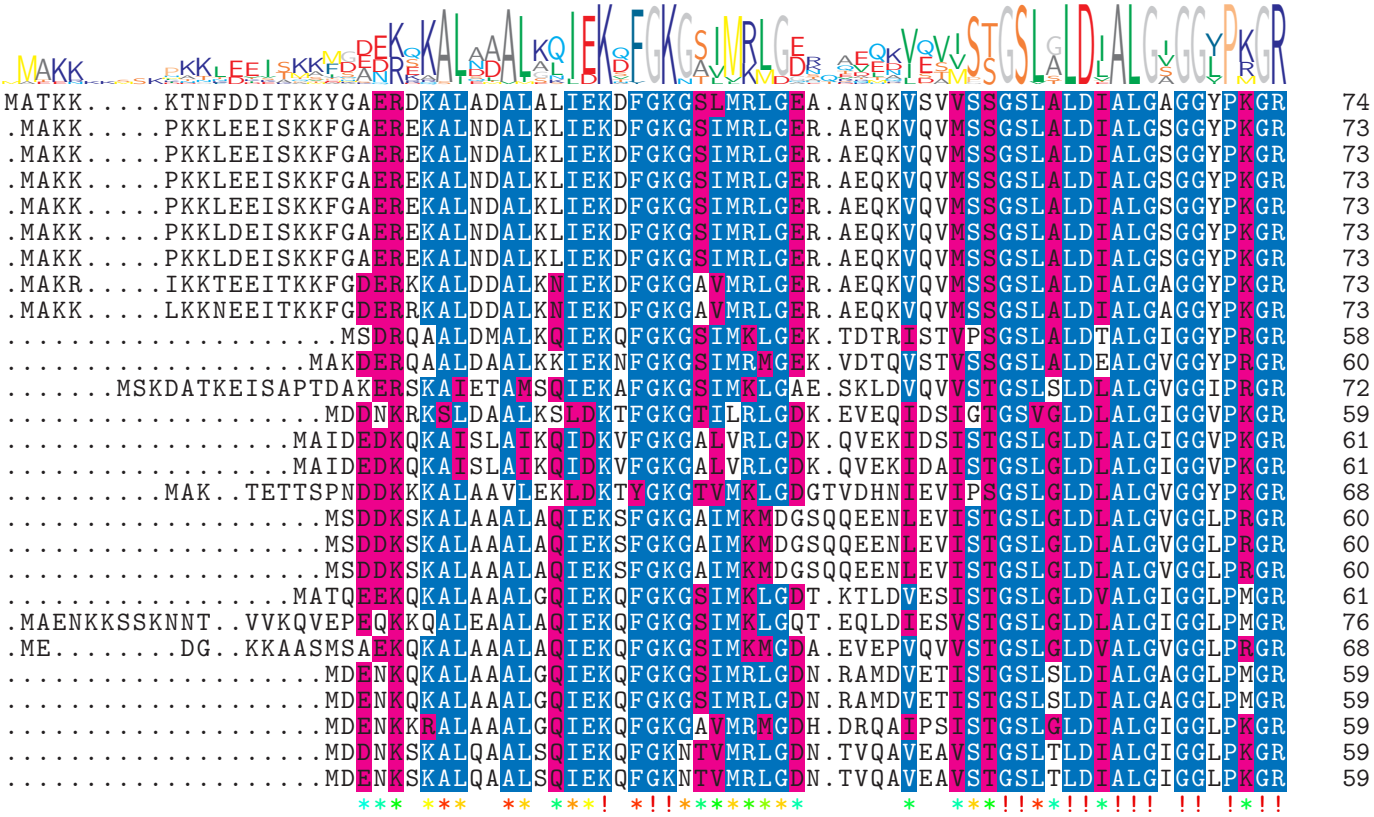


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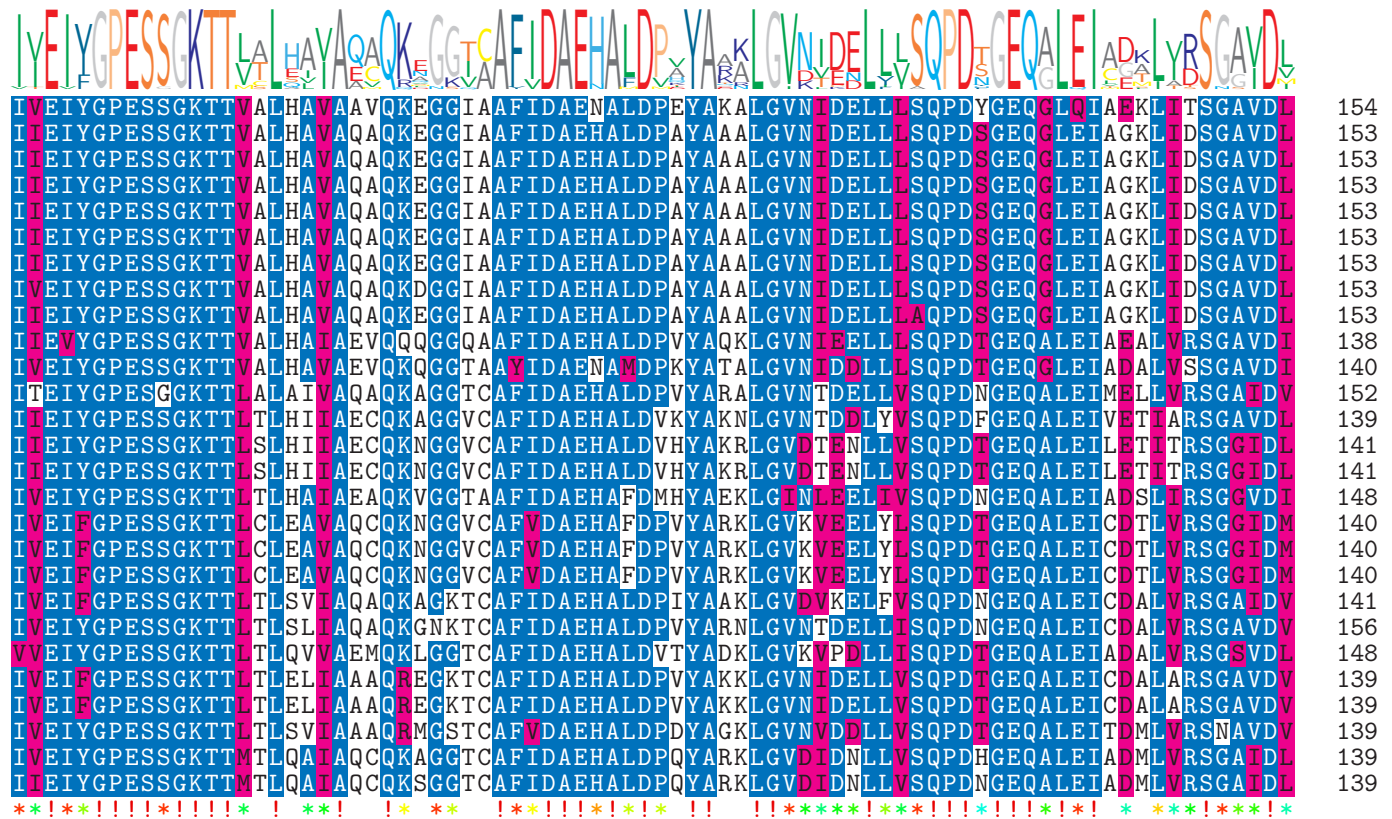
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consensus



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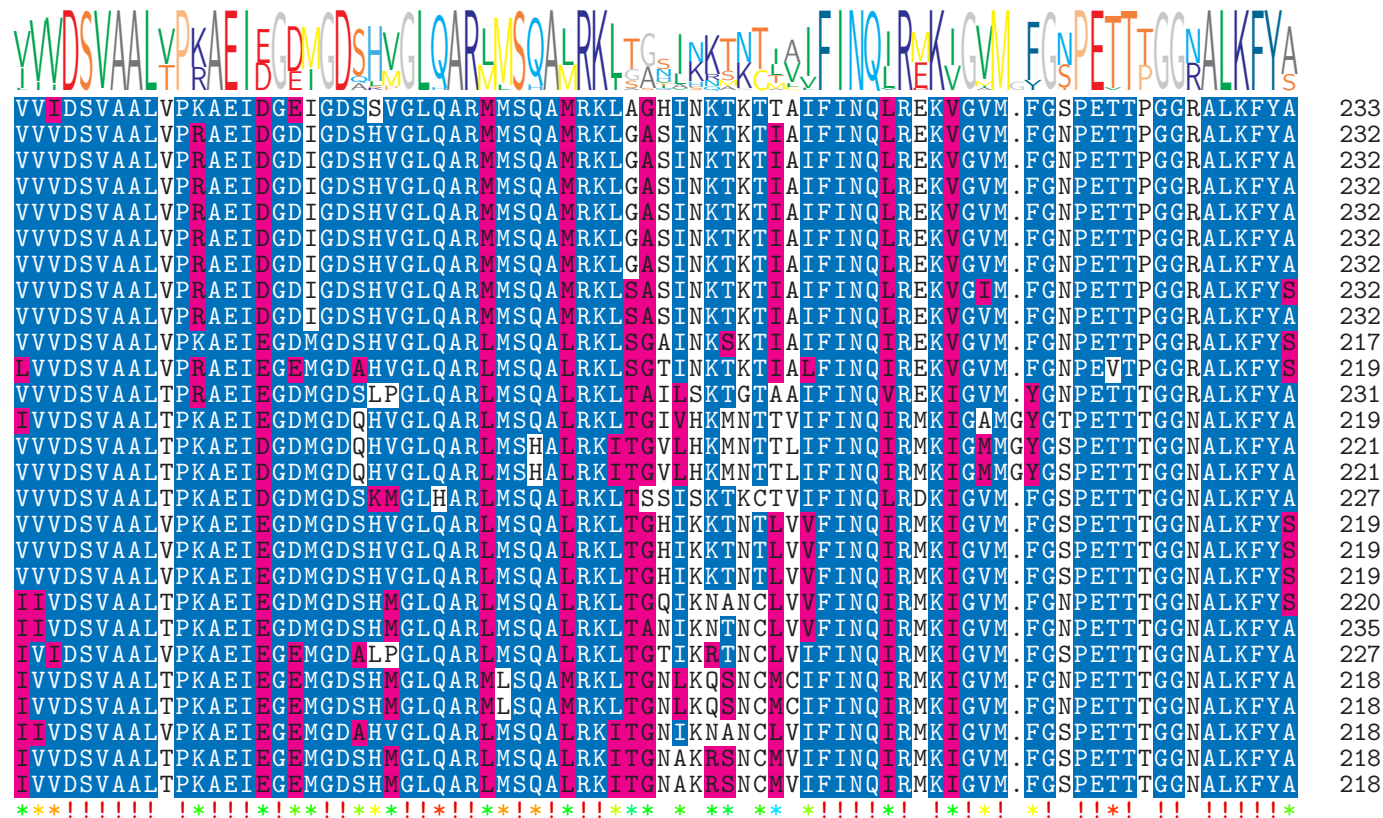
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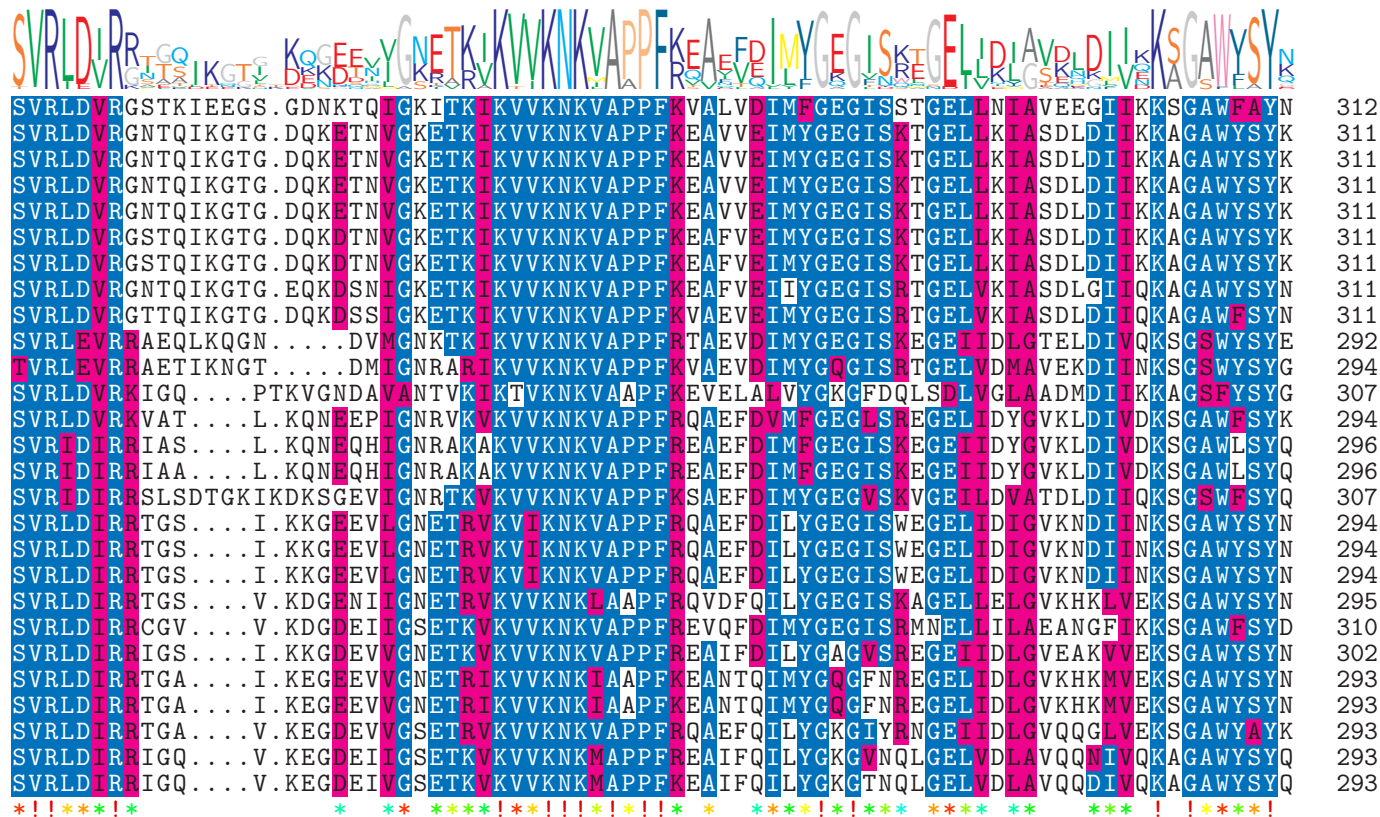
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consensus

