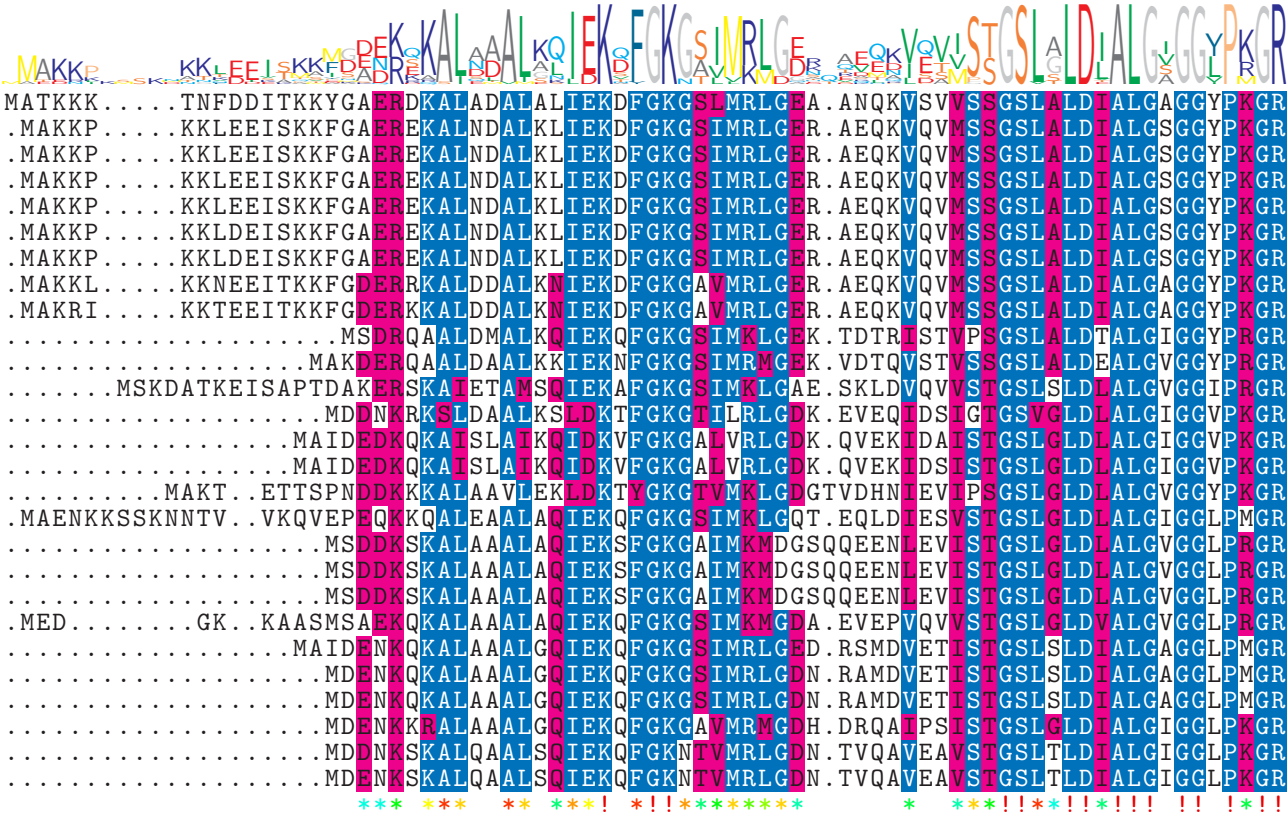


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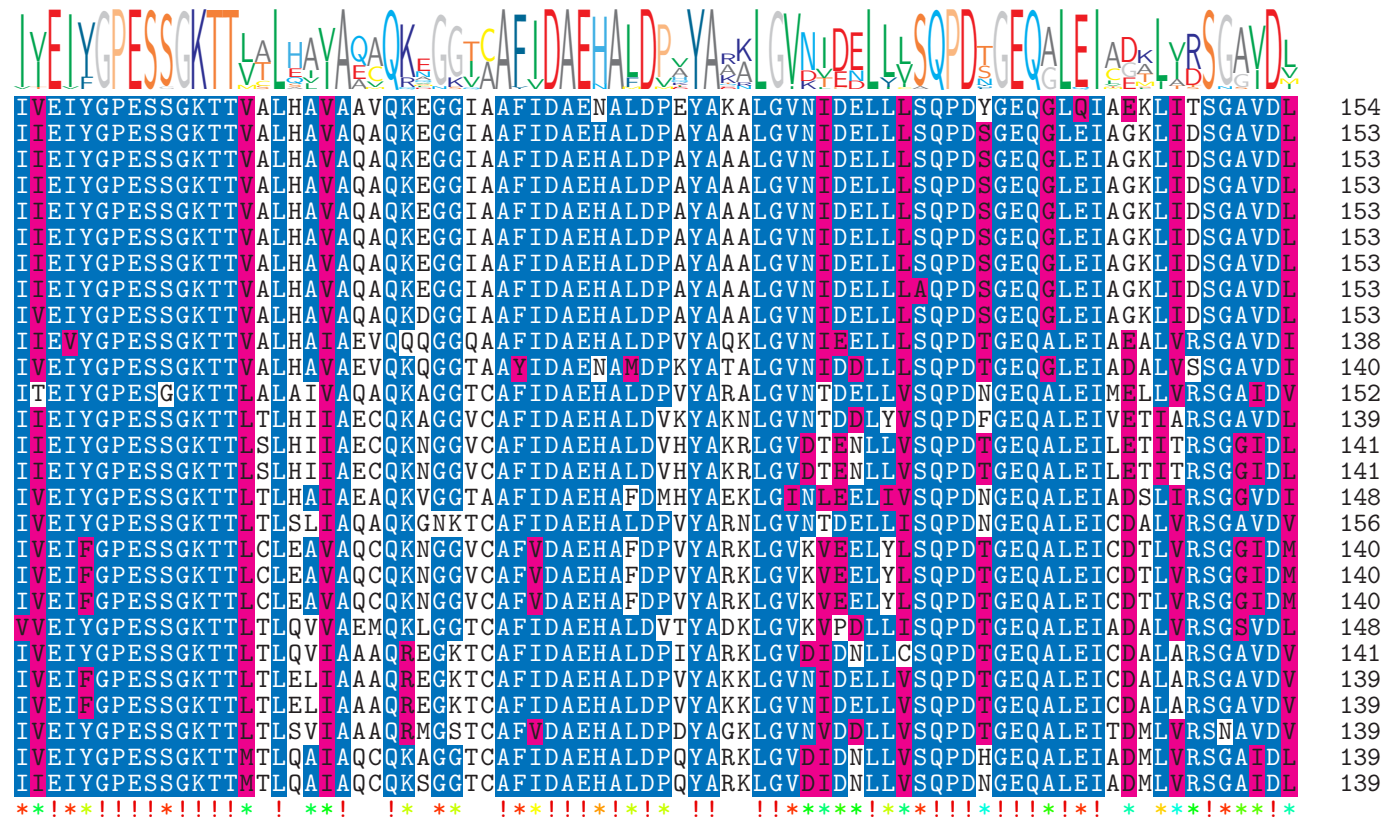


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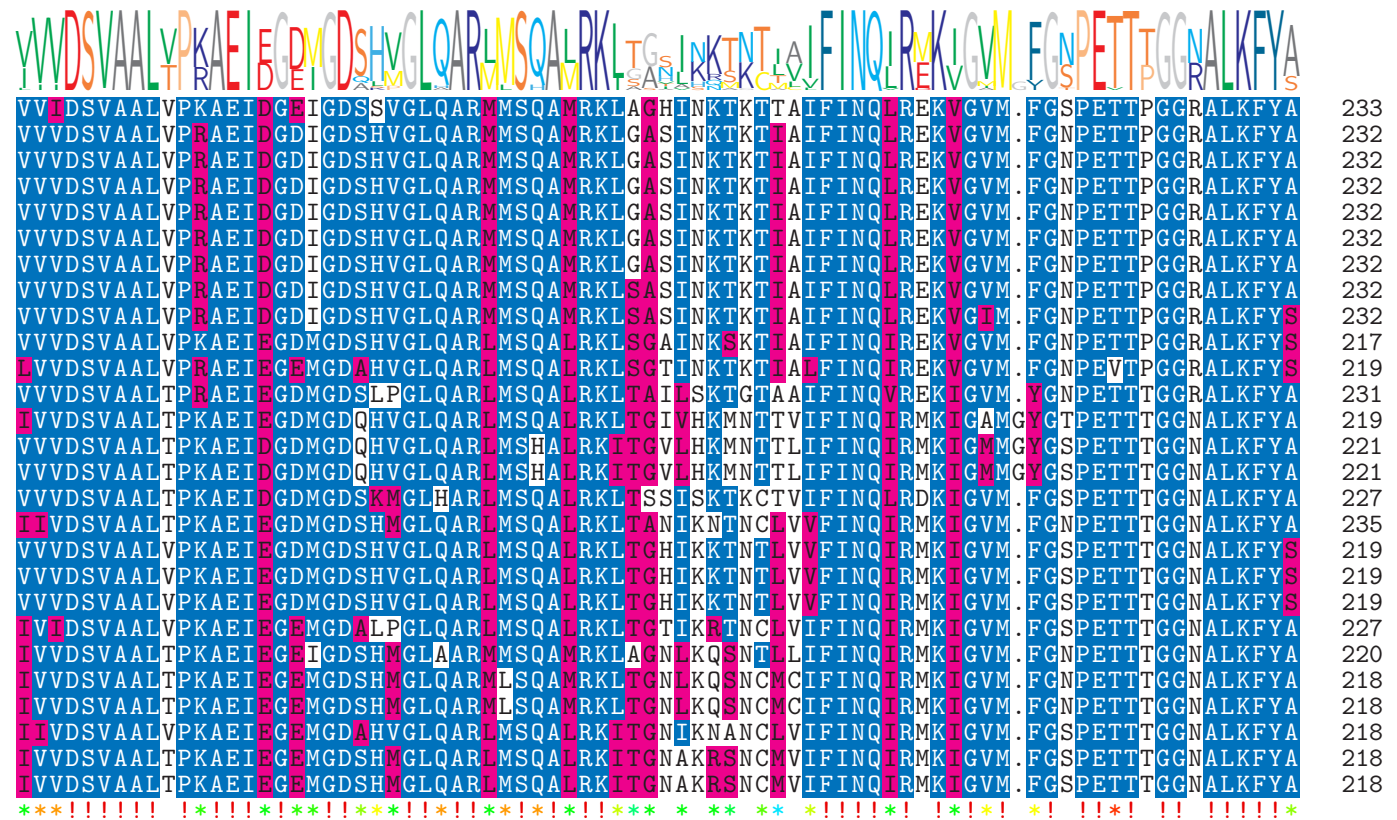
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consensus

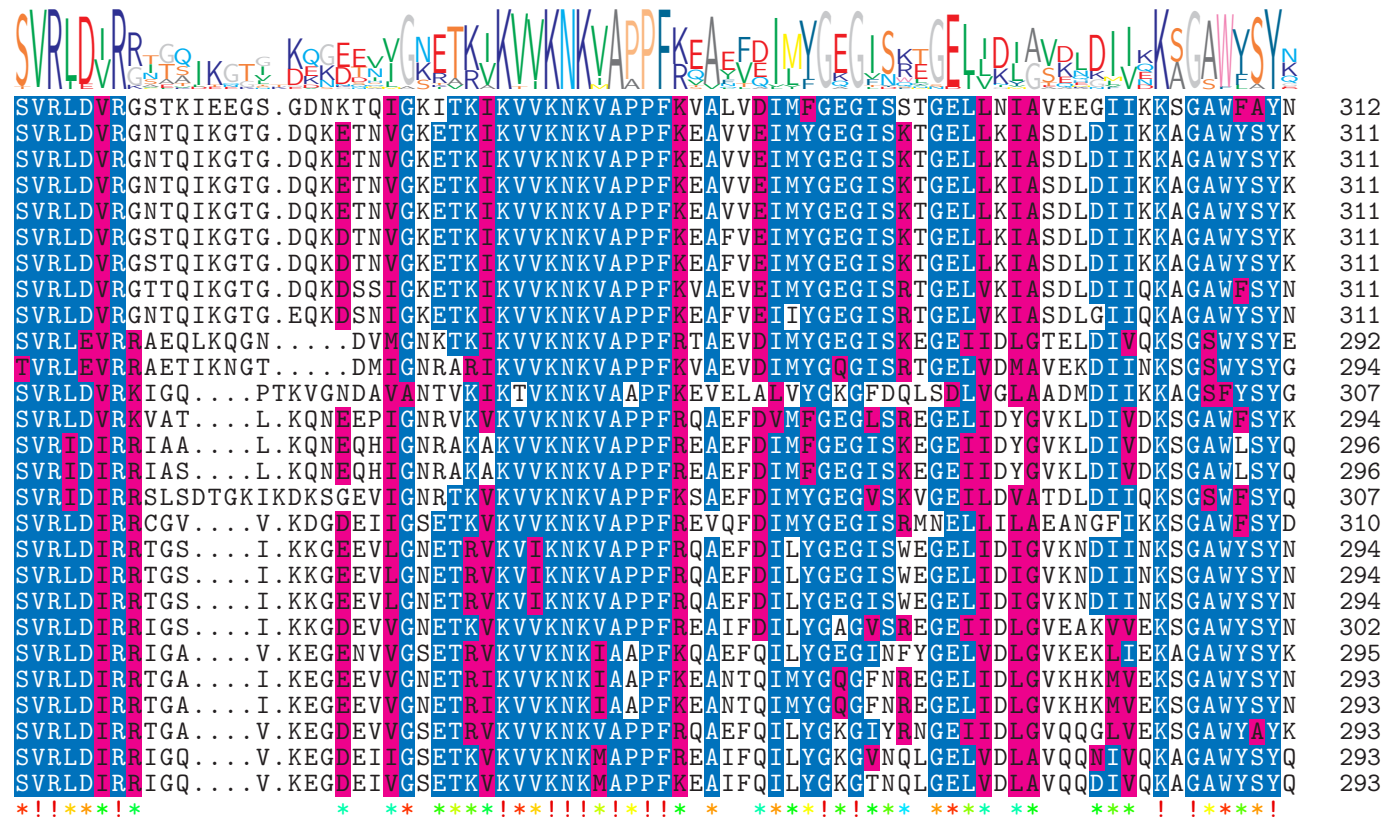
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consensus

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consensus

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Sequence	Score
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DEKIGQGSENAKKYLAHNPEIFDEIDHQRVVFGLIDGEEIAES...KKDE...AAQVDS..VNEEVTLDLGDLEIE	381
DEKIGQGSENAKKYLAHNPEVFAEIDHQRVVFGLIDGEEAAES...KKDE...VAQVDS..VNEEVTLDLGDLEIE	381
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GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EERLGGGRENAAKQFLKENKDIMLMIQEQIREHYGLDNGGVVQQAEETQEEL.EFE.E.....	348
SERIGGGRENAAKNYLADHEDVEDEVRLKVRAAAYGISDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
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DKKLGGGRENAAKALLKEDKALADEITLKIKESIGSNEE....IMPLPDEPL.....EEME.....	347
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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