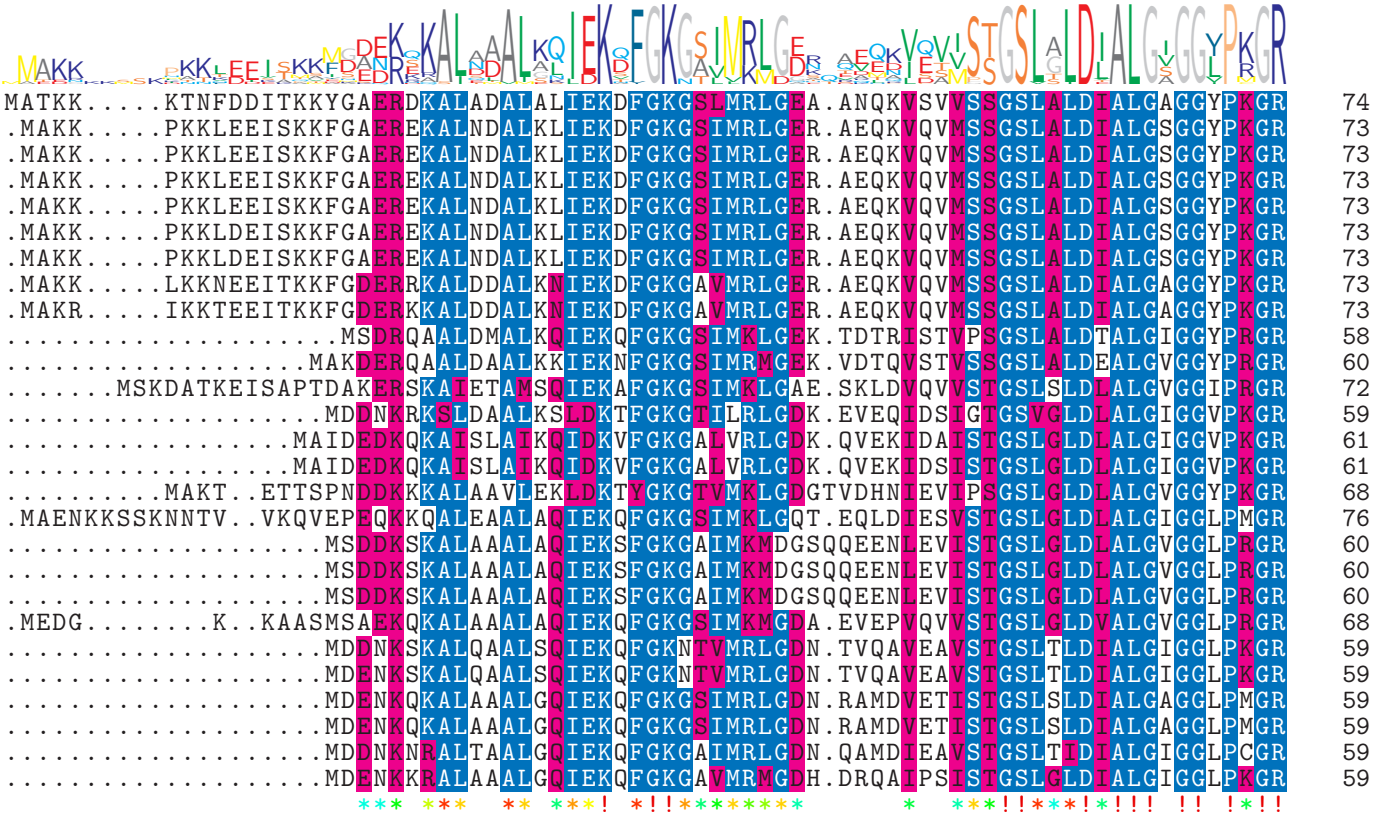
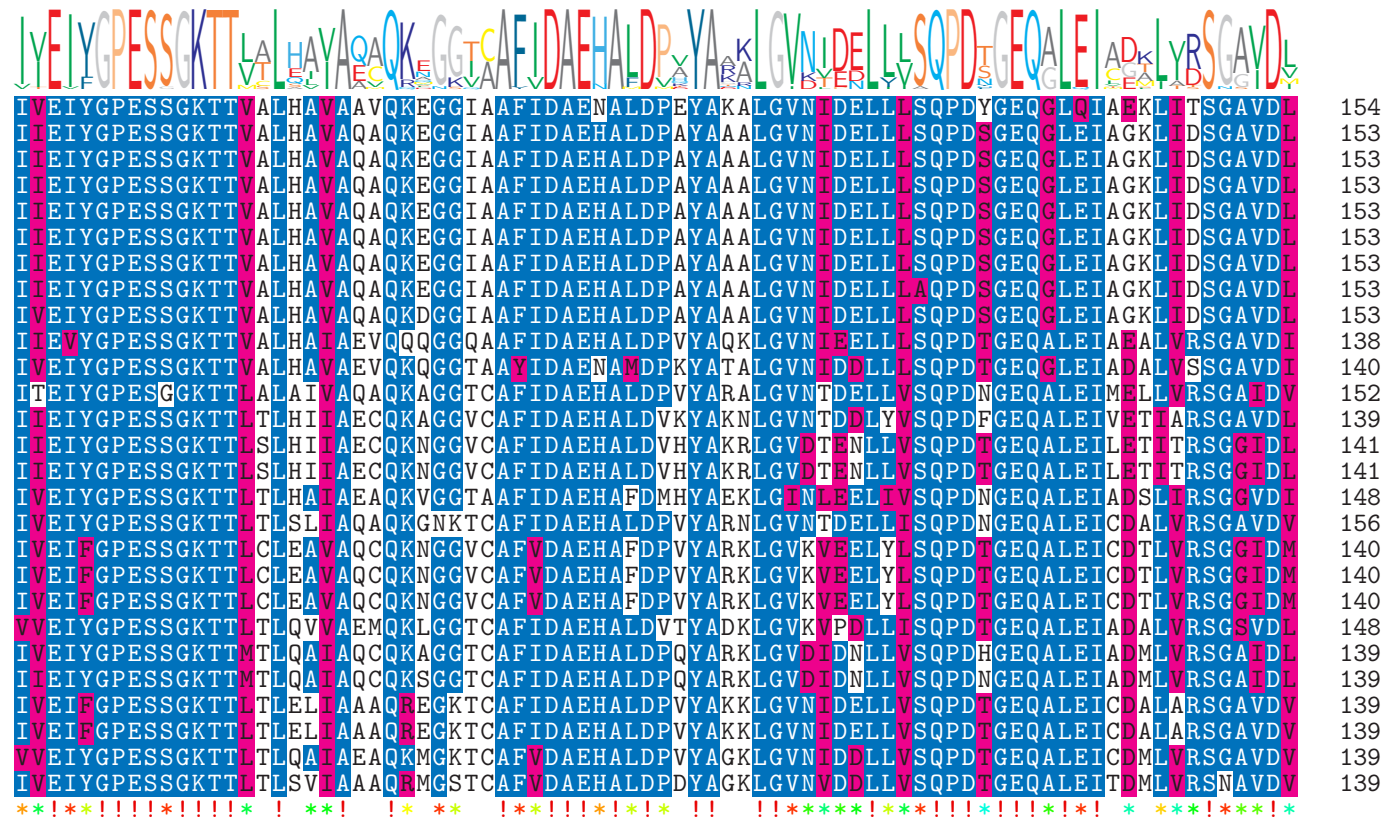


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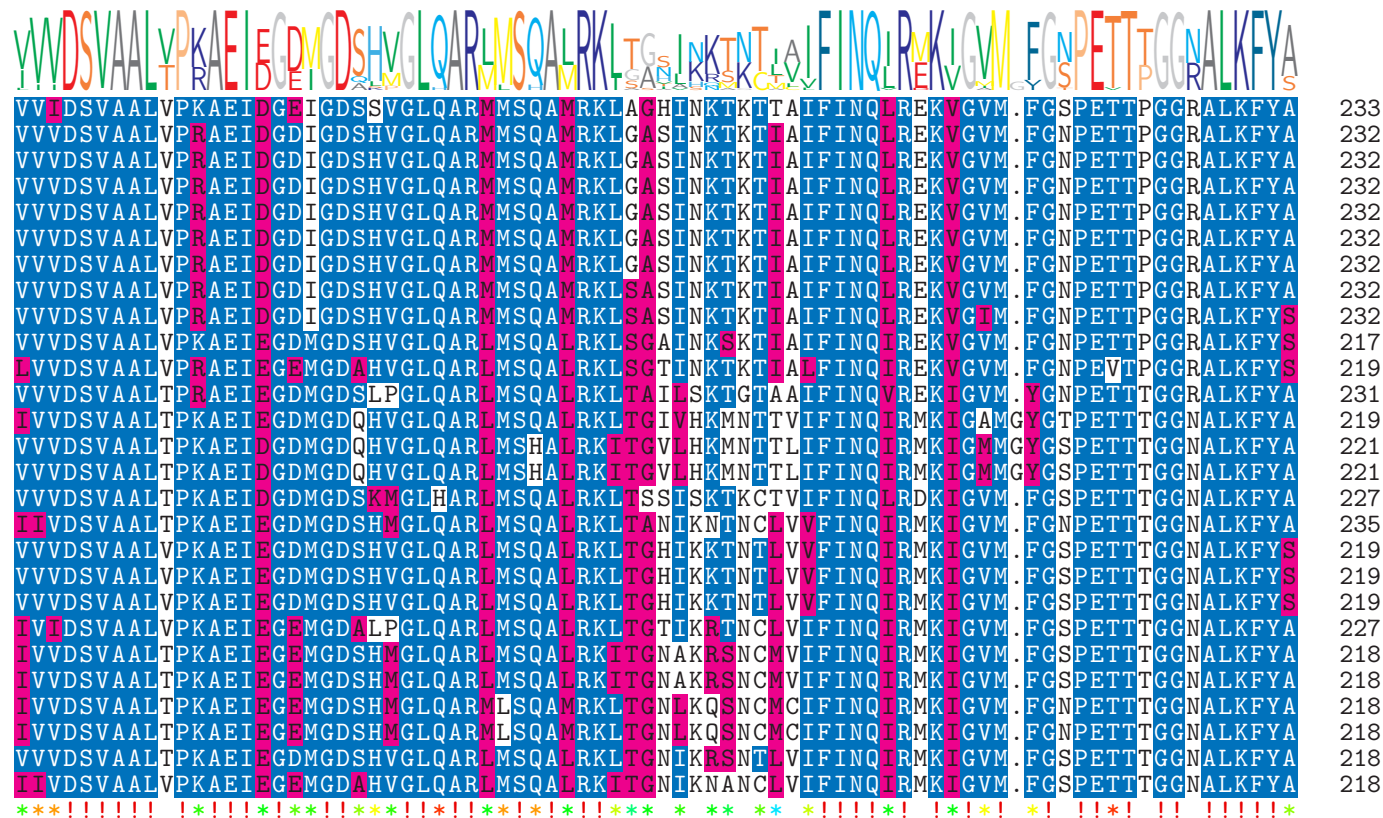
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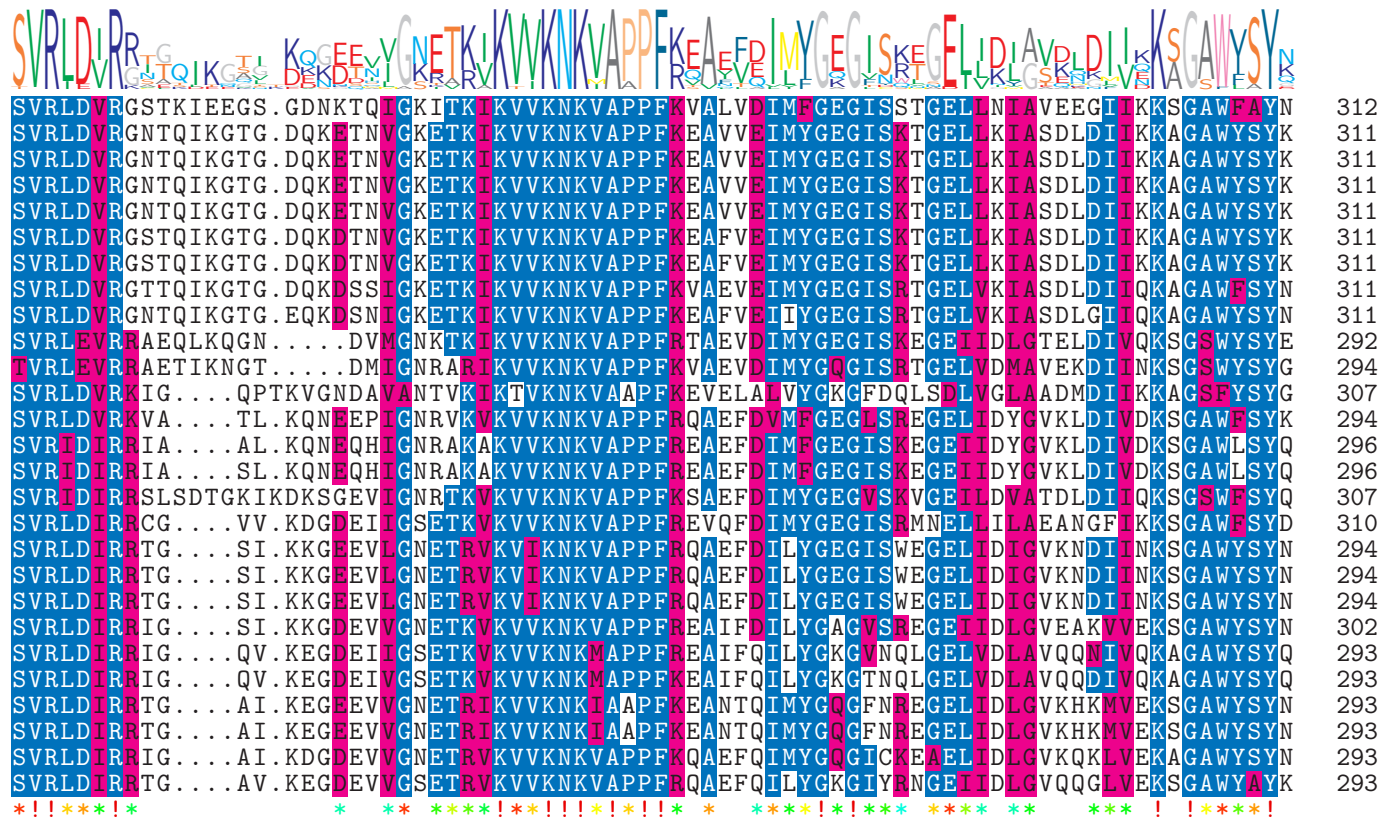
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consensus

Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDT.ENKKDE...PKKEEA..VNEEVPLDLGDELEI	384
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DEKIGQGSENAKKYLAHNPEVFAEIDHQRVVFGLIDGEEIAES....KKDE...VAQVDS..VNEEVPLDLGDELEI	380
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMA.VASE.....E.....TDDLALDLNGIEI	376
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQGLIEEDNTEEKQS.SKEK.....ETDEK..ADKNLVLEDDTIEL	381
EERLGGGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGVGVQQAE.ETQEEL.EFE.E.....	348
SERIGGGRENAKNYLADHEDVEDEVRLKVRVQGLSDVPEEDLPTT.EDE.QI.NILPDDST.....EE.....	355
DERIGGQKEKTIATIAERPMEQEIHDRVMAAIRAGNAGEAPALAPAPAAPEAAEA.....	363
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GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEG..TQDETGERP.....EE.....	348
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEG..TQDETGERP.....EE.....	348
GERIGGGRDNCREFLRENAELAREIENKVRHGLVTPMGAVT..LAEVEED.....	352
GNKIGGQKNNVIRYLEENPQISTEIEAVIREQLLTKASDQTA..AHDET.EEEPDLLES.....	349
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GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPNEMQLI..AETSSAADVEFGAVPEE.....F.....	354
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logo

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consensus

 non conserved
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 ≥ 50% conserved