logo

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NTDB id 1169 A1552VC RS11075 WP 000648511.1    ..........MKATQTLPLKNYRWKGINSNG.KKVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLA.RLTHRVKS   67
NTDB id 1402 DSB67 RS12670 WP 010643257.1      ..........MKTIAPQLKNYRWKGINSSG.KKTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFIT.KISHRVKG   66
NTDB id 1112 NGFG RS09215 WP 003689811.1       ......MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKT.....SSKRKITQ   69
NTDB id 1113 AAA85695.1 219..1451( )           ......MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKT.....SSKRKITQ   69
NTDB id 1252 GCO85 RS07730 WP 011213805.1      ..........MDKNSPPLLTFHYQGINKAG.QKMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFD.RKNKKITQ   66
NTDB id 1135269 MORIYA RS15625 WP 112716614.1  MVAVTKTTHNRRKPSAVKKRYPYHWQGVNRKG.KKVSGEMQAESISNLKVELRRQGINVLKAKRKSTGLFS.VGSKKIKA   78
NTDB id 1198 PSJM300 03950 AFN76868.1          ..........MAQKAIKNSVFTWEGLDRQG.AKIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKKIKP   65
NTDB id 1016 ACIAD RS01680 WP 004920476.1      ..........MAAKKTQVMPVFAYEGVDRKG.IKLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKVKP   68
NTDB id 1059 ABD1 RS01610 WP 000279215.1       ..........MAVKKAQMMPTFAYEGVDRKG.VKIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVTT   68
consensus                                                 *  *  * **!* * * *** !** * *   **  !***** * ****** *       ****
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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 GCO85 RS07730 WP 011213805.1      ADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGS   146
NTDB id 1135269 MORIYA RS15625 WP 112716614.1  MDIALISRQISTMLNAGVPLVQSLEIIARSNDNPAMRSLIGEVAAEVSTGTSLSNTLRKHPIYFDDLYCDLISAGEQSGS   158
NTDB id 1198 PSJM300 03950 AFN76868.1          MDIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGS   145
NTDB id 1016 ACIAD RS01680 WP 004920476.1      LDIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMREVVLGIKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGS   148
NTDB id 1059 ABD1 RS01610 WP 000279215.1       LDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGA   148
consensus                                       !!*****!!**!!* *!*!**!********  ** ****** ** *****!**** **** * *!* *** !***!!**!
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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 GCO85 RS07730 WP 011213805.1      LDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYW   226
NTDB id 1135269 MORIYA RS15625 WP 112716614.1  LDIMYDRIATYKEKAEALKSKIKKAMLYPAMVVAVATIVTLILLLYVIPQFKDIFAGFGAELPPFTLFVLSISDFVSQFW   238
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 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       WMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWCRTTATLFAAGVPLVDVLDSTAGAAGNLIY   309
NTDB id 1113 AAA85695.1 219..1451( )           WMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWCRTTATLFAAGVPLVDVLDSTAGAAGNLIY   309
NTDB id 1252 GCO85 RS07730 WP 011213805.1      YIIFGALGCVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIY   306
NTDB id 1135269 MORIYA RS15625 WP 112716614.1  YLVIGILFGIPIIYLKANQRSMKVKHITERTILKIPAIGPIMHKGALARFARTLSTTFAAGIPLVDSLTSAAGASGNIVY   318
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 1169 A1552VC RS11075 WP 000648511.1      ETAINEVYRDTAAGMPMYIAMRNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLGT   387
NTDB id 1402 DSB67 RS12670 WP 010643257.1        QLAIEEVYRDTAAGMPMYIAMRHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGV   386
NTDB id 1112 NGFG RS09215 WP 003689811.1         EEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGL   389
NTDB id 1113 AAA85695.1 219..1451( )             EEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGL   389
NTDB id 1252 GCO85 RS07730 WP 011213805.1        AKATDKIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGI   386
NTDB id 1135269 MORIYA RS15625 WP 112716614.1    KNAVMEMRNEVIAGLPMHIAMRSTNLFPDMVTQMVMIGEESGSLDDMLAKVAHIYEQQVDDAVDGLTSLIEPMIMVVLGV   398
NTDB id 1198 PSJM300 03950 AFN76868.1            RSATNKIKSDVSSGMQLNFSMRTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGV   385
NTDB id 1016 ACIAD RS01680 WP 004920476.1        EQAVLKIREDVSTGQQLNFAMRVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGI   388
NTDB id 1059 ABD1 RS01610 WP 000279215.1         EKAVMKIREDVATGQQLQFAMRISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGV   388
consensus                                        * !* *** **  !* *  *!* * *!! ***!!* !!!!!! !**!! !*! *!! *!***!**!* **!!*!***!!*
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NTDB id 1169 A1552VC RS11075 WP 000648511.1      VVGGLVVAMYLPIFNLMSVLG.   408
NTDB id 1402 DSB67 RS12670 WP 010643257.1        VVGGLVTAMYLPIFNLMSVLG.   407
NTDB id 1112 NGFG RS09215 WP 003689811.1         VIGTLLVAMYLPLFNLGNVVA.   410
NTDB id 1113 AAA85695.1 219..1451( )             VIGTLLVAMYLPLFNLGNVVA*   410
NTDB id 1252 GCO85 RS07730 WP 011213805.1        LVGGLVVAMYLPIFKLGSAV..   406
NTDB id 1135269 MORIYA RS15625 WP 112716614.1    IIGGLVIAMYLPIFKMGSIM..   418
NTDB id 1198 PSJM300 03950 AFN76868.1            LVGGLIIAMYLPIFQMGSVV..   405
NTDB id 1016 ACIAD RS01680 WP 004920476.1        LVGGLVIAMYLPIFQMGSVV..   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1         LVGGLVIAMYLPIFQMGSVV..   408
consensus                                        **!*!**!!!!!*!******
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X non conserved
X similar
X ≥ 50% conserved