

Peroxisomal

>urate oxidase Contig2211 (complete), 294 aa, 16C4 checksum.

MATLSANRYGKDLVRVVRVTRNGPVHDIKDVAVRVLLEGGKLETSYYNGD  
NSWVVPDITIKNTVYVLAKKHPFTDIEVFGITTIARHFLNEYAHYSKAEVT  
ISERPWNRMVIEGKPHDHSFLPGSGEERTAVVRLARESMDAPQVTSGMRN  
LLVMKTTGSEFVGFVKDKYTTLKEATDRIFKTTVTVEWDYVCQRKPVDT  
AVYNRAKETILHVFATTYSKAVQQTWEMGRQIIAKNDDVKNVHFTLPNQ  
HNWLFDLKPFLENNNEIFVPQADPQGYIQGTVSRDNGPKKAAL

>allantoicase ContigE80POFO01BBNJ0 (and 25798,16965,9568) (incomplete, with gaps), 638 aa, 12 checksum.

MPTPRSRSTSPCKQYVYQLVTSPPADYFTVFATRYLLAPFKLDLMEVER  
LGNVDRFPFLRMDNLMKGAELLFISNESFAPASNLLKETYPFVPHSFGS  
EGQIYDGWETVRHNMYPPDSFVHGVNIDTAHFDGNYAPGGSSVEGLVVER  
NKRLQLQKWVTLVPHSLLKGNRSRYFASIAATTVPVVSVKLNNFPDGGIARL  
QLFGAKTDEKVADMSNXEWTHLVAHEWIGKLOPTTGFPAHFQPPENSALD  
VAPPAPVTERQLKEALPSSFAWGKGDGLVDMKGAELLFISNESFAPALQP  
PQGNLDAPS FVHGVNIDTAHFDGNYAPGGSSVEGLVVERNKRLQLQKWVTL  
VPHSLLKGNRSRYFASIAATTVPVVSVKLNNFPDGGIARLQLFGAKTDEKV  
ADMSNXEWTHLVAHEWIGKLOPTTGFPAHFQPPENSALDVAPPAPVTERQ  
LKEALPSSFAWGKGDGLVDVSDAPGGGGKVVASSAHYSVPSNMLKAPR  
ALNMGDGWETARMRGQPDYGVFHLEGPVLS DYNWTLFKLSQECVIKKIGV  
DTLHFKNHNP IAFSLEGCEYEPGLTKDNYHSRGIKWTSLVKPKALQPHLEH  
PFDAEHEGRVTHVLLKIYPCGGISRLRLF GKPAKASAL

>acyl-coa oxidase Contig18106 (complete), 704 aa, 419 checksum.

MSATTPEFNSAAARAARRVQCVASHVQAGDQGLVAVQGVSAATEMVDGVT  
TLRAERAGGSFDVRAMTHLLDGGEEITRIKEEYVALLEREPLMLDAGFYD  
RTREQARYRVMQMKRFGELKPEDPLRSKIFNDLVALHDASFSTRMGVHY  
TLFIGALTGQATKELQEKYVPDARKLRVIGSFSMTEMGHGSAIRHFETTA  
HFDKQSDTFVINTPTLTATKWWIGGAAHISTHTICFARLIIDEKDYGVHS  
FLMQLRDRDGNILPGITIGDCGKMKGRDGDIDNGWLQFNVRVPRSQMLQK  
WAKVSREGVYSQPPKAQLAYGALLGGRVSLILNCNDQLKRGLTVAIRYCA  
VRRQFANKPGAPETQILDYQTHQIRLLEPLCGAFAWTFAGRTMEAQATKL  
QQDLANGDLTNLPDLHATSAGLKAICTWYITAALQARQCMAGHGYSAYS  
ALPTLVADITVNTWEGDNTVMLLQTAQYLVKSI SRVFEGKLVGSARYL  
ERTQEILTQSPLSVSSASDYENEELVVQLYERAAVKKIVRAARAVQREIK  
AGKPKDAAFNACLIDLVRASEAHCYLYAVHAFLQOVRAVEAGPLQAVLKK  
MFLFLFCLNRVANDASTHLADGWMNEKQLELLQEKVRQLLSEIRKDAVPLV  
DSFNLPDSLVSPLGRFDGDLKYHYFAEVRAAPNAEIKAPYWDELVKPCL  
RKDL

>fatty acyl-CoA reductase E80POFO01D5S9V (and 27140,15679,13458, E9BS9UA01BXDDK, 179, 25079) (from PGP), 1235 aa, 9E checksum.

MEGPGAPILDWPIQRLPGFINDFFDQGVVITGVTGFLGKILLEKMLRDL  
PGVSKYFVLIRPKKDCSAEERFQKEVLSSPLFNPLRKALGGDRAFAELVK  
DKVEVLKGDILDEDLGLSAEEMKKVVEEVTVFIHCAATISFTEPLLDAIN  
QNVVAALRVLKIAKSAKRKVI FTHVSTAYVGCNRTGFIEEKAYPFPEPE  
QLLNRLLT MHPKDVEKQTKKLLGRYPNTYFTFKSLAEHMFLKRRGNLPLA  
ICRPAIINAVNRDPVPGWIDTLAAAGGLYAACGFGILKFLPGHLENATDQ  
VPADFVNCIIAATAYNAGKDRYAIYHSGTSHRNPLRWSHIVKCLLPYWL  
MNPPKRMLGRPSFQFISGPYPMYEITYFLKWTVPAMIYQLLARTVGDKKV  
RKNAKMLDQIDKRLTKFTETFRHFTENWIFAVDNSDELLQSMTPEKEV  
FNFDAKLDWEDYLMRYAYGLRTYALNEKGLRPPKGDYLVYSGLSLTRK  
PFADIMFAMKSNLIVNAGISRTGEQLKLLVLS SPRVQRAIAREVSTKQV  
SIQVAESRAKNILEVMGAEASPAVLRSLAWAFRKYRRLYSGVVINQVGL  
EAVKELFGTTLKKEKSAVVLIPSHRSYIDFLIVSYIFYSFQLPVPPIAAG  
DDFLNMLLVRWIFRHS GAFFMRRSLGEDELYREIFTEYTQRLLLDGYVPE  
FFIEGTRSRSGKMIQPKMGLLSIITDPFFEMLKPNRSTRNAGSAKKQTL  
EDVHFVPIGVSYEKVVEESQHVKELMGESKQKPSLRALLAAAHWVLSLDF  
GRINVQFGNPI SLRSFMSQEVATNPDKRALGPHGDCPPLPFDIYSLPGLP  
TAVPAKVDAAGSPSESQVAVRPEAEPYNPWTNKNHRRRIAINNLAFKICQ

EIEANIVSMSTGIVAALVLTQRNGIKVEDLIEKFSWLKELIIAKGGWNDP  
ILHPVNYVVTRAIRLLQPLIIERNRRLEPNYITIQDQRNWVHLGYRNOI  
VHLFKDECIMAVALSFGFRSTVIGDAGAGQVGRKDELFAFLCSLLK  
FEFIPTGKEDYEQLLGFWIEKGLFQSKTSADHQHSLIFVPPHGERYFTFL  
CLLFWPFIDSYWLASLALFSALHDRTVQGTTLIDNAQWFADHLFKSGVLQ  
HFDANSKDTFHNAFTVFKHWGILKARGERYSGREVLLHLSPLYWQEEKAL  
DALVHHIGSFRREPLRQGVLDKALLADFPVVARL

>acyl-coa oxidase Contig25019 (and 8838) (possibly complete), 672 aa, 106E checksum.

MERTPTTSSSSAVRRVRMTEAHLRAPLQQRQEQELEGASAAAEGAGAALR  
THWTFAPTFDVREMRLLDHDNDHMRQRFRAFAXHPLFLVQNNIPLDKER  
EVALQRLQLICSDFLSVTDFSSNPKRIFAHAHEL TGLVDGSTATKMTVQF  
NLFGGTVLKLKGERHKKLLKLGIDSLKDIGCFALTELGYGNNAVEMRTDA  
ATDEFIINTPSVLAQKYWITNSAIHAKWAVVFARLLIHGQDYGVHAFLTR  
IRNDDHSVCKGVRVEDMGRKMGVNDNGKLVFDHVRVPRLLNLLDAHSQV  
AKGGAFTSSIKSARGRFLTVADQLLSGRICIASMLIGGSKTSLIIAIRYA  
SSRLAVGPTGKSDTPILAYQLQORALMPLLATTYAFNFGLDYVKDYFERT  
TVGDLKGDAMASKWLVILCCALKPVVWVWANEVSLVCRERC GGQYLACN  
RFSDAVGGAHAGMTAEGDNAVLMQKVAKELLDMLRAGQVNP SRDDS IKQ  
DLRSLEYLGYLFDLRFQORLLGLATSLQORQLGAGQPLFDVMMKQESDAIQ  
ATAKAYAHEHVTIGRFGENVGSSG PALQPILADLYRLYALTSIEKDLPWFL  
CHGILITIGQGREVGDAVRALCSALAPQALHLTDAFGIPDYVVQAPIALDW  
QKYNLVDNKGECVDYLKEEFRL

>acyl-coa oxidase Contig14462 (and 27341,13487) (possibly complete), 716 aa, 78F checksum.

MEKMNTNAAVSSRTAARRARAVARHMG LVTESMSGLAVNNAAKTKEVDQE  
KLRLKKEQRKQRREEERRQLGEERVEVFNVDMVMAEYVLGSKYRAQRRTVT  
ESVKANAELFPYNFELSKEDQRERVLQQRWIAAKGWASLDMLKEDPTMY  
CNSLEPFIGYDGSIAIKAGVHFLFLFGGSVVNLGTERHQKWDATNNLAEG  
GCFAMTELGHSNVQIGITTA VYDKATGEFVINTPTDVRKWWIGHAAHA  
KNAVVF AQLNVDGQEHGVHAFV VPLRPRDSNATYPGILIGDCGHKMG LNG  
VDNGWMMKFTNVRVPRENLLNRFADVQPDGQYVSSVKNPLKRFGRQLAALT  
CGRVCLVSGSSATLSVALTIAVRFAAGRKQFGPPGEPEQPILDYISHQRR  
LMPMLANCYAYRLMGHYLLDLYKNADSNNAKAIGELHSLSAGVKAAASWY  
TNVALQVCRESCGGQGYAAYNRFC HLRNDHDIYQTFEGDNTVLMQOVAKD  
LLTQYKKQFDGKPFSGMLKYL GKQMGHVI SESNPYVTNMA SWTHLRDQEF  
QKDAFDYRVARLLHNTAQLLQKRAKNNDFFTAWNQTLPELLHVAAEHVER  
VVVKQFVRRVNDPCPDINCKHVLKLLCDLYALTKIEKDLAVFSKEGYIKKR  
KANAISELITELCQEVRIHALHLVDAFEVDDFIVHAPLGLKPDGHDPLLR  
VLNYVQNTNYATYPQSS

>2-hydroxyphytanoyl-coa lyase Contig25374 (and 1569, 22838) (complete), 559 aa, BCD checksum.

MEGAAVVARTLKALEVTDVFGVGRPV TNIAMMAQAEGIHFWSFRNEQAA  
SYAAGAAGYMTGRPAVCLAVSGPGV VHALAGLGNAWANCWPMVLIGGATS  
TDHSEMGGFQEQEAPQIETVRPYVKMACRAESLARVPFYIEKAIRVAMYGRP  
GPTYVELPAEVIYDLMDESKLVLP RPVPPPPLTFADPKSVRAALELLKTA  
KNPLVIVGKGTAYARAEAEATHFVEKTGLPFLPTPMGKGVLSDEHSQVA  
AARNLALQSADVILLGARLNWILHFGQTPRYNKDVKFIHVEIAPEELNN  
SVRAEVALAGDIKAVLTQLNDLLAKSPFQFPKASPWWNALKDKVAKNKAV  
NAKLCADERMPLSYRALKGVHDTLPHDAIIVSEGANTMDIGRTIFDNRL  
PRHRLDAGTWGTMGVGMFAIAAQV VHPGKVVVAIEGDSAFGFSGMEIET  
MCRYGLNVCTVIINNNGISMGVEDLSGF EKPNVFFVYTPQARYEKLIEA  
FGGKGYVVTKPEEIEPAMRDALAQK CPTIVNIMIDTAATRKPQEHFELG  
ATLGKAKL

>catalase Contig15145 (complete), 487 aa, 1DD4 checksum.

MAQRPLFTTSHGSPVHDDNNSLSAGPDG PLLLQDYQLVDKLAHFDRERIP  
ERVVHAKGAGAHGYFEVTHDISKYCKAKFLNRVGRTPIFTRFSTVGGEK  
GSADTARDPRGFAVKFYTEEGNWDMTGN NTPVFFLRDPSKFPDFIHTQKR  
NPQTNLRDANMFWDFLSLTPESLHQVTILFSDRGIPKDYRHMNGYSSHTF  
KLVNKEGKQYVVKFHFHFKTEQGIENL TQEEGDRIAGENS DHATEDL FNSIA  
KGEFPAWRAFIQVMEYEDAWKYKFNPF DVTKVWSHKDYPLIPFGRLV LNR  
NPENYFAEVEQSAFSPASLIPGIEAS PDKMLQGR LFSYNDTHRRLGTNY  
LQIPINAPFATKVRNQERDGGMTVNGN QGSAPNYFPNSVEGSPAPCPQTL

DTHPFVSGPVARHRPNHPNDDFVQPGNLYRNVMTPEQRTLRVNNIVGHL  
KNARKDIQLKMVEIFSKADKDYGARIRDGLVAAGAKL

>peroxisomal membrane protein 2 Contig8150 (complete), 191 aa, 1BB1 checksum.

MSNSKPTTTASSPGLASLWEAYIFQLRKRPIILTKALTSVLSGLGNVAA  
QVAVERKGLRGLDVGRLWRFTALGLLLSPVSHYKFLWLENLFRFARGKTA  
VYGKLAIDQLVFGPIFNVLFFVLMAILLEGQPSAMGGLIKSNFWPTTVNSW  
KVWPIASFISFNYPVPAELRVLFVNVVVAFFVWIIISGIAARK

>sterol carrier protein 2 Contig22159 (and 15118) (complete), 235 aa, C19 checksum.

MASSVDQVFELITKNVAADPGLVKRVGGVYHFDIDGKVVTVDLKNGNGSV  
KSGKDGKADCTITIKGDDFLSLASGKLNQTAFMQGLKLGGMGLAMKL  
GQLFENRSGAAPQQQASSGAIEVAFNEIQKNISADLSLVNKINGVYQFDI  
TLASGDVQKWAVDLKTAPGSVSKGAPPKADCTLALKEEDFVNMLTGKADG  
QSLFMQGLKMTGNMGLAMKLGQVVANKQPKQAKL

>possible peroxisomal carrier protein PMP47 (mitochondrial carrier family) Contig17825 (complete), 320 aa, 1AC7 checksum.

MSERVSM DAVVAQLERDLASPAALAGAGGGAISLGLTYPLYTIVTKLQV  
RSNYGGPIDTFLHVLREEGWTSLYAGLAPALIGNAYAQQVYYYWYAFFRS  
VAEGKGPCKRAVGTFFASLLIGALAGAITVIFTNPFVWVTTTRLQGTRETTK  
KDDEVGFKTARPKQKQKILQVVQEIYQEGGLKAFWNGLVPSLILVINPALQ  
YMVFERVKAVWEKRTPGRQLSSSDFLLGAIKTVATVVTPYITVKTRL  
QAKGKYSGLDVLQKIYTQEGIGSFFKGIKESKIVQSVLTA AFLFMFQNKL  
ANSFLKLLVYIYIRRLPQRK

>3-hydroxyacyl-CoA dehydrogenase Contig8174 (mostly complete, but with internal gaps), 735 aa, 673 checksum.

MGDSLRFDGKVVVVVTGAGGGLGKTYALLFASRGASVVVNDLGTSHTEGGA  
GSKAADLVVEEIKKAGGKAAANYDSVENGEAIIKTAIDNFRVDIVINNA  
GILRDVSVFKMKQADWDLIYKVLHGAYSVTKAAWPYMRDQGFGRVIMTS  
SAAGLYGNFGQANYSAMKLALVGFAKTLAAEGKSRNIHVNTIAPVAGTRM  
TATVMPPELIEALKPEFVSPLVAFLCHESTPVTGGIFEVGAGWVSAVRWE  
RTQGNFYDVSKGLTPEAIRDNWAKVEDWTNSTHPASAQDGLTSIIAHINQ  
LKAAAKAAGGNENVDPQVVGFEFPVTKVQYTEKEVMLYALSIGAAKNPT  
DPAELKFAYENSDFSVLPTFGVTFPNFSNVLSIPGLKFNPMMLLHGEQY  
LEIRKPIPVNATLTNHRGVKHLVDKGGKALLVVEADTKDEKGEVVVHNES  
YLFIRGIGGFGGGERGSPGNENQPPNRPDAVHKEKTRDNEALVYRLASGD  
MNPLHADPSMAAMGGFDRPILHGLCSFGYASRAVLKHFCDNDPANFKDVK  
VRFKHFVFPGETLVTEMWKEGDKVIFQCKVEERGEYCITNAAVTVSSAAS  
SSSASASAAAAAASSAPAFKAEAVLNNLSKLLDVAGEAVVKKVNGIYHFH  
ITDGPNGAKESWVVDLKTGPKGTITRGAPTKPVGVTLTLGDSSFQQLFSG  
KLNAQQAFMQGLKIKGDMGLATKLGELIKQQAAL

>peroxisomal biogenesis factor 11 Contig12064 (complete), 219 aa, 21FC checksum.

MSLSKSKCFLAATDGRDKLYKFFHYGARFLSWFCLNTANNAQWAKYWSNI  
DSVMSDGRKLLRFLFKFLSEIEKLGTI REARPMLLVANLLKTLGMAGYFFF  
NNLSWAMKFNI VSGDEKKWGLKSFVAWTVGLLFALVLDVVKYRENSRRQO  
KALASSQTELAQLKKEQRELEYAMIREVANLQISTSLVEINPIKSAGVV  
GLAGVVEAGLASYQIWKKC

>cyclopropane-fatty-acyl-phospholipid synthase Contig10602 (complete), 292 aa, 1B4B checksum.

MVEQLEARMSDDLKPKIQEHYDEISPYHDLWGRHIHHGYWVKGETKED  
AQVRLIEEMISRGMRPGAKVLDVGCVGGSITHLAKNLKASMTGITLSP  
VQRDMAEKIAAEEGVQASTSFHRMDGENMTFDDQSFDFVWICEVLSHF SR  
KDKFFSSAQRVLKPOGRIILADWFKAPNLSQEQHDKYIVPIEQMLLPEL  
NTMGEYMRMMEKNGFKVVHFDITSHVSKTWDICAEILNPTLWKLAF TK  
GGEALAF LRAFQSMRAGYGSSTFRYGIIIAEKVATQTSTAKL

>peroxisomal assembly protein pex3 Contig841 (and 10633) (mostly complete), 193 aa, 193E checksum.

ASLHRLRLRGAFESTQSTCAGTVGFPRQAQRRRPTSRTSPPPP NYASA  
WQQAPKDGQDRYALWDHCKTQTYARLVVGVYGVLLSTFLRVQVNI LGRY  
LYLETLIATDPSARFRIPLDVAIQDQTKRYLGYSEYVVHTGLPQLVALV  
QATAHQVLSYPLQRQCTYDDVLAIIDAMRRKMEHAPFSPGLE

>hydroxysteroid (17-beta) dehydrogenase Contig2708 (complete), 305 aa, 522 checksum.

MGDSLRFDGKVVVVVTGAGGGLGKTYALLFASRGASVVVNDLGTSHTEGGA

GSKAADLVVEEIKKAGGKAAANYDSVENGEAIIKTAIDNFRVVDIVINNA  
GILRDVSVFKMKQADWDLIYKVLHLHGAYSVTKAAWPYMRDQGFGRVIMTS  
SAAGLYGNFGQANYSAMKLALVGFAKTLAAEGKSRNIHVNTIAPVAGTRM  
TATVMPPELIEALKPEFVSPLVAFLCHESTPVTGGIFEVGAGWVSAVRWE  
RTQGNFYDVSKGLTPEAIRDNWAKVEDWTNSTHPASAQDGLTSIIAHINQ  
LKARY

>Short-chain dehydrogenase/reductase Contig8758 (complete), 329 aa, 12F2 checksum.

