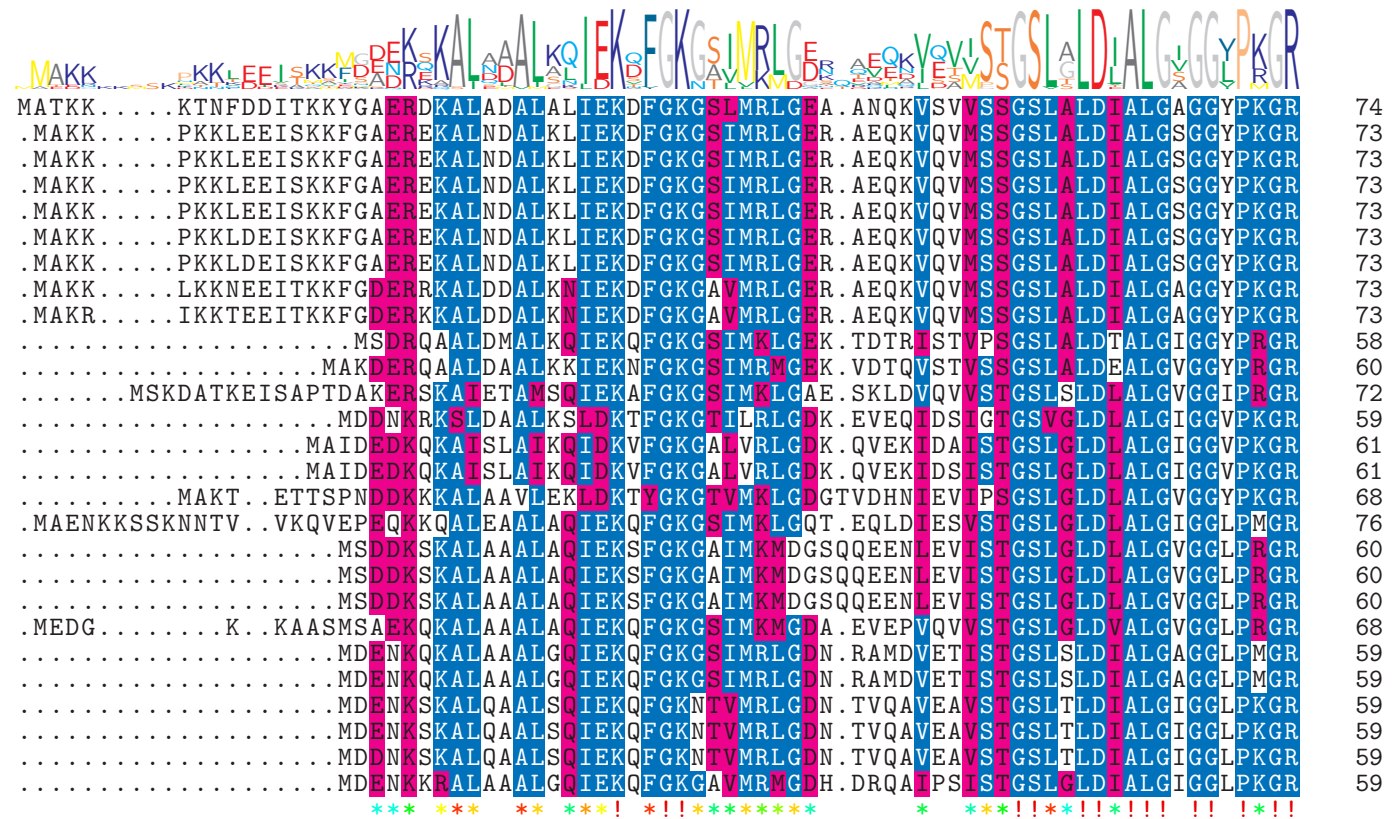


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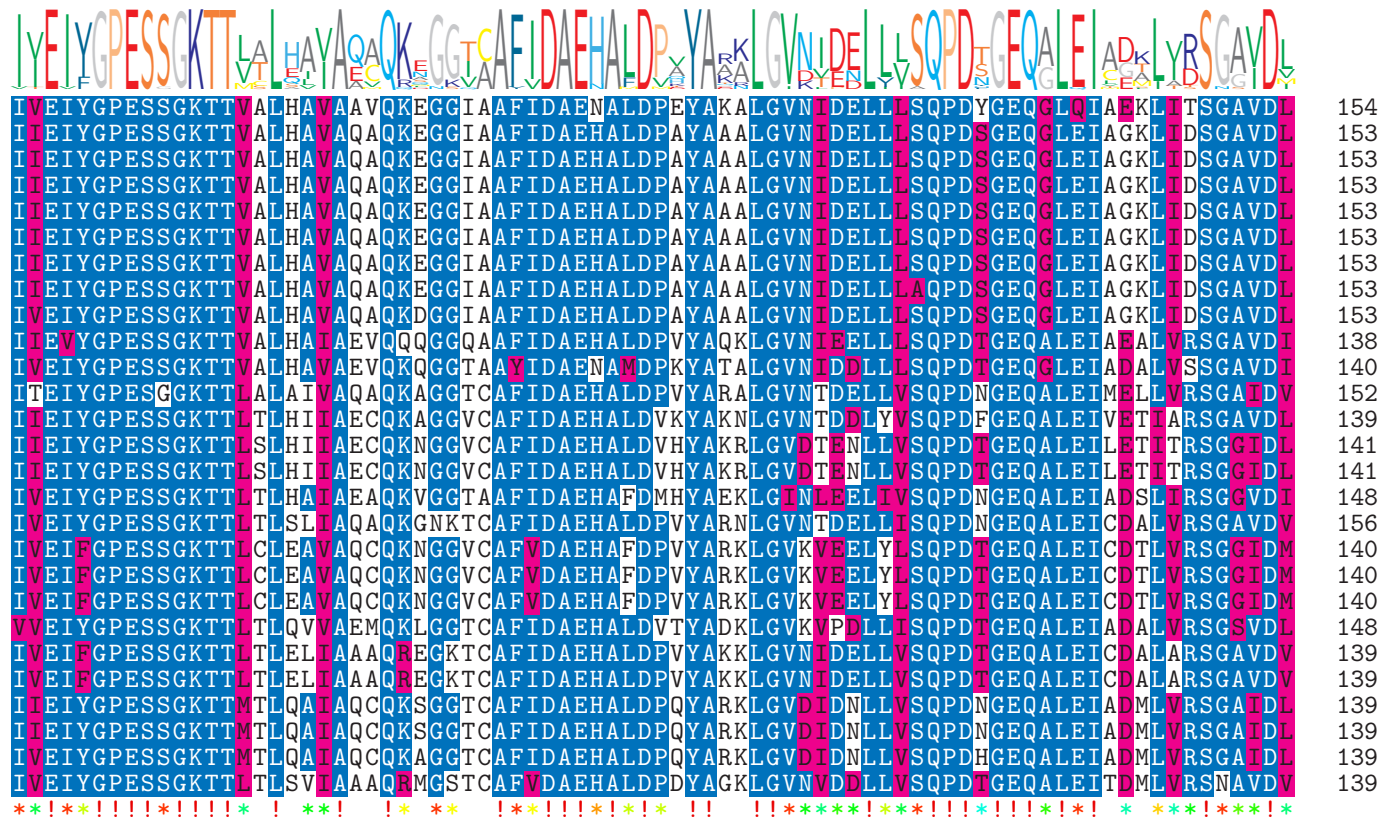
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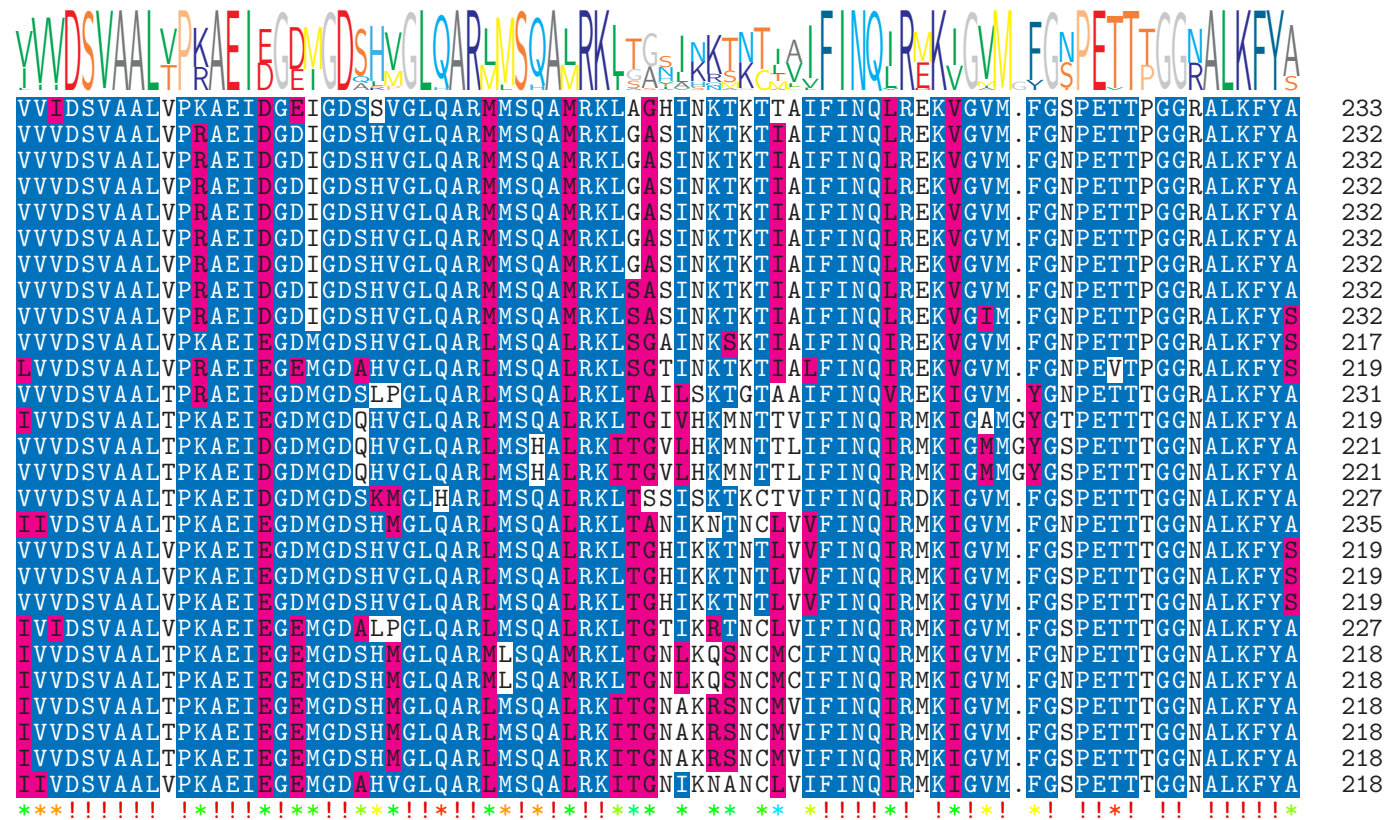
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consensus

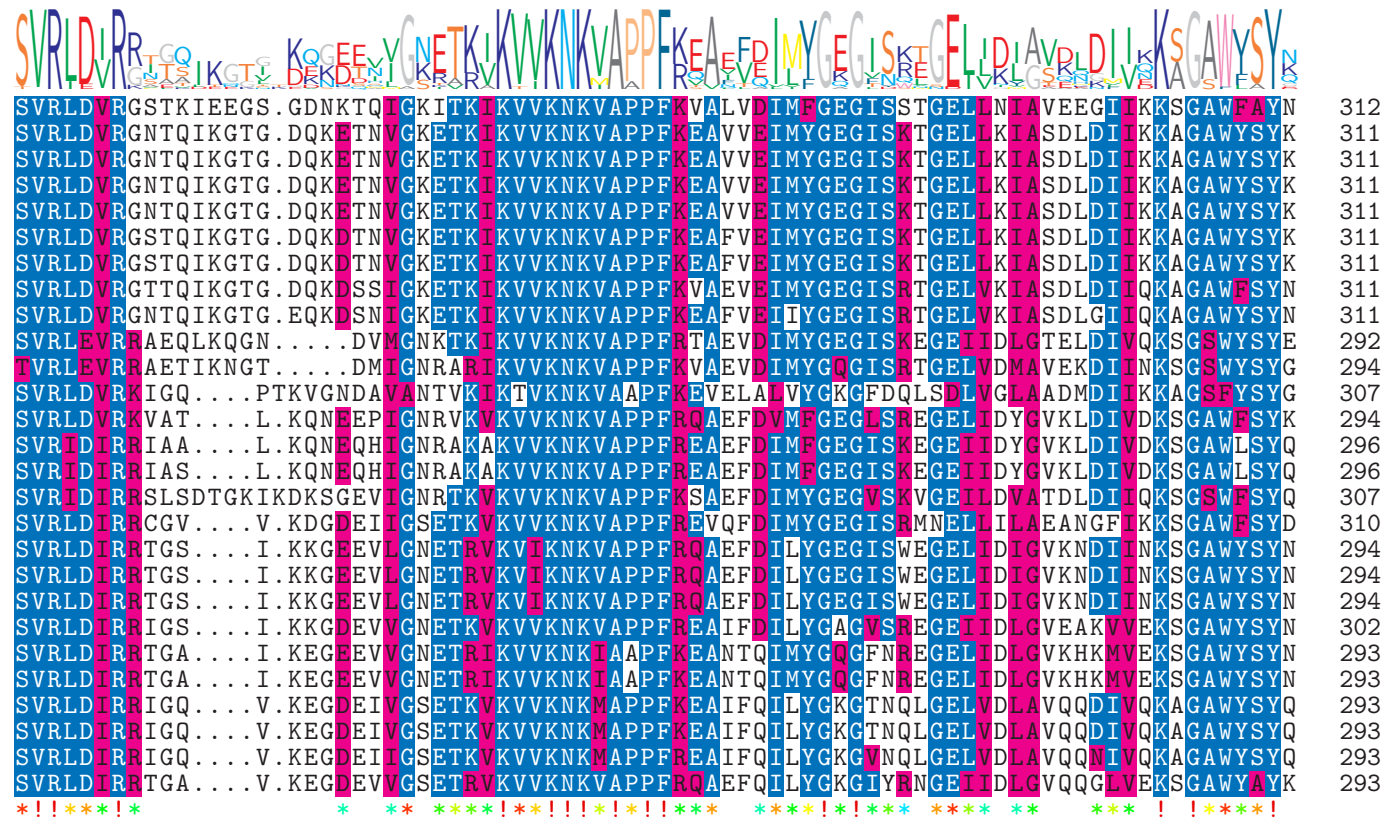
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consensus

