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logo
NTDB id 1029 TT RS02230 WP 011228203.1          ....................MPVYQYKARDRQGRL.VEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIPALER   60
NTDB id 1169 A1552VC RS11075 WP 000648511.1     ............MKATQTLPLKNYRWKGINSNGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.....LTH   63
NTDB id 1402 DSB67 RS12670 WP 010643257.1       ............MKTIAPQLKNYRWKGINSSGKK.TSGNVLAMIEIEVRERLDAQHIKIKKLKKGSISFITK.....ISH   62
NTDB id 1112 NGFG RS09215 WP 003689811.1        ......MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TS....SKR   65
NTDB id 1113 AAA85695.1 219..1451( )            ......MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TS....SKR   65
NTDB id 1198 PSJM300 03950 AFN76868.1           ............MAQKAIKNSVFTWEGLDRQGAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS......AGK   61
NTDB id 1016 ACIAD RS01680 WP 004920476.1       ............MAAKKTQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGL....LKK   64
NTDB id 1059 ABD1 RS01610 WP 000279215.1        ............MAVKKAQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGL....FKK   64
NTDB id 1000826 ABFT86 RS05315 WP 012437601.1   MSVARSAIKKQPVDRNTSMLQTFIWEGADKRGVK.MKGEQTARNANMLRAELRRQGIVPSVVKQKPKPLFGA.....AGK   74
NTDB id 1252 GC085 RS07730 WP 011213805.1       ............MDKNSPPLLTFHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.....KNK   62
consensus                                                   *  *  * ****** * * * *** * *  ***  !***** *  ****** *          *

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NTDB id 1029 TT RS02230 WP 011228203.1          GPGLKDLAIFSRQLATMLGAGLTLLQALAILERQTENRKFREILKQVRTDVEGGMAFSEALSKHK.IFSRLYVNLVRAGE  139
NTDB id 1169 A1552VC RS11075 WP 000648511.1     RVKSKDITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGE  143
NTDB id 1402 DSB67 RS12670 WP 010643257.1       RVKGKDITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGE  142
NTDB id 1112 NGFG RS09215 WP 003689811.1        KITQEDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGE  145
NTDB id 1113 AAA85695.1 219..1451( )            KITQEDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGE  145
NTDB id 1198 PSJM300 03950 AFN76868.1           KIKPMDIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGE  141
NTDB id 1016 ACIAD RS01680 WP 004920476.1       KVKPLDIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGE  144
NTDB id 1059 ABD1 RS01610 WP 000279215.1        KVTTLDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGE  144
NTDB id 1000826 ABFT86 RS05315 WP 012437601.1   KITPKDIAFFSRQMATMMKSGVPIVSSLEIIGEGHKNPRMKKMVGQIRTDIEGGSSLYESISAHPVQFDELYRNLVRAGE  154
NTDB id 1252 GC085 RS07730 WP 011213805.1       KITQADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGE  142
consensus                                       ***  !*****!!**!!***!*************** ** ****** ** ****!**** ****** *!* ****!***!!

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NTDB id 1029 TT RS02230 WP 011228203.1          TSGGLDLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLL  219
NTDB id 1169 A1552VC RS11075 WP 000648511.1     MSGNLPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWV  223
NTDB id 1402 DSB67 RS12670 WP 010643257.1       QSGNLSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWT  222
NTDB id 1112 NGFG RS09215 WP 003689811.1        TGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFF  225
NTDB id 1113 AAA85695.1 219..1451( )            TGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFF  225
NTDB id 1198 PSJM300 03950 AFN76868.1           QSGSLETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEAL  221
NTDB id 1016 ACIAD RS01680 WP 004920476.1       QSGSLEIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWM  224
NTDB id 1059 ABD1 RS01610 WP 000279215.1        QSGALETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWM  224
NTDB id 1000826 ABFT86 RS05315 WP 012437601.1   GAGVLETVLDTVASYKENIEALKGKIKKAMFYPAMVVAVAIIVSAILLIFVVPQFEEVFKGFGAELPAFTQLLVNASRFM  234
NTDB id 1252 GC085 RS07730 WP 011213805.1       KSGSLDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFM  222
consensus                                        *! !*******!***!*** ***!***!* !!* !***!********* **! ! ***  *!**!!**!**** *!***
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logo

