

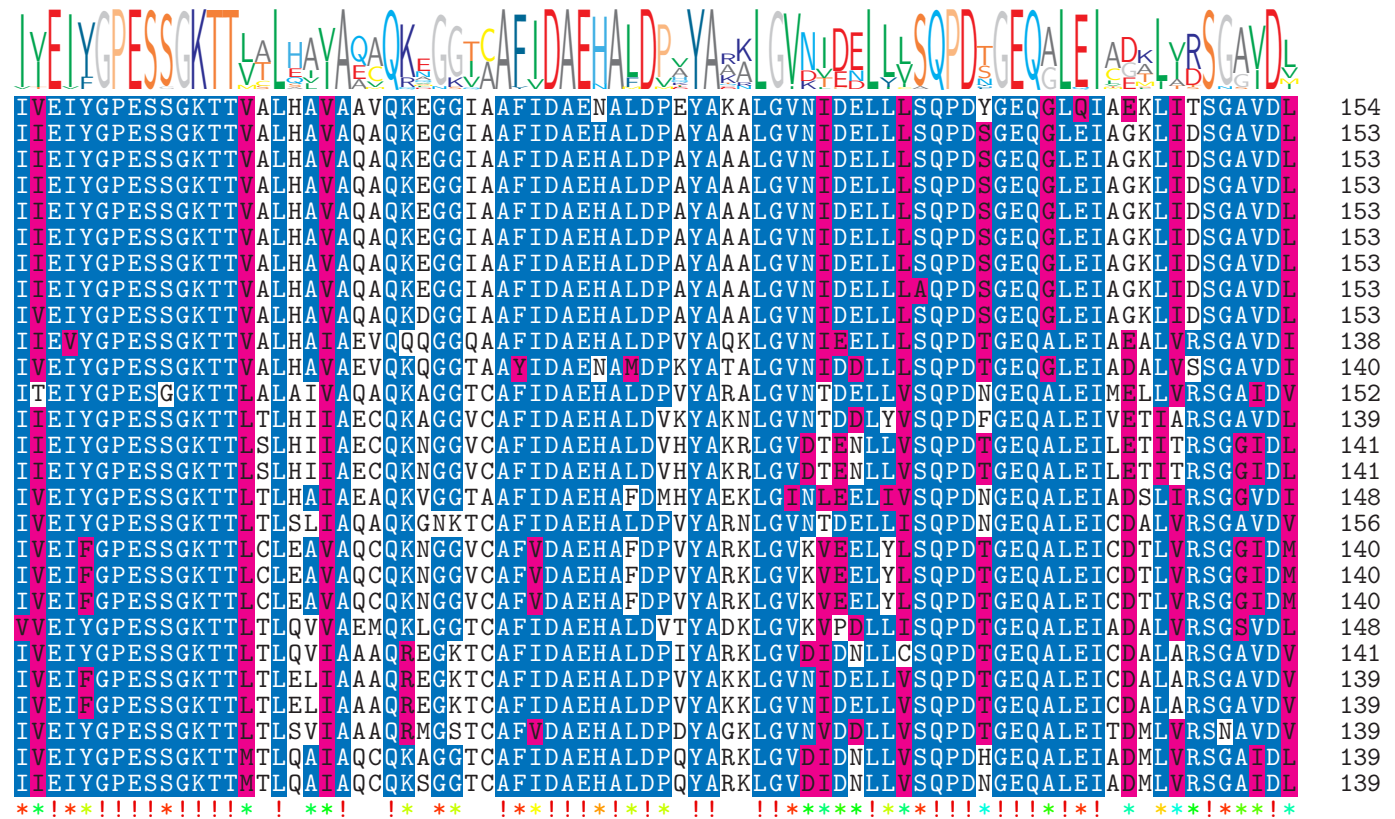
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NTDB id 453 Spy49 1753c ACI62003.1	.MAKKL....KKNEEITKKFG	DERR	KAL	DDAL	AL	KN	IEKD	FGKGA	VMRLGER	.AEQK	VQV	MSS	GSL	ALD	I	ALG	AGGY	PKGR	73
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NTDB id 625 LCA RS02525 WP 011374196.1	MAKDERQAALDAAL	KKIEKN	FGKGS	SIMRMGEK	VDTQ	VST	VSS	GSL	ALDE	ALGV	GGY	PRGR	60						
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NTDB id 1245 Cj1673c YP 002345041.1	MDDNKRKSLDAAL	KS	LDKT	FGKGT	ILRLGDK	EVEQ	IDS	IGT	GS	VGLDL	ALGI	GGV	PKGR	59					
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NTDB id 163575 AU099 RS11215 WP 000963143.1	MAIDENKQKALAAAL	GQIEK	QFGKGS	SIMRLGED	RSMD	VET	IST	GSL	SLD	I	ALG	AGGL	PMGR	61					
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consensus	***	***	*	***!	*!!	*****	*	***!!*!!*!!*!!*!!	!!	***!!									

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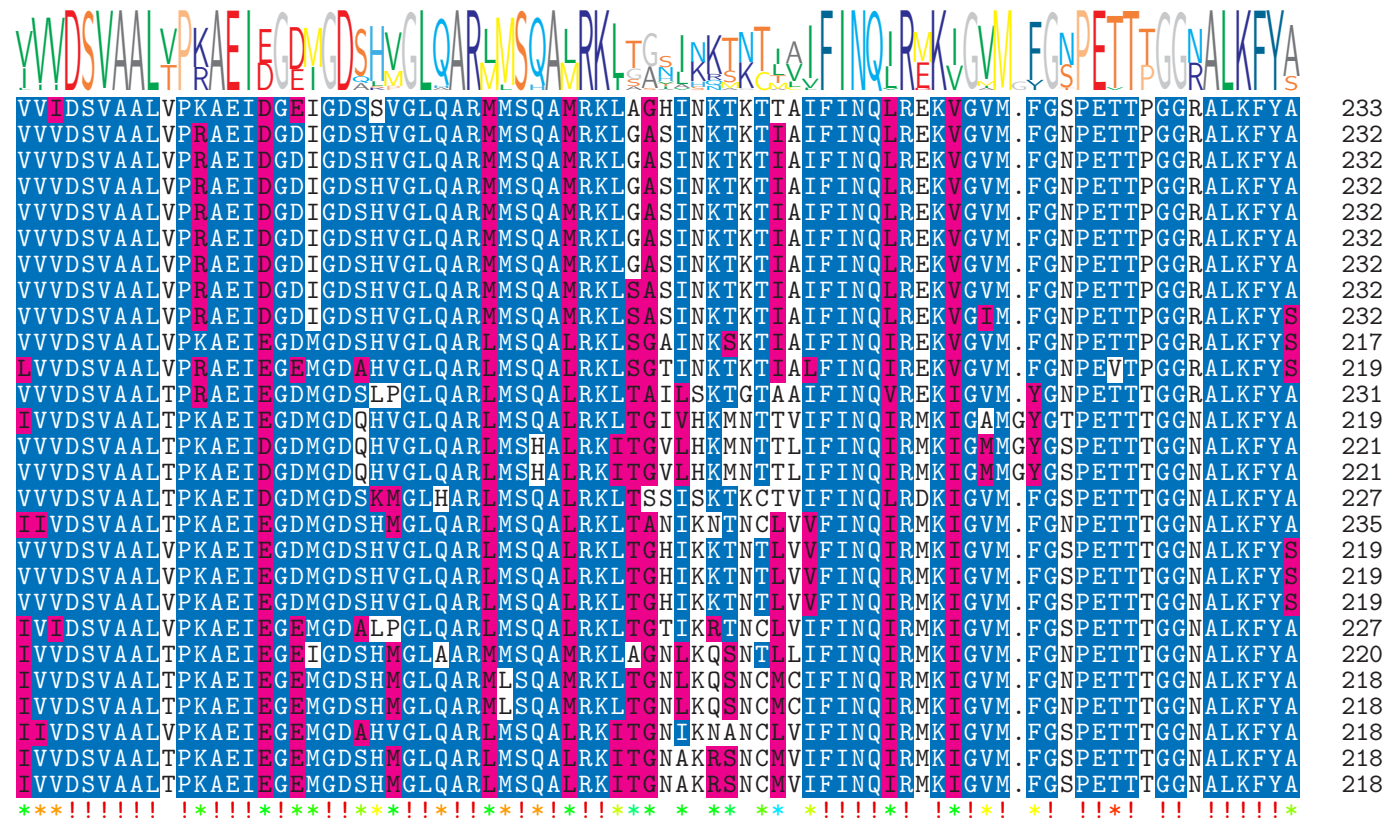
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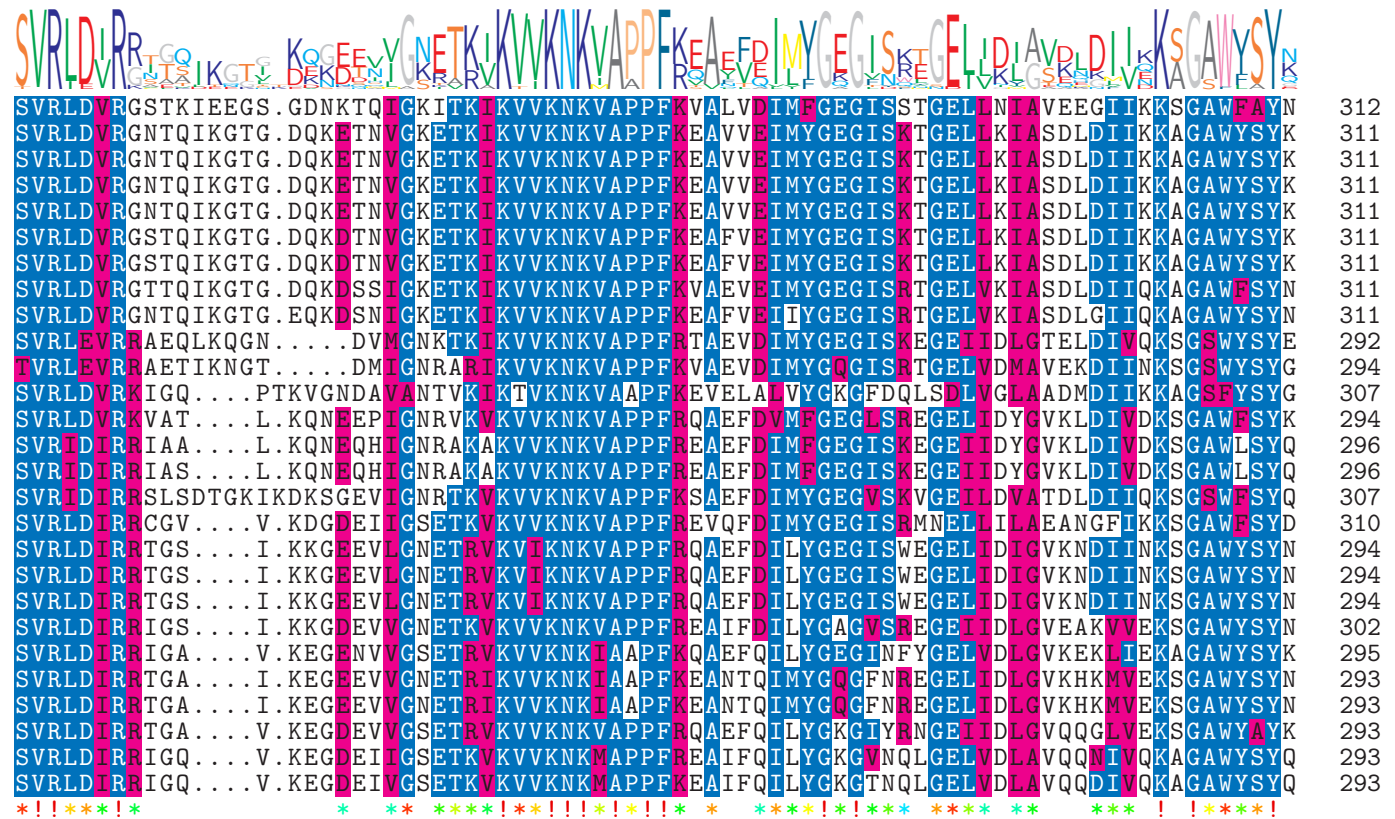
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consensus

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consensus

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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
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DEKIGQGSENAKKYLAHNPEVFAEIDHQRVVFGLIDGEEAAES...KKDE...VAQVDS..VNEEVTLDLGDLEIE	381
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EERLGGGRENAAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEETQEEL.EFE.E.....	348
SERIGGGRENAAKNYLADHEDVEDEVRLKVRRAAYGISDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGGQKEKTIATIAERPMEQEIRDRVMMAAIRAGNAGEAPALAPAPAAPEAA...EA.....	363
DKKLGGGRENKAFLENPEIADEITKATINSMGTIEGM.....ISGSEDDEG.....EE.....	343
DKKLGGGRENAAKALLKEDKALADEITLKIKESIGSNEE....IMPLPDEPL.....EEME.....	347
DKKLGGGRENAAKALLKEDKALADEITLKIKESIGSNEE....IMPLPDEPL.....EEME.....	347
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logo

		IEE	
NTDB id 600 KW2 RS01765 WP 011675413.1	...	387	
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consensus			

- X non conserved
- X similar
- X ≥ 50% conserved