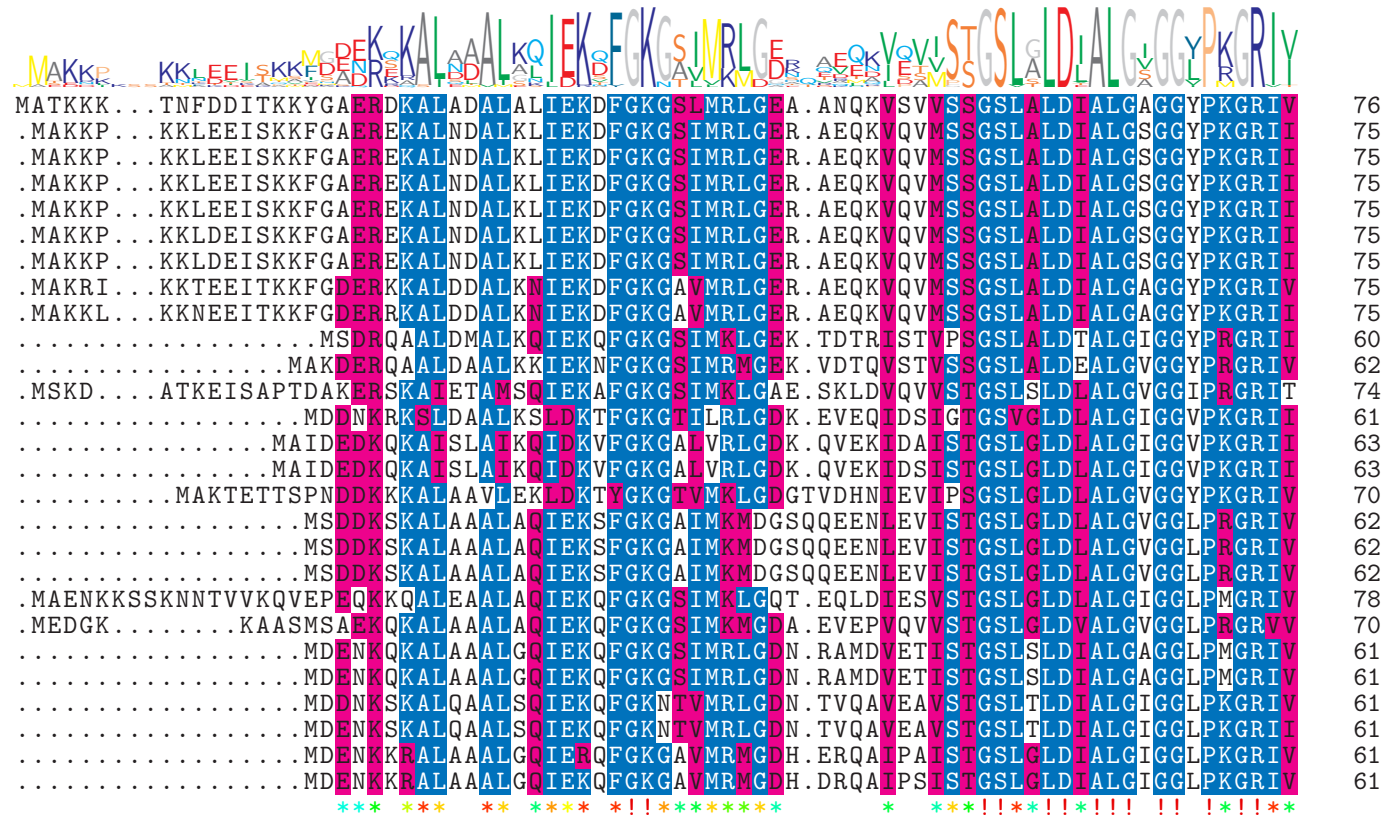


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consensus

