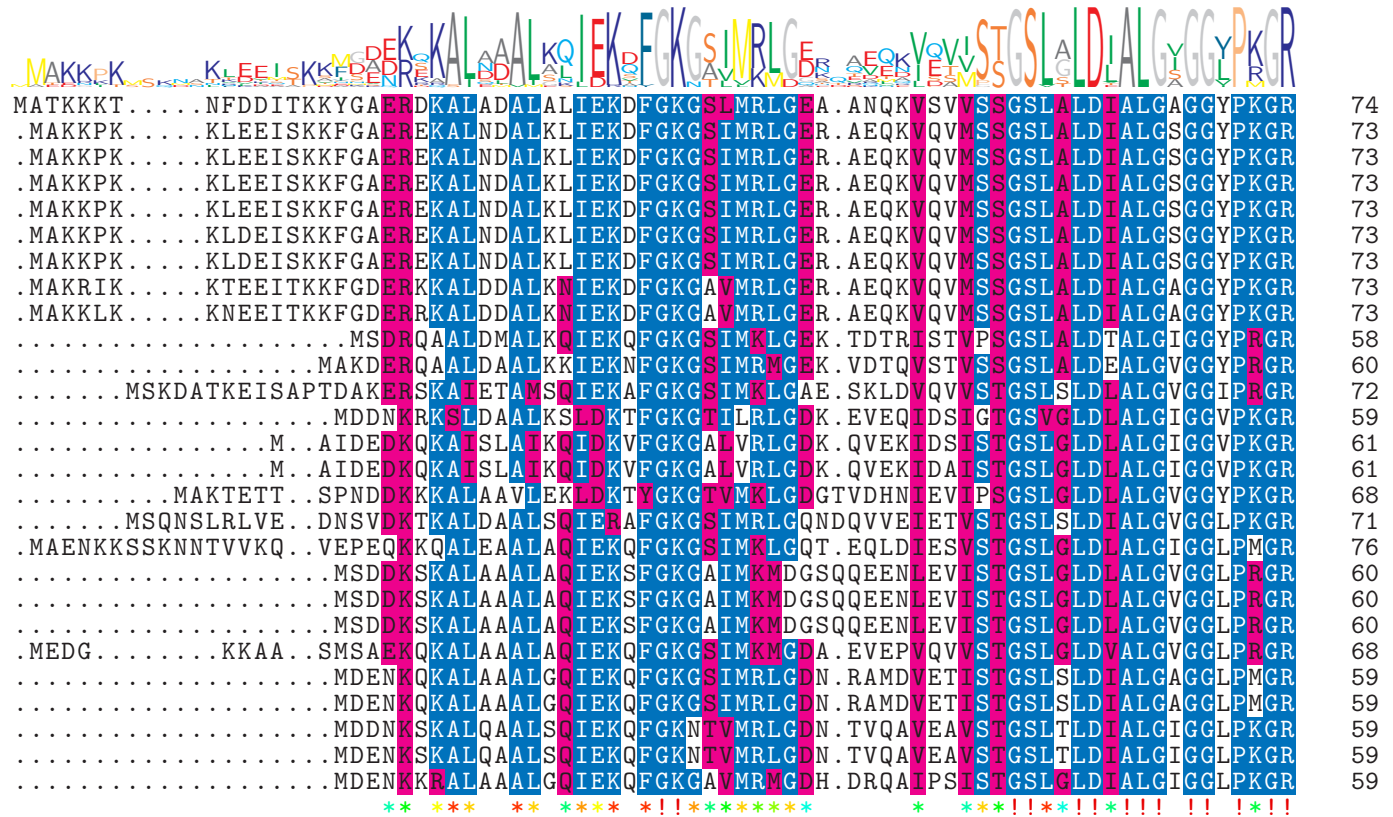


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consensus

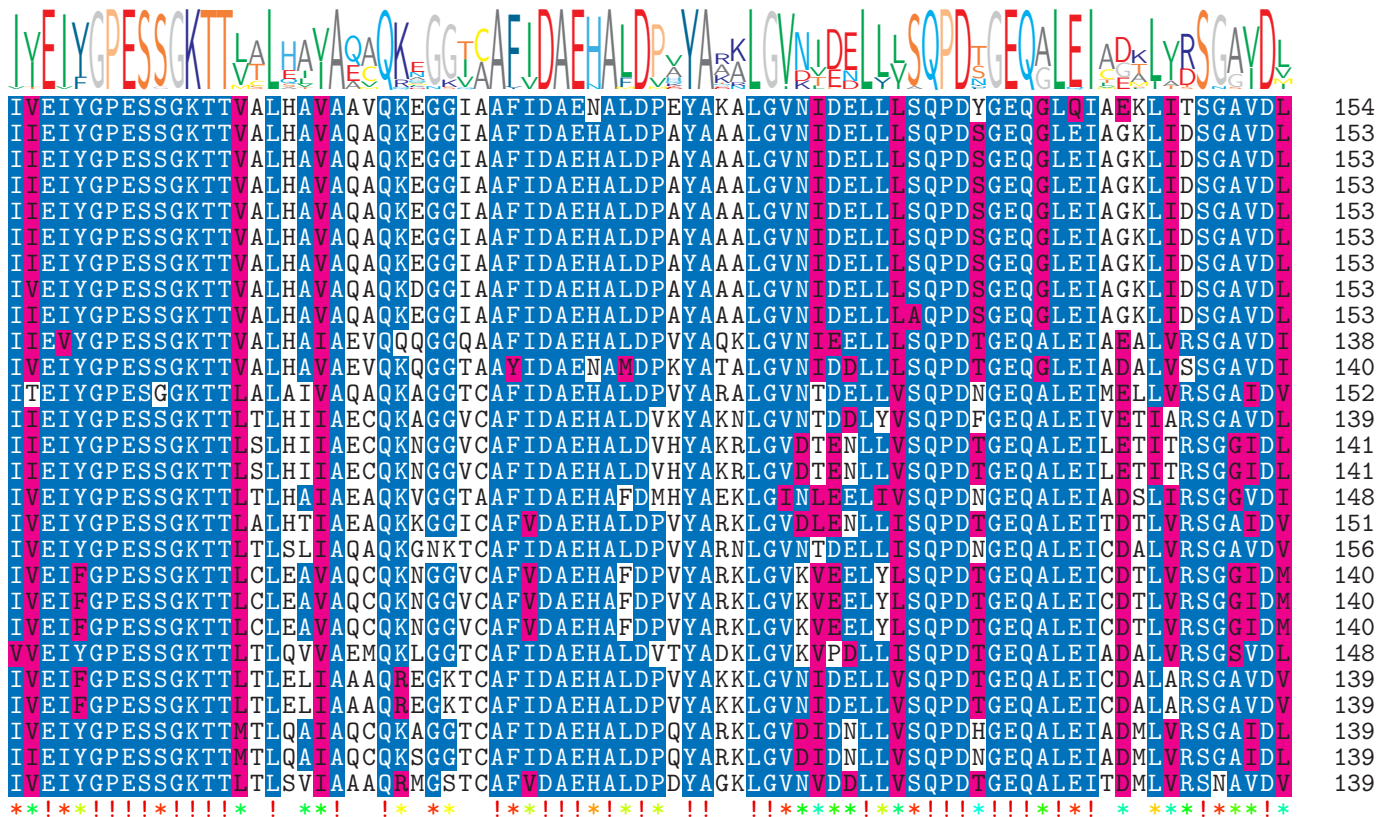
