```
logo
NTDB id 1029 TT RS02230 WP 011228203.1          ..............MPVYQYKARDRQGR.LVEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIPALERGPGLKD   66
NTDB id 1169 A1552VC RS11075 WP 000648511.1     .....MKATQTLPLKNYRWKGINSNGK.KVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.....LTHRVKSKD   69
NTDB id 1402 DSB67 RS12670 WP 010643257.1       ......MKTIAPQLKNYRWKGINSSGK.KTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.....ISHRVKGKD   68
NTDB id 1112 NGFG RS09215 WP 003689811.1        MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKTS.........SKRKITQED   71
NTDB id 1113 AAA85695.1 219..1451( )            MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKTS.........SKRKITQED   71
NTDB id 1252 GC085 RS07730 WP 011213805.1       ......MDKNSPPLLTFHYQGINKAGQ.KMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.....KNKKITQAD   68
NTDB id 1130254 DENOEST RS01415 WP 145771420.1 ...MATAKDDKKKEISFVWEGKDKAGR.IMRGEMRAGGEAVVQATLRRQGILVSKIKKQASG.........GGGKVTAKD   67
NTDB id 1198 PSJM300 03950 AFN76868.1           ......MAQKAIKNSVFTWEGLDRQGA.KIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS......AGKKIKPMD   67
NTDB id 1016 ACIAD RS01680 WP 004920476.1       .....MAAKKTQVMPVFAYEGVDRKGI.KLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGL....LKKKVKPLD   70
NTDB id 1059 ABD1 RS01610 WP 000279215.1        .....MAVKKAQMMPTFAYEGVDRKGV.KIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGL....FKKKVTTLD   70
consensus                                                 *  *  * ******* *  ** *** * ******  !***** * **** * **          ****  !

logo
NTDB id 1029 TT RS02230 WP 011228203.1          LAIFSRQLATMLGAGLTLLQALAILERQTENRKFREILKQVRTDVEGGMAFSEALSKHK.IFSRLYVNLVRAGETSGGLD   145
NTDB id 1169 A1552VC RS11075 WP 000648511.1     ITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNLP   149
NTDB id 1402 DSB67 RS12670 WP 010643257.1       ITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNLS   148
NTDB id 1112 NGFG RS09215 WP 003689811.1        ITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLE   151
NTDB id 1113 AAA85695.1 219..1451( )            ITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLE   151
NTDB id 1252 GC085 RS07730 WP 011213805.1       ITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSLD   148
NTDB id 1130254 DENOEST RS01415 WP 145771420.1 ITLFTRQLATMMKAGVPLLQSFDIVGKGSSNPAVAKLLFDIKTEVETGSSLNQAFRKYPMYFDLLFCNLVEAGEQAGILE   147
NTDB id 1198 PSJM300 03950 AFN76868.1           IALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLE   147
NTDB id 1016 ACIAD RS01680 WP 004920476.1       IAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLE   150
NTDB id 1059 ABD1 RS01610 WP 000279215.1        ITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALE   150
consensus                                       *****!!**!!***!****!****** *  ** ****** ** ****!**** **** * *!* ****!***!!**! !*

logo
NTDB id 1029 TT RS02230 WP 011228203.1          LILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAATLP   225
NTDB id 1169 A1552VC RS11075 WP 000648511.1     EVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSLW   229
NTDB id 1402 DSB67 RS12670 WP 010643257.1       QVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWGPF   228
NTDB id 1112 NGFG RS09215 WP 003689811.1        SLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYGWM   231
NTDB id 1113 AAA85695.1 219..1451( )            SLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGWM   231
NTDB id 1252 GC085 RS07730 WP 011213805.1       IMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWYI   228
NTDB id 1130254 DENOEST RS01415 WP 145771420.1 MLLDRLASYKEKILAIQSKIKSALFYPIAVVMVAFVVTAILMIFVVPQFKSVFSGFGADLPAPTLVVVGISDFFVKYWYV   227
NTDB id 1198 PSJM300 03950 AFN76868.1           TLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWWYV   227
NTDB id 1016 ACIAD RS01680 WP 004920476.1       IMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYWFI   230
NTDB id 1059 ABD1 RS01610 WP 000279215.1        TMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWFI   230
consensus                                        *****!***!!** ** !***!* !!* !***!********* **! ! ***  *!**!!**!**** *!**** ****
```

```
logo
NTDB id 1029 TT RS02230 WP 011228203.1          LLLLAVALFFAYRW.YYGTPQGRRVIDRLKLRLPVFGNLNRKTAVARFSRTLALLLSSGVNIVEALDITKGTAGNSVVEE   304
NTDB id 1169 A1552VC RS11075 WP 000648511.1     AFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNVHFET   309
NTDB id 1402 DSB67 RS12670 WP 010643257.1       IGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHYQL   308
NTDB id 1112 NGFG RS09215 WP 003689811.1        VLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEE   311
NTDB id 1113 AAA85695.1 219..1451( )            VLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEE   311
NTDB id 1252 GC085 RS07730 WP 011213805.1       IFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAK   308
NTDB id 1130254 DENOEST RS01415 WP 145771420.1 IFGGLGGGVYGFLNLWKRSRKVQIFMDRLSLKLPVFGDLLTKATIARWARTLSTMFAAGVPLVEALDSVGGAAGNYVYAT   307
NTDB id 1198 PSJM300 03950 AFN76868.1           VLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFRS   307
NTDB id 1016 ACIAD RS01680 WP 004920476.1       LILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQ   310
NTDB id 1059 ABD1 RS01610 WP 000279215.1        MIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYEK   310
consensus                                       ************ ** ** ***  *****!**!**!***  !***!***!!********!******!********!****
```

```
logo
NTDB id 1029 TT RS02230 WP 011228203.1          IVEAAKLKIQQGDPLNLTLAQHPFVFPPMVSSMVAIGEETGALDTMLSKVADFYEREVDEAVASLTAAIEPLMIIFLGVI   384
NTDB id 1169 A1552VC RS11075 WP 000648511.1     AINEVYRDTAAGMPMYIAM.RNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLGTV   388
NTDB id 1402 DSB67 RS12670 WP 010643257.1       AIEEVYRDTAAGMPMYIAM.RHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGVV   387
NTDB id 1112 NGFG RS09215 WP 003689811.1        ATREIRTRVIQGLSMTSGM.RATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGLV   390
NTDB id 1113 AAA85695.1 219..1451( )            ATREIRTRVIQGLSMTSGM.RATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGLV   390
NTDB id 1252 GC085 RS07730 WP 011213805.1       ATDKIREEVATGQQMFIAM.ENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGIL   387
NTDB id 1130254 DENOEST RS01415 WP 145771420.1 ATKQIQAEVSTGNSLTVAM.QNANVFPSMVLQMVAIGEESGQLDSMLSKVADFREAEVDDAVEALSSLMEPIIMAFLGVV   386
NTDB id 1198 PSJM300 03950 AFN76868.1           ATNKIKSDVSSGMQLNFSM.RTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGVL   386
NTDB id 1016 ACIAD RS01680 WP 004920476.1       AVLKIREDVSTGQQLNFAM.RVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGIL   389
NTDB id 1059 ABD1 RS01610 WP 000279215.1        AVMKIREDVATGQQLQFAM.RISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGVL   389
consensus                                       **  ** ** *!* * *** * * *!! ****!**!!!!*!*!**!! !*!***! !!***!**!* **!!*****!!**
```

```
<0
logo
NTDB id 1029 TT RS02230 WP 011228203.1          VGMIVAGMFLPLFKIIGTLSVQ   406
NTDB id 1169 A1552VC RS11075 WP 000648511.1     VGGLVVAMYLPIFNLMSVLG..   408
NTDB id 1402 DSB67 RS12670 WP 010643257.1       VGGLVTAMYLPIFNLMSVLG..   407
NTDB id 1112 NGFG RS09215 WP 003689811.1        IGTLLVAMYLPLFNLGNVVA..   410
NTDB id 1113 AAA85695.1 219..1451( )            IGTLLVAMYLPLFNLGNVVA*.   410
NTDB id 1252 GC085 RS07730 WP 011213805.1       VGGLVVAMYLPIFKLGSAV...   406
NTDB id 1130254 DENOEST RS01415 WP 145771420.1 VGGMVVAMYLPIFKLGAVV...   405
NTDB id 1198 PSJM300 03950 AFN76868.1           VGGLIIAMYLPIFQMGSVV...   405
NTDB id 1016 ACIAD RS01680 WP 004920476.1       VGGLVIAMYLPIFQMGSVV...   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1        VGGLVIAMYLPIFQMGSVV...   408
consensus                                       *!*****!*!!*!******
```

X non conserved
X similar
X ≥ 50% conserved