logo

```
NTDB id 1402 DSB67 RS12670 WP 010643257.1   ..MKT......IAPQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.ISHRVKGKDIT   70
NTDB id 1166581 AB5Y62 RS02690 WP 256799836.1 MSSKS......KQSQLKNYHWKGINSSGKK.VSGQSLALTELEVREKLKEQHIQIKKIKKSISAITR.LTHRVKAKDIT   72
NTDB id 1169 A1552VC RS11075 WP 000648511.1 .MKAT......QTLPLKNYRWKGINSNGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.LTHRVKSKDIT   71
NTDB id 1112 NGFG RS09215 WP 003689811.1    ..MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KTSSKRKITQEDIT   73
NTDB id 1113 AAA85695.1 219..1451( )        ..MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KTSSKRKITQEDIT   73
NTDB id 1252 GCO85 RS07730 WP 011213805.1   ..MDKN......SPPLLTFHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.KNKKITQADIT   70
NTDB id 1198 PSJM300 03950 AFN76868.1       ..MAQK......AIKNSVFTWEGLDRQGAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKKIKPMDIA   69
NTDB id 1016 ACIAD RS01680 WP 004920476.1   .MAAKK......TQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKVKPLDIA   72
NTDB id 1059 ABD1 RS01610 WP 000279215.1    .MAVKK......AQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVTTLDIT   72
consensus                                     ***         *  ** * **!* * * ! * !** * ** *** *!***** *******    *       ****  !!*
```

logo

```
NTDB id 1402 DSB67 RS12670 WP 010643257.1   IFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNLSQV   150
NTDB id 1166581 AB5Y62 RS02690 WP 256799836.1 ILTRQLATMLATGVPIVQAIKLVSDNHRKAEMKSILSHICKGVEAGTPISKAMRTASRHFDDLYTDLVATGELSGNLAQV   152
NTDB id 1169 A1552VC RS11075 WP 000648511.1 ILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNLPEV   151
NTDB id 1112 NGFG RS09215 WP 003689811.1    VFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESL   153
NTDB id 1113 AAA85695.1 219..1451( )        VFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESL   153
NTDB id 1252 GCO85 RS07730 WP 011213805.1   VFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSLDIM   150
NTDB id 1198 PSJM300 03950 AFN76868.1       LFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLETL   149
NTDB id 1016 ACIAD RS01680 WP 004920476.1   IFTRQLATMMKAGVPLVQAFEIVAEGLENPAMREVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLEIM   152
NTDB id 1059 ABD1 RS01610 WP 000279215.1    IFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALETM   152
consensus                                   ***!!**!!* *!*!**!********** ** ****** **   ***!********** * *!* *** !***!! *! !* *
```

logo

```
NTDB id 1402 DSB67 RS12670 WP 010643257.1   FERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWGPFIG   230
NTDB id 1166581 AB5Y62 RS02690 WP 256799836.1 FERLATYREKSEQLKSKVIKALIYPAMVVAVALTVSYLMLTMVIPEFESMFSGFGADLPWFTQQVLYLSHWMQAYSFYTA   232
NTDB id 1169 A1552VC RS11075 WP 000648511.1 FERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSLWAF   231
NTDB id 1112 NGFG RS09215 WP 003689811.1    LDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYGWMVL   233
NTDB id 1113 AAA85695.1 219..1451( )        LDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGWMVL   233
NTDB id 1252 GCO85 RS07730 WP 011213805.1   LDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWYIIF   230
NTDB id 1198 PSJM300 03950 AFN76868.1       LDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWWYVVL   229
NTDB id 1016 ACIAD RS01680 WP 004920476.1   LDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYWFILI   232
NTDB id 1059 ABD1 RS01610 WP 000279215.1    LDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWFIMI   232
consensus                                   ****!*!*!!** ** !***!* !!  !**!!* ******* !*! ! ***  *!!*!!**!* !* *! *** * ****
```

logo

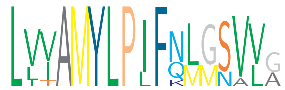
```
NTDB id 1402 DSB67 RS12670 WP 010643257.1   LSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHYQLAI   310
NTDB id 1166581 AB5Y62 RS02690 WP 256799836.1 IGIGLLILSFQQLRQRSYSIRLSTSRLGLRFPILGAVITKASIAKFSRTLSTSFSSGIPILTSLKTTAKTAGNLHYESAI   312
NTDB id 1169 A1552VC RS11075 WP 000648511.1 IAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNVHFETAI   311
NTDB id 1112 NGFG RS09215 WP 003689811.1    IALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEAT   313
NTDB id 1113 AAA85695.1 219..1451( )        IALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEAT   313
NTDB id 1252 GCO85 RS07730 WP 011213805.1   GALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAKAT   310
NTDB id 1198 PSJM300 03950 AFN76868.1       AGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFRSAT   309
NTDB id 1016 ACIAD RS01680 WP 004920476.1   LVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQAV   312
NTDB id 1059 ABD1 RS01610 WP 000279215.1    IAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYEKAV   312
consensus                                   **********  ** *! ***  *****!**!**!*** !***!***!!****!**!*!****! *******!**** !*
```

logo

```
NTDB id 1402 DSB67 RS12670 WP 010643257.1      EEVYRDTAAGMPMYIAMRHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGVVVGG   390
NTDB id 1166581 AB5Y62 RS02690 WP 256799836.1  IEVHRETASGMPMYIAMRNTNAFPEMVLQMVMIGEESGNLDDMLNKVASIYEFEVDNTVDNLGKILEPLIIVFLGTVVGG   392
NTDB id 1169 A1552VC RS11075 WP 000648511.1    NEVYRDTAAGMPMYIAMRNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLGTVVGG   391
NTDB id 1112 NGFG RS09215 WP 003689811.1       REIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGLVIGT   393
NTDB id 1113 AAA85695.1 219..1451( )           REIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGLVIGT   393
NTDB id 1252 GC085 RS07730 WP 011213805.1      DKIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGILVGG   390
NTDB id 1198 PSJM300 03950 AFN76868.1         NKIKSDVSSGMQLNFSMRTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGVLVGG   389
NTDB id 1016 ACIAD RS01680 WP 004920476.1      LKIREDVSTGQQLNFAMRVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGILVGG   392
NTDB id 1059 ABD1 RS01610 WP 000279215.1       MKIREDVATGQQLQFAMRISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGVLVGG   392
consensus                                       *** ****!* *  *!* *  !! ***!!* !!!!!! !**!!*!*! *!! !!***!* !* **!!*!***!!***!*
```

<0

logo



```
NTDB id 1402 DSB67 RS12670 WP 010643257.1      LVTAMYLPIFNLMSVLG.    407
NTDB id 1166581 AB5Y62 RS02690 WP 256799836.1  LVVAMYLPIFNLMSVLG.    409
NTDB id 1169 A1552VC RS11075 WP 000648511.1    LVVAMYLPIFNLMSVLG.    408
NTDB id 1112 NGFG RS09215 WP 003689811.1       LLVAMYLPLFNLGNVVA.    410
NTDB id 1113 AAA85695.1 219..1451( )           LLVAMYLPLFNLGNVVA*    410
NTDB id 1252 GC085 RS07730 WP 011213805.1      LVVAMYLPIFKLGSAV..    406
NTDB id 1198 PSJM300 03950 AFN76868.1         LIIAMYLPIFQMGSVV..    405
NTDB id 1016 ACIAD RS01680 WP 004920476.1      LVIAMYLPIFQMGSVV..    408
NTDB id 1059 ABD1 RS01610 WP 000279215.1       LVIAMYLPIFQMGSVV..    408
consensus                                      !**!!!!!*!*******
```

X non conserved

X similar

X ≥ 50% conserved