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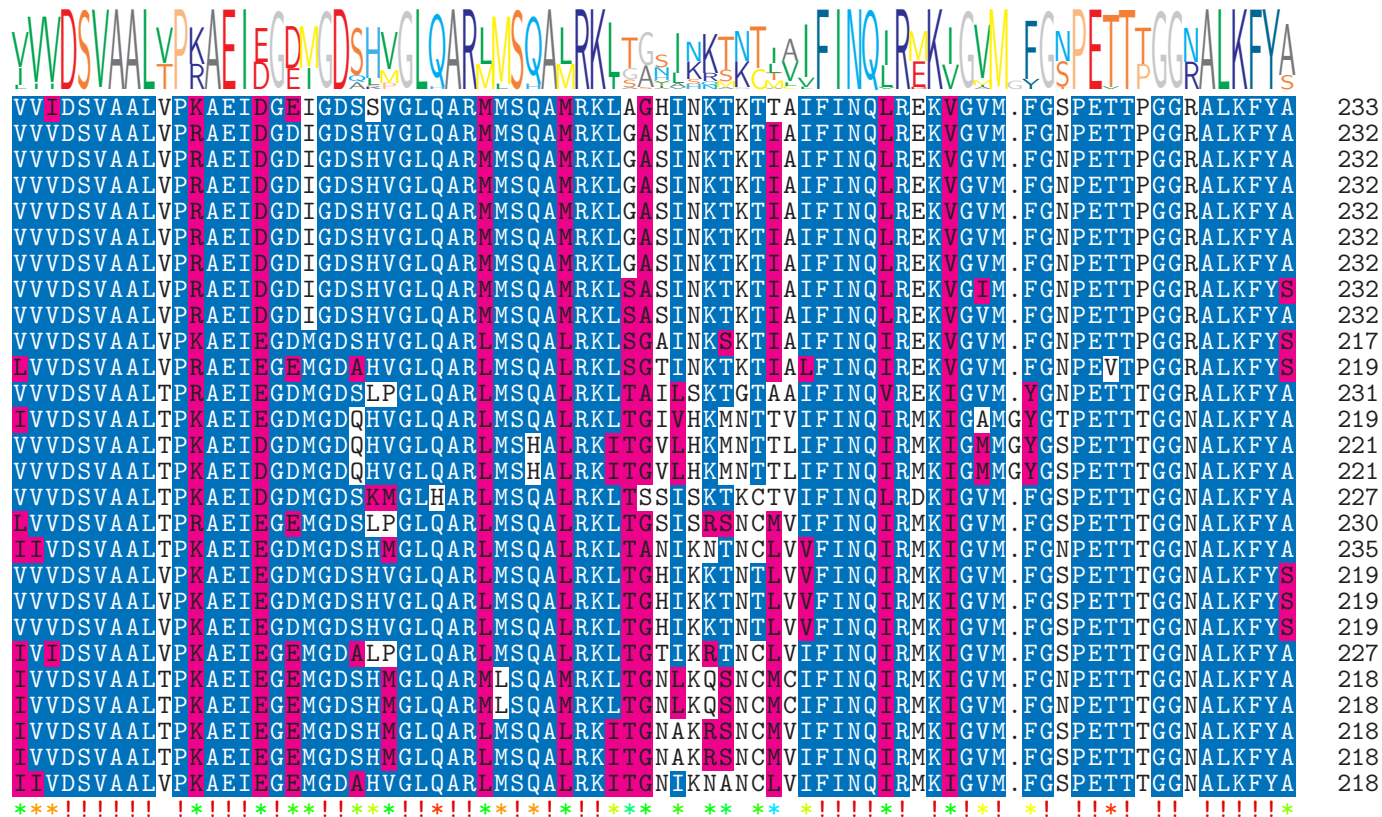
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consensus

