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logo
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NTDB id 1402 DSB67 RS12670 WP 010643257.1     ...........MKTIAPQLKNYRWKGINSSGKK.TSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.ISHRVKG   66
NTDB id 1112 NGFG RS09215 WP 003689811.1      ......MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVK.....TSSKRKITQ   69
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NTDB id 1198 PSJM300 03950 AFN76868.1         ...........MAQKAIKNSVFTWEGLDRQGAK.IKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKKIKP   65
NTDB id 1016 ACIAD RS01680 WP 004920476.1     ...........MAAKKTQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKKVKP   68
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NTDB id 1076866 ACJGEZ RS07700 WP 011408067.1 MSVARSAIKKQPVDRNTSMLQTFIWEGADKRGVK.MKGEQTARNANMLRAELRRQGIVPSMVKQKPKPLFGG.AGKKITP   78
NTDB id 1252 GC085 RS07730 WP 011213805.1     ...........MDKNSPPLLTFHYQGINKAGQK.MEGDIQARSLAIAKADLRKQGIVTNKVVKKRKPLFDR.KNKKITQ   66
consensus                                                  *  *  * **!* * * ! * !** * *  ***  !*****    *****  *      ****

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NTDB id 1113 AAA85695.1 219..1451( )          EDITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGV   149
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consensus                                      *!****!!**!!***!*!************ ** ****** ** ****!***  **** * *!* ****!***!! *!

logo
NTDB id 1169 A1552VC RS11075 WP 000648511.1   LPEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYS   227
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NTDB id 1059 ABD1 RS01610 WP 000279215.1      LETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYW   228
NTDB id 1076866 ACJGEZ RS07700 WP 011408067.1 LETVLETVATYKENIEALKGKIKKALFYPAMVVAVAIIVSAILLIFVVPQFEEVFKSFGAELPAFTQLLVNASRFMVSYW   238
NTDB id 1252 GC085 RS07730 WP 011213805.1     LDIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYW   226
consensus                                     !*******!*!*!*** ** !***!* !!  !**!!**** **** !*! ! ***  *!!*!!**!**** *! *** **

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NTDB id 1113 AAA85695.1 219..1451( )          WMVLIALGFAIYRFLKLKARSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIY   309
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NTDB id 1059 ABD1 RS01610 WP 000279215.1      FIMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIY   308
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NTDB id 1252 GC085 RS07730 WP 011213805.1     YIIFGALGGVVYSFFYAKNHSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIY   306
consensus                                     ************** ** *! ***  ****!**!**!*** ** *!***!!****!*!!*!****! *******!***
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logo
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NTDB id 1113 AAA85695.1 219..1451( )           EEATREIRTRVIQGLSMTSGMRATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGL   389
NTDB id 1198 PSJM300 03950 AFN76868.1          RSATNKIKSDVSSGMQLNFSMRTTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGV   385
NTDB id 1016 ACIAD RS01680 WP 004920476.1      EQAVLKIREDVSTGQQLNFAMRVSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHAVDGLTSMMEPLIMAILGI   388
NTDB id 1059 ABD1 RS01610 WP 000279215.1       EKAVMKIREDVATGQQLQFAMRISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGV   388
NTDB id 1076866 ACJGEZ RS07700 WP 011408067.1 EEAVFRMRDDVSVGYPVNMAMKQVNLFPHMVIQMTAIGEEAGALDAMLFKVAEYFEEEVNNAVDALSSLLEPLIMVFIGT   398
NTDB id 1252 GC085 RS07730 WP 011213805.1     AKATDKIREEVATGQQMFIAMENTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGI   386
consensus                                      * !* *** **  !* *  *!* * *!! ***!!**!!!!*!*!**!! !*! **!*!!***!**!* **!!*!****!*
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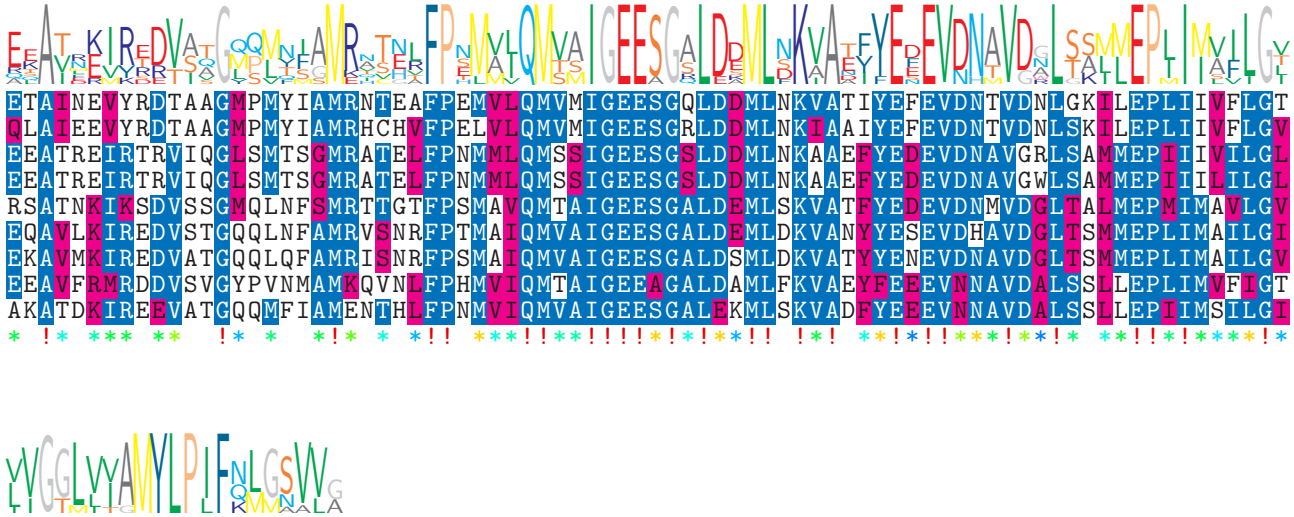

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NTDB id 1112 NGFG RS09215 WP 003689811.1       VIGTLLVAMYLPLFNLGNVVA.   410
NTDB id 1113 AAA85695.1 219..1451( )           VIGTLLVAMYLPLFNLGNVVA*   410
NTDB id 1198 PSJM300 03950 AFN76868.1          LVGGLIIAMYLPIFQMGSVV..   405
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NTDB id 1059 ABD1 RS01610 WP 000279215.1       LVGGLVIAMYLPIFQMGSVV..   408
NTDB id 1076866 ACJGEZ RS07700 WP 011408067.1 IVGGMVIGMYLPIFKLGAVVG.   419
NTDB id 1252 GC085 RS07730 WP 011213805.1     LVGGLVVAMYLPIFKLGSAV..   406
consensus                                      **!*****!!!!*!*******
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X non conserved
X similar
X ≥ 50% conserved