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logo
NTDB id 1402 DSB67 RS12670 WP 010643257.1     ....MKT......IAPQLKNYRWKGINSS.GKKTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.ISHRVKGKD   68
NTDB id 1169 A1552VC RS11075 WP 000648511.1   ...MKAT......QTLPLKNYRWKGINSN.GKKVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.LTHRVKSKD   69
NTDB id 1112 NGFG RS09215 WP 003689811.1      ....MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKTS.....SKRKITQED   71
NTDB id 1113 AAA85695.1 219..1451( )          ....MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKTS.....SKRKITQED   71
NTDB id 238490 CFN79 RS00725 WP 021479152.1  MATTAAKK......ANPGYIWEWEGKDKS.GKMIRGELRAESETVAKTQLRRQGINVAKIRRRRSG.....FGKRITEKD   68
NTDB id 1252 GC085 RS07730 WP 011213805.1    ....MDKN......SPPLLTFHYQGINKA.GQKMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.KNKKITQAD   68
NTDB id 1198 PSJM300 03950 AFN76868.1        ....MAQK......AIKNSVFTWEGLDRQ.GAKIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKKIKPMD   67
NTDB id 1016 ACIAD RS01680 WP 004920476.1    ...MAAKK......TQVMPVFAYEGVDRK.GIKLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKVKPLD   70
NTDB id 1059 ABD1 RS01610 WP 000279215.1     ...MAVKK......AQMMPTFAYEGVDRK.GVKIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVTTLD   70
consensus                                        ***       *  *  * **!* *  **** !** * ** ***  !***** * ****** **      ****  !

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NTDB id 1402 DSB67 RS12670 WP 010643257.1     ITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLLATGEQSGNLS   148
NTDB id 1169 A1552VC RS11075 WP 000648511.1   ITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNLP   149
NTDB id 1112 NGFG RS09215 WP 003689811.1      ITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLE   151
NTDB id 1113 AAA85695.1 219..1451( )          ITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLE   151
NTDB id 238490 CFN79 RS00725 WP 021479152.1  ITLFTRQLSTMMRAGVPLLQAFDIAAKGHSNPAVTRMLLEVRADVETGLSLAESFRKRPLYFDKLFCNIIAAGEAGGVLD   148
NTDB id 1252 GC085 RS07730 WP 011213805.1    ITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSLD   148
NTDB id 1198 PSJM300 03950 AFN76868.1        IALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLE   147
NTDB id 1016 ACIAD RS01680 WP 004920476.1    IAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLE   150
NTDB id 1059 ABD1 RS01610 WP 000279215.1     ITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALE   150
consensus                                    !****!!**!!***!*!**!********* ** ****** ** ****!**** **** * *!* ********!! *! !*

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NTDB id 1402 DSB67 RS12670 WP 010643257.1     QVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWGPF   228
NTDB id 1169 A1552VC RS11075 WP 000648511.1   EVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSLW   229
NTDB id 1112 NGFG RS09215 WP 003689811.1      SLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYGWM   231
NTDB id 1113 AAA85695.1 219..1451( )          SLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGWM   231
NTDB id 238490 CFN79 RS00725 WP 021479152.1  TLLDKLATYKEKVMAIKSKIKSAMIYPSAIVGTAFIITAVIMIYVIPAFKDLFSSFGANLPAPTLFVIWLSDQFVHFWWL   228
NTDB id 1252 GC085 RS07730 WP 011213805.1    IMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWYI   228
NTDB id 1198 PSJM300 03950 AFN76868.1        TLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWWYV   227
NTDB id 1016 ACIAD RS01680 WP 004920476.1    IMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYWFI   230
NTDB id 1059 ABD1 RS01610 WP 000279215.1     TMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWFI   230
consensus                                    ******!*!*!!** ** !***!* !!  ****!**** **** !*! ! ***  *!!*!!**!* !* *!**** ****

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NTDB id 1402 DSB67 RS12670 WP 010643257.1     IGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHYQL   308
NTDB id 1169 A1552VC RS11075 WP 000648511.1   AFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNVHFET   309
NTDB id 1112 NGFG RS09215 WP 003689811.1      VLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEE   311
NTDB id 1113 AAA85695.1 219..1451( )          VLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEE   311
NTDB id 238490 CFN79 RS00725 WP 021479152.1  IFGTLFGAVFAFFYAFKRTPKMQEQMDRILLRLPVIGDIIRKATIARWARTLSTLFSAGVPLVEALDSVGGAAGNQVYAE   308
NTDB id 1252 GC085 RS07730 WP 011213805.1    IFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAK   308
NTDB id 1198 PSJM300 03950 AFN76868.1        VLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFRS   307
NTDB id 1016 ACIAD RS01680 WP 004920476.1    LILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQ   310
NTDB id 1059 ABD1 RS01610 WP 000279215.1     MIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYEK   310
consensus                                    ************  ** ** ***  *****!**!**!*** !***!***!!*****!*!!*!****!********!****
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NTDB id 1402 DSB67 RS12670 WP 010643257.1     AIEEVYRDTAAGMPMYIAMRHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGVVV   388
NTDB id 1169 A1552VC RS11075 WP 000648511.1   AINEVYRDTAAGMPMYIAMRNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLGTVV   389
NTDB id 1112 NGFG RS09215 WP 003689811.1      ATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGLVI   391
NTDB id 1113 AAA85695.1 219..1451( )          ATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGLVI   391
NTDB id 238490 CFN79 RS00725 WP 021479152.1  ATRRIQSDVSTGSSLSYSMQRTDLFPNMVLQMTSIGEESGSLDQMLDKVADFYEEEVDNAVAALSSLLEPAIMVILGILI   388
NTDB id 1252 GC085 RS07730 WP 011213805.1    ATDKIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGILV   388
NTDB id 1198 PSJM300 03950 AFN76868.1         ATNKIKSDVSSGMQLNFSMRTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGVLV   387
NTDB id 1016 ACIAD RS01680 WP 004920476.1    AVLKIREDVSTGQQLNFAMRVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGILV   390
NTDB id 1059 ABD1 RS01610 WP 000279215.1      AVMKIREDVATGQQLQFAMRISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGVLV   390
consensus                                     !* *** ** *!* *  *!* * *!! ***!!* !!!!!! !**!! !*! *!!*!!***!**!* **!!*!***!!***
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logo

NTDB id 1402 DSB67 RS12670 WP 010643257.1     GGLVTAMYLPIFNLMSVLG.   407
NTDB id 1169 A1552VC RS11075 WP 000648511.1   GGLVVAMYLPIFNLMSVLG.   408
NTDB id 1112 NGFG RS09215 WP 003689811.1      GTLLVAMYLPLFNLGNVVA.   410
NTDB id 1113 AAA85695.1 219..1451( )          GTLLVAMYLPLFNLGNVVA*   410
NTDB id 238490 CFN79 RS00725 WP 021479152.1  GGLVIAMYMPIFKMGQVVG.   407
NTDB id 1252 GC085 RS07730 WP 011213805.1    GGLVVAMYLPIFKLGSAV..   406
NTDB id 1198 PSJM300 03950 AFN76868.1         GGLIIAMYLPIFQMGSVV..   405
NTDB id 1016 ACIAD RS01680 WP 004920476.1    GGLVIAMYLPIFQMGSVV..   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1      GGLVIAMYLPIFQMGSVV..   408
consensus                                     !*!**!!!*!*!******
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X non conserved
X similar
X ≥ 50% conserved