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logo
NTDB id 1169 A1552VC RS11075 WP 000648511.1  .........MKATQTLPLKNYRWKGINSNG.KKVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLARL.THRVKSKD   69
NTDB id 1402 DSB67 RS12670 WP 010643257.1    .........MKTIAPQLKNYRWKGINSSG.KKTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITKI.SHRVKGKD   68
NTDB id 1113 AAA85695.1 219..1451( )         ....MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TSSKRKITQED   71
NTDB id 1112 NGFG RS09215 WP 003689811.1     ....MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TSSKRKITQED   71
NTDB id 1252 GC085 RS07730 WP 011213805.1    .........MDKNSPPLLTFHYQGINKAG.QKMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDRK.NKKITQAD   68
NTDB id 1016 ACIAD RS01680 WP 004920476.1    .........MAAKKTQVMPVFAYEGVDRKG.IKLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKVKPLD   70
NTDB id 1059 ABD1 RS01610 WP 000279215.1     .........MAVKKAQMMPTFAYEGVDRKG.VKIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVTTLD   70
NTDB id 288593 DBO93 RS16090 WP 108457250.1 MAVTSTKTKDKKSKVKSVDVYKWQGLNRKG.KKISGELNATSILELKAQLRKQGITPGKISKKAKPLFGLGGDKKILPAD   79
NTDB id 1198 PSJM300 03950 AFN76868.1        .........MAQKAIKNSVFTWEGLDRQG.AKIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFSAG..KKIKPMD   67
consensus                                                 *  *  * **!* * * *** !** * *  ***  !*****   ******  *       ***   !

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NTDB id 1169 A1552VC RS11075 WP 000648511.1  ITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNLP   149
NTDB id 1402 DSB67 RS12670 WP 010643257.1    ITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNLS   148
NTDB id 1113 AAA85695.1 219..1451( )         ITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLE   151
NTDB id 1112 NGFG RS09215 WP 003689811.1     ITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLE   151
NTDB id 1252 GC085 RS07730 WP 011213805.1    ITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSLD   148
NTDB id 1016 ACIAD RS01680 WP 004920476.1    IAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLE   150
NTDB id 1059 ABD1 RS01610 WP 000279215.1     ITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALE   150
NTDB id 288593 DBO93 RS16090 WP 108457250.1 IAVVTRQIATMLGAGVPLVQTIEMISSGHSNGNMQKLLSTIGNKLQSGIPLSECLREHPQYFDDLYCDLVNSGEQSGALE   159
NTDB id 1198 PSJM300 03950 AFN76868.1        IALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLE   147
consensus                                    !****!!**!!* *!*!**!********* ** ****** **  ***!**** ***  * *!* *** !***!!**! !*

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NTDB id 1169 A1552VC RS11075 WP 000648511.1  EVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSLW   229
NTDB id 1402 DSB67 RS12670 WP 010643257.1    QVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWGPF   228
NTDB id 1113 AAA85695.1 219..1451( )         SLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGWM   231
NTDB id 1112 NGFG RS09215 WP 003689811.1     SLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYGWM   231
NTDB id 1252 GC085 RS07730 WP 011213805.1    IMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWYI   228
NTDB id 1016 ACIAD RS01680 WP 004920476.1    IMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYWFI   230
NTDB id 1059 ABD1 RS01610 WP 000279215.1     TMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWFI   230
NTDB id 288593 DBO93 RS16090 WP 108457250.1 TIYDRVATYKEKAEALKAKIKKAMTYPISVLVIAFVVTAILLIFVVPVFQEIFANFGAELPAFTLLVIAISEFMQAYWYF   239
NTDB id 1198 PSJM300 03950 AFN76868.1        TLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWWYV   227
consensus                                    ******!*!*!!** ** !***!* !!**!***!**** **** !*! ! **** *!!*!!**!**!* *!**** ****

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NTDB id 1169 A1552VC RS11075 WP 000648511.1  AFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILLASLKTTAKTSGNVHFET   309
NTDB id 1402 DSB67 RS12670 WP 010643257.1    IGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHYQL   308
NTDB id 1113 AAA85695.1 219..1451( )         VLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEE   311
NTDB id 1112 NGFG RS09215 WP 003689811.1     VLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEE   311
NTDB id 1252 GC085 RS07730 WP 011213805.1    IFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAK   308
NTDB id 1016 ACIAD RS01680 WP 004920476.1    LILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQ   310
NTDB id 1059 ABD1 RS01610 WP 000279215.1     MIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYEK   310
NTDB id 288593 DBO93 RS16090 WP 108457250.1 GLAAIFAAGYFFKKAHLNSLSFRDSVDKKILKLPIIGDVLKKAAVARYARTLSTTFAAGVPLPDALESAAGASGNAVFRD   319
NTDB id 1198 PSJM300 03950 AFN76868.1        VLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFRS   307
consensus                                    ************  ** *! ***  *****!**!**!*** !* *!***!!****!*!!*!****!********!****
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NTDB id 1169 A1552VC RS11075 WP 000648511.1   AINEVYRDTAAGMPMYIAMRNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLGTVV   389
NTDB id 1402 DSB67 RS12670 WP 010643257.1     AIEEVYRDTAAGMPMYIAMRHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGVVV   388
NTDB id 1113 AAA85695.1 219..1451( )          ATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGLVI   391
NTDB id 1112 NGFG RS09215 WP 003689811.1      ATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGLVI   391
NTDB id 1252 GCO85 RS07730 WP 011213805.1     ATDKIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGILV   388
NTDB id 1016 ACIAD RS01680 WP 004920476.1     AVLKIREDVSTGQQLNFAMRVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGILV   390
NTDB id 1059 ABD1 RS01610 WP 000279215.1      AVMKIREDVATGQQLQFAMRISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGVLV   390
NTDB id 288593 DBO93 RS16090 WP 108457250.1   AILEIRAEVTSGMQMNLAMRNCAIFPDMVIQMVAIGEESGAVDDMLAKVATVYEQEVDNAVDNLTTLLEPMIMAVLGVVI   399
NTDB id 1198 PSJM300 03950 AFN76868.1         ATNKIKSDVSSGMQLNFSMRTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGVLV   387
consensus                                     !* *** ** *!***  *!* * *!! ***!!**!!!!!!****!! !*! *!! !!***!* !* **!!*!* *!!***
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NTDB id 1169 A1552VC RS11075 WP 000648511.1   GGLVVAMYLPIFNLMSVLG.   408
NTDB id 1402 DSB67 RS12670 WP 010643257.1     GGLVTAMYLPIFNLMSVLG.   407
NTDB id 1113 AAA85695.1 219..1451( )          GTLLVAMYLPLFNLGNVVA*   410
NTDB id 1112 NGFG RS09215 WP 003689811.1      GTLLVAMYLPLFNLGNVVA.   410
NTDB id 1252 GCO85 RS07730 WP 011213805.1     GGLVVAMYLPIFKLGSAV..   406
NTDB id 1016 ACIAD RS01680 WP 004920476.1     GGLVIAMYLPIFQMGSVV..   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1      GGLVIAMYLPIFQMGSVV..   408
NTDB id 288593 DBO93 RS16090 WP 108457250.1   GGLIIAMYLPIFQIGMVV..   417
NTDB id 1198 PSJM300 03950 AFN76868.1         GGLIIAMYLPIFQMGSVV..   405
consensus                                     !*!**!!!!!*!******
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X non conserved
X similar
X $\geq$ 50% conserved