NTDB id 1029 TT RS02230 WP 011228203.1          RAATLPLLLLAVALFFAYRW.YYGTPQGRRVIDRLKLRLPVFGNLNRKTAVARFSRTLALLLSSGVNIVEALDITKGTAG   298
NTDB id 1169 A1552VC RS11075 WP 000648511.1     QAYSLWAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSG   303
NTDB id 1402 DSB67 RS12670 WP 010643257.1       QNWGPFIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSG   302
NTDB id 1112 NGFG RS09215 WP 003689811.1        VSYGWMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAG   305
NTDB id 1113 AAA85695.1 219..1451( )            VSYGWMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAG   305
NTDB id 1198 PSJM300 03950 AFN76868.1           QAWWYVVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATG   301
NTDB id 1016 ACIAD RS01680 WP 004920476.1       QDYWFILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATN   304
NTDB id 1059 ABD1 RS01610 WP 000279215.1        QEYWFIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATN   304
NTDB id 1000826 ABFT86 RS05315 WP 012437601.1   VSYWWLMLVVAVGSVVGFIFAYKRSPRMQHGLDRLILKVPVIGQIMHNSAIARFARTTAVTFKAGVPLVEALGIVAGATG   314
NTDB id 1252 GC085 RS07730 WP 011213805.1       QAYWYIIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATG   302
consensus                                       * ***************** ** ** ***  *****!**!**!*** ** *!***!!*******!******!********

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NTDB id 1029 TT RS02230 WP 011228203.1          NSVVEEIVEAAKLKIQQGDPLNLTLAQHPFVFPPMVSSMVAIGEETGALDTMLSKVADFYEREVDEAVASLTAAIEPLMI   378
NTDB id 1169 A1552VC RS11075 WP 000648511.1     NVHFETAINEVYRDTAAGMPMYIAMR.NTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLII   382
NTDB id 1402 DSB67 RS12670 WP 010643257.1       NMHYQLAIEEVYRDTAAGMPMYIAMR.HCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLII   381
NTDB id 1112 NGFG RS09215 WP 003689811.1        NLIYEEATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIII   384
NTDB id 1113 AAA85695.1 219..1451( )            NLIYEEATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIII   384
NTDB id 1198 PSJM300 03950 AFN76868.1           NVVFRSATNKIKSDVSSGMQLNFSMR.TTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIM   380
NTDB id 1016 ACIAD RS01680 WP 004920476.1       NTVYEQAVLKIREDVSTGQQLNFAMR.VSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIM   383
NTDB id 1059 ABD1 RS01610 WP 000279215.1        NVIYEKAVMKIREDVATGQQLQFAMR.ISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIM   383
NTDB id 1000826 ABFT86 RS05315 WP 012437601.1   NKLYEEAVFRMRDDVSVGYPVNMAMK.QVNLFPHMVIQMTAIGEEAGALDAMLFKVAEYFEEEVNNAVDALSSLLEPLIM   393
NTDB id 1252 GC085 RS07730 WP 011213805.1       NIIYAKATDKIREEVATGQQMFIAME.NTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIM   381
consensus                                       !**** ** *** **  !* ******  * *!! ****!**!!!!*!*!**!! !*!***!*!!***!**!* **!!***

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NTDB id 1029 TT RS02230 WP 011228203.1          IFLGVIVGMIVAGMFLPLFKIIGTLSVQ   406
NTDB id 1169 A1552VC RS11075 WP 000648511.1     VFLGTVVGGLVVAMYLPIFNLMSVLG..   408
NTDB id 1402 DSB67 RS12670 WP 010643257.1       VFLGVVVGGLVTAMYLPIFNLMSVLG..   407
NTDB id 1112 NGFG RS09215 WP 003689811.1        VILGLVIGTLLVAMYLPLFNLGNVVA..   410
NTDB id 1113 AAA85695.1 219..1451( )            LILGLVIGTLLVAMYLPLFNLGNVVA*.   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 1000826 ABFT86 RS05315 WP 012437601.1   VFIGTIVGGMVIGMYLPIFKLGAVVG..   419
NTDB id 1252 GC085 RS07730 WP 011213805.1       SILGILVGGLVVAMYLPIFKLGSAV...   406
consensus                                       ***!***!*****!*!!*!******
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X non conserved

X similar

X $\geq$ 50% conserved