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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 1252 GC085 RS07730 WP 011213805.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
NTDB id 23117 MAQU RS13725 WP 011786127.1
NTDB id 1198 PSJM300 03950 AFN76868.1
consensus

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NTDB id 23117 MAQU RS13725 WP 011786127.1
NTDB id 1198 PSJM300 03950 AFN76868.1
consensus

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logo

NTDB id 1402 DSB67 RS12670 WP 010643257.1	VTAMYLPIFNLMSV LG .	407
NTDB id 1169 A1552VC RS11075 WP 000648511.1	VVAMYLPIFNLMSV LG .	408
NTDB id 1112 NGFG RS09215 WP 003689811.1	LVAMYLPLFNLGN VVA .	410
NTDB id 1113 AAA85695.1 219..1451()	LVAMYLPLFNLGN VVA *	410
NTDB id 1252 GC085 RS07730 WP 01213805.1	VVAMYLPIFKLGS AV .	406
NTDB id 1016 ACIAD RS01680 WP 004920476.1	VIAMYLPIFQMGS VV .	408
NTDB id 1059 ABD1 RS01610 WP 000279215.1	VIAMYLPIFQMGS VV .	408
NTDB id 23117 MAQU RS13725 WP 011786127.1	II G MYLPIFQM GQ V VG .	406
NTDB id 1198 PSJM300 03950 AFN76868.1	IIAMYLPIFQMGS VV .	405
consensus	***!!!!*!***	



Position	1	2	3	4	5	6	7	8	9	10																																																																		
Sequence	KLRDVAAGQGMVYLAIRMRFPMAQVVA	GEESG	LDMLKVA	YE	EVDNAV	D	L	TAMMEP	L	MAV	LGVLVGG																																																																	
391	EYVRD	TAAG	MPMYI	AMRHCHV	FP	ELV	QVMV	MIGEESGR	LD	DDL	NK	IAAI	YEF	VDNT	VDNL	SK	LI	LEP	LI	IV	FL	GV	VGG																																																					
392	EYVRD	TAAG	MPMYI	AMRNTEA	FP	ELV	QVMV	MIGEESGR	LD	DDL	NK	IAAI	YEF	VDNT	VDNL	SK	LI	LEP	LI	IV	FL	GV	VGG																																																					
394	EIRTR	VIQ	GLS	MTSG	MRATE	LP	NM	MLQ	MS	S	I	GEESG	SL	DD	ML	NK	AAE	F	Y	E	D	V	N	AV	GR	L	S	A	M	E	P	I	I	V	I	L	G	V	I	G	T																																			
394	EIRTR	VIQ	GLS	MTSG	MRATE	LP	NM	MLQ	MS	S	I	GEESG	SL	DD	ML	NK	AAE	F	Y	E	D	V	N	AV	GR	L	S	A	M	E	P	I	I	V	I	L	G	V	I	G	T																																			
391	KIRE	VAT	G	Q	Q	L	F	A	M	R	I	S	N	R	F	P	T	M	A	I	Q	M	V	A	I	G	E	S	G	A	L	D	S	M	L	D	K	V	A	T	Y	E	N	E	V	D	N	A	V	D	G	L	T	S	M	E	P	L	I	M	A	I	L	G	V	L	V	G	L							
393	KIRE	VAT	G	Q	Q	L	F	A	M	R	I	S	N	R	F	P	T	M	A	I	Q	M	V	A	I	G	E	S	G	A	L	D	S	M	L	D	K	V	A	T	Y	E	N	E	V	D	N	A	V	D	G	L	T	S	M	E	P	L	I	M	A	I	L	G	V	L	V	G	L							
393	KIRE	VAT	G	Q	Q	L	F	A	M	R	I	S	N	R	F	P	T	M	A	I	Q	M	V	A	I	G	E	S	G	A	L	D	S	M	L	D	K	V	A	T	Y	E	N	E	V	D	N	A	V	D	G	L	T	S	M	E	P	L	I	M	A	I	L	G	V	L	V	G	L							
390	N	I	K	N	D	V	S	S	G	T	L	Q	A	S	M	R	Q	Q	G	V	F	P	V	M	A	V	Q	L	T	A	I	G	E	E	S	G	N	L	D	D	M	L	S	K	V	A	E	H	Y	E	G	V	D	D	M	V	N	L	T	A	L	M	E	P	M	I	M	A	V	L	G	V	L	V	G	L
390	K	I	K	S	D	V	S	S	G	T	L	Q	A	S	M	R	Q	Q	G	V	F	P	V	M	A	V	Q	L	T	A	I	G	E	E	S	G	N	L	D	D	M	L	S	K	V	A	E	H	Y	E	G	V	D	D	M	V	N	L	T	A	L	M	E	P	M	I	M	A	V	L	G	V	L	V	G	L



[illegible]

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