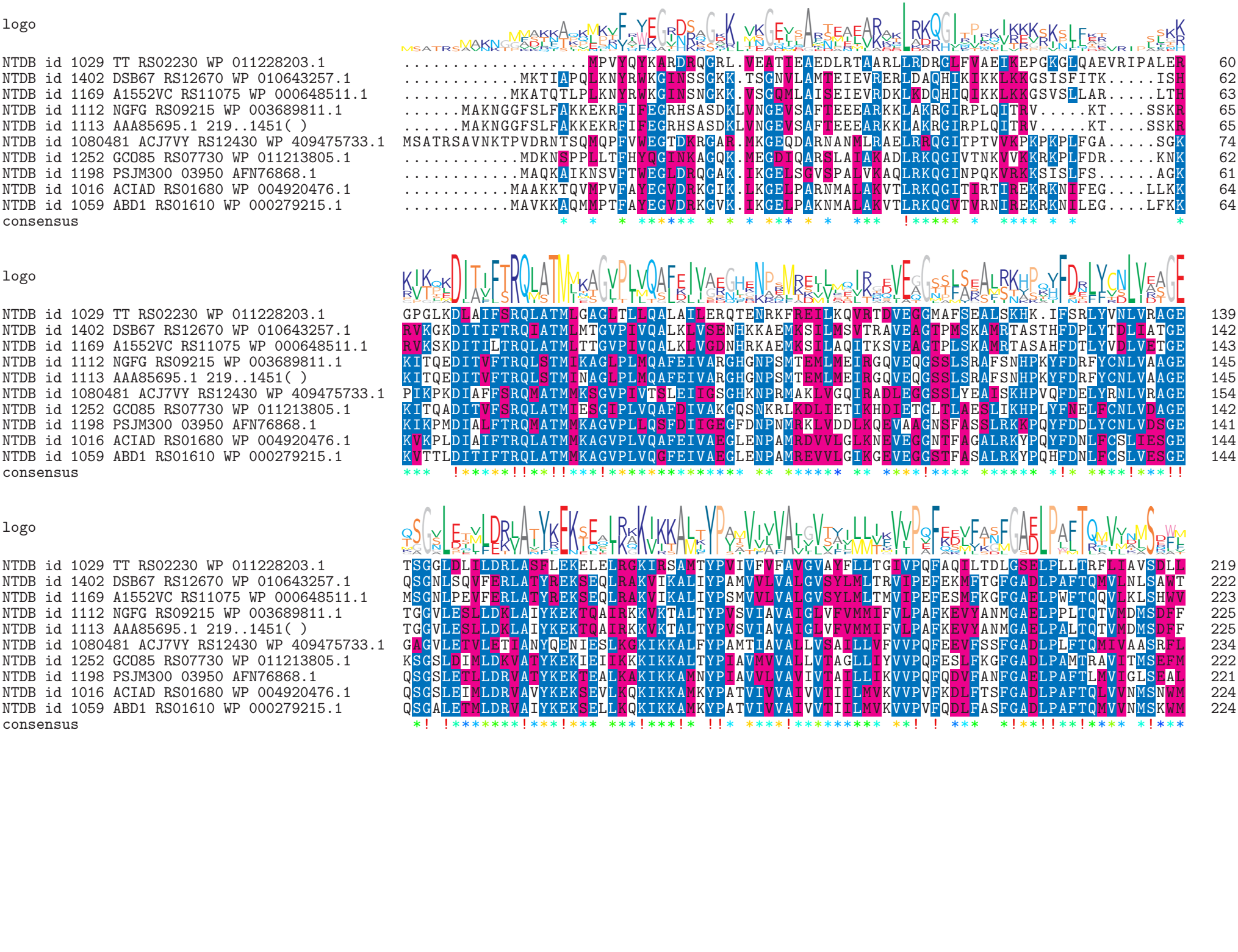
logo
NTDB id 1029 TT RS02230 WP 011228203.1 ..................MPVYQYKARDRQGRL.VEATIEAEDLRTAARLLRDRGLFVAEIKEPGKGLQAEVRIPALER 60
NTDB id 1402 DSB67 RS12670 WP 010643257.1 ............MKTIAPQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.....ISH 62
NTDB id 1169 A1552VC RS11075 WP 000648511.1 ...........MKATQTLPLKNYRWKGINSNGKK.VSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.....LTH 63
NTDB id 1112 NGFG RS09215 WP 003689811.1 ......MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KT....SSKR 65
NTDB id 1113 AAA85695.1 219..1451( ) ......MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KT....SSKR 65
NTDB id 1080481 ACJ7VY RS12430 WP 409475733.1 MSATRSAVNKTPVDRNTSQMQPFVWEGTDKRGAR.MKGEQDARNANMLRAELRRQGITPTVVKPKPKPLFGA.....SGK 74
NTDB id 1252 GCO85 RS07730 WP 011213805.1 ............MDKNSPPLLTFHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.....KNK 62
NTDB id 1198 PSJM300 03950 AFN76868.1 ............MAQKAIKNSVFTWEGLDRQGAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS......AGK 61
NTDB id 1016 ACIAD RS01680 WP 004920476.1 ...........MAAKKTQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITTRTIREKRKNIFEG....LLKK 64
NTDB id 1059 ABD1 RS01610 WP 000279215.1 ...........MAVKKAQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEG....LFKK 64
consensus
logo
NTDB id 1029 TT RS02230 WP 011228203.1 GPGLKDLAIFSRQLATMLGAGLTLLQALAILERQTENRKFREILKQVRTDVEGGMAFSEALSKHK.IFSRLYVNLVRAGE 139
NTDB id 1402 DSB67 RS12670 WP 010643257.1 RVKGKDITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIATGE 142
NTDB id 1169 A1552VC RS11075 WP 000648511.1 RVKSKDITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGE 143
NTDB id 1112 NGFG RS09215 WP 003689811.1 KITQEDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGE 145
NTDB id 1113 AAA85695.1 219..1451( ) KITQEDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGE 145
NTDB id 1080481 ACJ7VY RS12430 WP 409475733.1 PIKPKDIAFFSRQMATMMKSGVPIVTSLEIIGSGHKNPRMAKLVGQIRADLEGGSSLYEAISKHPVQFDELYRNLVRAGE 154
NTDB id 1252 GCO85 RS07730 WP 011213805.1 KITQADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGE 142
NTDB id 1198 PSJM300 03950 AFN76868.1 KIKPMDIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVDSGE 141
NTDB id 1016 ACIAD RS01680 WP 004920476.1 KVKPLDIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGE 144
NTDB id 1059 ABD1 RS01610 WP 000279215.1 KVTTLDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGE 144
consensus
logo
NTDB id 1029 TT RS02230 WP 011228203.1 TSGGLDLILDRLASFLEKELELRGKIRSAMTYPVIVFVFAVGVAYFLLTGIVPQFAQILTDLGSELPLLTRFLIAVSDLL 219
NTDB id 1402 DSB67 RS12670 WP 010643257.1 QSGNLSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLSAWT 222
NTDB id 1169 A1552VC RS11075 WP 000648511.1 MSGNLPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWV 223
NTDB id 1112 NGFG RS09215 WP 003689811.1 TGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFF 225
NTDB id 1113 AAA85695.1 219..1451( ) TGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFF 225
NTDB id 1080481 ACJ7VY RS12430 WP 409475733.1 GAGVLETVLETIANYQENIESLKGKIKKALFYPAMTIAVALLVSAILLVFVVPQFEEVFSSFGADLPLFTQMIVAASRFL 234
NTDB id 1252 GCO85 RS07730 WP 011213805.1 KSGSLDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFM 222
NTDB id 1198 PSJM300 03950 AFN76868.1 QSGSLETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEAL 221
NTDB id 1016 ACIAD RS01680 WP 004920476.1 QSGSLEIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWM 224
NTDB id 1059 ABD1 RS01610 WP 000279215.1 QSGALETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWM 224
consensus

