```
logo
NTDB id 1029 TT RS02230 WP 011228203.1        ................MPVYQYKARDRQGRL.VEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIPALERGP   62
NTDB id 1402 DSB67 RS12670 WP 010643257.1     ....MKT......IAPQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFIT.....KISHRV   64
NTDB id 1169 A1552VC RS11075 WP 000648511.1   ...MKAT......QTLPLKNYRWKGINSNGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLA.....RLTHRV   65
NTDB id 1113 AAA85695.1 219..1451( )          ....MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....T....SSKRKI   67
NTDB id 1112 NGFG RS09215 WP 003689811.1      ....MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....T....SSKRKI   67
NTDB id 1198 PSJM300 03950 AFN76868.1         ....MAQK......AIKNSVFTWEGLDRQGAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS......AGKKI   63
NTDB id 1059 ABD1 RS01610 WP 000279215.1      ...MAVKK......AQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG....LFKKKV   66
NTDB id 1016 ACIAD RS01680 WP 004920476.1     ...MAAKK......TQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEG....LLKKKV   66
NTDB id 1160747 R2K28 RS02965 WP 316367907.1 MAPPRKKA......KVKSHLYKWEGTDKKGAR.LSGESRGTDVNMVKADLRRQGVTPLKVRKKPTNLV......LTKQKI   67
NTDB id 1252 GC085 RS07730 WP 011213805.1     ....MDKN......SPPLLTFHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFD.....RKNKKI   64
consensus                                         ***        *  *  * ******* * * * *** * ** ***  !***** * ******  *         ****

logo
NTDB id 1029 TT RS02230 WP 011228203.1        GLKDLAIFSRQLATMLGAGLTLLQALAILERQTENRKFREILKQVRTDVEGGMAFSEALSKHK.IFSRLYVNLVRAGETS  141
NTDB id 1402 DSB67 RS12670 WP 010643257.1     KGKDITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQS  144
NTDB id 1169 A1552VC RS11075 WP 000648511.1   KSKDITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMS  145
NTDB id 1113 AAA85695.1 219..1451( )          TQEDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETG  147
NTDB id 1112 NGFG RS09215 WP 003689811.1      TQEDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETG  147
NTDB id 1198 PSJM300 03950 AFN76868.1         KPMDIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQS  143
NTDB id 1059 ABD1 RS01610 WP 000279215.1      TTLDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQS  146
NTDB id 1016 ACIAD RS01680 WP 004920476.1     KPLDIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQS  146
NTDB id 1160747 R2K28 RS02965 WP 316367907.1 TSADVTVFSRQLATMMAAGVPMVQAFDIVGRGHDNPSMQELILTIKADVEGGTALADALKKHPLHFEDLFVNLVRAGEHA  147
NTDB id 1252 GC085 RS07730 WP 011213805.1    TQADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKS  144
consensus                                     *  !*****!!**!!* *!****!****** ***** ****** ** ****!***  ****** *!* ****!***!! *

logo
NTDB id 1029 TT RS02230 WP 011228203.1        GGLDLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRA  221
NTDB id 1402 DSB67 RS12670 WP 010643257.1     GNLSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQN  224
NTDB id 1169 A1552VC RS11075 WP 000648511.1   GNLPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQA  225
NTDB id 1113 AAA85695.1 219..1451( )          GVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVS  227
NTDB id 1112 NGFG RS09215 WP 003689811.1      GVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVS  227
NTDB id 1198 PSJM300 03950 AFN76868.1         GSLETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQA  223
NTDB id 1059 ABD1 RS01610 WP 000279215.1      GALETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQE  226
NTDB id 1016 ACIAD RS01680 WP 004920476.1     GSLEIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQD  226
NTDB id 1160747 R2K28 RS02965 WP 316367907.1 GVLESLLHKIATYKEKTESIKGKIKKAMFYPAAVIIAAILVTAILLIFVIPQFESLFSSFGADLPALTRFVVNLSELVRD  227
NTDB id 1252 GC085 RS07730 WP 011213805.1    GSLDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQA  224
consensus                                     ! !*******!***!!** ***!***!* !!* !***!********* **! ! ***  *!**!!**!* ** *!****
```

```
logo
```

```
NTDB id 1029 TT RS02230 WP 011228203.1          ATLPLLLLAVALFFAYRWY.YGTPQGRRVIDRLKLRLPVFGNLNRKTAVARFSRTLALLLSSGVNIVEALDITKGTAGNS   300
NTDB id 1402 DSB67 RS12670 WP 010643257.1       WGPFIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNM   304
NTDB id 1169 A1552VC RS11075 WP 000648511.1     YSLWAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNV   305
NTDB id 1113 AAA85695.1 219..1451( )            YGWMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNL   307
NTDB id 1112 NGFG RS09215 WP 003689811.1        YGWMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNL   307
NTDB id 1198 PSJM300 03950 AFN76868.1           WWYVVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNV   303
NTDB id 1059 ABD1 RS01610 WP 000279215.1        YWFIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNV   306
NTDB id 1016 ACIAD RS01680 WP 004920476.1       YWFILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNT   306
NTDB id 1160747 R2K28 RS02965 WP 316367907.1    WWWAMLGGIIAFIYTFIYIWKRSRKFRHNVDRILLKVPVVGMVLDKSAIARFSRTLSTMSAAGVPLVEALDSVAGATGNV   307
NTDB id 1252 GC085 RS07730 WP 011213805.1       YWYIIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNI   304
consensus                                       ***************** ** ** ***  *****!**!**!*** !* *!***!!*******!******!********!*
```

```
logo
```

```
NTDB id 1029 TT RS02230 WP 011228203.1          VVEEIVEAAKLKIQQGDPLNLTLAQHPFVFPPMVSSMVAIGEETGALDTMLSKVADFYEREVDEAVASLTAAIEPLMIIF   380
NTDB id 1402 DSB67 RS12670 WP 010643257.1       HYQLAIEEVYRDTAAGMPMYIAMR.HCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVF   383
NTDB id 1169 A1552VC RS11075 WP 000648511.1     HFETAINEVYRDTAAGMPMYIAMR.NTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVF   384
NTDB id 1113 AAA85695.1 219..1451( )            IYEEATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILI   386
NTDB id 1112 NGFG RS09215 WP 003689811.1        IYEEATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVI   386
NTDB id 1198 PSJM300 03950 AFN76868.1           VFRSATNKIKSDVSSGMQLNFSMR.TTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAV   382
NTDB id 1059 ABD1 RS01610 WP 000279215.1        IYEKAVMKIREDVATGQQLQFAMR.ISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAI   385
NTDB id 1016 ACIAD RS01680 WP 004920476.1       VYEQAVLKIREDVSTGQQLNFAMR.VSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAI   385
NTDB id 1160747 R2K28 RS02965 WP 316367907.1    VYSDAVLRMREDVATGQSLQLAMK.QRNLFPNMVVQMVAIGEESGALDDMLNKVADFYEEQVDNAVDAMSSLMEPIIMVI   386
NTDB id 1252 GC085 RS07730 WP 011213805.1       IYAKATDKIREEVATGQQMFIAME.NTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSI   383
consensus                                       *** ** *** ****!* ******  * *!! ****!**!!!!*!*!**!!*!*!**!!**!***!**** **!!*****
```

```
<0
logo
```

```
NTDB id 1029 TT RS02230 WP 011228203.1          LGVIVGMIVAGMFLPLFKIIGTLSVQ   406
NTDB id 1402 DSB67 RS12670 WP 010643257.1       LGVVVGGLVTAMYLPIFNLMSVLG..   407
NTDB id 1169 A1552VC RS11075 WP 000648511.1     LGTVVGGLVVAMYLPIFNLMSVLG..   408
NTDB id 1113 AAA85695.1 219..1451( )            LGLVIGTLLVAMYLPLFNLGNVVA*.   410
NTDB id 1112 NGFG RS09215 WP 003689811.1        LGLVIGTLLVAMYLPLFNLGNVVA..   410
NTDB id 1198 PSJM300 03950 AFN76868.1           LGVLVGGLIIAMYLPIFQMGSVV...   405
NTDB id 1059 ABD1 RS01610 WP 000279215.1        LGVLVGGLVIAMYLPIFQMGSVV...   408
NTDB id 1016 ACIAD RS01680 WP 004920476.1       LGILVGGLVIAMYLPIFQMGSVV...   408
NTDB id 1160747 R2K28 RS02965 WP 316367907.1    LGVLIGTLVVAMYLPIFKMASVV...   409
NTDB id 1252 GC085 RS07730 WP 011213805.1       LGILVGGLVVAMYLPIFKLGSAV...   406
consensus                                       !!***!*****!*!!*!******
```

X non conserved

X similar

X ≥ 50% conserved