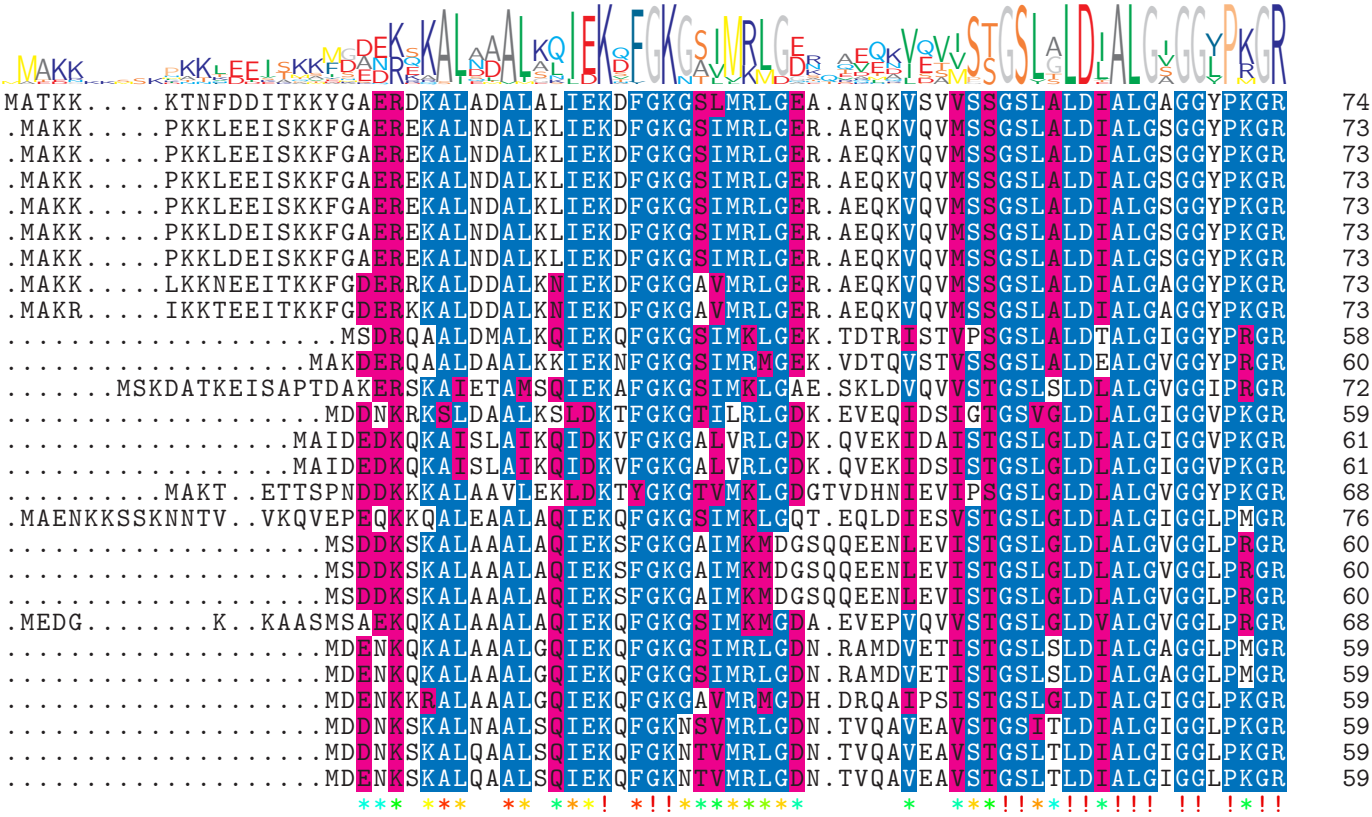


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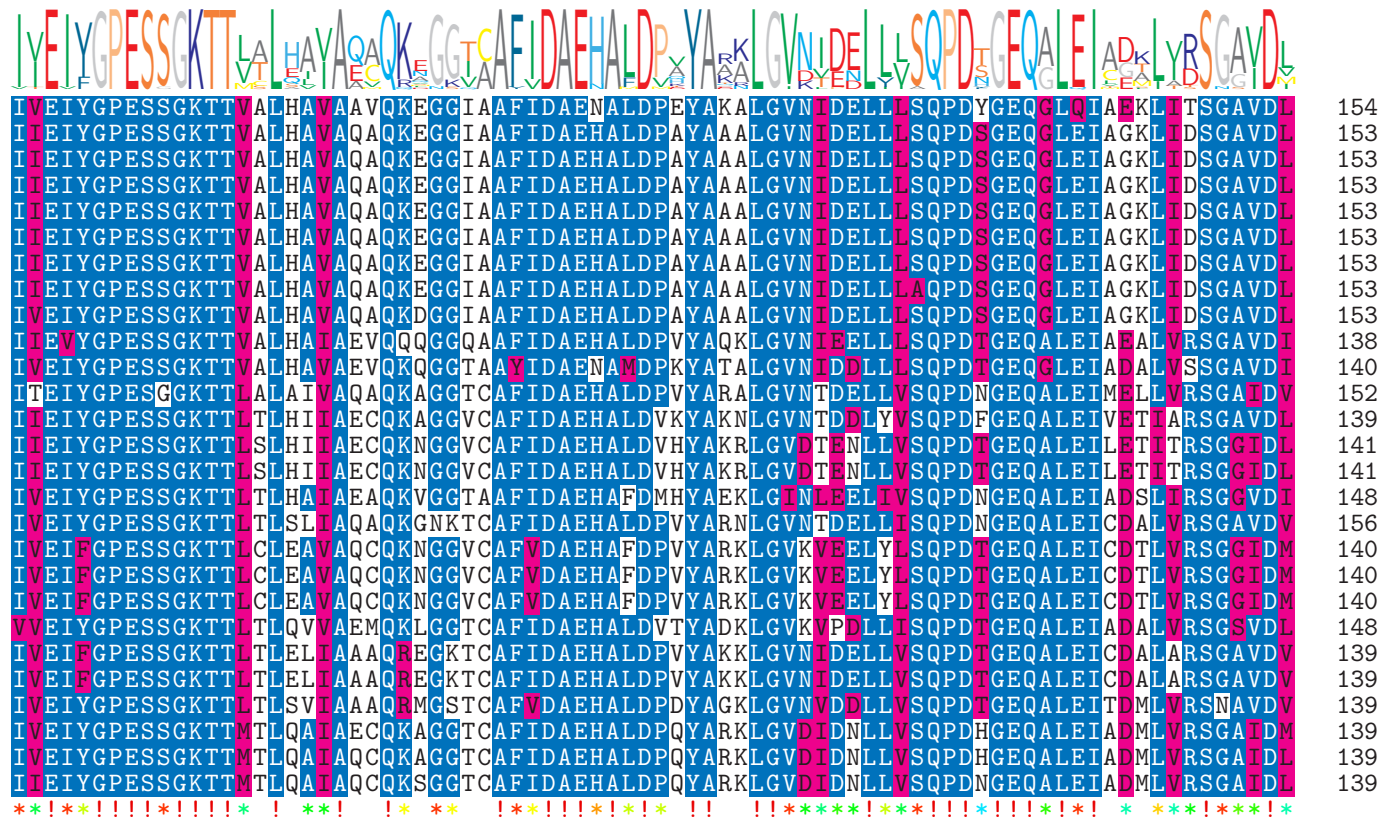
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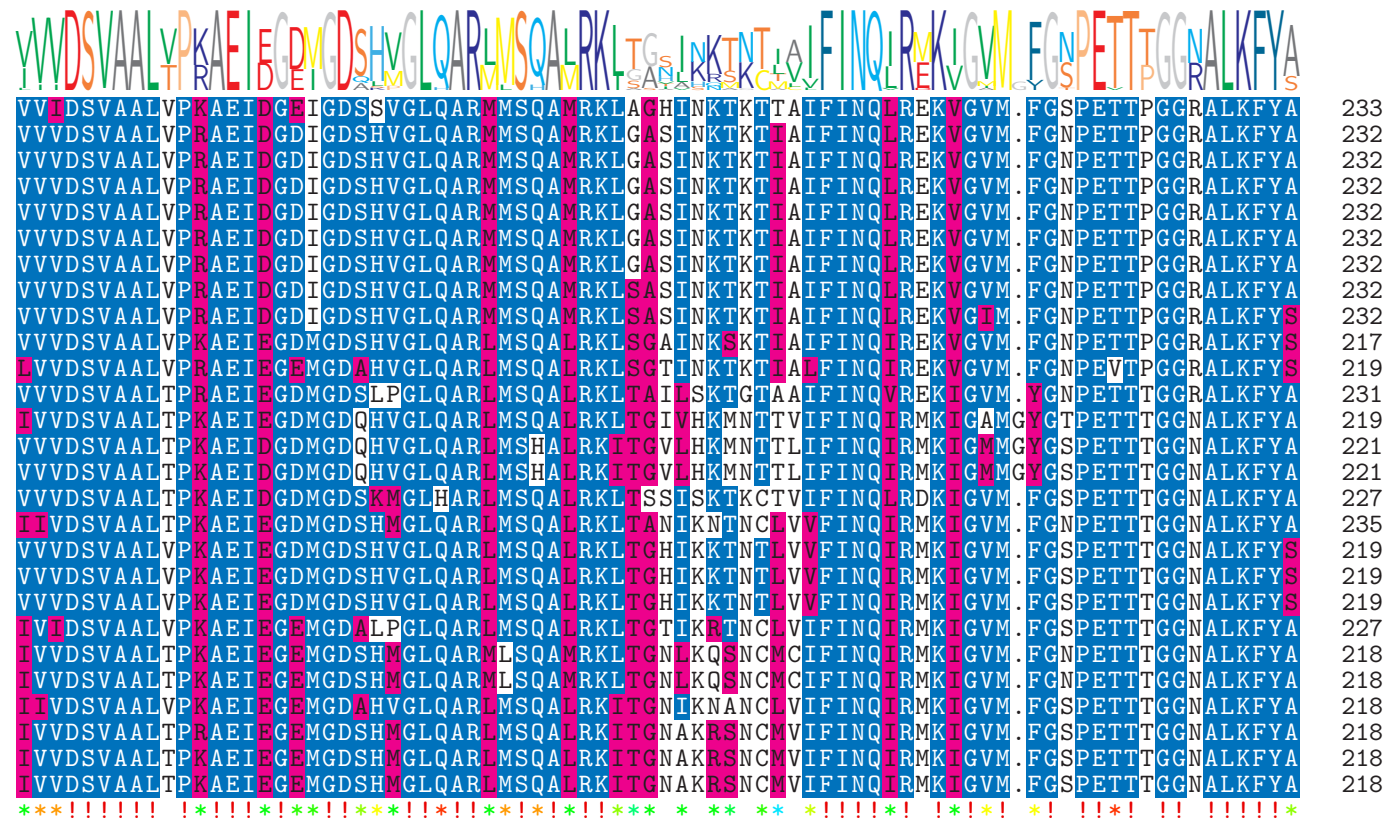
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consensus

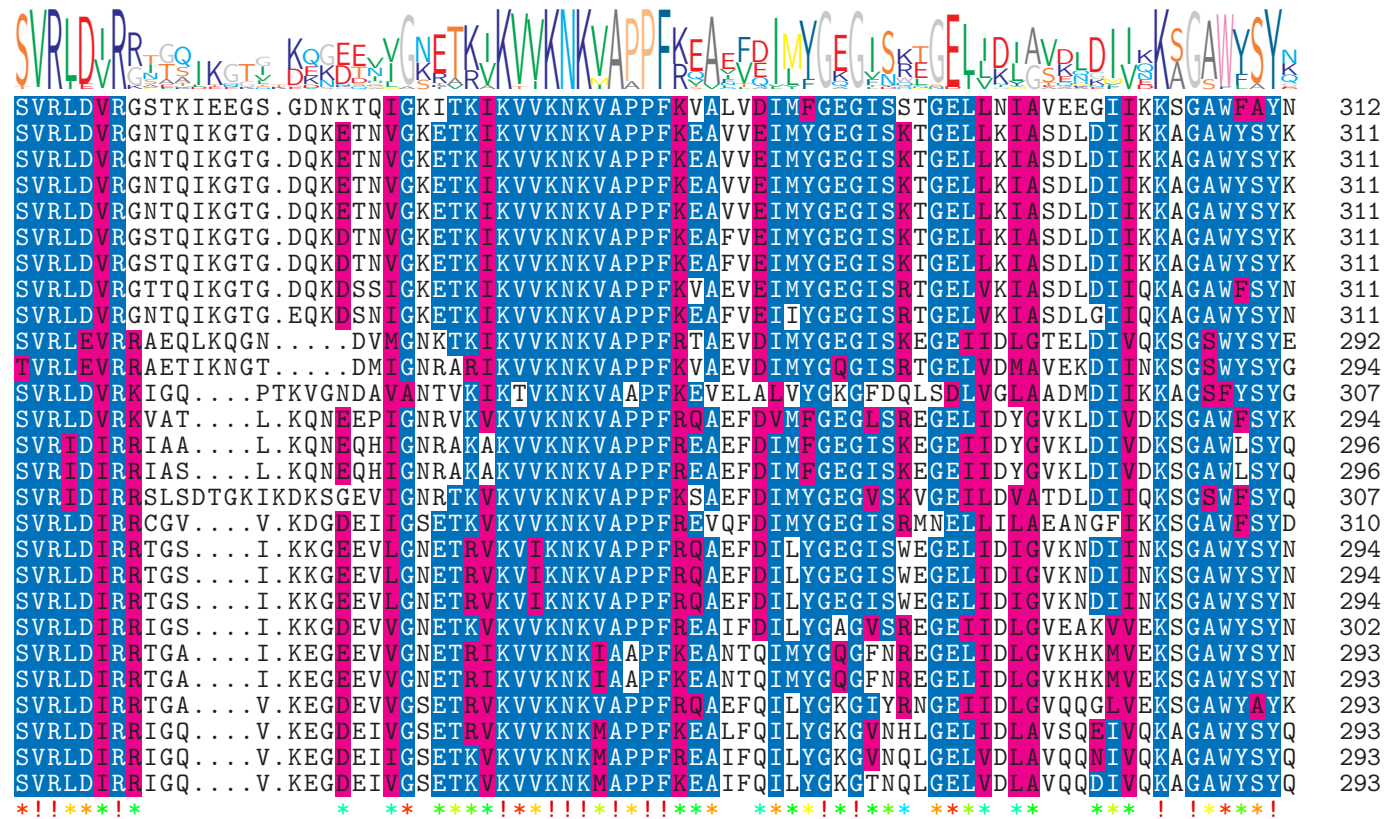
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consensus

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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENK...KDE...PKKEEA..VNEEVPLDLGDE	381
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DEKIGQGSENAKKYLAHNPEVFAEIDHQVRVQFGLIDGEEAAE...SK...KDE...VAQVDS..VNEEVTLDLGD	377
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GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEEEESAMAVAS...E...E...TDDLALDLNG	373
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKE...K...ETDEK..ADKNLVLELDDT	378
EERLGGGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEETQ...EEL.EFE.E...	348
SERIGGGRENAKNYLADHEDVEDEVRLKVRAAAYGISDVPPEEDLPTTEDE...QI.NILPDDST...EE...	355
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logo

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consensus		

-  non conserved
-  similar
-  ≥ 50% conserved