MSFFGLDLNACPAPLHSTVMVLGLLVLAKIAYFVASLVWRLLRPATDLR  
KYGAKSGGWAVVTGASDGIGKAYCIELAKRGNVMLISRTKSKLDEVAKE  
LEAKYKVETAVVAADLSSTDPKMYLDIAASINKLGKIGVLVNNVGLSYDW  
PTKYLNLPKETEEALIOMNIKTMHELTRIVLPLMVQNRKGAIINLSSFTG  
CIPTPLLSVYSAAKAYVNYFSVALAHEYKKDGIQVQSVTPGFVVSNSKF  
RKNLLGGVCNPDVIAKGSLSNAIGQDVHCNPFMHALIDWVNTAPENFI  
LEKIRATNQATETRALRRKQGAADVKKQK

>Alkyldihydroxyacetonephosphate synthase Contig1725 (and 22108) (likely complete), 616 aa, 1AA4 checksum.

MEKRDVWERLKWNGWGEKGVQYELNQNGNVEHSRTGVELPKIIPFAKDIF  
GLDDLENTPSVELDDIELAEPNPNEGFVSLKSFLSASQISFDKEQRICH  
AYGMSFRDLWRLRKGVI TDAPDCVLYPQSHEDVERIVQAAHVHRAHLIPS  
GGRTNIVGATEAERIENRFVSLDLRRMNRMLWVDKKTMTACFEAGILGP  
DLENGLKKEGLSLGHDPDSFQWSTLGGWLATCSSGMQSDKYGDIEDMCLS  
LKVVTPGVGTITTPFVPRNGSGPALKHLFIGTEGVMGVITQAVMRVHKIP  
AKQEFHGILFSPFEHGVAAIHTMVRKESHVAMVRLYDPDETRLSFHMKPK  
SSKLVSAFSELLKFKFLERFKNFDLQNICLMIVGVEGEVDNVNFQKKKVKF  
IAKEAGGFWIGQGPQKSWHEKRYDLPMLRDLLLLLEKGLWVDVAETAVSFSN  
LLLLLWKDVKESVLDLAFKERNAPGWIGAHISHTYTSVGCIFYHYASVQQLD  
KKDDVHGEEEDLSIYLDKAKKAATTAAILRNNGALSHHHGVGYEHVPPMSRYI  
GKSSIKLLSDIKKTLDPASVCNPGKLLPEAGKEDMDNEDHSFYKYGFASL  
TDQLKQASSVRAKSAL

>cycloartenol-C-24-methyltransferase Contig5964 (complete), 349 aa, 4BA checksum.

MSMEGDNKRATTIINYESLARDQVKKEVDGYIKLFTAEDASVEERKAKYE  
TLVNSFYDLVTNFYEGWGQSFHFAPRHRFESFEASIRHEMYLAHRLHL  
EKGQVALDVGCGVGGPARCIARFSEANIVGLNNDYQIGRAKLLTKEARL  
EHLINYMKADFMHI PAEDNTYDAVYSVEATCHAPDKVGVYSELFRVLKPG  
GLYATYEWVVTESFDENDPDHVKIKKGI EIGNLPELEKPSQIADALKQA  
GFEI IDNVDAKNADAETPWYLSLSGSFSLTGFKHTRIGRSVTHMAVSTL  
EYLKIAPEGTTRVSQMLCETADDLVEGGKKDVFTPMHFFLARKPLAKDE

>70 KDA PEROXISOMAL MEMBRANE PROTEIN Contig17179 (incomplete), 650 aa, 175 checksum.

FNSEQEVSSRAREEMGALS KLAPVVPNGSTSVGVGRVAEIIILGSRRTIG  
LVAIVASSMVYVVTTRNWAMKSNRPELLQTKKEDGAARQKVAVDGVFFSR  
LWRLKILIPGPF TPESGMVLVAAMMLSRTWCVDVWMLKNGTAIERTIIT  
RDFQGFVVVFLNFMVAFFPIALVNNLLRYGLNELALRFTRLTQHLYQY  
LNGFTYYKVS NLDNR IANADQLLTQDVETRLRRPIGKFTVNEQRLEGEFR  
FVNSRLITHSEEVAFYGGNEKERSVISKFRGLVNHLRYSIQFRALLGIV  
DSIIAKYCASCVGYLVVSRPFFDLNNAKLRNASQAELMEEYKSGRMLMN  
MALAVGRLVLAGRELTRLAGYTARVTELQNVLKDLNAGTYKRTMVSKNPA  
SGTSTRELKPNSGKIITQDHI IKFEDVPIVTPNGDLLIESLSFEVRS GMN  
VLVAGPNGCGKSSLFRI LGELWPLFGGTLTKPAKNKLFYVPQRPYLALGT  
LRDQVIYPHSHEQFRKAGGTDEDLVDYLRQVQLDYLVREGGWDAVSDWA  
DVLSSGGEKQRVAMARLFYHKPQFAILDECTSAVSVDVEGYIYTRCRELGI  
TLFTVSHRKS LQYHEYVLQFSGRGQYAFKQIDAETAFGSIWVVASLVK  
IQAVMNFMSRRQKASL

>acyl-coa oxidase Contig27272 (incomplete C-terminus), 283 aa, 1F3D checksum.

MEAGQVVRSGAGLLAAERKGASFPVRDLTLLLDPATPRRENFRALVAKDR

EFDNRDQHFRNRTERYQHALGLVKHLHLKYTKLGLNQTDMRLLTEEALTE  
FLPTLLHEIAFVFPFIRSQASPEQAQKWLPLAEQYRIIGAYAQTELGHGSN  
VQGLETTATFVPETDEFELHTPTLTATKWWPGCMGKTATHVVAMAQLIIH  
GKRVGVHAFIVPIRSLENHMPLPGVTVGDIGPKLGTDSNDNGYLRLDHVR  
VPRDHMLMGFAKVDREGRYSKPAHDKIDLTGLQ

>2-oxoacid dehydrogenases acyltransferase Contig18105 (complete), 306 aa, 127D checksum.

MHQSNLRLVLVAGLAVYAVWGTPQATLVYLVGLLFAFWFWASAGMPIRR  
KLQIATWGEPESESIHAKISLDATEKVKYIDEKRKTTRQHITITHVVGKA  
LGLALRNAPGLNGRIVFDRFLPFKTTIDISFLAMVEGGKNLAKVKVSNIDK  
KGVDOVATELDAGSQRRLRKGTDENFKKSMGPKLLPTWLIRLVVNTAAYA  
AGALGLSIPALGVEPHFPFGSCIIITSVGMGLGVDEAFAPFTPFARVPLLVI  
GAIHEGVKVEDGETKVTKKLLCCTIDHRFLDGAQGGAMAKVLRDVFNDP  
SMLDQE

>Pex11 Contig10122 (and 8822) (complete), 250 aa, 362 checksum.

MQDPNFLKYINTTIKLLSTHSGRDKVAKTLHYASRIWIWHLQNKGGKERA  
DQIESFRQAIGNSRRVGRFFSLLNSIPSIYQLVFPDPRTKDRESDLFRFL  
LVVANVSDMLYVSDNLTAAKYGFIKLSPETNYFWEELVGSWTWVSMI  
VYIAHDIKTYLKLQOQRLRLEHQVMKDSSTAKASASALAAATDEEIFNNRL  
SLIRNLADMQLAIYFCFPNSTWSSQVWGLFGVINAVTGGFQIWRGFHKAS

>citrate synthase Contig6506 (complete), 501 aa, 15A1 checksum.

MMMTTAPSTATVAARRLQRLAHLQISDVDLCPSTAAASGDKKETVTIT  
DNRTGKTIEVPIKNGTIAALNLKDLGLRAYDPGYLNTASATSRISYIDGD  
KGILRYRGPPIEELAEKSTFLEVAYLLVKGDLPNKQOYEEWTSRIMNHTY  
IHQNLISLLQTFRYDAHMPGMVVSSLAALSTFYPEANAALS GSGVFDLQ  
TRNKQIYRIVGKLPITIAACAYRHRMGRPYNEPVNHL SYVENFLYMLDHLQ  
EKDYRPHPKLVRALEVLFILHADHEMNCSTAAMRHITSSLADPFTAVAGA  
AGALFGPLHGGANEAVLRMLLESIGAKENVSKFLEEVKGRKKKLMGFGRHI  
YKNYDPRAAI IKKTAYEVFEVCGREPLIEVAIELERQALADEYFVSRKLY  
PNVDFYSGLIYKAMGFPTDIFPVLF TIPRAVGWLAHWVLLDDPENKIVR  
PRQVYLGHDLRHYP SMEERSAAKVTTTSKDYISQNSRRRIVSLQAHKQAHH  
H

>indigoidine synthase A family protein Contig22868 (and 1548) (incomplete), 716 aa, 24BE checksum.

MQHRAVHRLHTLNGHLTTEYHGEVDAAPTQKQKIARPRLPLVLLPEVAQA  
LAANRPVVALESTIISHGMPFPQNLLETARDVERVVERVVRDNGAVPATIA  
ILDGVIHVGLSPEGLEKLARAGKQVHKTSRRDLAAIVAGKLN GATTVSGT  
SYIANLVGISVFATGGIGGVHRGGEITMDVSADLTELGRTPIAVVCAGAK  
SLLDIGRTLEFLETQGVAVVGYGTDEFPAFFTPHSGHKTSCLDTPEQCA  
RLIHSGKALRLDSGVVFGVPIRKEDAAEASQVEKAIQQAIKEADERGVHG  
NDVTPFLLQRVNELTGGESLKSNI CLIKQNAKVAQA IASALSVIRAQEKD  
AGRSKKPKKRKTGRPVVVGAMDISARPYKGEAFIEGTSNPGIITHQWG  
GVGRNIAECMTRLSLPLLLISSVGDDELGHAYIKWADKMGMP TQGISFSD  
SESTGIYSATMQADGELMHAVAGMHIFKTTITPEQVLKFRKEIEEAAMVVV  
DGNISVETMRALVTTCAASDTEVWFEPSTSVVKSLLPAQAGVTAHLTYISP  
NVEELNMAAAALDGSAMDSARDMDTVVRNASKLLHAGVKNVLVTMGPDGA  
ILFRLGQEDGHLDAHHRFPDPSRAVVHVTGAGDCFVGGMVWALLARTAGD  
AEAAIPFGMAAAKFTVEWDGPVSPLISTRGVIAATTAKPGASSHQPARSA  
AGALWRDTQVLIINTTC

>cycloartenol synthase Contig6630 (complete), 715 aa, 119 checksum.

MEGFESGKEATDLRRWKLKVDEGRQVWHYIDGDEPVQQLTDKYTLGLLS  
DEDVPPTDPASTPLEAAEKAVAFYQQIQSEDGHWAMDYGGPMFLMPGLLI  
ACHVTGVELPRPVQIEMVRYLTNRQNA DGGWGLHIESPSTIFGTGMNYTA  
MRLLGVPMEDDRMRAREFLAANDGCKGIPSWGKFWLAVMGVYDWEGLHP  
IPPELWLLPYMLPIHPGRWWCHCRMVYLP MGYVYGRRI TAPESPLVLSLR  
KELYPNDDYAKINWYSIRS YVSPDLIYPHSTLLECLYVILDNYEKVHSS  
WLREKSVLLTAEHVAAEDKFTDWVCIGPVNKTINMLCSWHAQKDSKEFQ  
RHVDRVPDYLWLAEDGMKMQGYNGSQLWDTAFSVQAI IETGLGDQFQECL  
QKAYS YIDITQVREDVEQMEYFYRHISKGAWPFSTRHHGWPI SDCTAEGL  
KASLLLKQFSWVTPFEDQRYFDVAVNVILSLQNSDGGWATYELQGPSILE  
YINPAEVFDAIMVDYPPVECTSACVQALTMFVQHYPRHRATEITTAVKKA

VDLIKSKQRPDGSWYGSWVCFTYGTWFGVEGLMAAGEPSDSPYIQRACQ  
FLLSKQNHEGGWGETFESCSTKQYVQNEETQVVNTAWAVLTLKKAQWPDR  
RPVDRAVQVLMKRQLPNGNWPQEDIKGVFNANCAISYTAYKNIFPIWALG  
LYEHTQPQSQKTAKL

>malate synthase Contig26557 (and 23383) (likely complete ... from PGP), 550 aa, 2289  
checksum.

MNNEQRTTLLVRHGIEILGPIEKGYEQVLTVDALVFVAELHKRFDARRRT  
LLAARDERQSRIDAGEMPDFLHETRHIRESERWRCGSIPEDLKDRRVEITG  
PVDRKMIINALNSGAKVFMADFEDSSTPTWENGITGQINLYDAIRRTISM  
KVGEREYKLNQATATLMVRPRGWHLDEAHVLVHGKPVSGSLFDFGLYIYH  
NGHALLSRGSGPYFYLPKMESHLEARLWADAFRYAEQRLDIPHGSIKATV  
LIETILAAFEMDEILYELRDHSAGLNCGRWDYIFSTIKKFINHKDAVFPD  
RALCTMRSHMMASYVDLLIKTCHRRGIFAMGGMAAQIPRNDNAANQAAL  
AKVRDDKLEVKAGHDGTWVAHPDLIPIAMEIFNEHMKTPNQIHVRRDDV  
RVTSDDLLKFKPGDITLNLGRDNVRVCLVYLRAWLSGRGCVPINNLMEDL  
ATAEIGRSQVAQWIRHGVTDTGTQVTISLALKILKEETDALRGSTPASK  
TPSGAADSLALAHDIFAKVIVAAPATFYDFPPTLAYQHILTLQPPFHPRF

>5-hydroxyisourate hydrolase Contig11000 (complete), 190 aa, 155E checksum.

MEMMNAATSPERALSRLSSANRRLWTVGGHLDSSSPLISQRHVAADAGA  
HSAPSSTTTTATTSTNGSRKFLSSLSSHALDTTLGKPASSLPVTLFRLRP  
STGAVESNEEWEALFGAATDADGRVTSATFPPIAAGTWKLRFDTSAYFQR  
IGVAKFLYPYVEIVFQVETGQHYHVPLLLSAHGYSTYRGS

>peroxisomal-coenzyme A synthetase Contig2323 (incomplete), 277 aa, 1C01 checksum.

NECTWYSAVPTIHQILLARADKDYTTSGKLRFRIRSCSSALAPAVFKQLEE  
RFKAPVIEAYAMTENS HQMSTNQLPPGKRKPGSVGQGTGVEVTIRDDSGK  
ELAQGEKGEVCLRGPTVTRGYHNNPQANKTAFHEGRWFRTGDQGFDEDK  
FLVLTGRIKELINRGGEKIAPSEIDSALLSHPDVSEAVSFGVPSDKYGEE  
VEAAVVLKGGREGGKAVEEAAILKHCHAKLAAYKCPRRLYIAKDLPRATG  
KIQRHVATHFLKNSADSDKSLKKAKL

## Cytoskeleton

>actin Contig3705 (complete), 375 aa, 1F49 checksum.

MGDEVQALVIDNGSGMCKAGFAGDDAPRAVFPVIVGRPRHTGVMVGMGQK  
DSYVGDEAQSKRGILTLKYPIEHGIVTNWDDMEKIWHHTFYNELRVAPEE  
HPVLLTEAPLNPKANREKMTQIMFETFNTPAMYVAIQAVLSLYASGRTTG  
IVLDSGDGVTHTVPIYEGYALPHAILRLDLAGRDLTDYLMKILTERGYSF  
TTTAEREIVRDIKEKLCYVALDFEQEMHTAASSSALEKSYELPDGQVITI  
GNERFRAPEALFQPSFLGMESAGIHETTYNSIMKCDVDIRKDLYGNVLS  
GGTTMFPPIADRMQKELTALAPSTMKIKIIAPPERKYSVWIGGSILASLS  
TFQQMWISKEEYDESGPSIVHRKCF

>probably myosin light chain kinase Contig3837 (complete), 361 aa, 28F checksum.

MGCPGSKEAKDNGGGGAKPSKQVNDKPEKPVKPSAGASEAKATDDKCK  
EPPAERVIPOGEPIKLDLDELDFILFEPIEDHYELGEEIGKGGFSVYKA  
VRKSDHAEFAVKCIKKKMVEGDDIKLLRREIQIMKKNLHPNLIKLYEVYE  
DDEQFYLMELVKGKELFDKIVERGMYSERDAANIILQVVS AVRYLHENG  
IAHRDLKPENLLSAGEEENEIVKIADFGFSKSFADGEKLMTSCGSPGYV  
APEILTAESYDKSVMWSVGVIIYILLSGYPPFYADSAPALFKKIMDVKY  
DFDDSVWDDISDSAKDLIRNLLVKDPSKRFTASHCLEHAWVRGSAANERQ  
ILKMNRDNTKS

>suppressor of actin homolog Contig2877 (complete), 593 aa, 71 checksum.

MATVADKYHLHLPDAFLFEPVTTTEPAHLLIEERATGTFSLKTPRPGSFR  
SSEGIEEIFGLIGIIRLLAGPYLVVITARKRVGRLLGCDVWRVTGTKLLP  
FVKGRLHTERQRDEERYLALLQSILKGGHLYYSTHYDLTHRAQKQHALRD  
DHQDKPMWERADQRFWNRYLAQDFISSQLDGVVTPVMLGYVQIESHCTV  
NGHRFDYALISRRHTKRAGTRYHIRGADEQGHVANFVETEQVLVPAQDR  
IYSFVQTRGSIPVFWSQAPDITYKPKPRLTATEKRNAAAFKAHMDDLTRH  
YSRHVLINLINHKGAEAVIGKEYEKQVQLYGDESRYVWFDFHHECRKMR  
FENVSNIQOVKPEIEQFGYFLTENNEAVRKQEGVFRTNCIDNLDRTNVV  
QSTLAREVLNAQLLHAGVFORPSESIADHPAFRQIFNHVWANNADAISEQ

YAGTGALKTDYTRTGKRSFKGVLNDGLNSATRYLNNFKDGFRODAYDLF  
LGNYVVGQSPRSPFAHNYRPVATTLFVIALLLIGVVMLLASVVAPILQPEG  
TQSIYQFMVIVFWAVAMVGAYRVLKLYGRDLVDRPQLVPIPH

>coronin Contig12947 (complete), 403 aa, 7C checksum.

MSRVVRQSKYRHVFGTPOKPCENCYTDIRLSTNQWDSNYVTANTKFFAVCW  
EAAGGGSFAVVPWVQKGLKADYPLVSGHKGPVLDVDANPFNDYLFASAS  
EDGTAKIWKVPEDGLTETMRDPVQNLSGHKRKGVNRWHPTANNVLATSS  
TDYTVKVDVEKGAACHVDGHADIIQSIDWNYEGSLIATAACKDKKIRII  
DPRTGQVVSEAAAHTGVKGSRAMFLGRTEKVFTVGFSTRSDROYAIWDPS  
NMGTAQAENIDTGSGLLMPFFDPDSSIIFLAGKGDGNIRYYELTDNGSK  
IYFLSQYQSNVPARGMAYYPKYGVVDVGSCEISRLIKATTTGIEPISFNVP  
RKEGLDVFQDDIYPPATAAPEPTTTAAEEWFGGKTVPKQISLEGGFVARER  
PAD

>Actin-related protein Contig8946 (complete), 428 aa, 1123 checksum.

MSRSGLPAAVIDNGTGYTKMGYAGNTEPQYIIPATAIATKGIQKTPAAAP  
AAGGAPGAAGKNIADLDFFIGDEAYENSKVYQITMPVRHGOVENWTHMEQ  
FWEHCIFKYLRCEPEDHFFLLTEPPLNAPENREYTAEIFETFNVPGLYI  
AVQAVLALAASWTSKQVTEKTLTGTVIDSGDGVTHVIPVAEGYVIGSSIK  
HIPLAGRDITNFVLQLLRERNEKIPPAETLEVAKRIKETFSYVCPDIVKE  
FKKYDTEPKDFKTYEGIESVGKKPYNVDVGYERFLGPEIFFNPEIFSSD  
FLTPLPKVVDETIQSCPIDTRRGLYKNIVLSGGSTMFKDFGKRLQORDIKR  
AVDYRIKRSEELSQGRIKSKAVDVKVISHHMQRFAVWFGGSMLASTPEFY  
KVCHTKQOYDEVGPSICRHNPFVFGAMTM

>strumpellin family protein Contig13782 (incomplete N-terminus), 220 aa, 30F checksum.

