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logo
NTDB id 1402 DSB67 RS12670 WP 010643257.1        .........MKTIAPQLKNYRWKGINSSGK.KTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITKI.SHRVKGKDI   69
NTDB id 1169 A1552VC RS11075 WP 000648511.1      ........MKATQTLPLKNYRWKGINSNGK.KVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLARL.THRVKSKDI   70
NTDB id 1112 NGFG RS09215 WP 003689811.1         MAKNGGFSL...FAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKTS.....SKRKITQEDI   72
NTDB id 1113 AAA85695.1 219..1451( )             MAKNGGFSL...FAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKTS.....SKRKITQEDI   72
NTDB id 35163 CAP2UW1 RS20720 WP 015768571.1    MATALKLTKKAAPEVKEYVFLWEGKNKAGK.VIRGEQRASSVTVVQATLRRQGVVVSKITKQRFR.....GGRKISEKDI   74
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 1016 ACIAD RS01680 WP 004920476.1        ........MAAKKTQVMPVFAYEGVDRKGI.KLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKVKPLDI   71
NTDB id 1059 ABD1 RS01610 WP 000279215.1         ........MAVKKAQMMPTFAYEGVDRKGV.KIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVTTLDI   71
consensus                                                 *    *  *  * **!* * *  ** !** * *  ***  !***** * **** * **      ****  !!
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logo
NTDB id 1402 DSB67 RS12670 WP 010643257.1        TIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNLSQ   149
NTDB id 1169 A1552VC RS11075 WP 000648511.1      TILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNLPE   150
NTDB id 1112 NGFG RS09215 WP 003689811.1         TVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLES   152
NTDB id 1113 AAA85695.1 219..1451( )             TVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLES   152
NTDB id 35163 CAP2UW1 RS20720 WP 015768571.1    ALFTRQLATMMKAGVPLLQTFEIVGRGHDNPAVGKLLLDIKADVETGSSLSQAFRKYPLHFDLLYCNLVAAGEQAGILES   154
NTDB id 1252 GC085 RS07730 WP 011213805.1        TVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSLDI   149
NTDB id 1198 PSJM300 03950 AFN76868.1            ALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLET   148
NTDB id 1016 ACIAD RS01680 WP 004920476.1        AIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLEI   151
NTDB id 1059 ABD1 RS01610 WP 000279215.1         TIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALET   151
consensus                                        ****!!**!!***!*!**!********* ** ****** ** ****!**** **** * *!* ****!***!!**! !**
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logo
NTDB id 1402 DSB67 RS12670 WP 010643257.1        VFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWGPFI   229
NTDB id 1169 A1552VC RS11075 WP 000648511.1      VFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSLWA   230
NTDB id 1112 NGFG RS09215 WP 003689811.1         LLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYGWMV   232
NTDB id 1113 AAA85695.1 219..1451( )             LLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGWMV   232
NTDB id 35163 CAP2UW1 RS20720 WP 015768571.1    LLDRLATYKEKMIAIKSKIKSALFYPVAIIVVAFIITAVIMIFVIPAFKEVFKSFGADLPAPTQIVIAMSDFVVDYWWAL   234
NTDB id 1252 GC085 RS07730 WP 011213805.1        MLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWYII   229
NTDB id 1198 PSJM300 03950 AFN76868.1            LLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWWYVV   228
NTDB id 1016 ACIAD RS01680 WP 004920476.1        MLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYWFIL   231
NTDB id 1059 ABD1 RS01610 WP 000279215.1         MLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWFIM   231
consensus                                        *****!*!*!!** ** !***!* !!* ***!!**** **** !*! ! ***  *!!*!!**!**!* *!**** *****
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logo
NTDB id 1402 DSB67 RS12670 WP 010643257.1        GLSFVSLLISGKIMSQRSDSFRLLAAFSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHYQLA   309
NTDB id 1169 A1552VC RS11075 WP 000648511.1      FIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNVHFETA   310
NTDB id 1112 NGFG RS09215 WP 003689811.1         LIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEA   312
NTDB id 1113 AAA85695.1 219..1451( )             LIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEA   312
NTDB id 35163 CAP2UW1 RS20720 WP 015768571.1    FGGIAGSVFAFFYTWKRSEAMQIAFDRMFLRVPVFGDIIRKSVIARWTRTLATMFAAGVPLVESLESVGGAAGNYVYKVA   314
NTDB id 1252 GC085 RS07730 WP 011213805.1        FGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAKA   309
NTDB id 1198 PSJM300 03950 AFN76868.1            LAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFRSA   308
NTDB id 1016 ACIAD RS01680 WP 004920476.1        ILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQA   311
NTDB id 1059 ABD1 RS01610 WP 000279215.1         IIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYEKA   311
consensus                                        ***********    * *! ***  *****!**!**!*** !* *!***!!****!*!!*!****!********!**** !
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logo
NTDB id 1402 DSB67 RS12670 WP 010643257.1      IEEVYRDTAAGMPMYIAMRHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGVVVG   389
NTDB id 1169 A1552VC RS11075 WP 000648511.1    INEVYRDTAAGMPMYIAMRNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLGTVVG   390
NTDB id 1112 NGFG RS09215 WP 003689811.1       TREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGLVIG   392
NTDB id 1113 AAA85695.1 219..1451( )           TREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGLVIG   392
NTDB id 35163 CAP2UW1 RS20720 WP 015768571.1  TRQIQSEVSTGTSLTSAMQNVELFPNMVTQMVAIGEESGALDSMLGKVADFFEAEVDDAVEALSSLMEPIIMVVLGVLIG   394
NTDB id 1252 GC085 RS07730 WP 011213805.1      TDKIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGILVG   389
NTDB id 1198 PSJM300 03950 AFN76868.1          TNKIKSDVSSGMQLNFSMRTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGVLVG   388
NTDB id 1016 ACIAD RS01680 WP 004920476.1      VLKIREDVSTGQQLNFAMRVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGILVG   391
NTDB id 1059 ABD1 RS01610 WP 000279215.1       VMKIREDVATGQQLQFAMRISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGVLVG   391
consensus                                      *  ** ** *!* *  *!* * *!! ***!!**!!!!!!*!**!! !*! **! !!***!**!* **!!*!***!!***!
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   <0
logo
NTDB id 1402 DSB67 RS12670 WP 010643257.1      GLVTAMYLPIFNLMSVLG.   407
NTDB id 1169 A1552VC RS11075 WP 000648511.1    GLVVAMYLPIFNLMSVLG.   408
NTDB id 1112 NGFG RS09215 WP 003689811.1       TLLVAMYLPLFNLGNVVA.   410
NTDB id 1113 AAA85695.1 219..1451( )           TLLVAMYLPLFNLGNVVA*   410
NTDB id 35163 CAP2UW1 RS20720 WP 015768571.1  GMVIAMYLPIFKLGAVVG.   412
NTDB id 1252 GC085 RS07730 WP 011213805.1      GLVVAMYLPIFKLGSAV..   406
NTDB id 1198 PSJM300 03950 AFN76868.1          GLIIAMYLPIFQMGSVV..   405
NTDB id 1016 ACIAD RS01680 WP 004920476.1      GLVIAMYLPIFQMGSVV..   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1       GLVIAMYLPIFQMGSVV..   408
consensus                                      ****!!!!!*!*******
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X non conserved
X similar
X ≥ 50% conserved