

CI structural proteins:

>gi|11467066|ref|NP_042542.1| NADH dehydrogenase, subunit 1 [Acanthamoeba castellanii], 369 aa, 2706 checksum.
MVSLTVYFILLSLYLILNVILTVAFLTLFERKVLASIQKRKGNWTGFLG
ILQPLADALKLILKENPVPQONASSVLFVGGPLILLILSLSAWFVIPFNNE
TVVSDINIGILYVFMVSSLNLTNIIIVAGWSSNSRYAFLGALRSIAQVIAY
EVLVIGIIIIINIIVLSGSLNFKLVWAQKDLWYAFVLWAQFFLFFIAMLAE
TNRHPFDLAEAESELVSGYNVEHSSVLFALFFLSEYANIILLCHVATILF
LGGWTPDLYFFIKFFSVEYYVSIIDFFYTLRSNFYYITWIYHSLVYIIK
VYIYLFAFIWRATLPRYRYDQLMRLGWKVFVPLTIGLVFISISLTLFFD
GFPSEGGYINHHFFSSDIFI

>gi|11467058|ref|NP_042534.1| NADH dehydrogenase, subunit 2 [Acanthamoeba castellanii] -----
NOT DETECTED ----, 527 aa, F14 checksum.
MNVINFIYSIFDKKLFKCGTISRGLFYNDLNFFHFEEIYFLLALITFLIF
FVILSNKKNYRSYYYYLVGGIFSNLLPFVVILLIILNTNTNDSYYLAFAG
FYYNDAAVVFFKNIILIGFLIFTFAIKQYLSYFKYYDFEFILVLFISLFS
SLLILNSNDLISLFFIIEQLSLTFYILVASKQTSFSTESGLKYFILGCF
SSGIILFGISLIYGTGLLSYTDLTLFLSEVYVTNFILDSSFFSFGFLI
GFLLLTVGFLFKLGSAPFHMWMPDVYEGSPLLITAYLSTLPKISLIFVIF
KLYYYVFFEVFLFSQGLFTLTALFSILLGSIAAIYQVKLKRMLTYSMITN
TGYYYYLGLSFGDISGIYITIFYLISYIFIMIGLFFCFLSLRDRSSGLLVK
RINLFSNLLVNPSSLFSIFILLFSIAGIPPLLGFYSKFFLFLFSLKYKM
YWMTILFVIFSVVSVFYIRLVKLMYFNRTTGWIFLYDIPFLNSLIISFI
TIINCLFFFNPPLLKLIYNFSFYLYI

>gi|11467083|ref|NP_042559.1| NADH dehydrogenase, subunit 3 [Acanthamoeba castellanii], 118 aa, 508 checksum.
MTLEYIYIFIFFWGAFIFISCLLIFLSYFLVYQESDIEKNSAYECGFQPF
DTRSKFNVRYYLIAILFMIFDLEIMYLPWSISISTGSFFGVWAIFLFLI
ILTVGFIYEWQKGALEWD

>gi|11467057|ref|NP_042533.1| NADH dehydrogenase, subunit 4 [Acanthamoeba castellanii], 497 aa, 13C checksum.
MAFLLYYTLFISFMLWLAALLIISFSVYGSPEKVKLIKKTSLFFSFFQFI
LIIFFWILSDNISVLAEFDIYNFQFYKQWLFYLNHYVIGMDNISLLFLL
LTFFLTPIICILISWNSIKYRYNSFIICLIFITFILFNIFCVLDLVFFYIF
FESILIPMIFILIGVWGRQRKIHAVYQLFFYTLLGSLMLLGLILVIYSHI
QTTDIRVLYNTNFSFYRQLILWASFFFAFCVKVPLFPFHFWLPEAHVEAP
TVGSVILAGVLLKLGTYGLLRFVPIFCDATYFFLPLVYTLCLLGIYTC
CSTIRQVDLKKVIAYASVSHMSFVILGLFTSNIQIGGSVFLMLSHGIVS
SGLFFCIGCVYDRYKTRILRYSSGLVSTMPIFSLCLFILILSNISFPGTS
SFIGEFLILLGLFENNHFAAALIAATFSIILTAVYSIWLYNRIIFNRLVVNY
YLRFSDFSKKEFVVGFIFCFITILFGLKGSYIISLIEAPLYVYLSFK

>gi|11467062|ref|NP_042538.1| NADH dehydrogenase, subunit 4L [Acanthamoeba castellanii] -----
NOT DETECTED -----, 103 aa, 1873 checksum.
MTSFNIFLLFFSFVIFFLGILGIFITRKNIIIIILVSIELMLLAVNFNFA
IFSVLLEDMFGQVFILYTLTLAGAEAAIGLAILIIFYRIRGIISVNFVTS
LKG

>gi|11467054|ref|NP_042530.1| NADH dehydrogenase, subunit 5 [Acanthamoeba castellanii], 675 aa, B33 checksum.
MYLLPLLFPLLNLFISCILGKFLGKRVLFVLVINMLFSAIFSFWIFYEVG
INKSVCYIDLGPWFHIGLLKLNWLFVLDITSVMLVLVVVFVSLLVHLYSI
DYMGGDPHIIRFLGYLSLFTFFMLMLVTSGNFVQLFLGWEGVGLSSYLLI
NFWYTRIQAANKSAMKAIIVNRFGDFGIYFSLLVIFVFFKSFDFGVVFNLV
QFLDTQPRMSFLGFSNLRVDLIVIFLFLGAIGKSAQLGLHTWLPDAMEGP
TPVSALIIHAATMVTAGVFLIRSSPILEYSSTGLFLVSLIGGLTALFAGT
VGLVQYDIKKVIAYSTCSQLGYMFFACGMSNYSVGLFHLFNHGFFKALLF
LGAGSVIHALLEQDMRKMGLIKMLPLTYVAILVGSLSLTGFPFLTGFY
SKEVVLEIAFSKFSINSFFIYWLGVFAAFITSFYSIRLMYLVFFARPNSH
ARAVNSSHESSSIFIVLAFLGFLSIFIGFIFKDLFIGLGTDFWANSIFN
LYVNSDILYAEFLDYKYKLIPLVFSIVGLFFSLFVYFVIYDYTVFVVKNK

FFRYAYFFLAKKWFYFDLLYNNIFVFNLLSSFYLLTFKIIDRGLIELFGPL
SFVRLINKSSIIFFSSQTGFLYNYIFVVLLGLMFFIKLTSSLFFPSFNSF
FNFGLFICLLSLIIFLSFGNKKQNI

>gi|11467053|ref|NP_042529.1| NADH dehydrogenase, subunit 6 [Acanthamoeba castellanii], 260
aa, 19CA checksum.

MLTNYLLIIFCFLALFCSFMIIASKNPIHSILYLILVFCNVTFVLIILGV
EFIAIIFLIVYVGAIAVLFVVMMLNIKILELDEVFWRYIPAGLLISSC
FLFQLFTFVFNFSVVEVFGFFYNGFYNSINKLALNFSEIHTVPSGLLING
IYIFPNLSNLGIDQVFINSIYKEESFFCFVKLNEASTNLLGLSFELTNT
ILGWLVTYTYTFFIFLVVSLILLISMIGSIIILVNLQNNINIKRQVIFRQSLR
DLKSSVSLKN

>gi|11467085|ref|NP_042561.1| NADH dehydrogenase, subunit 7 [Acanthamoeba castellanii], 401
aa, A9 checksum.

MRKNQISPYIKTSKIKNFTMNFQHPAAHGVLRLILELDGELVRKADPH
IGLLHRGTEKLIYKTYIQALPYFDRLDYVSMMSQEHAYSLAIEKLLNCN
VPIRAQYIRVIYSELTRILNHILAVTTTHAMDVGALTPFLWLFEEREKLM
FYERVSGARMHAAYIRPGGVAQDFPLGLWNDIMQFVEQFFWRLVEVEELL
NGNRIWKQRLVDVGVITAEALSHGFSGVMLRGSGIAWDLRKNNPYEVYN
KLNFNPIPIGKNGDCYDRYLIRVYEMYESLNIKQCLTAMPAGLIKVNDDK
ITPPERTDMKYSMESLIHFFKLYSEGFNVPENETYACVEAPKGEFGVYVV
SDGSNKPYRCKIKAPGFLHLQSLNSMSKGHMIADVVTIIGTQDIVFGEID
R

>NAD8, Contig2253 (complete) 247 aa

MYAGRRAVSINRTSPLRGAFILPRASASSTLVATERSVVLATRGMAGGS
YQDEHKRTKLKGAAHAEPETLYEDLPTAHLHKNLTWSGLIEGSAHTFALSE
MMRGFMLTLAYMFKPKVTLNYPFEKGPISPRFRGEHALRRYPSGEERCIA
CKLCEAICPAQAITIEAEPRADGSRRTTRYDIDMTKCIYCGFCQEACPVD
AIVEGPNFEFSTETHEELLYNKEKLLANGDQWEPELAANLRADFLYR

>gi|11467084|ref|NP_042560.1| NADH dehydrogenase, subunit 9 [Acanthamoeba castellanii], 195
aa, 1465 checksum.

MGLNFFMSRKIYYIKLLTGLYKFKIKALIVKKNESNNAYLLVETANFYNL
VFSLQRSSLTQFKVLNDVCIVDYPEKIDRFELSYNLSSIKYNFRIKTY
TSAYVPSISTLFNANWIERECWDMFGVFFTNHPDLRRLTDYGFEGFPL
RKDFPLTGYIEIRYDDEKANIVYEPELSQEYRLFNFSTPWEKIK

>NAD10 Contig11752 (complete), 177 aa

MSSGVTQKLAHFGKQALTGLSKTEFVISKLDQIVNWIRKGSIWPMTFGL
ACCAVEMMHAAASRYDMDFRGIVFRASPRQSDVMIVAGTLTNKMAPALRK
VYDQMPPEPRYVVMGSCANGGGYHYSAVVRGCDRVVPVDIYVPGCPPT
AEALLYGLMQLQKKIARERNLLSWYRK

>gi|11467055|ref|NP_042531.1| NADH dehydrogenase, subunit 11 [Acanthamoeba castellanii], 675
aa, 498 checksum.

MKNISFKVNDFOYTINNKLTLIQACLKNKVDISRFCFHEKLSIAGNCRMC
LVEDLKQVKPLASCAINVSNSMNIYTNTLVKVKARESVEFLLANHPLDC
PICDQGGECDLQDQSVVFGSDRGRFYEFKRSVEDKDCGPLIKTIMNRCIH
CTRCVRFVSNEVAGVNILGVTGRGSKMEIGFYIENLMRSELSGNVIDLCPV
GALTSKPFRAFTSRPWELKSYNSIDVLDLSLHNSIRVDIRGTKIMRILPRVN
SELNEDWITDKIRFSYDSFRRQRLYDPMVKISGSFLKIGWKKAMLFIKKF
FCNFLGFNHSSFIPLRGYIGDYLDLETIYTFKKFLLLNGSNFFLPSSSYN
DLTALYSFNTPLTRLDEGDFCILLDVNLRVELPIVNSRIKQLVSKMLPV
FVLGFYSNFNYFVKHISNSSKTLHVLEGGSHWLSAKISKKFSSKPIFLIG
DSSLLKGLIIVPLFNFTNVICDNWNGLNIIISNDSSYLSTKEFNLSSSHS
QNSHLLNFPINFLVNYDKAVLVDSSAFQIYQGHGDTNAINSNLIFPSTS
FIEKNSFYNSLAIVQTKKILFSPGNSRDDWKILNALIDNFGFSYFKVR
NSFDLVSFLSESTPFILYKRSFSFKCFGFYEQLVYHFFNYFSVNNNYIY
DSITRNSKIMSLCFNKFKMKGYNFF

>Aca 24 kDa, Contig3477 (complete) 270 aa

MRRATSSLSAVPALRTTGMRATSSLFTSSSSAAMLKSRTLHSSVPRQGDH
GGLSQHRDTPDNTIDTPFDTEANTVEIKKILAKYPVNYQAATIPLLHL
AQYQTGGVWPLAAMNKIAKILEIPPMKVYEVATFYTMFNRTKVYKHYVQL
CTTTPCQLGGCGSTVILETIKKHLNIGVGETTADGLFTLVEVECLGACVN

