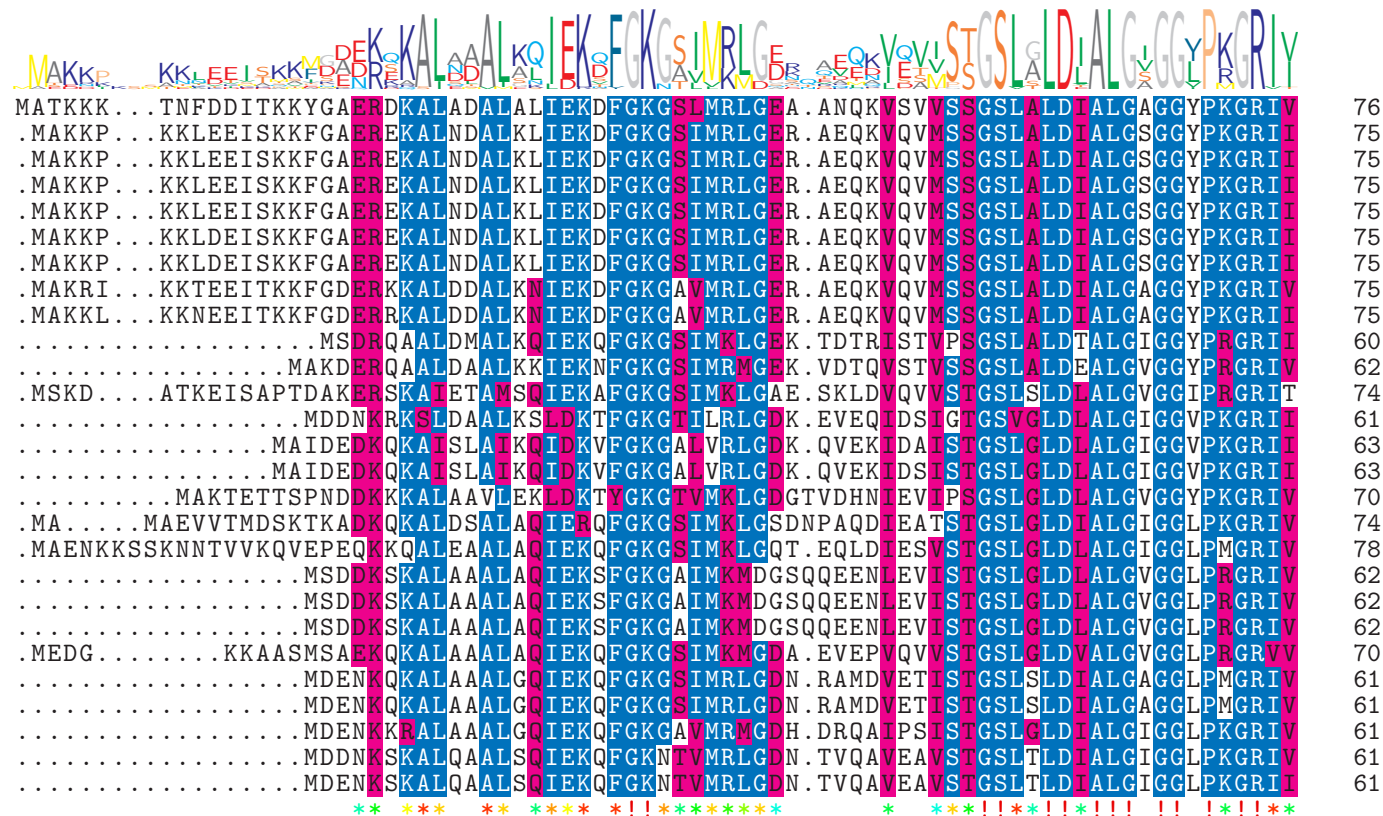


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consensus

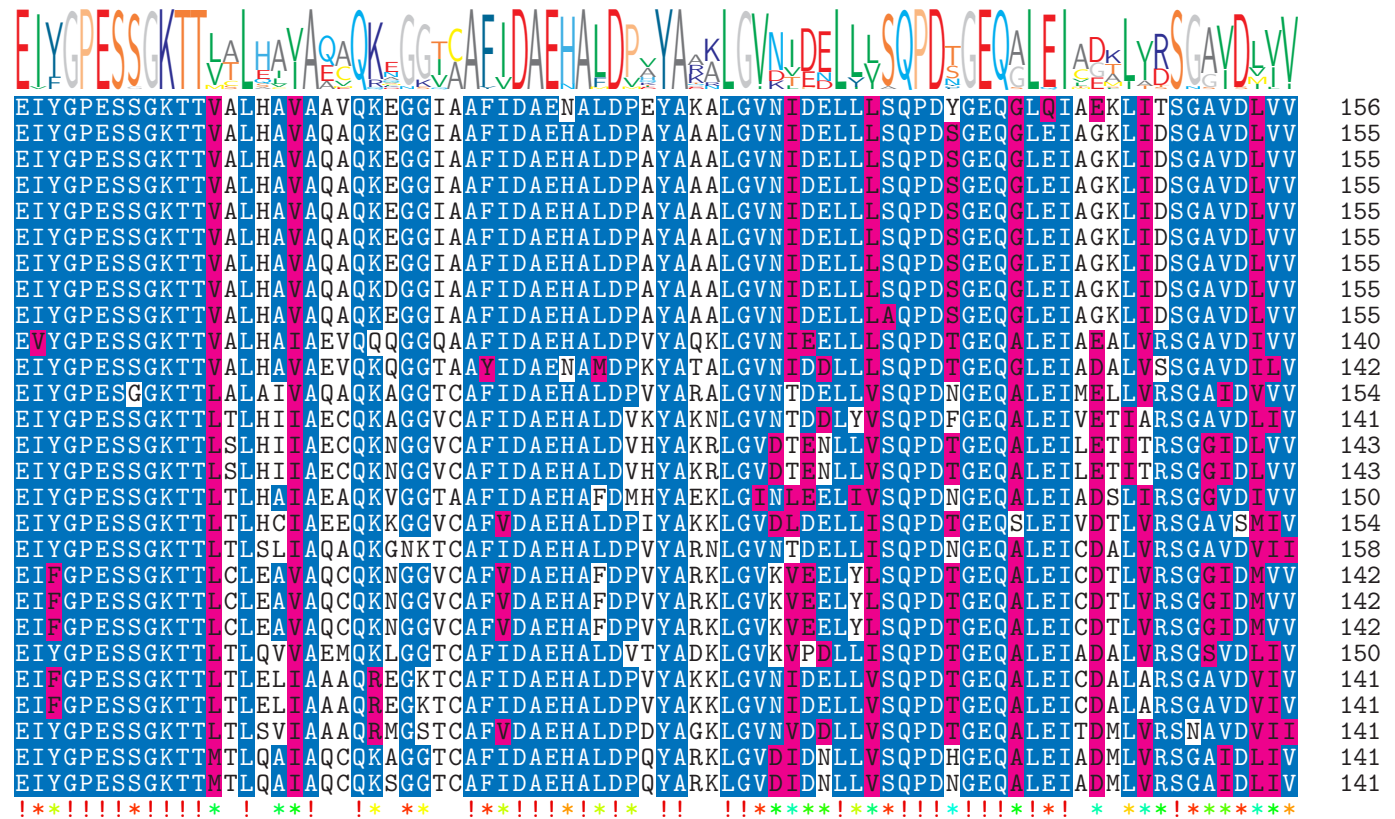
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consensus

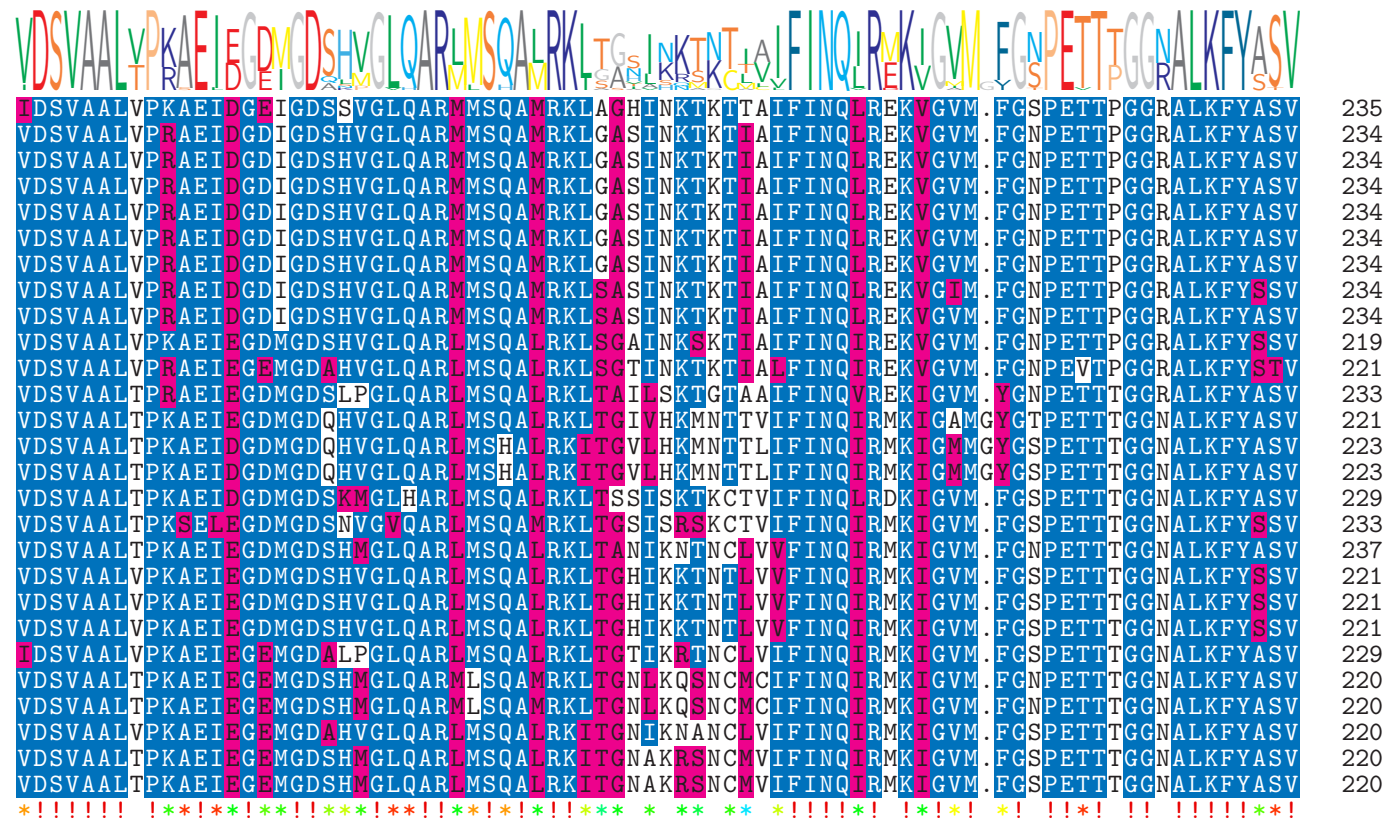
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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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logo

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NTDB id 269 KZH43 RS08665 WP 001085462.1	RLDVRG	NTQIKGTG	.DQKETN	VGKETK	IKVVKNKVAPPF	KEAVVE	EIMYEGEGIS	KTGELLK	IASDLDI	IKKAGAW	YSYKDE	313			
NTDB id 228 SPD RS09265 WP 001085462.1	RLDVRG	NTQIKGTG	.DQKETN	VGKETK	IKVVKNKVAPPF	KEAVVE	EIMYEGEGIS	KTGELLK	IASDLDI	IKKAGAW	YSYKDE	313			
NTDB id 194 SPR RS08825 WP 001085462.1	RLDVRG	NTQIKGTG	.DQKETN	VGKETK	IKVVKNKVAPPF	KEAVVE	EIMYEGEGIS	KTGELLK	IASDLDI	IKKAGAW	YSYKDE	313			
NTDB id 159 SP RS09750 WP 001085462.1	RLDVRG	NTQIKGTG	.DQKETN	VGKETK	IKVVKNKVAPPF	KEAVVE	EIMYEGEGIS	KTGELLK	IASDLDI	IKKAGAW	YSYKDE	313			
NTDB id 527 SMSK321 RS11065 WP 001085454.1	RLDVRG	STQIKGTG	.DQKDTN	VGKETK	IKVVKNKVAPPF	KEAFVE	EIMYEGEGIS	KTGELLK	IASDLDI	IKKAGAW	YSYKDE	313			
