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NTDB id 1113 AAA85695.1 219..1451( )          .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KTSSKRKITQEDITV  74
NTDB id 1112 NGFG RS09215 WP 003689811.1      .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRV.....KTSSKRKITQEDITV  74
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NTDB id 1059 ABD1 RS01610 WP 000279215.1      MAVKK......AQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVTTLDITI  73
consensus                                      ***        *  *  * **!* * * ! * !** * * **** !***** ***** *      **** !!**
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NTDB id 1112 NGFG RS09215 WP 003689811.1      FTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESLL 154
NTDB id 1144739 LPM7613 RS06950 WP 010947252.1 FSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSLDIML 151
NTDB id 1252 GCO85 RS07730 WP 011213805.1     FSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSLDIML 151
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NTDB id 1016 ACIAD RS01680 WP 004920476.1     FTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSLEIML 153
NTDB id 1059 ABD1 RS01610 WP 000279215.1      FTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGALETML 153
consensus                                      **!!**!!* *!*!**!********  **  ****** **  ****!**** **** * *!* ****!***!! *! !* **
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NTDB id 1113 AAA85695.1 219..1451( )          DKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGWMVLI 234
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NTDB id 1144739 LPM7613 RS06950 WP 010947252.1 DKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWYIIFG 231
NTDB id 1252 GCO85 RS07730 WP 011213805.1     DKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWYIIFG 231
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NTDB id 1059 ABD1 RS01610 WP 000279215.1      DRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWFIMII 233
consensus                                      ***!*!*!!** **  !***!* !!* !**!!**** **** !*! ! ***  *!!*!!**!* !* *!**** ********
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NTDB id 1113 AAA85695.1 219..1451( )          ALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEATR 314
NTDB id 1112 NGFG RS09215 WP 003689811.1      ALGFAIYGFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEATR 314
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NTDB id 1252 GCO85 RS07730 WP 011213805.1     ALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAKATD 311
NTDB id 1198 PSJM300 03950 AFN76868.1         GFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDILYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVFRSATN 310
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NTDB id 1059 ABD1 RS01610 WP 000279215.1      AIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYEKAVM 313
consensus                                      *********  **  *!  ***  *****!**!**!*** !* *!***!!****!*!!*!****!  *******!**** !*
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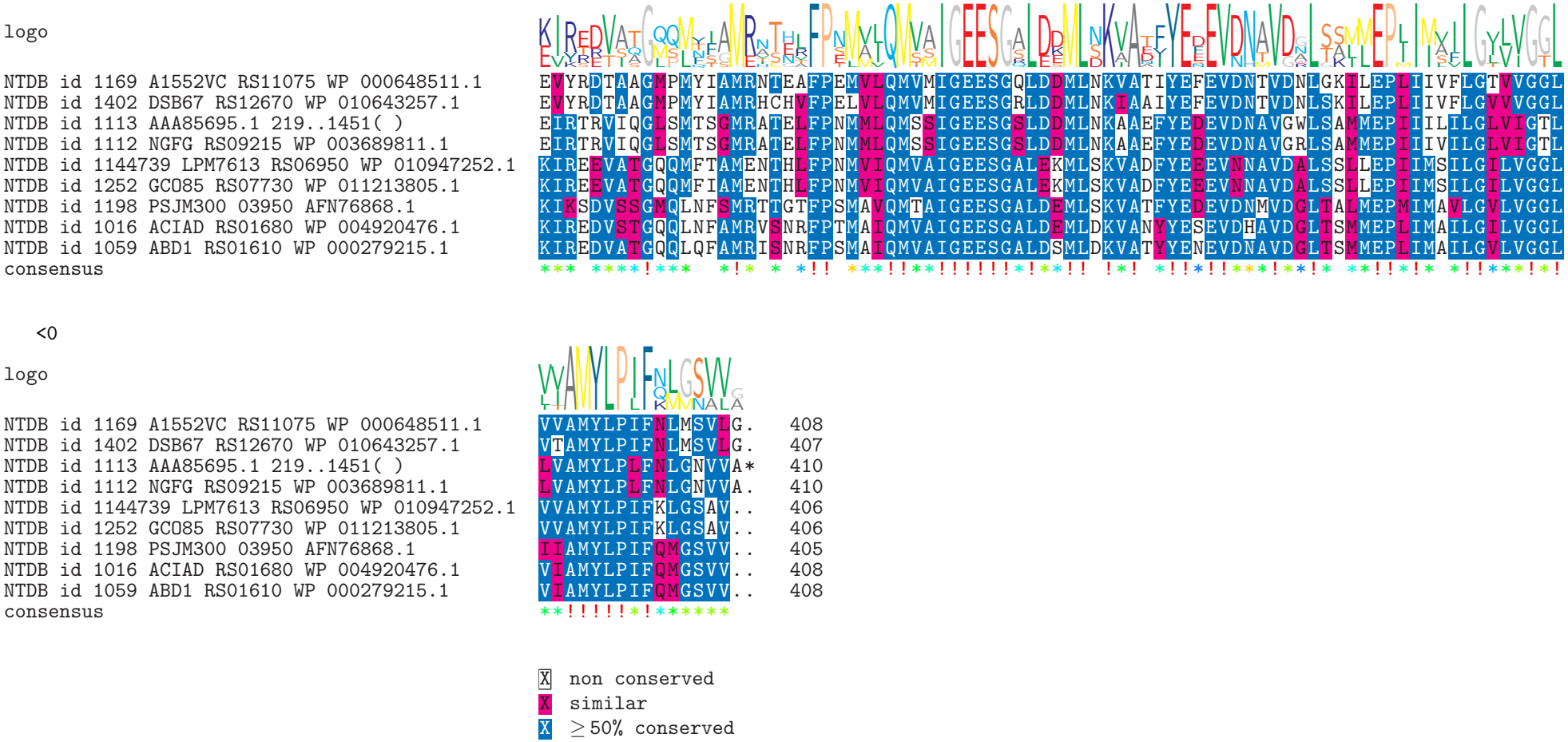
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NTDB id 1402 DSB67 RS12670 WP 010643257.1 EVYRDTAAGMPMYIAMRHCHVFPELVLQMVMIGEESGRLDDMLNKIAAIYEFEVDNTVDNLSKILEPLIIVFLGVVVGGL 391
NTDB id 1113 AAA85695.1 219..1451( ) EIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIILILGLVIGTL 394
NTDB id 1112 NGFG RS09215 WP 003689811.1 EIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGLVIGTL 394
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NTDB id 1252 GCO85 RS07730 WP 011213805.1 KIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGILVGGL 391
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consensus
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consensus
X non conserved
X similar
X ≥ 50% conserved