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consensus

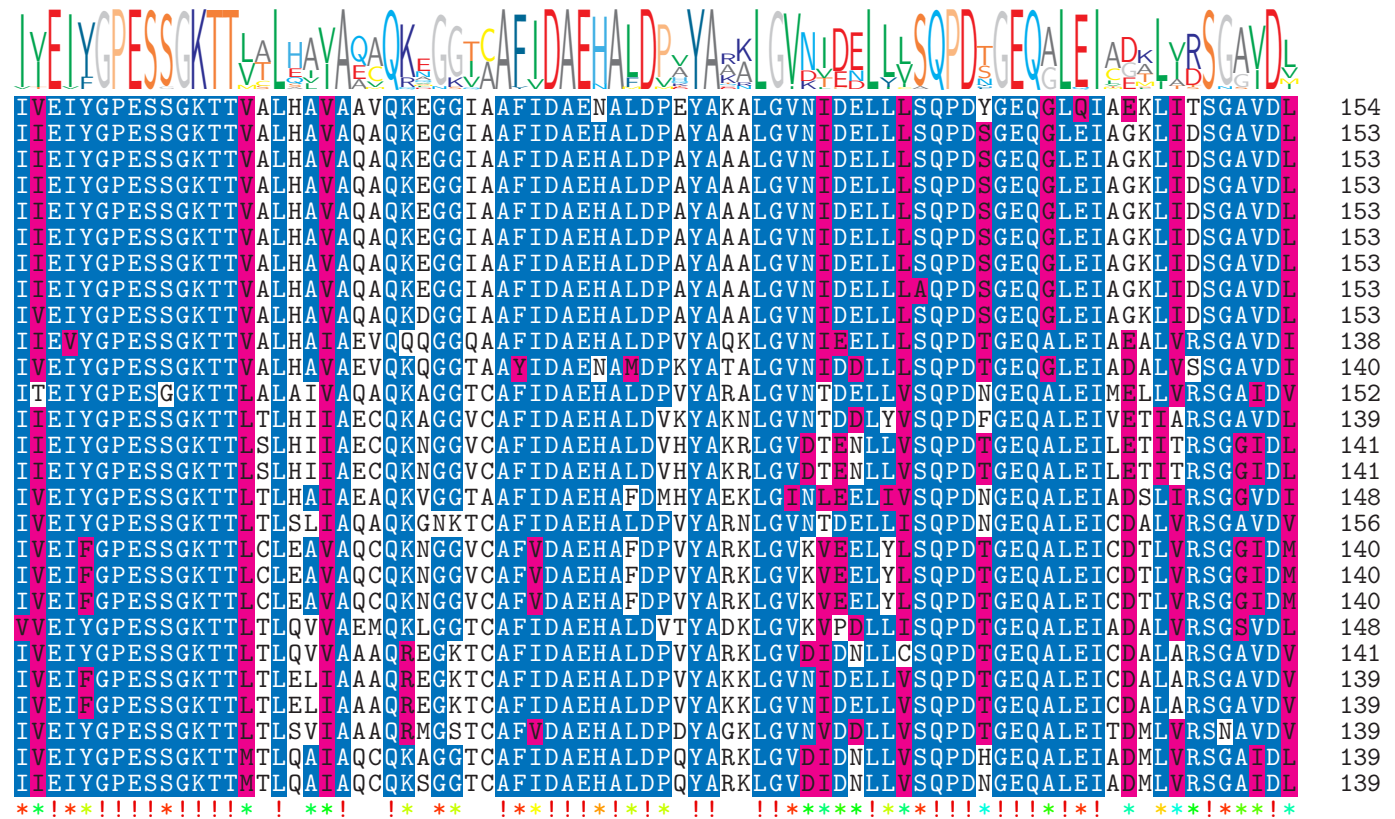
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