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NTDB id 1029 TT RS02230 WP 011228203.1 ..............MPVYQYKARDRQGRL.VEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIPALERGPGLK   65
NTDB id 1402 DSB67 RS12670 WP 010643257.1 .MKTI......APQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.....ISHRVKGK   67
NTDB id 1169 A1552VC RS11075 WP 000648511.1 MKATQ......TLPLKNYRWKGINSNGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.....LTHRVKSK   68
NTDB id 1113 AAA85695.1 219..1451( ) .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TS....SKRKITQE   70
NTDB id 1112 NGFG RS09215 WP 003689811.1 .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TS....SKRKITQE   70
NTDB id 1252 GCO85 RS07730 WP 011213805.1 .MDKN......SPPLLTFHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.....KNKKITQA   67
NTDB id 1059 ABD1 RS01610 WP 000279215.1 MAVKK......AQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGL....FKKKVTTL   69
NTDB id 1016 ACIAD RS01680 WP 004920476.1 MAAKK......TQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGL....LKKKVKPL   69
NTDB id 93109 AKN91 RS09280 WP 053105045.1 MEIKK......SPKSYMYVWHGKSRQGNK.LSGVINSHDINIVKAQLRKQGVLHAKVKKKGIT.FG......RDKKIKSM   66
NTDB id 1198 PSJM300 03950 AFN76868.1 .MAQK......AIKNSVFTWEGLDRQGAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS......AGKKIKPM   66
consensus                          *** *  *  * **** * * * * *** * ** ***  !***** * ******  *        ****
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NTDB id 1029 TT RS02230 WP 011228203.1 DLAIFSRQLATMLGAGLTLLLQALAILERQTENRKFREILKQVRTDVEGGMAFSEALSKHK.IFSRLYVNLVRAGETSGGL   144
NTDB id 1402 DSB67 RS12670 WP 010643257.1 DITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNL   147
NTDB id 1169 A1552VC RS11075 WP 000648511.1 DITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNL   148
NTDB id 1113 AAA85695.1 219..1451( ) DITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL   150
NTDB id 1112 NGFG RS09215 WP 003689811.1 DITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL   150
NTDB id 1252 GCO85 RS07730 WP 011213805.1 DITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSL   147
NTDB id 1059 ABD1 RS01610 WP 000279215.1 DITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGAL   149
NTDB id 1016 ACIAD RS01680 WP 004920476.1 DIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSL   149
NTDB id 93109 AKN91 RS09280 WP 053105045.1 DITVFTRQMATMMQAGVPLLQSFTIIIEGLDNSNMRKLLEAVRNDIAGGSSFAGALRKHSLYFDELYCNLVASGETSGAL   146
NTDB id 1198 PSJM300 03950 AFN76868.1 DIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSL   146
consensus                          !*****!!**!!* *!****!********* *** ****** ** ****!***  ****** *!* ****!***!! *! !
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NTDB id 1029 TT RS02230 WP 011228203.1 DLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAATL   224
NTDB id 1402 DSB67 RS12670 WP 010643257.1 SQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWGP   227
NTDB id 1169 A1552VC RS11075 WP 000648511.1 PEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSL   228
NTDB id 1113 AAA85695.1 219..1451( ) ESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGW   230
NTDB id 1112 NGFG RS09215 WP 003689811.1 ESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYGW   230
NTDB id 1252 GCO85 RS07730 WP 011213805.1 DIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWY   227
NTDB id 1059 ABD1 RS01610 WP 000279215.1 ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWF   229
NTDB id 1016 ACIAD RS01680 WP 004920476.1 EIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYWF   229
NTDB id 93109 AKN91 RS09280 WP 053105045.1 ETLLDRVATYKEKSEALKSKIKKAMNYPIAVVVVAAVVTSILLLKVVPQFQEIFEGFGAELPVFTQLVIGISELLQEYSL   226
NTDB id 1198 PSJM300 03950 AFN76868.1 ETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWWY   226
consensus                          *******!***!!** ** !***!* !!* !***!************! ! ***  *!**!!**!**** *!**** * *
