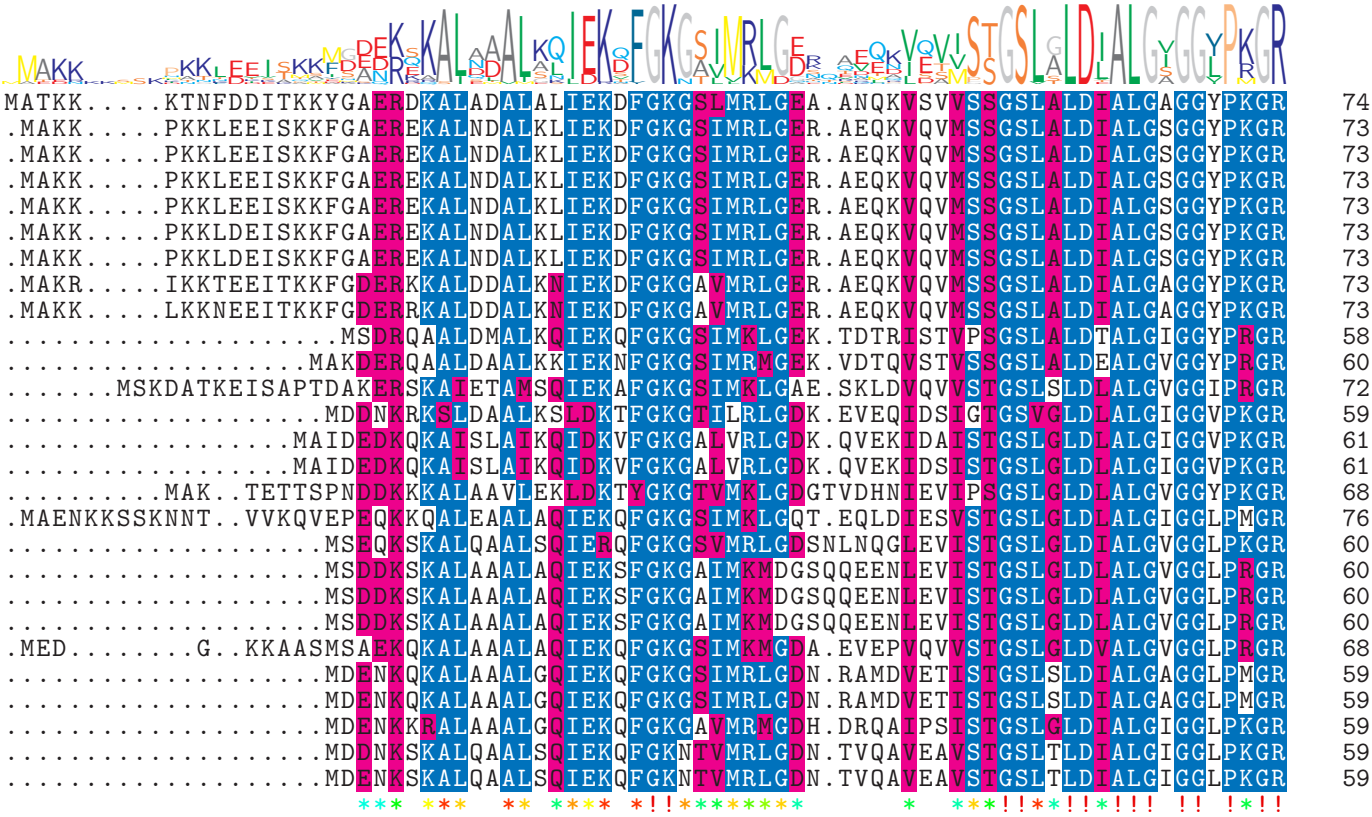


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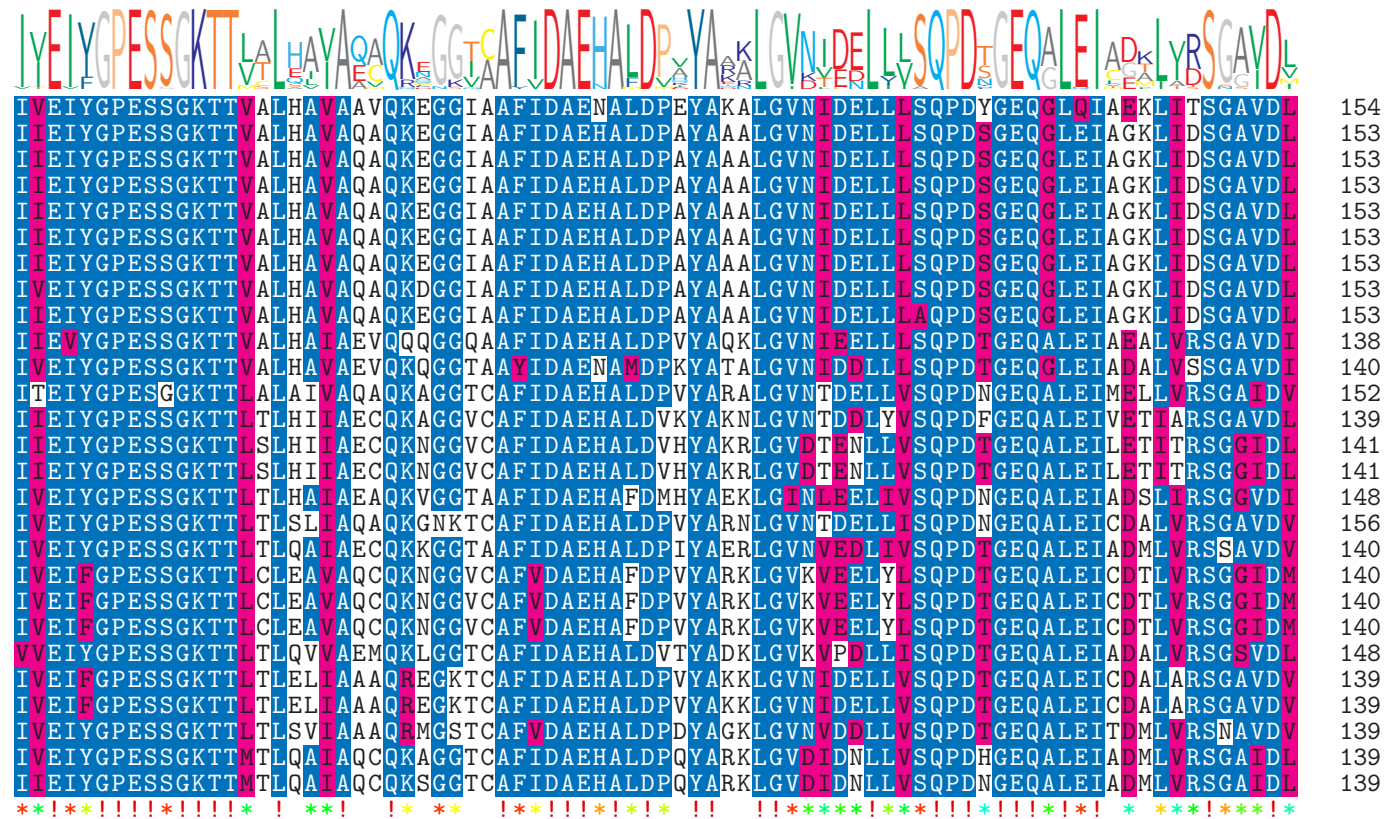
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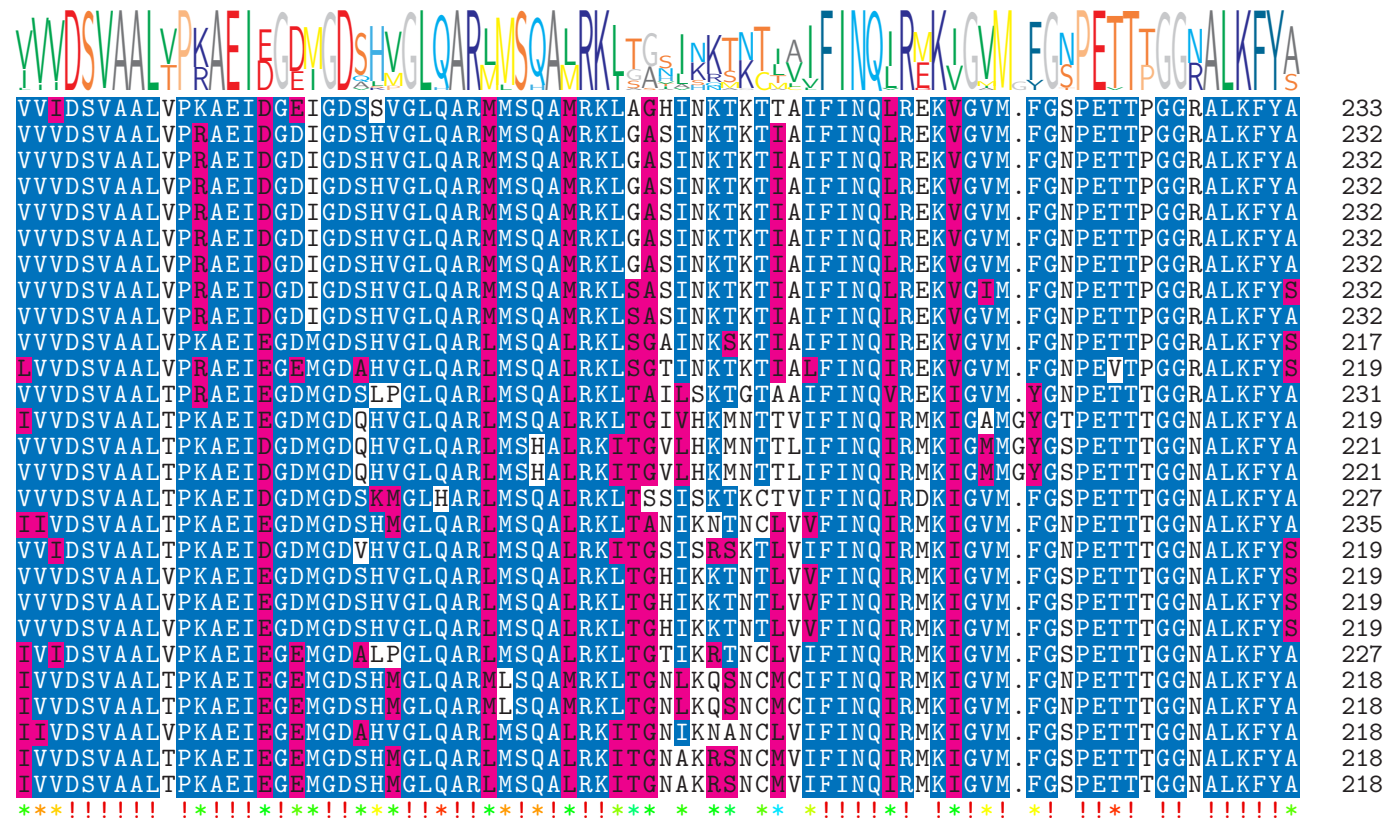
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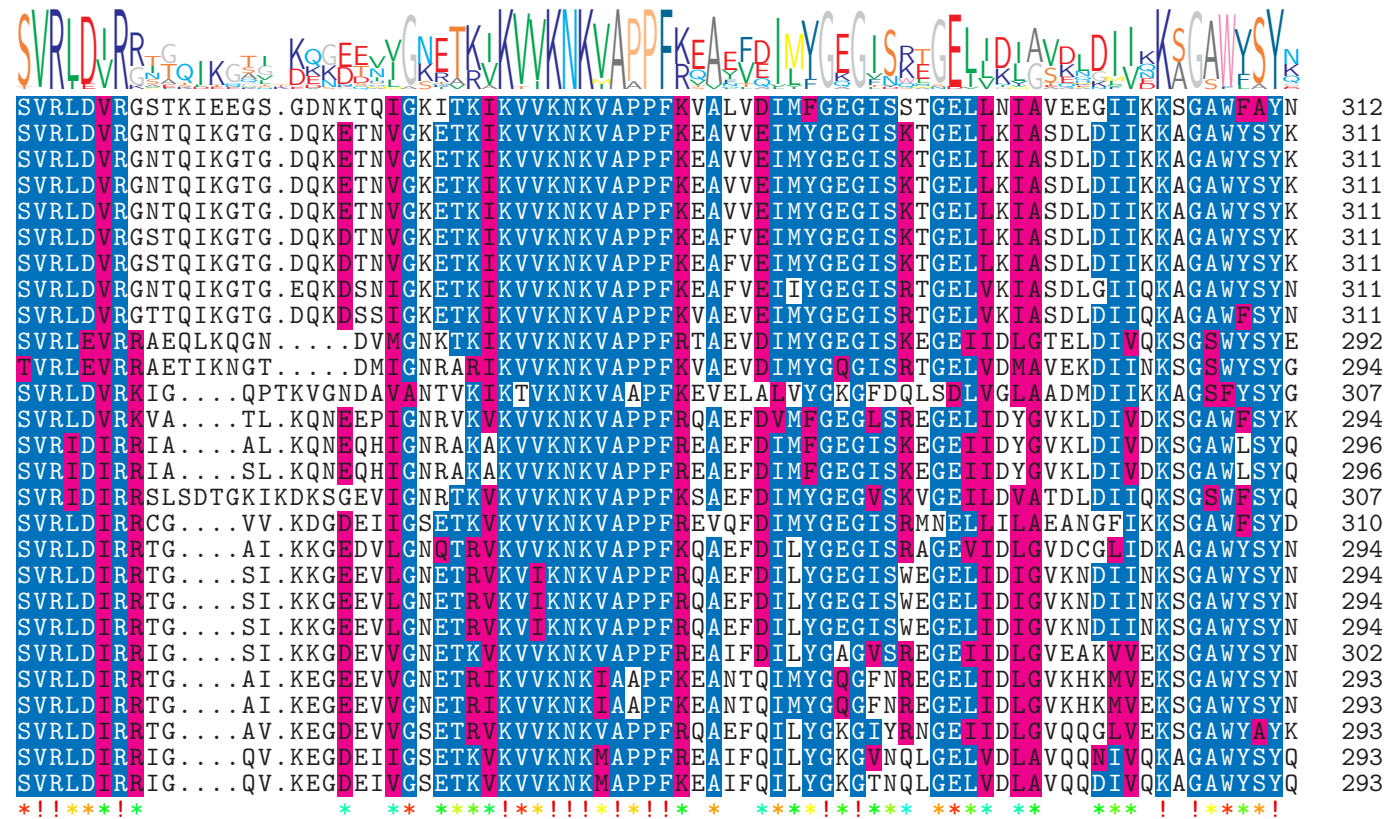
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consensus

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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENK.KDE...PKKEEA..VNEEVPLDLGDELEI	384
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GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEEEESAMAVAS.E.....E.....TDDLALDLNGIEI	376
EERLGQGRENAKQFLKENKDIMLMIQEQIREHYGLDNGGVVQQAEETQ.EEL.EFE.E.....	348
SERIGQGRENAKNYLADHEDVEDEVRLKVRAAAYGISDVPEEDLPTTEDE..QI.NILPDDST....EE.....	355
DERIGQGEKTIATYIAERPMEQETIDRVMAAIRAGNAGEAPALAPAPAAPAAEA.....	363
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DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPL..EEME.....	347
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GTKIGQKKNNAVKWLKENPEIAADKLEQIRNTLASNPNSVLK..ATASDSNDESVDVEEF.....SEEL.....	372
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logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved