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logo
NTDB id 1402 DSB67 RS12670 WP 010643257.1     ....................MKTIAPQLKNYRWKGINSSG.KKTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.    59
NTDB id 1169 A1552VC RS11075 WP 000648511.1   ....................MKATQTLPLKNYRWKGINSNG.KKVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.    60
NTDB id 1112 NGFG RS09215 WP 003689811.1      ..........MAKNGGF...SLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKT.....S    62
NTDB id 1113 AAA85695.1 219..1451( )          ..........MAKNGGF...SLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKT.....S    62
NTDB id 37733 RPSI07 RS11055 WP 013211405.1  MATRAPTANRSAAASARKTAAKKAPTQYIFEWEGKDRKG.KAFKGEMRAENLAEVNATLRKQGLSLITKSKRRRA.....A    74
NTDB id 1252 GC085 RS07730 WP 011213805.1    ....................MDKNSPPLLTFHYQGINKAG.QKMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.    59
NTDB id 1198 PSJM300 03950 AFN76868.1        ....................MAQKAIKNSVFTWEGLDRQG.AKIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..    58
NTDB id 1016 ACIAD RS01680 WP 004920476.1    ....................MAAKKTQVMPVFAYEGVDRKG.IKLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGL    61
NTDB id 1059 ABD1 RS01610 WP 000279215.1     ....................MAVKKAQMMPTFAYEGVDRKG.VKIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGL    61
consensus                                                          *  *  * **!* * * *** !** * * ****  !***** * ******  *

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NTDB id 1402 DSB67 RS12670 WP 010643257.1     ISHRVKGKDITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIA   139
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NTDB id 1112 NGFG RS09215 WP 003689811.1      SKRKITQEDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVA   142
NTDB id 1113 AAA85695.1 219..1451( )          SKRKITQEDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVA   142
NTDB id 37733 RPSI07 RS11055 WP 013211405.1  RGKKITPKDIAYFTRQLSTMLKAGVPLLQSVDIIARGHANPNFTQLLTEIRVDIESGSSMAQAFRRHPKYFDSLYCNLID   154
NTDB id 1252 GC085 RS07730 WP 011213805.1    KNKKITQADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVD   139
NTDB id 1198 PSJM300 03950 AFN76868.1        AGKKIKPMDIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVD   138
NTDB id 1016 ACIAD RS01680 WP 004920476.1    LKKKVKPLDIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIE   141
NTDB id 1059 ABD1 RS01610 WP 000279215.1     FKKKVTTLDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVE   141
consensus                                      ****  !!****!!**!!***!*!**!********* ** ****** ** ****!**** **** * *!* ****!**

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NTDB id 1402 DSB67 RS12670 WP 010643257.1     TGEQSGNLSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLS   219
NTDB id 1169 A1552VC RS11075 WP 000648511.1   TGEMSGNLPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLS   220
NTDB id 1112 NGFG RS09215 WP 003689811.1      AGETGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMS   222
NTDB id 1113 AAA85695.1 219..1451( )          AGETGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMS   222
NTDB id 37733 RPSI07 RS11055 WP 013211405.1  AGEQGGILDALLERLSLYMEKSIALKAQIKSAMIYPISVLTVAFLVTVMLIFVVPAFKGVFASFGATLPAPTLVVMGIS   234
NTDB id 1252 GC085 RS07730 WP 011213805.1    AGEKSGSLDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMS   219
NTDB id 1198 PSJM300 03950 AFN76868.1        SGEQSGSLETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLS   218
NTDB id 1016 ACIAD RS01680 WP 004920476.1    SGEQSGSLEIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMS   221
NTDB id 1059 ABD1 RS01610 WP 000279215.1     SGEQSGALETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMS   221
consensus                                    *!!**! !* *******!*!!** ** ****!* !!**!**!!**** **** !*! ! **** *!!*!!**!**!* *!

