

[illegible][illegible][illegible]

NTDB id	1402 DSB67 RS12670 WP 010643257.1	PFI ^T GLSFVSLIISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSTRLATSFSAAGIPILTALKTTSTKTSGNMHY	306
NTDB id	1169 A1552VC RS11075 WP 000648511.1	LWAFIAIAAAIFGLKALRKNSFQIRLKTSRLGLKFPIIGNVLAKASIAKFSTRLATSFSAAGIPILASLKTATAKTSGNVHF	307
NTDB id	1112 NGFG RS09215 WP 003689811.1	WMVLIALCFAYRYFLKLARSIIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIY	309
NTDB id	1113 AAA85695.1 219..1451()	WMVLIALCFAYRYFLKLARKSIKIQRMRDAILLRMPPFVGDIVRGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIY	309
NTDB id	1198 PJMJ300 O3950 AFN76868.1	VVVLAGVFCAAYAFAFKQAHTRESEKFRNWFDRLMLKVTVGGDILYKSSVARFARTLTSTTFGAAGVPLVDALDSVAGATGNVVF	305
NTDB id	1016 ACIAD RS01680 WP 004920476.1	FILILIITGAAIAGFLEARKRSKRFRDQLDLRLVLRLPVIGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNITY	308
NTDB id	1059 ABD1 RS01610 WP 000279215.1	FIMIIAICAVIAAFLEAKKRKKFRDGDKLALKLPVIGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIY	308
NTDB id	191899 BCV67 RS04905 WP 062166722.1	WIILLALVGSIVGFLYAYKRSPAMQHMTDKLILKVPVTIQIMHNSAIARFARTTGVTFFKAGVPLVEALGVAGATGNISVY	318
NTDB id	1252 GC085 RS07730 WP 011213805.1	YLIFGALCGVVYSFFYA ^N KHSLEFAQTIDRVMLKLPLVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIIY	306
consensus		*****~*****~**~!~***~****~!!~*****~*****~!*~*****~*****~!~*****~*****~!	

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NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 1112 NGFG RS09215 WP 003689811.1
NTDB id 1113 AAA85695.1 219..1451( )
NTDB id 1198 PSJM300 03950 AFN76868.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
NTDB id 191899 BCV67 RS04905 WP 062166722.1
NTDB id 1252 GC085 RS07730 WP 01123805.1
consensus

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logo

Sequence	Position
QLAIEEVYRDTAAGMPMYIAMRHCHVFPPELVLMQVMIGEESGRLLDDMLNKTAATYEFVDNNTVDNLSKILEPLIIVFLGV	386
ETAINEVYRDTAAGMPMYIAMRNTEAFPEMVLQVMVIGEESGQLDDMLNKVATYEFVDNNTVDNLGKILEPLIIVFLGT	387
EATREIRTRVDTAAGLSMTSCMRATELFPNMMLQMSIGEESCSLDDMLNKAAEFYEDVDNAVGRLSAMMEPIIIVFLGL	389
EATREIRTRVDTAAGLSMTSCMRATELFPNMMLQMSIGEESCSLDDMLNKAAEFYEDVDNAVGRLSAMMEPIIILILGL	389
RSATNKIKSDVSSGMLNFSMRTTGTFFPSMAVQMTAIGEESGALDEMLSKVATFYEDVDNMVDGLTALMEPMIMAVLGV	385
EQAVLKIREDVSTGQQLNFAVRVSNRFPMTAQMVAIGEESGALDEMLDKVANYYESEDVDAVDGLTSMMEPLIMAILGI	388
EKAVMKIREDVATGQQLNFAVRVSNRFPMTAQMVAIGEESGALDSMLDKVATYYENVDNAVDGLTSMMEPLIMAILGV	388
EKAVLMRRDDVAVGYPVNFAMKQVNLFPHVIQMTAIGEEAGALDAFLKVAEYYEQEVNAVDALSSLEPLMIMVFIGT	398
AKATDKIREEVATGQQMFIAMENTHLFPNMVIQMTAIGEESGALDKMLSKVADEYEEVNVNAVDALSSLEPIIMSILGT	386

[illegible]

-  non conserved
-  similar
-  $\geq 50\%$ conserved