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NTDB id 1018877 ABX013 RS02340 WP 084547381.1 MNKPVAVSKTKSSGTSFSFEGKNLKTEQIVRGEVVAKDEADARAKLTRRQIRVIQIAKVKK.....QRQKKISQADITVF  75
NTDB id 1112 NGFG RS09215 WP 003689811.1     MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKT.....SSKRKITQEDITVF  75
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NTDB id 1059 ABD1 RS01610 WP 000279215.1     .....MAVKKAQMMPTFAYEGVDRKGVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVTTLDITIF  74
consensus                                            * **!*   * * * !** * * * **  !*****    * * *  *       ****  !!***
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NTDB id 1112 NGFG RS09215 WP 003689811.1     TRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESLLD  155
NTDB id 1113 AAA85695.1 219..1451( )         TRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVLESLLD  155
NTDB id 1252 GCO85 RS07730 WP 011213805.1    SRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSLDIMLD  152
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consensus                                    *!!**!!***!*!**!****** *  ** ****** ** *** !**** ** *  * *!* ****!** !! *! !* ***
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NTDB id 1018877 ABX013 RS02340 WP 084547381.1 KLSVYKEKTQGIKKKVKSALTYPAVVVVVAIALVIVMMMFVLPSFGKVYEGMGVPLPGLTQFMMNISDFFVHYGVFVIIA  235
NTDB id 1112 NGFG RS09215 WP 003689811.1     KLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPPLTQTVMDMSDFFVSYGWMVLIA  235
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consensus                                    ****!*!!** ** !***!* !!  !**!!* ** **** !*! ! ***  *!**!!* !* ** *!**** * ******
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NTDB id 1112 NGFG RS09215 WP 003689811.1     LGFAIYGFLKLKAKRSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYEEATRE  315
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NTDB id 1252 GCO85 RS07730 WP 011213805.1    LGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIYAKATDK  312
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NTDB id 1059 ABD1 RS01610 WP 000279215.1     IGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYEKAVMK  314
consensus                                    ********   * *! * *  *****!**!* !*** !***!** !!****!!!!*!*** !***!****!**** !*
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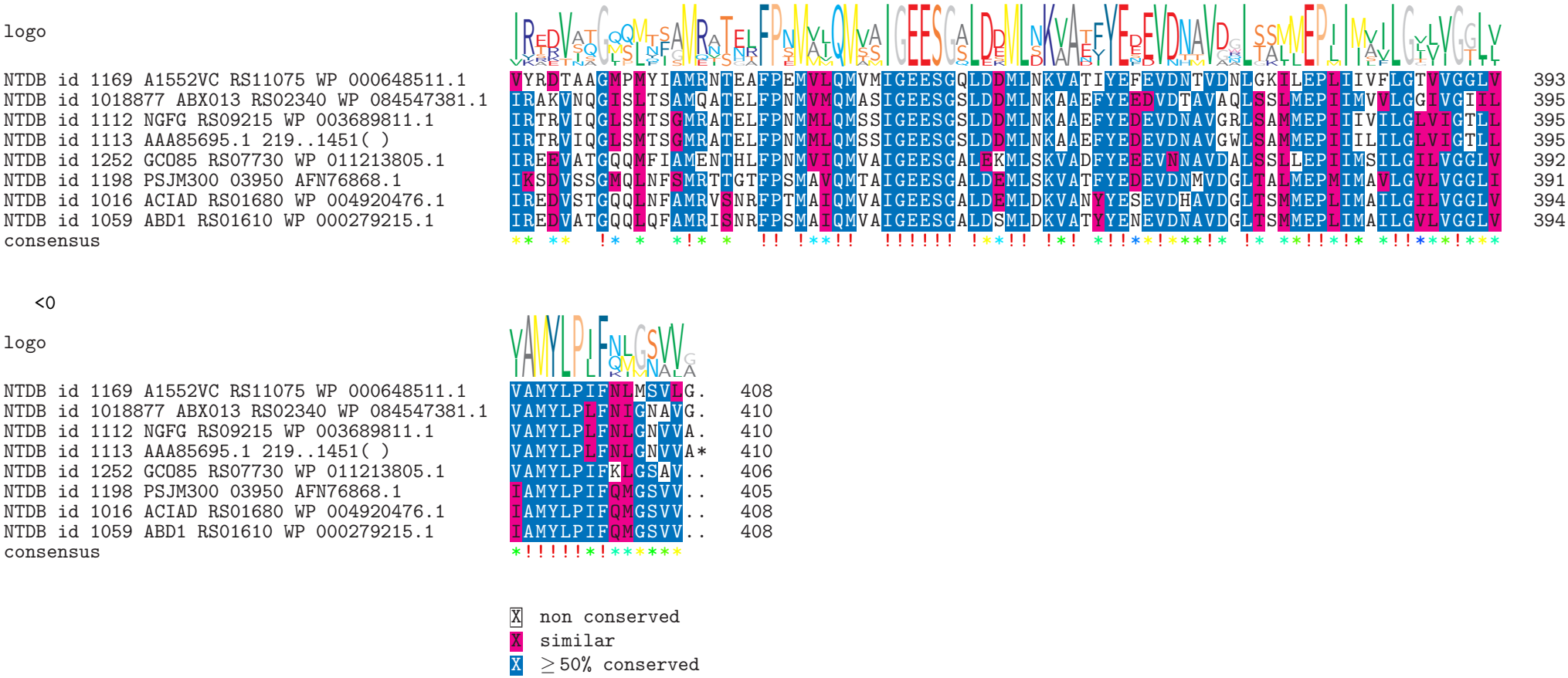
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NTDB id 1112 NGFG RS09215 WP 003689811.1 IRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGLVIGTLL 395
NTDB id 1113 AAA85695.1 219..1451( ) IRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGLVIGTLL 395
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consensus
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NTDB id 1112 NGFG RS09215 WP 003689811.1 VAMYLPLFNLGNVVA. 410
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NTDB id 1016 ACIAD RS01680 WP 004920476.1 IAMYLPIFQMGSVV.. 408
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consensus
X non conserved
X similar
X ≥ 50% conserved