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logo
NTDB id 1402 DSB67 RS12670 WP 010643257.1   ............MKTIAPQLKNYRWKGINSSG.KKTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.ISHRVKG   66
NTDB id 1169 A1552VC RS11075 WP 000648511.1 ............MKATQTLPLKNYRWKGINSNG.KKVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.LTHRVKS   67
NTDB id 1112 NGFG RS09215 WP 003689811.1    MAKNG......GFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TSSKRKITQ   69
NTDB id 1113 AAA85695.1 219..1451( )        MAKNG......GFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TSSKRKITQ   69
NTDB id 1198 PSJM300 03950 AFN76868.1       ............MAQKAIKNSVFTWEGLDRQG.AKIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKKIKP   65
NTDB id 1016 ACIAD RS01680 WP 004920476.1  ............MAAKKTQVMPVFAYEGVDRKG.IKLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKVKP   68
NTDB id 1059 ABD1 RS01610 WP 000279215.1   ............MAVKKAQMMPTFAYEGVDRKG.VKIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVTT   68
NTDB id 43132 DSUI RS06420 WP 014236420.1  MATAGKNTQNTKRADPSIKEFVFVWEGKDKTG.KIIRGELRATSETVVQATLRRQGVLVTKVSKQRF....K.SGGKITD   74
NTDB id 1252 GC085 RS07730 WP 011213805.1  ............MDKNSPPLLTFHYQGINKAG.QKMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.KNKKITQ   66
consensus                                                 *  *  * **!* * * *** !** * ** ***  !***** * **** *  *      ****

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NTDB id 1402 DSB67 RS12670 WP 010643257.1   KDITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGN   146
NTDB id 1169 A1552VC RS11075 WP 000648511.1 KDITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGN   147
NTDB id 1112 NGFG RS09215 WP 003689811.1    EDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGV   149
NTDB id 1113 AAA85695.1 219..1451( )        EDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGV   149
NTDB id 1198 PSJM300 03950 AFN76868.1       MDIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGS   145
NTDB id 1016 ACIAD RS01680 WP 004920476.1  LDIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGS   148
NTDB id 1059 ABD1 RS01610 WP 000279215.1   LDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGA   148
NTDB id 43132 DSUI RS06420 WP 014236420.1  KDITLFTRQLATMMKSGVPLLQAFDIVGKGHSNPAVGKLLLDIKADVETGSALNQAFRKYPLYFDSLFCNLIGAGEQAGI   154
NTDB id 1252 GC085 RS07730 WP 011213805.1  ADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGS   146
consensus                                   !!****!!**!!***!*!**!********** ** ****** ** ****!***  **** * *!* ****!***!!**!

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NTDB id 1402 DSB67 RS12670 WP 010643257.1   LSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWG   226
NTDB id 1169 A1552VC RS11075 WP 000648511.1 LPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYS   227
NTDB id 1112 NGFG RS09215 WP 003689811.1    LESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYG   229
NTDB id 1113 AAA85695.1 219..1451( )        LESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYG   229
NTDB id 1198 PSJM300 03950 AFN76868.1       LETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWW   225
NTDB id 1016 ACIAD RS01680 WP 004920476.1  LEIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYW   228
NTDB id 1059 ABD1 RS01610 WP 000279215.1   LETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYW   228
NTDB id 43132 DSUI RS06420 WP 014236420.1  LDTLLDRLAIYKEKILAVKSKIKSALFYPIAVIVVAFCITAVIMIFVIPAFKEVFKSFGADLPAPTLVVIAISDFFVAYW   234
NTDB id 1252 GC085 RS07730 WP 011213805.1  LDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYW   226
consensus                                  !*******!*!*!!** ** !***!* !!* !**!!* ** **** !*! ! ***  *!!*!!**!**!* *!**** **

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NTDB id 1402 DSB67 RS12670 WP 010643257.1   PFIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHY   306
NTDB id 1169 A1552VC RS11075 WP 000648511.1 LWAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNVHF   307
NTDB id 1112 NGFG RS09215 WP 003689811.1    WMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIY   309
NTDB id 1113 AAA85695.1 219..1451( )        WMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIY   309
NTDB id 1198 PSJM300 03950 AFN76868.1       YVVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVF   305
NTDB id 1016 ACIAD RS01680 WP 004920476.1  FILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVY   308
NTDB id 1059 ABD1 RS01610 WP 000279215.1   FIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIY   308
NTDB id 43132 DSUI RS06420 WP 014236420.1  YLIFGILGGGIYSFLESWKRSEAVQIAMDKALLRMPIFGPLIRKSVIARWTRTLATMFAAGVPLVEALDSVGGASGNHVY   314
NTDB id 1252 GC085 RS07730 WP 011213805.1  YIIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNLIY   306
consensus                                  ***************  * *! ***  *****!**!**!*** !* *!***!!****!*!!*!****!********!***
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NTDB id 1402 DSB67 RS12670 WP 010643257.1     QLAIEEVYRDTAAGMPMYIAMRHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGV   386
NTDB id 1169 A1552VC RS11075 WP 000648511.1   ETAINEVYRDTAAGMPMYIAMRNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLGT   387
NTDB id 1112 NGFG RS09215 WP 003689811.1      EEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGL   389
NTDB id 1113 AAA85695.1 219..1451( )          EEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGL   389
NTDB id 1198 PSJM300 03950 AFN76868.1         RSATNKIKSDVSSGMQLNFSMRTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGV   385
NTDB id 1016 ACIAD RS01680 WP 004920476.1     EQAVLKIREDVSTGQQLNFAMRVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGI   388
NTDB id 1059 ABD1 RS01610 WP 000279215.1      EKAVMKIREDVATGQQLQFAMRISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGV   388
NTDB id 43132 DSUI RS06420 WP 014236420.1     KMATRQIQSEVSTGTSLTNSMQNVNLFPNMVIQMVAIGEESGALDSMLSKVADFFEAEVDDSVAALSSLMEPIIMVILGV   394
NTDB id 1252 GCO85 RS07730 WP 011213805.1     AKATDKIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGI   386
consensus                                     * !*  ** ** *!* *  *!* * *!! ***!!**!!!!!!*!**!! !*! **! !!***!**!* **!!*!***!!*

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NTDB id 1402 DSB67 RS12670 WP 010643257.1     VVGGLVTAMYLPIFNLMSVLG.   407
NTDB id 1169 A1552VC RS11075 WP 000648511.1   VVGGLVVAMYLPIFNLMSVLG.   408
NTDB id 1112 NGFG RS09215 WP 003689811.1      VIGTLLVAMYLPLFNLGNVVA.   410
NTDB id 1113 AAA85695.1 219..1451( )          VIGTLLVAMYLPLFNLGNVVA*   410
NTDB id 1198 PSJM300 03950 AFN76868.1         LVGGLIIAMYLPIFQMGSVV..   405
NTDB id 1016 ACIAD RS01680 WP 004920476.1     LVGGLVIAMYLPIFQMGSVV..   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1      LVGGLVIAMYLPIFQMGSVV..   408
NTDB id 43132 DSUI RS06420 WP 014236420.1     LIGGMVVAMYLPIFKMGSVV..   414
NTDB id 1252 GCO85 RS07730 WP 011213805.1     LVGGLVVAMYLPIFKLGSAV..   406
consensus                                     **!****!!!!!*!******
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X non conserved

X similar

X ≥ 50% conserved