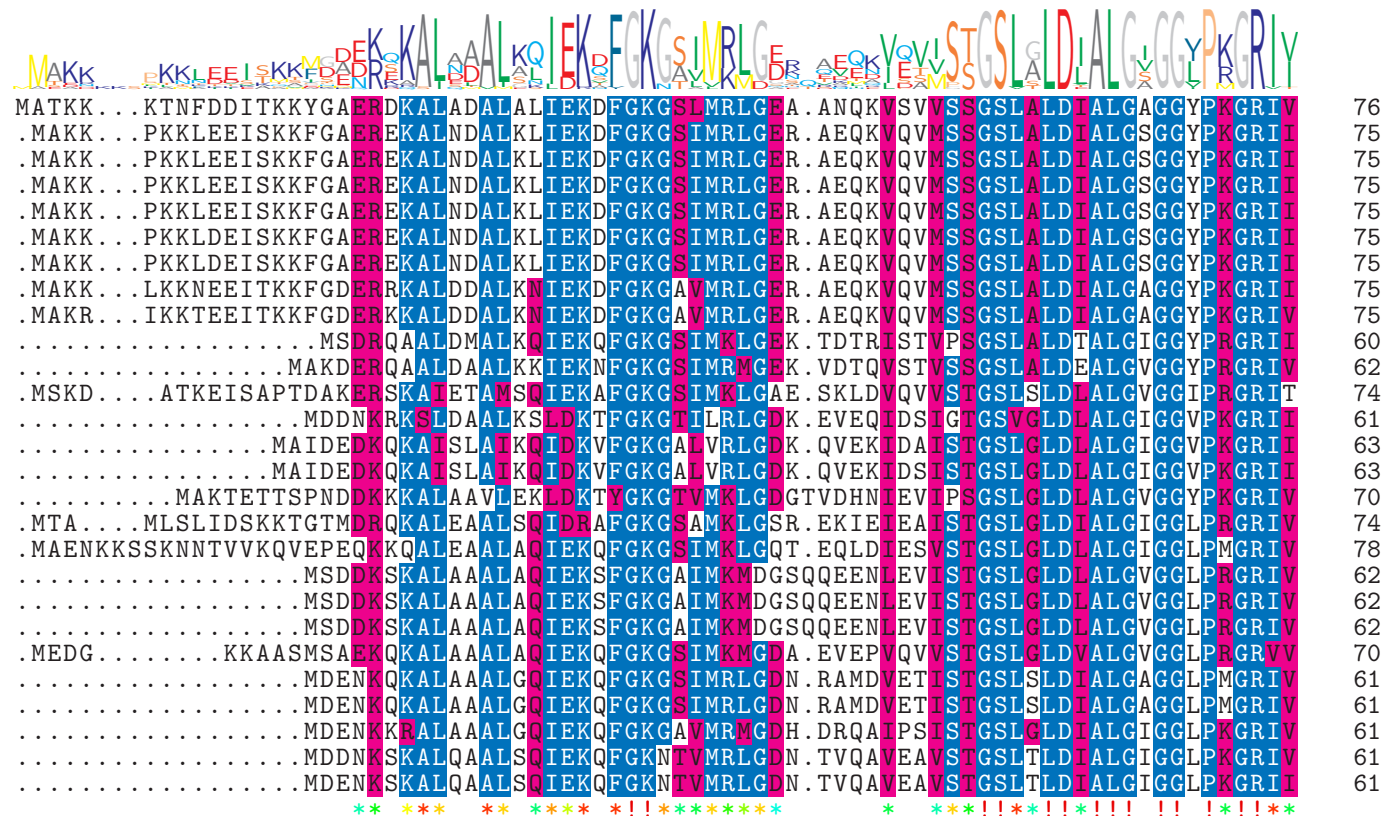


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consensus

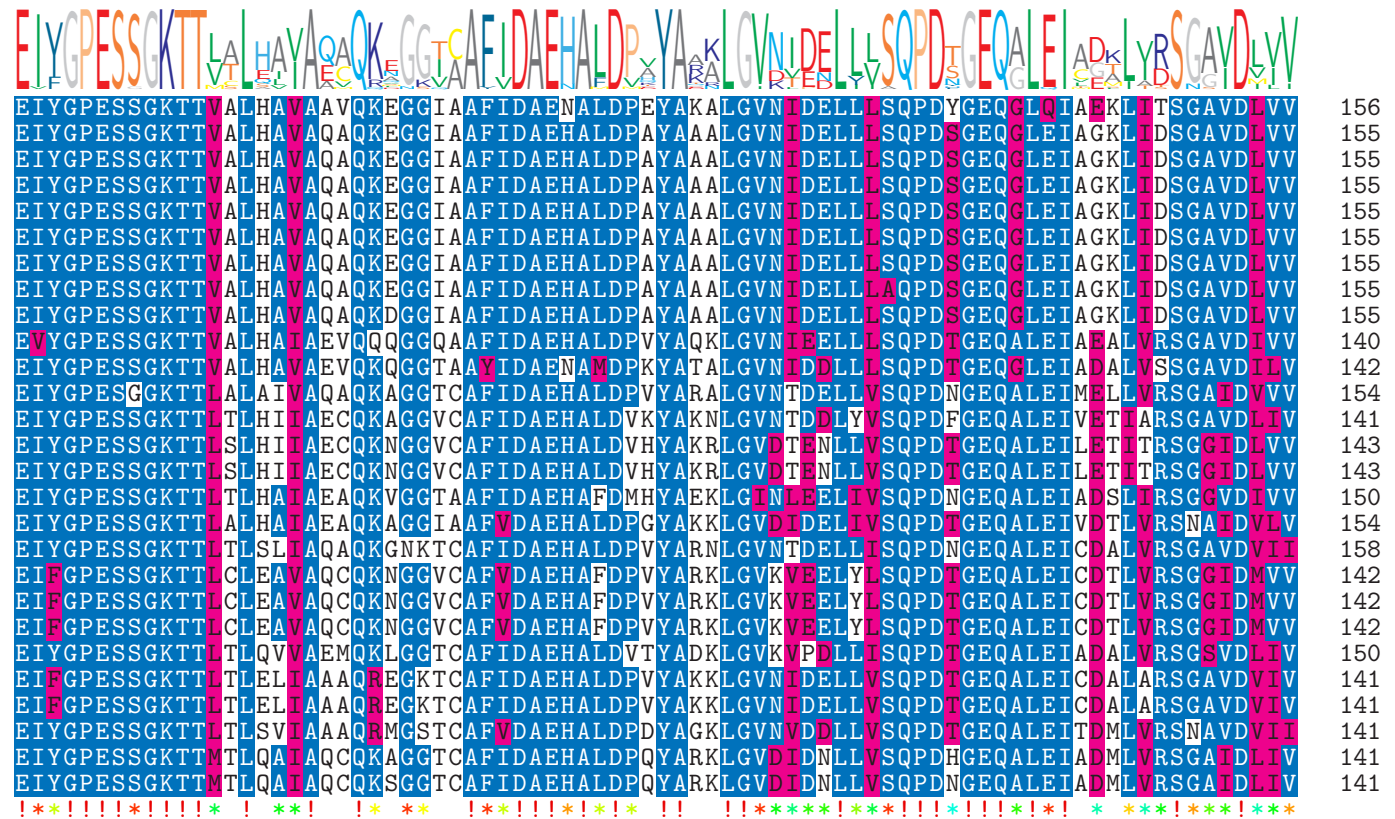
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consensus

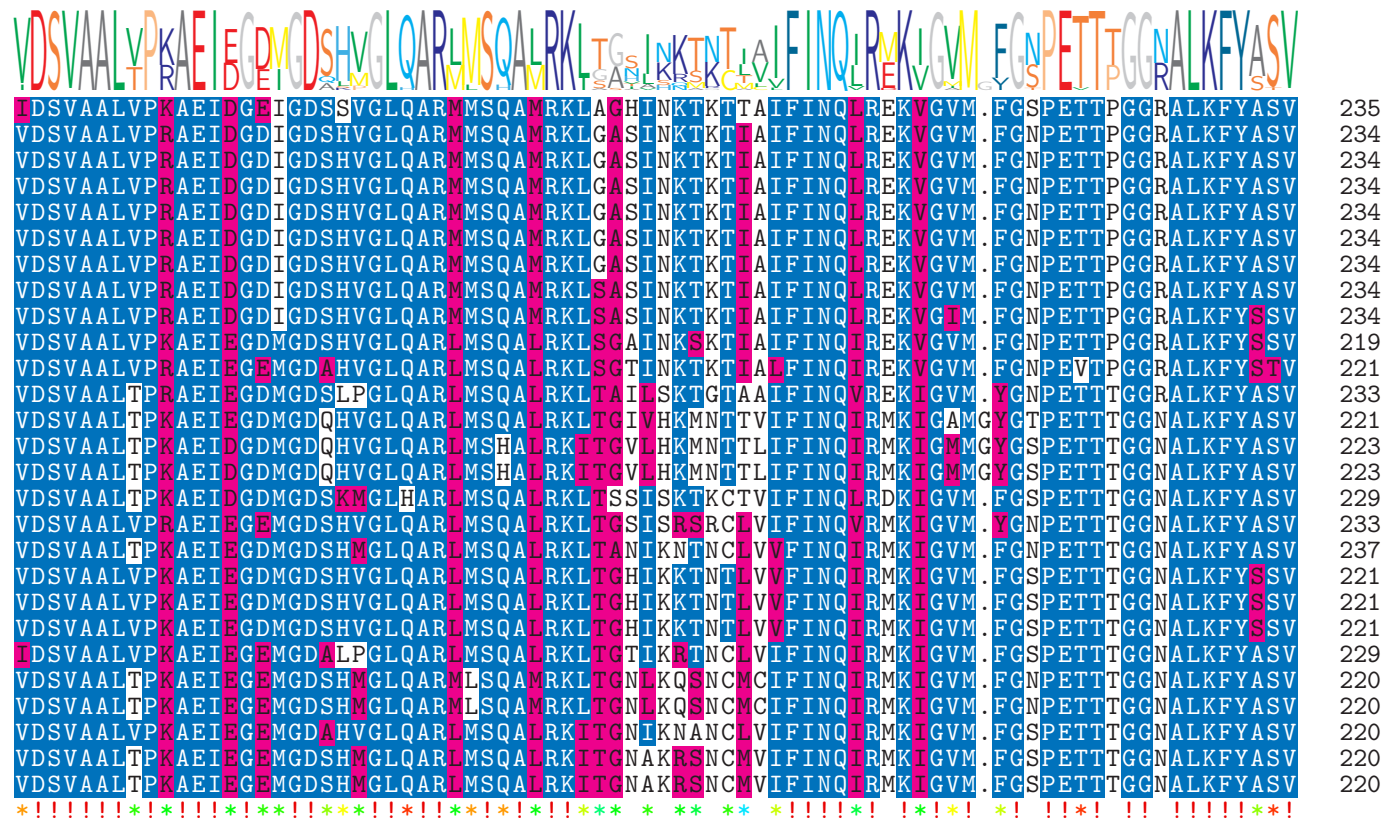
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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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logo

NTDB id 600 KW2 RS01765 WP 011675413.1	RLDVRG	STKIEEGS	.GDNKTQ	IGKITK	IKVVKNKVAPPF	KVALVD	IMFGEGIS	STGELIN	IAVEEGI	IKKSGAW	FAYNDE	314
NTDB id 269 KZH43 RS08665 WP 001085462.1	RLDVRG	NTQIKGTG	.DQKETN	VGKETK	IKVVKNKVAPPF	KEAVVE	IMYGE	GISK	KTGELL	KIASDL	DIKKAGAW	313
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NTDB id 194 SPR RS08825 WP 001085462.1	RLDVRG	NTQIKGTG	.DQKETN	VGKETK	IKVVKNKVAPPF	KEAVVE	IMYGE	GISK	KTGELL	KIASDL	DIKKAGAW	313
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NTDB id 1334 RAOC RS04870 WP 004918236.1	RIDIRRS	LSDTG	KIKDKS	GEV	IGNRT	KVVKNKVAPPF	KS	AEFD	IMYGE	GVS	SKVGE	309
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NTDB id 1389 A4U84 RS07560 WP 021112712.1	RLDIRRC	G....	VVK.DG	DEI	IGSET	KVVKNKVAPPF	REVQF	DIMYGE	GIS	RMNELL	ILAE	312
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NTDB id 1142 GTF74 RS11550 WP 000344154.1	RLDIRRT	G....	AIK.EG	EEV	VGNET	RIKVVKNK	IAAPF	KEANT	QIMYG	QGFN	REGEL	295
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consensus	!***!*			*	*	*	*****!***!!*!!*!!*	*	*****!*	*****	*****	*****


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consensus

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Sequence	Score
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KIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEE...KQSSKEK...ETDEK..ADKNLVLELDDTI	379
RLGQGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQ...QAEETQEEL.EFE.E...	348
RIGQGRENAKNYLADHEDVEDEVRLKVRAAAYGISDVPPEEDL...PTTEDE.QI.NILPDDST...EE...	355
RIGQGKEKTIAYIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAAEA...	363
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KLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIM...PLPDEP..LEEM.E...	347
KLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIM...PLPDEP..LEEM.E...	347
KLGGGRDITVKELIKDNPELAEELEAKIREKLQAK...	343
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KIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHIT...EGT...QDE.TDGER...PEE...	348
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KIGQGGKNNVIRYLEENPQISTEIEAVIREQLLTKASDQ...TAA.HDETEEEP.DLL...ES...	349
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logo

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consensus						

-  non conserved
-  similar
-  ≥ 50% conserved