logo

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NTDB id 1402 DSB67 RS12670 WP 010643257.1  .MKT.....IAPQLKNYRWKGINSSGK.KTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.ISHRVKGKDITI  71
NTDB id 1169 A1552VC RS11075 WP 000648511.1 MKAT.....QTLPLKNYRWKGINSNGK.KVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.LTHRVKSKDITI  72
NTDB id 1113 AAA85695.1 219..1451( )       .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TSSKRKITQEDITV  74
NTDB id 1112 NGFG RS09215 WP 003689811.1   .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TSSKRKITQEDITV  74
NTDB id 396436 GH742 RS07625 WP 108291623.1 .MEKA.....KNDIITYQWEGVNKAGE.KVNGVIDARSLAIAKADLRKQGIITKKVVKKRKPFFDK.KNKKITQGDITV  71
NTDB id 1252 GCO85 RS07730 WP 011213805.1  .MDKN.....SPPLLTFHYQGINKAGQ.KMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.KNKKITQADITV  71
NTDB id 1198 PSJM300 03950 AFN76868.1       .MAQK.....AIKNSVFTWEGLDRQGA.KIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKKIKPMDIAL  70
NTDB id 1016 ACIAD RS01680 WP 004920476.1  MAAKK.....TQVMPVFAYEGVDRKGI.KLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKVKPLDIAI  73
NTDB id 1059 ABD1 RS01610 WP 000279215.1   MAVKK.....AQMMPTFAYEGVDRKGV.KIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVTTLDITI  73
consensus                                   *** *  *  * **!* * *  ** !** * * **** !***** ******* *  **** !!**
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NTDB id 1402 DSB67 RS12670 WP 010643257.1  FTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNLSQVF 151
NTDB id 1169 A1552VC RS11075 WP 000648511.1 LTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNLPEVF 152
NTDB id 1113 AAA85695.1 219..1451( )       FTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESLL 154
NTDB id 1112 NGFG RS09215 WP 003689811.1   FTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESLL 154
NTDB id 396436 GH742 RS07625 WP 108291623.1 FSRQMATMIEAGIPLIQSFDIVAKGQSNQKMRDLIETIKRDVETGLTLAESLQKHPAYFNELFCNLVDAGEKSGSLEIML 151
NTDB id 1252 GCO85 RS07730 WP 011213805.1  FSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSLDIML 151
NTDB id 1198 PSJM300 03950 AFN76868.1       FTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLETLL 150
NTDB id 1016 ACIAD RS01680 WP 004920476.1  FTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEQGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLEIML 153
NTDB id 1059 ABD1 RS01610 WP 000279215.1   FTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEQGSTFASALRKYPQHFDNLFCSLVESGEQSGALETML 153
consensus                                  **!!**!!* *!*!**!********  ** ****** ** ****!**** **** * *!* ****!***!! *! !* **
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NTDB id 1402 DSB67 RS12670 WP 010643257.1  ERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWGPFIGL 231
NTDB id 1169 A1552VC RS11075 WP 000648511.1 ERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSLWAFI 232
NTDB id 1113 AAA85695.1 219..1451( )       DKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGWMVLI 234
NTDB id 1112 NGFG RS09215 WP 003689811.1   DKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYGWMVLI 234
NTDB id 396436 GH742 RS07625 WP 108291623.1 DKVATYKEKIETIKKKIKKALTYPMAVLVVAFLVTTALMIFVVPQFESLFEGFGADLPAMTRMVVDMSEFFQSYWYIMFG 231
NTDB id 1252 GCO85 RS07730 WP 011213805.1  DKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWYIIFG 231
NTDB id 1198 PSJM300 03950 AFN76868.1       DRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWWYVVLA 230
NTDB id 1016 ACIAD RS01680 WP 004920476.1  DRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYWFILIL 233
NTDB id 1059 ABD1 RS01610 WP 000279215.1   DRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWFIMII 233
consensus                                  ***!*!*!!** ** !***!* !!* !**!!**** **** !*! ! *** *!!*!!**!**!* *!**** *******
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NTDB id 1402 DSB67 RS12670 WP 010643257.1  SFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHYQLAIE 311
NTDB id 1169 A1552VC RS11075 WP 000648511.1 AIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNVHFETAIN 312
NTDB id 1113 AAA85695.1 219..1451( )       ALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEATR 314
NTDB id 1112 NGFG RS09215 WP 003689811.1   ALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEATR 314
NTDB id 396436 GH742 RS07625 WP 108291623.1 AIGGAIYAFIYFKNHSPQFAHSIDRAMLKFPVVGPILEKAAIARFTRTLSITFAAGLPLVEALKSVSGATGNILYAKATD 311
NTDB id 1252 GCO85 RS07730 WP 011213805.1  ALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAKATD 311
NTDB id 1198 PSJM300 03950 AFN76868.1       GFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFRSATN 310
NTDB id 1016 ACIAD RS01680 WP 004920476.1  VIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQAVL 313
NTDB id 1059 ABD1 RS01610 WP 000279215.1   AIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYEKAVM 313
consensus                                  ********** * *! *** *****!**!**!*** !* *!***!!****!*!!*!****! *******!**** !*
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NTDB id 1402 DSB67 RS12670 WP 010643257.1     EVYRDTAAGMPMYIAMRHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGVVVGGL   391
NTDB id 1169 A1552VC RS11075 WP 000648511.1   EVYRDTAAGMPMYIAMRNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLGTVVGGL   392
NTDB id 1113 AAA85695.1 219..1451( )          EIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGLVIGTL   394
NTDB id 1112 NGFG RS09215 WP 003689811.1      EIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGLVIGTL   394
NTDB id 396436 GH742 RS07625 WP 108291623.1   KIREEVSTGQQMQVAMDNTHLFPNMVIQMVAIGEESGALEQMLGKVADFYEEEVDNAVDALSSLLEPIIMSILGVLVGGL   391
NTDB id 1252 GC085 RS07730 WP 011213805.1     KIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGILVGGL   391
NTDB id 1198 PSJM300 03950 AFN76868.1        KIKSDVSSGMQLNFSMRTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGVLVGGL   390
NTDB id 1016 ACIAD RS01680 WP 004920476.1     KIREDVSTGQQLNFAMRVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGILVGGL   393
NTDB id 1059 ABD1 RS01610 WP 000279215.1      KIREDVATGQQLQFAMRISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGVLVGGL   393
consensus                                     *** ** *!***   *!* * *!!  ***!!**!!!!!!*!**!!  !*!  *!!*!!***!**!*  **!!*!*  *!!***!*!
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NTDB id 1402 DSB67 RS12670 WP 010643257.1     VTAMYLPIFNLMSVLG.   407
NTDB id 1169 A1552VC RS11075 WP 000648511.1   VVAMYLPIFNLMSVLG.   408
NTDB id 1113 AAA85695.1 219..1451( )          LVAMYLPLFNLGNVVA*   410
NTDB id 1112 NGFG RS09215 WP 003689811.1      LVAMYLPLFNLGNVVA.   410
NTDB id 396436 GH742 RS07625 WP 108291623.1   VVAMYLPIFKLGSAV..   406
NTDB id 1252 GC085 RS07730 WP 011213805.1     VVAMYLPIFKLGSAV..   406
NTDB id 1198 PSJM300 03950 AFN76868.1        IIAMYLPIFQMGSVV..   405
NTDB id 1016 ACIAD RS01680 WP 004920476.1     VIAMYLPIFQMGSVV..   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1      VIAMYLPIFQMGSVV..   408
consensus                                     **!!!!!*!******
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X non conserved

X similar

X $\geq$ 50% conserved