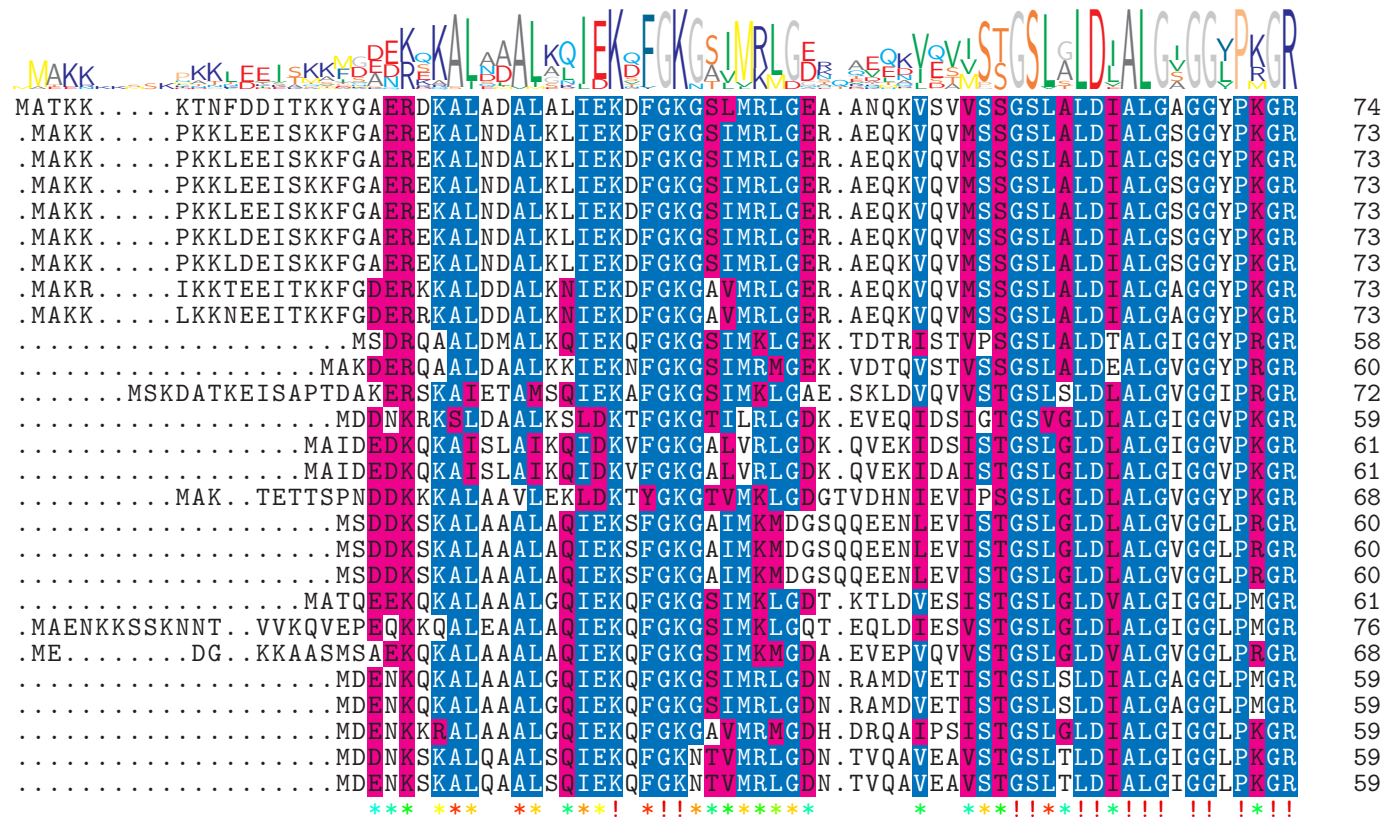


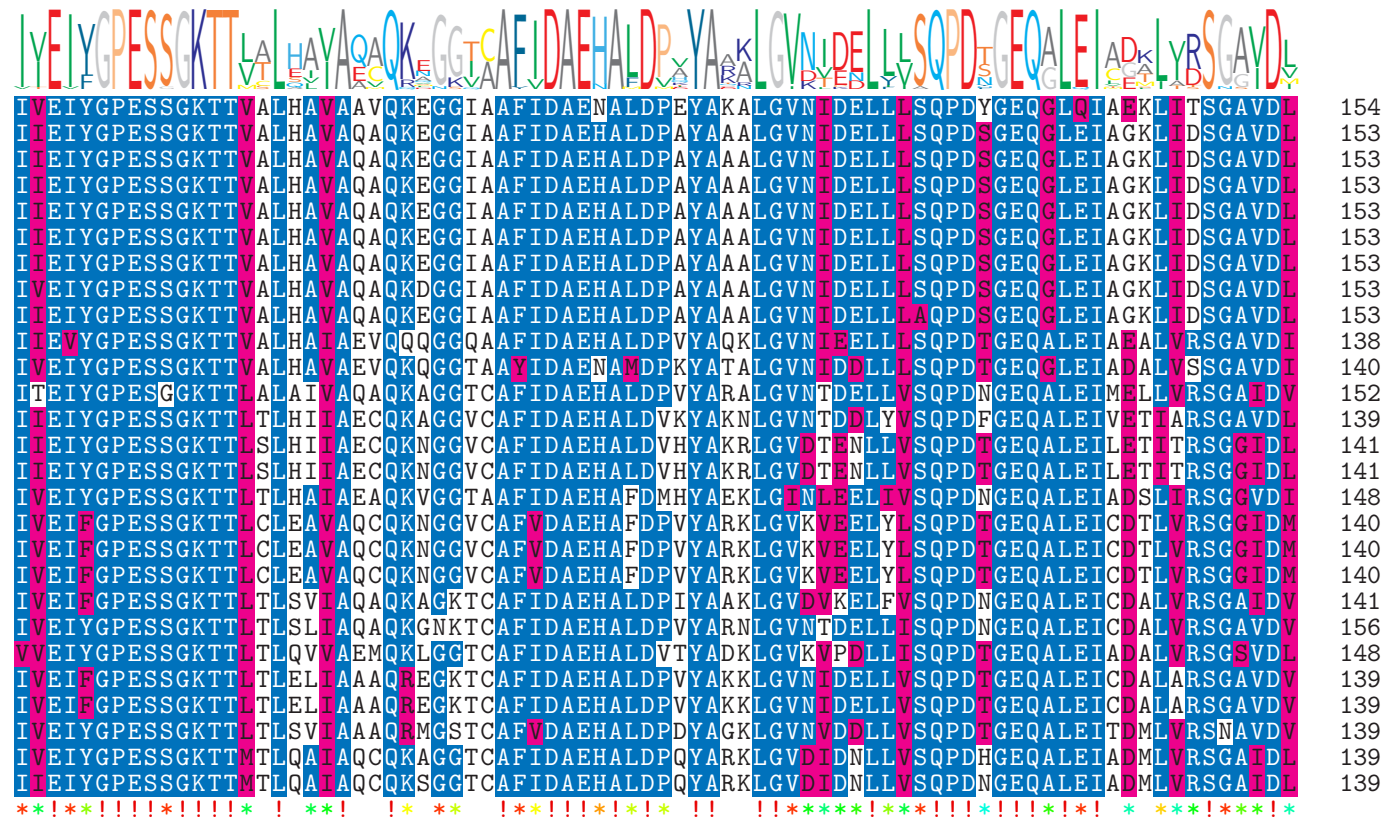
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consensus

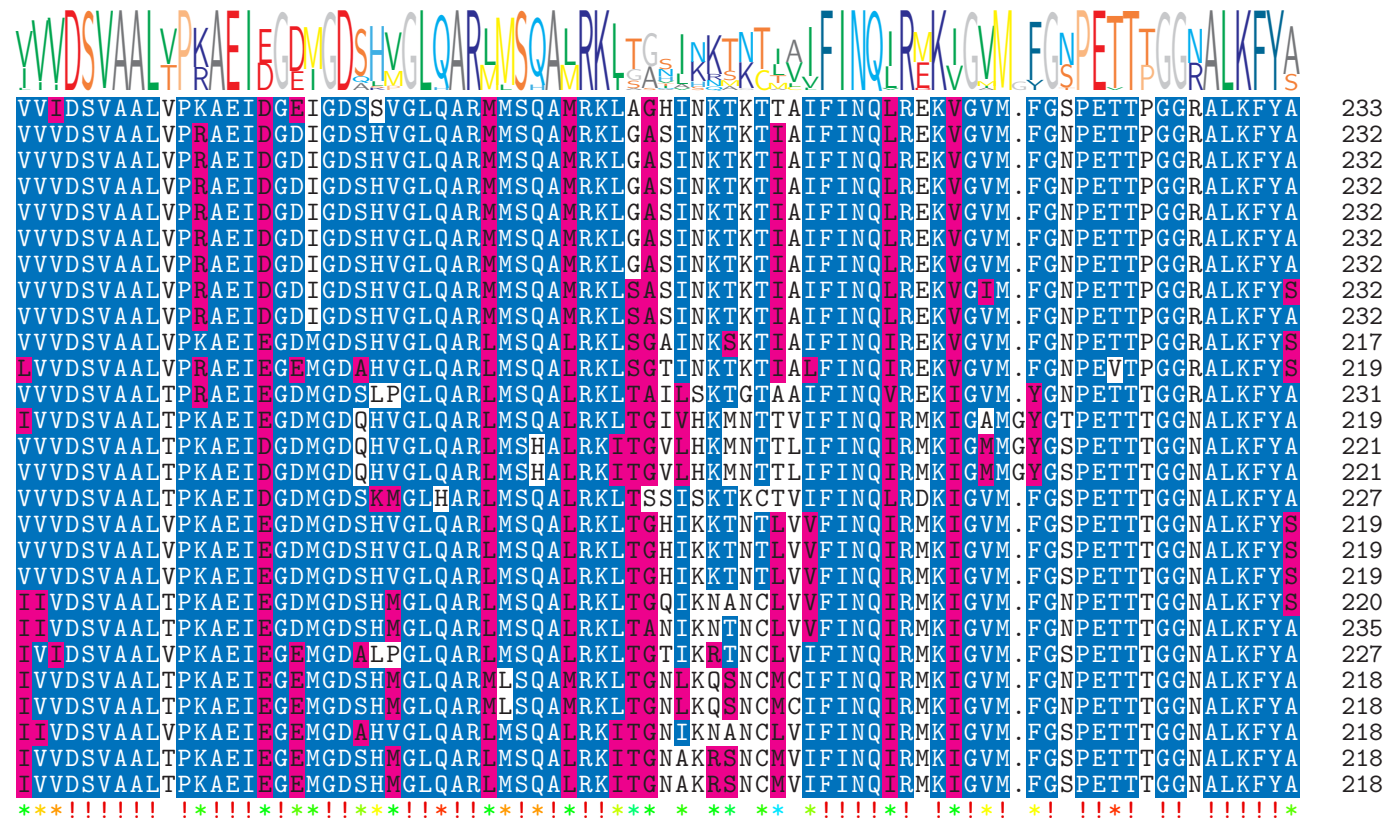
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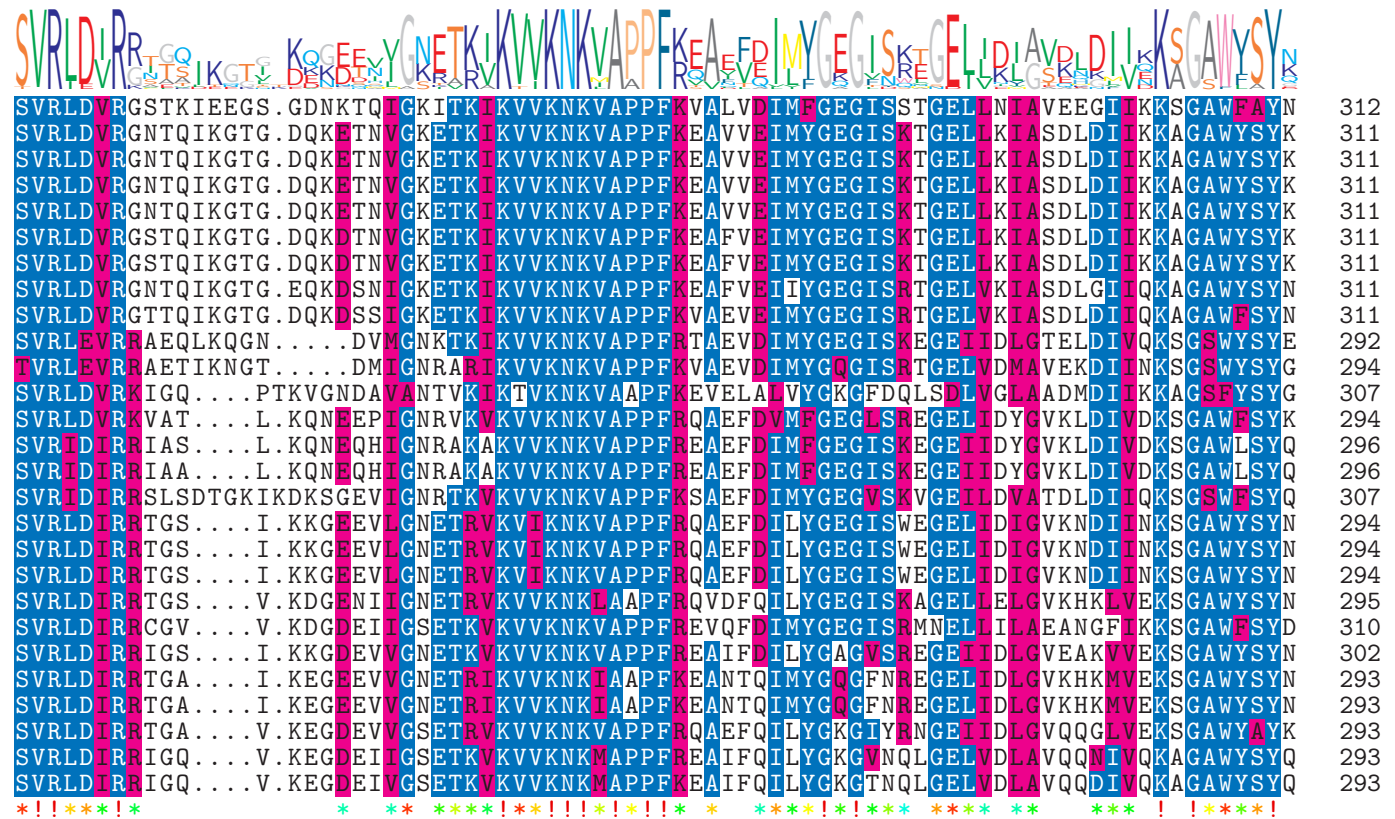
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consensus

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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
DKKLGGGRENKAFLENKEPEIADEITKAIQNSMGIEGMISGS..EDDEGE..E.....	343
DKKLGGGRENKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DKKLGGGRENKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DTKLGGGRDVTVKELIKDNPELAEELEAKIREKLQAK.....	343
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GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEG..T...QD..ETDGE.RPEE.....	348
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GTKIGGQKNNVAVKWLKENPEIADKLEQEIRNTLASNPNSVLK..ATASDSNDESDVE.EFSE.....EEL.....	372
GERIGGQKDNCRFLRENAELARIEENKVRHLGVTPMGAV..TLAEVEED.....	352
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GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPNENMQLI..AETSSAADDVEFGAVPE.....EF.....	354
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GNKIGGQKNNVIRYLEENPQISTEIEAVIREQLLTKASDQTA..A.HDETEEEPDLL..ES.....	349
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logo

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consensus		

-  non conserved
-  similar
-  ≥ 50% conserved