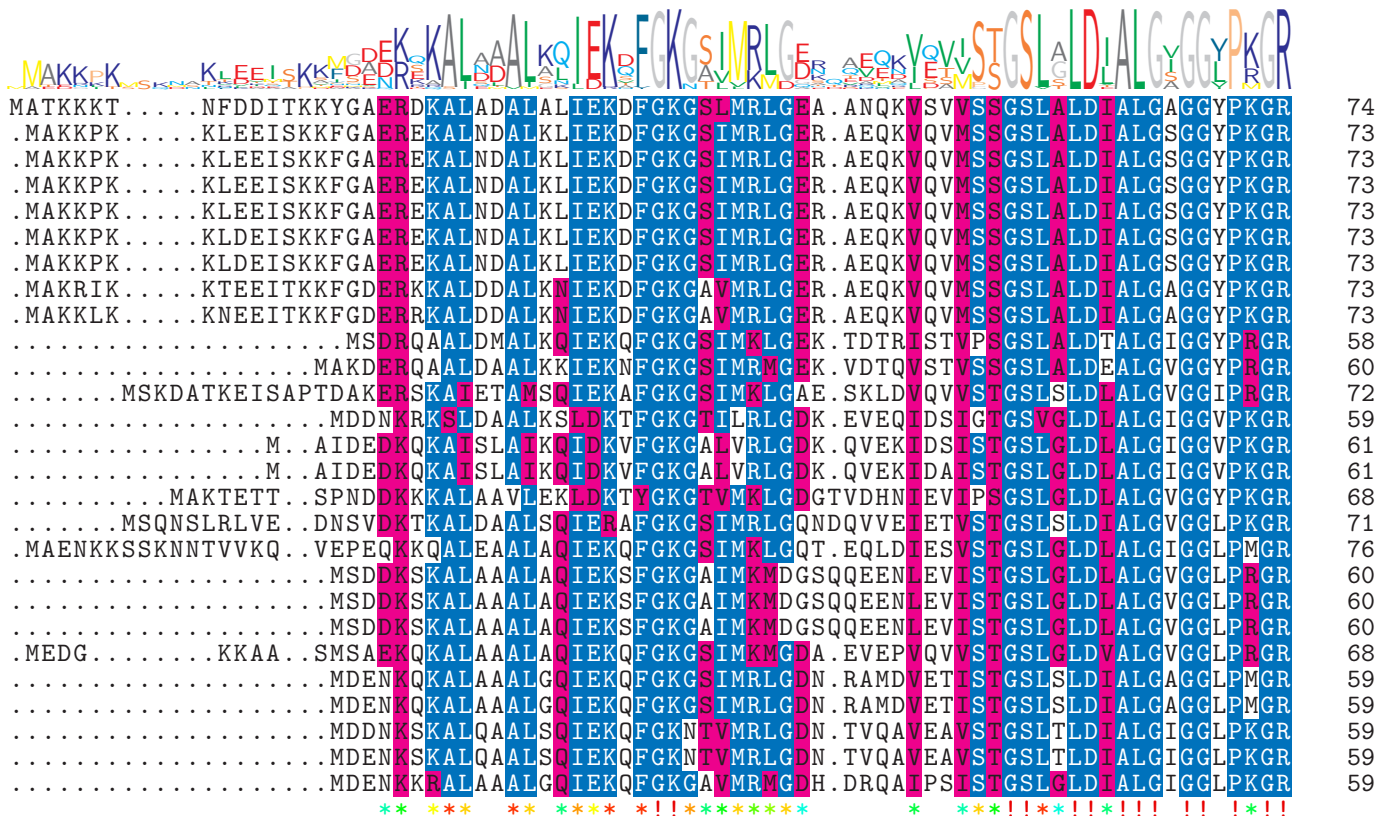


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consensus

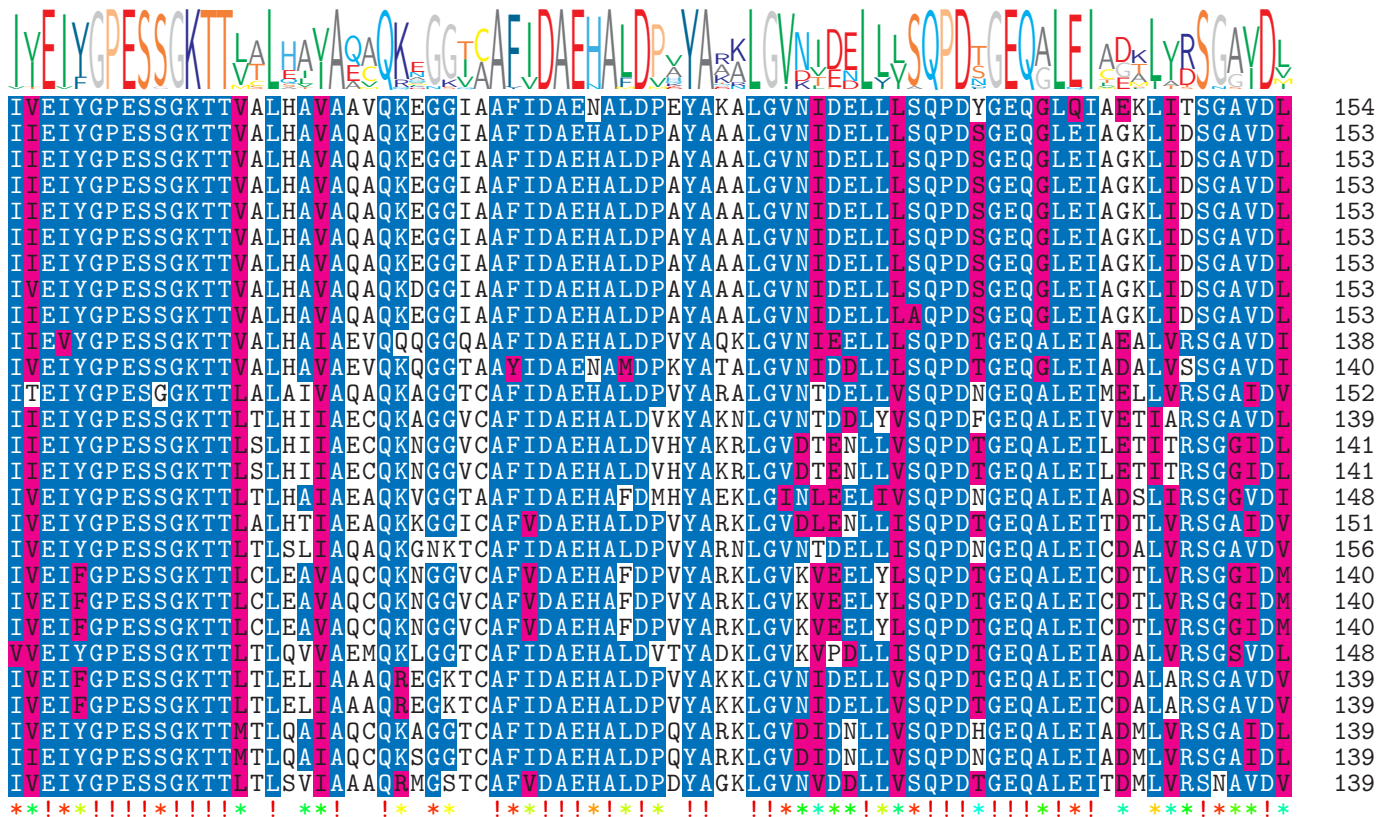
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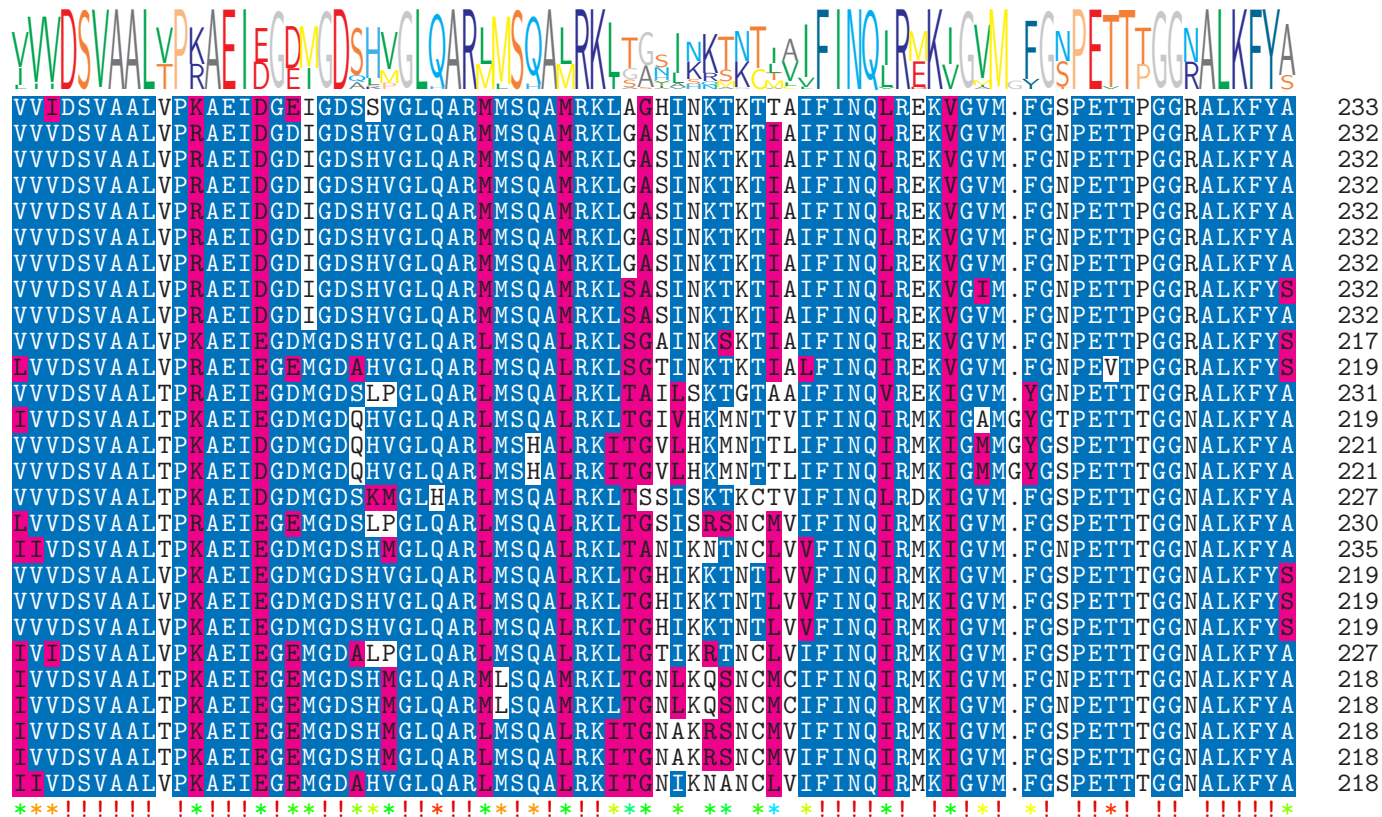
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consensus

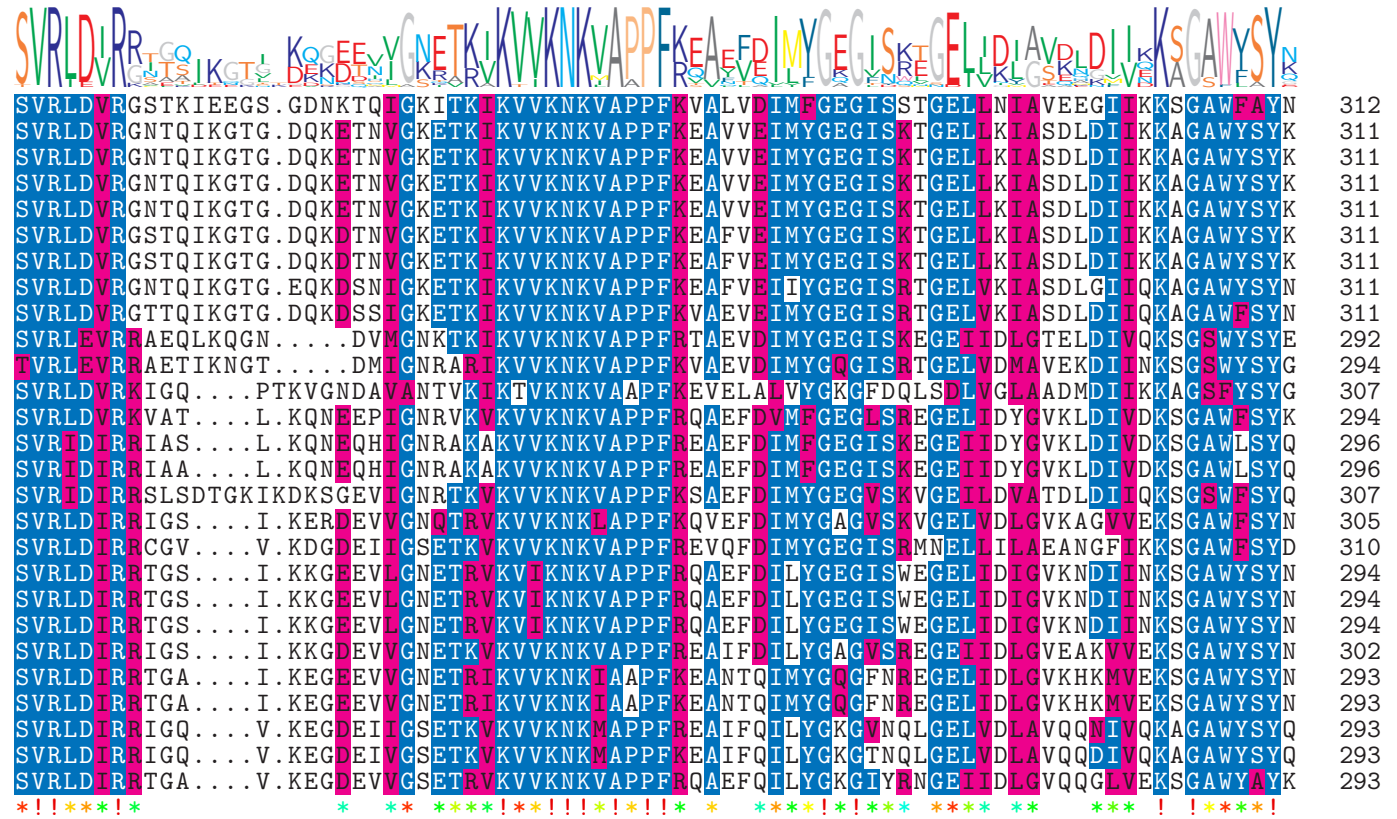
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consensus

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consensus

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Sequence	Score
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DEKIGGGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKK.DE...PKKEEA..VNEEVPLDLGDELEI	384
DEKIGGGSSENAKKYLAHNPEVFAEIDHQVRVQFGLIDGEEAAE...SKK.DE...VAQVDS..VNEEVPLDLGDELEI	380
DEKIGGGSSENAKKYLAHNPEIFDEIDHQVRVQFGLIDGEEAAE...SKK.DE...AAQVDS..VNEEVPLDLGDELEI	380
GEKIGGGSSENAKFLADNPEIFDDIDHKVRVQFGLIEEDNTEEEKSSKEK.....ETDEK..ADKNLVLELDDTIEL	381
GEKIGGGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESSEESAMAVASE.....E.....TDDLALDLNGIEI	376
EERLGGGRENAKQFLKENKDIMLMIQEQIREHYGLDNGGVVQQAEETQE.EL.EFE.E.....	348
SERIGGGSRENAKNYLADHEDVEDEVRLKVRVQFGLSDVPEEDLPTTEDE..QI.NILPDDST.....EE.....	355
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GSKIGGQKANAAYLEENPEIQEIEQQIRAKLLVTSANTKATP..VAEDLADADI.....	347

logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved