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logo
NTDB id 1029 TT RS02230 WP 011228203.1          ........................MPVYQYKARDRQG.RLVEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEV   53
NTDB id 1402 DSB67 RS12670 WP 010643257.1       ....................MKTIAPQLKNYRWKGINSSG.KKTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.   59
NTDB id 1169 A1552VC RS11075 WP 000648511.1     ..................MKATQTLPLKNYRWKGINSNG.KKVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.   60
NTDB id 1112 NGFG RS09215 WP 003689811.1        .............MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKTS.....   62
NTDB id 1113 AAA85695.1 219..1451( )            .............MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKTS.....   62
NTDB id 1029598 AB5B06 RS10335 WP 416049737.1   MATRAPAAAARKAAAPKGKPGRKAPTQYLFEWEGKDRKG.KAFSGELRAQSQAEVNATLRKQGLTVVKLKKRRAA.....   74
NTDB id 1252 GC085 RS07730 WP 011213805.1       ....................MDKNSPPLLTFHYQGINKAG.QKMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.   59
NTDB id 1198 PSJM300 03950 AFN76868.1           ....................MAQKAIKNSVFTWEGLDRQG.AKIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..   58
NTDB id 1059 ABD1 RS01610 WP 000279215.1        ...................MAVKKAQMMPTFAYEGVDRKG.VKIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGL   61
NTDB id 1016 ACIAD RS01680 WP 004920476.1       ...................MAAKKTQVMPVFAYEGVDRKG.IKLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGL   61
consensus                                                                *  *  * ****** * *** *** * * ****  !***** * ****** **
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logo
NTDB id 1029 TT RS02230 WP 011228203.1          RIPALERGPGLKDLAIFSRQLATMLGAGLTLLQALAILERQTENRKFREILKQVRTDVEGGMAFSEALSKHK.IFSRLYV   132
NTDB id 1402 DSB67 RS12670 WP 010643257.1       ....ISHRVKGKDITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYT   135
NTDB id 1169 A1552VC RS11075 WP 000648511.1     ....LTHRVKSKDITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYV   136
NTDB id 1112 NGFG RS09215 WP 003689811.1        ....SKRKITQEDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYC   138
NTDB id 1113 AAA85695.1 219..1451( )            ....SKRKITQEDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYC   138
NTDB id 1029598 AB5B06 RS10335 WP 416049737.1   ....RGKKITQKDIAYFTRQLSTMLKAGIPLLQSIDIIARGHANPNFTQLLSEIRFDIESGSSMAQAFRRHPRYFDTLYC   150
NTDB id 1252 GC085 RS07730 WP 011213805.1       ....KNKKITQADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFC   135
NTDB id 1198 PSJM300 03950 AFN76868.1           ....AGKKIKPMDIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYC   134
NTDB id 1059 ABD1 RS01610 WP 000279215.1        ....FKKKVTTLDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFC   137
NTDB id 1016 ACIAD RS01680 WP 004920476.1       ....LKKKVKPLDIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFC   137
consensus                                            ****  !*****!!**!!***!****!****** ** ** ****** ** ****!***  ****** *!* ***
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logo
NTDB id 1029 TT RS02230 WP 011228203.1          NLVRAGETSGGLDLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTDLGSELPLLTRFL   212
NTDB id 1402 DSB67 RS12670 WP 010643257.1       DLLATGEQSGNLSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMV   215
NTDB id 1169 A1552VC RS11075 WP 000648511.1     DLVETGEMSGNLPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQV   216
NTDB id 1112 NGFG RS09215 WP 003689811.1        NLVAAGETGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTV   218
NTDB id 1113 AAA85695.1 219..1451( )            NLVAAGETGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTV   218
NTDB id 1029598 AB5B06 RS10335 WP 416049737.1   NLIDAGEQGGILDALLERLSLYMEKTIALKSQIKSAMIYPIAVLTVAFAVTVILMIFVIPAFKGVFSSFGANLPAPTLVV   230
NTDB id 1252 GC085 RS07730 WP 011213805.1       NLVDAGEKSGSLDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAV   215
NTDB id 1198 PSJM300 03950 AFN76868.1           NLVDSGEQSGSLETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMV   214
NTDB id 1059 ABD1 RS01610 WP 000279215.1        SLVESGEQSGALETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMV   217
NTDB id 1016 ACIAD RS01680 WP 004920476.1       SLIESGEQSGSLEIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLV   217
consensus                                       *!***!!**! !* ****** **!!** ** ****!* !!* !***!********** **! ! ***  *!**!!**!***
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logo
NTDB id 1029 TT RS02230 WP 011228203.1          IAVSDLLRAATLPLLLLAVALFFAYRW.YYGTPQGRRVIDRLKLRLPVFGNLNRKTAVARFSRTLALLLSSGVNIVEALD   291
NTDB id 1402 DSB67 RS12670 WP 010643257.1       LNLSAWTQNWGPFIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALK   295
NTDB id 1169 A1552VC RS11075 WP 000648511.1     LKLSHWVQAYSLWAFTAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLK   296
NTDB id 1112 NGFG RS09215 WP 003689811.1        MDMSDFFVSYGWMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLD   298
NTDB id 1113 AAA85695.1 219..1451( )            MDMSDFFVSYGWMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLD   298
NTDB id 1029598 AB5B06 RS10335 WP 416049737.1   IAMSDFFVDHWYLIIGAPIIGITMYIRGLKRSEKVQRASDRLLLKLPIFGSLFRKAVIARWTRTLATMFAAGTPLVESME   310
NTDB id 1252 GC085 RS07730 WP 011213805.1       ITMSEFMQAYWYIIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALK   295
NTDB id 1198 PSJM300 03950 AFN76868.1           IGLSEALQAWWYVVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALD   294
NTDB id 1059 ABD1 RS01610 WP 000279215.1        VNMSKWMQEYWFIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALE   297
NTDB id 1016 ACIAD RS01680 WP 004920476.1       VNMSNWMQDYWFILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALA   297
consensus                                       * *!**** ***************** ** ** ***  *****!**!**!*** !* *!***!!*******!*******
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logo
NTDB id 1029 TT RS02230 WP 011228203.1          ITKGTAGNSVVEEIVEAAKLKIQQGDPLNLTLAQHPFVFPPMVSSMVAIGEETGALDTMLSKVADFYEREVDEAVASLTA   371
NTDB id 1402 DSB67 RS12670 WP 010643257.1       TTSKTSGNMHYQLAIEEVYRDTAAGMPMYIAM.RHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSK   374
NTDB id 1169 A1552VC RS11075 WP 000648511.1     TTAKTSGNVHFETAINEVYRDTAAGMPMYIAM.RNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGK   375
NTDB id 1112 NGFG RS09215 WP 003689811.1        STAGAAGNLIYEEATREIRTRVIQGLSMTSGM.RATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSA   377
NTDB id 1113 AAA85695.1 219..1451( )            STAGAAGNLIYEEATREIRTRVIQGLSMTSGM.RATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSA   377
NTDB id 1029598 AB5B06 RS10335 WP 416049737.1   SVAGAAGNWVYYDATKEIEQSVRIGTSLTNAM.QATHVFDSMVLQMTQIGEESGALDNMLLKVAEFYEREVDDAVAAISS   389
NTDB id 1252 GC085 RS07730 WP 011213805.1       SVAGATGNIIYAKATDKIREEVATGQQMFIAM.ENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSS   374
NTDB id 1198 PSJM300 03950 AFN76868.1           SVAGATGNVVFRSATNKIKSDVSSGMQLNFSM.RTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTA   373
NTDB id 1059 ABD1 RS01610 WP 000279215.1        STAGATNNVIYEKAVMKIREDVATGQQLQFAM.RISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTS   376
NTDB id 1016 ACIAD RS01680 WP 004920476.1       STAGATNNTVYEQAVLKIREDVSTGQQLNFAM.RVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTS   376
consensus                                       *******!**** ** *** **  !* *  ** * * *!* ****!**!!!!*!*!**!! !*!**!! !!***!****
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<0
logo
NTDB id 1029 TT RS02230 WP 011228203.1          AIEPLMIIFLGVIVGMIVAGMFLPLFKIIGTLSVQ   406
NTDB id 1402 DSB67 RS12670 WP 010643257.1       ILEPLIIVFLGVVVGGLVTAMYLPIFNLMSVLG..   407
NTDB id 1169 A1552VC RS11075 WP 000648511.1     ILEPLIIVFLGTVVGGLVVAMYLPIFNLMSVLG..   408
NTDB id 1112 NGFG RS09215 WP 003689811.1        MMEPIIIVILGLVIGTLLVAMYLPLFNLGNVVA..   410
NTDB id 1113 AAA85695.1 219..1451( )            MMEPIIILILGLVIGTLLVAMYLPLFNLGNVVA*.   410
NTDB id 1029598 AB5B06 RS10335 WP 416049737.1   LIEPLIIVILGVLIGGMVVAMYLPIFKLGQVV...   421
NTDB id 1252 GC085 RS07730 WP 011213805.1       LLEPIIMSILGILVGGLVVAMYLPIFKLGSAV...   406
NTDB id 1198 PSJM300 03950 AFN76868.1           LMEPMIMAVLGVLVGGLIIAMYLPIFQMGSVV...   405
NTDB id 1059 ABD1 RS01610 WP 000279215.1        MMEPLIMAILGVLVGGLVIAMYLPIFQMGSVV...   408
NTDB id 1016 ACIAD RS01680 WP 004920476.1       MMEPLIMAILGILVGGLVIAMYLPIFQMGSVV...   408
consensus                                       **!!*****!!***!*****!*!!*!******
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X non conserved

X similar

X $\geq$ 50% conserved