Supplemental File S3

Putative Nuclear Genome-Encoded, Contaminant Proteins Identified by Tandem Mass Spectrometry (MS/MS) of Purified *Acanthamoeba castellanii* Mitochondria

Key:

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

>C001_actin
MGDEVQALVIDNGSGMCK**AGFAGDDAPR**AVFPSIVGRPR**HTGVMVGMGQKDSYVGDEAQSKR**GILTLKYPIEH
GIVTNWDDMEK**IWHHTFYNELRVAPEEHPVLLTEAPLNPK**ANREKMTQIMFETFNTPAMYVAIQAVLSLYASG
R**TTGIVLDSGDGVTHTVPIYEGYALPHAILR**LDLAGRDLTDYLMKILTER**GYSFTTTAER**EIVRDIKEK**LCYV
ALDFEQEMHTAASSSALEKSYELPDGQVITIGNER**FRAPEALFQPSFLGMESAGIHETTYNSIMKCDVDIR**KD
LYGNVVLSGGTTMFPGIADR**MQKELTALAPSTMKIKIIAPPERKYSVWIGGSILASLSTFQQMWISK**EEYDES
GPSIVHR**KCF

>C002_similar_to_SSR_delta_subunit
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GEKGDLK**STALAFQALEYLGELQRQWVQDIFEK**VRTYLSK**HVQLADNAHFAFDEK**TLSTTSANYYGVVLGSYV
GFDFVSLPK**WAAFVAALQNQKEGGFYTGLDK**K**TTTLESTAHAISTLR**LLQQTK**GNTEQFVDVVSGEALANYVV
PIPR**DLR**SAAQAHLAVALTK**VFSRNFETR**VYYEFLR**ASGSADKK**VVQGTQLKPVISVK**TFDGMPHAGLDVEAT
ITHESTGEVVKAKLQIK**DGEHYTTNDFFDTTNHLGAMK**FQYTVRCYVVGVGEISFELDDVK**QIGYGVAVDSR**A
HLEVADKQFAQGETVAVGTEFTFGVALHNQTHKDLHSGDFNVVFSVLDSSLVAIHSESVDAKANAKPFRFAYT
LR**SSNLPSGDLVFKFEVVSATGVVHTTETVK**YQLSIPMIATQITFEGVAEGAPK**YKLGETARITIEPASFPDL
R**TVASYPAK**DVNGKPAAAQR**KFVMDVHSRKGALLRTVAGKAQTTESSSK**YVFEVPATATLDAIGLNVVSFR**YI
AASGR**SVELGSYDSR**LGELIEDASSLNYTVDANLQIVDIK**EQPQTTTFAYGQEVVFR**FRVKDALSGLYLHK**GE
NEQANVYLSLK**HADEAK**GKPFVSANVAAEEVVNAQGEK**EFVIEWVINPNAVQGAGVLSLSAQDADGNVLDLSD
ATTKKPVQLDVTVGGDIQVEHTSYSTSDASTYRETAFVVQFGLTCQNESLKNAQLRASVYR**DGQQVASFLPVA
TNDEGVYSVSWGGPHDATPSGVYTLK**FFREVDRKR**AVDAHEFQEK**RKKREEQLKQLEEGSETAHEETAQEELI
VENIVSPLFEISHSHVAPSTSKLPIRAEVILAFLLGGAFMAISYQKKHYLASK

>C003_aspartate_aminotransferase
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EFLARFAPGGAATPVYISDPTWGNHTNIFKDAHMPDVRKYRYYKEQTR**GLDFEGFIGDLK**AAPNGSVFILHTC
AHNPTGVDPTLEQWEAILDVIQAK**AHLPFFDTAYQGFATGDLDR**DAAPARMAIARGMELFASQSYAK**NLGLYA
ERIGALNIVCR**DAATADAVKSQLKTIIRPMYSNPPLHGARLVSKILSDKSLYNEWLVELKDMSDRIKRMR**HEL
YDAIK**KNGTPGTWEHIIDQIGMFSYTGLTKAQCEVMIKKHHVYMMTNGRISMAGLSSKNIPKMAAAIHDVVVN
VQ

>C004_urate_oxidase
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GMR**NLLVMK**TTGSEFVGFPK**DKYTTLKEATDRIFK**TTVTVEWDYVCQRKPVDYTAVYNRAKETILHVFATTYS
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AL

>C005_luminal-binding_protein

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GAYDEL

>C006_catalase
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TQKRNPQTNLRDANMFWDFLSLTPESLHQVTILFSDRGIPKDYRHMNGYSSHTFKLVNKEGKQYWVKFHFKTE
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>C007_nodal_modulator_2_protein
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>C008_fibrillin_1
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>C009_GAPDH

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VTQFGLSGKHFPAALVMAPHREKTFLLDEQTPITEEALKNFVDGVLDGTIAPSFKSDEAPASNDGPVTILVGN
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>C015_cytochrome_P450-like

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STSDITVAKDKLAVELTPR**FPLFGGWK**TEFIFGYDLPLSDFVFTDASDSSKLVLNTTFGKEIALDAVIDELTI
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>C022_calreticulin
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ILNYKGENHLIKREVRPETDIYTHLYTAVLFPNQTYEIRIDNEVK**QSGSLIEDWDLLAPK**QIPDPALSKPADW
VDEEYIDDPEAK**KPEDWDNTPK**QIADPEAKKPEDWDDELDGEWEAPMIANPDYQGEWQAPRVKNPAYKGPWVH
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>C023_hydroxysteroid_(17-beta)_dehydrogenase
MGDSLRFDGK**VVVVTGAGGGLGK**TYALLFASR**GASVVVNDLGTSHTGEGAGSK**AADLVVEEIKKAGGK**AAANY
DSVENGEAIIK**TAIDNFGR**VDIVINNAGILR**DVSFVKMKQADWDLIYKVHLHGAYSVTKAAWPYMRDQGFGRV
IMTSSAAGLYGNFGQANYSAMKLALVGFAKTLAAEGKSR**NIHVNTIAPVAGTR**MTATVMPPELIEALKPEFVS
PLVAFLCHESTPVTGGIFEVGAGWVSAVRWER**TQGNFYDVSK**GLTPEAIRDNWAKVEDWTNSTHPASAQDGLT
SIIAHINQLKARY

>C024_Sey1_homolog
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WFQDIGRWDAANYGLLKTVFELNLQLFGKHSSSAGSKTLLLFVIRDHVR**AVTPLEPLTQAVEADLEK**IWSGIS
KPPEFASSRVHDFFDIMYTSLSHK**ILDATTFAADVDTLK**ERFTNPEASDFIFKDAYAKDVPADGWPMYAER**IW
ETIQESK**DLDLPTQKEMLAMFRCDELMETAYR**SFNTAVEPVRQQLSNPEGSFVPAFGELVRQAEEEALSQYEA
PASR**YHTEVAARKGAALKEK**MLDASYALFLQQMR**RIYEAAIQHADTLAK**KLSPSTSDSKEGK**SPQVELSDLPT
RLHDLKDDAIAFFER**NAQASLVPGVSWKYDEERQALREHVEELVKRLREQYVDHLLKRRQQKLRSAIMNQLNK
QLDVASNEMWPRIADLHDHALEGAKAKLRVHLTR**LGLSEEELNTR**EEELRERAFAVIKDRLTEKSQHIQYQMQ
KKFDETFRLDPDGLPRRWSKADNIEETFKEARQQAYGVLDAYSIVRLRESDRHLSFFDSSLDPSSVDPSLVVI
SADQCNMTRDTFKRESDPAFIEAKREQEREIAVRIPPFFWAVMLILGFNEIMALLGNPLLLFLFVVLGLMAYA
AWLAGLLDVPLQIATELWSELTGRAK**SAAVQSVMGR**LTGSSGAPAANKDKKD

>C025_dolichyl-diphosphooligosaccharide-protein_glycotransferase
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AIVTYFFTKEIHSKSAGLVAAAMIAVVPGYISRSVAGSFDNEGIAIFALILTYYCWVKSVNTGSLFWAAMCSL
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FGLLQLYCFINWLRSFLPPDSFRIIFRTAILTGGALLALAVAVGTYTGYISPWTGRFYSLLDPTYAKDNIPII
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IAISTTLKTYSKFLKRSPSAKPKKGEAVYAGQKEIAWVVITGISILLIFYTFHCTWVTAEAYSSPSIVLAARG
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>C026_peroxisomal_membrane_protein_2
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>C027_Rab7a
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>C028_calcium-transporting_ATPase
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GQGFELHMLEELIGFVITAITIVVVAVPEGLPLAVTISLAYSMMKMLKDNNLVRHLDACETMGGATNICSDKT
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VEKLSGNYDQVRQTLKISQLYPFSSERKRMSILLEAEGNVHRLYTKGASEIVLQYCDKIVSPEGKVTPLSDEE
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IVLFFVLYRGESFFGVVSHSLEHTTIVFNTFVLCQVVNEINSRKIDHQLNVFSGILSNHVFLGILVFTLLFQY
VIVEFGGSFTATTHLTSDQWMKCAGVALLGFPVGVVIRLLSRPFVQTDPVTKQTVEVDPAIVKMMWQKVKRAS
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>C029_C-8_sterol_isomerase
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>C030_Rab8a
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GLADEYGIRFLETSAKTGAGVEDAFITLAKDIKKRLIDSTEKPIPPEGGGPTVQLNGNGTDPSKGAAKKNCCG