APMLQIGDDYFEDLTPESTVALLETLKAGKTPKVGPOQTGGRKNCEGPQOK
TTLFAAPAGPYCRPDLETCA

>51 kDa, Contig6370 (complete) 492 aa

MLRRVAVRSLAPVTENVAAPAAMALASRRDYTTTERSYPNLKSDRIFTN
LYGEHDIFIKGALARGDWYKTKELLRKGEDWIIKEIKNSGLRGRGGAGFP
SGLKWSFMPKVSDGRPSYLVINADEGEPGTCKDREIMRHPHKLVEGCLL
AGFSMKAKAAAYIYVRGEFVYEINNLRQRAIDEAYEAGFLGKNACGSGDFD
VYVHRGAGAYICGEETSLESIEGKPGKPRPKPPFANVGVFGCPTTVTN
VETVAVAPTILRRGAEFASFGRPKNSGTKLFCISGHVNNPITVEEEMSI
PLKELIERHAGGVGGWDLKAIIPGGSSVPLLPKSIDNVLMDFDALRD
VTSGLGTAAVIVMDKSTDVIAAARLSKFYRNESCGQCTPCREGSPWLWN
VMERMVTGDAKIDEIDMLYELSTQIEGHTICALGDAAAWPVQGVIRHFRG
EMEQRIHDYNSKHGQAIGSATVDEYASRQLHLAKQAPLTFVQ

>39 kDa, Contig21164 (complete) 376 aa

MKRVAQAQASFAGPRSIATSLSWEGAAGVRGLHVNLOGGRSSVSGVVATVF
GCTGFLGRFVVNRLGKIGSQVIVPYRGEESAFRHLKVMGDLGQIAPVWFD
LRDKETVRRAVQYSNVVINLLGKRWETRNFSFDDVHPEATRITIAEAAKEA
GVERFIQVSAAGADVNSPSAFARSKGESEKVLREIFPDATILRPTVLYGA
RDNFLVKWGMARIYWPVAVRVLTKDTKFQPLYVADMATALMNALADPETAG
KTYELGGPKVYTLLEEITELVTRLTFLEPSVVDVFPALRAFAQVTQPFLR
KPRFTVEELDYWKSQDVVVPENAPLTINNLNFSTEDLTVLEKEAVNFLRL
YRKPATMNLILEDQLDVKSPRARASR

>NADH dehydrogenase B14.7 subunit Contig22734 (complete), 196 aa, F9D checksum.

MAHEHDHHTAKDSKKDVEIPDLFGIDALDIHGGEPCLVQAKMAATSFIGA
GSFFGGVLVYWKDVGVVQKRGRFAALQGTLSIGSYGAFFALVGATYGT
FCALQHSRTKNDFNTVLASCAAGGVIGARVNGTVFGSVLGAVTGGLAA
MGEFFDWTLSPNSAKLFALREQKHQRLLRTSPGVGSDAASSDSDAQ

>15 kDa, Contig2142 (complete) 122 aa

MSTGFGFQAGRCYPIWRDFALCKNGSANPGECTPFFQDYITCTYGWADP
ENVELFKRQVALSEEQEKWQKQYQKMAAHVRTFETEAAAYEEWKESLGAK
VVETPATMDELNAFTKEKLNPO

>13 kDa, Contig14419 (complete) 134 aa

MRRAAPQLSRGMLPAYGRSSSSLLASRATLSSTASRAASSLKLKIPFLGD
TEIALKDDVFRPGVPENPGNLYAPMPAEELIHEIPPVTHGSTAVCDGGG
GALGHPRIFINLDKPGPHDCGYCGLRFIKEEEHH

>AQDQ, Contig797 (complete) 194 aa

MKRLTIARRPFTFAGATPLYRSAAPLSSQORFLKDIASNSANEAPPNTDA
AQVRLHMAIKGNADEVSEERRKSISAVMGTPVEHLKRRVRIYIPARCTMQ
SGVHSATFWKISYPPEEKNHWANPLMGWTATKDPVSNLHVKFDTKAAVA
FCKQHGLDYEIEDSTTPYENITPNKDYADNFKFKVERSLEPDIY

>PDSW, Contig9011 (complete) 96 aa

MSSGRAVPDFNDTDFDTEDPVAYQKAIRQRVVEHIVATEEMAELQQLSQ
CYYREGVNYRKKCRPLAEEYMKRLEKWKAYIPPEGEETDSVVRMRS

>PGIV, Contig13270 (complete) 178 aa

MASTRKEGEQLYADINAGGRTHLDVETDFNVLVAGAKYTSYMCAAEEELD
FLECKAKDENPRACVPENVALTECAHAALDKISRQCASEFDEVVDCLESP
SVHGELSACRQSERDLRVCVQARFGVDVVVEERKRRMASLQTWASTRRRP
QPTIIRPREQKKVDAAVAKYKKEHDITE

>SDAP (ACP), Contig16222 (complete) 145 aa

MNRIARPALLRASARAPAFAPVASSLRFSSISSAALSTTFARRSDAITT
FDYQRRHYGAAAGLSEADARERVIKVVKNFHKVDPNAVNEKSHFINDLGL
DSLDTVELVLGLEDEFCEIPEEQADKIQTIEDAVSYLVTPAAK

>B22, Contig8040 (likely complete) 129 aa

MNKGGLSSVANAAVGEAHRHVCHLYKRALKQLDVLVKRETWYPEANKT
RALFRQHMNETDPRTISRLVKDTENLLYTYRHPDPYVSPMSEGGTKWQRN
VPVPPEVAENGWAEFDYEEFEQPPPKADF

>B18, Contig112 (likely complete) 79 aa

MLISEEEMDAERLPIGYRDYCAHLLVPLNRCRQECFYLPWKCTHERHVEE
GCQYEEYKRRKKWMLIEKEKLRKRAQEKQA

>B17.2, Contig24514 (complete) 151 aa

D

>NADH dehydrogenase Nuum subunit Contig7424 (complete)
MGGGPRFPFPKVVWSPAGGWCCENPPNAQRNLRIVLGLNFIAIAGAVF
FISAANERRLLSHPTIPVPSQRWSAWTKVDDDPDYKRKLAAYHKNKKPLWERILPDAMIQD
EHGHH
>NADH dehydrogenase MLRQ ----- NOT DETECTED ----- Contig11127
MQAIRRTYNENTKAVWLTLPVVGGLWAAYIGFRTFA
THNDVVLKARGNEPYLMRDSPKLLSRDAAITLADKWSNEMGGDDQFQKPK
>hypothetical NADH dehydrogenase subunit Contig11 (and E9BS9UA01C9GEK) (complete)
MADENRDFPEYEAWVKKQSAFARWAIRTRAAIADQDETNNAEYLRHVAKNMIIMKEESYL
WSSSAQRPDYYKGRSPLTAAAYRDHGMFKSPYEIRAKELRGELIRWNHWHSWDLKPSATT
SYPKPPAKYDPLNPTRPNIRKQRLEREAH

CI-associated proteins:

>Ind1/mrp protein Contig23731 (likely complete)
MMRRSVVGAASSTRVAGWQKRGYAAMQLSRPVLHGGPQGRPLPNKIKLPGVKDIIAVAS
GKGGVGKSTVSTNLALAISALGKRVALLDADVFGPSIPRMLNLSEQKQVTDTOQLLPLS
NYGIKCMSMGFLAEKDSPMIWRGPMVMGALEQVPPVTCQSQLHSLTTRPRMVIDLPPGTG
DTQLTLTQRVQLTGAVIVSTPQDIALEDARRGANMFRKVEVPILGLVENMSYFACPKCGE
VSHIFGHQGARQTAKEMGMDFLGEVPLHMTIRETSDSGRPVVVSQPSSPQAEAFKHIAHQ
VLDKIQDPAFRKDQEAAPRIIS
>C8orf38 (phytoene synthase) ContigE80POFO01DU06I (and 2111) (likely complete .. mostly from
PGP)
MKAMQLSIQRARIVPATTVPLFSSVEQHLLLHRKRKLHSTSAALHGGGKCEHKPTTSGAI
PWTFTPHDEDATTKAPPVRAEKPFSTPPHPASTSEAGSADTAATAGQFERQGPAPAKQG
GISSLDYICITQSKKLDYEHYLCGMYLPKEARAPYSVLRAFNIETAIKDKIAKQAPLGLMR
IQFWRDLVDKSFKGNPPEHPVAIQIAAMVPRYKWTTRTFTRILNKRAEDIEGRPMPTLAA
LENFTEDTASSLLYLTLESIRNMDADHAASHIGKAVGISFLLRGTPYHLQORQTYLPM
DLLAKHGVSEEAIQGNLEHAQNLPEVVYEVASAAHAHLKHARELKVTPKEAYSALYSS
FIAEDYLNKLEKAKFNVPDPALRPTPQGSGLQAKLLYNHYVGHKY
>CI assembly methyltransferase C20orf7 Contig2501 (and E9BS9UA01A74BE) (complete)
MRRRAAVLQRANTRSLRPGAFSASSPFARGQIRRLSAEGCNRISCTTTRLAAAPVTMAWSK
RGLASSSDSAEEQRAMNVFNHRVVKRLQRDRAAADPESQDYDYLKEIAARLADRLNDILD
REFPSVLALGGAAAGVAEHLQEIPIGVKRIVQLDSSPLSLARDQHLADLAIKPERVVADE
ELIPFEEGTFDLVISNLALHVVNDLPGVLAQIRRVLKPDGLFLASMFGEETLWELRNAFL
VAEQDRDGGISNHVSPFAGVSDVGDLLTRAKFALPTIDQEEVVVDFADAFTLMRDLRGMG
ESNAQHFRRPYVPRSTMYAAAAAYKALYGKEDGRVPATFQVVYIMIGWCPHESQOKPKERG
SAQFSLKEFAHSVGEKLVVDDNGNEIAPARPGEPEAGGGDHSCGRH
>midA Contig13582.t1 (from 13582.t1) (likely complete)
MKRITAATRRLVLRGDAALVRCCTTSASLCRRGSNNHQIGGLRCNSTNGKPTDQSAQATEE
MTSRAISIDTSGLYKHKPHGPAGNKSADTPLLSHLRANIQVHLAPIVVPKPGAECLEAVS
CRWCLQLRGPISVATYMKREALTNPMHGYMKNDAFGQKGFITSPEISQMFGEVLKKTPE
LFGQMTIHMVEVSPYLRQQAATLGCPTLLSGDAAKETSSTEDTRDTKPTAGREETGHW
SSPVLTGADGVRVQWHRHFRDVPVPPFLVVAHELFDALPVYHFYTEKGLERLVDVDQD
EGPHHLRYVLSPGPTYATMALLRQAGVSTEPKPKLKQKAPTASFYSYRGGEDDDDDNDDN
RPTDGPVGDRIEVCAGMALASQISEKIAREQGRGAALVIDYQDRTREDTLRAIKNHK
IQDVLCEPGLADITADVDFSSLRRTAQOTRTPTLGFCRSRKSRRVVWPLMCVVCVCPD
SLDHDVREAAAGPVPAGARHRSAGHAPQERWRRQVRTVLLVQHTPPHTRHHAHAQRNRT
RCSAQAKDLIAAYERLVDDEQMGLTYKAMTICSLHNKQPPVGFSL
>Ndufaf1/Cia30 Contig5982 NOT DETECTED
MLGRSRAGVGSVKNLVREALAGPPLLREGAFGGPQARERMLYSFGAGADPAAWEAVTDA
DFGGRSRAKLEPTEQGTWVFGALDLSTEGTEMKQAGYAGLQPRQRKTIKSLEGFDALV
RAKTDGRVYIANIKTDSMVKHHLFQAFFTTTRKDEWTNVVLPFDRFTLTFQGVQVEGESLPI
DPRQFQAVSFLMAERKDGFRMELEWVKAINTRLRKGARYTGLVHDQD
>NDUFAF3 homolog Contig17448 (complete) NOT DETECTED
MAAAGPRLPGEYDVFVGGDGGEGSHGNKVMVDGYSGSRFSINGVLLPGPL
FLLPTLPLAWNVTSLDDLSPELALAYAIRPRVSILILGCGQRIKMINPQ
LRDFFRQKGISIEALDTWNAVATWNILNQEDRAVAAALMPFDYE
>Foxred1 homolog Contig27121 (and 22107, 24645) NOT DETECTED

MMKCRQPRHLLSARCASPAPAAVVRPVPRHRHSRLLSTSAGGAGGGSIVI
AGGGVVGSSVAYFVARALRSRGQTLASPPPVGSRSEWTVTVVERDPTYRF
ASSTLSASSIRHQFSTPENILIGQYGTEFLRNAGKLLSISDEDEARLSGR
LQEKPQQPQHPALLESNHQLQORDLGSDIRFLGSPSEIKAQFPYLHTDDLS
AGCFGASGEGWFDPATLLHGFKRKAALGVNFVHGEEVVGTELEADGPRQR
VSGVQVTTADGVAHKLSCSHLVNAMGPOAARLSQMMGLTLPVVPRKRCVF
VLRCRDEEVNQAKMPLVIDPSGVYWRPEGCGFIAGVSPLVDPDAHGDFFV
DHDLFEEVIWPVLAHRLPAFEAVKVVGHWAGHYDYNTFDQNAILGTHPSV
GNYYHANGFSGHGLQQSPAVGRAVAELLLLEGAYKTLDLSMFHFERVLENR
PIIELNVV