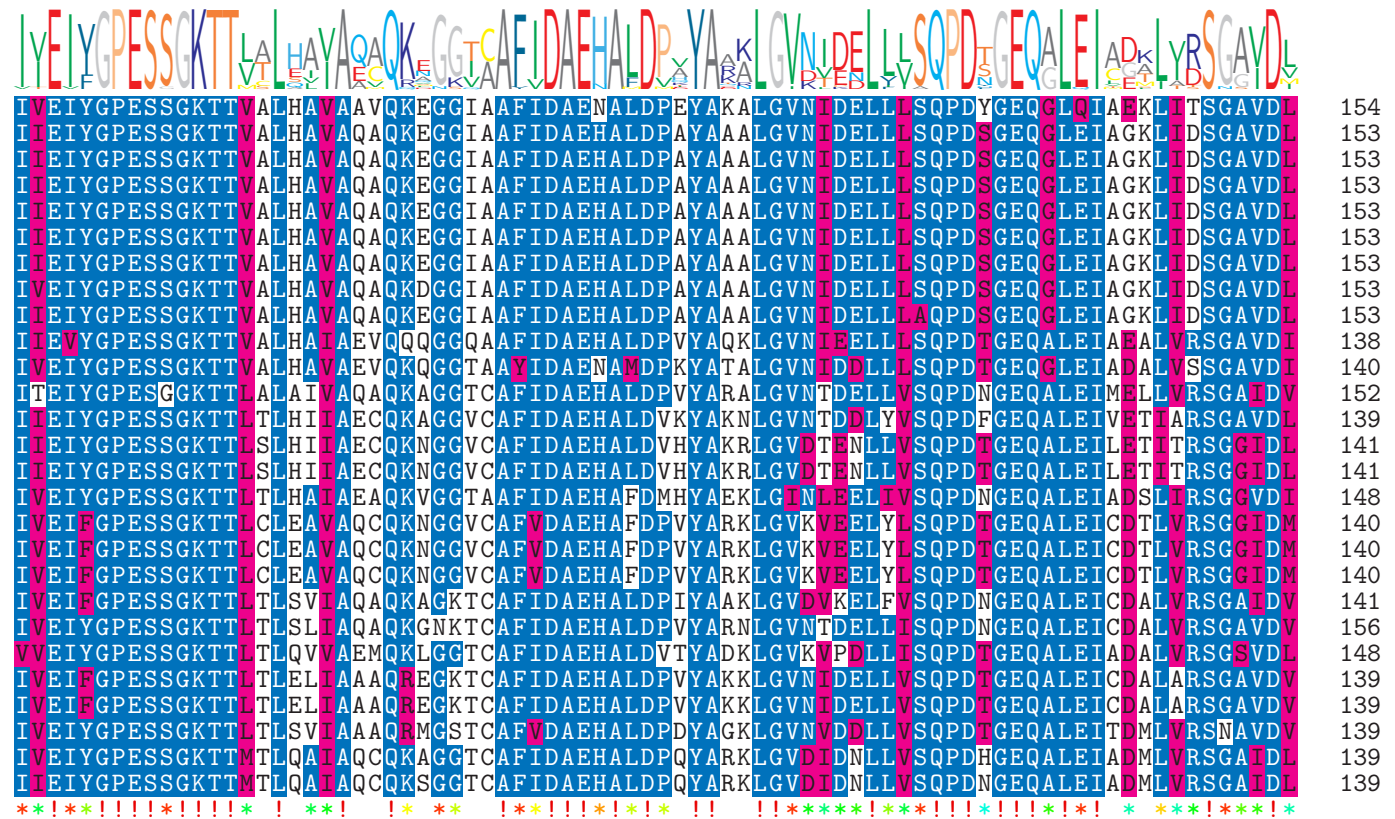


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NTDB id 159 SP RS09750 WP 001085462.1	.MAKK....PKKLEEISKKFGA	EREKALNDALKLIEKD	FGKGSIMRLGER	.AEQKVQVM	SSGSLALD	I	ALGSGGY	PKGR	73
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NTDB id 453 Spy49 1753c ACI62003.1	.MAKK....LKKNEEITKKFG	DERRKALDDALKNIEKD	FGKGAVMRLGER	.AEQKVQVM	SSGSLALD	I	ALGAGGY	PKGR	73
NTDB id 115 BSU 16940 NP 389576.2	MSDRQAALDMALK	QIEKQFGKGSIMKLGEK	.TDTRIST	VP	SGSLALD	T	ALGIGGY	PRGR	58
NTDB id 625 LCA RS02525 WP 011374196.1	MAKDERQAALDAALK	KIEKNFGKGSIMRMGEK	.VDTQVST	VSSGSLAL	DEALGV	GGYPRGR			60
NTDB id 1313 DR RS12030 WP 010888966.1	MSKDATKEISAPTD	AKERSKATETAM	SQIEKAFGKGSIMKLGAE	.SKLDVQV	VSTGSLSLD	I	ALGVGGI	PRGR	72
NTDB id 1245 Cj1673c YP 002345041.1	MDDNKRKSLDAALKS	LDKTFGKGTILRLGDK	.EVEQIDS	IGTGSVGLD	I	ALGIGGV	PKGR		59
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NTDB id 1074 ABD1 RS10195 WP 000344167.1	MDENK	SALQAALSQIEKQ	FGKNTVMRLGDN	.TVQAVEA	VSTGSLTLD	I	ALGIGGL	PKGR	59
consensus	***	***	*	***!	***!	***!	***!	***!	

