logo

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NTDB id 1402 DSB67 RS12670 WP 010643257.1   .MKTI......APQLKNYRWKGINSSGK.KTSGNVLAMTEIEVRERLDAQHIKIKKLKKGSISFITK.....ISHRVKGK    67
NTDB id 1169 A1552VC RS11075 WP 000648511.1 MKATQ......TLPLKNYRWKGINSNGK.KVSGQMLAISEIEVRDKLKDQHIQIKKLKKGSVSLLAR.....LTHRVKSK    68
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NTDB id 1113 AAA85695.1 219..1451( )        .MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSAFTEEEARKKLAKRGIRPLQITRVKT.....S....SKRKITQE    70
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NTDB id 55788 H045 RS00785 WP 004372350.1   ....M......NNASTTYDWEGINRKGR.RVSGQTTAHNPALVKAQLRQQGISPGRVRKRYPGLPG......LTQPIKPS    63
NTDB id 1198 PSJM300 03950 AFN76868.1       .MAQK......AIKNSVFTWEGLDRQGA.KIKGELSGVSPALVKAQLRKQGINPQKVRKKSISLFS......AGKKIKPM    66
NTDB id 1016 ACIAD RS01680 WP 004920476.1   MAAKK......TQVMPVFAYEGVDRKGI.KLKGELPARNMALAKVTLRKQGITTRTIREKRKNIFEGL....LKKKVKPL    69
NTDB id 1059 ABD1 RS01610 WP 000279215.1    MAVKK......AQMMPTFAYEGVDRKGV.KIKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGL....FKKKVTTL    69
consensus                                    ***         *  *  * **** * *  ** *** * * ****  !***** * ******  *         * ****
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NTDB id 1169 A1552VC RS11075 WP 000648511.1 DITILTRQLATMLTTGVPIVQALKLVGDNHRKAEMKSILAQITKSVEAGTPLSKAMRTASAHFDTLYVDLVETGEMSGNL   148
NTDB id 1112 NGFG RS09215 WP 003689811.1    DITVFTRQLSTMIKAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL   150
NTDB id 1113 AAA85695.1 219..1451( )        DITVFTRQLSTMINAGLPLMQAFEIVARGHGNPSMTEMLMEIRGQVEQGSSLSRAFSNHPKYFDRFYCNLVAAGETGGVL   150
NTDB id 1252 GCO85 RS07730 WP 011213805.1   DITVFSRQLATMIESGIPLVQAFDIVAKGQSNKRLKDLIETIKHDIETGLTLAESLIKHPLYFNELFCNLVDAGEKSGSL   147
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NTDB id 1016 ACIAD RS01680 WP 004920476.1   DIAIFTRQLATMMKAGVPLVQAFEIVAEGLENPAMRDVVLGLKNEVEGGNTFAGALRKYPQYFDNLFCSLIESGEQSGSL   149
NTDB id 1059 ABD1 RS01610 WP 000279215.1    DITIFTRQLATMMKAGVPLVQGFEIVAEGLENPAMREVVLGIKGEVEGGSTFASALRKYPQHFDNLFCSLVESGEQSGAL   149
consensus                                   !*****!!**!****!****!*********  ***  ******  **  ****!***   ****  *  *!*  ****!***!!**!  !
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NTDB id 1169 A1552VC RS11075 WP 000648511.1 PEVFERLATYREKSEQLRAKVIKALIYPSMVVLVALGVSYLMLTMVIPEFESMFKGFGAELPWFTQQVLKLSHWVQAYSL   228
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NTDB id 1113 AAA85695.1 219..1451( )        ESLLDKLAIYKEKTQAIRKKVKTALTYPVSVIAVAIGLVFVMMIFVLPAFKEVYANMGAELPALTQTVMDMSDFFVSYGW   230
NTDB id 1252 GCO85 RS07730 WP 011213805.1   DIMLDKVATYKEKIEIIKKKIKKALTYPIAVMVVALLVTAGLLIYVVPQFESLFKGFGADLPAMTRAVITMSEFMQAYWY   227
NTDB id 55788 H045 RS00785 WP 004372350.1   ETLLERVAVHQEKTEQLKARIRKAMTYPIAVIVVASVVCSVLLIHVVPQFEQLFAGVDGTLPGFTLLIIALSAFMQQAWW   223
NTDB id 1198 PSJM300 03950 AFN76868.1       ETLLDRVATYKEKTEALKAKIKKAMNYPIAVVLVAVIVTAILLIKVVPQFQDVFANFGAELPAFTLMVIGLSEALQAWWY   226
NTDB id 1016 ACIAD RS01680 WP 004920476.1   EIMLDRVAVYKEKSEVLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFKDLFTSFGADLPAFTQLVVNMSNWMQDYWF   229
NTDB id 1059 ABD1 RS01610 WP 000279215.1    ETMLDRVAIYKEKSELLKQKIKKAMKYPATVIVVAIVVTIILMVKVVPVFQDLFASFGADLPAFTQMVVNMSKWMQEYWF   229
consensus                                   *******! **!!** *******!**!!* !***!********** **! ! **** ****!!**!**** *!**** ***
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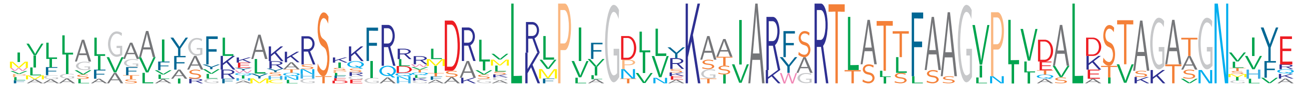

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NTDB id 55788 H045 RS00785 WP 004372350.1 LIALGLATVFFGVRHACLSSSGFRHRLDAGVLKLPLAGTLLKKSAVARYARTLSTTFAAGVPLVQALESVAGAVGNGLFK   303
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NTDB id 1016 ACIAD RS01680 WP 004920476.1  ILILVIGAAIAGFLEARKRSKRFRDQLDRLVLRLPIVGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVYE   309
NTDB id 1059 ABD1 RS01610 WP 000279215.1   IMIIAIGAVIAAFLEAKKRSKKFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYE   309
consensus                                  *************  ** ** ***  *****!**!**!*** !* *!***!!*******!******!********!****
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NTDB id 1169 A1552VC RS11075 WP 000648511.1 TAINEVYRDTAAGMPMYIAMR.NTEAFPEMVLQMVMIGEESGQLDDMLNKVATIYEFEVDNTVDNLGKILEPLIIVFLGT  387
NTDB id 1112 NGFG RS09215 WP 003689811.1   EATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGRLSAMMEPIIIVILGL   389
NTDB id 1113 AAA85695.1 219..1451( )      EATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEDEVDNAVGWLSAMMEPIIILILGL   389
NTDB id 1252 GCO85 RS07730 WP 011213805.1  KATDKIREEVATGQQMFIAME.NTHLFPNMVIQMVAIGEESGALEKMLSKVADFYEEEVNNAVDALSSLLEPIIMSILGI   386
NTDB id 55788 H045 RS00785 WP 004372350.1 QAIEHMRHDVSTGMPLHQSMA.SSGLFPRMAIQMTAIGEESGTLDHMLEKVASHYESDVDNQVDNLTSLMEPLIMVVLGG   382
NTDB id 1198 PSJM300 03950 AFN76868.1     SATNKIKSDVSSGMQLNFSMR.TTGTFPSMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGV   385
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NTDB id 1059 ABD1 RS01610 WP 000279215.1   KAVMKIREDVATGQQLQFAMR.ISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGV   388
consensus                                   **  ** ** *!* *  ***  * *!! ****!**!!!!*!*!**!!  !*! *!! *!***!* !* **!!*****!!*
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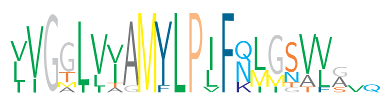

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NTDB id 1059 ABD1 RS01610 WP 000279215.1   LVGGLVIAMYLPIFQMGSVV...   408
consensus                                  **!*****!*!!*!******
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X non conserved

X similar

X $\geq$ 50% conserved