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logo
NTDB id 1402 DSB67 RS12670 WP 010643257.1      ..................MKTIAPQLKNYRWKGINSSG.KKTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.IS   61
NTDB id 1113 AAA85695.1 219..1451( )           ........MAKN...GGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TSSK   64
NTDB id 1112 NGFG RS09215 WP 003689811.1       ........MAKN...GGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TSSK   64
NTDB id 57130 R2APBS1 RS04440 WP 015447035.1  MATATATNINKARELGAQRAEVSKLTTYEWIALDKRG.KRMKGDMPAKNASLVKAELRRQGMNPQTVRERAKPLFGA.TG   78
NTDB id 1252 GC085 RS07730 WP 011213805.1      ..................MDKNSPPLLTFHYQGINKAG.QKMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.KN   61
NTDB id 1198 PSJM300 03950 AFN76868.1          ..................MAQKAIKNSVFTWEGLDRQG.AKIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AG   60
NTDB id 1016 ACIAD RS01680 WP 004920476.1      ................MAAKKTQVMPVFAYEGVDRKG.IKLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLK   63
NTDB id 1059 ABD1 RS01610 WP 000279215.1       ................MAVKKAQMMPTFAYEGVDRKG.VKIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFK   63
consensus                                                        *  *  * **** * *  ** !** * *  ***  !*****    *****  *

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NTDB id 1402 DSB67 RS12670 WP 010643257.1      HRVKGKDITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATG  141
NTDB id 1113 AAA85695.1 219..1451( )           RKITQEDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAG  144
NTDB id 1112 NGFG RS09215 WP 003689811.1       RKITQEDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAG  144
NTDB id 57130 R2APBS1 RS04440 WP 015447035.1  STVKPGDVAVFSRQIATMMASGVPMVQSFDIIADGQKNIRFKNILLDVKQNIEGGAALHEALARYPVQFDELYCNLVHAG  158
NTDB id 1252 GC085 RS07730 WP 011213805.1      KKITQADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAG  141
NTDB id 1198 PSJM300 03950 AFN76868.1          KKIKPMDIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSG  140
NTDB id 1016 ACIAD RS01680 WP 004920476.1      KKVKPLDIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESG  143
NTDB id 1059 ABD1 RS01610 WP 000279215.1       KKVTTLDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESG  143
consensus                                      ***   !***!*!!**!!* *!*!**!*******  ** ****** **  ***!  **  ** *  * *!* ****!*  !

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NTDB id 1402 DSB67 RS12670 WP 010643257.1      EQSGNLSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAW  221
NTDB id 1113 AAA85695.1 219..1451( )           ETGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDF  224
NTDB id 1112 NGFG RS09215 WP 003689811.1       ETGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDF  224
NTDB id 57130 R2APBS1 RS04440 WP 015447035.1  ETSGVLDTVLDTVATYKERTEAIKKKIKKALFYPMMVLVVVFLVCLIMLLFVVPVFAKTFQDAGAQLPAPTQLLVTASEF  238
NTDB id 1252 GC085 RS07730 WP 011213805.1      EKSGSLDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEF  221
NTDB id 1198 PSJM300 03950 AFN76868.1          EQSGSLETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEA  220
NTDB id 1016 ACIAD RS01680 WP 004920476.1      EQSGSLEIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNW  223
NTDB id 1059 ABD1 RS01610 WP 000279215.1       EQSGALETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKW  223
consensus                                      ! *! !*******! !*!*** ** !***!* !!* !**!***** **** !*! ! ***  *!!*!!* !**** *!**

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NTDB id 1402 DSB67 RS12670 WP 010643257.1      TQNWGPFIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTS  301
NTDB id 1113 AAA85695.1 219..1451( )           FVSYGWMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAA  304
NTDB id 1112 NGFG RS09215 WP 003689811.1       FVSYGWMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAA  304
NTDB id 57130 R2APBS1 RS04440 WP 015447035.1  MQSYWWVVIGVTVGGVAALIIAKKRSVKFAHFLDRMALKMPVMGNIVRNSAIARFARTLGVTFRAGVPLVEALDAVAGAT  318
NTDB id 1252 GC085 RS07730 WP 011213805.1      MQAYWYIIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGAT  301
NTDB id 1198 PSJM300 03950 AFN76868.1          LQAWWYVVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGAT  300
NTDB id 1016 ACIAD RS01680 WP 004920476.1      MQDYWFILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGAT  303
NTDB id 1059 ABD1 RS01610 WP 000279215.1       MQEYWFIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGAT  303
consensus                                      ** ************ *** ** *! **   *****!**!**!*** ** *!***!!****!*!!*!****!*******
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NTDB id 1402 DSB67 RS12670 WP 010643257.1      GNMHYQLAIEEVYRDTAAGMPMYIAMRHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLII   381
NTDB id 1113 AAA85695.1 219..1451( )           GNLIYEEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIII   384
NTDB id 1112 NGFG RS09215 WP 003689811.1       GNLIYEEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIII   384
NTDB id 57130 R2APBS1 RS04440 WP 015447035.1  GSVVYSDAVKQMREDISVGHQLQLAMKQTGLFPNMVVQMTAIGEESGSLDNMLFKVAEFYEEEVSNAVDTLSTLLEPIIM   398
NTDB id 1252 GC085 RS07730 WP 011213805.1      GNIIYAKATDKIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIM   381
NTDB id 1198 PSJM300 03950 AFN76868.1          GNVVFRSATNKIKSDVSSGMQLNFSMRTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIM   380
NTDB id 1016 ACIAD RS01680 WP 004920476.1      NNTVYEQAVLKIREDVSTGQQLNFAMRVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIM   383
NTDB id 1059 ABD1 RS01610 WP 000279215.1       NNVIYEKAVMKIREDVATGQQLQFAMRISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIM   383
consensus                                      *****  !   **  **  ! **  *!* * *!! ***!! *!!!!!! !**!! !*! *!!*!!***!* !* **!!*!*
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NTDB id 1402 DSB67 RS12670 WP 010643257.1      VFLGVVVGGLVTAMYLPIFNLMSVLG.   407
NTDB id 1113 AAA85695.1 219..1451( )           LILGLVIGTLLVAMYLPLFNLGNVVA*   410
NTDB id 1112 NGFG RS09215 WP 003689811.1       VILGLVIGTLLVAMYLPLFNLGNVVA.   410
NTDB id 57130 R2APBS1 RS04440 WP 015447035.1  VVLGTLVGGMVIALYLPIFKLAGTF..   423
NTDB id 1252 GC085 RS07730 WP 011213805.1      SILGILVGGLVVAMYLPIFKLGSAV..   406
NTDB id 1198 PSJM300 03950 AFN76868.1          AVLGVLVGGLIIAMYLPIFQMGSVV..   405
NTDB id 1016 ACIAD RS01680 WP 004920476.1      AILGILVGGLVIAMYLPIFQMGSVV..   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1       AILGVLVGGLVIAMYLPIFQMGSVV..   408
consensus                                       *!!***!****!*!!!*!******
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X non conserved

X similar

X ≥ 50% conserved