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>ADP/ATP translocator Contig25952 (and E80POFO01EIVE4) (complete)
MGDLNKKNDLTSFLIDFLMGGVSAAVSKTAAAPIERVKLLIQNQDEMLKTGRLAEPYKGI
GDCFKKVIAEEGFGSLWRGNLANVLRYFPTQALNFAFKDQFKRMFGYNKDRDGYWKWFAG
NLASGGAAGASSLLFVYSLDYARTRLANDNKSAKKGGERQFNGLFDVYKKTLKSDGIVGL
YRGFNISCVGIIVYRGLYFGLYDSLKPVLLTGSLSDSFFASFLLGWGITIGAGLASYPLD
TVRRRMMMTSGEAVKYRSSAHAFSEIVKKEGVKSLFKGAGANILRAVAGAGVLAGYDKLQ
VLVFGKTYGAGGG

>ATP synthase beta subunit Contig14918 (complete)
MLRNFSKRALPRTALSRGLATRTAAGLRQGANTTLATSSAPSKYAMWGSRTLATQPEPKT
ASKAEAESQAVDTDGKIVQIIGAVVDVKFPEDALPPILSALEIQDHNIKLILEVAQHLGR
GVCRTIAMDATEGLQRGQRVKDLKGPITVPVGAATLGRIINVIGDPIDEKGPIYSNKRNP
IHAAPPTLTEQGASDQILVTGIKVVDLLAPYAKGGKIGLFGGAGVGKTVLIMELINNIAK
AHGGFSVFAGVGERTREGNDLYHEMITSEVIKLKDPKTLKEGDHIGEGSKAALVYGQMNE
PPGARARVALTGLAVAEYFRDEEGQDVLLFIDNIFRFTQAGSEVSALLGRIPSAVGYQPT
LATDMGQLQERITTTMKGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSRQIAELGI
YPAVDPLDSTSRMMDAEIVGKEHYDVARAVQKTLQDYKSLQDIIAILGMDELSEEDKATV
YRARKIQKFLSQPFQVAQVFTGFEGKFVSLKDTISGFKSILEGKYDHLPEPAFYMVGDIE
EVVQKAQKLAADLGGGSAAKKDGKDASGAKVSGKRELTLDAFNDPSYPELKEGDFELNEK
SFRVFAEYTKNVAIPYARDHELKEFPEDAAKIKAKYDNILSKIDGETDELVKELHDASQK
HDAERKRKEQEAALKAQKAAAPQAAAH

>VDAC Contig17278 (complete)
MSYAPAKPVSVPVVVVPTVVRPAAPLYSNLGKGAKDLLSKGFPSTYKVEVTTSAENGVQF
VSSAEKKQANKTDVVVGTFQPKYKLASRGLELTGTFDTDNQIKAELALDNLFVPGVKGTF
KAQTGASHDLEAAFEYKHEVGTFTSTFVHNPTTAKTLLSATATVSRQSVTAGVESKYSLA
PAQPGTLTTVTGALNYKAATHDLTAFVKSDAGSVTDGGDAPRLYSLGAHLHYTPSKESSF
ASSLDYDLQKNTIKVTIGGSQKLDARTETKAKFSSDGRLGLGVAQQLTPAVKATLGTELN
TFDLAGSTPKFGVHFEVRA

>Hsp60 Contig14920 (complete)
MLRTAAPHARVAVRGSSRSASSLRLYASVAGKEIKFGSEARSLMLRGVDSLTDAVQTTLG
PKGRNVVLEQSFGAPKITKDGVTVAKHIEFKDKYMNMGAQLVRGVASKANDVAGDGTTTA
TVLARAIFSEGTKVVAAGMNPMDVKRGVDQAVSIVVGELKKLAKKVTTTEEIRQVATLSA
NSDDSIGSLIATAMEKVGSQGVITVTDGKTLENEVEVIEGMKFDQGYISRYFVTDPKTQK
CEYEDALFLLTDGKISSIHSLLPCLEEVSREHKKLVIISDNVEGEALATLIINKMRGLPV
VAVKAPGFGDNRKNNLQDIAVLTGATVVSEEMGLKLENFERSWLGSSKKVIISSDDTIIM
DGGGNSENIKERCEQITEALQRTTSSYEQEKLRERLAKLSSGVAVLKVGGATEVEVSERK
DRITDALSATRAAVEEGIVPGGGVALLHASKALEGVTGANADQTSGIQLVARAIRIPART
IATNAGKEGGVIVEKILQSTDAHWGYNAQTDEYGDMFKAGIIDPVKVVRTAIDAAASVSS
LMTTTEAIVVELPKESSMPAAPGMGGMGGMGGDMF

>putative TPR domain protein Contig17343 (and 17877) (likely incomplete)
MLYNYYLAWGNVKAERNEQAVKYLERYLDAAKVAKAPVESTLESIMSLVICYKEQGQLDA
AVKTVDRALQALKQIDEAEHPLLCLKQFYFLGLYCLNKLEQLDRARDLLERAYQLAKSNS
TLSKEMPWGTIAIDLAEAYHKLKMRQEALKMIETGLTALRERDTSLVPPALIRQAKIYSE
MGDKATAVRALEEALQVAEELKKKESATVGDAELGSGWLCRFLRFQLGKMYTLMGQLSKA
DALLTEAFNSFVGTTDLEIRTVVLATIASNLVQAGQKEAGLKKIQEVLDVLATPTTQKLN
QGDIRTELGECYLFLGDYAKAKQELESALEQFAKEKNEKSELLVLVRLAAIHDWLGEVDR
ALECLALAEKAKERDSSVIHLGSVGAGYALHHLTVGDIAKAQAQADQAAAYVDPACCGAT
PLNVLAFNGLLAETNFWSNRMEASIQHFQRCLQHIATFPYARENIVSILNVQTRLAALSL
YTENRDQDANALAMLGQLLPLARTRGSLHHVAQLLALTGLAKARALDNAEAEAAALFAEA
LSVAEETADRRTLAFVSRLAGAFYTRHAAADKADEGRKHLDQALALARQLGDQLLEAVVL
RDLAIVAVNEQTGSDEDKGRTWKEATADALAIAERTGNAYLANLLAHLPGQAPAAASLPL
EPLVVEQQTTTETAPAAPVEAVEEAKPEEKLPEVVAELTPTQTEEEDTKSSAEVVQEANE
EEAKAEAEEKEEAKQQEEQEQESRTEEESDTKTNAEVLQEANEEEANAEVEEKEEEATPA
QTEEESETKSFAEVVAEAEEKVTIEDVAEEEHDE

>Matrix processing peptidase beta subunit/Complex III Qcr1 Contig18201 (complete)
MSSIRSRAPSMLLPTKLGTSGRLGAAARRLSSGQPQAARDVEKRLRLPEYLLNVPPTQVT
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ALPNKFRVASEHKHGETATVGVWIDAGSVWETAENNGVAHFLEHLAFKGTKNRTKEQIEV
EIENMGGQLNAYTSREQTVYHAHVFKKDVPKAVEIISDIIQNSNLKEDDVERERGVILRE
MEEVESQTEEVIFDHLHSIAFQNTSLGYTILGPEKNIKKIKREDLVSYVGKHYTAPRMVL
SAAGAVDHDELVKLAEKHFSGLSSETNVDYSNREKLFDFTGSMVQVRDTSIPLVHTTVAA
KSVGWSDPDYFTFLVLQQLVGSWDRSLGGAKNLSSNLAETFATEELAHSLMSFNTCYHET
GLFGAYFVGEMERTSDAIFEVLREWVRIGSGVSEVEVERAKNKLKSTYLMQLDGTQAVAE
DIGRQLLTLGRRMPAAEAFMRIDAIDAKKVREVAYTYLNDVDVAVAAVGSVDSGLFPDYN
VLRGWTYWNRL

>dihydrolipoamide dehydrogenase Contig588 (and 23476 and 11795) (complete)
MRRGLIQASRSAVPTSASGVFASRAFPRTFIASRGFATAAEQDDVIVIGGGPGGYVAAIK
AGQLGLKVTCVEKRGKLGGTCLNVGCIPSKALLHASHIYEDTKKYFPDHGIVFDNVKLDL
GAMMKSKEKAVNGLTSGIEFLFKKNNVKYVKGFGKVSGANEVTVDLAEGGEKKLSAKNII
VATGSDVIGLPFLPIDEQRVVSSTGALALKEVPKKMVVIGGGIIGLEMGSVWRRLGTEVT
VVEFTDNLCGGAADGEVAKEFKRILAKQGMKFKMGTKVTGAKVEPSSITLITEPRDGGKT
EEVACDVVLCSVGRRPYLDGLGLENVGVKLDNRGRVAVDDHFRSNVPSIYAIGDCIPGPM
LAHKAEEDGIAAVEIIAGGHGHVDYNVVPSVVYTHPEVAWVGQTEEQLKAQGIQYKVGKF
PFKANSRARTNDDDEGFVKYLADAKTDKVLGVHMIGAMVGEMIAEPTLLMAYGGSSEDVA
RTCHAHPTLSEAVKEAAMATYDKAIHF

>phosphoenolpyruvate carboxykinase, GTP Contig13914 (complete)
MLRSGFRQGGAATAWGLRTSSRVASTSPAMLYPQAVRRWLASSSSSIEASTSNKKLIEWL
KTQQKLLQPSAVHICDGSVEEDERLKSELVKSGTLIKLNEAKRPNSYLARSDPGDVARVE
GRTYICSTNKADAGPTNNWVDPKEMRATLNGKFAGAMKGRTMYVVPFSMGPVGSPLSKIG
VEITDSPYVVANMRIMTRMGKQVFDALGSDGDFVPCVHSVGAPLQPGQKDVPWPCNPDKY
IVHYPETREIWSYGSGYGGNALLGKKCFALRIASVQARDEGWLAEHMLILGITNPEGKKK
YIAAAFPSACGKTNLAMMNPTLPGWKIETVGDDIAWMRFGKDGRLYAINPENGFFGVAPG
TSMSSNPNAMATTVKNALFTNCALTDDNDVWWESMTDKLPAHLISWKGKDWTPESKEPAA
HPNARFTTPADQCPVLDSKWEDPQGVPISAILFGGRRRTVVPLVYQAFDWEHGTYIGSSI
GSEVTAAAEGKRGEMRHDPFAMLPFCGYNMADYMQHWLNVGSRSAADKLPKIFFVNWFRR
GADGSFLWPGYGENSRVLKWIFDQTDNKSGNAKETPIGYIPKEGALDTSGLDVSPEAIKQ
LFEVNPSDWKEEVQEMRRYTEQFGDRLPAGLKKQMDALEKRLA

>malate dehydrogenase Contig10193 (complete)
MRRGLSTVSRSATVFGKQACLASSTLRVDRRAYATSPEDAALEAQIEKVLDLVKKQGNLG
SEKLTVRKLTELRQTVPEIDRALSSVGDSAVKYMAELEKPGAGPLSAVPPVRVTVTGAAG
AIGYAMLFRIASGEMLGKHQPVILQLLELEPAMKALEGVIMELKDCAFPLLHGVTASSDV
NKAFEGADFAMLVGAKPRTKGMERGDLLKENANIFSVQGKALNKVANRDTLRVCVVGNPA
NTNALIASANAPNIHPRRFTAMTRLDHNRGIAQLADKLKCKVTDIERFAIWGNHSATQYP
DISHTQINGKWAKDLVDEKWVKDTFIPDVQQRGAAIIAARGSSSAASAANAAIEHMRDWV
KGTNGQWTSMGVWTGNGKVGDYGTSPDIYYSFPVVCADGEYTIVQNVPVDKFSAERMQKT
NDELVSEKNGVGELAKRTTDPAALLKEQYKGGKQ

>Matrix processing peptidase alpha subunit/Complex III Qcr2 Contig18841 (and 14090) (complete)
MKPQHAARLSLAKGVTRASSPSASVLGSKSYSSWTATSSLKQAHSSVPQTWEATPQTLDN
VQTTTLDSGLKVTTVSSELPLAAVGLHVKAGARFETGESRGAAHFLRHLAFSRTSSRSPL
TVTREMEVATAAFDVSASRENISYSGQLMPDYLEDYVWMLRDLMHPLAWEYIVRDAAPQV
AAEVHEAETNPATALVEAIHREAYRDEGLGNSIYCPNYRVGAVTREAIIRYHHERYQASN
VALVGYGIKHEQLVAQANKYFPADAFAEDKAPWTTLEAADRKPGAVYTAASSYTGGELRL
PGPGNSRVALAFEGASLADPDVFAVRTLSSLLGGAARFTRDGPGVGLRSRLARNVLAKGD
YVLASSALNASYSDSGLFGVFVEALPGHGADAARLLSAELNSLAGSFSVDDAELTRAKNQ
AKASFFREVESRTGLVDYLARHTLAGTAPLAPAQYAARFDAVTRDDLARVARRVFSSPLT
LVSTGDIHGVPTKEELRPKLKA

>FAD-dependent pyridine nucleotide-disulphide oxidoreductase Contig27765 (complete)
MKTTQRSQLRLAARAPQGRVSGLRSASVLRRSVHSKAAHGSSPSVVQHDVVVVGGGAAGL
SVSHQLRRAMKGLDVAIVEPSSKHYYQPGWTMVGGGVINKRETERNEADLIPAGAKWIKS
AVDQFVPEENAVVTSDGQTVHYKYLVVCPGIQINWDNVKGLRDALGKKGVSSNYSYEYAD
KTWDHIKHFNGGNAIFTHPATPIKCGGAPQKIMYLAEENWRKRGVHADVSFYTGGPAIFA
SPYYGKVLTRICQERGIHTHFKHDLVEVRGANQEAVFKDLNTQELVTVPYDFMHVTPPMG
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PPSFVKSSPLADAGGWVDVDKHTLRHKKYANVFGLGDASNLPTSKTAAAVSSQAAVATAN
LLATIRDPNAALPESYTGYTSCPLVTGYGKLVLAEFDYSLQPCETFPVDQSKERRSMYHL
KKDVMPPMYWHGLIKGHWKGPRHHATTRLLKDLVNKPQQQQQS

>ATP synthase OSCP subunit Contig24806 (complete)
MYASRSSGMACRSRLASRVAPRMGNAARLVSARGFSQTLVTQQKKGEATTAAPVFKIDEE
FDDYKDVTASNEQVEKNYREPPVQVTSGKHGEFASTLYATASVLNAVEDVERDLKWLVDA
SQTIPMFQQFLSSGLPDKKVMRKLLQGVLKGADFHRLTQKFLVTELLEAGELKLVPDIAA
VYAQIMKAHRKEVPVVFTFASLPDKDFLTRQIERVKKYRLEADATPMWEFKINPALIGGF
TVEVGSNYKGNFALSSQFDLMRQQLKQAEDKWERVRPKELHINSFDTSSLFAPLSGVKIT
AADLDKTLADVLGSKKEAFQAADLDRTLKQALEDAQRDAGFSGDYEKNVLEQTRNLDFEK
LKTVKQLDLAQHEKHLMQKHNIADNDAEGKRKVKAKIEELKRFKELDTSFIGEVLKKHQP
ETYKKYQSVFQ

>2-oxoglutarate dehydrogenase, E1 subunit Contig813 (and 9386) (complete)
MLSSRARAGLLSRGPLAFTGMGRAGFAGSRVASSSLTGGASSRWYSLTTASRQAAASPTS
SSAVPLSRLSETFADGTSGAYVEDMYQAWKRDANSVHASWASYFRSVDAGRAPGEAFTAP
PTLRGATAAVPPPAGCRRRISVSDSMRLLLLVRAYQVRGHTLAKLDPLTGGPLSSFVPPE
LLPSTYGFTDADMDRPIHLGGESVISGFLSHGSATVTLREILVRLKQTYCSTIGVEYMHI
PDRHECNWIRERVETPEPFSFSPEQKFHLLDRLTWATLFERFLAMKYQNTKRFGLDGCET
LIPGMKTMIDTAADLGVESVVIGMPHRGRLNVLANVVRKPLDALLHEFDLEGNKDHSDDL
GLGTGDVKYHLGTSYDRPTASGKKVHLSLVANPSHLEAVNPVVEGKARAKQQYMGDTERT
RVMPVLLHGDAAFASQGVVYETLDLGIWKNFTTGGTIHIVVNNQVGFTTALRGSRTNTAS
SYPTDVAKTVNAPIFHVNGDDPEAVVHTLKLAAEYRQAFKKDVVIDIICYRRAGHNEGDE
PRYTQPQMYRMIEKHQSTLDLYRAKLKAEGVVDDARIKQMEDFVNEEHNKAFQASSTHVP
NKADWFSSYWKGFKSAHQYSSIRPTAIPDAVISKIGATVSSLPEGMKLHPNLEKLIKRKK
LMFESGKNIDWGTAEQLALGSLALEGNLIRLTGQDVERGTFSHRHAVLHDRETGETYQPL
RHIDPAQAPVFVHNSSLSEYAVLGYELGFSLENPNSLVLWEAQFGDFANGAQVIVDQFIS
SGEQKWQRQSGLVMLLPHGYDGQGPEHSSARLERFLQLSDSDPFVIPEMDPTERRQIQQA
NIQVVNVTTPANYFHALRRQVHRDFRKPLIVMSPKRLLRHPRCVSSLEEFSDKGTQPRFR
RVINDTAENPVSDDRIRKVLFCSGNVYYDLAERREKAAINDVAIVRVEQLAPFPFDRVAE
QALRYRNATTGWVQEEPMNMGAWTFVSPHMRTALAKAAHAHAEPAYFGRAVSASTATGSA
KAHKRQLTQLLDAAFS

>mitochondrial phosphate carrier Contig15406 (likely complete)
MATQQKQPIKLYSLEYFAACGLGGILSCGLTHTAVTPIDLVKCNAQANPE
HFKNTVQGFRAIYSGSLTSIGFGSGVSGLLKGWGPTLWGYSLQGLFKFGL
YEVFKHYFAEAVGPENAFKYRDLVYMGASASAEFFADIALCPFEAIKVRI
QTSPSFARGIIDGLPKFIKAEGFGNLYAGLGPLWARQIPYTIIKFVAFER
ICEAIYAMLPKKKEDMSKTEQMGVIFAAGYTAGIICGAVSHPADTMVSKI
NKIKSSGSLGEKMKLIYSGTPEAPGIGFAGLWKGFGPRVVMIGTLTGLQW
FIYGAFKAYVGLPTPGASAPAGDKKH

>succinyl coa ligase, beta subunit GDP Contig2792 (complete)
MRKTCRIGTAARATSGRVAATSARSFSSRTLSCGASGFLQSRTSVASSKLIRRAAPINST
QVRFLNLQEFSSKGLMDQYGVRTQKWKLATTPEEALAAAKELKKNPECKELVVKAQILAG
GRGKGVFDNGFKGGVHLCNTPEEAAQLTKQMLGHKLTTKQTGPEGTLVSKVMIAQSIDLK
RETYFAILMDRAFSGPVMVASPQGGMDIEQVAEETPDLIFKEAIDINQGIKPEQTRRLAI
AMGFDDEKKIADAQKQMAGLYELFLKTDATQVEINPFAETPEGEVYCVDAKINFDDNASF
RQKAVFDMGDDSETDQREVEAAKYGLNYIGMDGNIGCMVNGAGLAMATMDIIKLYKGSPA
NFLDVGGGANEQQVTQAFKILTDDHQVKAILVNIFGGIMKCDVIAQGIINAAKEVKLNIP
LVVRLEGTNVTIGKDLLEKSGLPIITANDLDEAAQKAVASIGHH

>aconitase Contig17472 (complete)
MQSLKRATIVTPCTRALPSSVRSALGERNYAALSRLEPSTTLPYEKMKSKLSDVRKRLDR
PLTLAEKILYSHLDDTKQEVVRGKTYLKLRPDRVAMQDATAQMAVLQFMTAGLPKVAVPT
TIHCDHLIEAHVGGAQDLKNAKDINREVYDFLASSSNKYGIGFWKPGSGIIHQIVLENYA
FPGGLMIGTDSHTPNAGGLGMVAIGVGGADAVDVMADIPWELKAPKILGVKLTGALSGWT
APKDVILKLAGILTVKGGTGYIVEYFGPGLDSISCTGMATICNMGAEIGATTSLFPFNHR
MSAYLKATSRADIASAAESFKDHLVADPGCEDLQNKLYDEVIEINLSELEPHVNGPFTPD
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LATPLSKFAEAVKKNNWPEKLAQGLIGSCTNSSYEDMSRSASIVQQAIDHGVKAKSGFII
TPGSEQIRATIARDGIINTFEKVGGTVLANACGPCIGQWKRDDIKKGDKNSIITSYNRNF
TGRNDANPQTHAFVSSPELVTAMSIAGDLTFNPLTDSLTGADGKQFKLKSPYGDELPARG
FDAGEDTYQPPAADGSKVTVVVDPSSQRLQLLPKFDEWNGSDAIENMPVLIKAKGKCTTD
HISMAGPWLKYRGHIDNISNNMFIGAINAENNKANCVQNQLTGEFGAVPDVARAYKKAGV
PWIVIGDENYGEGSSREHAAIEPRYLGGKAVVVRSFARIHETNLKKQGILPLTFANPADY
DRISGNDRITIVGLKDLAPGKPVTLRVTPKEGKPFDVVANQTLNEGQIAWWKAGSALNLM
GKQRASAQ

>succinyl-coa ligase, alpha Contig9628 (and 22544) (complete)
MRSNRASLLRTCATTSAPSFATRRLYAAASKPRVLINKDTKVICQGFTGKQGTFHSKQAI
EYGTKMVGGVSPGKGGSKHLDLPVFNSVKEAKENTGADATVIYVPPPFAAAAIIEAIDAE
IPLAVCITEGIPQQDMVRVKKRLMAPGCKTRLIGPNCPGIIKPGECKIGIMPGHIHTPGK
IGIVSRSGTLTYEAVGQTTAVGLGQSTCVGIGGDPFNGTNFVDVLKLFAEDPQTEGIILI
GEIGGSDEEAAAQWIKDNALVSKKPVVSFIAGLTAPPGRRMGHAGAIISGGKGTATSKIQ
ALQDAGVTISESPAKLGSTMLAAMRAAGKA

>malic enzyme Contig7726 (complete)
MRRFATRAGGMSSCRLAATSAFARPAQWARTLTNGPHKHLDYRKKSFIEPLLVEKKGVDL
IHDPIYNKGTAYPYSERDRLNIRGLVPPRCTTIEEQAKRVKTRFDHITDDLQKYSYISNL
RDRNETLFYRMVMDNIDEMAPIIYTPTVGKACIEFGSQFRRARGMYFSSADMGQMSAMIY
NWPEKHVDVIVVTDGSRILGLGDLGAHGMGIPIGKLSLYVAAGGIHPARTLPVTLDVGTN
NEKLLDDPFYLGRQHRRLTGEDYYNVVEEFMSAVKLRWPSCLVQFEDFSNANASNLLEKY
RDRHLCFNDDIQGTGSVALAGILTALRAQGKAAKEITKQRIVCLGGGSAGLGVINSLIDG
MVEEGLPREVANKNVWVVDADGLIAQGRSTISDAQKPFVRTDLPNGLKLKDTVDKVKPTI
LLGLSGAGRTFTEDVVRSMAANTERPIIFPLSNPTDHAECTAEEAFTWTDGRAIVASGSP
FDPVQYKGKTYYPSQGNNMYIYPGIGLGVVCCRAKKVTNAMFYAAAKKLASIVPEEDVQA
GRVYPDIAKIREVSKQIAIEVCKEAFASNLATIHPPNNERELEYLVENAMYIPEYAPLVH
APNIFSHAADPNPYD

>pyruvate carboxylase Contig23294 (and 27416,12686,4892,10179) (incomplete - internal gaps
likely)
MLRFARRSGGQHAVGQLATASLPSTIIAHASPALACGSSLVQTTWGRRHYASASSPTKPT
KSKLPYRPIHKLLVANRGEIAIRVMRAGTELGIRTVGIYSHQDEKSLHRQKADESYEVGK
GMSPVEAYLSIPEMVRVAKEVEADAIHPGYGFLSESGDFAQALALDNNIRFIGPAPEVVR
SMGDKVFARQMAIASGVQVVPGTDAPVSTVEEAELFCNKFGFPVILKAAFGGGGRGMRVV
HAREELHDAFERATSEAKSAFGNGSMFIERFVPKPAPHRGPSPGRQDWSGGALARTGLLR
PEETTRRWSRSPRLPSSPMLHQAETVLRRRQAGHVCRIRKRPAGTVEFLVDEQGRHYFIE
VNARLQVEHTVTEEITGVDLVQSQIRIAEGLTLQDLNLTQDKIHVNGAAIQCRVTTEDPY
HNFRPDVGRIDVFRTGEGMGIRLDGGNSYSGATISPYYDSLLVKARNHEEAAKKLQRALN
EFRIRGVKNNIPFLQNVLSHPKFLAGGVNTSFIDTIPELFQFHETQNRASKILNFLANVH
VNGSLTPLGTSNKPANITPQAPDVPHTDPPQGWRSIFLEKGPNEFAKAVRAHKTLLLTDT
TMRDAHQSLLATRVRTKDLLTIAPATAHLMAPLYSLEMWGGATFDVALRFLRECPWERLQ
RLREAVPNIPFQMLLRGANAVGYTNYPDNVVHRFCREAKTNGIDVFRVFDSLNYFPNMEL
GIDAVGNAGGIVEAAICYTGDVTRGLTEKDYKYNLDYYVDFAEKLVKRHIHVLCIKDMAG
LLTPQAARLLIGTLREKFPEVPIHVHTHDTSGAGVAAMVACAEAGADVVDAAIDSMSGMT
SQPSMGALVASLKGTPHDTGLKMDQLYPINNYWEQARTLYAPFECTTTMKAGSSDVYEHE
IPGGQYTNLHFQAYSLGLAHQWPSIKKAYAQANRLLGDIVKVTPSSKVVGDLAQFMVQNN
LDEESLLEKAEELNFPSSVVEYFEGLIGQPPGGFPEPLRTKVLKGRPSTNGRAGESLPPL
DFHKLKRELIEKHGKYHISELDVLSAAQYPKVFDEYMDFKRLYGNVSSLPTRNYLTGPEV
GEEIKADIEPGKSLHIMLKAVGAPNADHKREMFFELNGQPRSVFVEDKKATAKEGAGHAG
SSKSRERADPSNKKLVGAPMPGSIVGVKVKDGQEVKKGQPLLVLSAMKMETVVAAPADGK
VKRIIAKQGDSMTAGDLLVEME

>dihydrolipoamide acetyltransferase Contig7200 (complete)
MKRGVSRSSRVARGVKGTSATAQCLRATAVAQRSASTLSSTSRRSASPLFSGPVARSTAT
VQQFGVRSYATLPAHEVLGLPALSPTMTQGNLAKWLKKEGDKIQPGDLIASIETDKATVD
WEATEAGYLAKILIPEGSKDVTVGKPAVVTVEEEEDVAKFKDFSPEGGDAAAPAAPKEEA
PAAPKAAPAAPEQPKAAAPAAPKAAPAPQAAPAGGRVFASPLARKVAQEQGVDVAAVHGT
GSNNRVIRADVLDYAAKGPAFVPAATSVPTPAPGGLFTDIPNTQIRKVIAARLTESKQTV
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PHYYLSIECRMDKLLKVRQELNAKGEGAYKLSVNDFIIKAAALALQKKPTCNSAWFGDYI
RRYHNVDINVAVSTDEGLFTPIVQDADKKGLATIANTVKDLANKAKEKKLQPHEFQGGTF
TISNLGMFGVKQFAAVINPPQSCILAVGGTEKKVVPNEDKETSAAQPYATAHVMTVTLSC
DHRVVDGAVGAEWLKTFKELVEDPVKMLL

>aspartate aminotransferase Contig2676 (complete)
MRSCPQRRLLTLGFPSVSRTLGGRSSAVLVQRGYASSVWSHVPKGPEDPILGVTLAFNKD
TSPKKMNLGVGAYRDDNNKPYILPTVRQATSDLQKRLDEGKEDHEYLGIVGDPSFNKAAI
KLALGENSQHITDKKVVTVQALSGTGALRIAGDFLNRFYTHNKQIFVPTPTWANHIPLFT
DAGLEVKYYRYYDKAANGLDWKGLIDDINSAPNKSIILLHACAHNPTGQDPKLDQWKELE
KHIKTKEHLVVFDSAYQGFASGDPEKDAAAVRYFVEQGHNIVLCQSFAKNFGLYGQRIGA
VSFLTSTPEEAINVESQLKILVRPMYSNPPKQGAKIVSAILNNSELATEWRKEVKGMADR
IITMRDRLVHGLKEAGSTRDWTHITDQIGMFCFSGLSPEQVDRLANEFHIYMTKNGRISM
AGVTSHNVDYLAKAIHEVTKQ

>possible ATP d subunit Contig17555 (complete)
MRRISRVVASSARGTALNKSSRTAAVFSRGYAAPETPQTDFKVTDAGIRVYAHGVVHDMN
FLGDLPADAQEVLSGKEWVPQSVSDFTARWEKDAPELANQARQLESLITKFEKDPVQFGK
SEAYLRDIAIHTTLERAAARDVSPVEIALTHFWTAYSEVPSGGKLRESAPTQLERVKAFL
QSKKDPELSAQNSRARKTAAIVKFVQASSAEDKAAAAALLLGSEKGQALKAALKGVNDAA
KKEQIVKQHLQWDEATQAAAELTQRHPEFTELKEVLAHFPPLVHHIGEPSAVQYRFKHAT
DKAYKKWQQNYSLTSSDEVTEKDPLLKNLRELLYSGKPANTVADAKKAQALQRSFPGLLF
SRDVESFSNFVRKDEEVKSQLSTIYEDSLKEYPNDPALAVPKDLDQRVKLWSKHTQELAD
VQQQWLDAKIAFIDAKIQEGMVQMDKFVNGTVDDILADHPEWEKEIEDDIANHRWDPEME
KKEYDNALHHYYEHHTVHA

>phosphoenolpyruvate phosphomutase Contig15554 (complete)
MLARRSSSVAATSAVRLTSSTVTASGLVRPAASATAVISSRNASTKSKAQQLRDMLTSNQ
LEYIMEAHNGLSAKIVEEAGFKGIWGSGLSISAQLGVRDSNEASYTQVLEVLEFMSDNTS
IPILLDGDTGYGNFNNARRLIRKLEQRGVAGVCIEDKLFPKTNSLLEGVSQPLADIDEFC
GKIQACKDAQKDDAFSVVARCESFIAGWGLDHMMQRAEAYSKAGADAILCHSKRSDSSEI
QAFMKAWKERGNKTPVVIVPTKYYTTPSKDFQDWGVSLVIWANHNLRASVAAMQQTCKQI
YADQSLINVEGKIAPVNEVFRLQNNAELKEAEKKYLPKKDKKN

>Hsp70 Contig3529 (and 25050?) (complete)
MLRRVAATRRAPVSAASFLRSSWNAPAAARLYSAKSGDHIIGIDLGTTNSCVAIMEGSTP
RVIENSEGERTTPSVVAFVKDDHGTNRLVGATAKRQAVTNPTNTFFAVKRLIGRDFNDPM
TQKDLKMVPYKIVRHSNGDAWLEDSWGKKYSPSEISAFTLTKMKETAEGYLGTQVKKAVI
TVPAYFNDSQRQATKDAGKIAGLQVERIINEPTAAALAYGLTNKGGETVAVYDLGGGTFD
ISILEISKEGVFEVKATNGDTFLGGEDFDNTLMQHLVGEFKKAEGIDLSKDKLALQRLKE
AAEKAKCELSSTVSTEINLPFITATAEGPKHLHIKLTRAQFESLVDPLVQRTIDPCKSCL
KDAGLDKSDINNVLLVGGMTRMPKVQEVVKQFYGKQPSKGVNPDEAVAVGAAIQAGVLKG
DVKQLLLLDVTPLSLGIETLGGVCTKLITRNTTIPTKKSQVFSTAADGQTEVEIKVLQGE
RHMANDNKTLGSFILSGIPPAPKGVPQVEVTFDIDANGIVNVSARDKATGKEQAIRIQSS
GGLSESEIDRMVKDAETHEEEDRKRKDQTEARNHAESVIYDIEKNLNEFKEHVDQTEAER
LREQITELRKTLESADDHQAIKSGADSLQRESLKAFESAYKQKASSNDSGSSSSTENKED
DTPDADIKK

>aldehyde dehydrogenase Contig10187 (and 12335) (complete)
MLRTVPLASSRVAGTTAHGLSAARALATLPKIKHTKLFIDNEWVSSSSGSTFQTVNPTNE
EVLADIHEAGEADVERAVASARHAFDKGPWSKATCYDRSNLLNRLADLVELHRDELAALE
SADNGKPVHIANAADVGLTIQCLRYYAGWADKISGKTIPTASNDYFTYTRKEPIGVAAQI
IPWNFPLLMAAWKLAPVLATGCVSILKPAEQTPLTALRLAELIREAGYPAGVVNVLPGQG
NAGALLAKHNLVDKVAFTGSTEVGHKILAASAASNLKRVTLELGGKSPNIVLPDADLKEA
IAGAHFGLFFNHGQVCTAGSRVFVHKKQYDEFVEKSTELAKKRRVGNPLHAETEQGPQVS
QEQMERILHFINIGQKEGASMTAGGARVGDKGYFVAPTVFADVSDNMTIAREEIFGPVMS
IMKYSELDEVIECANDSVYGLAAGVWTRDVGKAHYVASKLRAGTVWVNCFNVYDSAQPFG
GFKRSGMGRELGEEALANYLEHKSVTTKLF

>prohibitin-1 Contig2302 (complete)
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MMQKLQALGPALNKVAIGAVSVGAVGYALNESMYTVDGGERAIIFDRLRNGTRDFIVKPG
THFLIPFLQFPIIYDTRTTPFNIKTETGSKDLQRVNITLRVLYRPDKKKLPYIYQRLGVD
YSANVFNSVGNEVLKAVVAQYDATELISRRETISNQIRQRLVKRAGTFGLKLEDVSITHL
TFSPEYVRAIEHKQVAQQLAEQAKFVVAKNEQEKLAKIIVAEGEAEAAALISKAMSGPGY
IALRRIEASRDIAEELSRSRNIVYLPSGTNVLMNLPQVGQQ

>ATP synthase gamma subunit Contig22783 (complete)
MRRPKSVLKIPFSECMPAQPSSLLCVVLQRQLFDSTAAPVVAHERRLLPWLGLLGHPLHQ
SNMRRVSSVGLRTSAFELRTSAVQTARTFERNELGPVGVRHYPGNLKELRLRLVAIKNIK
KITSTMKMIAAAKLNKAQAVLFKTRPYSESSQRFIQEFFPSPQEGEPNPAEEASAGKHLI
VAVTSDRGLCGGVNSSIIKASAAVLRNHPENTQLFLVGEKSKAALQREYANAIVYAVSEV
GANKKTSFTEVAQVAELIARQPADNVTLLYNHFNSVLSFTTTRKVFPSPKTFVEAERKFS
AYEFEGSHEEILADYWQFSVASQLYSAITESQTAEVATRMTSMDNATKNASEVLNKLTIK
YNRTRQAAITTELTEIVSGAAAIEEASS

>long chain fatty acid-coa ligase Contig26675 (complete)
MLQRSSSLLRSAPASRAASLVSGAQCYATKAGEAAPLLNKTVGELLSDQKAKYEHKDVLV
VSHQDIKWTHVELDKYVRGWGNGLPEARVTRKPAPATPDRVLSFLANDAENIVTQLGTAT
AGRIVVPASPETTASPAEVDAALKTLQARMVIVPARFEDRNNIDALNALDEEIPTWPLGV
ALNLKKYPNLKHVVNTGEQFYRGHTMWRDLMVYNPTPSNLPAAGSVSPSEAVLGYLSGGQ
TAMFSHSAVVNSGALFGSVVGLTSSDRICVASPLHTGHGLQAIVAAIAHGAVAVVPSLVF
EADQVLASLARDVCTVLQVSPQQLKAVLDSPVLAKHDLAALQKLVIVGSAHESSAEVAQL
VERATSALKVKEVVVAHTAPNVAGVLFAGSATQNASSPAAGRLLPHVEAKLVDGGKAVKP
GASGKLYVRGFNVTQGYWGAEKAAVDKEGWLDTGLQASASADGLYTIKH

>propionyl-coa carboxylase alpha subunit Contig20209 (complete)
MLRRAARCSTSASHVELLPKMGVRAFHRSLAPRQAEKLFDKVLVANRGEIACRVMRTCKR
LGIKTVAVYSEPDAQATHVRMADEAICVGPAASAQSYLRVDRILEAVKSTGAQAVHPGYG
FLSENEVFAKALEENGVQFVGPPSSAIRAMGDKIESKKLAKAARVNTIPGFLGEVNSDEE
VLKIAGEIGYPVMIKASAGGGGKGMRIAWNDEEALSGFRLSKAEAKAAFGDDRMLIEKFI
DNPRHIEIQILADTHGNVLYLNERECSIQRRNQKVIEEAPSPLLDPATRRAMGEQAVALS
RAVGYASAGTVEFLSDQHKNFYFLEMNTRLQVEHPITEKITGVDIVEEMLRVAAGHKLKL
RQEEVPLNGWAMECRVYAEDPYRNFLPSIGRLRTYKEPHAADGSIRVDAGVYEGGEVSVF
YDPLISKLVTWGPTRDECIKSMSYALDTYQIEGVNHNVPFLRSVMENQRFQSGKLSTNFI
PEEYPEGFKGHPVTPADIDELIASAAAIHLSRSRRDATISQQLHARPFTSENMDLVVTVE
GKNYPITLVQEPTASPAAGASTHPAIPSLEETDECEVVIKQDDGQERRVKVNYQWQLDSP
IFSAIVDGKDVTMQLAQALPVGYRLVHLGTKFDVLVRTPRQAELAVLMPKPVVQDFSSTV
RSPMPGLVISMRVKKGDKVTVGQEVAVVEAMKMQNVLRAERDGEIEDVMVTPGANVGVDE
VLITFKKADAAKEESKKQ

>Trans-2-enoyl-CoA reductase Contig9349 (complete)
MKRTFTITGVAPRTLTRSLQANPVVLSARLFATLPSEAKVIKYHATGQPEKVLKLETEKL
PQVGDNDVLVGFLAAPINPADLNMVEGVYPIGPKAPAVGGNEGVAEVLAVGSKVKGIAVD
DWVIPAKPGFGTWRTHAVAPESSLLKVKKDIKPEYAAAIAVNPCTAYRLLNDFADLKPGD
VIIQNGANSAVGQAVIQLAAQREVKTINIIRDRPDLGDTVERMKSYGAYMVVTEDKLGTP
AFHRLISDLPKPKLGLNCVGGTSATEIARVLEKDSTLVTYGGMSRKPVQVPTSLLIFRNI
QLRGFWLSRWVEEHSAEERLAMINTCWDLVKSKRLRMWAERYPLEDFAAALNRTTQAQRN
RKAILVMKP

>enoyl-coa hydratase Contig14367 (complete)
MRRSTKIVTSAMRGSAMPARMQVMGASMRLYTTESAAPQYTNILVEKKEGGVGLITLNRP
KALNALCDELIHELNDAARRFELDNEVGAIVLTGSKKAFAAGADIKEMSTKTYMDTYKNN
MFSAWDNLTKIRKPIIAAVNGFALGGGCELAMMCDIILAGDKARFGQPEIKLGTIPGVGG
TQRLTRAVGKSKAMELILTGDFMNAEEAKQSGLVSRVVPEDELLTVALDMAKKVASYSQP
IVSMAKECVNQAYESTLHEGVHFERRVFHSTFATNDQKEGMKAFIEKAQPAWTHS

>pyruvate:ferredoxin oxidoreductase Contig16068 (11768,E80POFO01A6MEI) (likely complete)
MNRLFARHTRPIVAQRTFPLSSAGTLRALSTPRWTAGPLRRLHGAVPMDGNTAAAHVAYG
LSDIHAIYPITPSSQMGELADKWSAEGRLNAFGNTPRVIEMQSEMGAAGTLHGAAVGGAL
VSTFTASQGLLLMIPNLYRVAGELMPAVFHVTARAISGQGLSIYGDHSDVMAVKQTGVAM
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LASASPQEAMDLALVAHLSSIRSSVPFVHFFDGFRTSHEINTVEPIKYEDMRKLLDEEAL
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FDYHGHPEPRHVIVACGSSVSTVEEAVNHRNAQGERVGLIKVRLWRPFSIKHLVDALPKS
VEKVAVIDRVRDYLASGGPLFQEVCTSLMMGGRRDVQLVNGRYGLGSKDFTPGMALAIFD
NLKQDQPLHNFVVGIKDDVTHKSLTVTEEPDTLPAGTKQSIFWGIGGDGTVGANEEAIKL
IVENSNMSAHKSGGVTVSHLRFGEKPINSTYQVQNADLIAVHTTPYLKKFPSLLGPLKEG
GTVILNSPWNDVAHLDRMLPDFVKRRIARRKARLINVDATAIAHEAGLRGRINMVMQAAF
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VAQWTNPDTCTQCNLCSALCPHAAIRPFLFTQEEAGSAPEGWEGRKAVGKAGKSYQYRVQ
VSPYDCTGCDVCVKACPTQSLAQVPFVDALDRGQARLWDFAAERLPIRSEVYPKESLKGS
QFAKPCLEFSGACAGCGETPVVKLLTQLFGDELYIANATGCSIVWGGMFPWSAYTTNERG
HGPAWGHSLFEDAAEYGFGIRHAVRYRREALRCAVQRDLTAGAYAAEHPVLAELLRRWDA
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GFGGLDHVLASGEKVNVLVLDNEVYANTGGQASKATPRASQVKFANAGKTTAKKDLGAMM
MQYGNVYVASICLEANPDHAVQALAEAEAFDGPSLVIAYAPCIAHGIKAGISTEVEEAKR
AIKAGYHILYRYNPSLVEQGMNPLSLDSSPPDDQLLQFLRGENRYEALRQQHPELTDEKQ
RLLVRDVADRYRHYALLKEQLEPKDDGEEEEEKADEAKEEATA

>succinyl-coa ligase beta subunit, ADP Contig20053 (and E80POFO01EK8OZ) (complete)
MWRRGARSVGMAGGMGRSLPARSALLQSNTATTLTSTSAQTGAARRWLNIHEYQSQELMR
KEGIRVPKGQVAASPEEAYKIAQQMQQGGDADVIVKAQVLAGGRGVGHFDSGLKGGVHTC
TSPEEVKDVASKMLGHHIFTKQTGPEGKPCNVVYLAERLFIRRETYFAILMDRAYNGPVI
IGSSKGGSDIETLSAEHPDAIFKIPIDIAEGVTPEKLELVADKLGFQSTKVKEQTKELVS
KLYDLFIKKDCTLAEINPLVEDHQGQIVALDAKLRFDDNAEFRQKEIFALRDESQEDPRE
VAASKFDLNYIQLNGNIGCLVNGAGLAMATMDIIKLKGGNPANFLDVGGGATEKQVTEAF
RIFSSDKSVKAVMVNIFGGIMRCDIIAMGILNAVKVLNIKVPLVVRLLGTNMKEAKDLLE
NSGARIIFASDLDEAAEKAVKVARIVDMAQEAQLNVSFELPL

>electron transfer flavoprotein alpha subunit Contig9513 (complete)
MLTRQARRCFSSSAVLRKTLVLAEHTNAALVDSTLPAITAAAKLGDVEVLVAGKNCKGVA
EQVSKLEGVKKVLVAENPAYEHGLAEDLAPLVANFSKKEEYTHILAPASAWGKNLTPRIA
GILDITALSDVISIEGQDTFKRPIYAGNAIATVQSGEKLKLLTVRTTAFEKAKEGSSSAE
VKEISVEGDANTKSTWVEEMQQKSERPDLTSANIVVSGGRALKSKENFKLIEDLADKLGG
AVGASRAAVDAGYAPNEWQVGQTGKVVAPQLYLAVGISGQIQHLAGMKDSKLIVAINNAA
DAPIFQVSDYGLVQDLFQAVPELTKELEKAKQ

>isocitrate dehydrogenase, NAD+ Contig8357 (complete)
MRRTSAVALSRTSTSAACNARTLSVGSQRMLATSTGTEAPPASLSTGVRRGLALGSEIPV
TLIPGDGIGKEIADSVVGVFGALRVPIKWEVFERVGDITQNFDLLTSLARNQLCLKGQLK
TDYEDSEHFKNNNLVLRKSLNLYANIVPIKSLPGITTRHSGIDMVVFRENTEAEYSGFEQ
EVTSGVVQSLKVVTRAACIRIAEAAFGYAAAAGRKRVHAIHKANIQKMSDGLFLESVREV
AKKYPTVEFKEMIIDNTCMQLVQNPKQFDVLVTPNLYGNLIINVGSGLVGGPGLVAGANY
GLHGEAVFEPGARHVAADIQGANVANPTGMLLSGVMLLRHVGLNEQAGRLEKAIHDILLR
GKVLTKDVGGFATTKEFTKAVINHL

>hypothetical protein Contig19158 (complete)
MRRASAQTWLASARSQPPLSQISTRIGARSAAILTGAAGSSSRSASLLSTVATATRPNLH
TPFTTAASATLRRLGLNGLAQPLRAGLRSKLPGGRRSYSTEVPAAAETAKVAETPASLDA
LRAEFYEFQKRTLNWNIGGVSVPKAVLWLVFFQFLGLAPYSFALERNESVVFVREYMEKV
QSMAESSGLPLGDDHNQHMPSFTRGLTGWERTALHSVASVATLSVIAFLWARRRTRRSFN
SFILSRALGEPTGTYPITMENVVRKGDALKIKGEGLKSVRSDVVRLAGLKAVQASVGLLL
ASTASSYAFTTWVDGKVRDGVIRFRRSDVLQGETALSLVLLFNFLVSWAVLVYQPYTIFP
FVISNVLMSYLRFTDSTYKHVTLPSKETPVVTEHKAVEEVDGGKEYITLTEKKSGSGCTR
TETRVFVPDAAEAGGNAQRTLDITTKTEGDADTQRSLDTTTKTDA

>citrate synthase Contig19816 (complete)
MRRATVIATKSAASPAAVAVQARALAQSQRLYATASLKDKFSEIVPKEQARVKKLKTEHG
DLPLGQVTLSMAYGGMRGIKGLVTETSLLDPEEGIRFRGYSIPECQAKLPKAKDGKQPLP
EALLWLLLTSEIPTEEQTQNLVHEISERSKKFPAHVSHILKNLPTTMHPMTQFTIGVNAL
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QTESQFAKAYLEGVNKAKYWEYAYEDMLNLISFLPRTAAEIYRNVYHGGKLIPSDPKLDM
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AGPLHGLANQEVLRFILKLREKFGGREVTDEELKKALWDLLNSGQVIPGFGHAVLRKTDP
RFTAQAEFASEYLPNDPLVKLVKQLYAVVPPVLTEQGKTKNPWPNVDAHSGVLLQYYGLK
EENYYTVLFGVSRALGVLPSLVLDRALGLPIERPKSVTTEWLEKEAKKHAAAAPKH

>SdhA Contig11902 (complete)
MRLSRFSRSSALKSSFAGSAGIRTAPSSGLFRRNYAVVSNATPQAGESQGTLTSSYDVVD
HTYDCVVVGAGGAGLRAALGLTEKGYKTACISKLFPTRSHTVAAQGGINAALGNADNDDW
RWHAYDTVKGSDWLGDQDAIHYMCREAPASVIELEHYGMPFSRTEEGKIYQRAFGGQSYN
FGKGGQAHRCCAVADRTGHALLHTLYGQAVRHNCTFFIEYFALDLIMENGECRGVVALCL
EDGKIHRFRSHQTVLATGGYGRTYLSATSAHTCTGDGNGMAVRAGLPCQDLEFVQFHPTG
IYGAGCLITEGSRGEGGILRNSDGERFMERYAPTAKDLASRDVVSRSITLEIRAGRGVGK
HKDHVLLDLSHIPADILAERLPGISETAKIFAGVDVTKEPIPILPTVHYNMGGVPTNYHG
EVVTKKGDNPDCVVPGLMAAGEAACVSVHGANRLGANSLLDIVVFGRAVANRVEETLKKD
TPHKPLPKNAGLEAIHNLDKLRFANGKYRTAEVRDKMQRVMQNNAAVFRTGETLQEGVKL
IDEVYDMFKEVKTVDRSLVWNTDLVETLELQNLLSQAVLTMHSAEARKESRGAHAREDFP
DRDDANWTKHTLSWMDMESGKVKLDYRPVHDKPLNDEMPYVPPVKRVY

>elongation factor Tu Contig9759 (complete)
MASRSFSRLGFSSQITAPARLTLPLRSRADFSRTLPCAYAGAQSYSTYRAKPHFNICTIG
HVDHGKTTLTAAITKVLADTGLAKFRDYQSIDKAPEEIRRGITINASHVEYETDKRHYGH
VDNPGHAEFIKNMITGTSLTDGAILVVDCSTGPMPQTREHILLARQVGVKNIVVWLNKCD
LIPDKELQDMVAMEIREELTRYEYNGDSTPIIHGSALEAIELKDTEYGIQAIRKLLATVD
ELPQPERQTDKPFLMAIEALYTISGRGTVATGVVEQGKVKIGDEVEVLGMQEDAKKIKGV
VTGIETFHKQMEEGFAGDSIGLLLRGPNRDDLKRGQVVGKPGTLSAHKKFEANVYVLTKE
EGGRHTPFGAGYAPQMFFRTANVTGKVMMEGDKVAVPGETMNVGFETIWPMPLSEGLKFS
CREGGMTVAAGVITKVFPMEEEGKKKKGK

>hypothetical protein, ATP synthase subunit Contig31 (complete)
MMKRGLRQVPRSVILGQRQSAQAMRLFASAAPSPNVDEIQFQVIGDTATAEYPTRPFTSK
SKAQLEEGVQRKANQTRGQFEAKFSADTPEGALFKDVVQIKPYDEQLLKAELEHVTNPTI
QPTVDTAVNTKNHNFLTEFMASRTAGYLEDPTLYFSYGENPSATLNPNWSTQLSGNLDAL
VKRELVDALAALSAEVKEIDALDQQAKKAHEELLQKLQADIDILTNKELFAKSLESSGMS
PLHVAQMTDIVTTDPLAVQALPLAQKQAAELAQFRQQSATFQQYSQLVADSRELVKQLQA
SGLQFDASKVSF

>pyruvate dehydrogenase E1 beta Contig19193 (complete)
MRRALSSVSRVASTSSAPLLGSAALRSRAVAALATAVEPKKISVREALREAIDEEMERDS
RVVMLGEEVAQYQGAYKVSKGLMEKFGRERVVDTPITEAGFAGIGVGAAMSGLVPIVEFM
TMNFSLQAIDHIVNSAAKLRYMSGGMYNVPIVFRGPNGPPRAVGAQHSQCFGAWYSSVPG
LKVVAPWNCNDAKGLLKAAIRDPNPVVFLESEIGYNETYELSPEAQSKDYVLDIGKAHIE
KEGSDITVLTFSRMVGVALEAAQKAAEKGISVEVVNLRSLRPLDLNTIVNSIKKTNRFVT
VEEGWPQCGIGSEIIALANEHCFDFLDAPPERITGADVPMPYTWPLEDEAMVQTQNIVNA
IERVCYRNTTNQ

>methylmalonate-semialdehyde dehydrogenase Contig2132 (complete)
MQSIARLSARSAPRKAGSIARFHTSTAPLASTTKLFIDNEFVESKATEFVDVFDPATQEL
VTRVPMATKDEMQAASDSAKKAYAQWSETPISARARVMFKLQALISENMEEIARCITKEN
GKTLVDARGDVFRGLEVVEHACSTGTVLMGETAENVGKNIDTYSYRQPLGVCAGITPFNF
PAMIPLWMFPLAVTCGNTFLLKPSEKDPGASMIIARLAREAGLPPGVLNVIHGAHDSVNF
ICDDPAIRSISFVGGDAAGRHIHSRGTSNGKRVQSNMAAKNHAAIMPDANKEATLNSLVG
AAFGAAGQRCMALSTAVFIGESKEWIPELVERARKLKLSSGFTPGADLGPLITKESKDRV
IRLIQSGVDQGAAIPLDGRNVSVPEFPKGNFVGPTVLTGVRPDMTCYKEEIFGPVLLCLT
ADTLEDAIQLINNNPYGNGTAIFTRSGAAARKYQHEIDVGQVGINIPIPVPLPFFSFTGS
RGSFVGASHFYGKAGVHFYTQTKTITSLWKEEDLSQFGTNMPILSKH

>cytochrome P450 reductase Contig20444 (complete)
MQRACRLSFRTHGGLPHSTHILPSTHSASGRLCQRHLHPSPKALAEVKSMKVLWGSQTGT
ATGFADDLARELSAQGITATSMDLRKYNSKKLATEKEPLALVLACYGQGEPTDNAKQFYD
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FVMAKERKQGSLKDVRYTVFGLGQSKAYPACYQAVGRSVDKRLEELGAQRIFARGEGDDS
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RVLDRSAAPASTYQRNPAEPISIVNPVEARIVENEELQSAASDRSTRHLEIELSNTGITY
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TGRPRKSLFARLSAFAGDEATRARLSSDDYAEFCVREKRGLYHILKDNPSLRLGLDSLLS
LAPPLLPRYYSIASSPKFKEGRMQLTVALAKTKAESGADHYGVCSRYICALKPGQTARLF
VKTSLFRLPKSPEVPIIMVAAGCGIAPFHGFMQERKLQCDQASLPYEKSKNVLYFGVYSK
SKDFLYESELTGYERDGLLKLRMAFSEDHAPNQPPTFAQHRMMEDMPMLWQLIEKEQANT
YVCGYCPLVCVLCAITQCS

>alanine-glyoxylate transaminase Contig8740 (complete)
MMRASVRRCQPQRVASLTATSAQLSARGLNVSAQAALTTKANRLEMPPTDFKPMPYTGPS
FDEVKALRAQHMPSAIFAFYKNPIMLVEGKMQYMWDEKGRRYLDLFGGIVTVSVGHCHPR
VTEAGVAQLKKLQHSTTIYYNPEVALFAKELADRLPSQLSVVYFVNSGSEANDLAMLMAR
AATGNFDFVALRNGYHGMSMNTMGLTALHTWKYNQPQGFGIHHAVCPNTYRGPYGPDEPD
VAQKYASDVADIIRSSTSGRVAGWISETIQGGGRHGGPARRVPQGGLQDGARRRRRLHRR
RGADRLRPPGLPLLGLPDPERHSRYCDDGQGHRKWCAAGGGGDDARDCGDAQAARALQHL
RRQPGVVRHGPRGAQGGGRGGHPAQGPLARRLLHARAERAQEAVPDHRRGAGQGPHAGRG
AGQGPDHQGAGHGRDGRHLRAGQGHGPPHRQGRPLRQRLPHQAPHVHHQARHRLLARGAR
PGLQGQRQGHVKRTHDDDDDDDAQQLQTKRMHF

>hydroxymethylglutaryl-coa synthase Contig11492 (complete)
MRRQSTLATLATATRRSATIAGVLRSVNATTTTTACGRGGIATMLATSPTTSARRGVATD
FSHYPRDVGIVALDVYFPSTYVSQADLETHDGVAAGKYTVGLGQTSMAFTGDREDINSIC
LTAVQSLLEKYNIDPKDVGRVEVGTETIVDKSKSVKSTLMDLFQKAGNTDIEGVDTTNAC
YGGTNALFNAINWVESSYWDGRYAVVVAGDIAVYEAGPARPTGGAAAVAMLIGKGAPIVF
ERGIRSTFMENAWDFYKPVMGSEYPLVDGALSNTCYLRALDQCFYTYAERFEKAHGKKLS
LDADVDYALFHSPYTKLVQKSWARMNYLEAVKNEAHALHESLKSQNKLQPETTYEDNNLM
KEAIKYSDATYKSKVGPSLTLPKELGNSYCGSLYTGLLSLVASHADAAATSEAEKRALMF
SYGSGLAASLFSVKLKSGLKKIADTSNFQARLAQRKKVAPADFVEALKRRETATSDDVPK
PFVPSDKVEDLFPGTFYLEQVDEKFRRTYARNQQ

>hybrid cluster protein Contig10665 (complete)
MKRLQHSTARASAVLRTSSSAAAGVSSRRLVASGAQSLTTSTRATALTSRALPRIAGTRA
LHASAGLRAAAAANAAGAPDMFCFQCEQTRDNKGCMTVGVCGKTPEVASLQDLLIHATKG
VSIYAKGARDLGGLSDREVDNFVLRALFSTVTNVNFDSARFNAFLKEAYDMKTRAKALYE
KAKASASPAALAKAQAEEQQEDQWHPTAFKFHSGMSLEELEAEGHRVGVLQRREVYGPDL
SGLQEMAMYGLKGMAAYAEHAFVLGQESDEVFAFCHEALARLSRKNEQTLEGLLQLCLDV
GKVNVEVMRLLDLGATTRYGHPKPTPVRTTAVKGKCALISGHDLRDLEELLKQTEGKGIN
IYTHGEMLPAHGYPGLKEKYPHLVGNYGGAWQQQKIEFSSFPGPILMTTNCIIEPRKSYK
NRIYTRSVVGWPGVTHIPDYDFSALVEQALAMDGFEEDEPEKNTTMTGFARNTVLSVADK
VVDLVKSGAIKHFFLIGGCDGAEGERNYFKEMALNTPQDTMVLTLACGKYRFNKFFDQFG
TIGGLPRMLDIGQCNDAYSAIQIASGLQQAFGLKDINQLPLSFVISWFEQKAVAVFLTLL
HLGIKNVYLGPQLPAFATPAMLDILVKSYGVKQINNVQADMKAMLARP

>ornithine oxo-acid transaminase Contig25959 (and 23813) (complete)
MQRSRITGATRLFGAPTRAALGARTFAASTQAKELPQTLKTSEDYIAVEDRYGAHNYHPV
PVVLSRGEGVHVWDVEGRRYLDFLSAYSAVNQGHCHPKIINALNEQAKKITLTSRAFHND
VLAPYTRFITSYFGYDRVLPMNTGVEAGETAIKLTRKWAYLKKKVPKNQAKVIFAANNFW
GRTIAAASSSTDPSCYEDFGPFTPGFEIIPYNDLNALREAVKDPNTAGFYIEPIQGEAGV
VVPDEGYLREAKRICKEANVLFIADEIQTGLGRTGKMLACDHEGVRPDILVLGKALSGGV
LPRLCRSDR

>isovaleryl-coa dehydrogenase Contig5198 (complete)
MRRTVQLSSRVLGSRTCTTSAASGAQLLRTASVARSYSVSANLRDTVAEGLFDDTQKELK
ETVHQFAQREIAPLAAELDRKNEFPMHLWRKLGEQSLLGITADPEYGGMGMGYTEHCIVM
EELSRASGSVALSYGAHSNLCVNQISRNGNEAQKKKYLPKLITGEHVGALAMSEPGSGSD
VVSMKLKAEKKGNKWVLNGNKFWITNGPDADVLVVYAKTDMAAGPKGITAFLVEKGFAGF
STAQKLDKLGMRGSNTCELIFENCEVPEENVLGQVGKGVYVLMSGLDYERLVLGAGPLGL
MQASLDVVLPYVHDRTQFGQPIGTFQLMQGKLADMYTTTSACRSYVYTVARACDKGQADA
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KECAGVILYAAEKATQVALDAIQALGGNGYINDYPTGRLLRDAKLYEIGAGTSEIRRMLI
GRDLNKLYGVERK

>hypothetical kelch repeat protein Contig21540 (complete)
MRSSTSRAARLTALPSIGTSSASSSAPSATALFLHHQRRTYAAKANARKCGEFKKDMFGH
HTIKVDDGHLLVLPSTRTLNPFARPSVYKVDTTKDEWHWEEKSVSAPFPQTGPRGHLFGQ
QLIVAGTLTTLGPLKRKGMVTLDMKDFTTSRVTMLDPASQKATKTVNMTNFVSEATHNPD
KVWFFGENYLNAKNENASCEVMVWNKGNNTLYSATANTLPIVGDGPKEKKELAVAAVGKD
KIYVISPDINSTKLETYVLDTERLEWSLVKTKGDKPVNPRAGFSITASGDKLVFLGYDMS
LSDKLMEVYVLDTDTSTWEKVEVTGDEISPRFGHTTTHLGGNQYAVIGGKGYGYFSTSVK
DFFKLQLDF

>acetyl-coa acetylase/transferase Contig19900 (complete)
MKRLQQMSARTTVVSAASAGRASAFGRRSYQGRPQMLSADDAVKVIKTGDRVFVHSVAAA
PQALIHAMTRRAPELRDVEVCHMHIEGDASYADKKYEGSFKNNNFFVGKNVRKGVQEGRL
DYTPVFLSEIPLLFRRGILPLDVALITVSPPDQHGFCSLGTSVDASLAAVQCAKTVIAQV
NPHMPRTHGDGFVHESAISFMVDGPAPLIEHKRGKVTETIGKIGKNVAQLVEDGATLQMG
IGVIPDAVLAELTHHKKLGIHTEMFSDGIIDLVERGVITGENKVIAPRTITVGFCLGTKR
LYDFVHENPAVQFRAIEWVNNPILIKENPKMTAINSAVEVDLSGQICADSIGSKLYSGVG
GQMDFMRGAALSHGGKPIIALPSTTSRGESKIVPRLKRGAGVVTTRAHVHWVVTEWGAVN
LFGKPVKERMKALISIAHPLHRPWLEKEVERGFWFDVDENSPKIPESAHVDE

>aldehyde dehydrogenase Contig14126 (complete)
MKRLSCASKQFVVPSRASLHLQGRRGLATGGSQYAKHARFLQSLGIEEGVNDGVCIDGKW
SKGSGEVVDSVNPAYNETITRVATAGLKDYERAIEATKSVEKMWAEVPAPKRGEIVRQIG
DELRKHLEDLGALVSLEVGKITQEGIGEVQEFVDVCDYAVGLSRSFSGQIFPSERPNHYM
LEQWNPIGTTGIITAFNFPVAVMGWNAALALVCGNPLIWKGAPSTNLCTLATQRIIQRVL
ERNGMPGSICVALTGGAEIGEAISKDPRVPLVSFTGSTQVGKIVATQVASRMGRSLLELG
GNNAITVLDDADLTLAVRSILFAAVGTAGQRCTTARRLFLHEKIHDEFLGSLKAAYEQLG
QKMGDPLEKNTLLGPLHRPSSVDLYKNAVAKAQEQGGKIITGGKVKTDRPGNFVEPTIVS
IKHDAPIALHETFAPILYVSKVPDLDTAIRYNNEVAQGLSSSLFTTNQQNVFKWIGPSGS
DCGIVNVNIPTNGAEIGGAFGGNKETGGGRESGSDSWKQYMRRSTCTINYGKELPLAQGI
KFD

>betaine aldehyde dehydrogenase Contig27079 (complete)
MATMLRTSTSSSTSTSASRVLGIRSFATKSDRAAAPLALAQRLSGKHFIGGLRPAKSGAV
FDVHNPATGETIGHAALGDEADINDAVTLASRAQKEWREQSVRARGALVAKCGEVLRAHV
EELAQLTSLETGKAIRTESRVEAGLISDTFSFFGGLAPEIKGQTIPFNPSVLTYTSREPV
GVVGAIIPWNAPLLLFALKLAPALVAGNAVVLKSAEAAPFGVLRVTELLNQVLPSGLVST
VSGYGKQAGTPLVRHPLVKKVTFTGSVDTGREIYKQAAEKLIPVTLELGGKSPMIVLEDA
NFEKAVNGAILSMRFTRQGQSCTAASRIYVHEAIHDKFVAALTEKINALKMGDPLDEATD
IGTVISKPQLDKIQRYIALGKGEQGATAHECSALPTDASLSKGLYVRPVVFTGISNQSRV
AREEIFGPVTCVFKFNDFDAVLDEANSTEYGLSASVWTNDLQKALHATRKLEAGVVQVNQ
NAVVQPNLPVGGWKVSGLGREGSLETMLEHFTHSKTVAINFA

>3-hydroxybutyryl-coa dehydrogenase Contig14727 (complete)
MLRNTSRLARASPVACSAPSLRTSAGSARRLYTTDNSTHGVKTLGVVGAGQMGGGIAQVA
SQVAGVRVVLVDSQQAQLERALQTMDHFLAKNIAKGKITEQAAQETKSRIAISTDVAKLQ
EADFIVEAASENVLIKEKIFKELARVAKPEAILASNTSSISITKIGAFTPRPEKVVGMHF
MNPVPIMQLVEIIPGLATSEHTLSTTLALAKAMGKTTAQSDDRPGFIANRLLCPYLNEAI
NALQDGLGSREDIDTTLKLGCNMPMGPLTLADFIGLDTVLAIMRVLHSELGEDKFRPSPL
LIKYVDAGWLGVKSGKGFYDYAKKQK

>nucleoside diphosphate kinase Contig27673 (complete)
MRRATSISARTATVARPAARSASRLQLSQVATRTFVSGTAQATSSSARTG
AMLIGAAAFAGASYYSFASVKADDKVPHTGLPGTRFERTFIAIKPDGVQRGIVGEIIQRF
EKKGYKLVGLKVVKPTKQFAEQHYADLSKKPFFPSLVNYFSSGPVVAMVFEGRNAIVNGR
KIVGATNPADAEAGSVRGDLCIDIGRNIIHGSDGPESAKDEISLWFKEGELANWESENAK
WVYEKL
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>NADH dehydrogenase 39 kDa subunit Contig21164 (complete)
MKRVAAQASFAGPRSIATSLSWEGAAGVRGLHVNLQGGRSSVSGVVATVFGCTGFLGRFV
VNRLGKIGSQVIVPYRGEESAFRHLKVMGDLGQIAPVWFDLRDKETVRRAVQYSNVVINL
LGKRWETRNFSFDDVHPEATRTIAEAAKEAGVERFIQVSAAGADVNSPSAFARSKGESEK
VLREIFPDATILRPTVLYGARDNFLVKWGMIARYWPAFVRTLKDTKFQPLYVADMATALM
NALADPETAGKTYELGGPKVYTLEEITELVTRLTFLEPSVVDVPFPALRAFAQVTQPFLR
KPRFTVEELDYWKSGDVVVPENAPLTINNLNFSTEDLTVLEKEAVNFLRLYRKPATMNLI
LEDQLDVKSPRARASR

>prohibitin 2 Contig2720 (complete)
MSKSPFQGLVKANLPGMGGKGLKTAMSLAVVGVGASAVAYNSLFTVEGGQKAIIFSRFSG
VLPKVYNEGLHFRMPWLHIPHVFNVRTRPTSIPSLTGSKDLQMVNITLRVLTKPKWEKLP
EIYKKLGTDYDQRVLPSIVNEVLKGVVARFNAAQLITQRELVSGMIQDRLRERAADFFID
LDDVSITHLSFGREYTAAIEAKQVAQQEAERAKFIVEKALQDKRSIVIRAEGDAESARMI
SEAVQSNPYYLELKTIEAARDIAGSLANSQNKVYLSSDMLMFNLLSSISGSNTASSLVGS
VLSAKDATIARQ

>NADH dehydrogenase gamma carbonic anhydrase subunit Contig11877 (complete)
MLKRFSYVLGNTVRETAYALDRVGCRLQGNYAFTEELSRHRRVMGLYDKQPAISQDVFIA
PNASVIGSVSLGEGANVWYGSVLRGDVNDISVGKKSSIGNRSVVHASGGLTTLAPTKIGD
NVVVGDGVVLHGCTLEDECRVDDGAVLNDNVVVEKHAIVGPGAVVTSGKRVPSGQVWAGN
PAKYVRDVSEEEKEFAGWAEKRYTQAKAHLAQTIKLAEEKEVDLLTEDILREMRPGTRFA
D

>universal stress family protein Contig14681 (complete)
MSNPKETTQQRAHVVALDGSEDADKAFVWALRNLPKNDKLVLVHGIHTQPLENPHMDWMD
QATTLSREERARLAKERHKALFSHYEKRCKEADRVCTFETIKFRSNGELANNICQVAEED
RASTVIAGSRGLGLYDRVMLGSVSTALLNRCRCSVLIARDSS

>SdhB Contig16868 (complete)
MRRITARSVTTPLFTSKTASLAGSARPLFGIVSAADKVVPKDGLVTVEVYRWSADEKEKP
YIQSYKLDVNNCAPMVLDALLKIKNEQDPTLSFRRSCREGICGSCAMNIDGTNTLACLKP
VAESVTNGKIKIYPLPHLPVVRDLVPDLSNFYEQHKSIQPYLQVDDHAALGSSKTEQLQT
REDRKKLDGLYECILCACCSTSCPSYWWAGNENKYLGPAILLQAYRWIADSRDQHTNQRL
RALAKEDMKVYACHTIMNCTKVCPKGLNPALAVAKVKKATLELDVQQKKQALAH

>mitochondrial ribosomal protein S28/35 domain protein Contig5565 (and 20000) (complete)
MLSSRAKIRHSAARLPHVQHHLQRQQRSAGALVLNARSYAATHEMTQQEESSDSIKHLLK
GPVTPLTIFATSPPPEPHPSTYQVPAAAADGATLDFRLSFAFPTVQKIKEERFKEEMGVF
KILYERPFLQEYKNVMQEKKQQKKSERAAAKKAKKEMKKLGLLPNDRKKTLFELEQDRQR
KLFLQTLHYPYQVPDMSVKGEELKKYFNFIATHSEKEIYDRLYPEFFGDTREHVENLVPH
KHDGYVWNTFFDPENPSDYPNQADAEGDVWETLNMSAEEQLSDLADAMEGEQEKEARLAT
WEMDPARFKGKWTPRAWTKEDLELSHIKQRARNLRYLREQLKKHGLLPEEDEATTREALM
SVESGGQASAAAESFDIDEIADKIDDNEESVLLLFEDDAQKKPAAVPEQKGTEDEIANLL
NAVLPPTEKDQSHAALLDALMPAGQPQEQAQPESGAAASEPTTTATEQELAEWRAKVDKF
QDGLKKRIRDGATEETIEEDVINFITAEGGGAQDEAEEDEIDWESRLQDIPGLDQPGEGG
FKVTGGREEAMQRSREREARLHKLQEHVKVLFDESPKKQVFANEPIPGEPAIEFIHSYTM
DPDVTMGSLARREFLQRKVVLKVHVPSLSLPPPVQQRLADLVGTRYDARSGWLKLVGDKH
PNRHLNQKHLTLLMRELLNESFLADSRFTPLTDLSIEDPSSLRRKYSLPTNLQNIFDGKT
GKGGWEYKMFTFSQLDGRFPSAQESTEEAAKLRQRLASALSL

>isocitrate dehydrogenase, NADP+ Contig11724 (and 13189, 26192, E9BS9UA01CI7L8) (complete)
MRRQAINVAKRSTPTTWALAQRHLGATAVALTHSQVRLAHKKIDVKNPVVELDGDEMTRI
IWKRIKEELILPFLNIDLKYYDLGIEYRDQTNDKVTIEAAEAIKQYNVGIKCATITPDEN
RVAEFKLKKMWKSPNGTIRNILGGTVFREPIICKNVPRLVPGWSQSIVIGRHAHGDQYKA
TDLVVPKAGTYDLVFTPADGSPKEVHQVYDFKTPGVIMGMYNTDESIEGFAHSCFQYALA
KNWPLYLSTKNTILKQYDGRFKDIFQAIYDKDYKSQFEANKQWYEHRLIDDMVAFALKTS
GGFVWACKNYDGDVQSDIVAQGFGSLGLMTSLLMCPDGKTVETEAAHGTVTRHYRMWQKG
QPTSTNPIASIFAWTKGLEHRAKLDNNTALAKFATALEEACVETVESGKMTKDLALCVHG
SKMTNKDWLTTDDFLAAIRDTFQSKVEKF
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>electron transfer flavoprotein beta subunit Contig27324 (complete)
MKRRVLVGVKRCIDYNVKIRVKPDNTGVLTQNVKFSMNPFDEIAVTEAVKMKKEGGFEEI
VAVSVGPKECQETIRRALAMGADRGIHVETDEELQPIAVARIFKKLAEKEQPQVVVLGKQ
AIDDDANQTGQMLAGMMDWSQGTHAYRLKFAPEEVECTRETDTGLQTLKLKLPSVITCDL
RLNEPIFAKLPEIMKAKSKPLQKFTPQELGVETATPVKVVKVTEPPKREAGKIVESVQEL
VAALKKEGAIQ

>phosphoenolpyruvate carboxykinase, ATP Contig15768 (complete)
MMLRSSVRGGRAVASGACVKATEVMGSSLVSARTLATAAAPAAAATAPSTQPRSSALFDY
RRLKNRKGWKKVVPDEDLDFVVFPRERLGKTYELNWTICKYAVIPNKDGEAFHNLHSRGL
QMLSNAAADKNKALHVTVPEEEYAFSHYFVLPSPPPAPAEGQAAPVDLMFVPENASVVND
GVAKNVSKEVRRFLSEGRYLFVHDGAVGSHSAAEEKVRFIVSSATTALLLKHLIPKQPTV
NIQDFEESITVFVAPELKATAEALGVSSDRFTLVNFKTNQVFVAGTNAPEAVQQAVSSLA
TYLLGKKGALPLQCDSALTKDGKSVLFFGPGLLQQKPRNDLFGAHGHFWTNEGVSRMYDG
ASVANPDASLALNRGDLVFHATKGGKTTKTSLSVPLSLQGHQAPHPSAIVFVSPNSAAGL
TKISAEEAAKHYLASFQYPVAVKPELLKQRFAYLLSNKNVTAYQVGAKSGKVNVDEINAQ
LHTALKQ

>glycine cleavage P protein Contig26495 (and 14613) (complete)
MKQSIRLAPSSARTVGRVAPLMRSRFLAAQGSRAVLYRSSSSKVFPPLDTFPRRHIGVTD
ASVQEMLSELQLKSIDELVHKTVPANILREPLNFKETGPRGESELLQEFRSNLQQKNKLL
RSFIGMGYYGTITPAVIQRNMLENPGWYTPYTPYQAEIAQGRLESLLNYQTMVTDLTGMD
IANASLLDEATAAAEAMAMCFAGTKKKGAQAGSFFISDDCHPQTIAVVKTRATALGVNLI
VGKPDTFDFKANEVVGAIVQYPTTDGRVVDYGDFVKRAHEHGVAVACGTDLLALSLLKPP
GEFGVDIAFGSAQRFGVPMGYGGPHAAFLATADKYKRNMPGRIIGVSKDVTGEVALRMSL
QTREQHIRREKATSNICTAQALLANMAAMYAVYHGPEGLKQIAQRVHTMTRVLAQGISQA
GYQLQGNEFFDTLTVHAGEGGADAVVQAALEKGINIRKLDGSRVGVSLDETVSDKDLVDL
LQAFTKAKTGKEGSVSLEQLLAAVQSGGSRALGDLSAHQRASGYLAHPIFNSYHTEHELL
RYLFRLQSKDLGLNTSMIPLGSCTMKLNATSEMFPITWPEVSQLHPFVPLDQAQGSIEMH
KELESLLSNITGFDAVSLQPNAGAQGEYAGLLCIKKYHETRGENQRDVCIIPTSAHGTNP
ATAVMAGMKVVIVPCDKDGNIDVAELRKKAEEHKDKLAALMVTYPSTHGVFEESIVDICN
VIHANGGLVYMDGANMNAQVGLTSPGNIGADVCHLNLHKTFCIPHGGGGPGVGAIGVAKH
LTPHLPNSPLVPVGGPKSIGAISAAPYGSSAILPIPYVYIKLMGAQGLRKATEVAILNAN
YMAAKLKDHYPIVYMGKQGMVAHEFILDIRPFKAATGVEAEDVAKRLMDYGFHAPTLSFP
IAGTLMIEPTESESKEELDRFVTALIKIREEIKEIEEGKLPRDNNPLHHAPHTQKVVCGE
TWERPYTRERAAFPAPWTKVHKHWPAVSRIDNAYGDRNLICTCPSPEAYAEHQ

>3-hydroxyisobutyryl-CoA hydrolase domain protein Contig13408 (and 4470,14938,22738)
(uncertain of completeness ... largely from PGP ... protein expected to be LARGE based on
position in SDS gel)
MQRGAQGGRFAFVGGRGALGKTIGGGATHPALALRNMNNKTATAAYSSGSGSKEDRDWFD
WSKYRTTSSKYDPFYQHITTDARFGMSDVWTQGMDPPQPIFPVDVKGRSKAYLPEVLSRK
HYYTKYAMLNRPQQLHALNLATIRHLTPVLKKWQAHKETTRAIVLTSSTPEHLSSGTDFV
DLLQAVRSGNQEFPKTYFKELYQLIYYINSLDKPFLPIMNGVTMGSGASLGYSSNSFKIT
TEQTVFALPEVGMGFFPDAGASYLLPRLADHVGTFLALTGKRIRGWDVLWSGIATHLVPS
DRIHIMYDQLDQLRDKFHSFDQIIHCVHSSAADKIEHPYLLKEKGYLDIIKRCFSQPTVP
EIMKALSHEKHPWAKQVLQRLQEQCPLSLAVTLRSLQEGATKDMGAALRARLSRDFAEGV
TARIVEKRQPNWTHKSVEDVHPDEVQAFFESLREDELDIRSLDEERAEDSAIQQLLDKQR
RFKKMMRRPWVQNEAKQYLAQELKSVQKELEARQSQTAGQLAAETEKQREEYQKKIEEGR
ARKGEALSFLQQLEDELVRRRNVEKEAVTKTTVDKLEWKRWEEDIKNVREAKGILTLDVN
TEYDEQLPTAALQTVLVDGIAEALSGTEDLAKQVSLVAASLDTAGKSALELKEHLFRRTP
EGVAEAEAEYERQYVEALQQDELRRTLREQMADIDIDAIRQAMNEDLGLLQPDERDQLDT
LLSSTEIVSHARQLHKQKQREQKQQQQQQQQQQRPEAEAGATVEPALTLDDIAKLVLGGD
HNDDAARVAETRAKIESGELAVSEETYAAAVQLMRERSLAAAEPSERATVEATFDTMHDE
IVNVVKAKVAGQSREQMVNALVGGEQGKSKLAQLMTQTAANLPHDSRVALTDPENQALIL
AEFQDFAKNLDSNASEGKVPLWKLEDKIANALARRDTEAAWPAEKRQELSRQIAQDRQLR
DLHAFPGLRGDDDDGADALQQATGQPGSSSSSEDLDLGKLVDDAAYELEHGRPAPIPVKL
MTEQQKDEFERNQSDMGLANYGKQFVYEKYADRIGHFKRIKERQDEFMSQVPDPISEPEQ
YRDWLVAVRLADLAMPALEDALGNWIDQQAKAGYNVKPIPEALRDDSVDGFVGTGSDDLE
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EVPTRRRRRSSSCGRWPRRRPPRATKPMRLSRR

>adenylate kinase Contig12348 (complete)
MQSSKPLRFVFLGPPGSGKGTQADLLKKQHTVCHLSTGDMLRAAVAEGNEIGRQAKEVMA
AGKLVSDEIMVNLIKDNLTKPECKDGFILDGFPRTVVQAEKLDEMLEKSNSKLTAALEFE
IDDEIVLDRLGGRYVHPASGRSYHVKYAPPKVAGKDDITGEPLIQRSDDNPETIKRRLAS
FHKDTVPVAAYYKKQGILEKLDAKRKPQEVHARVQKIIETRL

>ATP-dependent Hsl protease Contig14467 (complete)
MLKRAARLNAAVVGASSSSIPIMQRAAAARALRSSMREEALCLSSTSVHGNGRTEADRLR
FYSSENDTTTATVKSEEAAPPPVEEGKDEEQQEVAAPATPAEVERALLPSEIVNELDKFI
IGQAEAKKAVAIALRNRWRRRQLSPELATEIIPKNILMIGPTGVGKTEIARRLAKLAQAP
FIKVEATKFTEVGFHGRDVDMIIRDLVDVAVHDFTMKAREQEKQRVKQEVEERLLDILAG
AQAQERTKTMFRKMLQNGELEGKRVDFEVPQSTPATQMPFGSEMGAQGVFVQLDKIFGGA
KKQKRKMTIAECRPYLEEQEAEKLINKDAIVKNALEAVQSNGIVFIDEIDKICKDKNSYG
ADASSEGVQRDLLPLIEGTTISTKYGNVDTSKILFVASGAFHSCKPSDLLAELQGRLPIR
VQLKPLKKGDYYRILTETKFNQIDQAKALLLTEGVELDFTDDAIHEITKLTAEVNETVEN
IGARRLHTVMERILEEVSYECTPGKVTIDVAEVRKHLSELLLKTDLSRYVL

>acetyl-coa carboxylase Contig7031 (complete)
MRRALQCTTSTMTMTAAAGWRGGAAARMLHSSGARAALAASAEQRVETKRAEALVGGGLP
RIAAQHKKGKLTARERLELLLDPSSFREESMFVEHRSTDPAIVNQKYPGDGVVTGRGTIN
GRLVYVFSQDFTVFGGSLSETHAEKICKVMDQAMKVGAPVIGLNDSGGARIQEGVASLGG
YAEVFQRNVLASGVVPQISLIMGPCAGGAVYSPAITDFTFMVKDTSYMFVTGPEVVKTVT
HEDITHEGLGGARTHTSKSGVAHGSFTNDVEALSMLRQFVDFLPLSNKHEVPVRYTEDTR
ERCEESLDVLVPPDPNHPYDMHEVIDKIVDDANFFEIMPDYARNLIVGFARFEGRTVGVV
GNNPVELAGCLDINASTKGARFVRFCDAFNIPIVTLVDVPGFLPGTAQEYGGIIRHGAKL
LYAYAEATVPKITFITRKAYGGAYDVMSSKHLRGDANYAWPRAEIAVMGSKGAVEVLYRG
KAGVDMVKLEAEYRDKFANPLAAASRGFIDDVVSPRLTRRIICEDLEVLRNKQLDNPWKK
HGNIPL

>short chain dehydrogenase/reductase Contig19572 (complete)
MRRTIATHCNLAALPMRRGFASAVPAARRLEGKVAIITGAANGIGREASLIFARQGAKIV
AVDLGDARETVEGVKAEGGEAVYVKADVSKAGDCENMVQVAEKTFGKVNILFNNAGIMHG
DDNGATDTEEKIWDLTMNVNAKGVFFGCKYGIPALRRAGGGSIINTASFVAILGAATSQI
AYTASKGAVLSMSRELAVIHARENIRVNALCPGPLKTELLMSFLNTDEKKQRRLVHVPMG
RFGEAQEIAQSALFLASDESSYITGSTFLVDGGITAAYVTPQ

>alternative oxidase Contig2754 (complete)
MKQHCSQRIASLRGGGRDAFARLATTTASSLASGNGGVRASTLVQARRHLSLRLAPTTTS
RTSSATATTMTTRGRWCQGGALAWSRANTTSAAMTDGEPKQTQEEKKAAASNPSIAAQQT
VERAQQQSGKSTRVAYTLPHPIWQNEYVDAVEINHTPPENLTDKLALNTVRLMRFNFDWM
SGYSWGKLTEADWLRRIIFLETVAGVPGSVAAILRHLHSLRRLKRDHGWIHTLLEEAENE
RMHLLTGLKLKQPGKIFRTAVWVTQGIFFNFFFAAYLVSPRFCHRFVGYLEEEAVRTYTH
LLHDLDAGKLPEWKDTPAPEIARQYWKMGDDAKWRDVVALIRADEAHHREVNHTFANLQL
EQDNPFPPGH

>coproporphyrinogen oxidase III Contig22550 (complete)
MSETWKQPLSYLGVAALSAGAAVAGYRYLTGYRYTTVVPPPAAAAAVVPAVVDESTNADE
IELAFKAVQNHICQFLEDESGQRYKEDTWSYDKGSGGGISRVWEALSDDERHLLLEKGGV
NFSGIHGAAMPDSAATQFKIPPNTAFRATGVSLVIHPRTPHVPTIHANIRYFECGPRWWF
GGGVDVTPYYVNRERVVEFHKLLRALCEEWGYSYEAFKKQCDAYFLNTHRKEARGVGGLF
FDHLTTSDALPKSKKEICDFLVALGMLFPQLYGPFIHEGKDKEVTPEQREFQLYRRSRYV
EFNLLHDRGTKFGLQSEGRVESILMSMPPLARWKYNWHPEEGTPEAELYDIITPKDWASM

>NAD-dependent aldehyde dehydrogenase Contig12059 (and 11319) (complete)
MLKRQATVGRAFPIFVGGKPVTTATTLKVFDKYTKQVGYEVSLAGPQEIENALQLAHQAA
PAMRELPNYKRKEILLYCAAEIQRRQDELLHSLCVEAGKPLKDARAELGRAYDTFTIAAE
EAIRQYGEFLPLDVSVRNPGFTGLVRRFPVGLISMITPFNFPINLVAHKVAPAIAAGCPF
VLKPNDVTPVGALLVGDILSKAGLPDGAFSVLPCKLEDAKKLSTDPRIQVLSFTGSEQVG
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FALQRGAGRSKVLLELGGDAACVVDEGSDVDHVVSRIGFGAFYYAGQSCISVQRVYAHES
IYEELKQKLVAHVKTLKKGDPFDEDTFVGPLISEDSAKRLESWVQEAKEKGGKVLAGGSR
DGSVFDPTILEDVPDSAKLACEEAFGPICVLHKFSDFKEAIEQVNNSRFGLQAGVFTNEW
KKAWYAYDKLEVGGVVINDIPSVRVDAQPYGGIKSSGVGREGLRYTIEEFTEPKILLTKD
LGKL

>2-oxoglutarate dehydrogenase E2 subunit Contig8827 (complete)
MMKRTASMGRRPLFSACLVVQSNRGAAATLSGLRGVCSSSSHNGTGRIVASLTSHSRSGL
NVLPKRFYATAEVKTQAVPPMGDSITEGELKNWSKGVGEHVAVDDLVAVIETDKVAVEIR
AKEAGVIKEHFAEEGSTVSVGAPLFAYEAGAEAPKKAEVPKEEPAKKTEQAPKPEAAAPK
AEAPKTAAAPAAATEGKAAPKAEASKAPAPKTASPVAGGERKVKVTRMRERIAQRLKDAQ
NTYAMLTTFQEADMFNLINMREDFKEEFQKKHGVKLGFMSAFVKASAAALKEIPAVNAVY
DGSNREIIYRDYVDISVAVATPRGLVVPVLRDCDHLSFADVEKRLSELSVKARKDEITLE
EMAGGTFTISNGGVYGSLMGTPIINPPQSAILGMHAINKRPVVVNDQVVIRPIMYLALTY
DHRLIDGKEAVTFLRHIKHSIEDPRRLLLEL

>serine hydroxymethyltransferase Contig5591 (and 22804) (complete)
MRSVLARRGGVSAARGAVSAKSVGHTARRLVSSSTARPLSEVDPEVHSLIHEEYERQKYG
IELIASENFTSRAVLEALGSVMTNKYSEGYPGARYYGGNEVIDKNERLCIQRALDAFHLD
SAKWGVNVQPYSGSPANFAAYTALLNPHDRIMGLDLPHGGHLTHGYMSPKKRISATSIYF
ESMPYRLNESTGYVDYDELRRSALLFRPKIIIAGASAYPRNFDYARMRQICDEVGAYLMG
DMAHISGLVAAQQVPSPFDHCDVVTSTTHKTLRGPRSGVIFFRRGVKSVDPKTSKETLYD
LEERINFAVFPSLQGGPHNNTIAALAVSLKEAMSPEFVEYQVQVKKNCARLASSLQSKGY
TLVSGGTDNHLLLLDLRPQGVDGSRTETVMEACNITVNKNTVPGDTRPMVPGGVRIGTPA
MTTRGLKEAEFEVVSDFLHRSVQITQSLAKQGGGNLKAFKEQVEKEKSGGEIARLRKEVI
DFSGSFPLPS

>homo-isocitrate dehydrogenase Contig6170 (complete)
MNRCGARASLGLCRQRLASSPTAAARLYSSATVKIEKTGEPVKVALIPSDGVGKEVVPEA
RRVLEAVEPHLPFAFSWVPLHAGWETFQQQGVSLPKETIEGLKGCDGALFGAVSSPSHKV
EGYSSPIIGMRKALDLYANLRPVISAPIKTSRPDIDMLIVRENTECLYVKKERMENGPQG
RVAIADRVISEYASTRIAQMAFSQAERRAAVRAGSKRPARVTVVHKSNVLSVTDGLFREC
ALEVAKKYPHIEVEEQLVDSMVYKMILDPQRYDVVVAPNLYGDILSDAAAALVGGLGLAP
SANVSDSFALCEPVHGSAPDIAGKGIVNPLATIRAAALLLRHLRGPHADAAAQMGDVIEE
AVNRALAAGPLTPDMGGKASTTQVTDAVIEHLKSLLLNKH

>mitochondrial ribosomal protein s29 Contig26915 (complete)
MSMLRTAMHRSNGGRWGGRRAAASFQEWLTSSSTSSSTTTSSSSSALLPLRPHFVAGLAT
ASRPVYAKRMKNDGGNQSGREVSDLESTENQDDAEGVQDENDDDMRSLEKQVTKELSRIG
MADLKDEVLKQGKGEEEAVSESADPFDTVLREIADLHAKGLLGDHDTLTKYERYLHKKKS
HQGLVRDINASLAAMSPDQQSFLSHFVEFVKPVDVEAEAAAKAAAAALAAKQSEEAIREK
EAIAFAFAPGDATKLTVGKSLLRFSAQDQKQYLPEGVAGQLKNTQFKFGDESVVFRRAAY
DLIQELKRRQESGFLASAGNDSLILNGEGGSGKSTVLSQAVLWARKNDWFVVWIPDGRAW
TGGERIVPSTLEHAHYDQIEKAARFAARLNVTHGDKLKAIKLKGDYEIEDFHRKSDSTLF
DLLEFAYKHDKRAVNAVYYFRRELNRITEFPTLIAIDRYNYFWDNTGYFDPADVNRGNYR
HLDAQKLMLTKMFSDHQDHGLVNGTMVCALETTKPATIKPFLRRCGDKHMHEIPAYSLNE
FHEVMKHYKEIEYVNIDDTTKATERFIYQLCNGMPGLVFKYCGLQ

>succinyl-CoA:3-ketoacid-coenzyme A transferase Contig6520 (and 1179) (likely complete)
MRQSTMRGIVLTRGSRGFHTTSLLRSKIVGSAEEAVKDVKDGSKLLVGGFGLCGIPEKLI
GALRTTGVKDLTVVSNNCGVDDFGLGLLLQTRQIKRMISSYVGENAIFEKQYLSGELELE
LIPQGTLAERCRAGGAGIPAFYTPTGVGTFLEEGGFPIKYNTDGSVAIASKPREVREFNG
RKFIMEEAITGDFSLIKGWKADTRGNIVFRYTARNFNPPVATAGKICIAEVEEIVEAGSL
HPDEIHLPGIYVNRLIKGTGYEKRIEKLTLDKGQPAKGDAPKNEAAITREKIARRAALEF
QDGMYCNLGIGIPTLASNYIRSGIHIELQSENGLLGMGPFPKPGNQDPDLINAGKETVTT
LPGSSIFSSDQSFAMIRGAHVNLTILGGMQVSSNGDLANWVIPGKMVKGPGGAMDLTCSG
SRVVVTMEHKDKSGKPKILNRCNLPLTAQGCVNRIITEMAVFDVDRSGLTLIEVAEGVTV
DDVKKYTEPEFKVSPNLKKIAYA

>fumarase Contig5809 (and 4472) (complete)
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MRRLQPLLSSTAIAARSPACFAAAGPGRLIGLRALATAAPAKKSTPPAFEFEPLFQADPF
SATPYRKLFGPESGLIRTEKVAGREILHVEDEAIERLTFEAMRDISHLLRPGHLEQLNSI
LKDPPEASDNDRFVALELLKNANIASGMILPSCQDTGTAIVMAKKGQYVWTSGDDEAAIS
KGIYQTYTQTNLRYSQMAPIDMYKEVNTGTNLPAQIDIYASEGNAYKFHFIAKGGGSANK
TYLYQQTKALLNPDSLMKFVNENIRSLGTAACPPYHLAIVIGGTSAESTLKTVKLASTKY
LDTLPTEGNKHGRAFRDLELEKKILELAQKTSIGAQFGGKYFCHDVRVIRLPRHGASCPV
GIGVSCSADRQAVGKITPEGVFLEKLETNPAKYLPEITEDKLSDTVVNIDLNKPMSEIQA
TLSKYPIKTRLSLSGTLVVARDIAHAKLKERLDNGQGLPQYVKDHIIYYAGPAKTPEGYA
SGSFGPTTAGRMDSYVDMFMKNGGSLITLAKGNRSKQVTEACKKYGGFYLGSIGGPAARL
AQDCIRKVEVLEYPELGMEAVWRIEVEDFPAFVIVDDKGEDFFKNLSH

>adenylosuccinate synthetase Contig27123 (complete)
MRAFFGSTSPSAARCAVGQGSIRSFSLAANGTWSFAGRTAVLSRNLAARNYSTATSTTTT
EEAAPAAAVATPAAEAVEKPKVEEPKPATPKVEKKGNISRVAAEQVIAVMGGQWGDEGKG
KLVDVLGANFDIIARCAGGSNAGHTVIVEGKKYAFHLLPSGILHERPVCLIGNGTVVHVP
TLLKELTSLDEKGVNYKGRVKLSDRAHVVFDFHQQIDAFLEDAAKKGNKDGSIGTTRKGI
GPAYGAKIGRVGIRVGDLRFPDTLPEKLTKLVEYYQRSFPLEVNLNHEIEAYKAFAHKLQ
PMIVDSVHYINKAYGEGKRIMVEGANATMLDIDFGTWPYVTSSNASIGGAVTGLGLAPSK
IDGVIGIVKAYTTRVGAGPFPTELKDDLGESIRKIGHEFGTTTGRPRRCGWLDAFAIKYA
HMINNFTLLNLTKLDVLSDLDEIKIATSYKYNGEHLASYPSNLEILDQVEVEYETLPGWK
KDVSGVRYFEDLPAEARKYVERVEQLVGCPIGWVGVGPGREAMAIRKPK

>Sam50 Contig10559 (complete)
MSYTDEDEPIDLGVRGEDAWRVRRVWVKGNRRTRPDVVAACVKPVLKARTFDEVLARVAE
AAGELKGLGIFKSVNLVLDDLPDDVAAADPSACDLRVELVEHKLTRIEVKTSTTVGENEP
DVQATVGLCNAFGRAETVSVSAQVGASNWREHWSSAFSLAFKRPVLGQGPGPRHIEADAT
RASHRLPWCALTQTTHGLALRYSLPSHQVSYEASARHVIPESSAPLALRSHAGHSLKSAV
KYVYAHDTRDDPLTPTTGHAFTSSTELAGLGGDVRFVKQEMAAQLNLPLGKTRCSFNVLA
KAGYLHALDSGSRIVDRFFLGGPGSIRGFQYNAVGPSHQQRALGGGAYWAGSLHLSFPLP
LRDVPDFVSGHLFANAGNLRQPTPGRSVAANVQDLFSADDVRAAVGAGLVLRTMFGRVEL
NLSHPIRKAATDLVQPFQVGLSVRFL

>acetyl-coa acetyltransferase Contig8703 (complete)
MRASRVVNASGIRSAVVVSAVRTPVGSFGGVLSTVSGPRLAAACITAALQRTQGGQVDAA
EVTEAIMGNVISANVGQAPARQAAILAGLKESTVCTTVNKVCASGMKAIMYGAQSIMLGH
HEVVITGGFESMSNVPYYLEKARTGYRYGHGQLIDGVLKDGLTDAYDGQHMGMCAEKCAK
DHGFTREHQDEYAVTAYRRAAEAWKQGWFNDEVVPVSVPGGRGKETVVAEDEEYKKVNFD
KISSLKPAFHNEGTVTAANASSLNDGASAMLLMSEEKAKALGLKPLARILGFADAEQAPI
DFATSPSLAIPKALKHAGVEAKDVDYWEINEAFSVVALANAKLLGISLDRLNVHGGGVSL
GHPIGSSGARIAVSLTHILRQKGGRIGVASICNGGGGASAIVIEKL

>isocitrate dehydrogenase NAD+ Contig22692 (complete)
MRAASHLRLRSLPARLGSPLSHASSAPLVSRRLYADKPVENKTVTLIPGDGIGEEISEAV
VQIFAAAKVPVSWETVKVSTTTAKEGSLSSLLGGDVLESVKTTRLALKGPLATPIGKGHM
SLNLALRKQFNLYANVRPARSIPGVKTPYDNVNIVVIRENTEGEYSGIEHQVVPGVCQSI
KLITREASRRVAQYAFQYAETHKKDKVTAVHKASIMNLSDGLFLKSCREVACAYPFVEYE
EISVDKVCMQLVMAPEKFQVLVLPNLYGDIASDLCAGLVGGLGLTPSGNIGADSAIFESV
HGTAPDIAGQNKANPTALLLSAVMMLRHMGLYTHANRIERAAYDVLREGKVLTGDLGGSA
TTTQFTDAICKRVANDHEA

>aspartate aminotransferase Contig12222 (complete)
MFKRAATRTTSGSVSSAAVQQRLFASSSSARAASSLWAHLDVAPLDSNHATNAAFEADQS
PLKVNLGRGVYKDDNGKNWVLPSVRMAEEKIFAEKAGHDYLPFKGWDVFCKRTSEFAFGE
TNPLLKDKRVATVQAISGTGALRVGAEFLSRFLPPTHKGVSVYVADPTYVNHLPIFKLNG
FEIKRYRYYDPNTNGLDLKGFVEDLQNAPEGSVILLHACAHNPTGVDPSFEQWKLVSDAC
KERRHVVFFDCAYQGFASGDIDRDGAAFRYFAQEGHQVLVAQSYAKNMGLYGQRVGALNI
VTSDAKETEAVMSQLNQVIRPMYSNPPAYGARIVGTILSDPTLRAQWQKDVKTMADRIIG
SRQALVDNLEGLGSKKSWKHITNQIGMFAYSGLTPPQVQTLRTLHVYMNLDGRMSVSGVN
SHNVEYLAQAMHKATSQ
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>alkyl hydroperoxide reductase Contig15850 (complete)
MNRTASVSRTAFTVAARQTTVRGSQALFARSYAVGQNLLEGQANLKAVDGKDLSLTDLFK
GKKVVVFGLPGAFTPVCTSRHVPGYVDSADKFKAKGVDNVVCVSVNDPFVMKAWGESLKA
NNITLVADWDSSFTKLVDKELDLSAAGLGKRCRRYSLIVDNGKIVKENIENAPNDLQVTS
AEAVLAQL

>Rieske Fe-S protein Contig7171 (complete)
MKRTAISAAATLRASTAVSGSASATLTRMAPVLSSGSSKREVHEINVPDWGHYKREAQEG
GESGGRAFSYMVLGTAGVGYAAAAKHTVIKFLDSMNPAANVRAMANVEVDVSNIAEGTIM
TVKWRGKPLFIRHRTAEEIADAESAPLTDMRDPCPDAARRKADKPEWLIVLGVCTHLGCV
PLGGQGEYGGWFCPCHGSHYDTAGRIRKGPAPLNLEVPPYVFKDDSKVLVGVDSV

>mitofilin Contig3711 (complete)
MLRRGFNGSRARAACRLPASSTHARVPAARQVTSRRLFANAGATPPPSSGGGGVAFGVLV
GAAVGASAWTGYRYYTDPPFRARLNDFWASLSSSTTSSPSQPTAAASPKPSVTHEEQQQQ
EEAGAPLLAAQVLLAAAEEATALDAQEEAVVALPDSLVVQQQREHQQQEHHQQEQQQQEE
VEVEQMDPAATQSNDGEGEEETEQPAIIAAPAPLVVEVVGPEASHAHVATDGVAPEEAKA
AVPAAVVALVTESFAASDAHQEAVAAVAHDDHHHHHHHDKASPAEEQQQQQQQQQDAAN
PAEPAGEQRDHEGEQQQQEQQQEQQQQEEQQEQRQEQPAAEGATRLQELQAIKEIIAIQA
ESCERQVREKVERLRQKYEHKMAALRQHMDEVVAEHVDVERQKISDDYQNRLHQQLDTLQ
HQFVEERQRLYSEMEDVVAGLNARFVELVREEKQLLNEQLEESTRLHAHTLAYLQTLVDD
AQYRIRHLSEEREWWSWTERLASAVRALESAALGPEGHLASFQAELDLVRSLAATRPLYK
AVAHHIEAQASRGVYSVGRLRERFEQVEKHVRVAAQVPEGGGLLRHAVAPLLAATVSLNP
YHAPTPQELLLDSARRHLLDDDLLTALRDLEQLTGLAHELAHDWIEEARKRLVVEQAISV
ISADVTTLKPPTDL

>carboxymuconolactone decarboxylase domain protein Contig4383 (and 17744) (likely complete)
MLRQGSRSVIRGGAVNRGAWGLLSVSSRLPRATAVLSSSSTPAISSPRRQASATTPPAEP
PVVVNRSARKRYVRHPWNDSESMLSDDLRILTYLAGNTAAGNLSAVGRDWCYLDPAKHAA
GMDVILQTLVFAGVPKILNALQTVSELGVDNRQILEPTFPEGEEFKEPVSYGEFVERGEA
EMHLAFCHKYPRLRERMAELHPALDRWMVDTVWGRLRSRTGLAAKERQLCALAALAGNIV
WPQFKSSIIVALNSGCTLEEVRSVLDQTEKVWGTSAQIMVDALWTDLNKKSLHSWQDGSC
ESTLHNHGGSHIPASTPIPTSNHVKYATSGKHPFMYLNRMEDAIPQHLRVLALLAAHTAS
GNLTRVGVDWSYLGEEHHEAGLEIILQTTIFGGFQKAINALQVVHNIGVSPTAINYAAEE
VPEDRRANVKRGTELLKLIYQKQYPRLREKMRWMHADVEKVIVEWAYGRVLARPSPVLAP
KDRELCALACLSGQIVFPQLHSHILGALNAGARLEEIRAIFDQT

>ribonuclease III Contig22975 (and 11102) (complete)
MKRTTSSSLRLLASSSSFGARSAPLVLPRTSFAGLISSSSRSTGVHRTRLLATAAKASSS
TSSSPSSSKPAPRNADPEVLHEQLDAFAARIGFKWNNKKLLLQAFTHPSFSHDKEVSNQR
LEYFGDRTLNFLVCEHLVNKYPNLPARALAHATHLFTSNETLTTAGKRLGVQDFVRWTPH
EEEDRGEDIIVANTMEALVSSLYFDQGLKAAREFVVKHILPQDENLDLIPFLRQRLPRHT
LSDLLTRRGSGAPYYVVLQESARYSSKSTFVVGVYSDSQLLGQGSGQSIGKAETAAAQEA
LNKMWGAKAYTTLPPNDY

>1-pyrroline-5-carboxylate dehydrogenase Contig7268 (complete)
MRRIATRSHLVTPQQMASLAPLGARSMHAGGSLNIPKPTNEPNSINNEAQRNATLAKVAE
LRKGKLDVPLIINGKEVRTGNTGEIRPPHDHQHLLGVYHKAGEKEVKEAIEGSLAAHKHW
RNLAPEHRLGIFMKMASLLATKYRPLLAASTTLGQGKNLFQTEIDTPCEAIDFLNFNAHY
AEQIYNEQPASEYVDPYGRGSVRAWNRVEYRPLEGFTYAVTPFNFTAIALNLATAPAMLG
NTVVWKPSDHAILSNYYLTQLYKEAGVPDGVINFIPGDPQLVTKVVLENPKLSAIHYTGS
TDVFRLLWKGLGDNIDRYANYPRLVGETGGKNFVFVHQSADKDAVVTALLRGAYEFSGQK
CSAASRAYVPASMWKELKGKLVEGIKSFKVGNPEELDTMVGPVIHKASFERCKSFIQTAK
SDSNTYTIHAGGVCDDSKGYFVHPTLVETKDPHGVLMEKEIFGPILTVYVFPDEQIEDTL
HMAEKSTYGLTGSIFANDRYFVKKAMDVLEYGCGNLYINDKPTGAVVGQQPFGGSRASGT
NDKAGGKHNLLRFVNVRSIKENFVPDTNPFYPYMSAPKH

>2-oxoglutarate carrier protein Contig11386 (complete)
MATGERKAGKGMQFLFGGLSGMLATCVVQPLDLVKTRMQLSGEGGGAKAHKTSFHAMANI
ARTEGPSSLYKGLSAGLLRQATYTTARLGMYSIINDWLVARNNGNAAIPFYQKLVAGMMA
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GGFGAVIGTPAEVALIRMTSDGRLPPEQRRGYKNVFDALLRICREEGVLAMWRGCTPTVA
RAMILNAAQLGTYTQAKQVLMKNLPLQDNVYTHFLASLASGFLATAVSIPVDITKTRIQT
MKTINGVPEYSGVMDVLSKIVKTEGVTALWKGFTPYFLRLGPHTVLTFIALEQMNAAYNR
FAM

>2-oxodicarboxylate carrier Contig8220 (complete)
METQRAYSPVGASNLPFHKQVMAGALAGLCEVLCMYPLDVVKTRFQLQTAAEARYSSVLG
TFRDIIKTEGFSKLYRGIASPIMAEAPKRAMKFSMNEQYKKLFTNASGQLSGPGHVAAGG
CAGMTEALVNCPFELVKVRMQARSNAGLYKNTWHAARSVIQTEGALTLYRGFGSMLWRNG
VWNGAYFGIIQQVKRLLPVWSSERGQLATNFTAGTISGLIATMLNTPFDVVKSRIQNTLP
GQPRRYTYTLPALATVAREEGLCCALQGLRAQSP

>AAA family ATPase Contig2166 (likely complete)
MGNHPPSCNMMGLPPPTRETPTTTKMRTWDGSEGELAEEARGPVYTPSGKERAEIDQSTL
DEADDDDDVDEEDEDTELEGELDFRSSLVDVGREETNLDPAAQDKKDKKSNSVKNTVHKG
RYFEVESMDIMDPTTGKRVETVSKVIIKDATLEGTLQSFDVTLTYDAESSKLAAIFPWLK
KPPFCPLEALMMRLPILRNSTYGGAQMEELVKFLEKERPRMVRKIEAHLKKGLISYSGLW
YLFSKGNRFYVDIGKGILVGSSAEYTRYMPAVGLCAPNFYVQGPIIKSDGVKFFRQNRAF
DIPVFKGLMPISGLDVQPMTKQVLRILNKRGRVFQKVALKHHYMQYEKFMLKRGAFSDTW
IKADGRVMVDISTFNRMNPEYTEFGSSAHDTSTQQQLQQLMAAQQRFTGDYTQTTLPVAG
QKRISKAMRYQTWPYVAGFSFTAKRWGELLVESLSDIQFDDKAYDRLVLPEDKKALVKAL
VEDNKRVQEGRAGVSFSDVISGKGGGVIFLLHGSPGVGKTLTAEAIAEYLHYPLYSVSVG
ELGVTADHLESKLNDILELAGTWNAVVLIDEADIFLERRSDIDVLRNAMVGVFLRKLEYH
QGVLFLTTNRVKAFDPAFNSRINVAIRYHDLTKEARGQVWRNLLGHMGDDESSDLDFDQL
ADIEINGREIRTVIRLALALARCEGVALNAEHIKRTVAISQQFGKDLNSVEDW

>hypothetical protein Contig3831 (complete)
MSEPSPVAQTASGEIDWKKILGIGAAVVVGGAVLFYFLGGSDRRSNLKEAEQKFDEAAAK
KEEEDWETAEKLYHEALTILRRHLDKNDENIAEVYRELATCALNKMELDKAEQYSRDCLR
IKEHNHGHDSALICDSLVNLAGILAALKAADALEYAEKALRIYELPAEDERDYAGLSHAL
RTKAAIMMSNKKLPEAQEAAIRALECFEKVSSKGDAHSHYRDAMEGHLLLAKIYMKQDNR
EAAEGVYKGLVQRAKDTLGPVDTFVAYSLRNLGDFYEERNDVEQAEAAYKEALEVVREKH
GEDDSNVFAFLNYLAHFYWDHNRDSDAQDVFTKLRTMKCLPSPTNSRCLVTRLFAFTFTR
ARNDPHAIEPVYVGELLPTPKLPERAFLEVIYENPEDPSNPIRQERELTEDDRETIVLLS
PTVKGVKPQMYEIAIHVYKDRSKTEKVGEHHQMCQSVFDTDRIKTEEDLMLQIPKDRLI

>Zn-containing alcohol dehydrogenase Contig6146 (complete)
MRRTVTSQHAVMSRAAGATGQVASRSLKCAMPALQQQPQRYLATSTSRPSIPTTMRAAVV
EKFGAPLVIKNVPVPTPGKDEVLIKVHACGVCHTDLHAADGDWPVKPILPLIPGHEGVGE
VVAVGSGVERLKVGDRVGVPWLHSACGYCEHCLGGWETLCHSQQNTGYSVHGAYAEYTVA
PANYVGVLPDALSYVEAAPILCAGVTTYKGLKETGTRPGQWCVVFGAGGLGHVGLQYAKA
MGFNTIAIDISDQALALAKELGADMTINAAKQDPGQVVWKEVGGAHGCLVTAVAPKAFQQ
AVSTVRRGGTVALVGLPPSTFPLDIFNVVLNRITVRGSIVGTRLDLQECLDIAARGKIRA
RIETQPLDNINAIFEKMKKGKLEGRVVLSPL

>2-oxoisovalerate dehydrogenase beta subunit Contig5667 (complete)
MKKRISASIGSSATAHRLVGGSVSGASPARSLLQPSARAFHVSPAHAAATAHGGSSSTHQ
QQPQGEGEVARMNFFTAVNNALDIALGADPKAVIFGEDVAFGGVFRCTINLREKYGNSRV
FNTPLSEQGIAGFAIGMAAVGATPIAEMQFADYIFPAFDQLVNEAAKYRYRSGGQFDVAG
LTVRTPCGAVGHGGHYHSQSPEAYFCHTPGLKVVMPSTPKEAKGLLLSSIRDPNPVIFLE
PKILYRSAVEDVPLGDYELPLGKARIVKEGSDVTVVGWGSQLHVLTDACGLAEKEGISCE
LIDLRTLAPWDVDTVEASVKKTGRLVVSHEAPKTGGFAGEICSTIQERCFLHLESPIRRI
CGYDTPFPLVFEKFYVPDKLKNLEAIRSTVHF

>2-oxoglutarate dehydrogenase E1 Contig20262 (and Contig25463, 26471) (incomplete inner
portion)
MLRVGARGTRTQGSSFLSSSRFTGVTAAAAARFCPAARSQTLGLVGRYSSSTTTTAVEGG
KLTQEEVDNQNKHANVLRLVNAYRTYGHFDAALDPLGRRQRGAPEGVLDAARYGLGNEEV
QLRGLFFGLDKEKASVSEIVDALKKTYCSSVGVEFTHVENPEEQTWLARRFEAAMGRTAT
GATAQNALPAEDKKRILNLLQTSEEFDHFLHTKFRAVKRYGLEGCESMMACMDTIFSKAA
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ESSFDEAVIAMPHRGRLNFLTGILRYPASKIFAKVSGFNDFPTVEGAVRPGTGDVLSHIA
QSVDLEYQGKNLHVSLIHNPSHLEAANPVAQGKVRAKQDLGKGRKQALCIVVHGDAAMSA
QGVVPETLTLSQLPEYAVGGSMHVVVNNQIGFTTECHKGRSSWYCTDVLRSVHAPAIHVN
ADDPEAVVIATRLAMDYLTTFRKDIIVDLHGYRRHGHNELDEPSFTQPLMYDSIRVRPTI
AKLYGEKLITMGGKWQKMTAPQDMTKPVDTGYAEEELVKVGVASINPQGKTVHSRLQNFF
CKPRQAKLESKTGLDWATAESLAIGSLLLEKYNVRLSGQDVGRGTFSHRHVALTDQKTNE
RVIPLNLMSSDQGKLHVADSPLSEMAVMGFEYGYSMEDPSTLVLWEAQFGDFHNGAQIII
DQFLNSGEDKWWRQSALTLLLPHGYDGAGPEHSSCRIERFLQLCDGDRLNPGDISNLVPN
MQVINPTTPANYFHALRRQMKRSFRKPMVVVGPKTLLRHPQAVSDLAEMAPGTSFQPVIA
DTTVSPAQVKRVVMCSGKVYYDLVKHRETKKIDDVAIIRVEELSPFPYRALADELDKYRN
ADSYRWAQEEPQNAGMWDYVAPRFSRLSAPVKLVSRPASAAPAVGLGSIHAQQQKAILDG
AFA

>carnitine acetyltransferase Contig11131 (and 3023) (complete)
MMKRTALRFAGTTTATARPATVGLRHLQRARGLSSSVTSGEEAWAEHQKG
LRRLPVPSLEETVARYAEYVAPLVSEAEAAHARALAEEFARGEGRALQSE
LLALDRESPTSWLEGWWDTMYLTIRDPLPVNVNPFFIMQDDPERRSQVAR
AAGLANACAKFQRLVRTGQLKPDMEKTTPLDMSQYTKLFAAARIPRASRD
EMVYHPDSRHMAVLSHNHFYTVEIITEDGSVVPEKDIQRQLQQILNESAP
SGTREPGLGVLTADWRDSWASVRSELISSHGDNKHALEKIDSALFVLVLE
PEAPAKGDDIAKVFLHGDMRQRWFDKLQVIVAANGKAGINLEHTPIDGHT
GIRLPGEVPGLLQSQEGEANGPISARPQRLKWHLSPAVIKGLEKAEAVAD
ELVSHTEIRSLEFNHFGKKYITSKKLSPDGFVQMAYQLAYHQLTGKTVST
YESCMTKQFLHGRTETLRSVTRESAAFTRAFATPGATPKEKEQALRLAVQ
AHGNRAKEAKEGFGVDRHLFGLKNLAYHKQQRLPGYTIPALFQDKAYRVL
SASVLSTSNCGSDALTMFGFGPVVGDGLGLGYMIQNEKIPITVSSFQRQA
LPYARALEKSLLEMRDVLDASTTSTSA

>methylcrotonyl-coa carboxylase beta subunit Contig13448 (and 18847, 925, E9BS9UA01DA30H)
(likely complete)
MLQRGGLVMRRGGCAPTTLRCAATRFGRPTSIGFDGRAALPTVLVGREYHAERDFNVVDG
SVEMSQDEWRENGRVMLDLVNKLKHEVATVKAGGGESARNRHVAKGKLLPRDRILRLLDP
SSPFLELSQLAGHGLYEDHVPAGGIITGIGRVQGQECMIVANDATVKGGTYYPITVKKHL
RAQEVAQQNRLPCIYLVDSGGANLPRQDEVFPDKEHFGRIFYNQANMSAQGIPQVAVVLG
SCTAGGAYVPAMADECVIVKGNGTIFLGGPPLVKAATGEVVTAEELGGADLHCQTSGVTD
HYAHDEEHALALARRIVANLNPSHTKQRKASWEPEPVIEPRYPQTDLYNLIPSDARKPFD
MRKILARVLDDSRFDEFKALYGPTLVTGFGRIHGHPVGVVANNGILFSESARKGAHFVEL
CAQRGVPLLFLQNITGFMVGRSYEAGGIAKDGAKMVTAVACAQVPKITVVVGGSFGAGNY
AMCGRAYNPRFMFMWPNSRISVMGGEQAASVLTQIKREAMVKSKSSHQWSAEEEEAFRQT
MLAKYDKEGHPYYASARLWDDGIIDPAETRNVLGLTLAACRNAPIPQTQFGVFRM

>solute carrier 25 family Contig26983 (complete)
MHLSSAGIPFEKRPQLPAEPTVLAGFSADALTRTLLNGFYVVKTRLQVRRPRYHFCHAFV
ETQNLWREGIFGFLRGNAAGCLRAVPYSAAKYATHRAVEPLLKDRLPAARAEWVANGLAT
AVAVAVTYPLNTLQTRIALLPLEQARYAHIINELANSNGGLLDGLYAGILSVIPGQLAYQ
AGLHLADKLFLAVIGPTDESQHPTRAFVQSCLRATLANVLSYPFDTVCVRMQAGIFADKS
VLHCIKSIYEEQGVGGFYQGVGVTLLKVLPFALFMYFAFHFSNQWFEKHGRDERFSSLHS
YLHTYWRALSTHLETGSLQWRSHAQKQFHHAE

>Complex III Qcr7 Contig4544 (complete)
MAARKGSSGFLSRISSSFKPVSGYQAYGLRLEDFYNAENPEIQEVLRRLPNKTKEERDLR
IRRGHELHLKGTTLPESSWTTPEEDGQTYMEPYMSEVVQEIEERKDFRADFLLPVEKRHK
RK

>peptidyl-tRNA hydrolase Contig8428 (complete)
MKRSLGLWKRPYAGVNHLIVGLGNWYYPLSRESVGLYALERYAQRYSLVWDFIPNICSDA
LASKTGIALIKPKTYQQKDMGKAVAMATEAMNLTIDDVTILHYDANLPCGQVRYRTGALD
APNVAVQSIINMFDTERLNRVSIGIKPVSEDEVFVPTIVQAIDKRYLDNFNDIWIRNVLS
DTERPLVDKASDKVTDELLHSATNTTDNTFSRLNTL
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>Cox1-c Contig12260 (complete)
MRRCITSSTLRGSFSSRAISSARSLAAPAHAHASAQPDASVYRSKQGGSFEEALDINVVD
VEDLFNPASGYWENPANWNDMDYVWKLKVERLQQELNIPAEQAAKFRKEHDISKGYLTLE
WILPSPPPEHTFEELPILKETEEEPATSFEARAARLLESAHKAKTVSAEHTQTFESLAKE
FSFSDREKTAFKELLNRYAKGQTPSFPNEYEEHAHDEHH

>4-aminobutyrate aminotransferase Contig7954 (complete)
MSRYESSKKLLSPVWGHLSESIVERASGSFIYTTCGKKLLDFSTGIGVVNTGHCHPRVVA
AAQEQVGKLIHGQLNIVYHKPVLELVEELKPVVPEGLDTFFFSNSGAEAVEASIKLARHA
TKKQNIITFVNSFHGRTVGTMSLGNSKIVYKNQYGPLMPGVHVAPYAYCHRCPCKQQRKS
AEDCCNQPLLAVEMLLRQQTGPADTAAILLEPVQGEGGYVQPPKSFMQGLRKICDKHGIL
LIYDEVQTGFGRTGKYFAAELSGVKPDILVFAKAIASGFPLSGLVASKETHKHWQQGSHG
GTYGANAVACAAAVATQRVIKEEKLVENAAARGEQLTKLLLQLKDKYPQISDVRGPGLMI
GVEFYDERDNAYPFPGHDSKHTVKYGFTGALTKKCLDHGMLILNTGAHETLRFIPPLTVS
AEEIELGVELFEKGLKDTLKELAN

>armadillo repeat protein Contig4946 (N-terminus incomplete)
MSRQAPTHDAMRQLGLLQAMLAMLKPVTAGASSSS
GAGSSSGGGGGVGSSKHPLTDYESVMVELTKVVANLAANNGNRQVMGESGAIRDILRLLQ
DLPNEEIRENLLRTIMNLSIAAENEDRIREEGGLTLLLEFLQADDTSPALLLQTVRVLVN
LSCNETNKTIMQRAGVVDRVVVLLLGSTDVDTGLAHRLVRLLGTFSVGCDLAVYEKITDR
AVAQFLVTSLRKQMEKVEPDRDDKSFSEILLMAIWKITTERAPKFADALTRFQNLFIEES
EADGSCGIDFIFPYLRLTHPDDRTLVLSCLNTLQHLARGNDQVQAKIRGSGALGALKELY
NSREPVIAEKAVELVKSLSMIAALD

>FAD-binding monooxygenase Contig19652 (and 996, 11623, 6528) (complete)
MKMSRHAAVQQRGAALASLIVPRGGGLPAATMPTTSLLLRSYAAAATTTASSRGSLSSSG
SSGTPPAADEGRAVAHVRRREGGPLRVLISGATVGGLTLAHCLRARGIQAEVVEADSNYD
RFVGRSAVVSGDALRVLQGLGLRSVLEREGTVLAKAVTGLYSGKSIHQQNFEPPTQDQGA
GAVAIPAFALAELLAESWESRGGRINTSTAILTMREVAGTGVRCSFRDAKMGSRDYDLIV
LADGVNSGNTPEVLKEEIYQNPYMTATQVGAYGVWSTYLPRPFTIAPDQAVDVLGLGSRA
GYVPMPEDLLYFWATHRADMAPFLKGGAREAREWPSVGGGFEKGFSMRTVVQQVEQSDRT
CWVHYPRDMRIKQWTHRAGRVALLGSGAYSTAPLPLHEAALPIEDAAVLAHALATHPLPA
DALAAYAARRKPRVEAAQDWAWYLHTQATKTGRWQLALRNFWLTAGPGRLTFARRSSALA
RPLSSSSS

>hypothetical protein Contig22292 (complete)
MFASPHTSPSVLFQTTRVLINLVHNANNRALTTQEGLVQQAVQRLTASATVENIDFCLRL
LNLVGLFAVDCAPEVLAQIATKETAEAFNNLLSLSQSVDHVSTVLQATLKILARKHTQPQ
EVQPFIDALIEKTGPQPSGLEHVVAFYKNSDGPVLELARHVLADLAENNEKATSAINEID
PALLSLGSSPSTTDSADERAS

>pyruvate dehydrogenase E1 alpha Contig15930 (complete)
MRRTCAALRPASRFGAEGRAARVLVISRRGYAEEASAFSGAKAEDLGNGKYRFQVETPYA
AHKCDGPEQVCETTKDELLAMFKQMVRIRRTETEADKLYKQKEIRGFLHLYNGQEAVLVG
MEAALTLEDHIITAYRDHGHLLTRGGTPKQVLAELMGRADGCSKGKGGSMHMYSKEGNFY
GGNGIVGAQVPLGAGIAFSQKYLKTGRVSVSMFGDGAANQGQLFEAYNMAALWKLPAIFM
CENNKYGMGTSIERSSASTEYYKRGDYLPGIKIDGMDALAVKQGMLYAADWARNKGPIMV
EAETYRYGGHSMSDPGTSYRTREEINRMRSTRDPIEKIRYKMLDNNIATKEEIKAVEAEV
KAEVDEALKEALQAPFLPIEATYQHVLLGEEALGAVRAVELSKSYVHKH

>ATP-dependent metalloprotease FtsH (Yme1) Contig65 (and 1863, 1932)  (largely complete)
MSATPSATPNLTSLLKLRSTGGRIGGQYWNVHRKLPLSLYRTITSSSQRSGSPLFSSPHA
RLPLAAETPHSVERFPALNGRRTFFSGAGSKRLEGLERQVESGRASGTIWASYFRELNKM
DSPKEVIRQFERLEESAKTQEVVKEYLKALVLTGRLEGANLGHLLSRGASGGAGGNAGRL
TLVADSPIPITVTGGSLTGSAGGSTFSKIANVTGFMVSLAILYYLFTAMFKGGDSIMGVN
TKVKFAQKSNITFEDVLGVDEAKSELQEVVQYLKDPQKYTKLGAKLPKGILLVGPPGTGK
TLLAKAIAGEAGVPFLYCSGSEFDEVFVGVGPRRVRKLFEEAKKNAPAIIFIDELDSVGG
SRNRDHHQVYTHTINQLLTEMDGFQENQGVIVLAATNFPDVLDPALTRPGRFDKQVEVPR
PDVRGRKMILEHYLKKIVVAPDVNVDMIARGTPGFTGAELANLVNIAATKAATKGMEAVT
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TACMDEARDDVMMGVQRKSMIMSDDEKKLTAYHEGGHALVAIYTEGAKPLHKATILPRGR
ALGVTHFLPESDQLSLSRMQIMADVAVAMGGRAAEEVIFGPKMITTGASSDFKHATRLAN
AMVAQMGMSDKVGPIYRDERDLERASSETRQKIESEVEALLQGQYAVAKRILTDHQDELH
RLAQALLEHETLNKEEIMAVIKGKKLTNLFYQ

>aldehyde dehydrogenase Contig5888 (and 8877) (complete)
MKTTLASLRARSLPTGALSVRHFSASAASASRKLVMVNPATEQQETFAHEADTRESIQSK
FNAALQAQKEWGRPENLEKRVATLKKFLELINDDANVQEGARRLTQDMGKPISHAAGEVK
ATRARVQFFLDNIHSVLQHEVVNQKDALVEKISREPLGVIANIAPWNYPWFVSCNVYAPA
LLTGNAILYKPSEFALRTGEFQMELLHKAGVPKEVIAPVYGAGDVGAELLRLPVNGVFFT
GSVATGRKINEAVASRMIKVGLELGGKDATYVCEDANVKNAAASLADGAMFNAGQSCCSV
ERIYVQKEVYDEFVEEYVKTVKSFKVGDPMDSATYLGPLTRGSQLSFLEEQVKDAVAKGG
KLLLGGKRASVAKGYFFEPTVIVDANHSMSLMKDESFGPIIGIQKVSSEKEAIELVNDSD
LGLTGGVYTKDAERAKRVLGQYNTGTAYWNCCDRVAPALPWSGRNFSGLGATLGVEGIRT
FTIPKAWHLVSPQ

>D-lactate dehydrogenase Contig25235 (complete)
MRRFGSIGRSQRWAASSAGSTRLLPARGRSRTTATFSSSSSFTGSARRLWFLVPATMSAA
ALAATAYGFGLPDVQALDQAKASEAHHEQEQSKLPQGFIDELSAHLNTAGETRFVIERAE
RENHSKDASYHAQGMPDAVAFPKTPEEVQHIVTICAKYKVPIIPYGSGTSLEGHTLADHG
GVALDFTRYMNKVLKVHVEDMDVVVQPGLKREELNDYLKQYNLFFPLDPGPSASLGGMVG
TSCSGTHAVRYGTMKENILSLKVVLPNGKMVKTGQRSKKSSAGYDLTHLFVGSEGTLGVT
TEITLRLRRLPEKTAVAVCQFPTVHDAANTVIQAMQEGVQIGRVELIDELMIKAVNLSAG
LNEQEKPTLYFEFSGSPVEVDEQEKAMRRLSGANNGGVFTFAEGEKSEELWSARKNALWH
SLALRPGADMLITDVAVPISRLAECIDQTKEDLAGSYLLAPLVGHVGDGNFHLMILFDAK
NPKEVEEANRLNNRLVQRAITMEGTCTGEHGVGSGKKKWLAVEKGPEAVELMRTIKRSID
PENILNPGKIV

>mitochondrial DDX5 DEAD-box RNA helicase Contig12173 (and 20032 .. extreme N-terminus
inferred from genomic) (incomplete)
MFARNGAPARLPGASLRSLLPSSSSSTSSLQIAHLHRRLVSGYSPASSTSSTYRGDDSGS
AASGSFFDRIKNSRFEDLVGSLAKPKWEAKAGKLAHFKKDFYVEHPDVASMPEAEVARIL
EEAQIKVVDIKPGATPPPRPIVEFSQAGLPRAMVDRLSRNGITRPSSIQTQAIPIALSGR
DMVGRAQTGSGKTLAFALPACVHIGAQPPLRSGDGPVGLVLAPTRELALQIQAEVARYAL
LPDGSPLRSACVYGGASKVPQIKDLRRGVHMLIATPGRLLDLLQMGVTNLERVTYLVMDE
ADRMLDMGFEQQIRAIVDQIRPDRQTLMWSATWPKEVESLAQDYLNTPTTVTVGSTELSA
NPDITQIIDYCRPVEKKPKLLALMDELHKAGHKTLIFVNTKVSAELLSDELRAKGMKAAA
IHGDKTQVMRENVLYQFKRGHVDFLIATDVAARGLDVKNIECVVNFDFPGNLEDYVHRIG
RTGRAGAKGTAYSFLTNSHDKMIPKLVKILKQAKQEIDPTLLEMAARASSGQSFHETPSF
GQRRAPPGGNTRRYRSSDASSTRDSFRRSDFGRGGERKLKYAINSRGWSADHQ

>NADH dehydrogenase 51 kDa subunit Contig6370 (complete)
MLRRVAVRSGLAPVTENVAAPAAMALASRRDYTTERSYGNLKDSDRIFTNLYGEHDIFIK
GALARGDWYKTKELLRKGEDWIIKEIKNSGLRGRGGAGFPSGLKWSFMPKVSDGRPSYLV
INADEGEPGTCKDREIMRHDPHKLVEGCLLAGFSMKAKAAYIYVRGEFVYEINNLQRAID
EAYEAGFLGKNACGSGFDFDVYVHRGAGAYICGEETSLIESIEGKPGKPRLKPPFPANVG
VFGCPTTVTNVETVAVAPTILRRGAEWFASFGRPKNSGTKLFCISGHVNNPITVEEEMSI
PLKELIERHAGGVRGGWDNLKAIIPGGSSVPLLPKSICDNVLMDFDALRDVTSGLGTAAV
IVMDKSTDVIAAIARLSKFYRNESCGQCTPCREGSPWLWNVMERMVTGDAKIDEIDMLYE
LSTQIEGHTICALGDAAAWPVQGVIRHFRGEMEQRIHDYNSKHGQAIGSATVDEYASRQL
HLAKQAPLTFVQ

>mitochondrial substrate carrier Contig13899 (complete)
MAAAPQQEKEKAKVDVPPKGALMGAGSGLREGLFGFGCGVLYGMTSPLIGHPFDTVKTKM
QAQEGYRTGGMMRTFATVIKNEGFFALYKGLLPPLIGSGIFRSVQFGVYNSSWAMLRDWS
FGRKEIPGTGGLEVRVVAAGVVASTARTVIETPLELIKVRRQMGQTWKFNELYRGFNVTW
IRTCGLMCTFFILVDSGVRHLPNLINAPYVGPFLKGGLCSTISWWIIWPFETLKSQVQGN
TPGPKGIFSRLAFVAQTGGLAGLFRGIVPGSTRSLLANGCSMIVFTQCQSLRHHFIGDEQ
PPEGESLPHAPLDADGNAIIEPAISPPASSTEK
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>rotenone-insensitive NADH dehydrogenase Contig7058 (complete)
MRSRVTTSTARTSTSTLLAVAYRPAAHTATALPLSGPRFVRALATTTTVDGGKQRKKLVV
LGNGWAGYRLILDVDISKYELSVISPRNYFLFTPLLTSTTVGTLEFRGVIEPVRTARPGL
NYIQAGATSVDTTNKVVTFESVYEERETDEEVPVHPAASIKYDELVIAVGAAPNTFGVPG
VEKYCYFLKSVADARNIRQRIIECFERASSPTTTEAERSRLLHFVIVGGGPTSVEFSAEL
HDFLRKDVHKIYPDLEKQVQITLIEAGKTLLSTFDQRLSDYTMRTFRKRNIDVRTSVSVK
QVKRHEMVLSDGAVIPFGLGVWSTGLSTRKIPFIKGLPFPKDRSGRLLVDEYLHVKAPDV
EGVYAVGDCAAFETNPLPATAQGAEQEGKYLAQALNAKARGEEPKKFQYHHKGMLAYVGG
YRALIDSPLIKRSGFLTWIMWNAAYITKLVSIKNKMMIPMYWFKSFVFGRDIYPNY

>NADH dehydrogenase PGIV subunit Contig13270 (complete)
MASTRKEGEQLYADINAGGRTHLDVETTDFNVLVAGAKYTSYMCAAEELDFLECKAKDEN
PRACVPENVALTECAHAALDKISRQCASEFDEVVDCLESPSVHGELSACRQSERDLRVCV
QARFGVDVVVEERKRRMASLQTWASTRRRPQPTIIRPREQKKVDAAVAKYKKEHDITE

>glycine cleavage T protein Contig11793 (and 11666) (complete)
MAMASMRRGGVRAAQNSMTTTRRAFLATDAAPLKRTALHADHVALGGRMVPFCGWDMPVQ
YKESIIDTHTHTRTHAGLFDVSHMGQLKLHGRDRVEFMESLVVGDIKGLATDNARLSLFT
NEQGGIKDDTVITNGADWLYVVVNAGCADKDLAHIQEHLARFKASGKEVDLEILSPDYSL
VALQGPEAAAVVGEHIAGGPESLRGLAFMSGRDTRFDSLPVRITRCGYTGEDGFEISVPT
SDAVTLWRTLLQHTGKVMPVGLAARDSLRLEAGLCLYGNDITEETTPIEAGLAWTIGKRR
RAEGGFPGADVILKQIKEGVTRKRVGFVLAEGIARAHATVHDEKGELLGEATSGGYGPSL
KKAVGMTYLPTALAKNGTPIQVQVRKKFYPATVAAMPFHPTNYYKPTQ

>acyl-coa dehydrogenase Contig4616 (and 20682) (complete)
MRRIGSSLISQRLVTAAITSTRASARAATLRSTHSEASRPAVTTLSEDEEMLRSSVEQFA
RERIGPKVRSMDEKSELEPALVKECFEQGLMGIEIPQQYGGGGMSFMSAILAIEEVAKVD
GSVSVFMDVQNTLVNNAVIRWGTEKQKEQWLPRLAQDTVGSFCLSEWSCGSDAFALKATA
KKDGDGYLLNGTKAWITNSKEAGLFLVMATVDPSAGHRGITTFLIDKNTPGISIGKKEDK
LGIRASSTCEVVLENCRVPASQVLGEVGKGYKIAIETLNEGRIGIGAQMLGVAEGCFDHT
MKYINERKAFNSSIADFQGVQFQYASMYSDILAAKLMVYNAARLKEAGQPFVIDAAIAKL
RASEVAEKVASLCINLMGGVGFTKEFPVEKYFRDCKIGQIYEGTSNIQLQTIAKYIQQQY
K

>acyl-coa oxidase Contig4602 (and 13717) (likely complete)
MRRSRFARCAAALDLPDVSNGPAVMASERSQASFNVRELTHLLDGGERGTQRKHAAYELV
RNEPVFIDPGYYDRSRDEARYRVMQKLKRFAELVQKDPEQNYLLHNIIGIYDPAFYTRYG
VHAYLFGGAIAGQGTDEMVAKYMDDVDNMRIVGVFGMTEMGHGSAIRDFETTATYNKAKD
VIVINTPTITATKWWIGGAAHIATHTVVFGRLLVDGKDYGVHSYVVQVRDINGNLMPGVV
IGDCGKKMGRDGIDNGWMQFNNVEVPRTNMLMKWAKLSPEGVYTKPPKAQLAYGALLKGR
VGLIMNSAHNLEKALIIAIRYSVIRRQFASTSKGLETQILDYQTHQIRLLEPLAAAFAWH
FVALRVDKDIRHLSKSLAQGELGNIADIHAALAGVKASCTWYVAEALEQVRQCLGGHGYS
SYSGLPSLIADYAVNQTWEGDNTVMSLQTAQYLIKSLSQVMRGKTLTGSVQYLERTVAIL
GQAQWRATTEQDLSDASVLAEALERAAVKSVTRVAERLQREMQGGKSKAEAWDCCLIDLV
QAASHHSYVYVLDAFVQSVEKARNKCKDSNVSAILSKLLELFVLNRINKVSQIFLMDGFM
NEKHIDLIEKKIRGLLLEIRKQAVPLTDAFDLPDFLVNSPLGKSDGDIYNAYMQTVKSAP
GAMSKAPYWDELVKPCLRKDLA

>methylmalonyl-coa mutase Contig26933 (complete)
MLSLRRSARASTLVRTPAPLLALRSTGAPSTARHFSMSSRVLASTAENEAEWKKRATKEL
KGSPKHEGKDPLESLSFETPEGIRMKPLYTPTDVAGLDLTTNPYPGLFPYTRGPYATMYT
NRAWTVRQYAGFSTAEESNKFYKQNLAAGQTGLSVAFDLATHRGYDSNHPRVKGDVGMAG
VAIDTVEDMKVLFKDIPLDKVSVSMTMNGAVLPVLAMYIVAAEEQGVKQALLSGTIQNDI
LKEFMVRNTFIYPPKPSMRVVGEIMAYTSKNMPKYNSISISGYHIQEAGADASLELAYTI
ADGLEYVRTGMAQGLSVDNLAPRFSFFFGIGMNFYMEIAKLRAARKVWSQLIKEKFSPKD
ERSLLVRTHCQTSGWSLTEQDPYNNIIRTTVEAMAAVLGGTQSLHTNAYDEAVGLPTVTS
ARVARNTQLILRDESGIPKVIDPWGGSYMMEKLTDDLANTALDIINEVESMGGMSSAVEK
GFPKLRIEQVAAKRQAAIDSGEQVIVGVNKFRLAKEEKMDVRQIDNTIVREAQIKQLEQI
FAGRDKAKAEQCLANLTKAAAGELSGNLLELAVEAARARCSVGEISDALEKVFGRFQLND
SLVSGVYAASHPQQDLIHRIQGLSEQFLKDEGRRPRILVAKMGQDGHDRGAKVIATGFAD
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LGWDVDVGPLFQTPAEVARQAIDADVHAVGISSQAAGHKTLVPDLVAELKKQGAEDVVVV
VGGVIPPDDYDFLYKSGVSCIFGPGTRIPDAAEQVISSIKKKHLKSAVTAQ

>mitochondrial ribosomal protein S15 Contig10103 (complete)
MKSGRTMKGARLVLLPQLRQPLSLVRGYSATSASDGGSKATNRFAAQFNALGRTTPSSDD
KSSSKPEKSVDPATEKQAMENIFSSISLARSTPASSAIKTSREPRFIPKTLEVTKRRLWL
TDLKHFKLYPKTIKEWVIDCKTPCGVWWKDGTWRASVSLENEEKDETSAETAAQAREREI
LLGAKVLPADLRDRYRFGVMEEDIAALNLQGPQANKLKEILSFKYAGRAEINQFRIAESL
KKWSRKPNDTGSSEVQIAVLTEKIRYMTDHLKGHHKDQRTKRALGITIDKRRALLKHLKK
QNVSTYYHLLRDLNLRDMVSI

>stomatin-like protein 2 Contig26002 (complete)
MRRACAQPSHYGALARCATGAIRSTSASSTLATRLRPLETRSLRLYAVGRYSRQRLPTNL
GVLFVPQQEGWVVQRFGKYKEVLEPGLRFLIPFVDRVAYRHSLKMVTLEIPNQVGITKDN
VNIEIDGILYYRIVDPYKASYNIDDPEFAIQQLAMSTMRVEVGKLDLEKIFEEREIMNRA
IVNEINKSVDSWGLHCDRYEIRDIKPPVKAMRAMELQMIAERRRRQKVIRSEAERTAVVN
RGEGQRTATILAAEAKKLEKQLYAEGEANAIRARAEATAEGLERVAKALHQSKASDAVSL
VIAEQYVKAFGELAQKGNTLLLPTNAGDVSSMVAQALTIYQNISAAQQKRSGSSTSTNAA
GSETGAQTEDNTPPSSDSSSFDLPFTPKQ

>hypothetical protein Contig27269 (complete)
MADERRQALTRIIGERLSNCFGLGNAADQCVAVKGENDEECLQLESLRLHCFAELLCPQQ
AQRAVTCLQTRRNPSLCQDDIKALRACTGPAFDHFVDRYPQHSLVDRTEKACAGPSDKLT
SCIEANKGDASKCQVELKEVDLCVGSVICPAEGRTLGECLRNGTEDSCASQRQAFSACVA
EGRLKFWEELGIPVNEFAAKQ

>hypothetical protein Contig25938 (and 23690) (complete)
MDTRAVAVPTSVVVSTQASSSSSSSSSWWPLSTKGWLIVGGAVVSGLVLYLLRRRTRAAN
AWQSPPGEYDDILKSLRSSEPQQTVALKQLYEYSRYPKKHDSIRQTGVLEILLQILAQHP
DNDVLLLHLTRVVANLAINEENRLV

>hypothetical protein Contig6706 (complete)
MLMRRSFRQASPRPSALLSSVAAGREGSARLALAATSSQQLWSTRALATMPISATLREAQ
KKLDGNGLAGIERLTAEEAYEVLQSRFAEYGTIRAGFVTHLFRKADALMGVHWKAQNFEG
LRSLVEQTSDTTRSLDGALYASLAHLQANNVSAAADLVRQAVTATPATTEQFEKWANTLA
EEATSANLAQPAAGLLRALTGVAPADAALEELAAQLDAEAASAAAAAAAPETTEQAADSE
PAAAEADGAEKKEEAQA

>mitochondrial phosphate transporter Contig1954 (complete)
MSQQQTAIPAPVVAHHAPVFDLMYYVKAAVAGGLCCSVTHGAVCPIDVVKTRMQLDPQKY
NKGMISAFRQVVSTEGAGALATGLGATAAGYFVQGWFKFGGVEFFKVNIAHAVGERAAWE
NRTGIYLASSAMAEFIADLFLCPLEAIRIRSVSDSTFPKGLGAGAARMFSTDGLLGFYAG
LGPILFKQIPYTMAKFAVQGKAAELIYKSANTSPDKATKGTNLSISLLSGVIAGVVAAIV
SHPADTLLSKINKKGAGGSGSTTSRLFTIAREMGFAKLCLTGLPARCIMIGTLTAGQFGI
FDSVMAAIGAQKFHFHNPDEKH

>mitochondrial ribosomal protein L46 Contig5841 (complete)
MRKAWSGVRQQLAVPPCAVVGPSTTGMSRQFVRGITHSQHERAYLQRLRQMEAEAAAGKT
WRLVGGIAVQRLPLIIPTPDPIEDQYEQFRFDRDNYFSINVERNLELMEEDRRKGSKISK
TQKKKKEKKEGVSDAGPAGGKQKGGEQDEADSLYQKAEETAYREETLEDVRAKMERLSPR
ITAADLANDRKSLNRALASRLYLIVQKPRTEHAWQFPQGGRESGETMRQCCERELREEIG
TKVKVHFWSNAPAGCYSYPYPDNYSHNDGHHGSKVFFYHAEYVSGEPHPDNKEVVDFAWV
TRDELQEYFDPQLFKFVRDMLPA

>glutaryl-coa dehydrogenase Contig2223 (complete)
MRRATSVVAPVARRGISARINAIGARTFATGTEKVTFDWADPLNFEAQLTEEERAIRNQV
ADYCQEKLLPRVTLANRNEKFDREIFNEMGELGMLGATIDGYGCSGVNYVTYGLIAREVE
RVDSGYRSALSVQSSLVMYPIYAYGTEEQKQKYLPDLATGKKVGCFGLTEPNHGSDPGGM
ETRARKDGDSYVLNGSKTWITNSPIADVFIVWAKDDENVIRGFILEKGMPGLEAPKIEGK
FSLRASETGMIMMENVRVPAANLLPGAAGLKGPFGCLNNARYGISWGTLGAAEFCFHAAR
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DYTMQRKQFGKPLAQMQLIQKDLAEMQTEIALALHSCLHLGRMKDAGKATPEMISMMKRN
SCMKSIHIARTAREMLGGNGISDEYHIIRHVMNLEAVNTYEGTNNVHALILGRAITGLQA
FSS

>cytochrome c oxidase subunit IV Contig15163 (complete)
MSRILRRGALSNTSATLNATAFAARRSFAASALRLASLKEPATSLDVESQDDTDARHTGM
ERLEKVPWTKLYEGDAILTGKFGTLEEPTIVHSWFPSRIVGCQGSADHPHDILWHEVRRG
RDTVCLECGQVFRLRPNLFHQLSEVEADLFPPTEAKESAAH

>NADH-cytochrome b5 reductase Contig12918 (likely complete)
MALLLALSDFINLSDPTVIGGLIVGAITIFAVGRFLFASDSAQPAKKADNVVGKGKEVSK
DVPAARPAPVRTGVLDPSKFQKFALKERIELNHNTRLYRFALPNETDVLGLPIGQHMSFR
AVIDGKEVYRPYTPTSSDDDLGHFDLVIKVYPQGKMSQYIDNMKVGELIDVKGPKGLFTY
TPNMKRAFGMLAGGTGITPMLQVIQAILKNPADRTQVSLIFANVAEDDILVRSTLEDLAA
KNPDRFKLHYTLDKPPADWKYSQGFITADMVAEHCPAPADDVMILMCGPTPMVNAQIGNL
QKLGYSENQYFKF

>hypothetical protein Contig1063 (likely complete)
MKSTRGTWGLLRSSRPTPASAAAETLRVPFPRRTYALSTDGRNITSSSSLLRVGSSLRKT
YLRAEDAKELEQRYLKWITPAGKDPWEYNRHLLPSWKGLMGDANVAFSAIKTPERLLTTF
LTHMTYPSELGHNPRINTDPSGIFSHKRLYHWADENIFGLPPVAVVRLSYRNTLRQREIL
VAEVHWWRRILRVIKMEKVYLRDGQDSVDHILGEVSEDDYELRKEAAEYVIPPRWLHEFK
KLRWPEPPSVEELRFPDLDAEEPPPKTLLPYNTEPFPHPQASMLGRPFRADETEAELESL
DTRLDPSDETAADLAVGNIFVKVENEEDATAALPRS

>putative MAM33 domain relative Contig20395 (complete)
MRRFSSSIVASGRIASSSALVRTAVLGQGRLAATYATKKRNAETELHSYFEKEVELLDQD
EEAKTQDQELQKRLDDWAKRFHFNVNMGATEIVATKKDAALNADVTVKIDPNIEEADNYG
DEEDAEDEEGEEGEDAEEAEKAEGEEGDEEEGDEEEEEPEADGFGSVHFTVEVKKPEQTM
LLYGVVSESAVTVTEVALQAADGTEKSAYDAQRLDDEGQEKFRLYLSSLGVNDSFVPAAY
AAAHLHDEHAYHKWVKDVMAFTKQ

>NADH dehydrogenase gamma carbonic anhydrase subunit Contig17251 (complete)
MMRGLLRRLRPSTPAAVLPTRNGADIPDVPLEKFGLTVPVQATAYNDLYNKHTTLVNLPG
KRPQISSESFVAPSATLVGNVEVWDRASVWYDCVINADTKLIRIGAGTNVQDGTVITEAD
EELTEDHDGSTIVGHWVTIGHRCVLKACTIEDHCLVGMGSVLGAGSYMESHSILGAGSVL
PAWQRIPSGQIWVGNPAKYLRDLTEEEFDFLEKSSAHYTVLSKQHAYEFYLPGHAYIDAE
KKGIQVGYQVEPLSGEESVLLAPNYKEKVSVH

>Glycine cleavage system regulatory protein Contig12744 (complete)
MRRTGRLASSSLRQLGAPRRFLYSTQSEPKQARLVLTAAGPDRVGVTAAITKAVVDAQGD
VDSGRLTSLGGDYCIHMLVSVPETQEQAFRKEAQAAVGKFGDWDLSIRKNTPRAAVGPSL
RQRLVALSGEDKPGIMHAVSSFFADKGINILSMNVYNEPAPFASSRLFKLQALVQVPQGM
SDDQLEEGIDAVGENEGVDMWLESSQQPSTPPAALHEAAPQSHRA

>hypothetical protein Contig9150 (likely incomplete - uncertain of N-terminus)
MLPGSMLPFAFDAGGVDLGATLQAVRGPWALGMDCQVRTMWLDLTGGRCFLNSVVAYQKP
TFALTMNMHGFGERFIASAVANPVGLYRALCKTNTAKDEDLYNCTWLAGVEADTAQRNGV
FSTRCLSFALTRRNTSPYPFSAPHTTKTTEAEVFKVDEPLLRDGENKIKFDILNLGVGNN
AYRLSVHSSSLVRLYRNTHVKLSSSLQADVLPFDPNTARIGLSLVFVV

>Hsp90 ContigE80POFO01D2V4R (and 16204, 12961, E9BS9UA01DIVA4, 9423) (likely complete)
MRSAAVKNSSRPHRAVLRAPAPAHHVPARPLAEVAGTHNKVVVVGRRSRSCVPSALQVNH
TAGAKRAYRSTAIGMRAAGAREPEEAELVRTAEAAATPESARAGGAVSEAEEGKETLIEE
TETVSGQAETLPFQSETAKLLRIVAHSLYTDKEVFVRELISNASDASEKLRHLDVTGKEY
DDKYLPLEIHIATDDKNKTITIQDFGIGMKKEELIKNLGTIAHSGTQEYLRQLEGKDASN
IIGQFGVGFYSAFMVGNRVKVYSRSAAPGSKGYCWTSDGTGAYTIAEAEGVSRGTKIIIQ
LLEGQEHFAKKQTIDSIIKKYSNFVGFPIKLNGERVNTVRPLWTLPKQSISEEDHKQFYQ
FLAHSYDLPIYRLHFTSDAPFSIQSLFYVPEQHQEKYGMGRMDPGVSLFSRKVLVKPKMK
ALVPDWLRFMKGVVDCEDVSLHLSREHFQDSDLIKRLGNVVTGRLLKLFQDEAASDPDKY
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NAKFWKEYGSFIKEGICTDAKWKDELGGLLRCESSATGEGDVTSLEAYAKRMQDQQTAIY
YLCVPSRTFAESSPYYEAFKQRGVEVLFLYTSMDDFVMQNLAEYAGKRILSIESAQLPAE
LARPASTTTGNNNNNDASSSPQAHAGELSLDPQEVEELAKWMKTTLLDRVSSVKETKRLV
SSPAIIVDHESASFRRMMKFVDPSRAPKLPKQRLEINAAHPIITRLNSLRRREPSFAKAV
AEQVFDNALIAAGLMDDPRSMLARLNSILEAAARNSDTTSTTSTSTA

>putative mitochondrial ornithine carrier Contig16912 (complete)
MSAASAQPGLPYYPMPRGGGVGAGGGPIPSGPAGYPQPGVPVATGTPAVEEPQFLSLSSI
VTRLVLKVGEYSLVNVPSRTLYERQIAAAASAARMGGPGRTLDEQVQAKDENVVNTLLNY
YKEEGAVRIIGATSLAFTNDLFYGVIASISYVFCRMVPVLLGMTSGEDVDWQTSAVTYPL
FLASYQVRHHAWTGFSGLLPSGENFYGKLRDNVVAHLAEMVTLHTIRPAIVDTLYVLFGE
WLLAKADGETLADQAAYHVGIRGVHFMGSLFVGLIHLPVSTIVTKLRAHPDAYDSLWDCI
KKTWKTQGLKGFYGSAFWYLLANNQLIMP

>mitochondrial ribosomal protein L15 Contig26943 (complete)
MRRFSTPFSCSGGVMNLRSTFNLAAASPLRPSSSAWAAALASCNSTSMARAYATRARKGV
RSSSPTSYLGGGLPYLTRKLELEAQRELEPFDPFSIALNKIADNPGAHKKARKVGRGTGS
SKGKQCGRGTKGQKARGRGKVSPGFEGGQTPLYKRVRKHGFTNAMFRSEFVGINLGQLQQ
WIDAGRLSPEGKITMATLQQSGLSSKLTKSYEKGIKLLAGGSEFFAAKLDLEVSKVSQAA
REAIEKNGGSVQEVYYHPRQLRMALRHPENPLPPPQEYRTRP

>Short-chain dehydrogenase/reductase Contig16221 (and 18706) (complete)
MEIDKLFGVKGKVVLVTGGGRGIGFMISQGFVRNGATVYIASRSKKECDKAAEELTAAGP
GKCVALSSANISTAEGRKKVVEELSSLEDHLDILVNNSGCTWGMPIEDFTESAWDKVMDL
NVKALFFLTRDLLPLLQKKATAVDPARVINLGSIDGIRIPTLETYPYSASKAAVHQLTRV
LANRLASMNITVNAVAAGPFESKMMAETLRTFGELLKANVPRGRIGEPEDIAGACIFLGS
RAGAFLTGAVIPLEGGILSAARL

>pyrroline-5-carboxylate synthetase Contig8676 (and 19737) (incomplete - internal gap)
MSARREFQSKKRILIKAGTGVITDESGGVSLGRFGHLVEQVAELKKRGKEVIIVSSGAVA
MMRSEGRSNFRETVDELIRLGAVPILNENDVISSRKTPYTDSEKRIFWDNDSLAALVAGE
TNADLVILLSDVEGLYKEPPSASGKKGELIDTYQHDAKFTIGAGSRTGRGGMQAKIEAAR
YALSRGAFAVVIASGYTLNVITNIVAGARIGTLFVEHPERELATARQMASCSRKAAQALL
ALGPQRRQALLGAIATNLTAAKAQILEANQRDIANARENNLRPALAARLVLDDKKLHTLA
SGVRQIAAGEDPIGKVLKRRELADGLVLEEVRVPIGVLLVIFEARPDVLPQVAALAIRSG
NGLILKGGKEALHTNTVLHGIITRTVEQFGVDPQLVGLVQTYEQIDELLQLKEIDLVIPR
GSAELVSHIQHNTRIPVLGHSEGLCHVYVDQAADLDKATRIAVDSKTDYPAACNAAETLL
LHRDLLADRRAHAVLDALARANVKLYAAPHAATHFPDLPRAQSLRTEYSDLGMTVEVVDS
LEAAIAHVNEYGSGHTDAIITEDKEAAQKFSQFVNSACVFHNASTRFSDGYRFGLGAEVG
ISTSRIHARGPVGIEGLLSSKWVLVSQTGGSVASDFSAGKRTFTHRDIYPPFAPQPASVF
ADFQPKL

>cyclophilin Contig10776 (complete)
MWKRLFTTNAAPVTANPRVFFEVTRENKPLGRIVMELYKDKTPKTAENFRALCTGEKGVG
SIGKPLHYKGSIFHRVIPNFMIQGGDFTNFNGTGGESIYGAKFADENFVMKHVEPGTLSM
ANAGRNTNGSQFFITTVPTPWLDGRHVVFGKVVEGMDVVQKIEAARRDSNDRPLEIIKIS
DCGELKQ

>ROK domain kinase Contig17891 (and 20436) (likely complete)
MRRTSWIRSSVSRAVSCQAVGARTTATALRAHSAPLASTNSSCARRALGTAAQSGGQRTG
FAGSSSSFLVGAAAAVGVALGAILYYDEQNQVVYAVQKDGTVKRYFLGVDGGGSKTNVTC
IDEEKKVVGEGTSGCTNFNSVGQEKASQHLREAILSALKAAGVPEDQVAGICLSMSGVDR
PADKQLMRSWITPILPKARIDVHNDAVAALVSGTDGNLFGLVVISGTGTITYGVNKEGET
TRAAGWGPMLGDRGSGYQIGYEILTAVVRALDGRGPATSLVEAVLTKLNLSKGEELIPWA
YSSVAWERYAQLAPLAAIAARNGDKVAEQILEGQAQDLVVSIQAVAKRLHIENQPFPLVL
AGGNFTHEGSYLTALLKKKVNQQLPQVTVLLPTLKPEYAAALLARNNATAKH

>long chain fatty acyl CoA synthetase Contig16463 (likely complete)
MRAIRGAVAYFYWCFRQFLSPEARDRRSAATSSATAQTRTGPVLKWPQKRKMESLHDVWD
EYGTAITATGLAVVGAAAAYHLLGSAKPAPTGPQSVMMPPEKKGESHVYRSIHSPDTLVE
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TFVPETTTLYENFKRGFTLNPEGNCLGWRQGDGPYQWLSYRQVQDRFLALGAGLLELGFK
PKDTVGIYSRNRPEWVITEQAANAFSMVVVPLYDTLGEEAVEHILRETSLKLVFCTNEKV
QQLIRVLDKSDITHIVTFDSFDDEEAKSVLQERNISLHTIDELIELGKKNPAKPIPPSRD
DLCTICYTSGTTGTPKGAMLSHGNFIANVAGVFVLKPDLVTSSDVVISYLPLAHVFERIL
QAAVFLQGASIGFYRGTVPELFDDIATLRPTVFPSVPRLFNRLYDKVMAQRATLTGVKKM
LFERAWAAKVQLLKEGKVSSPLWDRLVFSKIAAKLGARVRLIISGSAPISADVKDFLRIC
FSAELLEGYGQTECCAAACATMPGDTTSGHVGAPLPNSELKLVDVPDMKYFATDKPNPRG
EICFRGPAVFSGYYQNPEKTAEVLEDDGWLHSGDIGEMQPNGTLKIIDRKKDIFKLSQGE
YIAPDKLESAYVKSPFVAQIFIYGSSLKASLVAVVVPDPEILLPWAKEKAIDGDLAELCR
KDQVKKEIMASLKKAGEAAHLKGFERLADIHLEPEAFSSDNGLVTPTFKLKRPQLHEHYK
EQIDAMLAKLD

>Methylcrotonoyl-CoA carboxylase subunit alpha Contig7170 (and 21123) (likely complete)
MLRRAARCSTSASHVEVLPKMGVRAFHRSLAPRQAEKLFDKVLVANRGEI
ACRVMRTCKRLGIKTVAVYSEPDAQATHVRMADEAICVGPAASAQSYLRV
DRILEAVKSTGAQAVHPAGYGFLSENSRFANLVEQSGLVFIGPPASAINS
MGSKSESKKIMSNAAVPIIPGYHGEKQDVDYLMAEAEKIQYPVLIKAVMG
GGGKGMRIVETKEDFVEALLSAKREAMSSFGDENVLVEKYITKPRHIEFQ
VFADKYGNVVHLFERDCSVQRRHQKIIEEAPAPGMTEELRARMGEAAVNA
AKAVGYVGAGTVEFIMDSTTKGFYFMEMNTRLQVEHPISEMITGQDLVEW
QLKVASGQHLPLTQDQLKINGHAFEARIYAENPRKGFLPGTGKLVHLSTP
EPSSQVRIETGVRQGDQVSIFYDPMIAKLVVWDTDRTSALRRLNASLGHY
QVVGLNTNIEFLGKLATHPSFIEGDVETGFIEHHRNELFPAISAPSEKVL
ALAALSVLSEERAANLKEAERNSADAHGAWSLPGWRLNEEQTRELRFVAQ
VGEEESAEFAVLATYRPDNTVSMKCKKVVAQEKGKKAHHHEEDSAEFTVT
GQVGPTGEIKASVGDETITDGRVVRHKNTLNVFLKGVHHEVNLALPKFLS
AGTEGRKGGLTSPMPGKIVKLFVQPGEEVKKGQPLIVMEAMKMEHTIRSP
ADGKVKSVGVSVDQFVEQNVALVQVE


>carnitine o-acyltransferase Contig20641 (and 23311) (likely complete)
MEDKYRREVVPQGSRNVQPYPWLEVTTLPRLPIPTIEETARRYDEYLQPLLAEASPADLA
RTRRFVADFVKHDAAGLQADLHNLARVSPTSWLEGWWDTGYLEFRVPSFINVNPFFVFKA
DPANPAQTARAAQIVGSAVRFYKKVATKGGLTPDLERKTPLCMTQYGRVFATARIPLPGR
DAVYSWTGVRHIVVLRKRQFFTLDVLTSAGEAVAESHIHAQLDAVVREADRPGTHQSFPI
GALTAEDRDAWSAARAELVRAHPINVASLEVVDRALFVLVLEDEAPADLDATARLFLHGD
VRNRWFDKLQFLVCANGVAGVNMEHSPIDGHTILRLLTEIHNEVLARNGTILTEGPTAPA
PRRLEWIVPASSPVADALEAAKVHAGELIAKTDTSVLIFKDFGQKRIVERKVSPDGFVQM
AYQLAYYKLYKKTASTYESVQMKQYYHGRTECLRSVTNESVHFTKTFTCPKADNAKKEAA
LRQAIEAHGRRAKECKEGRGVDRHWLGLKSIARHKEQWYPGFVMPEMFSDPSYSKLFGSV
LSTSNCGTRALDLFGFGPVMDDGFGLGYMIHPEAIHICVSNFHGQAAAFAAALRESLVQM
LAILSTSTPAQARL

>hypoxia-induced family protein Contig27074 (complete)
MSKKHDDLPDQGGSLDYRGNYVPFYPNPEENLNLWERVMRYPWVALGAFSTAGILGAGLW
TLKTGNSALGQKLMRARVAAQFTTVVLLLGASGVITLNSLNSDKPKPKAVAAPISSSSSS
TSETH

>mitochondrial elongation factor G Contig26230 (and 27675,1208) (mostly complete)
MYSASRRASSNPSASGFMRHSAGLMRPSTSSASTLCLNRAPSAMINLPLLSRFSTDAEGS
APQKELHKIRNIGISAHIDSGKTTLTERILYYTGRIQKIHEVVKGRDNVGAKMDSMELER
EKGITIKSAATYARWGENHINIIDTPGHVDFTIEVERSLRVLDGAILVMCGVSGVQSQTI
TVDRQMKRYDVPRITFINKLDRMGADPFKALRQMKEKLTHVKSAALQIPVGLEDHFQGVV
DVITREAYVYEGGSGEVLSKVAVPENVRAEMEARREELLETLYEVDDVLAEVVIAEGREP
SVEEIKAAIRRATIALKFTPVLMGSAYKNKGVQNLLDAVVDYLPNPTEVPSVGYDLDNNE
APVNLVPEHDKPFVGLAFKLEENPFGQLTYMRMYQGVLKKGDTIVNMSTTKRTKVPRIIR
MHSDEMEDIQEVGAGEICALFGIEWLLRHHLHRRQHPPLHVLHVRPDPVLSLAIWPKAKG
QDKNLSKALNRFQREDPTFRVHTDPESNQIIISGMGELHLEIYMERMRREYNVDLDSSPP
RVAYRETLTGKGAFDFTHKKQTGGQGQYARVAGYVEAIEEEDLEEHEQKALASGKRVLFQ
NQTIGGSIPPNFIPACEKGFFEAATEGPLIGHPIQGVRVTLTDGGWHPVDSSELAFKIAC
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INAFKQGMLKANPQVLEPVMGVEITVPKEFQSTVVSSIGKRKGVILNSENMTGTDYTRVD
AEVPLSNMVGYSTDLRSTTQGKGEFSMEFKKYAIVPRDSMEKLIAKYKEDKAKEKKD

>Tom40 Contig13048 (complete)
MDKLPTPPAAAPSALPSVPVMPPLPPLAGAGSPSEPIAPAETHKEAPPSFWRRVLDHGPL
PYPGKFDDLSKESKGILDSRENFDGFNFDVSRTITANFDMTHAIHFGSQTEPPSYNFMTR
YFSPTGMFLDGKLSPGPMLLNGTVQGRIAFPLKTWYRTTPGGRSKPVSKLSLRLTGVVGK
PSAKPIPPQFNMELDMKGSDYQAQFKWHNPGMYELSYAQSVHPNVALGLHGLFDSRMGRT
ELTAAGRVAWNGRKCIATASMASYGHLTSSYTQVMEDGRKSWSTDMQLIHLEDHGVWEAV
YSAGYAYNLLQSRVRGRVDSNWCCSAILEEKVLDTVTLLICGDMNYAKDVYKVGFGFSFH
L

>possible mitochondrial glycoprotein MAM33 Contig11585 (complete)
MLLNRTSNAAKNRNNFSKMMISMGQRYPTLRGARHLHHQESSLDHHLAISASRSSSSTAA
AAPHLVHSTRLRTLATTVFIRGIATRSGKDSMAQMKAEADPLPLGEFKKEVTKLIDQEVK
ESSSALDPAAEYLAELNYKLFVSDGVATLKRTQGKQVVELSFAVEEEDEEGENEEGEEKE
EEESEEEDEEETAEGFQAQDINPLMGVQDLYIPTEVKITIVDKMDKEVSSMSLACSAFES
RFFIDTLYSADGKNSVHFEQLSDGLQEKIYDYLESLKLDHRLGTFIFEYTRNYHAHKSAQ
VLSDLKQFVSHLRDE

>conserved hypothetical protein Contig25108 (complete)
MRRSSGRLLSGAQTRLGGAVVSAPRQATTAAHVGWRRLASGPAQPLVPPFTEQTARAKVQ
AAENLWNTKDPSKVALAYTEDSVWRNRDRFLQGRAAIRAFLEEKWAKEHDYRLRKELFCF
AGDRIAVEFNYEYRDDNGRWWRAYGLEHWTFDERGLMHTRQASINDVPIEEKDRIVQ

>hypothetical protein Contig8784 (complete)
MRRAATSAWRRQANPPHGGSGGGGGRMVRYAVGLPIAFKLGLDLGNLVSPLQSHYLEDEK
EKKTDVWNAVGSDLVEQVKTSTPLQAQLGSEPASRVQVSDVLSLSKSHLKWQFFTHCSPD
DSKEESLWDMVTNNRVVMATEELQLQVPLKTRSKGASDLSLVVDTHNDGRGWKVDNAWVE
TQGEGAVCVPLTPPRHA

>ClpB ATP-dependent protease Contig3786 (and 8341) (likely complete)
MRRAALGGTRSGSALSGLLSRRAPQQAGAVRRVLSSEPAASSRSSAMRTSAASRWPAALG
TSTVLLHPPALVFPLCRGYANGYTRGGQPIPPPYVNPDAAVPGDALKKYGKDITALAKEG
KLDEVIGRDEEIRRTMQVLSRRTKNNPVLIGEPGVGKTAIVEGLATRIIHGDVPDSLKGK
KVIGLDMGTLVAGAKFRGEFEERLKSVLKDVHDLKGEVILFIDEMHTLVGAGASEGSMDA
SNMLKPALARGELHCVGATTLNEYRKYIEKDPALARRSSRSLCREPTVQDTISILRGLKE
RYEVHHGVRITDGAIVCAAVYSHRYITDRFLPDKAIDLVDEAASRLRLQQESKPEQIEDL
DRQIITLKIELEALRKETDPASAERRQKVESEIARVEGKSQELTRAWQEERDKLHKIKNL
KEQLKRAKLDLQRAERNGDLARAGELAYGIIPTLERQLPKDQGAETTMLGEAVTDNDIAL
VVSRATGIPVHNLLMGEREKLLHMEQVLASRVKGQNDAVGAVSNAVRISRAGLHSHSRPL
GSFLFLGPTGVGKTELCKQLASFLFDSENAMVRIDMSEYMERFSVSRLIGAPPGYVGYEE
GGTLTEAVRRRPYQIVLFDEFEKAHRAIHNILLQILDEGRLTDSQGRKVDFRNTIIIMTS
NLGAEILADLPPGHSSSEARDAVMGAVRGAFTPELLNRIDEIVLFNRLSHEDMDSIVNIQ
LKDVSNLLADRRIQVELTPEAREWLAERGYDPVYGARPLRRIIQKHILNPLSREMLKGDV
LDGDLIRISRKAVDPEEVLKNTAATDSWSSALEELDLEVVHTEQSTPEVHNAKPLLKAEF
GVEDD

>NADH dehydrogenase subunit 8 Contig2253 (complete)
MYAGRRAVSINRTSPLRGAFILPRASASSTLVATERSVVLATRGVMAGGSYQDEHKRTKL
KGAHAEPETLYEDLPTAHLHKNLTWSGLIEGSAHTFALSEMMRGFMLTLAYMFKPKVTLN
YPFEKGPISPRFRGEHALRRYPSGEERCIACKLCEAICPAQAITIEAEPRADGSRRTTRY
DIDMTKCIYCGFCQEACPVDAIVEGPNFEFSTETHEELLYNKEKLLANGDQWEPELAANL
RADFLYR

>solute carrier 25 family protein Contig17837 (complete)
MRGNVPLLEDGVWANLHYASPWAKTGLYMSSLGAHVVAGTAEVCLTDVALRTLRHAYRGF
LTRQQAASGATRRRGEQLPGTHVDRLRAKLNYATVVSALQVVASFAVHTLLFPLLTVRMR
LEAQGGVDDEPVTALRHLGLVECVRSIWANEGGAGFYRGFGAHVLTFAGNALWIGIIYGL
TEAYINLDVDEDD
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>rotenone-insensitive NAD(P)H dehydrogenase Contig27704 (and 7318) (complete)
MLRSSNKVASTRGMQRACFASRTTISHGSKQLQVPSGGRLYSSTTSTAGSASRQSAFRWP
VVAAITAVGVGGGLYLLQGHVFAAESQPKPKLVILGSGWGALSVVRELDTSKYDVTIVSP
RNYFLFTPLLPSVTVGTLEPKAIIEPIRKYCRRSHADVDYFEAVATDVDPTNKTVSCHVS
TPGLDDSARDFTLPYDKLVVAVGAINNTFGTPGVEENCLFLKEIDDAMAIRNKMLDCLEL
ASLPTTSEEEKKRLLHFVVVGGGPTGVEAAAELRDFVQSNVHKWFPKLEPHVSITLVELM
DHILSTYDAKISTYTTSHFKNTNIDIRTKSRVVAVKPGDVIIQRTDTKETQHIPYGLCIW
STGIGTSPLINKIREKLPQDIQTNRRALLTDQFLRVKGADGIYALGDCATIAQEAMLGKL
NDLFKEADLNKDNHLQIEEFRSLIDKYKKTYPQIDVYGKKAEEIFQEADVDKTGALSLEQ
FENLVKKIDSKIKQLPATAQVASQEGQYLGKLLNRVANKSVELDTGFHYKHLGSFCFIGS
EHAVAEFAEGLVLEGFGAWWLWRSVYLSKQYSLRNKLYVGVNWLKTWIFGRDITRA

>tetratricopeptide repeat protein Contig16161 (and 27169) (likely complete)
MKRTVAACRVNGVAYNLPQSRSLVRLASQPTRSSSLLIAQQPRLLASSAFPASVRFTSRR
GYSAQAAPQDFSEEEKEIAKLRQQGAKSPAAQSSVNQRRIEELFNSANGYVSEEKWTQAE
DKLSTILDLQSSAKADDTLLGRVLINLAFVEQNIGKREKAEKHYEEGIAALKKTLGEDHH
EVARGLLNYAEVLAFLSKVEQAEAVSRQAIPIFEKNYGPKSELVGALLSNLGGYLCAQKK
LEEAEPVLKRALEVLDSALGCDNEYTSACLGNYARLLKDLDRNDQLNELKAKYSSNAATF
TATEALEKDVNDPEMKAMVDQFKGLADSRAFNPEGLFKPDAFHKDELKKFITQWESKHKE
KLDPALIPAVLEELEAMPREEIDKMCADALKELAESKRGGPAVDPSRLNAIADEIDDEAL
AEEEGDEGDDSSSSDSDDEEGEDEDDEIMERLDQGDEDEGDLWRATEAHEREAAKNIEID
MSHIELTDDKKQQ

>alpha-aminoadipate aminotransferase Contig13167 (and 6207) (complete)
MQRALASSGASRITDYEPFLSVTSKRRQPSPIRSLQPLLELPGMISLGGGMPNTSFFPIK
GVDVHLTDGTTLPIQGVDMNAALQYSSSYGVTEFVEWLKDYQTREHHPPYASRKDWHVCV
TNGSSDANAKAFEMLIDPDDYVLVENPTYSGSLAGLRPLGCRLVGVETDHSGLSPTHLRS
LLDSWPVDRPKPKVLYVIPTGQNPSGATLPEERRREIYGIAQQHNLIIILEDDPYFHLQLD
KQQDDEPLKSFLSMDVDGRVVRFDSFSKIISSGFRIGWATGPAPLIERIQLHQQASTLHV
SGLSQVVLLTLLKNWGEEGFKRHIAMVQEGYRQRRDLFCKLAEKHLTGLAEWHPPSAGMF
VWFKALGVRSTEKMIKERALAQKVLLVPGVAFTPNGEESSFVRASFSTASPDDMDEALRR
FAALLHEERNAHHQ

>fatty aldehyde dehydrogenase Contig20942 (and 13022) (complete)
MEGRYTAVDSIPGLVAGLRKTWKSGKTLNLEWRLQQLRQLIKLLKENENQIIAALKADLR
STDLIAGSEVDSSIKEATAAIKNLPEWSKPEEKSVPLMHKPGSGFIVKEPYGLVLIISPW
NYPISLLLKPLVGAISAGNVACLKPSEVSVNCSRVLFDLIPRYLDQEAVVVVEGAVEETQ
ALLKEAWDYIFYTGNGKVGREVMKAASANLTPVTLELGGKSPVILDSHVNLDVAARRLCW
AKFTVNAGQTCVAPDYILVTKDMEKPLLEKMAATLKEFYGNNPKATADYSRIINERHTQR
VAALIEGHDVFVGGEVDVEDRYIAPTILTNVDTNAKVMQEEIFGPVLPIVPVDSVEQAID
FINDRPKPLALYIFSNSSATQDKVLKNTFSGGVAINDAILQVVCPELPFGGVGESGMGAY
NGKHTFDTFTHRKSVLKRAVWSDPSLRYPPYTESKLKWLKLLGGDLKIPRWVVIALLAVP
VIAFVFSRYGFLFNNASSSGRL

>mitochondrial ribosomal protein L20 Contig3567 (likely complete)
MQNQARRAVVGSARTTPLLAGPLPLQRLHLRWRHGGGLVSEQPMVVRTEALSGVQLLGGG
AVFAHRLQAPAHAPPSRPGLGQLAEAEVAEMRRLRAEDPSRWTQRRLAERFGVNALLVAR
LAPAPAERFAQLEEEEQLRELRRVFGDRGGASARPAHKSYSESDQQRINRAKFQQQVAEQ
GGLKATLKQHNAVPKRRRQGVRPPFMQVADQEVVVDTAEFQPGVVGPEVDFAKATRPLTV
RSPTPDEAAAIRRHLAETAAKAPLDPAAAKAAADEFERDLQAVRSEAKAQGIQRKYRRK

>inosine-5'-monophosphate dehydrogenase Contig10390 (likely complete)
MKRATSTVVGRTAATLNGRRAPYATIREGSIRLGLTYDDVLLVPKRSPVRSRKAVSVKTK
LSRNITLNNPLVSSNMDTVTEAEMAIAMARNGGIGIIHRYLSVDEQAKEVEKVKRAEGYV
IDHPYCIDPSATYKDLDEKMEEAGVSSILVVQEGKLMGVVTRRDVALIDDPNEPVSKIMT
PRKELIVGRPGIGFEEARDIVQANRIKILPLVDEENRLKGLVTSKDILNQMRRPFASLDK
RGQLLVGAAVGVKEGFLQRAERLIKSGANALVIDIAHGHSDLAIDALVALKKHFPTMDVI
AGNVATAEGTRDLIDAGADGIKVGVGPGSICITRIVTGCGVPQLTAVMECAAVGREMGVP
IIADGGVKTSGDITKAIAGGASTVMLGSSLAGTDESPGQTLIKGGKKVKIIRGMAGYGAN
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LSNKERQQLKDDVFEIVPEGVEGVVPYRGAVSGIIRQLVGGLCSGVSYCGAHDIEGMQAN
AEFIRITPAGRKESGSHDISEI

>acetyl-coa c-acyltransferase Contig14459 (complete)
MEGLSAAFTSAVGVKSPDDIVIVKAVRTAVGKAKRGSFKNTGPDNLLAPVLKHLVQTTPQ
IKPELYGDVVIGTVLPPGAQGATEVRVASLLAGLPDIVPCTTVNRQCSSGLQAIANVASA
IKAGYYDIGIAGGVESMSSNSMDRWDGGINQEALQHPSAKGCYLNMGQTSENVAERYGVS
RETQDQFAALSHKKAAEAIKAGKFRDEIVPVTVTVEDDKGNSKTITVSQDEGVRADTTAE
KLGKLRPVFKEGGSTTAGNSSQVSDGAAACIVTKRSVAQKLGLPIFGVFRSFAAVGVEPA
VMGIGPAVAIPAAVQKAGISLQDVDVYEINEAFASQAVYCVQKLGIPVEKVNPNGGAIAL
GHPLGCTGARQTATLLNELKRRNARFGVVSMCIGSGMGAAAVYEREN

>hydroxymethylglutaryl-coa reductase Contig4017 (complete)
MRSSLRIARASAPSSFGSLRTTRLSLGGSLYTRTSALASARLYADDASKAKKKIDLTDKS
DEEIIELVTAGKLHSHKLEEYLPGNLERAVRIRRLGLEAHVQAKSDHKPDLSKLPYQSYN
YDSVYGACCENVVGYVPIPLGMAGPLLVNGKLVHIPMATTEGCLVASTHRGCKAITESGG
ATSVVIADGMTRGPAVRLPSAKRASEVIAWVKNTDNFYLLASAFNSTSRFARLNSIKTGI
AGRTLFLRFKSATGDAMGMNMISKGVEKALDVITDYFPDLEILSLSGNYCTDKKPSAINW
LEGRGKSVVAEAIIEERIVKEVLKTTVQSLVDLNIQKNLVGSAVAGSIGGNNAHASNIVS
AMFLATGQDPAQNVESSNCMTLMEVAPNGKDLFISCTMPSIEVGTIGGGTHLGPQSTCLD
IMGVKGSNLTNPGANARALAEAICAAVMAGELSLMSALAAGHLVRSHMAHNRKKDPQVSE
PHKLPDFTNTPSENDSPKEEKFGACVVGDKK

>pentatricopeptide repeat protein Contig3088 (and 1348) (uncertain of completeness... GenScan
inference)
MWRAGGQGPRLACRSHHGGGGGGARLMCGDVLPAEHRRRGSGGALLRFAATSTRTTPATA
TATLRRGQWAASLVVRRAITGRPGAAGVLAEDMEGAVGAVGRLLASPHARDQEAGRTLAT
DLLARQPLPPGGGAPSALLASARCSPSVLQAIATNSPAEVRTPQPPLLLPFFFPPRSYAR
RRRRRDSCCRCRCRLGRGTTPDSATYALGIEVRAPVPWPRHRARLPHHHHHHHHAGAVQL
DGKLLASMLTALAHKEAYDDALRLRRQLQTAHPHLASPPHAQDVQRGLISASAVKGDLRT
CLEAAHELQRLMRAPPDLNTLTTILQCYSRSSLFEQEHSMLLRYLASLRSLDPAHQKEKE
AHGQLRASGTEASPPTTITTGGGGGGGRAEGASWQDVVHRALARGPASKAGAPSSSDPGD
GALHLLEEILRSEGSFLGEQLTLRQFNPAIYALVRTAHTTRDTTRRATPHDARMAHTHGA
PQEEKSDGAPRLGQVDRALTLVEDIQTHGLQPDIATHNTILKGFALRGDAVGAVRYYNAM
LRKARTFLSLLSKSLLYARYTRHTTHDTHLYLLSISIFPYSCGKPRGAAFPLGHRIPPSP
LACTWTAAAAAAAGQSEVVAREVGSLQPAALVTAQLYNFDESNVLRAASPGHIQDAYSQL
LLEMQAH

>CBS-domain-containing protein Contig5121 (complete)
MRRMSRYQYVRDIMAKPVLTTTPDTALNVALGTMLQKRIHRLPVVDSSNPNKVVGIVTER
NLRLAADSPFLEESAQEVLEHLAKHKVGEIMRSSVTTVTEDASIVEAAKMMRVSNVGGVP
VLDKQGQLVGIITRTDMIDHLIRVLEPLDEGQRE

>putative pyruvate dehydrogenase phosphatase Contig3418 (and 931, 6270,E80POFO01EX230)
(incomplete, but with internal gap)
MLRLRQLASRSGPARGATSHVLKTTSGGYAFASPWASSPLFSTSAATATDKRVPDKSRVV
IIGGGVIGTSVAFHLAKLGWTDVVLLEQGTLGCGTTWHAAGLIGQLRANETETKLSRYGI
QLYADLEKETGQGTGWKQCGGVTVARTQERMTHIKRTLSRMRAFGIEGHLVSPMWAKQVG
RLAGVNVPLHTCEHFYISTKPIDGVDSYLPVLRDPDGYIYFREWSGGIIMGGFEPVAKPC
FADGVPNDFQFQLFDEDWDHFSILMNSALERCPALETAEVRQLLNGPESFTPDNQYILGE
APEVRNFFVAAGFNSSGIASAAGAGKALSEWLIQGYPTMDLWSVDIRRFGKYHANDNFQK
QRSMETLGLHYQIPWPKYELQSGRPLRVSPLYERLAARGAQFGSKMGWERPNYFLPSSVS
PSSIKYTFDRPAWLPYVGEEHKATRDEVALFDQTSFAKFVVKGRHVESFMQRLCANDVAV
PVGRVVYTPMLNPRGGYETDCTVTRVSEDSYFVVSSTAQATRDYDWISRNIQEDEEVSIV
DVSPQYSTLSLMGPKSRELLSRVIADRDLSNEAFPFGTSQEVPLGITQVRASRITYVGEL
GWELYVPIESTLLVYDLLHAKANEGTRIGLRDAGYYAIDGLRLEKGYRAWGSDITPDDTP
LEAGLGFAVDLKNETKNFLGKDVLLRQKKEGLEKRLAVFVIDNDQEVYPHGGEPIFRDGQ
VCGYLTSVAYGHTVGRSVGLGYVRKLANTATKEDRLVTPDWVKAGRYEVEVASKRVPASV
SLQPPFDPKNERVRM
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>NADH-cytochrome b5 reductase Contig11258 (complete)
MRRIASTNTRSFARASTFTSTTLSSSSSSAASLSLPLHRRFASSEDNKQQKQDDQQSSGS
GFLTTLVVAAAFAAGGYHWYKEVVGEPFEERKKVAPVAAVAQEGKKEAEAAEVKPLPPVS
LNKDEFREFELVEVEDLTPNTRRLRFALPSRDHVLGLPVASCVVTKANIGENGKPVIRPY
TPVTNDKSDKGYFDFVIKDYPTGVMSSHIYHLKKGEKLQVKGPIPKLAYSKNMKKHLGML
AGGTGITPMLQVLEEVLSEDDDKTHVSLVFANNTEQDIILKDRLDALAKKHPNRFEVHYV
VAQPADAASWKGHTGFINADIIKKHIPGPAEDVMVYVCGPPPFYKALSGSKAPDYSQGEL
DGVLKDLGYIKEQVFKF

>superoxide dismutase, Fe Contig26548 (complete)
MRRTAATRAVQTTTSFTRTAAGARSLFTLNDPPYLKTGLTPAISANTLNFHFNGHHKAYL
NKTNDLIKGTPLENKSLEDVILVAKTTNNAALFNNSAQLWNHSFYWDCMAPVGETGEISA
ELEQLIKESFGSVAEFKNKFTDSAVANFGSGWTWLVNINGKLEIQNTSNAESPVTLRVKP
LLTLDVWEHAYYLDHQNRRPEYINKWWDVVNWNFVNKQLKQ

>conserved hypothetical protein Contig17715 (uncertain N-terminus)
MFLNAEAGGQALRSAARSKADKPLRPKFDVLTSHKSVFEYTLGCTLGLAGGYIIWGQELK
KKADAIRELKEALKPEIVEVDPLQRLDQSHSDSQVYTVVLTGGPCGGKSTALATLTKHLR
AQGYEVYSVPEIPTLVFTAGVPTISSMNEEQLLAFEKQILTTQIQLEESMKKIASAMDKP
TVILLDRAALDISAYLPYSFWKKLLQDLDITEKQLRERYTAVVHLVTAANGAESYYTTAN
NAARTEGIEQARELDDKVKHAWIAHTRTFVADNTTDFPGKMQRVCSFLDDVLTSQHKAAP
TKETPEVK

>dihydrolipoyllysine-residue acetyltransferase Contig10054 (complete)
MKAANRAIAGFHIRQTAVAGLRGSTFTVGSGLPRLCTRRGISTKPYLEEPYGYEPVLSPA
VAMLVANNGIKNAHTVIKGSGPKGRILKSDVLAFLKGEQPPLAAFAQQIRPAAAAAAPKA
AAPKQAQPLVPPKGGKYEDLPNSNVRKIIASRLTESKSTIPHHFLSADCKLDNLLHVRKL
LNETEGVKLSVNDFIVRAIALALRDVPEANASWAGESIRRYKSVDVSVAVATDKGLLTPI
IKNAHQKGLATIAKEIRELASRAREGKLKPEEFQGGTVSVSNLGMFGISEFSAVINPPQG
AILAVGEGRQVVLPSGSSSSGPSHFDNADDIVLDEEETLLAPPKLATVVSVTLSCDNRAI
EADVAGRLLHTFQSYVENPELMA

>beta-lactamase protein Contig8207 (complete)
MRRVLSAAATSTTTCRSATHNSLLRLHLRPNLLRAGMATTTSNESHLLLELNGGEACKTY
LIADRQRRKAALLDPLKQNIPKYLGVLAYHQLQLEYIFDSHSHADHFTAGFELAMLTEGK
LAMHENAPAPKVKVHVRDGDVLRVGDIEVKVMHTPGHTPDSIALYLPRLGHLYSGDTLMI
GGTGRTDFAGGDPGQSYDSIQRMFALPEDTVLWPGHDYRGNVSSTIGHEKRTNPRAGGGK
TRDEYIHIMNNLGLPLPQKIMEALQCNVSASNDTAMKFPTIAELNEIRQLEPKLVRQLLA
ESDDKRPVVVDVRQPDEVDGELGHIPGSITLPLSELTKRYQELEQYKGRNIICVCRAGVR
STTAAALLTGLGFPNIHNMRGGMLAWNQKESATA

>Glycerol-3-phosphate acyltransferase Contig7181 (uncertain of N-terminus)
MADVTEASGGPHGHGEAEEQVQISNEEESTEAQNIEGEKGTAAVPVQEEEMLGQQRLNAA
EYSHENLFRQRRIRSENFVVRRLVGNFFDLWKAYAGYQHLPGAHEPFPRTENIIKNAILK
DERVIRATQKYAIEKKMSEEAAKRHVAEMIGNMIASFSSRITRSFEYVMTKILKRLFVSI
HVDDQGLRMVKELEEKGVPVVLIPTHKSHIDYIVMSIICFHYNLPLPYIAAGDNLNIPIV
GYLFRRAGAFFIRREFAGDPLYSLLFRCYVEQILNESSVLEFFIEGGRSRSGKVLRPKMG
MLSVITNTVLEGQVDDAMVVPVAISYDKVIEGEAYKKELLGGQKEPETVAGVIRAARLLK
FKFGRVDVNIGDAISIKQFIANQYVRHQLRAETGPDDPAVRRLVSALAYRVLYECNKVTV
ARPTALVATALLTHTGRGLPITQLRNKVLQLRQMIVERGGFVASLKEDKISALRITENAL
NVLDNLVEKHKQGTHETVYQPKQRLELTFYKNSIIHWFVLEGIVSAALYASIKPHIRVAQ
PEDISKFKVNKRDLLNDVRFVSQLLKLEFIYKPSPDIEVNFEQTLNQMQERGILKQEQVA
RTALPEEEQEDEESPTMVSIQASEDAQEMFLFLCSLFWPFIDSYWLVINAFKSLLPSIIM
EKNSFLERVRVFSMAQYYSGELSFIEALSTEGLSNALEFFHEQRVIRLGPRVAFQGGDDQ
AAPPVSPGPGRKAGGAHLQHRPLPPCHLPRPGLHLQDQEGEEAHQLP

>acetoacetate decarboxylase Contig20803 (complete)
MLRRSHSAARSVLSGAPCVLATSGTRCLASSTLNGGLTREQILALPSMPAISPSYPMGPY
RFVNREYFIVTYETDMDSLRRVIPEPLEPISNQVLYEWIAMPDSSGFGSYQESGTVVPCL
YEGKPVNYTVQMFLNDEPPIACGREIWGFPKKYAEAELRVEKDTLTGILTYGGRRAMGT
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MAYKYNRLDKTTATNSLSKLNCNLKIIPGYDFKPQIAQLVAYNLQDIEVMEAWEGPARLH
LIPHVNAPAADLPVRKIVGGKHIRANLTLPHGFVLHDYISERKKSEANFYMNGNPLAAAA
EKAKATEKEKAKVAPQDDKAGLTREKVLNLPSMPAICPSYPAAPSQMSNREYMIISYKTD
PEAVRRWVPELLQPDDNVHLSWVKTESSGYGVYQKMTASVGCKYNGEDCTFPLMAIVNCS
SAITAGREVHGQPQKFGFPSLTVDKDTLYGETKYGQQEVATGSMVYKHHRLDLSQAYKFF
EKPEINLKVIPSVTGEAEIAQLISLLPKDVKIKDAWRGPARLNIIPHVNAPLADLPVVEG
TCEGHYIVVEDMVLPEGTLIHDYTLDAGKEDHQQQSEPAEASAAAPQPGTGDASDSASQE
ERFRRRMERFLQMPTIVQ

>Tim17 Contig25569 (complete)
MDAYRDPCPSRIVTDCGSAFAMGAIGGSLWHGVIMGWPQAPRGMRMSSAITALKTKAPSL
GGSFAVWGGLYSSFDCTFAYLRGKEDFKNSIMSGAATGAVLAARTGWKGSLKSGVVGGGL
LALIEGIVFVISRQSPAQQQDFGYAPPPPPLEDVLDVEEKGGFFSSLTNLFSKKEESKPF
EMEEETTMDDFGQETKEDDFGDLFQPPPATSW

>pantothenate synthetase Contig17484 (and 1319) (complete)
MQRRVKVVREVAEVRALREAWRREGRRVGFVPTMGALHAGHISLISHALPHSDALFCSIF
VNPTQFGVGEDFDKYPRDVAKDVLAIEQGLSAAAAAQGDGGRDVEAVVFAPSVRELYGDR
FSTRVDIGLMADTSEAHARPQFFSGVATVVSKLFNITQPHRAYFGQKDALQCVAVRRLVE
DLNFGLEVVVCDTLREADGLAMSSRNVYLSAEERKRAPILYKALCAGRSRYLDGERSAQE
IIKATKEALEKGEHWWAAGPPRPEVQYVSIADAGFGHELDYIDPKGPGAFLSTAVRLGST
RLIDNIVLPPL

>hypothetical protein Contig23466 (complete)
MASSKTPGLWSRIRAALRPNFTLHPVPTAPDYVQYPTNFRVPYSKTEYSPETIPAKAHRD
LSTIYYWRHAAGKRSPPVPRKPDVLKELEKEGSATGPARVGGLTDITELRITRPPGEMRK
WNEIPNELYQ

>similar to NADH dehydrogenase 20.8 kDa subunit Contig12533 (and 19549) (complete)
MSRDPAVAAASFGFVNHRCAKDVKAFQEQKGSSEAVKACFAKETKTLTSTCGKEVHAFAE
CLADPESGSCSRPEWDLRVCVRSNFGFDSALEQKKQAARLSKSTVPTELADSEKLETAAS
RWK

>rhodanese-related sulfurtransferase Contig24868 (complete)
MWRRGTGSVLAGALGQRATTATASSWGAQRLMSSHTRTTPWVSVDELRRVLAEPKAHSKE
RVVLVDTRGAEAYDKGHLDGAVRIEECFTHLATSDPAGLASLEATFRDLFGRRAGITGAA
NERVVIYEEGLTSGFAQSCRGYFLLKWLGHPNVSVLQGGLAAWRNAGGELSQQAPQVTPA
QLKTQVDASLMATKDDVLQALKDKSKDAVLLDVRDQDEWIGTSSSPYGKDFCPRKGRLPG
AKWLEWYKLHDRKDGVAYTKPVDEVKATLTDMGIKPEQDVIVYCFKGSRASNTLMQLRHA
GFKATNYFGSWNEWSRDDSLPIESSLLSTPHA

>Lon protease Contig2814 (and 24099) (likely complete)
MKTCLGRLTPRPAAAQSHRYASSMLRGNASRLVGLRASAGARRPPLSTSSPLICGSHHGP
AYRFGFVRAVHDQAGGNGRKNGGGGTNNRGVGAAATDKKPSLVLSQADTGAMLRNMATMP
TPQTVYILPLTLNPVFGGTSYYALVDRRTLERMQDLQAKGDLFLGLFLQKDPNPNVKVAD
VSQLYQVGQLGCAIGAVQYTSNPDVHLLQITPLSRRIRIKAPVPGAERENDATLLAVEIE
ELIEGEYNRKDPVIRTNHEAIVSAIQQLHEHDPSSHYQKLLDEMDPDNPAEFVDLAAAVM
TSEPEMQQAVLETTDVKQRQLKCLELLHKKLEMFKKQKDVRTENMEQEAKLEAAQKKLYL
ERKKKAIEKELKLDVEDSDKLIEDFKKKLETLQVPEEAMHVINEEMNKLTSLERSSSEYN
ITRTYLNWLTTLPWGLHSKENLNLSHAISVLNEDHFGLKDIKERILEFIAVGNLKGSVQG
KILCFVGPPGVGKTSIGQSIARALDREFFRFSVGGMSDVSEIKGHRRTYVGAMPGKIVQS
MKNLKSANPVILIDEIDKMGNSRQGDPASALLEVLDPEQNKTFLDHYLDVPFDLSKVLFV
CTANVSDTIPGPLLDRMEVIQLSGYILEEKMNIAKKYLVPQIMKDSGLQPGQIAVNDSAL
HALIQSYAREAGVRELYKHIEKIFRKVAYKVAKERKLATDATDATPAGGDGAEKTKKRSR
KTKKPSKADEEEGKETKSEGESGDGQTQPVVITASNLTEFVGQPKFTSDRFYDVTPPGVV
MGLAWTAMGGATLYIETVNDRPLYSALKRSQPAELEHAKEGDAEGDKDRGVKTFGGAGGA
MRLLTTGQMGSVMQESTSIAFTFARNFLEDVSPRNEFFDRAALHMHIPEGATPKDGPSAG
CTMVTSLLSLATGRPVPPDIAMTGEITLTGKILTIGGVKEKTIAARRSGVKRLFFPDGNR
KDWEELPDYIREGLEARFVKDYRQIYDVIFADPDPAASSTSTTTTSTTAIDGETTSTTTK
SPGPPAGGSRQTRKRSCCDDSAHYKVAKERKLATDATDATPAGGDGAEKTKKRVRKTKKP
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SKADEEEGKETKSEGESGDGQTQPVVITASNLTEFVGQPKFTSDRFYDVTPPGVVMGLAW
TAMGGATLYIETVNDRPLYSALKRSQPAELEHAKEGDAEGDKDRGVKTFGGAGGAMRLLT
TGQMGSV

>cytochrome c oxidase subunit VIb Contig12762 (and 11210) (complete)
MSSTRIYSVVEDHEDKKAEEVEEEAPVEEEVQEEEAQEEEEEAGERTLGSILKPGVTTVE
QFLQFLHPHTPAYNPHFPNTNQTKHCWSSYINYTQCTKLKGEGDAECRRFYVSARSLCPD
EWLDSWAEAKEEDKFASPYDVTSEKSAH

>rhodanese-related sulfurtransferase Contig24350 (complete)
MQRRLISSSASGAFGSRSLFNRSYASWIRHRPDQAFHATRRGYFPQFVDVREEDEHFKER
LTGTLNVPLTKLKAETKDADTADKLAYLDRSRPVYVHCDGGERAEEGATLFCNLGFTDVK
LLEGGVFEISRDSGLIIERE

>pentatricopetide domain protein Contig19095 (and 454) (likely complete)
MQRSMSLGSRMWGSQCSAASSPVAFAMRNHLQRTVVRSPAAAPWGRGSSCLELASSSSSS
SSSSGLRSSGSHRRGYATEAARDLVRREVELLEDAYRAGVPVGRKRVVQAVQLCARTRDT
ELVKKMADLGVRLLPRDRVVRNSIVGAHANVSGGTRVGEAMEAMEAVGLAGVKPNRVTWN
TLVASYAKAGQRGQALTALDRMQEAGVLPDRVTFNTLIKAHVAVGDIEDALATFELMKAR
RIAPNERTYATLIDGHLKQGHNDRATQLLQEMEGRRIQPNRVTYTAIIEGMCRNGLGQQA
LLVFNEMVDRHGIAPDVLTYTSLLKGTERQPERAWTLYQDMLTRGVIPDAVFYRDLIRTQ
RQSADDATLNQLVDKAIEVGARMAPTMNAAGCQRLLRVLSERPASALHAWRAMLQAKLPL
DREVFEVASQIIGQTGDSQARAELQATARDYFKEE

>mitochondrial ribosomal protein S23 Contig23412 (and 3216) (complete)
MVHAGKGGGRMFVNAARINGRKSNFSLLEYIQSEVRAGESPVPPWMPATLISPPPTIPNV
PHPGPLTYPEDKLRQVWFDRHPEARKIKLKTVYVGEHRYWQHPATSFVHRQSKLIKKGYS
EQDAYDVVEAEDKKAARYRELERLMAIEQAKELGFDDLETARDLLAPPDLTQARERMLEE
LIDVLKAKGVPNVVPELLPKGMKWRDVLAFVHKYPQHAHFFSLGFMATHAIETMNPEIAD
AYNWIYGGEVLLDDDSVPLEEQEELNAFLDEEGFETVEDGDELDQQDLREQERLTSEAVA
QYEPVVAGASLVEEGLFFDEDEGEDEDESEAAREEEHDEEQRIAMVKKEGEQFKAILKRI
EKIYRPEQFPTTADTPWADLVNLLALRPQAPDVKLAQDAEQKLRKANQVKRPSGGSSRPQ
SQQPNKPTKGKEVELQ

>enoyl-coa hydratase Contig5196 (complete)
MRRATLKVVAGRGAVPAGQAVRSCFGRRAFTTAAASTEVKQKYDFINVEDKGEVRWVSLN
RPDTHNAFNELVIGEITDAFRTIQRDAAQEKFRAVVLTGNGKSFSAGADLNWMKKMASYT
QKENELDSHKLFDMFNSIYACPMPVIGRINGNAIGGGSGLVSACDFAFSVNKAVFGFTEV
KLGLIPAVISPFVMMKIGKGNCSRYFLTGERFYATEATRLGLIQGSFETVEELDKAVDSV
LTEIKANSPAAMRSCKQLINNVYHSLGSPKKGEGLSDVKEQLASEIARIRVSKEGQEGLS
AFLEKRKPSWIVS

>ferredoxin-sucrase-like Contig517 (and 9146) (probably complete)
MDDKTKIVQLTALAGAGAVLLGAYYLGTRHATAPAATSSSAAAETCECGLTVAQGGCAPA
SSSSASLYNSQLLGTVKKYEKHFIICSGTEPDEWGAKIDKDEGSFAQLAKQAISARKAEL
TFKFKLTNSDERSKGSEGTDLIVFPERIRYLGVTAETMPFIVEDHLVNGHVSERVKHEPF
ESELVLVCCHNNRDTRCGAEGPIIVSAFDRLLAARGLGEDKVMVRSSSHLGGHKYAGVVV
VYPRGDWFGFITEQQVEKLLDNYIEHGSMVPEHWRGRMGIDKQEAKDLADSVTLAVETSS

>rotenone-insensitive NADH dehydrogenase Contig10971 (and 16696, 210, 21921) (mostly
complete/correct, but some ambiguities)
MRAACTRSLVAPGCAARGRAATTAGSRLFCGGGGWVQQRRALATSSAGGRGGWRGVGTVA
GLVVAAGALGAVALEGLQDDENDSLLSRTPFVSAVRAEEKTTPNAKAPPSIVSQNPPVDR
AVQREQQGGADKPMRTKKRVVILGSGWAAVGVLRELDNEAYEVVVVSPRNYFLFTPLLPS
VTVGTLDSRSVVESIRRTFKRAGASDVQFLNAECTAINHQSNSITCNDVSGDGAVRSFDL
EYDQLIVAVGCDNTTFGTPGVEKYCHFLKELNDARRIRQQITQNFEVAGLPGQPEEEIKR
LLHFVVVGGGPTGVEFAAELHDLLVEDLEKWFPRSLTQHVRITIIQSAAHILNTYDAKIS
DAEKRFGRDDINVKPLCRVLSVDEKTLSYNDKQTNKTETLPYGMCVWATGIGPRPLVKKF
CSTIKEQTNRRAIVTDSHLRVLGTTNVYAIGDCGTVEQRRLLSKFVDLFDQADENKDGVV
SFDELSALVVKNKDEYPQLLIYAAKMQELFETVDLDKNQVLDREEFKALLTEVDKNLVEL
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PATAQVASQEGKYLGQALNALARGQEVEQFHYKPLGSLAYIGARESVLELPGGFSFGGFT
TWFAWRSAYLAKQVSWRNKFMVAMDWMKELLFGRDISKC

>leucine aminopeptidase Contig27148 (complete)
MQGKAKCLLWGAASFRSSLRAGAASSSAACIFTRSATHRSPLLSHSLSPSGTKLIFVAPS
TCGTTKTCYSTAAGDKQVDGVVVGIFEGGELTPAGQAIDKSTSGALTRRIKLSKKAAKGE
VGSGEVFLDLGEDYPRVAVVGLGKHPRDVKLTSEQEDYREGQPKPSDAVRQGAARGARLL
RDAGSKVIGVESFGQFTDLPSVQLAAEGALLGLHKFDELFSKKDDEPVDVQPWGVEADKQ
EEWNRGKIIATAQNFARVLTDTPANLMTPTIFSQKVEEKFASLPNKADVKIFAHDKAWAE
EQGMGCFLGVTRGSEEPPKFLEIHYNPLGDEAQDVAPIIFVGKGVTFDSGGISIKPSEGM
GMMRGDMGGAAAVVSTVWALASLQIKTKAICLTPLCENMPSGTATKPGDVLRAKNGKTVE
VDNTDAEGRLILADALVYANSFKPAAVIDVATLTGAMVVALGAGATGVFTTSDKLWREMD
EAGWKTDSRVWRMPLFSSYKRQIKSAYADLKNVGGRPAGSSTAALFLKEFVETPAWMHMD
IAGVMHSDDRNAYTPKGMAGEPVRTLVQWVRDKVEKH

>beta carbonic anhydrase Contig216 (complete)
MRRGLASSISLRSSAIARGGVSVLPRMAASSPLHSTTSTCLCARCATATTLPQRSISTDD
KLKDEMLRMRESYNDLINGNKEWVAQQLEKDPDLFKRLSAGQSPQVLWIGCSDSRVPANV
ITGSDPGSIFVHRNIANTVVHTDMNLLSVLQYAVDVLQVKHVIVCGHYGCGGVIASMTNN
QFGMVDNWLRNLKDEYMLHREELESIPNDADRAKRMTELHVIEGVYNVCRTSIIKDAWER
RKSANVFPHVHGWVYGIHDGFVRDLNVSVRGPDDVPLLVRKPVNPSKC

>xanthine dehydrogenase Contig9689 (and 10260, 18531, 4043, 4459, 5030) (incomplete .. still
lots of problems)
MMLRHGRRLPSSSSRAALLARNHVASSSTSLQRNGASSVMTRRSNASNTPSKPTQMSAAA
AEEMLKTARVPTSAPSSAPSGLPSASQSALKETRHEVVFYINGKRHAPKSVEPDLTLIDY
LRDQGLTGTKLACGEGGCGACTVTVAHWDQERGEVVHRALNSCLVPVCFVDGMEVTTVEG
LGSTRSGKLHPVQDKMANLFGSQCGFCTPGFVMSIHSALQKFPAPSLHQLEKSIDGNLCR
CTGYRPIVDALRSLEKEYKGKQSETLKKLHHFPQELIERSTHPLAITGTRAAWFRPTTLE
HLLELKATHHHAKIVVGNTEIGIEQRFGRKHYPILISAAHIPELNQVAFLDGGVEVGSAV
PLTTLWESLEHTNTYLTKNDQGKDAFKTRSLAAITEQLQWFSGTSIRNGACLGGNIVTAS
PISDLNPVFVALNAQFRLKSMERGERVVNASDFFQPGYRKVDLHHDEVLTSVVIPYSHEN
QYVEAYKQARRREDDIAIVNAGFNVALDDSGRVTSARLAFGGLAPFTLQAKETQAFLVGK
QWNQDTFEKAVDVLRKEVTLKEGTPGGMEKYRTTLALSFFFKYYLAVAQKMKNGPVIPPS
YLSALWPLTAESPKGKQVFAGSDQPVVGQSIVHASAERQVTGEAVYIDDMPRLQGELNGS
LVVSQRPHAKLRKVDASKALQVPGVIGFFSHKDIPGEKIIGDIVHDEEVFASEVVETVGQ
PIRYPALPWWYVVDEVTAKHAAHLVEVEYEDLEPIFSIEEAVAKQSFFPLEKKIEKGNVA
KGLAESKNVVEGRVRIGGQEHFYFEPQITIAQPLDTEMVLYASTQNANKTQKHAAAVLDM
PENKVSCSLRRIGGGFGGKESSNIIYSCCAAVAAHHLNRPVRLLLGRDEDMEWTGKRHPF
EGTYKAGYDNEGNITAVDVQLYNNGGYSHDLSWPVLERALFHSDNVYNVPHFRVKGRVCK
TNLPSNTAFRGFGGPQGMIVTEAWVEHIAHQLKMEPEDVRKKNMYLYEDKTHFGQPINLK
LHELWDQCEAQSDLRQRKKAIAEFNRENRFRKRGISMIPTKFGISFTFTPLNQGSSLVNV
YTDGTVLITHGGVEMGQGLHTKVMQVAANALGVGMKDVHVSETATDKIPNASATAASQGT
DLYCMATFNACEIVPSPPPAPLYPEARRLTLSVPWLNERLAPFREKMPGASFKELVQAAW
FDRVNLSAQAFYKVPVSGFNFETGEGKPFCYFTSGVAATEVQIDTLTGDYRPLRTDIVMD
VGKSINPAIDVGQIEGAFVQGAGWLTMEELVWGDKDHPWVRPGRLRTNGPGAYKIPSCDD
IPREFNITLMKDSSNPSAIHSSRAIGPPLFLGSSALFAIRNAIGAARKDEGLDNWLP

>hypothetical protein Contig10869 (probably incomplete)
MKKGDAMEVEEEVSMVDDRATDLTNREAEDEGEERSSPVLEGDGEALSHGGLVRHRVSGA
TETEDSVFDAEVDEISGGQKRFIF

>aconitate hydratase Contig806 (and 26672,5046)  (incomplete, due to some internal gaps ...
largely derived from genome)
MRANRACTTFFGPARLPTMTVCPSHHISPLRCLNIFHSRECANAPKADLSSPPPQGANRL
FGTSRGVLQRPAAMSRWELEDPATSADIQRGKTYLKLKPDRVAMQDASAQMALLQFISSG
LTSTAVPASTHCDHLIEAETGAAQDLESAKVTNKEVFEFLSSASQKYGIGFWKPGSGIIH
QIVLENYAFPGAMMIGTDSHTPNAGGLIAIGVGGADAVDVMAGMAWELEQRAPNVLGVKL
TGKLRGWASPKDVILKLAGKLTVRGGTGSIIEYFGPGVETLSCTGMATICNMGAEVGATT
SVFPLTESMLSYLAATGRKDIADTITAAKEIRGHLRADEGCHYDEVIEINLDELEPYING
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PFTPDLATPLSQFADAVKKNQWPEKISAGLIGSCTNSSYEDMSRAAAIARQASEKGTKAQ
SVFTVTPGSEQIRATIERDGQMQALRDIGGLVLANACGPCIGQWKRSDAKGEKNSILTSF
NRNFSARNDGNPNTHNFLASPELVTAMSLAGSLTFNPTTDYLTDAQGNKYKLKSPDAVDG
YDQATATLPAAGFDAGRSQDTYLAPPPADQRASLEVAVSPTSDRLQLLEPFAPWPKGEKD
IRDAAVLIKVQGKCTTDHISAAGPWLKYKGHLENIANNTLIGAVNADTGKVNAVVSQLTG
KEGTVPDVAREYQKAGVPWVVVAGKNYGEGSAREHAALQPPLPRRTGHHLPELCAHP

>mitochondrial calcium-binding protein Contig8180 (and 6963, 9989,13768) (C-terminus
incomplete)
MRKGLVVRRSNTVSSRLLGGGRQGGSASLLRLPRRSIITDNQPIRTHAQEEVASSNGSSG
VIKRILAIGVGAGLVVTALTLPLADEITNREEKPLALLEKLFTKYASAERNGVKFMTRRD
FIASMMPPDSELGPALALDTFRELFPTDDTLISFSEFVLFDALSSSTKKALATSFQVFDT
DSDGLLAKDEFRKVVASTGVGPRLMFDLDDPYWERYFGKDGKGKISEAELGLIFGSLKEG
ILAQEFSRNSFESDKNAIPMEAFARVLLVNVPSTRIPKRVVDNLKTVSAAFKDASVTFDR
FREFNIFIYRLSEFERALKMAMVANSGNITRDDFRRTARVSTGVELNPSEIELVFHLFED
QNKRGMLDCNAFLDIMEFRRARRLYDIQQLKVIKHAVNPGRAMVKAMESFAIGGFAGAIG
ATFVYPIDLVKTRMQNQRRTKGGIVPPGRVIYTSSWDCAAKVLKYEGFKGFYKGLGPQLI
GVTPEKALKLAVNERLREALEEEDGSITLPHEIMAGGGAGFCQVIATNPMEIVKIRMQVQ
GTLPPENRKPAAQIVKELGIRGLYKGTPVTLLRDVPFSFIFFPAYANLKAIFSDADGNIG
LVRLFLSGAFAGATAAGLVTPADVVKTRVQVENSRYTSIPQCAATVLREEGIAAFWKGVV
PRMAVQAPMFGIALMAFELQKKFILAHQNPTSKKVFQLP

>carnitine-acylcarnitine carrier protein Contig17816 (complete)
MSQSQGVIKDTIAGGFGGACLVLVGHPLDTIKVRMQTMVVQPGVPPPYTSTWDCAMKTMK
AEGPLALYKGMVAPLTGVTPMYSLCFLGYSFGQKIFCKEDTYKNLDLVRIGLAGATSGIF
TTPILAPLERVKCLLQIQGKTGQYKGPWDCAVKLYKEGGIANVNKGYMATMLRDSVASFF
YFSTYAILKHAMTPEGQAQPSAWGTLFAGGMAGIFNWLGCIPIDTLKTKLQTAPEGKYPN
GIRSVFKDVIKNDGWRALYRGIGPILIRAFPANAACFLGVETAMKAMNYVGL

>mitochondrial ribosomal protein S5 Contig17756 (complete)
MRRISLLGPSAESSRIVPPHAASTEGRSLLYRRAGGLSFGSKSLHHPYHSGGGTLVNGSS
RRQLATSSSSSKPASSEQTTAAKKGGLVGDAAAASTIQTHTATWVDEDEALSLDPRDYAF
DQDDSQDQWERLAGVSDNPLMGDRSGAPRGHGRAKERLAKKFPIEYADEDEEDEDEDNLP
GLGGGRRQSAAQQQQQGQEGEEEREDLTPLELRHRAKEEEKEKKWTQIINPLKDDLEAQI
SAGKHVPLWHPHVDEYDGDGYDDYARTLQGAWEDDSPFHRDYEYNEKEFKNHFAFSVSGN
QHILNVGRHTKTTKAGRVFSYLCHRD

>putative citrate transporter Contig5427 (complete)
MSEVKPLTVYSPAPTSKKRHPVKSIISGGLGGAIEICITMPTEYIKTQMQLYPAKYGKEG
VMYCVRDTVKNHGVLGLWRGLGPLVVFAVPKNAVRFFFVEMIRNQLRNDKGAISLSGNFF
AGLCGGLMEAVLVVTPQETMKVRLIHDRLSPNPRFHGTFHGITTLLKEQGISGCYKGLTA
TMIKQGSNQALRFTTFYQLKTWMLGDPALDFDRSTIKAVFQTIFAGATAGAVSVFGNTPI
DVIKTKMQGLEASKYRNTWDCVQQTWKADGLKGFYKGTVPRLGRVCADVAITMFLFDYIT
MALDAVWKTE

>translation initiation factor 3 Contig19975 (and 15548) (complete)
MKTTTRRLSLVTPRLSHGVGLGSAQPFRSYSRPASYCGHERACSSLVAQFNLYRSHQPLV
TSSFTAGQRRAYAGGYRKTRVRALLVDDAITSDVVQLVSLEGRNLGEVALADAKLLAKQK
GLRLACVVPLANPPVCRLQRIPVVPEVDELDDRRPDPEDEIDDFDEDGMPIHRPSSASSS
SSSYNEAAGGGVAKDVPDPNGNIKRRPKGEKELRFSDTIAEHDVQNKVNQLRRFLDKGLR
VRVSVYFKSVAQFDPDLARALLDNIVTRADDLGRVEGDINIANRFASLLLVPTSPDAATK
DK

>kynurenine 3-monooxygenase Contig10749 (and E9BS9UA01EFIYX) (probably complete)
MDSGTSTGAGENSGNENKSIIVVGAGLAGSLLAVYLAKRGYKVDVYERREDIRTAEIVEG
RSINLALSTRGLTALEKAGMGHIGRQLGTPMYGRIIHAQEEDPKLQFQQYGVDPKQHLMS
ISRTVLNERLITAAEEYPLVKFHFKHRCLKTDFAKTSIQFLNEETGETVTATADVILGSD
GAYSSVRAALQKTQYFNFSQYFLDHAYKELTLSPAADGSYQLPSNGLHIWPRENFMLIGL
PNLDKSFTITLFMPVKMFESLQTKEDVRRFFSIYFPDALRLMPNVPDQYFANPTGSLVWI
KCDPHHKDHVAILGDAAHAMVPFYGQGMNCCFEDVRVLDELLEKYNDDWDQVLPALTATR
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TKNTDAICQLSYRNYKEMSSHVSHADYLLRKKFDTMMNYFFPASWIPLYSMVTFSNIPYS
EVIERSEWQDRVVGKIKTAAPVVALGAASLLALYFPRSRAFVRQALTNLADRL

>peroxiredoxin Contig12041 (complete)
MSTHAVIGKPAPDFDEEAVLGQDFTRVKLSDFNGKYLVLFFYPLDFTFVCPTEILAFSDR
ADEFRKINTEVVGVSVDSKYSHLAWINTPRKQGGLGGALKIPLVADLTKSISRKYNVLME
EAGHTYRGLFIINPKGVLVQATLNDAPVGRSVDETLRLVQAFQYVDEHGEVCPVNWTPGS
ATMKADPKESLAYFEKVNQ

>mitochondrial ribosomal protein L24 Contig1378 (complete)
MLRAGSRNLRSNQIKNPITSWKIVRGDTVQVMQGADHGKKSVVIKVSRKTNRVVVRGIKL
AKRRIKATEESQGGFVYREQPIHYSNVSLVDPSDGKPCKISMSYLADGTKVRVSKRTGTV
IPKPAELTAKRFKNYLDGVKDTKPEVVTLKTFDETSLVPELDELTIAKVHEKLLLEKEEA
EQKRLAREQARVAYGFSSSSDEPRNVGSDSKKEEAEVV

>ADP/ATP translocator Contig22121 (complete)
MSFWMDFLLGGLSAAVSKLGAGPVNRAKIVHQAQGELLRQGRLGRPYGGLADALARTVRA
EGPLSLWRGAMYDVISYFPTQALNFALKDSFKKLFPFDRRQHGYGLWFFGNIMSGGLAGA
TSLLIVTPLQLATTVLAADVLAPELGRTTYQYTGMADVISKTFQHSGPLGLFNGFGVSVA
GIVLYRGAYFGLYDTLRPLVPQNNFLASFLVGWGVTIAAGLATYPLDTIRRRMMIAGATP
MAYSSALECTLTIWREEGVAGFFRGALSNIVRAIIGAMILVLYDQLQAALTAPPAPPPAP
APAANGDSE

>NifU Contig10864 (complete)
MQAALKRAFARTSPRFLPAASLARGRGGSTLWSTTTLTSSARGEGSWRWTAGGARSMFIQ
TENTPNPDSLKFVPDGNVVLESGTMDFPDARSSLSSPLAKSLFTVTGVQRVFFGNDFITV
TKKPDVEWHEIKAQIFANIMDFYASGESVVSEQQDTSNTTILPTDSETVAMIKELLEVRI
RPSVQEDGGDIEYKGFDEEAGVVYLKMVGSCSGCPSSSVTLKSGIERMLMHWIKEVTGVV
AVESDDELDRLTKQEFAKLEKKLGEEGKGDDTAKESTVA

>amine oxidase Contig17220 (likely complete)
MGLCALFFSVSHARTSFSTMQHPVVIVGAGAAGLYAAHVLQKEHNIPVELVEAADYVGGR
VKQDWKFSGNGRPIEIGGELVHGENNMLGKMVRELGLDTADVFSVFQVNTSRPEYEYFYL
GRERKLFGLHSDDADLKHLYKLIGELEENPPKGDVSFMQWLVDHGLPYRMLGVADALYAK
TWGTTVDKLSAVQFAVEQAAANEEEGEGNLQVKQSYAPVIQRLQKDLKIHLNWPVKKIDY
TNPDAIKVTNARGETVLASQVIITVSLKVLQEGDIQFVPSLPQDKLRGIAGLRMDAGMKI
FAKFNKIFWQEKHHLVICADTFVPQFWTYGKDVPIVTGFVTGDQAAAASALPPRQAADSF
IKQLDAVYGTESNPRPATDAFVDFMIQDWTKQPYVRGSYSAPSVGGNGCREALAKPIGRS
IFFGGEATSLSAAATIHGAMATGQRAAEDLLKARQQKVAKL

>pentatricopeptide repeat protein Contig12805 (complete)
MSRFSAFGRRAPVQLLPSAMRINGNSFWLAGRPKHEALPLESATYTALIDVFARAKRLDKA
HSLLRDMEAKGVSPSLAACIGVVRAANRPDSVGVADAVYDKLVDEGATLDAEFYDAYISSL
VGARKFRRAHQIYFHMSKRQKLPATATTYKNLITIYGESKRWDLVQDVLRKMASRNVLTEA
VHYSAAVLAVAKAEGIDEAFAWVERLGAEREKYPAPNEKVYNSLIEACCLDADTLDRSWRA
LRNMKKAGVRPSTRTYNAILAGHSKFGRSGEISTVLEEMTKDEVPKDSYTYSLLVRAYASA
ADMRKAFDLYSDYKAAGFPPRHDLCNHLLNGLRQQVAAHTSHGEQGADSACQEGVSEALAH
ADALFDEMVQADMQINAFSFFNLIQANHLARNNGKALELYDEMKRRGVQLNARLVHLMGAV
IATETDRLVLNGQF

>glutamyl-tRNA synthetase Contig20313 (and13024, 27108) (incomplete due to internal gaps)
MKSSTLVLRSRFVPAGARLGGVLGRLPTTTAGRFPYTPSSTGRLHSTCSAESSSPASGLI
DPGRRVRVRYAPSPTGQMHLGGLRTALYNFLFARKHGGDYVLRLEDTDQSRKVEGASANF
DRILEWAGIPYDEGPSKGGNYGPYVQSERLPLYHKHAHDLIEVYLHTFHSFMVSLLLGLT
EERLDQLKRSSNIRGIPPLYDRFCLNLTPQEVQHKLMSGVPHTVRMKVPSGVTSFTDIVR
GAVSFNNAFVNDQILVKSDGFPTYHLASVVDDHLMEISHVIRGEEWLASTPKHVMLYNQF
GWDVPRFAHLPLLLNPDKSKMSKRQGDASVDHYIEREYLPESVVNFVAFIGWAPEDTQEI
FTLEQLIEKFSLERVHKGGAIVNINKLDWFNGTDDIDWVSARVRPVLEQALPSSASFPDA
YLHQVIRLNKDRAQNFTDFVEPSRFFFEEADLASPEAQKARSTLWKPGQSETLVRALLDR
LEKADVPMEHDPLLALVKEVCKEHGAGSKVLFHALRYLLTGGKEGPGVVDTMATLGRPRT
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LHRLRQAFSPAAPPS

>mitochondrial ribosomal protein s34 Contig12316 (complete)
MTTGLPTGYKQFSLVVPKPSSRVKKGKNLFDIAFSFKNFGVGARFTRTGWQYPEPCYWTV
TSVKPRKNEPDMKRGKAWGVLTWRGVTDATPRRIRTTTKKDWSYIKEGEEVPTYSLDEET
HSRRYNYFEGGVAEPEPHVTEGAEHVFRATRRGVTEDIKPRLAPWKVENFTDEEIDKMIA
NVGKRSKSQATEGENKEKSDLS

>D-2-hydroxyglutarate dehydrogenase Contig10618 (26215 and 1873 and 7974) (likely complete)
MKALRATTSRSAFTCSGGVVPGTSLLTQRSGKSAATRIAIWSMHRPVAASTTVACSRRSY
ASMEKPPRDARYAKLEERDVQHFRSIVADPQASVVTDPDALAPLNEDWLHKYRGYSKLGL
QPRTVEEVARILKYCNERKLAVVPQGGNTGLVGGSVPVHDEIILSMSKMNKVLSFDPVSG
VLTCEAGCVLQTLDEYLEEKGFTMPLDLGAKGSCHIGGNVATNAGGVRFLRYGSLHGNVL
GLQVVLPDGTILDSLNGLRKDNTGYDLKQLFIGSEGSLGVITAVSLLTPARPKSVNVAVL
SVPSFEAVQKAFVEVKQDLGEILSAFEFWDRQSMELEMQQLPHIRDPLSSPSPFYILVET
HGSNEAHDTEKLNGFLERAMGEGLVTDGTVAQDTTQFRALWQIRESFAEAGSKAGFNYKY
DLSIPINKMYDLATEVRERLGDKAQTIAYGHVGDSNLHLNMVTPKYDAEVHGLIEPFVYE
WTSKQGGSISAEHGLGLMKRDCLHYSKPEQAIRYMRVIKETFDPQLILNPYKVIPLQ

>dihydroorotate dehydrogenase ContigE80POFO01C2Q3D (and E80POFO01ET2BL and E80POFO01CQJQU)
(likely incomplete - partial - very little EST data ... mostly inferred directly from nuclear
genome)
MMKRGSALGLAVAGAATGAGVWWGMRDAQSPLYPGLVMPFLTSRFLDPEVSHRLAVKSAA
LGLTPVDEWKDDPRLGVTVWGRHFEHPLGLAAGFDKNAEAMEGMLGMGFAFVEVGSVCLK
PQPGNPKPRVFRLFDEKAIINRYGFNSDGVLAVAERLDQFRERQKRVIETASLPIDGAGG
VRGQADSAKKRGLEKGVVGVNFGKNKDRVMGGTDGEGLGDDYVELMQRLSPYADYLVINI
SSPNTPNLRLLQVRVPHTHAHAHTTHTHARTHSGSELQKILEQAQAEDIAAAALKYKVDG
IIVSNTTVSRPLRVHNEQEETIAKEAGGLSGRPLLEMSTQLLRDMYRLTEGRIPLIGVGG
ISSGKDAYDKIKAGASLVQLYTGLVYEGPGLVGRVKKELVELLDRDGFRTIEEAVGHDHH
KEVETK

>alanine-glyoxylate transaminase Contig10009 (complete)
MKSSRRVGSALALGGRVQRGQRMGATALGSLGASRRSVQTTPGETKGAKPLLMIPGPIEF
SEGVLQSISLPTLSHVSPDFIEQFGQALEQLRSVFLTEKGQPFVLAGSGTLGWDMAACNL
LQKGDKALVVNTGYFGDRFGECLTAYGADVTHARTDIGNCPSVADVTQLLGQRDSFKMVT
LTHVDTSTGVLVDIESFAQAIRKHSPNAIVVVDGVCASGGEELRMDEWDVDVVLTASQKA
IGVPPGLAILMASQRAMSLFKSRTAPVANYFCDWSKWLPIMESYEGRKPAYFATPPVNLI
RGLHTSLYEILSEGEGAMDKRFKAHQTAGKAVREAVKALNLTTVAVSDKLAANTITAVRF
PQGVSGPALLPKVKAHGAELAGGLHQAIKAEYFRIGHMGVSVTDLNRGHLEQTIRAVEQG
LVECGYTGFERGAPVKALQRVLTAQ

>coiled-coil domain protein Contig21977 (and 12139) (incomplete - internal gaps)
MHRAATARTAASRLCGLATTSSMACAPSSALLRGFAASGALLRPSAAVRRLPSRRYASIA
EVKEPLEDVLRKAQYRQVTDALERDGSRVRVATLPGTTWRRRRRVSCVKSLHKSGRVLHY
ENSPELAATVIVRPDALAASFVKLLDVQGEYTKGFVQAKQQELDALRQELQELEVTRQGL
ETKAYQRADNWIRLGLAYIVLQAGLVARLTWWELSWDIMEPVTYMLTFTTGIGAMAYFTH
TGTEYTYEALRRHLAEGRLKKLYRKHNFDINRYQELQRAVVQTEVELAAPEVHLLKFQTL
ALQ

>citrate lyase beta subunit Contig2805 (complete)
MQRARSVVRATGVWSGGAQWGPSSQLWVGTRRLFATSATGHGALRSWLFVPGRQDMLLKV
LQKKGDMALPDVLVPDMEDSVPLAEKASARQAIASLLPQLAQLGAHTKVLPRVNSLDTGL
MEDDLQAVIAQGGLIFGVSVGKVGSAEDMRRIDEIVSALESKNGVRAGKIHIVPWLETAA
GVVNAHEICKSSSRIIGVAYGGDDFLTDMGVQGASDQTPSGLVTYARSAISVAARAANVL
SLETPYVNFRSAEGLRAQATDVKRLGYRGMFAIHPNQVQTINECFSPSAQEIEYAKKVVA
AYEEAERQGKGSTSVDGKMVDAPVVKRAYALLKTLPQP

>mitochondrial ribosomal protein L45 Contig593 (complete)
MASSRLILRTPIARIFPQTAGGSPMLLSATAVLPSQRRPLFPATCGMTTRHYAQTSKRVG
GMSYKPRIFVASLGQIADPAIPPSGAELLNPKKLWARLMSSMRNYASLWQVRKLLKKEKY
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PTSAWLIVGRWTAEAANQYRAFCEARANGNKQALQKLTTDEFFDVVKGSLIDPSSKLKRE
WQSQDLRVKVLALRMVMLQEPDVKFVQMLFRFTSQQKLKITDSKGALIAGSDSAVPVTEY
YVLERPLQDIHLFDWKFMGKLDPSHKEPLAKPLLEQ

>cysteine synthase Contig10433 (likely complete)
MKHMTPRSLMPSRRAGSLRHTTSPSFSPATLLSLHRSSSFSRRWSTFNNGLVEGFPGAVG
NTPLIKLRGLSEETGCEILGKAEFMNPGGSVKDRAALYIVRDAEERGLLTKGGTVVEGTA
GNTGNTTCPSPSSIHRRRRSTSYDPSVPRSLPVPAVAYDNPANYNHQARDFAQATPNCVW
TDQFDNVANRYGHFSTTGPEIWFQTQHKVDAFTCSTGTGGTLAGVGLFLKQKKPSIKIIL
ADPPGSVLYSYVKEGKLEREGSSITEGIGQGRITKNLKDAPIDDAIQIPDEETMSMFFRL
LDEEGLFVGASAALNVVAAVKVAKKLGPGHTVATVLCDGAQRYYSRLLNKKWLDEKKLLH
TLPDKYLQFLH

>DNA-binding protein Hu Contig12508 (complete)
MSKGPLIEAVFKQHSLANKTGKTISKAAIGRIVDSVFEQVGKQIVGKGYFRYPGFGSFLI
KDRSARTMYKALPRTKGQTMDRSEANKITVPARGVVGFKPAPPLKESVKDLKRVKRAKAS
KKEQEIV

>branched-chain amino acid aminotransferase Contig12291 (and E9BS9UA01BNIBK and 7815)
(complete)
MRRTISVASSSSFLVARSGRLAASASCRSLATSGVPQPKQDVDWEAMGFNLTKTDFMYVA
NTPKGSDFSRGEIRKYGPLELEPAATVFSYGQSLFEGLKAFRTANNRIVIFRPTENCKRM
NEGAARFLMSPIPEDVFMDGIKETVKANAHYVPPFGKGALYLRPIVFGSGPALGVAPSPV
FTFVIYASPVGNYFKGGIRGINLIASEDVHRAAPKGAGYVKAAGNYAPCFQIQQASKKAG
YDEVLFLDAKEDKYVEEAGASNFFCVTPDDTIHTPSLRGTILPGVTRKSLIHLAREKGIK
VNEGSVSIDTVCQAKEAFCSGTGASVTPVASVTYKGNKYLFNNGEVGKVT

>isochorismatase domain-containing protein Contig26021 (complete)
MQQVRRLGKLQAHSSVLMVCDVQERFRSVITHMPSVLHVARTMVKAAPLLRVPVLVTEQN
PKRLGRTASELGVDETEGVRVFEKLKFSMLTDEVRQTLERDHPERKDVLLLGIEAHVCVL
QTVLDLLEGGYNVHVLADGTSSSRQADRLLALQRFSQAGAYVTTSESALFQLMQSAEHPS
FKAISALVKEERPDSGLSRL

>hydroxymethylglutaryl-CoA lyase Contig9803 (probably complete ... N-terminus partially
inferred)
MKRTSVMASRRRLVPCLGSTYTTRGMMPAAQGARFLSTSSSSSSLEDEPR
FSWFGPLPKKVKMYEVGPRDGLQNEKEVIPTEVKVELIERLSRTGLSVVE
ATSFVSPKKIPQMADSVEVMTSIKREPGVIYPVLVPNDKGYENAVKTGCS
HIAVFTAASETFAQRNINSTIGDSLARYRELCKKAAKDGLQVRGYLSCVL
GCPYEGHISPKKVADVAAELHEMGCYEISLGDTIGVGTAGSTHRMLDEVL
KRVPLEKVAVHYHDTYGQALANILTSLQFGVATIDASVSGLGGCPYAVGA
TGNVATEDVVFMLHGMGIETGVDLEGLVDAGDFISKQLRRPSHSRVAVAL
VQKKKDHMMRRARGLLDELSNGKFSAPTTKTTSTSTSTSTTSTSSTACV


>ATP synthase delta subunit Contig2942 (complete)
MRRISASSRVLGMSAAAGGRFGPRTASVLTTTTRRSYATDDAQREAHEKAVKEGKLIFTL
ACPHETLINAEPVRIATVPSATGDMGILAHHVPTIAQLKPGVVKVTKFDESGATRDADYF
ISGGFVTVYPDSHCNVNVVEAFPLDQLDPEKAKKGLEDFTKELASASDAEAKTVATIGVE
VYKAMCSALKV

>hypothetical protein Contig4941 (incomplete C-terminus)
MTAQVLEMMEGAGVMPNQHTYTTLINVYANFTQHTAFPRGPPWLSPRNTPELREAGREAL
MKALSVYFSMRRQHLREQAASPSSSARGVPTATFNSLVKLVGTEDLLDVSCHDIDHLHDE
LLLLAAHHDAPAPPPPPRAKQQRGQQQQQQDEAEAWTRLPLAELQKRYAERPLPLPAYLP
AERTASQMTPLELLAWRDLAANGASPDRVTYNHLIFHLTASGRLPHAEHYLRFLLLHHHH
HHHHSPPPTHENPSSAASSSSSGPAAQAADGGGGRPDFLGRQLNPKYSSYLIKQRNDRRA
QFAKLLAKTPPSAAVGTAHHEQQQRQQQEEAQESTDVFGFDEAPGVEAGAHHHPLFLR

>mitochondrial phosphate transport protein Contig16437 (complete)
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MGEHLVSAVGGALTAALSHVTSFPLDVLKVRAQVGRSWLPLGEGFRHGLAASLVGWSLHG
GAKFLGYNMLREELHDVLPWGPSNTYLFASLTAETVATLLLAPFHTCEVKLVSDPLFAPS
LIAALLKIIRLSGVRGLFAGLPVLLLRQLVAGFCKFHLFEKCARASFNYLEPGYAKDRKI
KRYHRVAGVLFSSLVTSAVCAIVSNPFDVIYTHIAASPSPLSVLDVYAQVGLTGLFAGVG
YRVASTTLNNFFIWVYYDLFKELIAM

>mitochondrial ribosomal protein S9 Contig25384 (complete)
MRGSSKSTAVLGLPFPSPAGSKAALCTASSSRISSRVLPPARLHSLASSPLLPLSVLSSQ
RRHYAVKSKNFERKEARYDFSEITNRVWPRHPPPQIDYRNYVPAEEEDEEDDWKPEEDYP
EPTFTADQTSDQYIYPVITPQTVPVKIDSRTGAFLGTGRRKAAIARAALVSGQGKITING
RSFLDYFPCFFERGAVLAPFVAIERPNTFDVNVNVSGGGTKGQAEAIQLGIARALQSYNL
AFRPALKKAGCLERDPRVVESKKAGRVKARKRPQWSKR

>MAPEG family protein Contig12437 (complete)
MASGFPILRDVVAYPTLAVAASLVVYQWQCVAVGLARHKYGVAAPKTTGNDDFERVFRTQ
QNTLEALVIFVPSVYTFSYFVHPVGAGVLGGVFAVGRLIYGLGYAKQAEKRSAGFALSLL
ANAVLLGGTVYGVGRYLLTRPC

>Tim44 Contig12315 (and 15550) (likely complete)
MSFWSEFVKSFKEQAENSKELNESMAELKKLQESESLKKTKESVEKLKDKSAEGLAQLKN
LSEKAAATGGRVTARVSDSVTSTLGDITQRVGMDEKLEKTKEGFEKVADSLNKARENIEK
VGENIKTSAEESELVKKVKEKVPFGLLDGSDAAAGEGSGGEGAVAGARSQLVVKTQEVQT
AIEKRLQDARDRLRATGAFKKALALREKIVESDNPLIQRVLDLGDGITRTTSKLFSENDH
AKTIKLIHELDPTFSPEKFKQKMASSFVPTLRSALLRGDPAPISALMSKRLAEHELEAYK
EWDAHGYRSHSKLLNLDTVEILNAHTRDDGRPTLLIHFVSQENHCIRDSSGAVVEGAPDN
IQDVEQTWAMQINSQGEWEVIEYMVVASRPSW

>hypothetical protein ContigE80POFO01BSS7G (and 10698) (complete)
MWASDVDFEASLLQQGDAATDLVEHMTWRTRRFPGLHLPNRAALAREWAVARGTSTRLLV
TTLRDPDFFANTPAQTAAASGAWVPWLSFVHSQPEAALGVMGDGMRAQVVGALDVVPGVR
LSTNFGVIPASANDPRGSLLNKGIGLIPKTESELECYAIDGLQLSLTHATASLEGVDYVV
NATVSVNPMALARRFAAASKLETPTRAFLERWQLEARVTRIKPLNQPALGLPSLAVQYSH
PLGPAPGDGRRVPRLVLTAKAQALNTLRLSVTYDPVDILAALDEGASQGKPAVTGVCASG
VLSVSPSARAMQCLGTLRYYGDGYRATATAGWAVDPRQPSAAWTGTLSWVQRARNTSVGA
FVSGGRFNDQLVTPRFGITLTHHI

>hypothetical protein Contig15309 (and 17225) (complete)
MSDIEYQAPHSLRAAEAEAAAEQPNLSSSHSDSSGSTSSSSSSPTAPRRQRRASSLSTSA
PSGPAASMQASGERRISRRERLSGRGFMPPASGGGGGFDEELDDYEDGDVGTTDVLLYLA
RRIACEFGANLAFNLPLRLVSLRQAARPLGHPQHSLAHEVKSLISPSSSSADSWKYVLGT
SAFIGMSEVVAGLFSGGVSMYFDSGHIPTVDEWHEHEKPTIYGVSRKQLAVFAGKLLTGVFFYPF
FAVAPILLATHRWPGTGQFFRDLAYNRNGFWNALAERGQVQHHRSGAVPGDQALPLPPA
GARGGRGGRGRVGGGEQLPLLGQALHQIRPLLHLDGVGVPALRSARCAHHADGGLPDAVF
RRGRLRQEGVGRRRPQGALPRLLGQPVERTGAALHLMNQERERDLVL

>leucyl-tRNA synthetase Contig9820 (and 12901,4046, 11402) (probably incomplete)
MLRALSRSPSGAVANAGLRTRLPTTVSGGVAANACGASSRFLRSHNAKTP
DFFRFRFFQRAYTAEAPKEAGSWAATYQHKAVEDKWRKVWTELQHQKQQR
QKLGADEQATAAAAKDKQYVLSMFPYPSGQLHMGHVRVYTISDCLSRYHQ
MKGKEVLHPMGWDAFGLPAENAAIERGIAPHTWTHSNIATMKSQMLRLGI
QFDWDKEVTTCEPEYYKWTQWIFLQLHKAGLAYQKEAAVNWDPIDKTVLA
NEQVEQKLMKQWFFKITEFADALVEDLAGLKGWPEQVKLMQQHWIGKSKG
AYLEFPIKRELSASSGAKAEEPLRIFTTRLDTLLGVTYVVLAPQHPLVQE
IAKNTEDAKLRAFVDEFAKSKRSLQEDYGKSKKGMKLPGVTAVHPVTKES
LPVYIADYVLMDYGEGAVMAVPAHDTRDYEFAKQFDLPIKTVITPDQHTE
EHKEGDPFCGEGRVVNSGPELDNLTSEEARRKLLRILGEQGVGGEYTNYR
LRDWLISRQRYWGAPIPMVYCEADCGVVPVPEKDLPVVLPVDGLEFSGRG
GSPLGSLEHWLHTDCPKCGGRAKRETDTMDTFVDSSWYFLRYPDANNTDA
PFDKAVTNKWMPIDVYIGGIEHAILHLLYSRFITKFLHAQGHLNFSEPFP
NLLTQGMVQGRTFKDPHTGAFLKPDTVEKVGDKFIHKPTNQEVAISWEKM
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SKSKYNGVDPDRIVDEWGADTARLFVLFKAPPHLELEWENAGITGAYRWI
GRLWNLVNTFVQRDPSADTPSPPPSVTERAKEEKDLLALTHETITSVTKA
LDAAPYSFNTAVADLMKLSNKITTLPADSPQYYLSLRSLVLLLHPFAPHV
SSEMWQALVAHGPAHESAWAGSSAAPELSRQLWPVANEEFMKKDEVVVAV
QVKGKTRGTFVMPAAEVGDKAAVERYARESAVGKKALWQRDVKKVVIPPN
GKIVNFVC


>Acyl-CoA dehydrogenase family member Contig14716 (and 13138) (complete)
MKRSAIATATARSASAATVRRSTAVPLVLRSATRSAMVSAPRFSAISGAGQAHPGFAALS
SILPRRCGYSTYIPDMSVGLSDEQREIQQVALDFARKEMLPHAEKWDEEEIFPEDTLRKL
AELGFAGIYIKDDIGGSGLSRQDAAIVFEALSTACPSTTAYLSIHNMCAWVVDQYGNQEQ
REKYLPTLLSMEKFASYCLTEPGAGSDAAALKTTAAKDGNDYVLNGEKAFISGGGASDVY
IVMARTGQSGPKGISCFVVDKNTPGLSFGKKEKKLGWNSQPTRAVIFENVRIPSTNLIGK
EGEGFRIAMKALDGGRINIAACSVGAAQACFELARDHVQVRKAFGAPLSANQTIQFKLAD
MATSITASRQMIHLAARKIDSGAEDLTAYCAMAKRFATDEGFQVCNDALQLFGGYGYLKD
YALNRYLRDVRVHQILEGTNEIMRLIVARQVLKDAPPA

>acetyl-hydrolase Contig17691 (and 20112, 5495) (complete)
MSSRVVEYFLRFPHRQLARVVVCCEQVSMNKVAGFFVVLLAVVVGLVVLYPGAAQRALVT
GLIKADVLLLKHWYNVTSTERSLESIALEHLLRFQAYTLDVAATRSNLDAYGRLLPLGPG
VVAERVNISRHDGTVLPAYWITPPGYNNKTILFYLHGGAYIAGSFTSHGGSVAELARRAG
AKVLFVEYRLAPEHPFPAPVEDAITAYKWLVYDQKVAANRTVFVGDSAGGGLVLLALLAL
QDEDKGTIPAPAAAVTLSAVTDMSADRPSYLKNAESDTLVKEAFVTWAASQCTKTRPEDR
AARKSHKVSPIFAAADKVAKLPPLYMSVGESEILHDDTAHFAGKALQAGGDVKLVAAPFM
QHVFPYFYHFVPEADQELTQIANWVKKQQQKI

>mitochondrial genome maintenance protein MGM101 Contig17629 (and 5920) (complete)
MQRTMMRGGLNRGASAVIRTSRSSSGASRLTALSVPLSSDSSAVRPLRLGALQQRGYARR
RAFPFVDAQMAMNDEGGAEEDNETEDDEDEDYADDGETTQYSPFFGNAAAAPAAQPRHTE
NSFDGISTRAFPRKVADRLVAPVDPNIVEIKPDGTVYLPEIMYRRILNSAFGPGGWALMP
RGPATHGDKFLTREWALFCHGRFVAQASGESEMLTSFTGPATALEGVKSQALVRCCKDLG
VASELWDMAYVTDWKNKYAVAVWCENQKTGQKKTLYRRLDRPPFPYPWKESQLTTSTAAS
SPSSSSSSSPAPKTSTSAATSSSSATSAGAAKAAYSTAAEPFDMEALLPRELKKFAGKRW
SEVVSTDEGQKYLDYIANNFEGAARGLAQRALDSHHASRK

>glutamate dehydrogenase Contig3678 (and 9294) (likely complete)
MRRATAALPYARSAAPMRSSALLACRPYSTTPATAAREMSFLESVLHNFNKAAALTGLSE
PQIANIRKCAAVFRVKFPVRVNLNEKTGEYDTMIVEGFRVQHSHHRLPCKGGIRYSEHVD
QEEVMALASLMTYKCAIVDVPFGGAKGGIKINPRELGVSQIEAITRRYASELIKRNMLGP
GMDVPAPDMGTGPREMAWIKDTYEAFHPQDVNSLACVTGKPISQGGIRGRTEATGLGVFF
TVREAVNYEEDMKALGLTTGLKGKRVVIQGFGNVGSYSAKFMHEAGAKIIAIGERDGGLY
NKDGIDITALWNHIGEKKPFLSFPGAAVVKNPESLLEEECDILVPAALENQINATNALRI
KAKIIAEAANGPVTATADEMLEKRGIIVIPDILCNAGGVTVSYFEWVKNLSHVRMGRLER
RYDQRSKERLLEHFSNITGRKEDVPAGVVSGANEADLVHSGLEDTMIEGYANVRSVSKLK
NCSMRTAAFVDAIRKVARSYAELGVFP

>acyl-coa synthetase family member Contig27430 (and 19719,6022, 7656)  (likely complete)
MLRRATAITTTTTTGGASSFRRSSSAAVRRLAAALPPLRGLRALHSSPAA
LRAAPALLPRLGLVERAVGHRQRTAVVAPADAAVDSTANQRERSYGRLLA
DATALAGHLRQLAGVAPEKDMKEGRVAFLCPADYSYVATQWGIWSAGGVA
VPIGVHHPGPEVEYVISNSEASAVVIHPTFEQLVEPIARRLNVPVLTLAP
QLFPARPAELEPSFFDVDLDRGAHIVYTSGTTGRPKGVYTTHRNVEAQVS
ALVDAWGWTPDDHILNVLPLHHVHGIIAVLTSALWSGAKCEMMSKFDASA
VWRRFTDTTQPQLSLFMAVPTVYAKLIEAYDQMTPEQQRHATDACRHFRL
MVSGSAALPETIMARWQEISGHLLLERYGMTEFGMAISNPLHGQRRPGCV
GTPLPGYKVRILPAAAEGQAAASAATTEHGVSGDLQVTGPAVFKEYWKNP
EATAKEFTNDGWFKTGDIAEYVDESGVIRILGRSSVDILKSGGYKISALD
VERVLLEHPAIAECAVVGLPDPSFGQTITAVVVLKQGEKELELGALKEWC
QDRMSGYKVPRKLLALAQMPRNAMGKVNKKDLVKSIITTTATA
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>O-glycosal hydrolase family protein Contig21208 (complete)
MPKKFTIKTHHGKYICSEPSHTIVGNRDSADAWEHWEVIKLGGGKVYLKSAHGKYLSAET
NGTVVANRDTPKEWETFHVHKLGNKKVQFKTHHGKYLCVEPSGKVIADRAAPKEWETFEF
RKVGHCC

>lon protease Contig10152 (and 3185, 21213,14877,1398,5437) (incomplete, with many internal
gaps .. large part genscan inference)
MLRSRSWLKHSATPSLLRTGGRGWAPQCRSGLSVAGALPSPRGANLPFSTTPLPALRCSR
GPTGTSGSSLSVQTWRDRQWRNAAAAAPNGARRGFRTTAPAAAAAGDDNDDNENNKKKDE
PEYREDSDDDDDDDDFSDGEQDGEDVMPPRDMPLQVMVKTVTTPEQVLVVPVIKTSIMPG
TMGRATVRDPEFLKELQELRQKHPSPYIGLFIVKDAEEAKQKGVQITTLDQLHQTGVLGV
LTNVVPMRPSQQKDGVVGVIQFLSVHKRIKIDETVSGTKRLVAKVSELQDKPYDPKDPQI
RGFQAELEAIVHRIGAKGDVFARDNAAQLLLNFWTFHNPLNAAESADFVAGIITHIALDD
AAMQAQQAVIEELDVSERLKKTLALTKRELSLSDLTQKIKEDINAKMEERHRQMTLRDEL
KAIRTELGLEQPQTETLMAKFKERIKDKQVPEHAAKVINEEMEKFQHLSPSSTEYNVVRT
YLDWLTTLPWDTLTKDNLDMHHAEKVLEDEHYGLKDVKERILEFIAVGALKGEVTGHRRT
YVGAMPGKLLQALKRVKTSNPVVLLDEVDKVGTSSYKGDPSSALLEVLDPSQNTKFLDHY
LDVSYDLSKVLFICTANVLHTIPRPLLDRMEVIRLSGYVEEEKVAIAERYLVPKAVSEAG
LSEIKVNFEREALHKLIHSYAREAGVRNLQQQIDKIMRKVAHQVVVEQEKRQEGAVEGSD
GKKGAKGGVRKGRGKKKSTQERADESAQPGSSEALTLEKDQHGAIVIKPAGLGQFLGKPP
FSNDRYYDTTPPGVVMGLAWTSMGGSTPYIETVVDKHQLLVRKEEKRKRREAKEKLEKNK
KTNDDVASSESPATASSEDDAEEEGGSGSGRLITTGQMGEVMQESCSIAYTCAKIFWNKL
GAKRARSPQGATQGEDEGFDEGFFRDVTLHMHLPEGATPKDGPSAGIGMVSSLLSLGLGT
ALRQDVAMTGEITLTGKVLPVGGIKEKVIAARRAGVKTLVFPEGNRKDWDELEPFLREGL
DAHFVDYYGDVFQVVFPDAPKEYHQALRRTSA

>Hsp70 Contig14215 (complete)
MRATGRLNPMQGKMAFASLGGCRATAASSSASALFNRSAAMRSTFAGPVFSRRYTSTSDP
LVMGIDLGTTNSCVAVIENGKPRVIDNVDTGYNTTPSMVAFTKDKATGQQTMLVGDPAKR
QCVLNPRGTVYGVKRLIGRRFDSEEVAKIKKHVPYEIVKAANNTGDAWVSVGGKSYSPSQ
IGAFILQKCKESAEKHVGQTISKAVITVPAYFNDSQRQATKDAGAIAGLDVLRIINEPTA
ASLAYGFSEENSKERQRLAVFDLGGGTFDISILEIGDGMCQVVSTNGDTFLGGEDFDETV
LQYLMNEFKKKEGVDLSKDVFAIQRLREGAEKAKKALDHMPNYEINLPFITRDKNFSYSL
TKEKFNELIKPLVDRTIKPCQSALKDAGLDKVDNVILVGGMTRTPAVIEKVKEVFGLNPS
KGVNPDEVVAMGAAIQGGVLSGKVNSLILLDVTPLSLGVSVKGDLFSRIIKRNSSIPCSN
TQTYTTAADGQRQVVFDLLQGEREIASANHLLGQVTLPVMPAPKGIAKIDVTFNIDVNGI
VHVTAKDPVLNKVATVQIQANSGLSQRDIDRMLKEAELQKERDQQIKELAEVKNEAETLI
RSAETDYLHNDVVPEEDKETIRQAVSQLQTAMDGNSDELKTIYASLKDTILNVGAKLYQQ
GGASSSSSNDGHNHDNNNQETKQ

>mitochondrial ribosomal protein S17 Contig7327 (complete)
MKRVAVMQPMRFAGVAAARTNAWGLAMPRLSTVAQRRWTSSTPSTEDRAAAVESAPKEGE
GEEKMTPNAYKQEAAFRKDPIQPYIDGRTRDPLYNPVVDDWVDYNNPRWKALKHTFNRPG
PFFIGKCVSTKTAKTSMIEVPYWVRSMKYGKHMAVRRTTRFMAHDEDQICEPGDVVEIRQ
SKKWSKRKNTVVTRILKKDPGNAFIAEHPEFAIVRSRADLRKRIEQMREDELASAGLDVG
QGKRKTDSSEGSESGQQHQQQ

>enoyl-coa hydratase Contig19014 (complete)
MQRASLRLRHARPSCASALARFYSTAGSSANSEQLVRLEADHLPDGRPSGVYVMTLNRPD
KFNALTEAVGEEFRAHVADLAAMPPRSLRSLVLTGAGPAFSAGGDLDFLWARTKTPAEDN
TEIMLKFYKRFLSIRSLPVPVIAAINGPAVGAGFCLAMSSDLRIAAKDAKLSANFVKLGL
HPGLGATHYMPRSLGPQVANRLLFTGETLTGDEAARLGVVLEAVEKNQVLPHALNLARTI
ALNSPSAVRLLVRTLRYDDDVQLERALLREADGQAHSYASADLQEGLTAIKAKRPPTF

>pentatricopeptide repeat protein Contig14408 (and 4431) (likely complete)
MRRSSELSRTLWQRGPRVLPCATSFSSRATHTPALLFPSSAPRPATGVSLLRRMLATSAQ
PSAASAKSIPASTMTDEDDDVEDFAKLSQRSLFENRLQTLEANSNEVAPRQLATLLRAMV
LGKREKLKEFQPRVLALHKRVRGGTKLDGTAVLAALSYIGNLEATYAEYERLRAENIKSF
ELNYGYLIEVSSSQGNLKQAFSVVDLMRRDRDLLVESRPSTFVFNRLIIACGRNQSLGRA
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YRAFELMHEEGLRPTPTTFAAYIDACARTGDLQSGLKVLSQMKRILRLSPEKYQLDASYY
TGLIPACHQPQDFDRIVAEMIREDIAPAEETLAALIKDCATNGGLSRALGMFKELRLFQE
VTQQQQSQKKDHKQARAELAEERRKVVHKPSLGSIFF

>GTP-binding protein TypA/BipA Contig1617 (and 775, 15798)
MLRSALSRSSSSSPLAGSASSRSSLVRAFSSSRSTAASSSASSSSSSSGNRLHRCLAAPS
TSSSAQPSSSTLISSQRPLGASLRRTAPWSALRQVGHGWPSLASHHRSGVVGGRALARRW
LSTEAEGAEDLGEGVRNEKLRNIAIIAHVDHGKTSLVDKLLSQSGTTSLRGGERVMDSNA
LEQERGITIMAKQTSIKYKDYTINIVDTPGHGDFGGEVERVLGMVDGVVMLVDGTEGPMA
QTKFVLSKALGYGLKPIVVLNKMDRDTIRPDEVESELFDLFVSLDASDEQLDYVTLYASA
REGWAVKNRTAPRTDMTELFETIIEKVPPPLTYPDAPFSMLVTTMEYDMHLGRILVGRVR
SGSVTTGDQLHGLSREAKELEKSKVLKVLGRRGLERSPIERGECGDIIGIAGFGACSVTD
TICAPSVVHALPANPIDPPVLSVVLSVNDSPLAGREGTKLTSTLLRQRLYRELESNVTLQ
IGDTGREGALEVKGRGELQLAVLIENMRREGFEISVSPPKVLFKQEEGELLEPQEEVTVD
VPTEFSGVVLERFGLRKGELVEMKTDGDKARLIFMCPSRSLIGFRQELNQLCRGTVVLHH
LFHSFIPHKGVIENVRKGVLLSNTNGTTTTYALESLEQRGTMFVGPGTTVYMGMIIGENS
KKGDMDVNPVKAKALTNMRTLLKDENVRLTPPRILTLEEAITYIADDELVEVTPSALRMR
KEILDTSTRETMARRAKKSG

>mitochondrial ribosomal protein L12 Contig24290 (complete)
MRRSTVHVFPRLALRQGQQTSALCLFSNGSRTAVSSETNMASIARNYAAPAKGGKGAPAA
AKPAEDEPAEPLKLETVTFPDFGEDKAFTADISDFPAPKDWKYVSDWKEFEFSPRVRKIG
EALFQLNQVEMFELVKLLQLRFDVPDSALMGGGVVVQAAGAGAPAAAAEPAAEEPKEEKK
EKMIFDVQLTAVAEADKFKVLKEIRALKPGMKLLESKEMVEKLPSMLKQNVPKEEAEQMV
AKFKELGGTVELK

>monoamine oxidase Contig249 (and 13233,4140) (complete)
MDAYDCIVVGAGLAGLQAATKLAERGHTVLVLEARDRVGGRTLNIQVGQDAWDGGAGWIG
AQQPLVKGLCEQLGIATYPQYDEGKHILMINGKVSTYTGNISSLNRSDLGELEQVVQQWD
ELMLKVPLDKPYACANALEWDSMNLEVWERQNMKSEVAINLLNFIIRTVFAVEPSQVSFL
FFLFFLRSGFGYNCLSDIRGGAQQERVVGGTQSISLALAQVLGSKILLNAPVRKIEQWAG
GVVVHSDLGVHRSKYVVVAVPPVVAGSIQHSPPLPAMRDQLTQRMPMGCVIKCYALYDRP
FWREKGFSGEVLTTSSPLCLYYDATNYRGSAALVGFTAGDGAVNWSGREAELKAAIIEQV
VSLFGEEGRRPREVIIKDWMQEQPWSRGCYVGVMPSGMLSSFGKALREPVGRIHWAGTET
AMEWIGYMEGALSSGLRAADEVVARLHTDPVPARL

>putative transmembrane protein Contig20328 (uncertain of N-terminal completeness)
MSNVEVGAVAAAAAGGVPVIAQAEAEAVAVEAADEALLEEEEAANSKRVGEDEAGVARTM
RRWTASGCGEVHWERSCGAHFLRSFARNFAVGSGVKTLLNLVGFLLRKRRKGKGVPKRLV
PKLVKLVDLRWGFFLGSLAAVWKAVSCLSRRAIIAHAGADPCDLAQVRALQPRFAAADLV
AGAATGLSLICVRPEDRRTLAIYSLVRSMEFFFAFLGRQQILPAWLLRFSSHLDVLLMCA
TAGQVLYCYAFEQDTLAPSYRNFLNVHGGKDPRVRGFIKHTHFGLPLELDHLKSFSRERK
IDPEVARQNLLNFNICTVLHPHETCVQHFFTFAWAGFKRALPLYAPLHIVTTLVVLLAKL
TSKVKESVKRAGSFSNLSRSFSIDDFIEATDAQQQTHDGAHAPVPAQPPARKEPLQAALD
KAQAFAARMLKVLTKRRILRVTSFTLALVRRVIFNIVRSSVFLGVYCSAAWLAACFAHNM
SGVKGPFWVRLHLMFSGLACLLEAKSRRIELAMYCIPQALNSAVNEAIKYNKLPRWLVNL
RHLDVLFFCLASAVTVFCYKNDPKSIRPSFYFLMKWLWA

>nucleoside diphosphate kinase Contig11656 (and 50 and 14904) (complete)
MRTARWLPCQRPTALLSGHALGRATGGPSTAALVFPSAHNSSHQKRHTSIHRVRQGEQLS
FALITPKSLAKSLTGGIIARLLATPELQFVGARMLRPSAKLTDEFFLEMQRAAHEDGVID
PYEDTFLKAYPTIFGEEELKESGVANHTMLLLFAGGAQTRQVLADVVGANVPNPNDFGKT
IRGTYGDYFKDRTGKINLFQPAVVVPPSDESNRRCLEVLAKYLDSDHALRTINAEERNQP
LGWAKQTGLVMIKPDNLERPSSLPGHIIDLFGTTGLQLIGARVFCMSVRRGMEFYGFLEN
VFVKKLKPNLEEAMKQRLASAFEYEVTDQDYAKMADVVINRHARCEVAKIIHYMTGVHPD
DAKTDELFRKPGPAKCFALLYRGDNAIEIIRSKLGVTDPKKARAGTIRSDYGHDLMRNGA
HASDSPEGALRERRIVGLMGDEPSEEKAVILEWLHASSAPLSRQ

>conserved hypothetical protein Contig21421 (and 14063) (complete)
MRRGLVVQRFGGSSGSTGSLFAASAASSCGRRQLVLTGPALTRSFRTTPCSAAPEDLEDD
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KDGVEINAEDVEGEEYVSNSNESQADKKRRSKEARYAAENAELDFLAKALIWDYRGQHAP
RPMLAEETKEELYRLHKEDPKRWDLENLSLYFGLRKDRVQAILTFMGMRDVAVRNGEVLN
GGVVELLEQEFGVVGRLADKRVLDEERAGGRPGSGLPLEEDAIDNDARLLDHARAVRLAR
APRGAPLKELPPQPPKAADGSQVPEAKPHVLRRPTPTEPRSFKGTIFMERDSRRPPWGRR
RRYNDATRIMYISEPDGTLRTPTWDERRLLTSADKHIPTTARYAVGENRFFKDDN

>Electron transfer flavoprotein-ubiquinone oxidoreductase Contig9397 (incomplete - internal
gaps ... N-term from PGPs)
MKRLSARLSPSASAAALGVRVSSRHLHLARTAQVQSSSSLLPRAPITSSLRSFRTSPSLR
QDDDPRKQPRESDNVDVLIIGAGPAGLSAAIRLKQLANEQGKEIRVVVLEKGAEVGTFLF
SGGAHTLSGAVIEPRALNELIPYWKDKGAPIYTEATEDHFVFLGEGFHVRLPTPPQMHNQ
GNYVVSLGNVVRWLGEQATELGVEIYPATPAAEVQVLYNEDGSVKGVATVDMGVSKTGEP
KDSFTRGFELHARVTMFGEGCRGSLTKSVDKKLGTSGLGIKELWQVDPKKHKPGKIVHTI
GWPMDFSTYGGSFLYHLENNYVAVGYVVGLDYTNPYLNPYREFQRWKHHPFVKDTFEGGQ
CISYGARALVEGGIQSVPRLAFPGGLLLGDSAGFINLQVRNIRPYMAKGLVPGLALSAVD
TYVFRGNAPWTLNHHKPDHEATKPAKECKPIEYPAPDGKLSFNLLENVARSGTNHGHDQL
CHLTLKDSTVPEKINLYAAPESRYCPAGVYEYVDSKLVINYQNCVHCKTCDIKDPTQNIN
WVVPESGGPLYSYMVTTSKDYISQNSRRRIVSLQAHKQAHHHFNPTEVKSVEDEGPASEK
ELRAEWRKQKDRIAFLESELAKKDALLKNQGN

>hypothetical protein Contig24337 (complete)
MEKRNLYSLCEAHFEGFKERCLTYDGDPALKPRECQGTYDFLSECVGVATISCCEKEAAD
FRTACDAVEAGADGGRPWENTQPCYENTRRLVRCMTGTYGIKERIDLQNAEDRDLDRRAR
ELEKEAARVEALQRNHNPRS

>Glycine-rich RNA-binding protein Contig11262 (and E80POFO01D3VP1) (complete)
MNRLCLASRPAASLLIARQGSSAANRMAIRRFTEDINPSRLFIGGLSWGTDENKLKEAFE
GFGEVRHVRVVVNRETGRSRGFGFVTFQSPEDAAAAAEAMHDKELDGRRLSVSYARNTPR
EGGFRQRPVEGKEEESM

>3-hydroxyisobutyryl-coa hydrolase Contig7435 (26279 and 15441) (incomplete - internal gaps)
MKATLRVATSNVRSAGSTRVCSAASSFRSQRRCYSESAETEVLVQPLGKGQEVVLNRPKA
LNALNLNMVHLLRPHYTHWEKDPHTAFVLMKGAGGKAFCAGGDIRAIYDEGIAARQAGKN
AGGDPASLGYRFFHDEYVLDYQIATHPKPQVAFLNGITMGGGVGLSMHNKYKVATEHTVF
AMPETAIGFFCDGGGSHFLPRLSPGFEVGMYLALTGARLKGYDLYVPSSKTQVLEEKLKN
AENEDHVRHTLAELNEHDTANDANSELIKHADAIHKCFGKASVEDIIVALEREGSEWATH
TRNALSKLSPTALKVVFRQLHHGKQLPLNKCFEMEFRMAQRFMAGHDFFEGVRSVLVDKD
RNPQWKPARLEQIADSEVDSYFEPLADPSLELHLHPIEHHLQ

>cox11 Contig16747 (complete)
MRRTAAARGLTSRPLRSWFSSSPSSTTAPLRLFSTTRPLGSLRSSPSRSGLWSPASLLRS
GTCRLPSSSPFLLTIRRAYATPGGKGGSKQEWQQKNKNMGMILTTLILGGIAISYASVPL
YQRFCQVTGYGGTTRRVEESNMSSPDRWKKRPERPLTVKFYSNTNSNIPWVFYPLQNEVK
LVPGESTLAFYRAENPSPDDIVGIASYNVVPAKAGIYFQKIQCFCFEEQLLPAKKGVDMP
VYFVIDPDFVDDPNMHDVESISLFYTFFRAKDFDDLNAQAYDESQQQKEQQTPHQLAQLQ
AVVEKKEETQT

>esterase/lipase/thioesterase family protein Contig15224 (and 3060,11112,11325,15745) (likely
complete)
MRRTPLRGALLFHNKSGSVSSLSSILAPSRILPTPAIHSASSCASSVRLVSQARLLATQA
NSKNLKISNEENQIEKDWKQEAKELREELRLLKEAVRLLQQREASSTKPVRAKKSAAAAA
THLEDAASPPSTLATELPPLPPATTTKVEVTVTDASVKEDRVNRDVKEMVKRALLALRGP
ADATVTPDAANSNWQARLKKLMRQDDVAWVDRLLASNVAKRLPSETDWDRLLEQTKNLSK
EVKEVKVKKWLAEHKAVAWLQTRLEKLNTVNPKVEWEQVLTRLKAIPPGILSLDHVRTLQ
QQSKTLDGDAQVNRKQLEWMAKVAARLAKNQAKRKVNLPEVPAPTKYPIVLAHGLGGDKP
FLKCFMGIPEDLKPLGVPVYTPKVARYGTVFARAETLKEQIMQVLEETRAPKVNIIGHSM
GGLDARHFISNLGGHEVTASLTTLGTPHRGSSYSDWIIAMTDAIGLERLFQAQILPFPME
GHHHVTPKFMKDVFNPQTPDHPDVAYFSMGGSKKIARTHPLFICQRILSKYEGLENDGLV
SVESSKWGEYLETLDMDHAAMINWSYQYDARELYRRLVNLLRDKGF
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>aminopeptidase N Contig3296 (and 19646, 2341, 22716, E9BS9UA01DOPF5) (incomplete and internal gaps)
MLRRRCTTATAPAEQQSAELGLTWLADYRPPLYTVDDVHLTFGIEDAHTTVSSILHCRHN
PKAGEMAPIVLDGGPPSDMKLLSVTLDRVPLQAGSDYKVPPGSNKADRVAQCPQWCVLTQ
VQVDEASGRLHISKRPAQPAFTLEIATAIEPKKNTALEGFRRITYFFDRPDVLAKYTTTI
VADKVKYPVLLSNGNLVAEGQTEGGKHWAKWEDPYPKPAYLFALVAGQLHYLEETYTTAA
SKRKVTLRIYTEEENVYKVGHAMASLRRAMKWDEDKYGLEYDLANMNIVAVNDFNMGAME
NKGTRPFPSVHIRYKSLLVYFHNYTGNRVTLRDWFQLSLKEGLTVFRENQFMADHHSPAV
QRINEVTTLRNSQFREDSGPMAHSVRPASYIDISNFYTTTIYEKGAEVVGMLHTLLGDDT
FTRGVQTYLRENDGKAATVEDFVRAMETVSGRTLSQFYRWFGLHSRALSVRYDQAGTPEV
KVAKESFDERARQYKLTLAQSPASTPGQPAESKRPFLIPVTVGLLGRYPLRHIWARPEAR
LTNRGVMCVDDRDGQPIHSQLSDSDPELASHTLELSDVEQSFVFNNVASKPVLSVLRHFS
APVKLVHQQTKEDRLLLLRHDTDAFNRWESCQHLALDAALALVEQQATSPDVDPSQVDPQ
FVEALGSVLKSVLDSPGLNDNAFIARLLSLPSESYIGQQMAVLDVVRVHKARKALKAVIG
KEHRKHLERVYDKFHELVPIDFSDEPGRGKREVKNMALDYLMHGDLHEGRTDATSRCTQQ
FGDARNMTDKTLLAHMPQTQREAVKALDKSLQE

>NADH dehydrogenase B8 subunit Contig16297 (complete)
MSWRARLSTNMQELRFIMCTTSPNSGGVRSFLNSNYAELKKLNPRLPILMRTGEQAPPKV
YARYDWGEERGFDLHNATEKEVEDRVRELTLMGEKMEKSFESIPKDRDLIDESDVRKFDT
Y

>Heat shock protein HslV Contig17806 (and 5657) (likely complete)
MKSFARRGAITTAGLGARSSIATTGNGSRPLLAPMTNGIITSSAAAAASYHSEGGSGRHP
GFWGPDNPAYATTILCVRKGNSVVMVGDGQVTLGSTVVKPNARKVRQIRPGIVAGFAGAT
ADAFTLFERLEEKIEEHQGQLLRSCVDLAKQWRTDKYLRRLEALMVVADKNISLTLTGTG
DVIEPNDGIIAIGSGGTYALACARGLIDLPDIDAETIALKSMKVAADLCIYTNHNFVVER
ISIDADEAKEKGGSNILSAPDQHKEEP

>2-oxoisovalerate dehydrogenase alpha subunit Contig8973 (complete)
MMRLTRPTAFAASSSAAASSSLLPRFFASSVASSSRLFSKSAEPVASSACTPLAPPDYTT
GIQFIAHRETFPVYRIMDDEGEVLDAAQLPEVGQELTQKMYKNMVTLNVMDGVLYDAQRQ
GRISFYMTASGEEATHVGSASVLDPEDVIYAQYREAGVLMWRGFTIADFMNQCFSNELDM
GKGRQMPVHYGSRRLNFQTISSPLGTQIPQAAGTGYALKLAGRSNVCICYFGEGAASEGD
FHPALNFAATLRSPTIFFCRNNGYAISTPVKEQYAGDGIAGRGPGYGVATVRVDGNDVWA
VYNVTKAARKIALEESRPVLIEAMTYRVGHHSTSDDSSAYRSKEEVQSWAQNNNPISRLR
KFMEKRGWWSQEQEDEIRKAARKEVLEQLKLAEQRPKPHVDELFTDVYDSVPKHLQEQKA
ELEAMMRKYPDHYTAASH

>putative degp2 serine endopeptidase Contig16074 (and 16936, 3997, 4088) (incomplete)
MRQGFISTLARGWAEQGGHLRSSRTVKALGQSYGPLTRRDYSAAASSKMKINNNPAVSSS
VRTKEVTKRAPRGLGKRKAEAEVLAAPQLIGSEMAGDKTTAASAPVPVATVGQNEALRSV
VRLEVAAAEPDYSLPWQKGDPYYTSGSACVIESPPGKLRILTAAHVVANNTFVRAQRQDT
ARFFSATVVAINQDCDLALLEVSNPKFFDGLKPLQFVDTPSLQNTVVVFGYPEGGESLCA
TRGVVSRLELQQYQIVRSFKDEGLKLLTLQIDAAINPGNSGGPVLDQENKIVGVVFQKMG
GMWTESVGYVIPTEIIRHFLTDVENGRSPQFCSAGFEYQKTDNDSLRKWAKLKKGQTGVM
VTKVDELSSAKSVIQPGDVITRVEGVEIGNDGTVSLSESKDKENLRLSFEYFVTKKFVGE
KLSLTLVRNGEEHSVKVTAEPRKYLIPPHEEQHGVAVPNYFIHAGLVFIGLNENYVGHVD
AEPIVGRYYYQNTKRFEDEQVVVMTKILQDQVNAGFSQEHAHQLLSLNGCDIRNLRHLID
EVERCAEPFLEFRFDSGERIVLATQPARKATERILRKYGIRSAKSSNFLPVKAKATTKKK
TATKAQTSSPRMKKKKEKKNDSSTEKKEEELS

>nicotinamide nucleotide transhydrogenase Contig17333 (and 12263, 14225, 4088, 25832, 21690) (incomplete)
MKARACLPLGGASSPNLSLFKRIGSYVPGRAYFTTRPSASAVSSASNGGVPYSRLTIGVP
KEIHHTERRVAISPANARLLTKQGFKVVIEDNAGFNAKFLNEEYVANGAEIAANSTETLA
AADIVLKVRPPLENKELGRHEVEMLKDRSTLISFLWPAQNRDLVDRMVAQNKGLNVFAMD
AIPRISRAQTFDALSSMANIAGYKSVVLAANHFGRYFTGQITAAGKVPPAKVLVIGAGVA
GLSAVATARSMGAIVRAFDTRPAAREQVQSLGAEFLEVLIKEEGEGGGGYAKEMSKEFIE
AEMALFAKQLKEVDIVITTALIPGKPAPRLITKAMVDAMKPGSVLVDLAAETGGNIEVTR
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PGEIYTYKDITCIGLTDLPSQLPTQSSTLYSNNITMTSAAFTAALALGTFSPPGFDTALT
TFALASIVGYQVVWGVTPALHSPLMSVTNAVSGVVGIGGLHLMGGGYLPDDMPSLLAASA
VYMSAVNVFGGFKVTGRMLDMFKREGDPKDYGYLYTIPTGLFIGGALAAQSIYGPQSLHS
LAGLVSAGSCIGALACLSNQKTARLGNTLGQVGVAIGVAATLSHIAPSPEVLAQMALISG
LGGATGLAISKKVAITDLPQLVAGFHSLVGLAAVAVSVAQYMLDYDTFAMDPMGNVEKGA
IFLGTFIGGVTFTGSLTAFAKLQGLLNSKPLQLPGRNVLNAGLALSNVGAFAGFMSTADP
IAGLGYLAYSTISSFALGAHATASIGGADMPVVITVLNSYSGWALCAEGFMMGNDLLTIV
GALVGSSGAILSYIMCKAMNRPLLSVIFGGYGISTAPQTQLSGTVQECNVDEAVEMLTNA
KSVIITPGYGMAVAKAQYAIAEITKLLRENNVNVRFGIHPVAGRMPGQLNVLLAEASIPY
DIVHEMEEINEDFPKTDLALVIGANDTVNSAAEEDPNSLIAGMPVLQVWKAKNVIVMKRS
LAGGYADVPNPVFYKPNTSMLFGDAKKTCDALLAKIALHYNVDREQPARKATERILRKYG
IRSAKSSNFLPVKAKATTKKKTATKAQTSSPRMKKKEKKNDSSTEKKEEELS

>NADH dehydrogenase B14.7 subunit Contig22734 (complete)
MAHEHDHHTAKDSKKDVEIPDLFGIDALDIHGGEPCLVQGAKMAATSFIAGSFFGGVLVY
WKDVGVVQKRGRFAALQGTLKSIGSYGAFFALVGATYGTAFCALQHSRTKNDPFNTVLAS
CAAGGVIGARVNGTVFGSVLGCAVTGGLAAMGEFFDWTLSPNSAKLFALREQKHQRLLRT
SPGVGSDAASSDSDAQ

>homocitrate synthase Contig17695 (and 124) (complete)
MNRTTALRNPIFNACSASRRAASVTSSVARSQLPSVIATRRDFSKITAKKHVSNVTNFKI
IESTLREGEQFANAFFTTDKKLEIATLLDDFGVEYIELTSPAASAQSLHDCQKVAALPLR
KSKTLTHIRCTMEDAKLAIESGVDGIDLVFGTSSVLREFSHGKDIEYIIDQATKVINYVK
DAGKEVRFSSEDSFRSDIVDLLKIYSSVNKLKVDRVGIADTVGVASPLQVMEMVKTIRGV
VDCDIEFHAHNDTGCAIANSFVALEHGVTHIDTSILGIGERNGITPLGGFVARMYSVDRE
YVKNKYNLKLLRELENLVADCVSVQVPFNNYITGYTAFTHKAGIHAKGHPQQPRDL

>saccharopine dehydrogenase Contig9003 (and 1940, 8281, 12023, E80POFO01BQLBH) (likely
complete)
MFMRRLTRVSTSSAAPTGRTASALRGQVPCRRLLATSPDGDGIGALKAELKAAEDRVATL
KEAIVSHKDPAKKSILVLGAGRSSSFLINYLLQNAARERWAVKVGDEDEHTARRKVQDHP
DGTAFRFNINDTRQREEEIRRADVVVSLLPAFMHPVVAAECVKQGAHMVTASYSAALAPF
DEQARRAGVTILMECGLDPGIDHMSAMEVIDAIKRDGGQLTAFRSYTGGLVAPESDDNPW
GYKFSWNPRNVVVAGQGVCQYLQQGEYKYVPYHQLFRRTDEIRVPGHGTFEGYPNRDSLS
YRTIYGIPDCPTVLRGTLRKPGYCSAWNVFVQLGMTDDTYTIENADSLTYRDFLNSFLPY
RPHDTVELKLAHYLGLDINSPEMQKIKWLGMFGEQKISLKSATPAQVLQQILEKKWALQE
GEKDMIVMYHHFVYTNKNGELKETKSSLVVKGDGTDTGTAMAKTVGLPLAVATRMVATEQ
VKGKTGVHVPTTPDLYEPILRELEKDHGIIFSHQHDTVHQA

>ribosome recycling factor Contig11098 (likely complete)
MKRSVDWLTEEFAKLRVGRANTEILNRIKVEGAPLAKKGSVYVKDSFTL
AITPFEKEQTKKIVEALRDADMDLNPQTDGDNIIVRLPKATDEYRQSLLKQATKMNEEVK
NSIRRARQGALTDLKKHKDAVSKDDMKKLENEVQKITDEYNKKTEQLHKAKEQAITGAGN

>universal stress family protein Contig6212 (likely complete)
MAEKRAQKTKKDGDGNYEEDLDTYFVDRLRFLNQRDHTTQHLKQRFKERNGRLEAQEETG
DADKATTTQRQVVDDEGLAVVCVDGSPAADEALRFTLAQMPHARSLVLAHGIRVSLTSSS
SSSSGSTHAPFGEDEETEALHQALERRYLKMCRDAGRHCMVKHFTYTTRGGFGHAVCYLA
DKKDAAAVVIGQRHPRPLLGASGTAVMKYCGQRPVILVPESRASVATDREKEKPTAVGHH

>NADH dehydrogenase PSST subunit (Nad10) Contig11752 (complete)
MSSGVTQKLAHFGKPQALTGLSKTEFVISKLDQIVNWIRKGSIWPMTFGLACCAVEMMHA
AASRYDMDRFGIVFRASPRQSDVMIVAGTLTNKMAPALRKVYDQMPEPRYVVSMGSCANG
GGYYHYSYAVVRGCDRVVPVDIYVPGCPPTAEALLYGLMQLQKKIARERNLLSWYRK

>kelch repeat protein Contig12233 (and 1719, E80POFO01BKQVY, 6426,14050,19627) (incomplete and
internal gaps)
TTIKKSTARTLNVIDGHTGVSSVITARPDATSPIGASCRHLIAPTAPTST
DASSTDGVDGNAEAAATQNEPGLGWAISMAKHSGSRRATLLSLAMSAGWV
DIARLLIAEVKRRDKRKLKTFVTQRAADGTQLLHSACYFGSVECVDLLLL
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LSLRDDVTGEPLIDADGPDSDGVPPIFYASLSSAACIARLLEEGAPPTVN
SGKTVLHMCANTGNVPAVEMLLQGWKENKWGLRDKLDLNAEDPNAAGSTP
LHAAIFSTSALAHKNVAALLDAGVDPKKRLHNGSLSLGIHTARAAWAQLA
GPFGPEIDRFFHGNQQWSRADDGSLLLHAARSGTAKAVEELLLRNFDVEE
ADSFGSTPLTAALARQYPTLATSGQQVLLRLLEAGAKVKWGATPLVDVEC
YINTGSPEENMKSGHTATYYDAGRSAYQVVVGGHFNGVHPPGIYFLSTHY
RAWDATYFDNVRLLSCRRRTRHTRRTRRTTHDTHDTHDQPKQVSPQQSTQ
NVFVNRRGHTCTLVGDTIVLFGGLRYAPLPRTHFNDVYFISAVNGRVTKP
LILGEAPLARESHTATLVGRKIYFMYGCSATAFMDDIVVLDMDSLEWSRP
SVTSLKRPSMRFGHTATLVNDHEIWLYGGINRVVNVAGRTHLVSTDPDWH
VFDTHTLQWRTINASVAVPASGKGSPAKLPTPRANHTATLVGEEIYVFGG
DAVRREHLEIVLRFIYTDVIDVDNIPGFPPSGTHCAAPPFVRDLIDAAKL
YAAERLGQFVARLLRQSMPFHRDTADYEPRSLLAFLNNIEYSDVRLVCEG
KIINAHKAILSRCPYFDAMLRMSSSSFFGSESDESEDDVEELVITDTSHD
ILQVILRYLYELADENPVGEGAFVTEETAVEVLITAEKYGLDTLKLWCEK
LIVEVMEEQNIPYFLQLGDTYHAPHLRRYCLSALSAQYDHIDAVLRAAPG
SAGGVEEQIESDELRAEVLGIVHERRRKRNALLADYEDVNDKVYFNTVLP
TLADSRQPLGRASAVFGVMVGVAAAWAFLGGI


>porin 3 family protein Contig3292 (and 25969) (likely complete)
MKRRASICYEQQYISDEMTKAAEDEDSPPSSPPASPPTSRAGLNRRNLPYSFVEAHEREY
DEAGKEVRRYPPLFTVGAPFDRNTTRHDQRQDCYAEIHHPYQSVGGNTIEGSALFTVRSE
PMTVEGLLFSKNGGGASITLGYRTKDDSTTSYVAAEHMVNKPGGGSGTDLKAGIFYRYKY
LSCGASVTSPLDLTLNAASQRGGLQALRQRVDGNVWAMFKQGTVALGTACQLVDGRPDAL
NGVICYRNQWTRPDEPCTELTIRTTQKIADGQSAPTFHGSYYQRMVTRRKVQNPFEEANV
QFITNYVDLGVETTVAATGTKMAVGAAWQVNKNTLVKGKIGNSAFSFLVAAKSWWDPSAT
VALTVSKPFDGASRGTRIGLAFSIENWGGIGYHRPSDTYKRYVPMQMDRVSDETEPDTAE
ALLRRQKTAAN

>glutaredoxin protein Contig25663 (complete)
MQKATSSLAMRGAVRSTAQRRLFSTALNRSRSVVTSRAALLSLRSVSSPCSYAPIAPRQQ
RWYTTDDNKEVGSEVATDSVQDAIKKVVSEYPCVVFMKGTPDAPQCGFSNATIKALNTVG
AHYEAFDVLQSAELRDGIKKFTDWPTIPQVFIGGEFVGGCDITLQHLRSGELTTLLEKAK
ALKSQQ

>hypothetical proteins Contig3310 (uncertain of N-terminus)
MGATWALTRTVRGIEEAQKLDYFLQSGALVPTAALRDFIDAMRPRPLWNVAVWTSFVASV
GSLAVWTYRLPAGCTERSLVGVSAAFLVFATAHLARFAADQSDAEQWTLFRLPSRRASSS
TAGDN

>glutamine synthetase Contig264 (and 16989 and 23957) (likely complete)
MRSAVLRRTQSHVIRGSATAHQLGQRGLATARPLQGMLNYDEFKRAVEAE
ELDTVIVAFTDLTGRQLGKRYDAEYVLDHYHDFESHACDYLLTIGVDMNP
LDGFKAANWQRGYGDFHLVPRMGSLRHAAWLDRTAYLVCDVADRDTHQLL
THAPRTVLSKQVEQAQKDGFGALCASELEYFIYNDTYETAFKKGYKNLQT
AGWYSEDYHILQGTRTEDLQKAVRYYLKKSGIPVESSKGEFGRGQHELNV
AYSDILTMADNHVLYKQCFKEVAEAQGKSVTFMAKPHHDEAGSSCHIHLN
LTSAETGKNAFAGDKDLQGIKCSDTFRHFLGGWIKYTPEIMPFLAPTINS
YKRYQTASWAPTSLAWSPDNRTAGFRIVGSGKSLRIECRIPGADVNPYLA
FAGSLAAGLEGVRKGIEPPPMMSGDAYRAPSTTKVPVTLNEAAHALEESK
FARQAFGDDVVDHYAHYYKKEVEAFRKSVTDWEKQRYFEQI

>thiosulfate sulfurtransferase KAT Contig5309 (and 13795) (complete)
MRRGASVAIARCSVPVGRTLHSGTVLRSSALHLSAPHRRHIATTEENAGGRPANVVWDSD
HSWKKKDARSLPSDQLVTRAQLKALLANNSSGALLLDLRSVGECKVEPGIPGATNIPSED
LVRSVALDEGKWRARYGFAKPRPDTHLIIYTTPEQKAKAIETVDTLLQHGYGRVSVYEGG
AREWNKFENATC

>SAP DNA-binding domain protein Contig11180 (and E9BS9UA01BXD9U) (complete)
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MTAVLNSLGLETLEELYYHDDPHAAKEEKKKLKKKDIVDAISDKIDTYAIEVFIASLPLA
QLKTVAEKAKVPFKEEDNKNSRSVLSRRLTEQVVSAGFDEFLETVDADTLKAVAEDFDVK
ADKKAIAEAARTFAAERYFGNFDVESLRALAEELKLKQAAKTSSKRKLVEAIVTQEDAEP
VEAPKKKKQKTDVGKKKALEKGITYDEIFQHYYVEELRDFVKSKGIKVSGKKPVLIKRIL
AYLAGETEGIMAGDKTEKAKKKKKATTKKAAAAKKGAASTSAKGKGKKEENGNGDE

>hypothetical protein ContigE80POFO01BUV1F (incomplete C-terminus)
MLRVSASSCRAWAPPPDVGVASTPARPSQNSFSSSQLHPRGVNPVTALGSLSAFSTPSPA
SGSAASSSSFAGTPSTGGLPRFSPSSIAASVARMQLSSISALSTPSSASRGGYSSRGSTP
SFVV

>malonyl CoA-acyl carrier protein transacylase Contig19196 (likely complete)
MLRTRLGARLRLASWPALQPGGCARCFTSYDQPFIRVSRHTKDDADLQRRDREKHPRVKR
AVVFPGQGTQYVGMGADLAKEFPEARRVFEEVDEALGFRLSQIMWDGAQQELTMTENAQP
AILAHSLAVFRVLQKELGLSAPRGYASMLGYSLGEWSAICASGALPLWDTARLVHYRGRV
MQEAVPLGEGAMVALMPIDVPTASAIAKKAAEETGGLTCQVANINSPKQIVLSGAAGAID
KAVEIAKREHKRIKLVQKLNVSAPFHCEMMRPAAQKLQDYMADSTNKVKFADPSVPIVSN
VTARPITQAGELLDLEVKQVTDAVQWLDSIRLLAYPATAAASSEDVMRHAAGRPAWKEIE
EEEKLWQWKGFDDFLELGPGKTLSGFVRQIGTELQATNVGTAQEVIDYCKHYRE

>hypothetical protein (possible guanylate kinase) Contig13727 (complete)
MRAALVKRSTSRLHPLTRGPCASSLRWFGTAKKETAKATTAHASTPLEASNLPDPRAFAQ
EKAFWATQEPLKQKRLQAKEKGEPHFVFLEGSGGAGKKDLLWRLNKMGHEVVFHPYLTFL
LDSQYPYTPTRDHDILQVRWGNKIINALENIASLSKTGKAYKSNLVFVHRSPISSYHYAR
DRNPDEAALYLSLMRQITTAFSSSVVLCKADPLRVQERLGERLMVPPEKEKALRRELGES
TDLDVIQREIDAYERLLLTPPSTEREHHGIGATVVHTTSSKQATAQILKTYGVEMNWVWE
DLKKTSSPPAH

>conserved hypothetical protein Contig10587 (and 2970) (complete)
MQNPSARRRRRRRSGPRKMPKWAAKISTTRRHPGNQWRASNGGTAKRASKKKAARRATST
AIDEEQDPEGARQQQEEEEVRRLQQLRLERAEMGRDQRDEDNRPRAREERKKCLAYCTAD
AYVLHKLYRALRADDVIASEWKISYIRRDRKYIRLRCLDDSEIYIFPFGSFVCWDVDDAD
FIRVRQLIRACERGERTELYEDFDFVYGSDTAVDPEDDELILKEDDSTAKWPVSFALAQS
IKLDYFEKEVKDTFQEMQALSHYLARNGSIPLGPKKIVQEMGKIMELLVNVNLGETDFVS
DIPDEFWEDTESANTWKIFNSHLGVKNRAKVLDSQLKMFNDFYSMLSSEVHVKKSTRLEW
AIIFLISIEVVFGVADHSDWLASFIP

>mitochondrial substrate carrier Contig1057 (complete)
MSDAVKDFIAGTFGGMALVITGHPFDTLKVRLQTAPPGYFSSFGDCVKQTYTKEGAKGFY
KGVGSPLVGVSAINSVLFWTWGRSQRLFQPDKSIPLTTSQLIGAGAITGLVVAFAEGPVD
LIKSKMQVQYGAGGQYKNSFDCARQLVSTYGIRGLYQGIVPTILRNIPANAAYFAGYEYM
RRKFTGDDGGAGEKKLSAGAVLAAGAIGGVGYWVSSFPFDVVKSRIQTQPTDLSQRQYKS
TWDAMVQLNKAEGWRGFWRGFTPCMLRACPANAACFFAYETARSLLG


>Rab32 Contig15453 (complete)
MSHGHGGKAAEGPATEYLYKILVVGDIGTGKTAIIRRCVENQFSESYKTTIGVDFALKTI
QRSNATIHLQLWDIAGQERYGNLTRVYYKEAVGAFVVFDLTRNSSFEAVKRWKEDIDNKV
RLPNGDPLPVVLLANKCDLVKTPLSEEVMNDYCKENGFLAWFATSAKENINIDEAVNFLV
ENIIVHGSNDAIKGPGPDALKVGGERGGAPDSNACGC

>peroxiredoxin Contig27495 (likely complete)
MSLGDVAPSFALESDEGQVVHLHDFRGRSVVLFFYPGDFTSVCTKEAEHFRDSIDAFNAK
GAVVLGVSKDPVESHRKFKKEHKLPFTLLSDLTGKVHRKYRVAGSLGGLLKGRKTFVIDK
EGIIVHIFESALNWKMHVSEALAHC

>CBP3 ubiquinol-cytochrome c reductase complex chaperone Contig10140 (and 4561) (likely
complete)
MRIMRKTLYRPHLSAGALTMATPSCRALSITSRCNSSMARHPIVHRSRAGAINGCMPIRG
HVPSFLLFGRCSSTLRGTPEMPASSFGGRAEASATTGPSADPDLTYMSPVIFARRTPEER
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RRDELGVQKILEVAKERANQGESEDGLLRFLGYYGKKNQSLRSGSALYANVFYRSLDEEF
YDLLGYEEKGLLPWFLISTLHMWMTSVRLRKDASSRALDTRAYFADSFWMDVEEKLNNVG
VNYVGMGKAFKQMPNLYAHATLSLDKALKSTTDDQLGDALFRHIFFNRLPRQSHMTALIA
YVRQELAHLDTIPNNLLLHGYLPWGSLPRVDASPVSAASPSPSPQNDTSETGAAR

>mitochondrial ribosomal protein L9 Contig7807 (complete)
MRSSVFRVGGVSPLALSSYAPLRAGSLYRTSSILPQHDWTALVSSRGYATKKTAAPAKAK
PKSKASGPQKSNKPVKNKKIKIVLTSDVPSVGVKGEDVEVAKGFARNYLFPQKLAVYCTE
ENLKLYEADRANIDYEKRQKLQELAKAKKRLSKVEVLMKRQIIQVQPEQILHAPVTADNI
VEKLWLQHKIQLAKDQLDLEAPISQLGTFSVPVKLEDIDVPLKVRVQAR

>hypothetical protein Contig22991 (complete)
MEGGGNQNEACAGLFAHADSVCGTATATTTNDALAPACREATARALSCLRAKSTFMGPRA
RVVLECVAEHRRDPSPCNGLREDFERDTTHIREQAKLDEGWQKRMVELCEGPFTRLHKCH
ALMAARGGEQRLAEVCEEPLDEMSACIQRVACPARLSAVRACLQSSGGREEVCEVEVDRW
VGCTLNTAVESLRGLSGSRA

>hypothetical NADH dehydrogenase subunit Contig11 (and E9BS9UA01C9GEK) (complete)
MADENRDFPEYEAWVKKQSAFARWAIRTRAAIADQDETNNAEYLRHVAKNMIIMKEESYL
WSSSAQRPDDYYKGRSPLTAAYRDHGMFKSPYEIRAKELRGELIRWNHWHSWDLKPSATT
SYPKPPAKYDPLNPTRPNIRKQRLEREAAH

>3-hydroxybutyrate dehydrogenase Contig6244 (and 17396) (complete)
MKRTLAMMERSGLAAASTSGSRVTGTRAFATSSTPGLHLSLTGKTALVTGSTQGIGLGIA
EELRKGGVALVVTGFGDAAEVERTRQRLADLIPGDDRVHYVPADLGKAEDVEHLIKESEK
KLGGPIDIVVNNAGIQHLSPIEDFPVEKWNQIIEINLNSVFHTMRLTLPAMKERGYGRII
NISSVHGLVGSKHKAAYVAAKHGVVGLTKVAALEYAGSGVTINCINPGWVLTDLVRKQIE
ARAESLGVSYDEASRSLLAEKQPSETFATPSQIGQLAVFLSSDAASQITGISLPVDGGWT
AQ

>cytochrome b5 family protein Contig27736 (complete)
MAAPAKTYTLEELKKHNTTEDIWIAIQGRVYNITPFLEEHPGGDGVLVDNAGLDCTGEFE
AVGHSDEARATLEQFYIGDLVTADGAPVKSEKAPVQPKVSLADTKAPKPKVAAPAPAVWK
QAAVPLLIIAVGFVLRYYFSS

>5' nuclelotidase domain containing protein Contig3046 (and 23866) (mostly complete)
MRRALAGINRPQCIRSITTSRATSAFGGRRFATTTTSVRARTLTSSPSTSSGIFQGAHRC
QSVQAPGHQLRTYAVRSSEFASSNAGDNGTPLPNGRLKTLCDELRGIRAAAKASKAQGGE
GLHPDIVRLLVDFEEMTEMHKRYVKELPLANPQDIFTNGEIRLDELDILGFDYDYTLASY
TDKVSYFIYDKALQYLLRNHGYPQELKHKTFDPTFAIRGLHYDTKKGYMMKLDYLNLIQA
DTVHFGRTKLTEDRLYSAYPSLFIYMAENMRLLIDIFGQPEACLIADIIQYLADRKTEFD
PAYVYEDVSKAIQHVHASRLLHTEIMNHLDVYLNANPALGETLWRVKEAGRQVRSNFLTC
SDEPLAQRCSCTAKCCDINHLLPTIQLFLATNSPFDFVNAGMEFLLQGHLPNGVKHWTEM
FDLVMTSCRKPSFFLHNRPFRVYDPATGRVTWDRPNPKNYSGQVLVEGSLNQLIALTGWK
GDRVLYFGDHIFHDLKEPSSVAGWKTGVIIRELEKEVEIQNSSVYRSVLAELLEVERLMK
KCMFISGEWSQEVVFALRQHRIRLRKDLKNCMNPTFGSAFRTHKHASHFAYLLQRYCRVY
TSKLENFLNYPTHYVFYPERTFLPHEA

>adenylate kinase Contig8413 (and 17529) (likely complete)
MRRNLPPFSISSCLSPPLRPPQAVLRRAQGAGSATRSCVGEQQQRFCTTRLTAGPPRAAR
GTTSWLSLQRPYSSTATAAAAGAKTVKDALSAVPSAPDMTGKPSATVTSPKDGKDKSDGE
IKNSQLMFDSVWNKLKAKYTEERMVFPKEIIWLMGAPGSGKGTNTPFILEARGITASPVV
LSDLLDSPEFRVIKAEGGMISDAQVTETLLETLLQDQYRVGALVDGFPRTEIQVDHVSLL
YDRMLTLKRQNPQLYPRPVFRMSVLFVEERTSIERQLARGKRATIHNAKVKETGIGELAP
ERPTDMSEKAAAKRYAIFKQHFATLTTLQQRFPFHLINAQDSIEQV

>metaxin-like protein Contig19964 (complete)
MHLSLLEEGSLPCLALLFILGAIGARAVFRFLREEPEPKTSDVIDRGDSSVTHIKLHTFK
QPASAQTACSLSPFCEKLELFLRMAALDFKAIDGNVVTAPKAKLPMIEHGENLVPDSELA
IRYLINTFGENKTHLGRIRIKLTPEEQARSVLLTNVTNDSLYQLLLHARWVDLSVWNVVK
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GLYFGDLPLPFRLLIVPSIRRNMVGWLWGHGYSRYSQKDRVWLARREIDALATILGDHPY
FNGDEPTPVDAAVFGILDNCIYGIGSVYGIRDHVQTKKNLVAFVEGIRQEFF

>monoamine oxidase Contig15703 (likely complete)
MDTAPLEQGSNWDVVIVGSGLSGLTAATRILQENKERKVLIVDAVDWFGGRTRSIELAKY
DSKVSIGGTFALFEHNDTLQLAKEINCSPTETLKISDVNFNQFSKALFDPSGLPLFFKLM
YKGAKIVKEGKIDWSCKTAKELEKISLEDWISKHWILNKFNPNFTREFFYLLETFPNLHG
VSALVCAIALYVRFRGIPRNGIEIPPKVLRWEGGTGVFTQALVESLSHHENFRLKLNSPV
EQIIQPAINAGANAGPYPVQVVVNDNHTGSVTVNAQYVVVATSPLAAAPANLGGTINYTP
ALEPGAAQLFSSMEATPTVSRQILVVYKNRWWKKQGGGMFIMPPYATHVNEMGVWGNVVD
GSMKDERKAGIVRIFVDSRRLDGMSPKQVEQSTIDFLKHLFPKQHDLVEGYEEIIFHDWN
TAKPTIPGVTFTYAPTNNGVLSKFGKYFTQPYGRIHWGGSERSVWGANWMEGAVERGNDV
SEELMKMAGWVGPDYNVRKTAATLRVAKRAMPVAAMGAFAVETSAEEDDLEAEPDLEPIK
LLPTPTSPLGLAESLQPDDGDKLDIHELYTRVSQVEKPRLLQENDVWISPQMCLDALREL
EKAKLLKKKRAAEAEAEAEAEDEAEVASSSSSSSSSVPHPATSSSPLLAGVTPRPAHLPE
GTTPFSSSSNEKPTVQQLQAVPTLRGEVPAFLLGLTVGVFVTMAAFRFAKGSSQ

>pitrilysin presequence protease Contig2181
(23044,16875,23840,23534,18838,2992,E80POFO01EPXMF) (incomplete, with many gaps .. mostly
genscan inference ... little EST support)
MKRLLATTARGRSLSARAAAASAGIVDASRHALPTGAAATRLLRSRLSGSSGATRPQRRG
WATQAAAPSTTSQSTSIDFTGLKRGEERERPALAAGDKLHGFRVLKVVPIPERNFMTYQL
VHEKTGARLFHVDCSDTNNVFCVTFKTVPTDSTGVAHILEHTTLCGSEKYPVRDPFFNML
KRSLNTYMNAYTAPDHTSYPFSTQNVKDYYNLLSVYLDATFFPKLEPFDFMQEGHRLEFE
KIDGTPIANRGMCQSPLTHTLSIGDSHQLDPSSALKFKGVVYNEMKGAMVRSVCVTIFTG
PDLRPADRVPSKPLPPVQRLVRIAPAFLCFLNDSLLAVLPITDHTILWNIRFYTYGDLSL
EHRLQQINENVLSRFSQIDPGTDLPDEVRLTQPKRVEAVYPPVAGSDPKRQEKFTVAWLT
NKTTDPFENMSMNLLSRLLLNGPNAPMYKVLIDTNIGLDYAPSTGYDSGAREAPFAIGLS
GMNEKDVPKVEEGIMSTLKQVAAEGFPEERIQSVLHQIELSQKHVTTDFGMSVGHAINYT
WIHGADPAEVLSVNKKIERLKQELEAGPYFQHKVKQYFLDNPHMVSLLMKPDEKYLEKLD
KEEQARLEKIRASLSQAEIDDIIAKAKFLKERQEQQQSALSFWEAHFTNLKRPRLTRNAP
SVRLQMCRFCLRFTFRMCPGKRPTRTPGSNERRFLWRTRPTRYPTRLCGAAAWNVGQGLT
HRTDRVCHVLPLQIPLLSVPQPTNGLTYFRGMASLNSLPSELEVPLFCSAMASMGAGSMD
YRQLAQKIESHTGGIEFSPVCSTHHSDLSKFRAGIYVSSFCLDRNLDHMFELLHTVLSAP
RFEDVERLKSIIYGNTSDMQESLVESGHSYARSLAASVFSRASALHETWSGISQVTLMQQ
LAQSEDVSTVIPHLKAIAEHVLDASLMRCSIVGEEGSLPQAEQKLTHLLGGLKSSSSAQP
TAAADYRESEYAPLSRPHRLFVPIPAQVNFVSQILPTVPFTHPDFPKLKALSSLVSSSYL
HPEIREKGGAYGSGAMSGEGLWSFYSFRDPNTTKYVVVVSTHAHTHTTHSTHARAISVVI
DNAHLFVFVFIAGRQNVGRVFVVAGMDEEGRRLSGQGHRRGQAPAVLLHRPPRRPVPTRL
TTMNYEKKKKKKKLTNRCEYVCV

>hypothetical protein Contig21500 (complete)
MRRAACAFRPAPTHSLCTAVLSSPAVGRTLATVTRNARPKFVFPADGLPLYTANRRGEFL
IQAGVAVISCMAYGTYALTQYEAKKQTGEFVGSSDTVTKVAIGLGAFCVVTTPLFTWAST
RRAVRRLWAVPRSANTNVASALRVETHSFFGGPGKTTDVQISEIVPVGHINPAERLVRFQ
LRDNKLFVMTRDRGEFHNEEALQRLLNNKPVTFS

>phosphatidylserine decarboxylase domain protein Contig11474 (and 9362 and 611) (uncertain of
N-terminus)
MWRSGTRLAPSSSRCSLHQGWRPSLCGLPVWATSISATTRAARPLSHRVGGILITRGSLS
KPAPSSTPFSFKRHSANKTGNENVEQIPKEPIRLNTLGKTPEAAAKPLRAAENGGKTKKG
TTRRVIKYVLLGSAVGIGVATFAFLNQSEPATPRQVRFLTAIPSRAISALWGKANDVELP
LWLRTQLFLLWTWMYDCKLDEMRDPLESYKNLGEFFTRHLKEGVRPMGDGMVSPVDGRVL
IFGEIKDAQVEQIKGLTYELESLLGDTKLHLKVQDKNEAQGRPDKKLYHVVIYLAPGDYH
GIHTPVDMTVTHRRHFPGHLFPVAPTVVNLIKGLFALNERVALLGKWEHGFYSLIPVGAT
NVGSIALTIEEGFRTNLATHKVGRGDGNQNFYERIYAQPIKLAKGDEVAFFKLGSTVVLI
FESPEFEWTIQPGQKIKLNETIGRVVSNKKN

>mitofusin GTPase Contig10205 (incomplete due to internal gaps)
MRRTTAATMAQGRVVTTATFSTSAWLRRCGSETTSALMPSTSSLGRSAASRGVASARLHY
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PRPRTSLFGDAPGSRGAAAISSSLAFNRHLLPAASSCRRRQATATEVSLQKQGEGKEGLR
RVLNADQAALLQQEICLLEDVLAFLQKIGADQEDVELLKQTREQLEELFLLVVVGEFNAG
KSAFLNAMLGKKYLKEGVIPTTSKITSIRHGETASSVLPTEEPDREVIYLPVDWLKDLNL
VDTPGTNAILKYHQQITEHFCPTQRHGSVCHQLRPSAERKRTPIPEQDSPVEEERIFPVS
ARLALKAKQLMAKENASAEEKAEAAALWEKSRWAELETYILKSLDAGERSKLKLKNPLGI
AHNLLNKYKDVTESRLQVLAKDITSIEHIEEQLEEYRKEMKRDYEFQQNRIDNVLLELAN
RGDAFFDEHLSLSNVRLSAHTIAAILPLIVFRRFFRIFALARSEKLRGEFERTVVAETAI
QIER

>Mdm38/LetM homolog Contig17709 (and 2982, 21306, 7920) (incomplete … with mistakes)
MAARSRYLATTTYMATPSATIVGTPFVRMSQTSMLRLGATSRGISSSAVALALPRGTSGS
CAFLLGPHAAASWRRSGRSSATVLQWPGAGSSAAAGRLRVSEAACARYYATGGSLPDSNQSPKAVSAED
DKEAVPKKTLVGRAVHSTKKVVTFIKEGIHHYWLGSKLLALNVRTAFNIAVRLKNGHTLTRR
ERQHMIRTTADLFRLVPFAVFVIVPFMEFLLPIALKIFPNMLPSTFQDTMKKEEDMRKQLLLK
LKMASFLQDTLQEMAETGETHADIPKEEFLDFMKRVRGGGEVSGEEVLKFAKLFKDDFTIM
NLSRAQLSSICKFLNLRPYGTDAFMRWQISRRVSKLREDDTMIAQEGVKSLTFEELQQACIA
RGMPATGLSK

>pentatricopeptide repeat protein ContigE9BS9UA01EGS4T (and 9824) (uncertain of completeness)
MIWEIIHACRRAGEPRRALELFVNSAKYRVWPLARQFNRLMADFMAAGDH
EGAVLTYGALRKRQVVPNAQTFGLLVRAHAAQGNADQALAAADEAKRALQ
TETLPGPVADALMGVHWKAQNFEGLRSLVEQTSDTTRSLDGALYASLAHL
QANNVSAAADLVRQAVTATPATTEQFEKWANTLAEEATSANLAQPAAGLL
RALTGVAPADAALEELAAQLDAEAASAAAAARRAGNHRASRRQRTCRCRG
RCWARDQIELLHLRSSSSSSGSYHFEVTDKCLDAGEATVGDLKALLQSSP
DYGGPYRRFSFVTSALESAADDAPLALFDLAQGVDIEAFTSPSPHDPEQQ
KRQKHQQHLQYQYYRRQRQQEALEVIASAVGDHGRLHPDYEAPAPGDFSP
EQRRHSTPDGDDGDDGAAAAADEHDTAGGGAEGEKKKKPKGMLRLFRRNS
DMGPRSWVRGWSSSSSSSSSSSSSSSSSSSSTSSTQPSKHG


>hypothetical protein Contig21840 (complete)
MMRRSMAAGLPLVAVPWGAHVAWRTTTSAKGALLVGFVAGTAIPAGSAMTRVARVVGGQR
RHYAQMGAQFAPGPKSFSEMRSAAVSIKRRYMRLAVYLSVGFFFVVFPVSTLAAQAWEQR
NWPTLQAKIVEVVPIEGTNKRRVTYRYKVLGRVVEKTQVNWNVPWWDRINNTQLDFKVGD
FVTIYHHPHNVMLSIFKPGNFAHPNFGRLKGEVIEDTTKPARRTLPQVGPH

>hypothetical protein Contig5577 (complete)
MSLPTIEELEDLTSQCLARTFSDQQVQAIISHSRQLASFGVTDYVDREDLRKIFKDEKDK
KDKKKDKKKDKKDKKKKKGKKDKKKDKKKKKSKKDKKKSKKDKKKDKKHKKKDKKDKKKY
KEGYKEQPWRPAEWSLSKEASAEGKEYDFDEDETRYVRTRLQEVREKLLHRREASVSNFA
PCMLLYTEGSEPDVKETKLDAQCTLLRKASTHALKSEQCWSQYLAKMDECLHHRTGEYCL
RAFRPLERQCAQSGWRSVNDLRKLTRLRSKEEVDLQ

>NADH dehydrogenase B14 subunit Contig8248 (complete)
MATSGVATTASRSFADAAARNQHLYRSAMRAAPRIIQMYDLPYNVGQVRSRIAEEFRKHQ
NVRDPVTMDMLWFKGKSELDETLLTWKQRPHILHYFAPKKKEESDFLRKFYANEDID

>Thymidylate kinase domain protein Contig21908 (incomplete)
PSLLESYVRGIKECIDPTIGLVFILVILLQLNKIRLVIPQIIAVELFNDDSYAAWIFSTY
SLGGVIGSGVYALVKNTFTPAMNMVFASTGVLILAVSWWPALAQASIIPFLSHKDEWLLW
VLLGAMLFSIVKQSARTSMQSIFQYALKDSKSAADIMALNRFGVNGLATGLRFALGIPFI
FLSVTTAFLSISGGLAVIATVMFIGTYLLTKLPINNQNLKKDKDEKKEKDVDDSEDEDKK
IKKLKKRKPSKKLNRKLSDEEIAQLVDIPKDTGVLIVFEGLDGAGKSTQVERLKSFMQGE
GYVSLVTTWSKSAHHYDLIRQLKRQTPMRSILLTVVQAMDFQQMIKQDVIPALRAKKVVL
CDRYFYTGIARGVARGLSKTWLRQLFTADVNL

>hypothetical protein Contig17198 (uncertain of completeness)
MAEPPGGTGHQSIKSGPPAAPSLHQHLLQLSTKTHKANNHSPLFQASARRHYKTMMSRIA
VCIGAFVVLLVASALAGPVTLNGAKISATFNPTGGSVKIWETGTNRIFTHSFTKIQEVAA
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DGGVVNAVNSFADLTFNDPTTPQQETFQGVNSTVVSLSGNVNVAVAGSNATTTANVNVRF
YVFNDEGKITYGTKTYPVAPGSIEIIYTISGWPVEDTGNKLNFFVRIGTPGKTASWNSPE
LRFFDGASLIFAPDSANSNGQAAVKVTPTMGSGAVNIQMQFQAANSIEYDPLWSVEGESS
SAATLSPFITSVLF

>Coq3 3-demethylubiquinone-9 3-methyltransferase Contig7187 (and 4107, 180, 1254) (likely
complete)
MKRTLLLAGRCGSTATALPSCTRVCRTTAAAWRVPTRAAFQSVRSTATAHGSPQQQQGAA
TGGSTVDEEEVQRLSESARLRWWDPEGEMKPLHRMNPKRVAYLRTCLTKRLGLPPLAPQP
FTGLRFLDVGCGPGLLTESLARLGGEVLGVDASAANIQTAIKHSSGDSSLSTLAYRHGTA
EGLAAEGQQFDVVSSLEVIEHVNNPELFINSLSGLVKPGGSLFLSTINRTMKSYALAIVG
AEYILGWVPPGTHQWNKFVQPTELGVLLQRAGMNLEELTGLAYQPWNGSWSFTTDTSVNY
LLWATKPLAQ

>pyruvate dehyrogenase phosphatase catalytic subunit 2 Contig27417 (complete)
MLRVAGVGCRGARGHCLTNDLHLHHPSSTTASALSRSFVPHSTLPASAPAKKATTQSAPV
ATAAALPTSSSSTSPSSTATASPSTLLASHSHSPRAIPTLNSLFVLRNARPIAVSGVGRG
PMAFGVAARRRMSASTGPNPNELPQFPHTSTPATSSIFKKLSRPLFIGGVGIASFAASYG
YFEYQKKKRKYATSASPILDALTPSVSPDLVEQVTRKINANAQAFTVAPGNCHITEFHTN
TIASNSPIEDRHNQLLHDPQIYDGSLFGMYDGHGGWAASEFVKNELFDFVKLELGILKLK
QEKFIDSIVKEKELRDRIVDFLAKDPASPQLYEDLKGIIAKQSQLDEAHREQLLTPLDAL
FNPERNISQCLQLAFLRADSYFLYEALLDPEKLRDGFSGACVLLSYFLNDHIYVANAGDC
RAVLGRKRDSSGDPIKGADTRRVWEAIELSHDHGTENLEERKRLIEAHPNEDDIVLDERV
KGSLQPTRGIGDGLFKDPNFNDALARKLENWHPPYTTAMPEVISHKITPADQFVVLATDG
LFDFFTSQEVVDMVGHYLEHMQRDPKDDSHNSVQQPPSSELKLKLQENASSYLIGKVLNK
AGYGKTPEVRMNFCITLPKEAKRGFFDDTTVTVIFLGPHITSGAVQDEHGQEDTEAGTGS
GGSEPVLAKPAVMERVEGLIEQKVREDQESGMMWKAWHQSFAGGRSG

>hypothetical protein (possible ATP synthase e subunit) Contig24711 (complete)
MATPLQVPCGCRNSLQSFGAAAAFTVAFVWTSQSVQVKRNAYFSNLKSEIDTLKKKNHDL
EHEVELLKNPPEPKEAHTDFAADFESGNIDFEKILEQVASDH

>single-stranded DNA-binding protein Contig6662 (and 24410) (complete)
MKRAALQSIALRSEEAALRNPFVAKASRGINKVILLGNAGAEPKMRTYNDGTASVTYFPL
ATNQIYTNKSGERVNKPQWHNIVIYNDNLSQVAQKTVKKGSLVYVEGALSTRTYKDATGA
EKTICEIILPKYKGDLNVLSKREGQDEEAGHEVDHHDLVEDKENVTLA

>mitochondrial ribosomal protein L28 Contig7313 (likely complete)
MIRRSALQETTCRGWTKRSQRGLFAGRTVVFGNQISFSHKLTRRTWKPNVHKKKLFSELL
NETFHINVTTAALRTIDKMGGLDNYILYTKDHKLDSLFGLQLKERLKEVYELKHGVKFQA
KAAPAVSVKDQWQQIIDNYNRKKEGSSSSSSSTASATSSPPPVAQREQSEVV

>SAM-dependent methyltransferase Contig7269 (and 14088) (likely complete)
MARRALLKRMNAGPATTVLPALHPTLAARLFPNSDHSSPEQPPRRVWSLPENCVPQLQGS
GTTAASRPPPQGFVAVTNPLTSTSAGPADDRAVLLVDPTLSPPIRVVGYGMSAVDEAYVE
GALREALTYRRQLAGEGRLELDDARHTSAFRLVHELGDGLTALAIDVYGRYADVQTYSVH
WDRFLPFIRDKLWSPEFLPFLRGITVRRRFRKKRPTARFYYNPAFFNDEQEDDVGAAAGD
ADDLDEEDDVEGFDDEELDGGGDDRERAQQQLRAGDRSAEFRDVVVEEDGLKYHVDLRTS
ALSSGLFLDQRENRKWMLENVFTRPKMSLLNLFAHTGAWSVSAAVKAKALTTSVDHSAMC
LDVAMANFRLNGIPLAFSADKSKSRGADKKGWQGGRKRGEGHEFVARDAFQELIALRAKS
RKFDVVLLDPPALARTSALSGSVWSAKSDYGRLVKLAAPVVAPSGYIVAFNNTRSRSEEA
WVREIMEKGLKDESGRWRRVTALGQAADFRWRAGDERVGKYLKGLVLQKV

>hydroxyacylglutathione hydrolase Contig19835 (uncertain of N-terminus)
MSTYRVVPVPVLSDNYAYLLIDERDKVAAAVDPVEPKKVLEAAEKEGVPIKAIYTTHHHW
DHAGGNEELLKALPAGTPVYGADDRIPGLTHKVANAEVLQLGSTGVKVLFTPCHTAGHVL
FLAGSDHAPRALFSGDTLFIGGCGRFFEGTAQQMYHALHDVCAQLPQDTQVWCGHEYTVK
NLQFAQSVEKDNQELQAKLKWAEERRSQEPPLPTIPSTIHDELQCNPFMRVNRESVKRAL
GLATEADPIEVMAKLRHMKDKW
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>hypothetical protein (weak EF-G domain hit) Contig2056 (complete)
MMKRVGVCGSAAERFGARGGFVAAGAARSLFSNSRGAISSSSRFYTTTTLAEGGSRTPWI
PGNPPTLEQASEGAEWTRETIYQVMYPGHVEVADEIARGVSLRSVVQGLFKKAVREGGLP
PRQEERVWSKWHAALERLEHERGVTTLADLAGLNRVAWWRTRVPHALRTALNTYVYHHRL
PAAVLPSSSSSSTASSA

>cobalamin adenosyltransferase Contig17827 (complete)
MKRFVAGTRVGRFSRPLFSNCRPVLCTSHAWADSRRGVKIYTKTGDGGESSLFTGERRAK
EDVVFHALGTTDELNSFVGLAREYCEQSKNGLDEKLQMIQSLLLDIGANVATPRNAADAD
ARLRRTEFSDVHVTTLEKWIDELDAELPPLKNFILPSGGLASSHLHVCRSVCRRAERLVT
PLVKDGQASPAVGRYLNRLSDFLFVAARHAAKAEGKEEVIYKKPKD

>4-aminobutyrate transaminase Contig24940 (and 18011, 10969,6919, E80POFO01A62A8) (likely
complete)
MRRISQQVAGASTVATGQRTASLALRLTAAQHVRLLSSPPSTPMPAFPGEATEPTIKTEV
PGPASKAARAAMEQFQDVRTGHFFADYGKSLGNYVVDADGNVLLDVFSQIASLAVGYNNP
VLLKAATSPEWGRFLVNRPALGIMPPADWGNTLHDTFMSVAPKGLHQVFTAMCGSCANEC
AYKAVFMNYMHKKRGGRAFNEEELNSSMQNLPPGSPELSILSFQGGFHGRLFGSLTTTCS
KPIHKVDIPAFDWPKAPFPKIKYPLDKYEAENRKEEDRCLEEVRRVIKTHKVPVAGLIVE
PIQAEGGDNWASPYFFQGLRNITKENDVAFIVDEVQTGVCATGKFWAHEHWNLSSPPDIV
TFSKKMQAAGYFHNIQYRPSEGYRNFNTWMGDPVRVLLMKSILGEIRDQHLLENVQITGK
YLKEGLLELQDKHAALLSNVRGLGTFLAFDLPTAQSRDQLIHTLRQKGVESGGSGTASVR
LRPQLVFGPRHAHQFLSILDDALKVHPKQ

>mitochondrial ribosomal protein S10 Contig1037 (complete)
MSWRKAELVISGYHKRVAKVAQDIATAAEMVGMKRVGPIPLPTRHKRFALLRSPFKHKKS
YEHFEIRTHKRLIWIEGPPEQVRKFIDFTVDTMEPIASVKVREHNYHHLSSFYSPPTTAT
QALQEARQAALGSPSTPPS

>thioredoxin protein Contig16529 (complete)
MRRSLSSSARSASVRRAASSCASSQPLRAYTLQRNGRNLISSICARSSSSSPLLPVLAPS
AGRRFYATAENGASSDSAPVTAPQPTVSPIISIQTPEEYQKLVLDVSKTRPIIVDCYADW
CKPCKDLTPVIEAVIKSREGKVTLAKVDIDKVSEVAVQLSVSSIPAVFAIYKKETISKFV
GLKSKAELEDFVDAVLKKTTQS

>glycine cleavage H protein Contig25099 (complete)
MRRTATLLKTRPVSHQRLSTASAGLLKPSSAWAFLASRSYSSNVPTDLKYTKSHEWVRMT
NGVATIGITDHAQEALGEVVFVDLPETGATYGQKESFGAVESVKTVSDIYAPVGGEVVEV
NADLKDKGSVNINSDPYGNGWMVKLKVSNQAELNDLLDAKAYEEHCASEAH

>elongation factor Ts Contig3833 (and 9737,E80POFO01CE59P,E80POFO01DE9EK,E80POFO01EPRIT)
(incomplete - internal gaps)
MKSAFACRAAFALAAATTGSGRGAAVFAVRSSSSLVSLRTPASGGCSNSRAFADAAAGGG
GGGMMGQIKELRARTGAGVMDCKEALAASAGDPAKAELWLLDKARSRFAKKAERPTTEGT
LALALASSEALLLELNSETDFVGRLEGFQKLALDAAAAALARAGQVAADGQGPHHLDSAW
LSALPLGDGTPKTVGDGVVGLFMQVGENMKARRAVLLRTAGSEGALGTFIQGTGLPHTGT
LAALVALQAQPSGGGGAAVGEKLVPLANALAKHIAGINPRYLSLEDVPETEAKEVGKEHV
VLEQEVTYGEETGRVRELLEREGAKLGARVSIVHFVRWKVGDGLEKPTTDFAAEVEKELQ
RSTKH

>Mitochondrial substrate carrier Contig10123 (complete)
MVHQARTTEEHRGAPMPEPEQDAGLAVAAVGVMCGVMGKIVQDRSALSVLVRGNAHWRGL
AAALVDDAVLAAQETKQLWREDGLLMLVKWPVLVVGTMVPFGIFGMATQPLFDQALGVGE
EDIAEQTIRFHTSRVLNTTLLMLVVHPYNVLLASYVARNFPSWKVALVDRVVKGKDHFYS
SWLASAAVGPVMCGFDFVRAKLLHWHKAALFPDFMPPRAGDDEEDDIDSDEDDSEEELGE
PSTARRVAYVASTALALVTTCSLGAVLLTPLETITMRMAAQPHVYGPLGTLGTMAAIYRQ
EGVWGFLHGLVPSIIFQCSLGLLAVESEANTGHVAL

>hypothetical protein Contig19791 (complete)
MNRVIASEGLGSVAARATGPNWQRWNIPIALAARPQLINGSWRKPLISRRHLAKLRNEHL
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ENGRPWEEPAANYSVTKVRNPDKPLYKGHKRLRPETIAKRQKMIETKMKEIPAVEKAQKK
IRDEYKQRPLKGLELFYVKPARKEVAKIKAKCRGGSGGSAQPEAD

>Hsp10 Contig24909 (complete)
MSKRLFPLSDRVLIRKAKPVERIGGIVLPESAQKRLNHGTVLAVGPGARNREGALIPTTL
KEGDNVVLSEYGGTEVEIDGEELHLFREDDILGILKK

>hypothetical protein Contig16904 (complete)
MATNDERFDFEAVLSTQAKDWACASDLQNLTRCFNNRNLAACQGFMDAFDRCTAQAPFPR
KPAAADDGDDDDDDEEMAGGPVSKVAIALAPQVFIGDAPRRKTWLSTTLERLMPKIFTEG
GDDDDDDGDDGKGKDKDDKNDD

>cytochrome c Contig7440 (complete)
MSFTPPAGMDKACIPGDVDNGEKLFKARCTQCHTINKGGGNKQGPNLYGLIGRKSGMVPD
YKYSPANKNAGVTWTNDTLYNYLENPKKYIPKTKMAFAGFKAPQDRADVTAYIVKAAQE

>NADH dehydrogenase B22 Contig8040 (likely complete)
MNKGGLSSVANAAVGEAHRRHVCHLYKRALKLQLDWLVKRETWYPEANKTRALFRQHMNE
TDPRTISRLVKDTENLLYTYRHPDPYVSPMSEGGTKWQRNVPVPPEVAENGWAEFDYEEF
EQPPPKADF

>NADPH-cytochrome P450 reductase Contig26819 (complete)
MFRSAKRRAHQLLTPPRLANAHSSRHLAPPNLQQQQQRWYRAVPPAAAPVNLNVMFGSQ
TGTAMGFAQQLGKMARKKSIKARVVDLEEFEPADMLGKPSEVYVFVQATFGQGEGTDNAK
GFFEWLKANEREDDKSRFSPLRFAVFGLGMSQTYPARYQAAAKWVEKRMLELGAQEIVER
GEGDDNGDIETNFEEWVDKLFPKLQELDDTSSASENKDVGARTTTAAAVEEEKLFSLKVL
PRTDVKQLAASRPFDPTRAVDIRNPYPAPLLTKVELHTQTSTRSCKHIELDISNAPNMRY
MTGDYLGVFPRNHPELVTQYAERLGLPLDTVMDFNVKPDTKVTLPFATPCTLGTYLAHYA
DLSAPLKKAHLSSLLPFVARPAEKEQLESVIADNEVVKRMVDEEQILLDVMNRYASIDVP
LGGFVELAPPLQPRYYSISSSDRVHPQHIHLTVGLTQHKTRADRLHRGVCSDYLCNRVEV
GDRVPIFVKNSLFKLPDSSHPIVMIAAGTGLAPFRAFVQDRTYLHDHEGKMLGGTVLYFG
CYHQDQDFLYRDELAKEIDRGNLQLVTAFSHAQEERVFVQHKLMQNADRIWHLIHHEDAN
LYVCGATQMAMGVEDALVSIVEKCGKMERPLAEQYIRTLKEKNHYQEDKFG

>putative ATP synthase j subunit (or 6 kDa) Contig19534 (and E80POFO01BMSND) (complete)
MSARNFGLTEGEIQELKKRPYPRFAPAPMQRLISQAKVIWPFAVGWAVTLFLYSRIPISD
DDRAKSHYQYQLDVLDGKIKPEDHPIHGHHGH

>putative mitochondrial carrier Contig3787 (complete)
MESPSLFSSLWGNLAGTVIAFPLSILTWQLHTDNWRGWGSLVPFTSLGRLHWRALPAKYF
ELLALNVLKVRLADAVTSVTGIGCEPLGWLASDVKNHQDDPDFYDEREERSTARVIVDRA
RLWAIGTVGSWLSSLVLVGMQVPAAIVCHRMLAEPGRFGSVVECVRHIWASEGLSGFYRD
LPLFSLLIINELM

>SdhC Contig5019 (and 2707) (complete)
MLRQATARTAPLFAVRGTVTGLQVLSRSPVALATRTLATLPSDASTEAKPNRPLSPHVSI
YRFPLPALTSITNRATGGALTAGIYTAGALALFGAHDLPVYIDAFKAAVPLLVYPTKLLV
SFPFVYHTLAGIRHLYWDYTAKGLTLPEVYTSSYALMGATALLTLGLTFYSI

>Tim21 Contig1844 (complete)
MQRSAVCTSGRALLGGRVSLATACTRPVGIVGRRGVWEGALYSRPQPQQQSLGRRRFATD
SNGGQKEPPSGTKGGLQAAKPSGQGTAVTVAQKVVEGGKDAGYGLVILGGVVLLGAAAYQ
LFSAGFAPSSPQHVYSKASDLLRRDPEVQKLLGPNIKTYGEETSRRRRGLQSTKYFNAAT
QRDHVRVLFSAEGDVNAADVIADVTASGQFYLLTVEVPVTGEKLVYTNTGKFERR

>hypothetical protein Contig3449 (complete)
MATQGDASSADSSKKEEQHDNDQQQKEQKEKQDDERKEEDQKKEDWEKSRGGGYKQEVNT
FQKLLAVGIPVTAIVLGVKVLLDMQATGAEDDTLQVDMNVIMGHVFQNTVYNVLDSKRLV
GLLGDPLLVEPSKAKFSFTKDSAWVCYPLYAPQGHVCTVTVDLLRIDPKGKDVKTKKPHM
WYVAQVEVDLNNGKKVLMSTRMSDGLRQPFNVLTLFAKLYHDLKKQEQEFLQQQAAAALN
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QGPAPQ

>hypothetical protein Contig23117 (and 9466, 5375, 21747, 22005) (complete)
MRRVASTRSLARASCLRRSHSLLPKTCYLSTTGCVLARLALVGVKQQRYSEELHSNHGIS
VGDQLAGPHQRDPHEYLKQLSTKWSWPPPSAKLKAPPTATHFLYRAQDRMDSVEALWRGV
VQPSWQAYRSGYFDDKKAWSTGFIHGASGVGKTRFNLEFLALLADYLTSDASKAYRSPDD
EVESLHAALKNSKTVVLDIRHNGLALKVDETEWPPEVILGLRLAHNYWWPHVPYSEVYDA
FRWQHKAAPTRDDPSPRIPSMLHIAIDEIQSVFDTMAPYGGGSSVRSAPEPLSTALNRAL
QGAISQSQGLYVLGTLSGTAARHATEVLHATDATSTGVLLSPLSAKTVRQIVASFQFRFE
PQPGQPEMVSGQEWLEKGGKPFERLLTTIGGNARALECLERVLKTQGSPSKPLRLNQITT
ELTKEVRNTFNIESWGRKGSGQFGLLLALAGIPVTRESVVAFEEPSTPQQPPRPITVAEL
EKIGVVHLRPPPPSDPGQPDSWVNTWDVQELAVMEMPFVLAKAALDLAVKSKRHQRHQLH
QLLKEASRLLADFYPTAASFEKLALEHRVLRHNVASEWARRQGLTYVDAADLFCGTICHP
SLTELSFVPAATVRHVSEPAGAGVWWRAAKGGGPQASKEVPPTSVILEDGTTVELGSTSP
YALLLSGSNAVDGVLNEQLSHTPPKNVRVYIDTKHTQIGAPADDALSYSDDIKALISKRR
YLAEQFPEEEHIMVITSNKRAQQPGGKPHTAATLLRVPTAGRNETTSVDPRTCIITVTDD
SLAWAMSPTLAHFLVLE

>glutamine-fructose-6-phosphate transaminase Contig10312 (incomplete due to internal gaps)
MSKSSAAVARRLGVLERHLKDSPSTFNALLNNDVCGIIAFVGSEPAAAPVLIEGLKVLES
RGYDSAGIATINPATHELAMSKYASVGKTNNAITLLEQHLGKHDAHVAGIAHTRWATHGA
RTDENAHPHLDQSGRIAVVHNGVIENSNELKKELQTQHGIHFRSETDTEVIAQLLGVYVN
QGMSLLEAVKKTQDRLEGTWGLAILDKEHPDQILAVKNGSPLLVGIGEGKMFIASEAAFS
RYTKEFIDLEDKEVAVLTAKGHSLDRSRIEHAPQEHIQISPAPWPHWTIKEIMEQPAAIS
RALNYGGRILDESSTMLGGLDANRAVLSGVQHLVIAACGTSFYAGIAGAQYMRHLNAFKT
VQNIPCFSVVNAVGSQIARHSACGVYLNAGREHAVASTKAFTCQVTVLALVAIWFSQVNA
PQDKQKRRVMIEALHRLPTNVGMTLQSMRETIKKIAHKLFTMGPGGKIVEHMFILGKGAA
HPVALEGSLKIKEISYIHAEGYPGGALKHGPYALIEKGTPIVLIVLNDKHAAKMKTVAEE
VRARGAYTIVITNNAQMFEHELEASKGADFDLIKIPSNGPMTNLLSVLPFQLLAYELSVM
RKENPDRPRNLAKAVTVD

>MORN repeat-containing protein Contig11917 (possibly complete)
MMRRSSSTLPFRQLLRSNSPALRPATGVVDGSRRLLHNRGGQPAGKLISTSCTPRPVGVV
AVIPHLALDDCHHLTHSTSCVVQLRGGFRRALASQVPPEADERANKPKKQLTLLPFRSDV
DEMFATPEDSGQHWLQMTINDDWERAPEGPDMTEPADLNLAKYLGTLDERGLPTGRGKLF
SQDNQEGISIYYFGEFKNGKFHGRGRSVNIEHIELTKEERNMLPKNVYQWTGKEKLLQLG
TVYEGNWEEGKMHGKGRLTSRDGSVYEGDFSMGQRTGLAKMISDEGYYFYTGEFEDGAYH
GKGTLRSKAGDQFEGEFERGMMRQGKGKMVLEEGFIYEGEIFDGAPSGYGKQYHPNKKEG
YEGHFNDGEYQGRGKLLTPDGSFCRGHLRQGHARRTRHPLRCQW

>Dihydrodipicolinate synthetase Contig22655 (likely complete)
MKLRLSHRLALTSSVRSCGFAAVRGFGSVTGGQEPLFRGVFPPITTPFVEGTEDVDHAAL
AHNVQRYARKGERTLGLGGAGEVLRTAKLEAAKAEQETGHKLRLIAGTGCVSTRETIELT
NAAKDLGYDAVMLVTPYYYTNTMQNNLQHHYTEVAKNVGGMPIILYNVPPMAGGVAFTVP
LIRDLAEIPNIVGIKDTSGNIVQLTEIVQKVKLPLASKGKSFSVLAGSGSYFFPALTVGA
DGGVMALANIIPHVLSQLYKDFHAAEAQPHLLHQCQKVQHAVVELNQKITAEFGTPGMKR
ALDLSNVYRGGVPRRPLRSLSDERAQVLVSVLERTGKDLGHLGLKL

>Sdhd Contig22329 (complete)
MRRATALFSARAAPSAAGASRGAARRLYATSTESSVLDTVLPATGAGKHRLYHYTSIGLV
TLIPIALVAPSSVVLPVDLALGFLLPIHAHIGMAHIVEDYVPKAGRTAAGWGLMLATGIA
VAGLLKLNVTGSGLTSSVKTLWRKEPLTTTQKESSTA

>cell division protein FtsH Contig24281 (and 20121, 1341, 7222) (incomplete due to internal
gaps)
MMRMGTRAAHGSGYAMPRTLSLLGRTSYSPSALSRLPRHPLLSSTSTQTTLYPPRVLGVR
RGLTTPAGGPPPGGNLPYGWERWRNVAPNGQQTPKQSASGTGGSRPWGVIALPLLLAGLG
APTPTGSEISFQQLTNELLPEDKIAKLEVVNGNRVRVYLKDDATRDPRTGELQHTKAAYT
ITIGSVETFEKQLEEVQRLLEIDPHQFIPVTYTTLPDWGGMLANWLPPLLLVGFLVWMTR
SSLKAAGGPLKGMFDAASNPAKLYNKETGVKLSFSDVAGLEEAKEEIMEFVSFLKFPEQY
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RALGAKIPKGALLVGPPGTGKTLLAKATAGEASVPFYSVSGSDFIEMYVGVGPARVRGLF
EEARKNAPCIVFIDEIIDAVGRARGKGKFKGGGNDERENTLNQLLVEMDGADIANVCNEA
ALIAARHNKLAVDEQDFEAAIDRVIGGLEKKNKVLNPEEKRTVAYHEAGHAVAAWFLRHC
DPLLKVSIVPRGQAALGYAQYLPKDTYLVTQEELFDRMCMALGGRIAEQLEFQKMSTGAS
DDLDKVTRMAYSQVIGYGMNERVGPIAFNPNEESSGRPYSENLAEIVDEEVREMVKKAYA
TTRALLQDKYEGLKQVAELLLQKEKIRGEDLEAVLGPRPFKDTALEDIRHLLPAGYDEME
KAREKLFHDERERIQQREQELREAGGSSTPPSATQPQP

>hypothetical protein Contig14134 (complete)
MTLDSIKAGGSALLASLLQGGGESTPTGLLAGLGVTAAALGLGAAYMLVLRQPSYASFQL
NASFPTVPPNVLFDFLVEPANYYDPRINRKGYRPVVVEREAGKIAYVLEDDALGGLLHFS
TPVVRRFYEHPDGRDSTDGEDKRHSGSRVLILDCCALGVFVKIIWHFVGTNMEGEGGGEG
GGEADVGTDVKIKVSLQGPWWKLKLMQTGMKKEIGAKLAKLQLLAEQEGGLN

>adenylate kinase Contig18341 (and 18852) (likely complete)
MYGRSAVAGRAGSIKILRANCAQQFRFFTTNGSGSASALRLIIIGPPGGGKGTQAERIER
DYGLSQISTGQLLRAERDKKTPLGLVIEEKLTKGELVADDLMLDLVNNAVASHTNPKGWL
LDGFPRTTAQAQMLKTLLDQIAKPITGVLYINVDKNVIAERLKDRYIHPGSGRTYNLQYN
PPKVAGKDDVTGEPLVQREDDKPETVLSRLTVYEEKTRPVLDYYAQTGLLHTIDSPNSDV
GYERIKKLMDQLLRQ

>NUDIX hydrolase Contig11762 (and 21071) (likely complete)
MRRASVLASAQGTHPWTSGGSRVVGARTLTTSAGAGSAADRWKKNFKKVVPEGDSKERAV
CQECGFINYQNPKIVAGVVALSSTGKVLLCKRAIEPKTGYWTLPAGYMEVGETVQAGAAR
EAREEANATVEAGSLLTMYDVPRIGQVHMYYRAKLLSDEVSAGEETLDVALVDLDEIPWD
QLAFPTVRHTLEFFLKTGRHSADAIDFKSITEQLYLIDSSSTNTISSHLQVTFSYRPI

>antibiotic biosynthesis monooxygenase Contig10994 (and 9979) (complete)
MARPGFVRTNIVRWVKEGSEASFLSQMRDLRRLALNADGFIGSEHLWSVEHKHKHLTTQT
WTSLDAWHRFKSHPDRVHMVKKLQDHLTEEPLEDVYTPYVKERFSIDLEALQSGRHGN

>metaxin 1 Contig18718 (and 15904, 11378) (complete)
MASSSSAAPAVLKLHQYGARWELPSFDPFCLSAQAYMRLAGVTFEEVPSNNPDVSPTSNL
PLVQLGDDYVAGTNAIFTYVGNKTGKSLDSALNAEQKATAAAFIHLIETKLHPTLLYNWW
AEKQNMGQTLVLPHFNSMVFPLGYVLPRLKQRNVQSYLYTLNLTQDEKVYNDAEECYAAL
ADFLGDKHFFFGDSPSSLDAVAFGHLAIHLVAPQSHKLRSRLLQHKNLEAFCKRVMTLYL
GQDFPAIPAPPPATEDKDQKQEMSQHKKTGMYLLTGAGLLILLHYLTKQHQAAHQ

>L-gulonolactone oxidase Contig14564 (likely complete ... termini from PGPs)
MMMQQHEMDQAAPRTGHAHRTSSITRIANYQWRNWAGIHTATPKYLYKPTSAREIVEVLA
TARAAKEHVKVVGYSNSPGDIAVTDGYMISLENYRRVLSVDRKTGLVKVEGGIKLQDLID
DAARHGLAMSNLGSITWQSIAGALSTGTHGTGIKLGILATFVRELELINAQGQVLRCSAT
ERPELFNAARCGLGALGVISTVTIQLEPAYQLHAVEVPMTLEAVLSSLNTIIHSAEHARF
WWVPHTNKCWVWQANRTKEKAAPPRFPAWQNLLHILVERKLYEFLLWLGTFFPRLVPYIN
KLYSRILFSKRRETIDRSDKQLTFDCLFQQHVSEWSIPVANTATAMLRLRDLIKDLDLKV
HFSVEVRFTKADDIWLSPSYGRDSAWIGIIMYRPYGRDMPGTKVYFDAFEELMKELDGRP
HWAKAFKMSEVEFRQTLPHWDDFKRVRAEMDPTSTFSNAYLDRLFPTQKQPTS

>malate synthase/isocitrate lyase fusion protein Contig25389 (and 25906, 15037,2615, 13622,
22548) (incomplete due to internal gaps)
MLTARNSLLRGGGRSILSSSGLTVTSRALGSTLWRTYARKTERDLSHDINRSLQTDGIEI
LAPVNEERASVLTPAALHFVASLSRQFEPTRQELLGSRERVQQELNAGKLPDFLEETRHV
RESEWKVAPVPEAIQDRRVEITGPVDRKMIINALNSGASCFMADFEDSNSPTWTNNVDGQ
VNLRDAVNKVIGYTNEQGKSYQEQTATLFVRPRGWHLPERHMLVDGKPVSGSLFDFGLYF
FHNAKTLARQQEGPFFYLPKLEHYHEARLWNDVFNFSQDRMGLSRGSVKATVLIETILAA
FQMDEILYELRDHSAGLNCGRWDYIFSFIKKFRERPDFVLPDRSEVTMTQPFMKAYVDRL
IQTCHRRGAHAMGGMAAQIPIKNDPQANEEAMKKVREDKEREVKAGHDGTWVAHPGLVPV
AKEIFDAHMKAPNQINTPRRDEAKVAAADLLRVPQGNITEKGLRHNVSVGLQYLELRGQG
CVPIFNLMEDAATAEISRMQVWSWLRHQAPVTWSDGKKKELSRDTLSKVLEEELGKVYKQ
IGKKAYDESKFKLASKLFIDMCTSSKPPEFLTSYAYPFIIDPSLTRHMVADGQLMNGQEE
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SNFWLEVEDVRRWWQDERWADTVRHYSPEDVVRQRGTLQQDYASNQTAKKAWKLFSHLRE
TKGYSHTFGALDPVQVISMAPYLSTVYVSGWQCSSTASTSNDPGPDLADYPMDTVPNKVD
HLFRAQVFHDRKQRHARFMMSREERNATPPVDYFRPIIADGDTGHGGNTAIMKLTKLFIE
RGAAGVHFEDQKPGTKKCGHLAGKVLVSTREHIDRLAAARLQADIMGTDTLVVSRTDAEE
AATLLDSNVDERDHPYILGTPNGALPALNDLLTDAIAKGATKEDIQSLTEKWMEEAQLST
YHEAVANHLQNEKRDAASYLKEWEKARKLGHSKARELAKDLGVSLPWCWDKPRTREGYYR
LQNGIPVSIDRAIAFRPYADLLWMETSVPHLKDAKEFAEGVKRVYPNAMLAYNLSPSFNW
SAHGMTDSDIENYTKQLASYGFVWQFITVAGFHSDGLIATQLARDYAKRGMLAYVERIQR
TEEREQIPTLTHQKWSGTQLIDAAVQTITGGAASTLSMGKGVTEVQFGKEKSE


>L-lysine 6-transaminase Contig3139 (likely incomplete - uncertain of N-terminus)
MSSSAPLTREQVKNLKPNQVHETLGRKLLVDGFDVVYDLDKSKDLYLHDARTGRDFLDFF
SFFASWPISHNHPKMSDPDFKQRLLKAALHNPANSDIYTVEMAQFVATFERVAMPPQFKH
LFFIQGGSLAVENAMKAAMDWKVRLNFQNGLKQEKGKKVLHFKEAFHGRGGYTVSVTNTA
DPNKYKYFALFDQWPRITNPKIKFPLAGENLVQAIKDEEKAIAEIVHHLETDGDDVCCIL
LEPIQGEGGDNHFRPEFWQQLRQIANKYDVLLIADEVQSGMGLTGKFWAHQYYDVVPDVI
VFGKKSQVCGFMATDRMDIVKENVFVVPSRINSTWGGNLVDMVRSRHFLEIIEEDNLVQN
SAQTGAYLLQLLHGLQREFPHLINNVRGKGLLCSFDTVTPEVTNKLKAFAYEKNMLIISC
GTQTVRFRPVLDSKKEHFDIAARILREALVHIDRENKKAAL

>proline oxidase Contig1215 (and 18178,21767,21105,10132) (incomplete)
MKMSIGSPATMWRSRTPFSISCINPTSTTLCRARYLASSSAPDNSSSSSPSSSSSSSSLK
WLDFEDGEAAFKNRTTSELVRAWTVFHVCAWTPVVRRARRLLALAEAVVGARAVTWVLRR
TFFAHFCAGETQTELLPVIDRLRAAGVGAILDYAAEADLPPAPTTTNGNGAANAANAAKP
QAQTQAQTADPFPYPSTPASPSGPPPPAEFFRPDKSLDRREGVVSARTYYYEDEAHCDAN
AEIFHSCINSAGMRPDGFAAIKVTALCPPVLLMRISHILEESMSRPNFIKVLGMLNVSLS
PAEQADLFAAMDVDKNGVVDYVEWLESVQPNDATLHPFFCANGGSGGESTLLPKLNPREA
QQMDNMVDRLERLAERAAAQRVHLMVDAEQTYFQPAIDHMVLNLQKKFNRDFPAIYNTYQ
CYLTNTAGRVDIDLARAERHGYHFAAKLVRGAYMVQERKRAAKFGYKDPIFPVIQDTHEN
YHRVMDAILRANVSRGAQVMVATHNERSVRFAVEKMH

>methylmalonyl-CoA epimerase Contig20639 (complete)
MRRSSALARGFAPLRSTNAPASALFTTRRTLTTSAGASQLAVGVGKLNHVAIAVPDLEQA
TSLYRDVMGAKVSEPLALAEHGVTTVFIELGNTKLELLHPLGENSPIANFLKTKPSGGIH
HICLEVKDIHAALEVLKAKGIRAIDQKPKIGAHGKPVVFCHPKDLNGVLVELEQV

>SPRY superfamily protein Contig9767 (incomplete)
LAQLGWATRQSSFNKSTGVGDTGSSFGFDGFRCRAWHDLKSSPYGQRWKAGDIVGCELDR
SNDQISFYLNGQPMGVAFTKIGDDIKLFPAVSVDATERCRLNFGGRGGEGFRHLPDGCKS
LCDLIPRLRRASPTGSCAP

>Dimethylaniline monooxygenase Contig13065 (complete)
MEVSVKERTHPAIAKLLAKGTKPRVCIVGGGWNGLYALKWFVEEGLDDVVLFEQTNSIGG
VWVYTPDKPGGCFKGTRTTASKSYLHASDFPMPESFGHFPNHVEVLNFLKDYANHFNLHP
YIKLQQTVHKARKTEDGAQWKVVTVPTKEGHNDDEGNAKKEEHYFDILVCCSGQHQVPRS
THKDHPFNQFTGEMMHSHAYKKPTKAMKGKTVLVVGGGESASDVAAEVCEKAGRTILAIR
SGTWFQDRTVGANQPADMVFTKHQRLLGFSDFQSWLVWIGRYTMIEMMWGKGGSGLKEWQ
PSCAYFHGFLNKSRDIVDKAALGKVVARRGVERIEGKRVWFTNESKPEDVDLIIFATGYL
SNLPFLAPELDFTTQAYKLVFDPQDPTLCYVGTARPMIGSIPALGELQARWAVKVYTGQV
ALPSTDAMLTQLAADKIRHKRVFPADDHHLPQLVNHWEYSDEIASYFGAKPDLVRWFFRN
PFKWWTIISAPWSAHIYRVEEPKARDEAIANINRTWLPDHYSFNFFNKAMLAFDLWLVLN
VVAVFCLLYVYLFLM

>Mitochondrial substrate carrier Contig18671 (likely complete)
MENTTGETTLKAPSETFLAHLLCGAGAGLISDAIVHPIDTCRTRLQVQRG
VGSGLFYKNTADAFTKIVRQEGAKALYKGFTIVASFTVPAHALYFWGYET
AKRTLQPSVPLEEKGALVHFVSGMFADLMGSFIWVPQDVVKQRLQVQKTS
LASAAADTVKYKGSLHCIKTIIKEEGFLALWTGFLPALAVYCPFVGIYFM
TYEQAKRVFQKTRGYASVDDLPLPYQLVGAASAGAIAAAVTSPLDIIKTR
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IQVGSDYKGAVDAARRIWTEEGPRAFTKGMGARILWIAPATTITMAAYEQ
LKHVVPF


>aldehyde dehydrogenase Contig2067 (complete)
MDASSAAHTVTLNGKAISFPTRLFINNEFVESVSGKTFAAIDPATEQEICQLAEGDKEDV
DRAVAAARFAFEEGEWSELSSKQRGDLLYRLAELIDQEKEALALLESLDVGKPFFESFNF
DLKQVVDTYRYFAGWADKIHGKSIDIPGNNVCYTRHEPLGVVGLIVPWNFPLQITAWKLA
PALAAGNTVILKPAEQTSITALKLAELVKKAGFPAGVVNVITGFGPKAGAAIAAHMDIDK
VSFTGSTFTGRKVMELSAASNLKPVGLELGGKSPIIVFDDVINMEKAITDSYYALFWNAG
QCCSAGSRIFVHEKIYDEFVEKSVAMAKARIEQTGNPLLDTTMHGPQVSKLQFDKVMGYI
ETGKKEGARLLCGGARVGDKGYFIQPTVFADVEDNMTICREEIFGPVMAIIKFKDVHEVV
RRANDSIYGLVAAVYTRDVEKAMFLSKKLKAGTVWVNTYNVITPQTPWGGFKQSGHGRDM
SEYALAQYTAPKCVIIEYQTPKM

>mitochondrial substrate carrier Contig24831 (possibly complete)
MGLWTAGGLIVAATIGWSSYAPHVVLAHRLTYATSSISLPYPAFTHQFHL
RALHHEAKLIDSHARRLRQPLNLLHPGVLAHTAQAWAQSVVELVTAAVCS
PSSDASQLRRLGAKALGLLLGSLASFPFFIAQNRLFAQLAGEVTVLPLKY
TGLGQTLSSINYADTFRYAFIPHLLTSVVSDAIYSYYSPREETIANWIYR
KLPPFKSRSKKVNKTKRLIASTASNILFSVLGDLVLSPLYVVSTTMAIQG
SGLEVALGTPRYSSGLHCAEDIFVRHGPLAFWQGLVPVLYSELVPQAMAT
TFTALVFNAFAYLREE


>inorganic pyrophosphatase Contig25083 (and 14394/E9BS9UA01A2VJ9) (likely complete)
MAEGPAMTTSVRSADVEAREVGTPDTPGYRVFFYNTEGKKISPWHDIALTEPGTRIEQGV
LRYVVEIPKGTDQKMEIATDEPWNPIKQDTRKDGALRYLKHGPVLCNYGAFPQTWEDPSA
EAHPQVNLAGDNDPIDVIEIGSRVAQRGEVVKVKVLGAFALVDEGELDWKVLAIDVNDPK
AASLNDVSEVEKQMPGTLGAVQEWYRVYKVAEGKQKNSYAFDDKALDRAFTLSVLQHGHE
SWRKLFTARSSPKFAFDSTSGAQ

>mitochondrial ribosomal protein L25 Contig16304 (complete)
MRKSSVVLTRNPYWRTSILQFKGYNDSWDRVVQSLSVVEHLEAVPRPFLGQKACEKYRKR
GLVPGVLKGLGAGYFDIPIALRISDLVSFRERGGFLNREYKLIIENKIKYVKPVDIVLDQ
TSMAPEHIVLQELRELTPPPVLTEEEEKTKAKLERLMTSHFYGAKTYGPKNPIPLWYKED
GGVV

>mitochondrial ribosomal protein L51 Contig8446 (complete)
MSRSGIWQLRKLKLQYCDFGGSSRGMREFLETRLPEFQKKNPQVLVDVVKRRNRHPHLSG
EYLIGREKSVGVGGLEADEVEHYIYHLRNQWGLKSRRLGAGQIVSQRRSVQGVWNPFVKY
D

>AGF3 protein 2 Contig9344 (and 1852, 15971) (incomplete due to internal gaps)
MLRLRSGWSVAGRASCSAGQLGGGSRLLLSRNAALHSSYISTSAPQLASKSSAWRWSCVG
QRINTLGGRNNEIDFNTFRTEYLENGKVREIVIVNGERARITLENEVRPTLYFNIGDLHN
FERKLEEAQRNMGLDPFDFVSVRHVREENLAGDLLAVALPTLLLIGTLIWVSRKTASSMG
GGLFSVGKHKATLFTKDMKVGTTFNDVAGCDEAKQEIMEFVAFLKNPDKYRQLGAKIPKG
ALLVGPPGTGKTLLARATAGEAGVPFFSISGSDFIEMFVGVGPSRVRDLLFAAARKNAPC
IIFIDEIDAVGRARSKSGYNDERENTLNQLLVEMDGFNPTLNIVVLAGTNRPDILDDALL
RPGRFDRQVSVDLPDVKGRQAIFNVHLKPLKLAEELVGTIGDKLAVLTPGFSGADIANVC
NEAALVAARHRKPAVELIDFEKAIERIIGGLEKKSRILSREERTRVAYHEAGHAICGWFL
EHTDPLLKVSIVPRGVAALGYAQYLPKEQNIYTKEQLLDRMCMMLGGRAAESLIFGKITT
GAQDDLQKVTKLAYSQVSRYGMSEEVGTISFAFAEGDGERPQVDKPYSQATARLIDDEVR
SVIMNAYKRTEQLLREKQSQLESVAKLLLTKEVLSADDMISLLGQRPYGLPRKVDPNPEF
KVEL

>similar to MPP beta subunit Contig27020 (and 7554, 25735, 23118) (incomplete due to internal
gaps)
MKASLHNVRPVRLPRFVGLESANHLRRSLNFSGSALLLASAQRRWATTAATDVRPLKPKL
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ERGPSMKSPLLDMPTPLAHVSQLKTPSTRITTLRNGVRVATEETYGQATAMGVFIDAGSR
NETFETNGTTHVLQRMGFKATTNRTSAEIVQKLESLGVNAISSSSREAMVYTAEVVRGDV
EEVVEVLADSVTNPLLLEEDLQEQKIAVGRELEDMVHDPPSWLPEILHELAYGPEGLGLS
HLCPPSNLEHHIGREQLHNFVKTYYVGPRVVVAAAGVEHDSFVKLCAKHFDSLPAAEGGK
PLHVPSVYKGGAHVEFMSPENEKRLQELQAESDKPPPSHVALVFEGSGLNDPDLYATCVL
QSLLGGGSSGRQRAVLCDDIGRQVLSYGERKSAQELSDLIEKVTIEDVMRVARRILSTKP
TLVVYTPEKYATLVPSHERLCAWFDAINDKLNGKESSESK

>mitochondrial ribosomal protein L20 Contig6876 (complete)
MSGMNKKKLLKFVKGFRGRAKNCPSVARERAYKALQYAFVGRKLKKRLFRETWIQQINAA
TRIHDLSYSRFMQGCVLSDVKLNRKMLSELAIYEPYSFSAVTKLVGERLKKEEVAKEVER
RAAAKKNIHPGNRDLTADQKEWLLAQKLKEMQIV

>putative ATP synthase g subunit Contig14600/E9BS9UA01COP0N (complete)
MNRLCGSLAKGAQKFQALEQSTTSCACNKQLYGYLGTQFGCWSNRWQAFPADAKALWRRV
ITGQITVGEVGRGVRASTPILLAALAGNFLGRGEFLYSPIVGASYTYPEY

>NUDIX family hydrolase Contig18587 (complete)
MLARGRARLSLYSGRGGRSHFSTSSISFQPTAALWQRWSGLRVDGTEDPDPNDSDYESDG
EEPNADAGADVQNRHHHHDEIVGFAINGLNRFHAHHLRRDDEWLRYALHESPNSRFLAFH
KLRPMVEHRTPPTHLGPILAWQERGEVLPAITDAKSTVLLLGQSLRETNSDRSIQEQLSD
ESNQINVFAFDLDPIVGDDEQEAQRYAAAHQTHLEVRTTFEEPRAIVPHLPPWEGGVVAQ
ARSLLHWHKKNGFCAACGSTTKSVEAGYVRKCNDDKNASCGMDHYPRTDPCIITMVVSSN
RDKCLLGRKSSWPAGRFSLLAGFMEPGETIEAAVLREVYEEAGLLLDYDKVAYKLSQPWP
FPASLMIGCVATMHEAEIQRQKVSVDYHELDEARWFDVKEVAAMLARSTQEGAPEGELHL
PPPLTISHHLVKLWLHERKTKRIK

>probable mitochondrial folate carrier Contig20361 (likely complete)
MDETNTTLRDLVQWTSPSITYLLHPLVVAGHRRSVTPYSGVSFVTGAVTG
MVGWADEARLVRRQTGLFGHPAYWAWVGALEGVLDVLLTAASLSVEEVVC
PPPVGGAAATKKPSPYVHNWQMALLAVSERLVWTFLTRPLRIASNRLHAQ
LPGPEGKYPLEGLLHVLRLLWAEDGLAVFTRSFGPAAAHEVVSSMAFSVY
DAAAPFRSLALQNRISNRLVNGGLQSLSLAADECARALLVALLTRPLQTV
VRRLDIQGCGLALWNAPYRGALDCITRIWNEEGVPGFYKGFVPELLTDLA
PAGVLFLADLAISAIFEPSVLFGV

>hypothetical protein Contig6062 (likely complete)
MIYLLSTCQRKNMTRKYKRKKFFVLLSRTMLDDLLPLVVEGLLALISLGCLGLLAIQPFK
NPPPISLRYVALVGLLPVAVTAGLMAASRYDMRYAAASLLTFYTSAVAETTGALALAVAL
YSEVHRNSNISPQWYALPTGSSPLALISNYVPSSYIQLAIFTVLGAYLLSAARELPDKAD
SLRLSAFAFLGAAASRVVLDRFDFLLDAVNSNLLGVVGVQLSSYLVYEFMMVVAVFFLFL
HLLKTYQGTSIKLKGK

>hypothetical protein Contig18606 (complete)
MKLARSQFTVTPRRAGLVLATSGGAAMLGSRFSLPSVHAHEKDVAVDEEQPEAVAVAAEA
EESPVVSQQQWEEVWEEEKGTFLRPYITSVRIAAQETLADACGQWKSFKEKTDLDHKWGT
TKHFATRYYWLLTGQKLGPEIAFAATTGVLTLVATRKVLRLPFRLALLSGGVATAALLPP
YEKTVPYLVHQYETFEWAKVADKFDPVAIKDAAIDELKASLPLRPRQVDEEECGEGAA

>mitochondrial ribosomal protein L3 Contig21518 (complete)
MRGWRSSVNKDQVEARRTAVDPRTLSDPSTGWDQRKRRTGLVAIKVGMTSEYSEYMEWLP
LTVLQVVDCQVVQVKKERHNEYEEEKVGLQVGAVDGKWRRLAKAQRGHFFHAGVNPKKVL
MEFKISPDAVVPVGTELRAEHFVPGQLLDLTGKTKGKGFQGVMKRWGFSGGPASHGNSAS
HREPGSTGQHSIPSKVWKGKKMPGRMGNKYRTTKNLLLWKIDTKNNLLYVKGPVPGAPGS
YIRVRDAKNKLHSLVPPYPTYMRQPEEVLPEVITANSPEPMWYKKMMARQAAFAEDLSKN
TDDNQTAVQVVLAHKEAFPSYDKWKKGLLPPGPNPSKHHSCLSVGEPMEFPWLADTIADY
EDPSTAEEDQLQIHYAES

>NADH dehydrogenase B17.2 subunit Contig24514 (complete)
MAKMLTNLRSEVSRRGVLGTLMAWHRGYLRPGVNSVLVGTDERGNRYFEATELPFGQDRW
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VEYSTSDDWGHDYDASQVPPAWHAWLHHVHDKPVPHQAVYSKPHKENKTGSQEAYHPHNY
VYGPRVKSTTDPNCEEWDPTRHSPFKENELR

>coiled-coil domain-containing protein Contig1265 (likely complete)
MELKEEDLIPCEDFNFFEARLTALRKSDDLISIELNKIDVNSQAECGNIWKKLTAGYELR
DRSIHRCVEAAMSSVAALRAEVKAKPRTTPTSNLTFCANRTSSATSSPSSRWSRS

>thioredoxin protein Contig24775 (and E9BS9UA01EU3KM, 11405) (uncertain of N-terminus)
MRRVAAISHKGGNGPLLARSIRSSGVPLARRGNASAADSTSQLLRSSRSVVPARAFNQWR
GLATQTQPPPTASSFAQKKTNSPPQQKSSSAADSNIYEVNEANFLKEAIEASDKRVVLID
CYADWCAPCKQLAPLLEAAVRNSGGRLALAKLNVDNNPTLSRQMQVTSLPTVMALSGRKV
VDSFVGLLKPAELTKFVEGLLQDFAPAAPAEEAETGGNLLEEAEAELAKGDVNQAAAKFS
QALEKDKECTHLVYAGLARCALAENNLQAAQHLVKELKDKYKAKLNDPAVGKAIAAVELR
AELADKSGGSAQDLEAKVTEWRAKLQADANDHQARYDLAHALFSTGQTEEALDQILDLIK
RDKHWNDEAARKLMLKIFSALGPNNELTTKARKRFASIWFC

>short chain dehydrogenase ContigACL00000399 (and 1728) (likely complete)
MNSNKIDLGLKGKTIFITGASRGIGLAIALRAAKEGANVIVASKTDSPHPALPGTIYSAA
KEIEAAGGKALALKCDIRNEEDVKKAVEEGAKHFGGIDICINNASAIFPKGTLDVPVKRY
DLMQGVNTRGTFITSQACLPYLIESAKKGRNPHILTLSPPLNIDAKWFKDHTAYTISKFG
MSMCVLGMSAEFKDRGVAVNALWPKTGIATAAIRNVLGGDDLMNQCRTPDIMGDAAYYIL
TSPATECTGNFFVDEKVLRAVGQTNFDHYAYVPGTKEFWPDFFIEEQDGDGVGLRKARL

>hypothetical protein (likely Tom22) Contig16787 (complete)
MVRLNIEELKQPQKKGFFGSIGLPEPVRRVANTWSNGLYAASMYAQQGLGYVSSFAWIFA
TAAVVIYLPLLRAMDSDRETIRAIRAEMVQKTAGMVPGAAPRGPDLGNLDISGLDFKIQL

>ubiquinone biosynthesis methyltransferase COQ5 Contig16532 (likely complete)
MRKASTTTVPMFAGMGAVNRTVSNASFCLLPSFSFASNGAKSAVIGSLLQRTYSTSPSPA
AASLHASPPPANAAPKQREEEEEVTHFGFKNVRAKEKASMVGEVFHRVASNYDLMNDVMS
AGVHRYWKDRFVTTLNPLPGTRILDVAGGTGDIAFRCLDRMKSTSTFFSKAPGTGQRASS
SVTVCDINPSMLAVGKERGIARGYTESTDPSVAWVVGDAEQLPIDDASMDAFTIAFGIRN
CTHIDKVIKEAYRVLKKGGRFMCLEFSHLENHLMQQVYDTYSFQVIPVMGHVVAGDMDSY
QYLVESIRRFPRQEVFADMIGQAGFRAVTFENLTFGVAAIHSGWKL

>hypothetical protein Contig13114 (and 12519) (likely complete)
MRRIVYSASAATRAGSPFHGSTLCRLNFDSHRSLSTSLVLQAAKAGSAVEATKETKVKKA
KQEKTNAESTLVTKQKEKKEKVAKAKETKPKKAKKETNAAVSAIEQAATGEEVARFLHGV
EREGHVSAALAHAGMPQEDQMQLKGFVDALEKIGKTRPADKPWGVFKIQDDGQVEPLGLF
RTEQEANVAFGDDQEPATKPKKEKKEKSADGENQKSRKEKRDEKKAKEKVKKEEKAKKAE
DKKLAKVAAKETKADKPKSTKKGSKKAETASGKEEELK

>AAA-ATPase homolog Contig25138 (complete)
MLRHTKRSQLPAAVARDLFLSWRHTSAAKASFAGGQQSYATTPQRRQNPSLPTVMGAFQA
SSRKRMECFGSIERASSPLLEALKAKAVVSLRNRRMGKTLWIDTLAHYYDVAHKGRFKEL
FGHLEIGKAPTQLANTFHVLPLTFAGIKSHNFDDFRRSLNAALNQAAADFKERYNLSFEL
NDRDAAITFQGLVDELKRKNEKLYVLIDEYDVSINKALGDLPLVSALQVSEKGLLKSMEN
TYAEFFSRIKTACDRNVARCFVTGVTPLALNEFTSGFNIAEHITRDRRFASLYGFTEADV
RNGLARLHRLQPEVVDRIVDSWRRDHNGYHFHPRQEVALYNPTRVLHGLRQLEQVLSFDP
PLSTLRPEEAADFLLNEIQSDPNSMPAEATLEAIKSSPYASLVVAEALSSDDAELECAGG
VANQFRLSHMHELNTGRTPLLSFMFYTGALTYARSPPKLKHSLRIPNNVARKEFTVELQR
LLDIDEIGVQQLRGAIVKMVDGRQVEPFCQAVSRFLLRGLDRRDALSGEDPFAQAVYNAM
LLARRPGDCVRKEYKVDPVARHSNTSGPALDVVYIGQQAVAPQKPQHYCFTLKNVKVQGL
VLGQGVQSWEKQVEISRTIDNMGGDDEAVLDLPLAKGDNFRKPGSTVRTVLEEAIQEARG
KYVPALQAEVGEANVHCWALVRVGMTRIVCKKVLPVEQQQ

>valyl-tRNA synthetase ContigE80POFO01A7STM (and 19665, 14725, E80POFO01A4SJK) (incomplete at
termini and several internal gaps)
MLQSLRRKKAGGGLASIHASGALIPRLEIRSSAVLFRSTFVRSSTTSRRTLTSASRTKPP
TQGPLAAAYDPVRTLCPHQQAPTLTCLVTRHTRHTPARTQKAIEGAGWYQWYESQGYFRG
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KNGVPPGHNFSMVIPPPNVTGTLHIGHTLTVAIQSPQDSIVRWRRMMGDNVLYVPGTDHA
GIATQTVVERRLQKEKKLTRHDLGREAFIDEVWKWKETHGNHINNQLRRLGTSLDWSREV
FTMDPQRSKAVTEAFVRLHDEGLVYRSTRLVNWCCFLQTVISDIEVEYESLSRRTMIALP
GKGTKKYEFGVIHHFLYRVEGGGELEVATTRPETILGDSALAVHPEDPRYVDFIGRRAIH
PFTGQPIPIVADPILVDRELGTGVVKITPGHDFDDFACGVRHNLPRINLLRNDGTLNQHG
LHFQGLDRMEARRKVIEELEQMGLYKDKKDHESRIALCSRSGDVLEPLLKPQWYVACQDM
GADAARMVRDGTIELIPDFHKHEWYRWMENVEDWCVSRQLWWGHRVPAYKVVAEGEERAA
ANNKDNDTLPEDWQKERWVIARNQEEALEKAKALYPDIAAPKLEQQDEDVLDTWFSSSLF
PISALGWPDNTQDLKEFYPLSVMETGADILFFWVARMAMIQVYLHGMVRDAHGRKMSKSL
GNVIDPLHVIEGIPLEQLLQNLNHNLLDEAERKKATAGIKSDYPAGIPQCGTDALRFTLV
NYTQQTRNINLDINKVVANRHFCNKMWNATRFVLSYAESTPVAQPEPDDLASKWILSRLS
QVVTKCNQGMSDSEFHVATSSLYDFFLNEFCDVYLEYAKASLLQPRPRQAQIKNVLNTCL
ESYFRLLHPFMPYVSEELWQRLPEDCLMHAAYPLAANQVAAWRNEEAYEKPMEEVLRVLH
AVRSLRDGHGATPLKYSVSIHTTDASLYDLLSNEASVIRHLAR

>FAD-dependent oxidoreductase Contig20819 (incomplete C-terminus)
MQAGGKRRVAVVGAGVSGLACARALVSAGLEVRLFDKGQRAPGGRVHSRSVRLDAQDQVV
PHRSSPHEEKKAVAEVLSFDDGAQYFTARAPEFRAFVEECVARGCVVREWAPLRVAVIDR
EGEVVLKPDDEGKKKEEKEAENNARYVGSPTMQAFIPFLAQPVAHTIQQSVRVADIQRRE
GGDGGERWGLVGEKGEDLGDFEAVVVGVPAPQAVDLLRAAPNLRAKAASVHMNPCWSVAH
FFFFVRLSVCSLTRAMSCVFGGARVLRQLTMCVVCACVRVGRWAWRLMARRRACSSTGPS

>zeta crystallin homolog Contig2433 (and 5342) (likely complete)
MRSTRTTTLTTLASSCSPYRLPLAQHQRSAAQYFTGLHPHINTSYTTLTSNMRAIIVSKQ
GDPSVLELKHDLPLPTPAPGQVLVEVKAAGVNPVDTYIRSGGNGYSVSLPYTPGADGAGV
VVDAPAPSAFKPGDRVYFASTLTGSYASHALAKESQLHPLPEKVSFGQGAAVNVPYSTAY
RALIIKGKARPGQTVLVHGASGGVGIAAVQIAASLGLRIIGTASTKEGQELVLREGAHAV
FNHRDEDYLQRIKESTRDGAGVDIVIEMLANVNLAKDLDVIKRGGSVVIVGSRGEINFAP
RLIMAKEAIVTAVALAQSTPEELAEHHAFIGAGLANGTLRPVVDKEFALGDAPKAHEEVI
SGTHAGKIVLLP

>mitochondrial ribosomal protein L23 Contig10987 (complete)
MRRFEKLNPTKYWLPNIPLTLMPPARNLPSNKFVLRVQPNITKVELQNYISQLYGVSVTK
VNTMNYEGKLKRAPRRGKFYSTKRYKKAIITTDDSIRADDFQEEGRRGAGFIEGEVVPTK
RR

>RNAseII Contig2190 (and 2090) (extreme N-terminus inferred from genome and internal gaps)
MRRLCRVQRLPSPKARPGQTKPLSCTVGATPASRFLSQFRCISREAGWRGINARLGVSTR
QHSTTTLPRHALCTSSSYSTRAFEPAIGEVPEDEPNLAEEGRVIEYIEDGVPKLGLLLQK
LEEHERESKSLWIVGSQDARKFALSQAKFSYVWPEMPQLGLVDGITAQAVRGNAKQLAAL
AKEAEDLRATIAPERLQALWEEAQLTGDSPDSPRKTITPVQAAQFLFGSTGPLETYAAHG
LLWETRVYFKPRGKTFVCRDREMAEELKDSLQDRVDSVKHSKLFLIKMRHKLERAVGGDQ
APSAFLPDIADLSKEYQACWKSLNYAEDRASTDVDLVAGGMDSLTEKQHLDFLKKYAAMI
ISETPSSEPIDVTEHTPLEGLLKEGANSVDLFNAMVQLGVFSEKENLDIILHRRPLHFPE
EASTWVNEVLAQPPPDSDGGKRLDLRQLPVYTIDPHDAYEIDDGLSIQTDEDGDTWVYVH
VADPTRWITPDSPLDLLARDRAQSLYLPNGVSLPLFPPKFTSQAVALRPNTRSCALTFAA
KLDRESGEIKDYKIAPTLVENVHGLTYGQADSLILSGQEKYAKATAQYLPLHLQEEQQLL
AVPDADEREERKNDIKESLRRLGLNHKLGKKKGEASRKEAPHRTLDLQRVESADTFSNRE
LARPGVDKEAAMGAVWGLHEMAKLRRRYREQRGAVIVSLPTTAIRIDDVAQHRGVRVRRL
ESKVTEEGANLGQEGASEEGEEEEEIEGMQESTGARMMVEELMLLAGEIAGKFAEARGIP
IPFRVQQRPPGDSKYLDYLVRGKEKKAVVKSWKSLVGLPPTKYSSVPGPHFSLALDSYAQ
VTSPMRRYADVLAHHQIKAALRGEEPPFLSWHFVPMFQTMIQRKQEFASLVEVISRRWII
QYLKENKDRPFRAVVLEVQEKRAGGNLIGDSRATVLLSELGWRTIVTVPKSVKQGHALTL
RVRTADPWTNYVSFFKLRQ

>NADH dehydrogenase AQDQ subunit Contig797 (complete)
MKRLTIARRPFTFAGATPLYRSAAPLSSQQRFLKDIASNSANEAPPNTDAAQVRLHMAIK
GNADEVSEERRKSISAVMGTPVEHLKRRVRIYIPARCTMQSGVHSATFWKISYPEEEKNH
WANPLMGWTATKDPVSNLHVKFDTKEAAVAFCKQHGLDYEIEDSTTPYENITPNKDYADN
FKFKVERSLEPDIY
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>adenylosuccinate lyase Contig27007 (complete)
MKRAGVVTKCAWPLGSASTMRSGLVGASSASRLLLRQAGGESLLLATARPLATSSHRDVF
ENPLVSRYASRAMSGNWSPQKKFSTWRRLWLALAEAQKELGLPITEKQLAEMRAHLDDID
FAAAEKKEKEVRHDVMSHIHAFGTVCPTAMPIIHLGATSCYVTDNTDLIQLRDGLRIVQQ
HMLQLMQHLREVSLRYKDLPTLGFTHYQPAQLVTVGKRATLWLQDLLFDYEQLSERANRL
PFLGVKGTTGTQASFLELFNGDHNKVRELDRRVTEMMGFNKSLGVSGQTYTRKIDYQVLS
SLSAVAQSLNKMAVDIRLLMNLKEIEEPFESKQIGSSAMAYKRNPMRCERICGLARYVIS
LTDNAAHTHANQWFERTLDDSANRRLSLPEAFLATDVILRVACNVVDGLQVWPLVIKKHI
DAELPFMATENILMAAVKAGGDRQALHESIREHSMEAGRLVKEQGLDNDLIERIRNDPHF
AAVRHKIDDMLDPAKFVGRAPQQVEEFVRDEVDPVLARDAHLLRDFDHKTAAQLHV

>Pyrroline-5-carboxylate reductase Contig21589 (complete)
MRSCRRAFVLQAQLSPLTATVPYPIYKRPLPEHLIYIGPNNTSSSTHQQPPARSNNKMSE
PRIAFLGAGQMATALARGFIDANVTRPENIIASDAYEPQLPRFQKDTGGSTKTTKSNLEA
VENSDVVILSVKPQVMSTLLKEIKDAVASSPHLIISIAAGITIDTITKQLGSDTRVVRVM
PNTPCLVGKTAAAFSLGGKATPEDGKLVAHLLSSVGLGTEVPERLLDAVTGLSGSGPAYV
YQFIEALSDGGVAAGLPRDVAAKLAAQTVLGAAQMVVQTGEHPGVLKDKVASPGGTTIAG
IHALENGRLRATVMNAVLAATERSKELAKSE

>universal stress protein family Contig20243 (complete)
MATNEPKEEEEEERGVERRRKEEENESSGIIPLTSSHGRPIERPLDRDEEDEDEAERRAA
EKHWERTLDRLKSELVPVTHVVAIDGSPNSDRAFSWAVRSLPRHDRLLLVYGTRKVPMPG
LEVTLLERRSADEQRRKQRRKARTLAQHYAHRCEDAGRECYFERLEYWGSGDLAGQICRA
ADVNGAHTVVAGSRGLGPMQRWMLGSVSTALLHQCHSTVVIARDAPEPEREIQPDPSHRL

>hypothetical protein ContigE9BS9UA01BE0AK (likely incomplete)
MRKRGKNSARLVFSHTTPTNSRLVFGMNGVGQLE
GELFSSFAAGAAEEEEEATAAGVDEPASHVEDGRGVRWGYDAGFEAVNNC
PAPSYIDFFWEHSYHISTNNYLRGGFVVGGMLPGSMLPFAFDAGGVDLGA
TLQAVRGPWAVLGANLEIGNRSVSCALGMDCQVRTMWLDLTGGRCFLNSV
VAYQKPTFALTMNMHGFGERFIASAVANPVGLYRAFCKTNTAKDEDLYNC
TWLAGVEADTTQRNGAFSARCLSFALTRRNTSPYPFSAPHTTKTTEAEVF
KVDEPLLRDGENKIKFDILNLGVGNNAYRLSVHSSSLVRLYRNTHVKLSS
SLQADVLPFDPNTARIGLSLVFVV

>Bax inhibitor-like Contig26404 (complete)
MRRTFAFCSSSPHFAKVASNGLALKRAARPLITLSPAATGCMRPPLTCTASSSSSSSSSF
LLAHLKSSAIRPSSSSGRRQLFTATSNRTAAKTTSTTPLLASGGHRFGAATKTAIRSIRI
EGRPPRSYNGLMGDVGVVAPRDNTAWLLIGGLAALGLGGIALAGYVNQETTTIPTHGDLT
THRLRATYGYMLGGLATTAASAAVLFRAGAAHRVVAMNPWLFMGASLLGTIGSLMVMQSL
PPENTVARHLAWGVFNACNGLALSPVAMLGGAVVTKALVATGAVVGSLSLVAAAAPSESF
LWMGGSLGVGLGVVIAASMGQMFFPASAFLTGITLYGGLGLFGMMMLYDTQRVMHKAKTD
EVYDPMTQSIAIYLNTINIFVRMATIMANNQGNRRR

>hypothetical protein ContigE80POFO01AS94G (likely incomplete ... from pgp)
MEEEKRIKAQWGPVWKRTAGATAVGMVVGAAVARRRLRLALEAGPAQEIAASTLLAAAAS
KPPSTIIFTSALAGGLTAGTTTGLFLVSRELLRVDMQWEGMVPSLYAGMATGALLGAATG
GPYPALLGMSTLGGLAAVGEGGVALWNRWYNKKRQQIFQQRLIEKRQTLLRQRAQAAQSE
LEHIDQQLETIAYHLNAQKEKEEAAHESVMSWMSLKVPSWFPIQPVTEETQKKKQEAEAL
EK

>hypothetical protein Contig12279 (complete)
MQRQGTKIVAGIAVGRGAARLGRVAATASVLSSRATFHGYAQSTTTRSAGWKLARTAPFS
GPAGLLLHRRCLASSATPSRGDNKQKKAEVEEEDTEEEETDDDEDDEEEDEDTEEETDDE
EEEEDEDEDEEKSKGAPAPAGVSQAELAKQRKEAKDLKRLERKERQQKKKDIRKEQLQRR
REQDAKKKEKEELKSREGARKKEKKEAVVSDIDWEEDLEAGTTAAAQAAKKSNKKTSKKR
QKDAAFVPAVNPNLFNPE

>mitochondrial 2-oxoglutarate/malate carrier Contig26588 (likely complete) 310 aa
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MASTQAKNPYDTLIQFVGGGVGGCVASICTHPVDLLKVRLQVQGSASGLA
APQLGLWKTTVSVFKEGGMVALYQGLSASLLRQATYTTTRFGCYMYLRDL
LADSQGNLPFYQKVLASMLAGAGGAVVGTPADVTLVRMQADGRLPPEKQR
RYKHAVDGLIRIVREEGFFTMWKGCLPNVYRAMFMTAGQLASYDQAKMLL
LATNIFKDDPVTHFTASTIAGLIAAVITSPLDVVKSRVMNAEKGYYKGSI
DCTLRTLRAEGPLAFYRGFLPYAIRLTPHTIITFLAFEQFNKACIWLLKK
AGKLPTDVAA

>tetratricopeptide repeat protein Contig5100 (likely complete .. from pgp)
MASTEEVDVGMEATAARLRGSSSKDVAALGNEAWTVQEQLFVAALDSNDLPLANEVLARL
TAKFPGSARVRRLTAMKLEAEGEFEEAISIYNSLLIDDPADTATMKRRVCIWKARKETRP
RAIEELNDYLKIFMADTTAWQELGDLYLDEQQYEFAAFCYEELILAEPLNHHYINRYAEA
CKALASKKGGAKPKDNGELATLAAGKLRASYKAAAPEHLPVVDAVLAKLQ

>mitochondrial ribosomal protein L4 Contig11830 (complete)
MKAAGRHCARAPRSNQRLISSAALSLGVPSPSSTAGHLRFIASRTPLISMRYPRMSPILA
QMGVHSSVPSSSIFGGVKEEQKEHNKAAASDEEDEEEDAELDAAEDEAEATAVVQRATGL
IDGTQRWAPTLELPVESFLNEEQQGPLGSVTLNPNIFMVPIRRDILHRVVVWQLAKRRQG
THKSKTKAEVRGGGRKPRPQKGSGRSRQGSIRSPLWVGGGHAHAKKPRNYYFPLLRKVRK
LGLKTALSLKFAQGKLKIVRSTHVDEAKTKNLARVVEGKDWSKALVIDGKSVDDSFRKAS
NNLPSVKVLPVGGCNVFDILNHDLLVLSLEAMQHLEELLLEENEPTFYPEPATFQAKEET
LA

>hypothetical protein ContigE9BS9UA01ECYOD (likely incomplete/incorrect ... from Genscan)
MQRHLRRHFPRLLVLVLSSSSLRSSCASLPRPLRRTFTAAGSSSSLRTLPSSRTTTTTTA
TAAAAAGSAKRPLRREVGVEQAVARLTALRTAGRRAARETSVGVAETPDLVGRTLRPGDL
RAGLEAVEAAHALAVRRVREAGVPMGLDHYHLCLRFHRRSPEHARHLLEDLLRDGVRPTA
ATFDVRPPHPPTTSHHHHMRSHQRACVMVVDIYGVGRPRAHWLSEAVQLFHRYAHTSCPA
PRSTCSLVSYVVSLIACRVVGRVRWWLVVAGATGRDPLADGRVGRAFELHEGLRGLGLRA
DMDTYISLLALAHRCGDAERVKKLWTMITLAGIEPNTRLVNSFIANCNSPERALIAFNKC
GSPPPRPRPHLTPAALLPPDLPLTDGERRQDGRG

>hypothetical protein Contig21951 (and 12989) (likely complete ... from PGP)
MKARSSLLATVRCASGAGGRLPAPRLSATTLGAGHLRSGRTATATLARCSLRPSHQPWQL
SSVLLPRRDFTASAAPSSGQPEGEATSPALIKETSELFYQQLFVAKDEKAAFHLYKILNS
LTRNRAFAVEFGQREGGRAIDQLFRLFREAATTHYSQEKILAVLTNLARHDATQRRAIAV
SGAEPLRQALVCKTTLRGVVAQAVQLLNVTLQSKAELPSSLFEGYVPATMDLMVDFADKP
ELQLDLIHLLGLLSTDCAFEDYKKLSPLGAAMLIRNMQAYIFEPQSDSFIARQMTETLQA
LHRILSRRPAGGEHSEEESKLAQAFQNTFLEHDSKARYAVLNGLNCVVLLTKSTNPTVSS
LATEVVELLGRDNPGVFAEVAKIRSSQE

>pentatricopeptide repeat protein ContigE9BS9UA01BXXPB (and 2016, 11354)  (likely complete ...
from PGPs)
MSFLAQSKNGFMPRRLAGLTSTSLPSPPAPTLHLARSFRTLPASAVSSIGCGSATLRWLA
SSSSRGRAPVVTEDKGNRMVILGKGMIPLDVLSTQELRNEVDRLERAEHAVIQPRRYCSL
LVSCTNPKLRARVLRLADKVTDVSAADSAAHGYALIFHTLWKSRVLQRRELDPLVATILS
TMRDQEVQVNGQCLNYLLNLYFAYGDVAKACDLFDLLREGEGRWRAEPNVMTYTTLVRGL
AGRDAGGQLDGSVRPDLPRALRYFEQMVKRDGVRPDRVAFTALLHVCAAEADLPRALQVW
DEMKRAGVAPDTFAFNSLLHVCNRALDLDLALKLTDGMQSRQLEPNDVTYSSLIDLCCRV
NDFGRAHELLNEMKERGIAPTVITFTSFISAYGQAGDVERCFDVLALMAQERVRPNQITL
AGLVQACLNAGDFRKAVQTLGDMKRRYGLAPSAYVLYHLIHKAGPKAKTTDLLRLLERIE
ATEGVPLETRTYSELIKLCGTRNELELAFLIHEKAQQQQRGGNADAGQRLVDRSLFNACI
QNQNPRKALEIVDAIMQRESLKERDVAQVDGEEVVLDEEDTRDPVNVTMFNALLRTVDTN
TVESVIDRMKRLHVAPNMATIDLLITHYESSGRLDRMWAVLRDLQDHKVIEREDLIYNSF
IKVFLRRDDTDKAYTVFTELLTRNTPLPPATYHLFLDTRDSRTAAAGNISDNGMDGVDGD
EQHAALGAESEEERAVRLRRVGERAALIPSLVKLLYERDPSAPPTALLPFIRFCVLHYKP
AELQPLVDRLERDAGRGAALVERIQEAYIMLHEADRAIELIHTLRQRGLKVDASLYNALV
RLATPESPGSALRLRALMRADRIPDEDTQDPFAPLELQPQAARPRYYNRPQQQQQHQPYQ
RRQRLAPDYRTPAAAERHDMEVEVDLLDPEGEYGQSATTTTTREAVKDAAAERKRRKKEK
RLLNTEKADEEEGVKKEKERAKVEPIKRPKVTGDLLSLSFSLLGQQAKKRE
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>ABC transporter Contig15439 (and 3384) (uncertain of N-terminus ... may be internal gaps)
MLRHQVRRSWSTGTGLASRSVAHTGAEGMQAARLFRSSSAKIASPSWPSAGNQHQACRLR
TGLQSELRLSALTRRFFASPSYADKMKARVKDQKVKETGKEANKAERLQKKGKGQKVGGR
FVFSCEGLSKTLPDGRPLFTDLSFSLYERSKIGVLGPNGAGKSSLMKVIAGLDDDFDGRA
HVHDGVKVGYLPQEPELDPTKDVRGNVLAGVQDKLDILEEYNEVCRKLEGEKEEDDDDDD
SEDEDEEELLERKAELEAQVEQLGIKDLSWRIDRAMHATRDDDVAMVVQGERRRVALCRL
LISEPDLLLLDEPTNHLDAESVAWLERFLSEYKGTVMAVTHDRYFLDNVAGWILEIDRGD
CFVYEGNYSTWLTEHQKRIDLEQKKDVALSKQIDQELKWIQQTPKARQSKNKARVKAYEQ
LLEQARVKPFQPGTILIPPGPRLGRVVAEAERLRKQIEDRVLIDDFSFSLKPGAIVGVIG
PNGAGKTTLLNILSGEDKDFEGDLKIGESVVPGYVTQHRQDLTEGNTIYEEISEGDDYIE
ISPNNTIHTRQYVAAVLNPPSPPLPTVVIFFVIVTHHRLRFSFFVFVLRSSSSSVPVLES
AAGEDG

>hypothetical protein Contig27470 (uncertain of completeness)
MSDSVVAVPPSSSSSSSASTQGVQTRLSTSGAVVPIRQLGFISRFTKSIKKYLLQPFVVG
FAVALGMSFGYSAYDAIVHRVATFWKS

>Iron-sulfur assembly protein IscA-like 2 Contig20123 (complete)
MARTPTSAASFMRGYSALALPARTLHTSLPAALRSSAMNRVAVPSTSASSGPSCTTVPSL
GRVRSRCVPSALSIGTRFVPASSTSRRGTASAAAPLQDLHPQTHPMAPSASTFDTTPVSL
ILDTASATRAVPSTQTILLSDRAKKKLRGLTSKREGGAILRVEVQSGGCSGFSYKFTVED
RPLTEEDILIEEEGARVVVDDVSLPLINGATLDWDEKLIGSKFQMLANPHSAGECGCKYS
FTPKD

>DEAD/DEAH box RNA helicase Contig18558 (and 16878)  (likely incomplete N-terminus and
possible internal gaps)
MKARKTRRTTGTMTTDEEEEEDEEIRESDTLVMPTPKGAKVRSKREQLLAQKMRADHMAA
QMPGGASGGAQQYQSPVAPGGLLDLGFVESLVLDECDKMVELGFFPAIKQLYRLLPKPKK
ILRGGKKKGDMQTCLFSATLSPRIEDVISRFSPKSQLINLNVDLQPPSQVKHLVFPVSNR
RKRALLTYFLKRKGSPFMKDQKALIFCRTKQRAERLAQTLEEDGFKALPIHKGLTVTQRR
NAIQMFRDGEVQLLCSTEVMARGIDIPDLPFVINFDVPPRGEDYVHRTGRTGRAGNAGTA
INLVATAPYTLKLGGRVCEINEQHYLKDIETFLDARSLEIRKVPGPWKDEPIDIAQDPEA
QKQKQLREEGVLTLLKRKKSALNEKQKSDRRKAGLVDDEDDEAAEEQKTSPAAGRKMMKK
KSASGESLLPSLRNFKEGRYEDLLVEFDKKKARKAGVAVESPDKTEQKRQQRKKLRKAVR
HMEQRGLFDGDHKKAH


>Grpe co-chaperone Contig881 (complete)
MRAAVRRLPNVASHSAASRGIFALNVPLRSRTLAIARPFSTEQNGEQKVEGEHPPAQQQA
EGENKEQQQEQQDPQAAKIDELQNKVKDLEEQNKELNGNYLRSLADLDNMARIGKTNVEN
AKLYSIKSFAEGMLEIADNLSRALESLPEEKRGLPDVKVLFEGVAMTERVLQQVFARYGI
KKFNPLNEKFDPTKSSALFEIQDPTKAPGTVAFVQAPGYTLHDRLLRAAQVGVVAQPPDE
PSSSDQA

>hypothetical protein Contig19074 (likely complete)
MQRSVVLGGLRPFSPLRGTVAYSSSLRSSTPLALTQRRFYAEEAAVTPQEGEAAPVKKEK
KKKEKKEKKAAKAEAEDETLTAGGQKLHVKRKLCRTPPKKKVWTIIGEGRLLEFEFQNDD
LLDHPTFVTPYPYGDEDEDADEVAEAFANRGKKGQQDRGDSDE

>cyclophilin protein ContigE9BS9UA01CKKR0 (and 8624, 20522) (complete)
MSNPRVFFDISIGGNAAGRIVFELYSDVTPKTCENFRALCTGEKGMGGSGKPLHYKGSSF
HRIIPGFMCQGGDFTRGDGRGGESIYGAKFADENFKIKHSGLGTLSMANAGPNTNGSQFF
ICTAETSWLDGKHTVFGKAIEGLDVIKAMEKVGSQSGATAKKVTIADCGQL

>mitochondrial ribosomal protein L13 Contig13107 (complete)
MTTSFAPCKQPLTNTHMWHVVNGRGLKVGHAASRIARLLIGKHKPTYNPAFDAGDYVVVT
NAEKLIFTGDKWKQKLYRWHTGYPGGLKEVKAKDMLYKHPDAIIRTAVSKMLPKNKLRWE
RLKRLRVFVGEEHPHEGQVSQGYHYQVEPQSRSAVDPALAAFRDQVVADPDAFVRKYGGG
KFSIVPQEQGMAVVATKIKGTHAHAVRSFGNTRSLRAARLDRLRKVVEDIQSAQAREAAK
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RDPL

>Twinkle helicase Contig2699 (and 25131, 11050, 10375) (complete)
MRVGGQRIAAGRNAELCRQPAGLWLGRTEASVMGWSRWTSAPPPLGHARPVLEPLLRSRG
CSPRWLGRSFATRSAPASSSSYARKSAVPSSSFASSARPVGSVSGGGAPFVSSHFSISED
EITHFFSRKSLVWKRSGEELVVQTCPTCPDHKYKMDNLFKLYISKRTGQFFCHRCGNKGS
WFDFKRLYGEIPYTAPMSAPVPASGEVAHDHQHHQHAPAPGLQEEREKPLPDHDVVSKYP
LALFNEYPQVLTFLTGNKTKVQRHLSEEVIRKYKVGATKYAFGGDSEQCVTFPWIDADAE
GRNSIRRLKIRSIKNKANQRLTPAGGQWGFFGWHTVPADAKEIVITEGEFDAMAVYQATG
LPAISLPNGAHSLPVELLPRLERFEKIYLWMDDDIPGQEGAAKFAQKLGIKRCLLVRTKQ
GDPEGPKDANDALRAGKDLNAILKKAGRTPHQQVISFQDIADEVYRNICSPDELAGVPSK
MFPSLTKILKGHRKGELTVFTGPTGVGKTTLLSQLSLDFAMQGVRTLWGNFEIKNTYLAQ
KMLLQYAGKNLAELQDRAQWDEASRAFSDLPLYWMRFHGSTSVDQVLDAMDYAVYVHDVE
HVVLDNLQFMLSGQAWGQEGVAAGNKFDIQDRALEEFRRFASTKNVHITLVIHPRKTEDD
RPLNVASVFGSVKATQEADNVLILQYNKGEDWKWLEVAKNRFDGELGPIALQFNKRNKSY
REMPTTGLLNKARKGASKGASNQPDDPQPATASSATSTTPPTKAG

>carnitine O-acetyltransferase Contig23994 (and 25287,5608, 17086) (complete)
MLRRSARASSQGLVAARGGGSTARTAALIRPHFVRGTSSSAAGKKTWRTFEYQSQLPSLP
VPALEATVAKYVENARLFLSPQELERTRQEAERFLQGPGPVLQQKLLERADLKKKENKSW
LIDWWNSWAYMDYKDSVVINVSYAFNFVEPRLGRVSQNPQGRPSSFTAPSSSSNSFTMTR
CSRTWAKDGPMCMNMYQLMFNTTRIPSAKTDHWATYHDDPEARRKVLVAHKNRFFIVDVY
DQSNQLLSVPELEMQLEKVKSLGSTKEEWAVGVLTSDNRVQWAEARDLLLRDQQNRASLQ
QIEKTLFGVCLDEGAKSGLELERNFWHADGKNRFFDKSFQFIVMEDGLAGLNGEHSGVDG
SPAWRMTNFVLDWEEEFQRNPEHAANKNRNSAALSPVEASFNITDDVKPYITNAEKRLAK
AASEVDLQVKYFNKFGKDAIKSWKISPDAFCQMAMQLAVHSLTGEIYPTYESGQTRKFLW
GRTETVRSVSAESVEFVKSMKRTDLKDSDKLELLRKACNRHTQTNQDACDGLGIDRHLLG
LRLIAAEQGVEEPGLYKDPAYSRISTWRLSTSQLTSPHFQVVFGPVAEDGIGCCYGILDN
GLHFKASTALKCKTNATAFVNAVEDSLVQMAKICATGTTHASKAKL

>glyoxylate reductase/hydroxypyruvate reductase Contig22627 (complete)
MKTRAASTTRAWWAAARPAGPSQGVPSMARRFYGGAAAATAAKVVVTRALPDATLEALRA
GGCAWEGRYWSEPETAIPRSTLLSWLSPDTLGLYCLLTDKVDGEVLDRAPNLRVVSSMSV
GVDHIDLAACKARGVHVGHTPGVLTDSTADLAVALTFATVRKIVPGVAAVKNGEWKTWSP
FWMASPFDVSGSTVGVVGLGRIGAAFAKRMAHGFGCKILYSGSRPKPEEAEPLGATYVPL
DELLQRSDIVSVHCPLTPETRGLFGKEAFARMRSSAVFINTSRGPVVDQEALYDALASNT
IAAAGLDVTDPEPLPTSSPLLGLPNLVVVPHIASATYPTRMKMAMMAADNLVAGVQGKTL
PFAVKL

>CI assembly methyltransferase C20orf7 Contig2501 (and E9BS9UA01A74BE) (complete)
MRRAAVLQRANTRSRLPGAFSASSPFARGQIRRLSAEGCNRISCTTTRLAAAPVTMAWSK
RGLASSSDSAEEQRAMNVFNRHVKRLQRDRAAADPESQDYDYLRKEIAARLADRLNDILD
REFPSVLALGGAAAGVAEHLQEIPGVKRIVQLDSSPLSLARDQHLDADLAIKPERVVADE
ELIPFEEGTFDLVISNLALHWVNDLPGVLAQIRRVLKPDGLFLASMFGEETLWELRNAFL
VAEQDRDGGISNHVSPFAGVSDVGDLLTRAKFALPTIDQEEVVVDFADAFTLMRDLRGMG
ESNAQHFRRPYVPRSTMYAAAAAYKALYGKEDGRVPATFQVVYMIGWCPHESQQKPKERG
SAQFSLKEFAHSVGELKVVDDNGNEIAPARPGEGPEAGGGDHSCGRH

>hypothetical protein Contig12615 (complete)
MMRRATLALREQGSGCMLISRLPAVSSPFTSGSRSLSTSADDLLHLFKQAASKSAPSAPA
APAQQPRPVSAGRGRMPTSAVTTSSGNWAQQLANQLDDRAIESPASHPAAKPLYQGQDEK
KRKFRPARHAFDPSAPRGGSMEDVASPLSRGGRGRRMRGGVSLGFDDARFQDAAEEGEDD
DFDMRMVLREEKDDAKDLVSLSSAMDEGGDDDWEAMAAEINAWGKKLQNSLRPHIEVLNK
HTKTRRMRRQKYRAFLERCLARREAKRGGAPKPAGWPWPKERDLVYNTDLFVPLNLELKG
IEEEGEDLHALLTQQMEDAARAIGHNASWPLEEKRKLMLGLKRFYEQAVRSGPGSYDLFA
DHRHALDDDDFIGGGGGPSSSE

>branched-chain amino acid aminotransferase ContigE80POFO01C7FZU (and 5142, 25705) (incomplete
due to internal gaps)
MRRRGIAHFTSAGIASRTTQIGARSFEGIRRGLYSTSAQLAELDHNKLVIDRTKAPKPKI
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PNEQLVFGTQFSDHMLTVEWDKEKGWDKPHIKPYQNLSLDPASSVFHYALECYEGMKAYK
EANGKVRLFRPMENMKRFNRSCSRLVLPTIKEEELLECIKELVRIDKDWVPQGKGYSLYL
RPCMIATQGKVRLFRPMENMKRFNRSCSRLVLPKALCFVILSPVGPYYRSGWKPVRLIAD
TKFVRAWPGGTGNSKVGGNYGPTVLSQKEAEKMGYNQILWLYGPDHQVTEVGTMNMFVAF
QHKNGEKELVTAPATSEGVVLSGITRDSIIQLVKQLPGWRVTERPYTMKEIVDAHDEGRL
IEAFGCGTAAVVSPIQAIGYNGKEISFPLGNSGQAGNLTQHLADTLAAIQYGEVPHDWSI
VID

>putative Tim50 Contig18694 (complete)
MRRIASGTPRSYAAMSGVWTSGAAAAASFSSQSLFKCATSSAAPLFTRSASLATPSTARL
FARTTKPLGLAGRPLQQRFASTTAEGVQASGSGRARITAIGVLIAAVGGVTGVVYAAEGG
NQGEEAGLFANLKKKFTAQTNKLLNIDENKKILPDAHPPPYGKPITVVISDDVLLVQEYQ
PLSGGMLTKKRPGVEFFLAQLSQDYELVIWSLQQVMSFGPVIEKLDPNHHAAHRVYVDAT
VVNAEGMNVKDLKFLNRPLDKTIVLDISPDHVVQKENLIVAPKYDGRLEDVYLLEMLNFF
RLLAASSKSQSGVPDVRNWVAAMNKKGPQYFKELYADAVKKAKDRAEEERKKREEQLQMR
DVGNTGRKW

>serine/threonine kinase Contig364 (incomplete at termini)
MGFRSVYEGRLNISRLKEEGLESSPLLMLASSSGEDGSSKSASTRGQMMKVVVKELKDPK
SCGDVKAHFREVAIERRLRHPSIVPYVVSCSISPRYTLVSEYMEGGTLSVGITPNMASRT
YLSIMLDLAKGLEYLHYGVESGYTLIHDDLNPEQILLNANRTRGYITDFNLASWIRSGER
WGVRRYWWPKGGSWKWFAPEKLRQHYYWEAADIWSYGVLFYQTLVRANNQPDEWAATVIR
PFYEERILNAAVDGWRPSKPHFRSDRVVLDKAWGLVEECWRYDPYARPTPPGSSPPSKIS
CDNSPSLD

>hypothetical protein ContigE80POFO01CXI69 (likely complete .. from PGPs)
MSRSIIQSARGNAHYRGLAAALVGDASLATQEARQLWREDGLLMFVKWPALMIGTTVPFI
FFSMGVQPLLDQALGVSEEDIEERSSSFHISRMLNSALVMLAIHPLSTLLACYIAGTLPS
WKVALVDRVVKRKDHFYSSWLASAAIGPVTHIADVVRANALHWHKATFFPDFMPPRGSDD
HGDDDNIGSEGENEAEEDEEEEPSTARRMAYGASTALVLVLLCSARTLLN

>NFS1 cysteine desulfurase Contig23289 (complete)
MKRNSSSITHRGALLRKGWPRAAPSAAPIRLSSGAARMASSVPSATQGGRSVYLDMQATT
PVDPRVLDAMLPVYTEAYGNPHSRTHHYGWETQDLVEDAREKVARLIGADAKEVVFTSGA
TESNNAAIKGVARFYGEKRKHIITTVTEHKCVLDSCRVLEAGEGVRGDVPAGGEERGAGR
GQARGGDEARHGAGERDGGEQRDRGHPARRRDRAAVPAAGRVLPLLSISGHKLYGPKGVG
ALYVRRKPRVRLHPIISGGGQERGLRSGTVPTPLVVGLGKACEVALEEMERDGAWVKHLF
HRLYDGIRARVPEVYLNGDLERRYHGNLNISFAYVEGESLLMALKEVALSSGSACTSASL
EPSYVLRALGVSEDMAHTSLRFGIGRFTTEREVDHAIELCAKHVDRLREMSPLWEMVKEG
VDISKIQWTQH

>putative sodium/alanine symporter Contig2629 (likely complete)
MRRTSLRTLAQPLARSSTLSSSALRCGSVSGSFLTSRGFASEPPAATKLKPDQPHPSWND
YSQLLNNFMDKLVHKERMGYKWWVRPNPSAQTESPSNYHLWFDEDQFPEGKTVVAMASYA
PDRLERTLTINWKTWEMTIAQKDLVDNTLSATRTIQIPPDWLLAMKKVRWPLLEQAKKNA
QESVPAKLPLIRSKDLYTIAKQKFKDEEELAYLKEKLMAAHI

>phenylalanyl-tRNA synthetase Contig21167 (N-terminus incomplete)
TKQIDVTAHRSASTSIHCASRRAGASLTLGSSRGVSLQLRPRVLGTPASGSVLATRCHLL
EQAQPLRLSSAAKRFYASSFSFKEHGIEPDEVTNVTDRILGKIGTNLHKEDKHPLNTIKK
RIEQYFVNKYTTEDNKPLFNIYDSFKPVVSVKQNFDDLLFPVDHVGRSANDTYYLNKSTL
LRTHTSAHQAELMRSGERPRSGERQFLVTGDVYRRDAIDKTHYPVFHQMEGVRIFTPEQL
KAQNKTPEEFVAADMKDALEGMISAVFGKVQVRWVDAYFPFTHPSWEMEIFFENKWLEVL
GCGIVNPQIVRNCGMPISEDWAFGLGLERLAMVLFDIPDIRLFWSQDRRFLDQFASGENV
KFQSYSKFPPCYKDITFWVPDHFHENAFFELVGQVAGDLVECVEVVDKFTHPKTNRTSLC
FRITYRSMDRSLTNEEINELQAKVRDEVPVKLGVELR

>3,2-trans-enoyl-CoA isomerase Contig6638 (likely complete)
MKLHRHRCRLAGSLVLSCGRTAGVSTAWTLGHRAAPLTTSAEYGGWAIEKRGSDEKAEVR
VVRMASNPVNCINPAFLDQLDATLERLEGENASSQPSPVVFASASEKTYCAGLDLKTVLA
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MSRDELTHFIDRLNASYVRLLTLDCPTVAAVNGHAIAGGALLALSADYRVAAAPGKSWFG
VNEVQLGIPFPCGPWAVMHHVALTHPRLYDLTRSGDLVSLDAAHHQFGLVDHLLPAGADL
TEGSVDYARTKVAHHSLRAFVAVKQVLQRPIVERYDSERRAGDLDRTFVDIFFSDAARGA
IKKRLEGLKG

>alanyl-tRNA synthetase Contig25588 (and 8930,22115,) (incomplete with internal gaps ..
largely inferred by genscan)
MWRRSAGAGGKWAVAGGRRVNGGGPSPQHLLLQLEAQRGLSTTSPSSRASSSASSSSAPG
RGAGWVRGSFMDYMSRAGHEGRASAPLVPPRGDGSLLFVNAGMVPYKDSFLGRVVPPAPR
VASVQKCVRAGGKHNDLDNVGHTARHHTFFEMLGNFSFGSYFKEDAIRLAWTYLTRELGL
PKERLLVSVHHDDREAANIWHAQEGVPLDRIVYKYAKKGDEDNFWSMGDGPGPCGPCTEI
FWDQQQEVDGDSFLEIWNLVFMQYQRTESGELQPLARPCVDTGMGLERIASVLQGVRENY
DIDTIRGLVHGTRTILHDKFGGVHQPQAQLSPQESVALKVRASCFLIGDGVIPSNVSRGY
VLRRIIRRAARYANTLAPNRNQGLLADVGKLVIAQMGEAYPDLFTRQNVILHLIEKEEEA
FLATLEQGLAYLQDALRNNPGTDLPPEVVIHLYIRLGFPIDLTHLIVKENNKTFDMNAVD
RLMDEEREKSRAHAFSLSSSAPSSVKLGEGGVPTAVKEWMAEGIAPEFTGYARQVEEETS
VVALLPDLQRRTLWLSISPCPFYGMAGGQVGDKGRLIVSGGSGKTLSELRLRVEDSLIPY
EGGLVLRVKVDKGEQGQEVSEGELKELADKLIKGQVGLRAEVDDRHRRGVRAHHTATHLL
HASLRQVLGTSIVQAGSLVDANRLRFDFTHHSPLTDDQLQRIEHNVREVIAAQDTPVATD
MREYAKAVESGAMCLFSEKYPPVVRVVSVPGFSTELCSGTHAASTGEIRPFKITGQTSVA
LGIRRIEAVAAEAADQWYDAQYQYLSSLGRTLEVAPVKIEERVKRLLARERELEKEVGVL
QRKLASSAANSSASQSLAGTYSGHPLAVHVYPEGDDDKVLAKKAEQLREKEPGSVHVVVS
GRKVICTLATDQLPALKANKVLQDMLATVG

>conserved hypothetical protein Contig5256 (likely complete)
MRRAVRLNAFAFRQFDDPAFSGTKLMGFDKQAFEDHINQLFNMGSATLVDGYAPFCKHLF
VPNFTGAKVGAVTITDSNKHLLRSGYVARRASELPVLTRWFEAKDVEVPTAKYLDIILYS
RAQIEEEDAALPSDQKEAAKDYEWGIVSVKAQDEDYETPMTPITAMRNSLGREEGGSGAP
LDREAYLKAVAYWDTHAAVQ

>ATP10 (assembly factor) Contig2185 (likely complete)
MRHFALPSSAPTRPGLLVCRVPSDLRPGAAAPLTSGSLRVRPPFWHGPRHMHTPLLGVLP
AQATSRGARHEHWGTLKRFKELAKTPEELALKEELDKGYWGDANELLKNREGKFFFAVPK
LTPKKEAIKLLDAIPASLPTYKPFDFSKVNIEEAMHTKAPTLVLVTCKRMFATAMLDSWR
KPFEAEFPHLNCYELELVQQVGYWWFGGLFRMFAAKEIEPSRMNKVLYYNGIRKTKRMRW
DLNIKNRYCAYAFLCDEDGLVRWRAVGLANTEELAMLNKMVNKLQQEKGGVSSSNNLASR
SGLEHQQKAD

>hypothetical protein Contig9910 (complete - uncertain if this is a real protein .. on same
contig as rab protein)
MVSARRRNALLTLSPSLALVSRKSASLFLANSFAFRWSTDLSSSRSLLLPTIMRAAFGGA
CISTSFNQYSLICEKLLGSVMS

>signal peptide peptidase SppA Contig12810 (and 7961) (likely complete .. N-terminus inferred
from genome)
MLRGYRAASPLYSGGVTSMGLPRYLCSSHVGGSASFLARSGQQLRRLAQTQATPPPPPPP
QGEVPPPTAGAQLKRVGEAGAKVFRVVRGIAILAAVGYGVLLYSAYKAAEAIPTDVVLKL
NFERPFPDVSQTSQLFPVLTLQEVVDGLDAAAKDPRVRGIIATVGSEVMELPMAQVQELR
DALKKFREAHKAAVCHSEGFGGNNTDYYLATAFDQIVMQPSGWLNLTGVAMSATFLRGLF
EKLEIEPRLLQRHEYKSFANTFNEKGFTPAHKESVDAMATSLHKQLLQDISDARGIAPKK
LQALMDQGPLLPRDARDAGLIDEVAYRDKAYSLITGKVLDSLKHEQQGKPTPEVELAKAV
LAVPAKKVKFMSFKKYVKKTKEEKELEKLKKKKETATLMAADTANFQALKQVYDKQEHPE
QGDPETQKTSRRLARRAERGKTGVPKVAVIYATGEISSGHHEKTGVVASKTFSTILRTVV
RDKDVKAIVLRVNSPGGSAVGSDTIWWETIRAKEAGLPLVVSMGDYAASGGYYISAAADR
IIAQPGTITGSIGVIFGKMVLGKFLANKAGRPETR

>carnitine/acylcarnitine carrier protein Contig11454 (possibly complete)
MSAEIEMPAVVAAATTSRPVSRAWQDLVSGIASGVSIVVAGHPLDTIKVR
LQTQGGERSFNGLLDCFWKTLAKEGVRGLFKGMVSPLMGVPPIYAVVFGV
YGSTKRLMGETADTPLAINKIALAGAITGLATVAFAAPAEAIKARLQVQY
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SSAAGSARYSGPVDCAKQMYRAGGIRGVFKGTAITAYRDVPGNAIYFGVY
EMVKRCFIPAGGSARDVGPLPMMLAGGLAGTATWLTVYPLDIVKSRVQID
VTGKYAHGHRGLWQAYKEIVAESGSVRGLYRGITPALLRSFPANAACFLG
YEMSMRLLHFLSPS


>3-mercaptopyruvate sulfurtransferase Contig24454 (complete)
MMRRGIYCAAWAQHQARRCPFGRAVRTFASEANNSHGAVVSTEWVRANVDRIKVIDASWS
LGKRSQHTVKLPGAIYFDIDEIADKRTWLPHMLPTTSMFAAKMEELGITNEDQLLVYDES
DGQFVASARVWWTFRVFGHNDVKVLAGGLKNWPKGLQIQKTAADPKEHGLKFAVRKEPAL
VWSKYDMLDNLSPTNSDQSQIVDARSRERFYAQVDEPRADIPRGSIPDSMNVPFGSLFQT
THSEQGEPMHVLKSPSELQRIFEQAG

>pentatricopeptide repeat protein Contig22061 (and 22096, 26926, 2336, 26990) (uncertain of
completeness ... largely from PGP)
MRSARLSQPSVPLCWRGHSFVSRSNSLLVHYRQPLFTAPLPPLVSSARPGLHVGLPVVRR
FATRPAKSHPNHGAVKPPSETSGARVSLPTKENEQMVKKLTNLLRNKNPVTARQFVGFLR
KTSDQREPTILSDKVVSLLPQLTFEDERTRAKERYEQQAKELKKDSRQGSNAAAKKPAVP
KRKESAEEREYKARELLIKEDEDERRKFTIILASLGKMRKIEGMLYVVYNMLKSRERQEDE
RIRQALDEAASRKEKAPVMEDSRWKVDVYMYNLVLDALAKAGYLGKMEEILQDMAQSRVD
KDRVTYSVLYGAYSSRGDDTRADQVWQEMKDRGVEMDLAGYNGLMNTFARRDDVDRVLET
YKQMQTAGIQPDQGTFSILLECCARDALEFRTRTSAAAAAATETEKAGDEEGEAVKTGEE
EDDDGLYAMDEKERVRILQSKRRRMEAVMRAMKKAKVRLDNILVNSIIRCYASLGEVEEM
FSVVRFLVEEENIKLAEDNYSLMVYCAGREKAIDVGRLTKVLEEMKWSNVQPTAKTINAA
IHSFAFAGPQQLEAFILPPSAPTTNEAGAAAGDDGKNESEAEKAKKRKADGAKEKKEEQQ
VSLWQLIKKYGVVVTDDILFDLLKVYATNEAAPVAPAGADVVGIVEGARRQLDRARLAKL
LHKMKEEGFGSSLTVFNSLMRFHAAYGENRVREVTVLYSQMKKRQVRPNLQTYLVMVDTI
LSTERKVQPEQRPASSGKASGEEKEREKERAELSYLLFSEMQSEGVQPNLKLFNGLIELS
GFEERRRRASVVDSTTHNVDGDRSAALGEEEFRQKVLSILTEMRRLGIRPNTKTLKCISS
ACAVAGAGEALGPAIFDELPRLFA

>2-amino-3-ketobutyrate CoA ligase Contig41 (complete)
MRRVVSKCPVTLGQRAAAQGAIRLYAGKSSGASVYAATLQPRLDQALKEIEEAGLYKRER
TIVTPQSSSISVKERSEPVINFCANNYLGLADSQELIDVAKDHLDKFGLGLASVRFICGT
QSIHKDLEKKIAEFHKTDDTILYTSCWDANGGIFETVLGEGDAVISDALNHASIIDGIRL
CKAKRFRYKHLDMADLEEQLKKADGEGAKVRMIATDGAFSMDGDVAPLDKICALADKYNA
LVMVDESHATGFFGPTGRGVPEYFDVMDRIDVTNSTMGKALGGATGGYTTGRKAIVDLLR
QRSRPYLFSNSLPPALVGATLRTFELLTTSTKLRDQLEANTARFRQGMKKAGFNVLGNDA
HPICPVMLGDARLASKMAEEMLAHNIYVIGFSFPVVPKGEARIRVQLSAIHTPEQIDKAI
AAFTAVGKKLNVIA

>glycerol-3-phosphate dehydrogenase Contig16845 (and 19873 and 2793) (likely complete)
MWRRLKRVTIYAGVGSAVAAGGLLLYASSPFTGVNASTSLTGPRKTTLIPDFPAPATTVP
TRDEQLAKLQEGKEFDLLVVGGGATGAGIALDAATRGLNIALVEKYDFSSGTSSRSTKLV
HGGVRYLEKAIKNLDYEQYKMVREALHERATVLKVAPHLSYQMPIMLPIYKWWQVPYFWA
GSKLYDVFAGSQRLESSYFLSKKALEKFPMLRSDSLVGAMVYYDGAHNDSRTNIALALTA
ATYGATVANHVEVRSLTKLEVVSLIRAKVTDESGKEKEVVSGAVVRDTLSGKTWEVKAKG
VINATGPFTDAVRKMDEGDKCENLVIPSAGVHIVLPDYYSPRDMGLLDPATSDGRVIFFL
PWEGNTISGTTDTPTTLSDQPRPLEEEISFILKEVSNYLNQDVTVRRGDVLAAWSGIRPL
VKDPTKLGKAGTQGLARNHIITISDSKLLTIAGGKWTTYREMAEEAVDKAIAEYGLKPRN
ICVTTDVYLLGARDWTPTMFIKLIQNYGIQREVAQHLASTYGDRAFEVAKVATPTGKRWP
VLGRPLAEGYPYLEEEVRHAVHHEYACTAEDVLARRYTRLAFLNANVALDVLPRVIDIMA
EELRWDDARKKHEYENTKKFLRTMGLEDINSRGVFNNMDILHYRECFDAIDTEHKGHISK
QKLKEFVKSEKKD

>hypothetical protein Contig7100 (likely complete)
MATSMETVSSFPSKWAWIFGGAAVALAAGGIAFLLSRQRPNKHIQTLVTPDRRLTDNFKA
KLAEIFAAQLDLDGDGALNDAELDRLVFLTEGQRITPEMAEFIRSHFETNDEGWLTLSGF
VASYEWILQHLTDDSAAEQAFAKDLQAYGYTYARFKQN
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>AMP-dependent synthetase and ligase-like Contig2282 (and 3527, 14114) (mostly complete)
MASRGGSAAPSSSSVLPEWLRSVTAKQAALAGLGVSAALGYAYLNSMSPDLSKDFGTIMR
LARVKRKVDSALKNKQTVADMFNAVLQAHPNKEAIVFVDKQDHLTRNTKVSNTKVSYTYA
EVEAESNKVANWALSIGLKEKDVVALMMDNRPEFIFMWLGMTKIGVLTSLINTNLRGHVL
RHSMAVCKATHYFVGHEHMDVISRELVSDLGGKWYSCGGPAPEGNLFDLDSLLAVSNNTT
AIPRSFRANTSATDKLFYIYTSGTTGAPKAALVSHLKFLTAGLGFVDLMDVGENDRLYTA
LPLYHSAATLIGVSTTWNGMGTLILRRKFSANSFWEDIATHKATVFQYIGELCRYLLSHP
PKPSDSQHQLRLAIGNGLRPDIWAEFQKRFNIPQIGEFYAATEGNVALLNSFNKVGAVGY
LSPLIRMVHPGRLVKFDVESEMPVRDPKTGFCLECEQNEIGEMLGNIKPDDPLRQFLGYT
DSSATEKKVLRDVFTKGDMWFRTGDLLRIDREGYVYFVDRIGDTFRWKGENVATTEVAEV
ITTGNVGVQECNVYGVKVPHKDGRAGMACIIPVDRATFDMAALYKLVRTELPLYAAPLFV
RVTTAAMDVTGTFKHKKTELVEQGFNPHVHHRRRALLPGRPQGRLRAADQGPLPAHHQQH
HRSQALNVETILFGC

>hypothetical protein Contig11296 (likely complete)
MRTGILGDSTSLERLVGVPKQLQVLRHDGHINWVETAAMAAAEGGHHRHGAVFTSTLLDN
NRELLRVASGAASTEEGDHLDLDLIVFSFAAADRCSLEDRNFKAAFQWADAYFRARNKPA
QVGVLLVDYAVNKPAGPARADDDRIIGLVAGDPYLEALMRARRIVRWNATTPALDDHDHH
DGLPDLSDDLARVLADFCRRPVVSLQAASGSSLRGGSGGARAGGDRFVNGLLVCSLAVLV
ALLVLHLSPSLQALAAGALLPESAAELTRLRLENGAQEAMTVGLQKDNELLKEINARQKK
HNDELTKDVTDLKHRNTRLQAQVDQLTAAQLAATQTLTDRTLVISSLCQGCCQGETAVGG
SMCRLCSSAPAA

>neurolysin metallopeptidase M3 family ContigE80POFO01AOL9H (incomplete - ** this gene
prediction has lots of mistakes ... I am not even sure the peptide is part of this protein)
MKRIQRYTTRRNHPRLPTHATNIRVGVAATASAPHVLSTTSPASATASRAVVVESLFAAN
PSSSSSLSTTIASRRASTTLTASTPAIHRLPPPQVLLPAVVALRHSPFASRIHLDMLHAD
EHLWNLLRLHSMQGSRQERGTDALARQIFYQLQRAASNAQSARSRRSDAMAGLLPSVMER
GREVHIANRASISTDRKSKSIHKSFSRPDKMLRALRAGLALACGCASSSHGRHLGGVCSL
LTARDSQMXLRFDLSAAEIAKTSHEVMESYKKVSGRFTEYYNHTMPQETLTPVQRRRTAH
RPLFTTFHFFRLIYGSDALIEKTMHDFKKNGLMLSPEKREQLKAMRKMSDNAITFQKNLN
EDSGRRRRGEQGPQRVGHRDRHAVCRTSHLLSDVLSHTTCAPRVIGRTSLKRSRSTTTIR
CRRRHSLPCSDGVLRTALYSLHSTTTAFYFSREELDGLPQDFLDGLEKVDGQEGGATKYK
VSLRYPELLPVMRYANNAETRRKLDTANAARSMRENTPLLEETLALRHEAALLLGYEDHA
SYVLEDRMAKNPAHVLDFINELSVKVEPLARREWEKMIALKKATVGGSDNVTIDSHDFTF
YNQRILERDYQVDENLIKDYFPFETVTEGMLGVYQDILGLRFEELNDAHTWHRDVRMYAV
YDRSTNAFMGQFYLDLWPREGKYPHAAVFPLVPSHHFPSGSSSDIPASFLAHLHPVT

>alanine aminotransferase Contig6469 (and 7030, E9BS9UA01BR434) (complete)
MRRAATTPQLPRTAALRMSLPGRAASPSASLLLGTSRRPLSTAPSASAAPSGPIRGRLTT
ASMNQAVVGAAYAVRGELVMKADQYQRVLADPAQRDTLPFKEIIYCNIGNPQQLQQKPIT
FFRQVLSCMEYPALLDHPAAAQIYPQDVLQRARHLLANFSGGTGAYSHSKGERIVREHVA
GFLQKRDGYAAEPEDIYLSDGASGSVSKALNILIHSRRDGVMIPIPQYPLYSATIPLLGG
TQLNYYLDEENSWGLQVSELESLVEDAHKKNVNPRALVIINPGNPTGQCLAESNMQEVID
FCRRRGIVLLADEVYQTNAYTKPWLSFKKVLRDMGPKYKDVELISFHSVSKGVIGECGHR
GGFMELVGIDEEVKQQFYKLASISLCPNLPGQVVVDLMVRPPVAGEPSYDLYHQETTGIF
ESLKRRALRLTEAFNKLEGVTCNEAEGAMYLFPRVRLPAKAVHEAVKQKKTPDSFYCLAL
LDQTGICVVPGSGFGQKDGTYHFRTTFLPPEDKIDAVAKSIAKFHHDFMQKYRD

>conserved hypothetical protein with IGR domain Contig27311 (complete)
MRRAATLHRATPGAAAFSSRISFPSSSVLAATSSARIQLGTSSNAIAPSHPLVIIGARGL
RLRKGREDWYNEQEGKPHPGAEYPWGVRRIYPESWIREPRGSLFPLVPEPRKGETVESFF
QKIKLTDHASKFSSWEELFTTKTRAMRAKGIKKSKDRRLILSWVEKYRQGVDPGTSKYLL
YYPKGSW

>methyltransferase ContigE80POFO01BMTPQ (and 23076) (likely complete)
MASRRQRTTIAAVARQTSASTSWESAGRWYDGIVGKEGHHFHQQLVIPGVLRLLRLDSSP
KVASSLLDLGCGQGVLGRQVPKGVEYVGVDASKFLVRKAQAYDTAPQHRYAVADVTRPYD
VAPKSTGGGFSHAAFVLSLQNMRDQAAALRIAGERLGDQGRLVVVLNHPCFRVPRQSRWE
VDPQNNAQYRRVDRYHSPLEVPIMVHPGVKKGGGATEPSSSAAAKSEGASPTTYSYHYPL
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DHYFRWLSDAGMAVELIEEWYSDKTSEGSQAKRENRARTEFPLFLAISSFKLQQATQ

>carnitine O-acetyltransferase Contig26263 (and 15386, 1814, E9BS9UA01AKGJZ) (likely complete
... largely genscan/homology inference)
MLFVPLCTTTAAPTYAYQDKLPSLPVPPLEETLAKYLRSLQPFEMLGIFSPEEMKRTRAL
AEEFKAAGGRGQRLQSKLVARSQQKRNWLEEWWLKYAYNIWRCPTPVNVSYYFLFDEKVQ
GPERPDVSQSLVASLCIKGVLDFKAVLDKQGVPAEMMRGTVPLDMSQYSKLFTTARYPQQ
GEDYIATFEPEPYVLVLSNKQFYVLDVLDKASNRALTVKELQAQIERILQASQESNDGLG
VGILTGEDRDKWAKARQELVSISATNARNLDVIDKALFVLCLDEDEESPRDVDTAGHLCL
VGNGENRWYDKIVQYIVFKNGRGGLNGEHTPIDAPTAGAMTDHMLRYLRRAQESSLPSEE
QSVASDLRAPTKLQWTLSPSLRTAQEEAVESYGKVGQDVDFRLLHFRTYGADWIKEKAKL
SPDSYVQMALQLAYYKLYHTGTATYETGQTRQFYHGRTETVRSFCAESVEWTKAMTDASA
PKQKRIDLLRKAIEHHSKALMADATNARGVDRHLLGLKLVAMEDEEEKSLGMPELFKDRA
YAESSTFRLSTSNMPGKLYISGFGPVAADGYGVCYGTRNDMLQFTITSLRSCPTTDSARM
RETLHNTLVEMGALFADAGQAKL

>hypothetical protein Contig21433 (complete)
MRGAARSNLLLRGGGRRAAVLRPSLPQAAPIRIGGPQSNHIFSSSATASSQRPFHASTRA
LWAISSAEGENGDNASPTEEVQTESDAAFEEKERSEAYARWVESVRRELKHIEEMVLKRA
PAAADSEEGIEKLEEIFLSNPRMQLTESLFPDEARPAPSRIITFDKETRRPTQMPYVMLD
PKWYQGTTDEERLQQVLAWRPFTARAVAAEKADHQFREDPFRNKSHAFSGRVVSDAFRRQ
RLDKYLNEELANKRKGVLERQGGGGGGLQCDLG

>mitochondrial carrier domain protein Contig15699 (uncertain of N-terminus)
MVLSPSSMSQQQPPYNQQDLAQGSEGEDATAALMGVGTYFGLFALVIPARVVYDRTAASV
GTSHLYRGFLATLRGGFSDLVGGYRQLWREDGLRMFAKWPALGFAIGVGAFAIQEGAQQA
CHRLLGVTQEDMEARSHKWHLSKAMCLISTGVLLYPATILWTVHSTNRMPSWTVYLRDKV
WKGKDYFYSAAPLSSLSFLVFFLSDIIRAKVLHWNKKTFFPELLASPPQTEDEVYDEEPT
QQAALVGGAYRPLLHQITNLSLYTLSSMLSAMLTGPIDAVTARMIANPLLYGPLGILGTV
KTIYREEGVWAFFKGFVPNVVFLLGTYYAGISEEADTGKPPL

>enoyl-coa hydratase ContigE9BS9UA01DQAGT (and 19417, 10772) (complete)
MKATRLMGAGGRATAGRAATVAVTPCWGSGGHNQWRRSALATTATATSRVSLEKSTSHQG
VAFLTLTNARERNALSVEALEELKATLADVESHRSFGDVRVVVLRAQGPVFSAGHNVKEM
RGSERDPAYFARCFALCSEVMQAVRGLRVPVIAQVDGLATAAGAQLVASCDLVVASEDSH
FATPGVKIGLFCTTPAVALGRAINSEKKMMEMLLTGEPITAQEAHTYGLVNKVVPKAQIE
EATLELAKKIVSYSPSVIGLGKKAFYQQMAQPDISQAHKFAEGVMCANAVAEDAYEGMSA
FVEKRKPTWKPTH

>mitochondrial ribosomal protein L49 Contig5677 (and 525) (likely complete)
MMRRGTAVLGSCVRPSTTGAYAAAAGWRRTIAGSTSTSATSETVVPLGSLRYPPPHSEEA
VTGAGPTGYKPPLGNTDALPFRVLRTKSGRLPIYTDYKNGRTKKITILRKFSGDRKELRE
EVWRVLGGPKNPGLEVVERAGSLEIKGDYTWQLQMWLKRLGF

>methylmalonic aciduria type A protein Contig19977 (likely complete)
MRATSAGAWRCRGSQWAVLPSRVGTGCKLPQQMCLRPAGLLLPDLANPLRRPYTTNSEEE
ERVSALAGRVMRGERRAVAQAVTLVESSRHRDRRTAEALLARLAAATAAPTSSSSCLSRH
PTTSTFRVGISGPPGVGKVGLSPLFSCPLANDLSKRSAVDPSSARTGGSILGDKTRMLRL
SNHPDAFVRPSPTRGTLGGVTRYMSETIAICEGAGYDTIIVETVGVGQSETAVEAMVDMF
LLLVSPGGGDELQGIKKGVMELADLIVVNKADGDLADAARKTQFEYQSALKLIHPKSFDW
MPRVMACSAATGKGVDDVIATFEEYRKTMMETGELWRRREEQKRQWLWRLIADELVDRFK
QDPN

>oxa1 Contig3549 (complete)
MLARRGVNPRLVGLEGRAGSVSRYGIASSPAARHLAFPTRTFATTTRSSSSSSSSAPSLA
RRRLPSIISRGSVFSSTSSSSSISSSVSAAMLIRHERRCYATETVEEGATAAAEAATQTG
AAVERGSDAMASFIAADPVTSLTPAALEVVERTTSSFPPINWLVDAMTFVHYTVPLSWAA
TAVCFTLAFRTMILPAVALTMQNSAKMRAVQPELEKIKAKYGPNVGKDVNVAMQYREEVR
KMMAQSGVSMWKTMVPFLVQTPLFVSFFFTTRKLAEEEPGLRDASFLFFNDLSAADPYYI
MPILTSLTMLATIELGSDGVGGQSNPALKNFLRLFSVLAIPATSSLPIFTHIYWFSSNLF
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SLCQLGLFKVPFIKKALGLPDYQGVSPMLGSSDPQPAKPEVTFQQKPRIIRTKNQK

>short chain dehydrogenase Contig10182 (and 21879,10571) (complete)
MEKDSGVGEEEYTSYEPEDSVPRDDAANGGFVPVIVITGASSGIGEAIALQYASSRACQL
VLAARSRDKLKAVAIKCRKLGCEVAIIPTDVSKPKQCKFLIKETIRIFGRLDYLVLNAGV
SMHIAFEELKDLEIFHKLIDTNYFGYVYTTHFALPFLRKSPQPKIVVIGSLSGETGVPLR
TGYCGSKFAVNGFFEALRTELGPAVPITIVSPGYVDTEIRQNAYGPKDFNPASGGMMSPK
RCAELIVEAADQRRRKVVLTLSGKLAYALRPFVPDIIDMLVKRKAHQKKKAAL

>NADH dehydrogenase ESSS subunit Contig19202 (complete)
MRSATRRATLAVPSARSIVSTSSLSSSSRLLATHAAPGVTSAGHDFKADEHHDDHHHDDH
HHEDGPTGYLWSRQPGVKYPRESWEMITYVGIAATLLLGWVAISKSGKVSVEEFGQMEIA
RRRREREQGQPQPEPLQLQVDPTKFRKTPQVTEHGPQ

>Tim23 Contig27058 (complete)
MGDSSYADSSSMPDFDAFPEPKLDNIGIDVDSISYTNPMYGLSGPKGAEYIFADDNQARK
MSWADRSTWLWGGAWLTGGVIGTTWGGLKGLRDAERGLPWKLRLNACLNGAGRKGGRMAN
GLGVLVLLYSGVETATAAARQKQDGLNIVAGTTMAPLIYWSGAGLIRSMAFGALGGVVGF
GLVLGHKYNVMGLRKILPADE

>acyl-CoA dehydrogenase-like protein Contig18143 (and 24384) (C-terminus incomplete,
N-terminus may be longer)
MEDIMAALPEPRWEPVSERSVALQKQLWRFLVDNVFPIERQVHDEVNQPGNRWKIPPVIE
RLKAKAQQAGLWNLFLPDRSNGGAGLSNSEYAPLAELMGYSPHLAPEIFNCNAPDTGNME
LLAHFGTEQQKKQWLAPLLAGQIRSCFGMTEPAVASSDATNIECRITRDGEHYVINGRKW
WITGAGDPRCKLCIVMGKTDPDTPNQYRQQSMVLVPMDAPGVKLVRPLTTFGYDDAPSGH
CELLFENVRVPLTNILGGEGKGFEMAQARLGPGRIHHCMRMVGLAERVLHTMRVRVQERI
AFGRPLAEHGIIQQNIAFSRIEIEQARLLTLKAAHMMDTVGNRHARKEIAMIKVVAPNMA
LKVIDRAIQAFGAAGLSEDFGLAAAFAGARSLRLADGPDEVHMMTIARLELQQHK

>hypothetical protein ContigE9BS9UA01BTEDZ (incomplete/likely incorrect .. some from PGP)
ATNGLLHVAHASLWTISVPFIQSSIIESAKDLLFGGYTLYGRVREALNPDFRPSLYAEIM
RPVTFAAKTVAYAASFPFFLCAYGVRNNKPEHWNKIPASFLPSRKKAIPSMTLPLFVLIA
HLNAHLLTAGGLRDLFFRLRVRLLPSTVTHDQALSPLAQQFLRHVEDLALCLAAGEAEAE
AEADGEAERLGLEEADADAEAEGDAEAEAEAEADGEAERLGLTEGEADSLGLTEAEGEAD
WLGLVEADAEAEGEADRLGLEEADADADGEADWLGLLDADGEADRLGLPEADADAEGEAD
WLGLVDADGEAD

>Ind1/mrp protein Contig23731 (likely complete)
MMRRSVVGAASTRVAGWQKRGYAAMQLSRPVLHGGPQGQGRPLPNKIKLPGVKDIIAVAS
GKGGVGKSTVSTNLALAISALGKRVALLDADVFGPSIPRMLNLSEQKPQVTDTQQLLPLS
NYGIKCMSMGFLAEKDSPMIWRGPMVMGALEQVPPVTCQSQLHSLTTRPRMVIDLPPGTG
DTQLTLTQRVQLTGAVIVSTPQDIALEDARRGANMFRKVEVPILGLVENMSYFACPKCGE
VSHIFGHQGARQTAKEMGMDFLGEVPLHMTIRETSDSGRPVVVSQPSSPQAEAFKHIARQ
VLDKIQDPAFRKDQEAPRIIYS

>alpha/beta hydrolase Contig15877 (likely complete .. N-terminus from PGP)
MAEEGFFVNKRNQRIFTRAWLPPALEKTKALVFLFHGLGEHSGRYNHVAAAFNARNYAVF
ALDHHGHGKSDGAPIFVERFEDFVEDALLFIDVVSARYPAHLPKFILGHSMGGAIAALTA
KQRPKAWAGVVLSGAAIKRGADVNALTVHAARFLSWATPTLGVKRIDPSTLSTDPAQVKA
YEEDPLVYHGPVTARMGHELLKAADTIENDFSGFTFPFLACHALDDKLTHPDGSKELYER
APSPVKDLILYGGMRHEIFNERDGARVIADVLRWVEKRYAAVGHSREHGRVISAL

>gamma-butyrobetaine hydroxylase ContigE80POFO01BNN45 (and 9345, 12185, 12875) (likely
complete)
MKKRIHLLSLLVGCRLVIDEDALKSGAELGEFFYTTPHADLFVLQQRIRFEIADALREAG
FHHTWLRHNCQCPKCLDSSSGQKLVSILDFPPRPVPRSVSLENGQVVVRWKDGHVSPFPQ
DFLRRYAYDQQSRHERRAMRRAAVPWTPEVLISESVALEIDYADLMNKDEAVWQWLQQLL
KFGYCLIRGVPQQEGEVARVAQRMGQLRDTIYGLTWDVKSIENAANIAYSSLPIPPHMDL
ISCTRLINQAEGGANIFLDTMQVAKVLKERDEKAFRLLATTPATFHYQRSGHHLVQRRPI
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IELDQETGDASAFRYAPTFEGPLDIEGEKVEEYYAAYRELVRIINQEPDLHLWRRPEEGD
LVSFDNRRILHARTAFSNGNRHLQGAYVDWDAFLDRYRVLQSQFAPTAAIPQ

>universal stress protein family Contig24076/4104 (complete)
MSVPLVITAVENEEKQRAKEESRNLPEHIVAVDGSEHSERAFEWACDQLPKDHTLVLVHG
VHKPEFRVEAMPDSEGKWMEKQRRKAFEDYEFMQSARTMHRYARLCRQHERKCEWMTVPY
RSATELSDNICSAAQRRGISNIVCGSRGLGTLERALLGSTSSGLVHNCPANVTVVRD

>hypothetical protein Contig12807 (likely complete)
MRACMHYRVRASIRESGHPRLYLRRGSWRLLQLGADEAGRPPGPSLRLHRRARESAVPTP
AEPLPGRQRGQQARDRLLSAHQRQLREVPAVEAVRDQRPLRGPDRARRRMRRLRRPATR

>MaoC domain protein dehydratase Contig461 (and 14045) (likely complete)
MNTQAVRRVQVIGNHMAGAESIGALAANSANALRDEVKGRSAPQNRSFANVDEMKKAVGT
EVGVSGWLEITQQRVNTFADATCDWQWIHTEPERAKKESPFGGPVAHGFLTLSLAPFLNA
EAIPRLEGVKMGVNYGLNKVRFIAPVHVGASVRTRVTLKEVTDVPGGIQVIIEGTFEVKE
KGKSEPSKKPVAIVEQIARYYV

>saccharopine dehydrogenase (NAD+, L-lysine-forming) Lys1 Contig3474 (likely complete)
MQRAAAAGATSRLVVPLPHHARVFPTTSGACRRMLAISASTPSSSSSSSSSSNASTTTTT
PEKHHFWLRAEAKKNERRSILLPEHVERLLLLQAGHHVTVERSRLRCAPDAEYQRLLKEP
LVEEGSWKKAPRDAIILGLKELPEDDDPIKHKHVYFAHVFKGQNGAEKVLKRYAKGGGKL
WDLEFLVDDKGARVAAFSGAAGKVGMGLAFAVWAHQKLTGRPYSLPPLNTPYDSFAHMAH
QMRELLDQAKAKVGHDPSVIVVGSRGRSGKGAVSFSESVGIKPTEWGREQTAKGGPFPEL
LNYDILINAIYLLPEVRLPAFITKGMIDHTPDRKLSVFSDVSCDVTNPHSVFPIYDHLTS
FVHPTECVAEQPTPLEVIAIDHLPSLVPRESSKEFGDLIVEHILQFDQTPVWSRALKLFD
EKVQPFLPPSPRAAA

>tetratricopeptide repeat protein Contig6158 (and 17346, 4180) (incomplete with possible gaps)
MGNLSYRQGDYETAEELYKRSVAIKEHILGRQHPDIAEYMHTLAYLYTTQGKYEEAKGLY
EKAFTILLQTFGMDHPLMALNLNNLAWIHFKQAQYGKAEELYSQSLAIREKTFGKRHPDV
ARSMHDLAELYHEQGKYKQAEKLVHKALVIREQLLGPDHSDVARSLTTLAKLHFSLGSYT
EAKREHKRALKITTQLLGPNHIKVGQSLHDLAKVYYRRGTYQRAEELFQRALQIREAALG
TNHPDVAQTRASLAYLFTTLGKFNEAEEYYKNALSIMESCFGSDHPEVAQSYNALAWIYY
RQARYQESEELYRRSLDIRSRYLGEHHPDTARSFHDLAMICLAQSKYTEAEDLNERALAI
REKVFGKTHVEIAYSMHNIAELYFARSRYAKAKGLYKQSMRMLEIVLGEDHIKVAVPMAG
LAKVHYKLGEYQQAKPLYQKGLAIQEKTIGKNHPNCAASLNDLAYLYATRGHYRKAKKYY
QRSLAILQSSYGGTNHPEIALGLSSLAWVYYKKRGKYNRAHLLYKQSYKMRIAAMGPEHPL
VARSLHEIAELYQKIGKYEEAETLNKRALSIRMKAHGTSHPDVARSLFNTGVLCYYQGKY
KQSEELHLGALRNLEKAYGQNNPKVAQCLDELAKTWAKMGKHDDSKVYLQRALTIRESCL
GGRHPDCAESLHHLAYLAATQGKYAESEQYYTKALEILKGTFATEDHPEIATTQADLAWV
YFRQGKYKEAEELYVQSLKVRQTALGDSHPDVARGLHDLAELYQKLGRYEEAEPLHQKAL
NIRESIFGRLHADTARSLNTLAVLYQLRGMDEESEKLQLRSIEVLKEVFGESHSKLAKGY
ADLAALYARKADYERAETLYQQALDMRAQTLGPTHPDYAQNLLELAELYTKQGQYERAIP
LYEK

>L-threonine dehydrogenase Contig23167 (and 3626, 2232) (likely complete)
MRRTAVFGVTAQGGLSLGGKSGARSATALFRSSSPIAATSDRRTYSVEKKQPKVLITGAL
GQIGTELVPLLRQQYGAENVVASDVRKASGPVGDGGPFAYLDILNMADLERLVVEHKIDW
LIHNASILSAAGERNPQLALEINVKGLTNALEAAKRHNLRIFAPSSIAAFGPSTPRDATP
DLTIMRPTTVYGVSKLYAELLGDYYHRRWDVDFRSLRYPGVLSSVAPPGGGTTDYAVDIF
YWALQKGEFKSFLNKDSALPMMYMPDCLKATTMLLEAPTEALKQRTYNVTAISFTPEELA
AKKRIPNFRITYEPDFRQAIADSWPASLDDSMARKDWGWKHDFDLEAMVDDMLAKLRIKL
GIKQ

>similar to brain protein 44 Contig26399 (complete)
MSGSAWTKLEQRFFAKYHGVEGGVLLKGPFWQNLAQKYPVFGKVNNALWAAPAFKWGLAI
VPLYGILEGKPAVKDLDLNQSLALSLTGLVWTYYGFLVVPRADLLIAVNVALLSVNGYNV
YRKINYDKQMQAAQAHA
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>pyrophosphate--fructose 6-phosphate 1-phosphotransferase beta Contig2318 (and 12660, 23471, 20072, (probably complete)
MSEVAEVSTLQRARLAHQPPVTPTLRGRTTLRRHAHPTSSLAQSEEIEKRLPHIFGQPRV
ELEAASTAGDDASHSPLRVFNNTQIGVVLSGGQAAGGHNVIAGLFDYVAAGHPHSKLYGF
IGGPIGLVKGGFIVIDAPLVAKYRNQGGFDIIGAIALHHSRVDQKNLLAESKRACVACVN
QVVGVPKTIDGDLKSSLGVEVSFGFDTACMIYSELIGNIATDANSSRKYYHFIRLMGRSA
SHITLECALQTRPNITLIGEEVAARKQTLSDLTNELCHVIVERAKAGKNFGIVLLPEGLI
EFVPEVHRLISELNELMAKGNSADVVGEKLTEESRAVFDFLPSAIRHELLLDRDPHGNVQ
VSKIETEKLFIHLVTKELKRRKANGQFKGSFSAMGHFFGYEGRCGLPSNFDSNYCYALGR
TAGALLDHGLTGYMASVSNLTAPPEQWKSGGLPLTALMNMERRKGKNVPVIRKALVDLDA
APYKELLRHREKWARGEHYRNPGPIQFYGPASGEVNITLQLEFGQAHRHPKAAL

>GRAM domain protein ContigE9BS9UA01BNNRD (incomplete)
HISLQATANRETMSTRKGSPKISAFQDNFKNKKLHATFKLPDGDNFIRDFPCAFTETEEG
LGDVNGRMFVTSGHLCFDANSMG

>glutamyl-tRNA(Gln) amidotransferase, A subunit Contig7721 (and 18873) (incomplete due to internal gaps)
MEATRKGGRAVYRLSRGARRCCFRETSDCGSRRLYSGTSGGSADLVRQSLADVGRALAEG
RTTSEEVTRACLLQADHTATLNAFVSRHSDEHLLSLAALSDKRRRDGHQVGKLEGIPVAV
KDSFNTHDLPTTCASRMLKDHRPPCDAAVVSALRKEGAIIMGKTNMDEFSMGSGNTQSYF
GPVINPWSPSTKPEEAFVAGGSSGGSAAAVASDSCFGALGGDTGGSVRLPGAYCGVVGFK
PSYGRISRWGLVAYGSSLDTPGVLTKTVEDAAIMLGVLAGMDARDSTSVDIEVPDYVKSM
NQPRKLSRSTPSRPTYILAPAEASSNLSRYDGLRYGYRGAGDSITEMYSSSRSEGFGEEV
QRRILLGTFTLSRRLYDSYYRKAQQIRRLVLNDFETAFGQGVDVLLHPTAPTPAFALAEK
LNPVDMYINDIMTIPASMAGLPAVSVPVRQSAASNLPQGLQLVGRYMDEGTLLAAARLLE
QAFPRAHALRPPLA

>alpha/beta hydrolase fold protein ContigE80POFO01EIEXI (and 7986,22914) (incomplete - introns remaining)
MQRQMRNRLLRSSVVNFNATPLASHARILSRTLSSAVSEEHPYLHTTAKAPPPEGTVVLH
NTAVTSRAPKAFSRPPLAIAHGLFGAGINWRSVAKKITRTCLALFAFYHLPTRLTFPSSC
CVPACNVNSLLLDLRNHGSSPHHPEHTYDAMIGDLHYLLTQRYGINTFSLMGHSMGGNMA
MRMALKYPDLIDRLIIVDFAPTSYQSIEKYKDYIEIMQSIDLTAIKSRGDVDKIMAHTIH
EPLLRAFLVSNLVHEADKSWRWRLNLDALKRFIGPIRSWDILGVRVRWCVCVCLSCCMCV
SCATEPQEGLQYKKPTLFVGGGKSQFIKPEYHEKIHAFFPNAKIEMIPDADHWVHFEKPN
EFCHAVESFLHRTQ

>maintenance of mitochondrial morphology 1 homolog Contig7284 (uncertain of completeness)
MELLSIVIGFLLGLVAAGAGVAYTLFVLLFRRRTDAPLPLAPAPSFAPQLASALLADAAV
SEDLELFEKAEWLNLFAGRIFAEVSTPAFQEHTWRLLTEKLNAVDKPNLIGPIVIEDFSF
GTGVPRIEGVASFKTGKELELVLDVSYDGGALFAVQTELWLNLPTLERLASLPVSMSVSL
AHFRGRVSLTVPLESDPECTLAFAEEPQLDFRIGSLIGYDYQLRDVPKISNFIINKIRSV
IREEAVLPKAFSFHLPLSGRPLDLKQVLRPPRELRRNTVEELKEAAVSASKAKLRERVKR
EKDSRKGRDAEENAVVVLNTSRALVRT

>Tim17 family protein (TMEM135 homolog) Contig8579 (and 7471) (uncertain of N-terminal completeness)
MQSEGLPPVLDTSVDEEAEKTRLKKV
DLAEVLERYSPYQAWCTFLRGFITGFGLRMGVSLALRALQLLRKKPSRLLSLADLVKDKK
ANQVKLDAVRLGLTIGGITGVHKLAYGLLARLRRTEDAWNSLISGALSGLPLLFQEKENR
RTPALYLLTRLAQCIYNELKRRNMWHFWGSDWAHGDSLLFISHLRSDHVRLRDATRDPAA
LLLQIHRSLRSDR

>chalcone isomerase (flavonoid biosynthesis) Contig5548 (complete)
MRRASSACTIGTGVGRRSLGYSSSAALRVANRPVGSAQRCLSNQLRSPVVRSTTSWGWGL
ASGVALAALASSCRSADESPLSPLATVLAATAAAGDVPADSVKEERSGFLFPKTLRLDDS
TEGQVLAVGIRTMYVFFTTYAIALYADPKDVRSALSSFKEHSAEDLKKNQAVYDALRDGP
FTKTIRLIPTGDTSGSHLRNGLVSAVAARMQDNKEEALKEFGNFFPAQLKKGMLIDFTWK
KGGSLSVSVDGKEVGVVDSPALSRAFFEVYLGEKSKTPDVREKWAVALAEWLR
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>short chain dehydrogenase Contig22217 (complete)
MEHNTNALAASRRVTAIARHVEASAPSAAELLDLHRTAATNQGGLLKGQVAIVTGSGQGI
GEATAHLFAAEGAKVVVTDLDKAKSDKVAADIKAKGGEAISVAGDVTDPKFPEHIIKATI
DAFGRLDILVNNAGYTWDGIAHRMTDKQWEAMLLVHNTAPFRLIRAAAPYMRDAAKQEIE
TSGKAAPRSIINVSSTSGLHGNTGQANYATAKAGILGLTKTIAKEWGAFNIRCNAVAFGW
INTRLTAAKGQENFIEVEGKKVALGIPGATNSAEAVAKTVPLARPGNVDDAAGSVLLLAS
PHASYITGHCLEVTGGAGI

>zn-dependent alcohol dehydrogenase ContigE80POFO01B2W6B (and 6774, 14659) (likely complete)
MRGVRLASFGEGDPHSRLEVRDDLLVPPLNPSTNDVLVRVEATSVNPIDLAMRKGYARKI
LFRARAKESPMTLGFDCVGTVVQTGKSAWSFKVGDRVWGSTSLFRDGCNAEYVLVEEPAL
AQAPANLTSVKAAALPTAAVAAWKALVESGQLGPVGSPSPLNPSATTDRQRVFINGDSDG
VGVIALQLLKHYGHHASAVCSAPNVPKFTQLIDAGGGEVIDHTREPDWAARLAGEGKEYD
VLLDTVGTDEAEAQCVKLLKRGGKYLSLRPLVLDLIHEHGPFMGAMKGWWSIVKKQVEMK
KEKDVLVNYVTCGPDGKVLEQVRRLVEEGVIRPDVDRVFDDLAQLPEAHALLERGEARGK
VVIKVQDPLTAAAAAH

>DNA-directed RNA polymerase Contig6776 (and 7498, 19858,1656, 10545) (probably incomplete ..
from PGP)
MSLLRARQPILGRSLTSGPILPRASLPSSTILRHDQLRSSTRLFTSSSASSPSSILFPLS
RTGPSSSRSSTTANFARAKHSTSTQPKEPVFIASLQSHKESAPVTKSASQTELEKQQREW
EAKRELENLEYEWETKSVEKAVERYKKISKSLKQLGLAFELLQGNQILGHWFEPLCAAIR
AEQNAALLKTSAADAAASPKKGKKKTQKAEDRELSAYLVTIPPEKLAVITIHETMCEILK
SHHPEGAPFAALVVAVGRAVEYEYNCERLAKEGWKPQLRNRSATPTKQQICSLIRTQSRA
QFEDASWGAALHAKIGSLLVQQLLGTATIARKAEEADVAAAQSSPARLLSGAPRKRPAFV
TKEEALLEPAFNHHQAMLRGKLTGFLGCHEQVLALMEHEEVQRGVMQARYMPMLVEPQPW
VAPNQGGYLVARTQVLRAKGSRMQTEVLRSASMDKVYECLNLLSSTPWRINNRMHEVICE
AWDNGGGIADLPSRTNLPELEPPADYYSDLEVKQKFDRERKKAKIANYNLHSLRCDVTYK
LQVAKECQDRTFYYPHNMDFRGRTYPIPPHLNHLGQDLCRGLLTFAEGKPLGESGLRWLK
VHLANVFGNDKITFEDRVRFVENNMEHIMDSASNPLGGQRWWLKADKPWQCLAASIELIN
AYNSGQPETYVSTLPIHQDGSCNGLQHYAALGGDEMGARQVNLLPSERPQDVYSGVVELV
VRRLEDDAANGVEIAQRLLGKVDRKVIKQTVMTSVYGVTFIGARQQIENALKDKGKVSDD
DMFLASRYLATSTFSSIKEMFSGAREIMTWLSDCATLIAKQGKPVTWVTPMGLPVVQPYR
TKGKQTQTVVTALQNVMLVKEENDSLPVNTRKQRTAFPPNYVHSLDSTHMMLTALQCHEA
GLTYASVHDSYWTHASSVDTMNHILRRTFVDLHSQPLLDDLLAHFKRTYPGIEFPPVPPK
GDLDLKEIINSPYFFQ

>superoxide dismutase, Fe Contig2154 (complete)
MMKRASATRPLLASTALRFGASSPSSSALVGGAAKWRVLSSSSSMQRRSIHKLPELNWLD
QPAALNTCFSEEAFKQHLKKHHMVHLQATNKLIEGTDMETLSLEELIVKASKNKSKTVLL
NHAAEAWNHNFFWQCMSPTPSAPSPTLINSFELHFGGLEQFKEKFEQFATVHLGSGWTWL
VDRDGHMEVINTSNSGTVITDPQYTPLLVLDLWEHSYFLDYRESRKDYLAQWWKVVNWKF
VAGQLKEAESKNTWMQSSTSAQALKPYPAS

>universal stress protein family Contig18339 (and 18000) (likely complete)
MDPPRLDGKDDDRAERAEVVIMKLQVKDPGPKDFVCVDGTLGADRAVKWAVANLPKDHRL
VMVHGIYAPITGWTADSLMLEHQTVEDKYAPMCEAAGRKCSFFSFPYLTKGTFGDTVCKL
ARYNSVNSVITGRRSELSPLRRQFVGSSSMALLSRCEVPVTVVTDAWAEGDLFNEDNSSS
ESLER

>NADH dehydrogenase subunit B18 Contig112 (likely complete)
MLISEEEMDAERLPIGYRDYCAHLLVPLNRCRQECFYRPLEVHPRASRLRRLPVRRVQEE
EEVDAHRKGEAQEGAGEAGVGVCPHRRLGLR

>Fe-containing alcohol dehydrogenase Contig27610 (and 7783,94) (incomplete due to poor genome
coverage)
MKRTCSARRAAVVCRSTAAVAQGSSTRSLHSAQPTQSGHRAIPPHHVHGPTCPCSAAHNP
QYFYRGLLGAEGAEARASLTRPGVRFARRTQSTPTTHARLSSSAATGGLSRSGPKESEAD
YAFEMAGSNIRFGVGATREVGLDLVDMGARHVCVFTDSTLKDLAPVITVLQSLQDAKVNF
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VLYDKVKVEPTDASFKHAIEFVTQTARKVTPTGHFDAFVAVGGGSVIDTCKAANLYATYP
PEDFFDYVNPPVGKGKPPPGALKPLIAIPTTAGTGSEATGVAIFDHVERNSKAGIAHRRL
KPTLGIVDPENTKSMPPQVAAASGFDVLCHALESYTAIPYDQRTPRPATPLLRPAYQGSN
PIADVWSLKSLEMLAKYFVRSVENRDDTEARAQMALAATYAGIGFGSAGVHLCVPISSSC
L

>conserved transmembrane protein Contig27791 (and 16183) (complete)
MRSKARALTLHVASRTTAAGFLRCASSWTSPAWQRDGFSFLPAQAEKVGQKPRPLVLTLG
WLGANERHLGKYSSWYSSQGYDTLSFISPATSILFPQFGRKHAAQLLDYAIDLSEQTKDG
KQEKRPILFHVFSNNGLYFYANVLQQVARSSQYERVLHSTLGCVFDSTPSHLSVEIFTKG
FGGALLGAMGITNDGRPAYDHWLVSPIIRALFSVALAPPFLRNNVSSLLESYVRFQPKCP
QLFLYSKGDELIPYTDIELAIRATNNLDIPATGKCWEDSPHVSHFRMHPEEYREAVAQFV
EGATERWHHHGQHTAIVQQQPAPLSHAGLDKVVEEWKRLIIHF

>C8orf38 (phytoene synthase) ContigE80POFO01DU06I (and 2111) (likely complete .. mostly from
PGP)
MKAMQLSIQRARIVPATTVPLFSSVEQHLLLHRKRKLHSTSAALHGGGKCEHKPTTSGAI
PWTFTPHDEDATTKAPPVRAEKPFSFTPPHPASTSEAGSADTAATAGQFERQGPAPAKQG
GISSLDYCITQSKKLDYEHYLCGMYLPKEARAPYSVLRAFNIETAIIKDIAKQAPLGLMR
IQFWRDLVDKSFKGNPPEHPVAIQIAAMVPRYKWTRTWFTRILNKRAEDIEGRPMPTLAA
LENFTEDTASSLLYLTLESLRIRNMDADHAASHIGKAVGISFLLRGTPYHLQQRQTYLPM
DLLAKHGVSEEAIYQGNLEHAQNLPEVVYEVASAAHAHLKHARELKSTVPKEAYSALYSS
FIAEDYLNKLEKAKFNVFDPALRPTPQGSLGLQAKLLYNHYVGHKY

>mitochondrial substrate carrier Contig23931 (likely complete)
MATSTSASPPAAPPETQPKPQNAAPLISPWIKVLAGSLGGAMEAVLLQPLDVTKTRLQLD
SNSRYRNSFLYCAKTIYKEEGAGALYKGLTPFVTHLTLKYALRMGSFTFFRGLLGSQATS
PSGAPKKKPSEKMVMWNNFGSGLCAGVLEAFLIVTPFEVIKTRLQQQEGFHNRKYKNTVH
AAVTILREEGVRALWKGVAPTALRNGSNQACNFMVVGIFNKWVWKKEEGKQIAVWKTMIS
GAIAGAMGPCLNCPLDVIKTRLMGQKIEPGQPPKYRGVMGTIGTIYKEEGLFALWKGLVP
RLMRLAPGQAIMWTVVTRVTTYFEEQAQRRIEEEQRPSSRGGGSSSSSSSSSPSSSSSSS
SSSPSITPAQPLPH

>AAA ATPase domain protein Contig446 (incomplete C-terminus)
MRLLKPKHIPPSAGPYPPFDRPNEAAVLRNYLNHPPAGPCIFVGPDGSGKSHILEQAIEN
RKMVVYLDLQREPVINGEEILTQFINKISYILPPTKFIARIFLKDESKMVLSAEEINKAF
HCFEQVLSDQKRMGWPNGIPVICINDFHFLGSSNDLNLRSKNIYEDKQILKFMELVPLLD
RQQAVPRCLCDIVFVLPPGARHAFCIPIATGGAQVRLRVGVHGQAPLQEGQSVAHTALQG
TIDRIGDQTPRHVRGRPSQRSGHSHHGSPPRLHA

>3 beta-hydroxysteroid-dehydrogenase/decarboxylase Contig21357 (complete)
MSGKKYGVIGGGGFLGKWIVDELLNRGEKHVRVLDIRPSPTPDRPRRVRSGAVDVTKIDT
LRKGLAGLTTVIHTASPPHGKGYQMYYNVNVEGTKNVVEACVELGIKQLVFTSSASVVFD
GRHIKGGDESLPYCKTHLDGYTETKEKAERIVLEANGRKGLLTVALRPSGIFGPGDAQGW
PGFIEAAQNGKSKFQLGDGSNLMDWTYVENVAYAHVLAADKLVPGNDKVAGQAFFITNDE
PAPFWDMAKYIWKNLDYPTPTVVVPYWLAYYLALLLDWIVWLLSPLVSIHLTFTFFRVVY
AGAHRYFTIEKAKRDLGYKPKVALKEGMARTLKAFEHKRNPKATGSSQDKKKAK

>mitochondrial carrier protein Contig20482 (likely complete)
MTTTEHKGAVPAAVAPRKDPVRTANYLLYGAIAGICSKTATAPLERLRILQMVEHLHGGE
GRYQGILRPLLIIAREEGIRGYWKGNATNVVRIIPTSAARFYTFEIYKTFLRRFVRRDQL
NTGEVLLASASAGTTAAVVTFPMDFVRTRLTVQTAGNTYYRGVTNAVLSIYRQEGLLGFY
KGVTAAVLNTAPYIAINFTTYEKLKEYTQAGGGSPGTVLSLAMGAIAGTLATTISYPADL
IRKRIIVQEMGGKEGTYGGISDAVRKIMREEGPKGFYRGLTATYLKVVPSTAVTWWVIEL
CRSLSTNP

>ATPase inhibitor protein Inh1 Contig8833 (complete)
MMRRAATRSALCRPSFAPTAARGYSSVLEAGGRLGEREKAVEDRAIRGHDLELLKKLRDT
LGIQENQPIPETVVSQVSSSSSSLNPFAQRAQSQQPSSSSHNDEPLTRGEFLEFRREIVQ
RLRNLEDDIMDLQTRRK
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>deoxyuridine 5'-triphosphate nucleotidohydrolase family Contig371 (complete)
MSQQLVLRVKRLSPNAVLPFRATVGAAGYDLCSSENCVVPGRGKALVSTDLAMAIPPDHY
GRIAPRSSVSWKNHVDVGAGVIDADYRGHVKVCLFNHADADFTIQQGDKIAQLIVERISL
PDVEEVDDIDATVRGEGGFGSTGVSSKH

>lipoate-protein ligase A  Contig4679) (complete ... mostly from PGP)
MKRATAAWRSGTRLHLRGGRVAAYGSTTNRAYATDTSKVKVYVTSTTDPLFNIATEEWIF
REGDPTKQTLYLWRNAPTVPTSSLARRYSGGGAVYQDLGNTNFTFLSNVGAFDKVRNSGI
LINALKKRFNITASASGRNDILVDGKKISGSAYKISNGRALHHGTMLINVDFASLGKILN
PDKAKLKSKGVDSVQARVQNLKDLNPEVDHESMCDALVEEFYKTYEDRCEIEYLKHEMLA
SIPSLANTYATLQDWKWRFGETPAFEHSLEKRFTWGNIDLLINAKNGRITEVKIFSDSLY
PQMIDDLTLALHGRTYDKQGVTEAIEATQSKMKEVDNVEANLEELKEWLVHAM

>cytochrome b5 Contig21222 (complete)
MRRSTSLARSFGGAASSRPFLLSSTRSTALYTRRAYADDAHVPTPTAADVKTEPERLRTF
TRADVAKHAYEDDCWVIINNKVYNVSQWADIHPGGSAIIHAHAGGDATDLWVEVGHTPRA
RALMERYCIGKVAEPKRYMGASYGAMDLDESGYALPEGTPKEDILEDASSYRYSTR

>mitochondrial carrier protein Contig6061 (and 21609) (likely complete)
MNTAPAPAVDLRDLSRDNMSHLDNVPTPEFAVAGDEEGQQRAEEVGDEGEGGGGEATEKK
SNEAAAVQDIVSEQLAEDERRLQMQVASGGKAAPPVGKGRGGMLQQAFEAFLRHHQGNNR
IDAGQLQSVLQEAGLEMDTEQAAAILKAANVSATGELDFEEFYSIFVGLKIFKHLDQNKT
ACIQEHDLIRTLENYGLPTDRSMAEKMIQMVGEDEEGYVSFPAFFRIYLDVHHQHHRNID
LLEHAVRYWYSGASKDTILAQNQNLTPLQDFIAGTLAGVAITLVGHPFDTIKVRLQTQQQ
AYGSAIQATLKTVREEGIRGLYKGMGSPMATIPLINAIVFAAYGQAKAYLQDPNAPDADL
SIPQLALAGAWAGFVNAGVVTPVELIKIRLQNQTENTAAQFNLNLKERLRSGLRSSLFER
RIFYNGPIDCIVKIFKEKGFPGLWKGMSATVYREVPGYMGQFVVYEYIKQYLISRQGPEC
TVDDLHPLHLMLGRRHVRHRRLDRLLPHGLR

>ubiquinone biosynthesis protein Coq9 Contig14139 (and 3431, 7570) (incomplete)
RQPEEEDAIFEDRDGGFSDAVRTQVLDVALAQVGKYGWTVEALSLAAAEQGLSNLAHGLF
RRGPVELVEHFIAKCNARMLEELSALDMEHMTLKEKIRAAIHARLRQYAPHIATWPQAIA
ILAQPSNASTSFSLMFNTINDIIYVAGDSTIDFDWYTKRAVLAGVYTSTELFMLTDASDN
FADTWAFLNRRLEDVVTLSKYKAECETLTSLALGYLNAVVQKQHAAPTGESPFHHSPPPH
GTPPPPPPPAGPAGPFTPSPHDDSIPPRA

>adenosine deaminase Contig13294 (and 12878, 22579,24745) (likely complete ... lots from PGP)
MKRAVLNKHTPLSEDIIRKLPKAELHLHLDGSVRIGTIIELAEEQGVALPSTNYDELKDK
IYVGEDCTSLVDYLRAFDITLSVLQKPYAITRVMYEVCEDAVADGVRYLEVRFSPILHTK
EGMSLSQVMEAICEGQLMAEHNLPIFCRIIVCGMRQLDPKDTENLAEIAWRYKDKGVAGF
DLAGPEYGFRSKTHKPAFDIAQRNFINVTLHAGEAAGPESIQDSVRWCGAHRIGHGVTLR
QNPHLMHYIIDRRIPLECCITSNIQTRAIKTLEDHPIRQYFDAGAIVVPCTDNKTMSNCT
LTGEYALFQKTHKFNVEEMLRLIDYGFSAAFMQATHKRRLRGEVLHSCLQILHDEGYDLD
DIIGTSHYWHSIGVDLSHFAKSPAVRKQHGYWSGRVNPPITLDIVRALPKADLNCRIDGS
VSIPLLWQELQAAKIDMKQRFGLPCSSLEDLRRIVLSPTHDEASWTRVKRIFNSVLQHPD
QIKRATDDILRAAADENVRYIELVVRPRAHTHAEMTIAQVIDHMKEAADATVAALAAEGK
PLQYGLVVYSSLAKDDPIDFLQAAQLTVQSQSKGVCGFGVLGTRDLQASEYEFFRGTFDY
LKRNNANVNISAGRTDPSNVVKAIHEGGACRVSGAYQVHRSPDLMNYCANHSIPIELGLA
DRFSIYVSDVRTFAEVNVNDMVSTYNSDVRTFAGNPIRLFLDNLLPVAICSFKSSVSSKN
RSEVLFDLVNECNLSIAELMKLLSCSFENNFQPYDVRQKMVAKAWEEASTYLSAHGYSSL
YRQHYFPSLGKGMDSFSDA

>alanine racemase Contig431 (likely complete)
MRRVVWLKTSRAHFGLRTQRSILPSCRTMTSLAPSFNTRLASVRPAPAAVGDGVDSIQTP
ALILDKGALLANLRRLPALVRESSSSSVRIRPHFKAHKCGAIAKLQMEEGEASGFCFQKV
SEMEPLIRFFEEDSADSGKLLDLLVTNEVVERSKLRRLCELASHPSVKRVGVAVDDAGVL
QVLMDEARAASGGSSAASRVGVVIEIDVGQQRCGIDIASQQGEETFVALARRLIAAHRDP
SGHVSFIGLQAYHGGNQHVRAAADRERTV
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>Erv1 Contig2125 (N-terminus inferred from genome) (likely complete)
MEQFKKIKEKLQKEGDQLVVGGADEEDCGACKPRAGGLYGSDMRRRFRSQQQAREQRSAQ
EQDGGTTSTDATATSAGTEEDASNENTTECYDSEGYWEKQDAPDVIELGQAGWTLLHSMA
AYYPPKPSRQHQERMRSFLSLFPHLYPCKVCAKDFEETMDEIPPELESHDALSDWMCRAH
NRVNQQLGKPLFPCERVRERWGPSNAFHTKEQDDS

>ATM1 homolog Contig14471 (and 26685, 6308) (incomplete due to internal gaps)
MLRASGAGVASAAQHGGWWQRKPAALRKQLPRGWAAKPAAPPAGTTPATKAAGPTKLKGL
PDSGSGWAIMKSLSGYLWPKDNPAIKRRVLAAVALLVGSKILNVQVPFLFKEAVDLLNAT
TENVALVPIAILLAYGAARVGAAGFTELRNVVFSKVAQSSIRQVACNTFLHLLSLDLRFH
LSRQTGGLARAIDRGTRGINFVLTSMVFNILPTILEIGLVCSILTYQYGAQFAALTAGTI
GVYTAYTFGVTQWRTKFRKEMNAMESEASSKAIDSLINYETVKYFNNEKMEAERYDKYFA
KYSAASLKTNSSLGMLNFGQNFIFSAAITTAMILTAQGISAGSYTIGDLVMVNGLLFQLS
LPLNFLGTVYRELRQSFTDMETMFGLLSLNTDVKNEPGATDLRVSKGEISFEGVGFGYTP
ERTILNGATFNVPPGSKDTVLFNDTIFYNIAYGRPTATREEVLEAARLARIDDAIRQMPM
GYETVVGERGLKLSGGEKQRIAIARALLKDAPILLCDEATSSIDTATEREVQQSLAQLTR
GKTTLIIAHRLSTVVDADVVMVMKGGNVVESGSHHQLIARNGLYAAMWRHQLEAAHHGNP
TTATAPNQPSTPA

>conserved hypothetical ATPase  Contig5878 (and 20478) (complete)
MEGASGKVVRIGGASAFWGDSPTGAWQLVGSEGSNLHYLVADYLAEVTMAILARQNKEGG
GFVGEFVQSVWKPLMKQILANKTKVVTNAGGMNPVACKAAIEQAARDAGLPVPVVAAVAG
DDLMPRYEELSAKSAFTTFEEVPGEAEPKWHERGKLMSFNAYHGARAIAEALDRGAQIVV
TGRCADSALVLGPLVHEFRWTWADHDLLSSGSLAGHIIECGCQATGGNFTDWELSLAGGV
DGVESGRGWDNVGFPVVECRADGSFVVTKPKGTGGVVTTATVGEQMLYEIHNPAAYILPD
VVCNWEQVRMKQVGPNRVLVHGARGLPPTPFLKISATSVDGWKIGGTLFIGGIDARKKAL
AVADAILARTRRILV

>rhodanese domain protein Contig26234 (probably complete)
MQRSRLISRSSGSSLFQRRPACEHNVARLVTGGLGRRFLATSPAGDQAPAFGVLQATEAK
SHLPDFDLLLDVREPDEWAAGVIGTPKTITLGRVMRDVATDELQSLKGKKLLVYCRSGAR
SALACGVLAKNGFQVTNLAGGFRGWREANSSSSDAPPNKA

>hypothetical protein Contig2795 (and 5408) (probably complete)
MMRRRLRRVARESRDHRLPENVWGAFRQFEVLLAEPTRSLEEVQKAVDEWYGRLPFRPNF
RAELDMSKALHTYVPFWHFACNTACQYQGRARIGRRFAAKYGEKTSGTLSTAFPVLICAE
EPTPKRKPVLASIDDLKWHEVSAEGRLVSLTARSESSLKEVLDAHLRPTDRVMDLTLQPQ
AAWQREGRKRLEEVERELSERAIIESERARGVLRPNNDADGEAWEVDLDYVARTDQEREQ
GMGRVSLVLVPVYELHYRWHGFEYHLCVRDGDHAVGSPQPDSGERPLPLIEGARPYSYAK
ISLAGLAGLGVGLASYWMITH

>hypothetical protein (likely related to yeast CMC4 mitochondrial protein) Contig26556
(complete)
MSWTSWLSSGDSSARARNLTGAHIRWAAVTNHPQIAPYFSAAFRKDKATYAAMSCEADLV
ALAECEYKNPHDDGKCEPYRLRSLLCMESVVNPARAEQFTTCLRTAGNPSAVQAKCMPIF
EDVLKDLEKASEDAPLPLTPQEKQVVQECDQPDKGEEARMEEGMACFIPRVCASPYGNFH
SCVEANGGDIDKCVPEGQQVMECWGDFCVRMYRDQNVETAADH

>band7 protein  ContigE80POFO01ESZIC (and 26193, 15073, 26472) (likely complete)
MKRITTTPVSRTLTPRLARAAWPQASTLLRSGTASRTLTTTTGAGLRSTMTAGAARRSVP
LASGQRLARRAFSTSTSSPEREALQMVLDSMPKGSKRFWRALAGLGATAVVLATCQPWCV
VPAGHVGILDFFGDVSDQSLSPGFHLKNPLAKCVVFSTQTQRVETTASVPSREGLTVQLE
VSALYRLDPLKVQHIYKTVGRNYADVVLLPHFKSIIRELTSAHEAKGLYTAQVRTEISTF
LTKQLNDVLRERGIIIDETPINGITMPQRLVHAIEEKLRAEQESERMSWVLQREEAEAKR
KVIEAKGIADFQKIVTQGISEQLLRWKGIEATEKLATSSNAKMVVIGKSDGLPLVLAP

>hypothetical protein Contig3795 (probably complete)
MMRAGVRGGCLRGGLSASSTTTASSMLLAARSAVAAGAQREYAVHIFSPLPLPNAEKPVP
PVVERDNKAIFNVFDVPVFYTYQTTPRWRESPAMAHRRAERRRMTEVRKRATVYCNIELE
KERERFRQEREQMERWKALRLKKRREEWREKMVVREKVESQERAERAKLAAQNLQVHAEK
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SKLKEEAKREWLLCIKEELHKFDVADLPHLMSLKNYKYDTYESQEWYTKDN

>mrpl23 Contig27366 (complete)
MLRGGLFGRAAPFGQRAGWKRGMEEFIDNATKPGEYPIAGRAWKASELRLKSFEDLHKLW
FVLQKERNLLLTEKMLAKSEGKQMKAKGRRVKVRQSMARIKLVLGERQHIYKTFKREQIL
ALEQDRLEEVRGRQLAWAEQLKSQNDKLANVKLPKPQKEAASIK

>NapH domain protein Contig7524 (complete)
MSSARFERSFSLKDIGALQYLRHLTQLLATVFANGKLLGLASTGLIVPYLHVTQSPWSTV
HGAYESLEYTIARGVFPLLVLGVIYLTAVTVGRLFCGWACPFGLVQDILSYLPFKKEKLS
ASTTSQLKDLKWAVLGFSLISVILVAWRRASAMGHEDPMGVFSDSPFSVISPAGTLFAYL
PWLALWNTNVLLSAGLIAWIKLALCVAVLVPSVYIPRFFCRYLCPMGTLLEPLSSYKVLR
IARSSKTPVQDANKVLGDVCPMGVQLEKEDYVSDHPSCIHCGKCVTEAPATFAQTLFEKS
N

>hypothetical (similar to gamma proteobacterial membrane protein) Contig4773 (complete)
MARSLDYDALQESFVFLLVLAFFIERSLAVVFELRLWRGPLSNPGVKELVAVAVSYAVCT
WAEFDAFATLFNKDSVFLSKALNALLVAGGSKGAMKLMQDVLGVRKDVMENNIDRRKNRV
NYEENVNLKVTKTEE

>thioredoxin-related protein Contig23956 (and 19261) (likely complete)
MRSTARRGATSVATELAGAHRPALPLFAGTVSLPILQSSSQRLGRGVVLARPYASGAVKQ
TPLAAKSVWLPLGSVLVASTLGGMALSRRRVLAQEQSADSNADNAEKKPQDETNEGPQSN
KEDFVHYLLERPILLLLLDREDVDEKMDANLEEILADEELKAMHLLDYQFFSEDRKKFPP
NAIGLVYNYNTETKQVETYVYPADRELTAENIKQFLADVKEHKLDDLRLHPSEPRPAEDK
HPQVKDLKVVTKESFQDLVLNLDKDVLVYVHLPSQSVPTDLQVLANAYAGEDDIVITECS
SFLNELDPTYFGDTPIEGIKLFRKGHKNEPVTYHGKGDLLDVVAFIEQQRGTRGDVAYRH
LRKADTTRLLRDMEKTLGDYYMHTLAYKEFVPTSDKAKDLFNKLFDMYDQLNTNEDPFKR
SVAALKQQLKDELKSLERAGLRNIKIVDKDKYKEELEEARNKGKVVVFFWRKGCWPCKKL
NPMIGQLSQDFPEVTFLKVDADAEGLNATPAFWVYEAKKADDDTNANEEVKPSQLSGMKL
ITQFHPLARQRGLPGYAKWLPPAERSKLEEPVTEEAQSKHEEKEQKNDDNDGETKKDLEE
VRAPTDEEVTTKNESEQHEEDAKPSTLL

>acyl coa dehydrogenase Contig2647 (likely complete)
MEDGGQGFLQDPPRLGNQYIEDTPLREVLQRLLPEDVLQSIEPDLQRFGW
RVVEECTLHGKNIKQQPPVLVQYNAWGRIDQIRIGEGWKRLNDVSAEEGL
IAIGYERKQKEYSRVYQFAKMHLFGPYSAVYTCPLSMTDGATRLCEIMKP
RVGDDSGTPYSIHDLFDHYTSKDPAKFWTSGQWMTEKPGGSDVGNTETIA
RPVPGDKLMYRLHGIKFFTSATLSETAFALARVIDDKTGPTGVAGSRGLS
LFYIQLRDDEGNLKNIKIRRLKEKLGTKSLPTAELELCGTPARLVGQVGR
GVATIATLFNITRIYSASASVASMRKAIAVARDYAHRRHAFGKAIAELPL
HVQTLAQQEVAYRGCLQLLFHTVLLEVDFRVVCGVCAGKMETGRATKGEN
DLLRVLTTLGKLYTAKLSLATISECIEALGGNGYMEDATDLPELLREQQV
NTIWEGTTNVLSMDILRILDREPNAFVEYRNHINRVVALPSLSAPLKDCA
DQVRQAVKALTDIVEAITHDMDTDKRHVFSQSIARDVSYAMAAAFIAALL
IEHAAWPGGGEAGLTGAEDGVRTFAAQQWCARHLAGHVLALNDALNLAKL
NRKKASYEATRKLGLDVDPNGNFRGMGDLCPVTGKYRASY

>Transmembrane protein 147 Contig3813 (complete)
MTFLHFANCALLAFGPSFIFYKAGKLSEYNAFFPVAYAALIYVATQAIKLLLFATLVPAS
EEGQFEILHEVLKALVNAGDVVGIYFALNQKTVGGEARVLSVGLGWAVAESILMRLAPLW
IGARQLEFSWEYIQMSIEANFSLLRLIALTTLVWLYTHSRKEHTALSSIKMSAYAIILYF
AFPIAVSFLQLQLHVGSWYLVIASGLFSALMAYVANHLNALYSVERQTKAK

>methylisocitrate lyase ContigE80POFO01DI03R (and 11765, 18071, 2903)  (likely complete ..
mostly PGP)
MWLRGVNGLGVEATAGWRLREAVRVGVASKGGAWGGVVPVVGAPNAYAALLAERAGLPLL
YLSGSTLSASSFGLPDLGLTTLDEVVEDARRITRVSKLPLLVDADTGFGGVLNVARTIQE
LERVGAAGVHIEDQETQHKRCGHRPNKRVVTTGEMVDRLQAAVAARRDRSFVIMARTDSV
ASEGLDAALKRAQAYIDAGADMLFPEALTHIDHYKAFTSAFPDTPVLANLTEFGRTPLFT
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LEELSQAKVALALFPVSAFRAAARATQHVYETVAKDGSQSAAIPLMQTREELYDVLGYDE
YEKALDALYPPPATPAAQAPAAAAPAAVASLASSGGIGTEGQSVEEAKAKEEKNEEKEEE
EEEGEVLLVEENGEKKEEKVVSETAAPNNEDEKKEKKKEDEESEDEDEDDDTGVVITADS
AAAIEEELASGKEIKLKD

>hypothetical protein Contig12970 (likely complete)
MAFTWFSSVSTNARRAARRSSSSRSRSRFLLSVLFLLLRCRTPSSVFCFCFCFCFVVTPA
ELAGARANKVEWPPMLGELVLFSSSMAARCCLCTSCKRCLQAMLERVWGVSVGDVLLETC
VVCCEEWAYVGVTGQ

>ATP23 Mitochondrial inner membrane protease Contig3855 (uncertain of N-terminus)
MRERQHSQCETTIRDILIKDRVMQHLMAGMEDRGCRVFYKNFFHCKQCTGSDHGGYWDPD
EGVVICENNLEQKEMVRDTMLHEGVHAFDDCRANVDWSNCVHHACSEIRAANLSGDCSFR
AEVARGHFNVRAQQKECVRRRATLSVIKNPNCPGADADWAVNKAWERCYSDFEPFGQVPN

>mitochondrial RNA helicase SUPV3L1 Contig2610 (uncertain of N-terminus ... largely from PGP
... likely incomplete)
MWTSRLPYSSLRERGAREAAQTDSSTKKKKQQQQARKHEGWDEGKEKKMKKKTMTKKNGR
TGAGGGQQGNAYGAATAGVPPLRALTTGVGQVERDKDVVALRLEAFVRDASVRREVRARL
AARALQADQAPRGAAAAANDDDHERDDDDDEGDGYEEAEEQEEGARGRRRVREVKGHRSR
GERVMGLLGRERDLEAALALFEARTTSDDHLRRMPPALLSLLADPKRTHHECAEPLMEMF
VEFVWEHYYYGRPLKSSAGDEGGRGAVLLPPADDLRAETDEEEEEEKNAWRTFRRMATDL
RHPHAWYPLARALPGGRRIVLHVGPTNSGKTHEALTRLAASRSGVYCGPLRLLAEEVFRR
MNKEGVACSLLTGQRVVTDPTARHLACTVEMADVASEVECAVIDEIQMLGDQDRGWAWTR
ALLGLPAAEVHLCGNESIVPLVQKICQDTGERLHVHHYTRLSPLVVSDTPLGRKWYKSLR
AGDCVVAFSRADIHTLKREIERNTRHRCCVVYGNLPPQTRVEQAELFNDPASEYEVLVAS
DAIGMGLNLNISRVVFSTLHKFDGHKRRLLTDSEIKQIAGRAGRYRSIFPTGEVTAFDGA
DLPRIRRALLRELEPLPSAGLAPTFEQVSMFSRVYPQSPFYELLDELTLKAAVSSHYFLC
GNDDRVSVAKLIESVPLSLRERFKFSIAPVRSDDSSLMWHLLKFANSHASEGEVEMDLRP
ERGDSKSGRLAELESFHHVLDLYLWLSYRFDSFTGRDRAIRLKQETEQRIQELLVSQTEA
SKQSRAQKGSALDHIKGHLQRQQEGQRAAERPPVVLGTTTTAAGGGERRKARRRSSEATG
TDAPSPHEPAQWAQALNAALAASTTRRKGTPAKAQRKRNSREEEDDEDE

>hypothetical protein Contig22327 (likely complete ... uncertain of sequence)
MQLPQTSSAHDRLTPSPSLLHAGSQVMESYLRAGQRWLSESDVAAKLDFCSMLGIHVKTP
PKEGGGKLLEGVLIPFAFLKPLFDRLEDSEVTQRLAHLQPAVIGKDLNQRRELAIIYRKI
VEWCRGPHFTPEHLATLGRYLGIPASASKEQILTGFLYSFIFSASSPHLGYTSHITLNAG
DSVPLSLTPHAAAAAASTTTAASSARSSSPPPPPSFGSTVHTATSTKRADSPNSMPLVRV
KQEPRDEEDTDGGLARLAGGVEVKRERQPEGNMIDQLSSHFETDAQDSNKRRRTESTPTG
AATAEDAAQRERSMAGRRSLKRPLPSTLPPPPPSSSSSTSSAPASGPRASSGPPTSAFAP
LPSPFPQPLFAGPGGSSAMPIHPLYLSALQSAAPLTPQMLASLAGLPLIYPLPGSSSTPF
IQPKPSSSAASSSTGAPSALSSSSSSVPVSTATAQHSKATGKYTPIQPASGGGYPPILPL
PPILPFPSNAGSNGPMMPQHLSSSAPSVATLKRKAEKEVEEEKRRPLSRTAPVRVTSLSP
PSPSSFDTPFCSSFTETSSDSNPFSGATQGPFSPFSPLFASPTSYSSTVIPSTGAGTPSS
LFSLSASSAPSAIDVDLIGSESGNHGSRYYYGAPFPEIEAFEAAGEKKLDYLNVDVIVVP
KEESSANNGNNPGKAASDPSSPTRSGRGGRGSGRGRGRSGGLGRSTEGDNARGTLTASRG
SSSTTTTTTASSGSAERGTRSGSARSKGAGSGGRAMTATHPVYDASQGASPGSTLPPYVP
PKIRPAPIKSAAASPPRRARPAAAGTSVGAPKTSTSKRTSATTPTPTLEEAKRSEDEYTT
AGAADVTRVRQGPAVDEQHANDRARGGEEQRDERGARGRRGAQQLGRPAAGNQHHTHGCG
HHREREWQHGGSGGGGG

>Asparaginyl-tRNA synthetase Contig8636 (incomplete)
MPWRVSDILSKATPGQDLVIKGWVRTVRQQKQHAFVELSDGSHQTPLQIVATPELVKGAS
TGCSIEVEGKIVESPAGKQKLEMVASRLNIIGACDPEKYPLAKKKHSLEFMREIPHLRAR
TNTIGGVLRVRDTAASAIRDFFHENGFIELHTPILTSSDCEGAGEQFTVSALMPASSSEQ
GPREFFDRTVGLTVSGQLQAEMAACALSRVYTFGPTFRADNSMTRNHLAEFWMIEPEIAF
CDLNLNMRVAEHMVKAVIEAVLAKCDEDMAFFHKRVDEGLMARLHKTLAGPFQEVTYTDA
VKLLEKSGKKFEFPVAWGLDLQKEHERYLVEFEFDNRPVFVTHYPKDIKPFYMKLDEDGR
TVQAMDLLVPTIGELIGGSVREENLDTLQARMKAMNMNVDDYQCFGTVPHAGFGLGFERL
LQYVTGMDNIRDVIPVPRYRGYCRF
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>cardiolipin synthase Contig4341 (complete)
MRRCCSIAASRPQVLRLGTSARTLTASSSSPGGLPAKQFRTGARGVHLPWQQSGAVRSGV
IRLRSSVPLGGALAGRAWQPPATVLIRVYSTPKSAAEDDDKASQGNVNPPTTATANVEAT
TSSTRVLTIPNILTVSRMIASPFIGYWIIQEEFALAMGWFLAASATDAVDGFIAKRFNQK
SVVGSFLDPLADKLLMTIMVTTMAYKALLPLPLVGLILLRDVSLLAGGVIRRYRSLPRPV
TVSRFFSVSKVESIEIKPTVISKVNTVLQVGLVFLVLSAKGLDFTLDPMFMSGLEWSVAG
TTLFSGLDYLNSNAMQRIKTFQDRLTKRDP

>cytochrome c1 Contig11871 (and E9BS9UA01EO9K4) (complete)
MLRQRTLTSATGMAFRSQTRSFATSAGASAKRLHPNVLGLVIGAGAVGAAAGTLISRARC
SDDVLVAPAYPWSHKSEWKSYDVASLRRGHQVYKEVCAACHSLNYIAWRNLIETLYTEEE
VIAMAAETEVEDGPNDDGEMFTRPGKPTDYLPRPYPNEEAARSANAGAIPPDLTEMVKAR
EQGADYIFALLTGYMPAPAGLNVREGLYYNPYFPGGAIGMPPPLNDGMLEYEDGTEASVS
QMAKDVSAFLCWTARPEQDERRVMGIKVLIYLGALFGCSWYIKRFKWSVLKNRKVQFPGK
NWPTV

>AFG1-family ATPase Contig6445 (and 6044) (incomplete)
MFYEGAPVPKKRRVHFNAFMLEVHSKIHKWREGKRRALEKKFEEDREGPDLPNFNLGVSA
SLGEEEWGDPIPPLARELAAQAPLLCFDEFQVTDVADAMILHRLFSLMFTHGLTVVVTSN
RPPDDLYKGGLQRDRFLPFIDLIKRRCLVHDFGSGRDYRLRGNQNINIYQVYVQRPKYSH
FGDDTDPLLLCAYNSEKPGVDVAKNLETLFGELTHHVPAKSINISVGGRKLFVPRAERGV
AFFSFSDLCKQALGAADYIAISQEFHTVIVSGIPKMEDRHREEAKRFITLIDELYNHKVK
MICSAAAEPRQLFAGGVEKREWFDESTGKSVGTIWQGEEERFMFNRTVSRLIEMQSDDYL
QSPHKKEV

>3-oxoacyl-(acyl carrier protein) synthase II Contig23034 (likely incomplete N-terminus)
MSKRRVVVTGLGVVTPLATGVQATWGRLINAECGIRRITQFDVSDLPAKIAGNVLRGKDE
HGEFELDKWVDKRDQAHTPAFIQFALSAARQALDDARWQPTTDAEKERTGVAVGSGIGTL
DEIVSTANTLQTSGYRKVSPHFIPKILVNMAAGRISLAHGLRGPNHACITACATGANALG
DASRFIQYGDADVMVAGGTEACIHPLALAGFSRMRALASKFNDEPEKASRPFDEKRDGFV
MGEGAGIVVLEEYEHAKQRGAKIYCELAGYGLSADAHHITAPSPIGDGAYRAMTSALRHA
GLGVESVDYINAHATSTPMGDEIENRAIKRLFGDHAYKLAVSSTKGAVGHLLGAAGAVES
VFAILALHTNTAPPTINLTATGDSELDLNYVPLTAQQRTINVALNNSFGFGGTNACLAFT
KLSC

>hypothetical protein (possible thymidylate kinase) Contig18419 (likely complete)
MKSRKVALAGVLGWSSTGAPVRRGASVLLLRSFSTSSPAPLTAAGPKDEQIRRNRENKSL
QFVFIEGEAATGKSTICELLKRQGYTVQFEGFVELCKENSRYSPQGSVVSIKWVSSMFTA
MERLLHQFDEKQAEIKGGVVFFDRSFLTPYVYTRGSLNNLYVCDAMKEIKEVFPCTTVLC
KTALATIEDRLLQRYQQGDAQAKDIRKNLGELDHAYIQKVHNKYAELEQDGWFDHVLDTS
APGPQVVENLLSTLRQAAIINSHDTHISSH

>globin Contig3364 (complete)
MSASSSSTSSADEQTIYDAIGGSKAMELAVDVFYTKVLADQRVQSFFEGINMDRQRRMQV
HFLTFALGGPYKYNGRAMRLAHRRLVERQGLNDSHFDVILELLSGTLRELAVDERHIEQV
VAKCESIRDDVLCREPAKPMEDEPKTMEVEEKEVKWERVAGLVVVAAALLVYLLLASSQ

>hypothetical protein Contig9685 (incomplete .. seems to have CXXXC motifs)
TPGEDQAVSREAHRVVEAARHLCHLPCAHALEHDGAGLGLLPHCGRRCPPELPVRVASPR
PHDAVLFCPLRRMALLNLHRWFSSTPSQGPRNC

>glutaredoxin ContigE80POFO01EPD8X (and 10896) (complete)
MMSSATRRSAQYSFLLASARSSFAGRIVTASNRRSAPLISTSSSAPSFISSISSSRRHLY
STEAESPAAAVETAPEAAAAEKESEITQQEEEVKQESLAEFLERIEKEDQAKIDAALKAF
ESGNAIDEHISSLLGMKKYKCVVFMYGDEHAPADGQGYAVIKQLQRDHALFKTFDLNKYP
LLKEGLIKHKGSYVRGDEDIPQVYILGRPFGSLREVMDSVATGQLEARLRLTRSQRHFYA

>calcium-binding protein-like Contig10984 (probably complete .. inferenence from PGP)
MFVATRQRSASALAGRRLTTRAFSTASSSSRLFASNHSALPIDKDANWKEKWRARYNDKI
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KNWSTPEKIFNVFATVRKNGESFMTVEDFCDAILPADHRPPSEKGKIKRIPDFIRFADLD
GDELISFGEYSFFTTLLSLPEEHLKVAFQMFDLDGSGAISKQEFRKVLRVLRKESPLGSQ
QTTHKKEVEKSGIYAHFFGLDGKKELTYTEFENFIKSLHQGVLQLEFDRYDSKGEGKITA
RAFGMSVIGYVDPKDLPSFLTRVESLDNRKGELSFEDFVNFNRALKKLPEIGLAVKLYAQ
GGEINKKDFGRAVKAISGVDLKPVQIDVIYHVLDKDGNGKLDHNELVEVMAKRVEKGMAH
HRDVGVARFVNCLVTCCSRKAL

>thioesterase superfamily protein Contig25387 (and E9BS9UA01ERMEU) (complete)
MTSTPQHQDFYFVVEKIDVVPELRERAQQYEKSIRDSNAKHVGQLLGIHYTKITKDSVEA
TMPVTDRHHQVIGLLHGGLNAALAEDVASTAATLHVADMAKQFVVGSTITANHIRSVTSG
FVTATATVQHKGRRQQVWQVTIRNEKGEVACVSYCTLVVLDKKSVIGSAQRNHQQQQQG
QGKAK

>zinc-containing alcohol dehydrogenase superfamily Contig27133 (likely complete)
MQAVVVDHWLKGPEEIKVSVAAVPEPGDGEVLVDVAYAGANFYDILMVQGKYQFRPTFPF
IPGTEFSGVIGKLGSGVSGWKVGQEVYGMTMLGAYAEKVVVPANKIRPVPKGMSLVDAAG
FSMTYPTSYCALVYRANLLKGETLLVHAAAGGVGVAAVQIGKALGARVIGTVGSAEKVEV
AKKGGCDEVINYKDEDFVEKVKELTDGRGADVIYDPVGGEVFDKSTKVIAWGGRLLVVGF
AGGKIPSVQTNRVLLKNCSIVGVFWGSYEIHQPHKIEETFQALTEMYAKGHLKPVTCAVY
PLVELPQALKHIGSRQSYGKVIVQTSSNRGTTAKL

>isoleucyl-tRNA synthetase ContigE80POFO01CUGC0 (and 17388, 3605) (mostly from PGP)
MLRRVTNKGLGSPLHRGAPPLLPHRLGGNYNLQSLHFANSSARRLHRGFASSPASEANSA
AAAPAATANSKAFGHTLNLPRTTFPLYTTEKAQLQLEGSLLAEVSDNLYAWQVLFATFIP
CPRHNNNAKRASSCTMAHPTPTGHCTRVRFTHSQTPIVVPRPLNAGNLLVRTGHVMNKVL
KDIVNRYKLLRGHAIKYVPGWDCHGLPIELKAVDQAKSGSTLSPTEIRAKAHACAEEAIA
QQMKGFRSWGVMGEWNNPYATKDPKYEASQLGLFLDLYKKGYVYRGLKPVIWSPSSRTAL
AEAEVEYSDTHVSPSVYVAFSVKHLANKAGELSRFNNLHALIWTTTPWTIPANMAICVNP
NIEYSVVKTTDQHDKHYVIASDRLQAMQELLKQEIEVCARLPGSSLADTIYVHPLDGREL
KVLPGTHVTTESGTGLVHTAPAHGADDYVVCKAHGIPLRSFVDDNGKFTQDLPEFAGKFV
LGPGNELVIQALTDKGALVHQHKYTHKYPYDWRTKKPIIMRATEQWFVDLKDVVAPALDE
ISRVQMVPATGRTRLESFIRSRQEWCISRQRVWGLPIPVFYSRQGELLLTEESVGHVQKL
VAKHGSDCWWSMPTSELLPPSEKHNADKWEKGRDTMDVWLDSGVSWHSVLHNRELPFPAD
MYLEGSDQHRGWFQSSLITSVALTGKAPYRAVLTHGFVLDEHGRKMSKSLGNTIDPVALV
NGDEKKAGCGVDVLRMWVASSDYSRDTLIGPVVINKMKGSLRKLRNTARFLLGNLADYDR
RQAIPYDDLTGIDRYMLHKLHEFSHGVTTDYDDYQFSKVYRGLVNFATVDLSAFYFEVVK
DRLYADATDSLRRRSTQTVLRHTLDALTAALAPIAPFTAQDIHRHDAQAAAVAPNVFHLE
WPRAGDQWKQDGMAQQWDAIRDVRSQTYKVLEAARAHKVIGSSLDARVRLYTGSDDNQVA
RWLAEPTSDELAEILVTSAVDLVPEAPAFEVVDDRPPQADLTSGPTPSFVGGGLVHAVPV
GVEVVPASMHAVKCPRCWRYASAEENTPCPRCAQAMA

>Co-chaperone protein HscB Contig22279 (likely complete ... N-terminus inferred by Genscan)
MQRIRTSKMAATASSPSFSSLLPSSLPILSPAQMPPCCLMRAIGGSGAGRSAPCLMGSRE
IGHWAPLNRAQCYSALTSKPSPLFSSSSILSSTSRRFIRVRTASEADTASSTQHQPPSIE
EDQASNCADCGHSTQQHQHQHQHTTAPGCGSDKFGSHPKCWSCDNFVKGIPLFCTCCQKV
QPPSNYDFFELMGMPKRFAVDAGKLEKHYWALQRKLHPDNFHTATTRERNYSEGVSSIIN
EAYHTLKHPNRRAKYLMQLKGVPLDETTGTITDPDLLMEVMEIRMRLEDADDAELRALER
ENKQRLDRCYEEVGHALDASDMDKCRDVAVRLQYFVKIEEEIKRRKKVE

>mrpl22 Contig23422 (complete)
MRRGTAAMSGCGRRLLVASSSTSSSFTAGALQRTILSTHRYLPAIQSFGAARSYASPSLL
GDDIFTKAYEQVKQKEEETGERVRITEAKADSKNLPASMKRIDHLLRQIRRLSYKEAITQ
LKFSQKRVAPKVIATIEKARQKAELKFGLDPERLILDEIYATKGQYGNPQIYYHAKARIG
IMRRKRVHLTVKLKEVPFKGGREAAGQVRQGSQQRAAEGVGGEAGQSREGDGRAEARRHH
QAGRALGPLQGEDPQQEARDCHRPRRRRRHQRRRQGIVCINNTHNASVAVQLTSL

>coiled-coil domain protein Contig7406 (probably complete)
MGAASSRPHEEAEDWEDHFQHEYEQPTAANWAEDEEEEASVSVHLGPRLVRRLQQRQSGG
AAARRPQQQQREKQEQQQRFDEAALELDVDEALPPPLSEEELDSIAFSTPLPLLLGDDDV
EEEVRHGAGEASTSVVVPARRAGGVSQADREFAQQEVAEVRQRFRAEQEKISATEVEQLH
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KLRGLLDAMTRHRRASEDSCEAERSACLECYAKETDDPLACAAKARAFKQCATAPVRKGA
PV

>similar to PPOD peroxidase Contig11799 (likely complete)
MHHGHHHHHAVTISTESKVHLKSHHGKFLCAEPSGKVVADRSDCKEWETWTMRTTNGRA
TFQSAHGKYLCAEPSGKLVADRSSPSDWEHFHVVHQGAHTALRSHHGKYVCAEQNHHVVA
NRDALGPWEQWQVVPAGSHCHPSPPQHHHHQHSSESKVHLKSHHGRFLCAEPSGKVVADR
SDCKEWETWTMRTTNGRATFQSAHGKYLCAEPSGKLVADRSSPSDWEHFHVEHHGSQVAL
RTHHGKYVCAEQDHRAVADRSSASAWEQWHIVPVATYQIPHYAPPPQYPPAFGGGFPPAP
SSGYPPQQGYPQYPQSPMGGYPPQQGYPAGLNPPGQYPPGHY

>NADH dehydrogenase B13 subunit Contig11269 (complete)
MMRRGLTLFASAGVRTVPTSSSRLFLTTSRLASSDAAPSPVPRKNVKASTGIAGLDVVPN
AREVLIGLYNKYLAELQVIEPTSPYRKLVENMTRERLRIVEENEDIAKIEELIDNGQVEE
LIQEAMEDIKEVPWWAEHKPWEDSPHKRIPVFEREF

>carbon-nitrogen hydrolase Contig19772 (and 3026) (likely complete)
MQRTLRVGTAAAVRLGASSGTCARTLHASAAVGQSAASTNPEAVQVALIQFHSASANPDE
NQAKAEGFVREAARNGAQFILLPELYRTMLPREQMPQYAESIPDGPTSRRWAGLAKELGV
WLLGGSYMIEPVEGQPGKLYNTAVLFSDSGDLAARYRKIHLFDVCVPGVVDFQESALISS
GKETTTVASPFGKLGLSVCYDLRFPELFRHLAKQGMDILCLPAAFNYGTGQKHWLHLLKA
RAIENQCFVLAPNQVGEAPNKFKSWGHSLILDPWGDIVAEGGDGEEIVYGKLDLSLLGKY
REALPSLKHIRKDIFHV

>mitochondrial distribution and morphology 10 (MDM10) Contig673 (and 7019) (likely complete)
MDFEEAPEELPNNPGDYEGVDGRSTGIIDFDAMPGFGFRWGSQISSRFERSIRLMILPPF
PTIGFSYSSRPMPSMHQAMEEAMAREMEALHDEEDAGEGQAEGEAESAAEAKPLLRPLDV
AVLSKAGAEVTERPDNDDNTTSSEDEEEEEEEAEQKESGGHFMLSAEATFDGMVQGMYMQ
RFNKNWSTRHMILTSMEPGRSMLMSSLSYSGGSFTSKLSWSSERDRACFSHMQAITQRLS
VGGEVGYAMKDKQPVGWSVGGRYVIRKEEGGKFAATHITATYNHLGRVKTTYTLPFSETV
FASARYTVNAFSFKSNMAVGVESWPSATMPLMTKAKWDTDKGFGVSLGAHLGLAALMFSA
SYGKDGPMVGLHFEL

>hypothetical protein Contig4384 (likely complete)
MKMKTTTERTAVLMAAMVVAEDPTTTKMVRWAGASGRDVERASSTDGKCGRPSPDTTSRR
RRTSHPAEPYDDEGQDDNPKEKTMSPTTNRPSRRRSCSSPG

>hypothetical protein Contig14930 (probably complete)
MGKGIHLPASLRSFLYRQITVITVGSVVVGTAFGGWQSYTTRVADENMRQIRFKQAEKEA
RISHTLLTKGGLKKALEEQGFDMGFYEVDEADEEEIQ

>deg protease relative ContigE9BS9UA01B3LRE (and 22468,21474,3995) (incomplete)
MAHMLDTLVKNDELATARVVVMGDMNVDTGHKALQAFSDSQTWGLVLDNALDVSPVAKRS
SGTFTGWSKRSVGITIDHIFVRRHGGDPGARHSIMDVVRYEVGTNIDPKIEGVLALARKR
TSLFHTSSVVEARKASPALPPLVPDDVQEVPIEEANWEESTNMLPLEPVIKVYSHVTSPN
YVMPWQMKATSEKVGSAFALSGRRILTNAHVVADHTYIAVKKFSGTQKYPAKVLSVAHDC
DLALLTVTEDDFWTDITPLELGDVPHLQDTVAVVGYPTGGDTISVTRGVVSRIEPQRYAH
ASGHLLAVQIDAAINPGNSGGPVLKDDKVVGVAFQSLVNAENMGFIIPVPIIKHFLKDIE
LHGKYTGFGAMGIQCQPMDNPQLRHFHKMARDITGVLVNHVEAVSKAKGVLQKDDVLLSI
DGNRIANDGTVAFRKRERIFFDYVTSMKQVGEYCRLEILRNGEKQEVSVQLSPVQPLIKN
LKQLAKLVAANKQPYLRFDFDEHVVIILEADAAKKAEEAILTRHRIPSPHSPDLFDKKEE
TDVV

>Sco1 Contig13084 (probably complete)
MRSCRAASARNLTSAGFRACRQGASATRLYASGIIRDGCCKDNSLISTATRSLKTSVWPA
RSPLVRTQALPRRRAEEPSSTPGPAGGSNTRTSPPPPPEARPPQAPITWKSALLALGACG
VVLAYFEFEKAKRKPRIEIAVAGTPSIGGPFTLVDQDGHVVTNHTFRGRYMLVYFGFTFC
PDICPAELAKVTKTLKILEEEEGITPGLVVPVFISVDPYRDTVGKIRSYLKDFHPSFVGL
TGTPQQVESMARSFRVYSSTSQHSEEDEDYLVDHSIFLYLMDKEGSFLSHHGSQYDAHAL
AQRIATDVRSKGDCPPSLWAQLKERGSNFVATFIH
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>hypothetical protein Contig16980 (and 20409) (likely complete .. somewhat inferred)
MLRRNVRGGMSPTWAAASRGLHVHASTPLLARRREYDEEALREAAAALSVEGARQQRGRV
EVGKGRRRRAVGAHDDASEETNGHGVAARRQRETGAGPVVEEGEEVGHLKWLAGEEFVLR
EIQPGQLAYVRILKPGITPLMAFGQKRGNKRKRFAYKGHVSPYFRLSPKSPLWKLVIAEK
DLIEEGRRARLEYERTMWPKSKKKPQNWGENV

>hypothetical protein Contig7317 (and 9106) (probably complete)
MERTDEEVTTPTMSASTTTTTSGEAEIPDYWQRVDSPFSKSTIFAYAGGMLAFGAVCGAA
AALVIGQRPPKPSAAKTTTKAGTALCLTGALAVRWVVYTSMGVSTVEEFADKMRRWAPEK
AKKVGLVPSRESAYWTQKKLEEEGGAGEEGRRAIGVFEQWFGVKFDEGDNTDDEAAAEAS
T

>thioredoxin-dependent peroxide reductase/dienelactone hydrolase Contig23605 (complete)
MADHAHSAEELAPYTEEENKIYFIRESDWTQCPAYLFGQEDYLGIGVVVIQEWWGVNHQI
IDVAKHVADKGFRTLVPDLYRGKCAIDNENAGHLMDGLNWPAAVQDIKGAVQYLKATGSR
KVAVIGFCMGGALSLASAALVPEIDAAVPYYGIPPAQLADVSTIRVPILGHFAELDTYAG
FSDPQAARDLTEKLKSANVDSQIVMHKGVGHGFVNPIHGAPQSVIDESWEQTFAFIRKKL
NVASVGFPAPHFEEEAVVGQDFKTLKLSDYKGKYLVLFFYPLDFTFVCPTELLAFSDRIK
EFQALNTEVVGASVDSKYAHLAWLNTPRKAGGLGGALNYPLIADLRQKMARDYDVLIEGE
GHTLRGLFIINPQGVVVQITKNDSPVGRNVDEVLRLVQAFQYVDEHGEVCPVNWTPGAAT
MKPDPKASLSYFEKVN

>tim9 Contig18985 (complete)
MDIAPDAKKSEAAARNMVQLMNEMQMKSVLGMFNSMSERCFRLCMKNVDDDAPITTKEDS
CIKNCTEKWQRYSQRVQLIFAEENTRANTKADLMQDRPSSNLEGQD

>SMC domain protein Contig19833 (likely complete .. mostly from PGP)
MRRATVVVTRSRTLGTSATSFSAGWGRLPRATSSTAAPLVPLRLQPSSAAQHVRRWSGGV
LSSAAEVRVGQGSTTGRARSWVVACGVNIARGVVGVTAFASTPRSPSSLVVRDGFVCTPD
GKHAYLDQTKPVVVRRPTLWQRARYVVAKVMAAVLSAIGALYPASWLFFVQYKEVDIFTD
SWDWLNATPALIAGPLVLFVAAAYMWYRGCGTYFTVPELATFRDRALLSEYSEIVDEHGL
GQATKFVTPRELRIKLFKQARDKGILSCLKDASVVEWMNTGMLLPDEAQPVSQIQRSLQD
AHRRLKIETSALEQELAELTGKAATKRNRLIADAELSYAACAEAKLVELYSRNYRDRIAS
ARKERDNKIARLNNTANVSPTQRNAEKAEIERECDRIEEVEARLYQEQMRSNLPNLEKRA
RERDDAILSAREEFETHTQAVRIEKQIDLRLKRSQDTFAQQVAKLQREWDNLADSTLEKN
TARTPDSVPFVVPLVPFVAPTQ

>hypothetical protein Contig18159 (incomplete)
GDQTLRVGRKAGVEEGEAHIVKDETKVRRSVLHDLVNEEAVLSLVQRAVHQEKALVGAEK
DLSGRLPRQIAAGSSPSRLSGAFTTRGGGRRRCGAALAVREGKGEDLELGAQIERHIVHE
VLVVPSGRLRGI

>NADH dehydrogenase B16.6 subunit Contig3161 (complete)
MSQEKGRARYHQEPLFRPEGPEFEPIPLEKRKAFQFRRGPTGKALYAAYFGVLVAGHYVY
ATGAWEQRDLYAERQNVWGSVTTYLQAEADRKYLQTRKRSTDAEEKLLFPKEVSEGKRQL
NHEEAQYKTRWVRPATDPFQQWHYVKRTFDKAQE

>hypothetical protein Contig1374 (probably complete)
MSFFFSSSKHKKDADEASADRPATASSPRSTSSSAGSSRGEGSEVTPVTSFRGGGGGAGA
VGAVDGLGGGRHTAGIATGGEENLIVQLLVRQHEENRRWQEALLQSLDSLTKALLVSSSV
ARQPEPGVESEREDERKSASREKKKRKPDSLHVVIYSSSMTEHKQAQTLSEHLIAQVPGL
DIELCTAYSARPADVAIVLKRSEARIDMPEDSFLRQASQSTRFGNAISVKALQSNDPATA
PYSPKPSLVAEYSSGIGLKLENPTKAVVSLTFNFPLTSDKDPKPFLLRCKQNDENFGGLV
DLLRKAPR

>cytosolic type malate dehydrogenase Contig26422 (and E80POFO01EOQ35) (complete)
MSADSNATTRRAVSRMSRIAAHMGVGSQTGFEAAATSASRVVSQQPPVTVLVTGAAGQIA
YSLVFLVAQGRLLGEETPIKLHLLDLPQFVGALQGLAMELEDCAFPLLRGVVCTGDLKEA
FKGVDVALLVGSFPRQAGMERNDLLAKNAAIFKEQGRALDQYASKNVKVCVVGNPANTNA
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LIAQACAPSIPKENFTALTRLDQNRAKGFLAKKLHVSPGQIHNAIIWGNHSSTQFPDVSH
GQVSIDGRTVSLKEAVGGTEWVEKEFIPGVQQRGAAVIKARQKSSAASAANAVVGHVHDW
LVGTPQGEWVSMGVYSDGSYGIPPGVIYSFPLTCSRGNWAIVQGLPVDAAARKRMQATYD
ELHSEKETAFSFLGLDKKH

>hypothetical protein Contig969 (likely complete)
MPSRPSSHSSLPPTGAALGPLHGTGWLQRRRQHATRCGRRSSFVRLVSSSAPSTAFYETF
ARRTMTGLPSCRGCSAARPCCASRTSGVPSCSPSPCPGLPKWCGASRRSAATSAPSPTAR
LSSLPSPWEW

>hypothetical protein Contig23728 (likely complete)
MARASAGLRRLVAAPVALTAGRSMLATGGIAVQAAERTPTAQALHKHDAVLAQPLREVEE
KKDDAQRALAEAKRKEAEGRPPEWYVILMGFAGALVGYVTAVALKFVGRYVFYFAAAETT
ALLALTATGAITRQTAIEVAKYTMPPFTWALKTAIDLARGQFSRVFSASSLALRFFFVLS
FGLTLRYSRTGPKPSWK

>hypothetical protein Contig1521/10562 (complete)
MLRRSIAPVTGAGIQPATSSSCLVARTASAFVSSGSSQGQPILFKRNIQKYWSKEARQFK
GKRPVKVMSIKRAARLAARRAAEEAEAAHLDSKYGTRCTSAFLAERVRWNEDYEGPVIST
PTEEPKKTKREVPIATGAQEEKPSFFARLFGRSQIPPASLWKTICPPRGDHPAGDE

>Complex III Qcr6/hinge protein Contig14062 (complete)
MSENWAGCAIKKSLEEKAHPKCLKKWAEYDACGQRIKGDTTGEAQCSGQYFEYWHCVDAL
VANDLFKRLK

>B12-D-like protein Contig3636 (complete)
MQRSPMTVSTFCKRFMPVEVYPLLVPLGFACGLATYMSYRTLAGAPDVHLFGKKPRYETG
DHRADPHFAGIHSKASRFDPHPELGQAEAAFHKTYSASASSPTYF

>MIRO mitochondrial rho GTPase Contig7278 (incomplete)
MEEFKEVETCIECSAKSFLNVHEVFYFAQRAVLYPTAVLYDAGSRSLREECVAALKRIFK
LCDKDRDGILSDDELNAFQARCFGASLDPAELQGVKDVVRGNVENGLTEKGLTLTGFLFL
DNQPTLLIT

>mitochondrial protein S18 Contig26123 (likely complete - but other amoebozoans have
N-terminal extension)
MQSDLDKLMKKAKKCVFCRPSAQRPVLDPMNVSLLTMFLTPTGDIIGRRHNGNCRRHQRK
LATTIKRAKHMGIFSYKYGGFTIYSPFHEPPETYAEDDGEGDEEQYGESDEEGDY

>hypothetical protein Contig6167 (uncertain of completeness)
MFAVPPVYSIVCGVLYCPLMLSYSNAWNAWVRAINRPPTPSASGWDRVVGSPLKDFKAEA
VISNRSWKRFALLVGTDMLELLTALYAGLAVSLTLDD

>hypothetical protein Contig4457 (incomplete)
SSAISKARLDANIVNTSSYWRFFSVLGNVCLGAEASCTLQTRWSVSGHWWALAACAPATV
AYSTKTKPLDWPSLPRTIRTSDTGPHTSKAFRTAASSMLKGRPAPRTVRSWALVPSVSTS
LGLAVSLGLAF

>hypothetical protein Contig24539 (and 25611) (likely complete)
MQRAVGLRSQFLVAKNSTAALPLWARRSFVSEAHIQAELEAARRVKALEEKNARDRATML
STTPAPPQGKRSDEAPGQPARLPSAENNHQPARPSAQ

>Cox23 Contig3955 (likely complete)
MEEERKPVSAREAARRRRAEQNQKHQQAAGINRHPCYELHQASLKCLEENDYAQGACTYS
FAAYKECLANQNEAKRAGEQKSIFG

>CMC1 cytochrome oxidase assembly factor Contig15299 (complete)
MAQADASQTKTYRLSDDPSFLTNQEKNHIYRVQHKRAYKLCDPVVKPYVDCTKHRLISLL
WACRDEKAQMADCLHEVAERAREEVTEEYLRQRQAKRAAEDAALSKETAASS
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>hypothetical protein Contig2757 (complete)
MQRATNAALRKGVMPLHSRLKIATGRQLWESGLLPPLPTLRPLFLHLPPNVPSGLGWVDE
NAMEHRFTMFVQTAVGKMMLDHAPHHCTVHLPAVLPFELPHVKAKVAEKEYATVEEDIAK
YKCREVHWKDFVWPLWQLSRLHEMAHLDPEAEPLPLSPLSFRETVCGRDTHEFLHHVEAA
VQAQLLRLPRDKELTHEKAVHGKTSNHLSPEKMQRGIAAEKAAAKDLWLYPQLGTDLCPA
TAEFVIDDTVLNVSATTDPRRHWEKGLTELFAYAALARQQGMAVGEVGLFYPFSRHLVHV
PIHDWDHRPLFDRVLNSPDVEVGPATDDLYRAVDSR

>Gatb/YqeY domain protein Contig16382 (and 1895) (complete)
MRRATFVTVSAGGLRASAVPHSSGLLFRSSTRFVLATSARADARVFPLRSYTTTAEEFVG
KLMADLKEATMAKDKVRLGVIRRLRSEIMNKEKLNVDAKLEFGDCVKVVQQMAKQCEDSA
KEFDKINQADTAAKEREEARLLRTYLPAQLSEAEVQQLAEEAVKAVGATTIKDMKNVMAT
LGPKVQGKSDPSLVGEIVRKLLGGK

>brain protein 44-like Contig24712 (complete)
MASNQVMSPARRKWTQFVGTVGALANWGIPLAAISNIYNQQDPKKIDPRMTSALVFYSFL
FMRWSLAITPANYPLLVCHASNEVVQLVQLGRWANATWGGEKKDEVKAE

>hypothetical protein ContigE9BS9UA01BKURI (complete)
MGKSQGQQEKIPSKKRKIAIAKQNKTEVEFVNKIFPFIVAAMVGAFLVAIVLLFIKASAS
APDAAKDLIEGAVDQAAAAAGLD

>related to Protein-tyrosine phosphatase mitochondrial 1 Contig8605 (likely complete)
MSEHVRPKHYRKEPLGWAPQFMALWISRVLFYPTLIYNVTLYYLWPTKFRNWWDRVDDSI
ILGALPFYWHVPLLYNQGVRGVVNTCDEYAGPVQTYARYGIEQLRVPIVDYFPPTLEDVK
VALRFIRKHTNNGDSVYVHCKAGRGRSTTIVLCYLIERYPGVKPVEAQTHLNKKRPQVSP
NVWKRQVVFDFWDTVPQDEDASGTPVTIPEPGTSTSTSTAITSADGGAD

>ISD11 Contig21283 (complete)
MSSRLRLVAPPTRRQVLGLYKEMVVASRSFKHSDPQWFLARVRQEFYKTNREPAERIKWF
EKGQQLIRNKECIL

>mitochondrial ribosomal protein S25 Contig22353 (complete)
MGKRFWRAARQFGLEKGMPKPKTPEDWNRLYLKHQVYLHGIKSLELQMVKTGAGKTGARH
FHYWKVPPIRWWNPDVNIHEQKLLAGESKLIIEKVDGKKIELVVDGMKDEEIYNALLSHS
DAAPVASKEASVQ

>homologous to mitochondrial intermembrane space protein MIC17 ContigACL00004542 (complete)
MGRRGGSSRSSARPASKPTATAAPAKKAAPPATQQRAQPPATQQHAQTAPAMGGGGQSFL
GGVAQMAAGYAVGHVASRAIENVIFGGHNATPEQIQKAEEQVQQGPCARPYDGFLKCLKK
NEDDATECDWAYDMFKECQTTNRANRDFGYGGESKEQSATY

>hypothetical protein (possible mitochondrial homolog in plants/fungi) Contig17726 (complete)
MSATGPPSSSMNEGYVPPHMRKGGKQGGGPPPGAGGGARPPVPWRLRPGAKFLTAGLLAL
GVGWTFFYTMRSVSQDDFADIDDSGNKIRERPRV

>hypothetical protein ContigE9BS9UA01DFLBH (complete)
MNSSSRMTSLAFRTSTRSQLVGARLLPATTAQRTLFQGAGSEQKTEKKPLLDEDWKDLMV
VDYGTGATSSVPPTAIEETRHHPAAFESSSELRIFQHWSSGLVREVEDPLL

>hypothetical protein Contig19630 (incomplete N-terminus)
SQKQKRWTRRSWWVPLATGAIGLGSYYLVRPLANPWLRGVLASGSCAALTAYVCKDLPIG
SVSTMMTTSLCWMASIRLTHLMLLPDEERQALTLRDYAAKFLWFVFPRVEEPHASRGHAM
ARPRRIQCRSWAG

>MYND family protein Contig17432 (uncertain of completeness)
MEGGQARGGGVTGMSVGEGVALMAGVAIAAAGYVWWFNRKSTPTTERQRSSPAISAAPTP
TPKQQVKVCKSCGKTESGDRALVRCGRCHKVYYCSRDCQRQDWGRHKPECSSSDSAAAPK
KTPPPEPLPAWAQNLRLTSAEYANVEGSAQEER
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>mitochondrial ribosomal protein s36 Contig9471 (complete)
MASTGVRQLRQHVPLIKFPQRHGAAVQSLQDAALPSRHTGGVESTPLTAPPKTTTMQTSP
NLPTPAKFDIKSRGPVTHHESMDELPARYRRALLSEEVIDLIQMGGAVDH

>hypothetical protein Contig12707 (and 8072 and 1911) (incomplete .. largely inferred)
MRRWALAASRTGFGGSGIGGAGSARNWLASSTLPQAFRWSVLRGVHTQSAGVGRGLVGRV
RPRRNLSTQAPKEEPNPSTLPPPAEEPITHTVESLTESYYAFQDSVLNIQIMGNSVPRFW
VGLVAFGLFGLGKDLLSLGVADLSALAGDKEDFVLTQLPTAVSMSDPFTLLTLPLLSSLF
AASVGIWWGRFRIKKLFDKFVFMETKKGHVAPPEVIDGARKGIITRGSNEWKWTVPAGKE
GELQRKLPSDLELKAFSAASFVYFVFIQLLVLKFTPFVILPSLTALFPLTAVLAQSPVFL
RMQDKTKGKLETLEAKGVFGKLPSGEGKELDFDGEGADEGAYGLHSADHDDDDDLGSRPA
AGDGSLSTKPNNVFDKTAGATRVRAIVSRRKREQSADGAAGGGDEEHGKENQWGDVVLED
EQNQQQ

>mandelate racemase Contig10694 (and 25467) (likely complete)
MKRATSVSRTLVGLNKQVTGPRAGTMPLLSSRHFSSTTPVQREKPRVKELRAYVVQKDEA
GADYHRQQSGHWIIDTPISNPMSVYPPYRKSRVSWGIDVLGTVIVEAELEDGTVGVGTSI
GGEPACYLIENHFSRFVEGQDVRNVELMWDQMWRGSMPYGRKGLAIQALSAVDLALWDCL
GKLWQEPIYNLLGGKTKEKLPVYATTSRPDLAKKMGFHAAKFPLPYSHAEGEEGMRKNIE
CVRKHRESVGPDFPLMIDCYMSLTVPYAIALAKAVEPYKIKWIEEFLPPDDYDGYSQVKK
GKGEASCLLTTGEHEYTRYGFRELIERRCVDILQPDITWVGGLTEAKKIYSMAAAYDIPV
IPHGSSVFSYHLQFAYANSPMAEILIMSPKADKVVPVFANLFTNEPLPDDQGYLQLDENK
HGWGVDLNKDGLKLQRPYPRHQH

>mitochondrial ribosomal protein L52 ContigE80POFO01DTJO9 (and 21304) (probably complete)
MRAGQRVRLMQGVGRSGNEDGAFHDAPDWEYADGTPAPPSRKQIVWMTKRQETEERIQRL
REEVMEMEQKELERQSFYKDE

>hypothetical protein ContigE80POFO01CS520 (and 6672) (incomplete)
RPREPGLLPRRDALLRDDRHDQEPARQEGAEGDADRRLVAALARQPRRPEVAKLCHRSRR
SHRSAEHVSVCAQPRGSRGRGHLRLLQEAAVHHPLQDRRRPGGEQAARGAGGRCPDRALL
APGHRCQPGHPLGPGHHVDGQRHVREWSEAGELRAAEAAGDAVAGLVQDHDEQQPRRPGL
QLWPPHHRPQDALQEELHVSLPLMSAPPHRHTCCTHQVRHKEQTVSPPF

>hypothetical protein Contig19632 (uncertain of completeness)
MEMIEDRSKAREAWPHTPQVQCREETAVVERKENNTAPAIACRLYDSGWPL

>3-ketoacyl-coa thiolase Contig22255 (likely complete)
MKKALSRRTFVVGGRTLPFIGKGHPDFVWKKHPLFGKKENPSLEDYITQSVQAALKDTNT
PASAIEKAWIGNFAGELFSSQGHLGAALAGASPEFRFLPAMRVEGACASGGLAFASAVEA
IQAGTDVTLVCGAEVQNTVSAREGGDYLARASHYRSQRQLDDFTFPALFAQRMKHYCKTH
NVGPKDFARVSVKAYANANKNPLAHMHAVKMDLDTASTASDKNPNFLANEDLKPHLRTSD
CSQVSDGASAMVVVSEEGLRRLGKSPRDAIEVLAVQVAADNLYVDRDYDKFETTHAAAQR
AFQSTGLTAKDIGVFEVHDCFSIAEVLMYEALGLADHGKGTHFAADGHTHIDGKFPVNTG
GGLIGFGHPVGATGVKQVLEIYRQMKGQSGAYQIPNHESKLKLGLAANMGGSDKTAVVSL
FANH

>conserved hypothetical protein, similar to yeast fmp21 Contig22059 (complete)
MQRTKAYATMYSTRHIKSAAHLARPSFLCRFASSSSSPKATPSATHAAKAEPKSKFMSND
DKSLEELQAELDKINQEIEAFNAQEGKTADDEYEYKNPKTGEIGGPRGPEPTRYGDYAYA
GRVTDF

>hypothetical protein ContigE80POFO01DF64L (likely complete)
MRLRPARCVRRLPPPRWLEVTVSGLTRPRRTRAARTVWTGCSTRFPSSTRPCSGPTNPAA
WARNSWLISSKRFC

>hypothetical protein Contig5433 (uncertain of completeness)
MFVGKCSHVCNMHVVRVYNGMGRGHHVLLFSRQKRIFFLTRFLMVASCLLFGVFQAGWSA
RHRLIIRTMSSKASFTFCPVLAEHSSHPQLSFSARKRASSWLTWRWLSRSACEPRKTIGT
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>transmembrane protein 14c family Contig3840 (complete)
MSNKADSRRAAAVSEALPTFGVGAVVALMGIRGFTATKSIPSLLAGLGFGTLFGVGGYLI
QDPATSASGRTIALATSLTLAGVMGSRFARTRKLYPAGVLAAVGAGSSAWHGYSVFVRVE
HQVADALHSAKETGKHEVEKIERKLSGKD

>hypothetical protein Contig2000 (incomplete)
WGSALSTQGMWTIQLLQSTPGLALAQHADWLYAFGCENSERALDLAPRDQDGLRKHVLYA
DYCAELGTKPGGEGNAYLAKARVYYRRAIERAHAVQHKRIVKTTDGVSTFEIDTFQDVAT
IARAHSGIAIACLSAAEKLYESVVSSRAEREHKANQRTNEGNADDEACDEEEKENGEAGD
EQNEVAQMLELLLEGRERLMACVKIEPDQRDYLLSLCSVLTLLGEMTDDSDESEMYFSEG
VTNFERALTIADDGNADAQNEYGILLSKRAQRILKQLRREGFDPAAVNHTPAARAEPESD
TSSADSSAQPEGELPIETEEEKEAARRAARCAELVARANRYFDAAEAKFVELYETSVWFG
TINLACLAALRGREEETRRWLQVCRDQHDLAPEHLDDHDFDAYRDRAWFGELRAELAEQR
LAQQREEEAQREAELRQQAEEMAAVADAVDGHAEA

>NIPSNAP domain protein Contig14822 (complete)
MRRTSSIALGRGSPLMASASRSFASATPPSQAIWQSLTNARHSIVTSKKTEATTTPVEDP
HVHELRVLTINPGHLKEFVQVSEKALAHKTKEGAKLIGYFNVTLGECTNEVMQIWQWESY
KHREQATENLANNPAWEEYTKTVKPMLQHQKYSIILQFPFWPLNYSQTKGGIYELRTYRL
IPGAVWVWGDYWEQGLKHRSKYVQPVAAWYTEIGHLNTVHHLWRYDDMDQRRQLREAVWD
EPGWSEIVELTHPLIQTMDSRILTPTDFSPLQ

>conserved hypothetical protein Contig22941 (complete)
MRRVRPAMRSATGHLAAAAPLVLTSRRTYGVLYRTHKGEKSERAAPGTTAANSSSSSNNG
NSGEAGKKDKTGDTFQESAGVLVTTRGVIAHHEIVREVGIIVGSSVSSRHVGLDLLARVK
GVFGGSVVAYAEMMVDSSAEATHNLMREASRRGANAVLRVRYETAVSSDPAVWSSTFSYT
LAYGTAVVVRPVKGAKEATSWRDHHSDDDDTDDDDD

>hypothetical protein Contig6896 (incomplete ... uncertain of N-terminus)
QQRERLRSVGLRGRQQWHQLEQRGRPQHQPWLQGPLSLTLKALRRRS
SGRDNVGHDRGTKVTRTRAQCGGVTTAPPKELLSCGGAATGCRWVTFVEFVECARLAIRP
SVDGTESRWGQHAHNTRCCGVCCVTPCVTLVRVVLCGKKRAVSPCANASLPSFAVIRVAA
PNQKGRRPPNRGVNPHHSLF

>NADH dehydrogenase 13 kDa subunit Contig14419 (complete)
MRRAAPQLSRGMLPAYGRSSSSLLASRATLSSTASRAASSLKLKIPFLGDTEIALKDDVF
RPGVPENPGNLYAPMPAEELIHEIPPKVTHGSTAVCDGGGGALGHPRIFINLDKPGPHDC
GYCGLRFIKEEEHH

>Putative Mg2+ and Co2+ transporter CorD Contig12274 (completeness unknown ... used PGP)
MNGNSSLRPGLDFRSGESWEREVLRGRLVLGEKNEIRRLKGTLPSTVGSHLREDVALTGA
VVPSLTRQLWRDLNRPSHDDAPRRHPSADDDFSDAFASLRVLNDRTAALQQLVYEPHSQC
TTNGILIEVRSYPLPFRMDNNTTKYSRFEYRVEMTNLHPTKTFKLLSRHWLILDGDGQTE
EVRGPGVVGLYPVLAPGQNFHYKSSSETKVPNVLRRHNLPPFYRSEAKS

>hypothetical protein Contig8244 (likely incomplete)
MKVFFLNKNRGELSSLGSPVQAFISSAGFSSGSRQRSQSSFFSKRANVADSFSSRRSMTS
LSMASADAPASMANAFEFESMKCTRTTDLAIVWRSSLLD

>threonyl tRNA synthetase Contig6211 (and 15382, 5592) (likely complete ... mostly from PGP)
MRRGAGAASATAASVRRSMGRVPASSFLLTQQRTCAQKSGSMRTPAACFSRSVRVRPPSL
AGERPFLRRFASASVVTHRAVPAEARPGKAPSSLPPFMQRRLELWREEWERQQTGKEAQA
AAGEGPHPIKITLPDGRIIDTSSSTTPLQVAASISEGLAREVVVARVNGELWDASRPLEQ
DCRLELLKFDSPEGAGVFWHSASHLLGLAIEREYSPATGEHAESSAKVQLCDGPALSDEK
GGLGGFFYEFFLQPGEGATGASTEDFAELEKRVEAFAKEKRQFERMTVSRDFALQMFAYN
DFKREIIEAIPAGEELTLYKCGEFIDLCRGPHIPHTGLVKGFKLVKVSGAYWKGDSTRPL
LQREEAAKRDHRLIGKKQGLFMFHQWSPGNAFFLPPGAKIYNKLMNFVRDEYRVRGYQEV
ITPLVFNKELWETSGHWQNYKDDMFAVTGASHAHGHDHGHAREGHSCAHHHHSPSAGKEE
VMGLKPMNCPAHCLIFSGGHYSYRDLPLRLADFGVLHRNELSGALTGLTRVRRFQQDDAH
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IFCAEDQIESEIGGCLDFLRKVYSIFGFEFAVQLSTRPEKYLGELALWNKAEDALKQSLS
RFGHSWRINEGDGAFYGPKIDIEVTDALKRKHQCATIQLDFQLPLRFGLKYQGLDDAYHT
PVMIHRAIFGSVERMMAILLEHTSGKWPFWLSPRQSVILPVTDDHYDYAKQVHAQLQKQR
EDKFNEFFVDLDGRTKLTLPKRIKEAQEKQYNYILVVGERERTEGTVSVRTRDGVIHGAK
TTADLLTEWRQLLDAFQ

>pyridoxamine 5'-phosphate oxidase-related Contig27600 (likely complete, N-terminus inferred from genome/genscan .. est support exists in Baylor data)
MRRGAQHASRSGLMRTVLAEGHSTRRALPVSCAATRRFLSSSPALAPSTRTLHLSPISSL
PPLLRRYSNRPQSGQDDHQRLTVAELTRSLIESRKSGTLTTVQLYMAAEQPPLGGTLPLF
GSLMPYILVDDAVPIVGLRPDEKHVRNLEHLDMASLVVYPLTPANINPSSFALPRVNLAG
RLRKLDPADSNDAVTSVRRQYLVAHPGCQKIIDDLSFYKLEIEDTVYCSGGLQETTHVTA
DKYKATKPDVVMQSSRAILEWMNESKRAIYLKLFCQEYAQIEDVGEIFMFSVDRKGFDVM
AWRQTNRNWVELRFPFPYEMKSVDDCRGGLLDSCSFLHDKYLKKVEGGDKFDIEEERRLE
HERQRKQLEADEARRKELSEPEF

>hypothetical protein Contig25233 (likely complete)
MNMVKKGVVATPIGEAGQGFSTAQKVLRMSGALRQNWRGVHPLQPERQMQPSRARLLLRQ
RTNFRIWKTWAGKTKQLALSPRIYGSVTTVIVPTWTHTAHPVDESYGHDASNETFYPYKS
TVKGTRHRDEKTMLGIINDQ

>hypothetical protein ContigE9BS9UA01BYGVY (likely complete .. largely Genscan inference)
MLRQRRTLITSRPVALASLLGRPSAAGARALVRHGQAFSTNRSTAFSSSRWRSPLLLAAV
TAMSAEPQPGTEAEEYEDEGYQRLLMGLMDSARDDGEDGEGDLADAIVFEPEEEVKEEEK
EKDEEELLPASRVLGAGRAKIANEEAEARRQQLEAHLHEHIRSWAKFEKVCSQGGGDDGE
EGEEQDKPHAGAKVALRYPPWMQPGESNEVAQFTILGASPHGQKDGVVDMLTMLTTTPPV
HRMRDLYEFHRGIRDEIGKQARIVKPRMRWLVAGRPALGFVTAFTGWGKTLVSTYVVTAY
NKTGYVLVFNTIHDGEAPLPQCFARHQEESDEAFEYILRTVTFRPAPPPSPSASLPSSSF
FLSAYEKTK

>elongation factor P Contig26691 (likely complete)
MRRHLQQSTAGSLPSSVQHRRNYKAPISDIKRVWVIEHLGKLWEVTETSQSRKTAQRRAH
INMELRDLAAGTKKSERFRVEDRVETIILDVHKCIFSRSEGKKLLFTNAETGEEVSVKKE
MVGPAEAYLKPGTSVARLSVHNGEAVTVKLPGKAVVTVKEADSTQSATAGYKKAVLDNGR
TVRVPPYLEAGDVIIVSLPDEVYVGKSDGSALADDGDEEDDEEDDDDDTDTDDEDEDEDE
DEDDEEDEEDAKKK

>Alcohol dehydrogenase zinc-binding domain protein Contig6141 (likely complete ... largely from PGP)
MKAATTKLATRSRPVTPMLSPALLTRCSVGPTCTSQSLLARRFSSDVKKTMKAAVVPQYD
LEDSDEVHPASLIVRSDWPVPSLHDVESRHDEGDVLVQVAASSVNPIDSMLRRGYGRALL
EATAQGRSRLPFIPGFDVAGTVVDVGTGVWNWKKGDMVWGGAELFRNGAHAEYIAINQHA
LAPKPANLTMEEAGSLPFVALTSWRGLVDTAGLSSSTSKRIFINGGSGGIGVFSIQLLKS
WGHYVVASCGERNVEKLTKLGCDQVLDYRSPQFQQFLDTPESVDVVLDTVGGAKSEARGL
RVVKPGGHYLSLRGPLATMTDSGGLVGGLLGAATTIAQKKLAAFTQDRRHVHVDYVIYKP
NGDALREVGKLVEMGRIKPDIDRVFDLGDIREAHQYLEGGHARGKVVIKVM

>hypothetical protein Contig26894 (incomplete ... uncertain of N-terminus and C-terminus ... is this bogus?)
MPRTTVTTTVTAGLLALLTSRTAAASSATTASVVALLEHGGLGHPLGGLVDGLGRALDDD
LLIVVVAGGDLDLSAGLLDDLANGLTARADDQLVLVLGDPHRDASVVAAVELLLLRLPDG
FDFLALVDDLLDELAGLLRGLGAAADDDLLHLLVEREGDVGAAGGADALEGLAALADDEA
THGARDGHLDLDGGLAEDHELEALLLGVVLGQEARVVAQISVSAVLHEELDEVRIAAHNG
LVEGRRASVVGLVDVGALVDEELGHGEA

>frataxin Contig119 (likely complete)
MFGSARHARHLATSAEPPSA
GEFAKAAEETLEDLQDRLEEAGLDEDLDISYSDGVLTIRLGDKGTYVINKQTPNRQLWFS
SPISGPKRFDYVATEGKWLDTREREPLHQLLYAELEQLTGVSLS
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>AMP-dependent synthetase and ligase Contig10657 (and 23620, 26757, 23750) (likely complete)
MRGRMATSAASSCRRARARQWQAPGGTIPYGPIRGFHAGRACLAPYQKENPDALANLLPK
AHEDHVPAKAEPDHLPLPIHPPARPHAITLISHVKGDRSIPLISKPIGAFFDEQVDLYGD
KEALRVVHQDIRWSWNDLQRQVDAFSQGLLDLGFEKGDRLGIWLPNTAEWVVAEFATAKT
GIILVNVNPAYRVYELEHSLNLVGCKGLIVTDKLKSSNYFELLHELLPELEHSAAGELNS
TKVPTLKHLIQITDQHVKGMRRYVDVLSEKASSPDTRQNLKSLAQAQHVDDAINIQFTSG
TTGLPKGATLTHLNILNNGFFAGERMGLTPDDTLCVPVPLYHCFGLVLGNLAAFTHGAKV
VYPSPSYDPLKVLEAVQEEKCTGLHGVPTMFISELEHPRFKEFDLSSLRTGIMAGSPCPI
EVMKRVVNEMHMKDVTITYGMTETSPGSFQTEGNSPLEKRVETVGRVHPHTECKIVDTEG
RTVPVGHVGELCTKGYLVMKGYWNNPKKTEESIDAGGWMHTGDLAVFDEDGFCKIVGRSK
DVIIRGGENVYPREIEEFLYTHPAIEDVQVIGVPNRKYGEKVCAWIKKKDNTKARAVTAE
DIHAFCKDKIAHYKIPEYVVFKEEFPMTVTGKYMKHKMREQTIAELHLEKEVVATA

>enoyl-coa hydratase Contig20345 (possibly incomplete N-terminus)
MTSRDFGFGVSVREAEGAEGVFILHLKANENR
FNPDFMVAIDRALSHVEKHEGPTALVTVGEGKFYSNGLDLDYVGSHTDQVESFMNQYMAL
LAHFLIAGVPTVAAVNGHCFAGGFLLALSHDYRIMREDRGFCCLNEVDIGLNLCPGMAAV
ARAKLERTIFRDSILNATRYTAPEGVKAGFIDAAVPDAEVLARAVALAQKLAPRGANKTI
LSQLKQEMYIDAYDKLTTGGLGLAAGRFGGSKKKANL

>hypothetical protein Contig430 (incomplete)
LAVSSVTRSFLRKPRRLASSATSASFLAVTLMARNSCSAKASMRSRVLGPIAIAISSSLL
SKINIHTSFSCDPMPAPACFLLRSKYHSLFILNISPLSWNTSTKPSMPSDCFTRLSICST
SSTVPSSALTTGIPPLAAASVSAVYLRYRPVALWRIAMSIRKSSG

>hypothetical protein Contig26428 (incomplete)
LSLFICVGWDTAGPFRRLFCLRVSGRGVLLCSGGSCQLSPHLRHTPSSFAFSLFSALLPP
LRFPPLHVPAVLGVPERPDAAFLIACSLIHLLVPPPPSSSALLFFPHSSNACQLLKRRIP
RILCRPPATKLRHLQRSGTAPRRTCRGAGRAQAAMTSPYYITQRPRVKKKAKAAKLSSSM
TSLPLVDMSGSIAPSAGQTLQPPKMTSSSSSDLISDYMMTIPESG

>hypothetical protein Contig23141 (probably complete)
MWAWERGAGVERSLGGEDALSGLQQGRADEMRVHGGIYTKRVHGERLASFLHHLLVLAIL
LNMIHNLRSPSSPSIQLGRQHEEVFILGNRV

>zinc finger protein (possible Tim15) Contig327 (uncertain of N-terminus)
ATVAKGELALLARSVPSSALLGIRQSTLASRVSASPLHGAATRPRPWSPSCFLRISARSL
HASSTLQRSAKSSMVEATSADAPTDSAEAKETSAESAATPTTTTTLNIGRIQPKLELHYT
CGVCELRSTKQFSRVAYEKGVVIIRCGGCESLHLISDNLGWFGEDKNIEEIMRKRGEAVE
RGRRDAGGNILLDNNNTNTAGDDTITTDLEHDGTQTVVEESEDCILI

>hypothetical protein Contig24777 (complete)
MSSTKKTTAASAAADKKSKVVVFKVKDLENMPRKRLVSLAKRVGEKANQNSAALVEALTK
YHNEHQSEIEEKLKELSSKPKASETRSL

>Cox19 Contig22998 (incomplete C-terminus)
MTSHSMRNKAPLVLPPEKGSFPLDREQACSEKGSIYRTCLRDHNNSSSICRQKARDYFEC
RMDHGLMQREPWDKLGLGDDQIEEKSAPIDVHTKEQTGWVAGAKYR

>glutathione-disulfide reductase  Contig15901 (incomplete ... likely internal gap ... mostly
from PGP)
MKRFNFDLFVIGAGSGGVRASRIAAGQYGARVGICEESRVGGTCVIRGCVPKKLLVYASH
YPEEFRDARSYGYSKNRELNRLEGVYRNLLTKANVDLMEGRGVLLDPAHEHTITSNEALE
LESLPKQVAIIGAGFIACEFAGIFHGSGTDVTIIHRGPVLLSGWDEDVQKTVTSLHRERG
IKLASQSGVAKIEKDPRTGKLRVFTFDSKTKAEGPVVEADVVLSATGRAPKVEGLGLENA
GVKVNEKGAVMVDEWSRTSVPHIYAVGDVTDRVNLTPVALAEGHAFADTVFGKKPRQCDY
RHLPWAVFSQPPASAVGLTEQQARKELGDDGVDVYVSSFSPLKHTITKRTTDRVMMKLVV
DRKSDVVLGCHMVGPDAPEIIQGLAVALKCGARKAQFDATIGIHPTSAEEFVTMRTKRT
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>protoporphyrinogen oxidase Contig12031 (and 19315, 6296) (incomplete N-terminus and internal
gaps ... not sure if both ESTs are definitely part of the same protein, as 12031/19315 and
6296 are on different contigs)
CRFVQKRLQDSCSSGSKRIILIEQGQRLGGWLHSLRTPEGFVFEAGPSSIRTVGSKGRAT
LRLVDELGLRQHVVPCSSLAIKNRYLYTNGSLLRLPNHPLKVLGSPLMRSAVFAFLREWT
VPRSQQPDESIHSFFTRRFSPVVADTLTDALSIGIFGGRSQSLSIKSCFPFLHEYEQKYG
SIGLGMLREMLASRSGQEKNEKNQNTKTTKNEAAAEEEEETDEGYLSPAVQEMQKMQVYS
FREGVETLSRALEQKIREDEHTDILLNTAVERMDQERDGTMSLSLGHGMKVRAEKVISAL
PSHALAHCLRHHPTLEQDM

>hypothetical protein Contig24860 (likely complete)
MVHQAIVIYSIPASLLFLTWLVLFGVVPAFDTLLPITAVGMLIWTKIEFDKVNKLKAQAA
AMRKANKAAEDAASTNATAGNKKPAAKKQAKKAD

>LYR protein Contig27708 (complete)
MQRSQRALKVYRDLLRTQHTVFSGDALAQERARSLIRQEFEAHRGVQDAKEIDDLIARGN
DTIAYVRGHVVQAVKNDRGNWEMKLRPENKFIKSKDFPMCGVEF

>regulator of chromatin condensation Contig22000 (and 19707,24163) (incomplete ... used PGP)
MLYMAVNSKSVVHAEEHLPQATTSASHSPRAETDKPLASGGNVWVWGADGGTVPSAGSSP
ADSLVPRLAAKLSGKGIKGLAFGDKAAAAVTNKGELYLWRVGEEEPTLTEHKGVQQVACG
RNGLIAALTDKGDVLLWDARTHAEGGLHPSASSKEAGEADWKNVKRIDIASLSLPPASAT
ATPAASASSWWWPFGGSGSKAGAETITQVDCGSGHVAMVTSRGRVLVLGDNNYGQCGTQD
ASNETRGPGMVRPSPVVIDLGIAGGGHKAVGVSCGDTHTAILLDDGAVFMLGSVHLSGLK
GSTLYTDSPVLVPLTRDSKSVEKLGRIIKLSCGGEHTLALTNYGVLLAWGNGMYGQVPDN
QGKHINTAHPVLRAPFFNAEGKEFINNEVKELQCGNEHCLALTKGGDVWSFGRNDRGQCG
VGNRAHQKTPHKVTKLQSRKDKISAIACGQHTSAAIEEGAQKYEI

>histidine triad nucleotide-binding protein 2 Contig24241 (complete)
MRRAIGVGRRLDVLSRQLICPSAAATSSSSTLLLTSSPASSTLAQRQFTSRPPVRMASDG
DKHGATAAALKVEPKDTIFAKIVDGTIPAKKVFEDDTTIAFHDIAPQAPTHILIIPKKPI
GGIGDVKQDEEALVGHLMFVATQVAREQGLGDDGYRLVINEGTNGQQSVRWLHIHLLGGR
KLTWPPG

>leucine-rich repeat protein ContigE9BS9UA01E46QY  (incomplete)
TSTSLFDPLFETLKTNTTIHTLNLSDNGFDNTILPRLLDLLEYNQHLARIKLLDNALDVD
DLMTLFECIERCNFSIVDL

>hypothetical protein ContigE80POFO01A8VZC (incomplete)
LRRADMAEDPEGCALVERGRGASFVAEDGGKVAHVAGHGQEFAAQHGLGEVAVEVGRDVE
RRLVLRAPDLALARHHLERLLQLEHVLDVPLRLPLRQLALQIARLQQVLEPRLRRKHLEY
KVGRNAVL

>SAM-dependent methyltransferase ContigACL00002233  (likely complete ... largely from PGP)
MKAGASRGGGFGHLFTTQAASYAHFRPDYPASLYQRIWSFAGEGRGTGLAVDVGCGTGQA
TKVLATHFDRVVAFDPSPKQVEAATKIGTSHNVEYRVGLAEALEGIEDESVDLLTTAQAA
HWFQLEPFYRELDRVLKPKGCVAIWGYGLCRLPTPEADKLLSRYHTETLGPYWEKKRALV
DALYEHIQLPFARTHREVIENKKEVPFKHFVGYLGTWSSLKTFREKHPEGSDPVQDLCPQ
LFEALQLRSEEDVIHVTFPTVLILGQK

>LYR protein Contig11327 (likely complete)
MSQRVRKHSGLQKQVLSLYRQFMMSAYKRPEGPGRDSLLGRVRDEFKEGAKMSRFEVDAI
ERRLGMARKQLKMLNLPGTETVQRIGP

>X-prolyl aminopeptidase Contig7161 (and 25246, E9BS9UA01B4HZO) (likely complete ... some from
PGP)
MQRGRSVAARAFAGRARGAASSSAPSSCLSFSSAVGRRCRLVSAATPGGERRPFSSSSSS
RMGLSDSLAGKRPRPMNYGQPHPSTHPHLVKEGEITPGITAKEYAQRRENLMARVPVGTV
MIVPSHPEMMMSYDIPYSFRQQTDFYYLSGYQEPDALLVLAKRSDSEPIHFTMFLRPRDP
AREIWDGPRSGVEGAVSFFGADEAHPIDRLAEKLKDLTDGVKNILYSPDVHLEFTHQIFA
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LIPPEKIACPRNLLQTMRLIKSPAEIDVMRRSTEISGQAFREIMRATQPGITEGQLAALY
EYECRKRGSQRLAYPPVFASGIHANTLHYVANDDIMQDGQMVLVDAGGEYNMFSSDITRT
WPVNGKFTPAQLDLYNTVLDVQKKCIELCVSDGRMSPSALHQMSTQFITEGLKNLGLIKP
GQTSGVSRFYPHSIGHWLGMDVHDVHDVSTRVPFKPGMMATVEPGIYVPDDPDIPAELRG
MGVRIEDDVLITTGAPEILTAGAPKEAHDIEAVMRDRKPL

>3-hydroxyisobutyrate dehydrogenase Contig13456 (and 5116) (likely complete .. .from PGP)
MRRATRSFALRPTARQLWAGADSLTAHRGFVSVAKPETTRVGWVGTGVMGGHMCGHLLSA
GYQVTLYSRTAEKAQGLLGRGAKLAASPKEVAQQSDVVFTMVGFPHDVRSVILGSSGVLE
GLCSDGVVVDMTTSEPSLALDIYNEAKKKGVHSIDAPVSGGDVGAKEARLSIMVGGDEEA
VSAVKPLFDVMGKNIVHLGPASSGQHTKMVNQILIATTMVGMVEGLLYGHKAGLDLNQVI
EAVGKGAAGSWSINNLGPRIVKRNFDPGFFVEHFIKDMGIALKEAERMKLSLPGLGLAHQ
LYVAVAAQGHGRKGTHALQLALEKLNNMDHDHSSPKSGLPKAL

>SAM-dependent methyltransferase Contig302 (likely complete)
MSRLVAPKVKEVIAVDLTEEMMAVGKEQAQTAGLNNIHWVVSKAQQMPFMDNAFDVVVSR
LAVHHWDEPQSIVSEMARVCKPGGKVVLIDIVTPEDLTDAQGDRLNHLERLRDPSHVCFW
RLSELFGFLKKARPALSVLPLVDRRDNQVFLDQWLELTNTPSASRKAITDALQAELDGGG
QQKDTNSLVTGFRPDRSADGSLHFVHSYVLLSAQKQ

>acyl-CoA thioesterase Contig16554 (and 10626) (likely complete)
MRRNLSMNAAPLKLLRPRLCSSSSSLSLVARPRGVSYMSTTSTAKAKRPRDSLVERDLRF
STDPRLQEAFVNSSGKIRLGMVLEELDTLAARVGYAHVLGTPRVAQLEERRKEGLEVPTI
VTAACDRIMLLNPISIDRDLKLRGMTTWVGKSSSEVRVEVSSVRKDPQGNDEATPHLVAY
FVMVARRNGVNEAYPIPPLEPVSPVEKRHYDQGASNAARRKEAAATSLLIQPPKLDEIKI
VHDMFARQMHQGQAQQDASEVPMASACHSSTQWTHPQNRNIHGNIFGGFLMRQAFELAHV
TCGLFTGVMPTFLSMDDVSFLRPVHIGSVLALESQVVYTSTSTLDYESDQDRDQQSATGG
AKQQQQGFPLVQVRVQANVGNFGTAFEPSNVFHFNFKAGANQRKVVPNAYSEAMAYLDGR
RRMIREKTLRQDIASYLEGFGTAHVE

>fumarylacetoacetate hydrolase Contig7616 (complete)
MQQRGLASFHQWCRKVVCVGRNYAEHAKELGNAVPQTPVLFLKPPSSLVTHGSPVELPAA
AADDSHHEVELGLVIGKRGRDIPEAAAMDHIGGYALAIDMTARGLQNEAKNKGLPWSVAK
GYDTFCPVSRFIAKEELPHPEDTTLWLKVDDELRQNGSTKDMIFSIPFLVSHISSIMTLE
EGDLILTGTPSGVGPVKPGQRLTAGIEGISLDVSFPVLLRSRPSA

>copper/zinc superoxide dismutase Contig20273 (complete)
MATKTAVCVLRGFGDAAVEGTVRFSQTADDEPTTIDVEIKGLKPGPHGFHVHEFGDNTNG
CVSAGGHFNPFGKKHGGPDDEERHVGDLGNVVADETGVARTTIKDRLVTLGGPHSIIGRT
MVVHADEDDFGKGGFEDSLTTGHAGARLACGVIGLSK

>Kynurenine-oxoglutarate transaminase ContigE80POFO01BZ76L (and 10773,26175) (likely complete
.. some EST and PGP)
MRKCFVARSCLNSPVQGGLLKGGSLEAVSVLAPRLFAPLSSWASSSRQCRSYAAVTVPPS
EKFARAKRIETFGETVWSEFTPLAQKYQAVQLGQGFPDFPAPDFVLAAAQTAIHNNLNQY
TRMQGHPRLVKALANTYSPLFGRELDPMNDILVTVGATEGIFAVISALVNPGEEVIMLEP
FYDAYPTDTILNEGVPVYVPLRPPKVPKGTITSANDWKLDFDELESKITPKSKILIFNNP
TNIPGKVWTREEMEEVARLAKKHNLIVLSDEVYEWMTYDDATHIRMASLPGMWERTITLG
SAGKSFSVTGWKVGWAIAPPHFTTALGTIHQFDCFTHGTPLQEAIAVAFEQAEEKNYFPD
LKQMYWRKRDKLVATLRDCGLAPVVPKGSYFVMADTSSIPSSVFMGKGKAEPGIGGDGPK
EETRDYQFCRWLTRELGVGAIPPSAFFSKENAHIAENFVRFTFCKRDEVLDAAATKLHKL
RDLSAQ

>protein kinase ContigE9BS9UA01C4CKQ (complete)
MKTILGGSKKKAPPEPRPRLHHRRTQAKALIGKTIEVKNRRFKVKEILGEGGYSNVYRVV
EEGSNNVFALKRMLVSVDEMDLVKREVSLMKSIPPHRNLVHFECANVTTSAEQRKGEDLM
EANIIMEYADVRLFDVMEARHTEGKYFTEAELIAIMVDVCEGVAVLHQHRPPIAHRDIKV
ENVLLGNDGAYKLCDFGSATSVTHHPKTAAERDAAEADIERNTTMVYRAPEMLDLYAAKP
IDEKADIWALGCMLYKMCFFEDAFSIGGRLAILQANFSFPLAPKYSPELNECIKYMLELN
AEERPSITAVIRRLQRLKAGLGQDTPGKHRRSRTWGGSQDNLHIDDIPPAAANAEDKATS
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LHSSGASSNRGTGRSEEDKQRPRHIYSG

>hypothetical protein ContigE80POFO01DI3ZA (likely complete)
MPAKPCVQRAACFWKVAMSPAPVWARPAWMPPTSTFRTRTTLPLYSTRPSTPSGTIFWAW
PVVSSSAWLAPSR

>aldo/keto oxidoreductase Contig6592 (likely complete)
MRRSCSSSALFPSKACGALLPPYGSARRGYGDVVRAAGLRGHATPEGTAA
FHQRLGSKLPFRLVPRTQWSLAPFGFGGYRVSARTSSHRSALKKAIRLGC
NVVDTSSIYSDGDSELLFGQVVRELVDKEDIKREEVVIITKAGYLSEKAE
HNRSSAPSYSDKDVDHVSPGLDYSLSPRVLEDQISASLERLGMERVDLLM
LHNPEQLLEVHPHLGPAFYELVSKAFAHLEKEVQRGRIQYYGVSSNTLAV
PSSSPDHVCVDKLVQAANSVSEKNALAAVQYPFNLIESEVLTEGVSAKAK
AHGLIRFSNRPLNAVYEGKLQRIATFPSHDDKDLVQLLKEAFDYAIHLEK
NYPGADKASLPPASDYAWAQILAHNQATLGTIDRWVNALESTILPSYEPA
IARLEDHAQLRSWGDKYRVAIARLFERFTWVNEANASKNSEQLTLAADAT
WPELNERGMATLSQKALLAARSSDVADCVLVGMRRATYVREVLLNVGPSA
AVDTASDPARYAQFAAELQKAKAGP


>conserved hypothetical protein Contig24598 (complete)
MAGTSWGLRRSSSAAGRLTTSPRRCYTPGSATPADEAEQDKALREGVLRGFDQMHSLERM
EVEGKATLPDSQSGVSLILQGSGKILQVKVDQEVADNVENVEKLFVAASQNARQKIADRI
NSLLAASHQ

>hypothetical protein Contig3110 (likely complete)
MSLVMNPSGGGNDSSYGVGGTYYGGELVQSTGDAQRGGRNADQDSGDEFMTEMAKIRQNQ
AAESAPATGKYKQKLEEARRATVDEPDNGYKYPGYKARRRESLSADETPVVSAPADPPSG
DVFSQVRTRRQEDLLKAARTRKKTKEKKKAFGDQIKGVLAYLPFRTSHLSGFDG

>dihydrodipicolinate synthetase Contig22480 (and 16230, 21597) (probably complete ... largely
from PGP)
MRRRVVSSCVPWLPTRPGLAECRAAGGGSHALTARHNSTSSQTKRFEGFIAATLTPMDSN
AKPSLGRVKDYAQKLVSDGCSGVFVCGTSGESMSLTLDERKAALEAWVKNKGSLNVIAQV
GTTSLEQTRDLAAHAESVGAAGIATMAPFFFKPPDVSTLVDFCASVTSAAPKTPFLYYHY
PGITGVNLPVFDFFEKAHGVIPTLRGAKFTGTELGDYYRTLCFQGGRYDILMGFEYMHLP
CLPLGSKGGISLSFSFCAPVYAKLFKAYHQNDLETARKLQLVIAEFMAALAQYGFVPASK
LLMREWHGLDMGPCRLPLRALSPDEEKRFMALKVVQELHSLL

>hypothetical protein Contig11589 (complete)
MYSQRLLGSRSTAVPSLARTLPWAQTTGLRAGANGATPLAIFPSAQLEAQRETRRIPIMQ
KWRAGAIKTRDQVHKKAERTKRNQERCEYQRVKLHLKQGTLYEYIEGKTADEETKRKWFH
QHFGHVQPKSRLAEEVTTGSSSEGASSPPPQQQSFVDLDAESVRVSQ

>mitochondrial distribution and morphology 34 MDM34 Contig6411 (complete)
MSFQIEWPTLDEITLEKIKAQITEVMNKGELPDAICDVMRVTDLDLGNIAPTLQFMDIPD
VSEDGFEGHFKVAYAGNGSITLQTKVQVNPFAAKTVPSKRALRHLGGLIAHEPMVVPLRI
TISQVRIDGDLVLNIKKRAKAHDPRSDGSLILENTNTAVSAPAADSELSIPHIAAQFKVD
PLQSVNISSSFDDFGSVKDYLQEQVEGSLRKLFVEDFPQIVSGINKQLETAAHAKHNTVV
VLAPK

>ATP12 Contig13926 (complete)
MRRSCASVAAGGARWGRCGHQAASRFPTSMLRQAGSDGFRFLRPSLTTMRMLGATRSYAE
RVKVDYHYGHEKFGKDQAEPASEDTTKPKVKGAKLSGVQGGSKTRRWYKQVSVGEREGGW
APLLDGRVILTPMEHPLVVPSQHNALMIAAEWEMQQPYIKPDTMPITRLATTIMDRLVEG
KPEIRHALTLEMLDYIETDTICYRPDDREKEQVLYDKQQAQLRPFLKWFSSFFNMELMLH
FSVIPEAQPEETINGLRLLLHNTTDWELGCLDTLVSRTKSLVLGLALWKGPFSVDQCIAA
SRIEEDHNIAEWGECEGAHDLDKVDIYKHVAAATAFLRSLPPEQSSLKQW

>zinc-binding alcohol dehydrogenase Contig4172 (and 9647) (incomplete N-terminus, internal
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gap)
MNGDSNTKVLLVKRPGTGMPDASLFKIVEEPIPEPADGQFVVKNVYLSLDPAMRGWMNDV
KSYIAPVKLGDVMRGQTVGQVIGLLRVGLPKAGETVLVSGAAGAVGSVVGQIAKIKGCRV
VGIAGSDEKCKWLVDELGFDAVVNYKGKSADQLNDEIRQACPKGVDVFFDNVGGDILDVA
LKRIRKGARIVICGAISQYNAAQTKGPANYLSLLVHSARMEGFVLFDYIPEYPLAIRELG
QWVKEGKLKYAEEVVEGLERAPEYLNMLFTGANKGKLIVKLADEPAQFAQARL

>universal stress family protein Contig9417 (and 862) (likely complete)
MTKYMVAVDGSEHSNKAYAIAAKLLTNKDEVIFVTVGQKGKGAAAQDLLETWTKKAEADG
FTAKPLFLESADPRDAICNAVTEHGIDILVVGTRGLGTIKRMLLGSVSNYCVQHASCDVI
VAK

>hypothetical protein (possible ybab related) Contig10353 (complete)
MRVLATRTRSSAVPLLRTVQRGLATDDQGQPLGGGMFDHLQEIEVVGNSLSKSGGIVEVT
ARGGGTEVVKAQIDPILAGDAALLSKLLTQAAQDAYDQVQYEVKRKLVEVSMRDRRKQQM
KERDQMAIDLEAFKEK

>aldose 1-epimerase Contig25072 (complete)
MNQGKGGLERVVIGHAATGASAEVYLLGAHLTSFIPKRGGADLLFVSQKAEFAEGKAIRG
GVPIIFPQFSDMGPLTKHGFARTALWEVASAADSEVTLVLRSSEATRKLWPHDFEALFRI
ALVPHGEEAALETEFTVKNTGSSAFAFTVALHTYFAVKDIHVTRVEGLHREGEDLYYLDN
TQGRKKIKEESRDVGFTGETDRIYLHTADELRLNDTERAIVIKKSGLADAVVWNVWADKV
KSMADLGDDEWPRYACVEVAAVEHPVQLNPQQSWTGKQTLYEQSRSRSPSAL

>related to mitochondrial FeS cluster maturation protein Iba57 Contig13880 (likely complete
... could in introns/gaps)
MMSRAGRLRAWYRSTEVVRGAVVGKRGIHHAAPLWLVAREAPPLEQPAPPPLGWWVGEVG
GRAIVEVRGRDAARFLQGLTTNDLLAAAATSRAGREEGRYTAFLTPTGRLLADALVCQLP
PGQQQQGQQEGEQTFLVECDARAAPGLVVHLRRYRLRAHVDITPPAQRPAADEWAVGAVL
TRGHVQSSSSSSSGGGGSGEATPSPRDSLLQCLRSHAPSLPCFADPRTAAMGIRVYHRRS
SSFAPPPGLAEASAKEYRLHRILHAVPEGIDELEPNVAVPLECNLDALNGVSYDKGCYLG
QELTSRVHHTGVIRFVSSLIDRSLPSLATTNIASDKTELFLVGADGTPERRQVGRLCGGV
EAGLGFALLRLQHTTAVLTPSTTTAPFFLAKPLWPPPYPLP

>protein tyrosine kinase Contig13529 (incomplete ... largely from PGP)
MAQSALSSLFFVIVYVSALSADSIEWRKKGYAGTKFGNNSSTLPLLTLSDDWRIDYDDLE
IVEPLARGNFAEVHRGFWRGINVAIKTLYQTQMQHTELKQFENEVELLRQLHHPNIVLFI
GACMQAPHFSIVMEFMTQGSLYHVIHSDREITLHRKFLMGRDIARGMLYLHSHKPSIVHR
DLKSLNILVDDSLNLKVTDFGLSCKVNHTITAVGTPMYSAPEVLRSSVYTEKSDVYSFGI
IMWELMTREEPYVGINLFEIINKVVTEKLRPRLPAPSDEFPSCLLDIIQRCWDDEPEVRP
CFREILEYMEIKAEETRDPALVAASSCYVDLSSSGVRRTLTAGLRRSSSLSTSAGATTSA
ASSMPLPSLAAGAGREESVDDEDRRRTTTGSGEESGDGGPSSVRLQIDVPASWDDGASDA
ESRERTREEEVRRQRHQRHEQERSRQLQQQLQRQRQQDEREDNEERRGDDEDEDEDSRTR
RRLNINDADNP

>hypothetical protein (respiratory-interacting) Contig26576 (complete)
MAKVAAGPTRSEVRGLLRSLLREANEQMIPVSNNPLWRDSIMGAFRSASPSPAEAWNGFR
VGQAYLTLLESSRVEKDMFERYGLTPRPDDTRARLHRNAARVGLRLPQWLDEKEASRS

>ferredoxin Contig18230 (complete)
MMKRTTTLVTGGRRFAGLQSPVVPFAWAGRQATSSSASTLRSARLYSADADSKKTVHVTF
IDKDGTEIPLEAPVGKSVLELAHDNKIDLEGACEASLACSTCHVILDKEYYDKLPAPVEE
EEDMLDLAFGLTETSRLGCQIIISPELEGIRLKLPPATRNMMVDGYKPPHH

>NADH dehydrogenase 24 kDa subunit Contig3477 (complete)
MRRATSSLSAVPALRTTGMRATSSLFTSSSSAAMLKSRTLHSSVPRQGDHGGLSQHRDTP
DNTIDTPFDFTEANTVEIKKILAKYPVNYKQAATIPLLHLAQYQTGGWVPLAAMNKIAKI
LEIPPMKVYEVATFYTMFNRTKVGKYHVQLCTTTPCQLGGCGSTVILETIKKHLNIGVGE
TTADGLFTLTEVECLGACVNAPMLQIGDDYFEDLTPESTVALLETLKAGKTPKVGPQTGG
RKNCEGPQGKTTLFAAPAGPYCRPDLETCA
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>calcineurin Contig3684 (complete)
MGNDVGRISAKDFEGVEDFTEAELHKLHRRFQKLDKDGSGSISADEFLSIPELAG
NPLLSRIIAIFDTNKDEEIEFTEFVKALSTFTNRDNLEGKLRFTFQVYDIDNDGFISNGE
LFQVLKMMVGSNLTDAQLQNIVDKTILEADEDKDGKISYEEFVKLITNTEELGAKLTITL

>3-methyl-2-oxobutanoate hydroxymethyltransferase Contig3145 (and 4135, 23007) (likely
complete)
MRSLLCRVSPATVAHTSSRSLTTTTSTTSISTSSSSVARVQDGSGRRGYSAHPRPTSTKD
IGKRTTVLDLGEKYRKNIPLTMLTAKDFPSAVIIQQVGGIDLILVGDSLGMTTMGYESTI
PVTMTDMLHHAKCVHRGNQTSFLVGDMPFGSYEPSSALAVENAMRLIKEANMNAIKLEGG
KRMAARAKAIVEAGIPVMGHIGLTPQSIHSLGGFKVQGRTSGQATAILEDALALQDAGVF
AMVLECIPDRVATFITQQLRVPTIGIGSGNGCSGQVLVWDDMVGQSDIQSFQPKFLKKYA
NVGEEMRKAVEDYRNDVVARKYPEDGTHTFAIKDDEFDAFTKKAQAQHQTSAEPLTT

>asparaginase Contig4249 (likely complete)
MEAPSDSRAAAALLPPPSDVGLHKPPAAELVVDDHRRKPDILIIYTGGTL
GMKKDEAGSLRPVRGYLNSQLAAIEATKDPRVPTFDIINFDPPIDSSDME
PADWISIATVIEKNYWDYQGFLIIHGTDTMSYTASALSFMLENLGKIVVL
TGSQIPLENSITDARRNLIASMIIAKEVDMPEVVIFFNNKILRGNRSTKA
DNWGVAAFESPNYPPLGVLGVDIHIDYQFVASPPKGRFRVWKNFNTRVAV
LHLVPGFDVKAVENLLLPPLEGLIVKSYGSGNAPSRKRDLINALQKAIQR
GVVVIITSQCYKGRVRRADYETSLGTSGAIIGCDMTTEAAVTKLAYLLGK
GYPRETVRQLMLDSLRGELTVEEAKAQL

>homoaconitase Contig12386 (likely incomplete ... lacks ESTs ... largely Genscan inference)
MKRFFGFLRCLHLRQCPRIRLGARRYSVPGLQLPHFRSRLAATTESRREDCTKICCTLPP
LVLCIQRMGNSFHSLIASFLFDECKVDAGGREVQSLDFVTIRPRHVMTHDNTSAVIKKFK
SIAASVKDREVRVANPRQPVFTLDHNIQDRSDANLNKYKQIQVRHTTHRPALRLPLVCGV
CGVRADRLRPVRQQCQEFADKYGIDAYPAGRGIGHQVMCEEGYAFPGTMVVASDSHSNMY
GGLGCLGTPIVRTDAAAIWATGATWWQIPPVAKGTALSTTQSINTRRRSSLWCVELRGQL
PEYATGKDIIITLCGLFNKDEVLNHAVEFVGEGVGRLTIDDRLTIANMTTEWGALAVHSF
MSDLLTPPPNSDLNRIGVRRERVGSGPQRVLRQGARAGPLHGPPARFWVMHSVDDMERRG
IKVSKAYIVSCTNSRVQDLSAAANVLRAVIPPPQYEQGKKVAEGVELYIAAASSEVESDS
AKRGDWQALIDAGAIPLPPGCGPCIGLGAGLLKAGEVGISATNRNFKGRMGSREADVYLA
SPEVVAASALAGIIKAPGGPGANGLTAQGSVKVNSKDTQDSGEGETVAILPGFVEKLEGE
LVFCHQDNINTDGIYPGKYTYNEDISPQQQAEVSMENYDPAFTKKARKGDLLVSGYNFGT
GSSREQAATCLKHYGISLVLAGSFSETYKRNAFNNGYLVIEVPELVDYLKQKAASDKGTN
ELTQRTGLKAVLDFKSSVLSVDGRKFAFPPVGAVAQEIVLAGGLEQWVEKKL

>EF-hand domain-containing protein Contig14219 (incomplete - confused here ... may be
continuous with 8180)
FRCRAKRPAPRSRPTRFVRSSGSQASIGGASACFLRDIPFSGIYFPAYAKLKQSFRDEEG
RLSNTNLLLAGSLAGVAAASTTTPADVIKTRLQVEARLGEARYNGILDCFVQVLKSEGPT
AFFKGVVPRVFRSSPQFGITLLSYEFLQDMFHPEDIVVSAPTNAPVAQDDIKPAPSVIHL
SVAAAAKEEVEVK

>cytochrome oxidase assembly factor Pet100 Contig4380 (complete)
MDRFRSFVRRGLSLETFKFTLYLAIPAGITVALLYPGQVNRLVSHFPFVVYPPEDPTIRE
ANDRFRQQQLEALERQSREAEQKAKQQQ

>adrenoleukodystrophy related protein Contig19669 (mostly complete, with internal gaps)
MCRCESASAFRPLRERRVGIFTRTPMSSTPISVEALTRLLRENVTKRHLVSGLGILASVG
AGVYLTRKRVNQMEAEKEHRAQQDALEEATTGVVVKAKPQFNRQQFYKRLGRLLRIVLPS
IYSKEAGILGMHTFFLFTRTLLSIYVAYIDGQIVRSIVGRSPFAFMWLLAKWLALSVPAV
YTNSMIKYLEDKLAIAFRTRMSDHLYQKYMESETYYRVGNLDSRLTNADQCLTEDVSKFS
SHLASLYSQLSKPMFDVVLMVVQLWVLITRQAGFMSGLPPLAGGVMCVWLTSKLLRRMSP
PFGALVAKQAALEGQLRFVHSRLITNAEEIAFYRGHKIEHGVIARSYYALVKHMNLIFQQ
RVFYTMLEGFLMKYVWSAIGMNIIAFPTFLADYKQQKIEKATGTVEGLSSMGDRTQNYIV
ARKLLLDSADAVERIMLAQKQISELDGYVTRVTDMLDVFEDMHDGKFVKTMINNVDDDDD
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GAKAKRIKGEPDGEDSDEDDAEEESTTVKEKRIRHHDNGPAEPLDLTKPQGVVQEADYIQ
FDKVPIVSPNGDVLVESLSFEVTPGRHLLITGPNGCGKSSLFRILGGLWPVYRGSVVKPS
ISDMFYIPQRPYLAIGSLRDQVIYPHTVQDMHSANITDKDLDDIMEWVNLTKVVVREGGW
DAVSDWKDVLSGGEKQRVAMARLFYHRPKYAILDECTSAVSYHNYLLQFDGEGGWQFLPL
NATARMGLKEEKMRLEAQLQGMPTMHKRLRELCNLLGEDSIALQQE

>hypothetical protein Contig2052 (complete)
MRLPPFTNIVYVGLAGSVVGGFVGMYFAEQFMREAREREDAKLWAEIEQDRKRAAAQRAA
ATNPTRSLPSEQQ

>hypothetical protein Contig13920 (and 15712, 1671, 27102) (likely complete)
MMPGGDDPYGGGERWAPPEFPRLRWAMGIVGGLTLAAFVYHSLTAASRYRHQQAQKERET
RFMGFLHHEEANKRLVNGDLAGAVKHYSKAARFALRGEPGDDVAAAAAAAAGVDPAFIVP
DFDAPGAEGWALSLLQRAAAHWSTGDANSCARDCLAVLRVLPRQAASPVDESETISPPTP
EASEASEAQPEAGAGVAAVMTEAGPPEQGGEEEKVSKEEEEKRALEKEARMRKDRLERIT
ARATELLGRALAASGQPLAALLALQRCTQARSKRREAALVQFQHLKESLQNALAAENGQS
HWPVKVVVGHEGGARGVLVATEEIAEGGEILVEEPFLAAPWSAQDLVQKVYCVHCLRRLA
QPDVDGAPNKGIASAPVVAEARSGYCSSVCEAAAWLLHDHRPSSRPAQPAGPSSDQTGAE
ERTSLYLLAKRVLACLAYGEREPMLQPLWTTFDAAIRSLPTSEAEAKGVGHEHAELQAFV
ESLRNDVAQQSEQQAGPSTSETGWDASSLVSQLRGGALPVMEQQQQTEGCRGVGLYLLGS
HVGRSSPTAEPNARVVFSDADSTLRLVALRPIPANEAVVISSSASSPALASSA

>mitochondrial carrier domain protein Contig25783 (and  (likely complete)
MTRTAAAGSGAGGADASPRPFSDSLMTTLDMISPAFSVLALPLLMAYSNGWNAWVRAVNR
PPAPPSVSAWDRVVGSPVKTWKEEAWRTSRNWTRFGLLMATDLLEICAVNYAGALLGVSV
DTFHMTPAQLQLRDPESDISLTSALWGFTGAAVIGFPLSILGWQLHTDTWRGWGSLLPTS
ALGRQHWLALPAKIVDVVVFNVLFVRLVEAVRGKVGIVPQPLGWLTSDAENNREDPALYD
EEREERSTARVILDRARLFAISSAAGSACSLVLVGLQVPAIIVWNRMLAEPGRFASVVAC
VRHIWASEGLAGFYRDLPLFALNLINIA

>pentatricopeptide repeat protein ContigE80POFO01DIPB7 (likely complete ... largely from PGPs)
MKGSATGRLRVAGAILRNRCAAAGATMPADRPAALLLSPLHPTVRGHAAFFPRSSSSLIF
PSRHNILRCRAMATTATTTTHPAAEREAKAEGGGAKLPSTTASTRIVPALELNLRALEDR
LSRREPLDVKSVTAFFRSCGRQPDHYALAQRALALLGGVRWTTGTDLNLLMRAISLLPAH
PDAVPAGYVLLEAAERKGVVPSVHAFTSLVNVCAKSNNIPEAFHAVERMWKLKVVPDVNI
FTSLIQLCTRCKDVNRAFEVLELMRLFDVRPDAFVYTSLINAGAKAPLPSPRAGEPERAL
AVMEMMKTDGVKPSAITYNALISALASKENRDVEALVRLVDEMKSQGLTPSVVTYNTLIL
ACRGPSAHRGGGHDDGDDREEDEAEEERRLERALGLLHDMKREGLTPDVITLHSLVRVAI
HDDEGDAGNRTRRRRQKNAEDEDAGAGGGGDARRQRGEAAARQVDRALALIDRLTADFPG
LTPNAHLYNGLIALCQLGGRADKATALYRRMREAGLQPTIDTFRSLLSSLDHHNDDQAEA
QTAAAKQAMELLEEMKRDGPAPTPAIYGKVIEVVVRGRGRGGWDEACGLVREMEARGLLV
SAKVYNVLLGESVRAGDAQRAQEVLREMRRKDVPGDYKTSLLRKEAERLH

>Glutathione S-transferase-related protein ContigE80POFO01BKS5Q (incomplete ... largely from
PGP)
TPSEPQRALPFTAADIRFLPENKNDLNIVLYQYSYQPSSAQVRSYLDLRKLKYKAVEVNP
LTKNHLPCPPDQRKAKQIPLVHINNREISVAVHTILFLELYLNRNNPFQPSREESARVAD
LMYHIDQNLMQLVQADRYATLRSASRTLRPLRQASNLSVWERVSAPPMAALSLWWQWRHA
RRLLRGVYGDDLRLALVRELDAYCDLLGDREFFNGAEPGLVDVHLFGVLRSVADEATGHY
ALAHAHPRLPAWYQRMQRLTAHDDDQPTTTTTTTKS

>hypothetical protein Contig11068 (uncertain of N-terminus)
MGQMTSRGFRATPSTNNDIREALNAAFSFRPTPQSLEASTLLAKNNEVPAEIDFDLHLPL
LKSALSQHKKADVIRLMQDLARANAPARAFILQRVERYTKQMEEQMTQAQQKAASSSNAA
KISANAKNIDVQQPPSDKEAKEGSPAPSDKMSLQEAVLHGQLSARELEGVLRDLHRDITL
SPADEQQIKDEARALWEAGTAAVLAVDQSLPKHFTAMVIDAFPWADLLLADDVTKLVIES
PVSKAAARIRATEVLARQENIKKNMSWISRLILPSIAPSKIKKGQTPHVYDAALDAYIHN
DFDKLLSTPSGEKLTEATFRHVVQKFEDAPENIARTIAATLHDTFVGHFIARTMASGIDY
YSPKSFAKKLLTPMKPLNPYFAQRKRELDSTASASASASASA
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>tolA-related protein Contig10886 (and 11557) (incomplete)
TDDCTHSLSRALHRLEEAWVLRVRLQFKRATETLKRWTANSLYFVQGFAKKAAQASKEVA
AEIKAKESTKASGADHMKRGADLFETKPASGAGTAGTNWKPSFAEGLGGAGAKIPGYSLG
LLKNAITSVGGVILPRLEHAKDWLGCRRWYVALPFRVRCCVRAACVPLCYVELYVHCLMN
H

>phosphatidylcholine transfer protein Contig21519 (complete)
MEEVETFEPCSDEHVKEILALDASAHSDWSAISAVTDEEGNTIEVFRQRMDTGLDKLKAL
VTTVHITADVVHEVLYNIETRVNWDHGGKDMQVVEKIDDELDVIYFWAKAPPTFTNREFL
QSRLTRTLDDGTRVIIYRSVKHDKFPEKPKKFVRAYTKLSGYVIKPNPSGEGCRVTFLSQ
NDIKASIPSWVVNLLASFFMKKWLNTLRDACNNQLKENAKAKE

>mrpl27 Contig6392 (23699) (complete)
MQRMSSGAVGLRTSNVSSMGNGMMARTWGIAVGGSSSSTAATRMVGPSTWGDVWRRGATK
KTGGSSKNGRTSRPKYLGPKRGDGEEVKAGEILLRQRGTRIHPGPGVERGRDHTLYATTP
GVVSYTTSHYPVPDRRLLCVVPLSLALPRRIAVLRARPSQL

>calcium-binding EF hand family protein (Mdm38) Contig14024 (and 8425, 8848, 4882 .. also
Genscan) (incomplete)
MQRIRAATKGPVVGRAFAGPSGSLLGAPGAFGSFSTALVVRRSTTGCTASSSSSLRLRRL
HSPILPTALPSPPLVHLRHGGPCNYSLVSSPSSLSRLRCGELQPPGNVRSYTTPTTTTTP
TIGSSSPAVAAADTAPPSTPTATTATPQKVGLGQKVMDTLRHFWAGSRLLAANVKAASML
LRKKIAGQNLTRRERRLLTQTTVDLFRLVPFLAIVVIPFAELLLPVLLAVFPNMLPSTFE
DKIKKEEARRKAVQLKLEMAKFLEDALYLRSLQISHDTPSAATFAEAMKKVKEGQSLETK
EILGLSKLFEDKFTLEMLDRQQVVAMCKYMGLSRFGTTHYLRNQLRSKLHDIREDDDLIA
QEAALDKFTEAEMKQATQVRGMDYKDFNTAKAQMEQWLLLSAQHVPPSLLILSRAFALTS
AYSSLKPLEGQQVVTKKAETGEIALPKAMEEALHKTISALPDQLVADTKLTSATKTTQDM
VSKLEVLQEQIQAIKTEEKEKKEKEREEKAKAPATEAEAKQATKKDAAGAYSAEQMKVVS
EAVSLLFASAPSKIKREREALEQLKERKEERKEEREEELSAASASTDQPQHQPQPPPQDK
VVHTLETKLEKMIAKLDKEMDKIDQRAHTLMSIIDTNQDGQISFEEFQEAVSHLKAKYSP
EDITTMWRKLDTNNDGQVSLEQLEQLYSAGADEHHER

>Hsp20 Contig9184 (complete)
MQRTTSRTAAPAIRQRLLSSAATATRPSSALTAGTTQTMTSSSSSSSSSARGLSVHLRPR
HSHHHESFFDAFARDPFFRPLINELASTAKQVGRPAVPKEGPRPRPLHANVNVLETQQGF
AIEAEMPGIRREDIRVEVCEGDRLVIRGEKRFEGHTANNTNTNTNTNVRGELKEAKEAAE
PQQRYLTFERSYGTFERTFALPENVDASRIKASYTDGVLKVELPKAAKETPKSWTVEIN

>pentatricopeptide repeat protein Contig21159 (incomplete)
AALGTAGRVDDAERHFAQMAQLGVVPNAHCFSALIAALGTAGRVDDAERHFAQMAQLGVV
PDTHCFNALISGFAEAGRVDEAERWFAKITTVGRLKPDLISYNALIKANEVAARPERALK
LLQEMAHKGVRPDVVSYNTVISSLAKARRG

>hypothetical protein Contig20823 (complete)
MQNAAGAGRRAFGPRWFAKLGLISFAAGGLLEFAMIKSGFYEAVVATSSAPDWQNSWQEV
GAEVQRQLREKRERGDIPEPTRVERVLQQLEARYQQQLNQDQPPSAPSSSTSTSTQEQKE
SETIKWSSRRRE

>hypothetical protein Contig1298 (likely complete ... N-terminus from GenScan inference)
MQARPQRSGVRPNSPPQPPRPGPSQAVINGAALEDRVARILKRLGKWNVRRNIIMRDRYG
NTSEIDLSYGLFFRRYVECKNMPRIDLEHVAKFKEVLNLNKISPSRGLFVTTGYYGPRAI
TIGIKTINGSELRTWEERAMWVARLRRLVWAGCAVGAGWLAYTTYGPMHRWKDVDRALAR
FETDARRQVDKWKRTAREYWPW

>hypothetical protein Contig16682 (incomplete)
IGQGAVRCVAAPSALLNRGVVVLRCCGASVDGFPTAPSLETRKSEDEGGRGQAAQIPGFT
SVVGLRLVRDGWLAPGSLRHSLGLGRRLLPFIALLFLFIFVLAGIGPLPLLRTARRLLLF
LSLLLVAARRRGAEAQLGFDQFEDVEQCGQVGSVLGRPEGVQLRKEQHLVLFFFFMLPLH
HFKRPLARLPAG
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>calcium-binding mitochondrial substrate carrier Contig3356 (likely complete ... largely from
PGP)
MSATATTNTTATEAATIDNGGVMSKVREVFAKLDANGDGHLTRDELHDGLKLLKLPATEA
DVDALLARLDIDKDGNVSLLEFEAFAMAQSKLLRKVFDDLDADKSGTIDVEEVRGSLRRL
GMKYDDGAVTKLIKRIDVDGNGKIDFNEWQTFLLLVPSATVDAIFRYWEDAMMAFDSEDG
VILPPAHKPKTLMDSVAFLSSGAIAAMTSRTATAPLERIRTIYQVQSTKPSIDAISRQIY
AESGVSGFWRGNGANLLKVAPEKAIKFWTYETIKATFGKKDADISPHERFIAGAGAGVFT
HTLSFPLEVIKTRLAAAPNGTYTGITDVVRKIVTKEGPMAFFRGLTPSLLSTAPHSGIDL
TVYEVLKREYTKRNEGKSPGVITLLGCASASSVAGLLACYPLHVAKTRMIMQSMHGAPQI
YSGVWNVFTQTYSKEGFVGLYRGLVPSILKSVPSHCITFVTYEFLKKQFGVEKHSKH

>hypothetical firmicute protein Contig8036 (and 22740,27100,9128) (incomplete N-terminus)
PLQTVWFNILGLLDREGYGQSLETALRELGQLFTADPDSVREFLALKDEEALTKFLKFIG
CTAFELSKKKRVEQDLKNLDAVLACVRTIIATEEGKQAVADVKDALYDVYHATFYSPAAT
QAVAFAILRDMLHHSEKAYKEIVESMEDLMYNPIKEEFLLAQLFERLANTDSVPLLTAAV
SFVDALLKSPHAGEYSAMFRHHFEERGVQEKLQTISGQHSEVQAPIDSLVADLSEGDKAE
PSFHTTPHDTMSNYSHMFKSRIRFFSRVLGCLYTVLPGVLPAKMKPISDEVRMASIMRMK
NLRDSKRTGSFTPEEVQSMNREMSALTLGVEPAFFDDMMKRGMFSETRRFVDQAEAIENW
NHEELLQAGRNVWTCFGLQMIIYNEEVRLQDAYVGYSLLYPYTDNYLDDETIPKETKLTF
QNLFTQRIAGQDVKARSALEQKIWDMVSLVENVYDRTKFPDAFNSMISINEAQTRSLAQH
SKISLSEETLTDITMEKGGTSVIADGYLVHGVMTEEEALFAFGFGVCLQLVDDLQDTLKD
TEVNHQTLFTYGWTRKQSADVKAYKAFQLLYLFIDPDHYDIDEKGSDLRGALLKMTHTIM
LKAIAKYCYIFTEAFVEALAQFAPIPIQHLQRVNNMARMLQMVRNNQI

>lysophosphatidylcholine acyltransferase Contig25144 (and 10930, 23399,25223) (likely complete
... largely from PGP)
MRGLAKGLRHAASAPFTRLAPTGFTASGISSGPTANGYRRGAVLPICWREALVGRGHLLR
PLGQAALQRSGATRTPQRRIRLRLRHRAREGPSFGERLVYIAAVASFFVVPAVVWYRHGD
EIRAQLSSHKNAPAASSSAAGFDAASDQQDQHQQAQEQGLVSAADPSPAAVDGQQQQPEA
TSTVNPFIYDSPLTLYEKVKLTFGALVLLPIRVTLLVPALFLTYLLAKLSVVGLPRPVCE
RIVDGRTEVVVDNNAAGPIPAWRRVVFLNPCRLLVRYIMFLMGFHSISIKGTPASKREAP
IVVANHVSFVDPFYLFIAYLPAFVAKKDVENLPVVGTVALALQCLLVDRRSTTSRKDTLD
LICRRAGAVGHGSAAVEQKEQDGPATQPPEDEQHHHHHYWQQLLAHNSVALGFSRFLTYL
SALPKVAYQRQFGEDDYAQVVIFPEGTTTNGKALITFHQGAFVPGVPLQPVLIKYPHRHF
DPSFPVGISLARLMLSLLCQITNHLEIEFLDVYRPSDQEQKDPALYAHNVRNLMAEKLGV
EVTEYTYEDALLMVEALALNMKPDRVNIPVQRVKKLYQEMTLKDLKQLLWRFRHIDRDGD
GLISYAEFAHSLRLPEDSAYTRDLFSLLDTDETGAIDFRKFVVGMSSLNRKVNKQQIIEL
AFTAFDKEGRGFIEREQLRGLLHEVFPTIGEDQLDALFNAADADKDGLISREDFVRLAEE
QPGYVGIMENATRNHHRIARDATASAIQ

>hypothetical protein Contig22432 (uncertain of completeness .. mostly Genscan inference)
MSPPVRRFLIMGSIVVGILHCRLLMSPSTDRDTAHARHTHGTRGTHDTRHTRTTRHDTHG
TLRDISVYLTVGTTPAVGAANAWYRSSKKADAPSEASKPAAAITPSGTAPPLTQTHHSVV
ATFLISIVCVDLNIVLYQYSYQPSSAQVRSYLDLRKLKYKAVEVNPLTKNHLPCPPDQRK
AKQIPLVHINNVALCSHDIHATHTQHTTLDTTHDHTRHTTQREISVAVHTILFLELYLNR
NNPFQPSREESARVYTTLLSLFYFVYYLLYYVINNNNINKNTLTCYARVRADLMYHIDQN
LMQLVQADRYATLRSASRTLRPLRQASNLSVWERVSAPPMAALSLWWQWRHARRLLRGVY
GDDLRLALVRELDAYCDLLGDREFFNGAEPGLVDVHLFGVLRSVADEATGHYALAHAHPR
LPAWYQRMQRLTAHDDDQPTTTTTTTKS

>hypothetical protein Contig2224 (likely complete)
MLQGSPNCHELRRVRNGGAGHPHHRQGVRRQDLPGLLVRPRVPLRRPPVRALYRERTAKA
RHRRRRGAGCRAARPGRRRPVGGAGGHARVGQEHDGLGPRRGPGLEVHRHRRRV

>hypothetical protein Contig23045 (and 4890, 4949) (likely complete)
MHARQKLLVCRSTPPRQGKATVTAWVPWSPVPLPHSSLPPRCAARFLVITSCAVDSSSAS
SASPSAHIVAESGNGSNKGRSSSSSSSSSKEPEQPEHHFPSRHVELKQTINELSRKKYVL
PRHMARVVQYMEKHRSVFLEARVVSRVRLLLQRLTAGEVGDYNVVMNALAEMGLREDCFN
VFARMRNNLIKPDTETLNCLVLASVRDGRTQDIDDVVAHFKKTFNVKPNARTFAHRISEF
DKKKEGRRGSSGSAGGRKEEVKQAIQLLEAMKLEKPPIRPNLEVINSLIAVCVRHEHMGG
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AEQEERALQAFEDVKANHPDVALDAAIYGKVLDVLAGKWKEEDDYQIDDLWMANATRDGR
EGEVDEDWDREWTDEWEGAGNVEQMALFEEQEAERRREEMRKKEEDRLRREAEEREREER
EEEERKQKEREEEREMSEMEKQRRREANAQYVDKAFALLEDMSRGRNIDPDYATFFKLMSL
CLKRDNTTRALQVFDLFKREAERHKQHRDEAQWTGMEMQSVAKLLALKFVRGCEKNRDMQ
ALETFLTKHPHYIVPGDIYSAVVKAIANAYVPPLRKPTETDEERGWIDSLESGDHPSTRD
GGGVAEKGENKRQQQGEKGDWLYTQAWALFHEMPRHGIARSKDVYDAMIELACKRASIKR
ALALFREMQHEAEREQRESGKTTLKPGLRTYRSLIVHCLNNNYFNKEEEYNYRNDINHPL
TQRAFQLFEEMEDARIKPDLKVINAMLGCCARVEDKANGLKLLGLLVRSNLVADDQTLKF
KDRIQKL

>mitochondrial carrier protein Contig15750 (complete)
MASTKQDDDASMGKGPGEGLPSSSSSAPSLPPIPTPSMPTSSVEDEGKQKNEVAGALAGV
GRTLSRVLTRAVLGVGRGSIAGTLSGMAEETAGYPLDLVKTRMQAHGDHPTGAMGILRET
LQKEGVRGLFKGLGPPFLASSITTATIFGSYAHAVDFLHERYGSRGEVRLAHVALAGAVA
GFAQAFILCPVDVIKNRMQVGGFGHGGAAGPGNMEMVREVIATRGWRGLYLGMVPTLWRD
VPGYAVFFASYEFLKRSFAALPFLRAAPGAAEGADDDPHGAGGLSPVAVILAGGVAGMAY
HTATYPFDVVKTRIQIQSGSTPTYKSTLDCFRILYRQGGAGALFKGYVPTVLRSFPANAV
GFLVYELTLRFLP

>potassium channel tetramerization domain protein Contig6018 (incomplete N-terminus)
EFFGRACTRRCWSAAPCRGFLPLLWKAAVAFPVAIKTIDVALKGGQFYANWAKSRQVLQT
DWVTLNIGGALFKTTKKTLLADSSSLFYDILGEKNPAKEDVLKAMKGKPGITSTFIFTRT
KLKNGKERKTLRLIDHQVERAEMEKQKNILTLKSLSWKVEKKDGLITVNLDRDPHYFKPV
LNFLRYGNLFADAGIDLKGILEEAKFFQVDTLVKMLHKRGVWDEDNKYFKEGKEVTDAMP
GVHAEADTTKP

>hypothetical protein Contig6195 (likely complete)
MSLKFEPSEAQMESCRQQFLQEGGKALAKWGGAATLFTSAMSLWPAYRNLFNWRGQIFCV
MGAGIAGFWIRGEQAVLRCHHARDAQRLKDIYEGRTMG

>pentatricopeptide repeat protein ContigE9BS9UA01C30F3 (incomplete ... largely from PGPs)
MGLDHYHLCLRFHRRSPEHARHLLEDLLRDGVRPTAATFDMVVDIYGVGRPRAHWLSEAV
QLFHRFIGMGVEGIANLSAFRRLIQFCHRAGDINQCGDAERVKKLWTMITLAGIEPNTRL
VNSFIANCNSPERALIAFNKMAEADLQPDVHTFAALTTTLARAGHVEDLRRVYHLMRSLG
LGSPAIYTTLLWAHVGGSSANVWEAGRMWSDLVGSGLPITPSALSAMAHVHCSHSGARAA
LDFLATVRKGEGEGRGMAGSQDLYEELLGASASIEEAREVLHEMRALGYAPSSTTPFRRL
AARLPSRLPVSERTQVLDLMQESGVGGDGEVYRWLILHGHPDDGMGLLNRMLHEGLQPDV
RVYNALLLKTDGDEPKSAASSPPSRKSMHNIWHHGGRARAEALFRSMREGTVSTDRTYAY
NPKLNAESFMILLRKCRRHREPDMAIARLRHPPHRVECRHIPRESGMYGLLLASLQPSVV
SPASEAEAERYREHLGRVVAQMEADGVPLAGPHAASALVDSFVRHRGPPAAPASQSGTGG
GKGSLFAELQERLGPNSRYLKTSLMHMVEEGEVDLAAWSALVAGYVRNGRVEEALGVLYG
MLEQHGQVPPVSLLGQVGRALEQDGRLVQPGALRPLFTGTFADIRRQVFRVARHRRLDRD
AAFRQLAFNRFLYFHLTLLARRRRDGGPPSSPSAAARAPPPSFLPSLLSRIGIAGSGRGS
STATTGGGGGVERERRQERVDAQRTQLILGRMEDEDVYVSVPLQRLMASFISSSSPLGGP
EGRF

>mitochondrial 18 kDa protein Contig24116 (complete)
MDDPKATELDVLRDTWARYLGYANEVGEACRGVLPLSLVHASYGLVGLYVLADAIHKGRR
ASHRKHGSVAERRFDIVDNVADTLLWQTLASLLVPPLLINRTCKLTAFGLGKYFPPAAYP
SLTPRRRALVQTAVGLAVIPFIVHPIDHGVHFALDHTSRVLSGIIRRKYFPVPSSSSPPL
QTPQGSDNQQQHE

>D-amino acid dehydrogenase small subunit Contig7014 (and 17560, 3653, 13183,4451) (likely
complete ... some from genome)
MKAWSRGVAGARAKGATNSTTRPACWHHDATASALGLPLCRSSGVASPLPLHYSRPSTTP
SSAVPRGRQSLPIPTGRRAFHHHTHHEGAAAKGPTVTKLVAGAGLLGALIGGTAAVALYA
GDGGVLAAQQQLQTRPIASAAVASGPHKQPSPRPDGGGTGQVGLASAVAAEKEDRSGVVV
EGRGRGGKERVAVLGAGVVGLATAYYLARTGRYEVVVIERQPGPASGVVVEGRGRGGKER
VAVLGAGVVGLATAYYLARTGRYEVVVIERQPGPAMETSFANGGQNCVSDFMPMTDGTLP
RRVLAQQLLRLRFNMLSALENRPPPYYLVRLKALFDPLVAWSLWLLLRRSSDEAAVNSGR
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GILHLALSSQQCLQQIREEEQLQYDRGSPAGILHLYRSDDQFEEAKREVEMLQRTFGTKV
KPCAVWDADQCRTREPALRDSRASIVGGIWWEDNESGDCNMFTARLADTCRSKYGVTFLF
DTGVSLLMRDPANPHRVRALLTDEGREVEVDRVVVCLGSYTPLLLRRSLDVWLPIFPVKG
YSLTLRPDDAPLTSGGGHDAAPSLNIADIESKTYIARFGGILGDRLRVVGMGELCGYDQN
VDPAKEGVTNLTAVVGQLFPRLPSSASREASLWACLRPMTPDSLPIIGPVGRMENVYVNS
GHGSMGWTLACGSGKLTAALVAGTPTDLDPTPYAQARFS

>transmembrane protein Contig9597 (and 9953, 5105) (complete)
MEELSSRYPAKYDVQLMALADFFESKFGKASLGPAKLLDEKSFARKLEIPYAYLDDAVAE
ALQTWLATVPPTVMAEFTQFLLNEVFSAEKNHKTSGIGLRMLLAAIARGFPDVVRGAVDH
ASFVQKYLGDSPATYPKHEPNVLSEDTALLRANFVPVLVWYFGQTIEDHPALAFDLWAEF
LLPFLLISAPETIRTLVLDYFHLLFTDVGGKVKRADPVVTARALERLAAYRENVSENQLK
KGAINPIYLAIENAIVWRNSSSVHNYLNVYLRRAASANKHVRDEAQKKVLRALAVDKESY
QTWDSLYPRYVIQSTQVILFLTDKWDKYVLTQDKGTIQASDVAETVHNFLYTNEKLAESH
YRLTTRVKKGAKAKKEAKADQADVEASTAACRELLRRTGAKVSATASSRPTSRSRAQHAA
AASSRASSASSSSSGFLGTLVYLLLFVALVAAIAVLYLRQTQPETYEELLRTGLAYYREG
QAHATVLTAQASAKAQDLLAQAYELKAKYMAQAQPLLAQASAKAQELLAQAHELKAKYMP
ATASPAAAVAGKA

>conserved hypothetical protein Contig1150 (complete)
MRRSSSAFTSWGGGAIRSAASSSFSSATLASSSGSRFISSTSSPSSLSTLLKAQRSSASP
SSSLLNRSLATRPSMGGRLPFASAEANPSAARTGSIYGSVNATSLLAPLSVAATRVAGLA
TSSSKVESEEADEPSSRSRPSATASPPPDAQAALPSSAEAEAKPKLGKIRTFLKKYGAVG
VVTYFGLYGATLASFYGAYSSGLLFAGDVVGLIEFLHLGDFFDESLLTPKVGNFALAWVS
TKFTEPLRFAITLGITPSISRWWTGHHQHKLEAKREREEQQQKKEEEEENANSSTKH

>hypothetical protein Contig11808 (complete)
MLRASTIARCPQGKSGGRGLFWKKPSWNATRKANFKERARQVESVEYFLRKHNNNDHHKG
MPKRKLYEEYTADELPWYDRSLKVQRPEIGEGFHLPTSRALRHQLRPKYSPDLFLSEPKE
SD

>CIII Qcr9 Contig9630 (complete)
MNALKSSGASNWVYQNLFKRNSSYFALILVGAVVVESGVSRTVDFWWNSVNKGRTWNDFK
RTQLPKIQAKKAAAAEEEESDE

>putative NADH dehydrogenase B14.5b subunit Contig7901 (complete)
MATVCVLSGAALGLSSTLYANAIRKTYLLRAPWRHLGGIVGGGLLGYYYHKLDQHEDAKM
AALGKKYREMYGALDNPLLVQPPYLRTSSESKESSSDE

>DNAj protein Contig13849 (complete)
MRATKTASHVAAAKSIVHNQGANRSLASSLRSLNGSSSSSIIFTHSSCSNHTHCGIRNHS
TVSSFTAGNKTAASSTPLSFIVSWKQASLRQFHATSSTRKEEDLYETLGVPRTASADEIK
RQYYKLAMQYHPDRNKGDKKAEEKLQKINAAYTVLKDEDKRRQYDQFGSAAFDGSGGGGF
EGFDPNDIPVDMRDIFEGIFSGFGGGGGRRAKTKGDDVEVPLRINFHEAVNGCEKDISYM
GKLPCPTCHGSGAAAGSKAKKCPRCNGQGIEQIAHGFIPIATQCRQCGGEGTIISDPCGT
CKGQGIISGNRKIQVKIPAGVDDGANIRLVGQGDAGMKGGKPGNLFLRVHVSPDKVFKRD
GVNVHTDIPVTLAQAVLGGTVKVPTLSGAEVEIKVPPGTQPEEKRVLRNQGVSAVGQPGT
KGHHYIHFKVEIPTKLTPKQKELMEEWQKEEEQSGGIADKLKGYFKS

>hypothetical protein, likely ASHI NADH dehydrogenase subunit Contig18207 (complete)
MWKQSSRVAVVARSRAVVPSSSGLRRSAGALLPRRAGAETEPEWKLYEEGDPNLFDNWKG
KAPGALAEQVDIDPNDWHAMTPDYDTSVSIQHALISLGTAFGVLAGFYYFCKAIAPEPAL
IPRNDWRTVPPSIVNDQPGTPYTPRPQ

>aspartyl-tRNA synthetase Contig12808 (and 23127,16011) (likely complete)
MKARLGSTGVLRAGRTGRAASSAAVPARHAAGRASAPVREGISSSNSRPG
AIISGLRWGRPSSTWSPSSAAPQWPQLRSFSTSSSPAPKKAGLGSTTPAL
DRTHHCGRVCGRVTAADAGTSVRLCGWLTASRDFGGVLFLVVKDHTGPVQ
VLVDEKRLTPGLREQVASWRIESVVTVTGKVQLRPASMQNKDMPTGEIEI
VCEDIALLNPTSHTSLPFPSWSSPLHGDERDALPPEELRLRYRFLDIRRP
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YIQDNLRLRSQLSLAARNYLHGQGFSEIETPTLFRSTPEGAREFIVPTRT
RGKFYSLPQSPQQYKQLLMVGGIDRYFQFARCYRDEGIRFDRQPEFTQID
MEMAFVGDRDVCNLTEGLVRTMWKTAGHTLPDPFPRMSFRHAMETYGSDK
PDTRYDLLLRDVTDILQQSRVNVLTAPLTAGASTDAAAHKKGPGRCIKAI
NVRGMADLSREDSDGIQKRARDLGGKGVVEIRCGPEGKWRSPIEKHLTDG
ERRRLGDALEAQEGDLLLLCSGPERDDVSLILGGIRSHCAKLMKRRGKLS
IPDDQYNFLWVEEFPLFSFESASPGEAKRIVTTHHPFTAPHPDDIDLLMS
SDAEHDLLRVRGLHYDCVVNGVELGGGSIRVHNEAMQRHIFRVLGMSDNV
MTRFQHLLDALGMGCPPHGGLAIGFDRLMAILCHAESLREVIAFPKTATG
NELMTGAPSEPGLDELKEYHISVAAAPPS


>putative Complex III Qcr10 Contig26093 (complete)
MSIHKLDKTHATVNLEEAATRTGTIRSVPYHETIAYQRFYANVFTKATVFGKRLIPLTKN
YAPTAFRWGALAGLAAAYVIEPSFLTKYFTKSESK

>Adenosylcobalamin-dependent ribonucleoside-triphosphate reductase Contig337 (and 12090)
(likely complete)
MLRCSSAGAPGSVCLPGAASHTPRACFSRFVGGYVHSSRKASLLGGQDRLVMLISSTSPA
PSLRAHYSATAAPAVAKPAAATTKEQEELLEMDIHTFDQRASAPFRLSSKFVSKFKDKQP
PFGFNGLGEFVYRRTYSRLKKDGSKEEWHETVERVVNGTYNMQKKWIETHQLGWNPWKAQ
KSAQEMYTRIYEMKFLPPGRGLWAMGSNITEERGLYAALNNCAFVSTEAMREDASKPFVF
LMDASMLGVGVGFDTKGAGSMVVKGSRRDRTPELVKIPDSREGWVESVRLLLDSYFHGNP
CPEFDYSLIRKAGEPIKGFGGVSSGPESLKELHHTLREVLDKQVGEPISVTTIVDIMNLI
GRCVVSGNVRRSAEIAFGDPHLEEYLDLKNYGVNPQRAAYGWTSNNSVLAHIGMDYDDIC
KRIAINGEPGIAWLDNMQAFSRMNGVVDNRDSRARGGNPCLEQTLEPYELCCLVETFPGK
HESLEDFKRTLKFAYLYGKTVTLGKTHWPETNRVMLRNRRIGCSMSGIAQFISDRGLENL
RVWCEEGYNTIRHYDDLYSDWLAIPQVHQGHQHQAQRHVSLLAGATPGMHYPISSQYIRR
VRLSSNSDLLPALKEAGLKVEPAVGSESNTAVVEFPVSVGKGIRKANELSMWEQLALASF
LQRHWADNQVSCTVTFDPETEASQLKHALDYYQYQLKGISFLPRSTGVYPQMPYEEIDEA
TYQEMLAHFKQPDFRRSEAPQEAYPEKFCDTDVCTIDEAATPAAAVGAKTDSQ

>hypothetical protein (K+/H+ exchange?) Contig3489 (complete)
MQAATGKGGPRIRLLVVPVLRDRWVFSVPHHAEALASHDTSSPVSGWGPKGLQRKGAELL
GRAKDSFDRLPREGLKGRLKAGVDALNRRLDPSESMLKCLTAAHRTVAPAADEAVTTRGV
ANDEGNQPEGLTEAERELQLEVVYPAKLSGEQVRATLSQLVAARTKRHQNLAYGSTAMLP
VSLAMGLLPGPNVFLAWNVYRLYSHVQALRGGKLFLDLSSRNRISYSPSHELEEIVRTEE
RHEEPLSQAQIEELSATYGLRTLLEDVERLRIVGVAQRQDSGKEPTGK

>hypothetical protein, putative ATP synthase subunit Contig15510 (and E80POFO01B6VDY)
(complete)
MSKRLITRATLNGRLATAWAPSRSYAEAAVPKLGKDIQPKNYRRPDGTYEPCDEILFLSV
IGYGEDLRAVTNAKEGITNTLVLSRYNKTASQ

>putative CoxV Contig13338 (complete)
MASRAAARVTKNRFALPLDHRATRPGFQAPWGSIDPAQEVRQSSVLMGVLGGIFVSWGLF
ALTRRDNVRKLPESVKNKEWATVSEERLAKNRGA

>putative mitochondrial escape protein Contig11227 (and 6282, 9180, 1833,E9BS9UA01AD4KH)
(likely complete)
MFRFSTNRVGCGGAAHHLRLSPLPLSSSSSSLSLSLSGRLLPSSSLFTTSSSVTASTTIR
GLPAKRPLVWGTQSPTATTASSPFGSRSLLVNYSGCRRHNSTTPASSSESGATPPTAPPS
GAGSSAAEAAARKKAEAILQEYTALFRPGPQAPKEEFTARVLGAPFDVAFRGTVGVAVAV
LLILVTFGVAAKISDAWDVYQLARKLLDEDLPPSPKDCFGREEDVRKMESRLGERPEFIY
FVGGSPRSGLSTVVSRVLNDYAGNSYIINLRESSPMTGMEDVTHSLNKSLGFLEILPSFQ
SLKHHFSGWEIKGVLIPATEAQRVEALKSTLEKLTKALKFIRFLSRLKFSRTRENTYPII
AFDHFKEVMNIPESKQTLNVLLKWALYITHEAHLAHVILVSSDPKVAYALTNDELLSGRI
ISVNIDSIAKEPALKYLRKRLARSRYPREITEEEGEKIFSEIGSAFVDLNRVEAHLSSGP
HISVDQALDIMHRTTIAHIVGALGAEGRSWTPTQLWRTIKMLAESETGELDYFQLKTTVF
NGNERVLHELFDAGILLYRVFPFKPNGVQMTPVVTAYTPFVMFCCKQLANDLRLNTIMNR
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QMADEEAAASSLAGRLSSAMMMVS

>NADH dehydrogenase B12 subunit Contig20711 (complete)
MASNPKVSGPFGGPIESWRTHPMLRITHPRDVLPGFGTALGLFAIVCVGEWMWKSAGAPK
LRATGKSAWKDASAAHDDEKVLKSHSH

>Complex III Qcr8 Contig1256 (complete)
MGVRWTTYTLSPFRQKMFPGFWTGLIPRQIKRWKYNFPRVAPPILAGIAIYTWGNWKHDQ
IARSHWY

>acyl carrier protein Contig16222 (complete)
MNRIARPALLRASARAPAFAPVASSLRFSSISSSAALSTTFARRSDAITTFDYQRRHYGA
AAGLSEADARERVIKVVKNFHKVDPNAVNEKSHFINDLGLDSLDTVELVLGLEDEFCIEI
PEEQADKIQTIEDAVSYLVTNPAAK

>Tim13 Contig20011 (complete)
MAQITDQQRADFYRKQEESVGQQLFQQMVQTTKNRCFKTCVTRPGAALSKDEQKCLINCV
DRFFEARAIVMHSYNKVYQSMMQQEGGSDEF

>ATP synthase epsilon subunit Contig9766 (complete)
MSSWRSAGFSYLRYSNTCAILTRRALKEPFRAKAAERDSVNMKVEQWILGKGQDKVDVKR
ANEIAGSAGH

>hypothetical protein Contig10684 (and 4391) (incomplete)
MRRMARPAPARFLLAGPPLPTRGATSLLSAPSARSLSASLASKWPVRASGTRRFFVSSTI
IHRQARDNVVDAEPVQPNPGQSSPPRSELPQQQIDEQFDRVYEKLFNKKRPARGERDSHD
AANPFTQDWRERLFDIMFSNAGNLFMMTVVASLFFQIMREQGEHKEYKRLTTARLDDAQH
ALRVCQAQVHQAADARRQELASALERTNTAVPPEEVKRLVDQLLTSLVADIDASLTTDES
KATTQTEASSDSALVDTNTPATSSTAVATTAEGHQAGYHKVV

>cytochrome c oxidase subunit VIa Contig10747 (complete)
MQRTTPFLRSSAPSLLGRTSSRGFASAAGHGAHGNHAYGYYSAAGFGVVIVAHLIIALQA
HEHEHRHEYSHMHQMRKKFPFRDGTTPLFGLVDEEEHRDLYDTLVGIQTERVPDNYGWLY
DPFADKQ

>hypothetical protein (likely NADH dehydrogenase MWFE subunit) Contig15263 (complete)
MSKAYGLFYSWELLPALTVMGVFLTTVPMGTYAGFKLILGEPKKIAAKAIEYESELRNHN
HGVKKRYYGHSKTASSETH

>3-hydroxyisobutyrate dehydrogenase Contig19441 (likely complete)
MQQSRRFSSLAALSAVRGTTATTSGRISFALRCYSTGDKKPVGFIGLGNMGGFMAQNILK
AGYPLVVFDVNKGAVERLTSQGAKAAATPREVASQVHQLVTMLPSSPHVQEVYTSENGIF
NGIKEGSLLIDASTIEPAVARGVIAKAAEHKVTMVDAPVSGGVGGAEKGTLTFMVGGSQE
EFDRAKPLLSVMGKNIVLCGGAGSGQAVKICNNLVLAISMIGVSEGMNLGVKLGLEPKIL
AGIFNTSSARCWSSDTYNPVPGVMEGVPASRGYTGGFGVDLMAKDVSLAINAAHGVKAPI
PLGAVALQVYNMISTQGGGGKDFSSVFEFFNKGSAPKQ

>hypothetical protein (maybe some brain protein 44 similarity?) Contig12372 (complete)
MATLLRLSPLKPLRHLRNGTPLGAAFDLRATSRLINGPTEFAQVLDDAPHAAEAGHALPS
TAPGALPSLQLTSRTSVGVTRGPRVHVFSRRQFE

>thioesterase family protein Contig6705 (and 9814) (complete)
MNALRRGSGAARAGSRGSGATAAAAVLGRSQVVRMSSTSSAAGGKKEHKARWPLSITREV
NWGELDSFNHVNNVVHFRWFETLRCEQALKLGIDLSPTAGASLILAESNCRYLRPVMWPD
TVTISTRTTAIGETSWTTEFQVESKEQEAVCAVGYSRLVYYDYKEGKKTPIPQDLRDRIN
RLEGTNF

>Pam16 Contig10914 (complete)
MVVRLLLNILGVGSQVFGKAFLDAWRQAGLKAKQTGAGLSLAEAQKILGLRPPYELKEVT
KRYEQLFKSNDPANGGSFYLQSKVYRARERLEQEFKTNAEWQAKGGGTNAE
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>hypothetical protein (DUF543) Contig6530 (likely complete)
MGDRVPSEFLVAKRWDYCSEAILRSTGYGALFGSLSLFLFGKRWMRLVGIGASAGAGFGL
GVSECRASFNRATNYDPDRILVVPHGTKVQADGTPRH

>hypothetical protein Contig4878 (uncertain of completeness)
MQIVKFAIVALLVCFFVAAVCGQGRGGQDYETAAVTDDINEYHYGEIRQAVADHYNQRRR
GGKDIDVDIDIKKLEIEFEKNFFIVIKKDRS

>conserved hypothetical protein Contig3415 (likely complete)
MRNNSITCLLALSFVLAACLGVEGMTSFPANIRVPDGHTFAVSYFAAGFQIYRCNVSTGS
WVLNRPEADLWPSKIGHDLNETRVGYHRFVDGRPTWYTVSAKDYHVTDSRVTAKAEATAP
DAPNIAWVLLKTFSTEGCGPLSRVTYVHRVNTNGGTAPAGACSEGDGEYSSPYTAEYWYW
VATEDAVCGSASVRTSSIFSI

>hypothetical protein, putative ATPf Contig26899 (complete)
MSRSLITRSLPLRSSSHGALGGARPVFSEVPLKEVPSYVRLHVLGNTRRLTKEFVQWYWR
TYFHAGKADPIIHGILLVSGVGYLLHNHWHGSHP

>dihydrolipoamide branched-chain transacylase E2 Contig23284 (complete)
MRRFASASTSRAPASRSIFSRALRTNATRNVPRVECSASLMTGCRGVLAKETIPLSATIS
TARRGFHATRVASSGQTIQFNLADVGEGITECEVLKWHVKEGDRIEEFQPIAELQSDKAN
VEVTSRYTGKITKIHYAVGDLAKVHTPLVDILLDASESAAPAAAAAAPSPSSSSSSSSQS
SPSSSSSSSSGHSGPVLTTPAVRRIAKENSIDLSKVAGTGRDGRVLKEDVLAYLEGSPLA
HQAPPQFALPTAAGAVPPLPPSVTTTTTTEAGGLAHVVARKAVVGADREVEIRGLQRAMV
KTMTAANQIPHFGYSDEIVVDQMVALRDELKPIAEARGVKLSYMPFILKAISLALKSYPV
LNSSVNADVSKIIYKASHNLGVAMDTPQGLIVPNIKDVQVLTIFEIAQELNRLQRLGKEG
RLGKEDLTGGTFTLSNIGVIGGTYAKPVLMPPEVTIGALGKIQKLPRFDERGNVVPTHIM
IASWSADHRVIDGATMANFSNLWKNYLENPKAMLMDMQ

>pyridine nucleotide-disulfide oxidoreductase domain-containing Contig23726 (and 14526, 20458)
(likely complete ... mostly derived from gene predictions)
MRRVLGSVSREQQVVRSGVVATARSVRSYTTAAAASATVSGRKWDAIVVGGGHNGLVTAA
YLAKAGKKVAVLERRHVVGGAAVTEELLPGYKFSRASYLCSLFRPQIFKDLKLKEKYGVK
LYQRNPSSFTPLLDGRYLLMGGGTMEETQRAIAQFSKADAEAYPEYEAMLDKLVHFINPL
IDEIPPNLGESPFSGSPKQVLDKLASLSRLGLRTAKLGKDIAPLYEIVTAPAAQILNKWF
ESEPLKSTLATDAIIGAMTSPQVPGSGYVLLHHVMGETDGIPGAWSYVEGGMGSISRAIA
SAAADEGVTIVTDAAVKSIIVSERGASGVELADGTKLESDLVISNATPEVTFHSLLSQES
QARLPSSFRQQLKHYDYTSPVMKINIALNQIPNFTCLPNQAPGVAGPQHRCTIHLGAESM
ADIETAYQDALQGTPSRKPVIEMTIPSSLDPTLAPEGHHVASLFVQYAPYHIRGGTWDEK
TKEEYADRVFSLIDQYAPGFKQSVIFKDILAPPDLERVFGLTGGNIFHGAMGLNQLFFMR
PSSGFARYQTPIPGLYLCGSGAHPGGGVMGAAGKNCARAILNNA

>mitochondrial ribosomal protein L40 Contig17281 (complete)
MMKRLVVARPSAVGVAQSSLLSSSFSSTTTMCLRSSSVAGIQISSRSYAGSFTKKKKEKK
KSGGGEEGEAAEGKRFDEELWKLRPQWVTLTRTPEQLAEEEALIKSYAKLKMKQLHEESR
QLSKMLKLKLEALNELPPDLRAEALVEEVSNAPRERVLPLWTAPIPGYQDSLPPEKRDEP
FDFTKLGSIRKRSS

>NADH dehydrogenase 15 kDa subunit Contig2142 (complete)
MSTGFGFQGAGRCYPIWRDFALCKNGSANPGECTPFFQDYITCTYGWADPENVELFKRQV
ALSEEQEKWQKQYGKKMAAHVRTFETEAAYEEWKESLGAKVVETPATMDELNAFTKEKLN
PQ

>B12D homolog ContigE9BS9UA01AGAXA (and 23357/7569/8345/15555) (complete)
MKSMNKKATTSTMSSFVKKFVPPEVYPLLVPVTFACGFGTYIGYRTLVGAPDVHV
FGRQPRFESGHHRSDPHFAGIHSKASRFDPHPELGQAEANFHSSYASSDSNNSY

>hypothetical protein Contig24792 (likely complete)
MRSSVRNAAAARWASAPARFSSSLRLYRSSSLASAHTILRSTSSRTYSSSSVPPRPGHDQ
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DLQPPPGAKEGDIDYTEYLAKMDRLEKPKGGLPRANKIAALLTGIPMLLILYHMLFPTPI
EKNEWFQLEKEHRDRMVRAMEEANANANSKK

>NADH dehydrogenase PDSW subunit Contig9011 (complete)
MSSGRAVPDFNDTDFDTEDPVAYQKAIRQRVVEHIVATEEMAELQTQLSQCYYREGVNYR
KKCRPLAEEYMKRLEKWKAYIPPEGEETDSVVRMRS

>NADH dehydrogenase B15 subunit Contig14886 (complete)
MNSNKFYVPRGPRVEHAIKDPAIEEWAFYRENTHRYFRMNPKIARKALIWAVAVPYITYQ
LTKMAQIEQDNQNPRSQLAVPDRKYL

>Tim8 Contig15686 (and 20235) (complete)
MDDTTLRQRAAALQAEVMIQVSVLATTDDCWKVCMKGKTSFGTTLNKNEKECFHNCTMAT
VQSENFLTKRTAQHIEQQARQSGH

>hypothetical protein, putative CoxVIII Contig11857 (complete)
MNFLRRTPLSGVRTLFVRGHGPTHGPDGRLLGQGIGTTFPFSTAETAKKKYHTGRAVWGY
FVVGVVAPCWAVWFSANKEAK

>CoxVIb homolog Contig27789 (complete)
MEQRKEPAAASTTPSSGGEGAANAPLVDAQKRERCWAARDAYHACIDGSKTGGGE
EECGAALRLYAAECPRSWLLHFEKRRKADQERSAREAAYQNRQRG

>BolA related protein Contig11307 (complete)
MSKGTGVRRLGLAMKQKLESGLLPVKLNIVDESHLHAGHRFVKESGITQETHFKVFVVSK
AFEGKSLVARHRLCYSLIDQEIKEGVHAVALTTLTPEEDKEKEVV

>conserved bacterial protein Contig2900 (complete)
MAARRPPRGFEELFVRFPFFTPFRVVGWGTLALINAGLAESKGRSRLFWGGVSLGAGPLA
TAYIVFTPSHKHDHS

>cytochrome c oxidase subunit 17 Contig10134 (complete)
MSSATATSSTSAAPAAAAAPTTNAAGKRICCVCKDTKKVRDECIFQFGEEKCQEPIELHK
VCLRSEGFDIQ

>Ubiquinone biosynthesis monooxygenase COQ6 Contig12152 (and 3009) (likely complete)
MRAARGSVRAALWRRPGAGAAMVLHSAPHAASSPLRFMTTTRDDSDFDVVIIGGGMVGSA
LACALGSTPATGHLRVGLVETSVVAPLHPLPPTPDLRVVSVNPASARLLQAVGAWDAIVN
ARVAPFYSMKVWDTSGKASIVGMDYLGFLVENRVITSALFERMQQLPSVKLFSPMSVQRI
ELEENGKGDKHEVDWSSPQPTVGLHLKNGDKLRTKLLIGADGAQSIVRQTFNFGAVGWQY
SQRGVVATVTLPPHMANMTTAWQRFLPTGPVALLPLWDRYASIVWSTNLPHADHLLGLDE
KAFLEELNHAFHDPPAPTTGPLAFIEDKLPFNPFAGADPQPPVLQEVVGKRAAFPLRIAH
ATDYIRPRVALIGDAAHTIHPLAGQGVNLGFADVASLTNSVIDAVHTGRDVGDVSVLKQY
EEDRRVANAVMLTAVDGLKRVWGTSFLPLAALRNVGLKLTDSFSPLKKEMMKFAVGSFDT
SAIGAHVPDTTST

>hypothetical protein Contig26231 (probably complete)
MFAPSRRLALSRPSSVASTSFGRFPTFASSSTSSFTLPALGTRTYVTNVKRIARREKRRL
AEKALVKAEAEKQATEAAVAATKQQVE

>hypothetical protein Contig1118 (only from BN-PAGE) (likely complete - inferred from genome)
MMAWRGGGATRRLVISSSAVESSFQAWRSRYFTAPSPMGRNRS
SVLACGDSTPLVAASYSLADAEAARKERMARWASGGTSISSSTLCSRSPGRARVRVVSFC
VTSTDVKPRVEMLAGADSLSSLLSSAAAAGPAAKATWRSCRMAAATISMGEAVPSATRLL
RAGTMRNSSGGRKLRAASSPLSEDSMKGRKRSSHVVTSAVRRSMACLMTWDAPGEVVVPT

>hypothetical (likely Cox protein) Contig16044 (complete - only in BN-PAGE)
MSSALHSARPLANTVIRRSTEKLYGQQAHIGREAQHRVIFLRTGQDKFF
YGVATSVAGAGIATLLFGATRLATGNGKREE
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>hypothetical Contig26374 (incomplete N-terminus - only in BN-PAGE)
MNGCIVGKTAHIVVVGSHGGIGGGGALTLSRRLELALVVVRKRLPRTGPLLLRL
LPVVRSHERWAAVVIILARREEALGGDHGGGSLPRSGAGARG

>NADH dehydrogenase Nuum subunit Contig7424 (complete)
MGGGPRFPFPKWVWSPAGGWWCENPPNAQRNLRIVLGLNFAIAGAVF
FISAANERRLLSHPTIPVPSQRWSAWTKVDDPDYKRKLAAYHKNKKPLWERILPDAMIQD
EHGHH

>AarF domain containing kinase 1 Contig6358 (and 5578) (incomplete at C-term)
MWRAKASSWLCAGGVRCVALTSGIAAGGSLSLLRGAPGAAGRLRSSAPLL
GRPAHTAAAATAPLPKEGAAGLRRPCHKIYACRRHRTPLFLCFVVSWFGG
ALRLGCGRHRCATRHTSRVARGMVVPTRVGNVCRAGGGDSPGLQVEPPRT
RGGGAAAAIASRARAVPNPPPSLSAANGPLWCANNNDDNRSADRLLRLFQ
QNKGIYVKAGQHISSLDYILPYEFVFAMTPLHNQAPTCPWEDTVRVFREE
FDSHPDIMFAEFEREPVAAASLAQVHREFPDVTIPRIHWDKTTSRILTMD
FIHGVKLDDKEGIARMGLSTHKVAELLTTVFSKQIFLDGFVHCDPHPGNV
LIRRLRPHDPSSDDPELVLLDHGLYRELDDEFRINYCNLWVAIIHADEAK
IKDYARILCGPDASYQLFACMLTARAWE

>hypothetical protein Contig5488 (BN-PAGE only) (complete)
MSAARGVRTIIRPVNKGTYFGRFNQFWKEVTLEDPAISISFFLGGLGVAI
TFLSMPNVRGILVPFKSPKQSWFGEHY

>hypothetical protein Contig (BN-PAGE only) (uncertain if this is real ... on same contig (but opposite strand) as glycogen branching enzyme)
MSMELGLSSQALGSVKKDTPACMRLWPPYSAASVSSMISYLPGWVTPTR

>Nca2 Contig9 (likely complete .. from PGP)
MLFARRAQGTRQRIASLFGLIDGATHDLSFLPPDQEKLYRDACVALTKQSIDGHTLTHVA
TSVAPFIGYRHRHRGAPTGPATGGGGEAASQSSSAPADNSDAVVHHDEGKDKGKGKEKNR
SEPATDGEGSAASKEDLQDQVLFEAKLYVLCLIAIAQNQSVCDELLRLASSIQHHHREWS
LREDQPFWYLYEKTPWYWLNYLLLKRDETPHPITELREKLRHLRALEKNTFAFIGVGSRV
LSRYEAVGRTNYAERLSNLIRKDQQEEDGENEDVLFNLAQTVNLSYFDYHSADVIGETTT
ETTPNIPNLYAQLMENVKKAALFPTQMKHTLNEYKRPSALSTNWLRYSCITAGITVGVLS
VVKRREDIIDWLVDFKVLAKNFIQKNILLPLQDVYETIRYEKRAFTIMDARALDADVESL
QRMVDEYVRKLHPHISQAQLEEITTAAANSDISAIMPVYERELESPIKNALFGDLLSLLL
IQVHKAKVDVARAMLALDKLMRANELNFQLFAVTPAILLVGGLSRYLYRRITRIDIRRTT
HVQIRETLRNVERMLDLNLSSASSSVRHHHAGGPTNLSLSTSFSGWGRSSTNSLSTQGRP
ESDLRLEDTGRLLVSINELIRLALQMPRHDRKWLLEDLQDLQAEELQVAQKLATIHRMYH
THHFLSAV

>Radical SAM domain protein Contig7396.t1 (from PGPs g7396.t1 and g7394.t1) (likely complete)
MLQRATARNASLGSLRGGGNALGLTSFLHQRCPRLLVQTPVRLYAPQPRRRKPLSDQKLL
VKKEKKILRKLTKEEEKRAADAFYSAHEAQEAAGATATSTSSSAESGRPRTKKKKRATGG
DGDGAGEGATSAGSRFGRDQRLADSREALVERARQLARQSAARAGSGLAGARGQRRVEDL
PQSNPWLLYANEMGDMIDFPGLELVGAVAGEVTPHRLDRGDCISAPEGSRLLTLSQRAPV
GYQRDDQEAEVLSADPKTDRANMTKRDRTWPPEAVAVSLPAPYIATHYSSFNSLPGGQTL
PLFFYTPVGWWKKGSDFLAARERMERAKRGEPDPEGEEAQSLEPDDSFDKAKESLKVMKD
RGGFTSIRYMILPGLNDERKEVDELCRFIEETRIDMIQWRNIALDPEYYLTSIKYEPPAS
VVYAEKLGVKQLMETIRDKYPHVKHGYYNPCLDEKAHGYNLTAASPMCLGCPSLQKDRKD
LLARYKRIPFVPTADEIVEVAVEHLAKAPHAIIAFGQSCEGEPLLQADLLCEVIAKIRQR
TRRGTIHVNTNGTVTEAVARLRESGLDSLRVDVNSVRREYFNRYTRLNYEPVVERLRQAA
RERMERAKRGEPEPDPEGEEAQSLEPDDSFDKAKESLKVMKDRGGFTSIRYMILPGLNDE
RKEVDELCRFIEETRIDMIQWRNIALDPEYYLTSIKYEPPASVVYAEKLGVKQLMETIRD
KYPHVKHGYYNPCLDEKAHGYNLTTASP

>pentatricopeptide repeat protein Contig13581.t1 (from g13581.t1) (likely incomplete)
MALTALDELKTAGLTPTAAVMNAFMAVTPQRAPKVLAMMRDHNIEPTESTWNQLIYSVAW
RLKSESDKNESGNENETSWRGRELELLEEAFASADRLQQSSGSGPASVAYGYLLEACLYA
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AQRISARRESTTGTGVDADEDVSGGQAVLSADDRAELRRVAQLADRCWRDMLAHQPTAIT
REACAVRMRLCLRSASRLDPADAAEARAGLQGAIEAYGEMRRRGFLPSPLTYGALARTCA
RHGAFERVTQLVEDMRAQGVQPSTATLGATAQALTSSRSAGAAAALAALRDLVLPKSTAA
PTST

>AAA ATPase Contig3186.t1 (from g3186.t1) (likely incomplete)
MSFTSWRNCLVRIRVGWTGQGERLKVVAAMVVALVVATSCLLGMLHHDGPEHSCAFAATD
SCPTFASITSRSLRVTWRPPSRASLVRRYELYTAETYASAGEGGSSPPTKVYSGLKRSVE
LKDLSPSTSYNFTVKIIGHQDSIRSSCWRFTRTLGEEHGNLLANPSFEEVGGPLTPQMDY
GDQPFAAYWEPLMMPYSLKLLPKRGRTWYTHSNDAPNKRAAHQWVFLNHTEPTKMLLSGW
SKASEVSGEPDDGYSVYMDLKFVDGTFAYVESMEPECRKLHNVPSISLGCCPTRESILAT
DTPESDDVAIASQMTIDRLPVLESMAESWAGPISAVILLSNPEAELKQIHSLRNRSAVIR
KNVDFHLVHGEENVYALHTLGLYPVNSLRNEAVVKSRTAHVMVLDIDFIPSRDARENILR
LWDQLHEPQTVFVVASFEMDDFNMRDVPHTKDQLLRMVAQDRIRQVHKDKWFPAHGPTDY
EHWYSTRELYQVPYQRDYEPYYIVRKDVPLIDTQRVVGRWDERFVGYGFDKVSHSTELNA
AGYSFFVMPDTFIIHAEHGVPGWRGKGDFNRCGEVLLLPINRPELFEGRRSKLLQPPKGI
LLYGPPGTGKTMMAKAIAKEGKLAFININLATILNKWYGESEKIVRSIFTLAHKLQPCVV
FFDEMDCFFHNGASASGSQHSYHMQVESVFMTLWDGIVTDSKSRVIVIGATNRPYNLSAA
ILRRMPLQFLFDLPNKAQRAQILNVVLANEPLAPGFSIDALAQLTSGYSGSDLQELCKKA
AVAPLRHFLEEEERRQTATATTTTTGSDTHGLRPMHMQDFIEAMKEVAPTGKKAKQYHNF
AQKRERGGAKPDGDDDDNDEDEPSGASINMADVLQFWSAMMGGAAARGSSSSSSFTSAST
AQEKKSSKPKIEEIDVDDEGVALLDEEEEGEYDERIEKWSKRFEGKDGARLLEQLCGLVD
VDPSQPRPVVLKELAKHFLD

>Fe-S oxidoreductase Contig9200.t1 (from g9200.t1 and Genscan) (likely incomplete)
MMLRGRVLLRRPLHCAACLPPPATARLLAPSVPAAVRSWSTLSSPAVPVVRTPSCMPSTY
LMHLTHTTTTAAAGGQQLPENYAALARELRKFLREDQVVSDPLRTLAYGTDASFYRLIPK
LVVQVVKALGLAERFGAPITFRAAGTSLSGQAITDSVLLRLVPSKWSHIDVLDPEGSRVR
LQPGVIGGQANKVLGTYYLSSTNASTIQHLADAWAAIAGLYGRKIGPDPSSIESCMIGGI
TANNSSGMGAIERRPADPCQEPQAHARWYALSVRGAQGGGGRTTNRITCEAHSLVDQCIE
CGFCEKNCPSRELTLSPRQRIVIWREIQQLRRTKSDPARLAELEQQFRYAGDDTCAADGM
CATACPVNIRHLPTAPARLPFGLTRGGVSVNTGQLIKTLRATERSPWAQTVAQAAADHFA
LVNGMGRTALQAAHVGHRVVGARVMRALSDALHRVLPASPQWNPHLPRGGHAPSPPPPTA
TSKDQVVYFPSCANRVMGVSTSEKTEGRALPDVALSVLGKAGYDVIRNAGNDVSSAGGAG
GAVLRDGVRESRVPAPGAPEGRRAARRPLARIGPRPPPRPLRHEPLRPPRQDPQAHARYP
PPPSPGDFASSHDITRTTRTTRTTRTTRTTRTTRTTRTIIDESLGLPEAKKQQKLEIFEP
VEFTHDFLLSRLQWTPREEGLVYHTTCSSKRMAGVDQKFLSVLKQCTGEAPAKRLGSLLL
DSAVPCCGMAGDRGLCFPELPRSALKKLRERVASHPPGCSEGLLHAP

>midA Contig13582.t1 (from 13582.t1) (likely complete)
MKRITAATRRVVLRGDAALVRCTTSASLCRRGSNNHQIGGLRCNSTNGKPTDGSAQATEE
MTSRAISIDTSGLYKHKPHGPAGNKSADTPLLSHLRANIQVHLAPIVVPKPGAECLRAVS
CRWCLQLRGPISVATYMKEALTNPMHGYYMNKDAFGQKGDFITSPEISQMFGEVLKKTPE
LFGQMTIHMVEVSPYLRQKQAATLGCDPTLLSGDAAKETSSTEDTRDTKPTAGREETGHW
SSPVLTGADGVRVQWHRHFRDVPPGPFLVVAHELFDALPVYHFEYTEKGWLERLVDVDQG
EGPHHLRYVLSPGPTYATMALLRQAGVSTEPKPKLKQKAPTASFSYRGGEDDDDDNDDDN
RPTDGPKVGDRIEVCAEGMALASQISEKIAREQGRGAALVIDYGQDRTREDTLRAIKNHK
IQDVLCEPGLADITADVDFSSLRRTAQQTRTPTLLGFCSRKSSRVVWPLMCVVCRVCVPD
SLDHDVRPEAAGPVPAGARHRRSAGHAPQERWRRQVRTVLLVQHTPPHTRHHAHAQRNRT
RCSAQAKDLIAAYERLVDDEQMGLTYKAMTICSLHNVKQPPVGFSL

>pentatricopeptide repeat protein Contig3902.t1 (from g3902.t1) (uncertain of completeness)
MKEWRVRPSAHTFSILFNAYANLAQPSPSYLPKLKQLKDQEMPKYGVVPSVEIYNVLLKA
YLALDPEKSHQELKSVIAEMQEYRLKPDAITYTLWMATAARGIANNPKATVDVAAAFEVW
DEMKKNRVHPNLRGYNELLKICNEGSSEDRDIAFELYKEMLVEGVTPDHHTFDILLMTCW
KQRKFELANELFDKAVQLNADNKGKLVELDTHLCNSALRVCTRNEGKRGPGRKSGSAEAN
QYLLDVISKITKVMFRKHLPYDEETYALLISAYTRAGAKEKATSTFADMQSKGQVRISKK
TIGALLVTCRESNDVEEVKKVMDLAKDRRVRLTDSMVEEAKTIFIKNKRYQEWTRVERDL
AEWLPTATADYATKGKRRASAVEGGDEDDEDDINNDIEAASVSKHPKATTRRSSSAFGKP
ARPGPYAEGRSGSRERAREEGPRRPEGGEESARQERRRRWREERSGGAGGGEKAQRRSRP
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GREPKDRVSAKNYYKDTRVKSPSATGRKSFGGAPKPHAGRRKSPPSSLARNED

>mitochondrial sideroflexin Contig3994.t1 (from g3994.t1) (likely complete)
MEGTTTTPSPAKSLRLDLTKPRYDQSTFYGRWRHFLDVTDPRTLLVSEDELSRALTMIQD
YRSGRRDFMEEDLWRAKKIKDAIVHGDTGEKIFAPFRLSAFVPMNIVICAAMLMPNPSMA
SQLFWQWFNQSYNVGVNHANRNASNQMSNSQIMLAYGGAVAVSCSLAAGLSQLVKKAPSL
SPALRATLSRFVPFTAVATAGVVNVFLMRKNEMTEGIAVQDKDGNVVGKSQRAGLFALTQ
TSISRCLTTAMVMAVPPIIMAGAEKTLLKRYPKLHWPVNLVFPQNCSVSAKLLEPQFHNL
KDAKGNPIDTLSYNKGL

>BCS1 chaperone Contig612.t1 (from g612.t1) (likely complete)
MNGGPPSPLGGLLDTTNPYFSAGAGLFVLGGGATLLRGGWKYGAAYFQRNFMVKMEIPSK
DPSYSWVLNWITARAARQTQHLSVETFYQKDPTGRIKTSYNLIPSTGRHFIKHKGYWMVV
ERAREKAMVDLTSGTPWETVTFTTYGRNRELFLDILQEARDMALAKEEGKTLIYTANGFE
WKEFGQPRARRPLSSVILDGDQAERLAGDVKEFLANQSWYRDRGIPYRRGYLLYGPPGSG
KSSFITALAGELQYNICMLNLSERGMTDDKLAYMMSIVPTRSITVLEDVDAAAIRREQPT
REYQSCVTFSGLLNVLDGVASSEERLLFMTTNHIDRLDPALIRPGRVDVKLEMGNASADQ
VRRMFLRFYPDHERSADEFVARVEAAGKPVSMAQLQGHFMLFKEQPHNAVSNAELLSAE

>HydF Contig4978.t1  (from g4978.t1) (likely complete)
MTKRAGTVCGIPPKHAASWSRAYAGQPLLRTNIGIFGAMNSGKSTLMNLISQQETSIVDS
KPGTTADTKVALMEMHDLGPVKLFDTPGIDEEGLLGEKKRRKAFDVLKECNAAVVVVNPF
NPASLKAARDVIQEASAKQKKGDDSAQMRVMVVFNVFGQQTAEIRKATNTILDAAEKSLT
PDGTNLQITSIALDLNSPEAMGRVVKFVTTNTKPHSSNVSLLPSALQLGPDSVVFLNIPM
DAETPSGRLLRPQALVQEELLRQYASTFCYRMDLKKARSPIEEERREEEQRFRSSVDALK
SQNKLKLLITDSQAMDVVHKWTMEPGTAAPSDQGGQSSQETVPLTTFSVMMINYMSGGRL
SAFVEGIKRFETLKHGDKVLICEACNHDRIQDDIGTVQIPAKLRQRFGEGTIGVDHAFGR
EYQTKILNDYQLVIHCGGCMLDQQKMAARLSDIEGSGVPITNYGLLLSYLAAKQGLSRVL
RPWGL

>DNA polymerase A Contig301.t1 (g301.t1) (incomplete with gaps .. from PGPs and inference)
MTMRGRFQPSTATSLPLLRRSASTRAAPAPAIAIATEIERAVLESQQSQPNGAIKINGEL
NQPAPAELMPHTILIDGSFLTHRAYHTPIAEMTNGAGVAVTALFSYTRSMLKMLQDPHFR
ADYIGVFVDSGPSFRKQLYGEYKAHRSAPSAELRKQFPLVADATRALGIETIKAEGMEAD
DLIACYAKVAQAQGHRVTIISRDKDLMQLVGPTVKLYDPVGKKTFDEAEVRKKFQVEPRQ
VRDVLALMGDDGDNVPGVPGIGPKTAAALISEFNSVEELLANTAKITNKKRRQLIEEHVD
TIRRALALVELRHDIPMPVLLEDLQRQPINRDKFLAFLREHSFGSIISKLDKICPPTAAE
QAAEAAPRTSSTRGRPRLDNPTQEAVQAPPAPLSVAVALKRPKVEIEGVTIVDTPEEARR
VLRILRSPGVRERYHACDTEAIQNRTKLTPPSHAHAEVKHQSPYNYGEVICASVYCGPDV
DFGTGPNLWIDNMDDARGVLDLFKEYFEDEGIKKVWHNYSFDRAMMWRHGIDVKGFGGDT
IHMARLWDAARTSVGKKYSLEALTGELLEGETKRSIKEIFGRNKVLKDGTLGKEIVVPNL
DAIQRHAHSPPAAMEALNNWIYYSTYDTRGTYELRDKLEDQLREMPWVYEGKKALPGANR
TMWDYYQNYWLPFGEVLTDMEREGIKYINSSRVVSLVVSCRVVGRVVSCRDQVNVDYLAE
IEQVAVAEGKKHQIRFKEWASEYCQDARYMNPTSDAQKQQLFFAPCKNLKTDDMMPAERL
FDIENDEGTHAQAVCRARRISCACVVSCRAPLITHRFAGIPDPVTGKVKKKRQIRISGFG
LPAIAHTGAGWPAAGAEVLKQLAGKPFDNPPKYGVAYKAFSEGEAGAEACQAIDSLVKMS
SIDTLLSNFIVPLQHEVDPNNRIHASLNINTETGRLSCRRPNLQNQPALEKDIFKIRSSF
TCEKGNKLIVADYGQLELRLLAHMTKCRSMIDAFQKGGDFHSRTALGMYSHVQEAIQKGE
VLLEWGGEGKPPVPLLKDIFATERKRAKTLNFSIAYGKTAMGLSKDWGVSLQEAKDTLQR
WYARLCVSCGVCARVCGSLKVGAQENTIRTARKTGYTKTLMGRYRPLPDISHSKPMMRGH
AERAAINTPIQGGAADIVINAMVLAHHDELLRRWGWKMILQVHDELMLEGPAESAEEALA
RLIEVMQNPMPEGEELLVELAVDGKAGSTWYEAK

>putative NADH dehydrogenase 20.9 kDa subunit Contig12304.t1 (from g12304.t1) (complete)
MVVFTEEPKNAVINPKPTYPSILWHMRLSDWGILVGLTGAGVAWGYMAGKGARKSVALCG
GILGFLGGHSIAAQNSAQRLLGRKPNGRPISSEH

>Tim8 Contig6199.t1 (from g6199.t1) (complete)
MDHTTLARNLQAIQVAVESQKQLMETTDFCWPICMRNARIGTELDRSQKVCFSNCVVRSI
DAERMIAQRVLVAMKQSSTGEA
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>topoisomerase III Contig11413.t1 (from g11413.t1) (likely complete)
MQRCGGLARYPLLRGVAGRGSLPSAMLVGPRFTNSIIGSHLHFIPRLSFT
TRGRPRKSVEEVATPKEPKEAKNKHNVAGTSDPGPKVKSGAKAKKVAEGQ
TTEKKTKKEAPATEAKETVPKAKKARAEKAAKPTAKLPKTTVPPNDAKPL
PTADKATKARKKEAKPSETKNEAAATVAKTAKDVKAAKAAKETITSAKVT
QSLEAVKTAKKAATQRAEVEAPDELLNKAEAKAPEKRPKKGKVELTTQVA
TATGGAAERTEAVKEEKPARVVEAKRGETTKEDAEAALPKWEHLTQAQLK
EECKKRRLKVTGSKQQLVERLQEATRPPPAAAVEPQPQGPVIRIIVAEKK
SAAENIARALGIKKFKKEGAKEPGFIGNVELTPNGVQVVPDESGSGGATV
VTWASGHLFELQKYAMWKLDKLPMLPSEWTFSCKGPAQKRQFEVIRRLFE
SADEIVNACDAGREGELIFREIFEQAKPKAPFKRLWISSLTDEAIKEGFR
KLQAGTEYDSLYHSALARTKADWLIGMNATQVYTLSYRPKVPSFQGKEAV
SLGRVQTPVLKMIVDRWKAAHNFKPEPYWELHLRCRPQGSDEHLRLKYFS
PEAASERIASEQEAEDVRHALGPVCTVQQLTHKRRIEKPPKLFDLTALQR
EANRRYGYTAERTLGALQGLYEHHKLISYPRTDSRYLTKDIFNDVNTILD
GIGKHSMYAPAIEDVRNSKRLSLSNKAVFDAGKVSDHHAIIPTTNIPSEK
TLAHLSPDERKLYHLIVSRLLSCFMPDCEKQHTELVAVNKSKHFRGRGVE
LVKPGWRSVYSLSPFAAPQDGSSVDEKEVDDQSTTGDGGDSIGDGDEEEA
TTDDGNLCSIASKLKENDTLACVLPAEVKCEHTRPPPLLNEASLLFLMET
AAKYVAKKGAYDAENEADDGAEESLKEFGLGTPATRAQTIERLIAVKYVR
REGKKLVPTEKGKILIELLQKTHSSLTSPQMTGQWEKRLQDIAKGEGSHE
AFVEDIKRFTEQVVDEAKVGATRLPDFRKMMRTINQQEEGTPQTSEAAGA
EAATQARGGWEEEEEEVLGDCWKCGKGHVVSRARSNRWTCSTESCDFIIW
KTTASREMQREELKELLTEGVTPFLSGFKSRAGKPFEARLAINQDGKVVM
MFPFTVRRSAGGGSGGGHGRGGLSRRLPGITESSETDE
```

```
>ferrochelatase Contig12653.t1 (from g12653.t1) (likely complete)
MRRPTAVVMMNLGGPETLSDVRPFLQRLFSDQEIVQMPFPQKFQENVVEKQYAEIGGGSPI
RKWTEAQARQMEKLLDQSSPATAPHKAYIAFRYASPLTHEALEQMKKDGVKRAVAFTHLNE
LWRQLKKHDMENEFQWSVIDRWNTHPLFIESIAQKIRTSLETKFTSATDREKCIIVFSAHS
LPHKVIDRGDAYPQEVGATVHKVMELLVDPAGLATSPEGRTQAPVRNRYLLSYQSQVGPVA
WLGPQTVDVVGKLGKRGEKNVLVVPIAFTSDHVETLFEIDKEISHVAKESGVTNFVRSESL
NDDPRFARALADIVSQHLNTNELHSEQYTLRCPACVNPDCRNIVSPVRTYDHPQL
```

```
>ATP11 g4701.t1 (complete)
MLLMRRCLRSPAVITNTAGGGGRAAPVRWFSSGAAPPPRELAHVVKLDSL
HQETPERISQLWIDYHVKKEACVSAVAPAATYALINRRLAESPLFVLPLP
RESGFVSVLLQAHAEQDTVMFTELEQYQRAADKSAVPSCLHLRYYTDLAA
TKDIVLVRGEVDLARLTTTVKRKRW
```

```
>mmp37 g757.t1 (complete)
MAQREPAEWEVPLGLGEEDRQQLRRIIGAFPKLTFAAGYGSGVVPQADAT
KLTKKPMKDFIFAVEDSRRWHEANIATNGGHYSGVAWLGSSVVARLQEDV
GASIYYNTHVQLLDETIKYGVISSKHLISDLVNWDTLYVSGRMQKPGSDE
IMSANQANLESALSSALLLAPAQLPQRQLWETIAGLSYTGDFRMQFGENP
NKVKNIVTDKNAEAFRLMYRHSCDKLQHLLRLEDDTVVQDTSRAARQDLL
LRLPARLKANVERQTGQSLVDLSGAPVQTIASAVASGISTLVKSSSRSQS
LKGILTAGLVKTIVYSANKIAKMRNATK
```