>C031_cyclophilin_protein
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KAMEKVGSQSGATAKKVTIADCGQL

>C032_alkyldihydroxyacetonephosphate_synthase
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>C033_NADH-cytochrome_b5_reductase
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VIKVYPQGKMSQYIDNMKVGELIDVKGPKGLFTYTPNMKRAFGMLAGGTGITPMLQVIQAILKNPADRTQVSL
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>C034_peptidyl_prolyl_cis-trans_isomerase
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>C035_protein_disulfide_isomerase
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>C037_histone_H2B
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>C038_Rab1a
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SYYRGAHGIIIAYDITDEASFSHVRGWFQEIERYAQDNVRKLLVGTKCDLESKRVVDKARGQQLADELNVPFV
ETSSKNSTNVEQAFLLMAKEIKNKQGPPPAASTQKKVDLSGPTTPVGGDNGGCC

>C039_TRAP_beta
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IPTATWDKIAPGQNVSHYFVVQPKAGVANTVVRALPGYVQYRETAKGPLQISISTGVGSLPILSSSEGEVRSG
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>C040_dolichyl-diphosphooligosaccharide--protein_glycosyltransferase
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LSKYGDYLYDNLVIFAPQVEEFGSLSIDSILNFIDDGHHVLIAGDSQVSEPVRELALECGVEFGDDNTFVIDH
LHYDAADEGDHTLVVLGEENVAKASIITGQVTGPIVFRGTGLALEAGNSLLHPILSAHTTSYVYAPNTVVKDD
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GVLRASNVRHHLVGETEAPRVYTVREEVEYAVDVEEWDGAKWVPYDQTIQVEFVMLDPYHRLNLQREQGSATH
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HREAK

>C041_short-chain_dehydrogenase/reductase
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>C042_F-actin-capping_protein_subunit_alpha
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GGSVVVTICISSARFNPNNFWNGRWRAVWTCKFSPSGGNVDISGVLKVNVHYYEDGNVQLNTETPVKISATGS
DARGLADAVVKAIDKAESNFHKSLETSYNTMGDTTFKALRRVLPITRTKIDWTKIQNYKSGGDAGGKAAASRG
VRN

>C043_sphingosine-phosphate_lyase
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>C044_Rab2
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>C045_protein_disulfide_isomerase
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LSESNFKSEIVESDTDALVEFYAPWCGHCKKLTPEYEKVAAAYKNEAGVKVAKVDCDANSALCQQYGVSGYPT
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>C046_FAD-linked_oxidase_domain_protein
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TVAGARTGLEAGAVPELGGVVIDVSRMDAVLKLHREDLMVTVQAGIRKSALAEWLKDKGFMFMVDPGSDATIG
GYASTGASGTLSIKYGTIRDNVISMKVVLPTGEVIDTRSRVIKSSVGYDLNHLFIGSEGTLGIITELTVRIRS
VPRAVKAGILLFDSVANASAAVVAFLHADLPSLARCELLNIEALAAVNAFFNKTYALTPTLFLEFHAPTLEEV
EEEAKVALSVAQSNGLKSHMFADEEKERDALWHARRSAYYASAKYRNDFGRHQMRLWVTDVCVPLSHLAQVIS
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>C047_Sec61_alpha_subunit
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AANALMIIIQLFISGIIVILLDELLQKGYGLGSGISLFIATNICENIVWK**ALSPTTINTGR**GTEFEGALIALV
HLLITRTDKVRALKEAFYRQNLPNVTNLLATVLVFMVVIYFQGFRVDLPVKYQRQR**SGPGTYPIK**LFYTSNIP
IILQTALVSNLYFMSQLLYRRYPGNVFVNLLGQWHESEGAQHMQSVPVGGLAYYVSPPSSVAEIFHDPFHAVF
YLTFVLTACALFSK**TWIDVSGSSAK**DVAKQLRDQQMIMKGHRDSSLVKELNRYIPTAAAFGGLCIGALSVLAD
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>C048_long-chain_acyl-CoA_synthetase
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PTGARVGFYAKNSAEWVVGAEACNAYSLVNVALYDTLGEENRVFIVQQAEVLVIITTPDLVKNVASLVKECPT
LKAIVVIGELNNEQQALATEAGLEVRTFADVEK**AGEAAPVDLR**LPKPDDLAILMYTSGTTSTPKGVLITHTNL
VSAVAGVLQAVMPISSDDVFLSYLPLAHILERASEAAMFSSGASVGFYQGDVRKLDDDIR**TLAPTLFVGVPK**V
YQRVMLGIQKKVALSGPIARFVFYTAFAIQQKAIESGFTIGLLNKIVFAKVQEGLGGRLRQALSGGAPISAEC
HQFIRICFGCPIMQGYGLTETCGGTAVTPYTMPNPYGRAGVPISSCEVKLVDAGNYKTASNPPRGEVCVSGPC
VTKGYYKMEEKTKEDFREEEDGRVWFHTGDVGQWNEDGSLSVIGRTKDIFK**LDGGEYIAPER**LETIFAGCKYV
GNIFIYGDSTK**SFIVAVVVPEPIAAR**HWATEQGLKYKDEDFTATSVPEDLCENAQFKKAIADDLAKVANTAKL
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>C049_squalene_synthetase
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YKVPDFPKNLSEADIYSYKKLVKVSR**SFAAVIAELPEDLR**RPIANFYLVLRGLDTVEDDMSIPLEKKMPELRS
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EYCHYVAGLVGIGLSQMFAASGLESEKFGQMDELANSMGLFLQKTNITR**DYLEDVTAVNPR**IFYPKDIWGKYA
KNIGDLKEPENKEQALQCLNEMVTNAMAHINDCLDYMMLLTHPNVFKFCGLPQAMAIATLARIYNNYDVFKRE
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>C050_cycloartenol-C-24-methyltransferase
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>C051_cyclopropane-fatty-acyl-phospholipid_synthase
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SIHLAKNLK**ASMTGITLSPVQR**DMAEK**IAAEEGVQASTSFHR**MDGENMTFDDQSFDFVWICEVLSHFSRKDKF
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SKTWDICAELILNPTLWKLAFTK**GGEALAFLR**AFQSMR**AGYGSGTFRYGIIIAEK**VATQTSTAKL

>C052_Rab11a
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LSFIETSALDSTNVELAFQK**ILTEIFHIVNGGK**QLETK**KDSQSVDGETEVVQVGGDPAPK**KAGACCG

>C053_polyubiquitin
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>C054_Sec61_beta

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>C055_Rieske_domain-containing_protein
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PYPNAWYKVCNSHDIPKGESR**DFELLGHFFAVYR**GEDGKVRILDAYCPHMGANLGVTGRVVGNEIACPFHGWQ
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IVQVGPSMVHLHFATPFGK**VMLIETVTPVQPLLQR**ITHQVFAEWTVPRFFAKFIMGNTIVQFERDVPIWNNKT
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>C056_coronin
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ATSSTDYTVKVWDVEKGAAKCHVDGHADIIQSIDWNYEGSLIATACKDKKIRIIDPR**TGQVVSEAAAHTGVK**G
SRAMFLGRTEKVFTVGFSRTSDRQYAIWDPSNMGTALAQENIDTGSGLLMPFFDPDSSIIFLAGKGDGNIR**YY**
ELTDNGSKIYFLSQYQSNVPARGMAYYPK**YGVDVGSCEISR**LIK**ATTTGIEPISFNVPRKEGLDVFQDDIYPP**
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>C057_sulfite_reductase_(NADPH)
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TASVVRYETLGKKRTGVTTTFLCDRFDVNQRCPVFINKNPEFR**LPGDGATDIIMIGPGTGIAPFR**AFIHERVA
SK**AAGTNLLYFGCR**HRATDFLYREELEKLDGEGKIKLRTAFSRDQERKVYVQHRIAEDKDAIWSMLEGGAHVY
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>C059_endoplasmin_Hsp90
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>C060_nicalin-like
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HRFSHGTMPIMNIFKNSGYYWGFGALCGYFVNHPYFTNPEPTQVYTALAFFVLFELGNLISHIQLRNLRPEGT
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LFPFLY