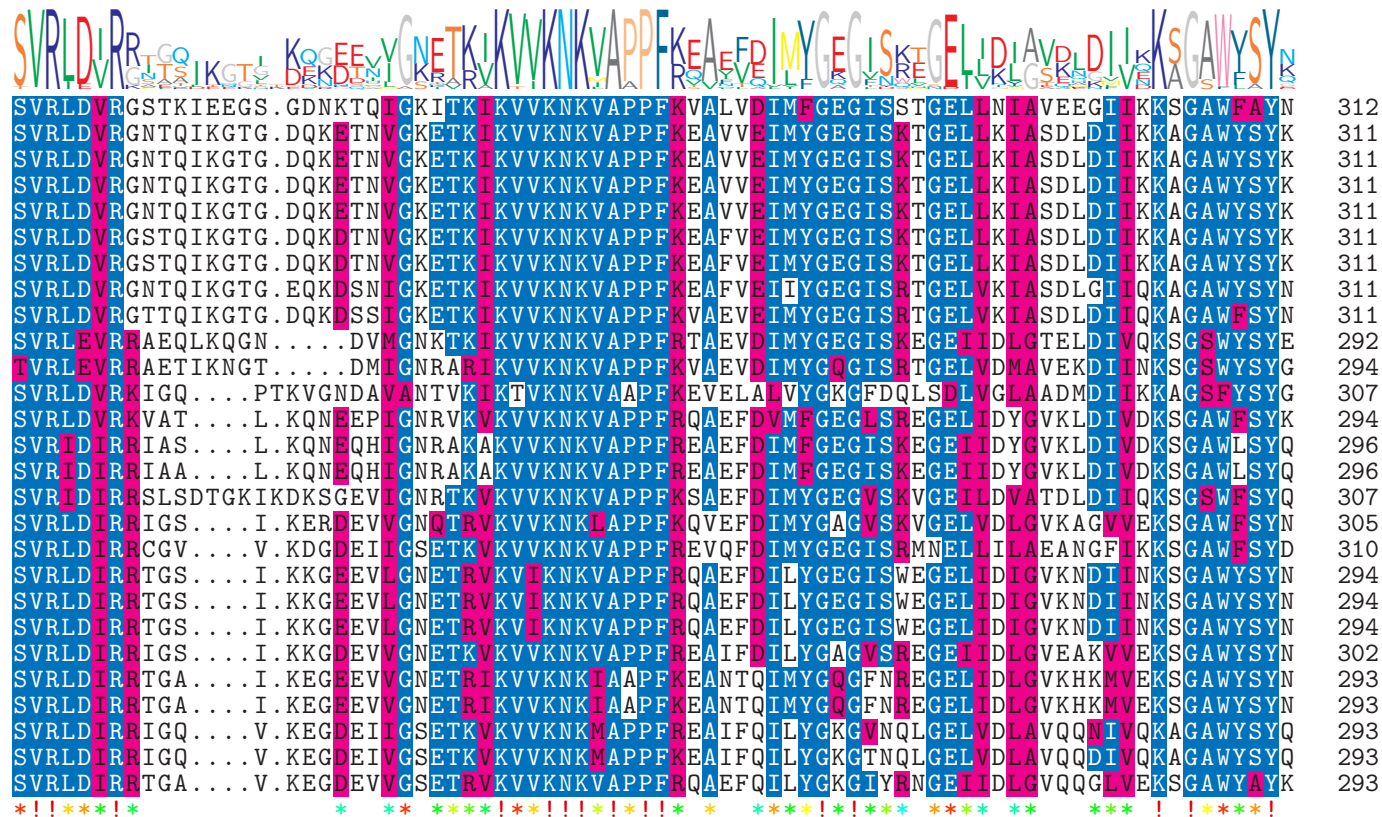
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consensus

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consensus

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Sequence	Score
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DEKIGGQSENAAKKYLAEHPEIFDEIDKQVRSKFGLIDGEEVSEQDTENKK.DE...PKKEEA..VNEEVPLDLGDELEI	384
DEKIGGQSENAAKKYLAEHPEIFDEIDKQVRSKFGLIDGEEVSEQDTENKK.DE...PKKEEA..VNEEVPLDLGDELEI	384
DEKIGGQSENAAKKYLAHNPVFAEIDHQVRVQFGLIDGEEAAE...SKK.DE...VAQVDS..VNEEVPLDLGDELEI	380
DEKIGGQSENAAKKYLAHNPVFAEIDHQVRVQFGLIDGEEAAE...SKK.DE...AAQVDS..VNEEVPLDLGDELEI	380
GEKIGGQSENAAKRYLADHPQLFDEIDRKVRVKFGLLEESSEESAMAVASE.....E.....TDDLALDLNGIEI	376
EERLGGGRENAAKQFLKENKDIMLMIQEQIREHYGLDNNGVVQQQAETQE.EL.EFE.E.....	348
SERIGGQRENAAKRYLADHEDVEDEVRLKVRAAAYGTSVPEEDLPTTEDE..QI.NILPDDST.....EE.....	355
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GDKIGGQKANACKYMLKENPEIAKTLDDKKIREMLLNPNMQLIAE..TSSAADDVEFG.....AVPEEF	354
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GNKIGGQKNNVIRYFEENNRIABEIERNIREQLLTGTNGAVQ...I.EDETEEPDLL.....LES.....	349
GSKIGGQKANAAYLEENPEIQQEIQIRAKLLVTSANTKATP..VAEDLADADI.....	347

logo

		ELEE	
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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved