```
logo
NTDB id 1029 TT RS02230 WP 011228203.1          ..............MPVYQYKARDRQ.GRLVEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIPALERGPGLK   65
NTDB id 1402 DSB67 RS12670 WP 010643257.1       .MKT......IAPQLKNYRWKGINSS.GKKTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISF..I...TKISHRVKGK   67
NTDB id 1169 A1552VC RS11075 WP 000648511.1     MKAT......QTLPLKNYRWKGINSN.GKKVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSL..L...ARLTHRVKSK   68
NTDB id 1112 NGFG RS09215 WP 003689811.1        .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV......K...TSSKRKITQE   70
NTDB id 1113 AAA85695.1 219..1451( )            .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV......K...TSSKRKITQE   70
NTDB id 1252 GC085 RS07730 WP 011213805.1       .MDK......NSPPLLTFHYQGINKA.GQKMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPL.F....DRKNKKITQA   67
NTDB id 116473 YC6258 RS10625 WP 044616970.1   ..MA......TAAKTFTYKYEGISRS.GRSVKGELSAVNPAIAKAQLRKQGINVKKMVKKSQSLSFL...GSGKKSIKSE   68
NTDB id 1198 PSJM300 03950 AFN76868.1           .MAQ......KAIKNSVFTWEGLDRQ.GAKIKGELSGVSPALVKAQLRKQGINPQKVRKKSISL.FS.....AGKKIKPM   66
NTDB id 1059 ABD1 RS01610 WP 000279215.1        MAVK......KAQMMPTFAYEGVDRK.GVKIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNI.LE...GLFKKKVTTL   69
NTDB id 1016 ACIAD RS01680 WP 004920476.1       MAAK......KTQVMPVFAYEGVDRK.GIKLKGELPARNMALAKVTLRKQGITIRTIREKRKNI.FE...GLLKKKVKPL   69
consensus                                        ***        *  *  * **** *  **** *** * * ****  !***** *******   *          *****

logo
NTDB id 1029 TT RS02230 WP 011228203.1          DLAIFSRQLATMLGAGLTLLQALAILERQTENRKFREILKQVRTDVEGGMAFSEALSKH.KIFSRLYVNLVRAGETSGGL   144
NTDB id 1402 DSB67 RS12670 WP 010643257.1       DITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNL   147
NTDB id 1169 A1552VC RS11075 WP 000648511.1     DITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNL   148
NTDB id 1112 NGFG RS09215 WP 003689811.1        DITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL   150
NTDB id 1113 AAA85695.1 219..1451( )            DITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL   150
NTDB id 1252 GC085 RS07730 WP 011213805.1       DITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSL   147
NTDB id 116473 YC6258 RS10625 WP 044616970.1   DIAVFTRQMATMMKAGVPLVQAFDIVAEGLSNKSMAELVTAMKADVSAGGTFGSALRKHPKYFDDLFCSLVESGEQAGAL   148
NTDB id 1198 PSJM300 03950 AFN76868.1           DIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSL   146
NTDB id 1059 ABD1 RS01610 WP 000279215.1        DITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGAL   149
NTDB id 1016 ACIAD RS01680 WP 004920476.1       DIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSL   149
consensus                                       !*****!!**!!***!****!********  ** ******* ** ****!**** ****** *!* ****!***!!**! !

logo
NTDB id 1029 TT RS02230 WP 011228203.1          DLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAATL   224
NTDB id 1402 DSB67 RS12670 WP 010643257.1       SQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWGP   227
NTDB id 1169 A1552VC RS11075 WP 000648511.1     PEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSL   228
NTDB id 1112 NGFG RS09215 WP 003689811.1        ESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYGW   230
NTDB id 1113 AAA85695.1 219..1451( )            ESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGW   230
NTDB id 1252 GC085 RS07730 WP 011213805.1       DIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWY   227
NTDB id 116473 YC6258 RS10625 WP 044616970.1   ETMLDRVAIYKEKSESIKRKVKSALKYPITVIVVAMIVTAVLLLKVVPVFAEMFNSFGAELPLPTQVVVSMSEWMQRNWY   228
NTDB id 1198 PSJM300 03950 AFN76868.1           ETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWWY   226
NTDB id 1059 ABD1 RS01610 WP 000279215.1        ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTILLMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWF   229
NTDB id 1016 ACIAD RS01680 WP 004920476.1       EIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTILLMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYWF   229
consensus                                       *******! **!!** ** !***!* !!**!***!***********! ! ***  *!**!!**!**** *!**** ***
```

```
logo

NTDB id 1029 TT RS02230 WP 011228203.1          PLLLLAVALFFAYRW.YYGTPQGRRVIDRLKLRLPVFGNLNRKTAVARFSRTLALLLSSGVNIVEALDITKGTAGNSVVE   303
NTDB id 1402 DSB67 RS12670 WP 010643257.1       FIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHYQ   307
NTDB id 1169 A1552VC RS11075 WP 000648511.1     WAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNVHFE   308
NTDB id 1112 NGFG RS09215 WP 003689811.1        MVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYE   310
NTDB id 1113 AAA85695.1 219..1451( )            MVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYE   310
NTDB id 1252 GC085 RS07730 WP 011213805.1       IIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYA   307
NTDB id 116473 YC6258 RS10625 WP 044616970.1   IGLGVIIVSTFLFSTAMKRSIKFRHGVQRFLLRLPVFGPIFKQSAYARYARTLSTTFAAGVPLVDALDSAAGASGNIVYE   308
NTDB id 1198 PSJM300 03950 AFN76868.1           VVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFR   306
NTDB id 1059 ABD1 RS01610 WP 000279215.1        IMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYE   309
NTDB id 1016 ACIAD RS01680 WP 004920476.1       ILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVYE   309
consensus                                       *************  ** ** ***  *****!**!**!***  **  *!***!!********!******!********!****

logo

NTDB id 1029 TT RS02230 WP 011228203.1          EIVEAAKLKIQQGDPLNLTLAQHPFVFPPMVSSMVAIGEETGALDTMLSKVADFYEREVDEAVASLTAAIEPLMIIFLGV   383
NTDB id 1402 DSB67 RS12670 WP 010643257.1       LAIEEVYRDTAAGMPMYIAMR.HCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGV   386
NTDB id 1169 A1552VC RS11075 WP 000648511.1     TAINEVYRDTAAGMPMYIAMR.NTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLGT   387
NTDB id 1112 NGFG RS09215 WP 003689811.1        EATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGL   389
NTDB id 1113 AAA85695.1 219..1451( )            EATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGL   389
NTDB id 1252 GC085 RS07730 WP 011213805.1       KATDKIREEVATGQQMFIAME.NTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGI   386
NTDB id 116473 YC6258 RS10625 WP 044616970.1   TAIQNVKHEVSSGGELAGSMR.AENVFPPMLVQMVSIGEQSGALDDMLAKAAAIYEEEVDTMVDGLTSMMEPMIMAFLGV   387
NTDB id 1198 PSJM300 03950 AFN76868.1           SATNKIKSDVSSGMQLNFSMR.TTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGV   385
NTDB id 1059 ABD1 RS01610 WP 000279215.1        KAVMKIREDVATGQQLQFAMR.ISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGV   388
NTDB id 1016 ACIAD RS01680 WP 004920476.1       QAVLKIREDVSTGQQLNFAMR.VSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGI   388
consensus                                        **  ** ** *!* *  ***  * *!! ****!**!!!**!*!**!! !*! *!!*!!***!**!* **!!*****!!*

   <0

logo

NTDB id 1029 TT RS02230 WP 011228203.1          IVGMIVAGMFLPLFKIIGTLSVQ   406
NTDB id 1402 DSB67 RS12670 WP 010643257.1       VVGGLVTAMYLPIFNLMSVLG..   407
NTDB id 1169 A1552VC RS11075 WP 000648511.1     VVGGLVVAMYLPIFNLMSVLG..   408
NTDB id 1112 NGFG RS09215 WP 003689811.1        VIGTLLVAMYLPLFNLGNVVA..   410
NTDB id 1113 AAA85695.1 219..1451( )            VIGTLLVAMYLPLFNLGNVVA*.   410
NTDB id 1252 GC085 RS07730 WP 011213805.1       LVGGLVVAMYLPIFKLGSAV...   406
NTDB id 116473 YC6258 RS10625 WP 044616970.1   VVGGLVVSMYLPIFQIGNVV...   407
NTDB id 1198 PSJM300 03950 AFN76868.1           LVGGLIIAMYLPIFQMGSVV...   405
NTDB id 1059 ABD1 RS01610 WP 000279215.1        LVGGLVIAMYLPIFQMGSVV...   408
NTDB id 1016 ACIAD RS01680 WP 004920476.1       LVGGLVIAMYLPIFQMGSVV...   408
consensus                                       **!*****!*!!*!******
```

X non conserved

X similar

X ≥ 50% conserved