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NTDB id 1402 DSB67 RS12670 WP 010643257.1     AWTQNWGPFIGLSFVSLLISGKIMSQRSDSFRLLAAFSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSK   299
NTDB id 1169 A1552VC RS11075 WP 000648511.1   HWVQAYSLWAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAK   300
NTDB id 1112 NGFG RS09215 WP 003689811.1      DFFVSYGWMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAG   302
NTDB id 1113 AAA85695.1 219..1451( )          DFFVSYGWMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAG   302
NTDB id 37733 RPSI07 RS11055 WP 013211405.1  DFFVQWWYIIVFTPIIGIILYARAFKRSEKVQRNTHKAILKMPIFGSIIRKATIARWTRTLATMFSAGTPLVESMESVAG   314
NTDB id 1252 GC085 RS07730 WP 011213805.1    EFMQAYWYIIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAG   299
NTDB id 1198 PSJM300 03950 AFN76868.1        EALQAWWYVVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAG   298
NTDB id 1016 ACIAD RS01680 WP 004920476.1    NWMQDYWFILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAG   301
NTDB id 1059 ABD1 RS01610 WP 000279215.1     KWMQEYWFIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAG   301
consensus                                    **** ***************  ** *! ***  *****!**!**!*** !***!***!!****!*!!*!**********
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NTDB id 1402 DSB67 RS12670 WP 010643257.1     TSGNMHYQLAIEEVYRDTAAGMPMYIAMRHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPL   379
NTDB id 1169 A1552VC RS11075 WP 000648511.1   TSGNVHFETAINEVYRDTAAGMPMYIAMRNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPL   380
NTDB id 1112 NGFG RS09215 WP 003689811.1      AAGNLIYEEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPI   382
NTDB id 1113 AAA85695.1 219..1451( )          AAGNLIYEEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPI   382
NTDB id 37733 RPSI07 RS11055 WP 013211405.1   AAGNWVYHDATIEIQQAVRIGTSLTNAMQATHVFDNMVLQMTQIGEESGALDNMLLKVAEFYEREVDDAVANISALIEPL   394
NTDB id 1252 GC085 RS07730 WP 011213805.1     ATGNIIYAKATDKIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPI   379
NTDB id 1198 PSJM300 03950 AFN76868.1         ATGNVVFRSATNKIKSDVSSGMQLNFSMRTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPM   378
NTDB id 1016 ACIAD RS01680 WP 004920476.1     ATNNTVYEQAVLKIREDVSTGQQLNFAMRVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPL   381
NTDB id 1059 ABD1 RS01610 WP 000279215.1      ATNNVIYEKAVMKIREDVATGQQLQFAMRISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPL   381
consensus                                     ***!**** !* *** **  !* *  *!* * *!* ***!!* !!!!!!*!**!! !*! *!! !!***!* ** **!!*

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NTDB id 1402 DSB67 RS12670 WP 010643257.1     IIVFLGVVVGGLVTAMYLPIFNLMSVLG.   407
NTDB id 1169 A1552VC RS11075 WP 000648511.1   IIVFLGTVVGGLVVAMYLPIFNLMSVLG.   408
NTDB id 1112 NGFG RS09215 WP 003689811.1      IIVILGLVIGTLLVAMYLPLFNLGNVVA.   410
NTDB id 1113 AAA85695.1 219..1451( )          IILILGLVIGTLLVAMYLPLFNLGNVVA*   410
NTDB id 37733 RPSI07 RS11055 WP 013211405.1   IIVILGVLIGGMVVAMYLPIFKLGQVV..   421
NTDB id 1252 GC085 RS07730 WP 011213805.1     IMSILGILVGGLVVAMYLPIFKLGSAV..   406
NTDB id 1198 PSJM300 03950 AFN76868.1         IMAVLGVLVGGLIIAMYLPIFQMGSVV..   405
NTDB id 1016 ACIAD RS01680 WP 004920476.1     IMAILGILVGGLVIAMYLPIFQMGSVV..   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1      IMAILGVLVGGLVIAMYLPIFQMGSVV..   408
consensus                                     !***!!***!****!!!!!*!******
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X non conserved

X similar

X ≥ 50% conserved