

CV structural proteins:

>F1 alpha gi|11467065|ref|NP_042541.1| H(+)-transporting ATPase, subunit 1 [Acanthamoeba castellanii], 522 aa, 15FE

MKKYQFLKSNLLQONINELFLOYLKNSNIGVIKSIVDGVVIEGLSNV
KAGEMLQFSNDIQGMALNLSSETVSAVLFGEDETKIKPGEYVEGTGNIISV
PVGMSLLGRVVALGQPIDNKGFDPGSELKQVEVKAPGIITRQSVNEPMI
TGVKAIDCLVPVGRGQRELVIQDRQTKTSICLDAVLNQKYENSKNKKNA
LYCIYTAIGQKRSSISKLVTLLEKTNLSLEYSIIVAATASEAAPLOYLAPY
TGCVIGEYFRDNGKHALIIYDDLKQAVAYRQMSLLLLRRPPGREAYPGDI
FYLHSRLLERAALKLNKFNFGGSLTALPVVETQAGDVSAYIPTNVISITDG
QIFLETNLFYNGIRPAVNVGLSVSRVGSAAQILAIKKLAGSLKLELAQYR
EALSFAQFGSDLDETTKNLLSRGNMLTELLNQNRFTPIPIENQFVLMYSG
IKGFLTNNVNNKVIKRSYENELFNRIISNYSVFNTNVILLNSNEYKKNKNNN
VVAFFISYFKFITTNIFGFSAK

>ATP synthase beta chain Contig14918 (complete) 720 aa

MLRNFSKRALPRTALSRGLATRTAAGLRQGANNTLATSSAPSKYAMWGTR
PPLSIKYRGERKQONERSHFVPPHRNFASFNEYAFSFLQSAQSRTPEPKTA
SKAEAESQAVDTDGKIVQIIGAVVDVKFPEDALPPILSALEIQDHNKLI
LEVAQHLGRGVCRTIAMDATEGLQGRQVVKDLKGPITVPVGAATLGRIIN
VIGDPIDEKGPIYSNKRNIHAAPPTLTEQGASDQILVTGIKVVDDLAPY
AKGGKIGLFGGAGVGKTVLIMELINNIKAHGGFSVFAGVGNLYHEMIT
SEVIKLLKDPKTLKEGDHIGEGSKAALVYGQMNPPGARARVALTGLAVAE
YFRDEEGQDVLFFIDNIFRFTQAGSEVSALLGRIPSAVGYQPTLATDMGQ
LQERITTTMKGSIITSVQAIYVPADDLTDPAATTF AHLDATTVLSRQIAE
LGIYPAVDPLDSTSRMMDAEIVGKEHYDVARAVQKTLQDYKSLQDIIAIL
GMDELSEEDKATVYRARKIQKFLSQPFQVAQVFTGFEGKFVSLKDTISGF
KSILEGKYDHLPEPAFYMVGDIEEVVQKAQKLAADLGGGSAAKKDGDAS
GAKVSGKRELTLDAFNDPSPYELKEGDFELNEKSFRVFAEYTKNVAIPYA
RDHELKEFPEDA AKIKAKYDNILSKIDGETDELVKELHDASQKHDAERKR
KEQEAALKAQKAAAPQAAA

>F1 gamma, Contig22783 (complete) 326 aa

MRRVSSVGLRTSAFELRTSAVQTARTFERNELGPVGVRRHYPGNLKERLR
LVAIKNIKKITSTMKMAIAAKLNKAQAVLFKTRPYSESSQRFIQEFFPSP
QEGEPNPAEEASAGKHLIVAVTSDRGLCGGVNSSIIKASAAVLRNHPENT
QLFLVGEKSKAALQREYANAIVYAVSEVGANKKTSFTEVAQVAELIARQP
ADNVTLNHFNSVLSFTTTRKVFPSPKTFVEAERKFSAYEFEGSHEEIL
ADYWQFSVASQLYSAITESQTAEVATRMTSMDNATKNASEVNLKLTIKYN
RTRQAAITTELTEIVSGAAAIEEASS

>F1 delta, Contig2942 (complete) 191 aa

MRRISASSRVLGMSAAAGGRFGPRTASVLT'TTTRRSYATDDAQREAHEKA
VKEGKLIFTLACPHETLINAEPVRIATVPSATGDMGILAHHVPTIAQLKP
GVVKVTKFDESGATR DADYFISGGFVTVYPD SHCNVNVVEAFPLDQLDPE
KAKKGLDFTKELASASDAEAKTVATIGVEVYKAMCSALKV

>F1 epsilon, Contig9766 (complete) 70 aa

MSSWRSGFSYLRYSNTCAILTRRALKEPFRAKAAERDSVNMKVEQWILG
KGQDKVDVKRANEIAGSAGH

>F0 OSCP, 409 aa, Contig24806 (complete)

MGNAARLVSARGFSQTLVTOQKKGEATTAAPVFKIDEEFDDYKDV TASNE
QVEKNYREPPVQVTSKGHGEFASTLYATASVLNAVEDVERDLKWLVDASQ
TIPMFQOFLSSGLPDKKVMRKLLOQVVLKGADFHRLTQKFLVTEELLEAGEL
KLVPDIAAVYAQIMKAHRKEVPVVF'TFASLPDKDFL'TRQIERVKKYRLEA
DATPMWEFKINPALIGGFTVEVGSNYKGNFALSSQFDLMRQQLKQAE DKW
ERVRPKELHINSFDTSSLFAPLSGVKITAADLDKTLADVLGSKKEAFQAA
DLDRTLKQALEDAQRDAGFSGDYKENVLEQTRNLDFEKLKTVKQLDLAQH
EKHLMQKHNIADNDAEGKRKVKAKIEELKRFKELDTSFIGEVLKHKHPET
YKKYQSVFQ

>F0 B subunit gi|11467082|ref|NP_042558.1| ORF25 [Acanthamoeba castellanii], 124 aa, 1953

MKYSILLFFTLFAINLLHYISEKVIIVIFIVFLFFLMGFLSNIINSEFK
SKIDYILNDINAYVNVVFNFLYINKLFLYLNKSLKTGFLSLNSILGKKID

SLKFYTTLSNKLNAISSTTVLLLL

>F0 A subunit gi|11467086|ref|NP_042562.1| H(+)-transporting ATPase, subunit 6 [Acanthamoeba castellanii], 247 aa, 587

MIFNPLEQFRISVLQKLFQGNIDISITNNTIILFVILIGFTFLFYVNYST
NTYIPSKWQYAVENIYLFVLQLFKQOINNIVALKYFPLVLFVFSFILFAN
LIGLLPYGFTITGHIIFTFQIAFSLFFGITLINFFNKKTEFFNLFVPSGV
PKPLIPFLVVIEVVSYLIRPFSLSVRLFANMLAGHTLLNLSAIFNFVK
KYALISFLPLLFIIVLEFCIAIVQAYIFSILTTCIYLNDIYNTSH

>Fo C subunit gi|11467060|ref|NP_042536.1| H(+)-transporting ATPase, subunit 9 [Acanthamoeba castellanii], 79 aa, A9F

MKNLEIILQSSKMIGSGLATSGLIGAGAGVGVIVFGCLILAFSRNPLOKE
LFSYALIGFALTEAIGLLALVMAFLILFI

>F0 A6l subunit (ORFB) gi|11467081|ref|NP_042557.1| ORFB [Acanthamoeba castellanii], 142 aa, 198E

MPQLDKLSFATQYFWLTLFFFGLYFLSVNFFVILVFKNLKLRNIIYKIWY
FFLYRFDYVDYNNKHKSLVNTSFSFIYYTLYINFFILTKINFIFEKTKSI
INKTQTLNQSQRLLMISLLNFFLNSNSVDFVKKFQELNIDEI

>Probable ATPG, Contig14600/E9BS9UA01COP0N (complete) 110 aa

MNRLCGSLAKGAQKFQALEQSTTSCACNKQLYGYLGTQFGCWSNRWQAFP
ADAKALWRRVITGQITVGEVGRGVRASPILLALAGNFLGRGEFLYSPI
VGASYTYPEY

>ATPi/j, Contig19534 (and E80POFO01BMSND) (complete) 92 aa

MSARNFGLTEGEIQELKKRPYPRFAPAPMORLISQAKVIWPFVAVGWAVTL
FLYSRIPISDDRAKSHYQYQLDVLGKIKPEDHPIHGHHGH

>hypothetical ATPase subunit, Contig31 (complete) 312 aa

MMKRGLRQVPRSVILGQRQSAQAMRLFASAAPSPNVDEIQFQVIGDTATA
EYPTRPFTSKSKAQLEEGVQRKANQTRGQFEAKFSADTPEGALFKDQVQI
KPYDEQLLKAELHVTNPTIQPTVDTAVNTKHNHFLTEFMASRTAGYLED
PTLYFSYGENPSATLNPWSTQLSGNLDALVKRELVDALAALSAEVEKID
ALDQQAQKAHEELLQKLQADIDILTNEKELFAKSLSSGMSPLHVAQMTDI
VTTDPLAVQALPLAQQAELAQFRQOSATFQOYSQVLVADSRELVKQLQA
SGLQFDASKVSF

>hypothetical ATPase subunit, Contig15510 (and E80POFO01B6VDY) (complete) 92 aa

MSKRLITRATLNGRLATAWAPSRSYAEAAVPKLGKDIQPKNYRRPDGTYE
PCDEILFLSVIGYGEDLRAVTNAKEGITNTLVLSRYNKTASQ

>hypothetical protein (possible ATP synthase e subunit) Contig24711 (complete) 102 aa

MATPLQVPCGRNSLQSFQAAAFTVAFVWTSQSVQVKRNAYFSNLKSEI
DTLKKKNHDLHEVELLKNPPEPKEAHTDFAADFESGNIDFEKILEQVAS
DH

>ATPd, Contig17555 (complete) 499 aa

MRRISRNVASSARGTALNKSSRTAAVFSRQYAAPETPQTDKFTDAGIRV
YAHGVVHDMNFLGDLPADAQEVLSGKEWVQSVSDFTARWEKDAPELANQ
ARQLESLITKFEKDPVQFGKSEAYLRDIAIHTTLERAAARDVSPVEIALT
HFWTAYSEVPSGGKLRRESAPTQLERVKAFLQSKKDPELSAQNSRARKTAA
IVKFVQASSAEDKAAAAALLLGESEKQALKAAKGVNDAKKEQIVKQHL
QWDEATQAAAELTQRHPEFTTELKEVLAHFPPLVHHIGEPSAVQYRFKHAT
DKAYKKWQONYSLTSSDEVTEKDLLKLNRELLYSGKPANTVADAKKAQA
LQSFPLGLLFSRDVESFSNFVRKDEEVKSQLSTIYEDSLKEYPNDPALAV
PKDLQORVKLWSKHTQELADVQQWLDKIAFIDAKIQEGMVQMDKVFNG
TVDDILADHPEWEKEIEDDIANHRWDPEMEKKEYDNALHHYYEHHTVHA

>ATPf, Contig26899 (complete) 94 aa

MSRSLITRSLPLRSSSHGALGGARPVFSEVPLKEVPSYVRLHVLGNTRRL
TKEFVQWYWRTYFHAGKADPIIHGILLVSGVGYLLHNNHWGSH

>malate dehydrogenase Contig10193 (complete), 454 aa, 63B

MRRGLSTVRSATVFGKQACLASSTLRVDRRAYATSPEDAALAEQIEKVL
DLVKKQGNLGEKLTVRKLTRELQTVPEIDRALSSVGD SAVKYMAELEKP
GAGPLSAVPPVVTVTGAAGAIGYAMLFRIASGEMLGKHQPVILQLELE
PAMKALEGVIMELKDCAFPLLHGVTASSDVNKAFFEGADFAMLVGAKPRTK
GMERGDLLKENANIFSVQKALNKVANRDTLRVCCVGNPANTNALIASAN
APNIHPRRFTAMTRLDHNRGIAQLADKCLKCKVTDIERFAIWGNHSATQYP

DISHTQINGKWAKDLVDEKWKDTPFIPDVQQRGAIIAARGSSSAASAAN
AAIEHMRDWVKGTNGQWTSMGVWTGNGKVGDTGSPDIYYSFPVVCADGE
YTIVQNVVPDKFSAERMQKTNDELVSEKNGVGEKAKRRTDPAALLKEQYK
GGKQ

CV-associated proteins:

>Inh1 homolog Contig8833 (complete)

MMRRAATRSALCRPSFAPTAARGYSSVLEAGGRLGEREKAVEDRAIRGHDLLELLKLRDT
LGIQENQPIPETVVSQVSSSSSLNPFQAQRAQSQQPSSSSSHNDEPLTRGEFLEFRREIVQ
RLRNLEDDIMDLQTRRK

>ATP10 (assembly factor) Contig2185 (likely complete)

MRHFALPSSAPTRPGLLVCRVPSDLRPGAAAPLTSGLRVRPPFWHGPRMHHTPLLGVLP
AQATSRGARHEHWGTLKRFKELAKTPEELALKEELDKGYWGDANELLKNREGKFFFAVPK
LTPKKEAIKLLDAIPASLPTYKPFDFSKVNIIEAMHTKAPTLVLVTCKRMFATAMLDLSDR
KPFEAEPHLLNCYELELVQOVGYWVFGGLFRMFAAKEIEPSRMNKVLYYNGIRKTKRMRW
DLNIKNRYCAYAFLCDDEDGLVRWRAVGLANTEELAMLNKMVNKLQOEKGGVSSSNLASR
SGLEHQKAD

>ATP11 g4701.t1 (complete)

MLLMRRCLRSPAVITNTAGGGGRAAPVRWFSSGAAPPPRELAHVVKLDSL
HQETPERISQLWIDYHVKKEACVSAVAPAATYALINRRLAESPLFVLP
RESGFVSVLLQAHAEQDVMFTELEQYQRAADKSAVPSCLHLRYTDLAA
TKDIVLVRGEVDLARLT'TTVKRKRW

>ATP12 Contig13926 (complete)

MRRSCASVAAGGARWGRCGHQAASRFPSTMLRQAGSDGFRFLRPSLT'TMRMLGATRSYAE
RVKVDYHYGHEKFKGDQAEPASED'TTKPKVKGAKLSGVQGGSKTRRWYKQVSVGEREGGW
APLLDGRVILTPMEHPLVPSQHNAIMIAAEWEMQOPYIKPDTMPITRLATTIMDRLVEG
KPEIRHALTLEMLDYIETDTICYRPDDREKEQVLYDKQQAQLRPFLKWFSSFFNMELMLH
FSVIPEAQPEETINGLRLLLHNTTDWELGCLDTLVSRTKSLVGLALWKGPFSDQICIAA
SRIEEDHNIAEWGECEGAHDLKVDIYKHVAAATAFLRSLPPEQSSLKQW

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

MRERQHSQCETTIRDILIKDRVMQHLMAGMEDRGRVIFYKNFFHCKQCTGSDHGGYWDPD
EGVVICENNLEQKEMVRDMLHEGVHAFDDCRANVDWSNCVHHACSEIRAANLSGDCSFR
AEVARGHFNVAQQKECVRRRATLSVIKNPCPGADADWAVNKAWERCYSDFEPFGQVPN

>Nca2 Contig9 (likely complete .. from PGP)

MLFARRAQGTRQRIASLFLGIDGATHDLSFLPPDQEKLYRDACVALTKQSIDGHTLTHVA
TSVAPFIGYRHRHRGAPTGPATGGGGEEAASQSSAPADNSDAVVHHDEGKDKGKGEKNR
SEPATDGECSAASKEDLQDQVLFKLYVLCIAIAQNQSVCEDELLRLASSIQHHHREWS
LREDQPFWLYEKTWPYWLNYLLLRDETPHPITELREKLRHLRALEKNTFAFIGVGSRV
LSRYEAVGRNTYAERLSNLIRKDQOEEDGENEDVLFNLAQTVNLSYFDYHSADVIGETTT
ETTPNIPNLYAQLMENVKKAALFPTQMKHTLNEYKRPSALSTNWLRYSCITAGITVGVL
VVKRREDIIDWLVDFKVLAKNFIQKNILLPLQDVYETIRYKRAFTIMDARALDADVESL
QRMVDEYVRKLHPHISQAQLEEITTAANSDISAIMPVYERELESPIKNALFGDLLSLLL
IQVHKAKVDVARAMLALDKLMRANELNFQLFVTPAILLVGGLSRYLYRRITRIDIRRTT
HVQIRETLRNVRLDLNLSSASSSVRHHHAGGPTNLSLSTSFSGWGRSSTNSLSTQGRP
ESDLRLEDTRLLVSVINELIRLALQMPRHDRKWLLLEDLQDLQAEELQVAQKLATIHRYH
THHFLSAV