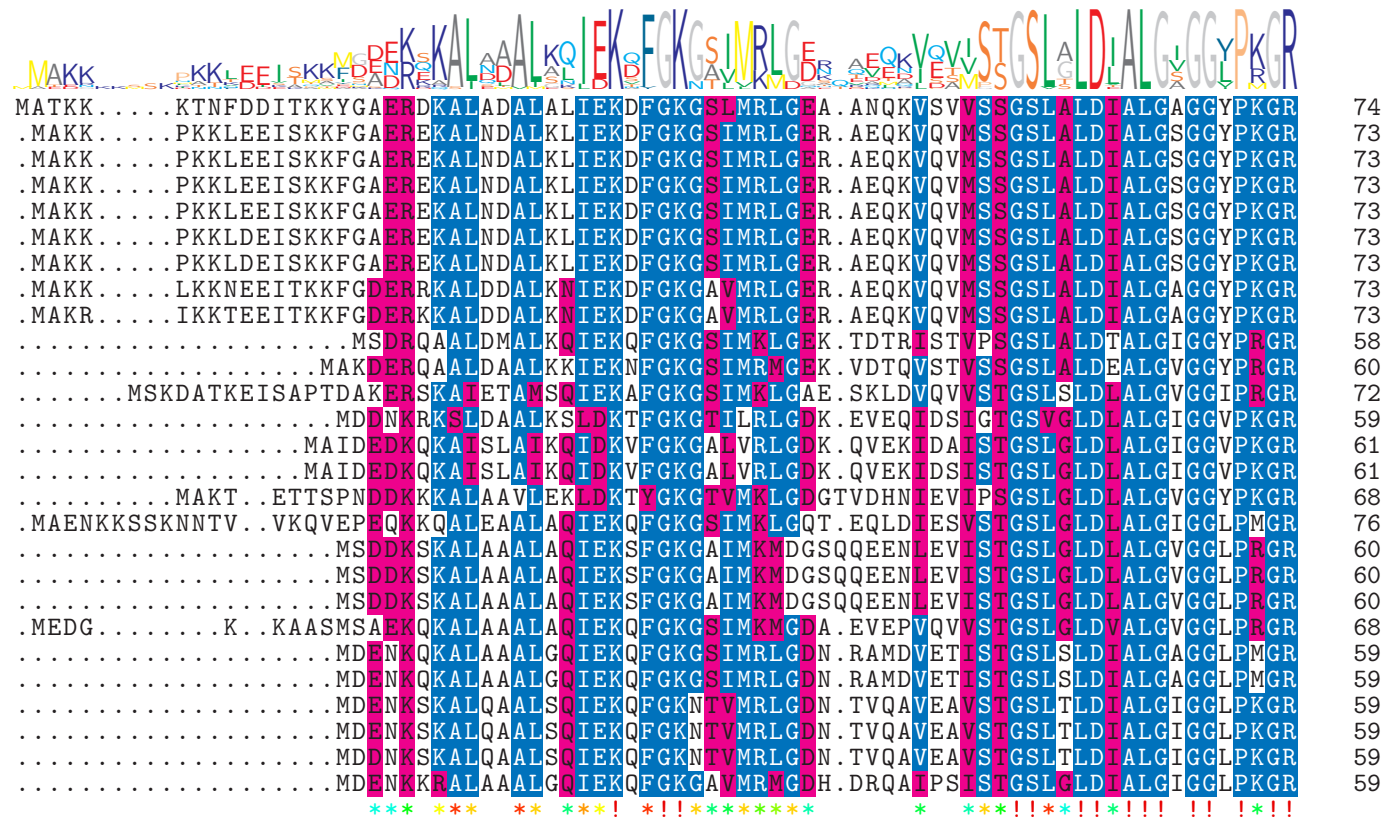


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consensus



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consensus

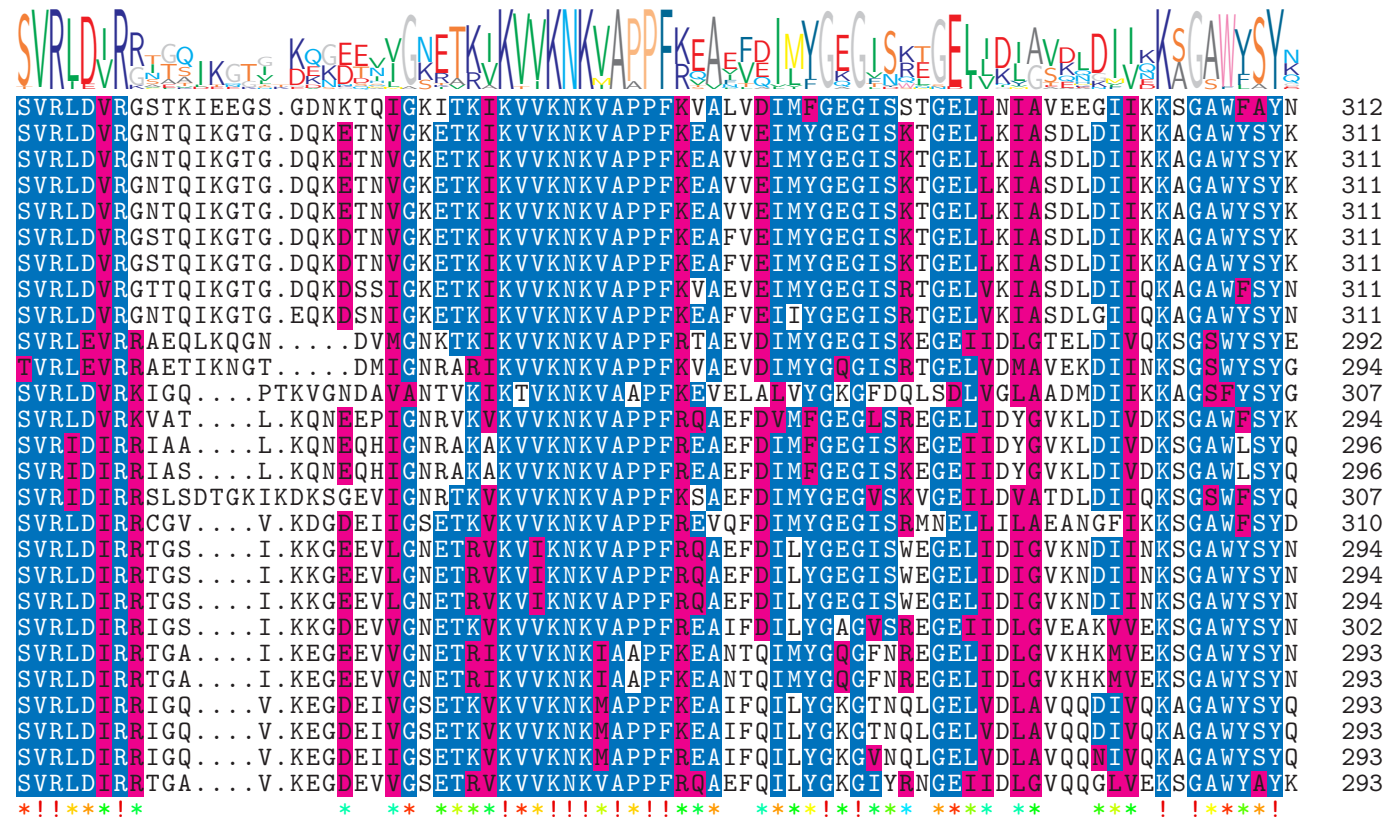
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consensus

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Sequence	Score
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DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTE.NKKDE.....PKKEEA..VNEEVPLDLGDEL	382
DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTE.NKKDE.....PKKEEA..VNEEVPLDLGDEL	382
DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTE.NKKDE.....PKKEEA..VNEEVPLDLGDEL	382
DEKIGQGS ENAKKYLAADNPVFAEIDHQVRVQFGLIDGEEAAE.....SKKDE.....VAQVDS..VNEEVPLDLGDEL	378
DEKIGQGS ENAKKYLAADNPVFEIDHQVRVQFGLIDGEEIAE.....SKKDE.....AAQVDS..VNEEVPLDLGDEL	378
GEKIGQGS ENAKRYLADHPQLFDEIDRKVRVKFGLLEESEEESAMAV.ASE.....E.....TDDLALDLNGI	374
GEKIGQGS ENAKKFLADNPVFEIDHKVVRVQGLIEEDNTEEKQSS.KEK.....ETDEK..ADKNLVLELDDTI	379
EERLGQGR ENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAAE.TQEEL.E..FE.E.....	348
SERIGQGR ENAKNYLADHEDVEDEVRLKVRAAAYGISDVPEEDLPSTE.DE.QI.N..ILPDDST.....EE.....	355
DERIGQG EKTITAYIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAPEAAEA	363
DKKLGGGR ENSKAFLKENPEIADEITKAIQNSMGI EGMISGS..EDDEGE..E.....	343
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DKKLGGGR ENAKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
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GAKIGQGDKNVRVWLKENPEISDEIDAKIRALNGVEMHITEG..TQDET.....GERPE.....E.....	348
GERIGQGRDNCREFLRENAELAREIENKVRHGLVTPMGAV..TLAEEVEED.....	352
GDKIGQG KANACKYLKENPEIAKTLDKKLREMLLNPNMQLI..AETSSAADVFEFGAVPE.....EF.....	354
GDKIGQG KANACKYLKENPEIAKTLDKKLREMLLNPNMQLI..AETSSAADVFEFGAVPE.....EF.....	354
GNKIGQG KNNVIRYFEENTQIAEEIERNIREQLLTGTNGAV..Q.I.EDEEPPD..LLE.....S.....	349
GNKIGQG KNNVIRYFEENNQIAEEIERNIREQLLTGTNGAV..Q.I.EDEEPPD..LLE.....S.....	349
GNKIGQG KNNVIRYLEENPQISTEIEAVIREQLLTKASDQTA..A.HDETEEPPD..LLES.....	349
GSKIGQG KANAAYLEENPEIQEIEQQIRAKLLVTSANTKA..TPVAEDLADAD..I.....	347

logo

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consensus								

-  non conserved
-  similar
-  ≥ 50% conserved