

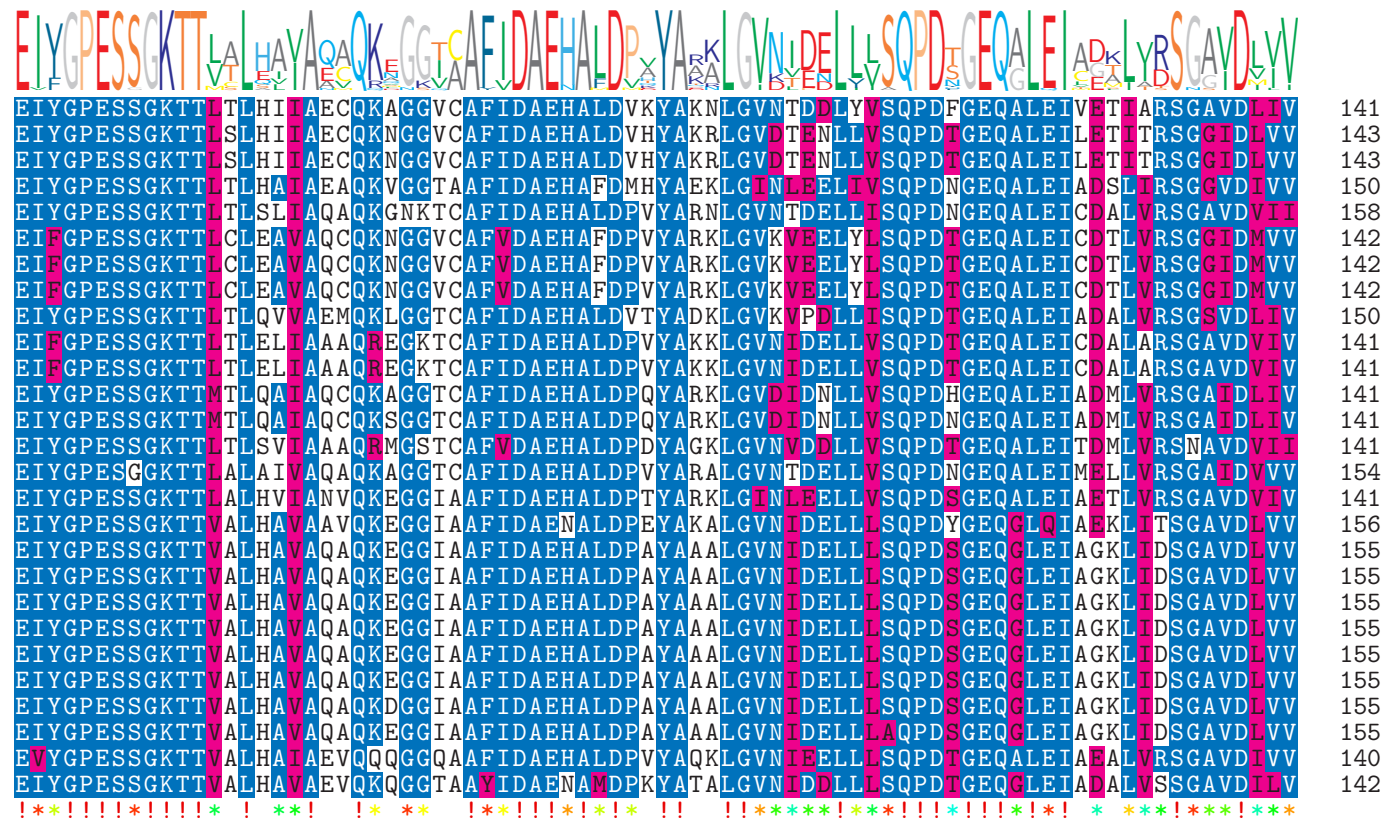
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NTDB id 1211 C694 RS00795 WP 000963128.1	MAID	EDKQKATISLAIKQ	IDKVFGKGALVRLGDK	.QVEK	IDS	ISTGSLGLDLALGI	GGV	PKGRI	63			
NTDB id 1334 RAOC RS04870 WP 004918236.1	MAKTETTSPN	DDKKKALAIAVLEK	LDKTYGKGTVMKLG	DGTVDHNI	EV	IPSGSLGLDLALGV	GGY	PKGRIV	70			
NTDB id 1389 A4U84 RS07560 WP 021112712.1	.MAENKKSSKNNTVVKKQVEP	EQKKQALEAALAQ	IEKQFGKGSIMKLG	QT.EQLD	IES	VSTGSLGLDLALGI	GGL	PMGRIV	78			
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NTDB id 39993 DESTER RS07550 WP 013639045.1	MQ	EEERRRVLEDALRR	IKKEFGE	SV	MFLG	EK	.PAEE	IPA	ISTGSI	SIDRATGI	GGIPRGRIT	61
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NTDB id 159 SP RS09750 WP 001085462.1	.MAK...KPKK	LEEISKKFGA	EREKALNDAL	KL	IEKD	FGKGSIMRLGER	.AEQK	VQVM	SSGSLALDIALGS	GGY	PKGRI	75
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consensus		*** **	*	***	*****	*	*****!!!!!!	!!	!!!!*			

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NTDB id 1130 NGFG RS03960 WP 003688695.1
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NTDB id 1123 OK783 RS03845 WP 003688695.1
NTDB id 1427 RS RS02760 WP 011000510.1
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NTDB id 1142 GTF74 RS11550 WP 000344154.1
NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
NTDB id 1205 PSJM300 05545 AFN77183.1
NTDB id 1313 DR RS12030 WP 010888966.1
NTDB id 39993 DESTER RS07550 WP 013639045.1
NTDB id 600 KW2 RS01765 WP 011675413.1
NTDB id 269 KZH43 RS08665 WP 001085462.1
NTDB id 228 SPD RS09265 WP 001085462.1
NTDB id 194 SPR RS08825 WP 001085462.1
NTDB id 159 SP RS09750 WP 001085462.1
NTDB id 527 SMSK321 RS11065 WP 001085454.1
NTDB id 499 SM12261 RS08315 WP 078228268.1
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NTDB id 115 BSU 16940 NP 389576.2
NTDB id 625 LCA RS02525 WP 011374196.1
consensus

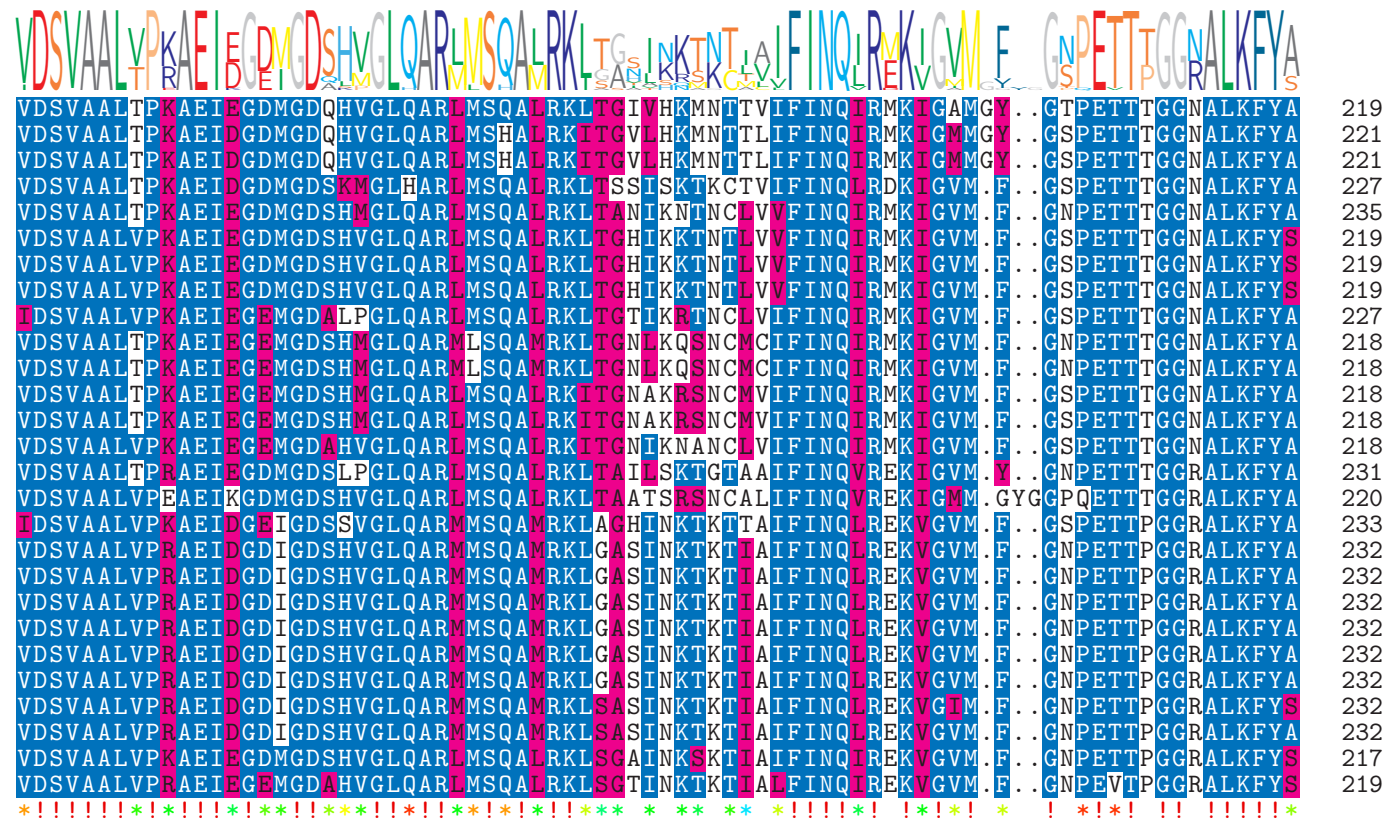
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consensus

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logo

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NTDB id 1334 RAOC RS04870 WP 004918236.1	SVRIDIRRLSDTGKIKDKSGEV	IGNRTKVVVKNKVAPPFKSA	EFDIMYGEGLSVKVGELIDVATDLDITQKSGSWFSYQ	307						
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NTDB id 1074 ABD1 RS10195 WP 000344167.1	SVRLDIRRIGQ....V.KEGDEI	IGSETKVVVKNKMAPPFRQA	IFQILYGKGTNQLGELVDLAVQQDIVQKAGAWYSYQ	293						
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NTDB id 499 SM12261 RS08315 WP 078228268.1	SVRLDVRGSTQIKGTG.DQKDTN	VGKETKIKVVKNKVAPPFKEA	FVEIMYGEGLSKTGELLKIASDLDIINKKAGAWYSYK	311						
NTDB id 408 SMU RS09530 WP 002262392.1	SVRLDVRGNTQIKGTG.EQKDSN	IGKETKIKVVKNKVAPPFKEA	FVEIITYEGEGISRTGELVKIASDLGIINQKAGAWYSYN	311						
NTDB id 453 Spy49 1753c ACI62003.1	SVRLDVRGTTQIKGTG.DQKDS	IGKETKIKVVKNKVAPPFKVA	EVVEIMYGEGLSRTGELVKIASDLDIINQKAGAWFSYN	311						
NTDB id 115 BSU 16940 NP 389576.2	SVRLEVRRAEQLKQGN.....DV	MGNKTKIKVVKNKVAPPFR	TAEVDIMYGEGLSKEGEIIDLGTELIDIVQKSGSWYSYE	292						
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consensus	**!*!!**!*~	~	**~	*****!!*!!*!!*!!*!!*~	~	*****!!*!!*~	*****~	~	***~	!!*!!*!!

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NTDB id 625 LCA RS02525 WP 011374196.1
consensus

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Sequence	Score
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DKKLGQGGRENAKALLKEDKALADEITLTKIKESIGSNEEIMPLPDE..PLEEM.E.....	347
DTKLGQGRDRTVKELIKDNPELAELEAKIREKLQAK.....	343
GTKIGQGGKNNAVKWLKENPEIADKLEQEIRNTLASNPNSVLKATASDSNDES.DVEEF.....SEEL.....	372
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GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEGTQDETGDGER.....PEE.....	348
GERIGQGRDNCREFLRENAELAREIENKVRHLGVTPMGAVTLA.EEVEED.....	352
GDKIGQGGKANACKYLKENPEIAKTLDDKKLREMLLNPNEMQLIAETSSAADVV.EFGAV.....PEEF.....	354
GDKIGQGGKANACKYLKENPEIAKTLDDKKLREMLLNPNEMQLIAETSSAADVV.EFGAV.....PEEF.....	354
GNKIGQGGKNNVIRYLEENPQISTEIEAVIREQLLTKASDQTAA.HDETEEP.DLL.....ES.....	349
GNKIGQGGKNNVIRYFEENNQIAEIEIRNIREQLLTGTNGAVQ.I.EDEEEP.DLL.....LES.....	349
GSKIGQGGKANAACKYLEENPEIGQIEEQIRAKLLVTSANTKATPVAEDLADA.DI.....	347
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DIRLGQGGKENARIFLKENPEIAVELEAKIMEAFSDRGA.....	334
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GEKIGQGSSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
GEKIGQGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
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SERIGQGGRENAKNYLADHEDVEDEVRLKVRAYGISDVPPEEDLPTTEDE.QI.NILPDDST.....EE.....	355

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NTDB id 115 BSU 16940 NP 389576.2	...		348
NTDB id 625 LCA RS02525 WP 011374196.1	...		355
consensus			

- ⓧ non conserved
- ⓧ similar
- ⓧ ≥ 50% conserved