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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQD.TENKKDE....PKKEEA..VNEEVPLDLGDELEI	384
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQD.TENKKDE....PKKEEA..VNEEVPLDLGDELEI	384
DEKIGQGSENAKKYLAHNPEIFDEIDHQRVVFGLIDGEEIAES....KKDE....AAQVDS..VNEEVPLDLGDELEI	380
DEKIGQGSENAKKYLAHNPEVFAEIDHQRVVFGLIDGEEIAES....KKDE....VAQVDS..VNEEVPLDLGDELEI	380
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQGLIEEDNTEEEKQ.SSKEK.....ETDEK..ADKNLVLELDDTIEL	381
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAM.AVASE.....E.....TDDLALDLNGIEI	376
EERLGGGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQQA.EETQEEL.EFE.E.....	348
SERIGGGRENAKNYLADHEDVEDEVRLKVRVQGLSDVPEEDLPT.TEDE.QI.NILPDDST....EE.....	355
DERIGGQKEKTIAYIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAPEAAEA.....	363
DKKLGGGRENKAFLENKEPEIADEITKAIQNSMGIEGMISGS..EDDEGE..E.....	343
DKKLGGGRENKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DKKLGGGRENKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DTKLGGGRDTPVKELIKDNPELAEELEAKIREKLQAK.....	343
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GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEG..T...QD...ETDGE.RPEE.....	348
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GDKIGGQKANACKYLKENPEIAKTLDDKKLREMLLNPNENMQLI..AETSSAADVEFGAVPE.....EF.....	354
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GNKIGGQKNNVIRIYFENNQIAEIERNIREQLLTTGTNGAV..Q.I.EDEEEPDLL..LE.....S.....	349

logo

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NTDB id 1074 ABD1 RS10195 WP 000344167.1		349	
consensus			

-  non conserved
-  similar
-  ≥ 50% conserved