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logo
NTDB id 1169 A1552VC RS11075 WP 000648511.1  ..........MKATQTLPLKNYRWKGINSNG.KKVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.LTHRVKSK   68
NTDB id 1402 DSB67 RS12670 WP 010643257.1    ..........MKTIAPQLKNYRWKGINSSG.KKTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.ISHRVKGK   67
NTDB id 1113 AAA85695.1 219..1451( )         MAKNGG.....FSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KTSSKRKITQE   70
NTDB id 1112 NGFG RS09215 WP 003689811.1     MAKNGG.....FSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KTSSKRKITQE   70
NTDB id 1252 GC085 RS07730 WP 011213805.1    ..........MDKNSPPLLTFHYQGINKAG.QKMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.KNKKITQA   67
NTDB id 175225 A3Q33 RS05870 WP 081179143.1 MAVSSTIKVKDKKSKVKALDVYKWQGLNRKG.KKISGELNATSILELKAQLRKQGITPGKISKKAKPLFGMSGDKKILPV   79
NTDB id 1198 PSJM300 03950 AFN76868.1        ..........MAQKAIKNSVFTWEGLDRQG.AKIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKKIKPM   66
NTDB id 1016 ACIAD RS01680 WP 004920476.1    ..........MAAKKTQVMPVFAYEGVDRKG.IKLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKVKPL   69
NTDB id 1059 ABD1 RS01610 WP 000279215.1     ..........MAVKKAQMMPTFAYEGVDRKG.VKIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVTTL   69
consensus                                                 *  *  * **!* * * *** !** * *  ***  !*****   *****   *      ***

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NTDB id 1169 A1552VC RS11075 WP 000648511.1  DITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNL  148
NTDB id 1402 DSB67 RS12670 WP 010643257.1    DITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNL  147
NTDB id 1113 AAA85695.1 219..1451( )         DITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL  150
NTDB id 1112 NGFG RS09215 WP 003689811.1     DITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL  150
NTDB id 1252 GC085 RS07730 WP 011213805.1    DITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSL  147
NTDB id 175225 A3Q33 RS05870 WP 081179143.1 DIAILTRQIATMLGAGVPLVQTIEMIGSGHNNANMQKLLSTIGNKLQSGIPLSECLREHPKYFDDLYCDLVNSGEQSGSL  159
NTDB id 1198 PSJM300 03950 AFN76868.1        DIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSL  146
NTDB id 1016 ACIAD RS01680 WP 004920476.1    DIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSL  149
NTDB id 1059 ABD1 RS01610 WP 000279215.1     DITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGAL  149
consensus                                    !!****!!**!!* *!*!**!********* ** ***** **  ***!**** ***  * *!* *** !***!!**! !

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NTDB id 1169 A1552VC RS11075 WP 000648511.1  PEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSL  228
NTDB id 1402 DSB67 RS12670 WP 010643257.1    SQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWGP  227
NTDB id 1113 AAA85695.1 219..1451( )         ESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGW  230
NTDB id 1112 NGFG RS09215 WP 003689811.1     ESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYGW  230
NTDB id 1252 GC085 RS07730 WP 011213805.1    DIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWY  227
NTDB id 175225 A3Q33 RS05870 WP 081179143.1 ETIYDRIAIYKEKAEVLKAKIKKAMTYPISVLIIALIVTSVLLIFVVPVFKDIFDSFGAELPGFTLFVLAISDFMQSYWY  239
NTDB id 1198 PSJM300 03950 AFN76868.1        ETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWWY  226
NTDB id 1016 ACIAD RS01680 WP 004920476.1    EIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYWF  229
NTDB id 1059 ABD1 RS01610 WP 000279215.1     ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWF  229
consensus                                    *******!*!*!!** ** !***!* !!**!***!**** **** !*! ! ***  *!!*!!**!* !* *!**** ***

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NTDB id 1169 A1552VC RS11075 WP 000648511.1  WAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNVHFE  308
NTDB id 1402 DSB67 RS12670 WP 010643257.1    FIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHYQ  307
NTDB id 1113 AAA85695.1 219..1451( )         MVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYE  310
NTDB id 1112 NGFG RS09215 WP 003689811.1     MVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYE  310
NTDB id 1252 GC085 RS07730 WP 011213805.1    IIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYA  307
NTDB id 175225 A3Q33 RS05870 WP 081179143.1 FGLAGIFITGYLFKKAHANSLNFRDSVDKKILKLPVVGDVLKKAAVARYARTLSTTFAAGVPLPDALESAAGASGNAVFR  319
NTDB id 1198 PSJM300 03950 AFN76868.1        VVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFR  306
NTDB id 1016 ACIAD RS01680 WP 004920476.1    ILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVYE  309
NTDB id 1059 ABD1 RS01610 WP 000279215.1     IMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYE  309
consensus                                    ************  ** *! ***  *****!**!**!*** !* *!***!!****!*!!*!****!********!****
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NTDB id 1169 A1552VC RS11075 WP 000648511.1   TAINEVYRDTAAGMPMYIAMRNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLGTV   388
NTDB id 1402 DSB67 RS12670 WP 010643257.1     LAIEEVYRDTAAGMPMYIAMRHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGVV   387
NTDB id 1113 AAA85695.1 219..1451( )          EATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGLV   390
NTDB id 1112 NGFG RS09215 WP 003689811.1      EATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGLV   390
NTDB id 1252 GCO85 RS07730 WP 011213805.1     KATDKIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGIL   387
NTDB id 175225 A3Q33 RS05870 WP 081179143.1   DAILEIRAEVTSGMQMNLAMRNCAIFPDMVIQMVAIGEESGAVDDMLAKVATVYEQEVDNAVDNLTTLLEPMIMAVLGVV   399
NTDB id 1198 PSJM300 03950 AFN76868.1         SATNKIKSDVSSGMQLNFSMRTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGVL   386
NTDB id 1016 ACIAD RS01680 WP 004920476.1     QAVLKIREDVSTGQQLNFAMRVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGIL   389
NTDB id 1059 ABD1 RS01610 WP 000279215.1      KAVMKIREDVATGQQLQFAMRISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGVL   389
consensus                                      !* *** ** *!***  *!* * *!! ***!!**!!!!!!****!! !*! *!! !!***!* !* **!!*!* *!!**
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NTDB id 1169 A1552VC RS11075 WP 000648511.1   VGGLVVAMYLPIFNLMSVLG.   408
NTDB id 1402 DSB67 RS12670 WP 010643257.1     VGGLVTAMYLPIFNLMSVLG.   407
NTDB id 1113 AAA85695.1 219..1451( )          IGTLLVAMYLPLFNLGNVVA*   410
NTDB id 1112 NGFG RS09215 WP 003689811.1      IGTLLVAMYLPLFNLGNVVA.   410
NTDB id 1252 GCO85 RS07730 WP 011213805.1     VGGLVVAMYLPIFKLGSAV..   406
NTDB id 175225 A3Q33 RS05870 WP 081179143.1   IGGLIVAMYLPIFQIGMVV..   418
NTDB id 1198 PSJM300 03950 AFN76868.1         VGGLIIAMYLPIFQMGSVV..   405
NTDB id 1016 ACIAD RS01680 WP 004920476.1     VGGLVIAMYLPIFQMGSVV..   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1      VGGLVIAMYLPIFQMGSVV..   408
consensus                                     *!*!**!!!!!*!******
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X non conserved
X similar
X ≥ 50% conserved