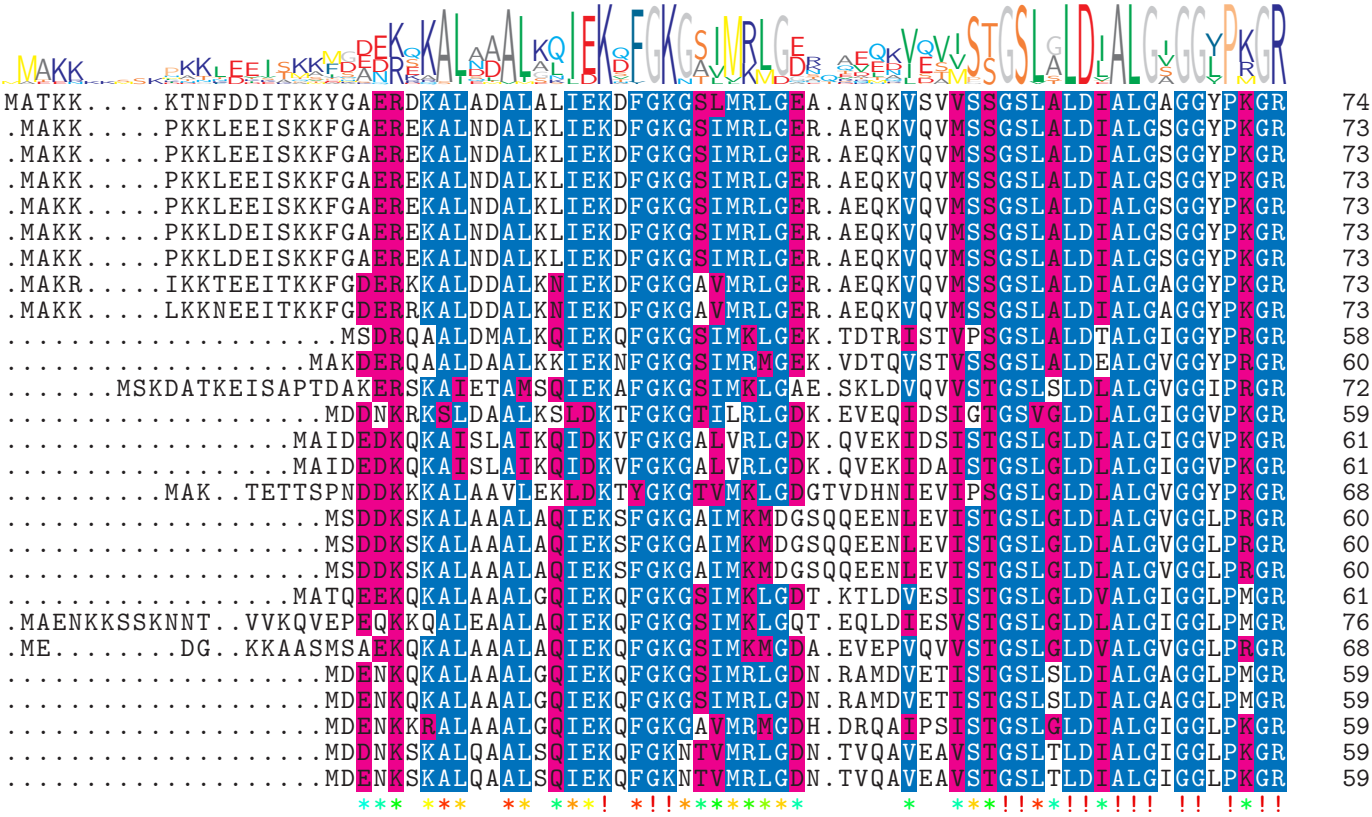


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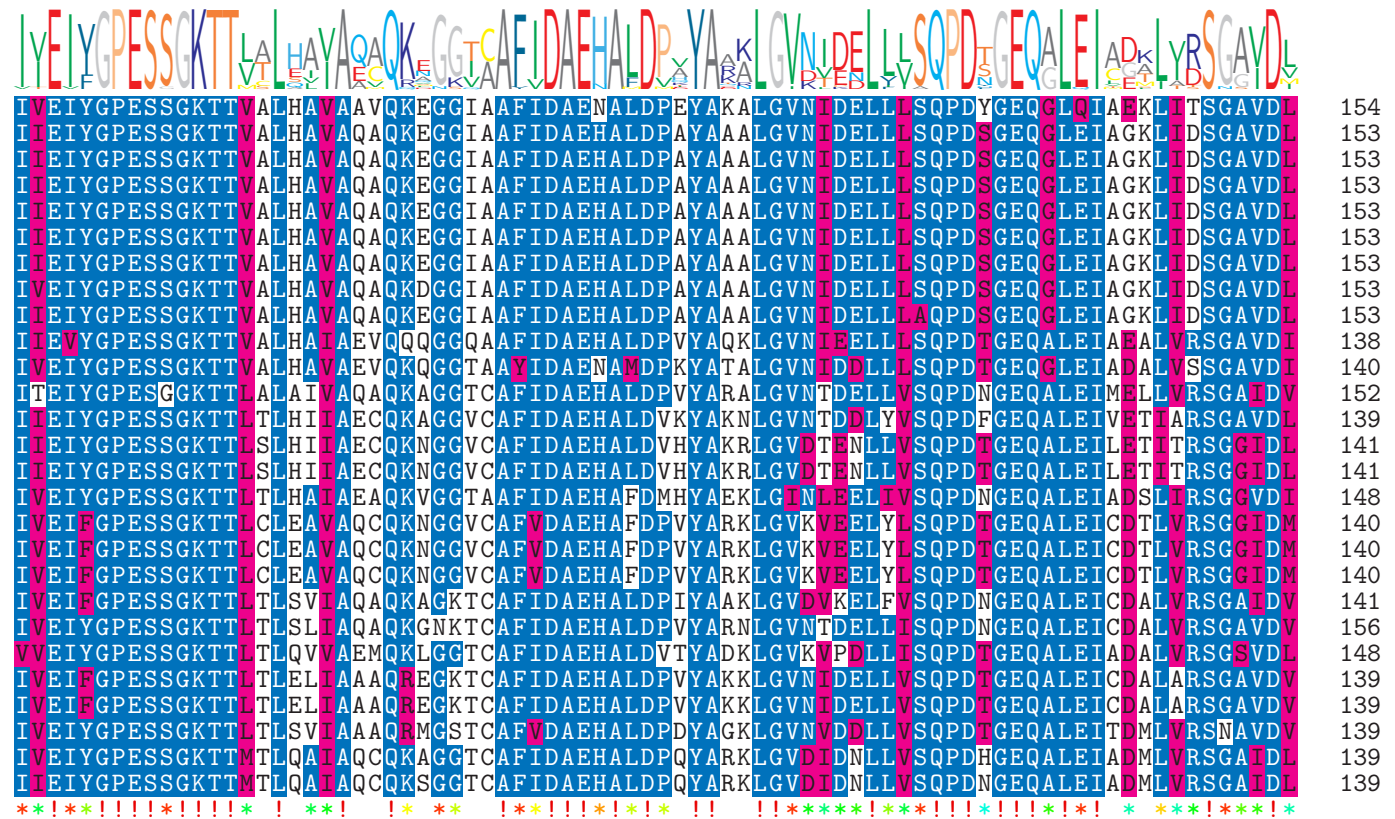
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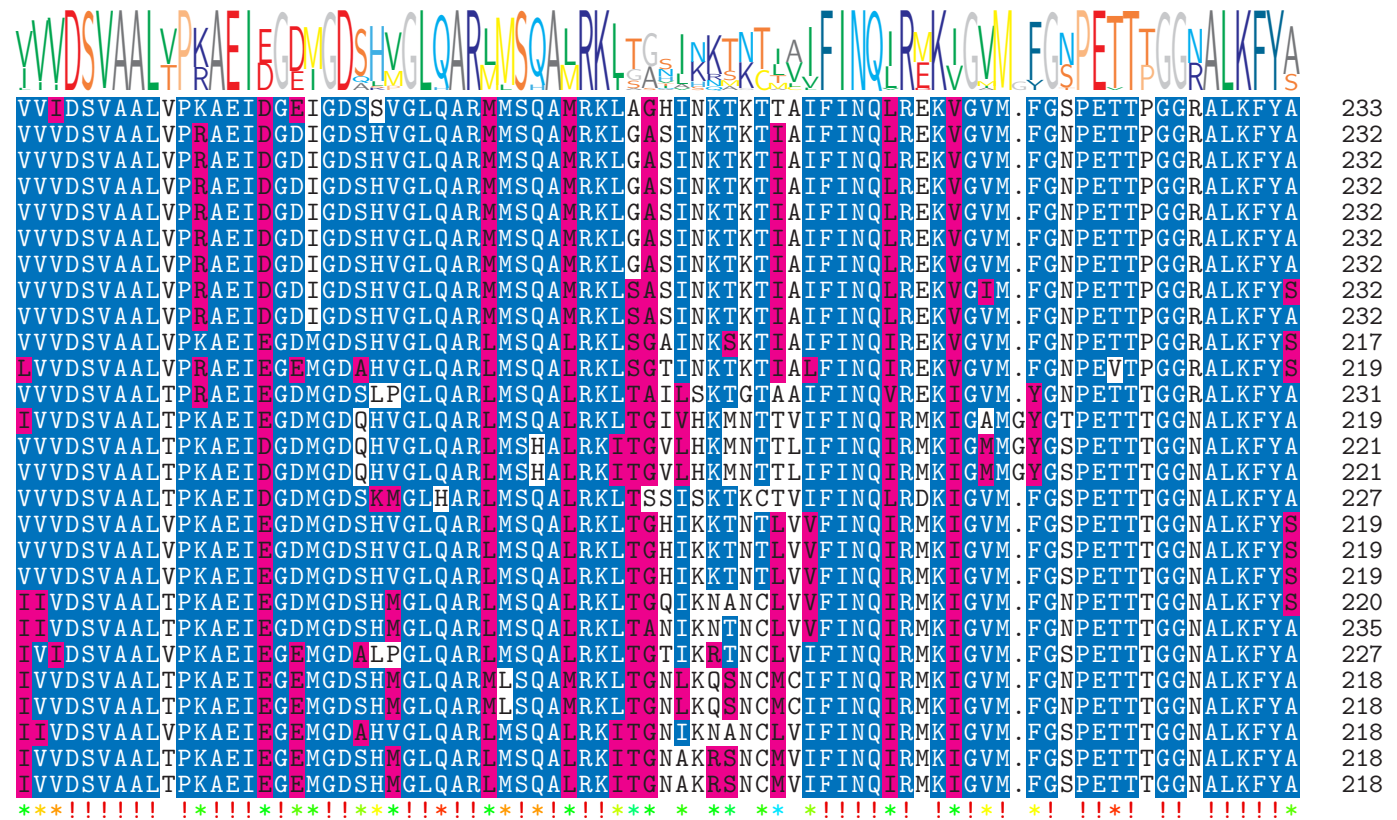
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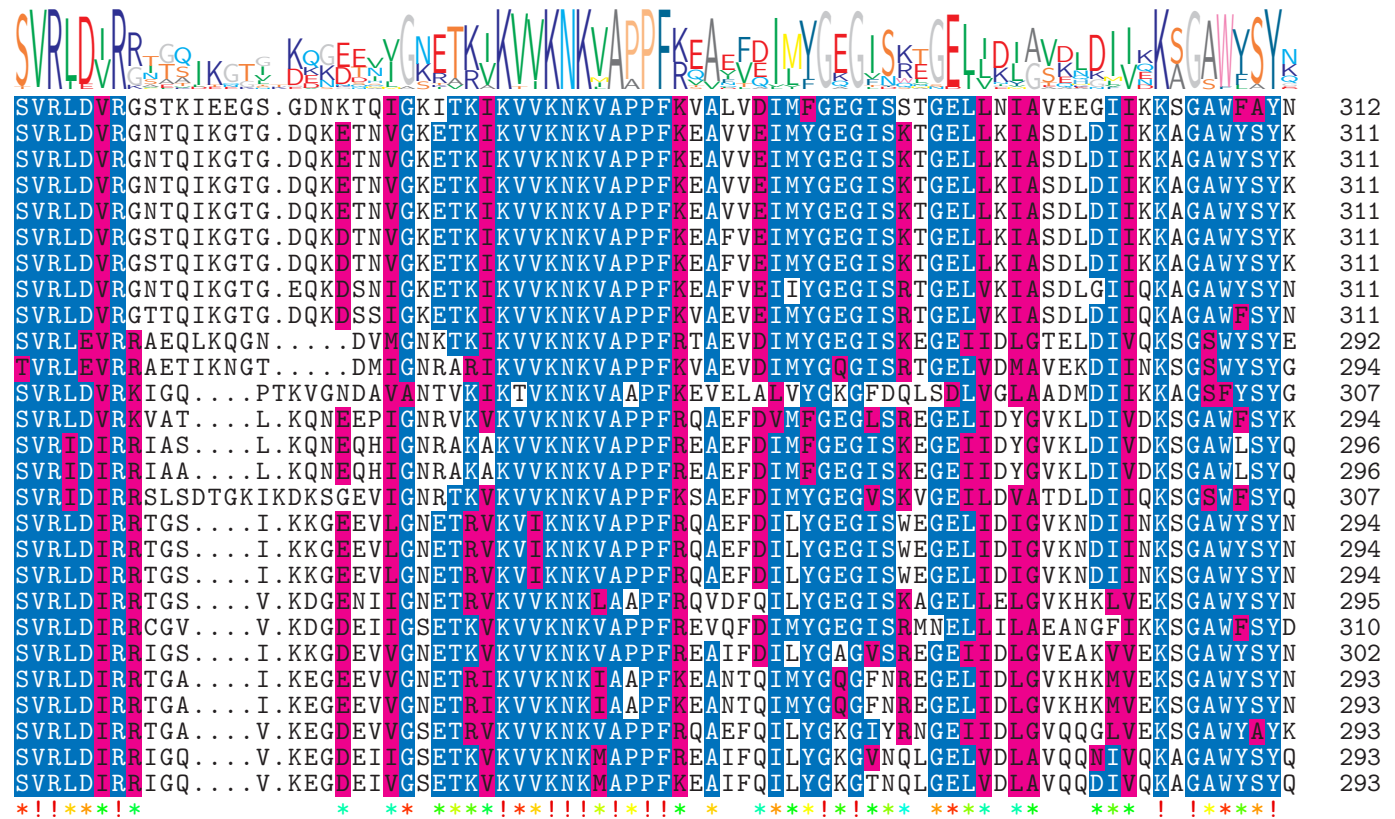
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consensus

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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQD.TENKKDE....PKKEEA..VNEEVPLDLGDELEI	384
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQD.TENKKDE....PKKEEA..VNEEVPLDLGDELEI	384
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQD.TENKKDE....PKKEEA..VNEEVPLDLGDELEI	384
DEKIGQGSENAKKYLAHNPEIFDEIDHQRVVFGLIDGEEIAES....KKDE....AAQVDS..VNEEVPLDLGDELEI	380
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GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQGLIEEDNTEEEKQ.SSKEK.....ETDEK..ADKNLVLELDDTIEL	381
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAM.AVASE.....E.....TDDLALDLNGIEI	376
EERLGGGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQQA.EETQEEL.EFE.E.....	348
SERIGGGRENAKNYLADHEDVEDEVRLKVRVQGLSDVPEEDLPT.TEDE.QI.NILPDDST.....EE.....	355
DERIGGQKEKTIAYTIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAPEAAEA.....	363
DKKLGGGRENKAFLENKEPEIADEITKAIQNSMGIEGMISGS..EDDEGE..E.....	343
DKKLGGGRENKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DKKLGGGRENKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
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GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEG..T...QD...ETDGE.RPEE...	348
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEG..T...QD...ETDGE.RPEE...	348
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logo

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consensus

 non conserved
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 ≥ 50% conserved