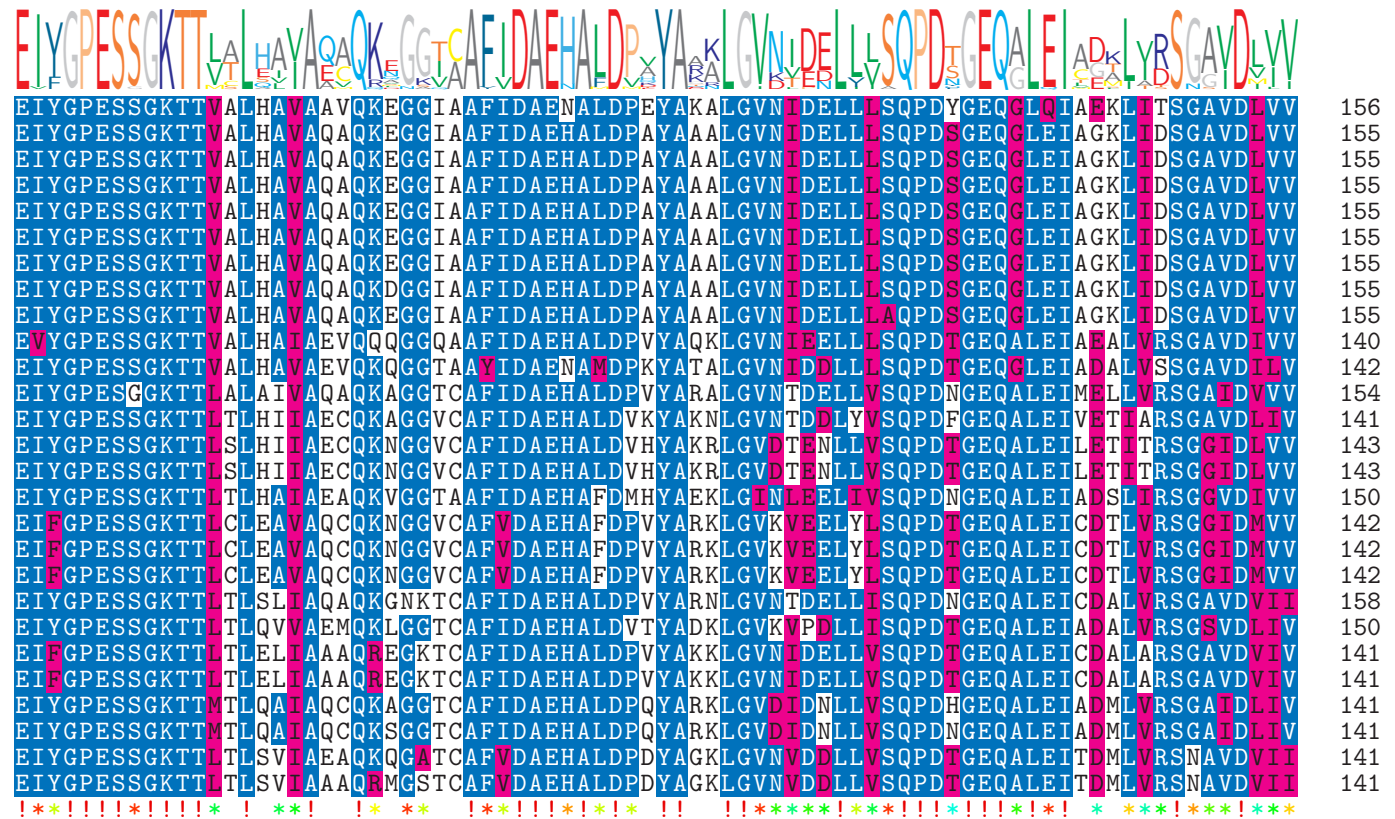
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consensus

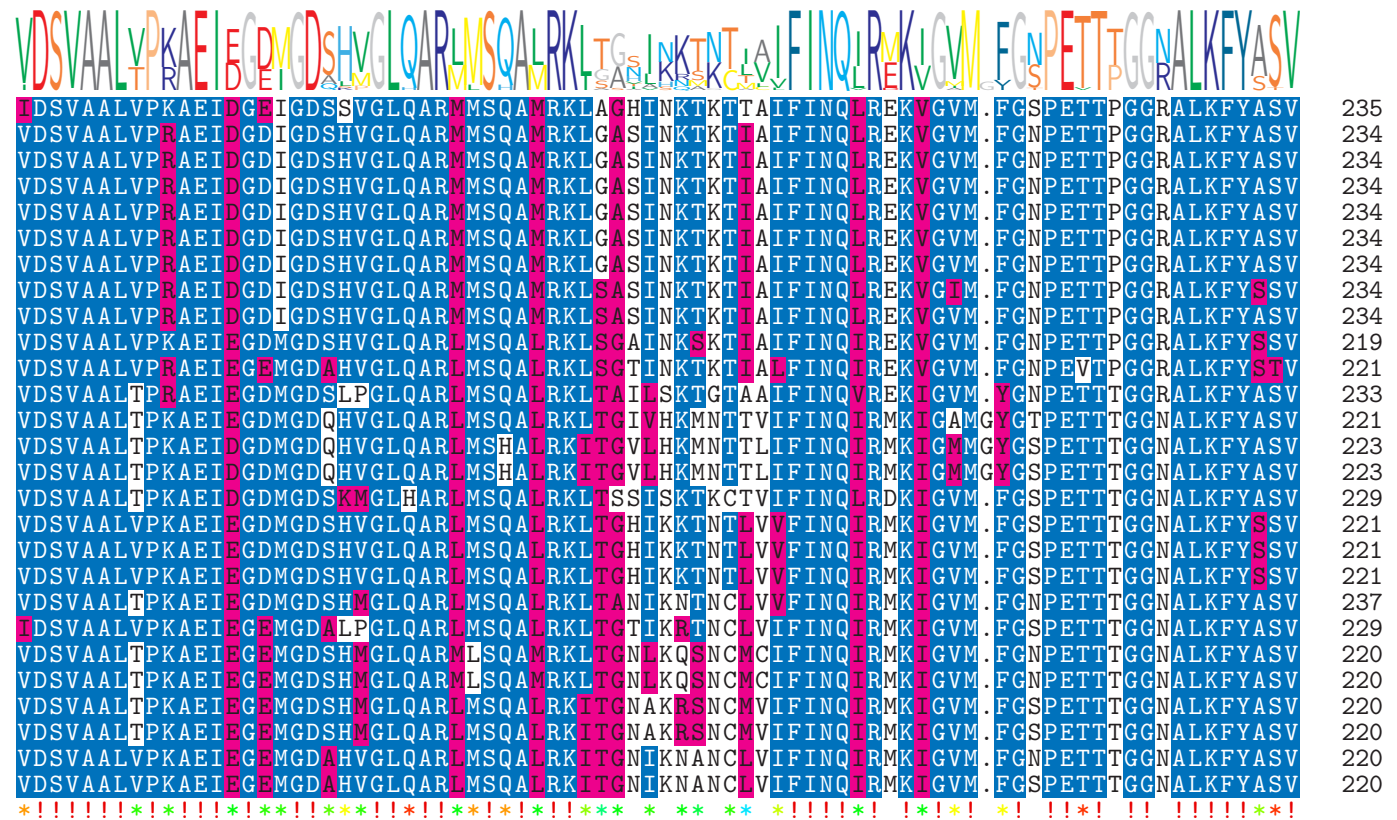
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NTDB id 294746 CSC33 RS00950 WP 003092260.1
NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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logo

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NTDB id 115 BSU 16940 NP 389576.2	RLEVRR	AAEQLKQGN		DVMGN	KTIKVV	VKNKVAPP	RTAEV	DIMY	GEGIS	KEGE	ITID	LGTE	L	DIVQK	SGSW	SYEEEE	294			
NTDB id 625 LCA RS02525 WP 011374196.1	RLEVRR	AAETIKNGT		DMIGN	RARIKVV	VKNKVAPP	KVAEV	DIMY	GGIS	R	TGELV	DMAVEK	DI	IINK	SGSW	SYSGE	296			
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NTDB id 1214 NCTC11637 00359 SQJ03206.1	RIDIRRIA	A....	L.KQNE	EQHIGN	RAKAKV	VKNKVAPP	REAEF	DIMF	GEGIS	KEGE	ITID	YGVKL	DIVDK	SGAW	LSYQ	DK	298			
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NTDB id 1130 NGFG RS03960 WP 003688695.1	RLDIRR	TGS....	I.KKGE	EEVLGN	ETRVKVI	KNKVAPP	RQAEF	DILY	GEGIS	WE	GELID	I	GVKN	DIINK	SGAW	SYNGA	296			
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NTDB id 1427 RS RS02760 WP 011000510.1	RLDIRR	IGS....	I.KKGE	DEVVGN	ETKV	VKNKVAPP	RE	AI	FDILY	GAGVS	REGE	ITID	L	GV	EAKV	VEK	SGAW	SYNGE	304	
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consensus	!***!*		*	*	*	*****!***!!*****!*	*		*****!*	*****	*****	***		***	!	!*****!				


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Sequence	Score
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KIGGQSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENK...KDE...PKKEEA...VNEEVPLDLGDELE	383
KIGGQSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENK...KDE...PKKEEA...VNEEVPLDLGDELE	383
KIGGQSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENK...KDE...PKKEEA...VNEEVPLDLGDELE	383
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KIGGQSENAKKFLADNPFEIFDDIDHKVRVQGLIEEDNTEEEKSSKE...K...ETDEK...ADKNLVLELDDTIE	380
KIGGQSENAKRYLADHPQLFDEIDRKVRVKFGLLEESSEESAMAVAS...E...E...TDDLALDLNGIE	375
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NTDB id 228 SPD RS09265 WP 001085462.1	IEIEE	388
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NTDB id 159 SP RS09750 WP 001085462.1	IEIEE	388
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NTDB id 1074 ABD1 RS10195 WP 000344167.1		349
NTDB id 294746 CSC33 RS00950 WP 003092260.1		346
NTDB id 1205 PSJM300 05545 AFN77183.1		347
consensus		

-  non conserved
-  similar
-  ≥ 50% conserved