```
logo
NTDB id 1029 TT RS02230 WP 011228203.1      ..............MPVYQYKARDRQGR.LVEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIPALERGPGLK   65
NTDB id 1402 DSB67 RS12670 WP 010643257.1   .MKT......IAPQLKNYRWKGINSSGK.KTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.....ISHRVKGK   67
NTDB id 1169 A1552VC RS11075 WP 000648511.1 MKAT......QTLPLKNYRWKGINSNGK.KVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.....LTHRVKSK   68
NTDB id 1112 NGFG RS09215 WP 003689811.1    .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....T....SSKRKITQE   70
NTDB id 1113 AAA85695.1 219..1451( )        .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....T....SSKRKITQE   70
NTDB id 1252 GC085 RS07730 WP 011213805.1   .MDK......NSPPLLTFHYQGINKAGQ.KMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR....K.NKKITQA   67
NTDB id 1016 ACIAD RS01680 WP 004920476.1   MAAK......KTQVMPVFAYEGVDRKGI.KLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEG....LLKKKVKPL   69
NTDB id 1059 ABD1 RS01610 WP 000279215.1    MAVK......KAQMMPTFAYEGVDRKGV.KIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG....LFKKKVTTL   69
NTDB id 215163 PspS19 RS23430 WP 159998015.1 .MAV......KAAKVSLYAWQGTDRTGR.KMSGESSAQTPALIKAQLRQRGIIPGKVRKKFAPLFSA......GQRVTAQ   66
NTDB id 1198 PSJM300 03950 AFN76868.1       .MAQ......KAIKNSVFTWEGLDRQGA.KIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFSA......GKKIKPM   66
consensus                                    ***        *  *  * ****** *  ** *** * * ****  !***** * ******  *           ****

logo
NTDB id 1029 TT RS02230 WP 011228203.1      DLAIFSRQLATMLGAGLTLLQALAILERQTENRKFREILKQVRTDVEGGMAFSEALSKH.KIFSRLYVNLVRAGETSGGL  144
NTDB id 1402 DSB67 RS12670 WP 010643257.1   DITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNL  147
NTDB id 1169 A1552VC RS11075 WP 000648511.1 DITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNL  148
NTDB id 1112 NGFG RS09215 WP 003689811.1    DITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL  150
NTDB id 1113 AAA85695.1 219..1451( )        DITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL  150
NTDB id 1252 GC085 RS07730 WP 011213805.1   DITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSL  147
NTDB id 1016 ACIAD RS01680 WP 004920476.1   DIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSL  149
NTDB id 1059 ABD1 RS01610 WP 000279215.1    DITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGAL  149
NTDB id 215163 PspS19 RS23430 WP 159998015.1 DIALFTRQMATMLKAGVPLLQAFDIIAEGFDNPRMRGLLEDLRQDVMAGSSLTTALRKKPQHFDELYCNLIDAGEQAGAL  146
NTDB id 1198 PSJM300 03950 AFN76868.1       DIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSL  146
consensus                                   !*****!!**!!***!****!******** *** ****** ** ****!**** **** * *!* ****!***!!**! !

logo
NTDB id 1029 TT RS02230 WP 011228203.1      DLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAATL  224
NTDB id 1402 DSB67 RS12670 WP 010643257.1   SQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWGP  227
NTDB id 1169 A1552VC RS11075 WP 000648511.1 PEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSL  228
NTDB id 1112 NGFG RS09215 WP 003689811.1    ESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYGW  230
NTDB id 1113 AAA85695.1 219..1451( )        ESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGW  230
NTDB id 1252 GC085 RS07730 WP 011213805.1   DIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWY  227
NTDB id 1016 ACIAD RS01680 WP 004920476.1   EIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYWF  229
NTDB id 1059 ABD1 RS01610 WP 000279215.1    ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWF  229
NTDB id 215163 PspS19 RS23430 WP 159998015.1 DTLLERVASYREKTQRLKARVRKAMTYPLAVLLVAVIVSAILLLKVVPQFEVMFQGFGAELPALTRGVIGLAEFLRHSGW  226
NTDB id 1198 PSJM300 03950 AFN76868.1       ETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWWY  226
consensus                                   *******!***!!** *******!**!!* !***!***********! ! ***  *!**!!**!* ** ****** * *
```

```
logo

NTDB id 1029 TT RS02230 WP 011228203.1          PLLLLAVALFFAYR.WYYGTPQGRRVIDRLKLRLPVFGNLNRKTAVARFSRTLALLLSSGVNIVEALDITKGTAGNSVVE   303
NTDB id 1402 DSB67 RS12670 WP 010643257.1       FIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHYQ   307
NTDB id 1169 A1552VC RS11075 WP 000648511.1     WAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNVHFE   308
NTDB id 1112 NGFG RS09215 WP 003689811.1        MVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYE   310
NTDB id 1113 AAA85695.1 219..1451( )            MVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYE   310
NTDB id 1252 GC085 RS07730 WP 011213805.1       IIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYA   307
NTDB id 1016 ACIAD RS01680 WP 004920476.1       ILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVYE   309
NTDB id 1059 ABD1 RS01610 WP 000279215.1        IMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYE   309
NTDB id 215163 PspS19 RS23430 WP 159998015.1   LLLGGLLAAALGVHQTQRRSPRFRDWLQTRWLDLPVVGPLLRKSAVARYARTLSTTFAAGVPLLEALNSVAGATGNRVFK   306
NTDB id 1198 PSJM300 03950 AFN76868.1           VVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFR   306
consensus                                       *************   * ** ***  *****!**!**!***  !* *!***!!********!******!********!****

logo

NTDB id 1029 TT RS02230 WP 011228203.1          EIVEAAKLKIQQGDPLNLTLAQHPFVFPPMVSSMVAIGEETGALDTMLSKVADFYEREVDEAVASLTAAIEPLMIIFLGV   383
NTDB id 1402 DSB67 RS12670 WP 010643257.1       LAIEEVYRDTAAGMPMYIAM.RHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGV   386
NTDB id 1169 A1552VC RS11075 WP 000648511.1     TAINEVYRDTAAGMPMYIAM.RNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLGT   387
NTDB id 1112 NGFG RS09215 WP 003689811.1        EATREIRTRVIQGLSMTSGM.RATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGL   389
NTDB id 1113 AAA85695.1 219..1451( )            EATREIRTRVIQGLSMTSGM.RATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGL   389
NTDB id 1252 GC085 RS07730 WP 011213805.1       KATDKIREEVATGQQMFIAM.ENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGI   386
NTDB id 1016 ACIAD RS01680 WP 004920476.1       QAVLKIREDVSTGQQLNFAM.RVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGI   388
NTDB id 1059 ABD1 RS01610 WP 000279215.1        KAVMKIREDVATGQQLQFAM.RISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGV   388
NTDB id 215163 PspS19 RS23430 WP 159998015.1   QAVLAIREDVCSGMQLHVAM.RNSGVFPNLAIQMTAIGEESGALDDMLGNVASYYEDEVETLVDHLTSLLEPLIMAVLGV   385
NTDB id 1198 PSJM300 03950 AFN76868.1           SATNKIKSDVSSGMQLNFSM.RTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGV   385
consensus                                        **   ** ** *!*** *** * * *!! ****!**!!!!*!*!**!! **! *!!*!!***!* !* **!!*****!!*

   <0

logo

NTDB id 1029 TT RS02230 WP 011228203.1          IVGMIVAGMFLPLFKIIGTLSVQ   406
NTDB id 1402 DSB67 RS12670 WP 010643257.1       VVGGLVTAMYLPIFNLMSVLG..   407
NTDB id 1169 A1552VC RS11075 WP 000648511.1     VVGGLVVAMYLPIFNLMSVLG..   408
NTDB id 1112 NGFG RS09215 WP 003689811.1        VIGTLLVAMYLPLFNLGNVVA..   410
NTDB id 1113 AAA85695.1 219..1451( )            VIGTLLVAMYLPLFNLGNVVA*.   410
NTDB id 1252 GC085 RS07730 WP 011213805.1       LVGGLVVAMYLPIFKLGSAV...   406
NTDB id 1016 ACIAD RS01680 WP 004920476.1       LVGGLVIAMYLPIFQMGSVV...   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1        LVGGLVIAMYLPIFQMGSVV...   408
NTDB id 215163 PspS19 RS23430 WP 159998015.1   IVGGLVIAMYLPIFQLGTAL...   405
NTDB id 1198 PSJM300 03950 AFN76868.1           LVGGLIIAMYLPIFQMGSVV...   405
consensus                                       **!*****!*!!*!******
```

X non conserved

X similar

X ≥ 50% conserved