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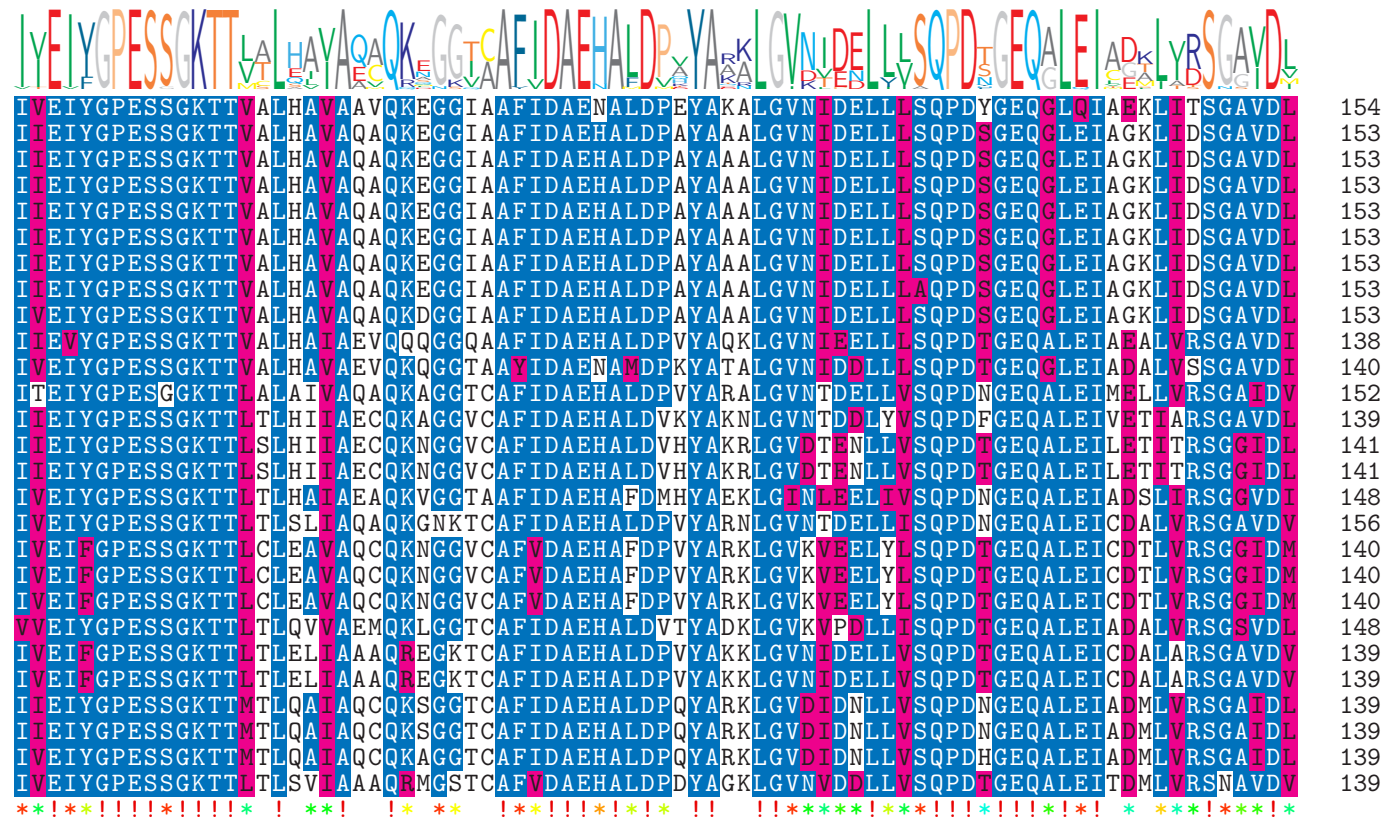
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consensus

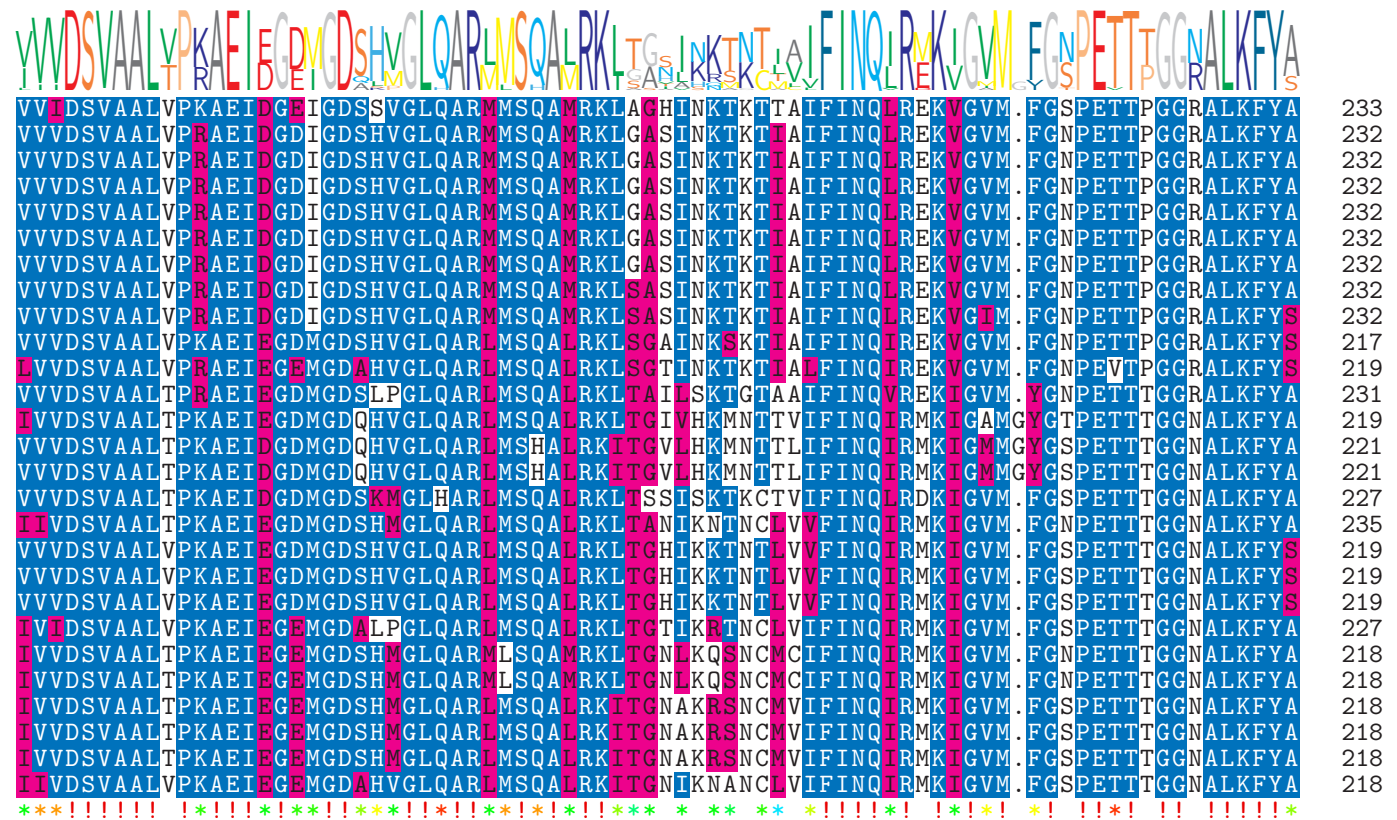
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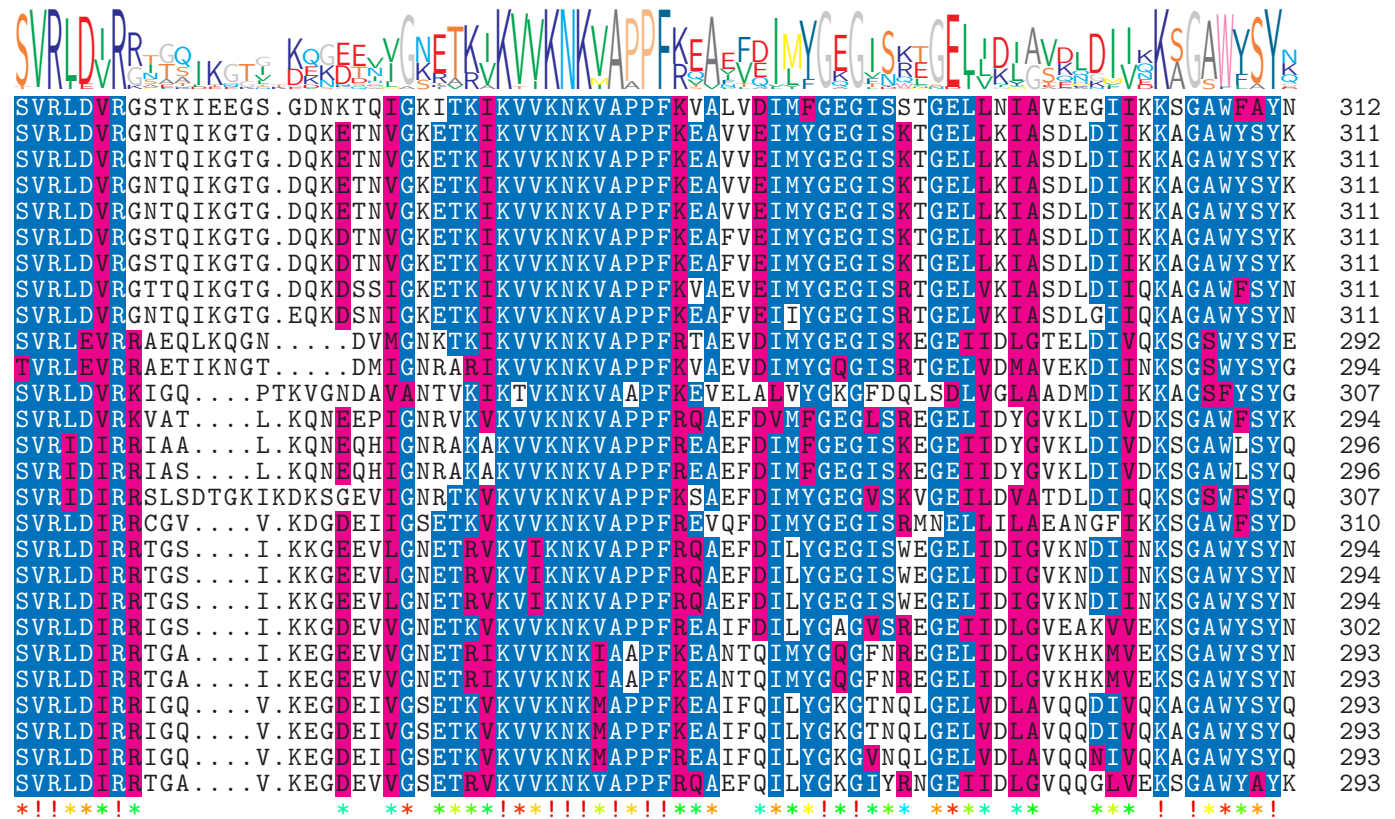
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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTE.NKKDE.....PKKEEA..VNEEVPLDLGDEL	382
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTE.NKKDE.....PKKEEA..VNEEVPLDLGDEL	382
DEKIGQGSENAKKYLAADNPVFAEIDHQVRVQFLIDGEEAAE.....SKKDE.....VAQVDS..VNEEVPLDLGDEL	378
DEKIGQGSENAKKYLAADNPVFEIDHQVRVQFLIDGEEIAE.....SKKDE.....AAQVDS..VNEEVPLDLGDEL	378
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEEESAMAV.ASE.....E.....TDDLALDLNGI	374
GEKIGQGSENAKKFLADNPVFEIDHKVVRVQGLIEEDNTEEKQSS.KEK.....ETDEK..ADKNLVLELDDTI	379
EERLGGGRENAAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAAE.TQEEL.E..FE.E.....	348
SERIGGGRENAAKNYLADHEDVEDEVRLKVRVQGLSDVPEEDLPSTE.DE.QI.N..ILPDDST.....EE.....	355
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DKKLGGGRENAAKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
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GTKIGQGKNNNAVKWLKENPEIADKLEQIRNTLASNPNSVLK..ATASDSNDESDVEEFSE.....EEL.....	372
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GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEG..TQDET.....GERPE.....E.....	348
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEG..TQDET.....GERPE.....E.....	348
GERIGGGRDNCREFLRENAELAREIENKVRHGLVTPMGAV..TLAEEVEED.....	352
GDKIGQGKANACKYLKENPEIAKTLDKKLREMLLNPNMQLI..AETSSAADVEFGAVPE.....EF.....	354
GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPNMQLI..AETSSAADVEFGAVPE.....EF.....	354
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GNKIGGQKNNVIRYFEENNQIAEEIERNIREQLLTGTNGAV..Q.I.EDEEPPD..LLE.....S.....	349
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logo

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consensus								

-  non conserved
-  similar
-  ≥ 50% conserved