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logo
NTDB id 1029 TT RS02230 WP 011228203.1        ........................MPVYQYKARDRQGR.LVEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIP    56
NTDB id 1402 DSB67 RS12670 WP 010643257.1     ..........MKT......IAPQLKNYRWKGINSSGK.KTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFIT.....    58
NTDB id 1169 A1552VC RS11075 WP 000648511.1   .........MKAT......QTLPLKNYRWKGINSNGK.KVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLA.....    59
NTDB id 1112 NGFG RS09215 WP 003689811.1      ..........MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITR.....VKT....    61
NTDB id 1113 AAA85695.1 219..1451( )          ..........MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITR.....VKT....    61
NTDB id 1252 GC085 RS07730 WP 011213805.1     ..........MDKNS......PPLLTFHYQGINKAGQ.KMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFD.....    58
NTDB id 306557 DWG18 RS00850 WP 115644634.1  MSASRSTAKTTARAG......DGMQTFTWVGKDKRGV.VMKGETPAKNINLVKAELRRQGITPQTVKPKGKPLFG.....    68
NTDB id 1198 PSJM300 03950 AFN76868.1         ..........MAQKA......IKNSVFTWEGLDRQGA.KIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS.....    58
NTDB id 1016 ACIAD RS01680 WP 004920476.1     .........MAAKKT......QVMPVFAYEGVDRKGI.KLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEG....    60
NTDB id 1059 ABD1 RS01610 WP 000279215.1      .........MAVKKA......QMMPTFAYEGVDRKGV.KIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG....    60
consensus                                               *** *         *  * ******* *   ** *** * ** ***  !***** *  **** * **
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logo
NTDB id 1029 TT RS02230 WP 011228203.1        ALERGPGLKDLAIFSRQLATMLGAGLTLLQALAILERQTENRKFREILKQVRTDVEGGMAFSEALSKHK.IFSRLYVNLV   135
NTDB id 1402 DSB67 RS12670 WP 010643257.1     KISHRVKGKDITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLI   138
NTDB id 1169 A1552VC RS11075 WP 000648511.1   RLTHRVKSKDITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLV   139
NTDB id 1112 NGFG RS09215 WP 003689811.1      SSKRKITQEDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLV   141
NTDB id 1113 AAA85695.1 219..1451( )          SSKRKITQEDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLV   141
NTDB id 1252 GC085 RS07730 WP 011213805.1     RKNKKITQADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLV   138
NTDB id 306557 DWG18 RS00850 WP 115644634.1  AAGSAIKARDIAIFSRQIATMMKSGVPIVGALEIIANGNKNPRIQKLVNTIRADIQGGQSFSEALGKHPVYFDELYQNLV   148
NTDB id 1198 PSJM300 03950 AFN76868.1         .AGKKIKPMDIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLV   137
NTDB id 1016 ACIAD RS01680 WP 004920476.1     LLKKKVKPLDIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLI   140
NTDB id 1059 ABD1 RS01610 WP 000279215.1      LFKKKVTTLDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLV   140
consensus                                        ****  !*****!!**!!***!*************  ** ****** ** ****!**** ****** *!* ****!*
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logo
NTDB id 1029 TT RS02230 WP 011228203.1        RAGETSGGLDLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAV   215
NTDB id 1402 DSB67 RS12670 WP 010643257.1     ATGEQSGNLSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNL   218
NTDB id 1169 A1552VC RS11075 WP 000648511.1   ETGEMSGNLPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKL   219
NTDB id 1112 NGFG RS09215 WP 003689811.1      AAGETGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDM   221
NTDB id 1113 AAA85695.1 219..1451( )          AAGETGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDM   221
NTDB id 1252 GC085 RS07730 WP 011213805.1     DAGEKSGSLDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITM   218
NTDB id 306557 DWG18 RS00850 WP 115644634.1  RAGESAGVLETVLDTVATYKENLEALKSKIKKAMFYPIMVVAVALLVSAILLVFVVPQFEDVFKSFGADLPAFTQMVVNL   228
NTDB id 1198 PSJM300 03950 AFN76868.1         DSGEQSGSLETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGL   217
NTDB id 1016 ACIAD RS01680 WP 004920476.1     ESGEQSGSLEIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNM   220
NTDB id 1059 ABD1 RS01610 WP 000279215.1      ESGEQSGALETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNM   220
consensus                                     **!! *! !*******!***!*** ** !***!* !!* !***!********* **! ! ***  *!**!!**!**** *
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logo

NTDB id 1029 TT RS02230 WP 011228203.1        SDLLRAATLPLLLLAVALFFAYRWY.YGTPQGRRVIDRLKLRLPVFGNLNRKTAVARFSRTLALLLSSGVNIVEALDITK   294
NTDB id 1402 DSB67 RS12670 WP 010643257.1     SAWTQNWGPFIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTS   298
NTDB id 1169 A1552VC RS11075 WP 000648511.1   SHWVQAYSLWAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTA   299
NTDB id 1112 NGFG RS09215 WP 003689811.1      SDFFVSYGWMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTA   301
NTDB id 1113 AAA85695.1 219..1451( )          SDFFVSYGWMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTA   301
NTDB id 1252 GC085 RS07730 WP 011213805.1     SEFMQAYWYIIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVA   298
NTDB id 306557 DWG18 RS00850 WP 115644634.1  SRFMVAWWWLMLVGAIGAVVAFIAAKKRSVAFQHFLDRLILKVPVIGQIMHNSAIARFSRTLGVTFRAGVPLVEAMDTVA   308
NTDB id 1198 PSJM300 03950 AFN76868.1         SEALQAWWYVVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVA   297
NTDB id 1016 ACIAD RS01680 WP 004920476.1    SNWMQDYWFILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTA   300
NTDB id 1059 ABD1 RS01610 WP 000279215.1      SKWMQEYWFIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTA   300
consensus                                     !*********************  **  **  ***   *****!**!**!***  **  *!***!!*******!***********

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NTDB id 1029 TT RS02230 WP 011228203.1        GTAGNSVVEEIVEAAKLKIQQGDPLNLTLAQHPFVFPPMVSSMVAIGEETGALDTMLSKVADFYERREVDEAVASLTAAIE   374
NTDB id 1402 DSB67 RS12670 WP 010643257.1     KTSGNMHYQLAIEEVYRDTAAGMPMYIAMR.HCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILE   377
NTDB id 1169 A1552VC RS11075 WP 000648511.1   KTSGNVHFETAINEVYRDTAAGMPMYIAMR.NTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILE   378
NTDB id 1112 NGFG RS09215 WP 003689811.1      GAAGNLIYEEATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMME   380
NTDB id 1113 AAA85695.1 219..1451( )          GAAGNLIYEEATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMME   380
NTDB id 1252 GC085 RS07730 WP 011213805.1     GATGNIIYAKATDKIREEVATGQQMFIAME.NTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLE   377
NTDB id 306557 DWG18 RS00850 WP 115644634.1  GATGNIVYEQAVLRMRDDVAVGYPVNVAMK.QTNLFPHMVIQMTAIGEEAGALDTMLFKVAEFYEQEVNNAVDALSSLLE   387
NTDB id 1198 PSJM300 03950 AFN76868.1         GATGNVVFRSATNKIKSDVSSGMQLNFSMR.TTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALME   376
NTDB id 1016 ACIAD RS01680 WP 004920476.1    GATNNTVYEQAVLKIREDVSTGQQLNFAMR.VSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMME   379
NTDB id 1059 ABD1 RS01610 WP 000279215.1      GATNNVIYEKAVMKIREDVATGQQLQFAMR.ISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMME   379
consensus                                     ****!****  **  ***  ***  !*  ******   *  *!!  ****!**!!!!*!*!**!!  !*!**!!  !!***!**!*  **!

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logo

NTDB id 1029 TT RS02230 WP 011228203.1        PLMIIFLGVIVGMIVAGMFLPLFKIIGTLSVQ   406
NTDB id 1402 DSB67 RS12670 WP 010643257.1     PLIIVFLGVVVGGLVTAMYLPIFNLMSVLG..   407
NTDB id 1169 A1552VC RS11075 WP 000648511.1   PLIIVFLGTVVGGLVVAMYLPIFNLMSVLG..   408
NTDB id 1112 NGFG RS09215 WP 003689811.1      PIIIVILGLVIGTLLVAMYLPLFNLGNVVA..   410
NTDB id 1113 AAA85695.1 219..1451( )          PIIILILGLVIGTLLVAMYLPLFNLGNVVA*.   410
NTDB id 1252 GC085 RS07730 WP 011213805.1     PIIMSILGILVGGLVVAMYLPIFKLGSAV...   406
NTDB id 306557 DWG18 RS00850 WP 115644634.1   PMIMVFLGVVVGGMVVAMYLPIFKLASVVG..   417
NTDB id 1198 PSJM300 03950 AFN76868.1         PMIMAVLGVLVGGLIIAMYLPIFQMGSVV...   405
NTDB id 1016 ACIAD RS01680 WP 004920476.1    PLIMAILGILVGGLVIAMYLPIFQMGSVV...   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1      PLIMAILGVLVGGLVIAMYLPIFQMGSVV...   408
consensus                                     !*****!!***!*****!*!!*!******
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X non conserved

X similar

X ≥ 50% conserved