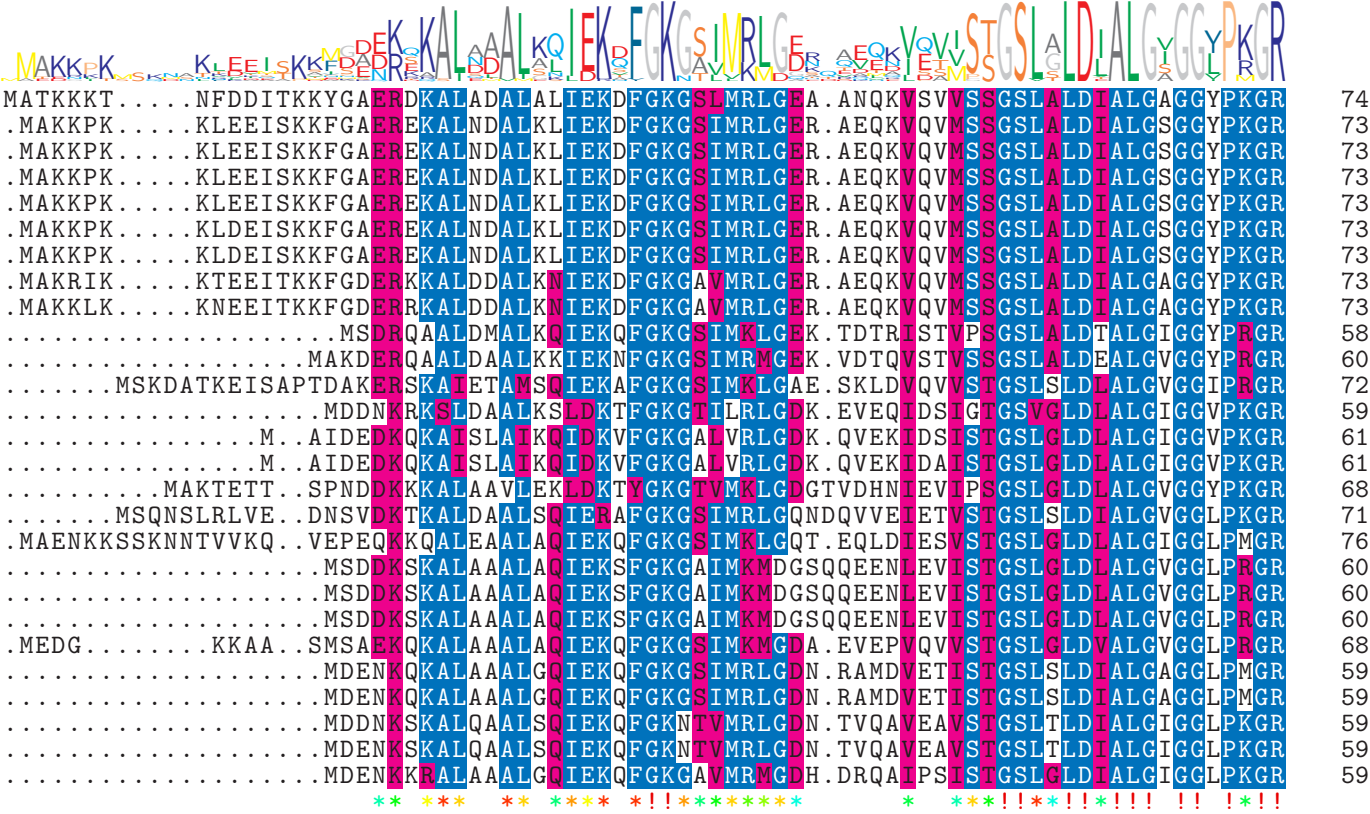


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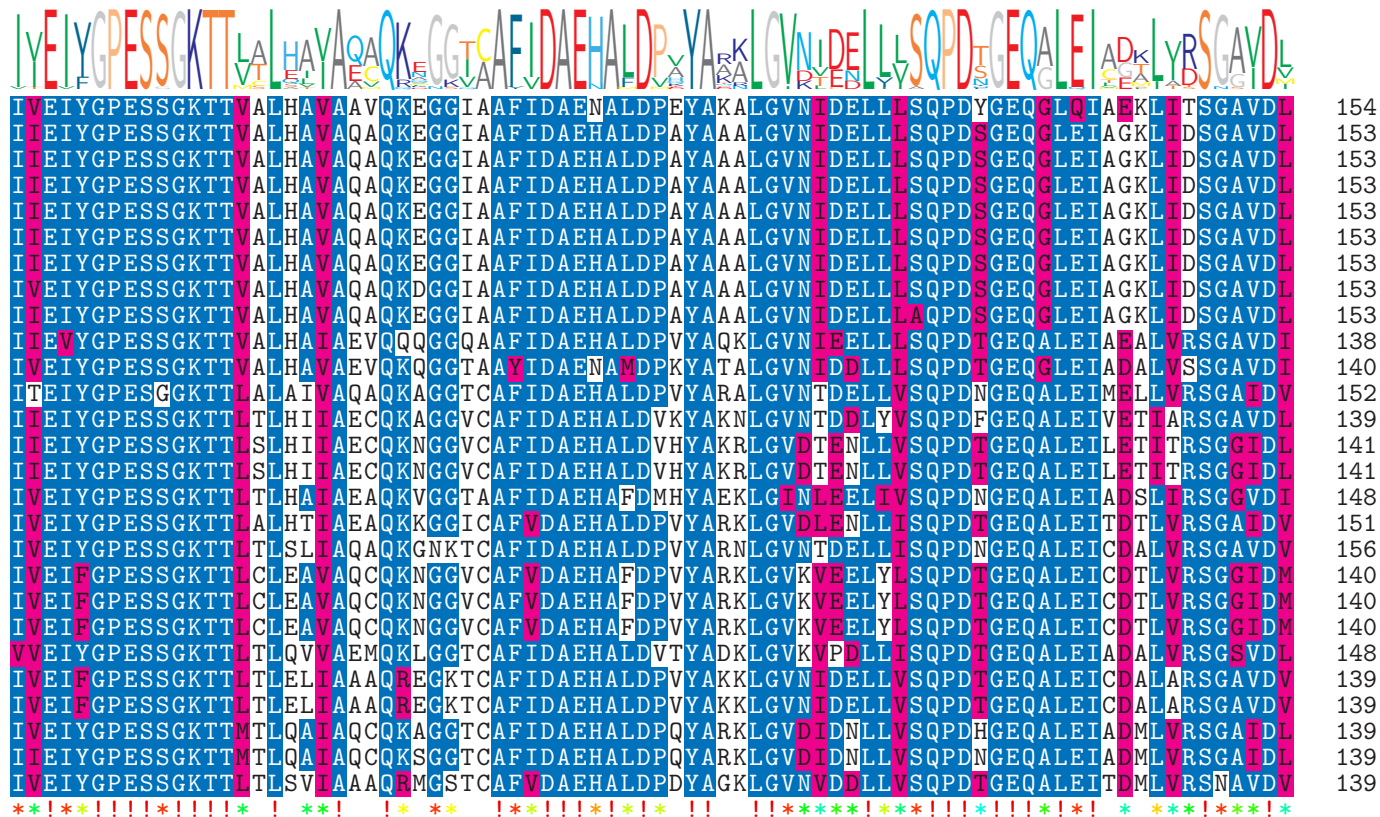
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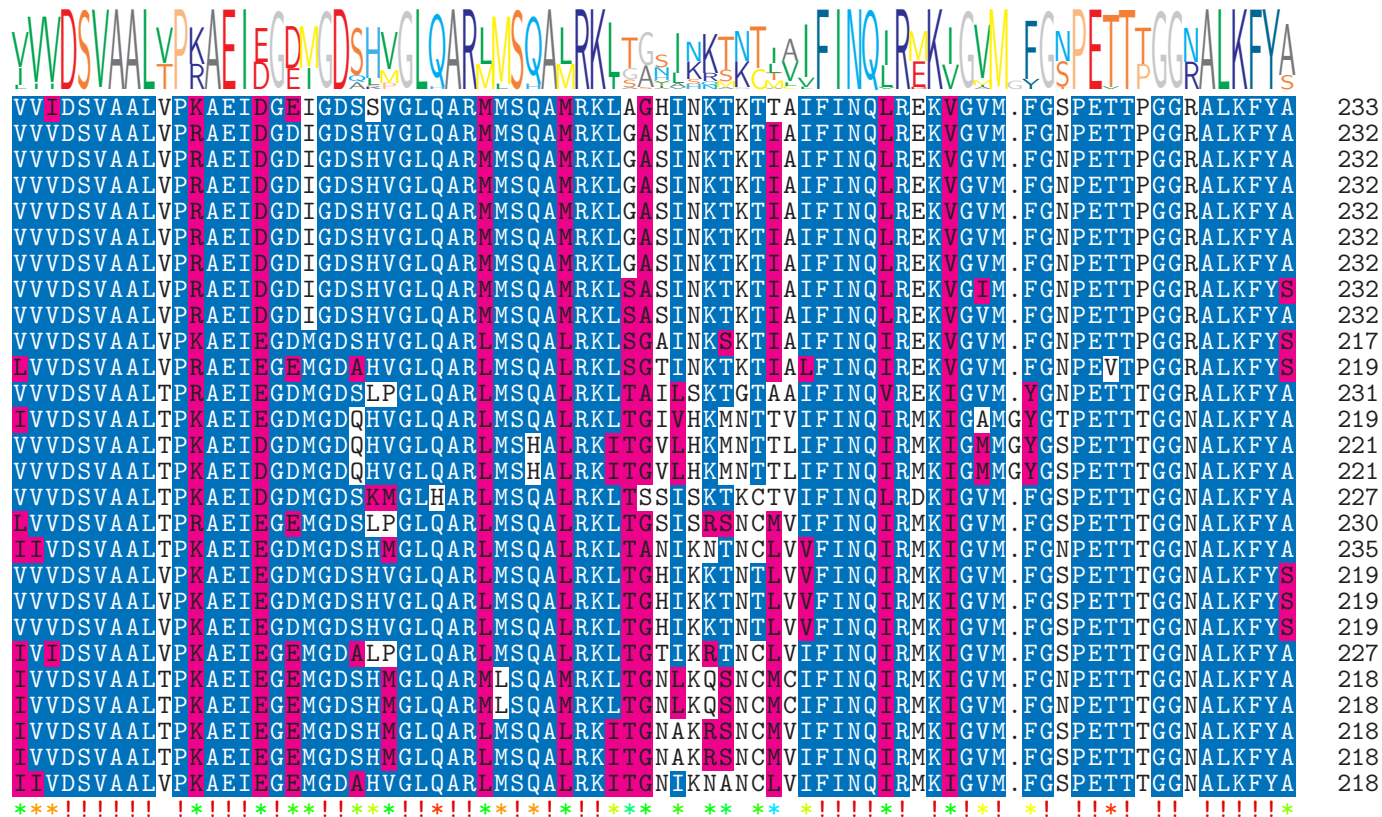
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consensus

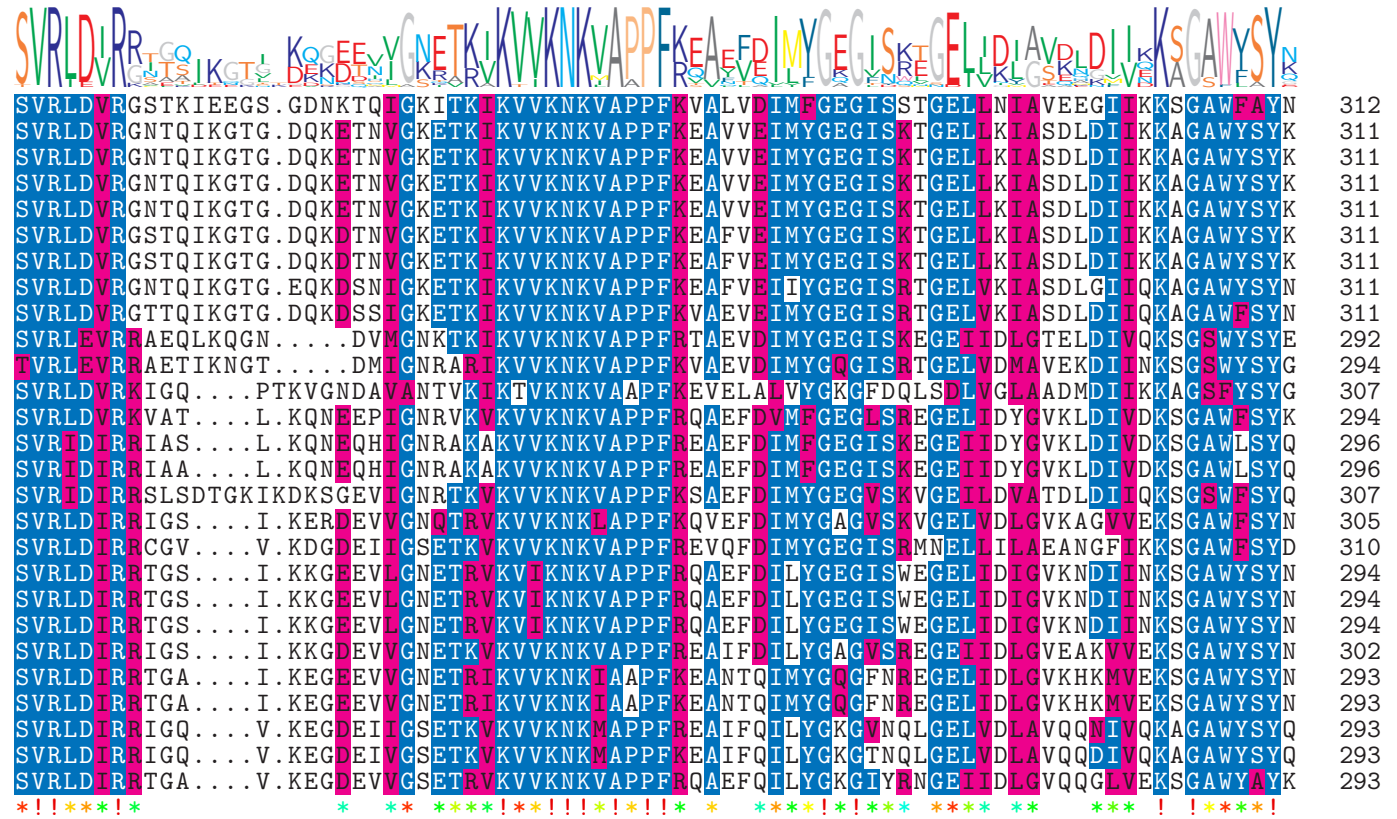
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consensus

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Sequence	Score
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DEKIGGQSENAKKYLAEHPEIFDEIDKQVRSKFGLIDGEEVSEQDTENKK.DE....PKKEEA..VNEEVPLDLGDELEI	384
DEKIGGQSENAKKYLAEHPEIFDEIDKQVRSKFGLIDGEEVSEQDTENKK.DE....PKKEEA..VNEEVPLDLGDELEI	384
DEKIGGQSENAKKYLAADNPEVFAEIDHQVRVQFGLIDGEEAAE....SKK.DE....VAQVDS..VNEEVPLDLGDELEI	380
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GEKIGGQSENAKFLADNPEIFDDIDHKVRSVQGLIEDNTEEEKSSSEK.....ETDEK..ADKNLVLELDDTTIEL	381
GEKIGGQSENAKRYLADHPQLFDEIDRKVRVKFGLLEESSEESAMAVASE.....E.....TDDLALDLNGIEI	376
EERLGGGRENAKQFLKENKDIMLMIQEQIREHYGLDNNGVVQQAEETQE.EL.EFE.E.....	348
SERIGGQRENAKNYLADHEDVEDEVRLKVRAAAYGTSVPEEDLPTTEDE..QI.NILPDDST.....EE.....	355
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GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEGTQ..DETDGER.....PEE.....	348
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GDKIGGQKANACKYLLKENPEIAKTLDDKKIREMLLNPNMQLIAE..TSSAADVEFG.....AVPEEF.....	354
GNKIGGQKNNVIRYLEENPQISTEIEAVIREQLLTKASDQTAA...HDETEEPDLL.....ES.....	349
GNKIGGQKNNVIRYFEENNQIAEIERNIREQLLTTGTNGAVQ...I.EDETEPDLL.....LES.....	349
GSKIGGQKANAAKYLEENPEIQQEIEQQIRAKLLVTSANTKATP..VAEDLADADI.....	347

logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved