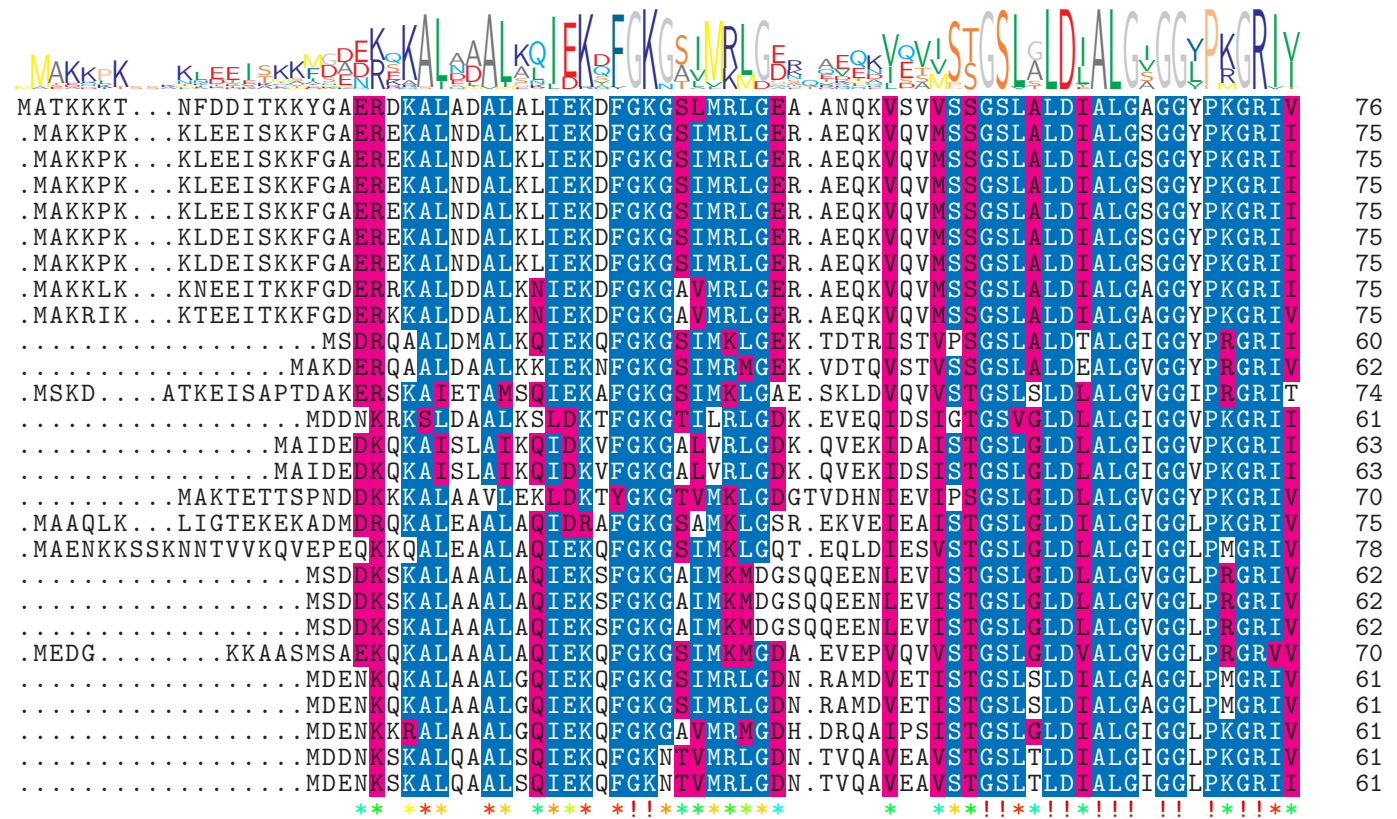


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consensus

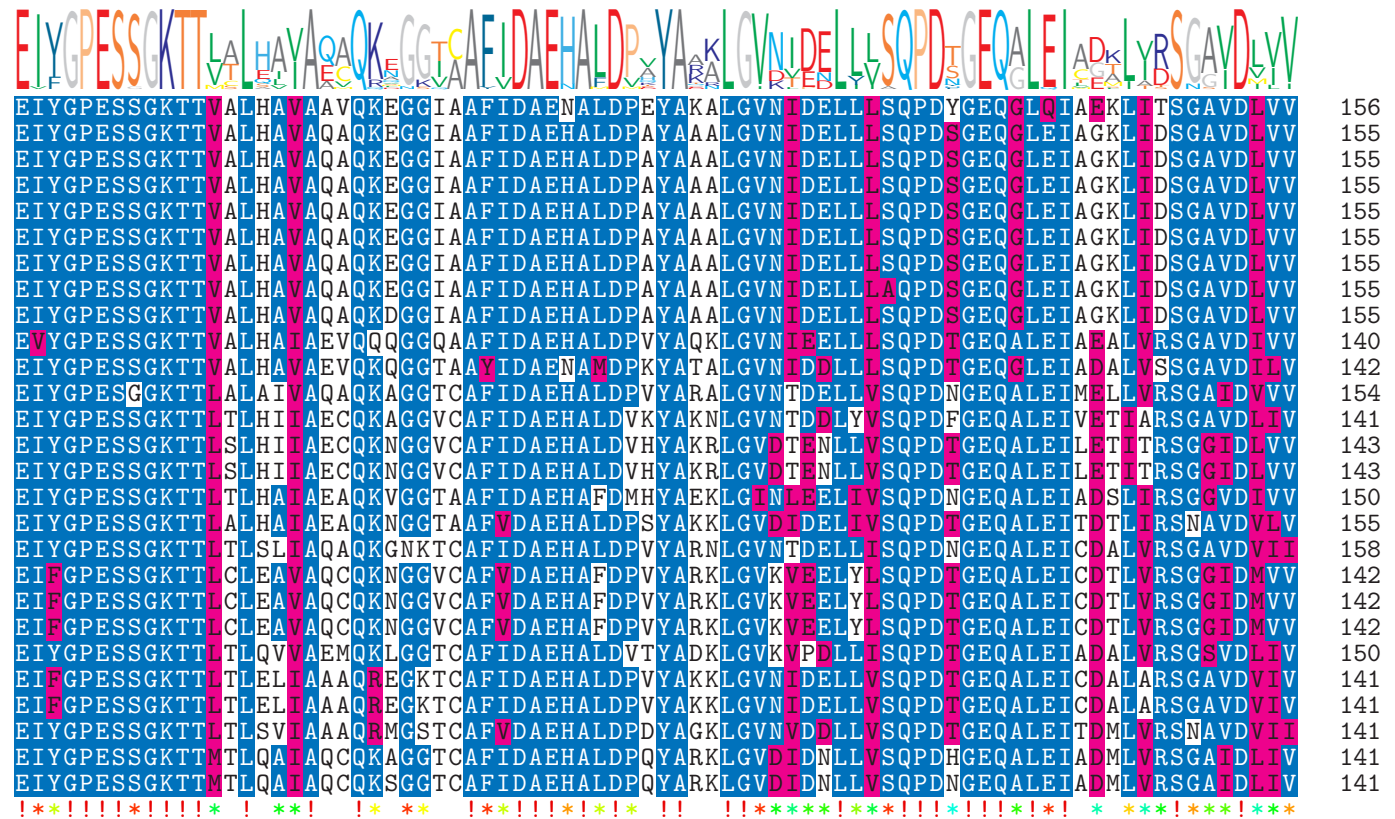
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consensus

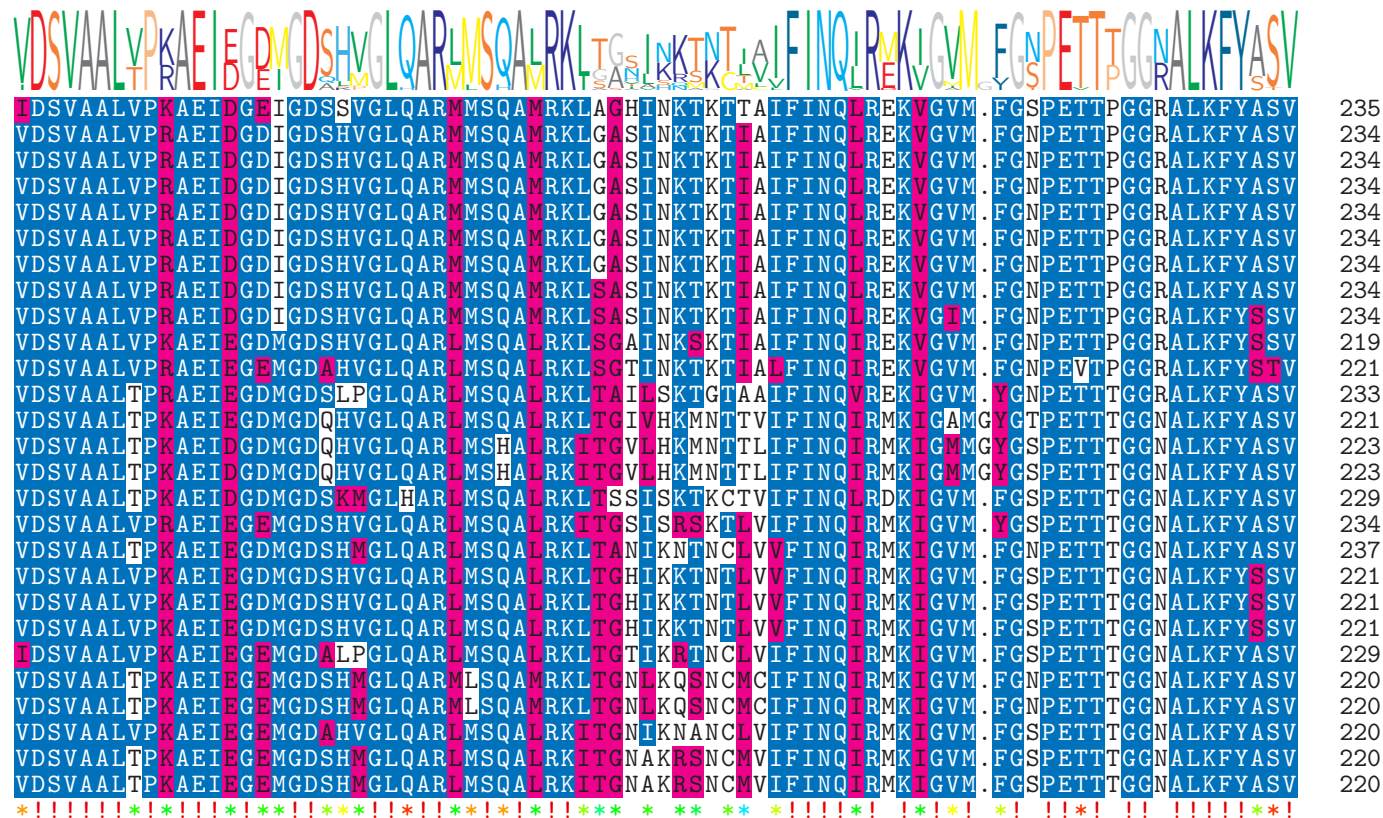
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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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logo

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NTDB id 527 SMSK321 RS11065 WP 001085454.1	RLDVRG	STQIKGTG	.DQKDTN	VGKETK	IKVVKNKVAPPF	KEAFVE	EIMY	GEGISK	TGELL	KIASDL	LDI	IKKAG	AWYS	YKDE	313		
NTDB id 499 SM12261 RS08315 WP 078228268.1	RLDVRG	STQIKGTG	.DQKDTN	VGKETK	IKVVKNKVAPPF	KEAFVE	EIMY	GEGISK	TGELL	KIASDL	LDI	IKKAG	AWYS	YKDE	313		
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NTDB id 1214 NCTC11637 00359 SQJ03206.1	RIDIRRIA	ALK	.QNEQH	IGNRAK	AKVVKNKVAPPF	REA	AEFD	DIMF	GEGISKE	GEI	IDY	GVKLD	IV	DKSG	AWLSY	QDK	298
NTDB id 1211 C694 RS00795 WP 000963128.1	RIDIRRIA	SLK	.QNEQH	IGNRAK	AKVVKNKVAPPF	REA	AEFD	DIMF	GEGISKE	GEI	IDY	GVKLD	IV	DKSG	AWLSY	QDK	298
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consensus	!***!*		*	*	*	***!***!!*!!*!!*	*	***!*	!***	***	***	***	!*	!***!			

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consensus

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Sequence	Score
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KIGGQSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTEN...KKDE...PKKEEA..VNEEVPLDLGDELEI	384
KIGGQSENAKKYLAHNPEVFAEIDHQVRVQFGLIDGEEAAE...S...KKDE...VAQVDS..VNEEVPLDLGDELEI	380
KIGGQSENAKKYLAHNPEIFDEIDHQVRVQFGLIDGEEAAE...S...KKDE...AAQVDS..VNEEVPLDLGDELEI	380
KIGGQSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVA..SE.....E.....TDDLALDLNGIEI	376
KIGGQSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSK..EK.....ETDEK..ADKNLVLELDDTIEL	381
RLGQGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEET...QEEL.EFE.E.....	348
RIGGQGRENAKKNYLADHEDVEDEVRLKVRAAAYGISDVPEEDLPTTED...E.QI.NILPDDST.....EE.....	355
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KLGGQRENSKAFILKENPEIADEITKAIQNSMGI EGMISG...SEDD..EGEE	343
KLGGQRENAKALLKEDKALADEITLKIKESIGSNEEIMP...LPDE..PLEEME	347
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KIGGQKNNNAVKWLKENPEIADKLEQETIRNTLASNPNSVL...KATASDSNDESDVEEF...SEEEL	372
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logo

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NTDB id 499 SM12261 RS08315 WP 078228268.1	EIEE	384
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NTDB id 1142 GTF74 RS11550 WP 000344154.1		354
NTDB id 1205 PSJM300 05545 AFN77183.1		347
NTDB id 1022 ACIAD RS06390 WP 004925639.1		349
NTDB id 1074 ABD1 RS10195 WP 000344167.1		349

consensus

 non conserved
 similar
 ≥ 50% conserved