```
logo
NTDB id 1029 TT RS02230 WP 011228203.1              ....................MPVYQYKARDRQGRL.VEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVR   54
NTDB id 1402 DSB67 RS12670 WP 010643257.1           .............MKTIAPQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK..   59
NTDB id 1169 A1552VC RS11075 WP 000648511.1         ............MKATQTLPLKNYRWKGINSNGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR..   60
NTDB id 1112 NGFG RS09215 WP 003689811.1            .......MAKNGGFSLFAKKEKRFIFECRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....T..   61
NTDB id 1113 AAA85695.1 219..1451( )                .......MAKNGGFSLFAKKEKRFIFECRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....T..   61
NTDB id 227696 XcfCFBP6996P RS15845 WP 099207232.1 MSALGSTVKKGAKPANRVNAMTSFVWEGTDKRGVK.MKGDELARNANMLRAELRRRGINPTVVKTKPKPLFGA..   72
NTDB id 1252 GCO85 RS07730 WP 011213805.1          .............MDKNSPPLLTFHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR..   59
NTDB id 1198 PSJM300 03950 AFN76868.1               .............MAQKAIKNSVFTWEGLDRQGAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS...   58
NTDB id 1016 ACIAD RS01680 WP 004920476.1           ............MAAKKTQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEG..   60
NTDB id 1059 ABD1 RS01610 WP 000279215.1            ............MAVKKAQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG..   60
consensus                                                          *  *  * ****** * * * *** * *  ***  !***** *  ****** *
```

```
logo
NTDB id 1029 TT RS02230 WP 011228203.1              IPALERGPGLKDLAIFSRQLATMLGAGLTLLQALAILERQTENRKFREILKQVRTDVEGGMAFSEALSKHK.IFS   128
NTDB id 1402 DSB67 RS12670 WP 010643257.1           ...ISHRVKGKDITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFD   131
NTDB id 1169 A1552VC RS11075 WP 000648511.1         ...LTHRVKSKDITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFD   132
NTDB id 1112 NGFG RS09215 WP 003689811.1            ..SSKRKITQEDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFD   134
NTDB id 1113 AAA85695.1 219..1451( )                ..SSKRKITQEDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFD   134
NTDB id 227696 XcfCFBP6996P RS15845 WP 099207232.1 ...TGKPIKPKDIAFFSRQIATMMKSGVPMVGTLEIIGEGSKNPRMRKMVGEIRTDIEGGSSLNEAISRHPVQFD   144
NTDB id 1252 GCO85 RS07730 WP 011213805.1          ...KNKKITQADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFN   131
NTDB id 1198 PSJM300 03950 AFN76868.1               ...AGKKIKPMDIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFD   130
NTDB id 1016 ACIAD RS01680 WP 004920476.1           ..LLKKKVKPLDIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFD   133
NTDB id 1059 ABD1 RS01610 WP 000279215.1            ..LFKKKVTTLDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFD   133
consensus                                               ****  !*****!!**!!***!*************  ** ******* ** ****!**** ****** *!*
```

```
logo
NTDB id 1029 TT RS02230 WP 011228203.1              RLYVNLVRAGETSGGLDLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTDLGS   203
NTDB id 1402 DSB67 RS12670 WP 010643257.1           PLYTDLIATGEQSGNLSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGA   206
NTDB id 1169 A1552VC RS11075 WP 000648511.1         TLYVDLVETGEMSGNLPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGA   207
NTDB id 1112 NGFG RS09215 WP 003689811.1            RFYCNLVAAGETGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGA   209
NTDB id 1113 AAA85695.1 219..1451( )                RFYCNLVAAGETGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGA   209
NTDB id 227696 XcfCFBP6996P RS15845 WP 099207232.1 ELYRNLVRAGESAGVLDTVLDTVATYKENIEALKGKIKKALFYPAMVMAVALIVSSILLIWVVPQFETVFSSFGA   219
NTDB id 1252 GCO85 RS07730 WP 011213805.1          ELFCNLVDAGEKSGSLDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGA   206
NTDB id 1198 PSJM300 03950 AFN76868.1               DLYCNLVDSGEQSGSLETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGA   205
NTDB id 1016 ACIAD RS01680 WP 004920476.1           NLFCSLIESGEQSGSLEIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGA   208
NTDB id 1059 ABD1 RS01610 WP 000279215.1            NLFCSLVESGEQSGALETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGA   208
consensus                                            ****!***!! *! !*******!***!*** ***!***!* !!* !***!********* **! ! ***  *!*
```

```
logo

NTDB id 1029 TT RS02230 WP 011228203.1                ELPLLTRFLIAVSDLLRAATLPLLLLAVALFFAYRW.YYGTPQGRRVIDRLKLRLPVFGNLNRKTAVARFSRTLA   277
NTDB id 1402 DSB67 RS12670 WP 010643257.1             DLPAFTQMVLNLSAWTQNWGPFIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLA   281
NTDB id 1169 A1552VC RS11075 WP 000648511.1           ELPWFTQQVLKLSHWVQAYSLWAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLA   282
NTDB id 1112 NGFG RS09215 WP 003689811.1              ELPPLTQTVMDMSDFFVSYGWMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTA   284
NTDB id 1113 AAA85695.1 219..1451( )                  ELPALTQTVMDMSDFFVSYGWMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTA   284
NTDB id 227696 XcfCFBP6996P RS15845 WP 099207232.1   ELPAFTQMIVNLSRFMVSWWFPILLVIIGSAVGLIMAYKRSPRMQHLFDRLILKVPVIGKIMHDSSIARFARTTA   294
NTDB id 1252 GC085 RS07730 WP 011213805.1            DLPAMTRAVITMSEFMQAYWYIIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLS   281
NTDB id 1198 PSJM300 03950 AFN76868.1                 ELPAFTLMVIGLSEALQAWWYVVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLS   280
NTDB id 1016 ACIAD RS01680 WP 004920476.1            DLPAFTQLVVNMSNWMQDYWFILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLA   283
NTDB id 1059 ABD1 RS01610 WP 000279215.1             DLPAFTQMVVNMSKWMQEYWFIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLA   283
consensus                                            *!!**!**** *!**** ***************  **  **  ***  ****!**!**!***  ****!***!!**

logo

NTDB id 1029 TT RS02230 WP 011228203.1                LLLSSGVNIVEALDITKGTAGNSVVEEIVEAAKLKIQQGDPLNLTLAQHPFVFPPMVSSMVAIGEETGALDTMLS   352
NTDB id 1402 DSB67 RS12670 WP 010643257.1             TSFSAGIPILTALKTTSKTSGNMHYQLAIEEVYRDTAAGMPMYIAMR.HCHVFPELVLQMVMIGEESGRLDDMLN   355
NTDB id 1169 A1552VC RS11075 WP 000648511.1           TSFAAGIPILASLKTTAKTSGNVHFETAINEVYRDTAAGMPMYIAMR.NTEAFPEMVLQMVMIGEESGQLDDMLN   356
NTDB id 1112 NGFG RS09215 WP 003689811.1              TLFAAGVPLVDVLDSTAGAAGNLIYEEATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLN   358
NTDB id 1113 AAA85695.1 219..1451( )                  TLFAAGVPLVDVLDSTAGAAGNLIYEEATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLN   358
NTDB id 227696 XcfCFBP6996P RS15845 WP 099207232.1   VTFKAGVPLVEALGIVAGATGNKVYEEAVLRMRDDVSVGYPVNLSMK.QVNLFPHMVIQMTAIGEEAGALDAMLF   368
NTDB id 1252 GC085 RS07730 WP 011213805.1            ITFAAGLPLVEALKSVAGATGNIIYAKATDKIREEVATGQQMFIAME.NTHLFPNMVIQMVAIGEESGALEKMLS   355
NTDB id 1198 PSJM300 03950 AFN76868.1                 TTFAAGVPLVDALDSVAGATGNVVFRSATNKIKSDVSSGMQLNFSMR.TTGTFPSMAVQMTAIGEESGALDEMLS   354
NTDB id 1016 ACIAD RS01680 WP 004920476.1            TTFAAGVPLIDALASTAGATNNTVYEQAVLKIREDVSTGQQLNFAMR.VSNRFPTMAIQMVAIGEESGALDEMLD   357
NTDB id 1059 ABD1 RS01610 WP 000279215.1             TTFAAGVPLIDALESTAGATNNVIYEKAVMKIREDVATGQQLQFAMR.ISNRFPSMAIQMVAIGEESGALDSMLD   357
consensus                                            *****!******!********!**** ** *** **  !* ******  * *!! ****!**!!!!*!*!**!!

   <0

logo

NTDB id 1029 TT RS02230 WP 011228203.1                KVADFYEREVDEAVASLTAAIEPLMIIFLGVIVGMIVAGMFLPLFKIIGTLSVQ   406
NTDB id 1402 DSB67 RS12670 WP 010643257.1             KIAAIYEFEVDNTVDNLSKILEPLIIVFLGVVVGGLVTAMYLPIFNLMSVLG..   407
NTDB id 1169 A1552VC RS11075 WP 000648511.1           KVATIYEFEVDNTVDNLGKILEPLIIVFLGTVVGGLVVAMYLPIFNLMSVLG..   408
NTDB id 1112 NGFG RS09215 WP 003689811.1              KAAEFYEDEVDNAVGRLSAMMEPIIIVILGLVIGTLLVAMYLPLFNLGNVVA..   410
NTDB id 1113 AAA85695.1 219..1451( )                  KAAEFYEDEVDNAVGWLSAMMEPIIILILGLVIGTLLVAMYLPLFNLGNVVA*.   410
NTDB id 227696 XcfCFBP6996P RS15845 WP 099207232.1   KVAEYFEQEVNNAVDALSSLLEPMIMIFIGTIVGGMVIGMYLPIFKLGAVVG..   420
NTDB id 1252 GC085 RS07730 WP 011213805.1            KVADFYEEEVNNAVDALSSLLEPIIMSILGILVGGLVVAMYLPIFKLGSAV...   406
NTDB id 1198 PSJM300 03950 AFN76868.1                 KVATFYEDEVDNMVDGLTALMEPMIMAVLGVLVGGLIIAMYLPIFQMGSVV...   405
NTDB id 1016 ACIAD RS01680 WP 004920476.1            KVANYYESEVDHAVDGLTSMMEPLIMAILGILVGGLVIAMYLPIFQMGSVV...   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1             KVATYYENEVDNAVDGLTSMMEPLIMAILGVLVGGLVIAMYLPIFQMGSVV...   408
consensus                                            !*!***!  !!***!**!*  **!!******!***!*****!*!!*!******
```

X non conserved

X similar

X ≥ 50% conserved