

NTDB id 598 KW2 RS08500 WP 021037660.1	MRTAIDENNKIINLLELDR	KELTGKIFYCPSCHSELLIKNGQIKVLHFAHKSLSKCNLWLENESCHLGLKKILYQWFKATDKVET	85
NTDB id 24747 SAK RS04640 WP 000903642.1	MLIAKDKQGNIINLLES..	HPGKGQGYFCPTCCSAVRLKAGRIMRRHFAHISLKNQCFYHENESNEHLQLKAKLYMSLSRENETML	83
NTDB id 155 SP RS04850 WP 000495909.1	MFVARDARGELVNVLED..	KLEKQAYTCPACGGQLHLRQGSPSVRTHFAHKSCLKDCDFFENESPEHLANKESLYHWLKKETKVQL	83
NTDB id 265 KZH43 RS04315 WP 000495911.1	MFVARDARGELVNVLED..	KLEKQAYTCPACGGQLHLRQGSPSVRTHFAHKSCLKDCDFFENESPEHLANKESLYHWLKKETKVQL	83
NTDB id 224 SPD RS04655 WP 000495911.1	MFVARDARGELVNVLED..	KLEKQAYTCPACGGQLHLRQGSPSVRTHFAHKSCLKDCDFFENESPEHLANKESLYHWLKKETKVQL	83
NTDB id 190 SPR RS04415 WP 000495911.1	MFVARDARGELVNVLED..	KLEKQAYTCPACGGQLHLRQGSPSVRTHFAHKSCLKDCDFFENESPEHLANKESLYHWLKKETKVQL	83
NTDB id 495 SM12261 RS04415 WP 000495920.1	MFVARDSRGELVNVLED..	KLEKQAYTCPACGGQLRLRQGSPSVRTHFAHKTCLKDCDFFSSENESPEHLENKEVLYHWLKKAEVQL	83
consensus	*****	*****	

NTDB id 598 KW2 RS08500 WP 021037660.1	ERYLP ELN QR P D L L V N D K I A T E I Q C S H L S I K R L K E R T E N Y K T H G F K V L W L M G K D L W L A E Q V T E L Q K N L V Y F S E N R G F F Y W E L D F Q	170
NTDB id 24747 SAK RS04640 WP 000903642.1	E H H L P E I N Q I A D L F V N E T L A E V Q C S R L S E Q R L R E R T K A Y L Q A D E F Q V R W L L G E K L W L K H R L T N L H K Q F L Q F S Q S I G F H I W E L D L R	168
NTDB id 155 SP RS04850 WP 000495909.1	EYPLSELKQIADVFVNGNLAEVQCSPLPQKV L KERSEGYRSQGYQV L WLLGQKLW L KERLTRLQQGFLYFSQNMGFYVWELDK E	168
NTDB id 265 KZH43 RS04315 WP 000495911.1	EYPLSELKQIADVFVNGNLAEVQCSPLPQKV L KERSEGYRSQGYQV L WLLGQKLW L KERLTRLQQGFLYFSQNMGFYVWELDK G	168
NTDB id 224 SPD RS04655 WP 000495911.1	EYPLSELKQIADVFVNGNLAEVQCSPLPQKV L KERSEGYRSQGYQV L WLLGQKLW L KERLTRLQQGFLYFSQNMGFYVWELDK G	168
NTDB id 190 SPR RS04415 WP 000495911.1	EYPLSELKQIADVFVNGNLAEVQCSPLPQKV L KERSEGYRSQGYQV L WLLGQKLW L KERLTRLQQGFLYFSQNMGFYVWELDK G	168
NTDB id 495 SM12261 RS04415 WP 000495920.1	EYLP L PE L KQIADVFVNGNLAEVQCSPLPQKV L KERSEGYRSQGYQV L WLLG K KLW L KERLTRLQQGFLYFSQNMGFYVWELDK E	168
consensus	***LPELQKQIADVFVNGNLAEVQCSPLPQKVLERSEGYRSQGYQVWLWGKLWLKERLTRLQQGFLYFSQNMGFYVWELDKSE***	

[illegible]

NTDB id 598 KW2 RS08500 WP 021037660.1	LTKKFEGP	YIAPLGLNLL	ENFTDEMT	ITTTFT	QIDQNV	KLYYEN	FLIN	QRN...	SL	EM	LYPP	RSY	AIMGKQKKEK	327		
NTDB id 24747 SAK RS04640 WP 000903642.1	LTQE	LMM	FFPQI		QPPRVD	DFCQIT	NSLTS	FYQNF	TNY	YQKN	KN	NLDQT	LYPPV	FYDKIVT	KN...	315
NTDB id 155 SP RS04850 WP 000495909.1	LT	YGLKEW	YPQI		RPI	..	VGKFFQ	IEQDL	TSYYQH	FYTTYQ	KNPQ	NDWQ	KLYPPAFY	QQYFLKNMVE	317	
NTDB id 265 KZH43 RS04315 WP 000495911.1	LT	YGLKEW	YPQI		RPI	..	VGKFFQ	IEQDL	TSYYQH	FYTTYQ	KNPQ	NDWQ	KLYPPAFY	QQYFLKNMVE	317	
NTDB id 224 SPD RS04655 WP 000495911.1	LT	YGLKEW	YPQI		RPI	..	VGKFFQ	IEQDL	TSYYQH	FYTTYQ	KNPQ	NDWQ	KLYPPAFY	QQYFLKNMVE	317	
NTDB id 190 SPR RS04415 WP 000495911.1	LT	YGLKEW	YPQI		RPI	..	VGKFFQ	IEQDL	TSYYQH	FYTTYQ	KNPQ	NDWQ	KLYPPAFY	QQYFLKNMVE	317	
NTDB id 495 SM12261 RS04415 WP 000495920.1	LT	YGLKEW	YPQI		RPI	..	VGNF	FCQIEQDL	IRYYLY	FQTTYQ	ENPQ	NDWQ	ML	LYPPAFY	QQYFLKNMVE	317
consensus	!	!	*****	*****	*****	!!	*****	!!	*****	!!	*****	!!	*****	*****	*****	*****

[illegible]



 EYPLSELKQIADVFVNGNLALEVQCSPLPQKVLKERSEGYRSQGYQVLWLLGQKLWLLKERLTRLQQGFLYFSQNMGFVWELDKG 170

KQVLRKLYLYQDLRGLHYQIKFEFSYGGGSLLLEILRLPYKKQKISHFTVSEDKDICRYIRQQLYYQNLFWMKEQAEAYQKGENI
 255
 LEVLRKLYLIYEDLRCHVYVLSKTCPLSGDVLAFLLKWPYQSKNLNFYKVKQDRNIRDYVRQQLRYGNQFWLRKQEKAYLSGQNL
 252
 KQVLRKLYLIYQDLRGLHYQIKFEFSYGGGSLLLEILRLPYKKQKISHFTVSEDKDICRYIRQQLYYQNLFWMKEQAEAYQKGENI
 253
 KQVLRKLYLIYQDLRGLHYQIKFEFSYGGGSLLLEILRLPYKKQKISHFTVSEDKDICRYIRQQLYYQNLFWMKEQAEAYQKGENI
 253
 KQVLRKLYLIYQDLRGLHYQIKFEFSYGGGSLLLEILRLPYKKQKISHFTVSEDKDICRYIRQQLYYQNLFWMKEQAEAYQKGENI
 253
 KQVLRKLYLIYQDLRGLHYQIKFEFSYGGGSLLLEILRLPYKKQKISHFTVSEDKDICRYIRQQLYYQNLFWMKEQAEAYQKGENI
 253
 KQVLRKLYLIHQDLRGLHYQIKFEPYGHGSLLEILRFPPYKKQKISHFTVSQDKDICRYIRQQLYYQNPTIWMKEQAEAYKKGENI
 253

[illegible]

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