

NTDB id 1169 A1552VC RS11075 WP 000648511.1	MKATQTLPLKNYRWKGINSNGKK.VSQQLLAISEIEVRDKLKDQHTQIKKKKGSVSLAR.LTHRVRK	66
NTDB id 1402 DSB67 RS12670 WP 010643257.1	MKTIAPQIKNYRWKGINSNGKK.TSGNVLAMTEIEVRERLDAQHTIKIKKKKGSISFITK.ISHRVK	65
NTDB id 1112 NGFG RS09215 WP 003689811.1	MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSFAFTEEEARKKLAKRGIRPLQITRV....KTSSKRKIT	68
NTDB id 1113 AAA85695.1 219..1451()	MAKNGGFSLFAKKEKRFIFEGRHSASDKLVNGEVSFAFTEEEARKKLAKRGIRPLQITRV....KTSSKRKIT	68
NTDB id 999804 ABFU18 RS05440 WP 057671824.1	MSVVRNAIKKQVVDRSTGQQQLFLWEGTDKRGIK.MKGEQTARNMNLRAELRKGGINPSVVKPKPKLFGA.AGKKIT	78
NTDB id 1252 GC085 RS07730 WP 011213805.1	MDKNSPPLTLTFHYQGINKAGQK.MEGDIQARSLATAKADLRKQGIVTNKKVKKRKPLFDR.KNKKIT	65
NTDB id 1198 PSJM300 03950 AFN76868.1	MAQKAIKNSVFTWEGLDKQGAQ.IKGELSCGVSPALVKAQLRKQGINPQKVRKKSISLFS..AGKKIK	64
NTDB id 1016 ACIAD RS01680 WP 004920476.1	MAAKKTQVMPVFAYEGVDRKGIK.LKGELPARNMALAKVTLRKQGITIRTIREKRKNIFEGLLKKVK	67
NTDB id 1059 ABD1 RS01610 WP 000279215.1	MAVKKIQMMPFTFAYEGVDRKGIVK.IKGELPAKNMALAKVTLRKQGVTVRNIREKRKNILEGLFKKKVT	67
consensus	* * * * *	

[illegible]

NTDB id 1169	A1552VC	RS11075	WP	000648511.1	NLP	E	F	E	R	L	A	T	Y	R	E	K	S	E	Q	L	R	A	K	V	I	K	A	L	I	P	S	M	V	L	V	A	L	G	V	S	Y	L	M	L	T	M	V	I	P	E	F	E	S	M	F	K	G	F	G	A	E	L	P	W	F	T	Q	Q	V	L	K	L	S	H	V	Q	A	Y	226				
NTDB id 1402	DSB67	RS12670	WP	010643257.1	N	L	S	Q	V	F	E	R	L	A	T	Y	R	E	K	S	E	Q	L	R	A	K	V	I	K	A	L	I	P	A	M	V	L	V	A	L	G	V	S	Y	L	M	L	T	R	V	I	P	E	F	E	K	M	F	T	G	F	G	A	D	L	P	A	F	T	Q	M	V	L	N	L	S	A	W	T	Q	N	W	225
NTDB id 1112	NGFG	RS09215	WP	003689811.1	V	L	E	S	L	D	K	L	A	T	Y	K	E	K	T	Q	A	I	R	K	K	V	K	T	A	L	T	Y	P	S	V	I	A	V	A	I	G	L	V	F	M	M	I	F	V	L	P	A	F	K	E	V	A	N	M	G	A	E	L	P	L	T	Q	T	V	M	D	M	S	D	F	F	V	S	Y	228			
NTDB id 1113	AAA85695.1	219..1451()			V	L	E	S	L	D	K	L	A	T	Y	K	E	K	T	Q	A	I	R	K	K	V	K	T	A	L	T	Y	P	S	V	I	A	V	A	I	G	L	V	F	M	M	I	F	V	L	P	A	F	K	E	V	A	N	M	G	A	E	L	P	A	L	T	Q	T	V	M	D	M	S	D	F	F	V	S	Y	228		
NTDB id 999804	ABFU18	RS05440	WP	057671824.1	V	L	E	T	V	L	D	T	V	A	T	Y	K	E	N	I	E	A	L	G	K	I	K	K	A	L	T	Y	P	A	M	V	I	A	V	A	L	I	V	S	A	L	L	I	F	V	V	P	Q	F	E	E	V	F	K	G	F	G	A	E	L	P	A	F	T	Q	M	I	V	G	A	S	R	F	M	V	S	Y	238
NTDB id 1252	GC085	RS07730	WP	011213805.1	S	L	E	I	M	L	D	R	V	A	T	Y	K	E	K	I	E	I	T	K	K	I	K	K	A	L	T	Y	P	I	A	V	M	V	A	L	L	V	T	A	G	L	L	I	Y	V	V	P	Q	F	E	S	L	F	K	G	F	G	A	D	L	P	A	M	T	R	A	V	I	T	M	S	E	F	M	Q	A	Y	225
NTDB id 1198	PSJM300	03950	AFN	76868.1	S	L	E	T	L	D	R	V	A	T	Y	K	E	K	T	E	A	L	K	A	K	I	K	K	A	N	Y	P	I	A	V	L	V	A	V	I	T	A	L	L	I	K	V	V	P	Q	F	Q	D	V	F	A	N	F	G	A	E	L	P	A	F	T	L	M	V	I	G	L	S	E	A	L	Q	A	W	224			
NTDB id 1016	ACIAD	RS01680	WP	004920476.1	S	L	E	I	M	L	D	R	V	A	T	Y	K	E	K	S	E	V	L	K	Q	K	I	K	K	A	M	K	Y	P	A	T	V	I	V	A	I	V	T	I	L	M																																					

