

## Acanthamoeba castellanii Mitochondrial Small Subunit Ribosomal Proteins

Key :

mtDNA-encoded

nuclear DNA-encoded, MS peptide(s) identified

nuclear DNA-encoded, MS peptide(s) not identified

**Boxed residues** denote nucleotide sequence heterogeneities, presumably due to allelic variation

**Red-highlighted residues** = MS peptides (underlined residues are MS peptides of questionable significance)

>Aca\_M-S2\_gi|11467059|ref|NP\_042535.1|\_[312\_aa]

MFNRIHITVNLQVSDFLGLYHIANWNPR**TNFFLIGK**YKNTNIFNLNYTYFLAKK**FIVFLSELFV**NKGHLW  
LVNENFSLFNRSSELYQLYSLFPEITFLNSKWCKGMLSNYKYVSIVKPAKFPHSIFVPNIQNNHYVINESF  
IINIPISIAIVDSIDNPSNVFFPIPGNSKSLKSLFFFYMVIAKSLFYSRYITSSK**FIFNSIN**RNLNGLNSKLY  
RNLFVR**DYFAFFK****RFLLENIIFL****FK**SGFFSKKKFNFLFRPKMHITSKTLFLFKWKMPLLILSSVFKNVLHW  
DIFNKIVLKKRLVVKNLQFFKTLMFVLI

>Aca\_M-S3\_gi|11467072|ref|NP\_042548.1|\_[298\_aa]

MGHIINPISYRLYNIRYWNWNWFSGLNYSYLNQDILIDRFFRKFLTTHLDSTNAGIIFVNLKIIRSFNN  
ISLYVYIHDSFLDLLFFNLK**NARFLLIK**RFLNKKFYKRYKALRQNKQLK**QGLFMLLKKR**VILRYSRKL  
FLFIKNIKILKIYWSFKTSLFYLRFSRSSFLSKIFIIGLSK**MNVNANIISEFFF**IRLTQYYTIWEVLRN  
**INFLFKSLM**KKRKLKVGKIKITCSGRFSRQRTTYSWK**AFGSLAFSTVKS****KL****DYSY**KTIALKYSSCTIKVWV  
RLGKKSNLVDFV

>Aca\_M-S4\_gi|11467052|ref|NP\_042528.1|\_[374\_aa]

MYKFYKHKLYK**KYQDELWGHII****SK**SFSYNKKSILLNYRDIILRNRLRIKTKFKYFRGFLKLNLYTLLLF  
KFFRKNIRVFSFKR**QSLVPLSLSS**KRFKTKRKFVFFKTSKIASLLKFNI FYANTVAFNKVFIK**HNYCLSS**  
**CSNIYTQT****KL****LYFPIISVNR**GLVIFYKSKNFLRVNQLQFVIKKNLNRKQKIFFYSVHIAAPKKKTKKWSLF  
ALKNIYYKVSLLFFGFRKVVDFFKVYNLAGALAK**GNSFAVFLMLEGRLENFL**MLRNLNLFPSIYFIKFFIEYG  
NVFVNKIINYSYHLNFNEIVSFNKKYKLYFFIKSKLRQKVIINAPSFVEVDYK**LLVAMLIR**NPDEL  
ALTKPLSFNLYTKFLSVNR

>Aca\_m-S5\_[468/469\_aa]{Contig17756}

MRRISLLGSPAESSRIVPPHAAS**M/T**EGRSLLYRRAGGLSFGSKSLHHPYHSGGGTLVNGSSRRQLAT**S**SS  
SSKPASSEQTAAKKGGLVGDAAAASTIQHTATWVDEDEALS DPR**DYAFDQDD****SQDQ**WERLAGVSDNPL  
MGDRSGAPRGHGRAKERLAKKFPYEADEDEDEDEDNLPLGGGRRQSAAQQQQ**Q/^**GQEGEEEREDLT  
PLELRHRAKEEEKEKWTQIINPLKDDLEAQISAGK**HVPLWHPVDEYDGDYDDYARTLQ**AWEDD**SPFH**  
**RDY**EYNEKEFK**NHF****AFSVSGNQHILNVGR**HKTTKAGRVFSYSATVIDGNGNGRAGWGYGK**GPTLSDAVLA**  
**AQK**DCEKNSFYIDRYKGCITESIRFSYKKSVELFALPEGR**VHPTSSQVMQLV****FN****AFGLK**YVAGKWLGST  
NKTTRIKTLFMALQQVEHPDYLSEKLGMKLFPKPRKVPKNGRVWTYD

>Aca\_m-S7\_gi|11467069|ref|NP\_042545.1|\_[337\_aa]

MGIRLKKNFKRFYFKSFYFKRILKSKIKR**YNSFLKLYNSAKSL****SQHS****FRR**RNKKGKFRVKKLRLGKFKRAL  
FVKRLYKLGKRY**FFCYLR**QRIESIRLKKFLVKYRWRNKQRLWKRIYRRGFKRLYFRFFKKSINFTARH  
FRTANSFYK**SHGLYFFL**KNFVKYSRLKLVARYGKIFKNKKKVICLKSADRVEKLILLNIFFOGLTSRQK  
**KLSISIFK**TLFLLKFKYK**KFIDCYLQ****FLEK**VRPLIYYKVMFIGGKYYKIPTLMPISKSYSTSIRWLIN  
NADKRDIATSLFSQINISLKNESLIKYRKEYHSASFENKSYIRFLRFLKTGF

>Aca\_m-S8\_gi|11467077|ref|NP\_042553.1|\_[127\_aa]

MSLLSNMISIVKVGYNAR**HLQVIVQNSK**LCINVLSVLYK**LG****YIRGFI****IKD**QKNITILLKYINNKPAVRNIA  
VISTPGRRTYLKHKKLEKFLTKK**DSGLILSTSKGILTDEESNM****FKIG****EALL****KIN**

>Aca\_m-S9\_[278\_aa]\_{Contig}

MRGSSKSTAVLGLPFPSPAGSKAALCTASSSRISSRVLPARLHSLASSPLLPLSVLSSQRRHYAVKSKNF  
ERKEAR**YDFSEITNR**VWPR**HPPPQIDYR**NYVPAEEDEEEDDWKPEEDYPEPTFTADQTSQYIYPVITPQT  
VPVKIDSRTGAFLGTGRRKAAIARAALVSGQGKITINGR**SFLDYFPCFFER**GAVLAPFVAIERPNTFDVNV  
NVSGGGTKGQAEAIQLGIARALQSYNLAFRPALKKAGCLERDPRVVESSKAGRVKARKRPQWSKR

>Aca\_m-S10\_[139\_aa]\_{Contig1037}

MSWRKAELVISGYHKRVAK**VAQDIATAAEMVGMKRVGPIPLPTR**HKRFALLRSPFKHKKSIEHFEIRTHKR  
LIWIEGPPEQVRKFI DFTVDTMEPIASVKVRE**EHNYHLLSSFYSPTTATQALQEAR**QAALGSPSTPPS

>Aca\_M-S11\_gi|11467080|ref|NP\_042556.1|\_[173\_aa]

**MKILKPITFR**KPRIISQKKVLRSKLSKVKKSPWYKAK**KNYVSFR**QRLVLAKKNPNKK**RYLFFSK**KRNNV  
FLTITDVIGRVVVSQAGSCKITTKKKRSPDTLKTVSASVAKIARAKNIKYLFK**FFMNTNQT**KIGKTIF  
ESFK**KTGLFILQGVV**KNKSHGLLMRKKKAKRL

>Aca\_M-S12\_gi|11467068|ref|NP\_042544.1|\_[127\_aa]

**MPTYHQILKNPR**RRKK**MHTNNV**KALEGCPQKKGVCVCLRIVKPKKPNSAQRKVAKLRLSTRMI IAYIPGQ  
GHNLQEYSSVLVSGGRAPDLPVRYRTLIGKYDFSWKESFERKKKLSKYGYSTKKKF

>Aca\_M-S13\_gi|11467079|ref|NP\_042555.1|\_[119\_aa]

MKKLQNFNTFVSDNKNKNI F SALKDIHGVLKINK**MGLVMGLDKFEKVS**SMNFEL**FLIKK**QAIFFYNLE  
ENK**IFNNVNKKK****IKNYTGMR**HILKLPVR**QORTHNAK**TPSKNIKKEL

>Aca\_M-S14\_gi|11467076|ref|NP\_042552.1|\_[99\_aa]

**MKYLLIK**NKKLYKLFK**FELKRLQYKSVMLNTRL**PNYIRQAFMYINKLDKNTSYVAIKQRCFLSNNGRS  
VLNHFKLSRIKLRLLISNNYVNGVKKFNK

>Aca\_m-S15\_[321\_aa]\_{Contig10103}

MKSGRTMKGARLVLLPQLRQPLSLVRGYSATSASDGGSKATNR**FAAQFNALGR**TTPSSDDKSSSKPEKSVD  
PATEKQAMENIFSSISLARSTPASSAIKTSREPRFI PKTLEVTKRRLWLTDLKHFKLYPKTIKEVIDCKT  
PCGVWWDGTTWR**ASVLENEEKDETS**AETAA**QAR**EREILLGAKVLPADLRDRYRFGVMEEDIAALNLQGPQ  
ANKLKEILSFKYAGRAEINQFRIAESLKKWSRKPNDTGSSEVQIAVLTEKIRYMTDHLKGHHKQRTKRAL  
GITIDKRALLKHLKQNVSTYYHLLRDLNLRDMVSI

>Aca\_m-S16(putative)\_[92\_aa]

MLINLKDRTMYTIRLKKKSNTK**TNNNSYDILLKDKHNLPIGSYNQ**SKMIITLDLESYIFAITKGCLVSEKF  
RKIFIKTTSNITNKKNVKIIF

>Aca\_m-S17\_[261/262\_aa]\_{Contig7327}

MKRVAVMQPMRFAGVAAARTNAWGLAMPRLSTVAQRRWTSSTPSTEDRAAAVESAPKEGEGEEKMTPNAYK  
QEAAFRKDPIQPYIDGRTRDPLYNP**V**VDDWVDYNNPRWKALKHTFNRPGPFIFGKCVSTKTAK**TSMIEVPY**  
**WVR**SMKYGKHMVRRTRTFMAHDEDQICEPGDVVEIRQSKKWSKRKNTVVTRILKKDPGNAFIAEHPEFAI  
VRSRADLRKRIEQMR**EDELASAGLDV**GQGRKRTDSSEGESGQQ**Q/H**QQ**Q/^**

>Aca\_m-S18\_[130\_aa]\_{Contig26123}

MQSDLDKLMKKAKKCVFCRPSAQRPVLDPMNVSLTMTFLTPTGDIIGRRHNGNCRRHQKRLATTIKRAK**HM**  
**GIFSYK**YGGFTIYSPFHEPPETYAEDDGEGDEEQYGESDEEGDYSYDDDEDEGQQNLH

>Aca\_M-S19\_gi|11467071|ref|NP\_042547.1|\_[78\_aa]

MRSVWK**GCFYKNNNGLSKS**STVINTMLKK**FTLHDGK**SYKS**SILIDRS**MVGLKIGEFV**TR**KMGVLHKKKV  
LKKKGKK

>Aca\_m-S29\_[585\_aa]\_{Contig26915}

MSMLRTAMHRNNGGRWGGRRAAASFQEWLTSSTSSSTTTSSSSSALLPLRPHFVAGLATASRPVYAKRMK  
NDGGNQSGREVSDLESTENQDDAEGVQDENDDDMRSLEKQVTKELSRIGMADLKDEVLKQKGKEEAVSES  
ADPFDTVLREIADLHAKGLLDHDTLTKYERYLHKKKSHQGLVRDINASLAAMSPDQQSFLSHFVEFVKPV

DVEAEAAAKAAAAAALAAKQSEEAIREKEAIAFAFAPGDATKLTVGKSLLRFSAQDQKQYLPEGVAGQLKNT  
QFKFGDES VVFR**RAAYDLIQELKRRQESGFLASAGNDSLILNGEGSGKSTVLSQAVLWARKNDWFVWVIP**  
**DGRAWTGGERIVPSTLEHAHYDQIEKAARFAARLNVTHTGDKLKAIKLKG DY EIEDFHRKSDSTLFDLLEFA**  
YKHDKR**AVNAVYFR**RELNR**ITEFPTLIAIDRYNYFWDNTGYFDPADVNR**GNRYRLDAQKLMLTKMFSHQ  
DHGLVNGTMVCALETTKPATIKPFLRRCGDK**HMHEI PAYS LNEFHEVMKHYKEIEYVNIDDTTK**KATERFIY  
QLCNGMPGLVFKYCGLQ

>Aca\_m-S33 [114 aa] {Contig20706}

MAVYLRSLRPAFEASAKIFGQRIGNGEHSGFKYLQALRKGEAMMKWYQEDLDQMKFPGWVSERRERKIIRT  
ASRAERGKAPRPKKGFGKIALRREKEEKRLAAKAAKGGGKKA

>Aca\_m-S34 [202 aa] {Contig12316}

MTTGLPTGYKQFSLVVPKSSRVKKGK**NLFDIAFSFKN**FGVGARFTRTGWQYPEPCYWTVTSVKPRKNEPD  
MKRGK**AWGVLTWR**GVTDATPRRIRTTTKDWSYIK**EGEEVPTYSLDEETHSRRYNYFEGGVAEPEPHVTEG**  
**AHVFR**ATRGVTEDIKPR LAPWK**VENFTDEEIDK**MIANVGRKRSKSQATEGENKEKSDLS

>Aca\_m-S36 [110 aa] {Contig9471}

MASTGVRQLRQ**H**VPLI**K**FPQRHGA AVQS**L/I**QDAALPSRHTGGVESTPLTAPPK**TTM Q T S P N L P T P A K**FD  
IKSR**GPVTHHESMDELPAR**YRRALLSEE**V/A**IDLIQMGGAVDH

>Aca\_Ribosomal small subunit Rsm22

MEELA EDEL D G S T D R E D E D D D F V E P A A G R S E E E G E R R E G S G A D D E H T G A L G D A I E G S A E A H D W L D S R R M R T  
Q H D H L K P M K L G M V V L P D A L K K R I G A T L K K V G R T G L R R T A G L L S E R L R E R T R L V P G Q P K S V M P D P V V Y R R E E  
A M A Y A A H R L P G V Y A C T F R V M N E I K L R R P E W T P K S L M D F G S G P G T A V W S A T E V W P E L D N I L A V E P S E A M I D V  
A N E L C K G K P V K W K R L L P T D P N E R Y D V V I A S Y V L S E L P S E E E R L A K I N A L W K H T R R G G I M I L V E P G T P V G F H  
N I K L A R S T V L G D L S H G L P N V L A P R M Q R I P V Q T Q S K Q N T S I N W E D E K F S Y V V L T K G N L L V D K N E A F D R L L I S  
P Q K R G R H V I M K T C G Q D G E I T T R I I A K S D G A I Y K E A R K A A W G D G F G F P D E T S K R D L A G K F R P K A F K Y R S L S K  
V G S V A P A T R S R R P P K P A A D A D A K E D S Q V M

## *Acanthamoeba castellanii* Mitochondrial Large Subunit Ribosomal Proteins

>Aca\_M-L2\_gi|11467070|ref|NP\_042546.1|\_[253\_aa]

MSTLLWKDRPIK**NLTFGLKRI**SGR**NNQGRITR**YHRGGGVKRMGRLIDYK**RYIWNIFGFVHR**VEYDPKRNSL  
IALIVYSNGVMSYILAPEGLLVGDCIFAKENIVLKPGNSTYLQHIPIGLK**INSIELSENKGAQFIRAAGSY**  
**ATIISKFEKIVILK**LKSGELRRVHSNCMATIGSISNFQYIYRNFYRLKQWLPVVRGAMNPVDHPH  
GGGQKTSGGRPSVTPYGVITKGPTRK**NKSAFIVR**RRKS

>Aca\_m-L3\_[378\_aa]{Contig21518}

MRGWRSSVNKDQVEARRTAVDPRTLSDPSTGWDQQRKRRTGLVAIKVGMTSEYSEYMEWLPLTVLQVVDQV  
VQVKKER**HNEYEEEK**VGLQVGAVDGKWRRLAKAQRGHFFHAGVNPKKVLMFEK**ISPDVAVPVGTELRAEHF**  
**VPGQLDLDTGK**TKGKGFQGVMKRWGFSGGPASHGNSASHREPGSTGQHSIPSKVWKGKMPGRMGNKYRTT  
KNLLLWKIDTKNNLLYVKGVPVPGAPGSYIRVRDAKNKLHSLVPPYPTYMRQPEEVLPEVITANSPEPMWYK  
KMMARQAFAEDLSK**NTDDNQTA****VQVVLAKHE**AFPSYDKWKKGLLPPGPNPSKHHSCLS**V**GEPMEFPWLAD  
TIADYEDPSTAEEDQLQIHYES

>Aca\_m-L4\_[362\_aa]{Contig11830}

MKAAGRHCARAPRSNQRLISSAALSGLVSPSSTAGHLRFIASRTPLISMRYPRMSPILAQMGMVHSSVPS  
SIFGGVKEEQKEHNKAAASDEEEDDEEDAELDAEAEATAVAVQATGLIDGTQRWAPTLELPVESFLNEE  
QQGPLGSVTLNPNIFMVPPIRRDILHRVVVWQLAKRRQGTHKSKTKAEVRRGGGRKPRPQKSGRSRQGSIRS  
PLWVG**G**HAHAHKPRNYFPLLRKVRKLGKLTALSFKFAQGLKIVRSTHVDEAKTKNLAR**V**VEGKDWSKA  
LVIDGKSVDDSRK**ASN****NLPSVK**VLPVGGCNVFDILNHDLVLSLEAMQHLEELLLENEPTFYPEPATFQ  
AKEETLA

>Aca\_M-L5\_gi|11467075|ref|NP\_042551.1|\_[177\_aa]

MR**FYNRYNSSL**KNYLLCSINSFNTNTLKIPLKPTLSAVFNTFRGERSLK**FIKLYLMILYISNQKPF**IKKVK  
FSYIKKKILKRFFISVSLNKKNSFNFFMYMLNFYNYFFHIIYQKCLKYNRNFENSLILYIDNIQFFFKNYNK  
**ONQKTQIK**CQLNLRNS**QASILFKYLN****NMFLIK**VKN

>Aca\_M-L6\_gi|11467078|ref|NP\_042554.1|\_[181\_aa]

**MELLKVIKSQDKITL**KTEKVNKNVFFYFKNKKKILLKITFSGELFLKERTLITLNNLNYSNYSNYIKFMAK  
NLETFYDQYNYFSKL**HMIGLGF**KNFILRKHLYILVGDCNYIIFRIPDSLKIFCKKNQVFILGESNVEIFN  
FMSNIKRVKKSNFYKGGVQLQFKNFKFTKLKVGKKQRFM

>Aca\_m-L7/L12\_[253\_aa]{Contig24290}

MRRSTVHVFPRLALRQGGQTSALCLFSNGSRTAVSSETNMASIARNYAAPAKGGK**GAPAAAKPAEDEPAEP**  
**LKLETVTFPDFGED**KAFTADISDFPAPKDWKYVSDWK**E/A****FEFSPR**VRKIGEALFQLNQVEMFELVKLLQL  
RFDVPDSALMGGGVVQAAGAGAPAAAAEPAEPEKKEKEMI FDVQLTAVAEADKFKVLKEIRALKPGM  
KLLSKEMVEKLPMSLKQNPKEEAEQMVAKFK**ELGGTVELK**

>Aca\_m-L9\_[229\_aa]{Contig7807}

MRSSVFRVGGVSPALSSYAPLRAGSLYRTSSILPQHDWTALVSSRGYATKKTAAAPAKAKPKSKASGPQKS  
NKPVKNNKIK**IVLTS****DVPSVGVK**GEDVEVAKGFARNYLFPQKLAVYCTEENLKLYEADRANIDYEKRQKLQ  
ELAKAKKRLSKVEVLMKRQIIQVQPEQILHAPVTADNIVEKLWLQHKIQLAK**DQLDLEAPISQLGTF****SVPV**  
**KLEDIDVPLK**VRVQAR

>Aca\_M-L11\_gi|11467067|ref|NP\_042543.1|\_[339\_aa]

MRINLNFHYDKLHLK**EIIILIPK**YHTNMVSFLTPIGLGYGINVKEFINDFEIKTRFINFDVIVPTLVKISK  
IKTFEIIKTPYVISILSNLNNFSVTKPNIDLLSVYK**ISLLKSVFHSN****FLDVFHR**RIYLSLRKYLSLVIK  
NFHLSVSSALAKK**SLSNLN****LLLLKFN****IQNNILFAK**LLNNRYGLFVSNSSASNLNLYL**TVLAIQ****NISIF**  
**KAKSNLLS**SLTGNKYFFGNIIYFIGATSLKYFIGFLKEVSLK**SFGSNFFPIFFK**IRSNLVSQPFVK**LFLSVF**  
**NSQVKLINFYALR**VIYTIKIKIFKNLNFN**KLTL****FLN****RNNSNS****NANISS****NIKES**

>Aca\_m-L13\_[244\_aa]{Contig13107}

MTTSFAPCKQPLTNTHMWHVNVNDRGLKVGHAASRIARLLIGK**HKPTYNPAFDAGDYVVVTNAEK**LIFTGDK  
WKQKLYRWHTGYPPGLKEVKAKDMLYKHPDAIIRTAVSKMLPKNKLRWERLKRRLRVFVGGEEHPHEGQVSQG  
YHYQVEPQSR**SAVDPALAARFDQVVADPDAFVR**KYGGGKFSIVPQEQGMVAVATKIKGTHAHAVRSFGNTR  
SLRAARLDRLRKVVEDIQSAQAREAAKRDPL

>Aca\_M-L14 gi|11467074|ref|NP\_042550.1| [129 aa]

MINVQTVLKVADNSGAVFVSCIR**LLNSSSRVAGVGDITIVVVK**SIKKNIKKSKVEVK**KGQVCSAVILRT**  
IKGVKR**WGNFFLRSSNSVALINK**YCLPIGSRLLGPFVREIRVNLKFSKIISIAQVTL

>Aca\_m-L15 [282 aa] {Contig26943}

MRRFSTPFSCSGVMNLRSTFNLAASPLRPSSSAWAAALASCNSTSMARAYATRARKGVRSSSPTSYLGG  
GLPYLTR**KLELEAQRELEPFDPFSIALNK**IADNPGAHKKARKVGRGTGSSKGKQCGRGTGKQKARGRGK**VS**  
**PGFEGQTPLYKRVRKHGFTNAMFR**SEFVGINLQQLQWIDAGRLSPEGKITMATLQOSGLSSKLTKEYK  
GIKLLAGGSEFFAAKLDLEVSKVSAAREAIEK**NGGSVQEVYHPR**QLRMALRHPENPLPPPQEYRTRP

>Aca\_M-L16 gi|11467073|ref|NP\_042549.1| [141 aa]

MRFKKYFKIKYK**NNNVYEHDLIHFGDFGLK**SLGNCNLTSQTLASLKAIKRVIKKKNFLIIK**ALPFWMLTR**  
KPRDVRMGRGKSPAVKVYPLKAGKIIFEFK**NVNETLLLRALKSSSLR**LPVPTKVVVKYDKRTDCIKSSW

>Aca\_m-L17 [158 aa] {Contig23660}

MRHLVAYRKLRSRPAHRQALLRNLVNAVVKHGRI RTTVPKAKELRRLA EKAVTLAKRGDANARRSAHGMLY  
EKPVLDKLFREMPTRMADRNGGYTRIVRLGRRLGDNAEMCYVGFVDVLP SRHDIEQRALEEKQRNTPPTDG  
KEQAIDDLFLLSSPTQ

>Aca\_m-L19 {99 aa}

**MAINQINK**KRKNLNNNNVIKTGMVLYIKYLLKEDIEKISSFIGLCVIAKKKSNITIVLKNNIKKEDIKLV  
NIHSPLIINIKIVKRYKKKFRLSKLYYK

>Aca\_m-L20 [154 aa] {Contig6876}

MSGMKNKKLLKFVKGFRGRAKNCPSVARERAYK**ALQYAFVGR**KLKRLFR**ETWIQQINAATR**IHDLSYSRF  
MQGCVLSDVKLNRKMLSELAIYEPYSFSAVTKLVGERLKKEEVAKEVERRAAAKNIHPGNR**DLTADQKEW**  
**LLAQK**LKEMQIV

>Aca\_m-L21 [234/236 aa] {Contig3572}

MKSLRSVAGASGVPRPTLPLLPFALQTRNATAGS**S/^**LLRTMSAAHFTSSTQFASRPLSIFSKRQLHSSGP  
VSQESASQSAEVPAPTPSYIVPESFAVVYVGGQYKVSKGDTIITERLLVDVGETIHLKKVLMVGSQNF  
TAIGQPLLTEAVVEAVVEEQTRAAKVVVFKFKRRKNHRRTRGHRQDITVLRISNVKLGYEQAAPD**AT/V^**TGL  
STVFGPTVPASAVLPPRASDDLKESILS

>Aca\_m-L22 [279 aa] {Contig23422}

MRRGTAAMSGCGRLLVASSSTSSSFTAGALQRTILSTHRYLP AIQSFGAARSYASPSLLGDDIFTKAYEQ  
VKQKEEETGERVRITEAKADSKNLPASMKRIDHLLRQIRRLSYKEAITQLKFSQKRVAPKVIATIEKARQK  
AELKFGLD**P**ER**LILDEIYATK**GQYGNPQIYYHAKARIGIMRRKRVLHTVVKLKEVPFKEGEKQLGKFVVRGVN  
SEQRKVWEEKRDRVAKEMGVPRLVVT**TKQVELWDLYKE**KIILNKKPATATDPAAADATNAADKELSA

>Aca\_m-L23 [122 aa] {Contig10987}

MRRFEKLNPTKYWLPNIPL**L**MPPARNLPSNKFVLRVQPNITKVELQNYISQLYGVSVTKVNTMNYEGK  
LKRARRGKIFYSTKRYKK**AIITDD**SIRADDFQEEGRRGAGFIEGEEVVPTRR

>Aca\_m-L24 [218 aa] {Contig1378}

MLRAGSRNLRSNQIKNPITSWKIVRGDTVQVMQADHGKKS VVIKVS RKTNRVVVRG IKLAKR**R**IK**A**TEES  
**QGGFVY****R**EQPIHYSNLSLVDPDGKPKISMSYLADGTVRVSRTGTVIPKPAELTAKRFKNYLDGKDT  
KPEVVTLKTFDETSL**V**PELDELTIKAVHEKLLLEKEEAEQKRLAREQAR**VAYGFSSSSDEPR**NVGSDSKKE  
EAEVV

>Aca\_m-L25 [184 aa] {Contig16304}

MRKSSVVLTRNPYWRTSILQFKGYNDSWDRVVQSLSVVEHLEAVPRPFLGQKACEK  
YRKRLVPGVLKGLGAGYFDIPIALRISDLVSFRERGGFLNREYKLIENKIKYVKPVDI  
VLDQTSMAPEHIVLQELRELTPPPVLTEEEEKTKAKLERLMTSHFYGAKTYGPKNPIPLW  
YKEDGGVV

>Aca\_m-L27 [161 aa] {Contig23699, Contig6392}

MQRMSGAVGLRTSNVSSMGMGMARTWGIAVGGSSSSTAATRMVGPSTWGDVWRRGATKKTGGSSKNGRT  
SRPKYLGPKRGDGEVKAAGEILLRQRGTRIHPGPGVERGRDHTLYATTGVSYSYTTSHYPVPDRR**LLCVVP**  
**LSLALPR**RIAVLRARPSQL

>Aca\_m-L28 [172 aa] {Contig7313}

MIRRSALQETTTCRGWTKRSQRGLFAGRTVVFNGNISFSHKLTRRTWKPVNHKKLFSSELLNETFHINVTTA  
ALRTIDKMGGLDNYILYTKDHK**LDSLFGQLKERL**KEVYELKHGVKFQAKAAPAVSVK**DQWQI**IDNYNRK  
KEGSSSSSSTASATSSPPPVAQREQSEVV

>Aca\_m-L30 [83 aa] {Contig8613}

MATAAGKAAVELGVRQVRVVGVTLLRSGWHQRPEVRSTLRALGLTKINRTIYHKNIQPIRGQL**L**KVKHLI  
AVHPLKEPESIV

>Aca\_m-L32 [109 aa] {Contig2995}

MQRFTSLGRLTAPRLPVGNLPAAVGSSFGRAVDVFLPSPGAIGGVGDAGGLITCAVPKKKVSISRSRKR  
HAPGKERRNISHIEDCRACGQPKLRQHVCVLCAGWKVS

>Aca\_m-L33 [62 aa] {4945}

MAKGKKNQNMVVKLVSMAGTGFFYTTTKNPAATRKLFLQKYDPMLGSHTLFFREERISRSKRK

>Aca\_m-L34 [163/165 aa] {Contig10244}

MQRRVLLGSRGAVAFRACGPSSSRFLFTSSANVESAFNSEAFALPTLS**T/I**SSPLPVSRRPVAAFNDVS  
PRMAMVPLDRTLEIAPTDRSVDMLVPLPLPLD**LD/^^**APLYPTTEGNAPMEAVKRTYQ PSTVKRHHTH  
GFLVRMRSKNGRRTIARKKEKGRHKLGI

>Aca\_m-L36 [45 aa] {Contig17064, Contig15385}

MKYRAALRRLCIHCRFVLRERRLFVVCANQRHKQGQIKAKKSSD

>Aca\_m-L37 [136 aa] {Contig24432}

MNRSMMMQRRAVSSAASRTILARPVVGHAGALPLLSQQRGYAKPGGRGGAVERPKKEYKGDQYIDEMPLVA  
YGLQVPTWDDIPEVWKAEVDLKKPKELTPLDGPLFWKKINRERIKQFNEDRTWGVVKGKWLGE

>Aca\_m-L38 [323 aa] {Contig24117}

MLRRTSTTLQPACRLGSRSAAPSASNLGVSRTALQSARTSRILQNSPVLASEGARRNISQIQIAKKNRAA  
LRSAPKWSPPFPGWKDPETEISKHKNIRKKAKLHKVFPDVLPEPFTPYFMLQVEYSPEVVVRKGFHFLPP  
AKLQTTPRVSWPSDPTKRWTIMATPDDPDLVPDDVEIVKPGWVVPHEEGRGKEVLHVLVTNIPGNDISQG  
QVLCDYLPMPKKGHGGHRYVFLLEQLDGETQDFAFPEGALKEFVQRKNWNTFKAQEKYGLRPKALAFFK  
ATWDAEVSAQYSRLNLPEPEGPAPVNLVYRPRKWLDPKSW

>Aca\_m-L40 [194 aa] {Contig17281}

MMKRLVVARPSAVGVAQSSLLSSSF**S**STTTMCLRSSSVAGIQISSRSYAGSFTKKKKEKKKSGGEEGEAA  
EGKR**FDEELW**KLRPQVWTLTR**TPEQLAEEELIK**SYAKLKMQLHEESRQLSKMLKLEALNELPPDLRA  
**EALVEEVS**NAPRERVLPLWTAPIPGYQDSLPEKRDEPFDFTKLGSIRKRSS

>Aca\_m-L41 [112/113 aa] {Contig9854}

MGVFGSLTRRTGLGARTTVGT**T/^^**GFTRGKVSANQGGRLTPKMTPRGWYKGVGCRSLGFHTKKGGYR**V**VP  
AKVPVYVIPDLTDCPLKPYVSWSTKRVVVQPLRLPSDKELAQLE

>Aca\_m-L43 [121 aa] {Contig8446}

MSRSGIWQLRKLKLYCDFGGSSRGMREFLETRLPEFQK**KNPQVLVDVVKRRNRHPHLSGEYLIGREK**SVG  
VGGLEADEVEHYIYHLRNQWGLKSRRLGAGQIVSQRRSVQGVWNPFFVKYD

>Aca\_m-L45 [276\_aa] {Contig593}

MASSRLILRTPIARIFPQTAGGSPMLLSATAVLPSQRRPLFPATCGMTTR  
HYAQTSKR**VGGMSYKPR**IFVASLGQIADPAIPPSGAELLNPKKLWARLMS  
SMR**NYASLWQVR**KLLKKEKY**PTS**AWL**IVGRWTAEEANQYR**AFCEARANGN  
KQALQK**LTTDEFFDVVK**GSLIDPSSKWKREWQSQDLRVKVLALR**MVMLQE**  
**PDVKFVQMLFR**FFTSQKLIKITDSKGALIAGSDSAVPVTEYYVLERPLQDI  
HLFDWKFMGKLDPSHKEPLAKPLLEQ

>Aca\_m-L46 [323\_aa] {Contig5841}

MRKAWSGVRQQLAVPPCAVVGSTTGMSRQFVRGITHSQHERAYLQRLRQMEAEAAAGKRWLVGGIAVQR  
LPLIIPTPDPIE**D/E**QYEQFR**FDRDNYFSINVER**NLELMEDRRKGSKISK**TQ**KKKKEKKEGVS**DA****G(P/A**  
**)**AGGKQ**GG****EQ****DEAD****S**LYQKAEETAYREETLEDVRAKMERLSPRITAADLANDRKSINRALAS**R**LYLIVQK  
PR**TEHAWQFPQGGRES**GETMRQCCERELREEIGTK**V/M**K**VHFWSNAPAGCYSYPDPDNYSHNDGHHSK**VF  
FYHAEYVSGEPHPDNKEVVDFAWVTR**DELQEYFDPQLFK**FVRDMLPA

>Aca\_m-L47 [164\_aa] {Contig27366}

MLRGGFLGRAAPFGQRAGWKRGMEEFIDNATKPGEYPIAGRAWKASELRLKSFEDLHKLWFVLQKERNLLL  
TEKMLAKSEGKQMKAKGRRVKVRQSMARIKLVLGERQHIIYKTFK**EQILALEQDRLEEV**GRQLAWAEQLK  
SQNDKLANVKLPKPQKEASIK

>Aca\_m-L49 [162\_aa] {Contig525}

MMRRGTAVLGCVRPSTTGAYAAAAGWRRTIAGSTSTSATSETVVPLGSLRYPPPHSEEAVTGAGPTGYKP  
PLGNTDALPFRVLRTKSGR**LPIYTDYK**NGRTKKITILRKFSGDRKELREEVWRVLLGGPK**NPGL**EVVERAGS  
LEIKGDYTWQLQMWLKRLGF

>Aca\_m-L52 [109\_aa] {Contig21304}

MSNGVVANAIWRRSMAGGMRGFASASLPMRAGQVRVLMQGVGR**SGNEDGAFHDAPDWEYADGTPAPPSR**KQ  
IVWMTKRQETEERIQLRREEVMEMEQLERQSFYKDE

>Aca\_m-L53 [149\_aa] {Contig23150}

MSTARWQWRLAQKRAHYELHFLKSLNFSFCPANNHPTVAEFLRRVSNDRARASNPDC EVTVEVLEDIKARP  
SIKAVYENGMEEVLDHEQRVEHLVDDFWKRRERLQFFSELQFSMKNEEEENPFLNAAAQEDARKKQQQAK  
GGAKGKK

>Aca\_m-L54 [136\_aa] {Contig24432} → possible homolog id by hmmer

MNRSMMMQRRAVSSAASRTILARPVVGHAGALPLLSQQRGYAKPGGRGGAVERPCKEYKGDQYIDEMLVA  
YGLQVPTWDDIPEVWVKA EVDLKKPKELTPLDGPLFWKKINRERIKQFNEDRTGWVVKGKWLGE

