logo

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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 1112 NGFG RS09215 WP 003689811.1     MAKN...GGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKT.....SSKRKITQEDI   72
NTDB id 1113 AAA85695.1 219..1451( )         MAKN...GGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKT.....SSKRKITQEDI   72
NTDB id 1252 GCO85 RS07730 WP 011213805.1    ........MDKNSPPLLTFHYQGINKAGQ.KMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.KNKKITQADI   69
NTDB id 51051 Q7A RS03040 WP 014705866.1     MATAAKAKRKPKKAELPNLFIWQGTNKSGR.KVKGEQAGESVQAVRADLRRQGITPGKVRRKPKDLFAP.RKPKIKPVHI   78
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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NTDB id 1169 A1552VC RS11075 WP 000648511.1  TILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNLPE  150
NTDB id 1402 DSB67 RS12670 WP 010643257.1    TIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNLSQ  149
NTDB id 1112 NGFG RS09215 WP 003689811.1     TVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLES  152
NTDB id 1113 AAA85695.1 219..1451( )         TVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLES  152
NTDB id 1252 GCO85 RS07730 WP 011213805.1    TVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSLDI  149
NTDB id 51051 Q7A RS03040 WP 014705866.1     AIFSRMLATMMSSGVPMMQSLQIIGEGHENASMQEMILAIKADVESGTSLAESLAKFPLHFDDLYISLINAGEQSGTLEA  158
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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NTDB id 1169 A1552VC RS11075 WP 000648511.1  VFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSLWA  230
NTDB id 1402 DSB67 RS12670 WP 010643257.1    VFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWGPFI  229
NTDB id 1112 NGFG RS09215 WP 003689811.1     LLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYGWMV  232
NTDB id 1113 AAA85695.1 219..1451( )         LLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGWMV  232
NTDB id 1252 GCO85 RS07730 WP 011213805.1    MLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWYII  229
NTDB id 51051 Q7A RS03040 WP 014705866.1     LLHEIATYQEKTEALKSKIKKALVYPTAIMVVAFIVTAILMIFVIPQFQALFTGFGADLPGLTKMVISISQVFQDYWWLI  238
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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NTDB id 1402 DSB67 RS12670 WP 010643257.1    GLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKITSKTSGNMHYQLA  309
NTDB id 1112 NGFG RS09215 WP 003689811.1     LIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEA  312
NTDB id 1113 AAA85695.1 219..1451( )         LIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEA  312
NTDB id 1252 GCO85 RS07730 WP 011213805.1    FGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAKA  309
NTDB id 51051 Q7A RS03040 WP 014705866.1     FGSIIGSVMGFMAARRRSRKVQHFMDRMLLKLPVIGDVLTKGAIARFARTFSVMFKAGVPMVEAMTSVAGATGNIVYNEA  318
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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NTDB id 1402 DSB67 RS12670 WP 010643257.1    IEEVYRDTAAGMPMYIAMRHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGVVVG  389
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 51051 Q7A RS03040 WP 014705866.1    TLEMRDDVSTGTQLNKAMTDTELFPNMVIQMVSIGEESGSLDAMLAKVADFFEREVDDAVDNMTALMEPFIMAFLGVLIG  398
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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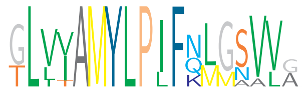

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NTDB id 1402 DSB67 RS12670 WP 010643257.1    GLVTAMYLPIFNLMSVLG.   407
NTDB id 1112 NGFG RS09215 WP 003689811.1     TLLVAMYLPLFNLGNVVA.   410
NTDB id 1113 AAA85695.1 219..1451( )        TLLVAMYLPLFNLGNVVA*   410
NTDB id 1252 GC085 RS07730 WP 011213805.1    GLVVAMYLPIFKLGSAV..   406
NTDB id 51051 Q7A RS03040 WP 014705866.1    TLVIAMYLPIFKLGAVV..   415
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