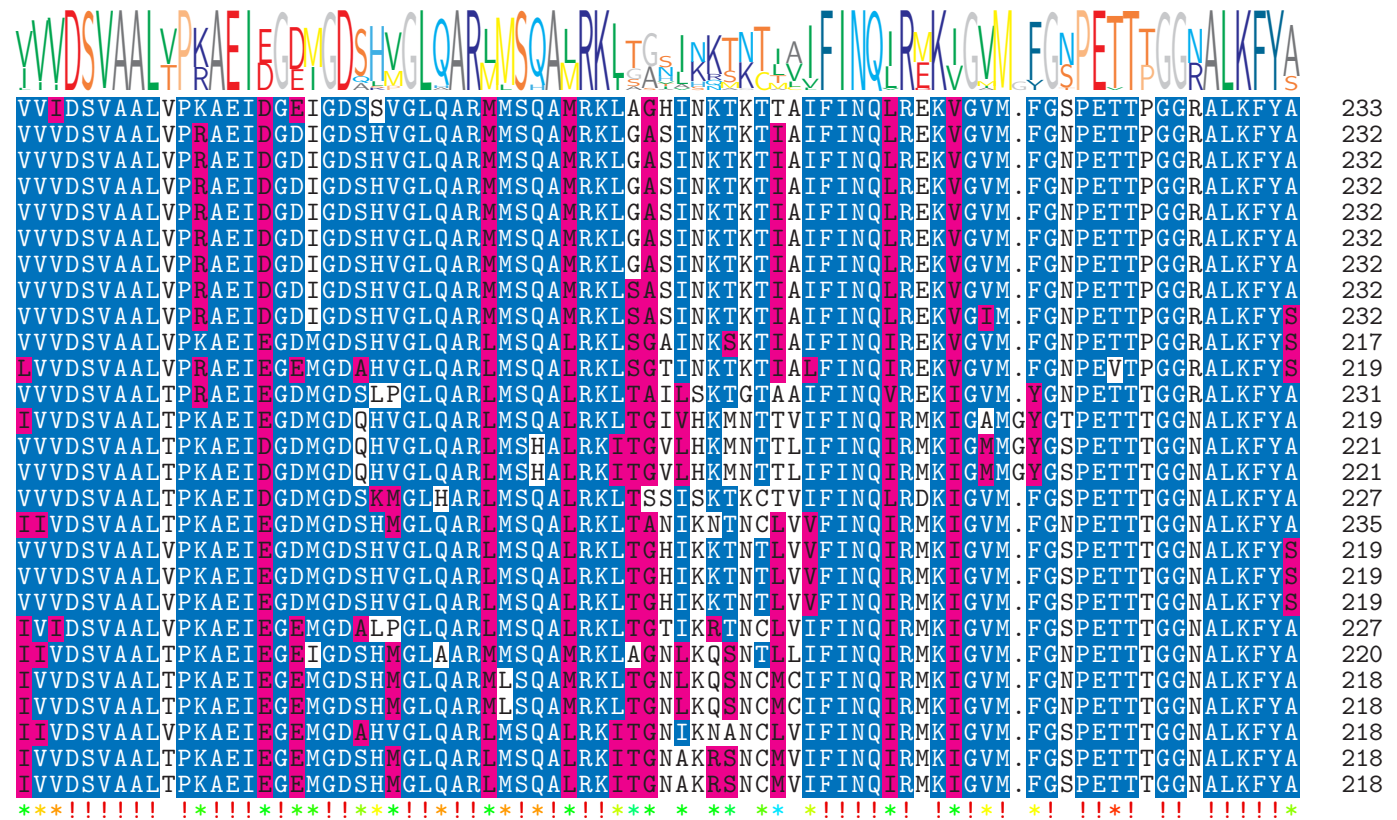
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consensus

