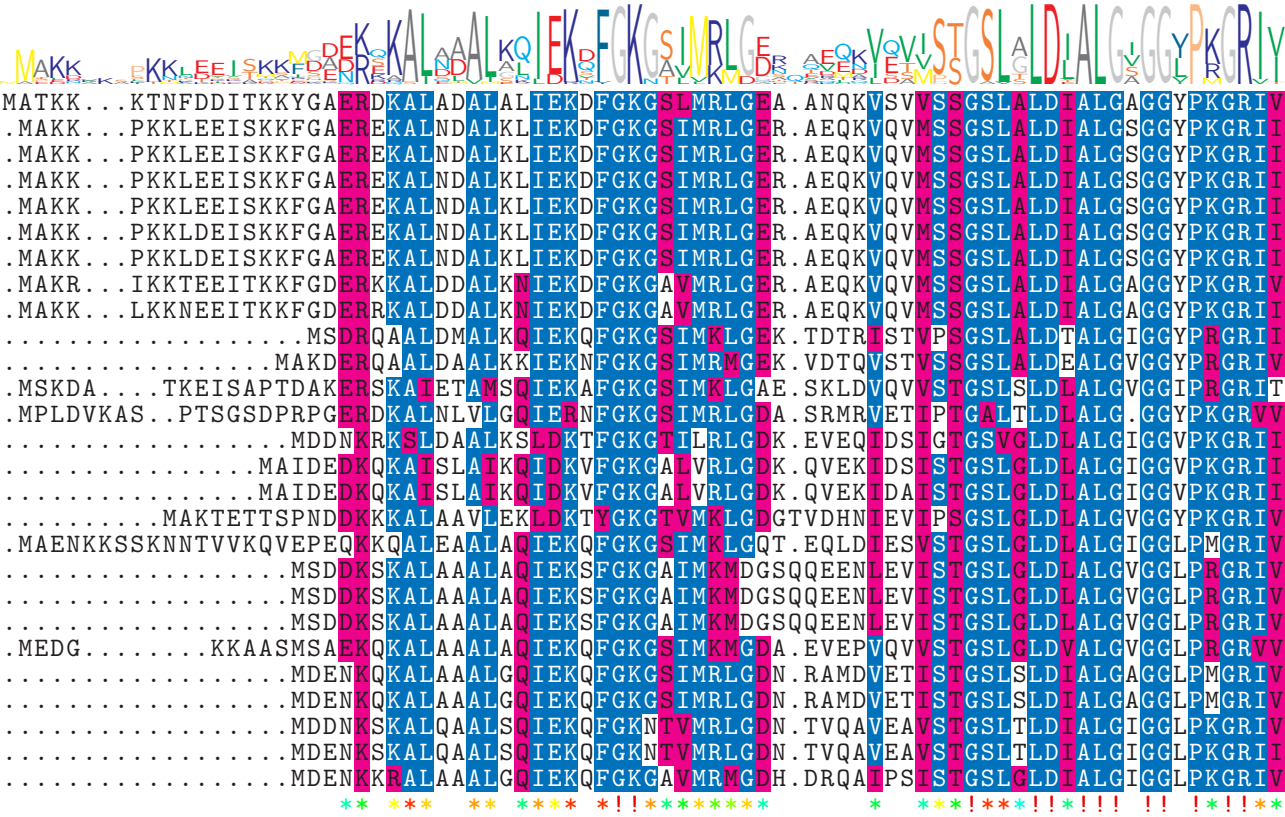


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consensus



logo

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consensus

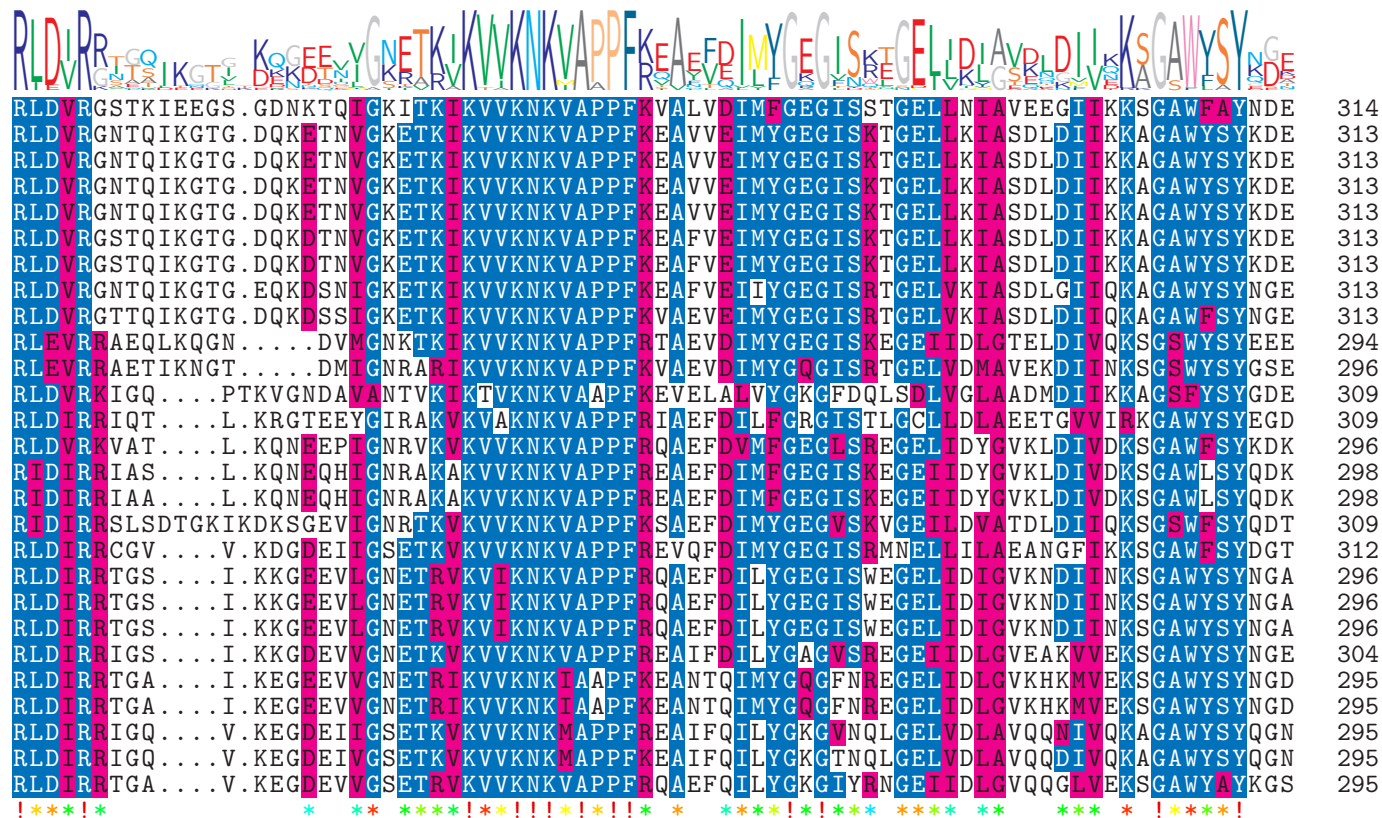
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EIYGP	ESSGKTT	V	A	L	H	A	V	A	Q	A	K	E	G	I	A	F	D	A	E	H	A	L	D	P	Y	A	A	A	L	G	V	N	I	D	E	L	L	S	Q	P	D	S	G	E	Q	G	L	E	I	A	G	K	L	I	D	S	G	A	V	D	L	V		155											
EIYGP	ESSGKTT	V	A	L	H	A	V	A	Q	A	K	E	G	I	A	F	D	A	E	H	A	L	D	P	Y	A	A	A	L	G	V	N	I	D	E	L	L	S	Q	P	D	S	G	E	Q	G	L	E	I	A	G	K	L	I	D	S	G	A	V	D	L	V		155											
EIYGP	ESSGKTT	V	A	L	H	A	V	A	Q	A	K	E	G	I	A	F	D	A	E	H	A	L	D	P	Y	A	A	A	L	G	V	N	I	D	E	L	L	S	Q	P	D	S	G	E	Q	G	L	E	I	A	G	K	L	I	D	S	G	A	V	D	L	V		155											
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E	V	Y	G	P	E	S	S	G	K	T	T	V	A	L	H	A	I	A	E	V	Q	Q	G	G	A	F	D	A	E	H	A	L	D	P	V	Y	A	Q	K	L	G	V	N	I	D	E	L	L	S	Q	P	D	T	G	E	Q	A	L	E	I	A	E	A	L	V	R	S	G	A	V	D	I	V		140
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consensus

Sequence	Score
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KIGQCKDNVVRVILKENPEISDEIDAKIRALNGVEMHITEGTQDET.....GE.R.....PEE.....	348
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KIGQCKANACKYILKENPEIAKTLDDKKIREMLLNPNMQLIAETSSA.....AD.DV.....EFGAVPEEF	354
KIGQCKNNVIRVILEENPQISTEIEAVIREQLLTKASDQTAA.HDET.....EE.EP.....DLL..ES.....	349
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KIGQCKANAAKYILENPEIGQIEEQIRAKLLVTSANTKATPVAED.....LA.DA.....DI.....	347

logo

NTDB id 600 KW2 RS01765 WP 011675413.1	E.....	387
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NTDB id 408 SMU RS09530 WP 002262392.1		383
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consensus		

- X non conserved
- X similar
- X ≥ 50% conserved