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NTDB id 1029 TT RS02230 WP 011228203.1          PLLLLAVALFFAYRW.YYGTPQGRRVIDRLKLRLPVFGNLNRKTAVARFSRTLALLLSSGVNIVEALDITKGTAGNSVVE  303
NTDB id 1402 DSB67 RS12670 WP 010643257.1       FIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHYQ  307
NTDB id 1169 A1552VC RS11075 WP 000648511.1     WAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNVHFE  308
NTDB id 1113 AAA85695.1 219..1451( )            MVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYE  310
NTDB id 1112 NGFG RS09215 WP 003689811.1        MVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYE  310
NTDB id 1252 GCO85 RS07730 WP 011213805.1       IIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYA  307
NTDB id 1059 ABD1 RS01610 WP 000279215.1        IMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYE  309
NTDB id 1016 ACIAD RS01680 WP 004920476.1       ILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVYE  309
NTDB id 93109 AKN91 RS09280 WP 053105045.1      YVLIGLVLLLYAARRTLRRSEQLRNRADKILLKMPIIGDILYNSAVARYGRTLATTFSAGVPLVDALDSVSGAIGNVVFK  306
NTDB id 1198 PSJM300 03950 AFN76868.1           VVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFR  306
consensus                                       ***************  * **  ***  *****!**!**!***  **  *!***!!*******!******!*********!****
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NTDB id 1029 TT RS02230 WP 011228203.1          EIVEAAKLKIQQGDPLNLTLAQHPFVFPPMVSSMVAIGEETGALDTMLSKVADFYEREVDEAVASLTAAIEPLMIIFLGV  383
NTDB id 1402 DSB67 RS12670 WP 010643257.1       LAIEEVYRDTAAGMPMYIAM.RHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGV  386
NTDB id 1169 A1552VC RS11075 WP 000648511.1     TAINEVYRDTAAGMPMYIAM.RNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLGT  387
NTDB id 1113 AAA85695.1 219..1451( )            EATREIRTRVIQGLSMTSGM.RATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGL  389
NTDB id 1112 NGFG RS09215 WP 003689811.1        EATREIRTRVIQGLSMTSGM.RATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGL  389
NTDB id 1252 GCO85 RS07730 WP 011213805.1       KATDKIREEVATGQQMFIAM.ENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGI  386
NTDB id 1059 ABD1 RS01610 WP 000279215.1        KAVMKIREDVATGQQLQFAM.RISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGV  388
NTDB id 1016 ACIAD RS01680 WP 004920476.1       QAVLKIREDVSTGQQLNFAM.RVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGI  388
NTDB id 93109 AKN91 RS09280 WP 053105045.1      SAVQQVKSDVSTGMQLHTSM.MSSGVFPPLALQLTAIGEESGALDTMLEKVAAYYEAEVDNAVDGLTALLEPIIMVVLGV  385
NTDB id 1198 PSJM300 03950 AFN76868.1           SATNKIKSDVSSGMQLNFSM.RTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGV  385
consensus                                         **  **  ** *!***  **  *  *  *!! *******!!!!*!*!**!!  !*!  *!!  !!***!**!****!!*****!!*
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NTDB id 1029 TT RS02230 WP 011228203.1          IVGMIVAGMFLPLFKIIGTLSVQ   406
NTDB id 1402 DSB67 RS12670 WP 010643257.1       VVGGLVTAMYLPIFNLMSVLG..   407
NTDB id 1169 A1552VC RS11075 WP 000648511.1     VVGGLVVAMYLPIFNLMSVLG..   408
NTDB id 1113 AAA85695.1 219..1451( )            VIGTLLVAMYLPLFNLGNVVA*.   410
NTDB id 1112 NGFG RS09215 WP 003689811.1        VIGTLLVAMYLPLFNLGNVVA..   410
NTDB id 1252 GCO85 RS07730 WP 011213805.1       LVGGLVVAMYLPIFKLGSAV...   406
NTDB id 1059 ABD1 RS01610 WP 000279215.1        LVGGLVIAMYLPIFQMGSVV...   408
NTDB id 1016 ACIAD RS01680 WP 004920476.1       LVGGLVIAMYLPIFQMGSVV...   408
NTDB id 93109 AKN91 RS09280 WP 053105045.1      LIGGLVIAMYLPILQMGNVV...   405
NTDB id 1198 PSJM300 03950 AFN76868.1           LVGGLIIAMYLPIFQMGSVV...   405
consensus                                       **!*****!*!!********
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X non conserved
X similar
X ≥ 50% conserved