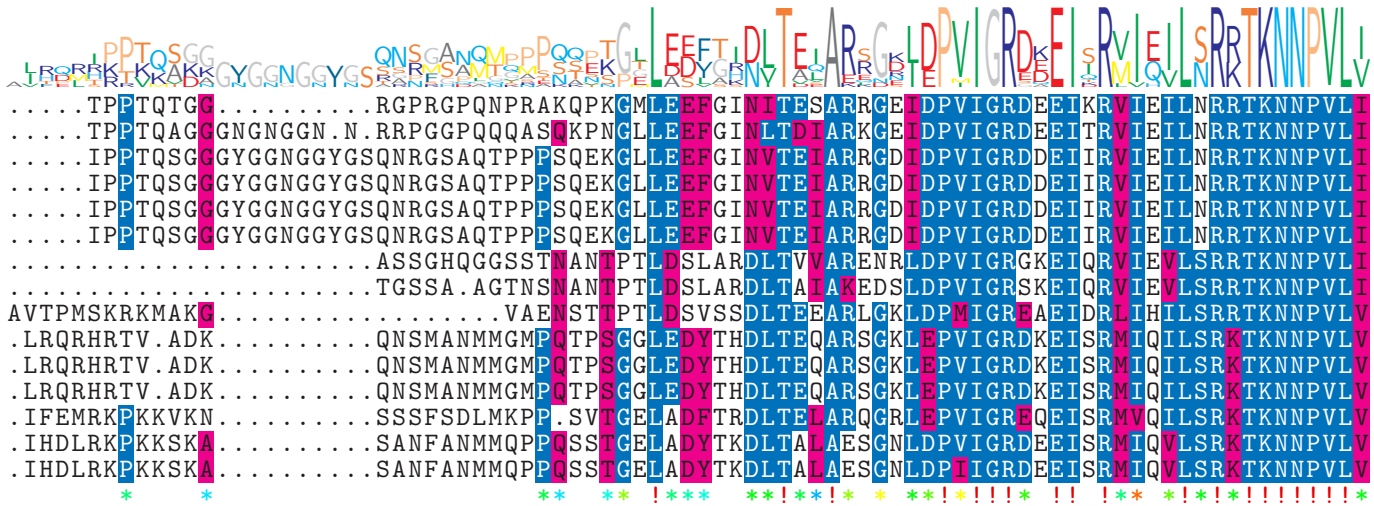


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NTDB id 327 STU RS10020 WP 011225298.1	MTIYSRKMQAIFHRAQLEAERFESPFL ETWHVLLAMVEVPGSVAYLTFTDFEDRIHSEEIETA AVLAMEKRPKDLSESDI	81
consensus	*** * * * * *	

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NTDB	id	281	KZH43	RS03550	WP	000882517.1	H	L	Y	T	N	L	N	G	K	K	K	Q	I	D	L	C	N	C	Y	K	I	...	I	K	T	D	P	N	N	S	.	L	F	K	G	M	T	.	D	L	N	N	R	D	...	F	D	P	.	F	G	D	.	F	F	N	D	.	L	N	N	F	R	P	S	S	N	..	T	P	P		77								
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NTDB	id	85	BSU	00860	NP	387967.1	Q	T	I	H	Y	T	P	R	A	K	K	V	I	E	L	S	M	D	E	A	R	K	L	G	H	S	Y	V	G	T	E	H	I	L	L	G	L	I	R	E	G	E	G	V	A	A	R	V	.	L	N	N	L	G	V	S	L	N	K	A	R	Q	Q	V	L	Q	..	L	L	G	S	N	E			146					
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NTDB	id	290	KZH43	RS10025	WP	001109677.1	T	E	L	P	F	S	R	R	L	Q																																																																							

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NTDB id 85 BSU 00860 NP 387967.1
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NTDB id 289 SPD RS10700 WP 001109677.1
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NTDB id 377 SMU RS09275 WP 002262344.1
NTDB id 297 STER RS00545 WP 011680614.1
NTDB id 329 STU RS10020 WP 011225298.1
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NTDB id 329 STU RS10020 WP 011225298.1
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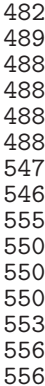
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NTDB id 79686 L6481 RS00525 WP 000971179.1	GAIDASNILKPSLARGEELQCIGATTTLDEYRKYIEKDAALERRFQPIHVDEPSLDESTQILKGLRDRYEAAHHRVSIITDDAIDAAVK	377
NTDB id 85 BSU 00860 NP 387967.1	GAIDASNILKPSLARGEELQCIGATTTLDEYRKYIEKDAALERRFQPIQVDQPSVDESTIQLQGLRDRYEAAHHRVSIITDDAIEAAVK	376
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NTDB id 289 SPD RS10700 WP 001109677.1	STLDAANILKPALARGTLRTVGATTQEEYQKHIEKDAALSRRFAKVTIEEPSVADSMTILQGLKATYEKHHRVQITDEAVETAVK	403
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consensus	*!!!!!!!!*!!!!*****!!!!!! !! * !!!!!*!!!!!! * ****!*****!! !** *!****! *! !****!	

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NTDB id 289 SPD RS10700 WP 001109677.1	MAHRYLTSRHLPDSAIDLLDEAAATVQNKAKHVKAADSDL....S....PADKALMDGKWKQAAQLIAKEE.....E....	467
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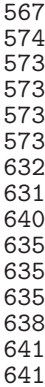
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consensus



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NTDB id 329 STU RS10020 WP 011225298.1
consensus

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logo

Sequence logo for the 10th position. The y-axis represents information content in bits, ranging from 0 to 0.4. The x-axis shows the amino acid sequence: K I K S A K A E V K S S E K E K. The 'S' at position 10 is the most conserved residue, with a height of approximately 0.35 bits.

NTDB id	Accession	Species	Gene	Protein	Length
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NTDB id 243	SPR	RS03635	WP 000882517.1	QIKSAKK.AEVKSSEKEK.	752
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consensus					

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