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logo
NTDB id 1402 DSB67 RS12670 WP 010643257.1     ..MKT......IAPQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.ISHRVKGKDIT   70
NTDB id 302964 DUN60 RS11595 WP 054547485.1  MSSKS......KQSQLKNYHWKGINSSGKK.VSGQSLALTELEVREKLKEQHIQIKKIKKKSISAITR.LTHRVKAKDIT   72
NTDB id 1169 A1552VC RS11075 WP 000648511.1  .MKAT......QTLPLKNYRWKGINSNGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.LTHRVKSKDIT   71
NTDB id 1112 NGFG RS09215 WP 003689811.1     ..MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KTSSKRKITQEDIT   73
NTDB id 1113 AAA85695.1 219..1451( )         ..MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KTSSKRKITQEDIT   73
NTDB id 1252 GC085 RS07730 WP 011213805.1    ..MDKN......SPPLLTFHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.KNKKITQADIT   70
NTDB id 1198 PSJM300 03950 AFN76868.1        ..MAQK......AIKNSVFTWEGLDRQGAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKKIKPMDIA   69
NTDB id 1059 ABD1 RS01610 WP 000279215.1     .MAVKK......AQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVTTLDIT   72
NTDB id 1016 ACIAD RS01680 WP 004920476.1    .MAAKK......TQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKVKPLDIA   72
consensus                                     ***       *  ** * **!* * * ! * !** * ** *** *!***** *******   *       ****  !!*

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NTDB id 1402 DSB67 RS12670 WP 010643257.1     IFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNLSQV  150
NTDB id 302964 DUN60 RS11595 WP 054547485.1  ILTRQLATMLATGVPIVQAIKLVSDNHRKAEMKSILSHICKGVEAGTPISKAMRTASRHFDDLYTDLVATGELSGNLAQV  152
NTDB id 1169 A1552VC RS11075 WP 000648511.1  ILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNLPEV  151
NTDB id 1112 NGFG RS09215 WP 003689811.1     VFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESL  153
NTDB id 1113 AAA85695.1 219..1451( )         VFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESL  153
NTDB id 1252 GC085 RS07730 WP 011213805.1    VFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSLDIM  150
NTDB id 1198 PSJM300 03950 AFN76868.1        LFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLETL  149
NTDB id 1059 ABD1 RS01610 WP 000279215.1     IFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALETM  152
NTDB id 1016 ACIAD RS01680 WP 004920476.1    IFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLEIM  152
consensus                                    ***!!**!!* *!*!**!********* ** ****** **  ***!********  * *!* ***  !***!! *! !* *

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NTDB id 1402 DSB67 RS12670 WP 010643257.1     FERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWGPFIG  230
NTDB id 302964 DUN60 RS11595 WP 054547485.1  FERLATYREKSEQLKSKVIKALIYPAMVVAVALTVSYLMLTMVIPEFESMFSGFGADLPWFTQQVLYLSHWMQAYSFYSA  232
NTDB id 1169 A1552VC RS11075 WP 000648511.1  FERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSLWAF  231
NTDB id 1112 NGFG RS09215 WP 003689811.1     LDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYGWMVL  233
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NTDB id 1252 GC085 RS07730 WP 011213805.1    LDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWYIIF  230
NTDB id 1198 PSJM300 03950 AFN76868.1        LDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWWYVVL  229
NTDB id 1059 ABD1 RS01610 WP 000279215.1     LDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWFIMI  232
NTDB id 1016 ACIAD RS01680 WP 004920476.1    LDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYWFILI  232
consensus                                    ****!*!*!!** ** !***!* !!  !**!!* ******* !*! ! ***  *!!*!!**!* !* *! *** * ****

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NTDB id 1402 DSB67 RS12670 WP 010643257.1     LSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHYQLAI  310
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NTDB id 1113 AAA85695.1 219..1451( )         IALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEAT  313
NTDB id 1252 GC085 RS07730 WP 011213805.1    GALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAKAT  310
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NTDB id 1059 ABD1 RS01610 WP 000279215.1     IAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYEKAV  312
NTDB id 1016 ACIAD RS01680 WP 004920476.1    LVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQAV  312
consensus                                    **********  ** *! ***  ****!**!**!*** !**!***!!****!**!*!****! *******!**** !*
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NTDB id 1402 DSB67 RS12670 WP 010643257.1     EEVYRDTAAGMPMYIAMRHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGVVGG   390
NTDB id 302964 DUN60 RS11595 WP 054547485.1   IEVHRETAAGMPMYIAMRNTNAFPEMVLQMVMIGEESGNLDDMLNKVASIYEFEVDNTVDNLGKILEPLIIVFLGTVVGG   392
NTDB id 1169 A1552VC RS11075 WP 000648511.1   NEVYRDTAAGMPMYIAMRNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLGTVVGG   391
NTDB id 1112 NGFG RS09215 WP 003689811.1      REIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGLVIGT   393
NTDB id 1113 AAA85695.1 219..1451( )          REIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGLVIGT   393
NTDB id 1252 GC085 RS07730 WP 011213805.1     DKIREEEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGILVGG   390
NTDB id 1198 PSJM300 03950 AFN76868.1         NKIKSDVSSGMQLNFSMRTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGVLVGG   389
NTDB id 1059 ABD1 RS01610 WP 000279215.1      MKIREDVATGQQLQFAMRISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGVLVGG   392
NTDB id 1016 ACIAD RS01680 WP 004920476.1     LKIREDVSTGQQLNFAMRVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGILVGG   392
consensus                                      *** *** !* *  *!* *  !! ***!!* !!!!!! !**!!*!*! *!! !!***!* !* **!!*!***!!***!*
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NTDB id 1402 DSB67 RS12670 WP 010643257.1     LVTAMYLPIFNLMSVLG.   407
NTDB id 302964 DUN60 RS11595 WP 054547485.1   LVVAMYLPIFNLMSVLG.   409
NTDB id 1169 A1552VC RS11075 WP 000648511.1   LVVAMYLPIFNLMSVLG.   408
NTDB id 1112 NGFG RS09215 WP 003689811.1      LLVAMYLPLFNLGNVVA.   410
NTDB id 1113 AAA85695.1 219..1451( )          LLVAMYLPLFNLGNVVA*   410
NTDB id 1252 GC085 RS07730 WP 011213805.1     LVVAMYLPIFKLGSAV..   406
NTDB id 1198 PSJM300 03950 AFN76868.1         LIIAMYLPIFQMGSVV..   405
NTDB id 1059 ABD1 RS01610 WP 000279215.1      LVIAMYLPIFQMGSVV..   408
NTDB id 1016 ACIAD RS01680 WP 004920476.1     LVIAMYLPIFQMGSVV..   408
consensus                                     !**!!!!!*!*******
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X non conserved
X similar
X ≥ 50% conserved