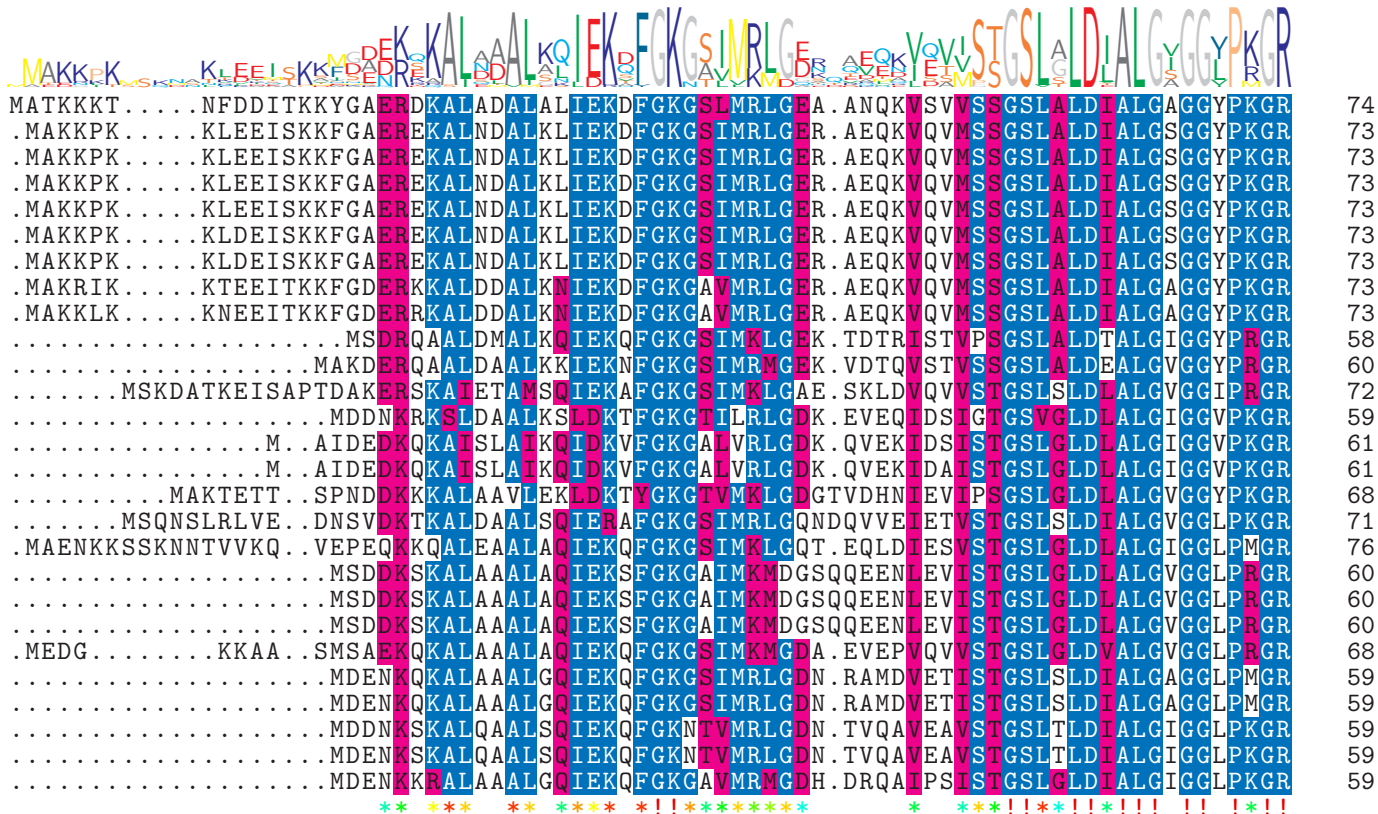


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consensus

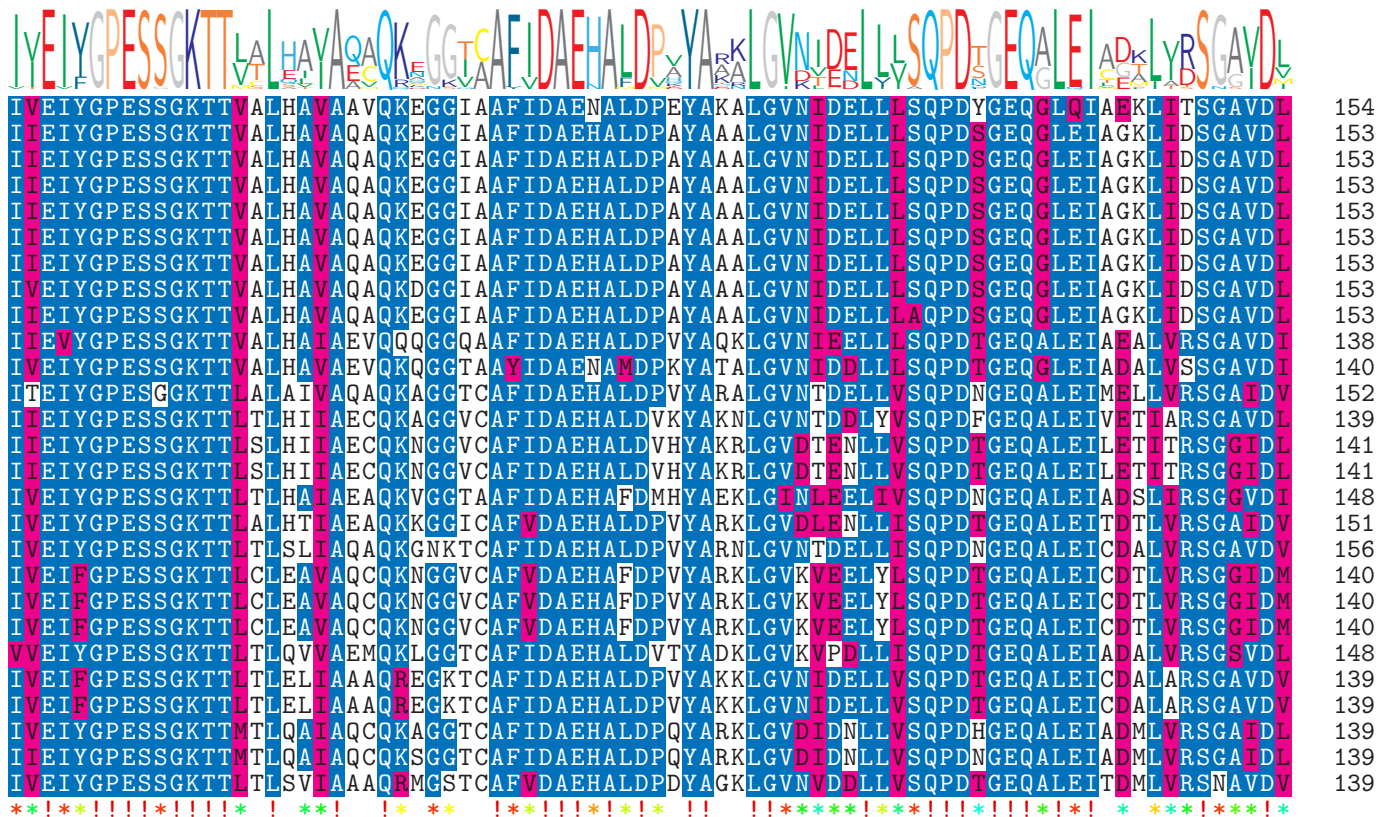
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consensus

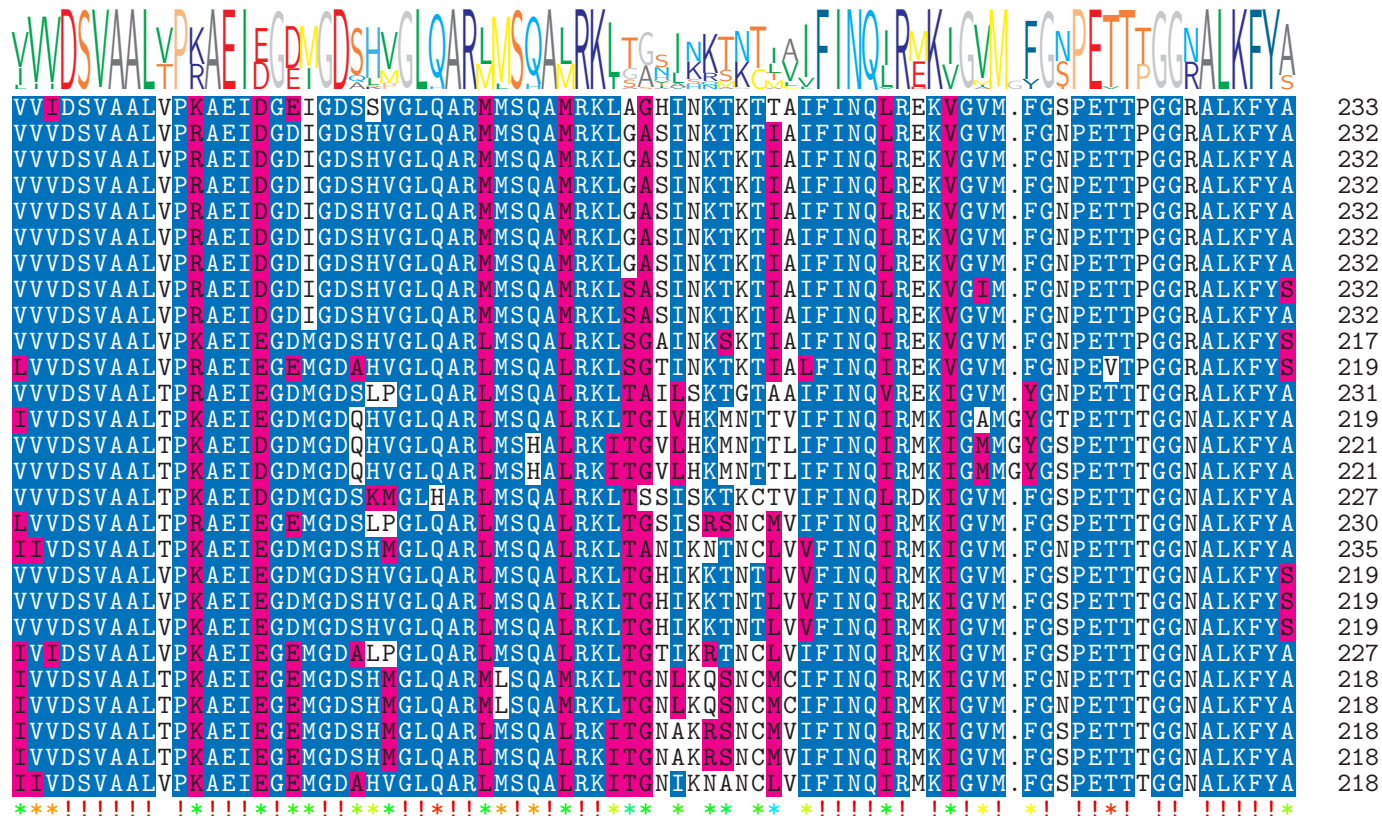
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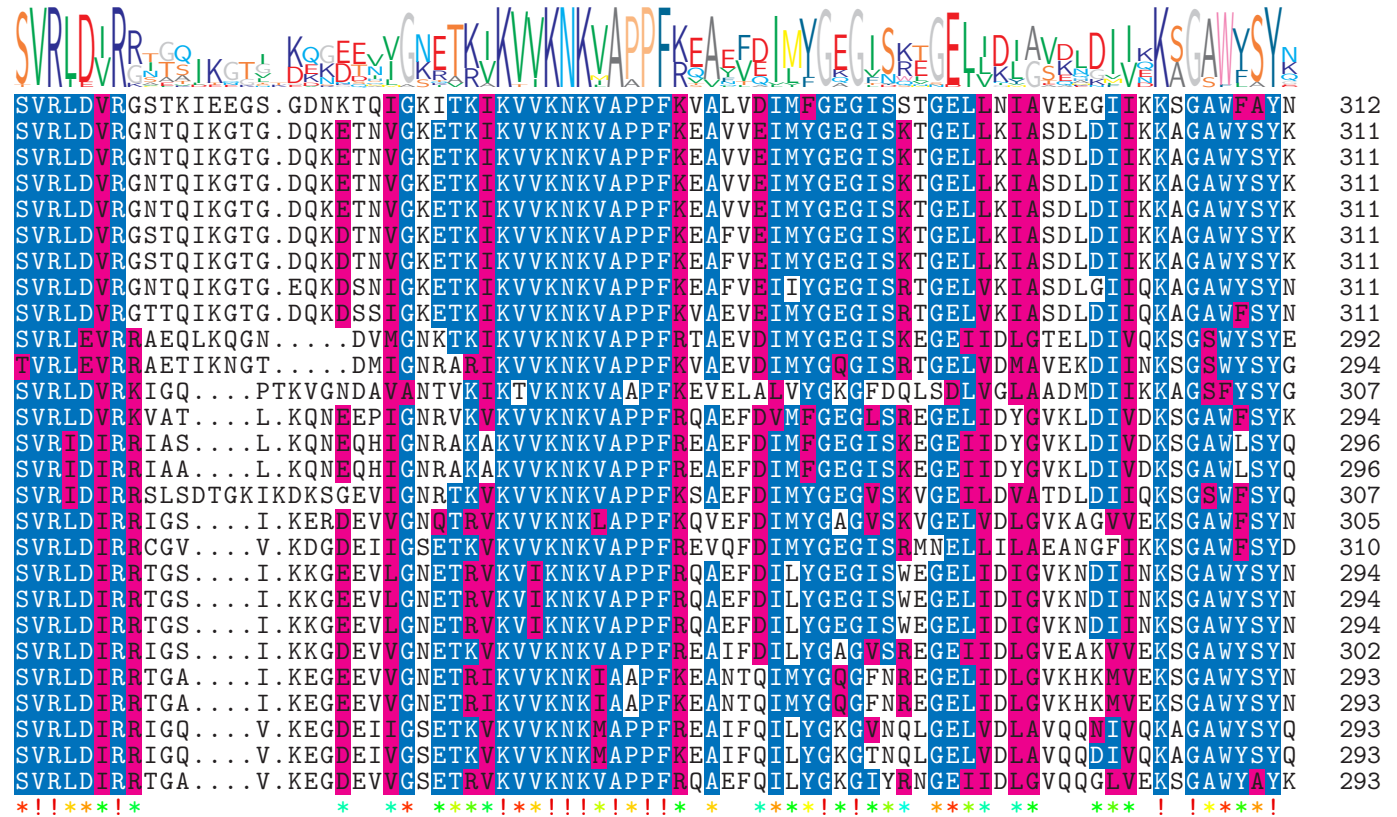
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consensus

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consensus




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Sequence	Score
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DEKIGGGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKK.DE...PKKEEA..VNEEVPLDLGDELEI	384
DEKIGGGSSENAKKYLAHNPEVFAEIDHQVRVQFGLIDGEEAAE...SKK.DE...VAQVDS..VNEEVPLDLGDELEI	380
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GEKIGGGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESSEESAMAVASE.....E.....TDDLALDLNGIEI	376
EERLGGGRENAKQFLKENKDIMLMIQEQIREHYGLDNGGVVQQAEETQE.EL.EFE.E.....	348
SERIGGGSSENAKNYLADHEDVEDEVRLKVRVQFGLSDVPEEDLPTTEDE..QI.NILPDDST.....EE.....	355
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logo

		ELEE	
NTDB id 600 KW2 RS01765 WP 011675413.1			387
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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved