```
logo
NTDB id 1029 TT RS02230 WP 011228203.1        ...................MPVYQYKARDRQGRL.VEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIPALERG   61
NTDB id 1169 A1552VC RS11075 WP 000648511.1   ..........MKATQTLPLKNYRWKGINSNGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.....LTHR   64
NTDB id 1402 DSB67 RS12670 WP 010643257.1     ..........MKTIAPQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.....ISHR   63
NTDB id 1112 NGFG RS09215 WP 003689811.1      .....MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KTS....SKRK   66
NTDB id 1113 AAA85695.1 219..1451( )          .....MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KTS....SKRK   66
NTDB id 1134996 XTG RS15520 WP 115677263.1    MAAIRGTLKGKPSGTVNQLSTFVWEGADRRGVK.MKGEQSARNVNLLRAELRRQGITPSVVKPKPKPLFGE.....AGKK   74
NTDB id 1252 GC085 RS07730 WP 011213805.1     ..........MDKNSPPLLTFHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.....KNKK   63
NTDB id 1198 PSJM300 03950 AFN76868.1         ..........MAQKAIKNSVFTWEGLDRQGAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS......AGKK   62
NTDB id 1016 ACIAD RS01680 WP 004920476.1     ..........MAAKKTQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGL....LKKK   65
NTDB id 1059 ABD1 RS01610 WP 000279215.1      ..........MAVKKAQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGL....FKKK   65
consensus                                                  *  *  * ****** * * * *** * ** ***  !***** *  **** * *          **
```

```
logo
NTDB id 1029 TT RS02230 WP 011228203.1        PGLKDLAIFSRQLATMLGAGLTLLQALAILERQTENRKFREILKQVRTDVEGGMAFSEALSKHK.IFSRLYVNLVRAGET   140
NTDB id 1169 A1552VC RS11075 WP 000648511.1   VKSKDITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEM   144
NTDB id 1402 DSB67 RS12670 WP 010643257.1     VKGKDITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQ   143
NTDB id 1112 NGFG RS09215 WP 003689811.1      ITQEDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGET   146
NTDB id 1113 AAA85695.1 219..1451( )          ITQEDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGET   146
NTDB id 1134996 XTG RS15520 WP 115677263.1    ITPKDIAFFSRQMATMMKSGVPIVGALEIIGSGHKNPRMRNLVGQVRTDIEGGSSLYESLSKHPVQFDELYRNLVKAGEG   154
NTDB id 1252 GC085 RS07730 WP 011213805.1     ITQADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEK   143
NTDB id 1198 PSJM300 03950 AFN76868.1         IKPMDIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQ   142
NTDB id 1016 ACIAD RS01680 WP 004920476.1     VKPLDIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQ   145
NTDB id 1059 ABD1 RS01610 WP 000279215.1      VTTLDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQ   145
consensus                                     **  !*****!!**!!***!************** ** ****** ** ****!**** ****** *!* ****!***!!
```

```
logo
NTDB id 1029 TT RS02230 WP 011228203.1        SGGLDLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLR   220
NTDB id 1169 A1552VC RS11075 WP 000648511.1   SGNLPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQ   224
NTDB id 1402 DSB67 RS12670 WP 010643257.1     SGNLSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQ   223
NTDB id 1112 NGFG RS09215 WP 003689811.1      GGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFV   226
NTDB id 1113 AAA85695.1 219..1451( )          GGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFV   226
NTDB id 1134996 XTG RS15520 WP 115677263.1    AGVLETVLDTVATYKENIEALKGKIKKALFYPAMVIAVAIIVSAILLVFVVPQFEDVFKGFGAELPAFTQLIVSASRFMV   234
NTDB id 1252 GC085 RS07730 WP 011213805.1     SGSLDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQ   223
NTDB id 1198 PSJM300 03950 AFN76868.1         SGSLETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQ   222
NTDB id 1016 ACIAD RS01680 WP 004920476.1     SGSLEIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQ   225
NTDB id 1059 ABD1 RS01610 WP 000279215.1      SGALETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQ   225
consensus                                     *! !*******!***!*** ***!***!* !!* !***!********* **! ! ***  *!**!!**!**** *!****
```

```
logo

NTDB id 1029 TT RS02230 WP 011228203.1        AATLPLLLLAVALFFAYRWY.YGTPQGRRVIDRLKLRLPVFGNLNRKTAVARFSRTLALLLSSGVNIVEALDITKGTAGN   299
NTDB id 1169 A1552VC RS11075 WP 000648511.1   AYSLWAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGN   304
NTDB id 1402 DSB67 RS12670 WP 010643257.1     NWGPFIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKITSKTSGN   303
NTDB id 1112 NGFG RS09215 WP 003689811.1      SYGWMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGN   306
NTDB id 1113 AAA85695.1 219..1451( )          SYGWMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGN   306
NTDB id 1134996 XTG RS15520 WP 115677263.1    AYWWLMLFVSIGCVAGFLYAFKRSLRLQHLVDRLTLRVPIIGQIMHNSAIARFSRTTAVTFKAGVPLVEGLGIVAGATGN   314
NTDB id 1252 GC085 RS07730 WP 011213805.1     AYWYIIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGN   303
NTDB id 1198 PSJM300 03950 AFN76868.1         AWWYVVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGN   302
NTDB id 1016 ACIAD RS01680 WP 004920476.1     DYWFILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNN   305
NTDB id 1059 ABD1 RS01610 WP 000279215.1      EYWFIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNN   305
consensus                                     ****************** ** ** ***  *****!**!**!*** ** *!***!!*******!******!********!
```

```
logo

NTDB id 1029 TT RS02230 WP 011228203.1        SVVEEIVEAAKLKIQQGDPLNLTLAQHPFVFPPMVSSMVAIGEETGALDTMLSKVADFYEREVDEAVASLTAAIEPLMII   379
NTDB id 1169 A1552VC RS11075 WP 000648511.1   VHFETAINEVYRDTAAGMPMYIAMR.NTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIV   383
NTDB id 1402 DSB67 RS12670 WP 010643257.1     MHYQLAIEEVYRDTAAGMPMYIAMR.HCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIV   382
NTDB id 1112 NGFG RS09215 WP 003689811.1      LIYEEATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIV   385
NTDB id 1113 AAA85695.1 219..1451( )          LIYEEATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIIL   385
NTDB id 1134996 XTG RS15520 WP 115677263.1    AVYEDAVLRMRDDVSVGYPVNMAMK.QVNVFPHMVIQMTAIGEEAGALDTMLFKVAEYYEQEVNNAVDALSSLLEPLIMV   393
NTDB id 1252 GC085 RS07730 WP 011213805.1     IIYAKATDKIREEVATGQQMFIAME.NTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMS   382
NTDB id 1198 PSJM300 03950 AFN76868.1         VVFRSATNKIKSDVSSGMQLNFSMR.TTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMA   381
NTDB id 1016 ACIAD RS01680 WP 004920476.1     TVYEQAVLKIREDVSTGQQLNFAMR.VSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMA   384
NTDB id 1059 ABD1 RS01610 WP 000279215.1      VIYEKAVMKIREDVATGQQLQFAMR.ISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMA   384
consensus                                     **** ** *** **  !* ******  * *!! ****!**!!!!*!*!**!! !*!**!! !!***!**!* **!!****
```

```
   <0

logo

NTDB id 1029 TT RS02230 WP 011228203.1        FLGVIVGMIVAGMFLPLFKIIGTLSVQ   406
NTDB id 1169 A1552VC RS11075 WP 000648511.1   FLGTVVGGLVVAMYLPIFNLMSVLG..   408
NTDB id 1402 DSB67 RS12670 WP 010643257.1     FLGVVVGGLVTAMYLPIFNLMSVLG..   407
NTDB id 1112 NGFG RS09215 WP 003689811.1      ILGLVIGTLLVAMYLPLFNLGNVVA..   410
NTDB id 1113 AAA85695.1 219..1451( )          ILGLVIGTLLVAMYLPLFNLGNVVA*.   410
NTDB id 1134996 XTG RS15520 WP 115677263.1    FIGTLVGGMVIGMYLPIFKLASVV...   417
NTDB id 1252 GC085 RS07730 WP 011213805.1     ILGILVGGLVVAMYLPIFKLGSAV...   406
NTDB id 1198 PSJM300 03950 AFN76868.1         VLGVLVGGLIIAMYLPIFQMGSVV...   405
NTDB id 1016 ACIAD RS01680 WP 004920476.1     ILGILVGGLVIAMYLPIFQMGSVV...   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1      ILGVLVGGLVIAMYLPIFQMGSVV...   408
consensus                                     **!***!*****!*!!*!******
```

X non conserved

X similar

X ≥ 50% conserved