SGKLVLFVRRVMEIIPKSMFFILNDIIELOTHKIKELPTRLEKVELKDFA  
QLDERNQLAKLTHGVSKFTEGILAMQTTLVGIIKVEPKQLLEEGIRKELV  
FKLASAMDKILIFKTGKIDEFESRLKQLASQLDGFSSRFQYIQDYVNIYG  
LKIWQEEFSRIVNYNVEQECNSFLKTKVYDHQSMYQSTAIPIPRFSPVDN  
SVNFIGRLARALLQHTNYNN

>Arp2/3 Contig1340 (complete), 348 aa, 2503 checksum.

MSFVNVGESTTCITCHAWNADRTKVAFCPNNNEVHIYKKQGADWVQEAFL  
QEHDQVVTGLDWAPKTNRLVSCSQDRNAYVWTFEQGRWKPTLVILRINRA  
ATQVKWSHDEKKFAVASGAKCVSICYFEEDNDWVWSKHIIKHKSTVTSVS  
WHPNNILIATGSTDFKARVFSAWVKGVDERPAPTPFGDKLPFGECLAEYE  
SSGWVHEVAWSPSGNRLAFVGHDSVTFIDAPNTQORLTLSTLPFRSVAFL  
LSENTIAAAGHDCNPAIFNAAGSAWSFTKVFVDEEKAAAAGGANAMSMWQ  
QKVDLGTTSNETTLSTKHQNAISNLQPVGAPGRITSFSTSAVDGKLV

>Actin related protein 2/3 complex, subunit 4 Contig11881 (complete), 170 aa, 81D checksum.

MATSTLAPYLNCRQTLTAAMCLENFASQVVERHNKPEVEARANKELLLN  
PVVISRNKNEKVLIEGSINSIRISICIKQADELETILCKKFMFLAQRAE  
NFVVLRRKPIKGYDISFLITNFHTESMFKHKIVDFIIOFMQDIDKEISEM  
KLGVNARARIVAQSYLKEFM

>myosin II heavy chain Contig13878 (complete), 1509 aa, 102 checksum.

MAAQRRRKGGEVESDYIKYLKYKNTGFQVSASDKTLAWWPTKDADRAFCH  
VEVTKDDGKNFTVRLNENGEEKSQPKNEKNFLGVNPPKFDGVEDMGELGYL  
NEPAVLHNLKRYDADLFHTYSGLFLVVVNPYKRLPVYTPPEIIDIYGRQ  
RDKVAPHIFAISDAAYRAMLNTRQNQSMILITGESGAGKTENTKKVIQYL  
AIAGRAEGGLLEQQLLEFNPILEAFGNAKTTKNNNSRFGKFIELQFNAG  
GQITGANTFIYLLKSRVTAQGAGERNFHIFIQILSKAMPEELKQKLLT  
KPEDYFFLNQACVYTDMDDAKEFDHMLKAFDILNINEERLAIFQOTIS  
AILHLGNLPPFDVNSETAGLKDEVELNIAAELLGVSAAGLKAGLLSPRIK  
AGNEWVTRALNPKKAMASRDALCKALFGRLFLWIVQKINRILSHKDKTAL  
WIGVLDISGFEIFQHNSFEQLCINYTNEKLQOFFNHHMFTLEQQEYEREK  
IDWTFVDYGMDSQDCIDLIEKKPMGILPLLDEQTVFPDADDTSTFKKLFQ  
THENHRNFRFRPRFDANNFKIVHYAGEVEYQTSAWLEKNRDPLEDDLSNLC  
KKSSVRFVTGLFDEDLMPFKAAPAEKAAAGGSRNRSTGRGKGAQFI  
TVAFQYKEQLAHLMSMLSSTAPHFIRCIIPNLGKKPGVSDQLVLDQLKC  
NGVLEGIARIARKGWPNRLLKYDEFLLKRYFLLKPGATPTSPSTKDAVKDLIE  
HLIAKEPTKVNKDEVRFVTKIFFRSGQLAAIEELREQAISKMVVSIQAG  
ARAFLARMYDKMREQTVSAKILQRNIRAWLELKNWAWYQLYVKARPLIS

QRNFQKEIDDLKKQVKDLEKELAAALKDANAKLDKEKQLAEEDADKLEKDL  
AALKLKILDLEGEKADLEEDNALLQKKVAGLEEEELQEETSASNDILEQKR  
KLEAEKAELKASLEEEERNRKALQEAKTKVESERNELODKYEDEAAAHS  
LKKKEEDLSRELRETKDALADAENISETLRSKLNTERGADDVRNELDDV  
TATKLQLEKTKKSLEEEELAQTRAQLEEEKSGKEAASSKAKQLGQOLEDAR  
SEVDSLKSKLSAAEKSLKTAKDQNRDLDEQLEDERTVRANVDKQKALEA  
KLTELEDQVTALDQGNAAAAQAKTLKTQVDETKRRLEEEAEASAARLEKE  
RKNALDEVAQLTADLDAERDSGAQQRRKLNTRISELQSELENAPKTGGAS  
SEEVKRLEGELERLEEEELLTAQEARAAAEKNLDKANLELEELRQEADDAA  
RDNDKLVKDNRKLKADLDEARIQLEEEQDAKSHADSSRRLLAEIEELKK  
RVAKETSQKQKADQKANYQRENESLKADRDSIERRNRDAERQVRDLRAQ  
LDDALSRLDSEKRAKEKSVEANRELKVVLDLDRERQSLESLSKFNSALESD  
KQILEDEIGDLHEKNQLOAKIAQLQDEIDGTPSSRGGSTRGASARGASV  
RAGSARAEE

>F-actin-capping protein subunit beta Contig1206 (complete), 271 aa, 1C24 checksum.

MGSELDLDCALDLMRRMPPSSIEDNLAGLIDLVPDLTEQLLSMVDQPLKVAH  
DSQARRDYLLCDYNRDGDSYRSPWTNKYDPSLPDQALPSAQLRQLEVQAN  
EVFDIYRDLYFEGGVSSVYCWDLDDGFAAVVLIKKTQDQSKKGQPMKGTW  
DSIHVVEVVDKGNNAHYKLTSTVMLFIETETKETGRVTLAGSLTRQDEKD  
FPVDKVNPHVANIGRMIEDMELKLRITTLQTIYFGKTKDIVNELRQVMPVS  
VLKRSALQQQIAGAIGGRGN

>F-actin-capping protein subunit alpha Contig8778 (complete), 295 aa, 1F7F checksum.

MSDITQEEIIVEIVTNFLLNSPPGEFMEVVTDVRGLLPDESILNDSAPATF  
REYNTDQMLQMQSPGNPHKFLITKFGVEVNGEYLDPRGRQVVHFDHIRQE  
VTGSRPISGELDNSVESFRAAFDDKATEYTNHEHYQNGTATIYGKKEGGSV  
VVTICISSARFNPNNFWNGRWRAVWTKCFSPSGGNVDISGVLKVVNHYYE  
DGNVQLNTETPVKISATGSDARGLADAVVKAIDKAESNFHKSLETSYNTM  
GDTTFKALRRVLPITRTKIDWTKIQNYKSGGDAGGKAAASRGVRN

>actin-binding protein Contig23436 (and 610,6438) (complete), 846 aa, 2562 checksum.

MRQIITISLVFLAVLALVHVAAGQIPSTAVRNFTYTGFVARDELDFGVE  
FNPVFGPENLKLMFYDPLGGDERIEVGAVWYKRRRAHLESFNVFTVVRMSN  
LSHTGVGNPDGFALVVQNHANAFGAGAGGIGYGATPDYEDLGVRRSVAV  
EFDTYLDENLGDPNNSNHISVHHTTPERVHNSAHEETALTPPGAVTNIPGI  
AGFTHKYNVQYIEKQLSVYIDDSASPAYQTTIDIPSIISLNSGAFVGLT  
AACMSTCEDVEVLDWSFNVAAILDATKSFVTNVKNSVAGRTSSFTVQGV  
DTNGYYYQTGGDASKWTFEFTRVSGSGSVVSPSVNVVDKNDGTYTISYAP  
TSAGVYDVTVYYNANALAGMPFRITVDPGAVDATKSDILGNINGGVAGQP  
LNITILGKDAFNVNPNNNPPATFTASFNNGGASASSSFIGNGTYLIQYT  
LTTARTYTMTVTYNGTAQQVKGSPFNAVITIPALPEPSASVASGTGIVGG  
TAGTTLTAVVLRDRFQNNITSNLPAGYQLTGFWDKPAAGNNVFTTVQPD  
GTLAGSYAISTAGTYRLTIVMAPTGLPISGSPFPVTISAETITSAAQSV  
TGAGLTTASAGNNASFTVQARDQFGNNMASSDASIAVSFSDDSGVPLQIA  
HTAVQNSADRSQWIVSYVPTNALSTRISVSLNGAPIKASPFIVNVHPGTL  
DPKNCFAEGLGLATPKTKVPLSFVVIADHFNNRLKSGGATIDVTLKEMK  
SGATVTGSVQDLNNGAYNVGFTLTRSGTYNITINANGVPIGKDTKYSMVV  
PNEGLGALGWALIVLAILALIAVVGGGAFWYLKYYKARSYDEIGA

## Ribosome

>cytoplasmic ribosomal protein L3 Contig173 (and 12087 and 27167 and 20599) (complete), 398 aa, 264E checksum.

MSHRKFSAPRHGSLGFTPRKRAARHRGKCKTFPKDDASKKPHLTAFLAYK  
AGMTHVVRDLDPKPSRMHKREVVEAVTILEAPPVVVGVIGYIDTPSGMR  
TLTTVWAQHLSAECLRRFYKNWYRSKKAFTKYQKALAANKARVFDREVA  
RLKKYCTVVRVIAHTQVRKLNQRQKKAHIMEIQVNGGSIADKVDFAVSLL  
EKPVVDNVFGDSELVDTIGVTGKGGYEGVTTTRWGVTRLPRKTHRGLRKV  
ACIGAWHPAAVQWSVPRAGQNGYHHRTELNKKIYRIGKGVROEGGKIVHN  
NASTEFDLTEKSITPMGGFPHYGEVNEDYLMIKGAVIGPKKRVIITIRKAL  
LRPTKRWQLEKIAPKFIIDTSSKFGHGRFQTKEEKEKFMGIRKKDKVVA



>cytoplasmic ribosomal protein L15 Contig11929 (complete), 204 aa, 1935 checksum.  
MGAYKYVQELWRKKQSDVMRFLARLRCWEYRQYPMVLRVSRPSRPDKARR  
LGYKAKQGFVIYRVRVRRGGRKRKIRKGRVHGKPATQGVNALKFQORSLRS  
VAEERAGRRRCGNLRVLNSYVWAQDATFKFFEIILVDPFHKAVRRDPKMNW  
IAAPTHKHREMRGLTSAGKKYRGLRGKGHNYTKSRPSRRAVWKRNNKVSL  
RRYR

>cytosolic ribosomal protein L15a Contig16226 (complete), 130 aa, 8A3 checksum.  
MVRISVLNDCLKSICNAEKRGKRQVLIRPSSKVIVKFLTVMMLKHGYIGEF  
EIVDDHRSGKIVVDLIGRINKCGVISPRFDIKLKHIEQWITDLLPSRQFG  
FIVLTTSSGIMDHEEARRKGC GGKVLGYFY

>cytoplasmic ribosomal protein L7 Contig7966 (complete), 248 aa, 23EB checksum.  
MSTATKTGA AVPPPETLLK KKHNEATAARLQKRKAEAAKARRNKRKLI  
FKKAEKYVKEYRSQERELIRARRTAKSAGHFFVEPEAKVALVVRIRGIMG  
VDPTTRKILQLFRLRQLN NATFVKLNKATINMLHRVEPIAYGYPNLKT  
KELVYKRGFAKINKQRIPIVDNSIVEGKLGKYGIICVEDLIHEIYTVGPN  
FKKANAF LWPFKLSNPRGGFTKKGTHFVEGGDAGNRESHINTLVRRMN

>cytosolic ribosomal protein L6 Contig18716 (complete), 245 aa, 177D checksum.  
MPRKPHAPRNHDLVRGISRYSRSAMFRRSGKAAVKKSGHQWKDVAATKKA  
PKSVEKTFNKTEKRTVVAKAKRFYPAEDVPRPIPSRKSHHKPAKLRSSIT  
PGTVLIVLSGRFRGRKRVIFLQQLQPSGLLLVTGPFKVNGVPLRRINQAYT  
IATSTKVDISGLEVPEKFNDA YFKKGKAAKKEKTEDEFFATGAOQKKTID  
AHRIADQKEFD AKVLEVVGKVPNLAAAYLNAKFSLTGKQFPHLIK

>cytoplasmic ribosomal protein L18 Contig23859 (complete), 185 aa, 25CD checksum.  
MGIDLEHKHRKNKNRSSPKTEDPYLLLLLVKLYRFLARRTGADFN RVVLKR  
LCMSRTNQPPSLIKLARFTKGKEDKIAVVVGTVTDDARLLKFPKLTVCA  
LRFTEGARTRILKAGGEILTFDQLALRAPTGANTVLLRGRKTARKATKHF  
GAPGVPNSTTRPKVANRSRKTERRARGRRKSVGFKV

>cytosolic ribosomal protein L0 Contig10235 (complete), 329 aa, 1963 checksum.  
MSKGGGKFQORKKEYFTKLSNLLVDYKVKVLI VAANNVGSNQLQVRQELRG  
KAVLLMGKNTMIRKCIRENLTKNPDLEALLPYVKGNVGFVFTNGDLSDMR  
TRIGAVKVKAAAKSGAISPCDVIVPAGPTGQDPAKTSFFQALTISTRISK  
GVIEIVNDVHLVKEGAKVTASQAALLQMLNIQPFEYALAVKTVYDDGSVY  
PVSLLDITDDDIINFRKGVANVA AISLRIGYPTVASVPYALTSSFRNLL  
SVSLATS YTFPQAEKLDLLANPEAF AAALAAAAPAGGAAPATATSAAAP  
AAAAAKVEEEEEEAEDMDAGGLF GGGDDDY

>cytosolic ribosomal protein L14 E80POFO01AVKL1/27081/6466 (complete), 150 aa, 22F8 checksum.  
MVFKRFEI GRVAVINYPDAGKLCV IIDVLDQNFRAFIDGPSSITGVQRQ  
AIPFKRLAL TDLKIKIQKSPRLKSLVKAYTEAGIQEKWEATSWAKKIALR  
KKRAALNDFDRFKIMLAKKEKSRVVRQELRKLTKEFHKKENDARVA AKKQ

>cytosolic ribosomal protein L23ae Contig12225 (complete), 210 aa, 944 checksum.  
MPKETKKAPAAATKAAPAKAAPAKAAAPKKDVAKAAPKKDKVNRAAKRAA  
APADKKADS AVAKKTTGQAAQARSKALKLQKTIKKGATKRVRKVRTNVHF  
FRPKTLRLPRNPKYPRRSVPRTNKL DQFRVLRHPLTTESAMKKIEDNNTL  
VFIVDLKANKRQIKDAVKKMYDITAEKVNTLV RPDGKKKAYVRLTGDFDA  
LDIANRIGII

>cytosolic ribosomal protein L11 Contig1590 (complete), 192 aa, 1228 checksum.  
MSQTKAAAAATPAGAAPT RTTKQNPMRKLKIDKLILNICVGESGDRLTRA  
AKVLEQLCGQTPVQSKARFTIRTF SIKRNEKIAVHV TIRGEKAAEILEKG  
LKVKEYELNARNFSDTGSFGFGIDEHIDLGIKYDPQIGIYGMDFFVVLAR  
PGFRVGRRRRCQNSVGTNHRVSKDEAIKWFEDKFE GVVLRKK

>cytosolic ribosomal protein L17 Contig19609 (complete), 176 aa, 14CA checksum.  
MGRGIYGREPENPTKAAKARGSDLRVHFKN TRETA AAIQGLGYRKAVQFL  
EDVVKHKQAVPFRRYNGGVGRHAQAKQHHLSTQARWPKKSAEFILGLLKN  
AESNAEVKGLDVDALVSWVQVNKAQKQRRRTYRAHGRINPYMSNPCHIE  
VILTEKATHVQKPKSDKKKADTTESA

>cytosolic ribosomal protein L9 Contig3420 (complete), 189 aa, 89B checksum.  
MKTIVASQVLP LKPNVTVSVNSRVVTVK GPRGELTRRFKHTDAEMEIIIG  
KKRKLKVTIWFGRKNLACIR TICTHIKNMIVGVTKGYEYKMKFVYAHFP  
VNCNIPDDGKFVEIHNFLGEKV VRRVHMLEGVKVT RSTEKDEIILTGNDL  
ELVSQSAANVHQSVLVKNKDIRKFLDGIYVSEKKVIGQE

>cytosolic ribosomal protein L13 Contig1776 (complete), 214 aa, 1CC9 checksum.  
MPKHNNLIPNQHFHKAQONHVKTWFNQPAKKKSRRVARAAKAAAIFFPRPV  
QGPLRPVVHCPTIKYNTKLRRLGRGFTLEELRGAGITKRFAQTIGISVDHR  
RKNKSEGPLADNINRLKQYKAQLVLPKRKESKKHPRKADEAAPEDREKA  
TQLTGAVLPVKQKEVVRVKAQVVEPMGKGSFAFVTLRRARADAKYIGIRKKK  
ALAREEKAKLKKKD

>cytosolic ribosomal protein L19 Contig4193 (complete), 309 aa, 2054 checksum.  
MVSLKLQKRLAASVMKCGQKKIWLDPNEVSEISMANSRQAVRKLVKDGYI  
IRKPPVMHSRARVRKNLLAKRKGHRMGVKGRRGTRNARMPEKVIWIRRM  
VLRLLLRKYREAKKIDKHLHYELMVKVGNVFKNKRVLMEYIWKAKAQKI  
KDKAEQEQGELRRQKNRQMRERRAKRLDERRKVLGEGDKKAVKKEETGKK  
AAAPAAAAAPKVSKNQKKKEAAKAAAAAAPAKAAAPAKAAAPKKEETKAA  
APKAAAPAKAAAPKKEETKAAAPKAAAAKPAKAAAPKKEAAKPAKAAKPA  
AKGGKKGK

>cytosolic ribosomal protein L12 Contig6683 (complete), 173 aa, 4EC checksum.  
MPPKLDPNAILIVRVVTGGEAGGVASLAPKVGPLGLSPKKIGDDIAKST  
QEWKGMKITVKKLIIQNRQAKVEVVPASAALLIKALKEPPAPTNOKKEKGA  
PGPKHDGNLTFDDVIEVAKTMRARSMAARTFAGTVKEMLGTCVSLGCTIDG  
RGARDMQKAVDDGEFDDRLAQFD

>cytosolic ribosomal protein L27 E9BS9UA01DRL9H/11387 (complete), 136 aa, D07 checksum.  
MPKFLKPGKVVIVLNGRYAGRKAIVENRDDGTKARPYGYAVVAGVDKYP  
KKITKSMGKKKIAKTKIAPFVKAINYNHLMPTRYGLDVELRSIVCKENA  
LEKQNKYKTKQALKKVFQTRYNSGKNKWFFTKLRF

>cytosolic ribosomal protein L24 Contig26518 (complete), 159 aa, 1E9D checksum.  
MKTEICQFSGYKIYPGHRRYARTDMKTFVFINAKAEKAFLLKSNPRKVL  
WTTVYRRIHKKGTTTEVQKKKTRKVVVQORDIVGATLDQIKQKRAQRPEI  
RAAAKEAALKEIKERQKKKEDLKKKAAPAPAKGAKGKVAAPKATKAKAP  
KAPKGQKGR