NTDB id 1169	A1552VC	RS11075	WP	000648511.1	SLWAFIAIAAATFGLKALRKNSFQIRLKTSRLGLKFPITIGNVLA	KASIAKFSRTLAT	SFAAGIPILASLKTITAKTSGNVH	306
NTDB id 1402	DSB67	RS12670	WP	010643257.1	GPFGLSFVSLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLAT	SFSAGIPILTALKITTSKTSGNMH	305	
NTDB id 1112	NGFG	RS09215	WP	003689811.1	GWMVLIALGFATYGFLLKARSIKIQRRLDAILLRMPIFGDIVRKGTIARWGRTTATL	FAAGVPLVDVLDSTAGAAGNLI	308	
NTDB id 1113	AAA85695.1	219..1451()			GWMVLIALGFATYGFLLKARSIKIQRRLDAILLRMPIFGDIVRKGTIARWGRTTATL	FAAGVPLVDVLDSTAGAAGNLI	308	
NTDB id 999804	ABFU18	RS05440	WP	057671824.1	WVIMIFVVGSIIGFIYAYKRSPSMQHAMDRLILRPVIGQIMHNSSIARFARTTAVTFK	AGVPLVEALGIVAGATGNRV	318	
NTDB id 1252	GC085	RS07730	WP	011213805.1	WYIIFGALGGVVSFFYAKNHSLEFAQTLDRVMLKLPVIGPILEKAAIARFARTLSIT	FAAGLPLVEALKSVAGATGNII	305	
NTDB id 1198	PSJM300	03950	AFN	76868.1	WYVVLACFVGAAYAFKQAHTRSEKFRNWFDRLMLKVPVVGDIYKSSVARFARTLSTT	FAAGVPLVDALDSVAGATGNVV	304	
NTDB id 1016	ACIAD	RS01680	WP	004920476.1	WFILIIVTGAATAGFLEARKRSKRFRDQDLRLVLRPIVGDVLYKATIIARYSRTLATT	FAAGVPLIDALASTAGATNNIV	307	
NTDB id 1059	ABD1	RS01610	WP	000279215.1	WFIMIIAIGAVIAAFLFAKRSKRKFRDGLDKLALKLPIFGDLVYKATIIARYSRTLATT	FAAGVPLIDALESTAGATNNVI	307	
consensus					*****	*****	*****	*****

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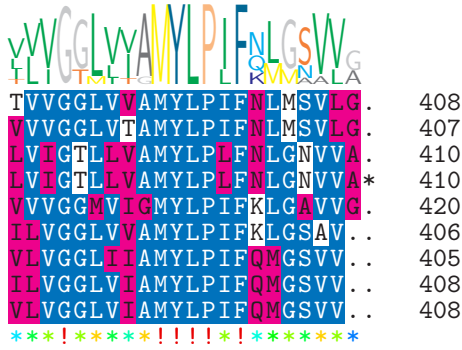
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NTDB id 1059 ABD1 RS01610 WP 000279215.1
consensus



 non conserved
 similar
 ≥ 50% conserved