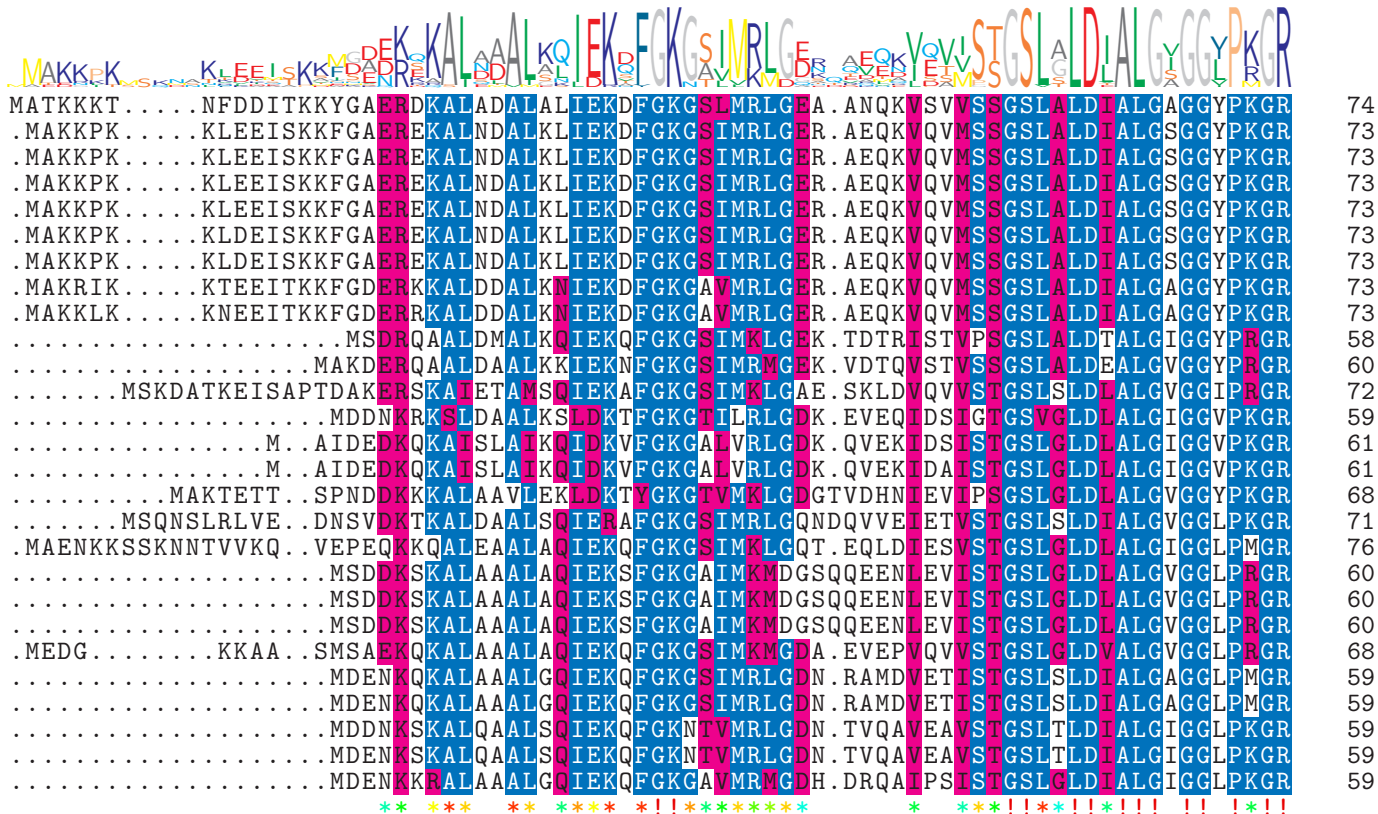


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consensus

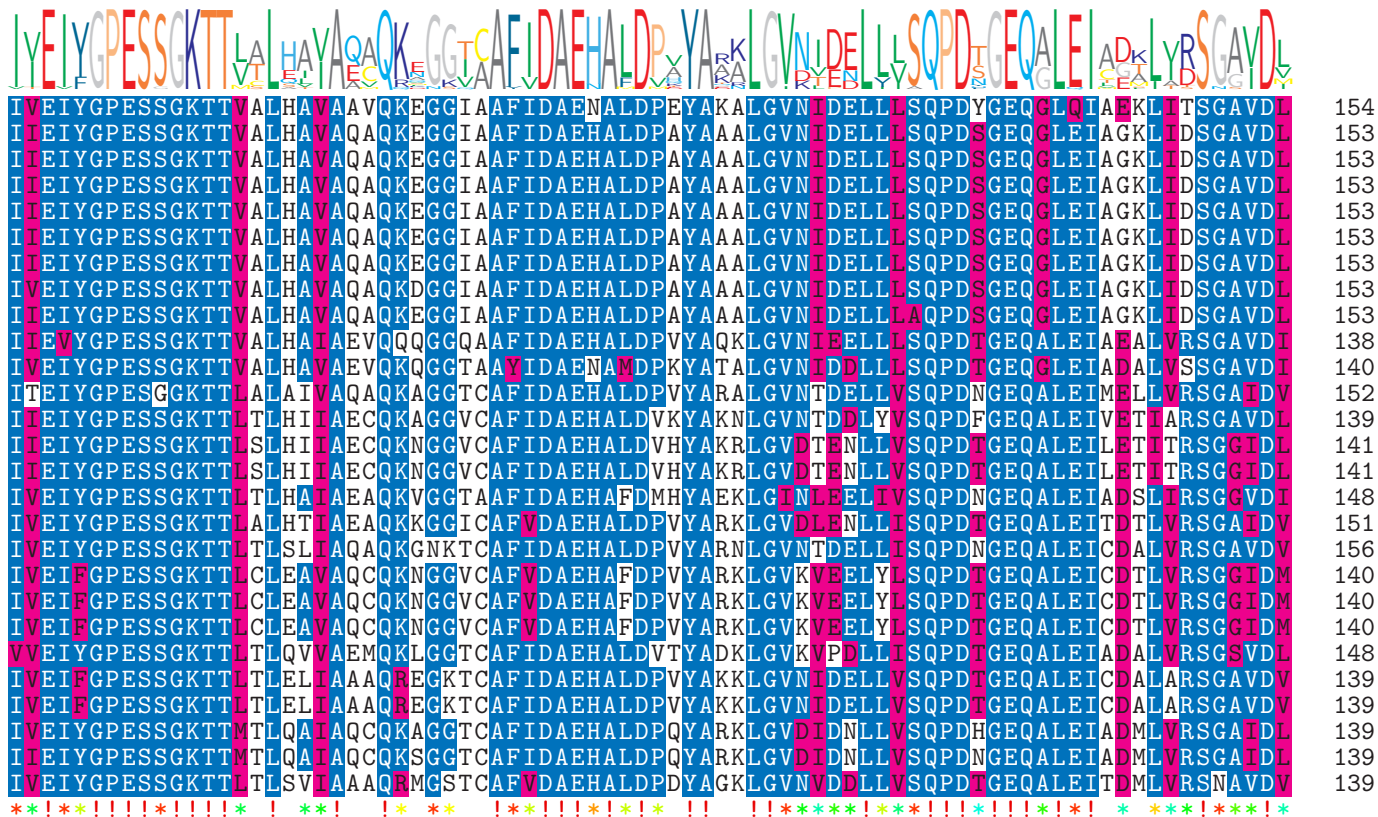
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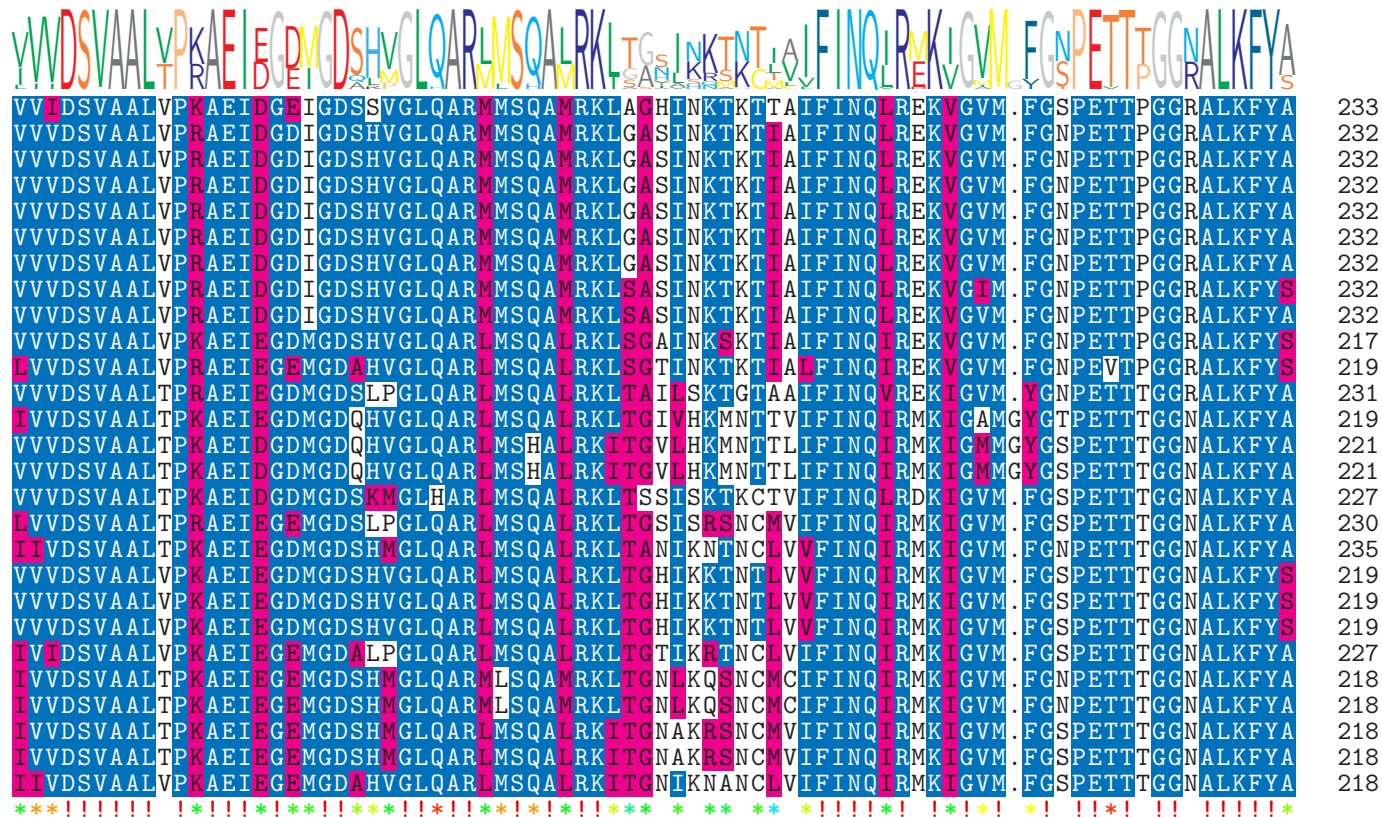
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consensus

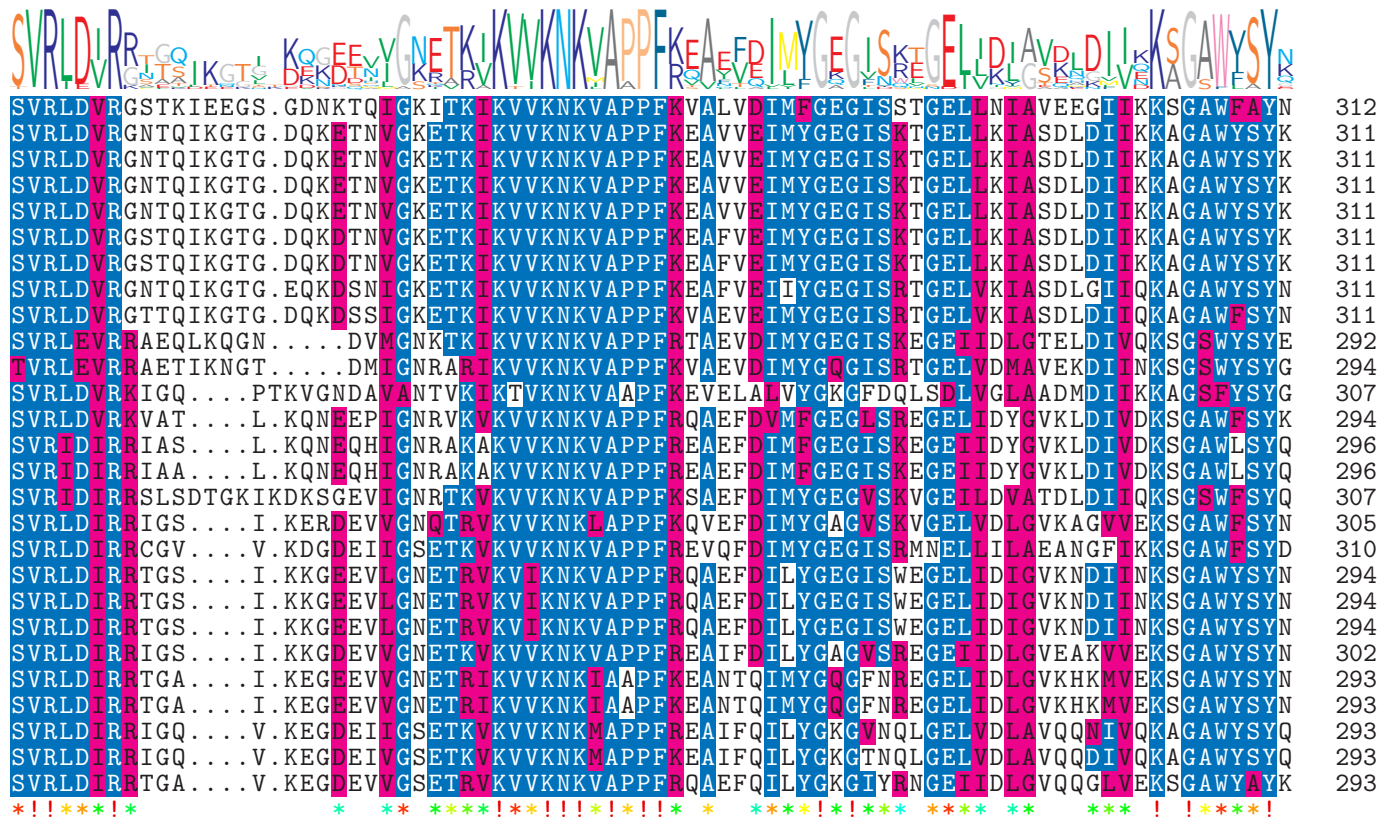
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consensus

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consensus

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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGLIDGEEVSEQDTENKK.DE....PKKEEA..VNEEVPLDLGDELEI	384
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGLIDGEEVSEQDTENKK.DE....PKKEEA..VNEEVPLDLGDELEI	384
DEKIGQGSENAKKYLAADNPEVFAEIDHQVRVQFGLIDGEEAAE....SKK.DE....VAQVDS..VNEEVPLDLGDELEI	380
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GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESSEESAMAVASE.....E.....TDDLALDLNNGIEI	376
EERLGGGRENAAKQFLKENKDIMLMIQEQIREHYGLDNNGVVQQQAETQE.EL.EFE.E.....	348
SERIGGQRENAKNYLADHEDVEDEVRLKVRAAAYGTSDVPEEDLPTTEDE..QI.NILPDDST.....EE.....	355
DERIGGQKEKTIAYIAERPEMEQETDRDRVMAAIRAGNAGEAPALAPAPAAPAAEA.....	363
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GNKIGGQKKNVIRYFEENNQIAEIERNIREQLLTTGTNGAVQ...I.EDETEEPDLL.....LES	349
GSKIGGQKANAAKYLEENPEIQQEIEQQIRAKLLVTSANTKATP..VAEDLADADI.....	347

logo

		ELEE	
NTDB id 600 KW2 RS01765 WP 011675413.1			387
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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved