```
logo
NTDB id 1169 A1552VC RS11075 WP 000648511.1  ............MKATQTLPLKNYRWKGINSNGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.LTHRVKS   67
NTDB id 1402 DSB67 RS12670 WP 010643257.1    ............MKTIAPQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.ISHRVKG   66
NTDB id 1112 NGFG RS09215 WP 003689811.1     ......MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TSSKRKITQ   69
NTDB id 1113 AAA85695.1 219..1451( )         ......MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TSSKRKITQ   69
NTDB id 1198 PSJM300 03950 AFN76868.1        ............MAQKAIKNSVFTWEGLDRQGAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKKIKP   65
NTDB id 1016 ACIAD RS01680 WP 004920476.1    ............MAAKKTQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKVKP   68
NTDB id 1059 ABD1 RS01610 WP 000279215.1     ............MAVKKAQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVTT   68
NTDB id 307028 LA08 RS08145 WP 011408067.1   MSVARSAIKKQPVDRNTSMLQTFIWEGADKRGVK.MKGEQTARNANMLRAELRRQGIVPSMVKQKPKPLFGG.AGKKITP   78
NTDB id 1252 GC085 RS07730 WP 011213805.1    ............MDKNSPPLLTFHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.KNKKITQ   66
consensus                                                 *  *  * **!* * * ! * !** * *  ***  !*****    *****  *      ****

logo
NTDB id 1169 A1552VC RS11075 WP 000648511.1  KDITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGN  147
NTDB id 1402 DSB67 RS12670 WP 010643257.1    KDITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGN  146
NTDB id 1112 NGFG RS09215 WP 003689811.1     EDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGV  149
NTDB id 1113 AAA85695.1 219..1451( )         EDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGV  149
NTDB id 1198 PSJM300 03950 AFN76868.1        MDIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGS  145
NTDB id 1016 ACIAD RS01680 WP 004920476.1    LDIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGS  148
NTDB id 1059 ABD1 RS01610 WP 000279215.1     LDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGA  148
NTDB id 307028 LA08 RS08145 WP 011408067.1   KEIAFFSRQMATMMKSGVPIVSSLEIIGEGHKNPRMKKMVGQIRTDIEGGSSLYESISKHPVQFDELYRNLVRAGEGAGV  158
NTDB id 1252 GC085 RS07730 WP 011213805.1    ADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGS  146
consensus                                     *!****!!**!!***!*!************ ** ****** ** ****!***  **** * *!* ****!***!! *!

logo
NTDB id 1169 A1552VC RS11075 WP 000648511.1  LPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYS  227
NTDB id 1402 DSB67 RS12670 WP 010643257.1    LSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWG  226
NTDB id 1112 NGFG RS09215 WP 003689811.1     LESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYG  229
NTDB id 1113 AAA85695.1 219..1451( )         LESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYG  229
NTDB id 1198 PSJM300 03950 AFN76868.1        LETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWW  225
NTDB id 1016 ACIAD RS01680 WP 004920476.1    LEIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYW  228
NTDB id 1059 ABD1 RS01610 WP 000279215.1     LETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYW  228
NTDB id 307028 LA08 RS08145 WP 011408067.1   LETVLETVATYKENIEALKGKIKKALFYPAMVVAVAIIVSAILLIFVVPQFEEVFKSFGAELPAFTQLLVNASRFMVSYW  238
NTDB id 1252 GC085 RS07730 WP 011213805.1    LDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYW  226
consensus                                    !*******!*!*!*** ** !***!* !!  !**!!**** **** !*! ! ***  *!!*!!**!**** *! *** **

logo
NTDB id 1169 A1552VC RS11075 WP 000648511.1  LWAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILLASLKTTAKTSGNVHF  307
NTDB id 1402 DSB67 RS12670 WP 010643257.1    PFIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHY  306
NTDB id 1112 NGFG RS09215 WP 003689811.1     WMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIY  309
NTDB id 1113 AAA85695.1 219..1451( )         WMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIY  309
NTDB id 1198 PSJM300 03950 AFN76868.1        YVVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVF  305
NTDB id 1016 ACIAD RS01680 WP 004920476.1    FILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVY  308
NTDB id 1059 ABD1 RS01610 WP 000279215.1     FIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIY  308
NTDB id 307028 LA08 RS08145 WP 011408067.1   WLMLIVTVGSVVGFIFAYKRSPRMQHGLDRLILKVPVIGQIMHNSAIARFARTTAVTFKAGVPLVEALGIVAGATGNKLY  318
NTDB id 1252 GC085 RS07730 WP 011213805.1    YIIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIY  306
consensus                                    *************** ** *! ***  *****!**!**!*** ** *!***!!****!*!!*!****! *******!***
```

```
logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1   ETAINEVYRDTAAGMPMYIAMRNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLGT   387
NTDB id 1402 DSB67 RS12670 WP 010643257.1     QLAIEEVYRDTAAGMPMYIAMRHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGV   386
NTDB id 1112 NGFG RS09215 WP 003689811.1      EEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGL   389
NTDB id 1113 AAA85695.1 219..1451( )          EEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGL   389
NTDB id 1198 PSJM300 03950 AFN76868.1         RSATNKIKSDVSSGMQLNFSMRTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGV   385
NTDB id 1016 ACIAD RS01680 WP 004920476.1     EQAVLKIREDVSTGQQLNFAMRVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGI   388
NTDB id 1059 ABD1 RS01610 WP 000279215.1      EKAVMKIREDVATGQQLQFAMRISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGV   388
NTDB id 307028 LA08 RS08145 WP 011408067.1    EEAVFRMRDDVSVGYPVNMAMKQVNLFPHMVIQMTAIGEEAGALDAMLFKVAEYFEEEVNNAVDALSSLLEPLIMVFIGT   398
NTDB id 1252 GC085 RS07730 WP 011213805.1     AKATDKIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGI   386
consensus                                     * !* *** **  !* *  *!* * *!! ***!!**!!!!*!*!**!! !*! **!*!!***!**!* **!!*!****!*

   <0

logo

NTDB id 1169 A1552VC RS11075 WP 000648511.1   VVGGLVVAMYLPIFNLMSVLG.   408
NTDB id 1402 DSB67 RS12670 WP 010643257.1     VVGGLVTAMYLPIFNLMSVLG.   407
NTDB id 1112 NGFG RS09215 WP 003689811.1      VIGTLLVAMYLPLFNLGNVVA.   410
NTDB id 1113 AAA85695.1 219..1451( )          VIGTLLVAMYLPLFNLGNVVA*   410
NTDB id 1198 PSJM300 03950 AFN76868.1         LVGGLIIAMYLPIFQMGSVV..   405
NTDB id 1016 ACIAD RS01680 WP 004920476.1     LVGGLVIAMYLPIFQMGSVV..   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1      LVGGLVIAMYLPIFQMGSVV..   408
NTDB id 307028 LA08 RS08145 WP 011408067.1    IVGGMVIGMYLPIFKLGAVVG.   419
NTDB id 1252 GC085 RS07730 WP 011213805.1     LVGGLVVAMYLPIFKLGSAV..   406
consensus                                     **!*****!!!!*!******
```

X non conserved

X similar

X ≥ 50% conserved