```
logo
NTDB id 1402 DSB67 RS12670 WP 010643257.1       .....................MKTIAPQLKNYRWKGINSSG.KKTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFI   57
NTDB id 1169 A1552VC RS11075 WP 000648511.1     .....................MKATQTLPLKNYRWKGINSNG.KKVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLL   58
NTDB id 1112 NGFG RS09215 WP 003689811.1        ..............MAKNGGFS..LFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKT...   61
NTDB id 1113 AAA85695.1 219..1451( )            ..............MAKNGGFS..LFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKT...   61
NTDB id 1021101 ABZP20 RS13995 WP 004633031.1  MATRAPAANRAAAAPNRTTGKTAKTKAPTQYIFEWEGKDRKG.KIFKGEMRAESITEVNAILRKQGLSITKSKRRRA...   76
NTDB id 1252 GC085 RS07730 WP 011213805.1       .....................MDKNSPPLLTFHYQGINKAG.QKMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLF   57
NTDB id 1198 PSJM300 03950 AFN76868.1           .....................MAQKAIKNSVFTWEGLDRQG.AKIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLF   57
NTDB id 1016 ACIAD RS01680 WP 004920476.1       .....................MAAKKTQVMPVFAYEGVDRKG.IKLKGELPARNMALAKVTLRKQGITTIRTIREKRKNIF   58
NTDB id 1059 ABD1 RS01610 WP 000279215.1        .....................MAVKKAQMMPTFAYEGVDRKG.VKIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNIL   58
consensus                                                             *  *  * **!* * * *** !** * *  ***  !***** * ******  *

logo
NTDB id 1402 DSB67 RS12670 WP 010643257.1       TK.ISHRVKGKDITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTD   136
NTDB id 1169 A1552VC RS11075 WP 000648511.1     AR.LTHRVKSKDITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVD   137
NTDB id 1112 NGFG RS09215 WP 003689811.1        ..SSKRKITQEDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCN   139
NTDB id 1113 AAA85695.1 219..1451( )            ..SSKRKITQEDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCN   139
NTDB id 1021101 ABZP20 RS13995 WP 004633031.1  ..ARGKKITPKDIAYFTRQLSTMLKAGVPLLQSIDIIAKGHANPNFTQLLTEIRVDIESGSSMAQAFRRHPKYFDTLYCN   154
NTDB id 1252 GC085 RS07730 WP 011213805.1       DR.KNKKITQADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCN   136
NTDB id 1198 PSJM300 03950 AFN76868.1           S..AGKKIKPMDIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCN   135
NTDB id 1016 ACIAD RS01680 WP 004920476.1       EGLLKKKVKPLDIAIFTRQLATMMKAGVPLVQAFEIVAEGLKNPEVEGGNTFAGALRKYPQYFDNLFCS   138
NTDB id 1059 ABD1 RS01610 WP 000279215.1        EGLFKKKVTTLDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCS   138
consensus                                        ****  !!****!!**!!***!*!**!********* ** ****** ** ****!**** **** * *!* ****

logo
NTDB id 1402 DSB67 RS12670 WP 010643257.1       LIATGEQSGNLSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVL   216
NTDB id 1169 A1552VC RS11075 WP 000648511.1     LVETGEMSGNLPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVL   217
NTDB id 1112 NGFG RS09215 WP 003689811.1        LVAAGETGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVM   219
NTDB id 1113 AAA85695.1 219..1451( )            LVAAGETGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVM   219
NTDB id 1021101 ABZP20 RS13995 WP 004633031.1  LIDAGEQGGILDALLERLSLYMEKSLALKAQIKSALIYPISVLTVAFLVTVVLMIFVVPSFKGVFSGFGADLPAPTLFVI   234
NTDB id 1252 GC085 RS07730 WP 011213805.1       LVDAGEKSGSLDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVI   216
NTDB id 1198 PSJM300 03950 AFN76868.1           LVDSGEQSGSLETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVI   215
NTDB id 1016 ACIAD RS01680 WP 004920476.1       LIESGEQSGSLEIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVV   218
NTDB id 1059 ABD1 RS01610 WP 000279215.1        LVESGEQSGALETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVV   218
consensus                                       !***!!**! !* *******!*!!** ** ****!* !!**!**!!**** **** !*! ! ***  *!!*!!**!* !*

logo
NTDB id 1402 DSB67 RS12670 WP 010643257.1       NLSAWTQNWGPFIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKT   296
NTDB id 1169 A1552VC RS11075 WP 000648511.1     KLSHWVQAYSLWAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFSAGIPILASLKI   297
NTDB id 1112 NGFG RS09215 WP 003689811.1        DMSDFFVSYGWMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDS   299
NTDB id 1113 AAA85695.1 219..1451( )            DMSDFFVSYGWMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDS   299
NTDB id 1021101 ABZP20 RS13995 WP 004633031.1  AISDFFVKWWIPIVLGPIAGIALFSRAFKRSENVQRSTHRFILKIPIFGDIIRKATIARWTRTLATMFAAGTPLVESMES   314
NTDB id 1252 GC085 RS07730 WP 011213805.1       TMSEFMQAYWYIIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKS   296
NTDB id 1198 PSJM300 03950 AFN76868.1           GLSEALQAWWYVVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDS   295
NTDB id 1016 ACIAD RS01680 WP 004920476.1       NMSNWMQDYWFILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALAS   298
NTDB id 1059 ABD1 RS01610 WP 000279215.1        NMSKWMQEYWFIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALES   298
consensus                                        *!**** ***************  ** *! ***  ****!**!**!*** !**!***!!****!*!!*!*******
```

```
logo
NTDB id 1402 DSB67 RS12670 WP 010643257.1        TSKTSGNMHYQLAIEEVYRDTAAGMPMYIAMRHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKIL   376
NTDB id 1169 A1552VC RS11075 WP 000648511.1      TAKTSGNVHFETAINEVYRDTAAGMPMYIAMRNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKIL   377
NTDB id 1112 NGFG RS09215 WP 003689811.1         TAGAAGNLIYEEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMM   379
NTDB id 1113 AAA85695.1 219..1451( )             TAGAAGNLIYEEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMM   379
NTDB id 1021101 ABZP20 RS13995 WP 004633031.1   VAGAAGNWIYHDATLEVQQAVRIGTSLTNAMQATHVFDNMVLQMTQIGEESGALDNMLLKVAEFYEREVDDAVANISTLI   394
NTDB id 1252 GC085 RS07730 WP 011213805.1        VAGATGNIIYAKATDKIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLL   376
NTDB id 1198 PSJM300 03950 AFN76868.1            VAGATGNVVFRSATNKIKSDVSSGMQLNFSMRTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALM   375
NTDB id 1016 ACIAD RS01680 WP 004920476.1        TAGATNNTVYEQAVLKIREDVSTGQQLNFAMRVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMM   378
NTDB id 1059 ABD1 RS01610 WP 000279215.1         TAGATNNVIYEKAVMKIREDVATGQQLQFAMRISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMM   378
consensus                                        ******!**** !* *** **  !* *  *!* * *!* ***!!* !!!!!!*!**!! !*! *!! !!***!* ** **
```

```
   <0
logo
NTDB id 1402 DSB67 RS12670 WP 010643257.1        EPLIIVFLGVVVGGLVTAMYLPIFNLMSVLG.   407
NTDB id 1169 A1552VC RS11075 WP 000648511.1      EPLIIVFLGTVVGGLVVAMYLPIFNLMSVLG.   408
NTDB id 1112 NGFG RS09215 WP 003689811.1         EPIIIVILGLVIGTLLVAMYLPLFNLGNVVA.   410
NTDB id 1113 AAA85695.1 219..1451( )             EPIIILILGLVIGTLLVAMYLPLFNLGNVVA*   410
NTDB id 1021101 ABZP20 RS13995 WP 004633031.1   EPIIIVFLGVLIGGMVVAMYLPIFKLGTVV..   424
NTDB id 1252 GC085 RS07730 WP 011213805.1        EPIIMSILGILVGGLVVAMYLPIFKLGSAV..   406
NTDB id 1198 PSJM300 03950 AFN76868.1            EPMIMAVLGVLVGGLIIAMYLPIFQMGSVV..   405
NTDB id 1016 ACIAD RS01680 WP 004920476.1        EPLIMAILGILVGGLVIAMYLPIFQMGSVV..   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1         EPLIMAILGVLVGGLVIAMYLPIFQMGSVV..   408
consensus                                        !!*!***!!***!****!!!!!*!******
```

X non conserved
X similar
X ≥ 50% conserved