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NTDB id 1402 DSB67 RS12670 WP 010643257.1     ..................MKTIAPQLKNYRWKGINSSGK.KTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.ISH   62
NTDB id 1169 A1552VC RS11075 WP 000648511.1   ..................MKATQTLPLKNYRWKGINSNGK.KVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.LTH   63
NTDB id 1112 NGFG RS09215 WP 003689811.1      ..........MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TSSKR   65
NTDB id 1113 AAA85695.1 219..1451( )          ..........MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TSSKR   65
NTDB id 350905 E2H97 RS17580 WP 133408340.1   MATASVASKRAKKKRAKSKSEPKMFTFEWKGTNRDGK.KTQGEIQASSVADVRVMLRTQGVMVKGVRKKSKSIFSG..DK   77
NTDB id 1252 GCO85 RS07730 WP 011213805.1     ..................MDKNSPPLLTFHYQGINKAGQ.KMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.KNK   62
NTDB id 1198 PSJM300 03950 AFN76868.1         ..................MAQKAIKNSVFTWEGLDRQGA.KIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGK   61
NTDB id 1016 ACIAD RS01680 WP 004920476.1     ..................MAAKKTQVMPVFAYEGVDRKGI.KLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKK   64
NTDB id 1059 ABD1 RS01610 WP 000279215.1      ..................MAVKKAQMMPTFAYEGVDRKGV.KIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKK   64
consensus                                                        *  *  * **!* * *  ** !** * * ****  !***** ** *****  *      *
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NTDB id 1402 DSB67 RS12670 WP 010643257.1     RVKGKDITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGE   142
NTDB id 1169 A1552VC RS11075 WP 000648511.1   RVKSKDITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGE   143
NTDB id 1112 NGFG RS09215 WP 003689811.1      KITQEDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGE   145
NTDB id 1113 AAA85695.1 219..1451( )          KITQEDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGE   145
NTDB id 350905 E2H97 RS17580 WP 133408340.1   PIKPMDIAMITRQIATMLSAGVPLVTTIEMLAKGHEKPKMRTLLGTILNELQSGVPLSDALRPHTRYFDELYVDLVAAGE   157
NTDB id 1252 GCO85 RS07730 WP 011213805.1     KITQADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGE   142
NTDB id 1198 PSJM300 03950 AFN76868.1         KIKPMDIALFTRQMATMMKAGVPLLQSFDILGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGE   141
NTDB id 1016 ACIAD RS01680 WP 004920476.1     KVKPLDIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGE   144
NTDB id 1059 ABD1 RS01610 WP 000279215.1      KVTTLDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGE   144
consensus                                     ***  !!****!!**!!* *!*!************ ** ****** ** ****!**** ***  * *!* *** !***!!
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NTDB id 1402 DSB67 RS12670 WP 010643257.1     QSGNLSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWT   222
NTDB id 1169 A1552VC RS11075 WP 000648511.1   MSGNLPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWV   223
NTDB id 1112 NGFG RS09215 WP 003689811.1      TGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFF   225
NTDB id 1113 AAA85695.1 219..1451( )          TGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFF   225
NTDB id 350905 E2H97 RS17580 WP 133408340.1   HSGALDTVFDRIATYREKSEALKSKIKKAMFYPIAVILVAIAVTIGLLLFVVPQFEEIFRGFGAELPAFTQMVLGISRWL   237
NTDB id 1252 GCO85 RS07730 WP 011213805.1     KSGSLDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFM   222
NTDB id 1198 PSJM300 03950 AFN76868.1         QSGSLETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEAL   221
NTDB id 1016 ACIAD RS01680 WP 004920476.1     QSGSLEIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWM   224
NTDB id 1059 ABD1 RS01610 WP 000279215.1      QSGALETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWM   224
consensus                                      *! !*******!*!*!!** ** !***!* !!* !**!!**** **** !*! ! ***  *!!*!!**!**!* *! **
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NTDB id 1402 DSB67 RS12670 WP 010643257.1     QNWGPFIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSG   302
NTDB id 1169 A1552VC RS11075 WP 000648511.1   QAYSLWAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKITAKTSG   303
NTDB id 1112 NGFG RS09215 WP 003689811.1      VSYGWMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAG   305
NTDB id 1113 AAA85695.1 219..1451( )          VSYGWMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAG   305
NTDB id 350905 E2H97 RS17580 WP 133408340.1   QEWWWVFVIGIIVGIVGFVNTHRKSQHFRDQVDAALLRIPLIGEILHKGAMARFARTLATTFAAGVPLIEGLESAAGASG   317
NTDB id 1252 GCO85 RS07730 WP 011213805.1     QAYWYIIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATG   302
NTDB id 1198 PSJM300 03950 AFN76868.1         QAWWYVVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATG   301
NTDB id 1016 ACIAD RS01680 WP 004920476.1     QDYWFILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATN   304
NTDB id 1059 ABD1 RS01610 WP 000279215.1      QEYWFIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATN   304
consensus                                     * ********************  * *! ***  *****!**!**!*** !* *!***!!****!*!!*!****!********
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NTDB id 1402 DSB67 RS12670 WP 010643257.1     NMHYQLAIEEVYRDTAAGMPMYIAMRHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIV   382
NTDB id 1169 A1552VC RS11075 WP 000648511.1   NVHFETAINEVYRDTAAGMPMYIAMRNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIV   383
NTDB id 1112 NGFG RS09215 WP 003689811.1      NLIYEEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIV   385
NTDB id 1113 AAA85695.1 219..1451( )          NLIYEEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIIL   385
NTDB id 350905 E2H97 RS17580 WP 133408340.1   NAVYRKALLQVRQEVMTGMQMNMALRTTKLFPDMLVQMVMIGEESGALDDMLNKLANIYEMQVDDAVDGLSSLIEPILMV   397
NTDB id 1252 GCO85 RS07730 WP 011213805.1     NIIYAKATDKIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMS   382
NTDB id 1198 PSJM300 03950 AFN76868.1         NVVFRSATNKIKSDVSSGMQLNFSMRTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMA   381
NTDB id 1016 ACIAD RS01680 WP 004920476.1     NTVYEQAVLKIREDVSTGQQLNFAMRVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMA   384
NTDB id 1059 ABD1 RS01610 WP 000279215.1      NVIYEKAVMKIREDVATGQQLQFAMRISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMA   384
consensus                                     !**** !*  ** ** *!***  *** * *!! ***!!* !!!!!!*!**!!*!*! *!! *!***!**!* **!!****
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NTDB id 1402 DSB67 RS12670 WP 010643257.1     FLGVVVGGLVTAMYLPIFNLMSVLG.   407
NTDB id 1169 A1552VC RS11075 WP 000648511.1   FLGTVVGGLVVAMYLPIFNLMSVLG.   408
NTDB id 1112 NGFG RS09215 WP 003689811.1      ILGLVIGTLLVAMYLPLFNLGNVVA.   410
NTDB id 1113 AAA85695.1 219..1451( )          ILGLVIGTLLVAMYLPLFNLGNVVA*   410
NTDB id 350905 E2H97 RS17580 WP 133408340.1   VIGGIVGALIVAMYLPIFQMGQVVG.   422
NTDB id 1252 GCO85 RS07730 WP 011213805.1     ILGILVGGLVVAMYLPIFKLGSAV..   406
NTDB id 1198 PSJM300 03950 AFN76868.1         VLGVLVGGLIIAMYLPIFQMGSVV..   405
NTDB id 1016 ACIAD RS01680 WP 004920476.1     ILGILVGGLVIAMYLPIFQMGSVV..   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1      ILGVLVGGLVIAMYLPIFQMGSVV..   408
consensus                                     **!***!*!**!!!!!*!*******
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X non conserved
X similar
X ≥ 50% conserved