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logo
NTDB id 1029 TT RS02230 WP 011228203.1      .............MPVYQYKARDRQGR.LVEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIPALERGPGLKD   66
NTDB id 1402 DSB67 RS12670 WP 010643257.1   ......MKTIAPQLKNYRWKGINSSGK.KTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.....ISHRVKGKD   68
NTDB id 1169 A1552VC RS11075 WP 000648511.1 .....MKATQTLPLKNYRWKGINSNGK.KVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.....LTHRVKSKD   69
NTDB id 1113 AAA85695.1 219..1451( )        MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKT.........SSKRKITQED   71
NTDB id 1112 NGFG RS09215 WP 003689811.1    MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKT.........SSKRKITQED   71
NTDB id 1252 GCO85 RS07730 WP 011213805.1   ......MDKNSPPLLTFHYQGINKAGQ.KMEGDIQARSLATAKADLRKQGIVTNKVVKKRKPLFDR.....KNKKITQAD   68
NTDB id 55319 TVNIR RS12230 WP 015259341.1  .........MAETETIYIWEGLNKKGT.RVKGETPADSEMLARAELRRNGINVLKIRKKPKSLFS......TKKRIKPVD   64
NTDB id 1198 PSJM300 03950 AFN76868.1       ......MAQKAIKNSVFTWEGLDRQGA.KIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS......AGKKIKPMD   67
NTDB id 1016 ACIAD RS01680 WP 004920476.1   .....MAAKKTQVMPVFAYEGVDRKGI.KLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEG....LLKKKVKPLD   70
NTDB id 1059 ABD1 RS01610 WP 000279215.1    .....MAVKKAQMMPTFAYEGVDRKGV.KIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG....LFKKKVTTLD   70
consensus                                             *  *  * **** * *  ** *** * ** ***  !***** * ******* *         *****  !
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logo
NTDB id 1029 TT RS02230 WP 011228203.1      LAIFSRQLATMLGAGLTLLQALAILERQTENRKFREILKQVRTDVEGGMAFSEALSKHK.IFSRLYVNLVRAGETSGGLD  145
NTDB id 1402 DSB67 RS12670 WP 010643257.1   ITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNLS  148
NTDB id 1169 A1552VC RS11075 WP 000648511.1 ITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNLP  149
NTDB id 1113 AAA85695.1 219..1451( )        ITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLE  151
NTDB id 1112 NGFG RS09215 WP 003689811.1    ITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLE  151
NTDB id 1252 GCO85 RS07730 WP 011213805.1   ITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSLD  148
NTDB id 55319 TVNIR RS12230 WP 015259341.1  IAYFLRQMTTMLSSGVPLVQAFDIVGRGHENPTMATLIMDLKSSVEGGETFAAALAKHPRHFDDLVINLVEAGEQSGTLE  144
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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logo
NTDB id 1029 TT RS02230 WP 011228203.1      LILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTLDLGSELPLLTRFLIAVSDLLRAATLP  225
NTDB id 1402 DSB67 RS12670 WP 010643257.1   QVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWGPF  228
NTDB id 1169 A1552VC RS11075 WP 000648511.1 EVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGADLPWFTQQVLKLSHWVQAYSLW  229
NTDB id 1113 AAA85695.1 219..1451( )        SLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGWM  231
NTDB id 1112 NGFG RS09215 WP 003689811.1    SLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYGWM  231
NTDB id 1252 GCO85 RS07730 WP 011213805.1   IMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWYI  228
NTDB id 55319 TVNIR RS12230 WP 015259341.1  TLLDKVATYKEKTESLKAKIKKAMFYPAAVIVVAIVVTAILLIFVVPQFEALFVGFGADLPAFTRMVVNLSELVQAWWWA  224
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 1029 TT RS02230 WP 011228203.1      LLLLAVALFFAYRW.YYGTPQGRRVIDRLKLRLPVFGNLNRKTAVARFSRTLALLLSSGVNIVEALDITKGTAGNSVVEE  304
NTDB id 1402 DSB67 RS12670 WP 010643257.1   IGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHYQL  308
NTDB id 1169 A1552VC RS11075 WP 000648511.1 AFTAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNVHFET  309
NTDB id 1113 AAA85695.1 219..1451( )        VLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEE  311
NTDB id 1112 NGFG RS09215 WP 003689811.1    VLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEE  311
NTDB id 1252 GCO85 RS07730 WP 011213805.1   IFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAK  308
NTDB id 55319 TVNIR RS12230 WP 015259341.1  ILAAMIALGLVFIQLRRRSPRFSRFVDLAVLRIPAIGPILRKAAVARFARTLSTMFAAGVPLVEALRSVAGATGNALYAE  304
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 1029 TT RS02230 WP 011228203.1      IVEAAKLKIQQGDPLNLTLAQHPFVFPPMVSSMVAIGEETGALDTMLSKVADFYEREVDEAVASLTAAIEPLMIIFLGVI  384
NTDB id 1402 DSB67 RS12670 WP 010643257.1   AIEEVYRDTAAGMPMYIAMR.HCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGVV  387
NTDB id 1169 A1552VC RS11075 WP 000648511.1 AINEVYRDTAAGMPMYIAMR.NTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLGTV  388
NTDB id 1113 AAA85695.1 219..1451( )        ATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGLV  390
NTDB id 1112 NGFG RS09215 WP 003689811.1    ATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGLV  390
NTDB id 1252 GCO85 RS07730 WP 011213805.1   ATDKIREEVATGQQMFIAME.NTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGIL  387
NTDB id 55319 TVNIR RS12230 WP 015259341.1  ATERMREETAAGAQLQWSMR.NTNVFPNMVVQMVAIGEESGSLDSMLAKVADFYEEEVDNAVDSLSSLLEPLIMVVLGVL  383
NTDB id 1198 PSJM300 03950 AFN76868.1       ATNKIKSDVSSGMQLNFSMR.TTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGVL  386
NTDB id 1016 ACIAD RS01680 WP 004920476.1   AVLKIREDVSTGQQLNFAMR.VSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGIL  389
NTDB id 1059 ABD1 RS01610 WP 000279215.1    AVMKIREDVATGQQLQFAMR.ISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGVL  389
consensus                                   ** *** *** !**** ***  * *!! ****!**!!!!*!*!**!! !*!**!!*!!***!* !* **!!*****!!**
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NTDB id 1029 TT RS02230 WP 011228203.1      VGMIVAGMFLPLFKIIGTLSVQ   406
NTDB id 1402 DSB67 RS12670 WP 010643257.1   VGGLVTAMYLPIFNLMSVLG..   407
NTDB id 1169 A1552VC RS11075 WP 000648511.1 VGGLVVAMYLPIFNLMSVLG..   408
NTDB id 1113 AAA85695.1 219..1451( )        IGTLLVAMYLPLFNLGNVVA*.   410
NTDB id 1112 NGFG RS09215 WP 003689811.1    IGTLLVAMYLPLFNLGNVVA..   410
NTDB id 1252 GCO85 RS07730 WP 011213805.1   VGGLVVAMYLPIFKLGSAV...   406
NTDB id 55319 TVNIR RS12230 WP 015259341.1  IGGLVIAMYLPIFMLGQVI...   402
NTDB id 1198 PSJM300 03950 AFN76868.1       VGGLIIAMYLPIFQMGSVV...   405
NTDB id 1016 ACIAD RS01680 WP 004920476.1   VGGLVIAMYLPIFQMGSVV...   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1    VGGLVIAMYLPIFQMGSVV...   408
consensus                                   *!******!*!!*!******
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X non conserved
X similar
X ≥ 50% conserved