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logo
NTDB id 1402 DSB67 RS12670 WP 010643257.1     .MKT......IAPQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITKI.SHRVKGKDITI   71
NTDB id 1169 A1552VC RS11075 WP 000648511.1   MKAT......QTLPLKNYRWKGINSNGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLARL.THRVKSKDITI   72
NTDB id 1112 NGFG RS09215 WP 003689811.1      .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TSSKRKITQEDITV   74
NTDB id 1113 AAA85695.1 219..1451( )          .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TSSKRKITQEDITV   74
NTDB id 1252 GC085 RS07730 WP 011213805.1     .MDK......NSPPLLTFHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDRK.NKKITQADITV   71
NTDB id 1016 ACIAD RS01680 WP 004920476.1     MAAK......KTQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKVKPLDIAI   73
NTDB id 1059 ABD1 RS01610 WP 000279215.1      MAVK......KAQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVTTLDITI   73
NTDB id 229977 MTMN5 RS14365 WP 126812063.1  .MAE......KAEKLQAFVWEGKDRKGNK.TKGEVSGTNLALVKAQLRKQGIIPDKVKKKPKPLFGG..SKKITPFDIAM   70
NTDB id 1198 PSJM300 03950 AFN76868.1         .MAQ......KAIKNSVFTWEGLDRQGAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFSA..GKKIKPMDIAL   70
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 1112 NGFG RS09215 WP 003689811.1      FTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESLL   154
NTDB id 1113 AAA85695.1 219..1451( )          FTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESLL   154
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NTDB id 1016 ACIAD RS01680 WP 004920476.1     FTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLEIML   153
NTDB id 1059 ABD1 RS01610 WP 000279215.1      FTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALETML   153
NTDB id 229977 MTMN5 RS14365 WP 126812063.1  LTRQLATMMKAGVPLVQSFDIVADGLENRGLQELVTNIRNDISSGTSFAGALKKYPRHFDDLYCNLVDSGEKAGALESML   150
NTDB id 1198 PSJM300 03950 AFN76868.1         FTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLETLL   150
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 1112 NGFG RS09215 WP 003689811.1      DKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYGWMVLI   234
NTDB id 1113 AAA85695.1 219..1451( )          DKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGWMVLI   234
NTDB id 1252 GC085 RS07730 WP 011213805.1     DKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWYIIFG   231
NTDB id 1016 ACIAD RS01680 WP 004920476.1     DRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYWFILIL   233
NTDB id 1059 ABD1 RS01610 WP 000279215.1      DRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWFIMII   233
NTDB id 229977 MTMN5 RS14365 WP 126812063.1  DRIATYLEKTEILKKKVKKAMTYPAAIVVVAIIVTAILLVKVVPQFESLFKGFGADLPVFTQMVVRLSEWLQTWWFVVLL   230
NTDB id 1198 PSJM300 03950 AFN76868.1         DRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWWYVVLA   230
consensus                                     ***!*!*!!** ** !***!* !!  ***!!**** *****!*! ! ***  *!!*!!**!**!* *!**** *******

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NTDB id 1402 DSB67 RS12670 WP 010643257.1     SFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHYQLAIE   311
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NTDB id 1112 NGFG RS09215 WP 003689811.1      ALCFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEATR   314
NTDB id 1113 AAA85695.1 219..1451( )          ALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEATR   314
NTDB id 1252 GC085 RS07730 WP 011213805.1     ALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAKATD   311
NTDB id 1016 ACIAD RS01680 WP 004920476.1     VIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQAVL   313
NTDB id 1059 ABD1 RS01610 WP 000279215.1      AIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYEKAVM   313
NTDB id 229977 MTMN5 RS14365 WP 126812063.1  GIVGTIFLFKEAIRRSQKFSDLVDKYVLKLPVVGEILDKSAVAKFGRVLSTTFAAGVPLVDALDSVAGATGNAVYRDAIQ   310
NTDB id 1198 PSJM300 03950 AFN76868.1         GFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFRSATN   310
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 1112 NGFG RS09215 WP 003689811.1      EIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGLVIGTL   394
NTDB id 1113 AAA85695.1 219..1451( )          EIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGLVIGTL   394
NTDB id 1252 GCO85 RS07730 WP 011213805.1     KIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGILVGGL   391
NTDB id 1016 ACIAD RS01680 WP 004920476.1     KIREDVSTGQQLNFAMRVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGILVGGL   393
NTDB id 1059 ABD1 RS01610 WP 000279215.1      KIREDVATGQQLQFAMRISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGVLVGGL   393
NTDB id 229977 MTMN5 RS14365 WP 126812063.1   RIKNDVSSGTQLQATMRQQDVFPVMAVQLTAIGEESGNLDEMLEKVAVHYEAVVDDMVDNLTALLEPIIMAVLGVLVGGL   390
NTDB id 1198 PSJM300 03950 AFN76868.1         KIKSDVSSGMQLNFSMRTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGVLVGGL   390
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 1112 NGFG RS09215 WP 003689811.1      LVAMYLPLFNLGNVVA.   410
NTDB id 1113 AAA85695.1 219..1451( )          LVAMYLPLFNLGNVVA*   410
NTDB id 1252 GCO85 RS07730 WP 011213805.1     VVAMYLPIFKLGSAV..   406
NTDB id 1016 ACIAD RS01680 WP 004920476.1     VIAMYLPIFQMGSVV..   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1      VIAMYLPIFQMGSVV..   408
NTDB id 229977 MTMN5 RS14365 WP 126812063.1   IIAMYLPIFQMGQVVG.   406
NTDB id 1198 PSJM300 03950 AFN76868.1         IIAMYLPIFQMGSVV..   405
consensus                                     **!!!!!*!*******
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X non conserved
X similar
X ≥ 50% conserved