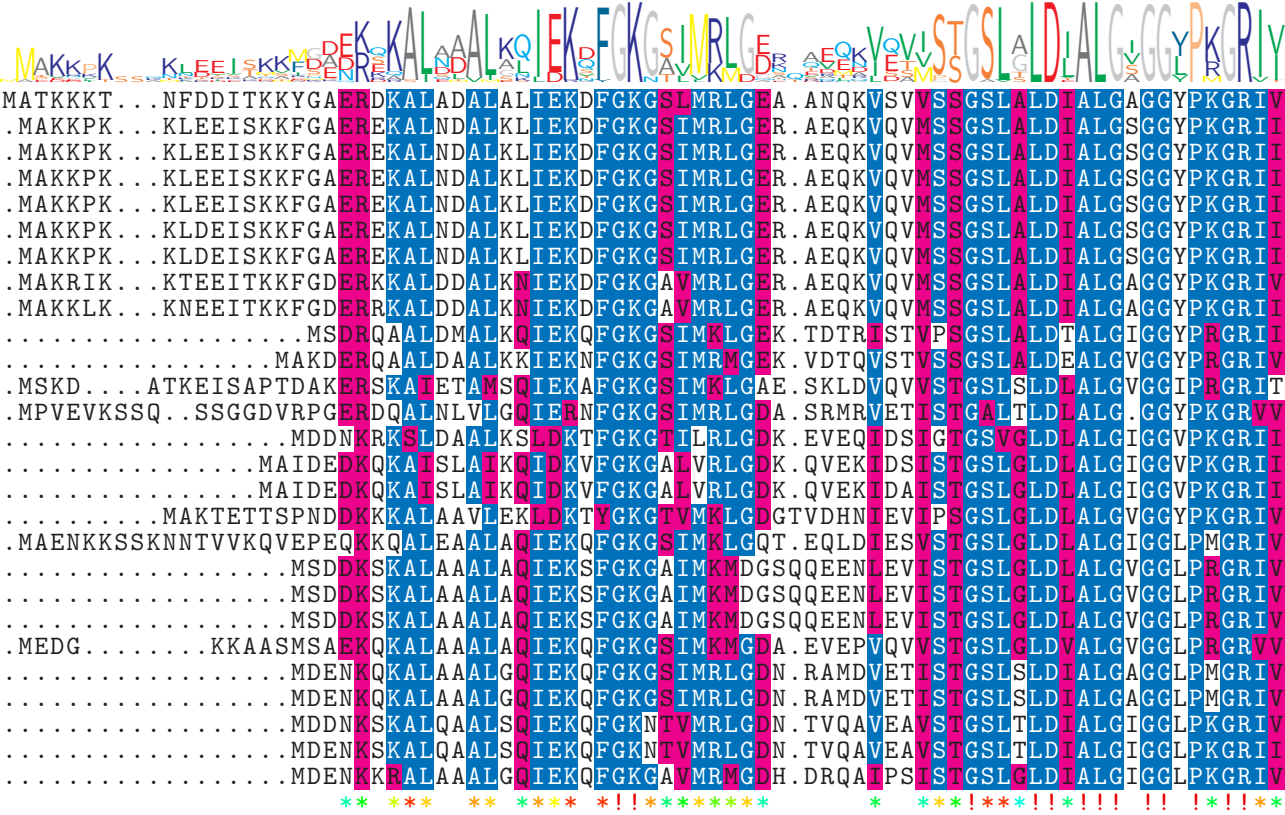


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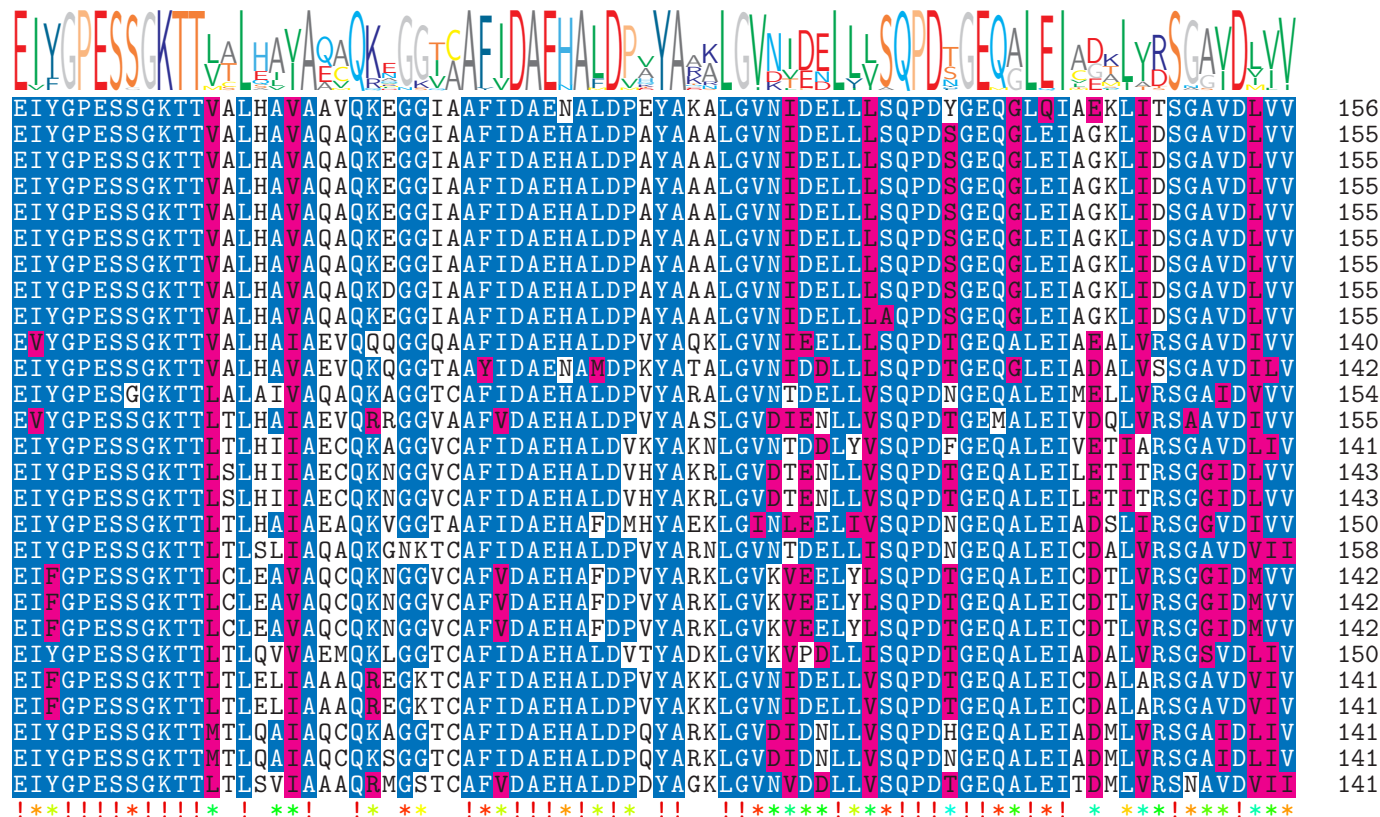
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consensus

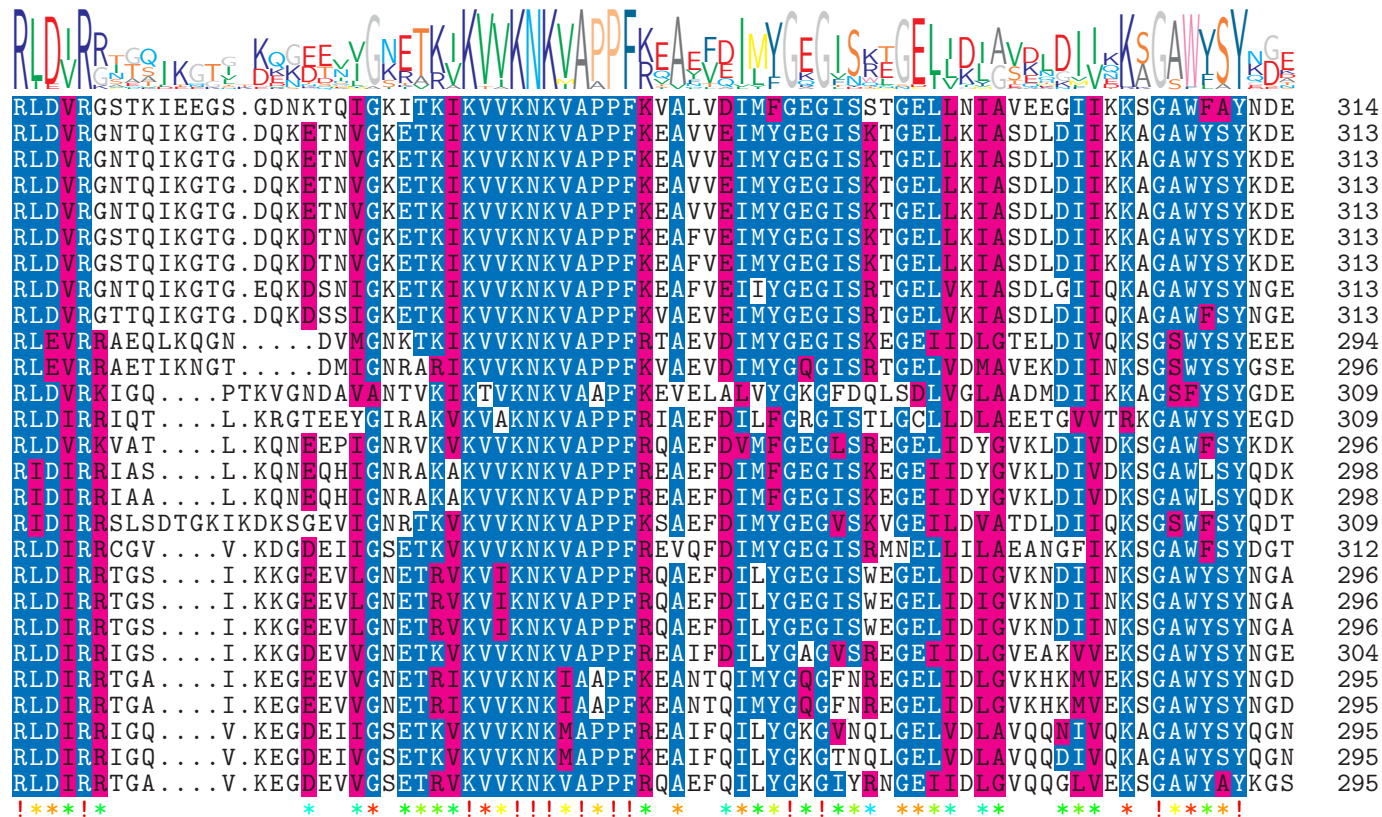


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NTDB id 499	SM12261 RS08315 WP 078228268.1	VDSVAALVPRAEIDGDI	IGDSHVGLQARMMSQAMRKL	GASINKTKT	TAIFINQLREKVGVM	FGNPETTPGGRALKFYASV	234	
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NTDB id 418640	SynPROS71 RS02570 WP 186596433.1	VDSVAALT	TPRAEIEGEMGDL	AVGSQARLMSQAMR	KITGNIGKSGCTV	IFLNQLRLKIGVT	YGNPETTTGGNALKFYASV	234
NTDB id 1245	Cj1673c YP 002345041.1	VDSVAALT	TPKAEIEGDMGD	QHVGLQARLMSQAL	RKLITGVHKMNT	TVIFINQIRMKIGAMGYGTPETT	TGGNALKFYASV	221
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NTDB id 1214	NCTC11637 00359 SQJ03206.1	VDSVAALT	TPKAEIDGMDGD	QHVGLQARLMSH	ALRKITGVLHKMNT	TTLIFINQIRMKIGMMGYGSPETT	TGGNALKFYASV	223
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NTDB id 1389	A4U84 RS07560 WP 021112712.1	VDSVAALT	TPKAEIEGDMGDS	HMLQARLMSQAL	RKLITANIKNTNCL	LVFINQIRMKIGVM	FGNPETTTGGNALKFYASV	237
NTDB id 1130	NGFG RS03960 WP 003688695.1	VDSVAALVPKAEIEGDMGDS	HVGLQARLMSQAL	RKLITGHIKKTNT	TLVFINQIRMKIGVM	FGSPETTTGGNALKFYSSV	221	
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logo

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consensus



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NTDB	id	228	SPD	RS09265	WP	001085462.1	KIGQGS	ENAK	KYLA	EHPE	IF	FEID	DKQ	VRSKF	GL	LIDGE	EVSE	QD	TENKK	.DE....PKKEEA..VNEEVPLDLGDELEIEI		386
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NTDB	id	453	Spy49	1753c	ACI62003.1	KIGQGS	ENAK	KRYLA	DHP	QLF	FEID	DRK	VRVKF	GL	LEESE	EEES	AMAVASE	E.....TDDLALDLNNGIEIED		378		
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consensus							***	!	!	*****	**	*****	*****	*****	**	**				*		

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consensus					

-  non conserved
-  similar
-  ≥ 50% conserved