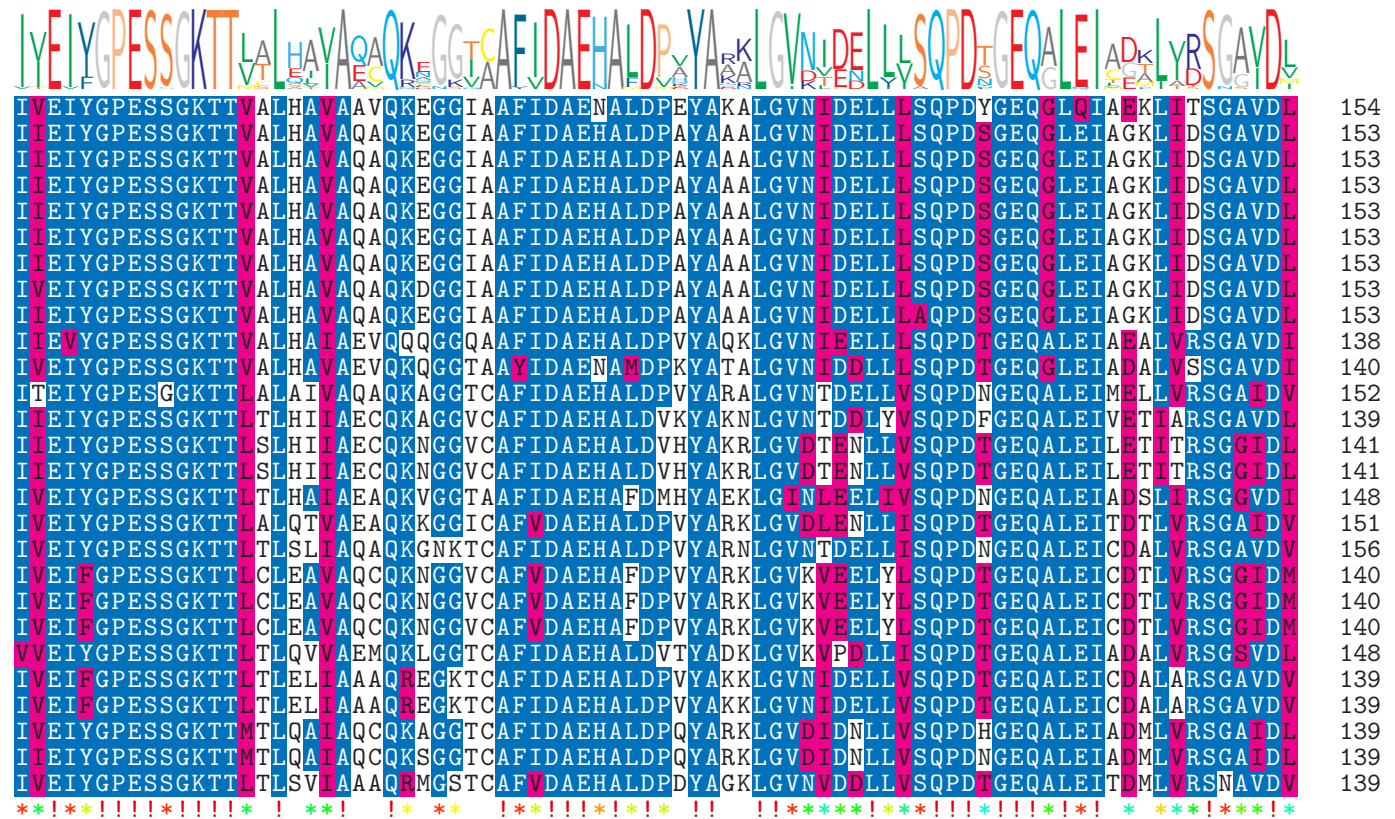


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NTDB	id	115	BSU	16940	NP	389576.2	MSDRQAALDMALKQIEKQ	FGKGS	SIMKLGEK	.TDTRIST	VP	SGSL	ALD	TD	ALGI	GGY	PRGR	58								
NTDB	id	625	LCA	RS02525	WP	011374196.1	MAKD	ERQAALDA	ALKK	IEKN	FGKGS	SIMRMGEK	.VDTQ	VST	VSSGSL	ALDE	ALGV	GGY	PRGR	60						
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NTDB	id	1245	Cj1673c	YP	002345041.1	MDDN	KRKSLDA	ALKS	LDKT	FGKGT	ILRLGDK	.EVEQ	IDS	IGT	GSVGLD	LALGI	GGV	PKGR	59							
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NTDB	id	1130	NGFG	RS03960	WP	003688695.1	MSD	DKSK	ALAA	ALAQ	IEKS	FGKGA	IMKMDGS	SQREEN	LEV	IST	GSLS	GLD	LALGV	GGL	PRGR	60				
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NTDB	id	1165	A1552VC	RS01565	WP	000344154.1	MDEN																			

