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logo
NTDB id 1169 A1552VC RS11075 WP 000648511.1      MKA.....TQTLPLKNYRWKGINSNGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.LTHRVKSKDITIL   73
NTDB id 1402 DSB67 RS12670 WP 010643257.1        .MK.....TIAPQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.ISHRVKGKDITIF   72
NTDB id 1112 NGFG RS09215 WP 003689811.1         MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITR.....VKTSSKRKITQEDITVF   75
NTDB id 1113 AAA85695.1 219..1451( )             MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITR.....VKTSSKRKITQEDITVF   75
NTDB id 1252 GC085 RS07730 WP 011213805.1        .MD.....KNSPPLLTFHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.KNKKITQADITVF   72
NTDB id 1198 PSJM300 03950 AFN76868.1            .MA.....QKAIKNSVFTWEGLDRQGAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLF..SAGKKIKPMDIALF   71
NTDB id 1146230 DABAL43B RS00380 WP 079690562.1  MAK.....AKTDMLLDFVYDGVNRRGQK.VKGETTSRSLELAKATLRKQGITVKGIKKKPKPLY..TFKKSIKPIDIAIF   72
NTDB id 1016 ACIAD RS01680 WP 004920476.1       MAA.....KKTQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKVKPLDIAIF   74
NTDB id 1059 ABD1 RS01610 WP 000279215.1         MAV.....KKAQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVTTLDITIF   74
consensus                                        **        *  *  * **!* * * ! * !** * *  ***  !***** ** ****   **    *****  !!***

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NTDB id 1169 A1552VC RS11075 WP 000648511.1      TRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNLPEVFE   153
NTDB id 1402 DSB67 RS12670 WP 010643257.1        TRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNLSQVFE   152
NTDB id 1112 NGFG RS09215 WP 003689811.1         TRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESLLD   155
NTDB id 1113 AAA85695.1 219..1451( )             TRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESLLD   155
NTDB id 1252 GC085 RS07730 WP 011213805.1        SRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSLDIMLD   152
NTDB id 1198 PSJM300 03950 AFN76868.1            TRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLETLLD   151
NTDB id 1146230 DABAL43B RS00380 WP 079690562.1  ARQLATMMKAGVPLTQSFEIVADSLDNPSMKDLVLQIKADIEAGGTFASALRRHPRYFDDLFCSLVESGEQSGALETMLE   152
NTDB id 1016 ACIAD RS01680 WP 004920476.1       TRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLEIMLD   154
NTDB id 1059 ABD1 RS01610 WP 000279215.1         TRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALETMLD   154
consensus                                        *!!**!!***!*!**!********  ** ****** ** ****!**** **** * *!* *** !***!!**! !*****

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NTDB id 1169 A1552VC RS11075 WP 000648511.1      RLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSLWAFIA   233
NTDB id 1402 DSB67 RS12670 WP 010643257.1        RLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWGPFIGLS   232
NTDB id 1112 NGFG RS09215 WP 003689811.1         KLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYGWMVLIA   235
NTDB id 1113 AAA85695.1 219..1451( )             KLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGWMVLIA   235
NTDB id 1252 GC085 RS07730 WP 011213805.1        KVATYKEKIEIIKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWYIIFGA   232
NTDB id 1198 PSJM300 03950 AFN76868.1            RVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWWYVVLAG   231
NTDB id 1146230 DABAL43B RS00380 WP 079690562.1  RVATYKEKSELLKAKIKKAMKYPIAVVVVALIVTIILLVKVVPVFSGLFESFGAELPAFTQMVVGMSEWMQAWWFLLLII   232
NTDB id 1016 ACIAD RS01680 WP 004920476.1       RVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYWFILILV   234
NTDB id 1059 ABD1 RS01610 WP 000279215.1         RVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWFIMIIA   234
consensus                                        **!*!*!!** ** !***!* !!* !**!!**** *****!*! ! ***  *!!*!!**!**!* *!**** ********

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NTDB id 1169 A1552VC RS11075 WP 000648511.1      IAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNVHFETAINE   313
NTDB id 1402 DSB67 RS12670 WP 010643257.1        FVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHYQLAIEE   312
NTDB id 1112 NGFG RS09215 WP 003689811.1         LGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEATRE   315
NTDB id 1113 AAA85695.1 219..1451( )             LGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEATRE   315
NTDB id 1252 GC085 RS07730 WP 011213805.1        LGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAKATDK   312
NTDB id 1198 PSJM300 03950 AFN76868.1            FVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFRSATNK   311
NTDB id 1146230 DABAL43B RS00380 WP 079690562.1  IGGTIISFSEAKKRSKKFRDVLDRAVLKAPIFGNIAYQAVIARFSRTLSTTFAAGVPLLDALDSTAGAANNVVFYNAIQQ   312
NTDB id 1016 ACIAD RS01680 WP 004920476.1       IGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQAVLK   314
NTDB id 1059 ABD1 RS01610 WP 000279215.1         IGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYEKAVMK   314
consensus                                        ********  ** *! ***  *****!**!**!*** ** *!***!!****!*!!*!****!********!**** !*
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NTDB id 1169 A1552VC RS11075 WP 000648511.1      VYRDTAAGMPMYIAMRNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLGTVVGGLV   393
NTDB id 1402 DSB67 RS12670 WP 010643257.1        VYRDTAAGMPMYIAMRHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGVVVGGLV   392
NTDB id 1112 NGFG RS09215 WP 003689811.1         IRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGLVIGTLL   395
NTDB id 1113 AAA85695.1 219..1451( )             IRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGLVIGTLL   395
NTDB id 1252 GCO85 RS07730 WP 011213805.1        IREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGILVGGLV   392
NTDB id 1198 PSJM300 03950 AFN76868.1            IKSDVSSGMQLNFSMRTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGVLVGGLI   391
NTDB id 1146230 DABAL43B RS00380 WP 079690562.1  IKNDVSTGQQLQFSMRSTNLFPSLAIQMVGIGEESGSLEEMLDKVAVYYENEVDNAVDGLTSLMEPMIMAVLGVLIGGLV   392
NTDB id 1016 ACIAD RS01680 WP 004920476.1       IREDVSTGQQLNFAMRVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGILVGGLV   394
NTDB id 1059 ABD1 RS01610 WP 000279215.1         IREDVATGQQLQFAMRISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGVLVGGLV   394
consensus                                        ** ** *!***  *!* * *!! ***!!**!!!!!! !**!! !*! *!! !!***!**!* **!!*!* *!!***!*!*
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NTDB id 1169 A1552VC RS11075 WP 000648511.1      VAMYLPIFNLMSVLG.   408
NTDB id 1402 DSB67 RS12670 WP 010643257.1        TAMYLPIFNLMSVLG.   407
NTDB id 1112 NGFG RS09215 WP 003689811.1         VAMYLPLFNLGNVVA.   410
NTDB id 1113 AAA85695.1 219..1451( )             VAMYLPLFNLGNVVA*   410
NTDB id 1252 GCO85 RS07730 WP 011213805.1        VAMYLPIFKLGSAV..   406
NTDB id 1198 PSJM300 03950 AFN76868.1            IAMYLPIFQMGSVV..   405
NTDB id 1146230 DABAL43B RS00380 WP 079690562.1  IAMYLPIFQMGAVVG.   407
NTDB id 1016 ACIAD RS01680 WP 004920476.1        IAMYLPIFQMGSVV..   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1         IAMYLPIFQMGSVV..   408
consensus                                        *!!!!!*!*******
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X non conserved
X similar
X ≥ 50% conserved