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>C064_conserved hypothetical protein

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QAYTIATSTKVDISGLEVPEK**FNDAYFKKGKAAKKEKTEDEFFATGAQQKKTIDAHRIADQKEFDAKVLEVVG
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>C068_Dap1
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AVAQPPVASIASRKRTPVEPRDFSPDELRKMNGTNGNPVYVAVLGVVYDVSSR**ASFYGPGGPYHIFAGR**DAAR
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>C069_related_to_UDP-glucose:glycoprotein glucosyltransferase
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FELQHILAEGQCIDVDKGSPAVGLQINLGNHQQSHITDTTVMANLGYFQLKANPGLWWLSLGKRFGDEQQEGV
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PYFLQLGDTYHAPHLRRYCLSALSAQYDHIDAVLRAAPGSAGGVEEQIESDELRAEVLGIVHERRRKRNALLA
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>C078_actin-related_protein
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GLYIAVQAVLALAASWTSKQVTEKTLTGTVIDSGDGVTHVIPVAEGYVIGSSIKHIPLAGR**DITNFVLQLLR**E
RNEKIPPAETLEVAKRIKETFSYVCPDIVKEFKKYDTEPDKWFK**TYEGIESVGK**KPYNVDVGYERFLGPEIFF
NPEIFSSDFLTPLPKVVDETIQSCPIDTRRGLYKNIVLSGGSTMFKDFGKRLQRDIKRAVDYRIKRSEELSQG
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>C079_Rab32a
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>C080_histidine_acid_phosphatase
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STRPHGREGVMDVNIVEGAAENMYPRSACARLNQLKKDARATPDYLKHREDRQPFQDKVEAALGRKVNSWDGL
NSTLQTIIRHR**LLLPDGVDQDIVDGVER**EAGYETAVKFSSPEICRLAIGR**FIGDVVDRVQTTVDGEDDVR**FAL
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>C081_cytochrome_P450
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GFAVPKGTSVWVPFYPLFTDAKLWEDPMAFKPER**FLDISSSDPK**YMPFSAGPRNCLGKAMAELELQIVLAGLL
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>C082_endoplasmic_oxidoreductin
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LVSGLHTSVSIHITEFYEQDEATGQWTRNETMFWDRVGNYPDRIRNLYFTYVFLLRAAYR**ASFFLENYDYNTG
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TDAMPGVHAEADTTKP

>C084_histone_H4
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>C085_indigoidine_synthase_A_family_protein
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>C086_histone_H2A
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>C087_Arp2/3
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TSVSWHPNNILIATGSTDFKARVFSAWVKGVDERPAPTPFGDKLPFGECLAEYESSGWVHEVAWSPSGNRLAF
VGHDSSVTFIDAPNTQQRLTLSTLPFRSVAFLSENTIAAAGHDCNPAIFNAAGSAWSFTKFVDEEKKAAAAGG
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>C088_3-hydroxyacyl-CoA_dehydrogenase

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PLVAFLCHESTPVTGGIFEVGAGWVSAVRWERTQGNFYDVSKGLTPEAIRDNWAKVEDWTNSTHPASAQDGLT
SIIAHINQLKAAAKAAGGNENVDPSQVVGFEFPVTKVQYTEKEVMLYALSIGAAKNPTDPAELKFAYENSDGF
SVLPTFGVTFPNFSNVLSIPGLKFNPMMLLHGEQYLEIRKPIPVNATLTNHGRVKHLYDKGKGALLVVEADTK
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QQAKL

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RISKGVIEIVNDVHLVKEGAKVTASQAALLQMLNIQPFEYALAVKTVYDDGSVYPVSLLDITDDDIINRFRKG
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>C091_PARN_nuclease_protein
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>C092_cytoplasmic_ribosomal_protein_L3
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REVARLKKYCTVVRVIAHTQVRKLNQRQKKAHIMEIQVNGGSIADKVDFAVSLLEKPVPVDNVFGDSELVDTI
GVTKGKGYEGVTTRWGVTRLPRKTHRGLRKVACIGAWHPAAVQWSVPRAGQNGYHHRTELNKKIYRIGKGVRQ
EGGKIVHNNASTEFDLTEKSITPMGGFPHYGEVNEDYLMIKGAVIGPKKRVITIRKALLRPTKRWQLEKIAPK
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AKKQ

>C094_F-actin-capping_protein_subunit_beta
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KGTWDSIHVVEVVDKGKNAHYKLTSTVMLFIETETKETGRVTLAGSLTRQDEKDFPVDKVNPHVANIGRMIED
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>C095_triose_phosphate_isomerase

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>C097_pyrophosphate-fructose_6-phosphate_1-
phosphotransferase_beta_[0.0795]
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EVSFGFDTACMIYSELIGNIATDANSSRKYYHFIRLMGRSASHITLECALQTRPNITLIGEEVAARKQTLSDL
TNELCHVIVERAKAGKNFGIVLLPEGLIEFVPEVHRLISELNELMAKGNSADVVGEKLTEESRAVFDFLPSAI
RHELLLDRDPHGNVQVSKIETEKLFIHLVTKELKRRKANGQFKGSFSAMGHFFGYEGRCGLPSNFDSNYCYAL
GRTAGALLDHGLTGYMASVSNLTAPPEQWKSGGLPLTALMNMERRKGKNVPVIRKALVDLDAAPYKELLRHRE
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>C098_TRAP_alpha_subunit
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TGRNYTNAAFNGTVDLVEPVVGWDAQSFFAVLAVLALLGVGGFFAYRSLSTWAKKQKSSKKVEYGTKVRQEVE
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>C100_ORMDL
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LFGLNSGPG

>C101_actin-related_protein_2/3_complex,_subunit_4
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>C103_Rab11d
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APPQPGCSC

>C104_Sar1

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>C105_Nop56
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>C106_strumpellin_family_protein
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LPATVVEMIIGRLRSDDIYSQMQCYPLPEHRSTALATQAAMLYVILYFAPQLLSSEQASMREIVDKHFADNWV
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>C107_cytoplasmic_ribosomal_protein_L15
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>C108_Rap1a
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>C109_peroxiredoxin_homolog
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IFYDMGHSNTRATLVEYHSIRIKKGAKNVTQPTMKVK**AVTYDTSLGGR**DFDYRLAEHLAGVAVTQMAAKGIES
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AAANTTVEEVGSMEVVGGSVRIPKVQAVLKQTLGLPELSKTLNGDEAAVLGAVFYAAHLSTSIKVPEHKIKDI
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KNVSFKKNVSNFTVELAYDDEAKLPEDAPRQLARFTVEDMNKLKKYNYTGKPKVTLAFRLTTSGLVELETAEA
EVVVIKYPEPEPSAKSTPAPTPEATEEDKAEAADAADEATGEEKEDSAANKEDEEAEKEEVAADDEEAEEESK
KKEKDEKKPKKEKKPKKTVHK**IALAVVTQK**LGIPERTYVEKSRARALLKQWEAKAVSKREKADAKNDLETYIY
DTKEKLWDDELEKVSTEEQRDEAREALGAAADWLEDEGIDVSVQEYKDKKAELVKLASAIFERKEELTKRPVQ
VAMLSYMLNHSRSSLVGITERLKVEVEERDEVLDLIEETEDWLKSKVKEQEGKEPHEEPAFKSEQVQAKASAI
EKTVRKLLKRKPRPTPTPATSSWPYTAADDDNKAAEETTETGEEASYRGQEEVVPPKEEAGEDIL

>C113_transmembrane_protein_TMP21
MMTRRTTFVLVVLVIGLVLGVHGIKFDISPNTERCLKEELSRDVLVLGNYSVEQQQPSLRLHFTIMDPSKGEI
FAKDADEAHFSFTTENGGEFLFCFNDITDQSRLAYGYSRRVALELKTGVDAKDYTELAGKENLSKLEVEMR**RI**
EDGVAEILNDLKYLRRREERMRDTNESTNSRVAWLSIFSVVTMVAVGAWQIYYLKRYFQQKKIL

>C114_Pex11
MQDPNFLKYINTTIKLLSTHSGRDKVAKTLHYASRIWIWHLQNKGKKER**ADQIESFR**QAIGNSRRVGRFFSLL
NSIPSIYQLVFPDPRTKDRESDLFRFLLVVANVSDMLYYVSDNLTYAAKYGFIKLSPETNYFWEELVGSWTWF
VSMIVYIAHDIKTYLKLQQQRLRLEHQVMKDSTTAK**ASASALAATDEEIFNNR**LSLIRNLADMQLAIYFCFPN
STWSSQWVGLFGVINAVTGGFQIWRGFHKAS