logo

```
NTDB id 1029 TT RS02230 WP 011228203.1          RAATLPLLLLAVALFFAYRWY.YGTPQGRRVIDRLKLRLPVFGNLNRKTAVARFSRTLALLLSSGVNIVEALDITKGTAG  298
NTDB id 1402 DSB67 RS12670 WP 010643257.1       QNWGPFIGLSFVSLLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSG  302
NTDB id 1169 A1552VC RS11075 WP 000648511.1     QAYSLWAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAKTSG  303
NTDB id 1112 NGFG RS09215 WP 003689811.1        VSYGWMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAG  305
NTDB id 1113 AAA85695.1 219..1451( )            VSYGWMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAG  305
NTDB id 1080481 ACJ7VY RS12430 WP 409475733.1  VGWWWLILLVTVGAIVGFIFALKRSSRMQHTMDRLVLKVPVIGQIMHNSAIARFSRTTGVTFRAGVPLVEALGIVAGATG  314
NTDB id 1252 GCO85 RS07730 WP 011213805.1       QAYWYIIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATG  302
NTDB id 1198 PSJM300 03950 AFN76868.1           QAWWYVVLAGFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATG  301
NTDB id 1016 ACIAD RS01680 WP 004920476.1       QDYWFILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATN  304
NTDB id 1059 ABD1 RS01610 WP 000279215.1        QEYWFIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATN  304
consensus                                       ********************  **  **  ***   *****!**!**!***  **  *!***!!*******!******!********
```

logo

```
NTDB id 1029 TT RS02230 WP 011228203.1          NSVVEEIVEAAKLKIQQGDPLNLTLAQHPFVFPPMVSSMVAIGEETGALDTMLSKVADFYEREVDEAVASLTAAIEPLMI  378
NTDB id 1402 DSB67 RS12670 WP 010643257.1       NMHYQLAIEEVYRDTAAGMPMYIAMR.HCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLII  381
NTDB id 1169 A1552VC RS11075 WP 000648511.1     NVHFETAINEVYRDTAAGMPMYIAMR.NTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLII  382
NTDB id 1112 NGFG RS09215 WP 003689811.1        NLIYEEATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIII  384
NTDB id 1113 AAA85695.1 219..1451( )            NLIYEEATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIII  384
NTDB id 1080481 ACJ7VY RS12430 WP 409475733.1  NKVYEEAVLHMRDDVAVGYPVNMAMK.QVNVFPHMVIQMTAIGEEAGALDTMLFKVAEYFEQEVNNAVDALSSLIEPMIM  393
NTDB id 1252 GCO85 RS07730 WP 011213805.1       NIIYAKATDKIREEVATGQQMFIAME.NTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIM  381
NTDB id 1198 PSJM300 03950 AFN76868.1           NVVFRSATNKIKSDVSSGMQLNFSMR.TTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIM  380
NTDB id 1016 ACIAD RS01680 WP 004920476.1       NTVYEQAVLKIREDVSTGQQLNFAMR.VSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIM  383
NTDB id 1059 ABD1 RS01610 WP 000279215.1        NVIYEKAVMKIREDVATGQQLQFAMR.ISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIM  383
consensus                                       !****  **   **  ***  !* ******   * *!!  ****!**!!!!*!*!**!!  !*!***!  !!***!**!* **!!***
```

<0

logo

```
NTDB id 1029 TT RS02230 WP 011228203.1          IFLGVIVGMIVAGMFLPLFKIIGTLSVQ   406
NTDB id 1402 DSB67 RS12670 WP 010643257.1       VFLGVVVGGLVTAMYLPIFNLMSVLG..   407
NTDB id 1169 A1552VC RS11075 WP 000648511.1     VFLGTVVGGLVVAMYLPIFNLMSVLG..   408
NTDB id 1112 NGFG RS09215 WP 003689811.1        VILGLVIGTLLVAMYLPLFNLGNVVA..   410
NTDB id 1113 AAA85695.1 219..1451( )            LILGLVIGTLLVAMYLPLFNLGNVVA*.   410
NTDB id 1080481 ACJ7VY RS12430 WP 409475733.1   VFIGVIVGGMVIGMYLPIFKLASVVG..   419
NTDB id 1252 GCO85 RS07730 WP 011213805.1       SILGILVGGLVVAMYLPIFKLGSAV...   406
NTDB id 1198 PSJM300 03950 AFN76868.1           AVLGVLVGGLIIAMYLPIFQMGSVV...   405
NTDB id 1016 ACIAD RS01680 WP 004920476.1       AILGILVGGLVIAMYLPIFQMGSVV...   408
NTDB id 1059 ABD1 RS01610 WP 000279215.1        AILGVLVGGLVIAMYLPIFQMGSVV...   408
consensus                                       ***!***!*****!*!!*!*******
```

X non conserved
X similar
X ≥ 50% conserved