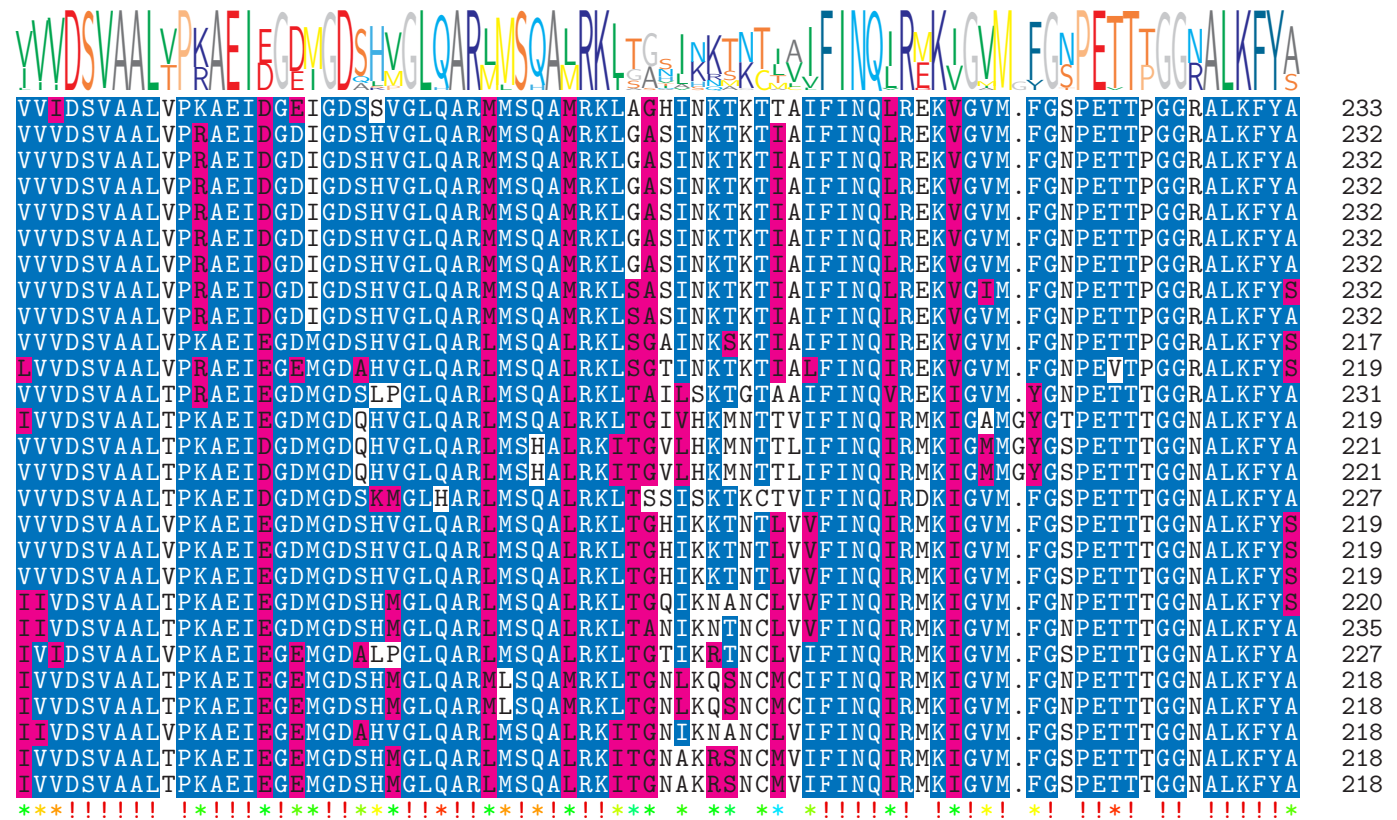
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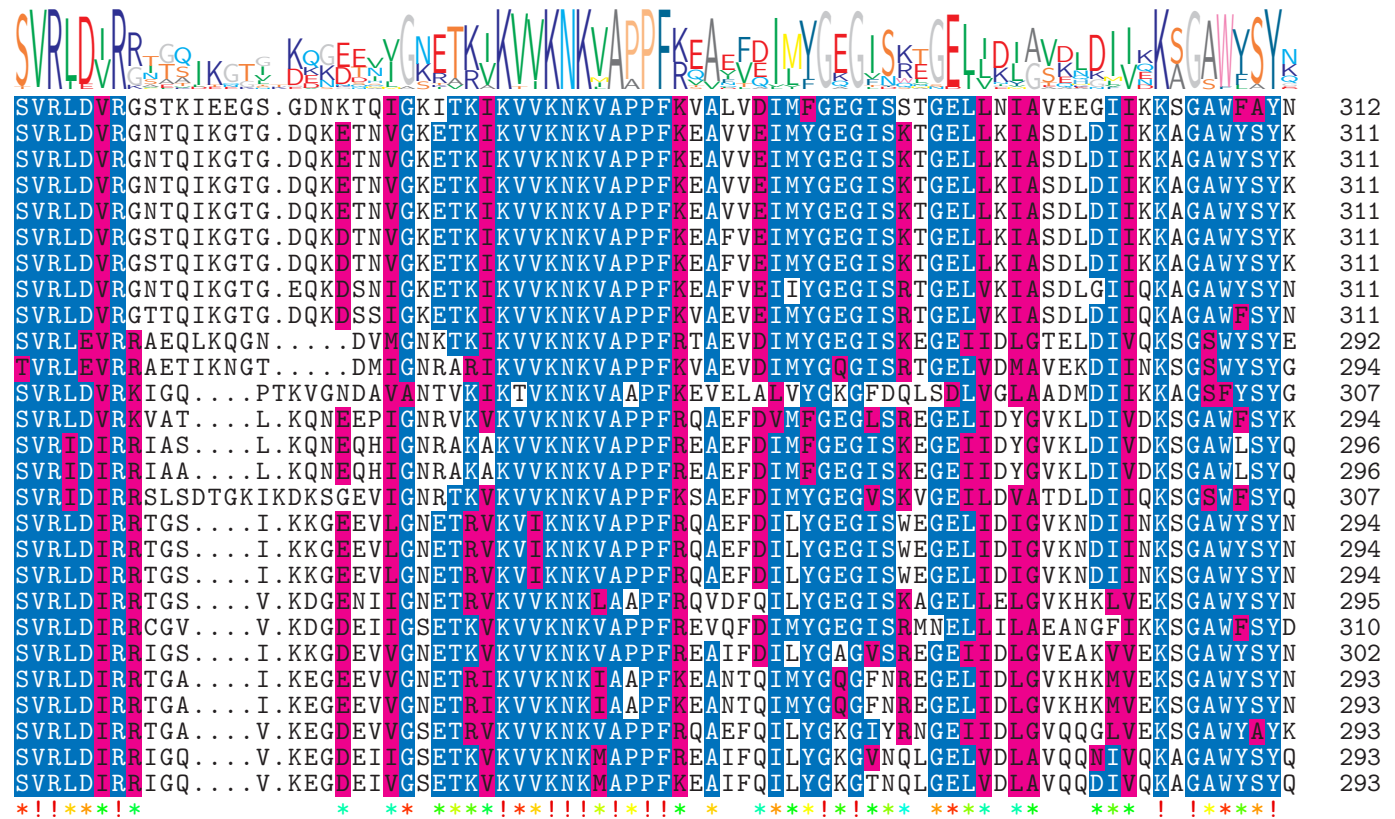
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consensus

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DEKIGQGSENAKKYLAHNPEVFAEIDHQRVVFGLIDGEEIAES....KKDE....VAQVDS..VNEEVPLDLGDELEI	380
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQGLIEEDNTEEEKQ.SSKEK.....ETDEK..ADKNLVLELDDTIEL	381
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAM.AVASE.....E.....TDDLALDLNGIEI	376
EERLGGGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQQA.EETQEEL.EFE.E.....	348
SERIGGGRENAKNYLADHEDVEDEVRLKVRVQGLSDVPEEDLPT.TEDE.QI.NILPDDST.....EE.....	355
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DKKLGGGRENKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DKKLGGGRENKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DTKLGGGRDTPVKELIKDNPELAEELEAKIREKLQAK.....	343
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logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved