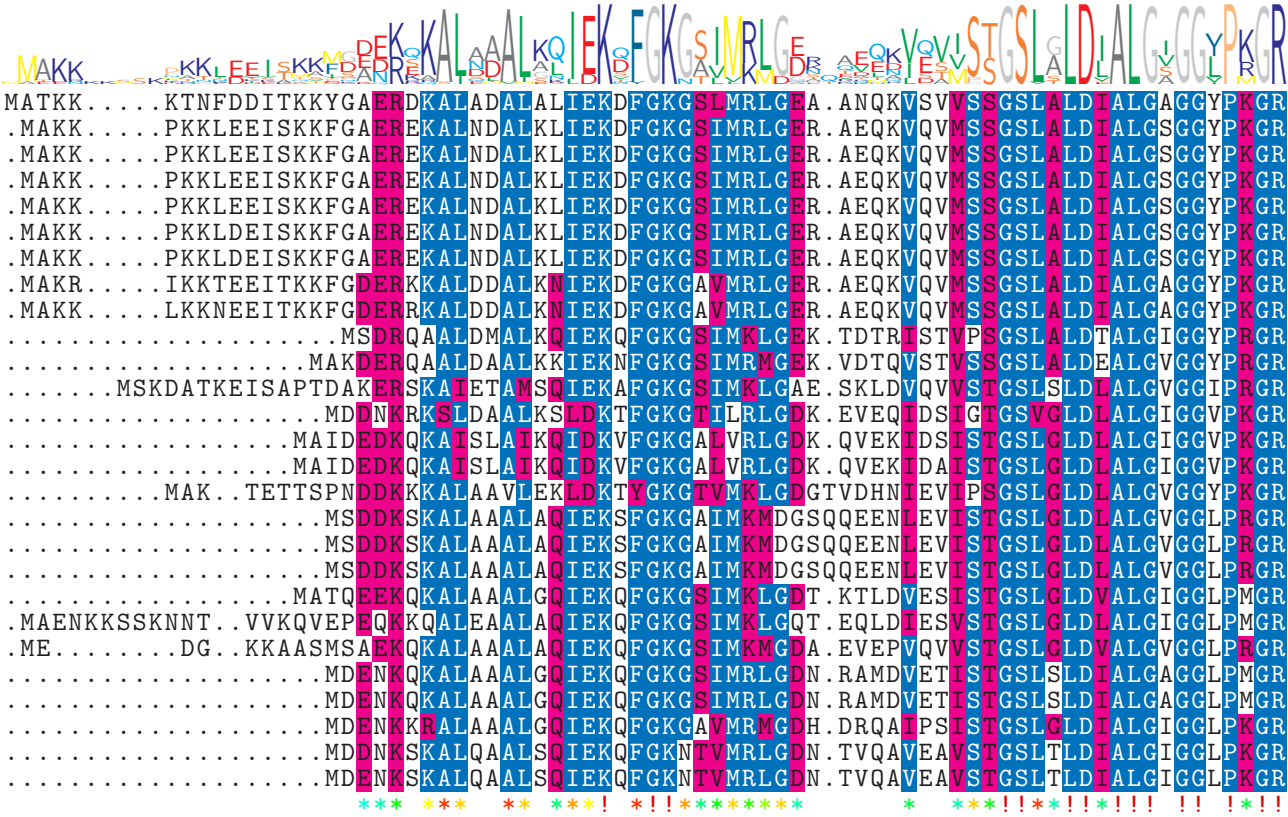


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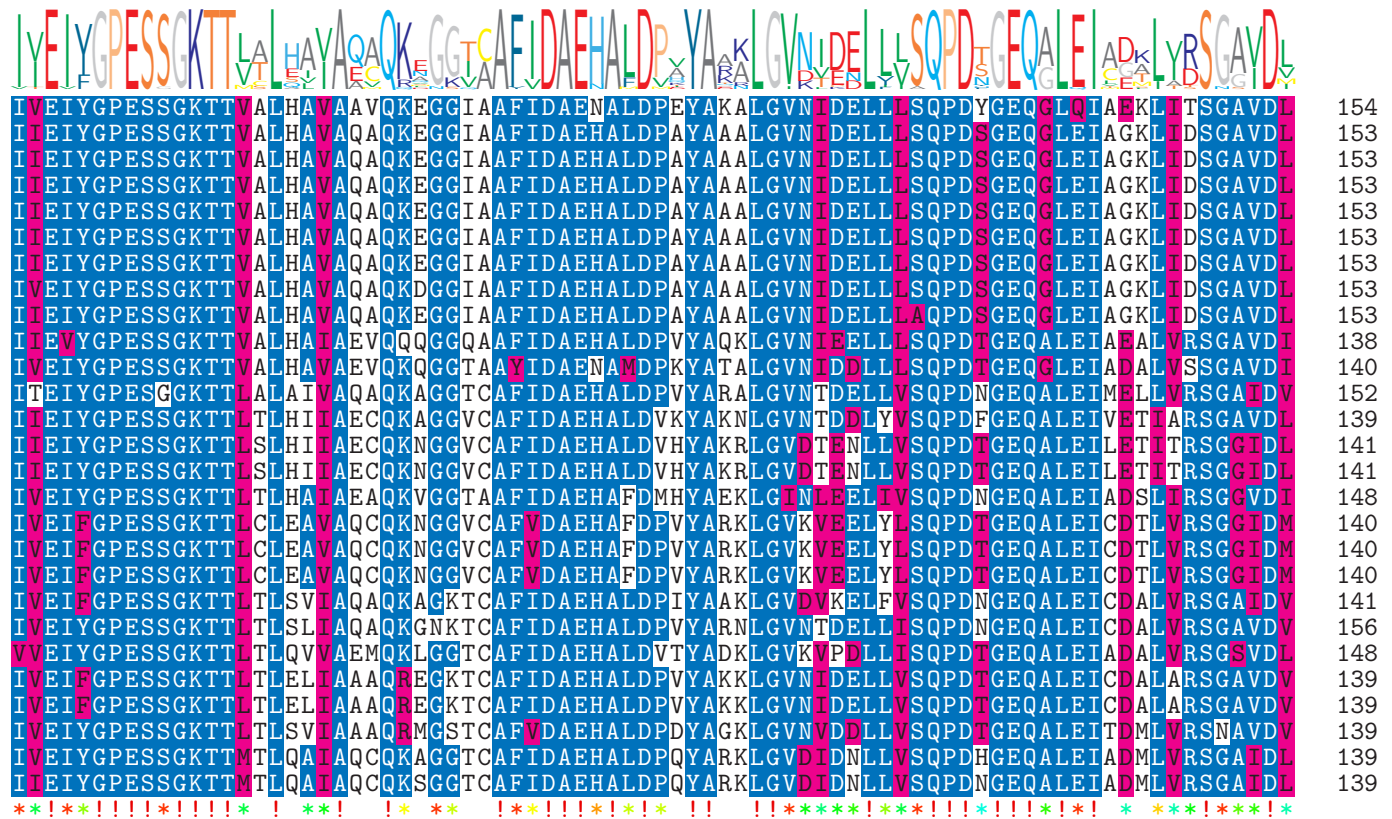


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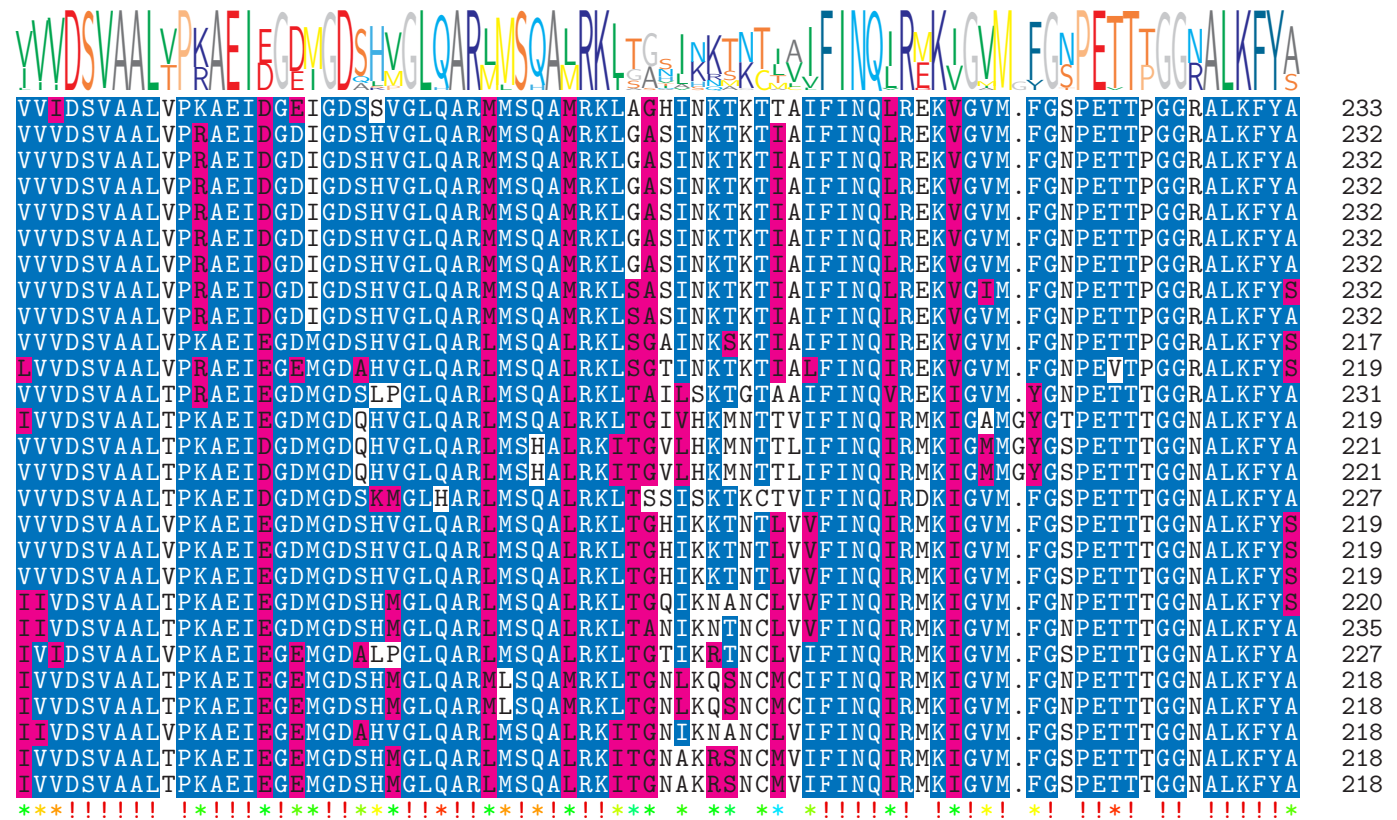
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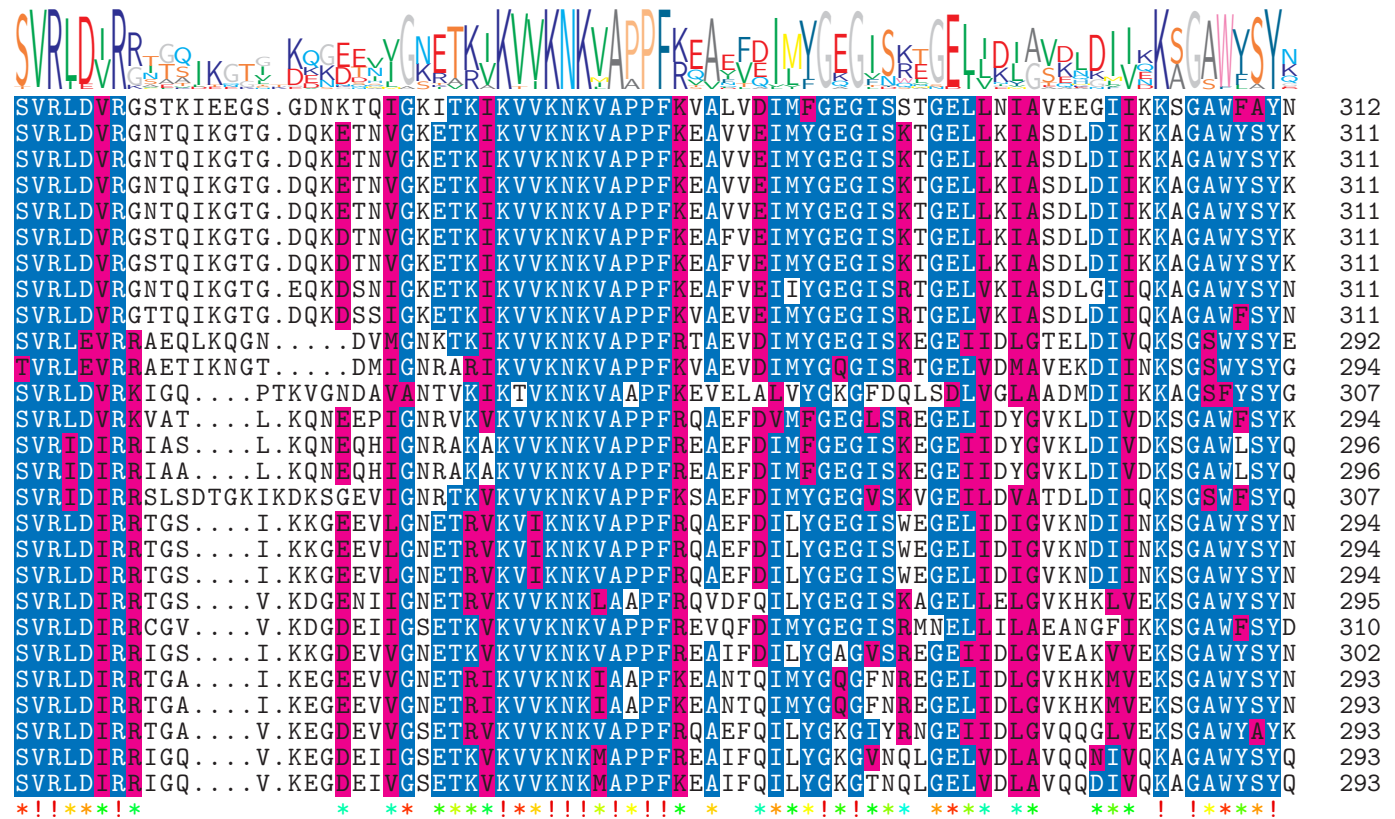
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consensus

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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQD.TENKKDE....PKKEEA..VNEEVPLDLGDELEI	384
DEKIGQGSENAKKYLAADNPEIFDEIDKQVRVQFLIDGEEIAES....KKDE....AAQVDS..VNEEVPLDLGDELEI	380
DEKIGQGSENAKKYLAADNPEVFAEIDHQVRVQFLIDGEEAAES....KKDE....VAQVDS..VNEEVPLDLGDELEI	380
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQGLIEEDNTEEEKQ.SSKEK.....ETDEK..ADKNLVLELDDTIEL	381
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAM.AVASE.....E.....TDDLALDLNGIEI	376
EERLGQGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQQA.EETQEEL.EFE.E.....	348
SERIGQGRENAKNYLADHEDVEDEVRLKVRVQGLSDVPEEDLPT.TEDE.QI.NILPDDST.....EE.....	355
DERIGQGKEKTIAYIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAPEAAEA.....	363
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DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DTKLGQGRDTPVKELIKDNPELAEELEAKIREKLQAK.....	343
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logo

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NTDB id 1074 ABD1 RS10195 WP 000344167.1		349

consensus

 non conserved
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 ≥ 50% conserved