logo

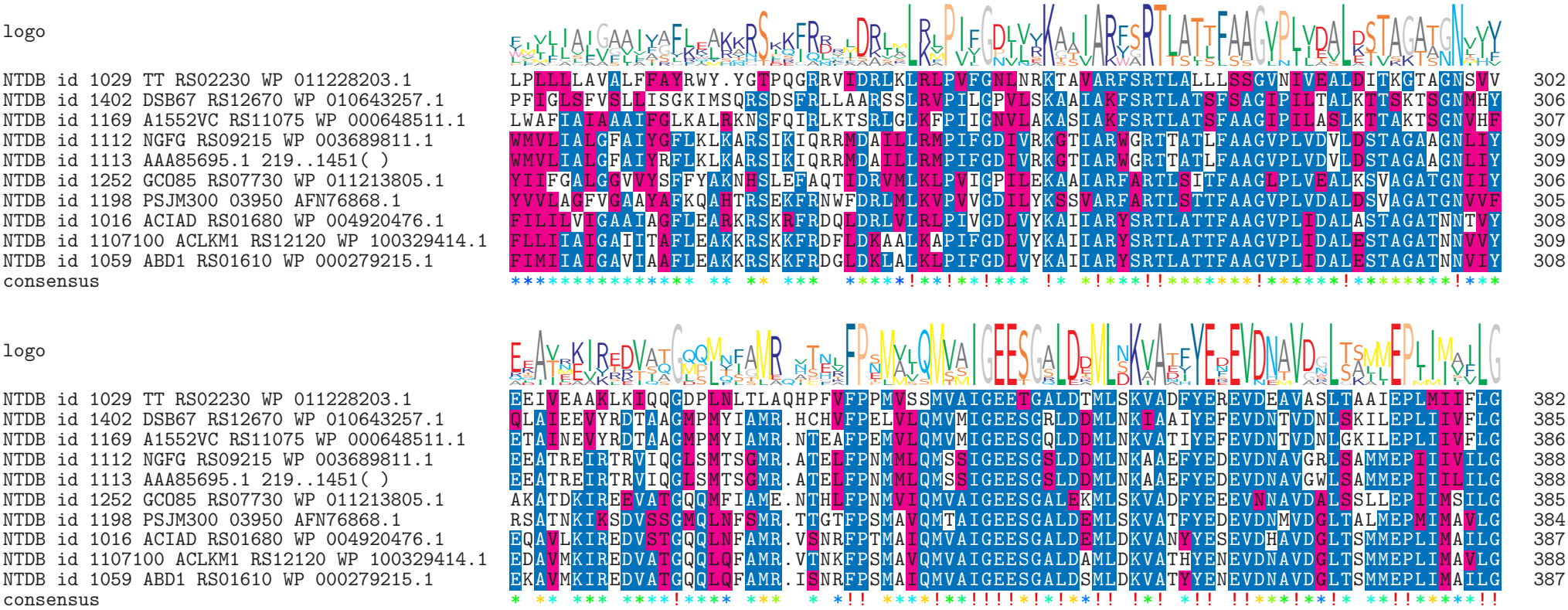
```
NTDB id 1029 TT RS02230 WP 011228203.1          ..............MPVYQYKARDRQGRL.VEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIPALERGPGL    64
NTDB id 1402 DSB67 RS12670 WP 010643257.1       ..MK......TIAPQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.....ISHRVKG    66
NTDB id 1169 A1552VC RS11075 WP 000648511.1     .MKA......TQTLPLKNYRWKGINSNGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.....LTHRVKS    67
NTDB id 1112 NGFG RS09215 WP 003689811.1        ..MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KT....SSKRKITQ    69
NTDB id 1113 AAA85695.1 219..1451( )            ..MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KT....SSKRKITQ    69
NTDB id 1252 GCO85 RS07730 WP 011213805.1       ..MDKNS......PPLLTFHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.....KNKKITQ    66
NTDB id 1198 PSJM300 03950 AFN76868.1           ..MAQKA......IKNSVFTWEGLDRQGAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS......AGKKIKP    65
NTDB id 1016 ACIAD RS01680 WP 004920476.1       .MAAKKT......QVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEG....LLKKKVKP    68
NTDB id 1107100 ACLKM1 RS12120 WP 100329414.1   MAAVKKG......QMMPIFSYEGIDRKGAK.IKGELPARNMALAKVTLRKQGISIKTIREKKKNILEG....LMKKRVST    69
NTDB id 1059 ABD1 RS01610 WP 000279215.1        .MAVKKA......QMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG....LFKKKVTT    68
consensus                                         *** *         *  * ****** * * * *** * ******  !***** ** **** * *         ******
```

logo

```
NTDB id 1029 TT RS02230 WP 011228203.1          KDLAIFSRQLATMLGAGLTLLQALAILERQTENRKFREILKQVRTDVEGGMAFSEALSKH.KIFSRLYVNLVRAGETSGG   143
NTDB id 1402 DSB67 RS12670 WP 010643257.1       KDITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGN   146
NTDB id 1169 A1552VC RS11075 WP 000648511.1     KDITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGN   147
NTDB id 1112 NGFG RS09215 WP 003689811.1        EDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGV   149
NTDB id 1113 AAA85695.1 219..1451( )            EDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGV   149
NTDB id 1252 GCO85 RS07730 WP 011213805.1       ADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGS   146
NTDB id 1198 PSJM300 03950 AFN76868.1           MDIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGS   145
NTDB id 1016 ACIAD RS01680 WP 004920476.1       LDIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGS   148
NTDB id 1107100 ACLKM1 RS12120 WP 100329414.1   LDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGNTFAGALRKYPQYFDKLFCSLVESGEQSGA   149
NTDB id 1059 ABD1 RS01610 WP 000279215.1        LDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGA   148
consensus                                         !*****!!**!!***!****!********* *** ****** ** ****!***  **** * *!* ****!***!!**!
```

