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logo
NTDB id 1029 TT RS02230 WP 011228203.1          ..............MPVYQYKARDRQGRL.VEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIPALER   60
NTDB id 1402 DSB67 RS12670 WP 010643257.1       .MKT......IAPQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.....ISH   62
NTDB id 1169 A1552VC RS11075 WP 000648511.1     MKAT......QTLPLKNYRWKGINSNGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.....LTH   63
NTDB id 1113 AAA85695.1 219..1451( )            .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KT....SSKR   65
NTDB id 1112 NGFG RS09215 WP 003689811.1        .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KT....SSKR   65
NTDB id 1252 GC085 RS07730 WP 011213805.1       .MDKN......SPPLLTFHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.....KNK   62
NTDB id 1198 PSJM300 03950 AFN76868.1           .MAQK......AIKNSVFTWEGLDRQGAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS......AGK   61
NTDB id 1016 ACIAD RS01680 WP 004920476.1       MAAKK......TQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEG....LLKK   64
NTDB id 313244 AhaeINNSZ174 RS01910 WP 005083853.1 MAAKK.....AQMMPTFAYEGVDRKGAK.IKGELPARNMALAKVTLRKQGVTIKNIREKRKNILEG....LMKK   64
NTDB id 1059 ABD1 RS01610 WP 000279215.1       MAVKK......AQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG....LFKK   64
consensus                                        ***        *  *  * ******* * * * *** * ******  !***** ** **** * *        ***
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logo
NTDB id 1029 TT RS02230 WP 011228203.1          GPGLKDLAIFSRQLATMLGAGLTLLQALAILERQTENRKFREILKQVRTDVEGGMAFSEALSKH.KIFSRLYVNL   134
NTDB id 1402 DSB67 RS12670 WP 010643257.1       RVKGKDITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDL   137
NTDB id 1169 A1552VC RS11075 WP 000648511.1     RVKSKDITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDL   138
NTDB id 1113 AAA85695.1 219..1451( )            KITQEDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNL   140
NTDB id 1112 NGFG RS09215 WP 003689811.1        KITQEDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNL   140
NTDB id 1252 GC085 RS07730 WP 011213805.1       KITQADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNL   137
NTDB id 1198 PSJM300 03950 AFN76868.1           KIKPMDIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNL   136
NTDB id 1016 ACIAD RS01680 WP 004920476.1       KVKPLDIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSL   139
NTDB id 313244 AhaeINNSZ174 RS01910 WP 005083853.1 KVTTLDITVFTRQLATMMKAGVPLVQGFEIVAEGLENPSMREVVLGLKGEVEGGNTFAGALRKYPQYFDNLFCSL   139
NTDB id 1059 ABD1 RS01610 WP 000279215.1       KVTTLDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSL   139
consensus                                       ***  !*****!!**!!***!****!******** *** ****** ** ****!***  **** * *!* ****!
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logo
NTDB id 1029 TT RS02230 WP 011228203.1          VRAGETSGGLDLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTDLGSELPLLT   209
NTDB id 1402 DSB67 RS12670 WP 010643257.1       IATGEQSGNLSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFT   212
NTDB id 1169 A1552VC RS11075 WP 000648511.1     VETGEMSGNLPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFT   213
NTDB id 1113 AAA85695.1 219..1451( )            VAAGETGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALT   215
NTDB id 1112 NGFG RS09215 WP 003689811.1        VAAGETGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLT   215
NTDB id 1252 GC085 RS07730 WP 011213805.1       VDAGEKSGSLDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMT   212
NTDB id 1198 PSJM300 03950 AFN76868.1           VDSGEQSGSLETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFT   211
NTDB id 1016 ACIAD RS01680 WP 004920476.1       IESGEQSGSLEIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFT   214
NTDB id 313244 AhaeINNSZ174 RS01910 WP 005083853.1 VESGEQSGALETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFSSFGADLPAFT   214
NTDB id 1059 ABD1 RS01610 WP 000279215.1       VESGEQSGALETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFT   214
consensus                                       ***!!**! !*******! **!!** ** !***!* !!**!***!***********! ! ***  *!**!!**!
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logo

NTDB id 1029 TT RS02230 WP 011228203.1          RFLIAVSDLLRAATLPLLLLAVALFFAYRW.YYGTPQGRRVIDRLKLRLPVFGNLNRKTAVARFSRTLALLLSSG   283
NTDB id 1402 DSB67 RS12670 WP 010643257.1       QMVLNLSAWTQNWGPFIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAG   287
NTDB id 1169 A1552VC RS11075 WP 000648511.1     QQVLKLSHWVQAYSLWAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAG   288
NTDB id 1113 AAA85695.1 219..1451( )            QTVMDMSDFFVSYGWMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAG   290
NTDB id 1112 NGFG RS09215 WP 003689811.1        QTVMDMSDFFVSYGWMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAG   290
NTDB id 1252 GC085 RS07730 WP 011213805.1       RAVITMSEFMQAYWYIIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAG   287
NTDB id 1198 PSJM300 03950 AFN76868.1           LMVIGLSEALQAWWYVVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAG   286
NTDB id 1016 ACIAD RS01680 WP 004920476.1       QLVVNMSNWMQDYWFILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAG   289
NTDB id 313244 AhaeINNSZ174 RS01910 WP 005083853.1 KMVVNMSVWMQEYWFILIIVVGAIIACFLEAKKRSKKFRDTLDKLALRLPIFGDLVYKAIIARYSRTLATTFAAG   289
NTDB id 1059 ABD1 RS01610 WP 000279215.1       QMVVNMSKWMQEYWFIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAG   289
consensus                                       **** *!**** ***************** ** ** ***  *****!**!**!***  !* *!***!!********!

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NTDB id 1029 TT RS02230 WP 011228203.1          VNIVEALDITKGTAGNSVVEEIVEAAKLKIQQGDPLNLTLAQHPFVFPPMVSSMVAIGEETGALDTMLSKVADFY   358
NTDB id 1402 DSB67 RS12670 WP 010643257.1       IPILTALKTTSKTSGNMHYQLAIEEVYRDTAAGMPMYIAMR.HCHVFPELVLQMVMIGEESGRLDDMLNKIAAIY   361
NTDB id 1169 A1552VC RS11075 WP 000648511.1     IPILASLKTTAKTSGNVHFETAINEVYRDTAAGMPMYIAMR.NTEAFPEMVLQMVMIGEESGQLDDMLNKVATIY   362
NTDB id 1113 AAA85695.1 219..1451( )            VPLVDVLDSTAGAAGNLIYEEATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFY   364
NTDB id 1112 NGFG RS09215 WP 003689811.1        VPLVDVLDSTAGAAGNLIYEEATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFY   364
NTDB id 1252 GC085 RS07730 WP 011213805.1       LPLVEALKSVAGATGNIIYAKATDKIREEVATGQQMFIAME.NTHLFPNMVIQMVAIGEESGALEKMLSKVADFY   361
NTDB id 1198 PSJM300 03950 AFN76868.1           VPLVDALDSVAGATGNVVFRSATNKIKSDVSSGMQLNFSMR.TTGTFPSMAVQMTAIGEESGALDEMLSKVATFY   360
NTDB id 1016 ACIAD RS01680 WP 004920476.1       VPLIDALASTAGATNNTVYEQAVLKIREDVSTGQQLNFAMR.VSNRFPTMAIQMVAIGEESGALDEMLDKVANYY   363
NTDB id 313244 AhaeINNSZ174 RS01910 WP 005083853.1 VPLIDALESTAGATNNVVYEEAVMKIREDVATGQQLQFAMR.VSNRFPSMAIQMVAIGEESGALDSMLDKVATHF   363
NTDB id 1059 ABD1 RS01610 WP 000279215.1       VPLIDALESTAGATNNVIYEKAVMKIREDVATGQQLQFAMR.ISNRFPSMAIQMVAIGEESGALDSMLDKVATYY   363
consensus                                       ******!********!**** ** *** ****!**** ***  * *!! ****!**!!!!*!*!**!! !*! **

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NTDB id 1029 TT RS02230 WP 011228203.1          EREVDEAVASLTAAIEPLMIIFLGVIVGMIVAGMFLPLFKIIGTLSVQ   406
NTDB id 1402 DSB67 RS12670 WP 010643257.1       EFEVDNTVDNLSKILEPLIIVFLGVVVGGLVTAMYLPIFNLMSVLG..   407
NTDB id 1169 A1552VC RS11075 WP 000648511.1     EFEVDNTVDNLGKILEPLIIVFLGTVVGGLVVAMYLPIFNLMSVLG..   408
NTDB id 1113 AAA85695.1 219..1451( )            EDEVDNAVGWLSAMMEPIIILILGLVIGTLLVAMYLPLFNLGNVVA*.   410
NTDB id 1112 NGFG RS09215 WP 003689811.1        EDEVDNAVGRLSAMMEPIIIVILGLVIGTLLVAMYLPLFNLGNVVA..   410
NTDB id 1252 GC085 RS07730 WP 011213805.1       EEEVNNAVDALSSLLEPIIMSILGILVGGLVVAMYLPIFKLGSAV...   406
NTDB id 1198 PSJM300 03950 AFN76868.1           EDEVDNMVDGLTALMEPMIMAVLGVLVGGLIIAMYLPIFQMGSVV...   405
NTDB id 1016 ACIAD RS01680 WP 004920476.1       ESEVDHAVDGLTSMMEPLIMAILGILVGGLVIAMYLPIFQMGSVV...   408
NTDB id 313244 AhaeINNSZ174 RS01910 WP 005083853.1 ENEVDNAVDGLTAMMEPLIMAILGVLVGGLVIAMYLPIFQMGSVV...   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1        ENEVDNAVDGLTSMMEPLIMAILGVLVGGLVIAMYLPIFQMGSVV...   408
consensus                                       ! !!***!**!****!!*****!!***!*****!*!!*!******
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X non conserved

X similar

X $\geq$ 50% conserved