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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        ......MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KT....SSKR   65
NTDB id 1113 AAA85695.1 219..1451( )            ......MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KT....SSKR   65
NTDB id 1076888 ACJGJ0 RS08230 WP 033483308.1  MSVARNVIKKQPADRSNSQMQPFVWEGTDKRGIK.MKGEQAARNVNMLRAELRRQGITPTVVKPKPKPLFGA.....AGK   74
NTDB id 1252 GC085 RS07730 WP 011213805.1       ............MDKNSPPLLTFHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.....KNK   62
NTDB id 1198 PSJM300 03950 AFN76868.1           ............MAQKAIKNSVFTWEGLDRQGAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS......AGK   61
NTDB id 1016 ACIAD RS01680 WP 004920476.1       ...........MAAKKTQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEG....LLKK   64
NTDB id 1059 ABD1 RS01610 WP 000279215.1        ...........MAVKKAQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG....LFKK   64
consensus                                                   *  *  * ****** * * * *** * ** ***  !***** *  **** * *          *
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logo
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 1076888 ACJGJ0 RS08230 WP 033483308.1  KVGPKDIAFFSRQMATMMKSGVPIVGSLEIIGEGHKNPRMRKMVGQIRTDIEGGSSLHEAISKHPVQFDELYRNLVRAGE   154
NTDB id 1252 GC085 RS07730 WP 011213805.1       KITQADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGE   142
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
consensus                                       **   !*****!!**!!***!*************** ** ****** ** ****!**** ****** *!* ****!***!!
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logo
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 1076888 ACJGJ0 RS08230 WP 033483308.1  GAGVLETVLDTVANYKENIEALKGKIKKALFYPAMVVAVALIVSAILLIFVVPQFEEVFKGFGAELPAFTQMIVAASRFM   234
NTDB id 1252 GC085 RS07730 WP 011213805.1       KSGSLDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFM   222
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
consensus                                        *! !*******!***!*** ***!***!* !!* !***!********* **! ! ***  *!**!!**!**** *!***
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logo
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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 1076888 ACJGJ0 RS08230 WP 033483308.1  ISYWWLMLLVIGGAITGFIFAYKRSPRMQHGMDRLVLKVPVIGQIMYNSSIARFARTTAVTFKAGVPLVEALGIVAGATG   314
NTDB id 1252 GC085 RS07730 WP 011213805.1       QAYWYIIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATG   302
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
consensus                                       * ***************** ** ** ***  *****!**!**!*** ****!***!!*******!******!********
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logo
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NTDB id 1029 TT RS02230 WP 011228203.1          NSVVEEIVEAAKLKIQQGDPLNLTLAQHPFVFPPMVSSMVAIGEETGALDTMLSKVADFYEREVDEAVASLIAAIEPLMI   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 1076888 ACJGJ0 RS08230 WP 033483308.1  NKVYEEAVLRMRDDVSVGYPVNMAMK.QVNLFPHMVIQMTAIGEEAGALDAMLFKVAEYFEQEVNNAVDALSSLLEPMIM   393
NTDB id 1252 GC085 RS07730 WP 011213805.1       NIIYAKATDKIREEVATGQQMFIAME.NTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIM   381
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
consensus                                       !**** ** *** **  !* ******  * *!! ****!**!!!!*!*!**!! !*!***! !!***!**!* **!!***
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logo
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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 1076888 ACJGJ0 RS08230 WP 033483308.1  VFIGTIVGGMVIGMYLPIFKLGAVVG..   419
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