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consensus

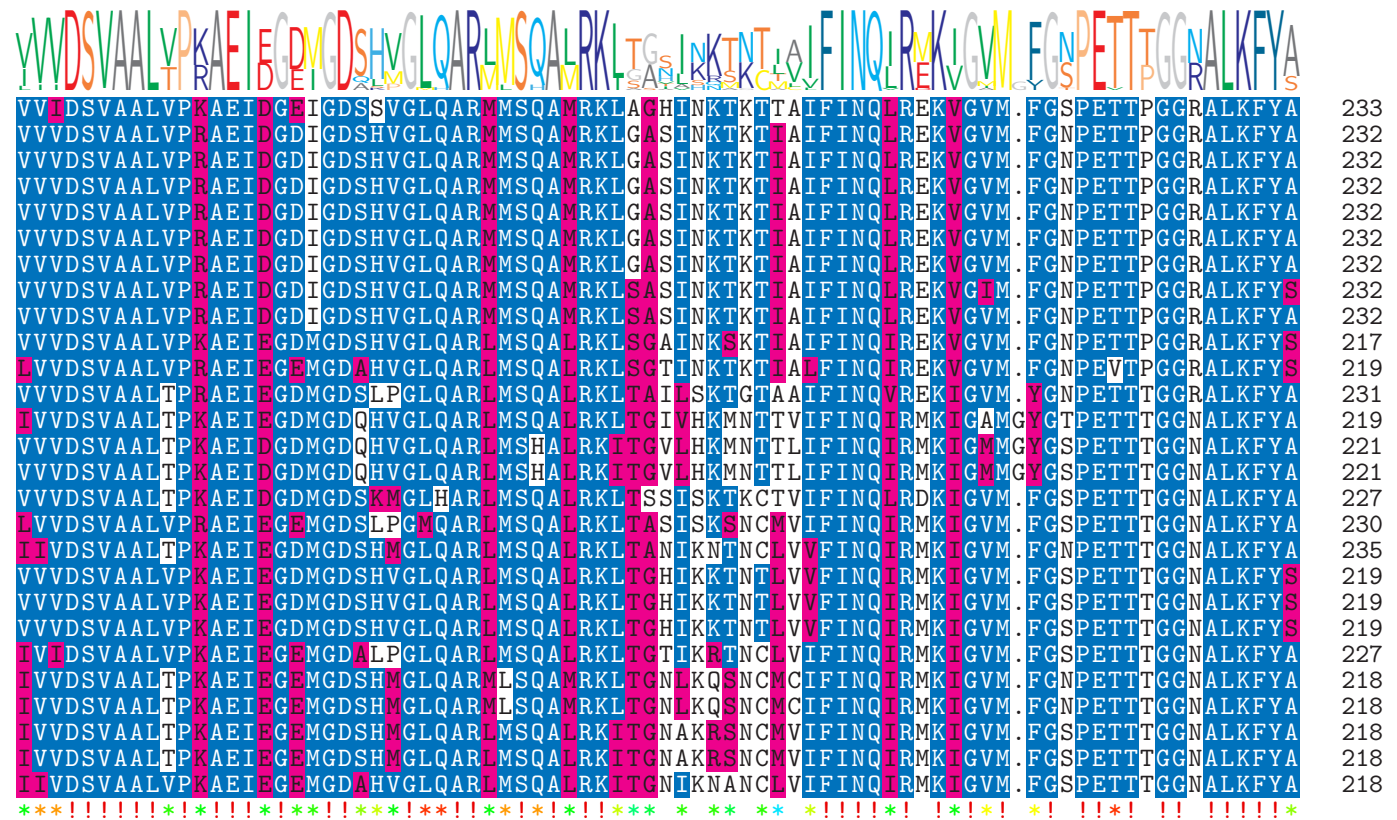
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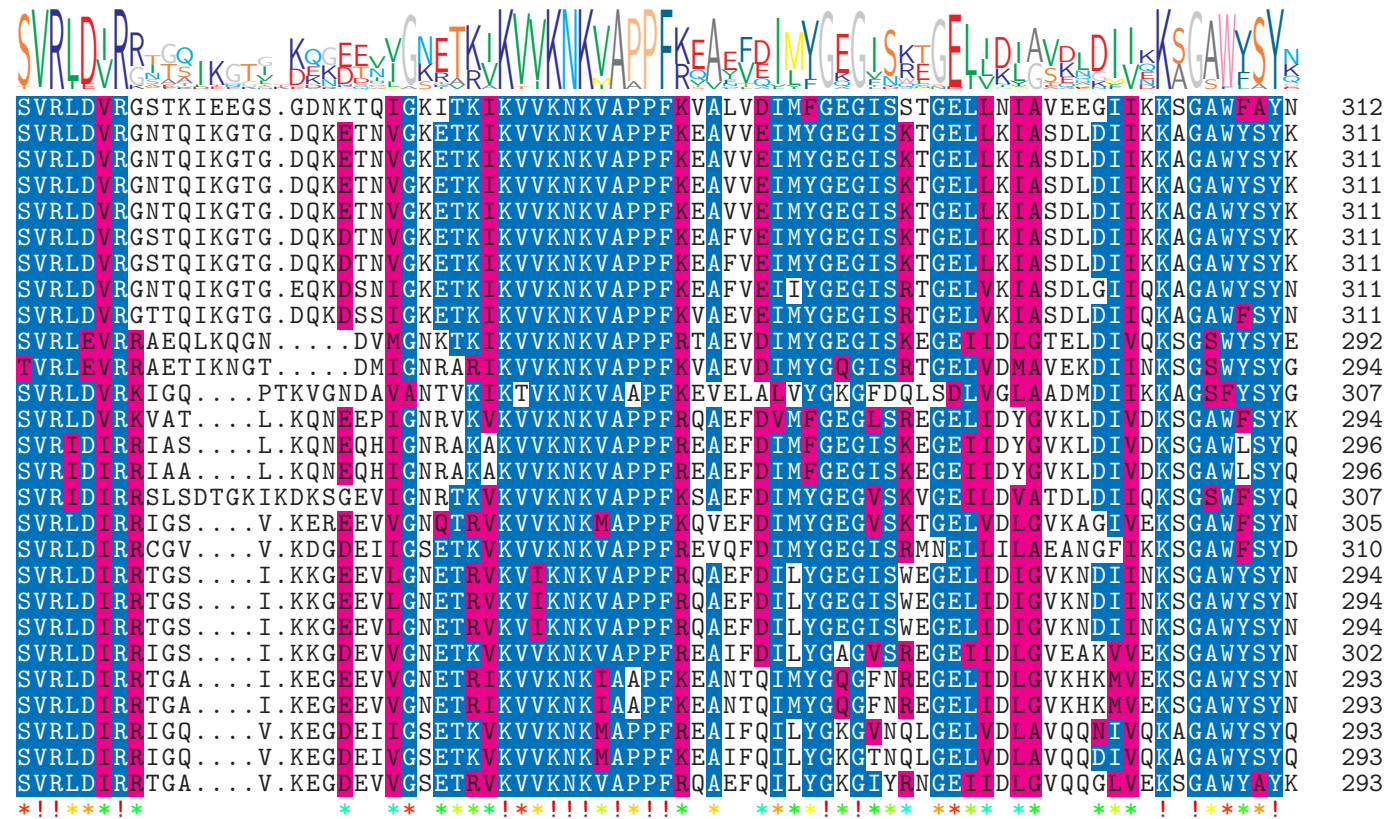
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consensus

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NTDB id 228 SPD RS09265 WP 001085462.1	DEKIGQGS	ENAKKYLAEHPEIF	DEIDKQVRSKFGL	IDGEEVSEQDTE	...NKKDE....PKKEEA..VNEEVPLDLGDEL	382	
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NTDB id 527 SMSK321 RS11065 WP 001085454.1	DEKIGQGS	ENAKKYLADNPEVFAE	IDHQVRVQFGL	IDGEEAAE	SKKDE....VAQVDS..VNEEVTLDLGDEL	378	
NTDB id 499 SM12261 RS08315 WP 078228268.1	DEKIGQGS	ENAKKYLADNPEIF	DEIDHQVRVQFGL	IDGEEIAE	SKKDE....AAQVDS..VNEEVTLDLGDEL	378	
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NTDB id 453 Spy49 1753c ACI62003.1	GEKIGQGS	ENAKRYLADHPQLF	DEIDRKVRVKFGL	LEESEEEESAMAV	...ASE.....E.....TDDLALDLNNGI	374	
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NTDB id 1214 NCTC11637 00359 SQJ03206.1	DKKLGGG	RENAKALLKEDKAL	ADEITLKI	KESIGSNEEIMPL	..PDEP....LEEME.....	347	
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NTDB id 300467 DQW09 RS08985 WP 034794574.1	SQRLGGG	RENAKTFLRDNPD	LAREIETALRQNA	GLIADRFLE	..NGGPEADDGDEP.....PET.....	362	
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NTDB id 1130 NGFG RS03960 WP 003688695.1	GAKIGQG	KDNVRVWLKENPEI	SDEIDAKIRALNGV	EMHITEG	..T..QDET DGER.....PEE.....	348	
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NTDB id 1205 PSJM300 05545 AFN77183.1	GSKIGQG	KANAACKYLEENPEI	IGQIEEQIRAKLL	VTSANTKA	..T..PVAEDLADADI.....	347	
consensus	***!!!*****	**	*****	*****	**	**	***

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved