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NTDB id 1029 TT RS02230 WP 011228203.1 ..............MPVYQYKARDRQGR.LVEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIPALERGPGLK  65
NTDB id 1169 A1552VC RS11075 WP 000648511.1 MKAT......QTLPLKNYRWKGINSNGK.KVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.....LTHRVKSK  68
NTDB id 1402 DSB67 RS12670 WP 010643257.1 .MKT......IAPQLKNYRWKGINSSGK.KTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.....ISHRVKGK  67
NTDB id 1112 NGFG RS09215 WP 003689811.1 .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKT.........SSKRKITQE  70
NTDB id 1113 AAA85695.1 219..1451( ) .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKT.........SSKRKITQE  70
NTDB id 1252 GCO85 RS07730 WP 011213805.1 .MDK......NSPPLLTFHYQGINKAGQ.KMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.....KNKKITQA  67
NTDB id 1016 ACIAD RS01680 WP 004920476.1 MAAK......KTQVMPVFAYEGVDRKGI.KLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEG....LLKKKVKPL  69
NTDB id 1059 ABD1 RS01610 WP 000279215.1 MAVK......KAQMMPTFAYEGVDRKGV.KIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG....LFKKKVTTL  69
NTDB id 35854 PPUTUW4 RS23545 WP 015096871.1 .MAV......KAAKISVYAWEGIDRKGT.KVTGELSAQNPALIKAKLRKQGISPGKVRKKNQSVFS......MGKRIKAQ  66
NTDB id 1198 PSJM300 03950 AFN76868.1 .MAQ......KAIKNSVFTWEGLDRQGA.KIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS......AGKKIKPM  66
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 1016 ACIAD RS01680 WP 004920476.1 DIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSL 149
NTDB id 1059 ABD1 RS01610 WP 000279215.1 DITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGAL 149
NTDB id 35854 PPUTUW4 RS23545 WP 015096871.1 DIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPAMRTLVDELKQEVAAGSSFAAALRKKPRYFDELYCNLVDAGEQAGAL 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 1169 A1552VC RS11075 WP 000648511.1 PEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSL 228
NTDB id 1402 DSB67 RS12670 WP 010643257.1 SQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQQMVLNLSAWTQNWGP 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 1016 ACIAD RS01680 WP 004920476.1 EIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYWF 229
NTDB id 1059 ABD1 RS01610 WP 000279215.1 ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWF 229
NTDB id 35854 PPUTUW4 RS23545 WP 015096871.1 DTLLERVATYKEKSESLKARIRKAMTYPLVVVFVAAIVTGILLVNVVPQFESVFKGFGAELPAFTVMVIGLSQFMQAWWW 226
NTDB id 1198 PSJM300 03950 AFN76868.1 ETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWWY 226
consensus *******!***!!** ********!**!!* !***!********** **!  ! ***  *!**!!**!**** *!********
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NTDB id 1029 TT RS02230 WP 011228203.1          PLLLLAVALFFAYRWY.YGTPQGRRVIDRLKLRLPVFGNLNRKTAVARFSRTLALLLSSGVNIVEALDITKGTAGNSVVE  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 1016 ACIAD RS01680 WP 004920476.1       ILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVYE  309
NTDB id 1059 ABD1 RS01610 WP 000279215.1        IMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYE  309
NTDB id 35854 PPUTUW4 RS23545 WP 015096871.1    VVLGALLTMAFGVRHILGKSPALRDRMDTWLLKLPLVGTLMHKSAVARFARTLSTTFAAGVPLMEALQSVAGATGNSVFK  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 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 1016 ACIAD RS01680 WP 004920476.1       QAVLKIREDVSTGQQLNFAMR.VSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGI  388
NTDB id 1059 ABD1 RS01610 WP 000279215.1        KAVMKIREDVATGQQLQFAMR.ISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGV  388
NTDB id 35854 PPUTUW4 RS23545 WP 015096871.1    HAVLRIRQDVSTGMQLNFAMR.TCGVFPNMAIQMTAIGEESGTLDAMLDKVAGFYEDNVDNMVDNLTSLIEPFIMVVLGV  385
NTDB id 1198 PSJM300 03950 AFN76868.1           SATNKIKSDVSSGMQLNFSMR.TTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGV  385
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 1016 ACIAD RS01680 WP 004920476.1       LVGGLVIAMYLPIFQMGSVV...   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1        LVGGLVIAMYLPIFQMGSVV...   408
NTDB id 35854 PPUTUW4 RS23545 WP 015096871.1    IVGGLVVAMYLPIFQLGSAI...   405
NTDB id 1198 PSJM300 03950 AFN76868.1           LVGGLIIAMYLPIFQMGSVV...   405
consensus                                       **!*****!*!!*!******
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X non conserved
X similar
X ≥ 50% conserved