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logo
NTDB id 1402 DSB67 RS12670 WP 010643257.1       ................MKTIAPQLKNYRWKGINSSG.KKTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.IS   61
NTDB id 1169 A1552VC RS11075 WP 000648511.1     ................MKATQTLPLKNYRWKGINSNG.KKVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.LT   62
NTDB id 1113 AAA85695.1 219..1451( )            ........MAKNGGFS...LFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KTSSK   64
NTDB id 1112 NGFG RS09215 WP 003689811.1        ........MAKNGGFS...LFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KTSSK   64
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
NTDB id 1009310 ABNK63 RS04390 WP 007809536.1   MATATATNIDKARALGAQRAEVSKLTTYEWVALDKRG.KRMKGDMPAKNASLVKAELRRQGMNPQTVRERSKPLFGS.SG   78
NTDB id 1252 GCO85 RS07730 WP 011213805.1       ................MDKNSPPLLTFHYQGINKAG.QKMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.KN   61
consensus                                                        *  *  * **** * * *** !** * *  ***  !*****    ****   *

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NTDB id 1402 DSB67 RS12670 WP 010643257.1       HRVKGKDITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATG   141
NTDB id 1169 A1552VC RS11075 WP 000648511.1     HRVKSKDITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETG   142
NTDB id 1113 AAA85695.1 219..1451( )            RKITQEDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAG   144
NTDB id 1112 NGFG RS09215 WP 003689811.1        RKITQEDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAG   144
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
NTDB id 1009310 ABNK63 RS04390 WP 007809536.1   STVKPGDVAVFSRQIATMMASGVPMVQAFDIIADGQKNVRFKNILLDVKQNIEGGASLHEALGRYPVQFDELYCNLVHAG   158
NTDB id 1252 GCO85 RS07730 WP 011213805.1       KKITQADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAG   141
consensus                                       ****  !*****!!**!!* *!*!**!******** ** ****** **  ***!***  **** * *!* ****!***!

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NTDB id 1402 DSB67 RS12670 WP 010643257.1       EQSGNLSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAW   221
NTDB id 1169 A1552VC RS11075 WP 000648511.1     EMSGNLPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHW   222
NTDB id 1113 AAA85695.1 219..1451( )            ETGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDF   224
NTDB id 1112 NGFG RS09215 WP 003689811.1        ETGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDF   224
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
NTDB id 1009310 ABNK63 RS04390 WP 007809536.1   EASGVLDTVLDTVATYKERTEAIKKKIKKALFYPMMVLAVVFLVMLIMLLFVVPVFSKTFQDAGADLPAPTQVLVNMSEF   238
NTDB id 1252 GCO85 RS07730 WP 011213805.1       EKSGSLDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEF   221
consensus                                       ! *! !*******!*!*!*** ** !***!* !!* !**!***** **** !*! ! ***  *!!*!!**!**** *!**

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NTDB id 1402 DSB67 RS12670 WP 010643257.1       TQNWGPFIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTS   301
NTDB id 1169 A1552VC RS11075 WP 000648511.1     VQAYSLWAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTS   302
NTDB id 1113 AAA85695.1 219..1451( )            FVSYGWMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAA   304
NTDB id 1112 NGFG RS09215 WP 003689811.1        FVSYGWMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAA   304
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
NTDB id 1009310 ABNK63 RS04390 WP 007809536.1   MQSYWWLVIGIIVGSIVAIVFAKKRSLKFAHFLDRLSLKLPVMGNIVRNSAIARFSRTLGVTFRAGVPLVEALEAVSGAT   318
NTDB id 1252 GCO85 RS07730 WP 011213805.1       MQAYWYIIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGAT   301
consensus                                       ** ***************** ** *! ***  *****!**!**!*** ** *!***!!****!*!!*!****!*******
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NTDB id 1402 DSB67 RS12670 WP 010643257.1        GNMHYQLAIEEVYRDTAAGMPMYIAMRHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLII   381
NTDB id 1169 A1552VC RS11075 WP 000648511.1      GNVHFETAINEVYRDTAAGMPMYIAMRNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLII   382
NTDB id 1113 AAA85695.1 219..1451( )             GNLIYEEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIII   384
NTDB id 1112 NGFG RS09215 WP 003689811.1         GNLIYEEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIII   384
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
NTDB id 1009310 ABNK63 RS04390 WP 007809536.1    GSIVYGDAVRQMRDDISVGHQLQLAMKQTGLFPNMVVQMTAIGEESGALDNMLFKVAEFYEEEVENAVDTLSTLLEPIIM   398
NTDB id 1252 GC085 RS07730 WP 011213805.1        GNIIYAKATDKIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIM   381
consensus                                        ****** !*  ** **  !***  *!* * *!! ***!!**!!!!!!*!**!! !*! *!!*!!***!* !* **!!*!*
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NTDB id 1402 DSB67 RS12670 WP 010643257.1        VFLGVVVGGLVTAMYLPIFNLMSVLG.   407
NTDB id 1169 A1552VC RS11075 WP 000648511.1      VFLGTVVGGLVVAMYLPIFNLMSVLG.   408
NTDB id 1113 AAA85695.1 219..1451( )             LILGLVIGTLLVAMYLPLFNLGNVVA*   410
NTDB id 1112 NGFG RS09215 WP 003689811.1         VILGLVIGTLLVAMYLPLFNLGNVVA.   410
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
NTDB id 1009310 ABNK63 RS04390 WP 007809536.1    VVLGGIVGGMVVALYLPIFKLAGTV..   423
NTDB id 1252 GC085 RS07730 WP 011213805.1        SILGILVGGLVVAMYLPIFKLGSAV..   406
consensus                                        **!!***!****!*!!!*!******
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X non conserved
X similar
X ≥ 50% conserved