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logo
NTDB id 1169 A1552VC RS11075 WP 000648511.1  .MKATQ......TLPLKNYRWKGINSNG.KKVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLARL.THRVKSKDIT   71
NTDB id 1402 DSB67 RS12670 WP 010643257.1    ..MKTI......APQLKNYRWKGINSSG.KKTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITKI.SHRVKGKDIT   70
NTDB id 1113 AAA85695.1 219..1451( )         ..MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KTSSKRKITQEDIT   73
NTDB id 1112 NGFG RS09215 WP 003689811.1     ..MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KTSSKRKITQEDIT   73
NTDB id 1252 GC085 RS07730 WP 011213805.1    ..MDKN......SPPLLTFHYQGINKAG.QKMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDRK.NKKITQADIT   70
NTDB id 1016 ACIAD RS01680 WP 004920476.1    .MAAKK......TQVMPVFAYEGVDRKG.IKLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKVKPLDIA   72
NTDB id 1059 ABD1 RS01610 WP 000279215.1     .MAVKK......AQMMPTFAYEGVDRKG.VKIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVTTLDIT   72
NTDB id 331275 EJ103 RS14345 WP 126008287.1 MAKKQE......DKGLDTFQWVGVSARG.KKLEGELTGSSVALVKAQLRKQGITPSKVKRKPKPLFGIQSVQKITPKDIA   73
NTDB id 1198 PSJM300 03950 AFN76868.1        ..MAQK......AIKNSVFTWEGLDRQG.AKIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFSA..GKKIKPMDIA   69
consensus                                      ***       *  *  * **!*   * *** !** * * ****  !*****   *****   *      ****  !!*

logo
NTDB id 1169 A1552VC RS11075 WP 000648511.1  ILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNLPEV  151
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NTDB id 1113 AAA85695.1 219..1451( )         VFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESL  153
NTDB id 1112 NGFG RS09215 WP 003689811.1     VFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESL  153
NTDB id 1252 GC085 RS07730 WP 011213805.1    VFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSLDIM  150
NTDB id 1016 ACIAD RS01680 WP 004920476.1    IFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLEIM  152
NTDB id 1059 ABD1 RS01610 WP 000279215.1     IFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALETM  152
NTDB id 331275 EJ103 RS14345 WP 126008287.1  LVTRQIATMLMAGVPLIQAIEMIGSGSTNKSVGKLMETIGDEVKAGQPLSQALRKHPRYFDDLYCDLVASGEQSGALDKI  153
NTDB id 1198 PSJM300 03950 AFN76868.1        LFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLETL  149
consensus                                    ***!!**!!* *!*!**!********  ** ****** ** ****!**** **** * *!* *** !***!!**! !* *

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NTDB id 1169 A1552VC RS11075 WP 000648511.1  FERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSLWAF  231
NTDB id 1402 DSB67 RS12670 WP 010643257.1    FERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWGPFIG  230
NTDB id 1113 AAA85695.1 219..1451( )         LDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGWMVL  233
NTDB id 1112 NGFG RS09215 WP 003689811.1     LDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYGWMVL  233
NTDB id 1252 GC085 RS07730 WP 011213805.1    LDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWYIIF  230
NTDB id 1016 ACIAD RS01680 WP 004920476.1    LDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYWFILI  232
NTDB id 1059 ABD1 RS01610 WP 000279215.1     LDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWFIMI  232
NTDB id 331275 EJ103 RS14345 WP 126008287.1  FDRVALYKEKSEALKSKIKKAMFYPISVLVIAGIVTSILLIFVVPQFQDIFAGFGAQLPAFTLFVIGISEFMQEYWWVIL  233
NTDB id 1198 PSJM300 03950 AFN76868.1        LDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWWYVVL  229
consensus                                    ****!*!*!!** ** !***!* !!**!***!**** **** !*! ! **** *!!*!!**!* !* *!**** ******

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NTDB id 1169 A1552VC RS11075 WP 000648511.1  IAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNVHFETAI  311
NTDB id 1402 DSB67 RS12670 WP 010643257.1    LSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKITSKTSGNMHYQLAI  310
NTDB id 1113 AAA85695.1 219..1451( )         IALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEAT  313
NTDB id 1112 NGFG RS09215 WP 003689811.1     IALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEAT  313
NTDB id 1252 GC085 RS07730 WP 011213805.1    GALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAKAT  310
NTDB id 1016 ACIAD RS01680 WP 004920476.1    LVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQAV  312
NTDB id 1059 ABD1 RS01610 WP 000279215.1     IAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYEKAV  312
NTDB id 331275 EJ103 RS14345 WP 126008287.1  IAIVGFGYAFKEAKLRSLKLRDATDRAILKLPVIGMILNKAAVARYARTLSTTFAAGVPLVDALDSAAGASGNAVYRYAI  313
NTDB id 1198 PSJM300 03950 AFN76868.1        AGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFRSAT  309
consensus                                    **********  ** *! ***  *****!**!**!*** !* *!***!!****!*!!*!****!********!**** !*
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NTDB id 1169 A1552VC RS11075 WP 000648511.1   NEVYRDTAAGMPMYIAMRNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLGTVVGG   391
NTDB id 1402 DSB67 RS12670 WP 010643257.1     EEVYRDTAAGMPMYIAMRHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGVVVGG   390
NTDB id 1113 AAA85695.1 219..1451( )          REIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGLVIGT   393
NTDB id 1112 NGFG RS09215 WP 003689811.1      REIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGLVIGT   393
NTDB id 1252 GCO85 RS07730 WP 011213805.1     DKIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGILVGG   390
NTDB id 1016 ACIAD RS01680 WP 004920476.1     LKIREDVSTGQQLNFAMRVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGILVGG   392
NTDB id 1059 ABD1 RS01610 WP 000279215.1      MKIREDVATGQQLQFAMRISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGVLVGG   392
NTDB id 331275 EJ103 RS14345 WP 126008287.1   LDIKAEVSSGNQMNWAMRNSKIFPDMVIQMVAIGEESGSLDGMLAKVATIYEQEVDDAVDGLSSLLEPLIMAVLGVLVGG   393
NTDB id 1198 PSJM300 03950 AFN76868.1         NKIKSDVSSGMQLNFSMRTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGVLVGG   389
consensus                                      *** ** *!***  *!* * *!! ***!!**!!!!!! !**!! !*! *!! !!***!**!* **!!*!* *!!***!*
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logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1   LVVAMYLPIFNLMSVLG.   408
NTDB id 1402 DSB67 RS12670 WP 010643257.1     LVTAMYLPIFNLMSVLG.   407
NTDB id 1113 AAA85695.1 219..1451( )          LLVAMYLPLFNLGNVVA*   410
NTDB id 1112 NGFG RS09215 WP 003689811.1      LLVAMYLPLFNLGNVVA.   410
NTDB id 1252 GCO85 RS07730 WP 011213805.1     LVVAMYLPIFKLGSAV..   406
NTDB id 1016 ACIAD RS01680 WP 004920476.1     LVIAMYLPIFQMGSVV..   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1      LVIAMYLPIFQMGSVV..   408
NTDB id 331275 EJ103 RS14345 WP 126008287.1   LIVAMYLPIFQLGSVI..   409
NTDB id 1198 PSJM300 03950 AFN76868.1         LIIAMYLPIFQMGSVV..   405
consensus                                     !**!!!!!*!******
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X non conserved

X similar

X ≥ 50% conserved