>C115_cycloartenol_synthase
MEGFESGKEATDLRRWKLKVDEGRQVWHYIDGDEPVQQSLTDKYTLGLLSDEDVPPTDPASTPLEAAEKAVAF
YQQIQSEDGHWAMDYGGPMFLMPGLLIACHVTGVELPRPVQIEMVRYLTNRQNADGGWGLHIESPSTIFGTGM
NYTAMRLLGVPMEDDRMKRAREFLAANDGCKGIPSWGKFWLAVMGVYDWEGLHPIPPELWLLPYMLPIHPGRW
WCHCRMVYLPMGYVYGRR**ITAPESPLVLSLR**KELYPNDDYAK**INWYSIR**SYVSPLDLYYPHSTLLECLYVILD
NYEKVHSSWLREKSVLLTAEHVAAEDKFTDWVCIGPVNKTINMLCSWHAQGKDSKEFQRHVDRVPDYLWLAED
GMKMQGYNGSQLWDTAFSVQAIIETGLGDQFQECLQKAYSYIDITQVREDVEQMEYFYRHISKGAWPFSTRHH
GWPISDCTAEGLKASLLLKQFSWVTPFEDQRYFDAVNVILSLQNSDGGWATYELQRGPSILEYINPAEVFDAI
MVDYPYVECTSACVQALTMFVQHYPRHRATEITTAVKKAVDLIKSKQRPDGSWYGSWGVCFTYGTWFGVEGLM
AAGEPSDSPYIQRACQFLLSKQNHEGGWGETFESCSTKQYVQNEETQVVNTAWAVLTLLKAQWPDRRPVDRAV
QVLMKRQLPNGNWPQEDIK**GVFNANCAISYTAYK**NIFPIWALGLYEHTQPQSQKTAKL

>C116_probable_myosin_light_chain_kinase
MGCPGSKEAKDNGGGGAKPSKQVNDAKPEKPVEKPSAGASEAKATDDKKKEPPAERVIPQGEPIKLDELDEDF
ILFEPIEDHYELGEEIGKGGFSVVYKAVRKSDHAEFAVKCIKKKMVEGDDIKLLRREIQIMKKLNHPNILKLY
EVYEDDEQFYLVMELVKGKELFDKIVERGMYSER**DAANIILQVVSAVR**YLHENGIAHR**DLKPENLLSAGEEEN**
EIVKIADFGFSKSFADEGEKLMTSCGSPGYVAPEILTAESYDKSVDMWSVGVIIYILLSGYPPFYADSAPALF
KKIMDVKYDFDDSVWDDISDSAKDLIRNLLVKDPSKR**FTASHCLEHAWVR**GSAANERQILKMNRDNTKS

>C117_hypothetical_protein
MMSRIAVCIGAFVVLLVASALAGPVTLNGAK**ISATFNPTGGSVK**IWETGTNRIFTHSFTKIQEVAADGGVVNA
VNSFADLTFNDPTTPQQETFQGVNSTVVSLSGNVNVAVAGSNATTTANVNVRFYVFNDEGKITYGTKTYPVAP

GSIEIIYTISGWPVEDTGNKLNFFVRIGTPGKTASWNSPELRFFDGASLIFAPDSANSNGQAAVKVTPTMGSG
AVNIQMQFQAANSIEYDPLWSVEGESSSAATLSPFITSVLF

>C118_phosphatidylinositol_synthase
MNPIYFFIPNLIGYVRIALAVVAFMYAMTNHKLFFVCYLLSELLDALDGHAARYYKQSTK**FGAVLDMVTDR**CS
TSCLIMILGLFYPEYMAFFLFAVALDITSHYAHLYSALSRGAKSHKDIDLKSQNWLLWVYYTNRTVLGVLCLF
NEIFFLGLYLCHFELGPLVANTGLGVWQIVTLVAFPLSMIKQLMNLIQLR**QAAMDIAELDLAERPPK**RLRRPG
TNSK

>C119_transmembrane_protein
MVWDCVQIFAISLASAVTAEVLSWLLIYRTESYSSLQGKVEKLTKKLEKKKDGPQSIDKKKSRDKR**IVQYEQQ**
LQEANRELTQSKMKSMFVIGITLVSLFGVINSSFGGLVVAR**LPFEPMPLVR**SISHRGLLGVDYYECSAAFIYA
LCSMSLRTSVQKLFGWAPPPGQDSMFGTPGTH

>C120_Rab21
MTTTNFKVVLLGEGSVGKTSLVTRYVQNTFNERHVTTIQASFLTKRLNVDGSRVNISIWDTAGQERFHALGPI
YYRESHGALLVYDITDNSSFVKVKNWVKELRSQLGMSVTLAIIGNKVDLEKSR**AVNKEEALSYAQSVGAK**HYD
TSAKLNK**GLEELFLDLTR**RMLEANKDGDSGRGAAKKDSILIDYEESQNTGAGGCSC

>C121_cytosolic_ribosomal_protein_L12
MPPKLDPNAIVELIVR**VTGGEAGGVASLAPK**VGPLGLSPKKIGDDIAKSTQEWKGMKITVKLIIQNRQAKVEV
VPSAASLLIKALKEPPAPTNQKKEKGAPGPKHDGNLTFDDVIEVAKTMRARSMARTFAGTVKEMLGTCVSLGC
TIDGRGARDMQKAVDDGEFDDRLAQFD

>C122_Rap1
MNTLK**IVVLGSGGVGK**SALTVQFVQGIFVEQYDPTIEDSYRKQVEVDGKQVMLEILDTAGTEQFTAMRDLYMK
NGQGFVLVFSIIAISTFNDLPDLREQILRVKDMDSVPMVLVGNKCDLQDQR**VISTDQGQQLAAK**FGNCSFLES
SAKTKTNVSEIFYDLIRQINRNKKPDGDSGGKKKKCLLF

>C123_Band_7_protein
MAARGRNPNGGFNWGLVVGPLLLLALVIVFNGVHQIPEGHVGLYWTGGALQDTISPAGWAVKLPLVSQVVNMQ
VTLQTDTVTDIPCGTSGGVMIYFDKIEVVNQLAQDHVLTTVRKYGVNYDSTWIFDRIHHEINQFCSSHTLQEV
YIDLFSTLDEALSESLQMDCNKHDVGITIIAVRVTKPRIPEEVRKNYEEVEKQKTSLLVAQQQQLVSLKKEET
LKQQARIQAEKEAEVAIINAQR**EASVATIVAQK**EANVSLINLEMTIKEKQAQQQRQAIDDQIYVANQKAVAEA
AHHR**ITLEAEANALR**LTPEYLRMVLYQSLANNTKIYFGEKIPQMFLDWAPGDSHMFLPQQQQQASKTVPVRAK
EVPAASKGPAASPAAQQ

>C124_acyl-CoA_oxidase
MERTPTTTSSSSAVRRVRMTEAHLRAPLQQQRQELEGASAAAEGAGAALRTHWTFAPTFDVREMTRLLDHDNH
DMRQRFRAFAKHPLFLVQNNIPLDKEREVALQRLQLICDSDFLSVTDFSSNPKRIFAAHELTGLVDGSTATKM
TVQFNLFGGTVLKLGTERHHKLLLKGIDSLKDIGCFALTELGYGNNAVEMRTTAEYDAATDEFIINTPSVLAQ
KYWITNSAIHAKWAVVFARLLIHGQDYGVHAFLTRIRNDDHSVCKGVRVEDMGRKMGMNGVDNGKLWFDHVRV
PRLNLLDAHSQVAKGGAFTSSIKSARGRFLTVADQLLSGRICIASMLIGGSKTSLLIAIRYASSRLAVGPTGK
SDTPILAYQLQQRALMPLLATTYAFNFGLDYVKDYFERTTVGDLKGDAMASKWLVILCCALKPVVTWNANEVS
LVCRERCGGQGYLACNRFSDAVGGAHAGMTAEGDNAVLMQKVAKELLDMLRAGQVNPRSRDDSIKQDLR**SLEY**
LGYLFDLRFGQR**LLGLATSLQR**QLGAGQPLFDVWMKQESDAIQATAKAYAEHVTIGRFGKNVGSSGPALQPIL
ADLYRLYALTSIEKDLPWFLCHGILTIGQGREVGDAVRALCSALAPQALHLTDAFGIPDYVVQAPIALDWQKY
NLVDNKGECVDYLKEEFRL

>C125_5-hydroxyisourate_hydrolase
MEMMNAATSPERALSLRSSANRRLWTVGGHLDSSSPLISQRHVAAADAGAHSAPSSTTTATTSTNGSRKFLSS
LSSHALDTTLGKPASSLPVTLFR**LRPSTGAVESNEEWEALFGAATDADGR**VTSATFPPIAAGTWKLR**FDTSAY**
FQRIGVAKFLYPYVEIVFQVETGQHYHVPLLLSAHGYSTYRGS

