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logo
NTDB id 1169 A1552VC RS11075 WP 000648511.1   ........MKATQTLPLKNYRWKGINSNGK.KVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.LTHRVKSKDI   70
NTDB id 1402 DSB67 RS12670 WP 010643257.1     .........MKTIAPQLKNYRWKGINSSGK.KTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.ISHRVKGKDI   69
NTDB id 1143805 A8Q77 RS07250 WP 004282575.1 MNQVKFGERMLTRKDKGKRFTFEGKNISTEQIVRGEVVAKNEEEARAKLQRRGIRPLRVSKV.....KAVRQRRITQADI   75
NTDB id 1112 NGFG RS09215 WP 003689811.1      ...MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KTSSKRKITQEDI   72
NTDB id 1113 AAA85695.1 219..1451( )          ...MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KTSSKRKITQEDI   72
NTDB id 1252 GC085 RS07730 WP 011213805.1     .........MDKNSPPLLTFHYQGINKAGQ.KMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.KNKKITQADI   69
NTDB id 1198 PSJM300 03950 AFN76868.1         .........MAQKAIKNSVFTWEGLDRQGA.KIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKKIKPMDI   68
NTDB id 1059 ABD1 RS01610 WP 000279215.1      ........MAVKKAQMMPTFAYEGVDRKGV.KIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVTTLDI   71
NTDB id 1016 ACIAD RS01680 WP 004920476.1     ........MAAKKTQVMPVFAYEGVDRKGI.KLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKVKPLDI   71
consensus                                                  *  ** * **!*   *  ** !** * ** *** *!*****   ****    *       ****  !!

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NTDB id 1169 A1552VC RS11075 WP 000648511.1   TILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNLPE   150
NTDB id 1402 DSB67 RS12670 WP 010643257.1     TIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNLSQ   149
NTDB id 1143805 A8Q77 RS07250 WP 004282575.1 TVFTRQLATMMKAGLLLMQAFEIVARGHSNPAMTQMLMQIRADVEQGSSLSKAFSKHPKYFDRFYCNLIAAGETGGVLEG   155
NTDB id 1112 NGFG RS09215 WP 003689811.1      TVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLES   152
NTDB id 1113 AAA85695.1 219..1451( )          TVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLES   152
NTDB id 1252 GC085 RS07730 WP 011213805.1     TVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSLDI   149
NTDB id 1198 PSJM300 03950 AFN76868.1         ALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLET   148
NTDB id 1059 ABD1 RS01610 WP 000279215.1      TIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALET   151
NTDB id 1016 ACIAD RS01680 WP 004920476.1     AIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLEI   151
consensus                                     ****!!**!!***!****!********* ** ****** ** ****!********* * *!* ****!***!! *! !*

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NTDB id 1169 A1552VC RS11075 WP 000648511.1   VFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSLWA   230
NTDB id 1402 DSB67 RS12670 WP 010643257.1     VFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWGPFI   229
NTDB id 1143805 A8Q77 RS07250 WP 004282575.1 LLEKLALYKEKTQAIKKKVKSALVYPVAVIVVAVALLIVMMMFVLPAFKEVYSNMGAELPGMTQIVMGMSDFFVANGWLI   235
NTDB id 1112 NGFG RS09215 WP 003689811.1      LLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYGWMV   232
NTDB id 1113 AAA85695.1 219..1451( )          LLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGWMV   232
NTDB id 1252 GC085 RS07730 WP 011213805.1     MLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVIAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWYII   229
NTDB id 1198 PSJM300 03950 AFN76868.1         LLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWWYVV   228
NTDB id 1059 ABD1 RS01610 WP 000279215.1      MLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWFIM   231
NTDB id 1016 ACIAD RS01680 WP 004920476.1     MLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYWFIL   231
consensus                                     *****!*!*!!** ** !***!* !!* !**!!**** **** !*! ! ***  *!!*!!**!**!* *!**** * ***

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NTDB id 1169 A1552VC RS11075 WP 000648511.1   FIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNVHEETA   310
NTDB id 1402 DSB67 RS12670 WP 010643257.1     GLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHYQLA   309
NTDB id 1143805 A8Q77 RS07250 WP 004282575.1 IIGLILAGFGLYKWHQHSPSFQRKVDVLLLKLPIFGPIVRKAIIARWARTTATLFAAGVPLVEALDSIAGAAGNALYEEA   315
NTDB id 1112 NGFG RS09215 WP 003689811.1      LIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEA   312
NTDB id 1113 AAA85695.1 219..1451( )          LIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEA   312
NTDB id 1252 GC085 RS07730 WP 011213805.1     FGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAKA   309
NTDB id 1198 PSJM300 03950 AFN76868.1         LAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFRSA   308
NTDB id 1059 ABD1 RS01610 WP 000279215.1      IIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYEKA   311
NTDB id 1016 ACIAD RS01680 WP 004920476.1     ILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQA   311
consensus                                     ***********   * *! ***  *****!**!**!*** !* *!***!!****!*!!*!****!********!**** !
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logo
NTDB id 1169 A1552VC RS11075 WP 000648511.1   INEVYRDTAAGMPMYIAMRNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLGTVVG   390
NTDB id 1402 DSB67 RS12670 WP 010643257.1     IEEVYRDTAAGMPMYIAMRHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGVVVG   389
NTDB id 1143805 A8Q77 RS07250 WP 004282575.1 THDIRSKVTQGLSLTSSMQSTDLFPNMVLQMASIGEESGSLDDMLNKAAEFYEDEVDNAVSQLSSLMEPIIMVVLGLMIG   395
NTDB id 1112 NGFG RS09215 WP 003689811.1     TREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGLVIG   392
NTDB id 1113 AAA85695.1 219..1451( )         TREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGLVIG   392
NTDB id 1252 GC085 RS07730 WP 011213805.1    TDKIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGILVG   389
NTDB id 1198 PSJM300 03950 AFN76868.1        TNKIKSDVSSGMQLNFSMRTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGVLVG   388
NTDB id 1059 ABD1 RS01610 WP 000279215.1     VMKIREDVATGQQLQFAMRISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGVLVG   391
NTDB id 1016 ACIAD RS01680 WP 004920476.1    VLKIREDVSTGQQLNFAMRVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGILVG   391
consensus                                    * *** **  !* *  *!* * *!! ***!!* !!!!!! !**!!*!*! *!!*!!***!* !* **!!*!***!!***!
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logo
NTDB id 1169 A1552VC RS11075 WP 000648511.1   GLVVAMYLPIFNLMSVLG.   408
NTDB id 1402 DSB67 RS12670 WP 010643257.1     GLVTAMYLPIFNLMSVLG.   407
NTDB id 1143805 A8Q77 RS07250 WP 004282575.1 FILISMYLPLFNLGNVVG.   413
NTDB id 1112 NGFG RS09215 WP 003689811.1     TLLVAMYLPLFNLGNVVA.   410
NTDB id 1113 AAA85695.1 219..1451( )         TLLVAMYLPLFNLGNVVA*   410
NTDB id 1252 GC085 RS07730 WP 011213805.1    GLVVAMYLPIFKLGSAV..   406
NTDB id 1198 PSJM300 03950 AFN76868.1        GLIIAMYLPIFQMGSVV..   405
NTDB id 1059 ABD1 RS01610 WP 000279215.1     GLVIAMYLPIFQMGSVV..   408
NTDB id 1016 ACIAD RS01680 WP 004920476.1    GLVIAMYLPIFQMGSVV..   408
consensus                                    *****!!!!*!*******
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X non conserved
X similar
X ≥ 50% conserved