logo

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NTDB id 1112 NGFG RS09215 WP 003689811.1     .......MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKT.....SSKRKIT   68
NTDB id 1113 AAA85695.1 219..1451( )         .......MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKT.....SSKRKIT   68
NTDB id 1169 A1552VC RS11075 WP 000648511.1  ............MKATQTLPLKNYRWKGINSNG.KKVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.LTHRVK   66
NTDB id 1402 DSB67 RS12670 WP 010643257.1    ............MKTIAPQLKNYRWKGINSSG.KKTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.ISHRVK   65
NTDB id 1252 GCO85 RS07730 WP 011213805.1    ............MDKNSPPLLTFHYQGINKAG.QKMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.KNKKIT   65
NTDB id 31814 SWP RS21145 WP 020914723.1     MATASSQLSKKRGAQKSQPKVVTYSWKGVNRDG.RRTSGELRGVSSAEIRAQLKAQGVIPKNVRKKSAPLFK..SEKKIK   77
NTDB id 1198 PSJM300 03950 AFN76868.1        ............MAQKAIKNSVFTWEGLDRQG.AKIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKKIK   64
NTDB id 1016 ACIAD RS01680 WP 004920476.1    ............MAAKKTQVMPVFAYEGVDRKG.IKLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKVK   67
NTDB id 1059 ABD1 RS01610 WP 000279215.1     ............MAVKKAQMMPTFAYEGVDRKG.VKIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVT   67
consensus                                                 *  *  * **!* * * *** !** * * **** !***** * ***** *       ****
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NTDB id 1112 NGFG RS09215 WP 003689811.1     QEDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGG   148
NTDB id 1113 AAA85695.1 219..1451( )         QEDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGG   148
NTDB id 1169 A1552VC RS11075 WP 000648511.1  SKDITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSG   146
NTDB id 1402 DSB67 RS12670 WP 010643257.1    GKDITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSG   145
NTDB id 1252 GCO85 RS07730 WP 011213805.1    QADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSG   145
NTDB id 31814 SWP RS21145 WP 020914723.1     PMDIAMVTRQVATMLAAGVPIVTTLELLGKGHEKPKMRELLATIVNDVQSGIPLSEALRPHRLYFDELYVDLVAAGEHSG   157
NTDB id 1198 PSJM300 03950 AFN76868.1        PMDIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSG   144
NTDB id 1016 ACIAD RS01680 WP 004920476.1    PLDIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMREVVLGIKGEVECGNTFAGALRKYPQYFDNLFCSLIESGEQSG   147
NTDB id 1059 ABD1 RS01610 WP 000279215.1     TLDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVECGSTFASALRKYPQHFDNLFCSLVESGEQSG   147
consensus                                      !!****!!**!!* *!*!************** ** ****** ** ****!**** *** * *!* *** !***!! *!
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NTDB id 1112 NGFG RS09215 WP 003689811.1     VLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSY   228
NTDB id 1113 AAA85695.1 219..1451( )         VLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSY   228
NTDB id 1169 A1552VC RS11075 WP 000648511.1  NLPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAY   226
NTDB id 1402 DSB67 RS12670 WP 010643257.1    NLSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNW   225
NTDB id 1252 GCO85 RS07730 WP 011213805.1    SLDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAY   225
NTDB id 31814 SWP RS21145 WP 020914723.1     SLDAVFDRIATYREKSEALKSKIKKAMFYPASVVIVAVIVTALLLLFVVPQFETIFQGFGAELPAFTQIVVNLSRWLQSS   237
NTDB id 1198 PSJM300 03950 AFN76868.1        SLETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAW   224
NTDB id 1016 ACIAD RS01680 WP 004920476.1    SLEIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDY   227
NTDB id 1059 ABD1 RS01610 WP 000279215.1     ALETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEY   227
consensus                                     !* *****!*!*!!** ** !***!* !! *!**!!**** **** !*! ! ***  *!!*!!**!**!* *! *** *
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NTDB id 1112 NGFG RS09215 WP 003689811.1     GWMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLI   308
NTDB id 1113 AAA85695.1 219..1451( )         GWMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLI   308
NTDB id 1169 A1552VC RS11075 WP 000648511.1  SLWAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNVH   306
NTDB id 1402 DSB67 RS12670 WP 010643257.1    GPFIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMH   305
NTDB id 1252 GCO85 RS07730 WP 011213805.1    WYIIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNII   305
NTDB id 31814 SWP RS21145 WP 020914723.1     WYIFVIAIIAAVWGFRRAHRNSQLFRDKIDEIILKIPLIGEILHKGAMAKFARTLATTFAAGVPLIDGLESAAGASGNAV   317
NTDB id 1198 PSJM300 03950 AFN76868.1        WYVVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVV   304
NTDB id 1016 ACIAD RS01680 WP 004920476.1    WFILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTV   307
NTDB id 1059 ABD1 RS01610 WP 000279215.1     WFIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVI   307
consensus                                    ***************  **  *! ***  ****!**!**!*** !* *!***!!****!*!!*!****!********!**
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NTDB id 1112 NGFG RS09215 WP 003689811.1     YEEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILG   388
NTDB id 1113 AAA85695.1 219..1451( )         YEEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILG   388
NTDB id 1169 A1552VC RS11075 WP 000648511.1  FETAINEVYRDTAAGMPMYIAMRNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLG   386
NTDB id 1402 DSB67 RS12670 WP 010643257.1    YQLAIEEVYRDTAAGMPMYIAMRHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLG   385
NTDB id 1252 GCO85 RS07730 WP 011213805.1    YAKATDKIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILG   385
NTDB id 31814 SWP RS21145 WP 020914723.1     YKKAVLNIRTEVMSGMQMNVAMRTTGLFPDMMIQMVMIGEESGSLDSMLNKVANIYEMQVDDAVDGLSSLIEPIMMVVIG   397
NTDB id 1198 PSJM300 03950 AFN76868.1        FRSATNKIKSDVSSGMQLNFSMRTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLG   384
NTDB id 1016 ACIAD RS01680 WP 004920476.1    YEQAVLKIREDVSTGQQLNFAMRVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILG   387
NTDB id 1059 ABD1 RS01610 WP 000279215.1     YEKAVMKIREDVATGQQLQFAMRISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILG   387
consensus                                    ** !*  ** ** *!***  *!* * *!! ***!!* !!!!!! !**!!*!*! *!! *!***!**!* **!!******!
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NTDB id 1112 NGFG RS09215 WP 003689811.1     LVIGTLLVAMYLPLFNLGNVVA..   410
NTDB id 1113 AAA85695.1 219..1451( )         LVIGTLLVAMYLPLFNLGNVVA .   410
NTDB id 1169 A1552VC RS11075 WP 000648511.1  TVVGGLVVAMYLPIFNLMSVLG..   408
NTDB id 1402 DSB67 RS12670 WP 010643257.1    VVVGGLVTAMYLPIFNLMSVLG..   407
NTDB id 1252 GCO85 RS07730 WP 011213805.1    ILVGGLVVAMYLPIFKLGSAV...   406
NTDB id 31814 SWP RS21145 WP 020914723.1     TVVGGLIVAMYLPIFQLGNVVGGG   421
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