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logo
NTDB id 1169 A1552VC RS11075 WP 000648511.1     .....MKATQTLPLKNYRWKGINSNGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.LTHRVKSKDITIL   73
NTDB id 1017587 ABX022 RS04410 WP 370580578.1  MNKPVAVSKTKSSGTSFSFEGKNLKTEQIVRGEVVAKDEADARAKLTRRQIRVIQITKVKK.....QRQKKISQADITVF   75
NTDB id 1112 NGFG RS09215 WP 003689811.1       MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKT.....SSKRKITQEDITVF   75
NTDB id 1113 AAA85695.1 219..1451( )           MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKT.....SSKRKITQEDITVF   75
NTDB id 1252 GC085 RS07730 WP 011213805.1      ......MDKNSPPLLTFHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.KNKKITQADITVF   72
NTDB id 1198 PSJM300 03950 AFN76868.1          ......MAQKAIKNSVFTWEGLDRQGAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKKIKPMDIALF   71
NTDB id 1016 ACIAD RS01680 WP 004920476.1      .....MAAKKTQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKVKPLDIAIF   74
NTDB id 1059 ABD1 RS01610 WP 000279215.1       .....MAVKKAQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVTTLDITIF   74
consensus                                                   * **!*   * * * !** * * * **  !*****    * * *  *      ****  !!***

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NTDB id 1169 A1552VC RS11075 WP 000648511.1     TRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNLPEVFE   153
NTDB id 1017587 ABX022 RS04410 WP 370580578.1  TRQLSTMMKSGLPMMQAFDIAAKGHSNPAMTQLLLQIRSDVEQGTSLAESFAKHPKYFDHFYCNLVHAGEAGGVLEAILD   155
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 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 1017587 ABX022 RS04410 WP 370580578.1  KLSVYKEKTQGIKKKVKSALTYPAVVVVVAIALVIVMMMFVLPSFGKVYESMGVPLPGLTQFMMNISDFFVHYGIFVIIA   235
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      KVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWYIIFGA   232
NTDB id 1198 PSJM300 03950 AFN76868.1          RVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTATLLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWWYVVLAG   231
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 1017587 ABX022 RS04410 WP 370580578.1  LIGGAIGLFKWYQNSDDLKKRFDYMLLKMPIFGQIVRKATIARWSRTTATLFAAGVPLVEVLDSVAGASGNIRYEEATQE   315
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 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 1017587 ABX022 RS04410 WP 370580578.1   IRAKVNQGISLTSAMQATELFPNMVMQMASIGEESGSLDDMLNKAAEFYEEDVDTAVAQLSSLMEPIIMVVLGGIVGIIL   395
NTDB id 1112 NGFG RS09215 WP 003689811.1        IRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGLVIGTLL   395
NTDB id 1113 AAA85695.1 219..1451( )            IRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGLVIGTLL   395
NTDB id 1252 GC085 RS07730 WP 011213805.1       IREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGILVGGLV   392
NTDB id 1198 PSJM300 03950 AFN76868.1           IKSDVSSGMQLNFSMRTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGVLVGGLI   391
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 1017587 ABX022 RS04410 WP 370580578.1   VAMYLPLFNIGNAVG.   410
NTDB id 1112 NGFG RS09215 WP 003689811.1        VAMYLPLFNLGNVVA.   410
NTDB id 1113 AAA85695.1 219..1451( )            VAMYLPLFNLGNVVA*   410
NTDB id 1252 GC085 RS07730 WP 011213805.1       VAMYLPIFKLGSAV..   406
NTDB id 1198 PSJM300 03950 AFN76868.1           IAMYLPIFQMGSVV..   405
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