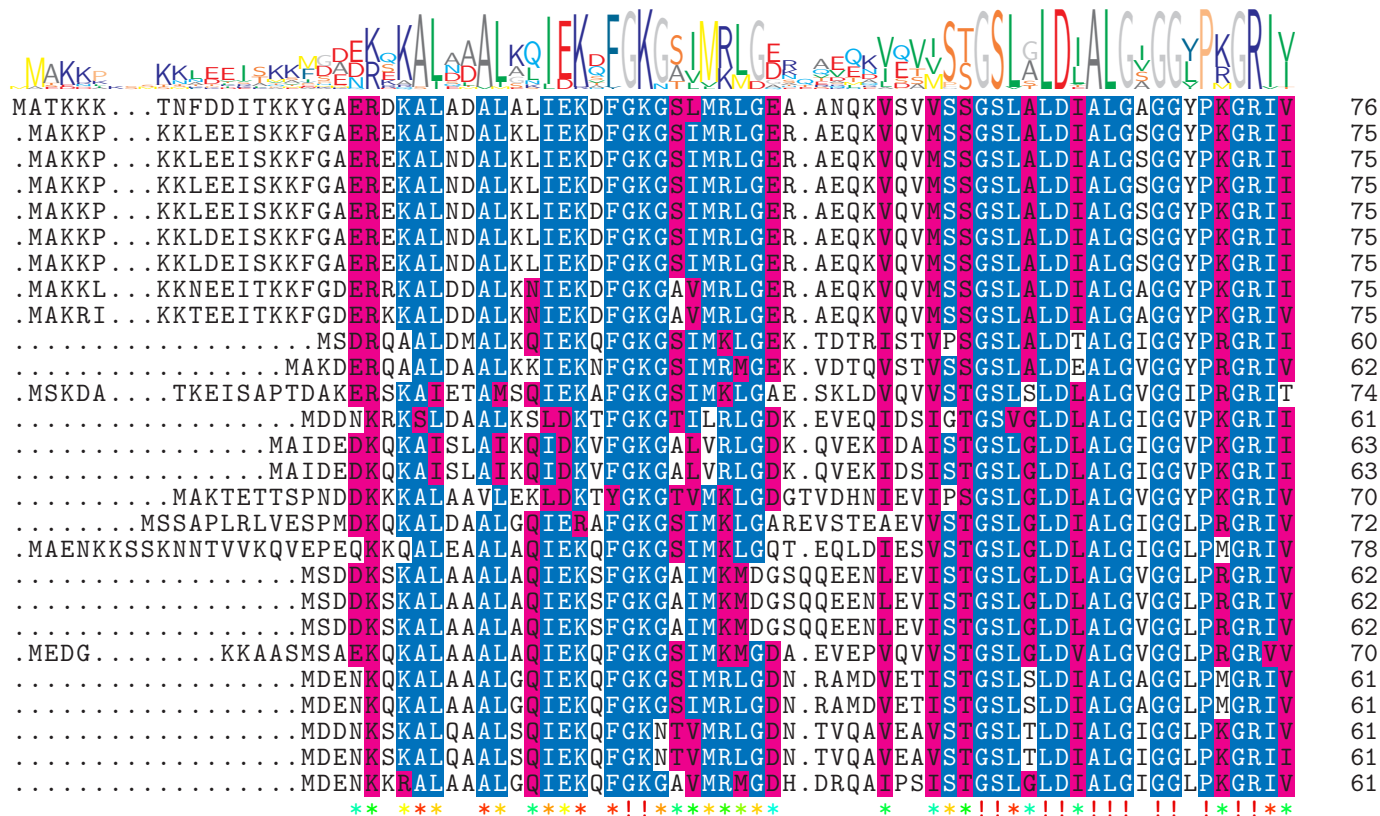


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NTDB id 115 BSU 16940 NP 389576.2
NTDB id 625 LCA RS02525 WP 011374196.1
NTDB id 1313 DR RS12030 WP 010888966.1
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NTDB id 1142 GTF74 RS11550 WP 000344154.1
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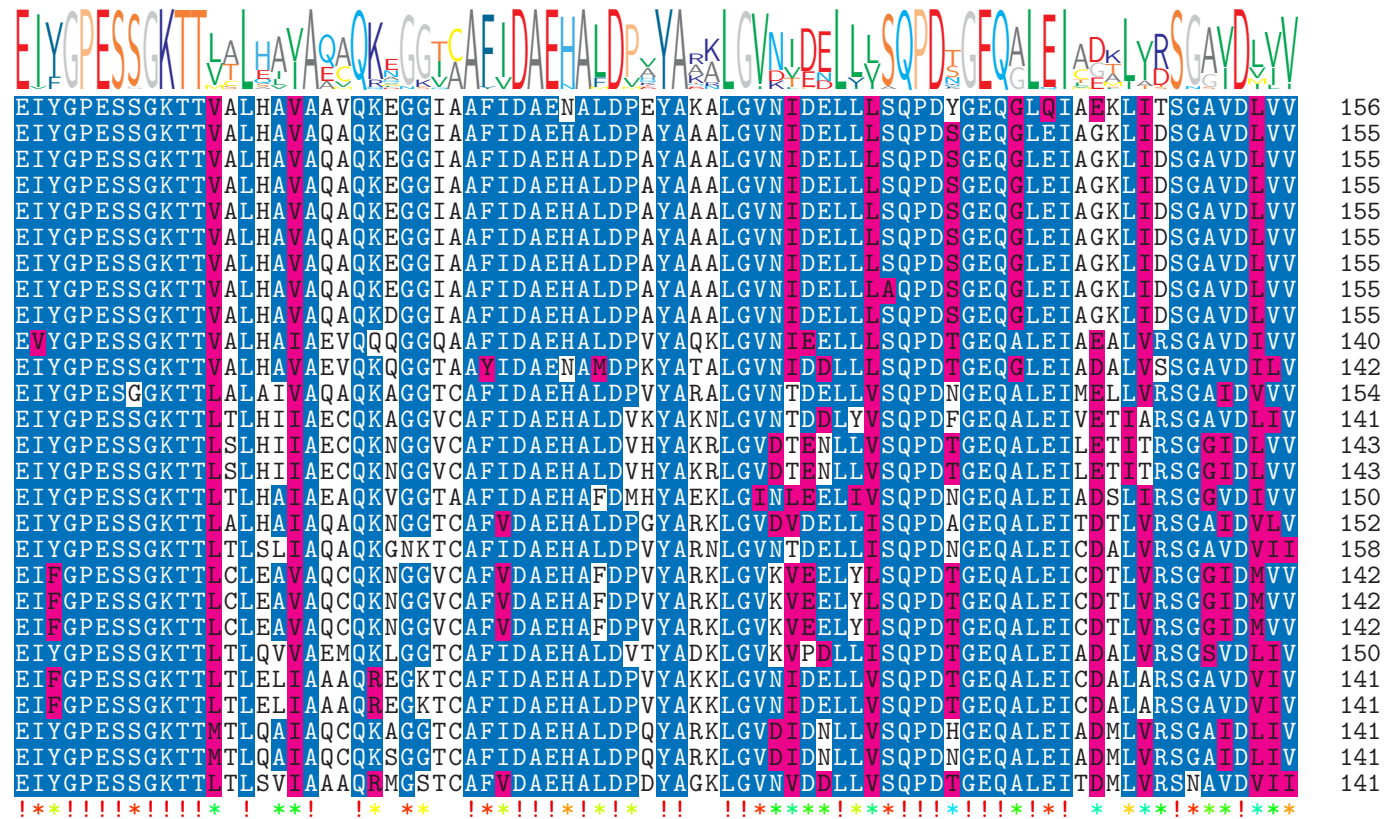
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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logo

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NTDB id 228 SPD RS09265 WP 001085462.1	RLDVRG	NTQIKGTG	.DQKETN	VGKETK	IKVV	VKNKVAPP	PFKEA	VVEIMY	GEGIS	KTGEL	LKIAS	DLDI	IKK	A	GA	WYSY	KDE	313				
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NTDB id 159 SP RS09750 WP 001085462.1	RLDVRG	NTQIKGTG	.DQKETN	VGKETK	IKVV	VKNKVAPP	PFKEA	VVEIMY	GEGIS	KTGEL	LKIAS	DLDI	IKK	A	GA	WYSY	KDE	313				
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NTDB id 1245 Cj1673c YP 002345041.1	RLDVRK	VVA....TLK	.QNEEP	IGNRV	KV	VVKNKVAPP	FRQA	EFD	VM	F	GEG	LS	REGEL	IDY	GV	KLDI	V	DKSGAW	F	SYKDK	296	
NTDB id 1214 NCTC11637 00359 SQJ03206.1	RIDIRRIA	ALK	.QNEQH	IGNRA	KA	VVKNKVAPP	FRQA	EFD	IM	F	GEGIS	KEGE	IIDY	GV	KLDI	V	DKSGAW	LSYQDK	298			
NTDB id 1211 C694 RS00795 WP 000963128.1	RIDIRRIA	SLK	.QNEQH	IGNRA	KA	VVKNKVAPP	FRQA	EFD	IM	F	GEGIS	KEGE	IIDY	GV	KLDI	V	DKSGAW	LSYQDK	298			
NTDB id 1334 RAOC RS04870 WP 004918236.1	RIDIRRS	LSDTGKIK	DKSGEV	IGNRTK	V	VVKNKVAPP	PFKSA	EFD	IMY	GEG	VSKV	GEILD	VATD	LDI	IQK	SGS	W	FSYQDT	309			
NTDB id 300475 DPR14 RS22405 WP 158047122.1	RLDIRR	IG....AIK	.DR	ENVGN	QTRV	VVKNK	MAPPFR	VVEFD	IMY	GEG	VSKV	GELL	DLGV	QAN	VVEK	SGS	W	FSYEGQ	306			
NTDB id 1389 A4U84 RS07560 WP 021112712.1	RLDIRR	CG....VVK	.DGDEI	IGSETK	V	VVKNKVAPP	FR	EVQFD	IMY	GEGIS	RMNELL	ILAE	ANGF	IKK	SGAW	F	SYDGT	312				
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NTDB id 1123 OK783 RS03845 WP 003688695.1	RLDIRR	TG....SIK	.KGEEV	LGNETR	VKVI	KNKVAPP	FRQA	EFD	DILY	GEGIS	WE	GELID	IGV	KNDI	INK	SGAW	SYNGA	296				
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consensus	!	***	!	*		*	*	*	***	!	*!!	!!	!!	!!	*	*		***	!	!!	***	!


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Sequence	Score
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KIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENK.KDE...PKKEEA..VNEEVPLDLGDELEIEI	386
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KIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENK.KDE...PKKEEA..VNEEVPLDLGDELEIEI	386
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KIGQGSSENAKKYLAADHPQLFDEIDRKVRVKFGLLEESEESAMAVAS.E.....E.....TDDLALDLNGIEIED	378
KIGQGSSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKE.K.....ETDEK..ADKNLVLEDDTIELED	383
RLGQGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEETQ.EEL.EFE.E.....	348
RIGQGRENAKKNYLADHEDVEDEVRLKVRVQYGLSDVPEEDLPTTEDE..QI.NILPDDST.....EE.....	355
RIGQGKEKTIAYIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAAEA.....	363
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logo

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NTDB id 1022 ACIAD RS06390 WP 004925639.1	..	349
NTDB id 1074 ABD1 RS10195 WP 000344167.1	..	349
NTDB id 1205 PSJM300 05545 AFN77183.1	..	347

consensus

 non conserved
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 ≥ 50% conserved