Figure S2: multiple sequence alignment of myxobacterial proteins assigned to COG2208

```
mxan4562    1   ---------- ---------- ---------- ----MSSTNT RLKSAPASDE FPDDAALPPS ERTGTQEVTS ARESTATRLT
sce1779     1   ---------- ---------- ---------- ---------- MHSRGFLQKQ SNLDAIRAIV KERQAWNTLL REEGNFTDFM
sce2617     1   ---------- ---------- ---------- ---MHDREPE AMTRKRRTLA FLIDNVVGDY QSELRAGIER GAAAHDVNLL
sce3610     1   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce3741     1   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce5198     1   ---------- ---------- ---------- ----MTGEPQ DKMKKRRTIA LVMDYVRGEY QSALRIGVER AAEAHDVNLV
sce5201     1   MQGGVPHRRE AGLATAEPDG HRAHVSGARL HRRYLTREPR EMSEKRRTIA FLMDYVGGDY QSEVRFGIER AAEAHDVNLV
sce5204     1   ---------- ---------- ---------- ----MKRGPQ DTMKKRRTIA LLMDYVRGEY QSEVRFGVER AAEAHDVNLV
sce6543     1   ---------- ---------- ---------- ----MRAGTP SLIDASSLIL ILDVSRKLAA PCDLTELLEL IIKTGREVIG
sce8427     1   ---------- ---------- ---------- ------MAEI DPLLARQLRR LGLEDLDAPP DKETWHKVVA RISEHYRHVA
sce9114     1   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
adeh0917    1   ---------- ---------- ---------- ----MFAFVA QRTRTSLRLR LLVATVALLA LALAAAAMAF ERVARSVVVD
sce0876     1   ---------- ---------- ---------- --MSGRRFGT HRRRSMSTPP PMVGPGRTMS PADDSLGPAP SSSDWKGHLE
sce1777     1   ---------- ---------- ---------- ----MTSPAD ETRKELRRRG FFFGLKKFNT KFMLVTGFSV LLGALLNVLV
sce2321     1   ---------- ---------- ---------- -----MAAKR HTIA LLTDYLCGEY QSEARFGVER AAEAHDVNLI

mxan4562   47   GPLGLAEGGT RTLIAPLEAG ELPNVAQIKG LRLDQILLLT TGVLVVLIVG LLAAL-SVAS TKSQFEETAL VSKERIQEQA
sce1779    41   ERCSALLEYV DKLKLDFDDL SLVHEAILEH ATSIENELEG YNRAIDDDLA VARQV-QRAL LPEASGAIAS SFDMAIFHKQ
sce2617    48   TAFSDPAMAR RPEVADRGTF YHLIGPETAD GVIVASSTLS PYGGMEVMRS FCRSF-APLP VCSIGTAIDG VPS-LMVDNA
sce3610     1   ---------- ---------- ---------- ---------- ---------- MTVAI-GTAC CVAAGEEIAG DEV-VVVR--
sce3741     1   ---------- ---------- ---------- ---------- ---------- MKLSV-EYAI LPKDGELVSG DAA-FVRA--
sce5198    47   IAVGETLSAH GPSEAAQNSI YRLVSAEAVD GIVVASATLC NFVGAEGVQR FCLDY-APMP LCSIGIPLEG IPS-IVVDNG
sce5201    81   IAFGETLALP GEGGAAQNSV YQLIGPETVD GIIVASATLC HHIGIEGMRE FFRAY-APLP VFSIGMAIDG IPS-LIVNNG
sce5204    47   IAFGETLALP GAASTAQNSM YHLIGAETVD GIIVASTTLC HHVGTEGMKR FCRSY-APLP ICSLGMAIDG IPS-LVVDNG
sce6543    47   ADRGSVFLYD EEAKELYSRV ATGEAQIRVS IDKGIAGECA RKRQTILVDD CYSDP-RFNQ EIDRRTGYHT KSLITVPLIG
sce8427    45   DDRSLLTRSL DLSTNEMGAL HRQLLAERDR --LRSVVVAI GDALTIFHDA ASSQV-EPSR PIEVGSTIST AKR-RFASKL
sce9114     1   ---------- ---------- ---------- ---------- ---------- -MRRC-GARG PHSHGGDIRG MGS-SSIGGC
adeh0917   47   AVHSHLAARA KEVHEAVVRF QGERALTVRN WAEAEAMQMS LDTGDPKFAE DYLRR-TIQD QGGAIGAAAL LAPDGEIRAA
sce0876    49   IRLGDLPGTR RPLTESHIVI GRAPGVQLTL DHYTVSRRHA ELFCDPFGRW WIRDLGSTNG TLVNDERINE KVLKPGDRIG
sce1777    47   ARQGLHELSQ KSAREIEGGL NEANREYLTN HLGDTAQQVN LKLGHAYADL RMLAA-IMQT MVDQGDQLDE LHKKVASTDF
sce2321    40   VAFGETRARQ GYTLDARGGI YSLIGATTVD GAVIMSSALT NHIGPEGAHE FCRSL-ASLP VCSVGLALDG VPS-VIVDNA

mxan4562  126   RELGQTVGQT IALTSATN-- ---------L RDNNYAFLEE VAGSIVKT-- --NPNILRVQ IFDPDGVRMA DSEGASEDKE
sce1779   120   LAQVGGDYYD FFYLPGER-- -------HAI GVYDISGHGV SSALIMAF-- --LKAQFAHA TKRLDSPGAI VD---WVNRS
sce2617   126   LGSEISVGHM ADEHGCRR-- ---------I AYIGGPSSSE EAALRADG-- --YRRALAAR ALPCDERLLV FG-GFTIPTG
sce3610    26   ---------- --QSPWVL-- ---------I GLADGLGHGP HAAQAASA-- --FCRYVEDH AS-MPIEDLL TG-AGEQLAS
sce3741    26   ---------- --GEDGVL-- ---------F AVIDALGHGE HAAAAANV-- --ALKALADA PSGEDVRALI DR-LHARLRG
sce5198   125   LGIEMAAGHL LDDHACRR-- ---------V AYIGGPVNNG EARIRADA-- --FRKALAAR AIPYDERLVA SG-QFTIDTG
sce5201   159   LGIDLSVGHM IDVHGRRN-- ---------I AYVGGPANNE EAKARADA-- --YWGVLAAR GLPLDERLFA VG-AFTIDSG
sce5204   125   LGLDLSVGHL VEDHGCQR-- ---------V AYIGGPPSNE EAEVRADA-- --YRRALADR SLRVDERLVA SG-SFTIDTG
sce6543   126   LDDKLVGVLQ MLNSKADH-- ---------F GPDERDVAEL LAAQAAVA-- --VQRTLLLE ERMIKLKLEH DLTIARDIQQ
sce8427   121   GELFSLSG-- -AAPGGAT-- ---------Q AAPGSATQDA AGASGSDE-- --AINEVRVQ LVALGDRLVQ LL-YDTAEKA
sce9114    28   IG-------- --PHAAIR-- ---------L RLPTRPAGHG EAELRVSG-- --YRSALAAR SIPCDERLVA HG-AFTIVTG
adeh0917  126   VRAAPGAAPR GIGLGEMRG- -------IVV DLPGLAHAGQ GAAVTADV-- --VPLARLLR GAPEGNALVL TAPVRDFAGD
sce0876   129   IGDYILEFQL TARAPRVP-- ---------I DPGGLHFEED KPTAIRKLGE LDPPRIAAKH LFTLMDLSRR LLSIEDATDR
sce1777   126   FRDKLVYNSK SNWWQNGPDE PTVVGVWGYL GKDGQILPDV QRAVDRTA-- --LLDLILPS FQKYGADKLQ VYYADSAEQP
sce2321   118   VGGEAAVAHV LDDHACKR-- ---------V AYISGPAHNE EAKLRAVA-- --YRRALEAR ALPYDERLFV YG-DFLIDGG

mxan4562  191   DVAPVRRAER RLVSAFYRGQ PISEIQEPID YGSSSGKGLV VISYSLGGLQ QQLASLEQDK RATVRATTLR MLGLGLGFVV
sce1779   184   AYSFLREVRR YATVNFVMFT DR-------- ---------F LRYVSGGGYG LLVRRGTPRS FNRVSN---- ----------
sce2617   190   RAAMRELLAR GVAFDAVVAA NDRMALAAIE VLKAEGRRIP EDVLVCGFDD VGIARFTKPS LTTVRQPIER LGGMAVSTVL
sce3610    78   TRGAAAALLR IDES------ ---------- ---------V GELEFSGVGN IAMKAITRTA MPSFCSA--- ----------
sce3741    79   TRGAAGMICR FRE------- ---------- ---------- GRLQGCGIGN VELMSHG-TR VQWLQSP--- ----------
sce5198   189   RAAMAEILDR GVEIDAVVAA NDNMALGAIE LLKARGLHVP RDILVCGFDD VGVARYAKPS LTTVRQPIKR LGEIALETVV
sce5201   223   RVAIRDILDR GVEVDAVVAA NDKMALGVIE LLAERGLRVP QDILVSGFDD AFIARFSKPS LTTVRQPMKR LGAQAMDTMM
sce5204   189   RAAMREIIGR GVAFDAVVAA NDNMALGAIE ELKAHGLSVP RDLPVCGFDD AVIARFAKPS LSTIRQPIKR IGARAVDIIV
sce6543   191   NILLRRLPRC PGYSLSAFSK PADDTGGDIY DVIRLDERVD MSPMLLLLAD AAGHGIGPAL SVTQFRAMLR IG--------
sce8427   182   SLKKQLEVAR AVQQMLVPSE D------VIE RPSLRLASHF QPAAECGGDW WTFHDLPDGR LLTVVGDVTG HG--------
sce9114    82   REAIREILDR G--------- ---------- ---------- ---------- ---------- ---------- ----------
adeh0917  194   LCGYVVGAVT RDALARLLGE VSGRDGDYRP VVADAAGALT FSTPGIDAAA LAPVLAVPAG TPGTLERLEP AGGDPALAVR
sce0876   198   FDALCQLMVR EDFHGSMALA LRLRQNGALT ILSGPHRPFQ SLRREDSVAP PYISRRVLAA VQDTREPVLA GNLVSDSATV
sce1777   202   FVRVAPYLDM GGTFDKLYPG HNEKRWYDFF YPGLVESWSE WLKEPGGLES RPVQTTVTAP YDDAGGGGMI MTAFHPIWSK
sce2321   182   RRAMRELLGR RVEFDAVVAG NDNMALGAMD TLKAHGIDIP RDVLVCGFDD VAVSRVTRPS LTTVRHPIKE LGALAVETVV

mxan4562  271   LAG------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce1779   232   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce2617   270   RMIDGEAVEA LQLARVELTQ RESCGCGYRA GDTFLQPVPS VRGFPRPIAD QRASLERALA SSVAIPSGAL DGWAGDLLAA
sce3610   119   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce3741   117   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce5198   269   RMLDGESVPE RNMQQIELTR RESCGCAYQA -IATRPLTNP PRLGAMSLGG RRDELERALE QAVGIPAASL DGWAGGLLSA
sce5201   303   RMLDGEVVED MALLDVELTC RESCGCRVQA SASLSPSAST PRDGPSLVAA RRESLETALR RSVAIPTGSL DGWPGELLSA
sce5204   269   RMIEGEPVPE YNLFPVELTL RESCGCGYQV EPAGAP-PSK AWSAPLPSAR QRDDLERLLE KSVAIPAGSL DGWAGLLLSA
sce6543   262   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce8427   247   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce9114    92   ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
```

Figure S2: multiple sequence alignment of myxobacterial proteins assigned to COG2208

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sce8427    247 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce9114    92  ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
adeh0917   274 TQAATAAPRW ATLMLVPERV AYGKLTWLRV VLGLLYAG-- ---------- ---------- ---------- ----------
sce0876    278 ELTMS----- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce1777    282 GRDKFAGALG LDLTLAQLVA SIKDVRLANA GFAFLTQADG NVLAVNDLGV TTLRLRAEGG AGQSEGVGVL QRRLKDSSDP
sce2321    262 RQLRGERVPE CSLLPVELTR RESCGCGYYA ALPRAT-GAP PRREPLSLAA QREPLERALA RCVTVPAASR EAWPRALLSA

mxan4562   273 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce1779    232 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce2617    350 MEAELAGDEG RFLRALQALL DGARRQGVLL EEFQGVISLL RSRVQGSPVG G-----DAAL EQLWHAARIL IGSECVHVEG
sce3610    119 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce3741    117 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce5198    348 LEEELKGHDG CFLHVLERVL DTAGREGVFL DLFQGVVTLL RARLRRPVEE GGDAAVNEAL EQLWHACRVL IGSASVRVEG
sce5201    383 LEDELAGREN RFRHALEALL DAAGRAGAIL DHFQGVIDVL RERLGRPPSG GGGVALYDAL ERLWHVSRMV ISSASMRVEG
sce5204    348 LEEELAGTEG RFLRAVESLL DAAGREGAIL EHFQGMITLL REQFRRGHGA LRDTVLDEAL ERIWHASRIV IGSASVRAEG
sce6543    262 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce8427    247 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce9114    92  ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
adeh0917   311 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce0876    282 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce1777    362 AVAMIALPSD DNVDYHERMI AG-------- EAYIIALQRL APVNSWAGPG ARIESQQWTL GFVVPKKELY ASLLASQRAI
sce2321    341 LEEELAGRED SFVTALQDLL DAAAREGVAL DQFQGAITLL RAKIGRTPGG ----APDDRL ERLWHTCRIL ISHASVRAEG

mxan4562   273 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce1779    232 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce2617    425 EQRLNVELAA IDVTYGARGF SACLSLPVLK GLLASELPRM RFSDVAVSLY D---DAQHAT MKPLFVMEDG HEVEVPAVSF
sce3610    119 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce3741    117 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce5198    428 RQRLDVEVAS IDLSWSGRWF STCLSLPLFQ RMLASEMPRL HFTRAAVSLY D---DAQRAT LKTLFLMEDG RAVAPPTESF
sce5201    463 ERRLTVELAA TYLSWSARSF STCLSLPSLK RVLASELPVL GISRAAVSLY DDAPEAQRGV MRSLFLMEDG REVDPPAASF
sce5204    428 QQRLNVELAS LYLSWSARSF STCLSLPILR RMMASELPRM QFSRVAVSLY DTAHDPQRAT MKALFLMEDG RELEPPAESF
sce6543    262 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce8427    247 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce9114    92  ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
adeh0917   311 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce0876    282 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce1777    434 EESRTSIVTK QILVTIASFL ALMLGVYLVS RKMTGALVAL STGATRMREG D--------- ---------- ----------
sce2321    417 EKRLYLERAS VNLSWTGMFF STCLGMPTLR RTLAAELPKL DLTHVAISLF D---DPQRAT LQSLFLMENS REVEPPPASF

mxan4562   273 --------VL VAYQSRRITR PLGMLTGKVM QLAAGNLSAR AGTAQGAGRE VVTLGVVFNH MAERIKVLLE DVRAKAQLER
sce1779    232 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce2617    502 PAHLLAPPGF LSADERISRI VLPVAFGDEE RFGVAVLDHR ASGMIYEVLR LQLGSAVKAA ALHRQVVREV ELRERLEQER
sce3610    119 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce3741    117 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce5198    505 PSRSLAPPGF LSSSERTSVV VMPLTFGDTE YFGVMALNSG MNEMVYDALR LQIGSAVKTV ALHREMVRQV ELRERLEQES
sce5201    543 PARRLAPDGF LGGRERTTMI ALPVAFGDEE KFGVAVFSSG AHELIYDALR LQIGSATKAA ALHREMVRQV EARERLEQER
sce5204    508 PARRLAPEGF LGGRERTSMI ALPVAFGDEE KFGVAVLNSG ANEMVYDALR LQIGSAVKAA ALHWEVVRQV ELRERLEQEK
sce6543    262 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce8427    247 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce9114    92  ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
adeh0917   311 -------VLL AAAGAGVAAV RQASRPLVDV SASMARVSRG DLTARVHAEY RDELGDLVRS FNVMVEEVAR SRDELQRTEA
sce0876    282 ---------- -----RDVMA LWVVACPLRV EEQMMNLLYV TLPPDFGSVE WLGLIALAAE VYQQAESAWE ARRHAQAHAA
sce1777    484 ---------- --YGVRIDVN SADEIGQLGV AFNDMASEIE AYTNNLEELV GERTRALEKA NEEISELNAK LAQENIRLGA
sce2321    494 AASCLAPPGF LSSSERWSVV AMPLTFGETE HYGIALVNGG ANEMVYDAAR LQIGSAMKAV SMHREIVRHV EVRERLEQER

mxan4562   346 EVSLARTVQE TLLPGREGVQ VGPLRIAGLV VTADACGGDW WFRAALDDRR -IVIGIGDVT GHGLSTSLVA TSATSGFASA
sce1779    232 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce2617    582 VRQESQVAAR IQTTLVPKQL SIEGLDLCAV MKPAAEVGGD YYDVIPANGG -GWLGIGDVA GHGLAAGLIM LMIQSMVSAL
sce3610    119 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce3741    117 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
sce5198    585 ERQETALAAR LQTTLVPERL HIEGLEISAA MTPAAEVGGD YYDVIATPEG -GWLGIGDVA GHGLAAGLVM LMIQSMVSAL
sce5201    623 VRQESVVAAR IQTTLVPERL SVAGLSICAV MKPAAEVGGD YYDVLATADG -GWLGIGDVA GHGLAAGLVM LMIQSMVSAL
sce5204    588 VRQESVVAAR IQTTLVPAQL SVEGLELSAV MKPAAEVGGD YYDVLATDEG -GWLGIGDVA GHGLAAGLVM LMIQSMISAL
sce6543    263 LRLSADMDAL MHHVNQQLIE DLPNDRFITA FLGILDPTTH QLRFHAAGQG -PLLHYRAAE GQVVWRDPST VPLG------
sce8427    247 ------ISSA IITGAAKAAC DVVRTFAREA IGPAQLLRVM NCSIFEAGQQ -KFLMTCAAC IFDPAAGSLT LANAGHPFPY
sce9114    92  ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
adeh0917   385 LRREVQIAHQ IQTAILPVSP AVPGYEVAAR MKPADDVGGD LYDILAFEDG -FWVLVGDVS GHGINSGLVM MMAQAAAYGA
sce0876    348 IERELEMAHQ IQRTFVPKRL EFKALDVALG FEPCRWVGGD YVDIVPMPDG RLMLAVADVC GKGLQAALIG SSVHTMVRAT
sce1777    553 ELNVARQLQL MVLPAPSELQ EIPGLDISGY MAPADEVGGD YYDVLRSDGL -VKIGIGDVT GHGLESGVLM LMVQTAVRTL
sce2321    574 VHQETLVAKH IQTTLVPAHL HVEGLELSAM MRPAAEVGGD YYDVLPTRDG -GWLGIGDVA GHGLVAGLVM LMIQSMVAAM

mxan4562   425 MTLREPSQVN AQMLITALNV TLANVGRGEH QMSSALAVID VSNGYIDYAA GAHPSPLVFN KRSGQIASLP ARG--PLLGA
sce1779    232 ---------- ---------- ---------- ---------- ---------- ---------- ---------- -------FIG
sce2617    661 TCNDPAASPA KVITALNKAI YKNVRDRLER DEHATLLLLR YERNGRVTFA GAHDDLVVCS ARTRRCGCIP SSGVWIGALP
sce3610    119 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ------GILG
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Figure S2: multiple sequence alignment of myxobacterial proteins assigned to COG2208

```
sce2617    661 TCNDPAASPA KVITALNKAI YKNVRDRLER DEHATLLLLR YERNGRVTFA GAHDDLVVCS ARTRRCGCIP SSGVWIGALP
sce3610    119 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ------GILG
sce3741    117 ---------- ---------- ---------- ---------- ---------- ---------- ---------- ------GILG
sce5198    664 TSRDPGASPS ELLAALNKAL YKNVRSRLKR DEHATLLLLR YERGGRVTFA GAHDDIIVCS ARTRRCVCIP SSGVWIGVLP
sce5201    702 TRRDPRASPA RVISAINAAL YENVRGRLMR DEHATLLLLR YERSGRVTFA GAHDDILVCR AKTRRCVCIP SSGVWIGTLP
sce5204    667 TRSDPRASPG DILSAVNGAV YENVRSRLKR DEHATLLLLR YERSGRVTFA GAHDDIIVCR AKTRRCVCIP SSGVWIGALP
sce6543    335 ---------- ---------- ---------- ---------- ---------- ---------- ---------- --------MF
sce8427    321 LVRNSAIRQL AAQGE----- ---------- ---------- ---------- ---------- ---------- ------PLGA
sce9114    92  ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
adeh0917   464 IAEDPRCSPR HVIAAVNRVV HENVRRRMGR DDYLTLMAAR HLGDGRFVAA GAHQPIFVVR -GPGAVEVVD SPGPWVGLTA
sce0876    428 VDAGRGITGM MDRLN----- --AYLCEYLP EHSFVTMVAV ALDPATGRME CVNAGHPPAL VATAEGGLRH LQAAVNPALG
sce1777    632 LAANERDPKK FLSIVN--KV IYQNIQRIRS DKNLSLTLLD YSDGELQLTG QHEDLIIVRK DGTLDRVETM GLGLPIGIDL
sce2321    653 TRRDPGARPG EVVSALNRAI YDNIRDRLKR DEHATLLLLR YERGGRVTFA GAHDDIIVCR ARTRRSECIP SSGVWVGVLP

mxan4562   503 SVESQFTSRQ AQLRPGDVVV WYTDGLTEAR DNAGKLYGTQ RLAAAVQAHA HL----SAEA LRDAVLADAR AFSAGQPQRD
sce1779    236 LRIKPFHEFE LPFEEDDVLA LYTDGMEEAQ DASGEIYSVQ RLNEIVVKHS EE----PVQV ILDRCIEDYT RFR--VADAD
sce2617    741 EIGALTRDAE LYLGDGDVLV LYSDGVTEAR NAHHEQFGLE RLCAVIEAVQ TE----PVGV IRDRILDAVE GWC--PSPDD
sce3610    124 RRVRRLRSFR FPISPGDVVL LHSDGISSG- ------FDLG -------AFR DL----DPEE MARRIVDAHK ------KSFD
sce3741    122 ASLSKVRIFD AQLARGDRLV VFTDGVSPR- ------FDLS -------LFR GM----KAAD ACRALMSRHR ------RSHD
sce5198    744 VIDEVTRDAQ FVLEDGDVLV LYSDGVTEAR NAHREQFGLE RLCTAIEAVQ TA----PVEA IRDRILREVE GWC--PSPDD
sce5201    782 SINELTRDAE FVLEDGDVLV LYSDGVTEAR DAHHEQFGLE RLCTTIEAVQ TE----SVVV IRDRILKEVE GWC--PSPDD
sce5204    747 AIDAMTRDAE FVLEDGDVLV LYSDGVTEAR NAHHEQFGLE RLCSTIESSQ SA----PAEA IRDRILGEVE AWC--PSPDD
sce6543    338 KDLDLPPTPP LVMAPGDLLV LLTDGFYEYQ DAAGQVFGKE RVGDLIHRLH AR----PTSD ILGALLAEVR RFAGSAKQID
sce8427    340 ASSAEYTSST IALEGGDALL WFTDGVTECE NESSEQFSEK RLRSLFQSVA AG----PPEE ARDAIVAAVS RFRGERALDD
sce9114    92  ---------- IVLEDGDVLV LYSDGVTEAR NAHQEWYGLE RLCAAIEAVQ AA----PVDA IRDRILEQVE GWC--PSLDD
adeh0917   543 GVPPGVTEYE FQVGPGELLC LVTDGMLEAP AAGGELFGED RLAQVLGDLH GA----SAPQ ALGTVFSAVE AFA--ASQED
sce0876    501 VGPVPMEAHQ SVLAPGEVLA MYTDGLTELR NSSKQMLGLH ALGTGFAKLC ATSAGRPVAS IADKLTHMLE EFRGDQLPED
sce1777    710 DISDFIGSIE VKLQPGDVVT LFSDGITEAE DSSEEQYGID RLCQVISRNH QR----TSRE IKDAIIEDVL AHVGYNKIHD
sce2321    733 SIDATTRDAE LLLEDGDLLV LYSDGVTEAR NAHREQFGLS RLCATVEAAQ DA----PVDD IRDRILREVD GWC--PSPDD

mxan4562   579 DITVVVAEFS PAA--
sce1779    310 DITLIILRRC A----
sce2617    815 DITIVVARYR APE--
sce3610    180 DATCVVAVVR DRGAA
sce3741    178 DSTVLIADIE P----
sce5198    818 DITVVVARYR APA--
sce5201    856 DITIVVARYR APRQP
sce5204    821 DITVVVARYS APRTL
sce6543    414 DLTALLVKRD A----
sce8427    416 DVTLVVARVS -----
sce9114    157 DITILVARYR APR--
adeh0917   617 DMTTVVLRRK NDDR-
sce0876    581 DRAFLLARRT -----
sce1777    786 DITVLVIKRV -----
sce2321    807 DITIVVGRYR APR--
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