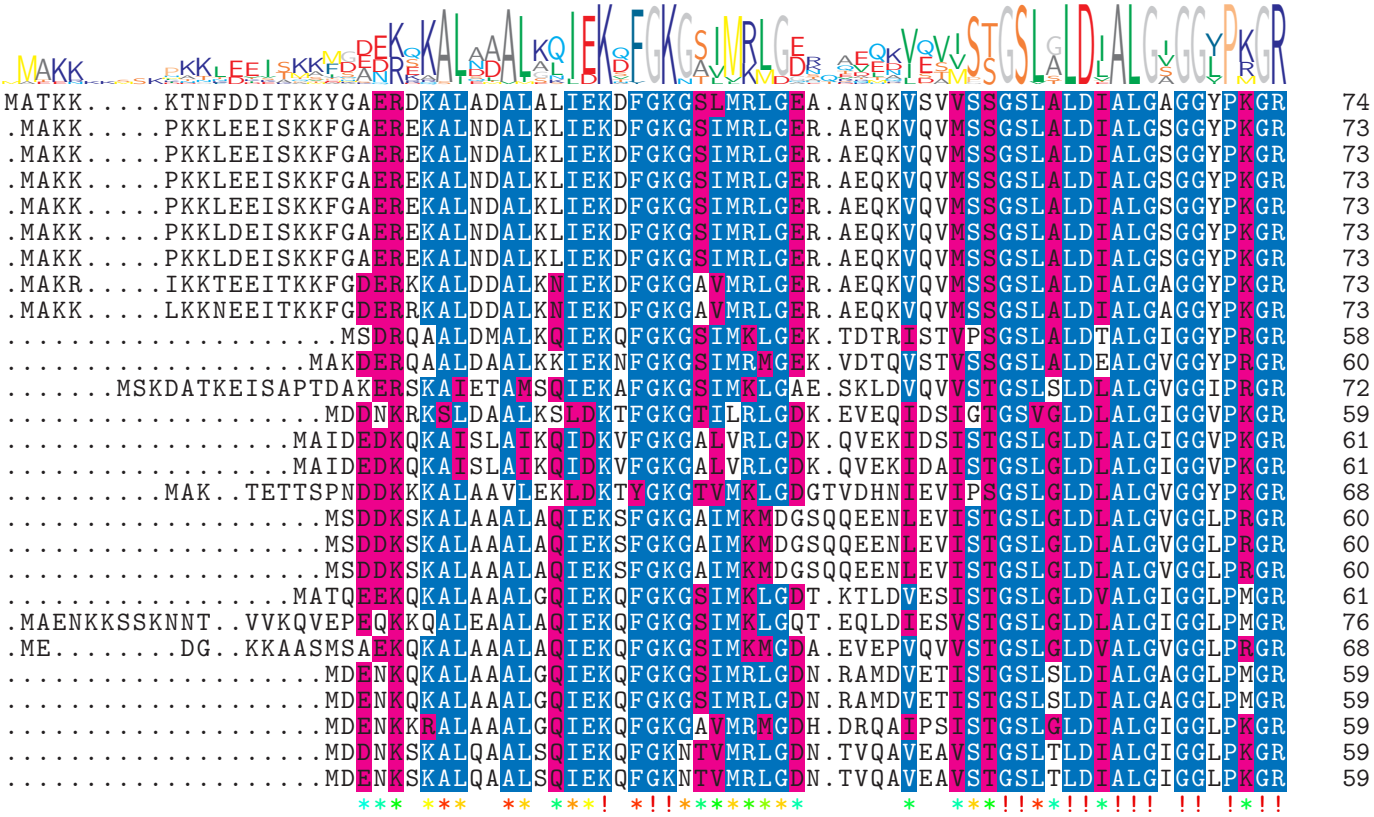


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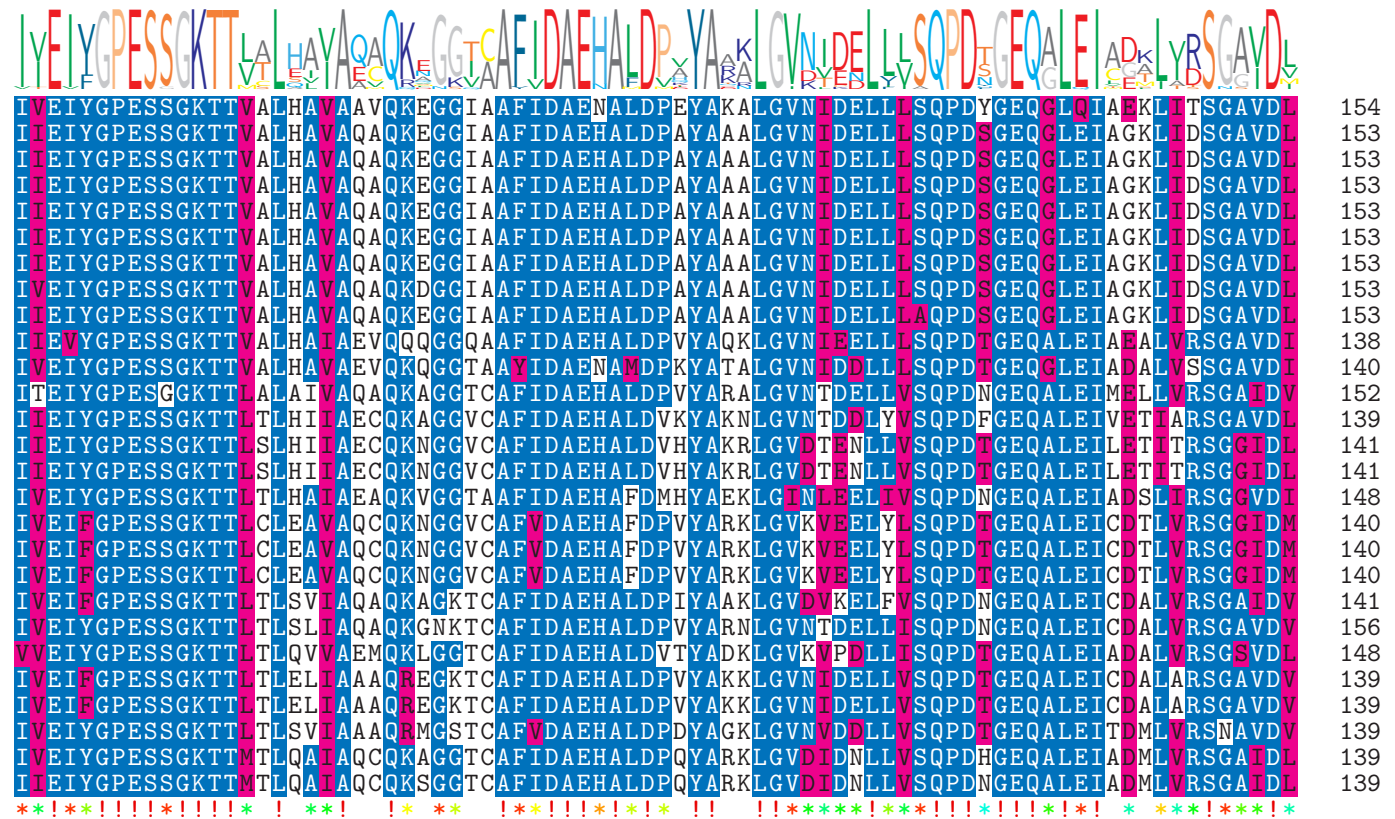
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consensus



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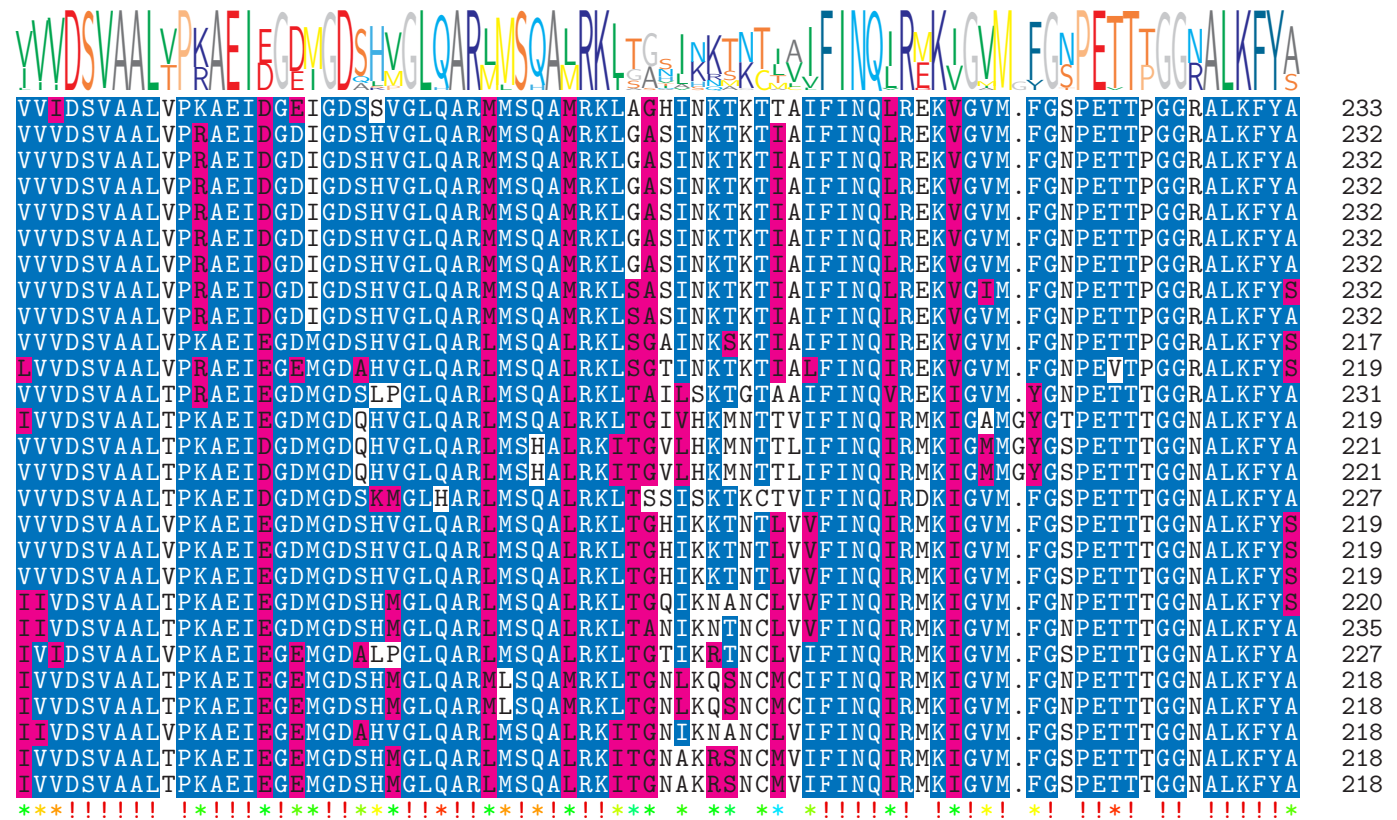
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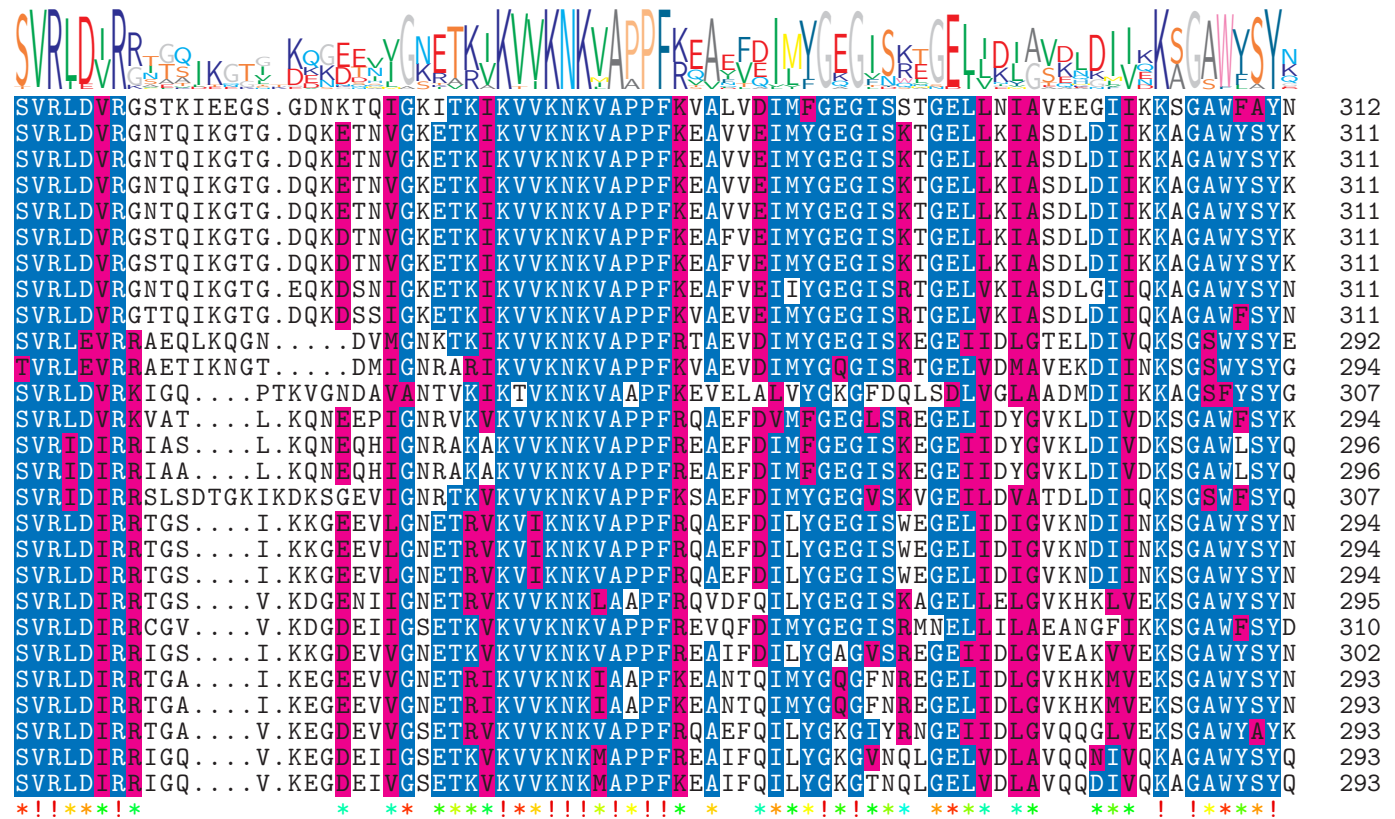
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consensus

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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQD.TENKKDE....PKKEEA..VNEEVPLDLGDELEI	384
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQD.TENKKDE....PKKEEA..VNEEVPLDLGDELEI	384
DEKIGQGSENAKKYLAHNPEIFDEIDHQRVVFGLIDGEEIAES....KKDE....AAQVDS..VNEEVPLDLGDELEI	380
DEKIGQGSENAKKYLAHNPEVFAEIDHQRVVFGLIDGEEIAES....KKDE....VAQVDS..VNEEVPLDLGDELEI	380
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQGLIEEDNTEEEKQ.SSKEK.....ETDEK..ADKNLVLELDDTIEL	381
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAM.AVASE.....E.....TDDLALDLNGIEI	376
EERLGGGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQQA.EETQEEL.EFE.E.....	348
SERIGGGRENAKNYLADHEDVEDEVRLKVRVQGLSDVPEEDLPT.TEDE.QI.NILPDDST.....EE.....	355
DERIGGQKEKTIAYTIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAPEAAEA.....	363
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DKKLGGGRENKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DKKLGGGRENKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DTKLGGGRDTPVKELIKDNPELAEELEAKIREKLQAK.....	343
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEG..T...QD..ETDGE.RPEE.....	348
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEG..T...QD..ETDGE.RPEE.....	348
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEG..T...QD..ETDGE.RPEE.....	348
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GNKIGGQKNNVIRYLEENPQISTEIEAVIREQLLTKASDQTA..A.HDETEEEPDLL..ES.....	349
GNKIGGQKNNVIRIYFENNQIAEIERNIREQLLTTGTNGAV..Q.I.EDEEEPDLL..LE.....S.....	349

logo

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consensus					

-  non conserved
-  similar
-  ≥ 50% conserved