logo

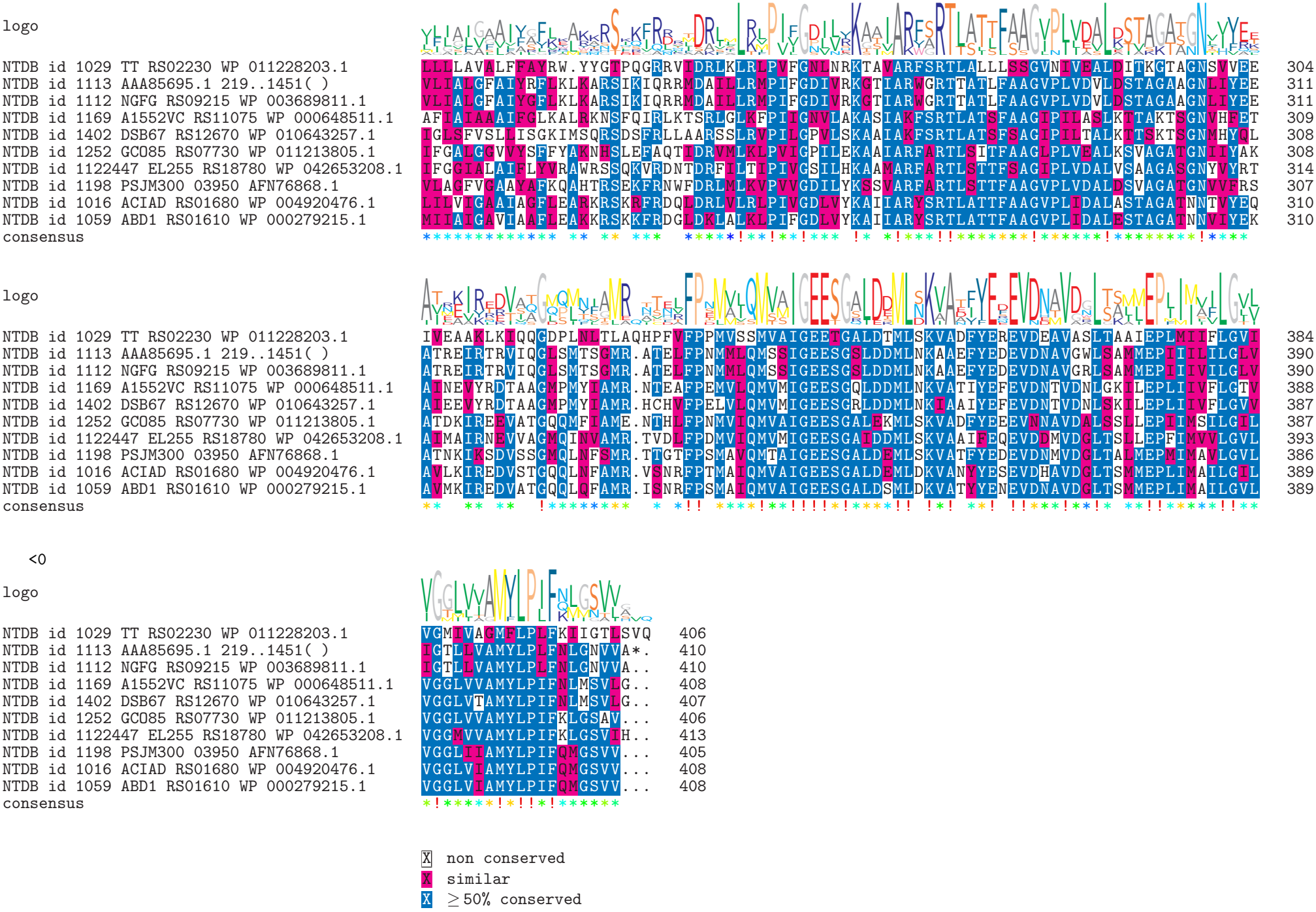
```
NTDB id 1029 TT RS02230 WP 011228203.1          .............MPVYQYKARDRQG.RLVEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIPALERGPGLKD   66
NTDB id 1113 AAA85695.1 219..1451( )            MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKTS.........SKRKITQED   71
NTDB id 1112 NGFG RS09215 WP 003689811.1        MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKTS.........SKRKITQED   71
NTDB id 1169 A1552VC RS11075 WP 000648511.1     .....MKATQTLPLKNYRWKGINSNG.KKVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.....LTHRVKSKD   69
NTDB id 1402 DSB67 RS12670 WP 010643257.1       ......MKTIAPQLKNYRWKGINSSG.KKTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.....ISHRVKGKD   68
NTDB id 1252 GCO85 RS07730 WP 011213805.1       ......MDKNSPPLLTFHYQGINKAG.QKMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.....KNKKITQAD   68
NTDB id 1122447 EL255 RS18780 WP 042653208.1    MATLAQKQNAPKKVFSFRWHGVNRKG.QKVSGELQADSINTVKNELRKQGVNVTKVSKRSQGLFSK.....GGAKIKPMD   74
NTDB id 1198 PSJM300 03950 AFN76868.1           ......MAQKAIKNSVFTWEGLDRQG.AKIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS......AGKKIKPMD   67
NTDB id 1016 ACIAD RS01680 WP 004920476.1       .....MAAKKTQVMPVFAYEGVDRKG.IKLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGL....LKKKVKPLD   70
NTDB id 1059 ABD1 RS01610 WP 000279215.1        .....MAVKKAQMMPTFAYEGVDRKG.VKIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGL....FKKKVTTLD   70
consensus                                                 *  *  * **** * * *** *** * **  **  !***** * ****** **          ****  !
```

logo

```
NTDB id 1029 TT RS02230 WP 011228203.1          LAIFSRQLATMLGAGLTLLQALAILERQTENRKFREILKQVRTDVEGGMAFSEALSKHK.IFSRLYVNLVRAGETSGGLD   145
NTDB id 1113 AAA85695.1 219..1451( )            ITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLE   151
NTDB id 1112 NGFG RS09215 WP 003689811.1        ITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLE   151
NTDB id 1169 A1552VC RS11075 WP 000648511.1     ITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNLP   149
NTDB id 1402 DSB67 RS12670 WP 010643257.1       ITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGEQSGNLS   148
NTDB id 1252 GCO85 RS07730 WP 011213805.1       ITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSLD   148
NTDB id 1122447 EL255 RS18780 WP 042653208.1    IAVISRQITTMLSAGVPLVQSLQIIARGHEKAAVRDLIGQIAADVETGTPMSEALRHPRHFDTLYCDLVEAGEQSGALE   154
NTDB id 1198 PSJM300 03950 AFN76868.1           IALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGEQSGSLE   147
NTDB id 1016 ACIAD RS01680 WP 004920476.1       IAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLE   150
NTDB id 1059 ABD1 RS01610 WP 000279215.1        ITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALE   150
consensus                                       *****!!**!!* *!****!****** ***** ****** ** ****!**** ****** *!* ****!***!!**! !*
```

logo

```
NTDB id 1029 TT RS02230 WP 011228203.1          LIILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLLRAATLP   225
NTDB id 1113 AAA85695.1 219..1451( )            SLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGWM   231
NTDB id 1112 NGFG RS09215 WP 003689811.1        SLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYGWM   231
NTDB id 1169 A1552VC RS11075 WP 000648511.1     EVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSLW   229
NTDB id 1402 DSB67 RS12670 WP 010643257.1       QVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWTQNWGPF   228
NTDB id 1252 GCO85 RS07730 WP 011213805.1       IMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLTYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWYI   228
NTDB id 1122447 EL255 RS18780 WP 042653208.1    TIYDRIAIYREKSEALKSKIKKAMFYPAMVILVAIIVTSILLLFVIPQFEEIFKSFGAELPIFTQFVIGISRFMQHWWYA   234
NTDB id 1198 PSJM300 03950 AFN76868.1           TLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWWYV   227
NTDB id 1016 ACIAD RS01680 WP 004920476.1       IMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYWFI   230
NTDB id 1059 ABD1 RS01610 WP 000279215.1        TMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWFI   230
consensus                                       ******! **!!** ** !***!* !!* !***!********** **! ! ***  *!**!!**!* ** *!**** ****
```


logo
NTDB id 1029 TT RS02230 WP 011228203.1 LLLLAVALFFAYRW.YYGTPQGRRVIDRLKLRLPVFGNLNRKTAVARFSRTLALLLSSGVNIVEALDITKGTAGNSVVEE 304
NTDB id 1113 AAA85695.1 219..1451( ) VLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEE 311
NTDB id 1112 NGFG RS09215 WP 003689811.1 VLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEE 311
NTDB id 1169 A1552VC RS11075 WP 000648511.1 AFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSGNVHFET 309
NTDB id 1402 DSB67 RS12670 WP 010643257.1 IGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHYQL 308
NTDB id 1252 GCO85 RS07730 WP 011213805.1 IFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAK 308
NTDB id 1122447 EL255 RS18780 WP 042653208.1 IFGGIALAIFLYVRAWRSSQKVRDNTDRFILTIPIVGSILHKAAMARFARTLSTTFSAGIPLVDALVSAAGASGNYVYRT 314
NTDB id 1198 PSJM300 03950 AFN76868.1 VLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFRS 307
NTDB id 1016 ACIAD RS01680 WP 004920476.1 LILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVYEQ 310
NTDB id 1059 ABD1 RS01610 WP 000279215.1 MIIAIGAVIAAFLEAKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYEK 310
consensus
logo
NTDB id 1029 TT RS02230 WP 011228203.1 IVEAAKLKIQQGDPLNLTLAQHPFVFPPMVSSMVAIGEETGALDTMLSKVADFYERFVDEAVASLTAAIEPLMIIFLGVI 384
NTDB id 1113 AAA85695.1 219..1451( ) ATRETRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGLV 390
NTDB id 1112 NGFG RS09215 WP 003689811.1 ATRETRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGLV 390
NTDB id 1169 A1552VC RS11075 WP 000648511.1 AINEVYRDTAAGMPMYIAMR.NTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLGTV 388
NTDB id 1402 DSB67 RS12670 WP 010643257.1 AIEEVYRDTAAGMPMYIAMR.HCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGVV 387
NTDB id 1252 GCO85 RS07730 WP 011213805.1 ATDKIREEVATGQQMFIAME.NTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGIL 387
NTDB id 1122447 EL255 RS18780 WP 042653208.1 AIMAIRNEVVAGMQINVAMR.TVDLFPDMVIQMVMIGEESGAIDDMLSKVAAIREQEVDDMVDGLTSLLEPFIMVVLGVL 393
NTDB id 1198 PSJM300 03950 AFN76868.1 ATNKIKSDVSSGMQLNFSMR.TTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGVL 386
NTDB id 1016 ACIAD RS01680 WP 004920476.1 AVLKIREDVSTGQQLNFAMR.VSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGIL 389
NTDB id 1059 ABD1 RS01610 WP 000279215.1 AVMKIREDVATGQQLQFAMR.ISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGVL 389
consensus
<0
logo
NTDB id 1029 TT RS02230 WP 011228203.1 VGMIVAGMFLPLFKIIGTLSVQ 406
NTDB id 1113 AAA85695.1 219..1451( ) IGTLLVAMYLPLFNLGNVVA*. 410
NTDB id 1112 NGFG RS09215 WP 003689811.1 IGTLLVAMYLPLFNLGNVVA.. 410
NTDB id 1169 A1552VC RS11075 WP 000648511.1 VGGLVVAMYLPIFNLMSVLG.. 408
NTDB id 1402 DSB67 RS12670 WP 010643257.1 VGGLVTAMYLPIFNLMSVLG.. 407
NTDB id 1252 GCO85 RS07730 WP 011213805.1 VGGLVVAMYLPIFKLGSAV... 406
NTDB id 1122447 EL255 RS18780 WP 042653208.1 VGGMVVAMYLPIFKLGSVIH.. 413
NTDB id 1198 PSJM300 03950 AFN76868.1 VGGLIIAMYLPIFQMGSVV... 405
NTDB id 1016 ACIAD RS01680 WP 004920476.1 VGGLVIAMYLPIFQMGSVV... 408
NTDB id 1059 ABD1 RS01610 WP 000279215.1 VGGLVIAMYLPIFQMGSVV... 408
consensus
X non conserved
X similar
X ≥ 50% conserved