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NTDB id 1029 TT RS02230 WP 011228203.1          ..............MPVYQYKARDRQGR.LVEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIPALERGPGL    64
NTDB id 1169 A1552VC RS11075 WP 000648511.1     .MKAT......QTLPLKNYRWKGINSNGK.KVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.....LTHRVKS    67
NTDB id 1402 DSB67 RS12670 WP 010643257.1       ..MKT......IAPQLKNYRWKGINSSGK.KTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.....ISHRVKG    66
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 1252 GCO85 RS07730 WP 011213805.1       ..MDK......NSPPLLTFHYQGINKAGQ.KMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.....KNKKITQ    66
NTDB id 1016 ACIAD RS01680 WP 004920476.1       .MAAK......KTQVMPVFAYEGVDRKGI.KLKGELPARNMALAKVTLRKQGITTRTIREKRKNIFEG....LLKKKVKP    68
NTDB id 1059 ABD1 RS01610 WP 000279215.1        .MAVK......KAQMMPTFAYEGVDRKGV.KIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG....LFKKKVTT    68
NTDB id 246641 PRUTH RS12710 WP 045979234.1     MAKQQ......QANQLDTFQWVGVSTRGK.KLEGELTGTSIALVKAQLRKQGITPSKVKRKPKPLFGL....SGEKKISA    69
NTDB id 1198 PSJM300 03950 AFN76868.1           ..MAQ......KAIKNSVFTWEGLDRQGA.KIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS......AGKKIKP    65
consensus                                         ***       *  *  * ****   *  ** *** * ******  !***** * ***** * *           ****
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NTDB id 1029 TT RS02230 WP 011228203.1          KDLAIFSRQLATMLGAGLTLLQALAILERQTENRKFREILKQVRTDVEGGMAFSEALSKH.KIFSRLYVNLVRAGETSGG    143
NTDB id 1169 A1552VC RS11075 WP 000648511.1     KDITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGN    147
NTDB id 1402 DSB67 RS12670 WP 010643257.1       KDITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGN    146
NTDB id 1113 AAA85695.1 219..1451( )            EDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGV    149
NTDB id 1112 NGFG RS09215 WP 003689811.1        EDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGV    149
NTDB id 1252 GCO85 RS07730 WP 011213805.1       ADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGS    146
NTDB id 1016 ACIAD RS01680 WP 004920476.1       LDIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGS    148
NTDB id 1059 ABD1 RS01610 WP 000279215.1        LDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGA    148
NTDB id 246641 PRUTH RS12710 WP 045979234.1     KDIAMFTRQLATMLLAGVSLVQAIDMIADGSENKSVKNLLRSIGEEVKAGQPLSTALRKHPKYFDDLYCDLVASGEQSGA    149
NTDB id 1198 PSJM300 03950 AFN76868.1           MDIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGS    145
consensus                                         !*****!!**!!* *!****!********* *** ****** ** ****!**** ****** *!* ****!***!!**!
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NTDB id 1029 TT RS02230 WP 011228203.1          LDLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAAT    223
NTDB id 1169 A1552VC RS11075 WP 000648511.1     LPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYS    227
NTDB id 1402 DSB67 RS12670 WP 010643257.1       LSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWG    226
NTDB id 1113 AAA85695.1 219..1451( )            LESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYG    229
NTDB id 1112 NGFG RS09215 WP 003689811.1        LESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYG    229
NTDB id 1252 GCO85 RS07730 WP 011213805.1       LDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYW    226
NTDB id 1016 ACIAD RS01680 WP 004920476.1       LEIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYW    228
NTDB id 1059 ABD1 RS01610 WP 000279215.1        LETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYW    228
NTDB id 246641 PRUTH RS12710 WP 045979234.1     LDRIFDRVALYKEKAEALKSKIKKAMFYPVAVIFVAAIVTSILLIFVVPQFKEIFEGFGAELPAFTLLVISISEFMQAYW    229
NTDB id 1198 PSJM300 03950 AFN76868.1           LETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWW    225
consensus                                       !* *****! **!!** ** !***!* !!* !***!********** **! ! ***  *!**!!**!**** *!*******
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NTDB id 1029 TT RS02230 WP 011228203.1        LPLLLLAVALFFAYR.WYYGTPQGRRVIDRLKLRLPVFGNLNRKTAVARFSRTLALLLSSGVNIVEALDITKGTAGNSVV   302
NTDB id 1169 A1552VC RS11075 WP 000648511.1   LWAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNVHF   307
NTDB id 1402 DSB67 RS12670 WP 010643257.1     PFIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHY   306
NTDB id 1113 AAA85695.1 219..1451( )          WMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIY   309
NTDB id 1112 NGFG RS09215 WP 003689811.1      WMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIY   309
NTDB id 1252 GCO85 RS07730 WP 011213805.1     YIIFGALGCVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIY   306
NTDB id 1016 ACIAD RS01680 WP 004920476.1     FILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVY   308
NTDB id 1059 ABD1 RS01610 WP 000279215.1      FIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIY   308
NTDB id 246641 PRUTH RS12710 WP 045979234.1   WIAVLVLGIGGYVFKQAHRRNKQLRDNVDKLILKTPIVGSILNKAAVARYARTLSTTFAAGVPLVDALDSAAGASGNAVY   309
NTDB id 1198 PSJM300 03950 AFN76868.1         YVVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVF   305
consensus                                     ***************  **  **  ***   ****!**!**!***  !*  *!***!!********!******!*********!***
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NTDB id 1029 TT RS02230 WP 011228203.1        EEIVEAAKLKIQQGDPLNLTLAQHPFVFPPMVSSMVAIGEETGALDTMLSKVADFYEREVDEAVASLTAAIEPLMIIFLG   382
NTDB id 1169 A1552VC RS11075 WP 000648511.1   ETAINEVYRDTAAGMPMYIAMR.NTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLG   386
NTDB id 1402 DSB67 RS12670 WP 010643257.1     QLAIEEVYRDTAAGMPMYIAMR.HCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLG   385
NTDB id 1113 AAA85695.1 219..1451( )          EEATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILG   388
NTDB id 1112 NGFG RS09215 WP 003689811.1      EEATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILG   388
NTDB id 1252 GCO85 RS07730 WP 011213805.1     AKATDKIREEVATGQQQMFIAME.NTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILG   385
NTDB id 1016 ACIAD RS01680 WP 004920476.1     EQAVLKIREDVSTGQQLNFAMR.VSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILG   387
NTDB id 1059 ABD1 RS01610 WP 000279215.1      EKAVMKIREDVATGQQLQFAMR.ISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILG   387
NTDB id 246641 PRUTH RS12710 WP 045979234.1   RDAILDIKAEVSSGNPMNWAMR.NSNIFPDMVIQMVAIGEESGSLDDMLAKVATIYEQEVDDAVDGLSSLLEPLIMAVLG   388
NTDB id 1198 PSJM300 03950 AFN76868.1         RSATNKIKSDVSSGMQLNFSMR.TTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLG   384
consensus                                     *  **  ***  **  *!*  **  ***   *  *!!  ****!**!!!!*!*!**!!  !*!  *!!  !!***!**!*  **!!*****!!
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NTDB id 1029 TT RS02230 WP 011228203.1        VIVGMIVAGMFLPLFKIIGTLSVQ   406
NTDB id 1169 A1552VC RS11075 WP 000648511.1   TVVGGLVVAMYLPIFNLMSVLG..   408
NTDB id 1402 DSB67 RS12670 WP 010643257.1     VVVGGLVTAMYLPIFNLMSVLG..   407
NTDB id 1113 AAA85695.1 219..1451( )          LVIGTLLVAMYLPLFNLGNVVA*.   410
NTDB id 1112 NGFG RS09215 WP 003689811.1      LVIGTLLVAMYLPLFNLGNVVA..   410
NTDB id 1252 GCO85 RS07730 WP 011213805.1     ILVGGLVVAMYLPIFKLGSAV...   406
NTDB id 1016 ACIAD RS01680 WP 004920476.1     ILVGGLVIAMYLPIFQMGSVV...   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1      VLVGGLVIAMYLPIFQMGSVV...   408
NTDB id 246641 PRUTH RS12710 WP 045979234.1   VLIGGLIIAMYLPIFQLGSVI...   409
NTDB id 1198 PSJM300 03950 AFN76868.1         VLVGGLIIAMYLPIFQMGSVV...   405
consensus                                     ***!*****!*!!*!******
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X non conserved
X similar
X ≥ 50% conserved