

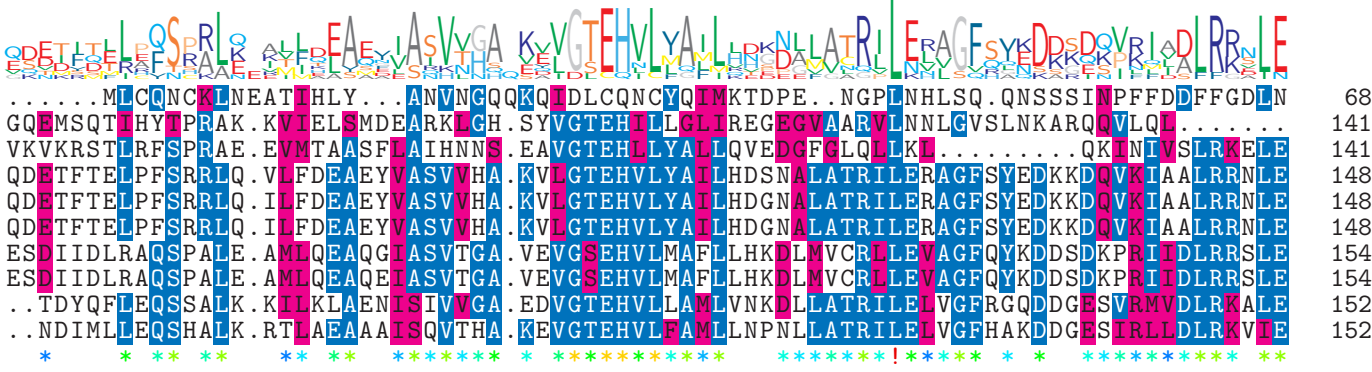
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NTDB id 85 BSU 00860 NP 387967.1
NTDB id 610 V4T04 RS10165 WP 012897346.1
NTDB id 287 SP RS11210 WP 001109712.1
NTDB id 290 KZH43 RS10025 WP 001109677.1
NTDB id 289 SPD RS10700 WP 001109677.1
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NTDB id 297 STER RS00545 WP 011680614.1
NTDB id 233988 BB194 RS09470 WP 017647770.1
NTDB id 377 SMU RS09275 WP 002262344.1
consensus



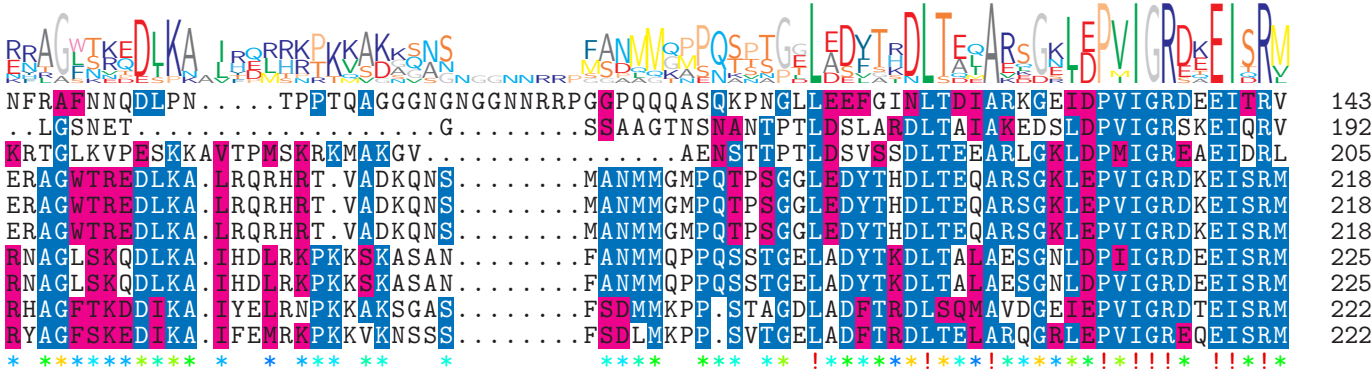
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IEILNRR	TKNNPVL	IGEP	GVGKTA	LV	EG	VGKTA	LAL	GLAQR	I	ASG	VP	F	ELADMR	VLE	LD	MS	WAGT	TR	FR	GDF	FEER	M	N	Q	I	AD	IE	DG	223																																																																						
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IHILSR	TKNNPVL	IGEP	GVGK	S	AI	IEGLA	QR	I	ASG	VP	I	GL	MS	R	I	AL	MA	TV	VAGT	K	FR	GE	F	FED	RL	T	A	I	285																																																																						
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IQILSR	TKNNPVL	IGEP	GVGKTA	LV	EG	VGKTA	LAL	GLAQR	I	ASG	VP	AE	MA	KMR	VLE	LD	LMN	V	VAGT	TR	FR	GDF	FEER	M	N	Q	I	KD	298																																																																						
IQVLSR	TKNNPVL	IGEP	GVGKTA	LV	EG	VGKTA	LAL	GLAQR	I	ASG	VP	F	ELADMR	I	LE	LD	MS	V	VAGT	TR	FR	GDF	FEER	M	N	Q	I	AD	305																																																																						
IQVLSR	TKNNPVL	IGEP	GVGKTA	LV	EG	VGKTA	LAL	GLAQR	I	ASG	VP	F	ELADMR	I	LE	LD	MS	V	VAGT	TR	FR	GDF	FEER	M	N	Q	I	AD	305																																																																						
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VQILSR	TKNNPVL	IGEP	GVGKTA	LV	EG	VGKTA	LAL	GLAQR	I	ASG	VP	F	ELADMR	I	LE	LD	MS	V	VAGT	TR	FR	GDF	FEER	M	N	Q	I	AD	302																																																																						

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[illegible]

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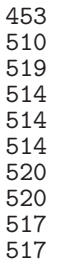
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QGLREKFEDYHQVKFTDQAIAKSAVMSLVRYMSTRKLPDKAIDLLDEAAAVKISVKNQKTRLDLEKELAEAAQEEISEAV	445
QGLKATYIEKHHRVQITDEAVETAVKMAHRYLTSRHLPDSAIDLLDEAAATVQNKAKHVKAADSDS...S...PADKAL	450
QGLKATYIEKHHRVQITDEAVETAVKMAHRYLTSRHLPDSAIDLLDEAAATVQNKAKHVKAADSDS...S...PADKAL	450
QGLKATYIEKHHRVQITDEAVETAVKMAHRYLTSRHLPDSAIDLLDEAAATVQNKAKHVKAADSDS...S...PADKAL	450
NGLRSSYEDYHRVTITDAAVETAVKAAHRYLTSKNLPDSADILLDEASATVQVRIKK...EAKREI...T...PLDEAL	455
NGLRSSYEDYHRVTITDAAVETAVKAAHRYLTSKNLPDSADILLDEASATVQVRIKK...EDKREI...T...PLDEAL	455
LGLKPAYEAFHNVTISDEAVMTAVKVAHRYLTSKNLPDSADILLDEASATVQVRIKK...NAPSL...T...EVDQAT	452
LGLKPSYETYYHVIISDAAVMAAVKGAHRYLSGKNLPDSADILLDEASATVQGLVKK...KAPAYL...T...LDHAL	452

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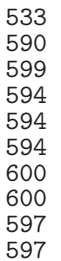
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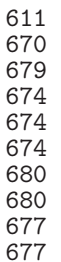
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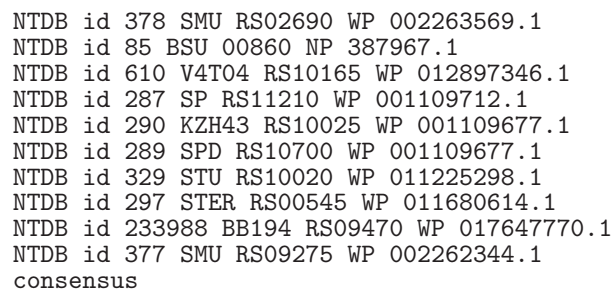
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Sequence	Position	Score
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IAEVEGFDPEYGARPLRKALQKQKVEDLLSEQLLSGEIKAGNHVSIGASNKKIKIAQIV	3	816
LANQGYDPMGARPLRRTLTQTEVEDKLAELLKGDLVAGSTLKIGVKAGQLKFDIA	4	810
LANQGYDPMGARPLRRTLTQTEVEDKLAELLKGDLVAGSILKIGVKAGQLKFDIA	5	810
LANQGYDPMGARPLRRTLTQTEVEDKLAELLKGDLVAGSILKIGVKAGQLKFDIA	6	810
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LAKDGYDIEMGARPLRRTLTQTEVEDKLSSELLGGQVVSQGLTKIGCSKDKLTFTTV	8	816
LAEDGYDIEMGARPLRRTLTQTEVEDHLSSELLANQVKEGQVTKIGVSKGKLKFDIAKS	9	815
LALAGYDAEMGARPLRRTLTQTEVEDKLAELLTSGKLASGQTLKIGITQKEKLKFDIV	10	813

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