>cytosolic ribosomal protein L10 E9BS9UA01EDWMT (and 10857) (complete), 208 aa, 6BA checksum.  
MGRPARCYRYCKNKPYIKSRYCRGVPEPKLRIYDLGRKKAGVDEFPFVA  
HLLSWEHEQISSEALEAARISCNKYITKMAGKDSFHMVRVHPYHILRIN  
KMLSCAGADRLQTMRGAFGKPGACVARVKIGQILFSVRSKDNSKAHVIE  
ALRRAKYKFPGRQKIVLSNKGWFTPLQREEYLQLKSEGRIIPDGVNAKVV  
KNKGVLGF

>cytosolic ribosomal protein L35a Contig18397 (complete), 108 aa, 64 checksum.  
MGRQPVRLYTKGTFVGFQQRGHRTQNPDVALVAIEGVQOKEDTEFYLGKRI  
AFVYRGHKKKQGTKIRVIWGRIARPHGNSGLVRRARFVNNLPPQAMGATLR  
VMLYPSRV

>cytosolic ribosomal protein L34a E80POFO01B2QY2 (and 5227) (complete), 114 aa, 584 checksum.  
MVQRLTYRRRHSYKTASNTTRVVKTPGGRLALQYTKKKKANGPKCGDCGVS  
LPGIAHLRSKEYARISKRQKHVTRAYGGSRCATCVRQORIVRAFLIEEQKI  
VKKVLKQOHATKAK

>cytosolic ribosomal protein L4 Contig25372 (complete), 399 aa, 2150 checksum.  
MASRPLVQVHGEGGAGATVLLPAVFTSPIRPDVVQEVHSALAKNRRQAYA  
VSRRAGMQSSAESWGTGRAVARIPRVPGGGTHRAGQGAFGNMCRRGGMFA  
PTKTYRRWHRKVVNVNQRFALCSALAASAVPALVMARGHKISQIPEVPLV  
VATEAVKDVTKTKHAVALKLLNAYEDVEKVKDSRKIRRGVGMNRNRRV  
QRRGPLVIYDQKSPLVFAFRNIPGVELCSVERMNLQLAPGGHLGRFVIW  
TKDAFEKLDIAYGTYTKKSTKTHFTLPRPLMTNADLTRIMTSDEVQSHL  
RKANRKPTRTIRKKNPLKNRGMVMIKLNPEKTRIRNQILQEKARAEKKDA  
ILAKKREHFKSKQIKKQRAEYKALLHNPRVYEGIYKKEVTEEAADQ

ER/Golgi

>prenyltransferase/squalene oxidase Contig24682 (complete), 365 aa, 4EA checksum.  
MNRKKNLRLTLLAFLSLALISLGASVSQONGYIHVVSHLDRFQTPAGGFS  
LVEGGKPSLEATSHALFISSFLGRKKINQQEVARYIQTLENGDYGYS  
AGLPSDLESVRQAVLSYQHLGLAVPNAGNVASFIKSLYDTQTNLFAARVG  
EKGDLLKSTALAFQALEYLGELQORQWVQDIFEKVRTYLSKHVQLADNAHFA

FDEKTLSTTSANYYGVLGSLVGFDFVSLPKWAAFVAALQNOKEGGFYTG  
LDKKTTLTLESTAHAISTRLLQQTGKNGTEQFVDVVSGEALANYVVPPIPRD  
LRSAAQAHLAVALTKVFSRNFETRYYYEFLRASGSADKKVVQGTQLKPV  
SVKTFDGMFHAGLDV

>protein disulfide isomerase Contig8202 (and 3106) (complete), 406 aa, 81E checksum.

MKQSFVVFILFGLCIGSLLTISVTGETTSDVVVLDNDFDEHTASGDWFL  
EFYAPWCGHCKNLAPVWEDLATQGKAKGLRVGKVDCTQNKIIGSRFGVKG  
YPTIKLLKDNQLYAYKGARKVDDFLQFAESGYKAVDPVVPVAPAVVVEEA  
EDVEGQTAGGAGEVQILTAENFTLATNGGKWFVKFYAPWCGHCKNLAPT  
EKAASELKGKVNIAKVDCTTDGFMQLFGVGRGYPTLKKFKGDGLVRDYS  
G VREVSDFSDFAKKGKQATAQDYPLPSFLMSPVVKFYQACEPIAAWINA  
NVGYSFAIAALSFIIFGLLVGRLSAGSEIRYVIPKELGPQWNEALLAKKKE  
LEEKKKARREKREQRKGGKEKITGEKKSQDATTPTSTPNETATSSPRRKR  
SKPKPEN

>dolichyl-diphosphooligosaccharide-protein glycotransferase Contig18004 (complete), 716 aa, 1C70 checksum.

MSSTKTVEERRSSPVATEGFGSLFKFKIPEAKYGVLLTALALSLIYIDAF  
ATRLFSVLRFESEVIEHFDYFNFNRSTKYLVYEGIEFLNWFDEGAWYPLG  
RIVGGTVYPGLMFTAGAVYHVLHALNITIDIRNVCVLLAPWFASNTAIVT  
YFFTKEIHSKSAGLVAAAMIAVVPYISRSVAGSFDNEGIAIFALILTY  
CWWKSVNTGSLFWAAMCSLSYFYMVSAWGGYIFIIINLIPLHVLTLITGR  
FSSRLVYAYCTVYTLGTLTLLSMQINFVGFQPVQSSEHMAALGVFGLLQ  
LYC FINWLRSLPDPDFRIIFRTAILTGALLALAVAVGTYTGYISPWTGRFY  
SLLDPTYAKDNIPIIASVSEHQPTTWSFFFDLHCLVFLFPAGLYFCFRK  
LTDANIFAILYGVTSVYFSGVMVRLMLVLAIPACVLSAIAISTTLKTY  
SKFLKRSPSAKPKKGEAVYAGQKEIAWVVITGISILLIFYTFHCTWV  
TAEAYSSPSIVLAARGHGGSKIIFDDFREAYYWLQNTKEDARVMSWWDY  
GYQLS AMANRTVIVDNNTWNNSHIAQVKGAMSAYEDVAYDVMQKLDV  
NYVLVIFGGLTGYSSDDINKFLWMVRIGGSTDPSIKEEDYYSKDKRFT  
IDRHGSDKMLNCLMYKLCYRFGQVYTEQGPQGYDRVRNVEIGNKNFELE  
HLEEAYTTQHWLVRIYKVLPPMNRG

>C-8 sterol isomerase Contig2678 (complete), 214 aa, 258F checksum.

MGFPPWKRSLALVLLVAFYYLDSIKHHGYIFEPKVLQEVASAIKNTS  
TAKTIDHIVKALDKHYPGHVKNVQEWVFNAGGAMGAMYLIIHASL  
TEYVIFIGTPVGTEGHTGRFLADDYFIILEGEQWAFYPGAFEKEVY  
TPGHMHLP RGFAQQYRMPDKCWALEYARGWIPLMLPFGGLADTFSS  
TLDFYTLAQTFKV YGKCVINELLQNKF

>calreticulin Contig12631 (complete), 408 aa, 2200 checksum.

MKAALLAFALFGLLAFASSTVHFQEDFDDSWESRWVYSTHDDASGNAGKF  
AHTAGKYFNDAEKDKGIQTSQDARFYKLSAKFPKFTNKDKPLVIQYSVKH  
EQSQDCGGAYIKVGPGLDQEKFEGETKYNVMFGPDVCGSTKRVHFI  
LNY KGENHLIKREVRPETDIYTHLYTAVLFPNQTYEIRIDNEVKQSG  
SLIEDW DLLAPKQIPDPALSKPADWVDEEYIDDPEAKKPEDWDNTPKQ  
IADPEAKK PEDWDELDEGEWEAPMIANPDYQGEWQAPRVKNPAYKGP  
VWHPLIDNPDY VADDQIYVFENEYVGFELWQVKTGTIFDHILITD  
DLAEAEAFATGYFAEQ QKGEKAAFEKQEEERNKAEERKKRDAETQ  
EADDDDDDDDDDDDDVADDH HGHDHEDL

>sec61 beta Contig6942 (complete), 97 aa, 1840 checksum.

MKTGTSVGSARPASAAAPRGAGALRRRKAAGAGGGGGGGARSASGSS  
ASGGILRFYSEDAEGLQVQPTVVIVVSLVFIGVVIFMHLWGRFFLRG

>FAD-linked oxidase domain protein Contig26698 (complete), 527 aa, 1A55 checksum.

MAKQSAQTSSAVVAVLTALVVGLLAFGVSYRHHHPPTCAVGADLPQYGE  
VDQALFASLAAVGPGRFVKLRSLPMTVASPLTPSGDEQSDAALKQRKV  
EEDELRAHSIDHSYHEASMPEAVVYPSTTAQVAAVVALCHEHRIPVTVAG  
ARTGLEAGAVPELGGVVIDVSRMDAVLKLHREDLMVTVQAGIRKSALAEW  
LKDKGFMFMVDPGSDATIGGYASTGASGTLSEIKYGTIRDNVISMKV  
VLPTEGEVIDTRSRVIKSSVGYDLNHLFIGSEGLGIIITELTVRIRSV  
PRAVKAG ILLFDSVANASAAVAVFLHADLPSLARCELLNIEALAAVNA  
FFNKTYALT PTLFLEFHAPTLEEVVEEAKVALSVAQSNGLKSHMFADEE  
KERDALWHAR RSAYYASAKYRNDFGRHQMLWVTDVVCVPLSHLAQVI  
SETEADFAQSAVK

LPCPIVGHVADGNFHCLVPFNSTDPFEVAEMRRLNERLVQRALAFEGTAS  
GEHGVGMGKIDALYQERGAVAVRVMVD

>cytochrome P450 domain protein Contig10279 (complete), 486 aa, 4D5 checksum.

MVAAAALFELFSAHPFIFGPLVLVALLLIVKRVREWRKYGGYNLPPVVSSL  
IPFVGSGLSFAGGPLYQYTTDAYKKYGDIFTMKVFGQRLTFLVGPDAHVPF  
FSQGAELSQDEPYQFSVPIFGPNVYVYADLAHRNQQLKFAASLSTKAL  
QSYVPLIVKEAEDFFAKWKDSTVDIRDALAEILILTASRCLMGKEIREN  
LFTFVAKLYQTLDEGLLPISVFFPYLPIPAHKRRDEARLAMVRMFKKIID  
ERRANPEVKHNDCLQVFMADARYRGEEQALNDEEITGLMIALLFAGQHTSS  
VTGSWTGLLLFEANNKKKFLPGVLEEQEEIRKEFGDELMEALNKMDKLH  
RCVKEALRMYPLLLFVMRKVIKPFYKDYVPEGDTVVFVSPALSMRVEEV  
FPNADQYNPERFVEEDKQAQKYRFVGFAGRHHGCMGENFAYLQIKTIWSV  
LLRNFDIELVGGELPKPDYAMVVVGAHPCLLRYTRK

>Dolichyl-diphosphooligosaccharide--protein glycosyltransferase Contig21595 (complete), 443  
aa, CDD checksum.

MGSKMSNRMSMGFAILLCSLLINASLSAQTHKRTLVLDDDLQIKSTHSI  
FFRSLEEKGHSLSHFFEAASPDQLSKYGDYLYDNLVIFAPQVEEFGSLSI  
DSILNFIDDGHHVLIAGDSQVSEPVRELALECGVEFGDDNTFVIDHLHYD  
AADEGDHTLVVLGEENVAKASITGQVTGPIVFRGTGLALEAGNSLLHPI  
LSAHTTSYVYAPNTVVKDDPALKGRTVALVAALQARNNARVLVSGSLAFF  
SDQFFGKVVQEVTFGADSANTEAASGNAALAVNLASWTFGDRGVLASNV  
RHHLVGETEAPRVYTVREEVEYAVDVEEWDGAKWVPYDQTIQVEFVMLDP  
YHRLNLQREQGSATHKVQFKVPDVYGIPTFRVEYQRPYGTGIDLREAVTV  
RPLRHNQYERFILLSAYPYAAAAASMMCALPVFALFFLYHREAK

>Rab2 Contig4844 (complete), 200 aa, 25CD checksum.

MSCCGGSPAAPPPSQALPYKYLKYIIVGDTAVGKSCLLLQFTDKRFQPV  
HDLTIGVEFGSRTLTIEDNQVKLQIWDTAGQEKFRSITRSYYRGAAGALL  
VYDITRRETFFEHLTSWLEDCRKYSNSNIVIMLIGNKCDLESKRQVSKEEG  
AAFAKEHNLLFLETSAKTAENVEQAFINTARTIYETTREGDIDWEHSTPK

>ribophorin Contig26348 (complete), 474 aa, DF0 checksum.

MKSFIGGFLLFAFLGLFISVHSAEVYRGWELQVDRQISLQTONVRHQIR  
IVAVNAGDKAASTFLLAIPSESASHLALVNAVHDGKLADVAPTTEARDG  
VTYFSVALNQAVSPKEQAVIDLIVVFTHVQPPYPTHVSNQNDPQLVVYADN  
HYFLSPYTVRSQKTVVKLPSASLESYSQDARPAVHKGDTITYGPIEQIA  
YQOSPLKIHFNNTPFLTITIKLVREVEVSHWGNVAITEHINMQHDGAKLQ  
GSFSRFDYQRTQRTSGAPIRSVLNLIPLSASEIYYRDEIGNISTSDITVA  
KDKLAVELTPRFPLFGGWKTEFIFGYDLPLSDFVFTDASDSSKLVLNFTF  
GKEIALDAVIDELTIRVILPEGSKNARFELPFAVDSEEATLHHTYLDTSG  
RPVVLVHLKKNVVAEHNQHFLVTYNFSKTSMLLEPLILVISYFVVFLFAML  
YVRFDLISISKEKVVVSKEAKQAKM

>luminal binding protein Contig9720 (complete), 663 aa, 61C checksum.

MKVAALVLLGIALLFASVHGQDENNKFEPIIGIDLGTYSVVGVIWKNGR  
VDIIANDQGNRITPSYVAFSDSERLIGDAAKNQAALNPENTVFDVKRLIG  
RNFADKEVQADAKLLPYKIINKNGKPYIGVEYKNEAKEFAPEEISAMVLT  
KMKEIAEAYLGKTVKNAVVTVPAYFNDAQRQATKDAGVIAGLNVVRIINE  
PTAAAIAAYGLNEVKGEKNILVFDLGGGTFDVSLQIDDGVFEVLATSGDT  
HLGGEDFDQRMQYMLKQFNKKTGLDAGKDKRAIQKLRREAENAKRTLST  
MKEVSIIEINFFEGQDLRERLTRAKFEDLNLDFKKTLPVQKVMEDSGL  
KKTEIDEVVLVGGSTRIPKVQELIKNFFDGKEPNKGVNPDEAVAYGAAVQ  
GGILSADKKDELNDIVLLDVTPLTLGIETVGGVMTTIIERNLTIPTKKT  
QTFTTYQDQOEAVTIQVYEGERAMTKDNHNLGKFDLKGIPPAPRGVPQIE  
VTFDQVNGILHVTAEDKSGTKKSITITPEKGRLTEEQIKRMVQEAER  
EEDDKLIRERVQARNGLESYVYQIRNTIQDKEKIEDKLSEDDLETLETLV  
KDSLEWLDHQAEDKDDYEEKRKEIDQVVSPIFTRMYGAAGAEGGFPGGA  
DGADEDFGAYDEL

>fibrillin 1 Contig1174 (complete), 827 aa, FB9 checksum.

MRSFFLFAAFALLALLSATPIAGLDEEELVAPEVEVKTVSPLSVDTGCI  
NETHSCHEKARCVIGLTGYECQCLKGYAGDGYSICADIDECDPSHRKCHP  
LAVCTNFEGGFECACPEGYQGDGVAECVLGDRGTFRPRPIDVSPPEPIKA  
PGLYLELRGGESISIDQKQATSYPKDPGWSVFKAGGALAEAEVWYELPQDL

NTGRVGTYEIEYQATDKEGNVAEKRYRKVEVTDIDECALGEHACSENAEC  
INTIGGYECVCKEGFAGDGFKCHDVDECKLGTHNCHEKANCTNTVGSYIC  
TCQDGYEGDGFTCVDIDECARNTAQCEHATCINLEGSYDCECEKGYKGD  
GWHCEAIDSCEEETHDCDEHAVCTKTNDTPEGYRCKCKRGFVGDGRICED  
INECLDPDLYNCPAHSCHVNTVGSYRCECDEGEFKAADDDYTCRDIDECLL  
EIHESCPHAICTNTMGSYECTCKPGYEGNGRVCAPLQPPLDIQLEGDNPL  
VLNKCETYNEEGFTLTNKEKNLRVTTTIPSALTAPFIQDLGNFTVYTYVY  
DGRERLGAMERLVVVAINPCELPVGHRCRHKCHPYAQCVFLGGSYDCE  
CREGFDKVIDPITGEVYCKDNQPPVIFLQGNPTILRACRVCQWYDPGES  
YSEEKHGGFFAYDNLDPGRQVDLTSRVRITNESLGANEWALYYNVEDAAG  
NQAETKTRIVRKEVEDVFEKIARMEQFLESRFEDFQPAFTTYNALYSYGR  
WFLQVIFFLFGFIVLVVLPVRLGLGRVLLFNPNPTFFPEFYAYDFYTYL  
TRPWWNQQEREKQTMVMWQKRKYDKHQ

>cytochrome P450 Contig22281 (complete), 478 aa, 1509 checksum.

MWGVAILTAVAAVLLAYYLLKPKAAKGYEWAANIPALTLTQGLRLAFSKD  
THLLLAEFANHHGPIFQIKNPDGVRMLVVTDPPAAKIAMKSEVKGSFYD  
PFKRFHAPVFLFLGEGDWRKQRRITSPVFSGSSVRALHGIMVEETQNLFN  
ALDAKPKGTPFDADDLFCRLTLDVIGRTIYGESFDALSGREVAVQAALAE  
GLLEIQKRISNPLRNYTYKGTQRLVENMHIVHSYGWKAIEKRRATENWEE  
INDLLTILLTSVDSETGEKMPDEQIARELGAFIAAGHETSHTLAWTLYH  
MLQNPVTERCRTEVDEVMGRSFPHTHEDLKKMKQLDLIMKESMRLTPVS  
PMGSARDLNADAEICGFAVPKGTSVVVPFYPLFTDAKLWEDPMAFKPERF  
LDISSDPKYMPPSAGPRNCLGKMAAELELQIVLAGLLRNYTFRLTPDAK  
VEGALEITLKPRGLMVLFFERRPATVSDA

>TRAP beta Contig6658 (complete), 191 aa, 3DC checksum.

MLHRLLLCVVGLVFLLSLCAELLVRKTLTNTTEILSSRAVVVKINIFNTG  
KTSAYDVELFDQDWLKNFDVKGIPATWTKIAPGQNVSHYFVVQPKAGV  
ANTVVRALPGYVQYRETAKGPLQISISTGVGSLPILSSSEGEVRSGLHA  
HWGIFSFLSVASLLVPPFGFWGFIQLNFEDGLKRKLLNKKSK

>squalene synthetase E80POFO01BG29D/19041 (complete), 503 aa, 162A checksum.

MTQWRKFSVSIFLICLLEFVFWAYCTVSAAGAAEEMVMVKGIETFKNVDG  
HDDTARLGSQAQEAASLVERTSNENNLKEADIIHHHGLGLFANTAIDGHNGV  
GRLGVWIAVAVGLLGFKWLFPHYVKKAEQELMAHPYEFYQMLKFKFFYKVP  
DFPKNLSEADIYSYKLVKVSRSFAAVIAELPEDLRRPIANFYLVLRGLD  
TVEDDMSIPLEKKMPELRSFYKHLYEKGWNVSGYGDNADERDLLERFHYV  
VDVFLDLKPAYQOVIADITRRMGEKMAKYAGEKTVVTTLEDYNEYCHYVAG  
LVGIGLSQMFASGLESEKFGQMDLANSMLFLQKTNITRDYLEDVTAV  
NPRIFYPKDIWGYAKNIGDLKEPENKEQALQCLNEMVTNAMAHINDCLD  
YMLLLTHPNVFKFCGLPQAMAIATLARIYNNYDVKREVKIRKGEAVQIM  
MYGGNYETIISYFVQYIKELEDKIPESDPNAEKMRHYIAVARARIAKGRG  
RQQ

>ribophorin ii Contig7499 (and 27461, 12214) (complete), 720 aa, FC checksum.

MKTSFLXLAFFALFAVSALALGTPSDFFSGADEAALRARLTEQLERRQSS  
DELIIEEDYYAVATLASLPKTTSPNSAQLCGKASTLLASASAKIVDAQAI  
HRALGVISALKCESQSPATLSSSLGTKLVESVLANDQAQLADLHAALAAL  
QQIQKTASPAVTVSSDVASEVAERIAADLMEPEGLFRAGSNDEEGTAGNAG  
LAYHALALLKRAAALNVAPKKGADGKSGPVDASKQAALKHIKTVAESISQ  
LLADVDEEDDNIIEFEDSQNPLRATALFWIGAEALTRSGESVTVTESQVA  
KLAEFFLRHKRVSNAVDAYHLLRALKTVASNVWKKSPVVTLPNSSVLAS  
SKGEDSLVKFRVTDVFGKFASKANVYITKVYPTANEKQVILHNQQATPVS  
TNADETLYSFNILAAKPDQGLYSIDLSVAPESKDAPVFGAVGVVRGVKVV  
VTADLSDVAVQVDALEDEDLEQAYKVSYPEKVAEVIKANPLQHVLVSFR  
VRSQGRPLPVQQAFFVVRHEESGHEVILPAQLTGKNKYVHLNLREAGRAF  
QGRSGKYSVHLLVGDFAFLHRPYFVFPVADVFLSLGKQREEPAAPSTEGLRP  
EIHQFRKPEKRPPPTVSMFTALVVGVPVVLVFLVGLFLVGANFSNFPLS  
GTGFLSAVGFLGCISAVIGLVLYWLQLTMVETLVYLAGLGLVTLVGVWQ  
ALRHRLYARLAASAKDKTRD

>rab11a Contig4320 (complete), 213 aa, EAD checksum.

MSKDDEYDYLKVVLLIGDSGVGKSNLLSRFTRNQFNLESKSTIGVEFATR  
SIKCDSKTIKAQIWDTAGQERYRAITSAYYRGAVGALLVYDISKAVTYEN

VERWLNELRDHADSNIVIMLVGNKSDLRHLRAVPTEQAAALAEKHGLSFI  
ETSALDSTNVELAFQKILTEIFHIVNGGKQLETKKDSQSVDGETEVVQVG  
GDPAPKKAGACCG

>rab7a Contig4656 (complete), 204 aa, 23D8 checksum.

MSTRKKVLLKIIILGDSGVGKTSLMNQYVVKKFSNQYKATIGADFLTKEV  
MVDDKLVTLQIWDTAGQERFQSLGVAFYRGADACVLVFDVNVAKTFENLH  
SWREEFLVQAGPRDPETFFIVLGNKIDLESSRVVSQKRAQTWCQSKGNI  
PYFETSAKEAINVEQAFQTIKAKNAMKEEEDVDLAGITDAIQLDKSEPSQS  
GCSC

>sec61 alpha subunit Contig1087 (complete), 475 aa, C85 checksum.

MSGVRFSLSLVRPFMGVLPEVAQAEKKIPFREKVLWTAVTLFIFLVCCQIP  
LYGIVSSDSADPFYWMRVILASNRGTLMELGISPIVTSGLVMQLLAGSHI  
IEVDQGLKEDRALFNQAQKLFGMIIITVQSIAYVWSGMYGDLASLGAANA  
LMIIIQLFISGIIVILLDELLQKGYGLGSGISLFIATNICENIVWKALSP  
TTINTGRGTEFEGALIALVHLLITRTDKVRALKEAFYRQNLPNVTNLLAT  
VLVFMVVIYFQGFVRDLPVKYQRQSRGPGTYPIKLFYTSNIPIILQ TALV  
SNLYFMSQLLYRRYPGNVFNLLGQWHESEGAQHMOSVPVGGGLAYVVSPP  
SSVAEIFHDPFHAFVYLTFFVL TACALFSK TWIDVSGSSAKDVAKQLRDQQ  
MIMKGRDSSLVKELNRYIPTAAAFGGLCIGALSVLADFMGAIGSGTGIL  
LAVTIIYQYFEIFVKEQQEFGDLFW

>Rab8a Contig9830 (complete), 219 aa, A32 checksum.

MAATHPPAGGKQAYDYLIKLLLLIGDSGVGKSCLLLRFSDDSF TSPFITTI  
GIDFKIRTIELEGGRIKLQIWDTAGQERFRITITAYYRGAMGILLVYDVT  
DEKSFGNIRNWIRNIEQHATESVNKMLIGNKSDMVDDKVIDTARGKGLAD  
EYGIRFLETSAKTGAGVEDAFITLAKDIKRLIDSTEKPIPPGGGPTVQ  
LNGNGTDPSKGAACKNCCG

>protein disulfide isomerase ACL00004759/21103, 358 aa, 1EA3 checksum.

MARLLL PFLLLSALLACASASNVVDLTPENFDKVL DGSKPAFVEFYAPWC  
GHCKNLIPVYEVFADAFAHAKDKVVIKVDADAH SALGSRFDVKGFPTLK  
FFPSGNPEESQKYEGGRSEDDLISFIEKNTGVKAKRAPAPPSYVTVLSES  
NFKSEIVESD TDALVEFYAPWCGHCKKLTPEYEVAAAYKNEAGVKVAKV  
DCDANSALCQQYGVSGYPTLKWFPKGEKASPVDYDGGRD LASFVKFINEK  
AGTERLANGHPGNAGR VADLDVVVKAYADAEDKAALLEKAKEVAAGLAG  
DAAKHAKIYIRALELLKTKPEYLT TETETERL TRMIESGSLSAAKVDEFVAR  
LNILAAFH

>nodal modulator 2 protein Contig5652 (and 11314,15940, 11020) (incomplete N-terminus) , 1130  
aa, A3B checksum.

WNFEPSSVLIDEGRCDSSRDYNFIVTGFVLSGTVRS LGQSSAEEGQK GPA  
GVVITLKNKANAKVADQTTTGTQDGAFHFSNVFPGTYEIVASHPSWTFVK  
DRTEVSFEW DNVRVKDELLVGGFEVSGSVQSDENAAVPGVDFILYSASD  
LKDLPLSCSTDGVSGAPEEKGLKAVCGARSDAAGKFVIKGVPCGQYTLVP  
HYRSSNTNYDLLPSRVDVTVSHANA EVSEPF RVAGFSVEGRVVDVDGAGI  
SGATVLF DGV EKATTDADGHYRVEKVRVGSYAVEVVKDHVFFDALKSVQL  
SPSKAQVPQIKAASYHLVRPREPLVGP RRREAEAGHRD VLLVDAVSGXEE  
RRSTDPTGAFCFEVVPGRYRVTPVISAAEERAGLLFVPAKREVTLNKSPV  
LDVNFQALVTVQGVVRCLEAPCDPSISITLTGTDIESHMTASLSPGEKQ  
EATYAIRDVLPGQYEVQIKHESWCWKQTTHKLDVKAE AETGKSHIQAPEF  
VHEGYQLSSVVDVVKLVASLDSAPKERQTFELTKGNRFCLNKPGVYTLT  
PVSCYKFERD TYKYDTANPRLLDLQATHYLLNASVLTAEPASNITIHVAV  
DHSQKAGRKDAAEHEEYVSTNEEQRSVEGGKHHYGFALWVAPGDKLTLTP  
KASTGSDLLFYPSSTTTLSKPECPSPLAPFQARPGSYVKGRVEPAIANV  
RISVYTTGEDGERRLVSESTTTASGNYSIGPLPDNTPYEIEAAHEGYFYK  
QTETGVFQ TQKLGTVAVTVKDEAGNALPGVVISLSGEGYRSNNPTNQGV  
FTVSALHPGSYYLRPLLKEYVFTPSATSVEVKEGLDEKVTISAKRVA YSC  
FGKVRSLNGEAEKFPVEAVSATGEVEETQ TDAEGNFRRLRGLQPGKEYRV  
RVKATADQRIERAAPSDGYLVTLAANEALTDVQNQDFLVFRRLPKTDLTG  
EVIAEPHVLSTLKVVEVFEDGKSEVVKSVGLGPSTFFNAGPLNRDAKYRVR  
LSSSLSSRSYSHAPQEVSVDLDSATHLKLNF TATMHDPLRHDLTSTPIFS  
FILAVLLIALVYFHKLALEV GKAALSGDINAVRGLLRPKAE EEEEDSATS F  
LSPHLLHPAKVGRAGARKNAPRPGYRPSRS

>similar to SSR delta subunit Contig3630 (possibly complete), 1004 aa, A8C checksum.

MNRKVLALLCWAFLSLALISLGASVSQQNGYIHVVSHLDRFQTPAGGFSL  
VEGGKPSLEATSHALFISSLFGLRKKINQQEVARYIQTLENGDYGYGKSA  
GLPSDLESVRQAVLSYQHLGLAVPNAGNVASFIKSLYDTQTNLFAARVGE  
KGDLLKSTALAFQALEYLGELOQVQDIFEKVRTYLSKHVQLADNAHFAP  
DEKTLSTTSANYYGVVLSYVGFDFVSLPKWAAFVAALQNOKEGGFYTG  
DKKTTTLESTAHAI STLRLLOQTGKNTQFVDDVVSGEALANYVVP IPRDL  
RSAAQAHLAVALTKVFSRNFETRYYEFLRASGSADKKVVQGTQLKPVIS  
VKTFDGMPHAGLDVEATITHESTGEVVKAKLQIKDGEHYTTNDFDFTTNH  
LGAMKFQYTVRCYVVGVEISFELDDVKQIGYGVAVDSRAHLEVADKQFA  
QGETVAVGTEFTFGVALHNQTHKDLHSGDFNVVFSVLDSSLVAIHSESVD  
AKANAKPFRFAYTLRSSLPSGDLVFKFEVVSATGVVHTTETVKYQLSIP  
MIATQITFEQVAEGAPKYKLGETARITIEPASFPDLRTVASYPKDVNGK  
PAAAQRKFMVMDVHSRKGALLRTVAGKAQTTESSSKYVFEVPATATLDAIG  
LNVVSFRYIAASGRSVELGSYDSRLGELIEDASSLNYTV DANLQIVDIKE  
QPQTTTFAYGQEVVFRFRVKDALSGLYLHKGENEQANVYLSLKHADAEG  
KPFV SANVAEEVVNAOGEKEFVIEWVINPNAVQGAGVLSLSAQDADGNV  
LDLSDATTKKPVQLDVTVGDDIQVEHTSYSTSDASTYRETAFVVQFGLTC  
QNESLKNAQLRASVYRDGQOVASFLPVATNDEGVYSVSWGGPHDATPSGV  
YTLKFFREVDRKRAVDAHEFQEKRRKREEQLKQLEEGSETAHEETAQEEL  
IVENIVSPLFEISHSHVAPSTSKLPIRAEVILAFLLGGAFMAISYQKKHY  
LASK

>rab7 E9BS9UA01D67RT/4587 (complete), 201 aa, 219E checksum.

MSKKKILLKIIIVLGESGVGKTSLLLLRYVERKFTMNTKSTIGANFLTKEVE  
VDDKVATCQIWDTAGQERFQGLGTAFYRGS DGVIFVFDVTVQRRTFEELEH  
WKEAFLIQVQEGNKDFPMII IANKIDLKEERVVSRKELQEWCAQYGLKF  
FEASAKEDENVEKAFFEEITRLVISKMKPEDIMYDVTVDLSVGEKKEDRGCD  
C

>protein disulfide isomerase Contig16593 (complete), 482 aa, 1155 checksum.

MNAKFLFAAFCLLGFVASMQASNVADLTDDSF AEFIANNEFVLAEFYAPW  
CGHCKQLAPEYEKAADQLLEAGSPVKLAKVDCTVQQQIAQQFEIQGYPTL  
KWRFRNGKATEYQGPRDASGIVAVWNKSGPPTH TLTDKAQLDAHIAAGTV  
VVGFFEKDSDAHKAFVAAAQSPQADSFTFVDVVS EDLIKEAGEKVGTVKL  
YRSFDEPLALEGEVTEQAVVSLVTGHGFYPYFEPAPVAWARLIGRGLEYIL  
LIVADVTEEDVWNPINTFATKLAQYADKVG FVYLTKEFFPRVTQFGLSG  
KHFPAAALVMAPHREKTFLLDEQTPITEEALKNFVDGVLDGTIAPSFKSDE  
APASNDGPVTILVGNTFEDLVINNDKDV LVEFYAPWCGHCKSLEPIYEEL  
GERFEDNDKIVIAKMDSTTNDNDHVAVKGFPTIVFFPAGSKDKPVTYEGP  
RTVEGFVSFLNQHATNLQGSPLAVEDPEHDEL

>sarcoplasmic reticulum glycoprotein Contig24049 (incomplete), 149 aa, 1EE9 checksum.

MKFLPHPLLKQVTLVDSPGMIDSVGEGRGYDFAEAVRWFADRADYV LFFF  
DGEKPGTTGETLKI FTQSLSGMDHKLLILMNKVDTFKNIGDFVRTYGTLC  
WNLAKVIPIYKDMPOIHTTFVPVDDVSGKSLAKHRPAPAAPASSSGAADS

>Sey1 homolog Contig21906 (and 4264, 4881, 5641)(incomplete N-terminus), 651 aa, 1F17 checksum.

SLFSLALAEIILINLWFQDIGRWDAAANYGLLKT VFELNLQLFGKHSSSAG  
SKTLLLVFIRDHVRAVTPLEPLTQAVEADLEKIWSGISKPPEFASSRVHD  
FFDIMYTSLSHKILDATTF AADVDTLKERFTNPEASDFIFKDAYAKDVPA  
DGWPMYAERIWETIQESKDLDLPTQKEMLAMFRCD ELMETAYRSFNTAVE  
PVRQQLSNPEGSFVPAFGELVRQAE EEAALSQYEAPASRYHTEVAARKGAA  
LKEKMLDASYALFLQOMRRIYEA AIQHADTLAKKLS PSTSDSKEGKSPQV  
ELSDLPTRLHDLKDDAIAFFERNAQASLVPGVSWKYDEERQALREHVEEL  
VKRLREQYVDHLLKRRQOKLRSAVMNQLNKQLDVASNEMWPRIADLHDHA  
LEGAKAKLRVHLTRLGLSEEELNTREEELRERAF AVIKDRLTEKSQHIQY  
QMOKKFDETFRLDPDGLPRRWSKADNIEETFKEARQQAYGVLDAYSIVRL  
RESDRHLSFFDSSLDPSSVDP SLVVISADQCNMTRDTFKRES DPAFIEAK  
REQEREIAVRIPFFWAVMLILGFNEIMALLGNPLLLFLFVVLGLMAYAA  
XLAXLLDVPLQIATELWSEL TGRAKSAAVQSV MGRLTGSSAAPAAGKDKK  
D

>TRAP alpha subunit Contig23193 (complete), 248 aa, D01 checksum.

MRSFLASILCFLLLFSFVAINAQSNLTPTNIADLLQEEAVLPTAAEDVVTS  
YVFPDNaARQFTAGEPVEVLVGFNRKGSRQYNITFIDASFNFQDFSYII  
QNFsrweYgmpVQATQEVTLsYmFRPDAMLEPRDFGLLVNvYyKDATGRN  
YTNAAFNGTVDLVepVVGWDAQSFFAVLAVLALLGVGGFFAYRSLSTWAK  
KQKSSKkVEYgTKVRQeVEDDwLAGTAADPALRKRKQOQPKKKVnkSG

>long-chain acyl-coa synthetase Contig14348 (and 338, E9BS9UA01DNFTE) (complete), 704 aa, ECF checksum.

MASFLASPLAGVAAVVSAYVASIFVVGGSFATFGLVLALVYYYYLVGWHK  
KTNEVSSYEVGSAKSGEGAVRRKLGvQELAIspYpGVtTLyENfQrgVEK  
FGDKNCLGTRTFEKNGTRGAYKWETyKQVSKRIRNFgAGLVGLFDLPTGA  
RVGFYAKNSAEVWVGAEACNAySLVnVALyDTLGEENRVfIVQQAeVLVI  
ITTPDLVKNVASLvkECPtLkAIVVIGELNNEQqALATEAGLEVRtFADV  
EKAGEAAPVDLRLPKPDDLAIlMYtSGTtSTPKGVLIthTNLVSaVAGVL  
QAVMPISSDDVFLSYLPLAHILERASEAMfSSGASVGFYQGDVRKLDDDD  
IRTLAPTLfVGVpKVYQrVMLGIQKkVALSGPIARfVfYtAFaIQKAIe  
SGFTIGLLNKIVFAKvQeGLGGRlRQALSGGAPISAECHQfIRICfGCPI  
MQGYGLTETCGGTAVtPYtMpnPYGRAGVPISSCEVklVDAGNYKTASNP  
PRGEVCVSGPCVtKGyYkMEeKtKEDfREeEDGRVWFHTGDVGQWnedGS  
LSVIGRTKdIFKLDGGEyIAPERLETIFAGCKyVGNIFiYGDSTKSFIVA  
VVVPEPIAARHWASEQGLkyKDEdFTATSVPEDLCENaQfKkAIADDLAK  
VANTAKLNRFEfVTALHLsAHMWTPEsGLVtAALKNKRPSLQqAFQsQID  
ALYA

>cytochrome p450-like Contig8486 (complete), 1185 aa, 1CBB checksum.

MAARQGLVWLTVLLLLLALAIaASLAADTPNNGGNKkNGPAKkVIDfLkGM  
VVGSDDLATKVEDLLDtnKwETLSKQAGSKKDSGKvKAQAATGVPNPFpD  
FGWEIDPKCLEskESyYyRSWdGScNwLRKqQAATGAQDQAYARDYtPPH  
YKPGTLGEPDGPVRELSnIFFKnrKtGYWdHTPwLLGyVEfLVHDLML  
SDAGREKGDLMNIDIPAGDPDFpPKTKLEfWRserAPGTGENgIPREQYN  
RRSNWMDLETIYGSTkEMNALLRQKDAAGALKCELILDDDYLPVnderfN  
FSLPGRPGQQRNLFAAGDLRANQDYLLMVyQTLfVREHNRmCGVLHGKYP  
DWNVEQRfQTTRIVMGAKMNMIGAAyFKAYfIDVPWPDDPTAIMRSWtGK  
TVLEINPLTMSyPQMLLNPKtGDPySLPNEfSVGYRWHDLIPASLQIFD  
KENNPTTLVNLAEtAFNATSfKQtGINSVVEAMSVtQIPDFHSGIQDtyR  
SMKfNFRNPDEGNfDLAAWAImHERERGLPTfNEYIRKvYDGVVPFKPR  
ATFEeFTSNyVfQqELKRLyKtPDDVDLWVGQELDEEwWPnTHIPRSMLI  
INfYTLfKAAAADRFGINWGMfWCISNyKpWNCPTtNVLQDLLWkPNPLP  
LFPNAKLpDSfWwEELDLQnQGTnLLHRMvTQNTGvKCLQKNLffVANAK  
SNPIECfSTGDMPSpDDDKSfLLDPFFKNDLHfLpFALWGSVQPFVDyT  
KQYGDVVKfKLSNDGNNILLsNANDLGKIFESDKyWLRsRMDySDfTYGR  
MVGyKDGtPFTALSNSHPSElyKwKRLRTIFDQtITPANINQLPTINvSA  
KLLLATFDQHVgKkyDAADDEtGVALELACSLAYGDDfCQRDPARLQqfV  
KYGKRWLKYfPDFLKYAPPYNNPILVLEgKtSKIKDAMDFfGQfSRDALA  
EVRKSPAGKtSWLAKWALTPTEDGSLLDDKEVIAATfDSFMGIPPTfSfI  
LGHGMYLLAKNPTVLERAYREvSAVLtTAARDLTiADfHRMPyLLKVVRE  
IYRYyPPGGQIYARvSMEDDtlRDWQVPAGtTYMIHTASIHQDPRfWANP  
TEFNpDRFDTPVANNTWIPfGGGkKDCPGKDLALQvSNAffAHLIRNFkK  
TYAGEDPPVIRMLLSAAPKDPFLfKlQRRSAKDEL

>fumarate reductase Contig23914 (and 23982, 26452) (complete), 619 aa, 1C0E checksum.

MNTVVLALLVAVVAALFYyPTfVRIpSAEEVSGNTAQRAATPTQAMSSAP  
SAQAQQTnAGSAAAPAGQVPSAPTASAVASPSQTPQASTAQVVELPPATG  
KKVIIVGGGLAGMSAAIEAVRAGAHVDMLEKtIRWGGNSEKASSGMNAAR  
TAAQIKLNLKDSVEEFyKDTIASGHGLSNEELVDVMTKESASAYDFLSSf  
DIDLtTVTKLGGHSRARTHRSERVtGNVgWEITStLSKYLATLPRDRLT  
MKLGARLTSLVVEDGRVVGVKYTKIVRDEKGHETGEELAELRGDSVILAT  
GGYSRADDLLRKYIPKIVDLPTtNGPFAEGDGIKVAEQINASLIHMDQVQ  
LHPTSFVSPKDLAKTKFLAPEALRGLGGILINQDGKRfVNELDTRDKVT  
QAIFKNCKPLIVEQEVNGQMKtVVGpVVAHLIMtDEAVKLfPNLQfYQAK  
GFLHGyLgVEEMAEGLELPNGTLKQTFAEyHECFVRQGNCADPFgKKDFP  
FGTRSNDVfHAMMITPAIHytMGGLEIDKEAHVLRaaATENKDEAAEAAT  
ATKEIIPGLFAAGEVTGGVHGanRLGGNSLLECVVfGRRAGRFAAAFTET



ATAPEVTSSSPSPASVV

>Rab1a Contig26930 (complete), 200 aa, 196 checksum.

MEYDYLKILLIGDSVGVKSALLLRFAADDEYSESYISTIGVDFKIRTINI  
DDKSVKQLQIWDTAGQEKFRITITSSYYRGAHGIIIAYDITDEASFHVGRW  
FQEIERYAQDNVRKLLVGTCKDLESKRVDKARGQQLADELNVFVETSS  
KNSTNVEQAFLLMAKEIKNKQGPAASTQKKVDLSGPTTPVGGDNGGCC

>rab32a Contig8456 (complete), 216 aa, 1A2B checksum.

MGEEGVSEYLYKVLVVGDMGTGKTAIRRYVNNMYSYKSTIGVDFALK  
EINWDSKTLVRLQLWDIAGQERYGNMTRVYYKEAVGAFVVDITRNSFE  
AVKKWKQDIDSKVTLHDQPIPVVLLANKCDLVKNPCNEEVMEYCREHGF  
AAWFTTSAKENVNVDEAVTALVSAISKRTGGTGGAAAAPAPSQQQENIKV  
AGGQPAADNKSSDCSC

>betaine aldehyde dehydrogenase Contig6718 , 592 aa, 2322 checksum.

MLEWLGDLFGLLWGAUVLVLSVDFLSDLLLLSVLYVVGRYVYVAFRGNIQ  
SGKPARSFKLSSEEFAGKELDAINPATNEKITTVRAFTPDEVNECVRRA  
RVAQAEWAETSFDERRAVLQDLMHAVVEQODTICHLSMQDTGKTRMEAEY  
GEILTTCERKIRHLIRNGEDALKSESRGVPLLLFLKKAWEYYPMGVIGII  
VPWNYPFHNVASAAVAALFAGNSAVIKVSECSLSSKDYFEKLFKRVLAAR  
GHNPELVTLIVGEGETGAALVKSGVDKILFIGSPAVGKRVMEGASANLTP  
VILELGGKDPFIVLEADLDHATEVALRGVFNCGQNCIAAERIYVHNKI  
LPKFEEVVAKKVAARFQGASVNGGCFDVGSMTPRQLEIVDELVQAAIQD  
GAKVLAGAKRDEKPLFYRPTVLSNVNHSRMRIVNEEVFGPVMLIIPFSSD  
DEAVRLANSTEYALGSSIFSGNAARAHEVARRVAGMATINDFGVGYLIQ  
SLPFGGTKISGFGRFGGAEGREFSRQKSVVTDVDFPGVLTAKAPFTKYPI  
PENGPAIVKNAIHFFYGPESPSGLWAKATHLCAMLQLLITLK

>DAP1 Contig11728 (complete), 206 aa, 15C4 checksum.

MENQRTSAFSTLAWWGCSTVVLAAVATADSIADSEYVVDVVAEESWL  
EIGAMGILLGVIGWLLKELLFPGAVAQPPVASIASRKRTPVEPRDFSPDE  
LRKMNGTNGNPVYVAVLGVVYDVSSRASFYGPGGPYHIFAGRDAARALAL  
GSLEEKDVEAPYPKLDDLQPSEREALNDWIGSYQAKYEVVGRRIIPSANSI  
ASSPSD

>endoplasmic oxidoreductin Contig281 (and 1632) (complete), 504 aa, 1090 checksum.

MHRLPVILLFAVVVALLLGCVTATASPAETAATAAVVGDVAVDGCYCELDT  
LAQVNHDLKPLLSQLVNKTFKFKYFKLNLYQECPFVWQEMLCGMQGGCNV  
CECDENEIPLPWKVPATDKVSSLRSNQFSQRWEEEDGEESKRRDVELLPW  
IWSDPLEEEECMSYVNLVDNPETNTGYTDGASNIWKSIEEENCFKPITQTN  
STHRDVL DGLCFEERVFYRLVSLGHTSVSIHITEFYEQDEATGQWTRNET  
MFWDRVGNYPDRIRNLYFTYVFLRAAYRASFFLENYDYNTGNVKQDKQV  
KDLMRRLHNLRECEPTFDERQLFDEEEREGLDELHRREIDKRELKQEF  
KMHFRNISRIMDCVGCCKIHKLQILGLGTALKILLEDRTCETLQORNE  
IIALVNTLYKFATSAEAVARYLSLVKEPTTGAAGDQVGANATSGGGWWQ  
QATQMYAAAPKDLLLGLFILSLSSVMGIVRLVMWQMERRQPNAADVDQD  
KKDN

>rab11d Contig23776 (complete), 228 aa, 963 checksum.

MNSDASDTPDYLLKIVIVGDSVGVKSNIMSRFTNDTFEESKTTIGVAFA  
TKNMAVETSNDSTKDCCKQVKLQVWDTAGQERYRALSSAYYRGAQALVV  
YDITSRESLDSIPKWLLEEDKYCTQDVVVTLVGNKLDLSENRCVSVVEEGK  
KVAARENMFFIETSAKDATNIEKAFTHLIKEIIQSNLSQANNDGKIAGKA  
PSDTGITLKPPEEPESDPNAPPQSGCSC

>band 7 protein Contig7478 (and 22166) (likely complete), 389 aa, 11F9 checksum.

MAARGRNPNNGFNWGLVVGPLLLALVIVFNGVHQIPEGHVGLYWTGGAL  
QDTISPAGWAVKLPVSVQVNMVTLQTDVTDIPCGTSGGVMIFYDKIE  
VVNQLAQDHVLTTRVRYGVNYDSTWIFDRIHHEINQFCSSHTLQEVYIDL  
FSTLDEALSESLOMDCNKHDVGITIIAVRVTKPRIPEEVRKCVALLTPNY  
EEVEKQKTSLLVAQQQQLVSLKKEETLKQQAARIQAEKEAEVAIINAQREA  
SVATIVAQKEANVSLINLEMTIKEKQAQQORQAIDDIYVANQKAVAEAA  
HHRITLAEANALRLTPEYLRMVLVYQSLANNTKIYFGEKIPQMFLDWAPG  
DSHMFLPQQQQQASKTVPVRAKEVPAASKGPAASPAQQ

>endoplasmin HSP90 Contig20290 (and 24498) (complete), 808 aa, 2653 checksum.

MLLSLQQAARLLPFLLVAAALVSALLLAPRVGASAEVSTDGEALLTADLKA

EKVALKTDDDDVAQREERSIAPSPAYTEEELKLLLEQTKKFEFQSDVSRIM  
NIIINNVTNREVFLRELISNASDALDKIRLQSLTDATKLDKKELEIRV  
QNAEDGTLTISDTGVGMTKAELVQNLGTIAHSGTKQFAEMLGSKDASSN  
LIGQFVGFYSAFLVADRVVVVVSKSNDADQWIWESTADSNYSIVKDPGR  
NTLGRGTSITMHLKDDADTQTFLLKSDKLRDLIIRYSDFISFPIFLWESHV  
ERVVPEEEAEDDAEEDDEEAEVDTDDEEETEDDEEKVVVETIPELVWDWER  
INDKQPIWTRRKDDIEDEEYENFFKAVTREDRPPLSYIHF'TAEGDNGAFK  
AIMFLPEAPPYSQFDSAARQKGVKLYVRRVFI TEVVPKYLAFLRGVVSDD  
LPLNLSRETLQEHKALEVIRNKLVRKTIAMFQQLGDAETAEEKAKYAKFW  
KSYGTNIKLGVIEDSGNRARLAKLLRYSSTTGENTSFDYVARMKEGQE  
DIYYLSGDSVEALKTSPLLEKLTEKGYEVLFAVDPIDEYTFQNLPKYDKY  
KLVNLAKEGVKLPGEEDDEDKHEEDLKEVITYLKKTFSKISRKVSRL  
SRSPCALVAESWGHTAQMEKVMRAQALSSKDDPKSRMWAGKKVLEINPRH  
PIVLELNRLVTADATDPTAKDVATLLLDATAAISGYNIDQPASFVTRVLR  
MISTSLDLPEAVIEDLAAPAAAEPAKKATEAEAEAEDEDDGGVDVLDLGE  
EDDEHDEL

>dolichyl-phosphate mannosyltransferase 1 Contig22937 (complete), 253 aa, AF checksum.

MSNKKEVRTTGYKPKYSIILPTYQESENLPYMLWLINKHLNKGIDWEVI  
VVDDASPDGTQKVCADLMEIFNTKDRDCIVLKPRPGKLGGLGTAYLHGIFK  
ARGSFIIIMDADMSHHPKFFIAQMIKKQOEKDYDVTGTRYVQGGGVWGW  
LRRKLTSRVANLADFLGLQVSDLTGSRFLYKREVFEELIKKTESKGYV  
FQMEMIFRSRQIGNSIAEVPITFVDRQYGESKMGKKEITQYLAGLVSFFF  
QAN

>rab7b Contig22376 (complete), 112 aa, E10 checksum.

MQEFLLIHAGPDDPEKFPFLVVLGNKVDLCRAQSPGTQPRRKPEVSEDEAKE  
WCKKHGNIPHLLVSAKEGTNLDEAFTLLADIAIQRLHAPLSTAASSVRSR  
HDKEGVYSSSPW

>Dolichyl-phosphate beta-glucosyltransferase Contig6660 (complete), 316 aa, 24F7 checksum.

MLDLLLSIPLWVPLLFFVIVAGVTLFYRHLPERSVLWYKNENMYIDARTND  
KKSFPPPSAEPAVYLSLVVPAYNEEKRMPTMLDEALAYLQORSAEDPQFT  
YEIIIVDDGSRDKTTDVALNYAKQHKLDTVRVLKLAKNRGGGAVRRGML  
VARGRYALMVDADGATKFSDLERLEKRLLOAEKNGLGAVGSRHHLQEK  
EAVAQRTFRLKTLGATFHMLVTFVANVHDTQCGFKLFTRRSAQLLFSNL  
HIERWAFDVELLYLAQQLNMPIEEVPVNWQEIAGSTLNPVTASIQMAKDI  
FYIRALYILGYWKIDK

>nicalin-like Contig1110 (and 6221,E80POFO01ATC2X) (mostly complete, with internal gaps), 563  
aa, 4D1 checksum.

MGYGSAPSPLRRALCIVLFFYLSFLLDFTAGLYSFDVFRMIQYDKAGAPF  
GSQRTSVSLQAVSISADIARKMVVAPYEQVDVTLIEEANAKAGLLILLP  
PRDVKLQRGVIEKWMVEEAQLNSRELRIPVYFAVVTPEIQEAMSTITSAG  
DEGAIVSGFLSSIYSDEYVMVASSADPSPITGVSLTNFQWIAAGSGARED  
DEEAAQTSTIALVAHYDTLGVAPELATGADANGSGVTALLELARLFSKLY  
SGMRTQOKYNLLLVLTGGGRLNFAGARVWADQADPRLLASIELTVCLDAL  
AAGDKLHLHVSRAKDPPIIGQLYSNLKAAGAAEGVEVELVHKKINISDPS  
IAWEHEVFAARKRIPAATISHFAQHSATLFSRSNVLDTTSQIDMDVFARNV  
KVVGEGLARYVYKLGNSGAVLEGSHAVHADFLRSWLATVASFPRVYPYL  
APASPLFGALEKALGDYAEVTRQTPWDGEVTPAAAADADVSRPASRAPS  
VVFYQPATASLAVHKVPGTFDLLLLTVVIAAYLGLVYVYFKGVDETMKQV  
QGLLTSKDKKKIR

>sphingosine-phosphate lyase Contig18815 (and 19955,20878) (possibly complete), 563 aa, 22CE  
checksum.

MERPSSTLAVLSQRVDEFVKQHKHLETVRNAIFLFFVVLRYGGKALWALYD  
VGLARMCRDLRAYLVTTTTFERARKIPYVVRKVAEEMDKVSASLRKTLLAG  
NEGMISHTRLPAEAI GAEDVLAELRTLQEMGHKWEGRVSGTVYHGGAD  
ITSISSRAYEMFIWSNPLHPDVFPGVRKMEAEIIAMIVHMYNGGPQACGT  
TTSGGTESILMAMKAYRDWGRKEKITAPEIVAPVSVHCAFDKAAHYFGM  
KLVHVPVDPQTRSVDRAVRAITSNTVAIVGSVPSYPHGAIDDIEALSE  
VALHYGVGLHVDCCGGFLIPFMDKAGFKLRPFDFRLPGVTSISCDTHKY  
GYAPKGSVVMYKTKELRSYQYFVASDWTGGIYASPTIAGSRPGALLAGC  
WATMISVGEAGYVACTREIIAAARKLSAAIKNIRGLKLYGNPQVCVAVFG

SDDFDIYLLGGEQLTKKGNLNSLQYPSSIHICLTYANKDSADDLIHDLTT  
LTAELMKTPGKVAQGAGAIYGMAQAVPDRITVDQIARCFIDTLYENVEEG  
APTTTTTPSSPHSD

>similar to synaptic glycoprotein/steroid reductase Contig6039 (likely complete), 298 aa, CFF  
checksum.

MGKLTIKSPSGKVLKELEVSESSTVAQLKAAYAKAFPKYYPDRQRFYLDQ  
GETRVSLEDEKKLSTYNLLCSKRDDVVYFRDLGPQIAWKTVFLVEYAGPL  
LIYLFYARPPFIYPASDAPHTWVQNLALLCWAGHYLKRELETIFVHRFS  
HGTMPIMNIFKNSGGYWGFGALCGYFVNHPYFTNPEPTQVYTALAFFVLF  
ELGNLISHIQLRNLRPEGTTVRRIPRGFLFELVSCPNTCEILAWVCFSL  
MTQSVAAFLFTLVGGGQMLVWAQQKHRRYKKEFPGYPKNRRILFPFLY

>ORMDL Contig374 (complete), 155 aa, BB8 checksum.  
MKTVDASLEENRNVTWFDSKGAWVAYLSLIIGFRIFLTFVPGISPSTAWT  
ITNLVHALGTWMAFHWSKGAFTGSDQDKYAKLTMWEQLDQGIQFSPTRK  
LLTVVPIVLFLLTTHYTQYNFLMLVINIVALIVLLVSKLPRMHKVRFLFGL  
NSGPG

>mannose-P-dolichol utilization defect 1 protein Contig3068 (complete), 260 aa, 12CB checksum.

MELKNLVEFMGEHCFKQLVVDHNFLLDVPCLKMLLSKFLSFGVVAGSLVYK  
LPQILKVQNSRSKGLAMGLVLELLSVTISFSYSYKGFPMFTYGESVF  
VAGANLLIICQILSFEHGGVGFQGLAGIALYGAAYVALLGGFVPPFSALQI  
MQGCVTPIVIASRLPQIWESYRNKSTGQLSFITWFLNFGGSLARIFTTLQ  
EIDDPLVLIGYIVGASLNAIIIGQIFLYWNNSGAKPSKPKKPAACKPATK  
AAAAKKKKAN

>hypothetical protein E80POFO01D09BM (and 14026) (complete), 244 aa, 599 checksum.

MRAALLYCAVVAALALTVVAAPSRPSFPSAYRATFSNLLVFTSDFNLT  
TNGLLAVSQALQAYKQSGIIYGVSAATLNLVYQOHISYVWTARSCSKPLS  
NTYQGADPLQIMIRYTSFAGAVRVNNVQTVWLFENANRDVRAIYVTDNA  
RQTPVRLFLETYGVGVQIDYSSFTAGASSDFQTPKACSTTARQPHEQQE  
EGRVHAVAASVAAKRSSLPESELEAEPHASGLAAVHAALASMLP

>hypothetical protein Contig3523 (complete), 183 aa, 1E28 checksum.

MKMRCVIVALLCLASLALFANAANLLEVSKTVEAGPKTGVYTVTIGYKV  
IGAPGRVANVNIADSLPEELDLVSGDLVVKAEADPSTEEWYYSYQVKKN  
VHLTIAEPEAVVELPPAEVSYTTGGNAVSTVSTDAVPLVIGVPPKGTFN  
LTPVIAFFTALPVLAAVYLIPYFSTSQLKRRK

>hypoxia upregulated protein Contig5732 (likely complete), 721 aa, 1ABB checksum.

MALSTRLLLLLVVGVSLAICFLPTARSLVFLDFGSRVWKMSVIRGNSFE  
IILDAQTKRKFMSGLAFHDDERFFAADA EKVMRSPQHTYQYLSQLLGS  
HNSSVVEALKPHLLYADEIVPNGERTVAIRYNENTTFAVEDLAGMVFNF  
ARETALAYVHSPVADVITVPPHWTAEERA AVIEAAELGGFHVLSLINDG  
TAIALHYAFGRFEFPKNVIFYDMGHSNTRATLVEYHSIRIKKGAKNVTQ  
PTMKVKAVTYDTSLGGRDFDYRLAEHLGAVTQMAAKGIESSVDQIKAN  
KRAWARLMTAASQAKTVLSANMETYAAVEGLVGSYDLKTTVSRAQFEEMC  
EDLFARAATPVKEVLAAANTTVEEVGSMEVVGGSVRIPKVQAVLKQTLGL  
PELSKTLNGDEAAVLGAVFYAAHLSTS IKVPEHKIKDITPYGVTATIKLA  
RPADALEASDKEDSVAGNQDGKGGDDDDDDDDIDEQAEDTGTVTKVLS  
LFFKPFGRVGAKNVSVFKKNVSNFTVELAYDDEAKLPEDAPRQLARFTVED  
MNKLKKNYNTGKPKVTLAFRLTTSGLVELETAAEAVVVIKYPEPEPSAKS  
TPAPTPEATEEDKAEADAADDEATGEEKEDSAANKEDDEAEKEEVAADDE  
EAEEESKKKEKDEKPKKKEKPKKT VHKIALAVVTQKLGIPERTYVEKSR  
ARALLKQWEAKAVSKRYGRIQ

>alpha/beta fold hydrolase Contig23416 (complete), 391 aa, 28 checksum.

MKLLLLVLVGLIAVLLGAVVYHDGAPSSPNDFATPASSADGIQOTRTYARI  
VERVPIHHEHFEAWLYLPLVPATKPPVIIMGPGLAAQKDFAGLTAYAER  
FVAEGWAVFLFDYRNFRGRSEGRPNLIDPIRHVQDYHAAIVHVNTNITE  
KVDVTRMALWGSSFSGGHVLVTASEFEAAVKAYPLNYILNQRPEHVNRTK  
PQLKAVFSQVPHLDPYAVIPTLNLQVARGFALAIADWIGSWFGLNVYVR  
IYASPAEVAIMNTPEAVEYGHVPEKPVGGWGKQGTGEVYPLRFSLQAAG  
LCGLHFYAHADDRSQRYPVPYHRRQRSRET PRQWKGSQVRRGPLRLLRG  
QATLRGDARAPDPIPRASLTLPLSPSPFLFAPSLLSSPFL

>phosphatidylinositol synthase Contig3726 (complete), 223 aa, 367 checksum.

MNPIYFFIPNLIGYVRIALAVVAFMYAMTNHKLFFVCYLLSELLDALDGH  
AARYYKQSTKFGAVLDMVTDR CSTSCLIMILGLFYPEYMAFFLFAVALDI  
TSHYAHLYSALSARGAKSHKIDILKSQNWLLWVYYTNRVTLVGLVCLFNEIF  
FLGLYLCHFELGPLVANTGLGVWQIVTLVAFPLSMIKQLMNLIQLRQAAM  
DIAELDLAERPPKRLRRPGTNSK

>peptidyl prolyl cis-trans isomerase Contig8450 (complete), 180 aa, 678 checksum.

MKIGFLLLALALLVSLVAAANMDKYNLRKKGKFEKKALEEGVVALPSGL  
QYKVVTEGPAGGKSPSAADTVSVHYRGTLDIGTEFDSSYKRGQPAQFGVG  
QVIRGWTEALQLMSVGDKWELYIPSDLAYGPSGPGSIGPNQVLIFEVELL  
DIVGGSSAQPAVAGGKKARKSKKKQAKEEL

>protein disulfide isomerase Contig9880 (complete), 210 aa, 1DAB checksum.

MRQTWLVVVLVVVGLLAVWCTTSAAAGASSDVIENDDNFEHLTQATSGS  
TTGNWLVEFYAPWCGHCKSLAPTWEALATELKGTVPVAKVDATLNPLVKK  
RFGIKGFPTIIFFKQKQYVYTGGRSLEQLKAFALSGHESVASAPIPAPV  
SAMDQIIEMLNEDVQHLANTKKLAVGAIFVVGGVVGLFVGFVLRGLTSSS  
SASKTSTKRE

>Peptidyl-prolyl cis-trans isomerase Contig19326 (complete), 202 aa, 13CB checksum.

MKLSLLLAVLVCVLSVLAQAEADKKGPKITNKVYFDIEIDGKLEGRVVFV  
LYGGTVPKTVENFRALCTGEKGVGSKGKPLHYKSSFHRVIPNFMIOGGD  
FTHGTGVGGESIYGDRFADENFKLKHHTTPGLLSMANAGKDTNGSQFFITT  
VATPWLDGKHVVFGKVLLEGYDIIKKLESLSQSGKPSATLTIADSGELPL  
SE

>histidine acid phosphatase E9BS9UA01DJC2M (and 1498, 11042) (likely complete ... from PGP),  
517 aa, 1B1E checksum.

MRRLLTCWTSVAVGAGMGLAAAGQCDGGLTIHATTTKTETATPSLPDVDL  
KVAPPAHAATSSPIATGPDGPASPLRLQLVLAVTRHGLRTPLSSTDQRN  
EWRCEHDQLLVQHYADADDALRLTHSDEPLPDHVPANLLTRRKLHGRQK  
LRGNCHVQQLTHLGLQLRRI GELLRERYVDELRLVPPVFDARTVVFVRS  
DTNRTIESAQSLWGLYPPSTRPHGREGVMDVNIVEGAAENMYPRACAR  
LNQLKKDARATPDYLVKREDRQPFQASTTTTTTTTSSSTALSTRPLRTNAW  
PRQDKVEAALGRKVNWDGLNSTLQTIIRHRLLLPDGVDQDIVDVEREA  
GYETAVKFFSSPEICRLAIGRFIDVVDVQTTVDGEDDVFALYSGHDNT  
LSPFLSAFNVDARQPPMASVIVLEVYKDAKDKHWVRFLYNGEEMVVQAP  
AKGAGA EKGELEPLTQRYPVAVVRDAGEAGERREAIALAPHERWRELATS  
LIPIDYDAECKESAPLA

>transmembrane protein E9BS9UA01B4UHH (and 346) (complete), 178 aa, 11C5 checksum.

MVWDCVQIFAISLASAVTAEVLSWLLIYRTESYSSLSQKVEKLTCKKLEKK  
KDGPOSIDKKKSRDKRIVQYEQQLQEANRELQSKMKSMFVIGITLVSLF  
GVINSSFGGLVVARLPFEPMPLVRSISHRGLLGVDYIECSAAFIYALCSM  
SLRTSVQKLFGWAPPPGQDSMFGTPGTH

>transmembrane protein TMP21 Contig14813 (complete), 210 aa, 2FA checksum.

MMTRRTTFVLVVLVIGLVLVGHGKFDISPNTERCLKEELSRDVLVLGNY  
SVEQQQPSLRLHFTIMDPSKGEIFAKDADEAHFSFTTENGGEFLFCFNDI  
TDQSRLAYGYSRRVALELKTGVDAKDYTELAKENLSKLEVEMRRIEDGV  
AEILNDLKYLRREERMRD TNESSTNSRVAWLSIFS VVTMVAVGAWQIYYL  
KRYFQQKKIL

>peroxiredoxin homolog Contig10531 (complete), 220 aa, 867 checksum.

MARMGLVALLLVAMAMTVLAVCPARVQKPAPAFTADAVVGSDFKSISSD  
FVGKYVVLFFYPLDFTFVCPTTEL TAMS DRVEEFKKN AEVVAVSVDSKFS  
HLAWTKLPRSEGGLGEMHIPLVADITKQISR DYGV LLEDGPDQGV ALRGM  
FIIDTTG VIRHITINDLPVGRNVDETLRLVKAFQHTDKHGEVCPINWQPG  
QKTMKASPEESKEYFKDIQL

>hypothetical protein Contig9997 (complete), 257 aa, 89 checksum.

MKMATSLLVFVLAFAALGCNMAIANSES GEFNAKEFLLGDWELELHRSPLT  
APSAFGFVATSSWKIKDGNETLYGVAIDEKDDERQLRVEFEGESKGQFLL  
AVADEESEEFVPVFAFAFTNR TAGHFVSQGEWKDEQRAETGVYQLAATSP  
NTFLLTLWLT DATGVGQEVVTITGKKFVEKPAQTFQRF GMPMAVVGMMI  
VSQVLKRSRAGAAAAAQPPQQAARPGQQAAGEDDDDDASEEEEEPRFTE  
ITDKKDQ

>Sar1 Contig27843 (complete), 190 aa, 2653 checksum.

MYLFDWFWGVLSFLGLYHKSakilFLGLDNAGKTTLHMLKDDRLAVHYP  
TFHPTMEELTLGSIRFRTYDLGGHTTARKVWKDYADVDAIVFLVDSVDR  
DRFPESKRELDGLLSADDLKTIPFLVLGNKIDIPKAASEAELRQALGLHQ  
TTGKNKTSLGDNIRPIEIFMCSVVKRSGYGEGFRWLSNYL

>related to UDP-glucose:glycoprotein glucosyltransferase Contig3876 (and 9531) (possibly complete), 1565 aa, 2222 checksum.

MPLPSISKLRTEFFAAETSQGFVAVVDGLHPGAAEDTDDTATTEETLYGK  
VMQLANALLPSSSKRLLHYALLSRYYSKPKVEMFRQYSRGOAHECRNAAWV  
HAGTHMLCTPEEVQRYLEQPNRNEGSVPEATLVFGDQEHLPNAAPSS  
APLLVLYGQVGSKFTQYHVSIRVAASASTVRYAVRHYTPEEPKRLMNV  
QGYVELAIKSTEYKVIDDKVPEKDKDGDDEQQSGQEODTTIEGFQFDKL  
KQRKPELATELDAFKEHLEMVSQQNEGFQQLRAWQIKSLGYQAAQRIMSA  
GEPLQLLRDIAHNFPPIANSLARLRVDADIRSEIEDNQEQLAGLHHLPGN  
FINMNGRNLAADQLSPYVLYEFIKDELSKLDALSVMRARPQGLGEAPFAA  
PATDDPNNVNGAIQFANNLEKDDAMYGHWPPIHALLQPVPYQGMRYIKKNI  
QTMILVIDPSSPQGLSVIGNFLYMLRQGLPFRVGFVVFSSGSTTESASTWE  
HSAENLAKLAKGESGDASQGSTESADNAPLPENLAATI IKTYFLLKQKRS  
EGVRPLDFFGFLGQSEEEATEVTEERVWQAFAMHQGGSIQSEWREG  
MKSEAVATEYRTMORYIEQKGIALLDRGSQYIFTNGKFQOIPADSSVGS  
LQNLMLQETFYGYSRFQEAAYKRELQHVDDLWSWILQESSPVFDRFSSLI  
FQTTGEDENGWVSLARHRELLAPATAYLSFPASEFNLKEYTHLVVGDLT  
RPGLTQALEAVLRLAEEGSEKVRVGFHLHNTQDSQQVPPERRENEFLVAR  
ALQAALTSGKTLKRVFPFVTRLLATALAVGPENVRAAHI EELALAAELKD  
LPALMSKTVAAAYAQFERDRNLASSALGLLPGQRAVVTNGKVTRLDPQVM  
LVQDLKLLAEFEGLARVDQIRATLDGVSEHFVDPDDL TSEFYSNELAAA  
VSVLSAETASSEQRVNLQPLTPSFVAGEQNDPTLKIVAVLDPLSKGAQOI  
APLLLSLVNNDMGIQVQVVLNPKRDLTELPLKTFYRYVLQDELVFDAAGR  
LARKGEAVFNNLPTSLLLTMNMDTPHSWVQAVRSVYDLNILLKDMGKE  
TRLSATFELQHILAEGQCIDVDKGS PAVGLQINLGNHQQSHITDTTVMAN  
LGYFQLKANPGLWWLSLGRKFGDEQQEGVSPYQLLSTDGRTVPVRLAAKI  
DRFTNTEYLQPYKVKRGAQQVEGTKEELAKQDGGMWGQWMSYFQDSQKD  
TAEAEAKKDETIHIFSVASGHLYERFLKIMMLTVLKNTKSPVKFWFLENY  
LSPKFKEYAPVFSQAYNTSIELVTYQWPSWLHHEKQORVIWGYKILFLD  
VLFPMDLRKFVFDADQIVRTDLKELYDMDLKGAPLAYTPFCSSRTEMNG  
FRFWDSGFWKNHLGGRPYHISALYVIDLKRFRMAAGDVIRATYQQLSQD  
ENSLANLDQDLPNFLQNRVPIFSLPQEWLWCETWCDESKARAKTIDL CN  
NPLTKTPKLENAVRIIPEWRDLDEEARSIEERYSSSFASSATATATTAPD  
AAAAVPTAPFEEIHA

>hypothetical protein Contig14206 (complete), 244 aa, 599 checksum.

MRAALLYCAVVAALALTVVAAAPSRPSFPAYRATFSNLLVFTSDFNLTT  
TNGLLAVSQALQAYKQSGIIYGVSATTLNLYQQHISYVWTARSCSKKPLS  
NTYQGADPLQMI RYTSFAGAVRVNNVQTVQVWLFENANRDVRAIYVTDNA  
RQTPVRLFLETYGVGVQIDYSSFTAGASSDFQTPKACSTTARQPHEQQE  
EGRVHAVAASVAAKRSSLPESELEAPHASGLAAVHAALASMQLP

>sulfite reductase (NADPH) Contig14693 (complete), 633 aa, 268C checksum.

MIIYIIIVAVVVVLI ALVLRPGA EVNGGSLDLFLGENSSDASDDDRKNAQ  
EAEEAKYSEVYTEEKQVLVLYATEYGFSEEVGKFLDHLIYAPPACQPRV  
VNARDREVF DLMKEQAVLIVSSTTG DGVPTDARDWLEDLVAKDRSSYDL  
SHLRYSVLALGDSNYTHYCKTGRTIDATLEALGAKRVVDKAEVDQEDWPV  
IDAWFAAVKAKLHEL DLDVRADYIVSRSGSAKQEKHGRLRPF AAEMVTKY  
DITDVPPEDEERKVIHAEFKLEAESELSYTAGDALGIYPLNPPPEVAAL  
LAALGQPGGDSLVPVPK MAYEPKPEKEMSLKEALLRFYDLKTIQPSLINL  
IKERTGDATERGQLEELLRDGGASISKNRRLKEYIELREVADVLEEFPSA  
IQHKKVSVDVLTNMKILQPRYSSISSPVIDKSIVSVTASVVRVYETL GK  
KRTGVTTF LCFDRFDVNQRCPVFINKNPEFR LPGA DGIIMIGPGTGIA  
PFRAFIHERVASKAAGTNLLYFGCRHRATDFLYREELEKLDGEGKIKLRT  
AFSRDQERKVVYVQHR IAEDKDAIWSMLEGGAHVYVCGDAKH MAGDVHNAL  
LTIIRDKSGCSDEAQQYMHKLEASKRYQRDVVV

>acyl-coa synthetase Contig3694 (and 27811, 26760) (possibly complete), 468 aa, 1FF6 checksum.

MSIFFDYDVTLAFAIITVTSALFFVVL PFLARDQQRGRIKPGPRKNTKFS

HQSYDVAPPEALGEGPIRRASDLKPDEELYDSLKDTENNLNLTENNLVVATL  
CQNFARSERLFGNCRCLGTRRFENDGTRGPYEFRTYKEIAALARYFGSGL  
KNLGAKRGEHIGIYSKNREEWVIADQACSAYSLSLTIIALYDTLGENAVAYI  
ASHASTRFVVSRESLRPLMGAAPDCPELKTIVILMEEPTDEERLAAEA  
LRLLLWFQDVVQDGKSRPVTIDPPTPDDLYSIMYTSGTTGDPKGVLLTHRN  
VMAMMAAVNQVAKSVATPEDAYLSYLPLAHIFERAIMQCAFSTRGTRVGF  
YQGSVLHIIDDVQELKPSFFVGVPRVYDKIYGKIVNLLPQQQKVRWWLF  
RRAVASMGEDPSGPARRAISGSGWSSTRPGRGLAATCGPCCPAAPHSPPW  
STSSSLACSDARSFRATA

>coiled-coil protein Contig2585 (complete), 194 aa, 9F3 checksum.

MYGRFCGMSRLFAVALFALLLALPAVFPQAKFQTDADWDEFEEEEFEAA  
VPVHTAKPGDAASPSHKDAAVKGAEEDKPAKLSFALTPALGDWFYVET  
ACIVLLTAFANYYFGRQANRRIALSWGRTFAQLLDSNFSRVGEGGGLLI  
KESENRYRVPATGRRNCHGLQATLNLGRRHDLFAQVYEFFMPAP

>rab21 Contig16061 (complete), 202 aa, 2622 checksum.

MTTTFNFKVLLGEGSVGKTSLVTRYVQNTFNERHVTTIQASFLT  
GSRVNI SIWDTAGQERFHALGPIYYRESHGALLVYDITDSSSFVKVKNWV  
KELRSQLGMSVTLAIIGNKVDLEKSRVANKKEALSQAQSVGAKHYDTSK  
LNKGLEELFLDLTRRMLKANKDGDSDGRGAACKDSILIDYEESSQNTGAGGC  
SC

### Cytosolic

>aspartate aminotransferase Contig23433 (complete), 440 aa, 7EE checksum.

MSHTESSVKKSVRRIVNSCIVSPNECSSNKKMSQYISNVPVAPEDPILGI  
NVAYKADPSTDKLNLGVGAYRTEEGLPLVNLVVRKVEQLVANDVSLNKEY  
LPIEGLPDFTAHTAKLIFGADSPALAEKRVATVQALSQTGALRIGAEFLA  
RFAPGGAATPVYISDPTWGNHTNIFKDAHMPDVRKYRYYYKEQTRGLDFEG  
FIGDLKAAPNGSVFILHTCAHNPTGVDPTLEQWEAILDVIQAKAHLPPFD  
TAYQGFATGDLDRDAAPARMAIARGMELFASQSYAKNLGLYAERIGALNI  
VCRDAATADAVKSQLKTIIRPMYSNPPLHGARLVSKILSDKSLYNEWLVE  
LKDMSDRIKMRHELYDAIKKNGTPGTWEHIIDQIGMFSYTGTLKAQCEV  
MIKKHHVYMMTNGRISMAGLSSKNIPKMAAAIHDVVVVNQ

>polyubiquitin Contig11231 (chimeric est) (complete), 128 aa, 23C4 checksum.

MQIFVKTLTGKTITLEVESSDTIENVKQKIQDKEGIPPDQORLIFAGKQL  
EDGRTLADYNIQKESTLHLVLRRLRGGVIEPSLQVLARKYNCDKVVCRKCY  
ARLHPRAVNCRKKKCGHSNHWRPKKKLK

>cyclophilin protein E9BS9UA01CKKR0 (and 8624, 20522), 171 aa, 40E checksum.

MSNPRVFFDISIGGNAAGRIVFELYSDVTPKTCENFRALCTGEKMGGS  
KPLHYKSSFHRIIPGFMCOGGDFTRGDGRGGESIYGAKFADENFKIKHS  
GLGTLSMANAGPNTNGSQFFICTAETS WL DGKHTVFGKAI EGLDVIKAME  
KVGSQSGATAKKVTIADCGQL

>PARN nuclease protein Contig14495 (and 19022) (incomplete C-terminus), 534 aa, 115F checksum.

MEVTKSNFAAVLPDVKEAIAASDFLSFDLEFTGLTLGGYLDNHPVDLLEE  
RYKKLKENS SAFTITQFGLSAFTWDATENKYVARTWNFYLFPRPYGWCDR  
RFTCQAASLQFLLEHKFDNFNFIYEGVGYLSRYVEGKMRPQVEEIIQKLL  
DAASQEALPDIVPTNPRDVEFVAGIKASIDGWLQDGAEPVLVIAPNSFL  
RRLVYQEVGRNYPELNVEKVQGTWDNMSISRMSSEEEKARRRAELVQQRD  
EFEAAIGFRQVWEARLLRAAPRPPRGRERLSSQKSNKIMEVTKSNFAAVL  
PDVKEAIAASDFLSFDLEFTGLTLGGYLDNHPVDLLEERYKKLKENS SAFT  
TITQFGLSAFTWDATENKYVARTWNFYLFPRPYGWCDRRFTCQAASLQFL  
LEHKFDNFNFIYEGVGYLSRYVEGKMRPQVEEIIQKLLDAASQEALPDIV  
PTNPRDVEFVAGIKASIDGWLQDGAEPVLVIAPNSFLRRLVYQEVGRNY  
PELNVEKVQGTWDNMSISRMSSEEEKARRRAELVQ

>cytosolic Hsp70 Contig23290 (complete), 666 aa, 14BE checksum.

MSKEVCVGDIDLGTYSVGVWQNDRVEI IANDQGNRVTPSYVAFTDSERL  
IGDAAKNQVAMNPHNTVFDKRLIGRNFSDPIVQADMKHWPFKVVQKPGD  
KPFISVEYKGETKEFSPEEVSSMVLIKMKETA EAYLGHPINSAVITVPAY

FNDSQRQATK DAGTISGMQVKRIINEPTAAAIAAYGLDKKSQ GEMNVLIFD  
LGGGTFDVSLLTIEEGIFEVKATAGDTHLGGEDFDNRMVTHFIQEFKRKH  
SKDISGNARAVRRLRTACERAKRALSSATQTNIEIDSLFEGVDFYTSITR  
ARFEELCADLFRSTMDPVEKVL RDAKMDKRTVSEVVLVGGSTRIPKIQQL  
VTQFFNGKEPCKSINPDEAVAYGAAVQAAILSGASTEGSVLGDVLLIDVT  
PLTLGIETAGGVMTALIPRNTTIPTKKTQVVFSTYSNDQPGVLIQVYEGER  
AMTRDNNLLGKFELSGIPPAPRGVPQIEVTFDIDANGILNVNAADKTTGR  
SEKITITNDKGRLSKEEIERMVKEAEKYKND DENAKEKVEAKNALENYAY  
TMRNTIRDDKIASKLDSGDKSKIEEAVDAAIKWLD TNQTAEKDEFEHKRK  
ELEDLCNPIFTKMYQAGAGGMPDMGGMGGGFP GGAGGFPGGAAPGGGA  
RPSGGSSAGPKIEEVD

>triose phosphate isomerase Contig15000 (complete), 258 aa, 228C checksum.

MSARRFFVGGNWKANGGQSFVRSVLVADLNAGNVPEDVEVVISPPSLYLAQ  
VQEQVRKEIAVSAQN CYHQDGAFTGEVTASMVKDLGLPWVILGHSERRSI  
FKESDELIGTKVAKCLGVGLKVIACVGEQLSERE EGKTTTEVVFSQLKAIA  
ANVTDPKGWENVVIAYEPVWAI GTGR TATPKQAQEVHAEIRKWLHDSASA  
EVAATTRIIYGGSVKPDNSDELASEPDIDGFLVGGASLKAADFFKIASAA  
NAKKSACL

>pyrophosphate--fructose 6-phosphate 1-phosphotransferase beta E80POFO01C3XLD (and 23471, 12660, 2318, 20072) (likely complete), , 554 aa, 23C7 checksum.

MSEVAEVSTLQARLAHQPPVPTLRGRTTLRRHAHPTSSLAQSEEIEKR  
LPHIFGQPRVELEAASTAGDDASH SPLRIGVVLSGGQAAGGHNVIAGLFD  
YVAAGHPH SKLYGFIGGPIGLVKGGFIVIDAPLVAKYRNQGGFDIIGTGR  
DKIETDKQLLASRVVCENLALDGLV IIGGDDSN TNAALLAEYFKSHHLKT  
NVVGVPKTIDGDLKSSLGVEVSFGFDTACMIYSELIGNIATDANSSRKY  
HFIRLMGRSASHITL ECALQTRPNITLIGEEVAARKQTLSDLTNE LCHVI  
VERAKAGKNFGIVLLPEGLIEFVPEVHRLISELNELMAKGN SADVGEKL  
TEESRAVFDLPSAIRHELLLDRDPHGNVQVSKIETEKLF IHLVTKELKR  
RKANGQFKGSFSAMGHFFGYEGRCGLPSNFDSNYCYALGR TAGALLDHGL  
TGYMASVSNLTAPPEQWKS GGLPLTALNMERRKGNVPVIRKALVDLDA  
APYKELLRHREKWARGEHYRNP GPIQFYGPASGEVNITLQLEFGQAHRHP  
KAAL

>Hsp90, cytosolic Contig3483 (complete), 716 aa, 247F checksum.

MAEDVETFAFQAEINQLLNLIINTFY SNKEIFLRELISNASDALDKIRYI  
GLTDKPALETNPELYVHLVPDKANKCIHIIDSGIGMTKADLVNNLGTIAK  
SGTKAFMEALQAGADVSMIGQFGVGFYSAYLVGDRVVVTTKHNDDEQYVW  
ESAAGGFTTIKRDTEGEPLKRGTKITVYLKEDQLEYLEERRLKDLVKKHS  
QFIQYPI SLWVEKTKEKEVEVEEEEEEKKAEEET TAEAPKIEEVTEEE  
EEKKEKEK KKKKVKETYHEWELLNKTKPIWTRNPQEVSEDDYKQFYK NLT  
NDWEDYLAVKHFSVEGQLEFKSIVFV PKRPPFDLFE TRKKRANVKLYVRR  
VFITDDCEELVPEWLN FVRGIVDSEDLPLNISREMLQONKILRVIRKNLV  
KKCIELFNEIAEKKEDDFK FYEAFGNIKYGIHEDSTNR TKLAELLRFHS  
TKSGAEMTSFKDYVTRMKENQKEIYFITGETKKAVESAPFVEGLKRKGYE  
VLFMVDPIDEY MVQQLKEYD GKKLVNITKEGLKLD ETEEEKKAEEETKKA  
NENLCKVIKDILGDKVEKVVISNRLVDSPCVLVTGEFGWSANMERIMRAQ  
ALRDSSMQTYMVSKK TLEINPDHAI VTELK KADADKNDKTVKDLVWLLF  
DTALLASGFSLEPPGGFAQR IHRMIKLGLSIEDTESDRVMGDDDLPPLES  
EEASAADEGSRMEEVD

>GAPDH Contig6882 (complete), 336 aa, 1835 checksum.

MSHIKVGINGFGRIGRLVFRAAVESGKV DVVAINEPFMSVDYMVYNLKYD  
SVHGAFKGAHEKDKNTLVVNGKEIKVFAERDPANIPWGSAGADYIVESS  
GVFTDADKAGLHLKGGAKKVIISAPSNNAPT FVMGCNESSYKPEYNVISN  
ASCTTNCLAPLAKVIHDNFGIEEALMTTIHAITATQKTVDAPAAKDWRS  
RAGLTNIIPATTGAAKAVGLVLP ELNGKLTGMAFRVPTIDVSVDLTARL  
KKEASYDEIKAAIRAAADG PLKGI LAYTEDEVVSSDFI HSSVSSTFDAKA  
GIALSKTFVKLIAWYDNEWGYSNRVLDLIVYINGKQ

>HECT ubiquitin ligase Contig20634 (incomplete), 232 aa, 67D checksum.

MEFFRDKSI VDVSCGLDHSAAVSKDGRVWTWGYGIDGQLGHNGTEDELKP  
KELTVIRGEGISRVICGTDFTGLLNETEGRLFTFGNGEAGQLGHGERGLC  
LEPSVVPLDNVKEVAAGGAHMLALTKD GQAWSWG WGEDGRLGHGATEDFL

KPEPIPTLGPVAVGVSVSAGGGHSLALTESGQVYGVGFNASGRLGLGNETS  
SVMTPTLIKALADKRVLRRAICGLDHSFLITQA

## Nuclear

>histone h4 Contig3839/7518 (complete), 110 aa, 1893 checksum.

MSHVGRGKGGKGLGKGGKGLGGAKRHRKVLDRDNIQGITKPAIRRLARRGG  
VKRISGMIYEETRGLVKVFLENVIRDAVITYTEHARRKTVTAMDVVYALKR  
QGRITLYGFGG

>histone h2b E80POFO01AOLNB (and 13209) (complete), 163 aa, 728 checksum.

MSSTPKKTGGKAPAKKPADTVEGAEKKTGGKTAATKKVGVKKTAGEGK  
KGTGKGGKSKKNYQSYSTFIYKVLKQVHPDTGISNKAMAIMNSFVNDIFE  
RIALEAGRLARYNKRNTISSREIQTAVRLLLLPGELAKHAVSEGTKAVTKY  
QSSLGSTAASQDE

>fibrillarin Contig9054 (complete), 307 aa, 1E43 checksum.

MSFSRPRGGRGGGFSRPRGGRGDRGGRGGGFGGGRGGDRGGRGSRGAS  
RGRGGGRGGGAGGMRGGKVVIEKHRLDGVFIARGKEDALCTRNLVLP  
GDSVYGEKRISVDEVDGSKVEYRVWNPFRSKLAAAIIIGGVENVVVKPGAR  
VLYLGAASGTSVSHVSDMVGPQGMVYAVEFVSHRSGRDLINVAKRTNVVP  
IVEDARYPLKYRMLVGMVDVVFADVAQPDQARIVAINAHQFLKNGGHFVI  
SIKANCIDSTAAPFAVFAKEVQKLRQENFKPMEQITLEPYERDHAUVVGV  
YRPEAKA

>nop56 Contig1712 (and 720) (complete), 509 aa, 172C checksum.

MVLYVLYESASGYALFERIESEEIADESPELQRSIQDFGRFSRIVKFKSF  
VPFVSAESALENVNAISEGLVHDVLDKLNFLNLPGGGKSKKVELGVTD  
EKLGGAINDSLEHVACVKSKAVALTRGIRLHFAKFIKEFKEGDYEKAQL  
GLGHSYSRSKVKFNVRADNMIQITINLLDNLKDLNFTSMRCKEYWSWH  
FPPELVKVPDNFQFARVVKFLKNKAEADESKIPGLVDITQDEAKAKEIID  
AAKASMGTDISDLMLNIEKFADRVIHLSTYQQQLQEYLSKMMHVIAPNL  
SELVGEHVGARLISHAGSLTNLAKYPASTVQILGAEKALFRALKTRGNTP  
KYGLIFHSSFIGRAAAKNKGRISRYLANKCSIASRIDAFSDVPTTKFGQK  
LNAQVEERLKFYDTGALPRKNVDMKEALSEALTEADQKQREDGMDVVST  
TAESTDKKRKRKAAEKDDSDSDEEESKDKKKSKKAKKSKKEEEKSKK  
DKKKKSKH

>histone h2a Contig1896 (complete), 159 aa, 215F checksum.

MSSKEGAKTTKKAEGAKKAPRSAPKAKPAPAGKDAAGEGHSRSFKAGLQF  
PVGRIHRQLKEGRYASRVGAGAPVYLAHVLEYLVAEILELAGNASRDNKR  
VRIVPRHIQLAVRNDEELNKLQDVTISSGGVIPNIHSVLIPKSKGKGGK  
AGESLSQEY

>appr-1-p processing domain protein Contig5482 (complete), 255 aa, B6 checksum.

MAHLVSNPVRVLAAGLLLVQCVSTLDEELINLAQAQPLINSCVWFRMTLLA  
GVAAFATSPVSTIVQATLPTGHTISVRHGDITSESDSDVIVNAANRHLRHG  
GGVAGAISRKGGPAIQAESNDWVARHGALNDGNVAVTSAGNLPARYVVHA  
VGPVWHGGGDQEEETKLEKAVLNSLKKAEELQARSVALPAISSGIFGFPKE  
RCAEIMVQTTTDFYHQKPTRLKDVRVLTNFDVETVGFVFKRKLTEKFPAAAR  
VHSEL

## Vacuole:

>vacuolar ATPase subunit F Contig20827 (complete), 140 aa, 1541 checksum.

MAAHGKTKLRSPETGSLLAIGDEDVTGFLLAGIGELNSKRTKNFLIVD  
NKTKLQGVVEAFREFTAREDLAILLISQHVANDIRHLLDEYDRLLPTVLE  
IPSKGAAYDMAKDSLMTKVLRLGTSADAPDIDDESTSHH

>vacuolar sorting protein 4 Contig4298 (likely complete ... some from PGPs), 428 aa, 83F checksum.

MGDNLLQKAITIVTQATEADNRKEYAEALRLYQLALEYFMTALKYKNER  
SKQVIRAKLKDYIDRAEKLKAYLKGNEGKPPVAQGGGGGEGDEDGDPEKT  
KLHKALQGAILTEKPNVRWDDVAGLYAAKESLKEAVILPIKFPQLFRGKR  
KPWKGILLYGPPGTGKSYLAKAVATEANSTFFSVSSADLVSKWLGESERL



VRSLFDMARQNKPSIIFIDELDSLCSRSRSDNESEAARRIKTEFLVQMNGV  
GNDEDGVLVLGATNIPWQLDAAIRRRFEKRIYISLPDAPTRARIFQIHLG  
NTPSNLTAQDYRMLGEMTEGFSGSDIATCVRDALMQPVRVAVQATHFKPV  
YEVDHNNPAVSREYLTPCSGSDPLAREMTWVDVPGEMLMEPRVMTMNDFLK  
SVKNSKPTVNTAELQKQIKFTEEFQEG

Unknown/other

>hypothetical protein 16998 (complete), 299 aa, 1C91 checksum.

MGRATAVLSYTLRSVAVFVATHVVFAYWLNLYLLNDPLNLGLVTLDAKPPLP  
AGQCEHFVVGNAVSNLLWFALWWGTHSILARKAVKQALGLWEHPLERPLF  
ATVAWVAWGLNVHTWRPVDTCAPWDPLAVSPYVVAASGAVFAAGVVLIIV  
GLLWSLPDHVFGTARYQYDQGRPHGDLILRFPYGLVVRHPAAAGFLWCYA  
VLPAAWTNVNHLFLAGLWITFIVVATGLEEGGLKGDDEFQORYEAYRRSVAA  
FHPSWAALKNILGIAPLKIVGSSGSKKKKSNGAAKEKEESASSKKKKQP

>SPX domain protein Contig24624 (complete), 182 aa, F78 checksum.

MKFGKHLSSALPAWLASLYDYKALKRAIKVQAQTGDTSLFDTLSSAEIK  
KADAFYKAREEDLLQLFSALIERPGSKRPSADEKTPLLTKGFSKSDVGAD  
ASGEAWRSMSREEVLQRLDEVEALATNLLKFSALNYTGVSKSLKKSFKKT  
GISSDAWLPRSSSTRPTSLSPASVTRCSPRPH

>Rap1a Contig4448 (complete), 198 aa, 1C8E checksum.

MAQKAASSHNEYRIVVVGAGGVGKSALTMVFIQGTFLTKYDPTIEDSYMK  
QVEVDGVACTLDIMDTAGQEEFGALRDQYMKTGQGFLLIVYSITTLTSFEA  
VTKFRNQILRVQEDRLDIPILVGNKKDLEEDREVPTEDGQALSEKFNCD  
FLEASAKTNTNVNEAFFRLVHRINKWREKHPQAPKPKPKKKKGCSLF

>rap1 Contig14992 (complete), 185 aa, 22F4 checksum.

MNTLKIIVVLGSGGVGKSALTVQFVQGFVVEQYDPTIEDSYRKQVEVDGKQ  
VMLEILDTAGTEQFTAMRDLYMKNGQGFVLFVFSIIAISTFNLDLREQI  
LRVKMDSVPMVLVGNKCDLQDQRVISTDQGGQQLAAKFGNCSFLESSAKT  
KTNVSEIFYDLIRQINRNKKPDGDSGGKKKKCLLF

>microsomal signal peptidase Contig9517 (and 7240) (complete), 195 aa, 1DA8 checksum.

MQKRKQAPPVVFTPAASEAVKVDVYDQNAVKQLLDDVIMTYVLETRGLEED  
LTYSNYKLALGGLSCLVAIASHAYPAPFPENAWVLKVCVVSIVLVSLLQ  
YVAFYMEGNTILATRPTQRGGTNNKKLIKPINVQTYFPKCEEAFIVQVTT  
TQGKPASHSISSSIGRWFPDGTFFIREAFISDLDQLFTTVEDASD

>regulator of chromatin condensation Contig22000 (and 19707,24163) (incomplete ... used PGP),  
465 aa, 74D checksum.

MLYMAVNSKSVVHAEHLPOATTSASHSPRAETDKPLASGGNVVWVGADG  
GTVPSAGSSPADSLVPRLAALKSGKGIKGLAFGDKAAAAVTNKGELYLWR  
VGEEPTLTHEKGVQOVACGRNGLIAALTDKGDVLLWDARTHAEGGLHPS  
ASSKEAGEADWKNVKRIDIASLSLPPASATATPAASASSWWPFGGSGSK  
AGAETITQVDCSGSHVAMVTSRGRVVLVLDNNGYQCGTQDASNETRGP  
VRPSPVVIDLGIAGGGHKAVGVSCGDTHTAILLDDGAVFMLGSVHLSGLK  
GSTLYTDSPLVPLTRDSKSVEKLGRIIKLSCGGEHTLALTNYGVLLAWG  
NGMYGQVPDNOGKHINTAHPVLRAPFFNAEGKEFINNEVKELQCGNEHCL  
ALTKGGDVVSFGRNDRGQCGVGNRAHQKTPHKVTKLQSRKDKISAIACGQ  
HTSAAIEEGAQKYEI

>calcium transporting ATPase Contig (very incomplete), 993 aa, 166E checksum.

MADFAFTADELSQLFDDRHFALAKAGGLQAIKGLKTNLETGLNEEQLS  
EEGRAGRVRVFGANKTDPKPKTLFELMLEALEDATLKIILVAALVSLAL  
GFYENPSSGWIEGTAILVAVVIVVLVTSNDYSKEQQFRRLSQVADDKLI  
KVMRCGQQQVSVYDLIVGDVVELGTGDEIPADGLVFASHNMKVDESSMT  
GESDAIKKNDNEPFLISGTPVTEGVGRMLVAVGAHSQKGIKALLQKEQ  
EDTPLQEKLEIVAAAIGNLGLVVAAILTLTVLVGQFGWRLYSSGQGFELHM  
LEELIGFVITAITIVVAVPEGLPLAVTISLAYSMMKMLKDNLLVRHLDA  
CETMGGATNICSDKTGTLTENRMTVTHVWLGRKMYGNSLPTQKDLAAEVH  
TALVEGISINSTAYITKSKDKNTTEFIGSKTECALLGFVEKLSGNYDQVR  
QTLKISQLYPFSSERKRMSILLEAEGNVHRLYTKGASEIVLQYCDKIVSP  
EGKVTPLSDEEKEEIRVDVIENFAAQGLRTICLAYGDVPPQDNSEEPPEQ  
GLTCIGIVGIKDPVRKEVPAAVAACKAGITVRMVTGDNILTAKKIAEEC

GIFYGEGIAMEGREFRQLSEEEMGNVVPKLQVLARSSPSDKYILVSYLRK  
LGEVVAVTGDGTNDAPALKESDVGFSGMISGTDVAKEASDIVLLDDNFTS  
IVAAMWGRNVYDSIRKFLQFQLTVNLVALLIAFVSAVTTGESVLTVPVQL  
LWVNLIMDTMGALALATEQPTKDLLHRKPYGRHDFLITKQMWCNIIIGQGI  
FQAIVLFFVLYRGESFFGVVSHSLEHTTIVFNTFVLCQVVNEINSRKIDH  
QLNVFSGILSNHVFLGILVFTLLFQYVIVEFGGSFTATTHLTSDQWMKCA  
GVALLGFPVGVVIRLLSRPFVQTPVTKQTVEVDP AIVKMMWQKVKRASV  
HMEITEDVEKRRANKFKDQVQRKIQLNRMLKEAKGKGDLLKHKQ

>fibronectin-like Contig2440 (complete), 480 aa, 197A checksum.

MSKLTALVVCLVVCALFGLSFGQENDFRETQSFKKRDLPLDPETIKECIG  
SAQFSQSVRTISSSYRGPQSIAAADFNKNGKQDVVAYATENKVYFVSNQ  
GEGLWSASVLTGTVNDASAVFAADLNGDGRIDVVAASETNDQVHWFKNVVG  
GWTHTILDAAISAPRSLFVADINDKNKPDIVAAGDAIAYLENQITNVQP  
NGWTINAVTYSGSPVDSIFAADLDKDGFTDLVLAASSTGDLVWLNNTSGSG  
TAFASNVIATATGVSQVFCQTDIDGDGYMDVVTADKSKNATTLYYNNLVIA  
THTLPSGNNNSAPAQSGWVGLYVDQDQONAPESVFVTDIDGNGYQDIVVAI  
TGADTIKWYDTSDFYTWDAHAVGDATSPSYVYARDIDGDYVKDVFASAT  
GNRLGWFEELCATSLPDGGDDHVVGWAVAGGVIGLLLILWILVAIAIAI  
HDYIKHQKASEQRKKEAKSMLPTEHDDL

>Rieske domain-containing protein Contig16785 (incomplete - uncertain of N-terminal completeness)

MAWKVAFCVLLAVVAHLLVDPFDISSLTKHKEDFLHRSPFADLQTGNSSSLSQVLF  
DAS TSVAGFKRLVAFLESTTNARALMGTWVAWVAVAFVLAAPWTLWAYDYFCCPLELTVSLE  
DVERRADGKKYPPWERPRRLRGAVPPPYPNAWYKVCNSHDIPKGESRDFELLGHFFAVYR  
GEDGKVRILDAYCPHMGANLGVTVGRVVGNEIACPFHGWQFDGEGKCTHIPYAEKVP  
GFMK TTAWPSTEMNGSVMLWHDAEGRPPLWMPSDIKEINSGRYKWHGAALH  
QVRAHIQEIPENG PDAHLNLYLHVPLVFRLLNKIGFHHAW  
EATWEAGKGVDEHLAFMRVIQSVEFRGRYIPGT RIDVDIVQV  
GSPMVLHFATPFGKVM LIETVTPVQPLLRITHQVFAEWT  
VPRFFAKFIM GNTIVQFERDVP IWNKTYLNNPGLVKEDGPIAKYRRWFAK  
NFYSENSEKVARDRAAATG SIDW