NTDB id 499 SM12261 RS08315 WP 078228268.1	RLDVRG	STQIKGTG	.DQKDTN	VGKETK	IKVVKNKVAPPF	KEAFVE	EIMYEGEGIS	KTGELLK	IASDLDI	IKKAGAW	YSYKDE	313			
NTDB id 408 SMU RS09530 WP 002262392.1	RLDVRG	NTQIKGTG	.EQKDSN	IGKETK	IKVVKNKVAPPF	KEAFVE	EITTYEGEGIS	RGTGELV	KIASDLGI	IKKAGAW	YSYNGE	313			
NTDB id 453 Spy49 1753c ACI62003.1	RLDVRG	TTQIKGTG	.DQKDSS	IGKETK	IKVVKNKVAPPF	KVAEVE	EIMYEGEGIS	RGTGELV	KIASDLDI	IKKAGAW	FSYNGE	313			
NTDB id 115 BSU 16940 NP 389576.2	RLEVRR	AAEQLKQGN		DVMGNK	TKIKVVKNKVAPPF	RTAEDV	DIMYEGEGIS	KEGEIID	LGTELDIV	QKSGS	WYSYEEE	294			
NTDB id 625 LCA RS02525 WP 011374196.1	RLEVRR	AAETIKNGT		DMIGNR	ARIKVVKNKVAPPF	KVAEVD	DIMYGGIS	RGTGELV	DMAVEKDI	INKSGS	WYSYGSE	296			
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NTDB id 1245 Cj1673c YP 002345041.1	RLDVRK	VVA....	TLK.QNE	EPIGNR	VKVVVKNKVAPPF	RQAEF	DVMFG	EGEL	LSREGEL	IDYGVK	LDIVDKS	GAWFSYKDK	296		
NTDB id 1214 NCTC11637 00359 SQJ03206.1	RIDIRRI	IA....	ALK.QNE	QHIGNR	AKAKVVKNKVAPPF	REA	AEFDIM	FEGEGIS	KEGEIIDY	GVKLDIV	DKSGAW	LSYQDK	298		
NTDB id 1211 C694 RS00795 WP 000963128.1	RIDIRRI	IA....	SLK.QNE	QHIGNR	AKAKVVKNKVAPPF	REA	AEFDIM	FEGEGIS	KEGEIIDY	GVKLDIV	DKSGAW	LSYQDK	298		
NTDB id 1334 RAOC RS04870 WP 004918236.1	RIDIRRS	LSDTGK	IKDKSGEV	IGNRTK	VKVVVKNKVAPPF	KS	AEFDIM	YEGEGV	SKVGEILD	VATDLDI	IIQKSGS	WFSYQDT	309		
NTDB id 330840 EI983 RS10075 WP 198389271.1	RLDIRR	IG....	AIK.DR	DEVGN	ATRVKVVKVKNKVAPPF	KQVEF	DIMYEGEGIS	KTGELL	DLGVKAG	VVEKSGS	WFSYGDE	308			
NTDB id 1389 A4U84 RS07560 WP 021112712.1	RLDIRR	CG....	VVK.DG	DEIIG	SETKVVVVKNKVAPPF	REVQF	DIMYEGEGIS	RMNELL	ILAEANG	FIKKSGA	WFSYDGT	312			
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NTDB id 1165 A1552VC RS01565 WP 000344154.1	RLDIRR	TG....	AIK.EG	EEVVG	NETRIKVVKNK	IAAPF	KEANTQ	IMYGG	GFNREG	ELIDL	GVKHKM	VVEKSGA	WYSYNGD	295	
NTDB id 1142 GTF74 RS11550 WP 000344154.1	RLDIRR	TG....	AIK.EG	EEVVG	NETRIKVVKNK	IAAPF	KEANTQ	IMYGG	GFNREG	ELIDL	GVKHKM	VVEKSGA	WYSYNGD	295	
NTDB id 1205 PSJM300 05545 AFN77183.1	RLDIRR	TG....	AVK.EG	DEVV	GS	ETRVKVVKNKVAPPF	RQAEFQ	ILYGK	GIVN	RNGEIID	LGVQQGL	VEKSGAW	YAYKGS	295	
NTDB id 1022 ACIAD RS06390 WP 004925639.1	RLDIRR	IG....	QVK.EG	DEIIG	SETKVVVVKNK	MAPPF	REA	IFQILY	GKGVN	QLGEL	VDLAV	QQNIV	QKAGAW	YSYQGN	295
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consensus	!***!*		*	*	*	***!***!!*!!*!!*	*	***!***!***	***	***	***	!***!!			

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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
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KIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDT..ENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
KIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDT..ENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
KIGQGSSENAKKYLAENPEVFAEIDHQVRVQFLIDGEEAAE.....SKKDE...VAQVDS..VNEEVPLDLGDELEIE	381
KIGQGSSENAKKYLAENPEIFDEIDHQVRVQFLIDGEEIAE.....SKKDE...AAQVDS..VNEEVTLDLGDELEIE	381
KIGQGSSENAKKFLADNPEIFDDIDHKVRVQGLIEEDNTEEKQS..SKEK.....ETDEK..ADKNLVLELDDTIELE	382
KIGQGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESASMA..VASE.....E.....TDDLALDLNGIEIE	377
RLGQGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQQAE..ETQEEL.EFE.E.....	348
RIGQGRENAKNYLADHEDVEDEVRLKVRAAAYGISDVPPEEDLPTT..EDE.QI.NILPDDST....EE.....	355
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KLGGGRDRTVKELIKDNPELAEELEAKIREKLQAK.....	343
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KIGQKKNNNAVKWLKENPEIADKLEQIRNTLASNPNSV..LKATASDSNDES.DVE.....EFSEEEEL..	372
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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
consensus			

-  non conserved
-  similar
-  ≥ 50% conserved