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logo
NTDB id 1169 A1552VC RS11075 WP 000648511.1   ..........MKATQTLPLKNYRWKGINSNGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.LTHRVKSK   68
NTDB id 1402 DSB67 RS12670 WP 010643257.1     ..........MKTIAPQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.ISHRVKGK   67
NTDB id 1112 NGFG RS09215 WP 003689811.1      ..MAKNGG...FSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KTSSKRKITQE   70
NTDB id 1113 AAA85695.1 219..1451( )          ..MAKNGG...FSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KTSSKRKITQE   70
NTDB id 1198 PSJM300 03950 AFN76868.1         ..........MAQKAIKNSVFTWEGLDRQGAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKKIKPM   66
NTDB id 1016 ACIAD RS01680 WP 004920476.1     ..........MAAKKTQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKVKPL   69
NTDB id 1059 ABD1 RS01610 WP 000279215.1      ..........MAVKKAQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVTTL   69
NTDB id 1112350 P3C48 RS16630 WP 275548358.1 MSVARNVIKKPVDRSTSQLQPFIWEGTDKRGVK.MKGEQTARNVNMLRAELRRQGITPNVVKPKPKPLFGA.AGKKVTPK   78
NTDB id 1252 GC085 RS07730 WP 011213805.1    ..........MDKNSPPLLTFHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.KNKKITQA   67
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 1112 NGFG RS09215 WP 003689811.1      DITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL   150
NTDB id 1113 AAA85695.1 219..1451( )          DITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL   150
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
NTDB id 1112350 P3C48 RS16630 WP 275548358.1 DISFFSRQMATMMKSGVPIVGSLEIICEGHKNPRMKQMVGQIRTDIEGGSSLHESISRHPVQFDELYRNLVRAGEGAGVL   158
NTDB id 1252 GC085 RS07730 WP 011213805.1    DITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSL   147
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 1112 NGFG RS09215 WP 003689811.1      ESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYGW   230
NTDB id 1113 AAA85695.1 219..1451( )          ESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGW   230
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
NTDB id 1112350 P3C48 RS16630 WP 275548358.1 ETVLDTVATYKENIEALKGKIKKALFYPAMVVVALVVSAILLVFVVPQFEEVFKGFGAELPAFTQMIVAASRFMVSYWW   238
NTDB id 1252 GC085 RS07730 WP 011213805.1    DIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWY   227
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 1112 NGFG RS09215 WP 003689811.1      MVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYE   310
NTDB id 1113 AAA85695.1 219..1451( )          MVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYE   310
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
NTDB id 1112350 P3C48 RS16630 WP 275548358.1 ALLVIVAGAVIGFIYAYKRSPRMQHGMDRIILKVPVIGQIMHNSAIARFARTTAVTFKAGVPLVEALGIVAGATGNKVYE   318
NTDB id 1252 GC085 RS07730 WP 011213805.1    IIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYA   307
consensus                                     ************** ** *! ***  ****!**!**!*** ** *!***!!****!*!!*!****! *******!****
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logo
NTDB id 1169 A1552VC RS11075 WP 000648511.1   TAINEVYRDTAAGMPMYIAMRNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLGTV   388
NTDB id 1402 DSB67 RS12670 WP 010643257.1     LAIEEVYRDTAAGMPMYIAMRHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGVV   387
NTDB id 1112 NGFG RS09215 WP 003689811.1      EATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGLV   390
NTDB id 1113 AAA85695.1 219..1451( )          EATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGLV   390
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
NTDB id 1112350 P3C48 RS16630 WP 275548358.1 EAVLRMRDDVSVGYPVNMAMKQVNLFPHMVIQMTAIGEEAGALDTMLFKVAEYFEQEVNNAVDALSSLLEPMIMVFIGTI   398
NTDB id 1252 GC085 RS07730 WP 011213805.1    KATDKIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGIL   387
consensus                                      !* *** **  !* *  *!* * *!! ***!!**!!!!*!*!**!! !*! **! !!***!**!* **!!*!****!**
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logo
NTDB id 1169 A1552VC RS11075 WP 000648511.1   VGGLVVAMYLPIFNLMSVLG.   408
NTDB id 1402 DSB67 RS12670 WP 010643257.1     VGGLVTAMYLPIFNLMSVLG.   407
NTDB id 1112 NGFG RS09215 WP 003689811.1      IGTLLVAMYLPLFNLGNVVA.   410
NTDB id 1113 AAA85695.1 219..1451( )          IGTLLVAMYLPLFNLGNVVA*   410
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
NTDB id 1112350 P3C48 RS16630 WP 275548358.1 VGGMVIGMYLPIFKLGAVVG.   418
NTDB id 1252 GC085 RS07730 WP 011213805.1    VGGLVVAMYLPIFKLGSAV..   406
consensus                                     *!*****!!!!*!*******
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X non conserved
X similar
X ≥ 50% conserved