logo

```
NTDB id 1029 TT RS02230 WP 011228203.1          LDLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAAT   223
NTDB id 1402 DSB67 RS12670 WP 010643257.1       LSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWG   226
NTDB id 1169 A1552VC RS11075 WP 000648511.1     LPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYS   227
NTDB id 1112 NGFG RS09215 WP 003689811.1        LESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYG   229
NTDB id 1113 AAA85695.1 219..1451( )            LESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYG   229
NTDB id 1252 GCO85 RS07730 WP 011213805.1       LDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYW   226
NTDB id 1198 PSJM300 03950 AFN76868.1           LETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWW   225
NTDB id 1016 ACIAD RS01680 WP 004920476.1       LEIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYW   228
NTDB id 1107100 ACLKM1 RS12120 WP 100329414.1   LETMLDRVAIYKEKSELLKQKIKKAMKYPAAVVVVALIVTIILMVKVVPVFQDLFSSFGADLPAFTKMVVNMSEWMQKYW   229
NTDB id 1059 ABD1 RS01610 WP 000279215.1        LETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYW   228
consensus                                       !*******! **!!** ** !***!* !!* !***!**********! ! ***  *!**!!**!**** *!**** **
```


logo
NTDB id 1029 TT RS02230 WP 011228203.1 LPLLLLAVALFFAYRWY.YGTPQGRVIDRLKLRLPVFGNLNRKTAVARFSRTLALLLSSGVNIVEALDITKGTAGNSVV 302
NTDB id 1402 DSB67 RS12670 WP 010643257.1 PFIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHY 306
NTDB id 1169 A1552VC RS11075 WP 000648511.1 LWAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNVHF 307
NTDB id 1112 NGFG RS09215 WP 003689811.1 WMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIY 309
NTDB id 1113 AAA85695.1 219..1451( ) WMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIY 309
NTDB id 1252 GCO85 RS07730 WP 011213805.1 YIIFGALGCVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIY 306
NTDB id 1198 PSJM300 03950 AFN76868.1 YVVLAGFVCAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVF 305
NTDB id 1016 ACIAD RS01680 WP 004920476.1 FILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVY 308
NTDB id 1107100 ACLKM1 RS12120 WP 100329414.1 FLLIIAIGAIITAFLEAKKRSKKFRDFLDKAALKAPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVVY 309
NTDB id 1059 ABD1 RS01610 WP 000279215.1 FIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIY 308
consensus
logo
NTDB id 1029 TT RS02230 WP 011228203.1 EEIVEAAKLKIQQGDPLNLTLAQHPFVFPPMVSSMVAIGEETGALDTMLSKVADFYERDVDEAVASLTAAIEPLMIIFLG 382
NTDB id 1402 DSB67 RS12670 WP 010643257.1 QLAIEEVYRDTAAGMPMYIAMR.HCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLG 385
NTDB id 1169 A1552VC RS11075 WP 000648511.1 ETAINEVYRDTAAGMPMYIAMR.NTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLG 386
NTDB id 1112 NGFG RS09215 WP 003689811.1 EEATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILG 388
NTDB id 1113 AAA85695.1 219..1451( ) EEATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILG 388
NTDB id 1252 GCO85 RS07730 WP 011213805.1 AKATDKIREEVATGQQMFIAME.NTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILG 385
NTDB id 1198 PSJM300 03950 AFN76868.1 RSATNKIKSDVSSGMQLNFSMR.TTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLG 384
NTDB id 1016 ACIAD RS01680 WP 004920476.1 EQAVLKIREDVSTGQQLNFAMR.VSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILG 387
NTDB id 1107100 ACLKM1 RS12120 WP 100329414.1 EDAVMKIREDVATGQQLQFAMR.VTNKFPSMAVQMVAIGEESGALDAMLDKVATHYENEVDNAVDGLTSMMEPLIMAVLG 388
NTDB id 1059 ABD1 RS01610 WP 000279215.1 EKAVMKIREDVATGQQLQFAMR.ISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILG 387
consensus
<0
logo
NTDB id 1029 TT RS02230 WP 011228203.1 VIVGMIVAGMFLPLFKIIGTLSVQ 406
NTDB id 1402 DSB67 RS12670 WP 010643257.1 VVVGGLVTAMYLPIFNLMSVLG.. 407
NTDB id 1169 A1552VC RS11075 WP 000648511.1 TVVGGLVVAMYLPIFNLMSVLG.. 408
NTDB id 1112 NGFG RS09215 WP 003689811.1 LVIGTLLVAMYLPLFNLGNVVA.. 410
NTDB id 1113 AAA85695.1 219..1451( ) LVIGTLLVAMYLPLFNLGNVVA*. 410
NTDB id 1252 GCO85 RS07730 WP 011213805.1 ILVGGLVVAMYLPIFKLGSAV... 406
NTDB id 1198 PSJM300 03950 AFN76868.1 VLVGGLIIAMYLPIFQMGSVV... 405
NTDB id 1016 ACIAD RS01680 WP 004920476.1 ILVGGLVIAMYLPIFQMGSVV... 408
NTDB id 1107100 ACLKM1 RS12120 WP 100329414.1 VLVGGLVIAMYLPIFQMGSVV... 409
NTDB id 1059 ABD1 RS01610 WP 000279215.1 VLVGGLVIAMYLPIFQMGSVV... 408
consensus
X non conserved
X similar
X ≥ 50% conserved