

CIII structural proteins:

>COB gi|11467061|ref|NP_042537.1| cytochrome b [Acanthamoeba castellanii]
MRFIKKYPLLNIVNSFLIDYPAPPNISYLWNFGALAAFCLGIQIVTGIFLAMFYVPSIESAFSSVQYIMR
DVNYGWLIRYIHANGASFFFCVYIHVFRGLYYNSYITPRELLWNLGVTILIVMILTAFLGYVLPWQMS
FWAATVITSLFSAIPVVGEYIWIWLGWGSVDNATLNRFFSLHYLLPFVIALLSLIHVAVLHESGSSNPL
NIALSVANKVPFHPYFIFKDLLGIIFFLIVFCYAVFFKPDSSIIDPINNVANPLVTPTHIVPEWYFLPFY
AILRSIPNKLGGVITLGLALIVLFLLPFITNNVFKGSFFFEISKILFWSFFSVCVLLGWIGFKPIEDPYL
MLGQMLTVLYFFYFFSLAVIVPTLQAYTFKNVFAK

>Matrix processing peptidase beta subunit/Complex III Qcr1 Contig18201 (complete)
MSSIRSRAPSMMLLPTKLGTSGRGLGAAARRLSSGQPQAARDVEKRLRLPEYLLNVPPTQVT
ALPNKFRVASEHKHGETATVGVWIDAGSVWETAENNGVAHFLEHLAFKGTKNRTKEQIEV
EIENMGQQLNAYTSREQTVYHAHVFKKDVPKAVEIISDIIQNSNLKEDDVERERGVILRE
MEEVESQTEEVIFDHLHSIAFQNTSLGYTILGPEKNIKKIKREDLVSIVGKHYTAPRMVL
SAAGAVDHDELVKLAEKHFSGLSSETNVDYSNREKLFDFGTGSMVQVRDTSIPLVHTTVAA
KSVGWSDPDYFTFLVLQQLVGSWDRSLGGAKNLSSNLAETTFATEELAHSLMSFNCTCYHET
GLFGAYFVGEMERTSDAIFEVLREWVRIGSGVSEVEVERAKNKLKSTYLMQLDGTQAVAE
DIGRQLLTLGRRMPAAEAFMRIDAIDAKKRVREYAYTYLNDVDVAVAAVGSVDSGLFPDYN
VLRGWTYWNRL

>Matrix processing peptidase alpha subunit/Complex III Qcr2 Contig18841 (and 14090) (complete)
MKPQHAARLSLAKGVTRASSPSASVLGSKSYSSWTATSSLKQAHSSVPQTWEATPQTLDN
VQTTTLDLSDGLKVTTVSSSELPLAAVGLHVKAGARFETGESRGAHFRLRHLAFSRTSSRSPL
TVTREM EVATAAFDVSASRENISYSGQLMPDYLEDYVWMLRDLMHPLAW EYIVRDAAPQV
AAEVHEAETNPATALVEAIHREAYRDEGLNSIYCPNYRVGAVTREAIIRYHHERYQASN
VALVGYGIKHEQLVAQANKYFPADAF AEDKAPWTTLEAADRKPGAVYTAASSYTG GELRL
PGPGNSRVALAFEGASLADPDVFAVRTLSLLGGAARFTRDGPVGLRSRLARNVLA KGD
YVLASSALNASYSDSGLFGVFVEALPGHGADAARLLSAELNSLAGSFSVDDAELTRAKNQ
AKASFFREVESRTGLVDYLARHTLAGTAPLAPAQYAARFDAVTRDDLARVARRVFS SPLIT
LVSTGDIHGVP TKEELRPKLKA

>cytochrome c1 Contig11871 (and E9BS9UA01E09K4) (complete)
MLRQRTLTSATGMAFRSQTRSFATSAGASAKRLHPNVLGLVIGAGAVGAAAGTLISRARC
SDDVLVAPAYPWSHKSEWKSVDVASLRRGHQVYKEVCAACHSLNYIAWRNLIETLYTEEE
VIAMAAETEVEDGPNDDGEMFTRPGKPTDYLPRYPNEEAARSANAGAI PPDLEMTVKAR
EQGADYIFALLTGYPAPAGLNVREGLYYNPYFPGGAIGMPPPLNDGMLEYEDGTEASVS
QMAKDVSAFLCWTARPEQDERRVMGIKVLIIYLGALFGCSWYIKRFKWSVLKNRKVQFP GK
NWPTV

>Rieske Fe-S protein Contig7171 (complete)
MKRTAISAAATLRASTAVSGSASATLTRMAPVLSGSSKREVHEINVPDWGHYKREAQEG
GESGGRAFSYMVLGTAGVGYAAA AKHTVIKFLDSMNPAANVRAMANVEVDVSNIAEGTIM
TVKWRGKPLFIRHRTAEIADAESAPLTDMRDPCDAARRKADKPEWLIVLGVCTHLGCV
PLGGQGEYGGWFCPC HSGHYDTAGRIRKGPAPLNLEVPYVFKD DSKVLVGVDV

>Qcr6/hinge protein Contig14062 (complete)
MSENWAGCAIKKSLEEK AHPKCLKKWA EYDACGQRIKGD TTGEAQCSGQYFEYWHCVDAL
VANDL FKRLK

>Qcr7 Contig4544 (complete)
MAARKGSSGFLSRIS SFFKPVSGYQAYGLRLED FYNAENPEIQEVLRR LPNKTK EERDLR
IRRGHELHLKGTTLPESSWTTPEEDGQTYMEPYMSEVVQEI EERKDFRADFLLPVEKRHK
RK

>Qcr8 Contig1256 (complete)
MGVRWTTYTLSPFRQKMFPGFWTGLIPRQIKRWKYNFPRVAPPILAGIAIYTWGNWKHDQ
IARSHWY

>Qcr9 Contig9630 (complete)

MNALKSSGASNWVYQNLFKRNSSYFALILVGAVVVEESGVSRTVDFWVNSVKNKGRWTWDFK
RTQLPKIQAKKAAAAEEEEESDE

>Qcr10 Contig26093 (complete)

MSIHKLDKTHATVNLEEAATRTGTIRSVPYHETIAYQRFYANVFTKATVFGKRLIPLTKN
YAPTAFRWGALAGLAAAYVIEPSFLTKEYFTKSESK

CIII-associated proteins:

>BCS1 chaperone Contig612.t1 (from g612.t1) (likely complete)

MNGGPPSPLGGLLDTTNPYFSAGAGLFLVGGGATLLRGGWKYGAAYFQRNFMVKMEIPSK
DPSYSWVLNWIARAARQTOHLSVETFYQKDPTGRIKTSYNLIPSTGRHFIFKHKGWYMMV
ERAREKAMVDLTSGTPWETVTFTTYGRNRELFLDILQEARDMALAKEEGKTLIYTANGFE
WKEFGQPRARRPLSSVILDGDAQERLAGDVKEFLANQSWYRDRGIPYRRGYLLYGPPGSG
KSSFITALAGELQYNICMLNLSERGMTDDKLAYMMSIVPTRSITVLEDVDAAAIRREQPT
REYQSCVTFSGLLNVLDGVASSEERLLFMTTNHIDRLDPALIRPGRVDVKLEMGNASADQ
VRRMFLRFYPDHERSADEFVARVEAAGKPVSMALQGHFMLFKEQPHNAVSNAEELLSAE

>CBP3 ubiquinol-cytochrome c reductase complex chaperone Contig10140 (and 4561) (likely complete)

MRIMRKTLYRPHLSAGALTMATPSCRALSITSRCNSSMARHPIVHRSRAGAINGCMP
HVPSFLLFGRCSSTLRGTPEMPASSFGGRAEASATTGPSADPDLTYMSPVIFARRTPEER
RRDELGVQKILEVAKERANQGESEDGLLRFLGGYKKNQSLRSGSALYANVFYRSLDEEF
YDLLGYEEKGLLPWFLLISTLHMWMTSVRLRDKDASSRALDTRAYFADSFWMDVEEKLNNVG
VNYVGMGKAFKQMPNLYAHATLSLDKALKSTTDDQLGDALFRHIFFNRLPRQSHMTALIA
YVRQELAHLDITIPNNLLLHGYPWGS�PRVDASPVSAASPSPPQNDTSETGAAR