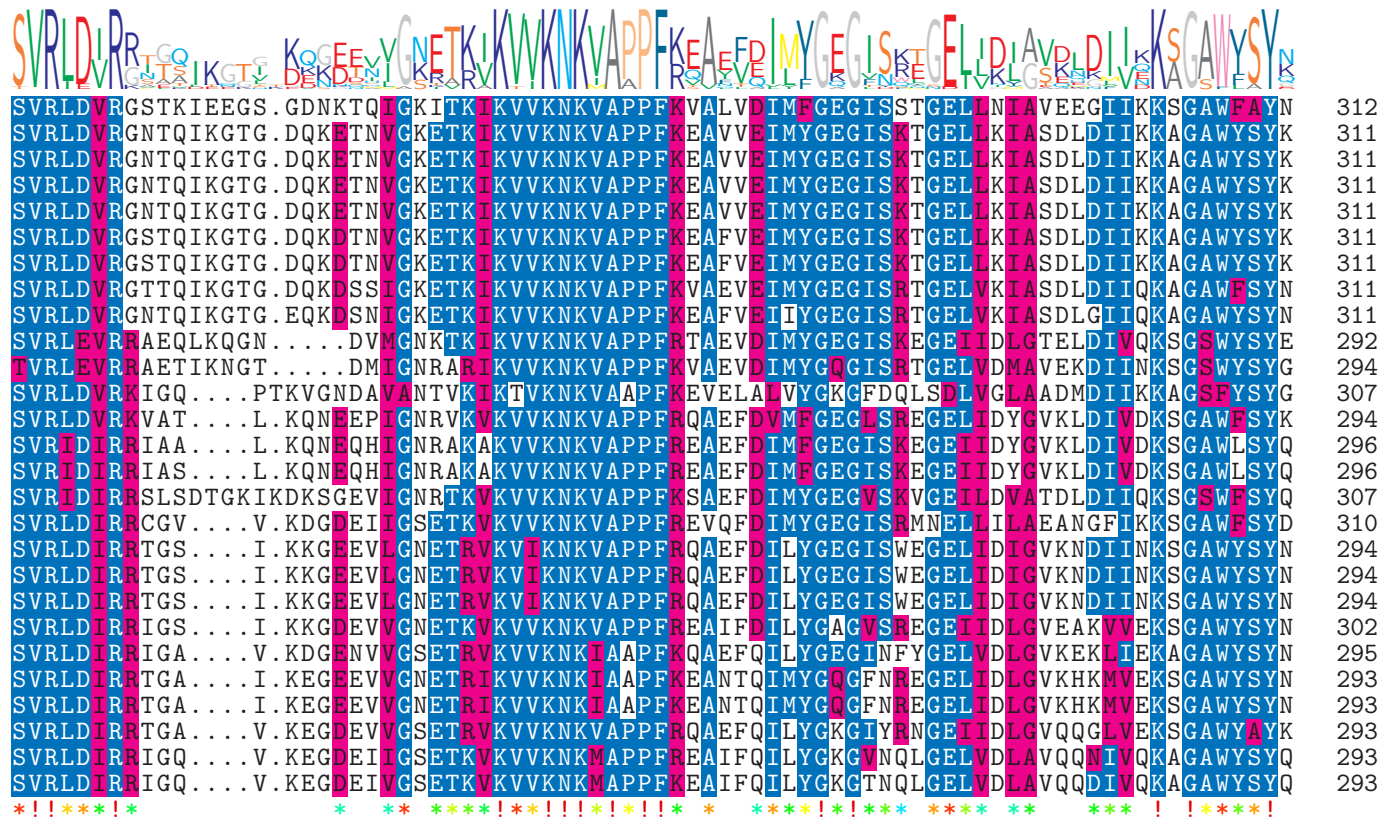
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consensus

Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAENPEIFDEIDHQVRVQFGLIDGEEIAES . . . KKDE . . . AAQVDS . VNEEVTLDLGDLEIE	381
DEKIGQGSENAKKYLAENPEIFDEIDHQVRVQFGLIDGEEIAES . . . KKDE . . . VAQVDS . VNEEVTLDLGDLEIE	381
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEEEESAMAVASE E TDDLALDLNGIEIE	377
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK ETDEK . . . ADKNLVLELDDTIELE	382
EERLGQGGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEETQEEL . EFE . E	348
SERIGQGGRENAKNYLADHEDVEDEVRLKVRAAAYGISDVPEEDLPTTEDE . QI . NILPDDST EE	355
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logo

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NTDB id 1074 ABD1 RS10195 WP 000344167.1	...	349	
consensus			

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