAVSAPAADSELSIPHIAAQFKVDPLQSVNISSSFDDFGSVKDYLQEQVEGSLR**KLFVEDFPQIVSGINK**QLETA
AHAK**HNTVVVLAPK**

>N477_NUDIX_family_hydrolase
MLARGRARLSLYSGRGGRSHFSTSSISFQPTAALWQRWSGLRVDGTEDPDPNDSDYESDGEEPNADAGADVQNRHHH
HDEIVGFAINGLNRFHAHHLRRDDEWLRYALHESPNSRFLAFHKLRPMVEHR**TPPTHLGPILAWQERGEVLPAITDA
KSTVLLLGQSLR**ETNSDRSIQEQLSDESNQINVFAFDLDPIVGDDEQEAQR**YAAAHQTHLEVR**TTFEEPRAIVPHLP
PWEGGVVAQARSLLHWHKK**NGFCAACGSTTK**SVEAGYVRKCNDDKNASCGMDHYPRTDPCIITMVVSSNRDKCLLGR
KSSWPAGRFSLLAGFMEPGETIEAAVLREVYEEAGLLLDYDKVAYKLSQPWPFPASLMIGCVATMHEAEIQRQKVSV
DYHELDEARWFDVKEVAAMLARSTQEGAPEGELHLPPPLTISHHLVKLWLHERKTKRIK

>N478_enoyl-CoA_hydratase_(crotonase)

MKATRLMGAGGRATAGRAATVAVTPCWGSGGHNQWRRSALATTATATTSRVSLEKSTSHQGVAFLTLTNARER**NALS**
VEALEELKATLADVESHRSFGDVRVVVLRAQGPVFSAGHNVKEMRGSERDPAYFARCFALCSEVMQAVRGLRVPVIA
QVDGLATAAGAQLVASCDLVVASEDSHFATPGVK**IGLFCTTPAVALGR**AINSEKKMMEMLLTGEPITAQEAHTYGLV
NKVVPK**AQIEEATLELAK**K**IVSYSPSVIGLGK**KAFYQQMAQPDISQAYKFAEGVMCANAVAEDAYEGMSAFVEKRKP
TWKPTH

>N479_uncharacterized
MRRWALAASRTGFGGSGIGGAGSARNWLASSTLPQAFRWSVLRGVHTQSAGVGRGLVGRVRPRRNLSTQAPKEEPNP
STLPPPAEEPITHTVESLTESYYAFQDSVLNIQIMGNSVPRFWVGLVAFGLFGLGKDLLSLGVADQIEHRPDLTTEQ
KLQLSALAGDKEDFVLTQLPTAVSMSDPFTLLTLPLLSSLFAASVGIWWGRFRIKKLFDKFVFMETK**KGHVAPPEVI**
DGARKGIITRGSTATAVGTMALTTTYISFYAIITRVWFRDYVEQMNEWKWTVPAGKEGELQRKLPSDLELKAFSAAS
FVYFVFIQLLVLKFTPFVILPSLTALFPLTAVLAQSPVFLRMQDKTK**GKLETLEAK**GVFGKLPSGEGKELDFDGEGA
DEGAYGLHSADHDDDDLGSRPAAGDGSLSTKPNNVFDKTAGATRVRAIVSRRKREQSADGAAGGGDEEHGKENQWGD
VVLEDEQNQQQ

>N480_acyl-CoA_thioesterase
MRRNLSMNAAPLKLLRPRLCSSSSSLSLVARPRGVSYMSTTTTSTAKAKRPRDSLVERDLRFSTDPRLQEAFVNSSG
KIRLGMVLEELDTLAARVGYAHVLGTPRVAQLEERRKEGLEVPTIVTAACDRIMLLNPISIDRDLKLRGMTTWVGKS
SSEVRVEVSSVRKDPQGNDEATPHLVAYFVMVARRNGVNEAYPIPPLEPVSPVEKRHYDQGASNAARRKEAAATSLL
IQPPKLDEIKIVHDMFARQMHQGQAQQDASEVPMASACHSSTQWTHPQNRNIHGNIFGGFLMRQAFELAHVTCGLFT
GVMPTFLSMDDVSFLRPVHIGSVLALESQVVYTSTSTLDYESDQDRDQQSATGGAK**QQQQGFPLVQVRVQANVGNFG**
TAFEPSNVFHFNFKAGANQRKVVPNAYSEAMAYLDGRRRMIREKTLRQDIASYLEGFGTAHVE

>N481_dihydrodipicolinate_synthetase
MQRSTLRRLSQRRSTAQKRNQQNVKKKKMRRRVVSSCVPWLPTRPGLAECRAAGGGSHALTARHNSTSSQTKRFEGF
IAATLTPMDSNAKPSLGRVKDYAQKLVSDGCSGVFVCGTSGESMSLTLDERKAALEAWVKNKGSLNVIAQVGTTSLE
QTRDLAAHAESVGAAGIATMAPFFFKPPDVSTLVDFCASVTSAAPK**TPFLYYHYPGITGVNLPVFDFFEK**AHGVIPT
LRGAK**FTGTELGDYYR**TLCFQGGRYDILMGFEYMHLPCLPLGSKGGISLSFSFCAPVYAKLFKAYHQNDLETARKLQ
LVIAEFMAALAQYGFVPASKLLMREWHGLDMGPCRLPLRALSPDEEKRFMALKVVQELHSLL

>N482_calcium-dependent_serine-
threonine_phosphatase_(calcineurin)_regulatory_subunit_B
MGNDVGRISAKDFEGVEDFTEAELHKLHRRFQKLDKDGSGSISADEFLSIPELAGNPLLSRIIAIFDTNKDEEIEFT
EFVKALSTFTNRDNLEGKLRFTFQVYDIDNDGFISNGELFQVLKMMVGSNLTDAQLQNIVDK**TILEADEDK**DGKISY
EEFVKLITNTEELGAKLTITL

>N483_lysophosphatidylcholine_acyltransferase
MRGLAKGLRHAASAPFTRLAPTGFTASGISSGPTANGYRRGAVLPICWREALVGRGHLLRPLGQAALQRSGATRTYV
SKAQQELRRRNPSAAANTPPPPPGKEGPSFGERLVYIAAVASFFVVPAVVWYRHGDEIRAQLSSHKNAPAASSSAA
GFDAASDQQDQHQQAQEQGLVSAADPSPAAVDGQQQQPEATSTVNPFIYDSPLTLYEKVKLTFGALVLLPIRVTLLV
PALFLTYLLAKLSVVGLPRPVCERIVDGR**TEVVVDNNAAGPIPAWR**R**VVFLNPCR**LLVRYIMFLMGFHSISIKGTPA
SKREAPIVVANHVSFVDPFYLFIAYLPAFVAKKDVENLPVVGTVALALQCLLVDRRSTTSRKDTLDLICRRAGAVGH
GSAAVEQKEQDGPATQPPEDEQHHHHHYWQQLLAHNSVALGFSR**FLTYLSALPK**VAYQRQFGEDDYAQVVIFPEGTT
TNGKALITFHQGAFVPGVPLQPVLIKYPHRHFDPSFPVGISLARLMLSLLCQITNHLEIEFLDVYRPSDQEQKDPAL
YAHNVRNLMAEKLGVEVTEYTYEDALLMVEALALNMKPDRVNIPVQRVKKLYQEMTLKDLKQLLWRFRHIDR**DGDGL**
ISYAEFAHSLRLPEDSAYTRDLFSLLDTDETGAIDFRKFVVGMSSLNRKVNKQQIIELAFTAFDKEGRGFIEREQLR
GLLHEVFPTIGEDQLDALFNAADADKDGLISREDFVR**LAEEQPGYVGIMENATR**NHHRIARDATASAIQ

>N484_mitochondrial_ribosomal_protein_S10
MSWRKAELVISGYHKRVAK**VAQDIATAAEMVGMK**R**VGPIPLPTR**HKRFALLRSPFKHKKSYEHFEIRTHKR**LIWIEG**
PPEQVRK**FIDFTVDTMEPIASVK**VREHNYHHLSSFYSPPTTATQALQEARQAALGSPSTPPS

>N486_cobalamin_adenosyltransferase
MKRFVAGTRVGRFSRPLFSNCRPVLCTSHAWADSRRGVKIYTK**TGDGGESSLFTGER**RAKEDVVFHALGTTDELNSF
VGLAREYCEQSKNGLDEKLQMIQSLLLDIGANVATPRNAADADARLRRTEFSDVHVTTLEKWIDELDAELPPLKNFI
LPSGGLASSHLHVCRSVCRRAERLVTPLVKDGQASPAVGRYLNR**LSDFLFVAAR**HAAKAEGKEEVIYKKPKD

>N487_L-gulonolactone_oxidase
MMMQQHEMDQAAPRTGHAHRSLQRLYIHCGHVVGERTISELAPVPTAASSITRIANYQWRNWAGIHTATPKYLYKPT
SAREIVEVLATARAAKEHVKVVGYSNSPGDIAVTDGYMISLENYRRVLSVDRKTGLVKVEGGIK**LQDLIDDAAR**HGL
AMSNLGSITWQSIAGALSTGTHGTGIKLGILATFVR**ELELINAQGQVLR**CSATERPELFNAARCGLGALGVISTVTI
QLEPAYQLHAVEVPMTLEAVLSSLNTIIHSAEHARFWWVPHTNKCWVWQANRTKEKAAPPRFPAWQNLLHILVERKL
YEFLLWLGTFFPRLVPYINKLYSRILFSKRRETIDRSDKQLTFDCLFQQHVSEWSIPVANTATAMLRLRDLIKDLDL
KVHFSVEVRFTKADDIWLSPSYGRDSAWIGIIMYRPYGRDMPGTKVYFDAFEELMKELDGRPHWAKAFKMSEVEFRQ
TLPHWDDFKRVRAEMDPTSTFSNAYLDRLFPTQKQPTS

>N488_tetratricopeptide_repeat_(TPR)_domain-containing_protein
MQAYVVEDEGAKEQSSFSIPPLQGLQNRTASLPSQSTNTRVSNHAVKEPEKRDWNEEFQKLLEFPTNTPQEAAERAM
AIKSFADGFVKTARPIAQTIIRERSQPVHTQTYKPVPDGKAATYNVDGMTFQFPTGSDGYPSTAEEDLKKEGHYMKS
LIALLSSGVDRVALPMTCLVQHLGFALRVSSSAPFGQADLVYGAEEGEDFKDTSPTGRAIVTNICSVFNIKPQIIEA
GGATREVYIPGVRVYLGKDGRYYFASLENLLPQMLEHGAVLHRQYIQRLPSPLSVGDKEAIRAAGKQLEEVNLEAFA
AKLSDREFTLTLAQLFDELHKEGINMCFLGRLRSKVTSKRISRLLLEKAVTRTVNKHLHEKLRATGDTTPQTVLVEY
FDLVFRPSEESTALWEGEIRQRLETKFPGVLSSGERASESGWKLRANVNMRDLFVSLSQRNGIQWKEGTAERVLENG
ATESLADAFVAAESTVKRFEVAFGETLHALGRYDDSELVHKERIAQREATGDPILTAAAVFHLACFYKANERYGDAE
EQFKKMVSLAEKVRPPTTSAAGGLSSPRGGTAASSRGQVHVATALLHLVDFYFFCGRFNDAEPVLQRAMDIRQKNLG
SAPLDYALCLEKVARMYRVMGKYTESERMAKRSLQIYMESLGVDYPAIEQRNTAAFVHFLEGNCAAAEEGFKNSLAA
SERSYGSSHLCVAQSLADLAIFYCKVKKYNEAEALFKRAITIREEVLGENNTRMAASLQQLAYLYTALGRYSEATDL
YNRSLAILQSCLDSSHPDITDALNKLAWLQLKCGNIKKADEIYGKLSEDNENSLGKEPPTIVRTLWELSELYQALGK
YDQAEEVIKRALIIKQNTPGQSVTDIAEWLNNLAELHYRKGNYGESLLLQQRSLDINIKTFGHNHVQVAEGLHNMGN
LSYRQGDYETAEELYKRSVAIKEHILGRQHPDIAEYMHTLAYLYTTQGKYEEAKGLYEKAFTILLQTFGMDHPLMAL
NLNNLAWIHFKQAQYGKAEELYSQSLAIREKTFGKRHPDVARSMHDLAELYHEQGKYKQAEKLVHKALVIREQLLGP
DHSDVARSLTTLAKLHFSLGSYTEAKREHKRALKITTQLLGPNHIKVGQSLHDLAKVYYRRGTYQRAEELFQRALQI
REAALGTNHPDVAQTRASLAYLFTTLGK**FNEAEEYYK**NALSIMESCFGSDHPEVAQSYNALAWIYYRQARYQESEEL
YRRSLDIRSRYLGEHHPDTARSFHDLAMICLAQSKYTEAEDLNERALAIREKVFGKTHVEIAYSMHNIAELYFARSR
YAKAKGLYKQSMRMLEIVLGEDHIKVAVPMAGLAKVHYKLGEYQQAKPLYQKGLAIQEKTIGKNHPNCAASLNDLAY
LYATRGHYRKAKKYYQRSLAILQSSYGGTNHPEIALGLSSLAWVYYKRGKYNRAHLLYKQSYKMRIAAMGPEHPLVA
RSLHEIAELYQKIGKYEEAETLNKRALSIRMKAHGTSHPDVARSLFNTGVLCYYQGKYKQSEELHLGALRNLEKAYG
QNNPK**VAQCLDELAK**TWAKMGKHDDSKVYLQRALTIRESCLGGRHPDCAESLHHLAYLAATQGKYAESEQYYTKALE
ILKGTFATEDHPEIATTQADLAWVYFRQGKYKEAEELYVQSLKVRQTALGDSHPDVARGLHDLAELYQKLGRYEEAE
PLHQKALNIRESIFGRLHADTARSLNTLAVLYQLRGMDEESEKLQLRSIEVLKEVFGESHSKLAKGYADLAALYARK
ADYERAETLYQQALDMRAQTLGPTHPDYAQNLLELAELYTKQGQYERAIPLYEKVIEIWEDKLGKDHPDLVTALESY
HACRRGQSRGPTPEKGSRDWSSLFLMASQRTHQPTASLAISLCRLLFGGTTAQKP

>N489_NUDIX_family_hydrolase
MRRASVLASVQGTHPWTSGGSRVVGARTLTTSAGAGSADRWKKNFKKVVPEGDSKERAVCQECGFINYHNPK**IVAGV**
VALSSTGKVLLCKRAIEPKTGYWTLPAGYMEVGETVQAGAAREAREEANATVEAGSLLTMYDVPRIGQVHMYYRAKL
LSDEVSAGEETLDVALVDLDEIPWDQLAFPTVRHTLEFFLKTGR**HSADAIDFK**SITEQLI

>N490_gamma-butyrobetaine_hydroxylase
MRSCGTRGFVAAAGKRALHGSVTTSNLLRCRSALLSSSGRSGFPSLLRSTSVVQARRAAHAQPEAHARSAAAAVHAE
DGRVEVQWRDGRTSPFHHTWLRHNCQCPKCLDSSSGQKLVSILDFPPRPVPR**SVSLENGQVVVR**WKDGHVSPFPQDF
LRRYAYDQQSRHERRAMRRAAVPWTPEVLISESVALEIDYADLMNKDEAVWQWLQQLLKFGYCLIRGVPQQEGEVAR
VAQRMGQLRDTIYGLTWDVKSIENAANIAYSSLPIPPHMDLMYYEVPPGYQFLHCLINQAEGGANIFLDTMQVAKVL
KERDEKAFRLLATTPATFHYQRSGHHLVQR**RPIIELDQETGDASAFRYAPTFEGPLDIEGEKVEEYYAAYR**ELVRII
NQEPDLHLWRRPEEGDLVSFDNRRILHARTAFSNGNRHLQGAYVDWDAFLDRYRVLQSQFAPMAAIPQ

>N492_mitochondrial_ribosomal_protein_L23
MRRFEKLNPTK**YWLPNIPLTLMPPAR****NLPSNKFVLRV**QPNITK**VELQNYISQLYGVSVTK**VNTMNYEGKLKRAPRRG
KFYSTKRYKK**AIITTDDSIR**ADDFQEEGRR**GAGFIEGEVVPTK**RR

>N493_uncharacterized_conserved_protein
MRRSSSAFTSWGGGAIRSAASSSFSSATLASSSGSRFISSTSSPSSLSTLLKAQRSSASPSSSLLNRSLATRPSMGG
RLPFASAEANPSAARTGSIYGSVNATSLLAPLSVAATRVAGLATSSSK**VESEEADEPSSR**SRPSATASPPPDAQAAL

PSSAEAEAKPKLGKIRTFLKKYGAVGVVTYFGLYGATLASFYGAYSSGLLFAGDVVGLIEFLHLGDFFDESLLTPKV
GNFALAWVSTKFTEPLRFAITLGITPSISRWWTGHHQHKLEAKREREEQQQKKEEEEENANSSTKH

>N494_uncharacterized
MQRAVGLRSQFLVAKNSTAALPLWARRSFVSEAHIQAELEAARRVKALEEKNARDRATMLSTTPAPPQGKRSDEAPG
QPARLPSAENNHQPARPSAQ

>N495_uncharacterized
MLRQRRTLITSRPVALASLLGRPSAAGARALVRHGQAFSTNRSTAFSSSRWRSPLLLAAVTAMSAGAAFGLHRHRSA
FALQPQPGTEAEEYEDEGYQRLLMGLMDSARDDGEDGEGDLADAIVFEPEEEVKEEEKEKDEEELLPASRVLGAGRA
KIANEEAEARRQQLEAHLHEHIRSWAKFEKVCSQGGGDDGEEGEEQDKPHVGAKVALRYPPWMQPGESNEVAQFTIL
GASPHGQKDGVVDMLTMLTTTPPVHRMRDLYEFHRGIRDEIGKQARIVKPRMRWLVAGRPALGFVTAFTGWGKTLVS
TYVVTAYNKTGYVLVFNTIHDGEAPLPQCFARHQEESDEAFEYILRTVTFRPAPPPSPSASLPSSSFFLSAYEKTK

>N496_zinc_finger_protein_(possible_Tim15)
MQRRVATVAKGELALLARSVPSSALLGIRQSTLASRVSASPLHGAATRPRPWSPSCFLRISARSLHASSTLQRSAKS
SMVEATSADDPTDSAEAKETSAESAATPTTTTTLNIGRIQPKLELHYTCGVCELRSTKQFSRVAYEKGVVIIRCGGC
ESLHLISDNLGWFGEDKNIEEIMRKRGEAVERGRRDAGGNILLDNNNTNTAGDDTITTDLEHDGTQTVVEESEDCIL
ITPTAAVR

>N497_mitochondrial_carrier_AcMC21
MPRNPSVRLSRSSSSLGAGGGPGKNSDDDEMGLWTAGGLIVAATIGWSSYAPHVVLAHRLTYATSSISLPYPAFTHQ
FHLRALHHEAKLIDSHARRLRQPLNLLHPGVLAHTAQAWAQSVVELVTVAVCSPSSDASQLRRLGAKALGLLLGSLA
SFPFFIAQNRLFAQLAGEVTVLPLKYTGLGQTLSSINYVDTFRYAFIPHLLTSVVSDAIYSYYSPREETIANWIYRK
LPPFKSRSKKVNKTKRLIASTASNILFSVLGDLVLSPLYVVSTTMAIQGSGLEVALGTPRYSSGLHCAEDIFVRHGP
LAFWQGLVPVLYSELVPQAMATTFTALVFNAFAYLREE

>N498_universal_stress_protein_family_member
MSVPLVITAVENEEKQRAKEESRNLPEHIVAVDGSEHSERAFEWACDQLPKDHTLVLVHGVHKPEFRVEAMPDSEGK
WMEKQRRKAFEDYEFMQSARTMHRYARLCRQHERKCEWMTVPYRSATELSDNICSAAQRRGISNIVCGSRGLGTLER
ALLGSTSSGLVHNCPANVTVVRD

>N499_uncharacterized_conserved_protein,_N-
terminal_pleckstrin_homology_(PH)_domain
MSTRKGSPKISAFQDNFKNKKLHATFKLPDGDNFIRDFPCAFTETEEGLGDVNGRMFVTSGHLCFDANSMGKKIQKI
LPWTDIKALNTTNDEQLLVTVGDEQLAFPKFGARLEEAFECIKEQWEQPHDQEETENGGASEEADASADANDANAAA
PAGEAETVNQASGEAEGEDHHDDHDEHHDEHDGEKKGSRRSRRRRKNRGKKGPHGDEHHDDHEAAAAHKKAEEEAAL
KKKQEEEEAEKKKKEDEEAAAQKKAEEEAEAERKRQQQEEEEAEKKRKEEEEAAAAQKKAEEEAEAERRRQQQQEEE
EAAAAAQKKAEEEAEAERKRQEEEEAERKRKQAEAEAAEAERVEKERREAEEAERKRREEEAAEAERQRLEAERLEK
ERQEAEERAKREEEERLRLEEEERQRQAELERQQREAEEKLRQEEEARKAREEAERVRQEAEEQARREEEEERLKREE
EERKRREEEERARAEEAEKKRREEEETERKRVEEERVRAEEEAKRHEEEQQKRIEEEQRAKAEAEERARREEEERLA
REAEEERRREEEERARAEEEQRVKAEAEERARKELEERLAHEEEERRKRDEAERARAEEEQRVKAEAEERERRAKEE
LLAREAEEERKRDEAERQRLEEEQLARQAAEERERRREKEEQLVREAEERRKREEEEKERQEEEARVKQEQEERERRE
AELKREEAEEKQRRAEEQAELEAQKQAEIEAEAARAVERARQIEIEAEVVQVQVTTATTIATTATSTPRSVPSSTVE
EAGGAWNTWVGVAAAVGVVAAAAVAAAIFMRNPRQK

>N500_Xaa-Pro_dipeptidase
MQRGRSVAARAFAGRARGAASSSAPSSCLSFSSAVGRRCRLVSAATPGGERRPFSSSSSSRMGLSDSLAGKRPRPMN
YGQPHPSTHPHLVKEGEITPGITAKEYAQRRENLMARVPVGTVMIVPSHPEMMMSYDIPYSFRQQTDFYYLSGYQEP
DALLVLAKRSDSEPIHFTMFLRPRDPAREIWDGPRSGVEGAVSFFGADEAHPIDRLAEKLKDLTDGVKNILYSPDVH
LEFTHQIFALIPPEKIACPRNLLQTMRLIKSPAEIDVMRRSTEISGQAFREIMRATQPGITEGQLAALYEYECRKRG
SQRLAYPPVFASGIHANTLHYVANDDIMQDGQMVLVDAGGEYNMFSSDITRTWPVNGKFTPAQLDLYNTVLDVQKKC
IELCVSDGRMSPSALHQMSTQFITEGLKNLGLIKPGQTSGVSRFYPHSIGHWLGMDVHDVHDVSTRVPFKPGMMATV
EPGIYVSDDPDIPAELRGMGVRIEDDVLITTGAPEILTAGAPKEAHDIEAVMRDRKPL

>N501_putative_Complex_IV_subunit_Cox7a

MSSALHSARPLANTVIRRSTEK**LYGQQAHIGR**EAQHRVIFLRTGQDKFFYGVATSVAGAGIATLLFGATRLATGNGK
REE

>N502_rhodanese-related_sulfurtransferase/oxidoreductase_family_protein
MMRRGIYCAAWAQHQARRCPFGRAVRTFASEANNSHGAVVSTEWVRANVDRIKVIDASWSLGKRSQHTVK**LPGAIYF
DIDEIADKRTWLPHMLPTTSMFAAKMEELGITNEDQLLVYDESDGQFVASARVWWTFRVFGHNDVKVLAGGLKNWPK
GLQIQKTAADPKEHGLKFAVRKEPALVWSKYDMLDNLSPTNSDQSQIVDARSRERFYAQVDEPRADIPRGSIPDSMN
VPFGSLFQTTHSEQGEPMHVLKSPSELQRIFEQAG

>N503_acyl-CoA_dehydrogenase_family_member
MYATEVHTSAVREAHVFDVERLTSFMAQQIPSFVPPLQVRQFKHGQSNPTFLLADGSGTKYVLRKKPPGKLLSSAHM
VEREYMVMKALKQVNFPVPDLLAFTADSSVIGTPFYIMQFVTGRIFTDPSLPGLPPQERAALFKEFIRVMAFLHSVD
YKKVGLGAYGKEGSYYARQVATWTRQYRASATEEVPAIESLITWLSRNVPEELPGDCTIVHGDMKFDNVIFHPTEPR
IIAVLDWELSTLGHPLADVAYSCLPYSVDLPGNSLIDKDMSGIPSQAEYVKQYCQHTGRAFPIPKWHFYVAFSAFRL
AGIAQGVYKRFLQGNASSTTAGVFGAVSKMCLEAAWSLVEAEESKLTTTGEANVRHGSPKKGVSTMEDIMAALPEPR
WEPVSERSVALQKQLWR**FLVDNVFPIER**QVHDEVNQPGNRWKIPPVIERLKAKAQQAGLWNLFLPDRSNGGAGLSNS
EYAPLAELMGYSPHLAPEIFNCNAPDTGNMELLAHFGTEQQKKQWLAPLLAGQIRSCFGMTEPAVASSDATNIECRI
TRDGEHYVINGRKWWITGAGDPRCKLCIVMGKTDPDTPNQYRQQSMVLVPMDAPGVKLVRPLTTFGYDDAPSGHCEL
LFENVR**VPLTNILGGEGK**GFEMAQARLGPGRIHHCMRMVGLAERVLHTMRVRVQERIAFGRPLAEHGIIQQNIAFSR
IEIEQARLLTLKAAHMMDTVGNRHARKEIAMIKVVAPNMALKVIDRAIQAFGAAGLSEDFGLAAAFAGARSLRLADG
PDEVHMMTIARLELQQHKGKALTQKGGATEAIKRYQTAIAETSGVLSVAEGQDLVEIYALFKQSSAGDNTTPQPNAS
DVRSYGKWMAWAGLKGMRQEEAQTKYADKIQELQRRKHATTKL

>N504_betaine_aldehyde_dehydrogenase
MDASSAAHTVTLNGKAISFPTR**LFINNEFVESVSGK**TFAAIDPATEQEICQLAEGDKEDVDRAVAAAR**FAFEEGEWS**
ELSSKQRGDLLYRLAELIDQEKEALALLESLDVGKPFFESFNFDLKQVVDTYRYFAGWADKIHGKSIDIPGNNVCYT
RHEPLGVVGLIVPWNFPLQITAWKLAPALAAGNTVILKPAEQTSITALKLAELVKKAGFPAGVVNVITGFGPKAGAA
IAAHMDIDKVSFTGSTFTGRKVMELSAASNLKPVGLELGGKSPIIVFDDVINMEKAITDSYYALFWNAGQCCSAGSR
IFVHEKIYDEFVEKSVAMAKARIEQTGNPLLDTTMHGPQVSKLQFDKVMGYIETGKKEGARLLCGGARVGDKGYFIQ
PTVFADVEDNMTICREEIFGPVMAIIKFKDVHEVVRRANDSIYGLVAAVYTRDVEKAMFLSKKLKAGTVWVNTYNVI
TPQTPWGGFKQSGHGRDMSEYALAQYTAPKCVIIEYQTPKM

>N505_TIM23_complex_homolog_Tim21
MQRSAVCTSGRALLGGRVSLATACTRPVGIVGRRGVWEGALYSRPQPQQQSLGRRRFATDSNGGQKEPPSGTK**GGLQ**
AAKPSGQGTAVTVAQKVVEGGKDAGYGLVILGGVVLLGAAAYQLFSAGFAPSSPQHVYSKASDLLRRDPEVQKLLGP
NIKTYGEETSRRRRGLQSTK**YFNAATQR**DHVRVLFSAEGDVNAADVIADVTASGQFYLLTVEVPVTGEKLVYTNTGK
FERR

>N506a_iron-sulfur_cluster_assembly_protein_Isa1_(Isca2)_isoform_1 **[paralog of N506b]**
MARTPTSAASFMRGYSALALPARTLHTSLPAALRSSAMNRVAVPSTSASSGPSCTTVPSLGRVRSRCV**PSALSIGTR**
FVPASSTSRRGTASAAAPLQDLHPQTHPMAPSASTFDTTPVSLILDTASATR**AVPSTQTILLSDR**AKKKLRGLTSKR
EGGAILRVEVQSGGCSGFSYK**FTVEDRPLTEEDILIEEEGAR**VVVDDVSLPLINGATLDWDEKLIGSKFQMLANPHS
AGECGCKYSFTPKD
>N506b_iron-sulfur_cluster_assembly_protein_Isa1_(Isca2)_isoform_2 **[paralog of N506a]**
MARTPTSAASFMRGYSALALPARTLHTSLPAALRSSAMNRVVVPSTASGPSCTTMPSLRVRSRWAMSGRSA**PSALSI**
GTRFVPASSTSRRGTASAAAPLQDLHPQTHPMAPSASTFDTTPVSLILDTASATR**AVPSTQTILLSDR**AKKKLRGLT
SKREGGAILRVEVQSGGCSGFSYK**FTVEDRPLTEEDILIEEEGAR**VVVDDVSLPLINGATLDWDEKLIGSKFQMLAN
PHSAGECGCKYSFTPKD

>N507_iron-sulfur_cluster_export_protein_Atm1
MLRASGWRGVRSSVTASRGGTLAWRSGSGATAAISIASRGCSAPLRSTTLRYNPALTPSWGGCGLGGPARRMVATEA
GGASKAAAEGVAAKPAAPPAGTTPAKAAGPTKLKGLPDSGSGWAIMKSLSGYLWPKDNPAIKRRVLAAVALLVGSK**I**
LNVQVPFLFKEAVDLLNATTENVALVPIAILLAYGAARVGAAGFTELRNVVFSKVAQSSIRQVACNTFLHLLSLDLR
FHLSRQTGGLARAIDRGTRGINFVLTSMVFNILPTILEIGLVCSILTYQYGAQFAALTAGTIGVYTAYTFGVTQWRT

KFRKEMNAMESEASSKAIDSLINYETVKYFNNEKMEAERYDKYFAKYSAASLKTNSSLGMLNFGQNFIFSAAITTAM
ILTAQGISAGSYTIGDLVMVNGLLFQLSLPLNFLGTVYRELRQSFTDMETMFGLLSLNTDVKNEPGATDLRVSKGEI
SFEGVGFGYTPERTILNGATFNVPPGSKVAFVGTTGSGKSTIFRLLFRFYDPEQGRVLIDGQDIRHVTLESLRKAIA
VIPQDTVLFNDTIFYNIAYGRPTATREEVLEAARLARIDDAIRQMPMGYETVVGERGLKLSGGEKQRIAIARALLKD
APILLCDEATSSIDTATER**EVQQSLAQLTR**GKTTLIIAHRLSTVVDADVVMVMKGGNVVESGSHHQLIARNGLYAAM
WRHQLEAAHHGNPTTATAPNQPSTPA

>N508_Twinkle_helicase
MRVGGQRIAAGRNAELCRQPAGLWLGRTEASVMGWSRWTSAPPPLGHARPVLEPLLRSRGCSPRWLGRSFATRSAPA
SSSSYAR**KSAVPSSSFASSARP**VGSVSGGGAPFVSSHFSISEDEITHFFSRKSLVWKRSGEELVVQTCPTCPDHKYK
MDNLFKLYISKRTGQFFCHRCGNKGSWFDFKRLYGEIPYTAPMSAPVPASGEVAHDHQHHQHAPAPGLQEEREKPLP
DHDVVSKYPLALFNEYPQVLTFLTGNKTKVQR**HLSEEVIR**KYKVGATKYAFGGDSEQCVTFPWIDADAEGRNSIRRL
KIRSIKNKANQRLTPAGGQWGFFGWHTVPADAKEIVITEGEFDAMAVYQATGLPAISLPNGAHSLPVELLPRLERFE
KIYLWMDDDIPGQEGAAKFAQKLGIKRCLLVRTKQGDPEGPKDANDALRAGKDLNAILKKAGR**TPHQQVISFQDIAD
EVYR**NICSPDELAGVPSKMFPSLTKILKGHRKGELTVFTGPTGVGKTTLLSQLSLDFAMQGVRTLWGNFEIKNTYLA
QKMLLQYAGKNLAELQDRAQWDEASRAFSDLPLYWMRFHGSTSVDQVLDAMDYAVYVHDVEHVVLDNLQFMLSGQAW
GQEGVAAGNKFDIQDRALEEFRRFASTKNVHITLVIHPRKTEDDRPLNVASVFGSVK**ATQEADNVLILQYNK**GEDWK
WLEVAKNRFDGELGPIALQFNKRNKSYREMPTTGLLNKARKGASKGASNQPDDPQPATASSSTTSTTPTTKAG

>N509_Complex_V_(ATP_synthase)_assembly_factor_Atp10
MRHFALGGSSAPTRPGLLVCRVPSDLRPGAAAPLTSGSLRVRPPFWHGPRHMHTPLLGVLPAQATIGGRRHEHWGTL
KRFKELAKTPEELALKEELDKGYWGDANELLKNREGKFFFAVPKLTPKKEAIK**LLDAIPASLPTYKPFDFSK**VNIEE
AMHTK**APTLVLVTCK**RMFATAMLDSWRKPFEAEFPHLNCYELELVQQVGYWWFGGLFRMFAAKEIEPSRMNKVLYYN
GIRKTKRMRWDLNIKNRYCAYAFLCDEDGLVRWR**AVGLANTEELAMLNK**MVNKLQQEKGGVSSSNNLASRSGLEHQQ
KAD

>N510_dihydroorotate_dehydrogenase
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ERLDQFRERQKRVIETAADSAKKRGLEKGVVGVNFGKNKDRVMGGTDGEGLGDDYVELMQRLSPYADYLVINISSPN
TPNLRLLQSGSELQKILEQVMAEKKRAEAASKSATAYPPVLIKIAPDLTKAQAEDIAAAALKYKVDGIIVSNTTVSR
PLRVHNEQEETIAKEAGGLSGRPLLEMSTQLLRDMYRLTEGR**IPLIGVGGISSGK**DAYDKIKAGASLVQLYTGLVYE
GPGLVGRVKK**ELVELLDR**DGFRTIEEAVGHDHHKEVETK

>N511_mitochondrial_carrier_AcMC22
MVHQARTTEEHRGAPMPEPEQDAGLAVAAVGVMCGVMGKIVQDRSALSVLVRGNAHWR**GLAAALVDDAVLAAQETK**Q
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YVARNFPSWKVALVDRVVKGKDHFYSSWLASAAVGPVMCGFDFVRAKLLHWHKAALFPDFMPPRAGDDEEDIDSDED
DSEEELGEPSTARRVAYVASTALALVTTCSLGAVLLTPLETITMRMAAQPHVYGPLGTLGTMAAIYRQEGVWGFLHG
LVPSIIFQCSLGLLAVESEANTGHVAL

>N512_methylmalonic_aciduria_type_A_protein_(probable_G-protein_chaperone)
MRATSAGAWRCRGSQWAVLPSRVGTGCKLPQQMCLRPAGLLLPGLANPLRRPYTTNSEEEERVSALAGRVMRGERR**A
VAQAVTLVESSR**HRDRRTAEALLAR**LAAATAAPTSSSSCLSRHPTTSTFR**VGISGPPGVGKSTFIEALGMRLVEREH
QLAVLAVDPSSARTGGSILGDKTRMLRLSNHPDAFVRPSPTRGTLGGVTRYMSETIAICEGAGYDTIIVETVGVGQS
ETAVEAMVDMFLLLVSPGGGDELQGIKKGVMELADLIVVNK**ADGDLADAAR**KTQFEYQSALKLIHPKSFDWMPRVMA
CSAATGKGVDDVIATFEEYRKTMMETGELWRRREEQKRQWLWRLIADELVDRFKQDPN

>N513_uncharacterized
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ETNGHGVAARRQR**ETGAGPVVEEGEEVGHLK**WLAGEEFVLR**EIQPGQLAYVRILKPGITPLMAFGQK**RGNKRKRFAY
KGHVSPYFRLSPKSPLWKLVIAEKDLIEEGRRARLEYERTMWPKSK**KKPQNWGENV**

>N514_proline_oxidase
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ELVRAWTVFHVCAWTPVVRRARR**LLALAEAVVGAR**AVTWVLRR**TFFAHFCAGETQTELLPVIDR**LRAAGVGAILDYA
AEADLPPAPTTTNGNGAANAANAAKPQAQTQAQTADPFPYPSTPASPSGPPPPAEFFRPDKSLDRREGVVSARTYYY

EDEAHCDANAEIFHSCINSAGMRPDGFAAIK**VTALCPPVLLMR**ISHILEESRRLFRSLSEEGGDPLGKSHASVPYLS
RMISRPNFIKVLGMLNVSLSPAEQADLFAAMDVDKNGVVDYVEWLESVQPNDATLHPFFCANGGSGGESTLLPKLNP
REAQQMDNMVDRLERLAERAAAQRVHLMVDAEQTYFQPAIDHMVLNLQKKFNRDFPAIYNTYQCYLTNTAGRVDIDL
ARAERHGYHFAAKLVRGAYMVQERKRAAKFGYKDPIFPVIQDTHENYHRVMDAILRANVSRGAQVMVATHNERSVRF
AVEKMH

>N515_enoyl-CoA_delta_isomerase_1,_mitochondrial-like
MKLHRCRLAGSLVLSCGRTAGVSTAWTLGHRAAPLTTSAEYGGWAIEKRGSDEKAEVRVVRMASNPVNCINPAFLDQ
LDATLER**LEGENASSQPSPVVFASASEK**TYCAGLDLKTVLAMSRDELTHFIDRLNASYVRLLTLDCPTVAAVNGHAI
AGGALLALSADYRVAAAPGKSWFGVNEVQLGIPFPCGPWAVMHHVALTHPRLYDLTRSGDLVSLDAAHHQFGLVDHL
LPAGADLTEGSVDYARTKVAHHSLRAFVAVKQVLQRPIVERYDSERRAGDLDR**TFVDIFFSDAAR**GAIKKRLEGLKG

>N516_SAM-dependent_methyltransferase
MWCRSQRVARVSRVVTPTATQAAVPSSCARGQRSLLSSAFGGEGGGAEEKGHAALVRKEFAKQAQRNYDNQAASSDA
MLSWISGHLAGDLQPSLRVLDVAAGTGRMSRLVAPKVKEVIAVDLTEEMMAVGK**EQAQTAGLNNIHWVVSK**AQQMPF
MDNAFDVVVSRLAVHHWDEPQSIVSEMARVCKPGGK**VVLIDIVTPEDLTDAQGDR**LNHLERLRDPSHVCFWRLSELF
GFLKKARPALSVLPLVDRRDNQVFLDQWLELTNTPSASRKAITDALQAELDGGGQQKDTNSLVTGFRPDRSADGSLH
FVHSYVLLSAQKQ

>N517_glutamine-fructose-6-phosphate_transaminase
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AMSKYASVGKTNNAITLLEQHLGKHDAHVAGIAHTRWATHGARTDENAHPHLDQSGRIAVVHNGVIENSNELKKELQ
TQHGIHFRSETDTEVIAQLLGVYVNQGMSLLEAVKKTQDRLEGTWGLAILDKEHPDQILAVKNGSPLLVGIGEGKMF
IASESAAFSRYTKEFIDLEDKEVAVLTAKGHSLDRSRIEHAPQEHIQISPAPWPHWTIKEIMEQPAAISRALNYGGR
ILDESSTMLGGLDANRAVLSGVQHLVIAACGTSFYAGIAGAQYMRHLNAFKTVQVLDAAELTEEDMPKENGGLLVIS
QSGETKDVYTAMALAQQRDIPCFSVVNAVGSQIARHSACGVYLNAGREHAVASTKAFTCQVTVLALVAIWFSQVNAP
QDKQKRRVMIEALHRLPTNVGMTLQSMRETIKKIAHKLFTMGPGGKIVEHMFILGKGAAHPVALEGSLKIKEISYIH
AEGYPGGALKHGPYALIEKGTPIVLIVLNDKHAAKMKTVAEEVRARGAYTIVITNNAQMFEHELEASKGADFDLIKI
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>N518_TIM23_complex_homolog_Pam16
MVVRLLLNILGVGSQVFGK**AFLDAWRQ**AGLKAKQTGAGLSLAEAQKILGLRPPYELKEVTK**RYEQLFKSNDPANGGS
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>N519_Complex_I_assembly_protein_Ind1_(MRP_like)
MMRRSVVGAASTRVAGWQKRGYAAMQLSRPVLHGGPQGQGRPLPNKIKLPGVKDIIAVASGKGGVGKSTVSTNLALA
ISALGKR**VALLDADVFGPSIPR**MLNLSEQKPQVTDTQQLLPLSNYGIKCMSMGFLAEKDSPMIWRGPMVMGALEQLL
RAVAWNNNGDVDVMVIDLPPGTGDTQLTLTQRVQLTGAVIVSTPQDIALEDARRGANMFRKVEVPILGLVENMSYFA
CPKCGEVSHIFGHQGARQTAKEMGMDFLGEVPLHMTIRETSDSGRPVVVSQPSSPQAEAFKHIARQVLDKIQDPAFR
KDQEAPRIIYS

>N520_uncharacterized_protein_affecting_Mg2+/Co2+_transport_(DUF525_superfami
ly_member)
MATKSNNKLGKLLYSSLLRSGESWEREVLRGRLVLGEKNEIRRLKGTLPSTVGSHLR**EDVALTGAVVPSLTR**QLWRD
LNRPSHDDAPRRHPSADDDFSDAFASLRVLNDRTAALQQLVYEPHSQCTTNGILIEVRSYPLPFRMDNNTTKYSRFE
YRVEMTNLHPTKTFKLLSRHWLILDGDGQTEEVRGPGVVGLYPVLAPGQNFHYKSSSGWMATPYGTMHGSYQFVDED
TGDLVEATIAPFGLNAGAESQTTSAYPHKERAVF

>N521_uncharacterized_conserved_protein_(YbaB/EbfC_DNA-binding_superfamily)
MAGTSWGLRRSSSAAGRLTTSPRRCYTPGSATPADEAEQDKALREGVLRGFDQMHSLERMEVEGKATLPDSQSGVSL
ILQGSGKILQVK**VDQEVADNVENVEKLFVAASQNAR**QKIADRINSLLAASHQ

>N523_mitochondrial_carrier_AcMC23_(probable_folate_transporter)
MDETNTTLRDLVQWTSPSITYLLHPLVVAGHRRSVTPYSGVSFVTGAVTGMVGWADEARLVRRQTGLFGHPAYWAWV
GALEGVLDVLLTAASLSVEEVVCPPPVGGAAATKKPSPYVHNWQMALLAVSERLVWTFLTRPLRIASNRLHAQLPGP
EGKYPLEGLLHVLR**LLWAEDGLAVFTR**SFGPAAAHEVVSSMAFSVYDAAAPFRSLALQNRISNRLVNGGLQSLSLAA

DECARALLVALLTRPLQTVVRR**LDIQGCGLALWNAPYR**GALDCITRIWNEEGVPGFYKGFVPELLTDLAPAGVLFLA
DLAISAIFEPSVLFGV

>N524_BAX_inhibitor_(BI)-1-like_family_protein
MRRTFAFCSSSPHFAKVASNGLALKRAARPLITLSPAATGCMRPPLTCTASSSSSSSSSFLLAHLKSSAIRPSSSSG
RRQLFTATSNRTAAKTTSTTPLLASGGHRFGAATKTAIRSIRIEGRPPR**SYNGLMGDVGVVAPR**DNTAWLLIGGLAA
LGLGGIALAGYVNQETTTIPTHGDLTTHRLRATYGYMLGGLATTAASAAVLFRAGAAHRVVAMNPWLFMGASLLGTI
GSLMVMQSLPPENTVARHLAWGVFNACNGLALSPVAMLGGAVVTKALVATGAVVGSLSLVAAAAPSESFLWMGGSLG
VGLGVVIAASMGQMFFPASAFLTGITLYGGLGLFGMMMLYDTQRVMHKAKTDEVYDPMTQSIAIYLNTINIFVRMAT
IMANNQGNRRR

>N525_uncharacterized
MARASAGLRRLVAAPVALTAGRSMLATGIAVQAAERTPTAQALHK**HDAVLAQPLR**EVEEKKDDAQRALAEAKRKEAE
GRPPEWYVILMGFAGALVGYVTAVALKFVGRYVFYFAAAETTALLALTATGAITRQTAIEVAKYTMPPFTWALKTAI
DLARGQFSRVFSASSLALRFFFVLSFGLTLRYSRTGPKPSWK

>N526_mitochondrial_alanyl-tRNA_synthetase_(AlaRS)
MWRRSAGAGGKWAVAGGRRVNGGGPSPQHLLLQLEAQRGLSTTSPSSRASSSASSSSAPGRGAGWVRGSFMDYMSRA
GHEGRASAPLVPPRGDGSLLFVNAGMVPYKDSFLGRVVPPAPRVASVQKCVRAGGKHNDLDNVGHTARHHTFFEMLG
NFSFGSYFKEDAIRLAWTYLTRELGLPKERLLVSVHHDDREAANIWHAQEGVPLDRIVYKYAKKWVVGDEDNFWSMG
DGPGPCGPCTEIFWDQQQEVDGDRFLEIWNLVFMQYQRTESGELQPLDRPCVDTGMGLER**IASVLQGVRENYDIDTI**
RGLVHGTRTILHDKFGGVHQPQAQLSPQESVALKVIVDHVRASCFLIGDGVIPSNVSRGYVLRRIIRRAARYANTLA
PNRNQGLLADVGKLVIAQMGEAYPDLFTRQNVILHLIEKEEEAFLATLEQGLAYLQDALRNNPGTDLPPEVVIHLYI
R**LGFPIDLTHLIVK**ENNKTFDMNAVDRLMDEEREKSRAHAFSLSSSAPSSVKLGEGGVPTAVKEWMAEGIAPEFTGY
ARQVEEETSVVALLPDLQRRTLWLSISPCPFYGMAGGQVGDKGRLIVSGGSGKTLSELRLRVEDSLIPYEGGLVLRV
KVDKGEQGQEVSEGELKELADMLIKGQVGLRAEVDDRHRRGVRAHHTATHLLHASLR**QVLGTSIVQAGSLVDANR**LR
FDFTHHSPLTDDQLQRIEHNVREVIAADTPVATDMREYAKAVESGAMCLFSEKYPPVVRVVSVPGFSTELCSGTHAA
STGEIRPFKITGQTSVALGIRRIEAVAAEAADQWYDAQYQYLSSLGRTLEVAPVKIEERVKRLLARERELEKEVGVL
QRKLASSAANSSASQSLAGTYSGHPLAVHVYPEGDDDKVLAKKAEQLREKEPGSVHVVVSGRKVICTLATDQLPALK
ANKVLQDMLATVG

>N527_TIM23_complex_homolog_Tim23
MGDSSYADSSSMPDFDAFPEPKLDNIGIDVDSISYTNPMYGLSGPK**GAEYIFADDNQAR**KMSWADRSTWLWGGAWLT
GGVIGTTWGGLKGLRDAERGLPWKLRLNACLNGAGRKGGRMANGLGVLVLLYSGVETATAAARQKQDGLNIVAGTTM
APLIYWSGAGLIRSMAFGALGGVVGFGLVLGHKYNVMGLRKILPADE

>N528_MaoC_domain_protein_dehydratase
MNTQAVRRVQVIGNHMAGAESIGALAANSANALRDEVKGRSAPQNRSFANVDEMKKAVGTEVGVSGWLEITQQRVNT
FADATCDWQWIHTEPERAKKESPFGGPVAHGFLTLSLAPFLNAEAIPRLEGVK**MGVNYGLNK**VRFIAPVHVGASVRT
RVTLKEVTDVPGGIQVIIEGTFEVKEKGKSEPSK**KPVAIVEQIAR**YYV

>N529_pyridoxamine_5'-phosphate_oxidase-related_protein
MRRGAQHASRSGLMRTVLAEGHSTRRALPVSCAATRRFLSSSPALAPSTRTLHLSPISSLPPLLRRYSNRPQSGQDD
HQRLTVAELTRSLIESRKSGTLTTVQLYMAAEQPPLGGTLPLFGSLMPYILVDDAVPIVGLRPDEKHVRNLEHLDMA
SLVVYPLTPANINPSSFALPRVNLAGRLRK**LDPADSNDAVTSVR**RQYLVAHPGCQK**IIDDLSFYK**LEIEDTVYCSGG
LQETTHVTADKYKATKPDVVMQSSRAILEWMNESKRAIYLKLFCQEYAQIEDVGEIFMFSVDRKGFDVMAWRQTNRN
WVELRFPFPYEMKSVDDCRGGLLDSCSFLHDKYLKKVEGGDKFDIEEERRLEHERQRKQLEADEARRKELSEPEF

>N530_uncharacterized
MLRASTIARCPQGKSGGRGLFWKKPSWNATRKANFKERAR**QVESVEYFLR**KHNNNDHHKGMPKRK**LYEEYTADELPW**
YDRSLKVQRPEIGEGFHLPTSRALRHQLRPK**YSPDLFLSEPK**ESD

>N531_uncharacterized
MQRSVLGGLRPFSPLRGTVAYSSSLRSSTPLALTQRRFYAEEAAVTPQEGEAAPVKKEKKKKEKKEKKAAK**AEAEDE**
TLTAGGQKLHVKRKLCRTPPKKK**VWTIIGEGR**LLEFEFQNDDLLDHPTFVTPYPYGDEDEDADEVAEAFANRGKKGQ
QDRGDSDE

>N532_uncharacterized
MRLRPARCVRRLPPPRWLEVTVSGLTRPRRTRAARTVWTGCSTRFPSSTRPCSGPTNPAAWARNSWLISSKRFC

>N533_iron-sulfur_cluster_assembly_protein_Grx5_(glutaredoxin)_form_2
MMSSATRRSAQYSFLLASARSSFAGRIVTASNRRSAPLISTSSSAPSFISSISSSRRHLYSTEAESPAAAVETAPEA
AAAEKESEITQQEEEVKQESLAEFLERIEKEDQAKIDAALKAFESGNAIDEHISSLLGMKKYKCVVFMYGDEHAPAD
GQGYAVIKQLQRDHALFKTFDLNKYPLLKEGLIKHKGSYVR**GDEDIPQVYILGRPFGSLREVMDSVATGQLEAR**LRL
TRSQRHFYA

>N534_Tiny_Tim_homolog_Tim8_form_1
MDHTTLAR**NLQAIQVAVESQK**QLMETTDFCWPICMRNARIGTELDRSQKVCFSNCVVRSIDAERMIAQRVLVAMKQS
STGEA

>N535_fascin_domain-containing_protein_(possible_peroxidase)
MHHGHHHHHHAVTISTESKVHLKSHHGK**FLCAEPSGK**VVADRSDCKEWETWTMRTTNGRATFQSAHGK**YLCAEPSGK**
LVADRSSPSDWEHFHVVHQGAHTALRSHHGKYVCAEQNHHVVANRDALGPWEQWQVVPAGSHCHPSPPQHHHHQHSS
ESKVHLKSHHGR**FLCAEPSGK**VVADRSDCKEWETWTMRTTNGRATFQSAHGK**YLCAEPSGK**LVADR**SSPSDWEHFHV**
EHHGSQVALRTHHGKYVCAEQDHRAVADRSSASAWEQWHIVPVATYQIPHYAPPPQYPPAFGGGFPPAPSSGYPPQQ
GYPQYPQSPMGGYPPQQGYPAGLNPPGQYPPGHY

>N536_thioesterase_superfamily_protein
MTSTPQHQDFYFVVEK**IDVVPELR**ERAQQYEKSIRDSNAK**HVGQLLGIHYTK**ITKDSVEATMPVTDRHHQVIGLLHG
GLNAALAEDVASTAATLHVADMAKQFVVGSTITANHIRSVTSGFVTATATVQHKGRRQQVWQVTIRNEKGEVACVSY
CTLVVLDKKSVIGSAQRNHQQQQQQGQGKAK

>N537_mitochondrial_carrier_AcMC24_(putative_carnitine-
acylcarnitine_transporter)
MASTKQDDDASMGKGPGEGLPSSSSSAPSLPPIPTPSMPTSSVEDEGKQK**NEVAGALAGVGR**TLSRVLTRAVLGVGR
GSIAGTLSGMAEETAGYPLDLVKTRMQAHGDHPTGAMGILRETLQKEGVRGLFKGLGPPFLASSITTATIFGSYAHA
VDFLHERYGSRGEVRLAHVALAGAVAGFAQAFILCPVDVIKNRMQVGGFGHGGAAGPGNMEMVREVIATRGWRGLYL
GMVPTLWRDVPGYAVFFASYEFLKRSFAALPFLRAAPGAAEGADDDPHGAGGLSPVAVILAGGVAGMAYHTATYPFD
VVKTR**IQIQSGSTPTYK**STLDCFRILYRQGGAGALFKGYVPTVLRSFPANAVGFLVYELTLRFLP

>N538_chalcone-flavone_isomerase_family_protein
MRRASSACTIGTGVGRRSLGYSSSAALRVANRPVGSAQRCLSNQLRSPVVRSTTSWGWGLASGVALAALASSCRSAD
ESPLSPLATVLAATAAAGDVPADSVKEERSGFLFPKTLR**LDDSTEGQVLAVGIR**TMYVFFTTYAIALYADPKDVRSA
LSSFKEHSAEDLKK**NQAVYDALR**DGPFTKTIRLIPTGDTSGSHLRNGLVSAVAARMQDNKEEALKEFGNFFPAQLKK
GMLIDFTWKKGGSLSVSVDGK**EVGVVDSPALSRAFFEVYLGEK**SKTPDVREKWAVALAEWLR

>N539_SAM-dependent_methyltransferase
MKAGASRGGGFGHLFTTQAASYAHFRPDYPASLYQRIWSFAGEGRGTGLAVDVGCGTGQATKVLATHFDRVVAFDPS
PKQVEAATKIDNVEYRVGLAEALEGIEDESVDLLTTAQAAHWFQLEPFYRELDRVLKPKGCVAIWGYGLCRLPTPEA
DKLLSRYHTETLGPYWEKKR**ALVDALYEHIQLPFAR**THREVIENKKEVPFKHFVGYLGTWSSLKTFREKHPEGSDPV
QDLCPQLFEALQLRSEEDVIHVTFPTVLILGQK

>N540_uncharacterized
MRCTLRTSQRFGHVSGRKNITCVVAFRRLHTSPLACTGHKEASDVSPADAPATAEEPHQHQHHQHVASSREQRRERR
RELLEAAKQELEWRVFIASRKSHESTTSATPPPPPSAVTIEPGPAPPVADAAASPTTKSGTTANDEEEHPERKREDL
GRRMMRRRLRRVARESRDHR**LPENVWGAFR**QFEVLLAEPTRSLEEVQKAVDEWYGRLPFRPNFRAELDMSKALHTYV
PFWHFACNTACQYQGRARIGRRFAAKYGEKTSGTLSTAFPVLICAEEPTPK**RKPVLASIDDLK**WHEVSAEGRLVSLT
ARSESSLKEVLDAHLRPTDRVMDLTLQPQAAWQREGRKRLEEVERELSERAIIESERARGVLRPNNDADGEAWEVDL
DYVARTDQEREQGMGRVSLVLVPVYELHYRWHGFEYHLCVRDGDHAVGSPQPDSGERPLPLIEGARPYSYAKISLAG
LAGLGVGLASYWMITH

>N541_SAP_DNA-binding_domain_protein
MTAVLNSLGLETLEELYYHDDPHAAKEEKKKLKKKDIVDAISDKIDTYAIEVFIASLPLAQLKTVAEKAKVPFKEED
NKNSRSVLSRRLTEQVVSAGFDEFLETVDADTLKAVAEDFDVKADKKAIAEAARTFAAER**YFGNFDVESLR**ALAEEL

KLKQAAKTSSKRKLVEAIVTQEDAEPVEAPKKKKQKTDVGKKKALEKGITYDEIFQHYYVEELRDFVKSKGIKVSGK
KPVLIKRILAYLAGETEGIMAGDKTEKAKKKKKATTKKAAAAKKGAASTSAKGKGKKEENGNGDE

>N542_uncharacterized
MSSTKKTTAASAAADKKSKVVVFKVKDLENMPRKRLVSLAKRVGEK**ANQNSAALVEALTKYHNEHQSEIEEK**LKELS
SKPKASKKRDMTKDLSTRIHYKDRVSDS

>N543_Tiny_Tim_homolog_Tim8_form_2
MDDTTLRQRAAALQAEVMIQVSVLATTDDCWKVCMKGK**TSFGTTLNK**NEKECFHNCTMATVQSENFLTKR**TAQHIEQ
QAR**QSGH

>N544_DNA_polymerase_A
MLRAADAWITKGTSRFASMAGGTVLRSTAALHVLDLPKRPLSSSISTIKMTMRGRFQPSTATSLPLLRRSASTRAAP
APAIAIATEIER**AVLESQQSQPNGAIK**INGELNQPAPAELMPHTILIDGSFLTHRAYHTPIAEMTNGAGVAVTALFS
YTRSMLKMLQDPHFRADYIGVFVDSGPSFRKQLYGEYKAHRSAPSAELRKQFPLVADATRALGIETIKAEGMEADDL
IACYAKVAQAQGHRVTIISRDKDLMQLVGPTVKLYDPVGKKTFDEAEVRKKFQVEPRQVRDVLALMGDDGDNVPGVP
GIGPKTAAALISEFNSVEELLANTAKITNKKRRQLIEEHVDTIRRALALVELRHDIPMPVLLEDLQRQPINRDKFLA
FLREHSFGSIISKLDKICPPTAAEQAAEAAPRTSSTRGRPRLDNPTQEAVQAPPAPLSVAVALKRPKVEIEGVTIVD
TPEEARRVLRILRSPGVRERYHACDTEAIKIEVKHQSPYNYGEVICASVYCGPDVDFGTGPNLWIDNMDDARGVLDL
FKEYFEDEGIKKVWHNYSFDRAMMWRHGIDVKGFGGDTIHMARLWDAARTSVGKKYSLEALTGELLEGETKRSIKEI
FGRNKVLKDGTLGKEIVVPNLDAIQRGEAGMEALNNWIYYSTYDTRGTYELRDKLEDQLREMPWVYEGKKALPGANR
TMWDYYQNYWLPFGEVLTDMEREGIKVNVDYLAEIEQVAVAEGKKHQIRFKEWASEYCQDARYMNPTSDAQKQQLFF
APCKNLKTDDMMPAERLFDIENDEGIPDPVTGKVKKKRQIRISGFGLPAIAHTGAGWPAAGAEVLKQLAGKPFDNPP
KYGVAYKAFSEGEAGAEACQAIDSLVKMSSIDTLLSNFIVPLQHEVDPNNRIHASLNINTETGRLSCRRPNLQNQPA
LEKDIFKIRSSFTCEKGNKLIVADYGQLELRLLAHMTKCRSMIDAFQKGGDFHSRTALGMYSHVQEAIQKGEVLLEW
GGEGKPPVPLLKDIFATERKRAK**TLNFSIAYGK**TAMGLSKDWGVSLQEAKDTLQRWYSDRPEVLQWQENTIRTARKT
GYTKTLMGRYRPLPDISHSKPMMRGHAERAAINTPIQGGAADIVINAMVLAHHDELLRRWGWKMILQVHDELMLEGP
AESAEEALARLIEVMQNPMPEGEELLVELAVDGKAGSTWYEAK

>N545_pentatricopetide_repeat_(PPR)_protein_AcPPR12
**MWRQLTTRHLASRSSGRLAKHACTAEASQLLVCRSTPPRQGKATVTAWVPWSPVPLPHRHFLHASPSAHIVAESGNG
SNKGRS**SSSSSSSSKEPEQPEHHFPSRHVELKQTINELSRKKYVLPRHMARVVQYMEKHRSVFLEARVVSRVRLLLQ
RLTAGEVGDYNVVMNALAEMGLREDCFNVFARMRNNLIKPDTETLNCLVLASVRDGRTQDIDDVVAHFKKTFNVKPN
ARTFAHRISEFDKKKEGRRGSSGSAGGRKEEVKQAIQLLEAMKLEKPPIRPNLEVINSLIAVCVRHYDMKTAGILFR
DIERGNLKPDRRSYDLMLRGFEIEADAKIIQKMIKEMQRAQVEPDASAYGHLIGAYGRAEQEERALQAFEDVKANHP
DVALDAAIYGKVLDVLAGKWKEEDDYQIDDLWMANATRDGREGEVDEDWDREWTDEWEGAGNVEQMALFEEQEAERR
REEMRKKEEDRLRREAEEREREEREEEERKQKEREEREMSEMEKQRRREANAQYVDKAFALLEDMSRGRNIDPDYAT
FFKLMSLCLKRDNTTRALQVFDLFKREAERHKQHRDEAQWTGMEMQSVAKLLALKFVRGCEKNR**DMQALETFLTK**HP
HYIVPGDIYSAVVK**AIANAYVPPLR**KPTETDEERGWIDSLESGDHPSTRDGGGVAEKGENKRQQQGEKGDWLYTQAW
ALFHEMPRHGIARSKDVYDAMIELACKRASIKRALALFREMQHEAEREQRESGKTTLKPGLRTYRSLIVHCLNNNYF
NKEEEYNYRNDINHPLTQRAFQLFEEMEDARIKPDLKVINAMLGCCARVEDKANGLKLLGLLVRSNLVADDQTLKFK
DRIQKL

>N546_thioesterase_family_protein
MNALRRGSGAARAGSRGSGATAAAAVLGRSQVVRMSSTSSAAGGKKEHKARWPLSITREVNWGELDSFNHVNNVVHF
RWFETLRCEQALKLGIDLSPTAGASLILAESNCRYLRPVMWPDTVTISTRTTAIGETSWTTEFQVESK**EQEAVCAVG
YSR**LVYYDYKEGKK**TPIPQDLR**DR**INRLEGTNF**

>N547_coiled-coil_domain-containing_protein
MELKEEDLIPCEDFNFFEARLTALRK**SDDLISIELNKIDVNSQAECGNIWK**K**LTAGYELR**DRSIHRCVEAAMSSVAA
LRAEVKANPDDTDLELDLLREQDKLSNIKSELTVEQIVKNRSLMLFKDKCHSFKEARSYRAAAREVAKDVVGPTKRK

>N548_neurolysin_(metallopeptidase_M3_family_protein;_Prd1_homolog)
MLRAMSKGRPRTCVRLCQQQPWQALGRRLFSADGKGFPNALR**FDLSAAEIAK**TSHEVMESYKKGYGRMVSVPSRERN
FQNTLQGIADLDAYCSAVSESCVFPSYVSVDAQVRDAAGAANKALSELAIETAMREDIFKAFTEYYNHTMPQETLTP
VQRRLIEKTMHDFKKNGLMLSPEKREQLKAMRKKMSDNAITFQKNLNEDTTAFYFSREELDGLPQDFLDGLEKVDGQ
EGGATKYKVSLRYPELLPVMRYANNAETRR**KLDTANAAR**SMRENTPLLEETLALRHEAALLLGYEDHASYVLEDRMA

KNPAHVLDFINELSVKVEPLARREWEKMIALKKATVGGSDNVTIDSHDFTFYNQRILERDYQVDENLIKDYFPFETV
TEGMLGVYQDILGLR**FEELNDAHTWHR**DVRMYAVYDRSTNAFMGQFYLDLWPREGKYPHAAVFPLVPSHHFPSGSSS
DIPASFLAHLHPVTGNACSPFARVIMVPRKLTRR

>N549_uncharacterized_conserved_protein
MAKVAAGPTRSEVRGLLRSLLREANEQMIPVSNNPLWRDSIMGAFRSASPSPAEAWNGFR**VGQAYLTLLESSR**VEKD
MFERYGLTPRPDDTRARLHRNAARVGLRLPQWLDEKEASRS

>N550_YqeY_superfamily_protein
MRRATFVTVSAGGLRASAVPHSSGLLFRSSTRFVLATSARADARVFPLRSYTTTAEEFVGKLMADLKEATMAKDKVR
LGVIRRLRSEIMNKEKLNVDAKLEFGDCVKVVQQMAKQCEDSAKEFDKINQADTAAKEREEARLLR**TYLPAQLSEAE
VQQLAEEAVK**AVGATTIKDMKNVMATLGPKVQGKSDPSLVGEIVRKLLGGK

>N551_uncharacterized
MRSSVRNAAAARWASAPARFSSSLRLYRSSSLASAHTILRSTSSRTYSSSSVPPRPGHDQDLQPPPGAK**EGDIDYTE
YLAK**MDRLEKPKGGLPRANKIAALLTGIPMLLILYHMLFPTPIEKNEWFQLEKEHRDRMVRAMEEANANANSKK

>N552_FAD-dependent_oxidoreductase
MQAGGKRRVAVVGAGVSGLACAR**ALVSAGLEV**RLFDKGQRAPGGRVHSRSVRLDAQDQVVPHRSSPHEEKKAVAEVL
SFDDGAQYFTARAPEFRAFVEECVARGCVREWAPLRVAVIDREGEVVLKPDDEGKKKEEKEAENNARYVGSPTMQAF
IPFLAQPVAHTIQQSVRVADIQRREGGDGGERWGLVGEKGEDLGDFEAVVVGVPAPQAVDLLRAAPNLRAKAASVHM
NPCWSVAHFFFFVRLSVCSLTRAMSCVFGGARVLRQLTMCVVCACVRVGRWAWRLMARRRACSSTGPS

>N553_alpha/beta_hydrolase_domain-containing_protein
MAEEGFFVNKRNQRIFTRAWLPPALEKTK**ALVFLFHGLGEHSGR**YNHVAAAFNARNYAVFALDHHGHGKSDGAPIFV
ERFEDFVEDALLFIDVVSARYPAHLPKFILGHSMGGAIAALTAKQRPKAWAGVVLSGAAIKRGADVNALTVHAAR**FL
SWATPTLGVK**R**IDPSTLSTDPAQVK**AYEEDPLVYHGPVTARMGHELLKAADTIENDFSGFTFPFLACHALDDKLTHP
DGSKELYERAPSPVKDLILYGGMRHEIFNERDGARVIADVLRWVEKRYAAVGHSREHGRVISAL

>N554_Tim17/Tim22/Tim23/Pmp24_family_protein
MQSEGLPPVLDTSVDEEAEKTRLKKVDLAEVLERYSPYQAWCTFLRGFITGFGLRMGVSLALRALQLLRKKPSR**LLS
LADLVK**DKKANQVKLDAVRLGLTIGGITGVHKLAYGLLARLRRTEDAWNSLISGALSGLPLLFQEKENRRTPALYLL
TR**LAQCIYNELK**RRNMWHFWGSDWAHGDSLLFILTSAQIMYAYVMRPETLPPSYYKFIVRSGPIDECVLEGVRRSNR
NKPIDVQTLVDYVTKLGTPATIAHAMGFLKSHPDGLLPVIPCSILHPRTSSCVGHNINTFLSTSKKTLPIYATLTFV
PMIVLQFFKLLRNPVTLLSRGLLSSLRSTVFLASFCAMYQVIICMQRNFVSRDHRIVYLLAGLISSFSIFIEKKGRR
SELALYTLPRAVDSIYMQMLDHKWMGSVPHGDLLLFCTAMSGLTYFYHNQTSVMSPTLLWVFKWLHKSKSD

>N555_Complex_I_(NADH_dehydrogenase)_24-kDa_subunit_(NUHM/NDUFV2/NuoE)
MRRATSSLSAVPALRTTGMRATSSLFTSSSSAAMLKSRTLHSSVPRQGDHGGLSQHRDTPDNTIDTPFDFTEANTVE
IKKILAKYPVNYK**QAATIPLLHLAQYQTGGWVPLAAMNK**IAK**ILEIPPMKVYEVATFYTMFNR**TKVGKYHVQLCTTT
PCQLGGCGSTVILETIKKHLNIGVGETTADGLFTLTEVECLGACVNAPMLQIGDDYFEDLTPESTVALLETLKAGKT
PKVGPQTGGRKNCEGPQGKTTLFAAPAGPYCRPDLETCA

>N556_short_chain_dehydrogenase_family_member
MEKDSGVGEEEYTSYEPEDSVPRDDAVNGGFVPVIVITGASSGIGEAIALQYASSRACQLVLAARSRDKLKAVAIKC
RKLGCEVAIIPTDVSKPKQCKFLIKETIRIFGRLDYLVLNAGVSMHIAFEELKDLEIFHKLIDTNYFGYVYTTHFAL
PFLRKSPQPK**IVVIGSLSGETGVPLR**TGYCGSK**FAVNGFFEALR**TELGPAVPITIVSPGYVDTEIRQNAYGPKDFNP
ASGGMMSPKRCAELIVEAADQRRRKVVLTLSGKLAYALRPFVPDIIDMLVKRKAHQKKKAAL

>N557_mitochondrial_threonyl_tRNA_synthetase_(ThrRS)
**MRRGAGAASATAASVRRSMGRVPASSFLLTQQRTCAQKSGSMRTPAACFSRSVRVRPPSLAGERPFLRRFASASVVT
HRA**VPAEARPGKAPSSLPPFMQRRLELWREEWERQQTGKEAQAAAGEGPHPIKITLPDGRIIDTSSSTTPLQVAASI
SEGLAREVVVARVNGELWDASRPLEQDCHLELLKFDSPEGAGVFWHSASHLLGLAIEREYSPATGEHAESSAKVQLC
DGPALSDEKGGLGGFFYEFFLQPGEGATGASTEDFAELEKRVEAFAKEKRQFERMTVSRDFALQMFAYNDFKREIIE
AIPAGEELTLYKCGEFIDLCRGPHIPHTGLVKGFKLVKVSGAYWKGDSTRPLLQRVYGIAFPKKELLKEWLTLQEEA
AKRDHRLIGKKQGLFMFHQWSPGNAFFLPPGAKIYNKLMNFVRDEYRVRGYQEVITPLVFNKELWETSGHWQNYKDD
MFAVTGASHAHGHDHGHAREGHSCAHHHHSPSAGKEEVMGLKPMNCPAHCLIFSGGHYSYRDLPLRLADFGVLHRNE

LSGALTGLTRVRRFQQDDAHIFCAEDQIESEIGGCLDFLRKVYSIFGFEFAVQLSTRPEKYLGELALWNKAEDALKQ
SLSRFGHSWRINEGDGAFYGPKIDIEVTDALKRKHQCATIQLDFQLPLRFGLKYQGLDDAYHTPVMIHRAIFGSVER
MMAILLEHTSGKWPFWLSPRQSVILPVTDDHYDYAKQVHAQLQKQREDKFNEFFVDLDGRTKLTLPKRIKEAQEKQY
NYILVVGERERTEGTVSVRTRDGVIHGAKTTADLLTEWRQLLDAFQ

>N558_iron-sulfur_cluster_maturation_protein_Iba57
MMSRAGRLRAWYRSTEVVRGAVVGKRGIHHAAPLWLVAREAPPLEQPAPPPLGWWVGEVGGRAIVEVRGRDAARFLQ
GLTTNDLLAAAATSRAGREEGRYTAFLTPTGRLLADALVCQLPPGQQQQGQQEGEQTFLVECDARAAPGLVVHLRRY
RLRAHVDITPPAQRPAADEWAVGAVLTRGHVQSSSSSSSSGGGSGEATPSPRDSLLQCLRSHAPSLPCFADPRTAAM
GIRVYHRRSSSFAPPPGLAEASAKEYRLHRILHAVPEGIDELEPNVAVPLECNLDALNGVSYDKGCYLGQELTSRVH
HTGVIRKRLMPVMCFSPEDEAREKELRVAERLLDFVHGRDQPSLERDHLLPSVLRSLPSLATTNIASDKTELFLVGA
DGTPERRQVGRLCGGVEAGLGFALLRLQHTTAVLTPSTTTAPFFLAKPLWPPPYPLP

>N559_uncharacterized
MIYLLSTCQRKNMTRKYKRKKFFVLLSRTMLDDLLPLVVEGLLALISLGCLGLLAIQPFKNPPPISLRYVALVGLLP
VAVTAGLMAASRYDMRYAAASLLTFYTSAVAETTGALALAVALYSEVHRNSNISPQWYALPTGSSPLALISNYVPSS
YIQLAIFTVLGAYLLSAARELPDKADSLRLSAFAFLGAAASRVVLDRFDFLLDAVNSNLLGVVGVQLSSYLVYEFMM
VVAVFFLFLHLLKTYQGTSIKLKGK

>N560_Complex_I_assembly_methyltransferase_C20orf7
MRRAAVLQRANTRSRLPGAFSASSPFARGQIRRLSAEGCNRISCTTTRLAAAPVTMAWSKRGLASSSDSAEEQRAMN
VFNRHVKRLQRDRAAADPESQDYDYLRKEIAARLADRLNDILDREFPSVLALGGAAAGVAEHLQEIPGVKRIVQLDS
SPLSLARDQHLDADLAIKPERVVADEELIPFEEGTFDLVISNLALHWVNDLPGVLAQIRRVLKPDGLFLASMFGEET
LWELRNAFLVAEQDRDGGISNHVSPFAGVSDVGDLLTRAKFALPTIDQEEVVVDFADAFTLMRDLRGMGESNAQHFR
RPYVPRSTMYAAAAAYKALYGKEDGRVPATFQVVYMIGWCPHESQQKPKERGSAQFSLKEFAHSVGELKVVDDNGNE
IAPARPGEGPEAGGGDHSCGRH

>N561_mitochondrial_ribosomal_protein_L52
MSNGVVANAIWRRSMAGGMRGFASASLPMRAGQRVRLMQGVGRSGNEDGAFHDAPDWEYADGTPAPPSRKQIVWMTK
RQETEERIQRLREEVMEMEQKELERQSFYKDE

>N562_uncharacterized_conserved_protein_(C-terminal_DUF1674_homology)
MQRTKAYATMYSTRHIKSAAHLARPSFLCRFASSSSSPKATPSATHAAKAEPKSKFMSNDDKSLEELQAELDKINQE
IEAFNAQEGKTADDEYEYKNPKTGEIGGPRGPEPTRYGDYAYAGRVTDF

>N563_mitochondrial_ribosomal_protein_L29/L47
MLRGGLFGRAAPFGQRAGWKRGMEEFIDNATKPGEYPIAGRAWKASELRLKSFEDLHKLWFVLQKERNLLLTEKMLA
KSEGKQMKAKGRRVKVRQSMARIKLVLGERQHIYKTFKREQILALEQDRLEEVRGRQLAWAEQLKSQNDKLANVKLP
KPQKEAASIK

>N564_uncharacterized
MGKSQGQQEKIPSKKRKIAIAKQNKTEVEFVNKIFPFIVAAMVGAFLVAIVLLFIKASASAPDAAKDLIEGAVDQAA
AAAGLD

>N565_iron-sulfur_cluster_assembly_protein_Yfh1_(frataxin)
MFGSARHARHLATSAEPPSAGEFAKAAEETLEDLQDRLEEAGLDEDLDISYSDGVLTIRLGDKGTYVINKQTPNRQL
WFSSPISGPKRFDYVATEGKWLDTREREPLHQLLYAELEQLTGVSLS

>N566_Hsp20/alpha_crystallin_family_protein
MQRTTSRTAAPAIRQRLLSSAATATRPSSALTAGTTQTMTSSSSSSSSSARGLSVHLRPRHSHHHESFFDAFARDPF
FRPLINELASTAKQVGRPAVPKEGPRPRPLHANVNVLETQQGFAIEAEMPGIRREDIRVEVCEGDRLVIRGEKRFEG
HTANNTNTNTNTNVRGELKEAKEAAEPQQRYLTFERSYGTFERTFALPENVDASRIKASYTDGVLKVELPKAAKETP
KSWTVEIN

>N567_Complex_IV_assembly_protein_Cox15
MMQRLSRPRSTWTTFSGGVERAGLFGTARSGSSSLSRTLFAATCPPSRALTVAGRLAPMRTSSSGVAPLFTSARPGI
AARVFPRLATATNGAALRPATLLRRANSTVTHQATQPGVMPKVAAATWHDVPTSMKVWIAGCTATVFGMVVVGGLTR

LTESGLSMVDWGVLQMKPPITQEEWEAEFDKYKQFPEYKKLNSKMTVEEFKSIYYYEWAHRNLGRFLGAAYTLPLLY
FTARGHVRGPLRTRLYAIAAGIGFQGLLGWYMVKSGLVEKDHPRVSQYRLAAHLGSAFVLYTAMLWTTFDFVLTPLT
TTAK**LTTSAAASAAAASAPTVLK**LQAKMRKYAHGVAGLVFLTAISGAFVAGLDAGLIYTDFPYMGGQVVPNEILDMD
PKWRNFTENDVTVQFQHRVLGITTFSSIVAMWLWSRKVPLPPRSRLAMNALLGMASLQVTLGIATLYTLVMTHVAAT
HQAGSLTLLSIATWLMHELKRLPK

>N568_mitochondrial_ribosomal_protein_L27
MQRMSSGAVGLRTSNVSSMGNGMMARTWGIAVGGSSSSTAATRMVGPSTWGDVWRRGATKKTGGSSKNGRTSRPKYL
GPKRGDGEEVKAGEILLRQRGTRIHPGPGVERGRDHTLYATTPGVVSYTTSHYPVPDRR**LLCVVPLSLALPR**RIAVL
RARPSQL

>N569_Complex_III_assembly_protein_Bcs1_(chaperone)
MNGGPPSPLGGLLDTTNPYFSAGAGLFVLGGGATLLRGGWKYGAAYFQRNFMVKMEIPSKDPSYSWVLNWITARAAR
QTQHLSVETFYQKDPTGRIK**TSYNLIPSTGR**HFIKHKGYWMVVERAREKAMVDLTSGTPWETVTFTTYGRNR**ELFLD**
ILQEARDMALAKEEGKTLIYTANGFEWKEFGQPRARRPLSSVILDGDQAERLAGDVKEFLANQSWYRDRGIPYRRGY
LLYGPPGSGKSSFITALAGELQYNICMLNLSERGMTDDKLAYMMSIVPTRSITVLEDVDAAAIRREQPTREYQSCVT
FSGLLNVLDGVASSEERLLFMTTNHIDRLDPALIRPGRVDVKLEMGNASADQVRRMFLRFYPDHERSADEFVARVEA
AGKPVSMAQLQGHFMLFKEQPHNAVSNAELLSAE

>N570_D-lactate_dehydrogenase_(Fe-S)
MMLRGRVLLRRPLHCAACLPPPATARLLAPSVPAAVRSWSTLSSPRSVHTEAHTAGKGCGPACSDPSHAHSSPRPTK
SGGQQLPENYAALARELRKFLREDQVVSDPLR**TLAYGTDASFYR**LIPKLVVQVEREDEVVKALGLAER**FGAPITFR**A
AGTSLSGQAITDSVLLRLVPSKWSHIDVLDPEGSRVR**LQPGVIGGQANK**VLGLYGRKIGPDPSSIESCMIGGITANN
SSGMCCGTRQNTYNTIEDIRIVLADGTVLDTASQESRERFSQSHGHLLSELSAMAHHVQHSNPDLLARIKRKYSIKN
TTGYSINALADFTDPFEILKHLIVGSEGTLAFISGVTMRTVPELPHKASSIMLFPDVITACEAVSALKLAPVDAVEL
MDRACLVSARDKLAQVGLSGEHGQDVAILLVETRADTTDELADRVEHVAKAVRPYRKVKEVQFTSDPRVFNLMWDVR
RGIIPSAGAMRPVSTSVILEDVAVEVPRLAAMTMDLQDMFKRHRYDDAVIFGHALDGNLHLLFAQGFDSRPEQERYG
AMMDELCAIVATKYGGSLKAEHGTGRNVAPFVEMEWGKDGYALMKDIKKAFDPHHLLNPGVLLNDDPQIHVKNLKPM
PAAHSLVDQCIECGFCEKNCPSRELTLSPRQRIVIWREIQQLRRTKSDPARLAELEQQFRYAGDDTCAADGMCATAC
PVNINTGQLIKTLRATERSPWAQTVAQAAADHFALVNGMGRTALQAAHVGHRVVGARVMRALSDALHRVLPASPQWN
PHLPRGGHAPSPPPPTATSKDQVVYFPSCANRVMGVSTSEKTEGRALPDVALSVLGKAGYDVILPEGLAGLCCGMAF
ESRGFPHQARQKADELHAVLWRASDHGRLPVLFDMSPCALHAKTHKPTPDESLGLPEAKKQQK**LEIFEPVEFTHDFL**
LSRLQWTPREEGLVYHTTCSSKRMAGVDQKFLSVLKQCTGEAPAKRLGSLLLDSAVPCCGMAGDRGLCFPELPRSAL
KKLRERVASHPPGCSEGVSNSRTCEVALSEHAGVPFRSVLYLVDRASSPLNPAAAPSTSAALHALLQRKAAAYAIDP
SGPAPPASPTLPSACTQADATPTPTGLLRNYK

>N571_universal_stress_protein_family_member
MDPPRLDGKDDDRAERAEVVIMKLQVKDPGPKDFVCVDGTLGADRAVKWAVANLPKDHRLVMVHGIYAPITGWTADS
LMLEHQTVEDKYAPMCEAAGRKCSFFSFPYLTKGTFGDTVCKLAR**YNSVNSVITGR**RSELSPLRRQFVGSSSMALLS
RCEVPVTVVTDAWAEGDLFNEDNSSSESLER

>N572_alanine_racemase_(PLPDE_III_superfamily_member)
MRRVVWLKTSRAHFGLRTQRSILPSCRTMTSLAPSFNTRLASVRPAPAAVGDGVDSIQTPALILDKGALLANLRRLP
ALVRESSSSSVRIRPHFKAHKCGAIAKLQMEEGEASGFCFQKVSEMEPLIRFFEEDSADSGK**LLDLLVTNEVVER**SK
LRRLCELASHPSVKRVGVAVDDAGVLQVLMDEARAASGGSSAASRVGVVIEIDVGQQRCGIDIASQQGEETFVALAR
RLIAAHRDPSGHVSFIGLQAYHGGNQHVRAAADRERTVQHVAALARKALDLLRANDCLPEGEFLVSGGGTGSFPYEI
ASGVYNEIQPGSYALMDRDYCLNKNAEDRTESPFKNSMFILSTVISTASAGRGWVTLDAGLKAYAVDSGLPVVWQND
ELDCEQAGDEHTKLIPRTPGNLAALAHFKVGDRVWLVPGHCDPTSNLYDWMVAVQEDKVTDVWAVSARGPGM

>N573_putative_Complex_IV_subunit_Cox6c
MGKGIHLPASLRSFLYRQITVITVGSVVVGTAFGGWQSYTTRVADENMRQIRFKQAEKEAR**ISHTLLTK**GGLKKALE
EQGFDMGFYEVDEADEEEIQ

>N574_amoebozoan-specific_protein_(no_putative_conserved_domains)
MSLK**FEPSEAQMESCR**QQFLQEGGKALAKWGGAATLFTSAMSLWPAYRNLFNWRGQIFCVMGAGIAGFWIRGEQAVL
RCHHARDAQR**LKDIYEGR**TMG

>N575_Complex_IV_subunit_Cox6b
MEQRKEPAAASTTPSSGGEGAANAPLVDAQKRERCWAARDAYHACIDGSK**TGGGEEECGAALR**LYAAECPRSWLLHF
EKRRKADQERSAREAAYQNRQRG

>N576_Nca2_regulatory_protein_(Atp6_Atp8_expression)
MLFARRAQGTRQRIASLFGLIDGATHDLSFLPPDQEKLYRDACVALTKQSIDGHTLTHVATSVAPFIGYRHRHRGAP
TGPATGGGGEAASQSSSAPADNSDAVVHHDEGKDKGKGKEKNRSEPATDGEGSAASKEDLQDQVLFEAKLYVLCLIA
IAQNQSVCDELLRLASSIQHHHREWSLREDQPFWYLYEKTPWYWLNYLLLKRDETPHPITELREKLRHLRALEKNTF
AFIGVGSRVLSRYEAVGRTNYAERLSNLIRKDQQEEDGENEDVLFNLAQTVNLSYFDYHSADVIGETTTETTPNIPN
LYAQLMENVKKAALFPTQMKHTLNEYKRPSALSTNWLRYSCITAGITVGVLSVVKRREDIIDWLVDFKVLAKNFIQK
NILLPLQDVYETIRYEKRAFTIMDAR**ALDADVESLQR**MVDEYVRKLHPHISQAQLEEITTAAANSDISAIMPVYERE
LESPIKNALFGDLLSLLLIQVHKAKVDVARAMLALDKLMRANELNFQLFAVTPAILLVGGLSRYLYRRITRIDIRRT
THVQIRETLRNVERMLDLNLSSASSSVRHHHAGGPTNLSLSTSFSGWGRSSTNSLSTQGRPESDLRLEDTGR**LLVSI
NELIR**LALQMPRHDRKWLLEDLQDLQAEELQVAQKLATIHRMYHTHHFLSAV

>N577_uncharacterized
MEEEKRIKAQWGPVWKRTAGATAVGMVVGAAVARRRLRLALEAGPAQEIAASTLLAAAASKPPSTIIFTSALAGGLT
AGTTTGLFLVSRELLRVDMQWEGMVPSLYAGMATGALLGAATGGPYPALLGMSTLGGLAAVGEGGVALWNRWYNKKR
QQIFQQRLIEKRQTLLRQRAQAAQSELEHIDQQLETIAYHLNAQKEKEEAAHESVMSWMSLKVPSWFPIQPVTEETQ
KKKQEAEALEKELMDRYYAQR**ELEYQQQLQR**QRGVTPSFPPAETKEVSNAQ

>N578_uncharacterized
MSARISLMGADDEDHLHGTAPDHADDGEGEYDEDEDEEEITLSQYLVELVWKDKRTRYQLWNCGKVIVLFGVTVWAM
R**RFPHFQDPER**LDQK**VVEYMDHQQR**MMMGGM

>N579_MYND_finger_domain-containing_protein
MEGGQARGGGVTGMSVGEGVALMAGVAIAAAGYVWWFNRKSTPTTERQRSSPAISAAPTPTPKQQVKVCKSCGKTES
GDRALVRCGRCHKVYYCSRDCQRQDWGR**HKPECSSSDSAAAPK**KTPPPEPLPAWAQNLRLTSAEYANVKALLKKNDE
QFELHLRGGPKPDSVDDIWEGLEPQEMQQLIEDTIWYKEFYKTNDASNVLSLLRRLASVQFWGSSPVAVAFFCLVFS
KQSEETLRSWVDQCATELAQDGWFRSAFLTFLRYADTPASRACYQPVLALLSSAVDQLEAQSMLSLTIPDFVARPLH
EPLHSPEAVDHMWANYFATGNVALLKKIIKEALPLAAQARVASNPVNAQLLMQTCNFAAVTLVNEGIFDEQVRNVCK
SERDALTSGTGQQNLGLMQMLQQIMMQQEGSIQQLATIPAEEVSRMRVEVEGHRPFLERMREIKHRQKVARLKQMPG
VRTVPTQFGNALWLPATTDHPEGLLFMTMEGESGAH

>N580_uncharacterized_conserved_protein_(YbjQ_1_superfamily,_putative_heavy_m
etal_binding)
MRRVRPAMRSATGHLAAAAPLVLTSRRTYGVLYRTHKGEKSERAAPGTTAANSSSSSNNGNSGEAGKKDKTGDTFQE
SAGVLVTTRGVIAHHEIVREVGIIVGSSVSSR**HVGLDLLAR**VKGVFGGSVVAYAEMMVDSSAEATHNLMREASRRGA
NAVLRVRYETAVSSDPAVWSSTFSYTLAYGTAVVVRPVKGAKEATSWRDHHSDDDDTDDDDD

>N581_mitochondrial_carrier_AcMC25
MATSTSASPPAAPPETQPKPQNAAPLISPWIKVLAGSLGGAMEAVLLQPLDVTKTR**LQLDSNSR**YRNSFLYCAKTIY
KEEGAGALYKGLTPFVTHLTLKYALRMGSFTFFR**GLLGSQATSPSGAPK**KKPSEKMVMWNNFGSGLCAGVLEAFLIV
TPFEVIKTRLQQQEGFHNRKYKNTVHAAVTILREEGVRALWKGVAPTALRNGSNQACNFMVVGIFNKWVWKKEEGKQ
IAVWKTMISGAIAGAMGPCLNCPLDVIKTRLMGQKIEPGQPPKYRGVMGTIGTIYKEEGLFALWKGLVPRLMRLAPG
QAIMWTVVTRVTTYFEEQAQRRIEEEQRPSSRGGGSSSSSSSSPSSSSSSSSSSPSITPAQPLPH

>N582_Complex_IV_assembly_protein_Cox23
MEEERKPVSAREAARRRRAEQNQK**HQQAAGINRHPCYELHQASLK**CLEENDYAQGACTYSFAAYKECLANQNEAKRA
GEQKSIFG

>N583_putative_Complex_III_assembly_protein_LYRM7
MQRSQRALKVYRDLLRTQHTVFSGDALAQERARSLIRQEFEAHRGVQDAK**EIDDLIARGNDTIAYVR**GHVVQAVKND
RGNWEMKLRPENKFIKSKDFPMCGVEF

>N584_long_chain_acyl-CoA_synthetase

MMLTKRAARRLRCMEAHLSGATESMMTLERGLDERSLARADEALLSLAYVVADKPSTAEEAAASSSGKLLGQEMGAL
ESLGERLRVYKTGAKMVTSVIKMGLDLHSALRRNPYTLADTWEDVSKQFVQNVALLFEDQSYTYGELNHAANRVANW
GREDAQLKAGDVVALFMQNRPEFFITWLGMAKLGVTTALINTNLNGKPLEHVLKVSQARTLIIGPEQLDHFETTRQT
LKTVDEGEWSVWVFQGREATAPNPLAWQWAKDMDVRLSAHDEYNTPSSLRAGVKMVDPLFLIYTSGTTGLPKPCKVS
HKKVWGYMQLWYRFANLTSRDRIYVTLPAYHSNGGTLSLSAWMAGGAIVLRRKFSASAFWDDARKYRATGFIYIGEL
CRYLYAQPPSPKDNQHPIRFMIGNGLRGDIWDGFRKRFGIETILEFYGATEGNIGLLNYNGRAGACGQLPYFLRPAV
PFRLIK**YDVENDAHIR**TADGFCIECPVGEVGEGIGRIDNDPNKMTGNFDGYTDPQATKKKILTDVFEKGDQWFRTGD
LLAKDFLGYFYFVDRIGDTFRWKGENVATSEVEMVINSLPNIVEVTVYGVPIPGKDGRAGMAAIAPTPGTTLDVEQY
LKVVTEQLPAYARPVFVRVMGEIDTTSTFKHNKAHLVKQGFDPEAITDAIYLVTYPGKHTASGSFTRLDRQLADAIA
QGKHDI

>N585_Complex_IV_assembly_protein_Cox19
MTSHSMRNKAPLVLPPEKGSFPLDREQACSEKGSIYRTCLRDHNNSSSICRQKARDYFECRMDHGLMQREPWDK**LGL**
GDDQIEEKSAPIDVHTKEQTGWVAGAKYR

>N586_mitochondrial_matrix_protein_Mmp37
MAQREPAEWEVPLGLGEEDRQQLRRIIGAFPKLTFAAGYGSGVVPQADATKLTKKPMKDFIFAVEDSRRWHEANIAT
NGGHYSGVAWLGSSVVARLQEDVGASIYYNTHVQLLDETIKYGVISSKHLISDLVNWDTLYVSGRMQKPGSDEIMSA
NQANLESALSSALLLAPAQLPQRQLWETIAGLSYTGDFRMQFGENPNKVKNIVTDKNAEAFRLMYRHSCDKLQHLLR
LEDDTVVQDTSRAARQDLLLRLPARLKANVERQTGQSLVDLSGAPVQTIASAVASGISTLVKSSSRSQSLKGILTAG
LVKTIVYSANKIAKMRNATK

>N587_ABC_transporter
MLRHQVRRSWSTGTGLASRSVAHTGAEGMQAARLFRSSSAKIASPSWPSAGNQHQACRLRTGLQSELRLSALTRRFF
ASPSYADKMKARVKDQKVKETGKEANKAERLQKKGKGQKVGGR**FVFSCEGLSK**TLPDGRPLFTDLSFSLYERSK**IGV**
LGPNGAGKSSLMKVIAGLDDDFDGRAHVHDGVKVGYLPQEPELDPTKDVRGNVLAGVQDKLDILEEYNEVCRKLEGE
KEEDDDDDDSEDEDEEELLERKAELEAQVEQLGIKDLSWRIDRAMHALRCPEPTKQVHFLSGGERRRVALCRLLISE
PDLLLLDEPTNHLDAESVAWLERFLSEYKGTVMAVTHDRYFLDNVAGWILEIDRGDCFVYEGNYSTWLTEHQKRIDL
EQKKDVALSKQIDQELKWIQQTPKARQSKNKARVKAYEQLLEQARVKPFQPGTILIPPGPRLGRVVAEAERLRKQIE
DRVLIDDFSFSLKPGAIVGVIGPNGAGK**TTLLNILSGEDKDFEGDLK**IGESVVPGYVTQHRQDLTEGNTIYEEISEG
DDYIEISPNNTIHTRQYVAAFRFWNQQQEKTVDVLSGGERNRVHLAKLLKRGCNLLLMDEPTNDLDVHVLRNLEEAI
EAFAGCAVVVTHDRWFLDRVCTDIIAFEGDGRVVYFEGSYGEYMDRREKLNGPTRHKFIKLK

>N589_uncharacterized_conserved_protein_(nucleoside/nucleotide_kinase_(NK)_superfamily;_thymidylate_kinase_domain)
MKSRKVALAGVLGWSSTGAPVRRGASVLLLRSFSTSSPAPLTAAGPKDEQIRRNRENK**SLQFVFIEGEAATGK**STIC
ELLKRQGYTVQFEGFVELCKENSRYSPQGSVVSIKWVSSMFTAMERLLHQFDEKQAEIKGGVVFFDRSFLTPYVYTR
GSLNNLYVCDAMKEIKEVFPCTTVLCK**TALATIEDR**LLQRYQQGDAQAKDIRKNLGELDHAYIQKVHNKYAELEQDG
WFDHVLDTSAPGPQVVENLLSTLRQAAIINSHDTHISSH

>N590_uncharacterized
MGSEGPSAVQKGAETLKRWTANSLYFVQGFAKKAAQASKEVAAEIKAKESTKASGADHMKRGADLFETKPASGAGTA
GTNWKSFAEGLGGAGAK**IPGYSLGLLK**NAITSVGGVILPGWSMRRIGWVAGAGFVVGFFVGKKFGGVHVHLTTPALP
PGYTLPPATQLAATSTAAAAPAATA

>N591_uncharacterized
MLWRRFRTLTPLISPCSPSFVESNKLRSNKRSAKDFSRPFSSFFGFIHSFIYVLFEVMVHQAHAAAGYWGAPEPEPE
QDGSLASLVVSVAGVGCGVLAKIVQSRSIIQSARGNAHYR**GLAAALVGDASLATQEAR**QLWREDGLLMFVKWPALMI
GTTVPFIFFSMGVQPLLDQALGVSEEDIEERSSSFHISRMLNSALVMLAIHPLSTLLACYIAGTLPSWKVALVDRVV
KRKDHFYSSWLASAAIGPVTHIADVVRANALHWHKATFFPDFMPPRGSDDHGDDDNIGSEGENEAEEDEEEEPSTAR
RMAYGASTALVLVLLCSARTLLN

>N592_tetratricopeptide_repeat_(TPR)_domain-containing_protein
MASTEEVDVGMEATAARLRGSSSKDVAAVRSLLKTLRNKNIRRPDLVLEFAPILLKSASQLGNEAWTVQEQLFVAAL
DSNDLPLANEVLARLTAKFPGSARVRRLTAMKLEAEGEFEEAISIYNSLLIDDPADTATMKRRVCIWKARKETRPRA
IEELNDYLKIFMADTTAWQELGDLYLDEQQYEFAAFCYEELILAEPLNHHYINRYAEILYTTGDYATARKYFAHSLE
LNRDSNNRALFGLALACKALASKKGGAKPK**DNGELATLAAGK**LRASYKAAAPEHLPVVDAVLAKLQ

>N593_protein_kinase_(possibly_serine/threonine)
MDVRSRTRREEGEEEVDRTTATATPPQFSYRRPPVARRGDQWWRSWWFVVGVAALVVALGWWLLVLKWEWYCFAWAS
WADPALHDARACRAVQPPCLERGRLLTAAYGFRSVYEGRLNISRLKEEGLESSPLLMLASSSGEDGSSKSASTRGQM
MKVVVKELKDPKSCGDVKAHFREVAIERRLRHPSIVPYVVSCSISPRYTLVSEYMEGGTLSVGITPNMASRTYLSIM
LDLAKGLEYLHYGVESGYTLIHDDLNPEQILLNANRTR**GYITDFNLASWIR**SGERWGVRRYWWPKGGSWKWFAPEKL
RQHYYWEAADIWSYGVLFYQTLVRANNQPDEWAATVIRPFYEERILNAAVDGWRPSKPHFRSDRVVLDKAWGLVEEC
WRYDPYARPNATRLVASLEDLLRQLPKSR

>N594_uncharacterized_highly_conserved_protein_(DUF3228_homology)
MRRAVRLNAFAFRQFDDPAFSGTKLMGFDKQAFEDHINQLFNMGSATLVDGYAPFCKHLFVPNFTGAKVGAVTITDS
NKHLLRSGYVARRASELPVLTRWFEAKDVEVPTAK**YLDIILYSR**AQIEEEDAALPSDQKEAAKDYEWGIVSVKAQDE
DYETPMTPITAMRNSLGREEGGSGAPLDREAYLKAVAYWDTHAAVQ

>N595_Complex_I_assembly_factor_6_(C8orf38)
MKAMQLSIQRARIVPATTVPLFSSVEQHLLLHRKRKLHSTSAALHGGGKCEHKPTTSGAIPWTFTPHDEDATTKAPP
VRAEKPFSFTPPHPASTSEAGSADTAATAGQFERQGPAPAKQGGISSLDYCITQSKKLDYEHYLCGMYLPKEARAPY
SVLRAFNIETAIIKDIAKQAPLGLMRIQFWRDLVDKSFKGNPPEHPVAIQIAAMVPRYKWTRTWFTRILNKRAEDIE
GRPMPTLAALENFTEDTASSLLYLTLESLRIRNMDADHAASHIGK**AVGISFLLR**GTPYHLQQRQTYLPMDLLAKHGV
SEEAIYQGNLEHAQNLPEVVYEVASAAHAHLKHARELKSTVPKEAYSALYSSFIAEDYLNKLEKAKFNVFDPALRPT
PQGSLGLQAKLLYNHYVGHKY

>N596_Complex_I_(NADH_dehydrogenase)_B16.6_subunit_(NB6M_GRIM19)
MSQEKGRARYHQEPLFRPEGPEFEPIPLEKRKAFQFRRGPTGKALYAAYFGVLVAGHYVYATGAWEQRDLYAER**QNV**
WGSVTTYLQAEADRKYLQTRKRSTDAEEKLLFPKEVSEGKRQLNHEEAQYKTR**WVRPATDPFQQWHYVK**RTFDKAQE

>N597_N-terminal_homology_to_plant_B12D_(Zea_mays)_protein
MQRSPMTVSTFCKRFMPVEVYPLLVPLGFACGLATYMSYRTLAGAPDVHLFGKKPRYETGDHRADPHFAGIHSKASR
FDPHPELGQAEAAFHKTYSASASSPTYF

>N598_Gem1/MIRO_mitochondrial_rho_GTPase
MKDQVRIVLIGDDGAGKTSLIATLLADSFQEVVEQVVPELTIPPSVTNDRVSTHIIDTSSRFQHKMDQQLRTADVVC
LCYAADSENVAERITHWLRHIRHTRQECRAPQVPVILVGNKIDLRGEDLTNPKLQEDMEPIMEEFKEVETCIECSAK
SFLNVHEVFYFAQRAVLYPTAVLYDAGSRSLREECVAALKRIFKLCDKDR**DGILSDDELNAFQAR**CFGASLDPAELQ
GVKDVVRGNVENGLTEKGLTLTGFLFLHHLFIQKGRLETTWTVLRQFGYDDNLRVDVASLCHSLPAPPPSHVYELSQ
AGVAFFSSLHRAFDKGAGLALDDLDDLFSTAAPGLPALWTSGELDPATATQLNAAHISLRGWLALWSYTTVHDHKTT
LEYLAWLGFESDPQLALALKPRREASALLCLVVGSPALTDAFLGDFLGKRDHEPSHATSTSITTTTRSPSSRLVALG
SLPDISGTEKYVAMRKYGLEETEALRTRLHEASLVIVLYDSSDSRSLSNTAHAGAELNSLCRNRDTPILHLALHHTD
GATVPDLSENGIHLEAFASYSTLLIKAHQLARREQEWQWLPTWPQAALLGAVAVLVGGILLYRHFKGSKQA

>N599_universal_stress_protein_family_member
MTKYMVAVDGSEHSNKAYAIAAK**LLTNKDEVIFVTVGQK**GK**GAAAQDLLETWTK**KAEADGFTAKPLFLESADPRDAI
CNAVTEHGIDILVVGTRGLGTIKRMLLGSVSNYCVQHASCDVIVAK

>N600_Mas2_form_2_(similar_to_MPP_beta_subunit)
MKASLHNVRPVRLPRFVGLESANHLRRSLNFSGSALLLASAQRRWATTAATDVRPLKPKLERGPSMKSPLLDMPTPL
AHVSQLKTPSTRITTLRNGVRVATEETYGQATAMGVFIDAGSRNETFETNGTTHVLQRMGFKATTNRTSAEIVQK**LE**
SLGVNAISSSSREAMVYTAEVVRGDVEEVVEVLADSVTNPLLLEEDLQEQKIAVGRELEDMVHDPPSWLPEILHELA
YGPEGLGLSHLCPPSNLEHIGREQLHNFVKTYYVGPRVVVAAAGVEHDSFVKLCAKHFDSLPAAEGGKPLHVPSVYK
GGAHVEFMSPENEKRLQELQAESDKPPPSHVALVFEGSGLNDPDLYATCVLQSLLGGGSSFSSGGPGKGMYTRLYRR
VLNNYGFVDSASCFNSFYLDSGLFGIYSTVQHKDIGNMLHIMSVELVDLTGFSAPIGQEEFDRAKNQLRSGIFMNLE
QRAVLCDDIGRQVLSYGERKSAQELSDLIEKVTIEDVMRVARRILSTKPTLVVYTPEKYATLVPSHERLCAWFDAIN
DKLNGKESSESK

>N601_uncharacterized_conserved_protein_(N-terminal_F-box-like_domain)
MAAQVCKEWNRLCSDDIIWREIYRRKWRKVDALMSLKYQTRVRASWQELYIERARIEKAYFHNPNVPDELKNDELAQ
ANFLFTEAKEIRYAATTQVGDDQLRKLAYAIVLLAISGEKFESLSLVDPANNDVFWSWGSALSTQGMWTIQLLQSTP

GLALAQHADWLYAFGCENSERALDLAPRDQDGLRKHVLYADYCAELGTKPGGEGNAYLAKARVYYRRAIERAHAVQH
KRIVKTTDGVSTFEIDTFQDVATIARAHSGIAIACLSAAEK**LYESVVSSR**AEREHKANQRTNEGNADDEACDEEEKE
NGEAGDEQNEVAQMLELLLEGRERLMACVKIEPDQRDYLLSLCSVLTLLGEMTDDSDESEMYFSEGVTNFERALTIA
DDGNADAQNEYGILLSKRAQRILKQLRR**EGFDPAAVNHTPAAR**AEPESDTSSADSSAQPEGELPIETEEEKEAARRA
ARCAELVARANR**YFDAAEAK**FVELYETSVWFGTINLACLAALRGREEETRRWLQVCRDQHDLAPEHLDDHDFDAYRD
RAWFGELRAELAEQRLAQQREEEAQREAELRQQAEEMAAVADAVDGHAEA

>N602_Complex_IV_assembly_factor_Pet100
MDRFRSFVRRGLSLETFKFTLYLAIPAGITVALLYPGQVNRLVSHFPFVVYPPEDPTIREANDRFR**QQQLEALER**QS
REAEQKAKQQQ

>N603_uncharacterized_conserved_protein_(SET_domain-containing)
MMPGGDDPYGGGERWAPPEFPRLRWAMGIVGGLTLAAFVYHSLTAASRYRHQQAQKERETRFMGFLHHEEANKRLVN
GDLAGAVKHYSKAARFALRGEPGDDVAAAAAAAAGVDPAFIVPDFDAPGAEGWALSLLQRAAAHWSTGDANSCARDC
LAVLRVLPRQAASPVDESETISPPTPEASEASEAQPEAGAGVAAVMTEAGPPEQGGEEEKVSKEEEEKRALEKEARM
RKDRLERITARATELLGRALAASGQPLAALLALQRCTQARSKRREAALVQFQHLKESLQNALAAENGQSHWPVKVVV
GHEGGARGVLVATEEIAEGGEILVEEPFLAAPWSAQDLVQKVYCVHCLRRLAQPDVDGAPNKGIASAPVVAEARSGY
CSSVCEAAAWLLHDHRPSSRPAQPAGPSSDQTGAEERTSLYLLAKRVLACLAYGEREPMLQPLWTTFDAAIRSLPTS
EAEAKGVGHEHAELQAFVESLRNDVAQQSEQQAGPSTSETGWDASSLVSQLRGGALPVMEQQQQTEGCRGVGLYLLG
SHVGRSSPTAEPNAR**VVFSDADSTLR**LVALRPIPANEAVVISSSASSPALASSA

>N604_[Fe-Fe]-hydrogenase_maturation_protein_HydF
MTKRAGTVCGIPPKHAASWSRAYAGQPLLRTNIGIFGAMNSGKSTLMNLISQQETSIVDSKPGTTADTKVALMEMHD
LGPVKLFDTPGIDEEGLLGEKKRRKAFDVLKECNAAVVVVNPFNPASLKAARDVIQEASAKQKKGDDSAQMRVMVVF
NVFGQQMAEIRKATNTILDAAEKSLTPDRTSLQITSIALDLNSPEAMGRVVKFVTTNTKPHSSNVSLLPSALQLGPD
SVVFLNIPMDAETPSGRLLRPQALVQEELLRQYASTFCYRMDLKKARSPIEEERREEEQRFRSSVDALKSQNKLKLL
ITDSQAMDVVHKWTMEPGTAAPSDQGGQSSQETVPLTTFSVMMINYMSGGRLSAFVEGIKRFETLKHGDKVLICEAC
NHDRIQDDIGTVQIPAKLRQR**FGEGTIGVDHAFGR**EYQTKILNDYQLVIHCGGCMLDQQKMAARLSDIEGSGVPITN
YGLLLSYLAAKQGLSRVLRPWGL

>N605_Complex_IV_assembly_factor_Sco1
MRSCRAASARNLTSAGFRACRQGASATRLYASGIIRDGCCKDNSLISTATRSLKTSVWPARSPLVRTQALPRRRAEE
PSSTPGPAGGSNTRTSPPPPPEARPPQAPITWKSALLALGACGVVLAYFEFEKAKRKPRIEIAVAGTPSIGGPFTLV
DQDGHVVTNHTFRGRYMLVYFGFTFCPDICPAELAKVTKTLKILEEEEGITPGLVVPVFISVDPYRDTVGKIRSYLK
DFHPSFVGLTGTPQQVESMARSFRVYSSTSQHSEEDEDYLVDHSIFLYLMDK**EGSFLSHHGSQYDAHALAQR**IATDV
RSKGDCPPSLWAQLKER**GSNFVATFIH**

>N606_Complex_I_(NADH_dehydrogenase)_13-kDa_subunit_(NUMM/NDUFS6)
MRRAAPQLSRGMLPAYGRSSSSLLASRATLSSTASRAASSLKLK**IPFLGDTEIALK**DDVFRPGVPENPGNLYAPMPA
EELIHEIPPKVTHGSTAVCDGGGGALGHPR**IFINLDKPGPHDCGYCGLR**FIKEEEHH

>N607_mitochondrial_carrier_AcMC26
MVQSSLSSHIDR**NEHQRPIDESGWETTLR**VVASLGSMASGWAVHGLGVLGYQWSVTPRPIVGQWLPATTFSAYWNLR
KEAATHPALRYGAFSAAGLWAGAVKAISHMFLQEYVFAPLLHIATSDEELDESFEAYDPIAPIKQGDMYQRGGWTGP
VCAMASAAGAILLSLPFLKAKFLLRTQSRRPDGSFKYTGLFQSIGVIWREQRWGLITNNLSAFISFGILYDVVGFLT
DRYKLSTLIMKIKTREGVLHNLKHALALAIDDIIEAAIIVAFTMPVNVVLRRLEAQAGGVAPFSADGVVYAGVLDCV
QQIFVREGLNGFYKGAMPELLERLLPRVFVDAAVDLGLNSFFGVPATYDNTEEHSHAD

>N608_mitochondrial_seryl-tRNA_synthetase_(SerRS)
MKRLSKGFSGLARRTRSAGVVPLCPASWAGLSASRTARFFAGQAAASGADETPMASHHTPQQPEYLFRHLDLKWMKE
HADELATSIRARKIEGADIHRTVALHDRFVRLDFEIQQMRAQRNRVTDELKQLKKKMNNKSLKGGDGNDADVERLVA
QGKELREQLHAAEKEVKEVEAELYREAKRIPNVCHPAVPHGSEDQARVVCHGGPAKKQHAADFGFEPVDHVTLCQRL
DLANFEAGSR**VAGNNFVFFR**NEAALMELALVQWVMGKAAARGFTPVLTPDVVRPVTAEGCGFQPRGTGTQTYSIEGS
DLCLVATSELALAGYYQMCALPPESLPVRMVAFSHCFRAEAGGTGLRDRGLYRLHQFSKVELFALTAPEQSDDVLES
IVQLQQEIFTELGLHYRVLDMPTEELGAPAYRKYDIEAWMPGRGSYGEVSSASNCTDYQSRRLNICYPKDDPSGRRR
DFVHTVNGTGCAVPRTILAILENHQTADGTVKVPRPLVPFMHGIDTIRPKTNPAPAPQLQHNVGHFYFHPMQ

>N609_uncharacterized_conserved_protein
MQNAAGAGRRAFGPRWFAKLGLISFAAGGLLEFAMIKSGFYEAVVATSSAPDWQNSWQEVGAEVQRQLREKRERGDI
PEPTRVER**VLQQLEAR**YQQQLNQDQPPSAPSSSTSTSTQEQKESETIKWSSRRRY

>N610_Complex_I_(NADH_dehydrogenase)_subunit_B18_(NB8M/NDUFB7)
MAHHGEKPEQSLEDMEAELSQPREMLISEEEMDAERLPIGYR**DYCAHLLVPLNR**CRQECFYLPWKCTHERHVYEGCQ
YEEYKRRKKWMLIEKEKLKRAQEKQA

>N611_uncharacterized
MSLVMNPSGGGNDSSYGVGGTYYGGELVQSTGDAQRGGRNADQDSGDEFMTEMAKIRQNQAAESAPATGKYKQKLEE
ARRATVDEPDNGYKYPGYKARRRESLSADETPVVSAPADPPSGDVFSQVRTRRQEDLLKAARTRKKTKEKKKAFGDQ
IK**GVLAYLPFR**TSHLSGFDG

>N612_uncharacterized_conserved_protein
MDVRTAAGQLAANFFVATPARVLFERAARDRPFIRAFIKSRIADASRITGIRGESSQHSFFTPFTSILSVLTGGGED
ATNGLLHVAHASLWTISVPFIQSSIIESAK**DLLFGGYTLYGR**VREALNPDFRPSLYAEIMRPVTFAAKTVAYAASFP
FFLCAYGVRNNKPEHWNKIPASFLPSRKKAIPAMTLPLFVLIAHLNAHLLAAGGLRDLFFRLRVRLLPSTVTHDQAL
SPLAQQFLHHVEDLALCLAAGAITVPLEVLLCTMLATRAGLASSVSAIWKEKGLSGFFSGFGWYLLAQYLTTW

>N613_putative_DegP2_serine_endopeptidase
MLRRWQQTGELMRHTSTVQRCAHGFNAARCTRARQGVLTLARKRTSPFHTSSVVEARKASPALPPLVPDDVQEVPIE
EANWEESTNMLPLEPVIKVYSHVTSPNYVMPWQMKATSEK**VGSAFALSGR**RILTNAHVVADHTYIAVKKFSGTQKYP
AKVLSVAHDCDLALLTVTEDDFWTDITPLELGDVPHLQDTVAVVGYPTGGDTISVTRGVVSRIEPQRYAHASGHLLA
VQIDAAINPGNSGGPVLKDDKVVGVAFQSLVNAENMGFIIPVPIIKHFLKDIELHGKYTGFGAMGIQCQPMDNPQLR
HFHKMARDITGVLVNHVEAVSKAKGVLQKDDVLLSIDGNR**IANDGTVAFR**KRERIFFDYVTSMKQVGEYCRLEILRN
GEKQEVSVQLSPVQPLVPIHRFDQRPSFFIHGGLVFTPLTQPYLQEYGEDWYNSSPRKLCMKALTEYMEEPDQEVVI
LSAVLVHEINYGYQQMTNLQLLRFNDQKIKNLKQLAKLVAANKQPYLRFDFDEHVVIILEADAAKQAEEAILTRHRI
PSPHSPDLFDKKEETDVV

>N614_radical_SAM_domain-containing_protein
MLQRATARNASLGSLRGGGNALGLTSFLHQRCPRLLVQTPVRLYAPQPRRRKPLSDQKLLVKKEKKILRKLTKEEEK
RAADAFYSAHEAQEAAGATATSTSSSAESGRPRTKKKKRATGGDGDGAGEGATSAGSRFGRDQRLADSREALVERAR
QLARQSAARAGSGLAGARGQRRVEDLPQSNPWLLYANEMGDMIDFPGLELVGAVAGEVTPHRLDRGDCISAPEGSRL
LTLSQRAPVGYQRDDQEAEVLSADPKTDRANMTKRDRTWPPEAVAVSLPAPYIATHYSSFNSLPGGQTLPLFFYTPV
GWWKKGSDFLAARERMERAKRGEPDPEGEEAQSLEPDDSFDKAKESLKVMKDRGGFTSIRYMILPGLNDERKEVDEL
CRFIEETRIDMIQWRNIALDPEYYLTSIKYEPPASVVYAEKLGVKQLMETIRDKYPHVKHGYYNPCLDEKAHGYNLT
AASPMCLGCPSLQKDRKDLLARYKRIPFVPTADEIVEVAVEHLAKAPHAIIAFGQSCEGEPLLQADLLCEVIAKIRQ
RTRRGTIHVNTNGTVTEAVARLRESGLDSLRVDVNSVRREYFNRYTR**LNYEPVVER**LRQAARERMERAKRGEPEPDP
EGEEAQSLEPDDSFDKAKESLKVMKDRGGFTSIRYMILPGLNDERKEVDELCRFIEETRIDMIQWRNIALDPEYYLT
SIKYEPPASVVYAEKLGVKQLMETIRDKYPHVKHGYYNPCLDEKAHGYNLTTASP

>N615_mitochondrial_ribosomal_protein_L33
MAKGKKNQNMVVK**LVSMAGTGFFYTTTK**NPAATRKLFLQKYDPMLGSHTLFREERISRSKRK

>N616_saccharopine_dehydrogenase_(NAD+-dependent,_L-lysine-forming)_(Lys1)
MQRAAAAGATSRLVVPLPHHARVFPTTSGACRRMLAISASTPSSSSSSSSSSNASTTTTTPEKHHFWLRAEAKKNER
RSILLPEHVERLLQAGHHVTVERSRLRCAPDAEYQR**LLKEPLVEEGSWK**KAPRDAIILGLKELPEDDDPIKHKHVYF
AHVFKGQNGAEKVLKRYAKGGGK**LWDLEFLVDDK**GARVAAFSGAAGKVGMGLAFAVWAHQKLTGRPYSLPPLNTPYD
SFAHMAHQMRELLDQAKAKVGHDPSVIVVGSRGRSGKGAVSFSESVGIKPTEWGREQTAKGGPFPELLNYDILINAI
YLLPEVRLPAFITKGMIDHTPDRKLSVFSDVSCDVTNPHSVFPIYDHLTSFVHPTECVAEQPTPLEVIAIDHLPSLV
PRESSKEFGDLIVEHILQFDQTPVWSRALKLFDEKVQPFLPPSPRAAA

>N617_ERMES_compondent_maintenance_of_mitochondrial_morphology_1_(Mmm1)_homol
og
MELLSIVIGFLLGLVAAGAGVAYTLFVLLFRRRTDAPLPLAPAPSFAPQLASALLADAAVSEDLELFEKAEWLNLFA
GRIFAEVSTPAFQEHTWRLLTEKLNAVDKPNLIGPIVIEDFSFGTGVPRIEGVASFKTGKELELVLDVSYDGGALFA
VQTELWLNLPTLERLASLPVSMSVSLAHFRGRVSLTVPLESDPECTLAFAEEPQLDFRIGSLIGYDYQLRDVPK**ISN**

FIINKIRSVIREEAVLPKAFSFHLPLSGRPLDLKQVLRPPRELRRNTVEELKEAAVSASKAKLRERVKREKDSRKGR
DAEENAVVVLNTSRALVRT

>N619_ERMES_component_mitochondrial_distribution_and_morphology_10_(Mdm10)_ho
molog
MDFEEAPEELPNNPGDYEGVDGRSTGIIDFDAMPGFGFRWGSQISSRFERSIRLMILPPFPTIGFSYSSRPMPSMHQ
AMEEAMAREMEALHDEEDAGEGQAEGEAESAAEAKPLLRPLDVAVLSKAGAEVTERPDNDDNTTSSEDEEEEEEAE
QKESGGHFMLSAEATFDGMVQGMYMQRFNKNWSTRHMILTSMEPGRSMLMSSLSYSGGSFTSKLSWSSERDRACFSH
MQAITQRLSVGGEVGYAMKDKQPVGWSVGGRYVIRKEEGGKFAATHITATYNHLGRVKTTYTLPFSETVFASAR**YTV
NAFSFK**SNMAVGVESWPSATMPLMTKAKWDTDKGFGVSLGAHLGLAALMFSASYGKDGPMVGLHFEL

>N620_Oxa1_complex_homolog_Oxa1
MLARRGVNPRLVGLEGRAGSVSRYGIASSPAARHLAFPTRTFATTTRSSSSSSSSAPSLARRRLPSIISRGSVFSST
SSSSSISSSVSAAMLIRHERRCYATETVEEGATAAAEAATQTGAAVERGSDAMASFIAADPVTSLTPAALEVVERTT
SSFPPINWLVDAMTFVHYTVPLSWAATAVCFTLAFRTMILPAVALTMQNSAKMRAVQPELEKIKAKYGPNVGKDVNV
AMQYREEVRKMMAQSGVSMWKTMVPFLVQTPLFVSFFFTTRK**LAEEEPGLR**DASFLFFNDLSAADPYYIMPILTSLT
MLATIELGSDGVGGQSNPALKNFLRLFSVLAIPATSSLPIFTHIYWFSSNLFSLCQLGLFKVPFIKKALGLPDYQGV
SPMLGSSDPQPAKPEVTFQQKPRIIRTKNQK

>N621_ubiquinone_biosynthesis_protein_Coq9
MRRAVSGQMWRQGGASRSAYWRNAAKPLSVTDASAAVRIRGRGCVLRSSGRPFFARTTGLWRGLFTSAESHGEQYRQ
PEEEDAIFEDRDGGFSDAVR**TQVLDVALAQVGK**YGWTVEALSLAAAEQGLSNLAHGLFRRGPVELVEHFIAKCNARM
LEELSALDMEHMTLKEKIRAAIHARLRQYAPHIATWPQAIAILAQPSNASTSFSLMFNTINDIIYVAGDSTIDFDWY
TKRAVLAGVYTSTELFMLTDASDNFADTWAFLNRRLEDVVTLSKYKAECETLTSLALGYLNAVVQKQHAAPTGESPF
HHSPPPHGTPPPPPPAGPAGPFTPSPHDDSIPPRA

>N622_uncharacterized
MMRAGVRGGCLRGGLSASSTTTASSMLLAARSAVAAGAQREYAVHIFSPLPLPNAEKPVPPVVERDNKAIFNVFDVP
VFYTYQTTPRWRESPAMAHRRAERRRMTEVRKR**ATVYCNIELEK**ERERFRQEREQMERWKALRLKKRREEWREKMVV
REKVESQERAERAKLAAQNLQVHAEKSKLKEEAKREWLLCIKEELHKFDVADLPHLMSLKNYKYDTYESQEWYTKDN

>N623_uncharacterized
MRLPPFTNIVYVGLAGSVVGGFVGMYFAEQFMREARE**R**EDAK**LWAEIEQDR**KRAAAQRAAATNPTRSLPSEQQ

>N624_pentatricopetide_repeat_(PPR)_protein_AcPPR8
MAQRWMRCRSITATAPSVLNRTPWPACRQLDLVAAGTLISARPAARFIPLIPNRSFAYAKSKGQLKFRLEATAAPST
TPQSPLPSPPPSPPPPSPTLAWLTKVEGKLQRGGQKVIEGARQRTQRALRGELADAVRSGDLNEAEHTWSELRARTG
SRLDEASCHTLMNAYAQRGHLRRALSLYARMKEWRVRPSAHTFSILFNAYANLAQPSPSYLPKLKQLKDQEMPKYGV
VPSVEIYNVLLKAYLALDPEKSHQELKSVIAEMQEYRLKPDAITYTLWMATAARGIANNPKATVDVAAAFEVWDEMK
KNRVHPNLRGYNELLKICNEGSSEDRDIAFELYKEMLVEGVTPDHHTFDILLMTCWKQRKFELANELFDKAVQLNAD
NKGKLVELDTHLCNSALRVCTRNEGKRGPGRKSGSAEANQYLLDVISKITKVMFRKHLPYDEETYALLISAYTRAGA
KEKATSTFADMQSKGQVRISKK**TIGALLVTCR**ESNDVEEVKKVMDLAKDRRVRLTDSMVEEAKTIFIKNKRYQEWTR
VERDLAEWLPTATADYATKGKRRASAVEGGDEDDEDDINNDIEAASVSKHPKATTRRSSSAFGKPARPGPYAEGRSG
SRERAREEGPRRPEGGEESARQERRRRWREERSGGAGGGEKAQRRSRPGREPKDRVSAKNYYKDTRVKSPSATGRKS
FGGAPKPHAGRRKSPPSSLARNED

>N625_mitochondrial_carrier_AcMC27_(carnitine/acylcarnitine_transporter)
MSAEIEMPAVVAAATTSRPVSRAWQDLVSGIASGVSIVVAGHPLDTIKVRLQTQPMPKPGEAPQFKGVIDCAAKTIR
HEGVRGLFKGMVSPLMGVPPIYAVVFGVYGSTKRLMGETADTPLAINKIALAGAITGLATVAFAAPAEAIKAR**LQVQ
YSSAAGSAR**YSGPVDCAKQMYRAGGIRGVFKGTAITAYRDVPGNAIYFGVYEMVKRCFIPAGGSARDVGPLPMMLAG
GLAGTATWLTVYPLDIVKSRVQIDVTGKYAHGHRGLWQAYK**EIVAESGSVR**GLYRGITPALLRSFPANAACFLGYEM
SMRLLHFLSPS

>N626_putative_SDH_assembly_factor_1_(LYR_family_protein)
MSQRVRKHSGLQKQVLSLYRQFMMSAYKRPEGPGRDSLLGRVRDEFKEGAKMSR**FEVDAIER**RLGMARKQLK**MLNLP
GTETVQR**IGP

>N627_putative_Complex_I_(NADH_dehydrogenase)_20.9-kDa_subunit_(NUXM)
M**VVFTEEPK**NAVINPKPTYPSILWHMRLSDWGILVGLTGAGVAWGYMAGKGARKSVALCGGILGFLGGHSIAAQNSA
QRLLGRKPNGRPISSEH

>N628_Complex_V_(ATP_synthase)_assembly_factor_Atp11
MLLMRRCLRSPAVITNTAGGGGRAAPVRWFSSGAAPPPRELAHVVKLDSLHQETPERISQLWIDYHVKKEACVSAVA
PAATYALINRR**LAESPLFVLPLPR**ESGFVSVLLQAHAEQDTVMFTELEQYQRAADKSAVPSCLHLRYYTDLAATKDI
VLVRGEVDLARLTTTEAQTLVNQLQVYYLADAKYAAVKTFNHDPAQFDYNAIIDDLRGGVGTDTVR

>N629_AAA_family_ATPase-like_protein
**MLRAARSGAGTAAGTVVTRSSGCRAIPSSSSTTSVLGMRGGCGDSTPLAHLPLCSSSYSASSLATTSASSKLLSSIH
RRHSSSLSSFNRIHGRPSHHHHGGGGGILSIASSSSSLSSTSSSAPCQYVITNLESRRHLSPWAWRT**IIGGVFGMGY
VSFHFFVRSVRAQKTWIKMRLLKPKHIPPSAGPYPPFDRPNEAAVLRNYLNHPPAGPCIFVGPDGSGKSHILEQAIE
NRKMVVYLDLQREPVINGEEILTQFINKISYILPPTKFIARIFLKDESKMVLSAEEINKAFHCFEQVLSDQKRMGWP
NGIPVICINDFHFLGSSNDLNLRSKNIYEDKQILKFMDWCLFLTDNKLCHVVFVTSFSFCHLELDTHSAFRSRREVL
KFGYASVSTVRHHFKKVNQLLTQHFKEPLTESEIKRLATFVGGQVK**DLDTVITGLLR**GYTPSQVIDYMISDSLQIVS
DSLESCLRPVISADGEEQALEKDDAFEKYLRLWRMIELIAQNSIVSRSDLLRIVFQENVSELEAYESSGLVAYVHKK
PISMSLSADIDAEDTVSSLARLAPEFMVSAGTPRLNMAFQILRKDEKAGAQKRSLEIKLKKKKLEKEEKELNETKKQ
LLEERKELVNETQSLLRYHQEFQSLFGEEEFTQRKADLLSGTRDITEKLRNVVRDQEEVKEGLRQLREEVKQLKKRS
EKDVVGEYPALSP

>N630_AarF_domain-containing_protein_kinase_1
**MWRAKASSWLCAGGVRCVALTSGIAAGGSLSLLRGAPGAAGRLRSSAPLLGRPAHTAAAATAPLPKEGGARWGRVLA
VTATAA**VVGGWSWGHHRPNHDDDDDDGVQLPAYVDRATRFTRAAATAVVIALDYKWSLRGLEGEERQRRLHLVHERS
ADRLLRLFQQNKGIYVKAGQHISSLDYILPYEFVFAMTPLHNQAPTCPWEDTVRVFREEFDSHPDIMFAEFEREPVA
AASLAQVHRARTHDGREVAVKVQFPQLRERCEGDVSTIAFLVDAMRKIFPDFDFQWLVGEFRLNLPLELDFAHEAKN
AEKTARLFREFPDVTIPRIHWDKTTSRILTMDFIHGVKLDDKEGIARMGLSTHKVAELLTTVFSKQIFLDGFVHCDP
HPGNVLIRR**LRPHDPSSDDPELVLLDHGLYR**ELDDEFRINYCNLWVAIIHADEAKIKDYARILCGPDASYQLFACML
TARAWESVKELDRPITQEEKRHLMSDAADRFKEINDILATVPSQLLLLLKTNDLLRALNRDLGHPVNTYSITAKYCV
KAVLAHSLEMDPSWRHRVWVRWEAVAWAVQIKATELVLRLLSFFSHLFGRFYQ

>N631_mitochondrial_ribosomal_protein_L54/L37
MNRSMMMQRRAVSSAASRTILARPVVGHAGALPLLSQQRRGYAKPGGRGGAVERPKKEYKGDQYIDEMLVAYGLQVP
TWDDIPEWVWKAEVDLKKPK**ELTPLDGPLFWK**KINRERIKQFNEDRTWGVVKGKWKLGE

>N632_adenosine_deaminase
MRPARARLQTSFAPYNTSTSALSAGGSTTFQSSFPSARFTNSRASSAATTRLVAPPRFALCNKYANLDRIVRSYHAS
AAASHQPHQKMKRAVLNKHTPLSEDIIRKLPKAELHLHLDGSVRIGTIIELAEEQGVALPSTNYDELKDKIYVGEDC
TSLVDYLRAFDITLSVLQKPYAITRVMYEVCEDAVADGVRYLEVRFSPILHTKEGMSLSQVMEAICEGQLMAEHNLP
IFCRIIVCGMRQLDPKDTENLAEIAWRYKDKGVAGFDLAGPEYGFRSKTHKPAFDIAQRNFINVTLHAGEAAGPESI
QDSVRWCGAHRIGHGVTLRQNPHLMHYIIDRRIPLECCITSNIQTRAIKTLEDHPIRQYFDAGAIVVPCTDNKTMSN
CTLTGEYALFQKTHKFNVEEMLRLIDYGFSAAFMQATHKRRLRGEVLHSCLQILHDEGYDLDDIIGTSHYWHSIGVD
LSHFAKSPAVRKQHGYWSGRVNPPITLDIVRALPKADLNCRIDGSVSIPLLWQELQAAKIDMKQRFGLPCSSLEDLR
RIVLSPTHDEASWTRVKRIFNSVLQHPDQIKRATDDILRAAADENVRYIELVVRPRAHTHAEMTIAQVIDHMKEAAD
ATVASLAAEGKPLQYGLVVYSSLAKDDPIDFLQAAQLTVQSQSKGVCGFGVLGTRDLQASEYEFFRGTFDYLKRNNA
NVNISAGRTDPSNVVKAIHEGGACRVSGAYQVHRSPDLMNYCANHSIPIELGLADR**FSIYVSDVR**TFAEVNVNDMVS
TYNSDVRTFAGNPIRLFLDNLLPVAICSFKSSVSSKNRSEVLFDLVNECNLSIAELMKLLSCSFENNFQPYDVRQKM
VAKAWEEASTYLSAHGYSSLYRQHYFPSLGKGMDSFSDA

>N633_cardiolipin_synthase
**MRRCCSIAASRPQVLRLGTSARTLTASSSSPGGLPAKQFRTGARGVHLPWQQSGAVRSGVIRLRSSVPLGGALAGRA
WQPPATVLIRVY**STPKSAAEDDDKASQGNVNPPTTATANVEATTSSTR**VLTIPNILTVSR**MIASPFIGYWIIQEEFA
LAMGWFLAASATDAVDGFIAKRFNQKSVVGSFLDPLADKLLMTIMVTTMAYK**ALLPLPLVGLILLR**DVSLLAGGVIR
RYRSLPRPVTVSRFFSVSKVESIEIKPTVISKVNTVLQVGLVFLVLSAKGLDFTLDPMFMSGLEWSVAGTTLFSGLD
YLNSNAMQRIKTFQDRLTKRDP

>N634_mitochondrial_ribosomal_protein_L22

MRRGTAAMSGCGRRLLVASSSTSSSFTAGALQRTILSTHRYLPAIQSFGAARSYASPSLLGDDIFTKAYEQVKQKEE
ETGERVRITEAKADSKNLPASMKRIDHLLRQIRRLSYKEAITQLKFSQKRVAPKVIATIEKARQKAELKFGLDPER**L**
ILDEIYATKGQYGNPQIYYHAKARIGIMRRKRVHLTVKLKEVPFKEGEKQLGKFVRGVNSEQRKVWEEKRDRVAKEM
GVPRLVVTTKQVELWDLYKEKILNKKPATATDPAAADATNAADKELSA

>N635_protoporphyrinogen_oxidase
MAEKVHRVAVVGGGISGLAACRFVQKRLQDSCSSGSKR**IILIEQGQR**LGGWLHSLRTPEGFVFEAGPSSIRTVGSKG
RATLRLVDELGLRQHVVPCSSLAIKNRYLYTNGSLLRLPNHPLKVLGSPLMRSAVFAFLREWTVPRSQQPDESIHSF
FTRRFSPVVADTLTDALSIGIFGGRSQSLSIKSCFPFLHEYEQKYGSIGLGMLREMLASRSGQEKNEKNQNTKTTKN
EAAAEEEEETDEGYLSPAVQEMQKMQVYSFREGVETLSRALEQKIREDEHTDILLNTAVERMDQERDGTMSLSLGHG
MTVRAEKVISALPSHALAHCLRHHPTLEQDMLKIPFASLALVHLAYTEPLLPAGVEGFGYLVPAMEKQPILGVQFNS
SAFPQQDPQPGCTRFTVMMRVEKGQENRTKDEWQAIALDSLQRHLRLPPAKTAALASPARVNVSVDLNAIPQYVVGH
AALVDSIRGALQRDFPSLHLVGNSWGGVGVNDCVENAWRTVHRLQL

>N636_lipoate-protein_ligase_A
MKRATAAWRSGTRLHLRGGRVAAYGSTTNRAYATDTSKVKVYVTSTTDPLFNIATEEWIFREGDPTK**QTLYLWR**NAP
TVVIGRHQNPFKECHLSVMERENVVLARRYSGGGAVYQDLGNTNFTFLSNVGAFDKVRNSGILINALKKRFNITASA
SGRNDILVDGKKISGSAYKISNGRALHHGTMLINVDFASLGKILNPDKAKLKSKGVDSVQARVQNLKDLNPEVDHES
MCDALVEEFYKTYEDRCEIEYLKHEMLASIPSLANTYATLQDWKWRFGETPAFEHSLEKRFTWGNIDLLINAKNGRI
TEVKIFSDSLYPQMIDDLTLALHGRTYDKQGVTEAIEATQSKMKEVDNVEANLEELKEWLVHAM

>N637_iron-sulfur_cluster_assembly_protein_Isd11_form_1
MSSRLRLVAPPTRRQVLGLYKEMVVASRSFK**HSDPQWFLAR**VRQEFYKTNREPAERIKWFEKGQQLIRNKECIL

>N638_uncharacterized_conserved_protein
MSSRPRGAPKPSGNRAMGIVLGGIVAVSFSYPFWLLLSNSSGSDSGRIDPTKGKLAGQAKIRGAFLNTGSK**DVGPDP**
NATTYLPTKEKNER

>N639_disulfide_relay_homolog_Erv1
MEQFKKIKEKLQKEGDQLVVGGADEEDCGACKPRAGGLYGSDMRRRFRSQQQAREQRSAQEQDGGTTSTDATATSAG
TEEDASNENTTECYDSEGYWEKQDAPDVIELGQAGWTLLHSMAAYYPPKPSRQHQERMR**SFLSLFPHLYPCK**VCAKD
FEETMDEIPPELESHDALSDWMCRAHNRVNQQLGKPLFPCERVRERWGPSNAFHTKEQDDS

>N640_dienelactone_hydrolase/peroxiredoxin_(PRX)_family_protein,_typical_2-
Cys_PRX_subfamily
MADHAHSAEELAPYTEEENKIYFIRESDWTQCPAYLFGQEDYLGIGVVVIQEWWGVNHQIIDVAKHVADKGFRTLVP
DLYRGKCAIDNENAGHLMDGLNWPAAVQDIKGAVQYLKATGSRKVAVIGFCMGGALSLASAALVPEIDAAVPYYGIP
PAQLADVSTIRVPILGHFAELDTYAGFSDPQAARDLTEKLKSANVDSQIVMHKGVGHGFVNPIHGAPQSVIDESWEQ
TFAFIRKK**LNVASVGFPAPHFEEEAVVGQDFK**TLKLSDYKGKYLVLFFYPLDFTFVCPTELLAFSDRIKEFQALNTE
VVGASVDSKYAHLAWLNTPRKAGGLGGALNYPLIADLRQKMARDYDVLIEGEGHTLRGLFIINPQGVVVQITKNDSP
VGRNVDEVLRLVQAFQYVDEHGEVCPVNWTPGAATMKPDPKASLSYFEKVN

>N641_uncharacterized
MFAPSRRLALSRPSSVASTSFGRFPTFASSSTSSFTLPALGTRTYVTNVKRIARREKRRLAEKALVKAEAEK**QATEA**
AVAATKQQVDAVMEEAANLAHADSSAQQQAGKGNLDRDIVKEMDGNVRMKPRHSPLSAA

>N642_fumarylacetoacetate_hydrolase
MQQRGLASFHQWCRKVVCVGRNYAEHAKELGNAVPQTPVLFLKPPSSLVTHGSPVELPAAAADDSHHEVELGLVIGK
RGRDIPEAAAMDHIGGYALAIDMTARGLQNEAKNKGLPWSVAK**GYDTFCPVSR**FIAKEELPHPEDTTLWLKVDDELR
QNGSTKDMIFSIPFLVSHISSIMTLEEGDLILTGTPSGVGPVKPGQRLTAGIEGISLDVSFPVLLRSRPSA

>N644_MORN_repeat-containing_protein_(possible_2-isopropylmalate_synthase)
MMRRSSSTLPFRQLLRSNSPALRPATGVVDGSRRLLHNRGGQPAGKLISTSCTPRPVGVVAVIPHLALDDCHHLTHS
TSCVVQLRGGFRRALASQVPPEADERANKPKKVNIDVDEMFATPEDSGQHWLQMTINDDWERAPEGPDMTEPADLNL
AK**YLGTLDER**GLPTGRGKLFSQDNQEGISIYYFGEFKNGKFHGRGRSVNIEHIELTKEERNMLPKNVYQWTGKEKLL
QLGTVYEGNWEEGKMHGKGRLTSRDGSVYEGDFSMGQRTGLAKMISDEGYYFYTGEFEDGAYHGKGTLRSKAGDQFE

GEFERGMMRQGKGKMVLEEGFIYEGEIFDGAPSGYGKQYHPNKKEGYEGHFNDGEYQGRGKLLTPDGSFVEGTFDKG
MLDGPATHFDANGNATPMVFKRGVPQQA

>N645_iron-sulfur_cluster_assembly_co-chaperone_Jac1_(HscB)
MQRIRTSKMAATASSPSFSSLLPSSLPILSPAQMPPCCLMRAIGGSGAGRSAPCLMGSREIGHWAPLNRAQCYSALT
SKPSPLFSSSSILSSTSRRFIRVRTASEADTASSTQHQPPSIEEDQASNCADCGHSTQQHQHQHQHTTAPGCGSDKF
GSHPKCWSCDNFVKGIPLFCTCCQKVQPPSNYDFFELMGMPKRFAVDAGKLEKHYWALQRKLHPDNFHTATTRERNY
SEGVSSIINEAYHTLKHPNRRAKYLMQLKGVPLDETTGTITDPDLLMEVMEIR**MRLEDADDAELR**ALERENKQRLDR
CYEEVGHALDASDMDKCRDVAVRLQYFVKIEEEIKRRKKVE

>N646_D-amino_acid_dehydrogenase_small_subunit
MKAWSRGVAGARAKGATNSTTRPACWHHDATASALGLPLCRSSGVASPLPLHYSRPSTTPSSAVPRGRQSLPIPTGR
RAFHHHTHHEGAAAKGPTVTKLVAGAGLLGALIGGTAAVALYAGDGGVLAAQQQLQTRPIASAAVASGPHKQPSPRP
DGGGTGQVGLASAVAAEKEDRSGVVVEGRGRGGKERVAVLGAGVVGLATAYYLARTGRYEVVVIERQPGPAMETSFA
NGGQNCVSDFMPMTDGTLPRRVLAQQLLRLRFNMLSALGRGDQENRPPPYYLVRLKALFDPLVAWSLWLLLRRSSDE
AAVNSGRGILHLALSSQQCLQQIREEEQLQYDRGSPAGILHLYRSDDQFEEAKREVEMLQRTFGTKVKPCAVWDADQ
CRTREPALRDSRASIVGGIWWEDNESGDCNMFTARLADTCRSKYGVTFLFDTGVSLLMRDPANPHRVRALLTDEGRE
VEVDRVVVCLGSYTPLLLRR**SLDVWLPIFPVK**GYSLTLRPDDAPLTSGGGHDAAPSLNIADIESKTYIARFGGILGD
RLRVVGMGELCGYDQNVDPAK**EGVTNLTAVVGQLFPR**LPSSASREASLWACLRPMTPDSLPIIGPVGRMENVYVNSG
HGSMGWTLACGSGKLTAALVAGTPTDLDPTPYAQARFS

>N647_lipid-binding_START_domain-
containing_protein/phosphatidylcholine_transfer_protein,_putative
MEEVETFEPCSDEHVKEILALDASAHSDWSAISAVTDEEGNTIEVFRQRMDTGLDKLKALVTTVHITADVVHEVLYN
IETRVNWDHGGKDMQVVEKIDDELDVIYFWAKAPPTFTNREFLQSRLTRTLDDGTRVIIYRSVKHDKFPEKPKKFVR
AYTKLSGYVIKPNPSGEGCR**VTFLSQNDIK**ASIPSWVVNLLASFFMKKWLNTLRDACNNQLKENAKAKE

>N648_SPFH_domain/Band_7_domain-containing_protein
MKRITTTPVSRTLTPRLARSAWPQASTLLRSGTASRPLTTTTGAGLRSAMTAGAARRSVPLASGQRLARRAFSTSTS
SPEREALQMVLDSMPKGSKRFWRALAGLGATAVVLATCQPWCVVPAGHVGILDFFGDVSDQSLSPGFHLKNPLAKCV
VFSTQTQRVETTASVPSREGLTVQLEVSALYRLDPLKVQHIYKTVGRNYADVVLLPHFKSIIRELTSAHEAKGLYTA
QVRTEISTFLTKQLNDVLRERGIIIDETPINGITMPQRLVHAIEEKLRAEQESERMSWVLQREEAEAKRKVIEAKGI
ADFQK**IVTQGISEQLLR**WKGIEATEKLATSSNAKMVVIGKSDGLPLVLAP

>N649_uncharacterized_conserved_protein
MATSMETVSSFPSKWAWIFGGAAVALAAGGIAFLLSRQRPNKHIQTLVTPDRRLTDNFKAKLAEIFAAQLDLDGDGA
LNDAELDR**LVFLTEGQRITPEMAEFIR**SHFETNDEGWLTLSGFVASYEWILQHLTDDSAAEQAFAKDLQAYGYTYAR
FKQN

>N650_UPF0041_domain-containing_protein_2_(putative_pyruvate_transporter)
MASNQVMSPARRKWTQFVGTVGALANWGIPLAAISNIYNQQDPKKIDPRMTSALVFYSFLFMRWSLAITPANYPLLV
CHASNEVVQLVQLGR**WANATWGGEK**KDEVKAE

>N651_AMP-dependent_synthetase/ligase-like_protein
MRGRMATSAASSCRRARARQWQAPGGTIPYGPIRGFHAGRACLAPYQKENPDALANLLPKAHEDHVPAKAEPDHLPL
PIHPPARPHAITLISHVKGDRSIPLISKPIGAFFDEQVDLYGDKEALRVVHQDIRWSWNDLQRQVDAFSQGLLDLGF
EKGDRLGIWLPNTAEWVVAEFATAK**TGIILVNVNPAYR**VYELEHSLNLVGCKGLIVTDKLKSSNYFELLHELLPELE
HSAAGELNSTKVPTLKHLIQITDQHVKGMRRYVDVLSEKASSPDTRQNLKSLAQAQHVDDAINIQFTSGTTGLPK**GA**
TLTHLNILNNGFFAGERMGLTPDDTLCVPVPLYHCFGLVLGNLAAFTHGAKVVYPSPSYDPLKVLEAVQEEKCTGLH
GVPTMFISELEHPRFKEFDLSSLRTGIMAGSPCPIEVMKRVVNEMHMKDVTITYGMTETSPGSFQTEGNSPLEKRVE
TVGRVHPHTECKIVDTEGRTVPVGHVGELCTKGYLVMKGYWNNPKKTEESIDAGGWMHTGDLAVFDEDGFCKIVGRS
KDVIIRGGENVYPREIEEFLYTHPAIEDVQVIGVPNRKYGEKVCAWIKKKDNTKARAVTAEDIHAFCKDKIAHYKIP
EYVVFKEEFPMTVTGKYMKHKMREQTIAELHLEKEVVATA

>N652_mitochondrial_tricarboxylate_carrier_protein_(sideroflexin)
MEGTTTTPSPAKSLRLDLTKPRYDQSTFYGRWRHFLDVTDPR**TLLVSEDELSR**ALTMIQDYRSGRRDFMEEDLWRAK
KIKDAIVHGDTGEKIFAPFRLSAFVPMNIVICAAMLMPNPSMASQLFWQWFNQSYNVGVNHANRNASNQMSNSQIML

AYGGAVAVSCSLAAGLSQLVKKAPSLSPALRATLSRFVPFTAVATAGVVNVFLMRKNEMTEGIAVQDKDGNVVGKSQ
RAGLFALTQTSISRCLTTAMVMAVPPIIMAGAEKTLLKRYPKLHWPVNLGVITGMLFAALPIAIAVFPQNCSVSAKL
LEPQFHNLKDAKGNPIDTLSYNKGL

>N653_thioredoxin_(TRX)-like/glutathione_S-transferase_(GST_C)_family_protein
MRAVRRTWPTASSTCVASGRVRGTPTALLRTGQKRWLASTPPRGGSSPSMSPPVRRFLIMGSIVVAVGAANAWYRSS
KKADAPSEASKPAAAITPSEPQR**ALPFTAADIR**FLPENKNDLNIVLYQYSYQPSSAQVRSYLDLRKLKYKAVEVNPL
TKNHLPCPPDQRKAKQIPLVHINNREISVAVHTILFLELYLNRNNPFQPSREESARVADLMYHIDQNLMQLVQADRY
ATLRSASRTLRPLRQASNLSVWERVSAPPMAALSLWWQWRHARRLLRGVYGDDLRLALVRELDAYCDLLGDR**EFFNG**
AEPGLVDVHLFGVLRSVADEATGHYALAHAHSRLPAWYQRMQRLTAHDDDQPTTTTTTTKS

>N654_pentatricopetide_repeat_(PPR)_protein_AcPPR9
MRSCQMRRAAVRQLPSGSPFPSTPPTTTATRAIRPPAASAGCPTTQLSTTTSTRLPLSSRQRSSNVVMCVTTRPPQR
FGALGAVRWSSHSTTTDESKVKRRAILASGLPFARYAEELTALEQLPSVPANSLSTIISEYAAAGKHEMILARLRPL
VPRLRGGAGAFGLIIKALQDVRGSVE**VAFAVMHQAATRPARSK**TDKATAPDARAYHCLIGVCARQGDYTDALRVGQL
MDDNRVAFTSGTYDCLINACARSLTDKLDSALVGVDSVAGANNVDTGARRHPGLDAAFALLDDMRQQRGLEPDRRIY
CSLMRVCLSYGDVARMRRTFDDMRQRAGIAPDIYAFNFLMQGCAVERDLGAAMRVLADMKLARVAPVTITYNMILNL
CAETAAAAASESADSVDSAGTQSVDSLAAAEQVLARMEQSRLAPPDQVTFNTLLKACANA**AASRSAAGAAAVGGFVE**
ALDKATAYVAAMKARDIDPDVYTYNTLLQVCSHCPRPWKRTTVDDADTGDDAAAAEHGQAAAAARVDKVVEEVMREM
NERGVRPDGATVTLLISHFGAREDPARAFAVLSDMKRANIKPYLPSFTALITACRHYSDPAMAEQMALTALDELKTA
GLTPTAAVMNAFMAVTPQRAPKVLAMMRDHNIEPTESTWNQLIYSVAWRLKSESDKNESGNENETSWRGRELELLEE
AFASADRLQSSGSGPASVAYGYLLEACLYAAQRISARRESTTGTGVDADEDVSGGQAVLSADDRAELR**RVAQLADRC**
WRDMLAHQPTAITREACAVRMRLCLRSASRLDPADAAEARAGLQGAIEAYGEMRRRGFLPSPLTYGALARTCARHGA
FERVTQLVEDMRAQGVQPSTATLGATAQALTSSRSAGAAAALAALRDLVLPKSTAAPTST

>N655_acyltransferase_(possible_long-chain-alcohol_O-fatty-acyltransferase)
MDTSKLVVPLATGAIGLGSYYLVRPLANPWLRGVLASGSCAALTAYVCKDLPIGSVSTMMTTSLCWMASIR**LTHLML**
LPDEERQALTLRDYAAKFLWFVFPVLKNPTPREGTQWLGHVAYNAALGLGKMVLRDWLGRWLLYSLEQVGGGEVVRQ
SYLLTLQYTAMFAVLVMASIPANDFQRALVSLLTKDRYEIQAFNDWMILSGSPREFWGRRYNRLVGSLLHESVFTPL
RKRAHFSATAASFAAFAVSGCLHAHVATACFGEAGLSSLLFFLIQGLACAIDTRYPLQQYLPRPFAIGLTQAFLLAT
APLYLSLFVFAGPAWQRNNATSPLPPFLALPIPSFYPK

>N656_AFG1-family_ATPase
MRRLAWQQSSRLGSSAISRTPLQPRRALPALLSSAPSSLQSLSFRFSIAPGRHIRCYADRSAAPDSSSSAPASPTTP
PVQDGHHHEHGGPLRTYDRLVQEKKVNDDPSQRRALQHLQALHDQLVAEQKARHHLHHQQPASAASLHVPHHPPRQE
PEPERAPWWKLASWFGSVDSEAAAATSPSSDSNAVKGVYMYGDVGCGKTFLMDMFYEGAPVPKKRRVHFNAFMLEVH
SKIHKWREGKRRALEKKFEEDREGPDLPNFNLGVSASLGEEEWGDPIPPLARELAAQAPLLCFDEFQVTDVADAMIL
HRLFSLMFTHGLTVVVTSNRPPDDLYKGGLQRDRFLPFIDLIKRRCLVHDFGSGRDYRLRGNQNINIYQVEKPGVDV
ANNLETLFGELTHHVPAKSINISVGGRKLFVPRAERGVAFFSFSDLCKQALGAADYIAISQEFHTVIVSRIPKMEDR
HREEAKR**FITLIDELYNHK**VKMICSAAAEPRQLFAGGVEKREWFDESTGKSVGTIWQGEEERFMFNRTVSRLIEMQS
DDYLQSPHKKEV

>N657_globin-like_superfamily_member_(specific_hit_Trunc_globin)
MSASSSSTSSADEQTIYDAIGGSK**AMELAVDVFYTK**VLADQRVQSFFEGINMDRQRRMQVHFLTFALGGPYKYNGRA
MRLAHRRLVERQGLNDSHFDVILELLSGTLRELAVDERHIEQVVAKCESIRDDVLCREPAKPMEDEPKTMEVEEKEV
KWERVAGLVVVAAALLVYLLLASSQ

>N658_AAA_ATPase
MKQQELQVVLLRSLISVATAAVGSLAIGYLLRRILAPKTSDADVQSALKKLYEIERQRGREVKELTLTEHECELIKD
VVSPSEIDVDFNSIGSLEDIKKSLREVLLLPINRPELFEGRRSKLLQPPK**GILLYGPPGTGK**TMMAKAIAKEGKLAF
ININLATILNKWYGESEKIVRSIFTLAHKLQPCVVFFDEMDCFFHNGASASGSQHSYHMQVESVFMTLWDGIVTDSK
SRVIVIGATNRPYNLSAAILRRMPLQFLFDLPNKAQRAQILNVVLANEPLAPGFSIDALAQLTSGYSGSDLQELCKK
AAVAPLRHFLEEEERRQTATATTTTTGSDTHGLRPMHMQDFIEAMKEVAPTGKKAKQYHNFAQKRERGGAKPDGDDD
DNDEDEPSGASINMADVLQFWSAMMGGAAARGSSSSSSFTSASTAQEKKSSKPKIEEIDVDDEGVALLDEEEEGEYD
ERIEKWSKRFEGKDGARLLEQLCGLVDVDPSQPRPVVLKELAKHFLD

>N659_SAM-dependent_methyltransferase

MASRRQRTTIAAVARQTSASTSWESAGRWYDGIVGKEGHHFHQQLVIPGVLRLLRLDSSPK**VASSLLDLGCGQGVLG**
RQVPK**GVEYVGVDASK**FLVRKAQAYDTAPQHRYAVADVTRPYDVAPKSTGGGFSHAAFVLSLQNMRDQAAALRIAGE
RLGDQGRLVVVLNHPCFRVPRQSRWEVDPQNNAQYRRVDRYHSPLEVPIMVHPGVKKGGGATEPSSSAAAKSEGASP
TTYSYHYPLDHYFRWLSDAGMAVELIEEWYSDKTSEGSQAKRENRARTEFPLFLAISSFKLQQATQ

>N660_3-oxoacyl-(acyl_carrier_protein)_synthase_II
MSKRRVVVTGLGVVTPLATGVQATWGRLINAECGIRR**ITQFDVSDLPAK**IAGNVLRGKDEHGEFELDKWVDKRDQAH
TPAFIQFALSAARQALDDARWQPTTDAEKER**TGVAVGSGIGTLDEIVSTANTLQTSGYR**KVSPHFIPKILVNMAAGR
ISLAHGLRGPNHACITACATGANALGDASRFIQYGDADVMVAGGTEACIHPLALAGFSRMRALASKFNDEPEKASRP
FDEKRDGFVMGEGAGIVVLEEYEHAKQRGAKIYCELAGYGLSADAHHITAPSPIGDGAYRAMTSALRHAGLGVESVD
YINAHATSTPMGDEIENRAIKRLFGDHAYKLAVSSTKGAVGHLLGAAGAVESVFAILALHTNTAPPTINLTATGDSE
LDLNYVPLTAQQRTINVALNNSFGFGGTNACLAFTKLSC

>N661_pentatricopetide_repeat_(PPR)_protein_AcPPR10
MKGSATGRLRVAGAILRNRCAAAGATMPADRPAALLLSPLHPTVRGHAAFFPRSSSSLIFPSRHNILRCRAMATTAT
TTTHPAAEREAKAEGGGAKLPSTTASTR**IVPALELNLR**ALEDRLSRREPLDVKSVTAFFRSCGRQPDHYALAQRALA
LLGGVRWTTGTDLNLLMRAISLLPAHPDAVPAGYVLLEAAERKGVVPSVHAFTSLVNVCAKSNNIPEAFHAVERMWK
LKVVPDVNIFTSLIQLCTRCKDVNRAFEVLELMRLFDVRPDAFVYTSLINAGAKAGEPERALAVMEMMKTDGVKPSA
ITYNALISALASKENRDVEALVRLVDEMKSQGLTPSVVTYNTLILACRGPSAHRGGGHDDGDDREEDEAEEERRLER
ALGLLHDMKREGLTPDVITLHSLVRVAIHDDEGDAGNRTRRRRQKNAEDEDAGAGGGGDARRQRGEAAARQVDRALA
LIDRLTADFPGLTPNAHLYNGLIALCQLGGRADKATALYRRMREAGLQPTIDTFRSLLSSLDHHNDDQAEAQTAAAK
QAMELLEEMKRDGPAPTPAIYGKVIEVVVRGRGRGGWDEACGLVREMEARGLLVSAKVYNVLLGESVRAGDAQRAQE
VLREMRRKDVPGDYKTSLLRKEAERLH

>N662_enoyl-CoA_hydratase_(crotonase)
MTSRDFGFGVSVREAEGAEGVFILHLKANENRFNPDFMVAIDRALSHVEKHEGPTALVTVGEGKFYSNGLDLDYVGS
HTDQVESFMNQYMALLAHFLIAGVPTVAAVNGHCFAGGFLLALSHDYRIMREDRGFCCLNEVDIGLNLCPGMAAVAR
AKLERTIFRDSILNATRYTAPEGVK**AGFIDAAVPDAEVLAR**AVALAQKLAPRGANKTILSQLKQEMYIDAYDKLTTG
GLGLAAGRFGGSKKKANL

>N663_Zn-dependent_alcohol_dehydrogenase
MQAVVVDHWLKGPEEIKVSVAAVPEPGDGEVLVDVAYAGANFYDILMVQGKYQFRPTFPFIPGTEFSGVIGKLGSGV
SGWKVGQEVYGMTMLGAYAEKVVVPANKIRPVPKGMSLVDAAGFSMTYPTSYCALVYRANLLKGETLLVHAAAGGVG
VAAVQIGKALGARVIGTVGSAEKVEVAKKGGCDEVINYKDEDFVEKVKELTDGRGADVIYDPVGGEVFDKSTKVIAW
GGRLLVVGFAGGKIPSVQTNRVLLKNCSIVGVFWGSYEIHQPHKIEETFQALTEMYAKGHLKPVTCAVYPLVELPQA
LKHIGSRQSYGK**VIVQTSSNR**GTTAKL

>N664_uncharacterized
MKKGDAMEVEEEVSMVDDRATDLTNR**EAEDEGEER**SSPVLEGDGEALSHGGLVRHRVSGATETEDSVFDAEVDEISG
GQKRFIF

>N665_dual_specificity_protein_phosphatase_family_protein
MSEHVRPKHYRKEPLGWAPQFMALWISRVLFYPTLIYNVTLYYLWPTKFRNWWDRVDDSIILGALPFYWHVPLLYNQ
GVRGVVNTCDEYAGPVQTYARYGIEQLRVPIVDYFPPTLEDVKVALRFIRK**HTNNGDSVYVHCK**AGRGRSTTIVLCY
LIERYPGVKPVEAQTHLNKKRPQVSPNVWKRQVVFDFWDTVPQDEDASGTPVTIPEPGTSTSTSTAITSADGGADDN
KKDQ

>N666_ferrochelatase
MRRCATASGLRGLRSLPRHESGSFLLRHASTDTPKPPTAVVMMNLGGPETLSDVRPFLQRLFSDQEIVQMPFPQKFQ
ENVVGPWIAKRRSPRIEKQYAEIGGGSPIRKWTEAQARQMEKLLDQSSPATAPHKAYIAFRYASPLTHEALEQMKKD
GVKRAVAFTQYPQWSCTTTGASLNELWRQLK**KHDMENEFQWSVIDR**WNTHPLFIESIAQKIRTSLETKFTSATDREK
CIIVFSAHSLPHKVIDRGDAYPQEVGATVHKVMELLVDPAGLATSPEGRTQAPVRNRYLLSYQSQVGPVAWLGPQTV
DVVGKLGKRGEKNVLVVPIAFTSDHVETLFEIDKEISHVAK**ESGVTNFVR**SESLNDDPRFARALADIVSQHLNTNEL
HSEQYTLRCPACVNPDCRNIVSPVRTYDHPQL

>N667_transmembrane_protein_14C-like_protein

MSNKADSRRAAAVSEALPTFGVGAVVALMGIRGFTATKSIPSLLAGLGFGTLFGVGGYLIQDPATSASGRTIALATS
LTLAGVMGSRFARTRKLYPAGVLAAVGAGSSAWHGYSVFVR**VEHQVADALHSAK**ETGKHEVEKIERKLSGKD

>N668_Tiny_Tim_homolog_Tim9_form_1
MDIAPDAKKSEAAARNMVQLMNEMQMK**SVLGMFNSMSER**CFRLCMKNVDDDAPITTKEDSCIKNCTEKWQRYSQR**VQ
LIFAEENTR**ANTKADLMQDRPSSNLEGQD

>N669_uncharacterized_conserved_protein_(C-terminal_Smc_multi-domain)
**MRRATVVVTRSRTLGTSATSFSAGWGRLPRATSSTAAPLVPLRLQPSSAAQHVRRWSGGVLSSAAEVRVGQGSTTGR
ARSWVVACGVNIARGVVGVTAFASTPRS**PSSLVVRDGFVCTPDGKHAYLDQTKPVVVRRPTLWQRARYVVAKVMAAV
LSAIGALYPASWLFFVQYKEVDIFTDSWDWLNATPALIAGPLVLFVAAAYMWYRGCGTYFTVPELATFRDRALLSEY
SEIVDEHGLGQATKFVTPRELRIKLFKQARDKGILSCLKDASVVEWMNTGMLLPDEAQPVSQIQRSLQDAHRR**LKIE
TSALEQELAELTGK**AATKRNRLIADAELSYAACAEAKLVELYSRNYRDRIASARKERDNKIAR**LNNTANVSPTQR**NA
EKAEIERECDRIEEVEARLYQEQMRSNLPNLEKRARERDDAILSAREEFETHTQAVRIEKQIDLRLKRSQDTFAQQV
AKLQREWDNLADSTLEKNTARTPDSVPFVVPLVPFVAPTQ

>N670_uncharacterized
MSFFFSSSKHKKDADEASADRPATASSPRSTSSSAGSSR**GEGSEVTPVTSFRGGGGGAGAVGAVDGLGGGR**HTAGIA
TGGEENLIVQLLVRQHEENRRWQEALLQSLDSLTKALLVSSSVARQPEPGVESEREDERKSASREKKKRKPDSLHVV
IYSSSMTEHKQAQTLSEHLIAQVPGLDIELCTAYSARPADVAIVLKRSEARIDMPEDSFLRQASQSTRFGNAISVKA
LQSNDPATAPYSPKPSLVAEYSSGIGLKLENPTKAVVSLTFNFPLTSDKDPKPFLLRCKQNDENFGGLVDLLRKAPR

>N671_putative_Complex_I_(NADH_dehydrogenase)_B9_subunit_(NI9M/NDUFA3)
MSAARGVR**TIIRPVNK**GTYFGRFNQFWKEVTLEDPAISISFFLGGLGVAITFLSMPNVRGILVPFKSPKQSWFGEHY

>N672_Tiny_Tim_homolog_Tim10_form_1
MSNEQYMTREQMLASAQQELVAFQDMYNRMQHQCWKKCVLRLGESELSVSEGLCADRCVKKYMEVHNRVGK**VLQGLQ
QQQPQPQ**

>N673_mitochondrial_carrier_domain_protein
MTRTAAAGSGAGGADASPRPFSDSLMTTLDMISPAFSVLALPLLMAYSNGWNAWVRAVNRPPAPPSVSAWDRVVGSP
VKTWKEEAWRTSRNWTRFGLLMATDLLEICAVNYAGALLGVSVDTFHMTPAQLQLRDPESDISLTSALWGFTGAAVI
GFPLSILGWQLHTDTWRGWGSLLPTSALGRQHWLALPAKIVDVVVFNVLFVRLVEAVRGKVGIVPQPLGWLTSDAEN
NREDPALYDEEREERSTARVILDRARLFAISSAAGSACSLVLVGLQVPAIIVWNRMLAEPGR**FASVVACVR**HIWASE
GLAGFYRDLPLFALNLINIA

>N674_uncharacterized
MYSQRLLGSRSTAVPSLARTLPWAQTTGLRAGANGATPLAIFPSAQLEAQRETRRIPIMQKWRAGAIKTRDQVHKKA
ERTKRNQERCEYQRVKLHLK**QGTLYEYIEGK**TADEETKRKWFHQHFGHVQPKSRLAEEVTTGSSSEGASSPPPQQQS
FVDLDAESVRVSQ

>N675_amoebozoan-specific_protein_(restriction_endonuclease_Mrr-
cat_specific_hit)
MQARPQRSGVRPNSPPQPPRPGPSQAVINGAALEDRVARILKRLGKWNVRRNIIMRDRYGNTSEIDLSYGLFFRRYV
ECKNMPRIDLEHVAKFKEVLNLNKISPSR**GLFVTTGYYGPR**AITIGIKTINGSELRTWEERAMWVARLRRLVWAGCA
VGAGWLAYTTYGPMHRWKDVDRALARFETDARRQVDKWKRTAREYWPW

>N676_Complex_IV_assembly_factor_Surf1/Shy1
**MRQQQRCWQSSLPALGKLTALPARQSTQQCRSLFTAARLGGCPPKARSGPTGLRLAMPPRSSLGRAPLRSFANESRE
D**IAARQQDLKNFVGGGNKAAATKPASGEAGQVMEGGLAAWFWIFPAITVCLGTWQVYRWQEKKEMIRYRKERLLEPT
VDLPPHLTDETLRDFEFRHVEVSGKFDPVREFVVRPRTR**DGQNGGLLLTPFR**RSDDGTIVLVNRGWIPAALMNDIVQ
RRAMLDRVSGDTRLFGLIRPGEKGGMFSPENKLADEQWYWFEVDKMRQALGLDYTPALLDFVAASAPAAKDSYPVPQ
PIVTKLRDNHLNYIITWYSLTVALVATMLLKGRGRVRR

>N677_putative_serine/threonine_protein_kinase
MKTILGGSKKKGSSRTKASSSSSKDAKAKALIGKTIEVKNRRFKVKEILGEGGYSNVYRVVEEGSNNVFALKRMLVS
VDEMDLVKREVSLMKSIPPHRNLVHFECANVTTSAEQRKGEDLMEANIIMEYADVR**LFDVMEAR**HTEGKYFTEAELI

AIMVDVCEGVAVLHQHRPPIAHRDIKVENVLLGNDGAYKLCDFGSATSVTHHPKTAAERDAAEADIERNTTMVYRAP
EMLDLYAAKPIDEKADIWALGCMLYKMCFFEDAFSIGGRLAILQANFSFPLAPKYSPELNECIKYMLELNAEERPSI
TAVIRRLQRLKAGLGQDTPGKHRRSRTWGGSQDNLHIDDIPPAAANAEDKATSLHSSGASSNRERRKVPVVPRKTSS
DLDTSIAASPPSPATEHKSSLRDSRRPRRDSGHGRRELHFDGPTAGSGATNGGIDPNPNIRGSPVSDRAFAFPAPPS
HRKGSISASASPLLMPDTFPSPVLSPSSALKPGQLIPGGSPMMGMMSITPLGSGGTASLPHGLGGLSMVPLGSGGGS
PSGGLTLTALPSGGHQGGLTMTPLASGGLTMTALASGGNQGGLTLAQRNSGGLSMNPLTSGGGNQGHGGLTMAPLTS
GGKTGIPTPYSSAASNGYGGHSLSPLASGDGAMGGMSIKPLASGGGTTAEAEAAAAAAAAARCRSFLRSAAPRGRRRA
RARSSRSRP

>N678_pentatricopetide_repeat_(PPR)_protein_AcPPR11
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AAAAAPQHHQNRRRSSPPTQSDNRGRRPPNTTATGTSAASPQQRKQPSPSDVQQTVQRIKRSGSASPPLNLILRLSP
WVPGARADRPPRHATPPPEWETAVELVELMPRHGHTPDLFVFSGLLQVLGKARQPDKALHYFAEIERSGLTPDTHCF
SALIAALGTAGRVDDAERHFAQMTQLGVVPNAHCFSALIAALGTAGRVDDAERHFAQMAQLGVVPDTHCFNALISGF
AEAGRVDEAERWFAKITTVGRLKPDLISYNALIKANEVAARPERALK**LLQEMAHK**GVRPDVVSYNTVISSLAKARRG
RRHMDQAQEVFDQMVQQGVRPDATTFGALIHGHALVGDLETARRRLQEMSTEFGLSPNAEIHTGAGSGDLPVQRIRA
RADPLRAGRNQRR

>N679_Tiny_Tim_homolog_Tim9_form_2
MQRGRMSK**DDEASISQMMER**MQMEDIITHYNRLADTCFTQCVGDFKSNALLQNEEVCVRRCVEKFTQFSTRFQRVFV
DHQTAANKQRQ

>N680_uncharacterized_conserved_protein
MERTDEEVTTPTMSASTTTTTSGEAEIPDYWQRVDSPFSKSTIFAYAGGMLAFGAVCGAAAALVIGQRPPKPSAAKT
TTKAGTALCLTGALAVRWVVYTSMGVSTVEEFADKMRRWAPEKAKKVGLVPSRESAYWTQKKLEEEGGAGEEGRR**AI**
GVFEQWFGVKFDEGD

>N681_Complex_I_(NADH_dehydrogenase)_NUUM_subunit
MGGGPRFPFPKWVWSPAGGWWCENPPNAQRNLRIVLGLNFAIAGAVFFISAANERRLLSHPTIPVPSQR**W**SAWTKVD
DPDYKRKLAAYHKNKKPLWERILPDAMIQDEHGHH

>N682_TOM_complex_homolog_Tom7
M**TLGGLDLEVMSAK**AARLYDKAVVVARVGFHWGFIPFIIFLGVRSMRREQSWLSLLVPTPYLQA

>N683_mitochondrial_ribosomal_protein_L38
MLRRTSTTLQPACRLGSRSAAPSASNLSGVSRTALQSARTSRILQNSPVLASEGARRNISQIQIAKKNRAALRSAKP
KWSPPFPGWKPDPETEISKHKNIRKKAKLHKVFPDVLPEPFTPYFMLQVEYSPEVVVRKGHFLPPAKLQTTPRVSWP
SDPTKRWTLIMATPDDPDLVPDDVEIVKPGWVVPHEEGRGKEVLHWLVTNIPGNDISQGQVLCDYLPPMPKKHGGGH
RYVFLLFEQLDGETQFDAFPEGALKEFVQRKNWNTFKAQEKYGLRPKALAFFKATWDAEVSAQYSRLNLPEPEGPAP
VNLYRPRKWLDPSKW

>N684_citrate_synthase_form_2
MMMTTTAPSTATVAARRLQRLEAHLQISDVDLCPSDTAASGDKK**ETVTITDNR**TGK**TIEVPIKNGTIAALNLK**DLGL
R**AYDPGYLNTASATSR**ISYIDGDKGILR**YRGYPIEELAEK**STFLEVAYLLVKGDLPNKQQYEEWTSRIMNHTYIHQN
LISLLQTFRYDAHPMGMVVSSLAALSTFYPEANAALSGSGVFDDLQTRNKQIYRIVGK**LPTIAACAYR**HRMGRPYNE
PVNHLSYVENFLYMLDHLQEKDYRPHPKLVRALEVLFILHADHEMNCSTAAMRHITSSLADPFTAVAGAAGALFGPL
HGGANEAVLRMLESIGAKENVSKFLEEVKGRKKKLMGFGHRIYKNYDPRAAIIKKTAYEVFEVCGR**EPLIEVAIELE**
RQALADEYFVSRKLYPNVDFYSGLIYKAMGFPTDIFPVLFTIPRAVGWLAHWVELLDDPENKIVRPRQVYLGHDLRH
YPSMEERSAAKVTTSKDYISQNSRRRIVSLQAHKQAHHH

>N685_Macro_domain-containing_protein_[Appr-1"-p_(ADP-ribose-1"-
monophosphate)_processing_activity]
MRRATWGASNRAAAAGGGARMTHLVSNPVRLAVGLLLVQMTLLAGVAAFATSPVSTIAQATLPTGHTISVR**HGDITS**
EDSDVIVNAANRHLRHGGGVAGAISRKGGPAIQAESNDWVARHGALNDGNVAVTSAGNLPARYVVHAVGPVWHGGGD
QEETKLEKAVLNSLKKAEELQAR**SVALPAISSGIFGFPK**ERCAEIMVQTTTDFYHQQKPTRLKDVR**LTNFDAETVGI**
FKRKLTEKFPAARVHSEL