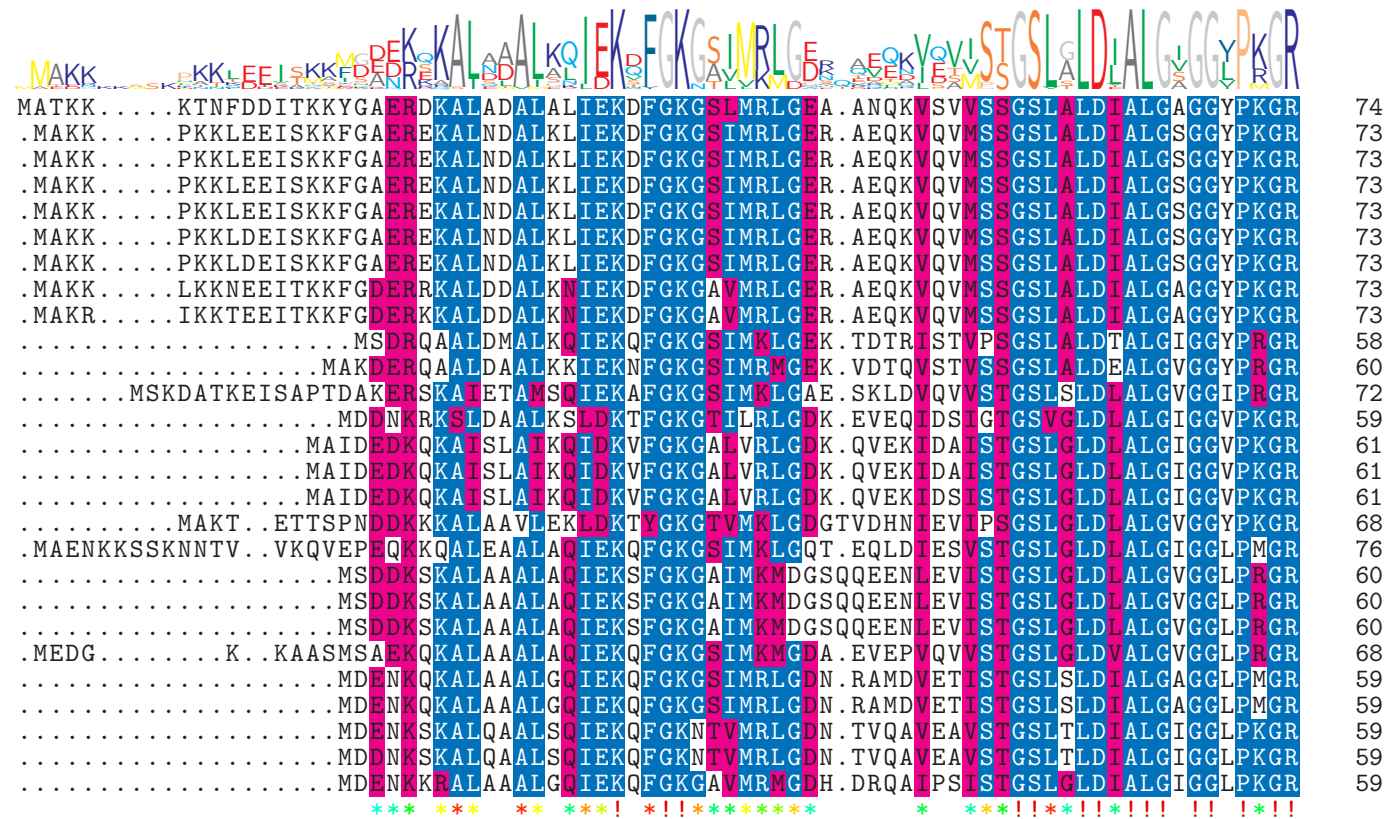


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consensus

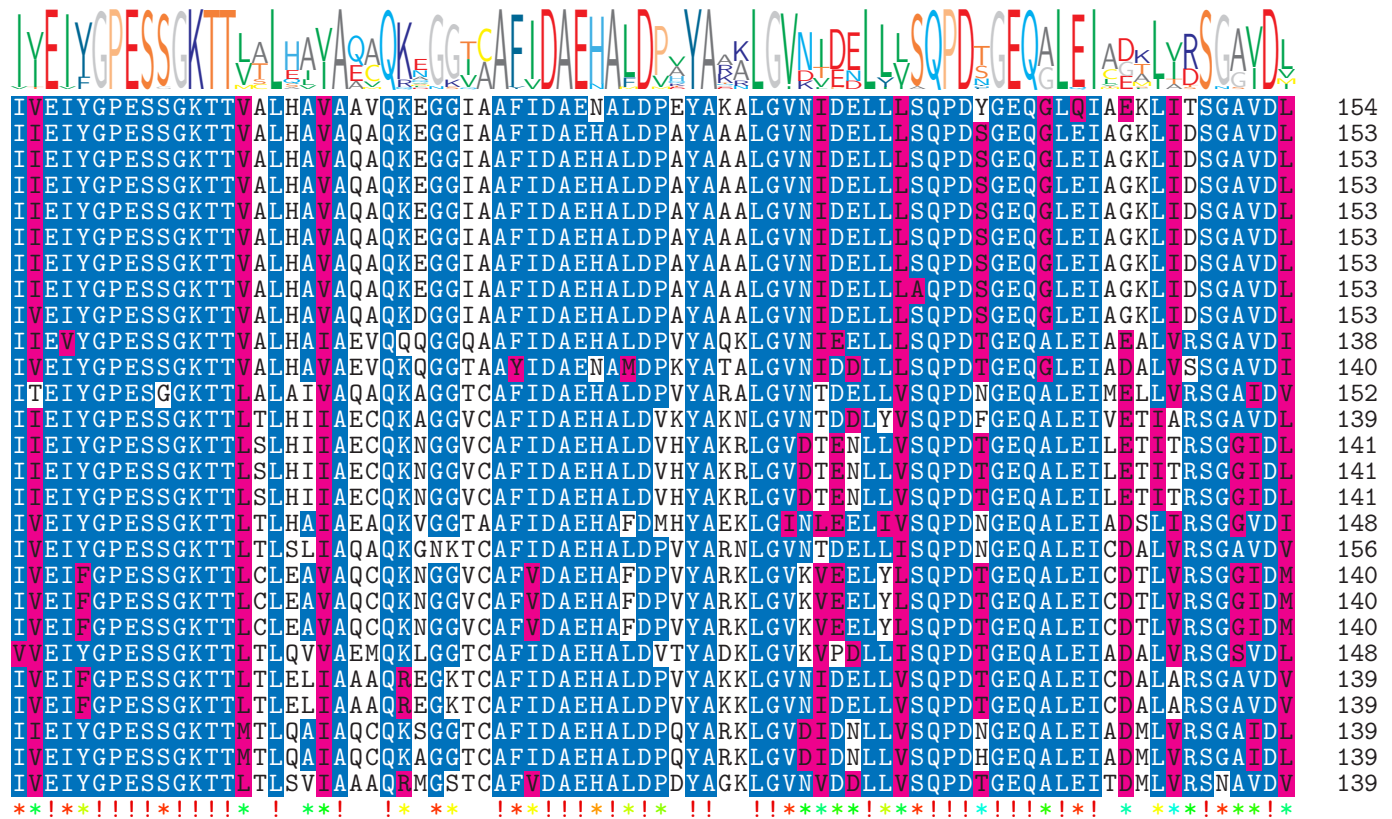
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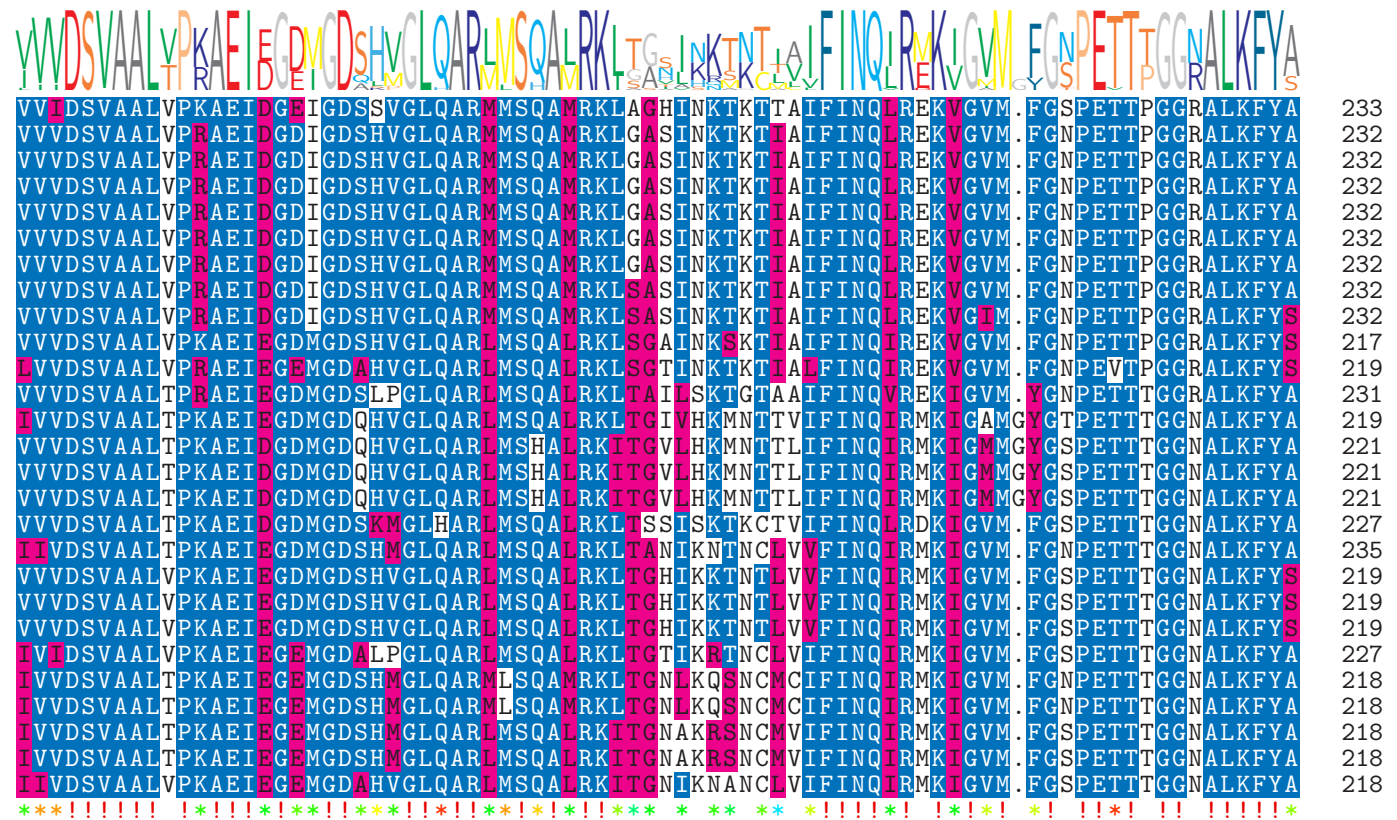
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consensus

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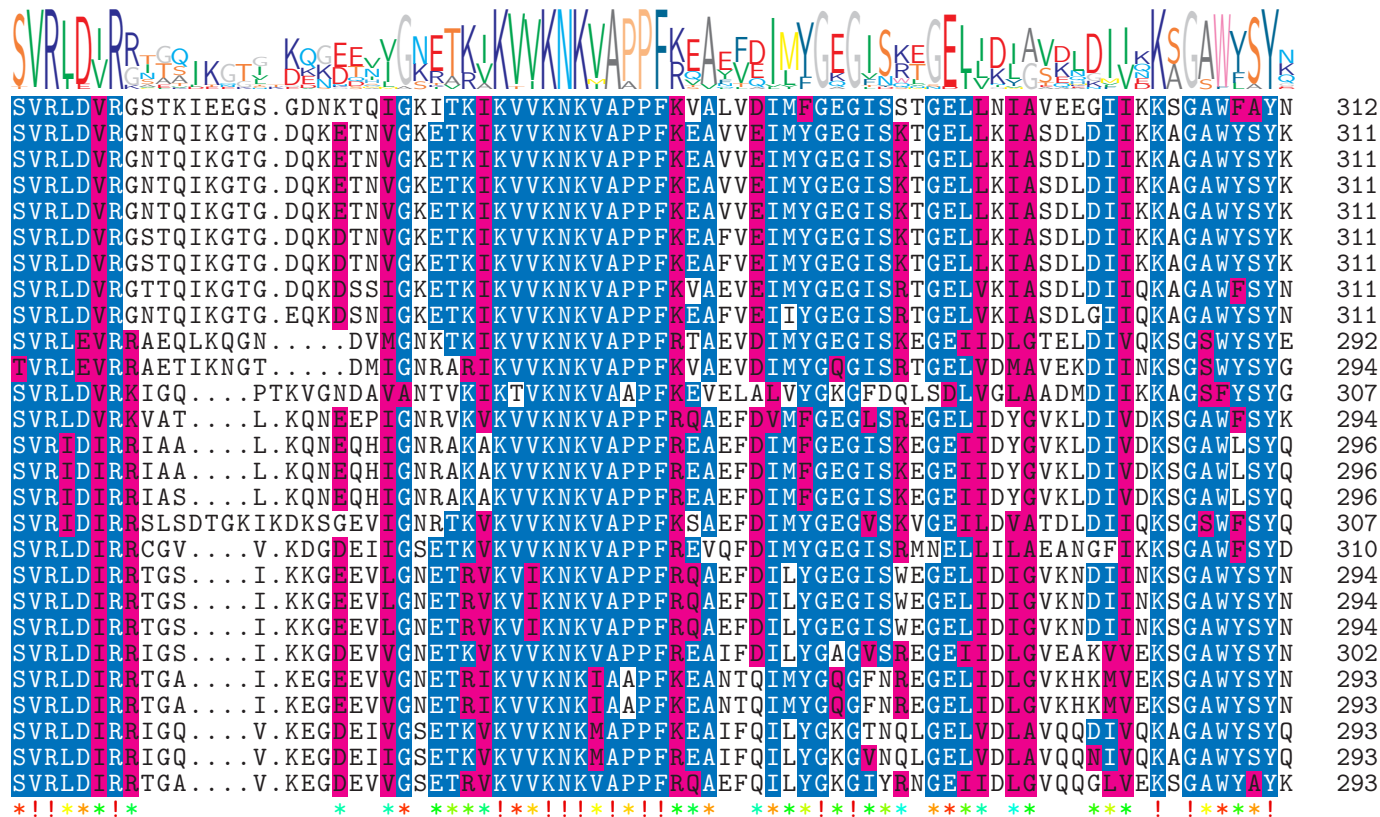
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consensus

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consensus

Sequence	Score
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DEKIGQGSENAKKYLAHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLDADNPEIFDEIDHQRVVFGLIDGEEIAES . . . KKDE . . . AAQVDS . VNEEVTLDLGDLEIE	381
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GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK ETDEK . . . ADKNLVLELDDTIELE	382
EERLGQGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEETQEEL . EFE . E	348
SERIGQGRENAKNYLADHEDVEDEVRLKVRVQYGLSDVPEEDLPTTEDE . QI . NILPDDST EE	355
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logo

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NTDB id 1205 PSJM300 05545 AFN77183.1	...	347	
consensus			

- X non conserved
- X similar
- X ≥ 50% conserved