>C126_myosin_II_heavy_chain
MAAQRRRKGGEVESDYIKYLKYKNTGFQVSASDKTLAWWPTKDADRAFCHVEVTKDDGKNFTVRLENGEEKSQ
PKNEKNFLGVNPPKFDGVEDMGELGYLNEPAVLHNLKKRYDADLFHTYSGLFLVVVNPYKRLPVYTPEIIDIY
RGRQRDKVAPHIFAISDAAYRAMLNTRQNQSMLITGESGAGKTENTKKVIQYLTAIAGRAEGGLLEQQLLEFN
PILEAFGNAKTTKNNNSSRFGKFIELQFNAGGQITGANTFIYLLEKSRVTAQGAGERNFHIFYQILSKAMPEE
LKQKLKLTKPEDYFFLNQNACYTVDDMDDAKEFDHMLKAFDILNINEEERLAIFQTISAILHLGNLPFIDVNS
ETAGLKDEVELNIAAELLGVSAAGLKAGLLSPRIKAGNEWVTRALNKPKAMASRDALCKALFGRLFLWIVQKI
NRILSHKDKTALWIGVLDISGFEIFQHNSFEQLCINYTNEKLQQFFNHHMFTLEQQEYEREKIDWTFVDYGMD
SQDCIDLIEKKPMGILPLLDEQTVFPDADDTSFTKKLFQTHENHRNFRRPRFDANNFKIVHYAGEVEYQTSAW
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EQLAHLMSMLSSTAPHFIRCIIPNLGKKPGVVSDQLVLDQLKCNGVLEGIRIARKGWPNRLKYDEFLKRYFLL
KPGATPTSPSTKDAVKDLIEHLIAKEPTKVNKDEVRFGVTKIFFRSGQLAAIEELREQAISKMVVSIQAGARA
FLARRMYDKMREQTVSAKILQRNIRAWLELKNWAWYQLYVKARPLISQRNFQKEIDDLKKQVKDLEKELAALK
DANAKLDKEKQLAEEDADKLEKDLAALKLKILDLEGEKADLEEDNALLQKKVAGLEEELQEETSASNDILEQK
RKLEAEKAELKASLEEEERNRKALQEAKTKVESERNELQDKYEDEAAAHDSLKKKEEDLSRELRETKDALADA
ENISETLRSKLKNTERGADDVRNELDDVTATKLQLEKTKK**SLEEELAQTR**AQLEEEKSGKEAASSKAKQLGQQ
LEDARSEVDSLKSKLSAAEKSLKTAKDQNRDLDEQLEDERTVRANVDKQKKALEAKLTELEDQVTALDGQKNA
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NAPKTGGASSEEVKRLEGELERLEEELLTAQEARAAAEKNLDKANLELEELRQEADDAARDNDKLVKDNRKLK
ADLDEARIQLEEEQDAKSHADSSSRRLLAEIEELKKRVAKETSDKQKAQDQKANYQRENESLKADRDSIERRN
RDAERQVRDLRAQLDDALSRLDSEKRAKEKSVEANRELKKVVLDRERQSLESLSKFNSALESDKQILEDEIGD
LHEKNKQLQAK**IAQLQDEIDGTPSSR**GGSTRGASARGASVRAGSARAEE

>C127_protein_disulfide_isomerase
MRQTWLVVVLVVVGLLAVWCTTSAAAGASSDVIELNDDNFEHLTQATSGSTTGNWLVEFYAPWCGHCK**SLAPT**
WEALATELKGTVPVAK**VDATLNPLVK**KRFGIK**GFPTIIFFK**QGKQYVYTGGRSLEQLKAFALSGHESVASAPI
PAPVSAMDQIIEMLNEDVQHLANTKKLAVGAIFVVGGVVGLFVGFVLGRLTSSSSASKTSTKRE

>C128_D3,D2-enoyl-CoA_isomerase
MGFTAITTEVKEGVLILRLNRPSRKNAFNHEQYEECIVALAQAAKDENVRAVLFTGAGDYFSSGNDLANFLRA
DSTDTTPAKDLLTRFVNAFILFPKPIVAAVNGPAVGIAATILGHCDLVYGSETCSLHTPFMQLAQSPEACSSL
LFPESMGALKANEMLLLGKKFSAREALKANLLNEVFTEKGDQFTEKVFAIARQLASYPPEAVQLSKRLIRNNR
R**LALLDAVNKEEVELLGER**WVSAECIQAVMNFMSRRQKASL

>C129_hypothetical_protein
MVHQAIVIYSIPASLLFLTWLVLFGVVPAFDTLLPITAVGMLIWTKIEFDKVNKLKAQAAAMRKANK**AAEDAA**
STNATAGNKKPAAKKQAKKAD

>C130_allantoicase
MAAAAQVSREGPIPAFDEYVPPAYLAALRSHPSMVTVGGVEGLQLATAPEAYADLLSPQALNFAVDLYRRSLT
FQHALQPALAHRKMKRNCLNRAASALAEASSQHKNQAKVALQDVRLDDGTVALGYRPDTKGLRDDLSWKVAPI
PASFARFHDTITAPPAALPIAKALGCGVHFLMVDFEDSSTVAYESLLAGLHACTLANRRQLVATSPKGKRYAV
TDDGKPISTEMLLRFEGLHLPNAHFLVDGFPMPAHIVTIALYLYHNWQPLQRIGKTPAFYIPKLETFEEAAYL
AELFRAAEAQLSTASRGAYRPGALRCLAIVENVFAAYQKEEILFALRDYIVGLNCGWHDYMASIGAVHQNLPS
FTMAPKSNLRIVVEHLEAYQMGVVDACKRRSAIPIGGMNGMVPPRGPHAKASWERIVPAFAQDFNVQVDRGLE
GCWLAMPKLAPVILKLIADMEERKRKQSPEQRKAEHMKIVERIRQITHEKMLVSGLDYEVSKEEDCERNLSDA
IQYLTSYLAGNGYVPITKTFPDGVPVTLVEDAATLERSRRELWSMLRYGKEVLLANGQKVPLSRELLDKLVKR
VVQKVKANKLDVPFNAHTKIPLDVAVHIVYQLVTSPQPADYFTVFATRYLLAPFKLDLMEVERLGNVDRFPFL
RMDNLMKGAELLFISNESFAPASNLLKETYPIFVPHSFGSEGQIYDGWETVRHNMYPPDFVILKLDAPSFVHG
VNIDTAHFDGNYAPGGSVEGLVLVERNKRLLQKWVTLVPHSLLKGNSR**NYFASIATTVPVVSVKLNNFPDGGI**
ARLQLFGAKTDEKVADMSNAEWTHLVAHEWIGKLQPTTGFPAHFQPPENSALDVAPPAPVTERQLK**EALPSSF**
AWGKGDGLVDVSVDAPGGGGKVVASSSAHYSVPSNMLKAPRALNMGDGWETARMRGQPDYGVFHLEGPVLSDY
NWTLFKLSQECVIKKIGVDTLHFKHNNPIAFSLEGCYEPGLTKDNYHSRGIKWTSLVKPKALQPHLEHPFDAE
HEGRVTHVLLKIYPCGGISRLRLFGKPAKASAL

>C131_cytosolic_ribosomal_protein_L4
MASRPLVQVHGGEGAGATVLLPAVFTSPIRPDVVQEVHSALAKNRRQAYAVSRRAGMQSSAESWGTGRAVARI
PRVPGGGTHRAGQGAFGNMCRGGRMFAPTKTYRRWHRKVNVNQKRFALCSALAASAVPALVMARGHKISQIPE
VPLVVATEAVKDVTKTKHAVALLKKLNAYEDVEKVKDSRKIRRGVGKMRNRRRVQRRGPLVIYDQK**SPLVFAF**
RNIPGVELCSVERMNLLQLAPGGHLGRFVIWTKDAFEKLDAIYGTYTKKSTEKTHFTLPRPLMTNADLTRIMT
SDEVQSHLRKANRKPTRTIRKKNPLKNRGVMIKLNPYEKTRIRNQILQEKARAEKKDAILAKKREHFKKSKQI
KKQRAEYYKALLHNPRVYEGIYK**KPEVTEEAADQ**

>C132_actin-binding_protein
MRQIITISLVFLAVLALVHVAAGQGIPSTAVRNFTYTGFVARDELDFGVEFNPVFGPENLKLMFYDPLGGDER
IEVGAVWYKRRAHLESFNVTFTVRMSNLSHTGVGNPDGFALVVQNHRANAFGAGAGGIGYGATPDYEDLGVRR
SVAVEFDTYLDENLGDPNSNHISVHHTTPERVHNSAHEETALTPPGAVTNIPGIAGFTHKYNVQYIEKQLSVY
IDDSASPAYQTTIDIPSIISLNSSGAFVGLTAACMSTCEDVEVLDWSFNYVAILDATKSFVTNVKNNSVAGRT
SSFTVQGVDTNGYYYQTGGDASKWTVEFTRVSGSGSVVSPSVNVVDKNDGTYTISYAPTSAGVYDVTVYYNAN
ALAGMPFRITVDPGAVDATKSDILGNINGGVAGQPLNITILGKDAFNNVNPNNNPPATFTASFNNGGASASSS
FIGNGTYLIQYTLTTARTYTMTVTYNGTAQQVKGSPFNAVTITPALPEPSASVASGTGIVGGTAGTTLTAVVL
VRDRFQNNITSNLPAGYQLTGFWDKPAAGNNVTFTVQPDGTLAGSYAISTAGTYRLTIVMAPTGLPISGSPFP
VTISAETITSAAQSVATGAGLTTASAGNNASFTVQARDQFGNNMASSDASIAVSFSDDSGVPLQIAHTAVQNS
ADRSQWIVSYVPTNALSTR**ISVSLNGAPIK**ASPFIVNVHPGTLDPKNCFAEGLGLATPKTKVPLSFVVITADH
FNNRLKSGGATIDVTLKEMKSGATVTGSVQDLNNGAYNVGFTLTRSGTYNITINANGVPIGKDTKYSMVVPNE
GLGALGWALIVLAILALIAVVGGGAFWYLKYYKARSDYDEIGA

>C133_microsomal_signal_peptidase
MQKRKQAPPVVFTPASEAVKVDVYDQNAVKQLLDDVIMTYVLETR**GLEEDLTYSNYK**LALGGLSCLVAIASHA
YPAPFPENAWVLKVCVVSYIVLSVLLQYVAFYMEGNTILATRPTQRGGTNNKKLIKPINVQTYFPKCEEAFIV
QVTTTQGKPASHSISSSIGRWFQPDGTFIREAFISDLDQLFTTVEDASD

>C134_malate_synthase
MNNEQRTTLLVRHGIEILGPIEKGYEQVLTVDALVFVAELHKRFDARRRTLLAARDERQSRIDAGEMPDFLHE
TRHIRESEWRCGSIPEDLKDR**RVEITGPVDR**KMIINALNSGAKVFMADFEDSSTPTWENGITGQINLYDAIRR
TISMKVGEREYKLKNQTATLMVRPRGWHLDEAHVLVHGKPVSGSLFDFGLYIYHNGHALLSRGSGPYFYLPKM
ESHLEARLWADAFRYAEQRLDIPHGSIKATVLIETILAAFEMDEILYELRDHSAGLNCGRWDYIFSTIKKFIN
HKDAVFPDRALCTMRSHMMASYVDLLIKTCHRRGIFAMGGMAAQIPIRNDNAANQAALAKVRDDKLREVKAGH
DGTWVAHPDLIPIAMEIFNEHMKTPNQIHVRRDDVRVTSDDLLKFPKGDITLNGLRDNVRVCLVYLRAWLSGR
GCVPINNLMEDLATAEIGRSQVAQWIRHGVKTTDGTQVTISLALKILKEETDALRGSTPASK**TPSGAADSLAL**
AHDIFAKVIVAAPATFYDFFPTLAYQHILTLQPPFHPRF

>C135_cytosolic_Hsp70
MSKEVCVGIDLGTTYSCVGVWQNDRVEIIANDQGNR**VTPSYVAFTDSER**LIGDAAKNQVAMNPHNTVFDAKRL
IGRNFSDPIVQADMKHWPFKVVQKPGDKPFISVEYKGETKEFSPEEVSSMVLIKMKETAEAYLGHPINSAVIT
VPAYFNDSQRQATKDAGTISGMQVKRIINEPTAAAIAYGLDKKSQGEMNVLIFDLGGGTFDVSLLTIEEGIFE
VKATAGDTHLGGEDFDNRMVTHFIQEFKRKHSKDISGNARAVRRLRTACERAKRALSSATQTNIEIDSLFEGV
DFYTSITRARFEELCADLFRSTMDPVEKVLRDAKMDKRTVSEVVLVGGSTRIPKIQQLVTQFFNGKEPCKSIN
PDEAVAYGAAVQAAILSGASTEGSVLGDVLLIDVTPLTLGIETAGGVMTALIPRNTTIPTKKTQVFSTYSDNQ
PGVLIQVYEGERAMTRDNNLLGKFELSGIPPAPRGVPQIEVTFDIDANGILNVNAADKTTGRSEKITITNDKG
RLSKEEIERMVKEAEKYKNDDENAKEKVEAKNALENYAYTMRNTIRDDKIASKLDSGDKSKIEEAVDAAIKWL
DTNQTAEKDEFEHKRKELEDLCNPIFTKMYQGAGGAGGMPDMGGMGGGFPGGAGGFPGGAAPGGGARPSGGSS
AGPKIEEVD

>C136_Rab7
MSKKKILLK**IIVLGESGVGK**TSLLLRYVERKFTMNTKSTIGANFLTKEVEVDDKVATCQIWDTAGQER**FQGLG**
TAFYRGSDGVIFVFDVTQR**RTFEELEHWK**EAFLIQVGQEGNKDFPMIIIANKIDLKEERVVSRKELQEWCAQY
GLKFFEASAKEDENVEKAFEEITRLVISKMKPEDIMYDTVDLSVGEKKEDRGCDC

>C137_cytosolic_ribosomal_protein_L10
MGRRPARCYRYCKNKPYIKSRYCRGVPEPKLRIYDLGRKKAGVDEFPFVAHLLSWEHEQISSEALEAARISCN
KYITKMAGKDSFHMRVRVHPYHILRINKMLSCAGADRLQTGMRGAFGKPAGCVARVK**IGQILFSVR**SKDNSKA
HVIEALRRAKYKFPGRQKIVLSNKWGFTPLQREEYLQLKSEGRIIPDGVNAKVVKNKGVLGF

>C138_hypothetical_protein
MGRATAVLSYTLSRVAFVATHVVFAYWLNYLLNDPLNLGLVTLDAKPPLPAGQCEHFVVGNAVSNLLWFALWW
GTHSILARKAVKQALGLWEHPLERPLFATVAWVAWGLNVHTWRPVDTCAAPWDPLAVSPYVWAASGAVFAAGV
VLIVGLLWSLPDHVFGTARYQYDQGKRPHGDLILRFPYGLVRHPAAAGFLWCYAVLPAWTVNHLFLAGLWITF
IVVATGLEEGGLKGDDEFGQRYEAYRR**SVAAFHPSWAALKNILGIAPLK**IVGSSGSKKKKSNGAAKEKEESAS
SKKKKQP

>C139_aldose_1-epimerase
MNQGKGGLERVVIGHAATGASAEVYLLGAHLTSFIPKRGGADLLFVSQKAEFAEGKAIRGGVPIIFPQFSDMG
PLTKHGFARTALWEVASAADSEVTLVLRSSEATRKLWPHDFEALFRIALVPHGEEAALETEFTVKNTGSSAFA
FTVALHTYFAVKDIHVTRVEGLHREGEDLYYLDNTQGRKKIKEESR**DVGFTGETDR**IYLHTADELRLNDTERA
IVIKKSGLADAVVWNVWADKVKSMADLGDDEWPRYACVEVAAVEHPVQLNPQQSWTGKQTLYEQSRSRSPSAL

>C140_cytosolic_ribosomal_protein_L19
MVSLKLQKRLAASVMKCGQKKIWLDPNEVSEISMANSRQAVRKLVKDGYIIRKPPVMHSRARVRKNLLAKRKG
RHMGVGKRRGTRNARMPEKVIWIRRMRVLRRLLRKYREAKKIDKHLYHELYMKVKGNVFKNKRVLMEYIWKAK
AQKIKDKAEQEQGELRRQKNRQMRERRAKRLDERRKVLLGEDKKAVKKEETGKK**AAAPAAAAAPK**VSKNQKKK
EAAKAAAAAAPAKAAAPAKAAAPKKEETKAAAPKAAAPAKAAAPKKEETKAAAPKAAAAKPAAKAAAPKKEAA
KPAAAKPAAKGGKKGGK

>C141_acyl-CoA_oxidase
MEKMNTNAAVSSRTAARRARAVARHMGLVTESMSGLAVNNAAKTKEVDQEKLRLKKEQRKQRREEERRQLGEE
RVEVFNVDVMAEYVLGSKYRAQRRTVTESVK**ANAELFPYNFELSK**EDQRERVLQQVRWIAAKGWASLDMLKED
PTMYCNSLEPFIGYDGSIAIKAGVHFLLFGGSVVNLGTERHQKWYDATNNLAEGGCFAMTELGHGSNVQGIGT
TAVYDKATGEFVINTPTDVDRKWWIGHAAHAKNAVVFAQLNVDGQEHGVHAFVVPLRPRDSNATYPGILIGDC
GHKMGLNGVDNGWMKFTNVRVPRENLLNRFADVQPDGQYVSSVKNPLKRFGRQLAALTCGRVCLVSGSSATLS
VALTIAVRFAAGRKQFGPPGEPEQPILDYISHQRRLMPMLANCYAYRLMGHYLLDLYKNADSNNAKAIGELHS
LSAGVKAAASWYTNVALQVCRESCGGQGYAAYNRFCHLR**NDHDIYQTFEGDNTVLMQQVAK**DLLTQYKKQFDG
KPFSGMLKYLGKQMGHVISESNPYVTNMASWTHLRDQEFQKDAFDYRVARLLHNTAQLLQKRAKNNDFFTAWN
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LITELCQEVRIHALHLVDAFEVDDFIVHAPLGLKPDGHDPLLRVLNYVQTNYATYPQSS

>C142_peroxisomal_assembly_protein_pex3
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GAFESTQSTCAGTVGSLVLKLNDAVLRLVPIPSPTELRLSLQQAPKDGQDR**YALWDHCK**TQTYARLVVGVYGV
VLLSTFLRVQVNILGRYLYLETLIATDPSARFRIPLDVAIPQDTQKRYLGYSEYVVHTGLPQLVALVQATAHQ
VLSSYPLQRQCTYDDVLAIIDAMRRKMEQPLSPDSDETVLNTFLLPQEDAEGSSGGNGKRHRDHKLTMLINET
RDVLESSEFNQILSRCLNLSFYAMAHQLHSCFPRQEQQALASSVDAERDLAAPAATAEPALPMAKLMPLVNKQ
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>C143_cytosolic_ribosomal_protein_L11
MSQTK**AAAAATPAGAAPTR**TKKQNPMRKLKIDKLILNICVGESGDRLTRAAKVLEQLCGQTPVQSKARFTIRT
FSIKRNEKIAVHVTIRGEKAAEILEKGLKVKEYELNARNFSDTGSFGFGIDEHIDLGIKYDPQIGIYGMDFFV
VLARPGFRVGRRRRCQNSVGTNHRVSKDEAIKWFEDKFEGVVLRKK

>C144_cytosolic_ribosomal_protein_L27
MPKFLKPGKVVIVLNGRYAGRKAVIVENRDDGTKARPYGYAVVAGVDKYPKKITKSMGKKKIAKKTKIAPFVK
AINYNHLMPTR**YGLDVELR**SIVCKENALEKGQNKYKTKQALKKVFQTRYNSGKNKWFFTKLRF

>C145_hypothetical protein
MKMRCAVIVALLCLASLALFANAANLLEVSKTVEAGPK**TGVYTVTIGYK**VIGAPGRVANVNIADSLPEELDLV
SGDLVVKAEDPSTEEWYYHSYQVKNKNVHLTIAEPEAVVELPPAEVSYTTGGNAVSTVSTDAVPLVIGVPFPK
GTFNLTPVIAFFTLALPVLAAVYLIPYFSTSQLKKRK

>C146_alpha/beta_fold_hydrolase
MKLLLVLVGLIAVLLGAVVYHDGAPSSPNDFATPASSADGIQQTRTYARIVERVPIHHEHFEAWLYLPLPVPA
TKPPVIIMGPGLAAQK**DFAGLTAYAER**FVAEGWAVFLFDYRNFGRSEGRPRNLIDPIRHVQDYHAAIVHVVNT
NITEKVDVTRMALWGSSFSGGHVLVTASEFEAAVKAYPLNYILNQRPEHVNRTKPQLKAVFSQVPHLDPYAVI
PTLNLLQVARGFALAIADWIGSWFGLNVYVRIYASPAEVAIMNTPEAVEYGHLVPEKPVGGWVNKAPARSILY
VSRYRPLDYVASIATPTLMIVANHDTLCPITAANEAEKLLANGKVLKYDVGHFDFYEGKPHFEETLEHQIRFF
REHL

>C147_peroxisomal-CoA_synthetase
MAACTRTNTGDTETLVDVLHPSHAGRTAVVLPEAAQSLTYAQLAHEVSHARDALSAAGLGRGDVVAMVLPNCL
EFVVCWLATTNGRSIAAPLNPDYRLDEFKFYLEDTEAKAVIVPRGGRAAVAVEAAQQLRVPVWETWAEVDASS
GRVRVGLESVEPLPVRRATASELRVAPEPEDVALFLHTSGTTGRPKGVPLTYRNLVTNLRNISRHYRLTPDDR
SLIVMPLFHVHGLIGCLLSTLYSGGSVVIQPGKFSATTFWRDFLSNECTWYSAVPTIHQILLARADKDYTTSG
KLRFIRSCSSALAPAVFKQLEERFKAPVIEAYAMTENSHQMTSNQLPPGKRKPGSVGQGTGVEVTIRDDSGKE
LAQGEKGEVCLRGPTVTRGYHNNPQANKTAFHEGRWFR**TGDQGFFDEDKFLVLTGR**IKELINRGGEKIAPSEI
DSALLSHPDVSEAVSFGVPSDKYGEEVEAAVVLKGGREGGKAVEEAILKHCHAKLAAYKCPRRLYIAKDLPRT
ATGKIQRRHVATHFLKNSADSDKSLKKAKL

>C148_Rab7b
MGLCESREEEEDGVRLATADTDAIVRSLGGDGKCVLLKVLLLGSSGVGKTSLIGQYCKGEFKERYKSTIGSDF
ATKDLSVDDRYVTLQIWDTAGQERFQSLGVAFYRGSDCCVLVYDVNNRESFKNLHQWMQEFLIHAGPDDPEK**F**
PFLVLGNKVDLCRAQSPGTQPRRKPEVSEDEAKEWCKKHGNIPHLLVSAKEGTNLDEAFTLLADIAIQRLHAP
LSTAASSVRSRHDKEGVYSSSPW

>C149_cytsolic_ribosomal_protein_L15a
MVRISVLNDCLKSICNAEKRGKRQVLIRPSSKVIVKFLTVMLK**HGYIGEFEIVDDHR**SGKIVVDLIGRINKCG
VISPRFDIKLKHIEQWITDLLPSRQFGFIVLTTSSGIMDHEEARRKGCGGKVLGYFY

>C150_cytosolic_ribosomal_protein_L24
MKTEICQFSGYKIYPGHGRRYARTDMKTFVFINAKAEKAFLKKSNPRKVLWTTVYRRIHKKGTTTEVQKKKTR
KVVKVQR**DIVGATLDQIK**QKRAQRPEIRAAAKEAALKEIKERQKKKEDLKKKAAPAPAKGAKGKKVAAPKATK
AKAPKAPKGQKGR

>C151_dolichyl-phosphate_beta-glucosyltransferase
MLDLLLSIPLWVPLLFVIVAGVTLFYRHLPERSVLWYKNENMYIDARTNDKKSFPPPSAEPAVYLSLVVPAYN
EEKRMPTMLDETLAYLQQRSAEDPQFTYEIIVVDDGSRDKTTDVALNYAKQHKLDTVRVLKLAKNRGKGGAVR
RGMLVARGRYALMVDADGATKFSDLERLEKRLLQAEK**NGLGVAVGSR**HHLQEKSEAVAQRTFLRKTLGATFHM
LVTFCVANVHDTQCGFKLFTRRSAQLLFSNLHIERWAFDVELLYLAQQLNMPIEEVPVNWQEIAGSTLNPVTA
SIQMAKDIFYIRALYILGYWKIDK

>C152_peptidyl-prolyl_cis-trans_isomerase
MKLSLLLVAVLCVLSVLAQAEADKKGPKITNKVYFDIEIDGKLEGR**VVFGLYGGTVPK**TVENFRALCTGEKGV
GSKGKPLHYKGSSFHRVIPNFMIQGGDFTHGTGVGGESIYGDRFADENFKLKHTTPGLLSMANAGKDTNGSQF
FITTVATPWLDGKHVVFGKVLEGYDIIKKLESLGSQSGKPSATLTIADSGELPLSE

>C153_3_beta-hydroxysteroid-dehydrogenase/decarboxylase_[0.1358]
MSGKK**YGVIGGGGFLGK**WIVDELLNRGEKHVRVLDIRPSPTPDDRVEFVQVDVTKIDTLRKGLAGLTTVIHTA
SPPHGKGYQMYYNVNVEGTKNVVEACVELGIKQLVFTSSASVVFDGRHIKGGDESLPYCKTHLDGYTETKEKA

ERIVLEANGRKGLLTVALRPSGIFGPGDAQGWPGFIEAAQNGKSKFQLGDGSNLMDWTYVENVAYAHVLAADK
LVPGNDKVAGQAFFITNDEPAPFWDMAKYIWKNLDYPTPTVVVPYWLAYYLALLLDWIVWLLSPLVSIHLTFT
FFRVVYAGAHRYFTIEKAKRDLGYKPKVALKEGMARTLKAFEHKRNPKATGSSQDKKKAK

>C154_hypothetical_(similar_to_gamma-proteobacterial_membrane_protein)
MARSLDYDALQESFVFLLVLAFFIERSLAVVFELRLWRGPLSNPGVKELVAVAVSYAVCTWAEFDAFATLFNK
DSVFLSKALNALLVAGGSKGAMK**LMQDVLGVR**KDVMENNIDRRKNRVNYEENVNLKVTKTEE

>C155_cytosolic_ribosomal_protein_L13
MPKHNNLIPNQHFHKAWQNHVKTWFNQPAKKKSRRVARAAKAAAIFPRPVQGPLRPVVHCPTIKYNTKLRLGR
GFTLEELRGAGITKRFAQTIGISVDHRRKNKSEGPLADNINRLKQYKAQLVLWPKRKESKKHPRKADEAAPED
REK**ATQLTGAVLPVK**QKEVRVKAQVVEPMGKGSAFVTLRRARADAKYIGIRKKKALAREEKAKLKKKD

>C156_acyl-CoA_synthetase
MSIFFDYDVTLAFAIITVTSALFFVVLPFLARDQQRGRIKPGPRKNTKFSHQSYDVAPPEALGEGPIRRASDL
KPDEELYDSLKDTENNLVVATLCQNFARSERLFGNCRCLGTRRFENDGTRGPYEFRTYKEIAALARYFGSGLK
NLGAKRGEHIGIYSKNREEWVIADQACSAYSLTIIALYDTLGENAVAYIASHASTRFVVVSRESLRPLMGAAP
DCPELKTVILMEEPTDEER**LAAEAINLR**LLWFQDVVQDGKSRPVTIDPPTPDDLYSIMYTSGTTGDPKGVLLT
HRNVMAMMAAVNQRVAKSVATPEDAYLSYLPLAHIFERAIMQCAFSRGTRVGFYQGSVLHIIDDVQELKPSFF
VGVPRVYDKIYGKIVNLLPQQQGKVRWWLFRRAVASMGEDPSGPARRAISGSGWSSTRPGRGLAATCGPCCPA
APHSPPWSTSSSLACSDARSFRATA

>C157_transmembrane_protein_147
MTFLHFANCALLAFGPSFIFYKAGKLSEYNAFFPVAYAALIYVATQAIKLLLFATLVPASEEGQFEILHEVLK
ALVNAGDVVGIYFALNQKTVGGEARVLSVGLGWAVAESILMR**LAPLWIGAR**QLEFSWEYIQMSIEANFSLLRL
IALTTLVWLYTHSRKEHTALSSIKMSAYAIILYFAFPIAVSFLQLQLHVGSWYLVIASGLFSALMAYVANHLN
ALYSVERQTKAK

>C158_cytosolic_ribosomal_protein_L34a
MVQRLTYRRRHSYKTASNTTRVVKTPGGRLALQYTKKKANGPKCGDCGVSLPGIAHLRSKEYARISKRQKHVT
RAYGGSRCATCVRQRIVR**AFLIEEQK**IVKKVLKQQHATKAK

>C159_regulator_of_chromatin_condensation
MLYMAANSESVVHAEEQLPQATTTTSASHSPRAETDKPLASGGNVWVWGADGGTVPSAGSSPADSLVPRLAAK
LSGKGIKGLAFGDKAAAAVTNKGELYLWRVGEEEPTLTEHKGVQQVACGRNGLIAALTDKGDVLLWDARTHAE
GGLHPPASSKEAGDADWKNVKRIDIASLSLPPASATATPAASASSWWPFGGSGSKAGAETITQVDCGSGHVAM
VTSRGRVLVLGDNNYGQCGTQDASNETRGPGMVRPSPVVVDLGIAGGGHKAVGVSCGDTHTAILLDDGAVFML
GSVHLSGLK**GSTLYTDSPVLVPLTR**DSKSVEKLGRIIKLSCGGEHTLALTNYGVLLAWGNGMYGQVPDNQGKH
INTAHPVLRAPFFNAEGKEFINNEVKELQCGNEHCLALTKGGDVWSFGRNDRGQCGVGNRAHQKTPHKVTKLQ
SRKDKISAIACGQHTSAAIEEGAQKYEI

>C160_hypothetical_protein
MRAALLYCAVVAALALTVVAAAPSRPSFPSAYRATFSNLLVFTSDFNLTTTNGLLAVSQALQAYKQSGIIYGV
SATTLNLYQQHISYVWTARSCSKKPLSNTYQGADPLQMIR**YTSFAGAVR**VNNVQTQVWLFENANRDVRVAIYV
TDNARQTPVRLFLETYGVGVQIDYSSFTAGASSSDFQTPKACSTTARQPHEQQEEGRVHAVAASVAAKRSSLP
ESLEAEPHASGLAAVHAALASMQLP

>C161_2-oxoacid_dehydrogenase_acyltransferase
MHQSNLRLVLAGLAVYAVWGTPQATLVYLVLGLLFAFWFWWASAGMPIRRKLQIATWGEPSEGSIHAKISLDA
TKVQKYIDEKRKTTRQHITITHVVGKALGLALRNAPGLNGRIVFDRFLPFKTIDISFLAMVEGGKNLAKVKVS
NIDKK**GVDQVATELDAGSQR**LRKGTDENFKKSMGPLKLLPTWLIRLVVNTAAYAAGALGLSIPALGVEPHPFG
SCIITSVGMLGVDEAFAPFTPFAR**VPLLVLIGAIHEGVK**VEDGETKVTKKLKLCCTIDHRFLDGAQGGAMAKV
LRDVFDNPSMLDQE

>C162_mannose-P-dolichol_utilization_defect_1_protein
MELKNLVEFMGEHCFKQLVVDHNFLDVPCLKMLLSKFLSFGVVAGSLVYKLPQILKVQNSRSAKGLAMLGVLL
ELLSVTISFSYSYSKGFPFMTYGESVFVAGANLLIICQILSFEHGGVGFQGLAGIALYGAAVYALLGGFVPFS
ALQIMQGCVTPIVIASR**LPQIWESYR**NKSTGQLSFITWFLNFGGSLARIFTTLQEIDDPLVLIGYIVGASLNA
IIIGQIFLYWNNSGAKPSKPKKPAAKKPATKAAAAKKKKAN

>C163_fibronectin-like
MSKLTALVVCLVVCALFGLSFGQENDFRETQSFKKRDLPLDPETIKECIGSAQFSQSVRTISSSYR**GPQSIAA**
ADFNKNGKQDVVVAYATENKVVYFSNQGDGLWSASVLGTVNDASAVFAADLNGDGRIDVVAASETDNQVHWFK
NNVGGWTHYTIPDAAISAPRSLFVADINGDNKPDIVAAGDAIAYLENQITNVQPNGWTINAVTYSGSPVDSVF
AADLDKDGFTDLVLASSTGDLVWLNNTSGSGTAFASNVIATATGSVQVFCTDIDGDGYMDVVTADKSKNATTL
YYNNLVIATHTLPSGNNNSAPAQSGWVGLYVDQDQNAPESVFVTDIDGNGYQDIVVAITGADTIKWYDTSDFY
TWDAHAVGDATSPSYVYARDIDGDYVKDVIFASATGNRLGWFEELCATSLPDGGDDDHVVGWAVAGGVIGGLL
ILWILVAIAIAIHDYIKHQMQKASEQRKKEAKSMLPTEHDDL

>C164_coiled-coil_protein
MYGRFCGMSRLFAVALFALLLALPAVFPQGAKFQTDADWDEFEEEEFEAAVPVHTAKPGDAASPSHKDAAVKG
AEEADKPASKLSFALTPALGDWFYVETACIVLLTAFAANYYFGRQANRRIALSWGR**TFAQLLDSNFSRVGEGG**
GLLIKESENRYRVPATGRRNCHGLQATLNLGRRHDLFAQVYEFFMPAP

>C165_vacuolar_ATPase_subunit_F
MAAHGKTKLRSPETGSLLAIIGDEDTVTGFLLAGIGELNSKRTKNFLIVDNKTKLGQVEEAFREFTAREDLAI
LLISQHVANDIRHLLDEYDR**LLPTVLEIPSK**GAAYDMAKDSLMTKVLRMLGTSADAPDIDDESTSHH