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NTDB id 1029 TT RS02230 WP 011228203.1          .............MPVYQYKARDRQGRL.VEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIPALERGPGLK    65
NTDB id 1169 A1552VC RS11075 WP 000648511.1     MKAT......QTLPLKNYRWKGINSNGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.....LTHRVKSK    68
NTDB id 1402 DSB67 RS12670 WP 010643257.1       .MKT......IAPQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.....ISHRVKGK    67
NTDB id 1112 NGFG RS09215 WP 003689811.1        .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KT....SSKRKITQE    70
NTDB id 1113 AAA85695.1 219..1451( )            .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KT....SSKRKITQE    70
NTDB id 1252 GCO85 RS07730 WP 011213805.1       .MDKN......SPPLLTFHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.....KNKKITQA    67
NTDB id 1198 PSJM300 03950 AFN76868.1           .MAQK......AIKNSVFTWEGLDRQGAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS......AGKKIKPM    66
NTDB id 1016 ACIAD RS01680 WP 004920476.1       MAAKK......TQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEG....LLKKKVKPL    69
NTDB id 980485 AAFA15 RS01145 WP 000279216.1    MAVKK......AQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG....LFKKKVTTL    69
NTDB id 1059 ABD1 RS01610 WP 000279215.1        MAVKK......AQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG....LFKKKVTTL    69
consensus                                        ***         *  *  * ****** * * * *** * ******  !***** ** **** * *          *****
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NTDB id 1029 TT RS02230 WP 011228203.1          DLAIFSRQLATMLGAGLTLLQALAILERQTENRKFREILKQVRTDVEGGMAFSEALSKH.KIFSRLYVNLVRAGETSGGL   144
NTDB id 1169 A1552VC RS11075 WP 000648511.1     DITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNL   148
NTDB id 1402 DSB67 RS12670 WP 010643257.1       DITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNL   147
NTDB id 1112 NGFG RS09215 WP 003689811.1        DITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL   150
NTDB id 1113 AAA85695.1 219..1451( )            DITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL   150
NTDB id 1252 GCO85 RS07730 WP 011213805.1       DITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSL   147
NTDB id 1198 PSJM300 03950 AFN76868.1           DIALFTRQMATMMKAGVPLLQSFDIICEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSL   146
NTDB id 1016 ACIAD RS01680 WP 004920476.1       DIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSL   149
NTDB id 980485 AAFA15 RS01145 WP 000279216.1    DITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGAL   149
NTDB id 1059 ABD1 RS01610 WP 000279215.1        DITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGAL   149
consensus                                       !*****!!**!!***!****!*********  ***  ******  **  ****!***   ****  *  *!*  ****!***!!**!  !
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NTDB id 1029 TT RS02230 WP 011228203.1          DLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAATL   224
NTDB id 1169 A1552VC RS11075 WP 000648511.1     PEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSL   228
NTDB id 1402 DSB67 RS12670 WP 010643257.1       SQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQQVLNLSAWTQNWGP   227
NTDB id 1112 NGFG RS09215 WP 003689811.1        ESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYGW   230
NTDB id 1113 AAA85695.1 219..1451( )            ESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGW   230
NTDB id 1252 GCO85 RS07730 WP 011213805.1       DIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWY   227
NTDB id 1198 PSJM300 03950 AFN76868.1           ETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWWY   226
NTDB id 1016 ACIAD RS01680 WP 004920476.1       EIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYWF   229
NTDB id 980485 AAFA15 RS01145 WP 000279216.1    ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWF   229
NTDB id 1059 ABD1 RS01610 WP 000279215.1        ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWF   229
consensus                                       *******!  **!!**  **  !***!* !!**!***!************!  !  ****  *!**!!**!****  *!****  ***
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NTDB id 1029 TT RS02230 WP 011228203.1       PLLLLAVALFFAYRW.YYGTPQGRRVIDRLKLRLPVFGNLNRKTAVARFSRTLALLLSSGVNIVEALDITKGTAGNSVVE  303
NTDB id 1169 A1552VC RS11075 WP 000648511.1  WAFIATAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNVHFE  308
NTDB id 1402 DSB67 RS12670 WP 010643257.1    FIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHYQ  307
NTDB id 1112 NGFG RS09215 WP 003689811.1     MVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYE  310
NTDB id 1113 AAA85695.1 219..1451( )         MVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYE  310
NTDB id 1252 GCO85 RS07730 WP 011213805.1    IIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYA  307
NTDB id 1198 PSJM300 03950 AFN76868.1        VVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFR  306
NTDB id 1016 ACIAD RS01680 WP 004920476.1    ILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVYE  309
NTDB id 980485 AAFA15 RS01145 WP 000279216.1 IMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYE  309
NTDB id 1059 ABD1 RS01610 WP 000279215.1     IMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYE  309
consensus                                    ***************  **  **  ***   *****!**!**!***  !*  *!***!!********!******!*********!****
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NTDB id 1029 TT RS02230 WP 011228203.1       EIVEAAKLKIQQGDPLNLTLAQHPFVFPPMVSSMVAIGEETGALDTMLSKVADFYEREVDEAVASLTAAIEPLMIIFLGV  383
NTDB id 1169 A1552VC RS11075 WP 000648511.1  TAINEVYRDTAAGMPMYIAMR.NTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLGT  387
NTDB id 1402 DSB67 RS12670 WP 010643257.1    LAIEEVYRDTAAGMPMYIAMR.HCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGV  386
NTDB id 1112 NGFG RS09215 WP 003689811.1     EATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGL  389
NTDB id 1113 AAA85695.1 219..1451( )         EATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGL  389
NTDB id 1252 GCO85 RS07730 WP 011213805.1    KATDKIREEVATGQQQMFIAME.NTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGI  386
NTDB id 1198 PSJM300 03950 AFN76868.1        SATNKIKSDVSSGMQLNFSMR.TTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGV  385
NTDB id 1016 ACIAD RS01680 WP 004920476.1    QAVLKIREDVSTGQQLNFAMR.VSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGI  388
NTDB id 980485 AAFA15 RS01145 WP 000279216.1 KAVMKIREDVATGQQLQFAMR.VSNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGV  388
NTDB id 1059 ABD1 RS01610 WP 000279215.1     KAVMKIREDVATGQQLQFAMR.ISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGV  388
consensus                                      **  ***  ****!****  ***   *  *!!  ****!**!!!!*!*!**!!  !*!  *!!  !!***!**!*  **!!*****!!*
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NTDB id 1029 TT RS02230 WP 011228203.1       IVGMIVAGMFLPLFKIIGTLSVQ   406
NTDB id 1169 A1552VC RS11075 WP 000648511.1  VVGGLVVAMYLPIFNLMSVLG..   408
NTDB id 1402 DSB67 RS12670 WP 010643257.1    VVGGLVTAMYLPIFNLMSVLG..   407
NTDB id 1112 NGFG RS09215 WP 003689811.1     VIGTLLVAMYLPLFNLGNVVA..   410
NTDB id 1113 AAA85695.1 219..1451( )         VIGTLLVAMYLPLFNLGNVVA*.   410
NTDB id 1252 GCO85 RS07730 WP 011213805.1    LVGGLVVAMYLPIFKLGSAV...   406
NTDB id 1198 PSJM300 03950 AFN76868.1        LVGGLIIAMYLPIFQMGSVV...   405
NTDB id 1016 ACIAD RS01680 WP 004920476.1    LVGGLVIAMYLPIFQMGSVV...   408
NTDB id 980485 AAFA15 RS01145 WP 000279216.1 LVGGLVIAMYLPIFQMGSVV...   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1     LVGGLVIAMYLPIFQMGSVV...   408
consensus                                    **!*****!*!!*!******
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X non conserved
X similar
X ≥ 50% conserved