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logo
NTDB id 1029 TT RS02230 WP 011228203.1          ...............MPVYQYKARDRQGR.LVEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIPALERGPGL   64
NTDB id 1402 DSB67 RS12670 WP 010643257.1       ..MKT......IAPQLKNYRWKGINSSGK.KTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.....ISHRVKG   66
NTDB id 1169 A1552VC RS11075 WP 000648511.1     .MKAT......QTLPLKNYRWKGINSNGK.KVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.....LTHRVKS   67
NTDB id 1113 AAA85695.1 219..1451( )            ..MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KT....SSKRKITQ   69
NTDB id 1112 NGFG RS09215 WP 003689811.1        ..MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KT....SSKRKITQ   69
NTDB id 1122387 EL239 RS02955 WP 126338045.1    MDKSKN......ANAIISYQWEGVNKTGE.KVNGIIDARSLALAKADLRKQGIITKKVIKKRKPLFDK.....KNRKITQ   68
NTDB id 1252 GC085 RS07730 WP 011213805.1       ..MDKN......SPPLLTFHYQGINKAGQ.KMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.....KNKKITQ   66
NTDB id 1198 PSJM300 03950 AFN76868.1           ..MAQK......AIKNSVFTWEGLDRQGA.KIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS......AGKKIKP   65
NTDB id 1016 ACIAD RS01680 WP 004920476.1       .MAAKK......TQVMPVFAYEGVDRKGI.KLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEG....LLKKKVKP   68
NTDB id 1059 ABD1 RS01610 WP 000279215.1        .MAVKK......AQMMPTFAYEGVDRKGV.KIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG....LFKKKVTT   68
consensus                                         ***       *  *  * **** * *  ** *** * ******  !***** ******* * *          ****

logo
NTDB id 1029 TT RS02230 WP 011228203.1          KDLAIFSRQLATMLGAGLTLLQALAILERQTENRKFREILKQVRTDVEGGMAFSEALSKHK.IFSRLYVNLVRAGETSGG   143
NTDB id 1402 DSB67 RS12670 WP 010643257.1       KDITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGN   146
NTDB id 1169 A1552VC RS11075 WP 000648511.1     KDITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGN   147
NTDB id 1113 AAA85695.1 219..1451( )            EDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGV   149
NTDB id 1112 NGFG RS09215 WP 003689811.1        EDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGV   149
NTDB id 1122387 EL239 RS02955 WP 126338045.1    GDITVFSRQMATMIEAGIPLVQSFDIVSKGQSNNRMRDLIEGVKKDVETGLTLAEALQKHPEYFNDLFCNLVDAGEKSGS   148
NTDB id 1252 GC085 RS07730 WP 011213805.1       ADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGS   146
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
consensus                                        !*****!!**!!* *!****!****** *   ** ****** ** ****!***   ****** *!* ****!***!!  *!

logo
NTDB id 1029 TT RS02230 WP 011228203.1          LDLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAAT   223
NTDB id 1402 DSB67 RS12670 WP 010643257.1       LSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWG   226
NTDB id 1169 A1552VC RS11075 WP 000648511.1     LPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYS   227
NTDB id 1113 AAA85695.1 219..1451( )            LESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYG   229
NTDB id 1112 NGFG RS09215 WP 003689811.1        LESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYG   229
NTDB id 1122387 EL239 RS02955 WP 126338045.1    LEIMLDKVATYKEKIETIKKKIKKALTYPMAVLVVAFIVTAALLIFVVPQFQSLFEGFGADLPAMTKAVVELSHFFQAYW   228
NTDB id 1252 GC085 RS07730 WP 011213805.1       LDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYW   226
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
consensus                                       !* *****!***!!** ** !***!**!!* !***!********* **! ! ***  *!**!!**!* ** *!*******
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logo
NTDB id 1029 TT RS02230 WP 011228203.1          LPLLLLAVALFFAYRW.YYGTPQGRRVIDRLKLRLPVFGNLNRKTAVARFSRTLALLLSSGVNIVEALDITKGTAGNSVV   302
NTDB id 1402 DSB67 RS12670 WP 010643257.1       PFIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHY   306
NTDB id 1169 A1552VC RS11075 WP 000648511.1     LWAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNVHF   307
NTDB id 1113 AAA85695.1 219..1451( )            WMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIY   309
NTDB id 1112 NGFG RS09215 WP 003689811.1        WMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIY   309
NTDB id 1122387 EL239 RS02955 WP 126338045.1    YLIFGVLGGLIYSFVYAKNHSPNFAQTIDRSMLKFPVIGPILEKAAIARFSRTLSITFAAGLPLVDALKSVSGATGNILY   308
NTDB id 1252 GC085 RS07730 WP 011213805.1       YIIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIY   306
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
consensus                                       ***************  **  **  ***   *****!**!**!***  !*  *!***!!*******!******!********!***
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logo
NTDB id 1029 TT RS02230 WP 011228203.1          EEIVEAAKLKIQQGDPLNLTLAQHPFVFPPMVSSMVAIGEETGALDTMLSKVADFYEREVDEAVASLTAAIEPLMIIFLG   382
NTDB id 1402 DSB67 RS12670 WP 010643257.1       QLAIEEVYRDTAAGMPMYIAMR.HCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLG   385
NTDB id 1169 A1552VC RS11075 WP 000648511.1     ETAINEVYRDTAAGMPMYIAMR.NTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLG   386
NTDB id 1113 AAA85695.1 219..1451( )            EEATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILG   388
NTDB id 1112 NGFG RS09215 WP 003689811.1        EEATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILG   388
NTDB id 1122387 EL239 RS02955 WP 126338045.1    AKATDKIREDVSTGQQMQVAMD.NTHLFPNMVIQMVAIGEESGALEQMLGKVADFYEEEVDNAVDSLSSLLEPIIMSILG   387
NTDB id 1252 GC085 RS07730 WP 011213805.1       AKATDKIREEVATGQQMFIAME.NTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILG   385
NTDB id 1198 PSJM300 03950 AFN76868.1           RSATNKIKSDVSSGMQLNFSMR.TTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLG   384
NTDB id 1016 ACIAD RS01680 WP 004920476.1       EQAVLKIREDVSTGQQLNFAMR.VSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILG   387
NTDB id 1059 ABD1 RS01610 WP 000279215.1        EKAVMKIREDVATGQQLQFAMR.ISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILG   387
consensus                                       *  **  ***  **  *!********   *  *!!  ****!**!!!!*!*!**!!  !*!**!!*!!***!*  !*  **!!*****!!
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logo
NTDB id 1029 TT RS02230 WP 011228203.1          VIVGMIVAGMFLPLFKIIGTLSVQ   406
NTDB id 1402 DSB67 RS12670 WP 010643257.1       VVVGGLVTAMYLPIFNLMSVLG..   407
NTDB id 1169 A1552VC RS11075 WP 000648511.1     TVVGGLVVAMYLPIFNLMSVLG..   408
NTDB id 1113 AAA85695.1 219..1451( )            LVIGTLLVAMYLPLFNLGNVVA*.   410
NTDB id 1112 NGFG RS09215 WP 003689811.1        LVIGTLLVAMYLPLFNLGNVVA..   410
NTDB id 1122387 EL239 RS02955 WP 126338045.1    ILVGGLVVAMYLPIFKLGSAV...   408
NTDB id 1252 GC085 RS07730 WP 011213805.1       ILVGGLVVAMYLPIFKLGSAV...   406
NTDB id 1198 PSJM300 03950 AFN76868.1           VLVGGLIIAMYLPIFQMGSVV...   405
NTDB id 1016 ACIAD RS01680 WP 004920476.1       ILVGGLVIAMYLPIFQMGSVV...   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1        VLVGGLVIAMYLPIFQMGSVV...   408
consensus                                       ***!*****!*!!*!******
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X non conserved

X similar

X ≥ 50% conserved