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Sequence	Score
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DEKIGGGS E NAK K YL A EH P E F ID D IK Q VR S K F GLID G EEVSEQDTE.NKK D E.....PKKEEA..VNEEVPLDLGDEL	382
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DEKIGGGS E NAK K YL A D N PE F ID D IH Q VR V Q F GLID G EEIAE.....SK K D EAAQ V DS..VNEE V TLDLGDEL	378
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EE R LG Q GR E NAK Q FL K EN K DI M LI Q EQ I RE H YGLD N NG V V Q Q A EE.TQEEL.E..FE.E.....	348
SERIGGGR E NAK N YL A D H DE V DE V RL K VR A AY G IS D VP E ED L PTTE.DE.QI.N..ILPDDST.....EE.....	355
DERIGGG K E K TI A Y I A E R P E M E Q E I DR D VM A A I R A GN A GE A PA L AP A PA A PE A PE A PE A	363
DKKLGGGR E NS K AF L KEN P E I AD E IT K AI Q NS M G I E G MISGS..EDDEGE..E.....	343
DKKLGGGR E NAK A LL K ED K AL A DE I TL K IK E SI G SNEE I MP L ..PDEPLE..E M E.....	347
DKKLGGGR E NAK A LL K ED K AL A DE I TL K IK E SI G SNEE I MP L ..PDEPLE..E M E.....	347
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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved