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NTDB id 1029 TT RS02230 WP 011228203.1        ................MPVYQYKARDRQ.GRLVEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIPALERGPGL   64
NTDB id 1169 A1552VC RS11075 WP 000648511.1   .MKAT......QTLPLKNYRWKGINSN.GKKVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLARL.....THRVKS   67
NTDB id 1402 DSB67 RS12670 WP 010643257.1     ..MKT......IAPQLKNYRWKGINSS.GKKTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITKI.....SHRVKG   66
NTDB id 1112 NGFG RS09215 WP 003689811.1      ..MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKTS.........SKRKITQ   69
NTDB id 1113 AAA85695.1 219..1451( )          ..MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKTS.........SKRKITQ   69
NTDB id 1252 GC085 RS07730 WP 011213805.1     ..MDK......NSPPLLTFHYQGINKA.GQKMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.....KNKKITQ   66
NTDB id 188313 BSY15 RS03400 WP 069103616.1  MATAA......SNIKEFVFEWEGKDRH.GKVVRGEIRASGENQVQATLRRQGVFPTKIKKRRMR.........SGKKIKP   64
NTDB id 1198 PSJM300 03950 AFN76868.1         ..MAQ......KAIKNSVFTWEGLDRQ.GAKIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS......AGKKIKP   65
NTDB id 1016 ACIAD RS01680 WP 004920476.1     .MAAK......KTQVMPVFAYEGVDRK.GIKLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGL....LKKKVKP   68
NTDB id 1059 ABD1 RS01610 WP 000279215.1      .MAVK......KAQMMPTFAYEGVDRK.GVKIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGL....FKKKVTT   68
consensus                                       ***       *  *  * ******  **** *** * **  **  !***** * ****** **   *      ****
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NTDB id 1029 TT RS02230 WP 011228203.1        KDLAIFSRQLATMLGAGLTLLQALAILERQTENRKFREILKQVRTDVEGGMAFSEALSKHK.IFSRLYVNLVRAGETSGG  143
NTDB id 1169 A1552VC RS11075 WP 000648511.1   KDITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGN  147
NTDB id 1402 DSB67 RS12670 WP 010643257.1     KDITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGN  146
NTDB id 1112 NGFG RS09215 WP 003689811.1      EDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGV  149
NTDB id 1113 AAA85695.1 219..1451( )          EDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGV  149
NTDB id 1252 GC085 RS07730 WP 011213805.1     ADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGS  146
NTDB id 188313 BSY15 RS03400 WP 069103616.1  KDIALFTRQLATMMKAGVPLLQSFDIVGRGNTNASVTKLLNDIRQDVETGTSLNAAFRKHPMYFDTLYCNLVEAGEAAGI  144
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                                      !*****!!**!!***!****!****** *   ** ****** ** ****!**** ****** *!* ****!***!! *!
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NTDB id 1029 TT RS02230 WP 011228203.1        LDLLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAAT  223
NTDB id 1169 A1552VC RS11075 WP 000648511.1   LPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYS  227
NTDB id 1402 DSB67 RS12670 WP 010643257.1     LSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWG  226
NTDB id 1112 NGFG RS09215 WP 003689811.1      LESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYG  229
NTDB id 1113 AAA85695.1 219..1451( )          LESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYG  229
NTDB id 1252 GC085 RS07730 WP 011213805.1     LDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYW  226
NTDB id 188313 BSY15 RS03400 WP 069103616.1  LEALLDRLATYMEKTEAIKSKIRSALMYPTSVIIVAFVVVAVIMIFVIPAFKEVFTSFGADLPAPTLFVMAVSEVFVKWW  224
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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NTDB id 1029 TT RS02230 WP 011228203.1        LPLLLLAVALFFAY.RWYYGTPQGRRVIDRLKLRLPVFGNLNRKTAVARFSRTLALLLSSGVNIVEALDITKGTAGNSVV   302
NTDB id 1169 A1552VC RS11075 WP 000648511.1   LWAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNVHF   307
NTDB id 1402 DSB67 RS12670 WP 010643257.1     PFIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHY   306
NTDB id 1112 NGFG RS09215 WP 003689811.1      WMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIY   309
NTDB id 1113 AAA85695.1 219..1451( )          WMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIY   309
NTDB id 1252 GC085 RS07730 WP 011213805.1     YIIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIY   306
NTDB id 188313 BSY15 RS03400 WP 069103616.1  WLIFGSIGATVYFFMQAWRRNEKMQMFMDRVLLKVPIFGALIDKSCVARWTRTLATMFAAGVPLVEALDSVGGASGNSVY   304
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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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 1112 NGFG RS09215 WP 003689811.1      EEATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILG   388
NTDB id 1113 AAA85695.1 219..1451( )          EEATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILG   388
NTDB id 1252 GC085 RS07730 WP 011213805.1     AKATDKIREEVATGQQMFIAME.NTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILG   385
NTDB id 188313 BSY15 RS03400 WP 069103616.1  AMATEKIQQEVSTGTSLTAAMG.NANVFPSMVLQMCAIGEESGSIDHMLGKAADFYEAEVDEMVAGLSSLMEPIIIVFLG   383
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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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 1112 NGFG RS09215 WP 003689811.1      LVIGTLLVAMYLPLFNLGNVVA..   410
NTDB id 1113 AAA85695.1 219..1451( )          LVIGTLLVAMYLPLFNLGNVVA*.   410
NTDB id 1252 GC085 RS07730 WP 011213805.1     ILVGGLVVAMYLPIFKLGSAV...   406
NTDB id 188313 BSY15 RS03400 WP 069103616.1   TLIGGIVVSMYLPIFKLGQVV...   404
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