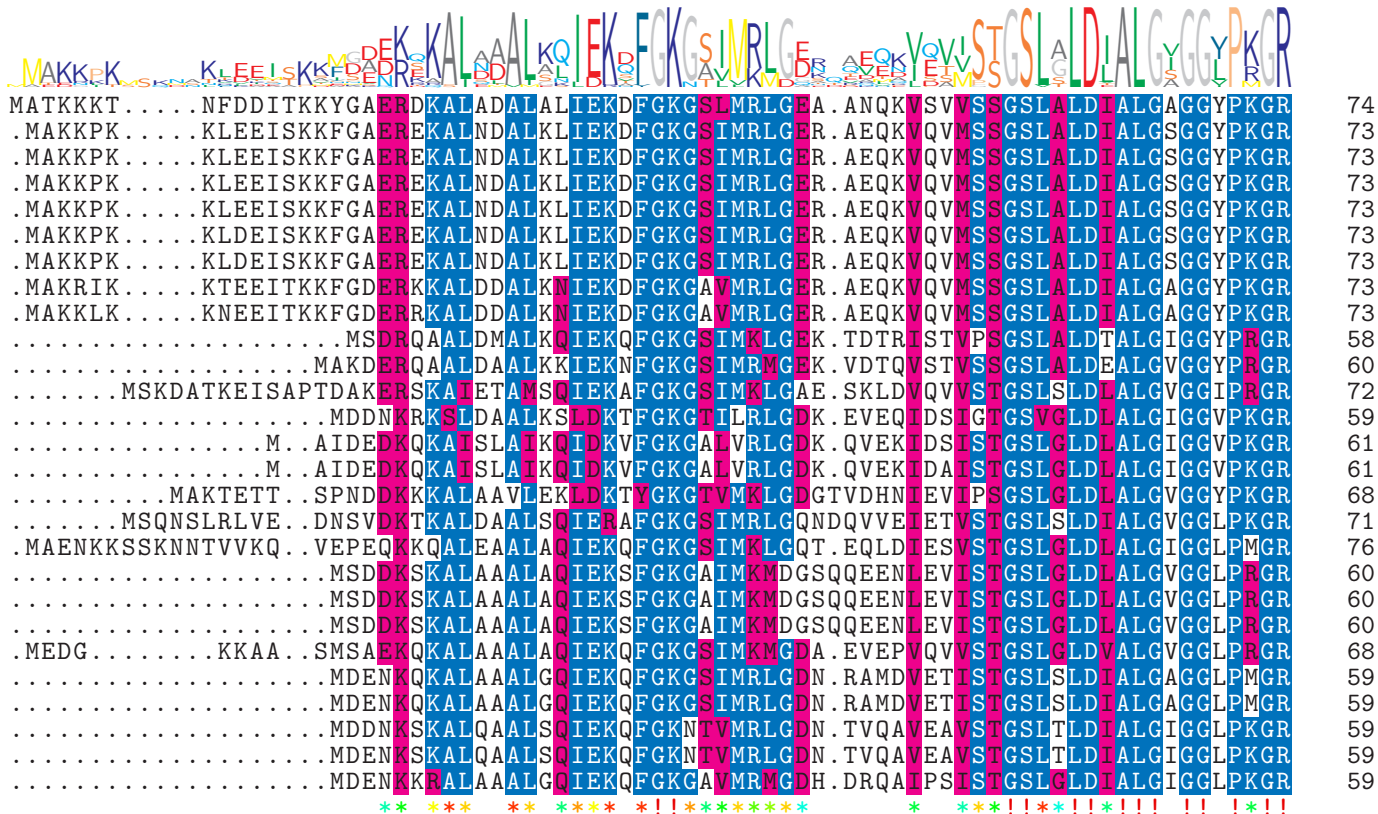


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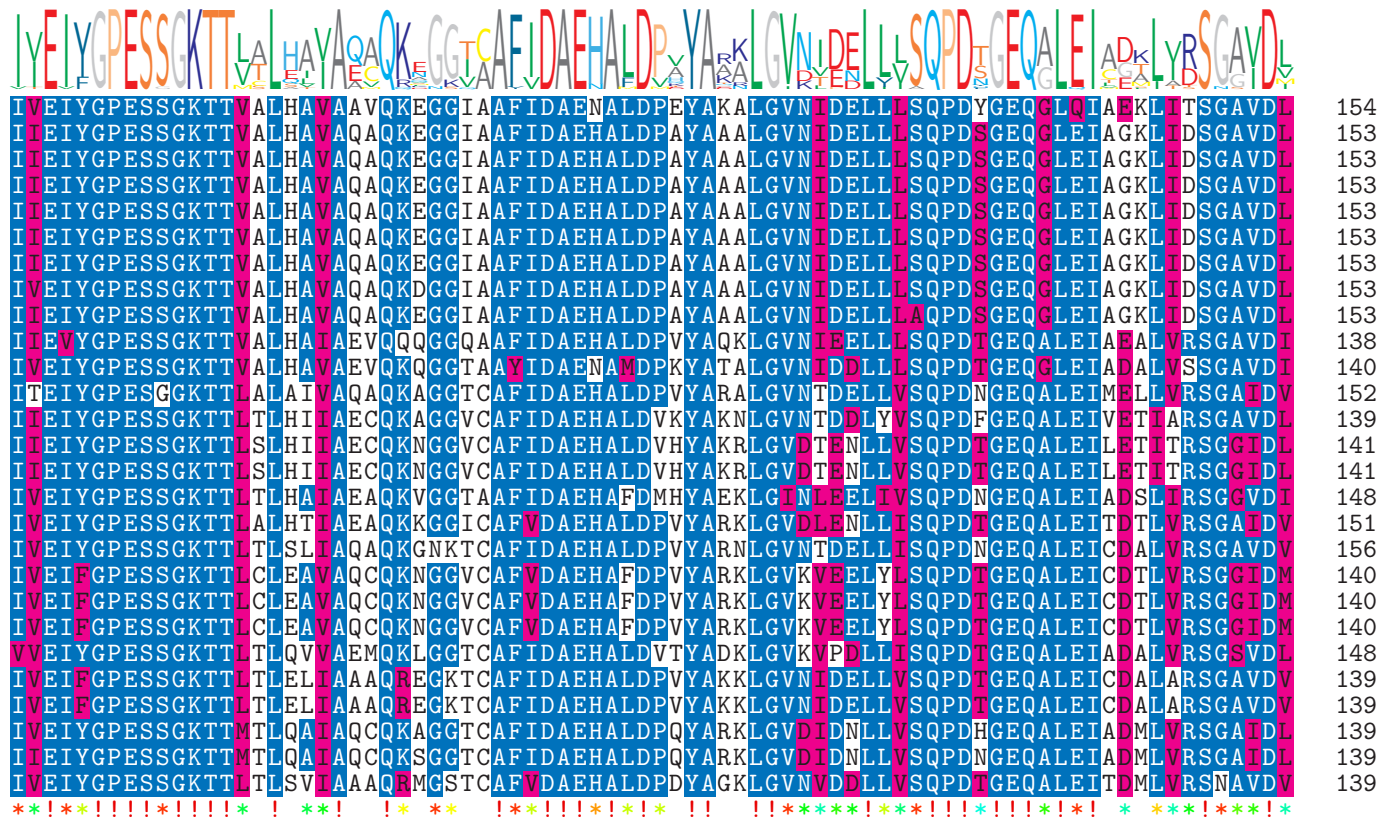
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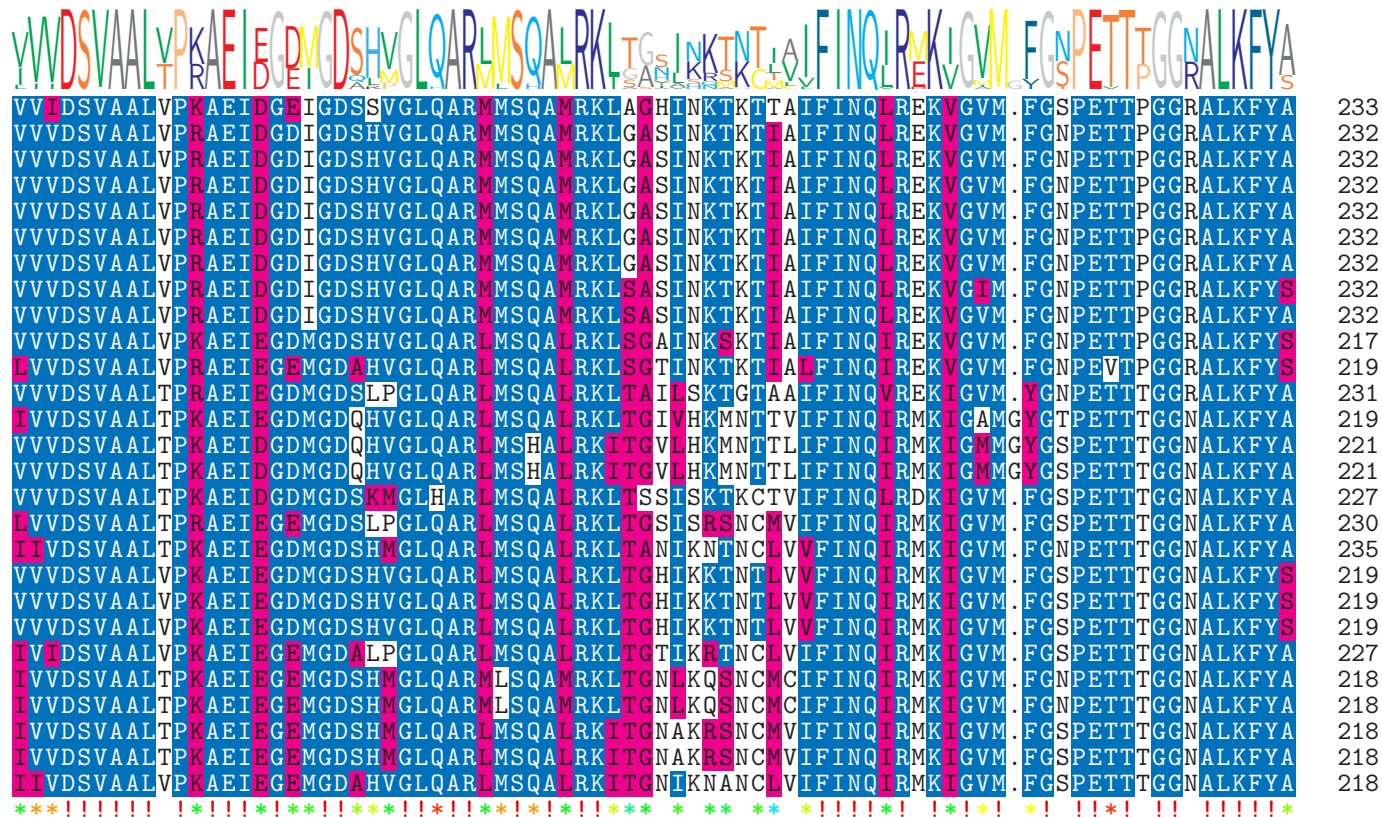
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consensus

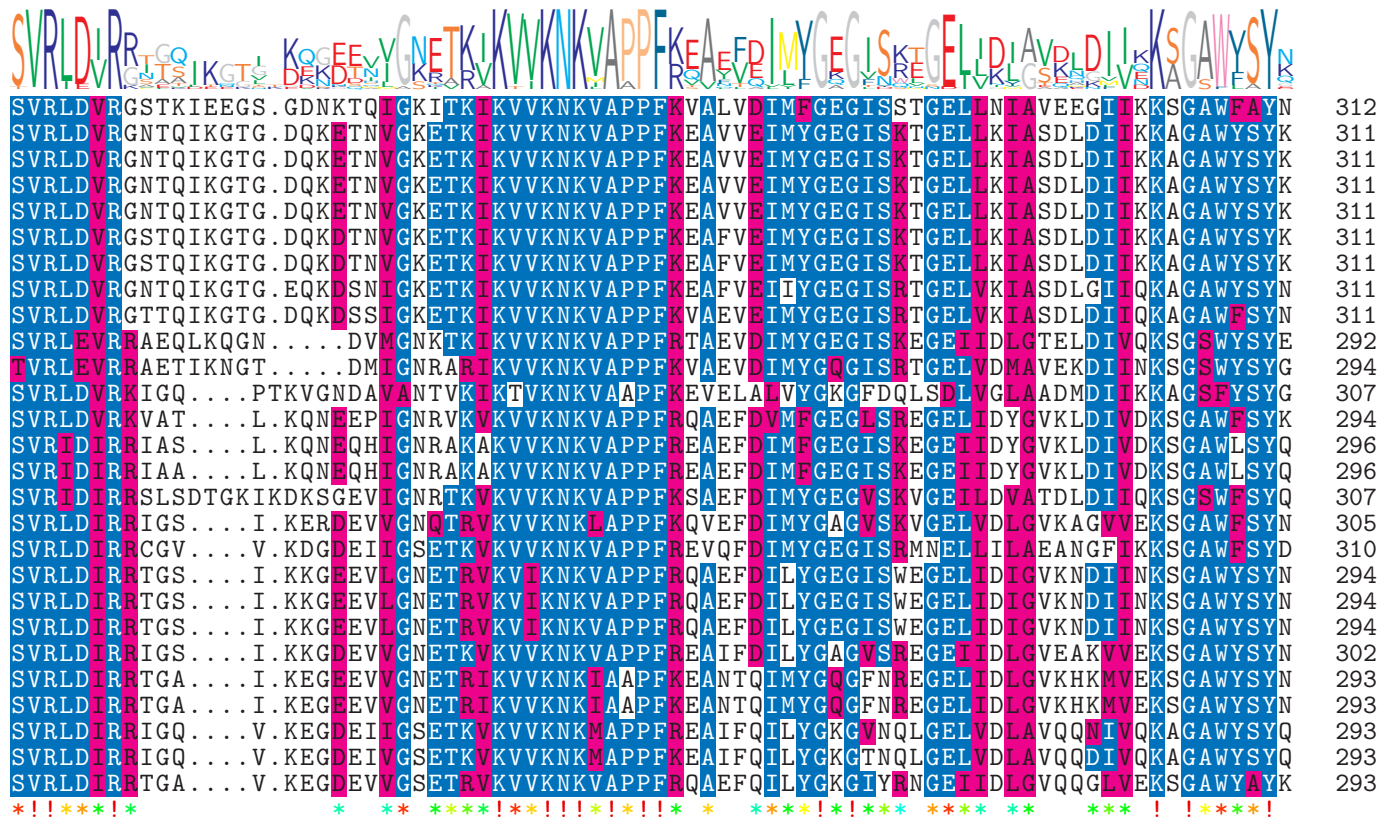
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consensus

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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
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DEKIGQGSENAKKYLADNPEVFAEIDHQVRVQFGLIDGEEAAE....SKK.DE....VAQVDS..VNEEVPLDLGDELEI	380
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GEKIGQGSENAKKFLADNPEIFDDIDHKVRSVQGLIEDNTEEEKSSSEK.....ETDEK..ADKNLVLELDDTTIEL	381
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESSEESAMAVASE.....E.....TDDLALDLNGIEI	376
EERLGGGRENAAKQFLKENKDIMLMIQEQIREHYGLDNNGVVQQAAETQE.EL.EFE.E.....	348
SERIGGQRENAKNYLADHEDVEDEVRLKVRAAAYGTSDVPEEDLPTTEDE..QI.NILPDDST.....EE.....	355
DERIGGQKEKTIAYIAERPEMEQETDRDRVMAAIRAGNAGEAPALAPAPAAPAAEA.....	363
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GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEGTQ..DETDGER.....PEE.....	348
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GDKIGGQKANACKYLLKENPEIAKTLDKKIREMLLNPNMQLIAE..TSSAADVEFG.....AVPEEF.....	354
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GNKIGGQKNNVIRYFEENNQIAEIERNIREQLLTTGTNGAVQ...I.EDETEEPDLL.....LES.....	349
GSKIGGQKANAAKYLEENPEIQQEIEQQIRAKLLVTSANTKATP..VAEDLADADI.....	347

logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved