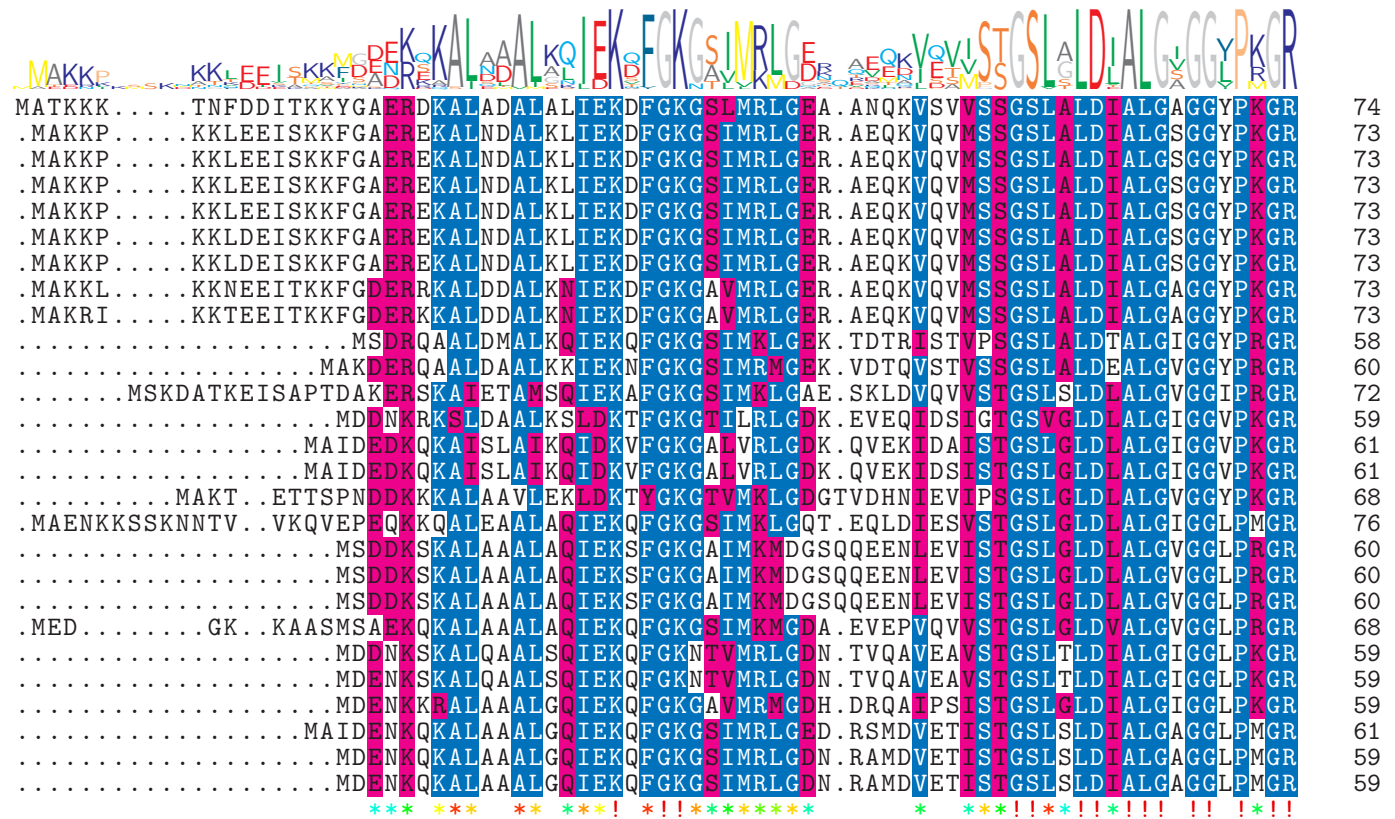


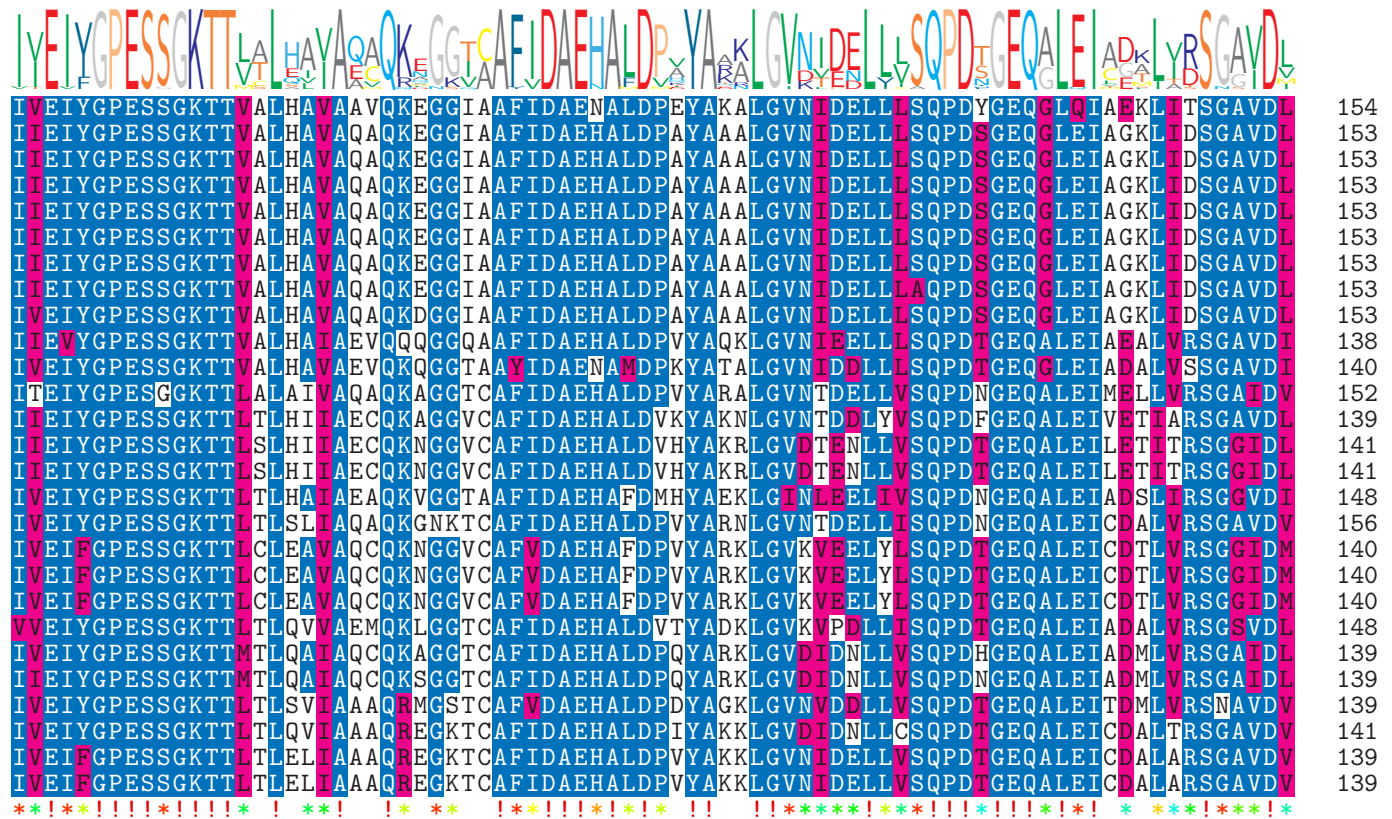
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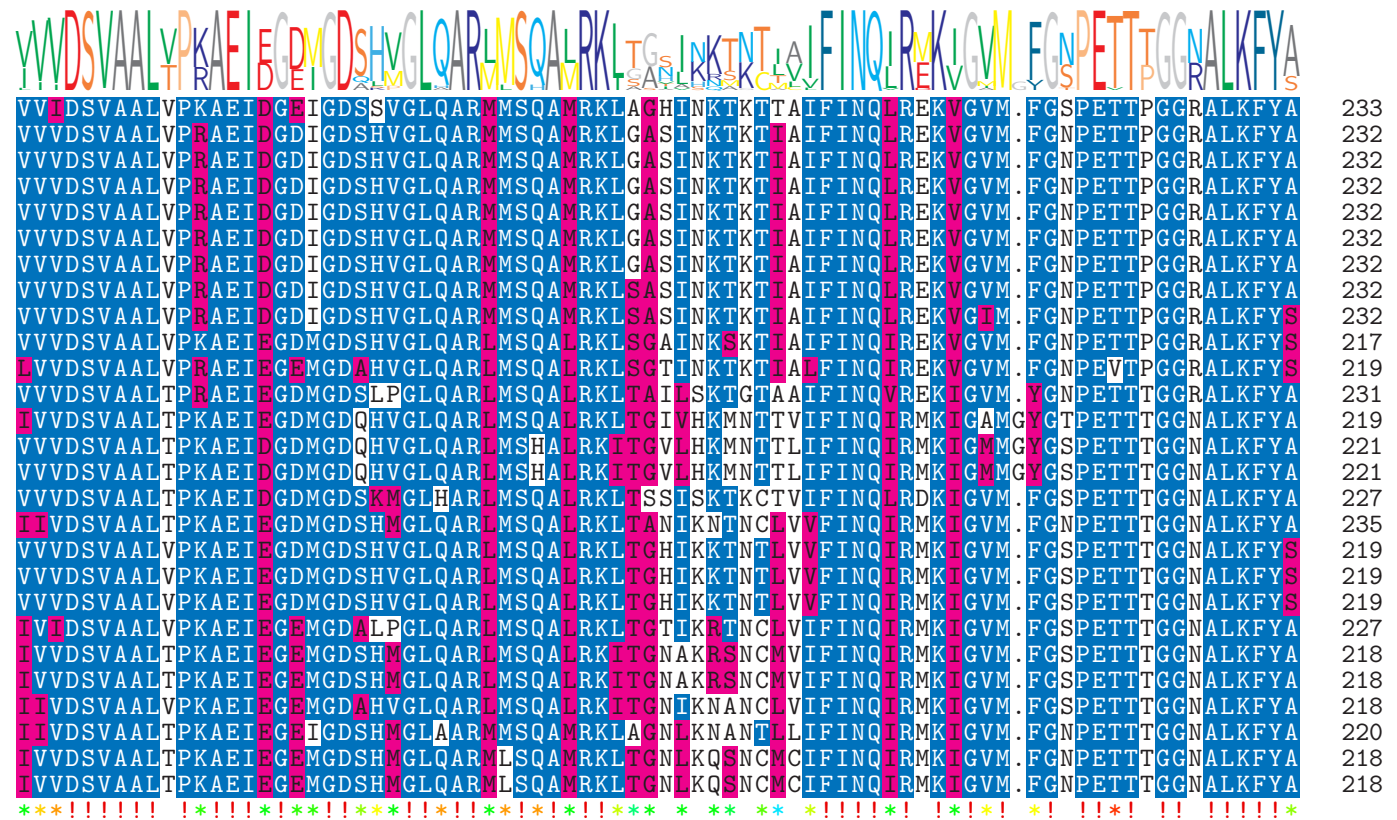
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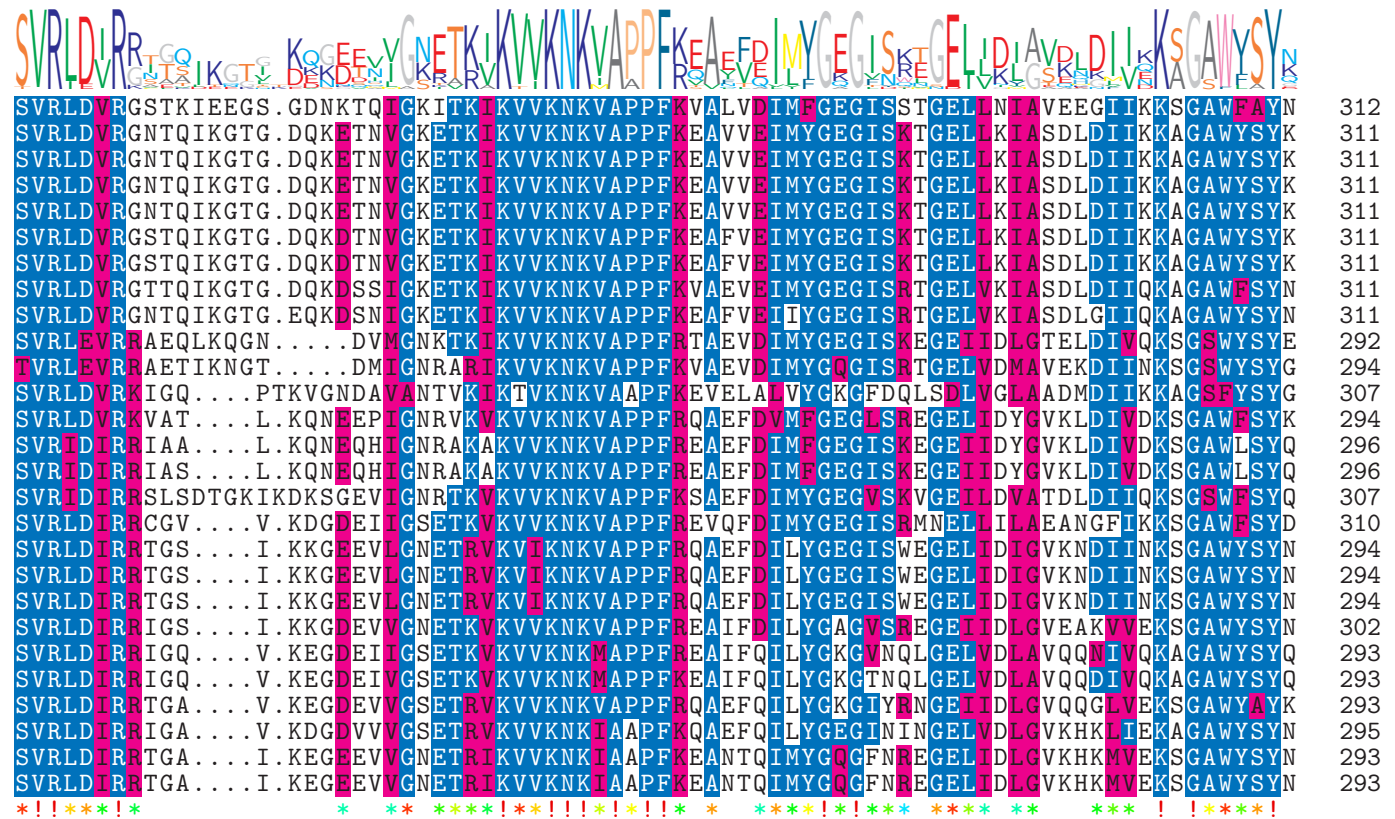
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consensus

Sequence	Score
DEKIGQGA EKAKNYLKEHQDVFEIDHKKVRAAHGLDDSEVAETEEETTASKTAKAKKKEEKAVETEEIELELED	387
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DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAADNPVFAEIDHQVRVQFGLIDGEEAAE . . . SKKDE . . . VAQVDS . VNEEVTLDLGDLEIE	381
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GEKIGQGS ENAKKFLADNPVFEIDHKKVRVQYGLIEEDNTEEKQSSKEK ETDEK . . . ADKNLVLELDDTIELE	382
EERLGQGR ENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEETQEEL . EFE . E	348
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logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved