logo

```
NTDB id 1402 DSB67 RS12670 WP 010643257.1 ..................MKTIAPQLKNYRWKGINSS.GKKTSGNVLAMTEIEVRERLDAQHIKKIKKLKKGSISFITK.  59
NTDB id 1169 A1552VC RS11075 WP 000648511.1 ..................MKATQTLPLKNYRWKGINSN.GKKVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.  60
NTDB id 1252 GCO85 RS07730 WP 011213805.1 ..................MDKNSPPLLTFHYQGINKA.GQKMEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.  59
NTDB id 1198 PSJM300 03950 AFN76868.1 ..................MAQKAIKNSVFTWEGLDRQ.GAKIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..  58
NTDB id 1016 ACIAD RS01680 WP 004920476.1 ..................MAAKKTQVMPVFAYEGVDRK.GIKLKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGL  61
NTDB id 1059 ABD1 RS01610 WP 000279215.1 ..................MAVKKAQMMPTFAYEGVDRK.GVKIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGL  61
NTDB id 1043387 ACEN2X RS12075 WP 014616068.1 MATRAPTANRSAAASARKTASTKAPTQYIFEWEGKDRK.GKAFKGEMRAESITEVNAVLRKQGLSITKSKRRRAA.....  74
NTDB id 1112 NGFG RS09215 WP 003689811.1 ..........MAKNGGFSLFAKKEKRFI..FEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKTS.....  62
NTDB id 1113 AAA85695.1 219..1451( ) ..........MAKNGGFSLFAKKEKRFI..FEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKTS.....  62
consensus                                      *  *   * ** **!* *  **** !** * *  ***  !***** * ****** **
```

logo

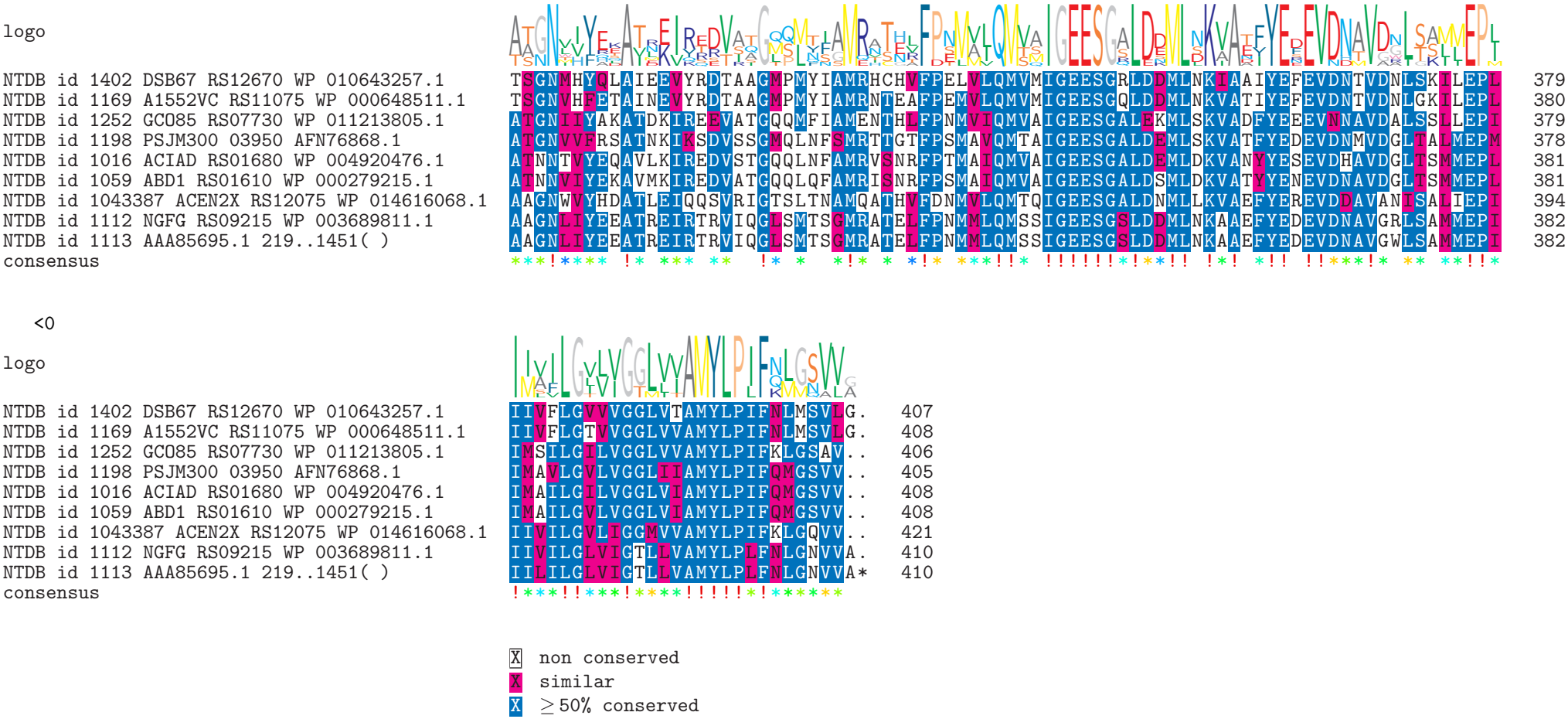
```
NTDB id 1402 DSB67 RS12670 WP 010643257.1 ISHRVKGKDITIFTRQIATMLMTGVPIVQALKLVSENHKKAEMKSILMSVTRAVEAGTPMSKAMRTASTHFDPLYTDLIA 139
NTDB id 1169 A1552VC RS11075 WP 000648511.1 LTHRVKSKDITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVE 140
NTDB id 1252 GCO85 RS07730 WP 011213805.1 KNKKITQADITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVD 139
NTDB id 1198 PSJM300 03950 AFN76868.1 AGKKIKPMDIALFTRQMATMMKAGVPLLQSFDIIGEGFDNPNMRKLVDDLKQEVAAGNSFASSLRKKPQYFDDLYCNLVD 138
NTDB id 1016 ACIAD RS01680 WP 004920476.1 LKKKVKPLDIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIE 141
NTDB id 1059 ABD1 RS01610 WP 000279215.1 FKKKVTTLDITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVE 141
NTDB id 1043387 ACEN2X RS12075 WP 014616068.1 RGKKITPKDVAYFTRQLSTMLKAGVPLLQSVDIIARGHANPNFTQLLTEIRVDIESGSSMAQAFRRHPKYFDSLYCNLID 154
NTDB id 1112 NGFG RS09215 WP 003689811.1 SKRKITQEDITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVA 142
NTDB id 1113 AAA85695.1 219..1451( ) SKRKITQEDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVA 142
consensus                                  ****  !*****!!**!!***!*!**!********** ** ****** ** ****!**** **** * *!* ****!**
```

logo

```
NTDB id 1402 DSB67 RS12670 WP 010643257.1 TGEQSGNLSQVFERLATYREKSEQLRAKVIKALIYPAMVVLVALGVSYLMLTRVIPEFEKMFTGFGADLPAFTQMVLNLS 219
NTDB id 1169 A1552VC RS11075 WP 000648511.1 TGEMSGNLPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLS 220
NTDB id 1252 GCO85 RS07730 WP 011213805.1 AGEKSGSLDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMS 219
NTDB id 1198 PSJM300 03950 AFN76868.1 SGEQSGSLETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLS 218
NTDB id 1016 ACIAD RS01680 WP 004920476.1 SGEQSGSLEIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMS 221
NTDB id 1059 ABD1 RS01610 WP 000279215.1 SGEQSGALETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMS 221
NTDB id 1043387 ACEN2X RS12075 WP 014616068.1 AGEQGGILDALLERLSMYMEKSIALKAQIKSAMIYPISVLTVAFLVTVVLMIFVVPAFKNVFASFGATLPAPTLVVMNIS 234
NTDB id 1112 NGFG RS09215 WP 003689811.1 AGETGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMS 222
NTDB id 1113 AAA85695.1 219..1451( ) AGETGGVLESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMS 222
consensus *!!**!  !* *******!*!!** ** ****!* !!**!**!!**** **** !*! ! **** *!!*!!**!**!* *!
```

logo

```
NTDB id 1402 DSB67 RS12670 WP 010643257.1 AWTQNWGPFIGLSFVSLLISGKIMSQRSDSFRLLAARSSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSK 299
NTDB id 1169 A1552VC RS11075 WP 000648511.1 HWVQAYSLWAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTTAK 300
NTDB id 1252 GCO85 RS07730 WP 011213805.1 EFMQAYWYIIFGALGCVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAG 299
NTDB id 1198 PSJM300 03950 AFN76868.1 EALQAWWYVVLAGFVCAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAG 298
NTDB id 1016 ACIAD RS01680 WP 004920476.1 NWMQDYWFILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAG 301
NTDB id 1059 ABD1 RS01610 WP 000279215.1 KWMQEYWFIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAG 301
NTDB id 1043387 ACEN2X RS12075 WP 014616068.1 DFFVKWWYIIIFAPVVGIFLYARAFKRSLKVQRNTHKAILKMPIFGSIIRKATIARWTRTLATMFSAGTPLVESMESVAG 314
NTDB id 1112 NGFG RS09215 WP 003689811.1 DFFVSYGWMVLIALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAG 302
NTDB id 1113 AAA85695.1 219..1451( ) DFFVSYGWMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAG 302
consensus **** ***************  ** *! *** *****!**!**!*** !***!***!!*****!*!!*!********** 
```


logo
NTDB id 1402 DSB67 RS12670 WP 010643257.1 TSGNMHYQLAIEEVYRDTAAGMPMYIAMRHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPL 379
NTDB id 1169 A1552VC RS11075 WP 000648511.1 TSGNVHFETAINEVYRDTAAGMPMYIAMRNTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPL 380
NTDB id 1252 GCO85 RS07730 WP 011213805.1 ATGNIIYAKATDKIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPI 379
NTDB id 1198 PSJM300 03950 AFN76868.1 ATGNVVFRSATNKIKSDVSSGMQLNFSMRTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPM 378
NTDB id 1016 ACIAD RS01680 WP 004920476.1 ATNNTVYEQAVLKIREDVSTGQQLNFAMRVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPL 381
NTDB id 1059 ABD1 RS01610 WP 000279215.1 ATNNVIYEKAVMKIREDVATGQQLQFAMRISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPL 381
NTDB id 1043387 ACEN2X RS12075 WP 014616068.1 AAGNWVYHDATLEIQQSVRIGTSLTNAMQATHVFDNMVLQMTQIGEESGALDNMLLKVAEFYEREVDDAVANISALIEPI 394
NTDB id 1112 NGFG RS09215 WP 003689811.1 AAGNLIYEEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPI 382
NTDB id 1113 AAA85695.1 219..1451( ) AAGNLIYEEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPI 382
consensus
<0
logo
NTDB id 1402 DSB67 RS12670 WP 010643257.1 IIVFLGVVVGGLVTAMYLPIFNLMSVLG. 407
NTDB id 1169 A1552VC RS11075 WP 000648511.1 IIVFLGTVVGGLVVAMYLPIFNLMSVLG. 408
NTDB id 1252 GCO85 RS07730 WP 011213805.1 IMSILGILVGGLVVAMYLPIFKLGSAV.. 406
NTDB id 1198 PSJM300 03950 AFN76868.1 IMAVLGVLVGGLIIAMYLPIFQMGSVV.. 405
NTDB id 1016 ACIAD RS01680 WP 004920476.1 IMAILGILVGGLVIAMYLPIFQMGSVV.. 408
NTDB id 1059 ABD1 RS01610 WP 000279215.1 IMAILGVLVGGLVIAMYLPIFQMGSVV.. 408
NTDB id 1043387 ACEN2X RS12075 WP 014616068.1 IIVILGVLIGGMVVAMYLPIFKLGQVV.. 421
NTDB id 1112 NGFG RS09215 WP 003689811.1 IIVILGLVIGTLLVAMYLPLFNLGNVVA. 410
NTDB id 1113 AAA85695.1 219..1451( ) IILILGLVIGTLLVAMYLPLFNLGNVVA* 410
consensus
X non conserved
X similar
X ≥ 50% conserved