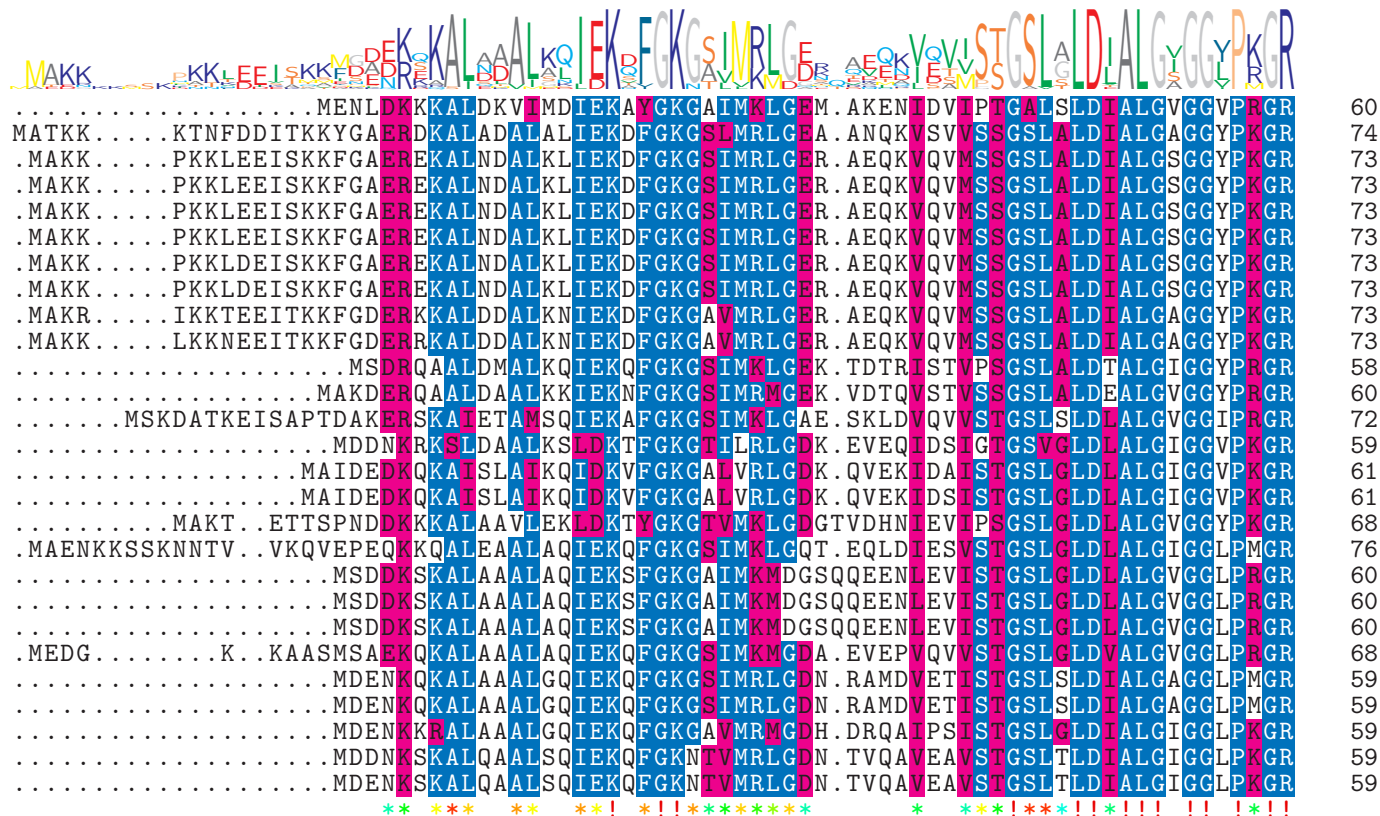


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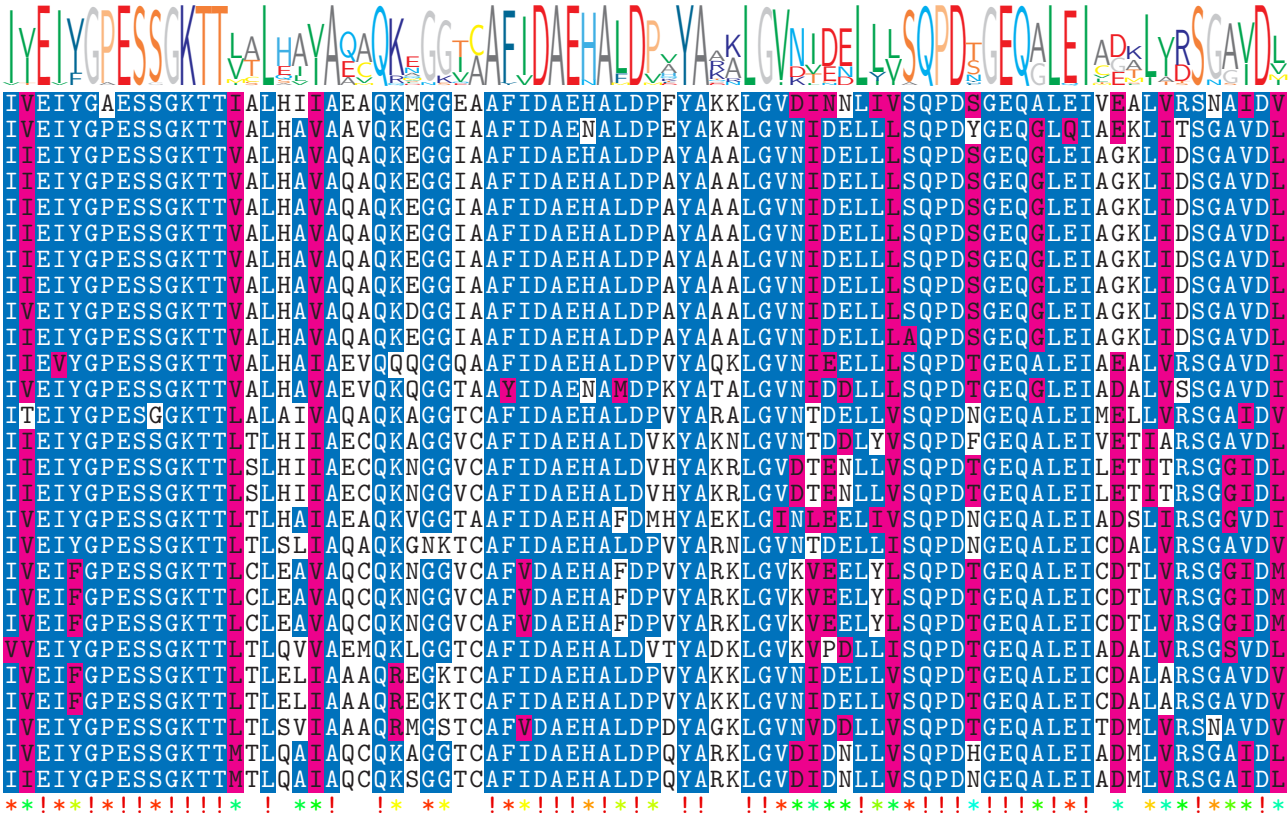
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consensus

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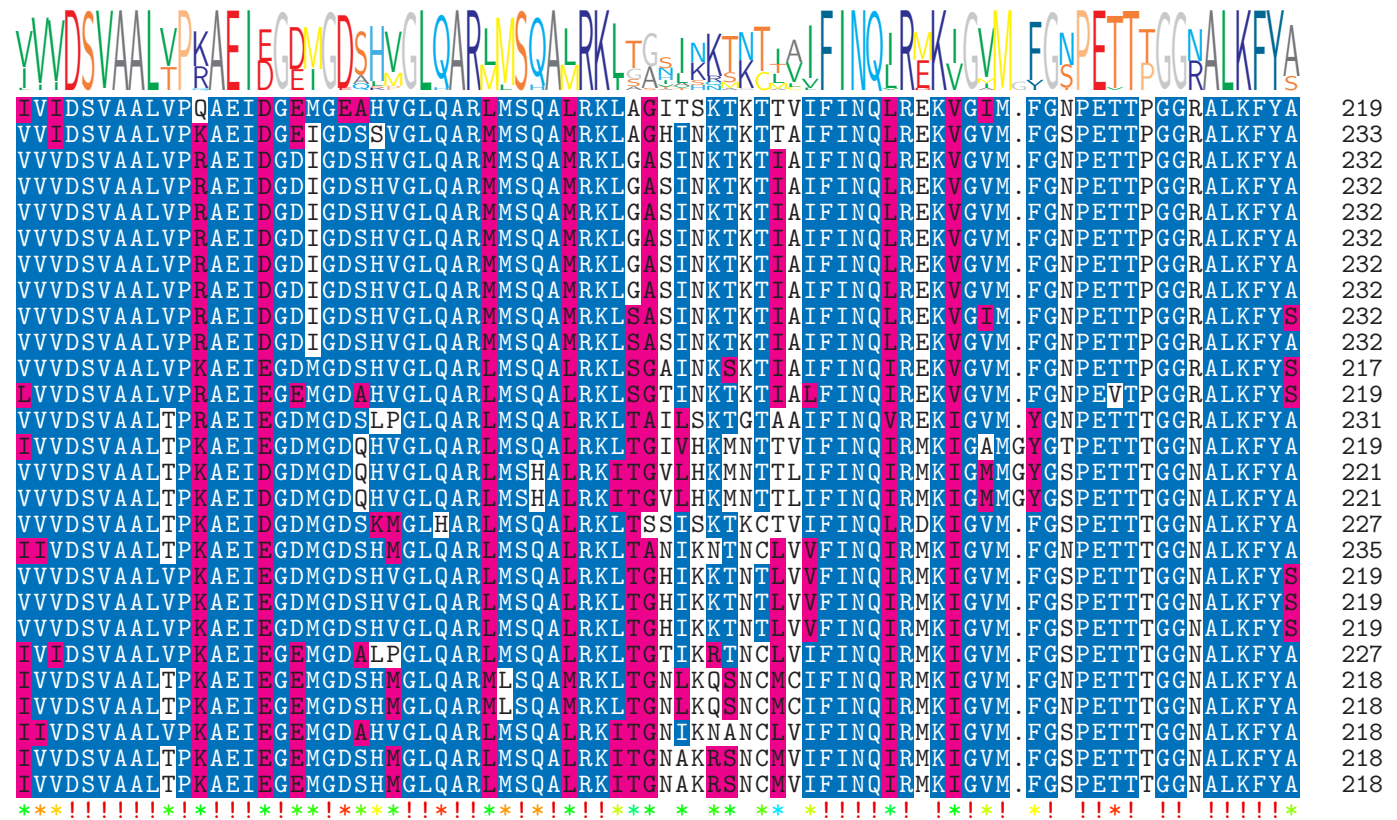
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consensus

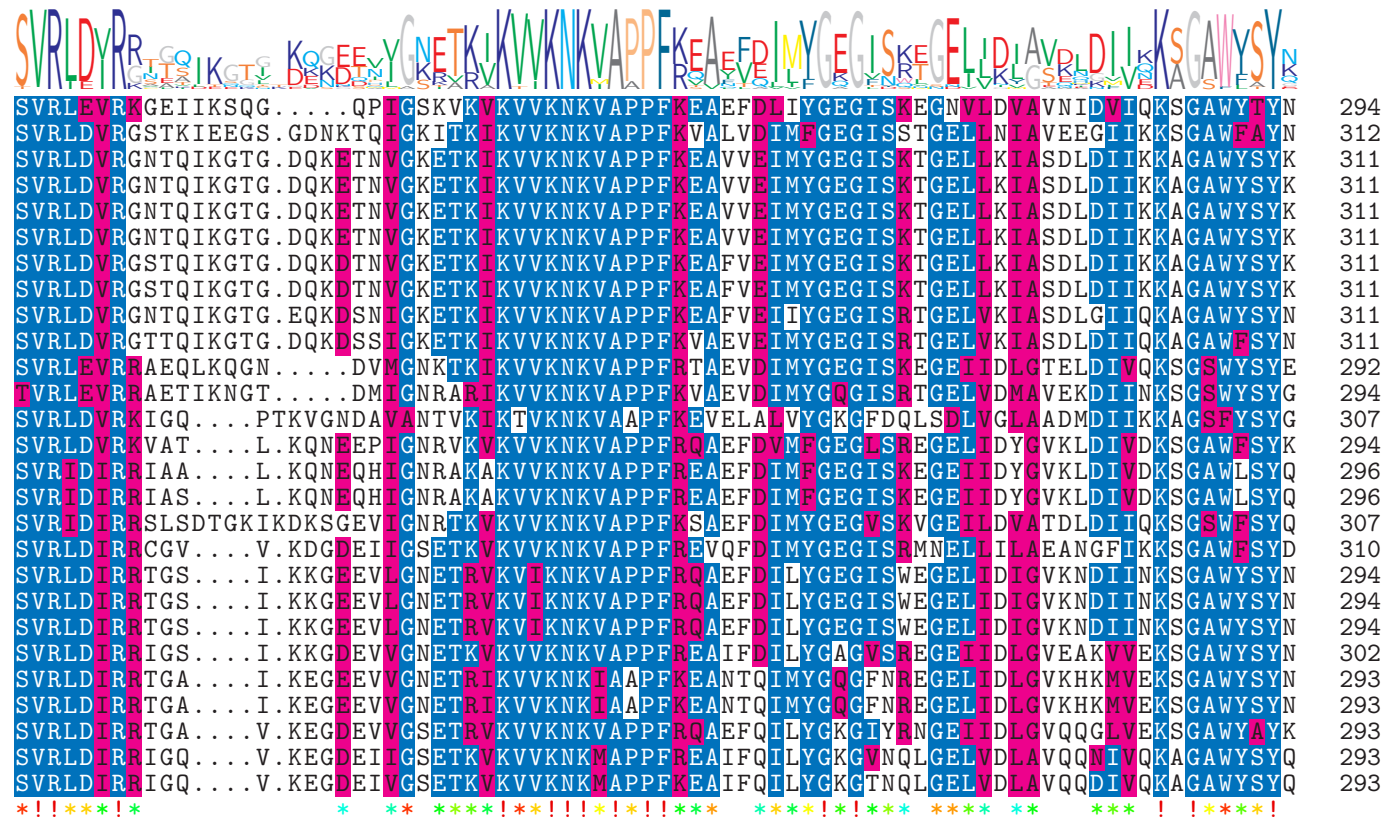


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Sequence	Score
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DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFG LIDGEEVSEQDTENKK...DE....PKKEEA..VNEEVPLDLGDE	381
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFG LIDGEEVSEQDTENKK...DE....PKKEEA..VNEEVPLDLGDE	381
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DEKIGQGSSENAKKYLANPEVFAEIDHQVRVQFGLIDGEEAAES...KK...DE....AAQVDS..VNEEVTLDLGD	377
GEKIGQGSSENAKKFLADNPEIFDDIDHKVVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDT	378
GEKIGQGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNG	373
EERLGGGRENAKQFLKENKDI MLMIQEIGIREHYGLDNNGVVQQQAETQE...EL.EFE.E.....	348
SERIGQGRENAKNYLADHEDVEVRLKVR AAYGISDVPEEDLPTTEDE...QI.NILPDDST.....EE	355
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DKKLGGGRENKAFLEKENPEIAD EITKAIQNSMGTIEGMI...SGSEDDE..GEE.....	343
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GA KIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI...TEGT.....QDET DGERPE.....E.....	348
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GDKIGQGGKANACKYLKENPEIAKTLDKKLREMLLN PENM...QLIAETSSAAD DVEFGAVPE.....EF.....	354
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GNKIGQGGKNNVIRYFENNQIAEIERNIREQLLTGTN...GAVQ.I.EDEE EPDLL..LE.....S.....	349

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consensus			

- X non conserved
- X similar
- X ≥ 50% conserved