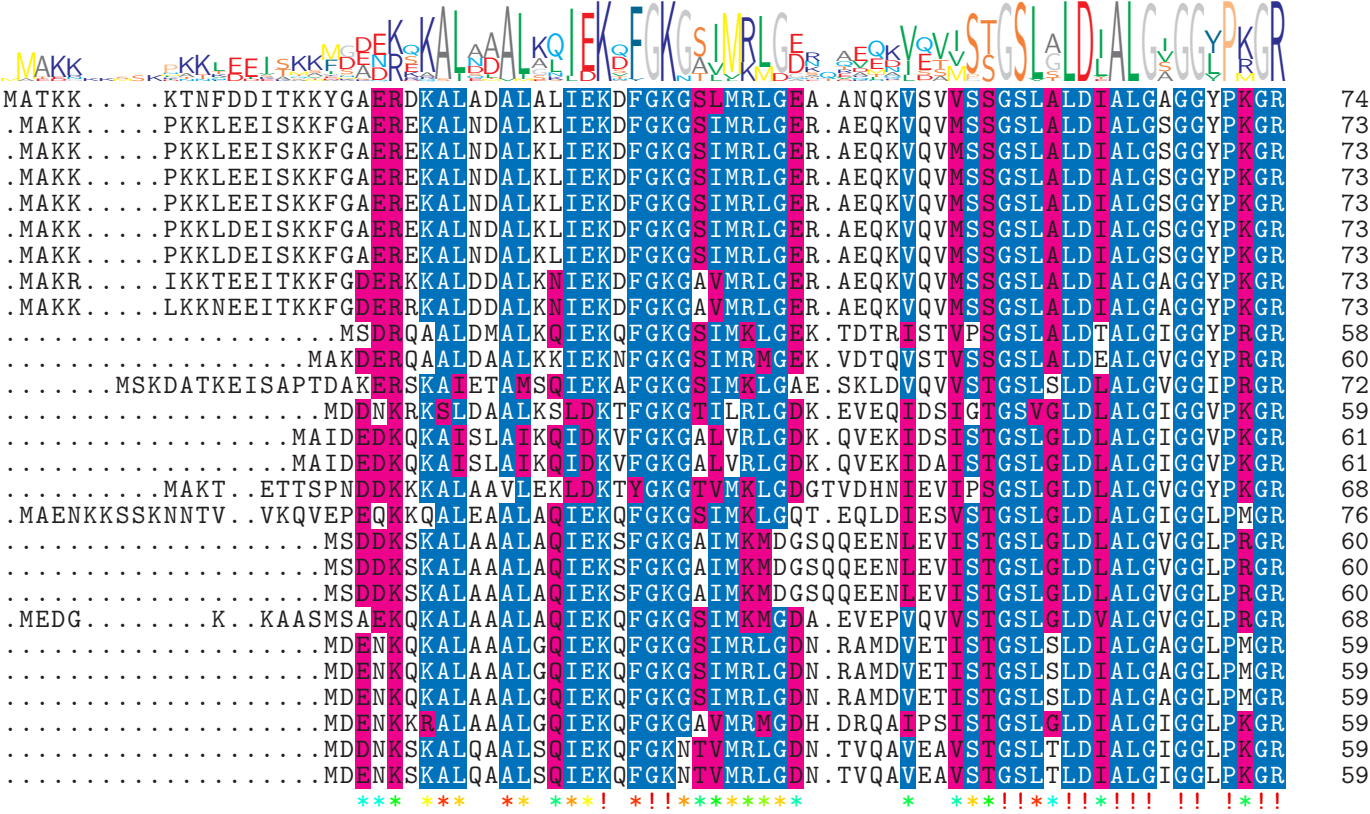


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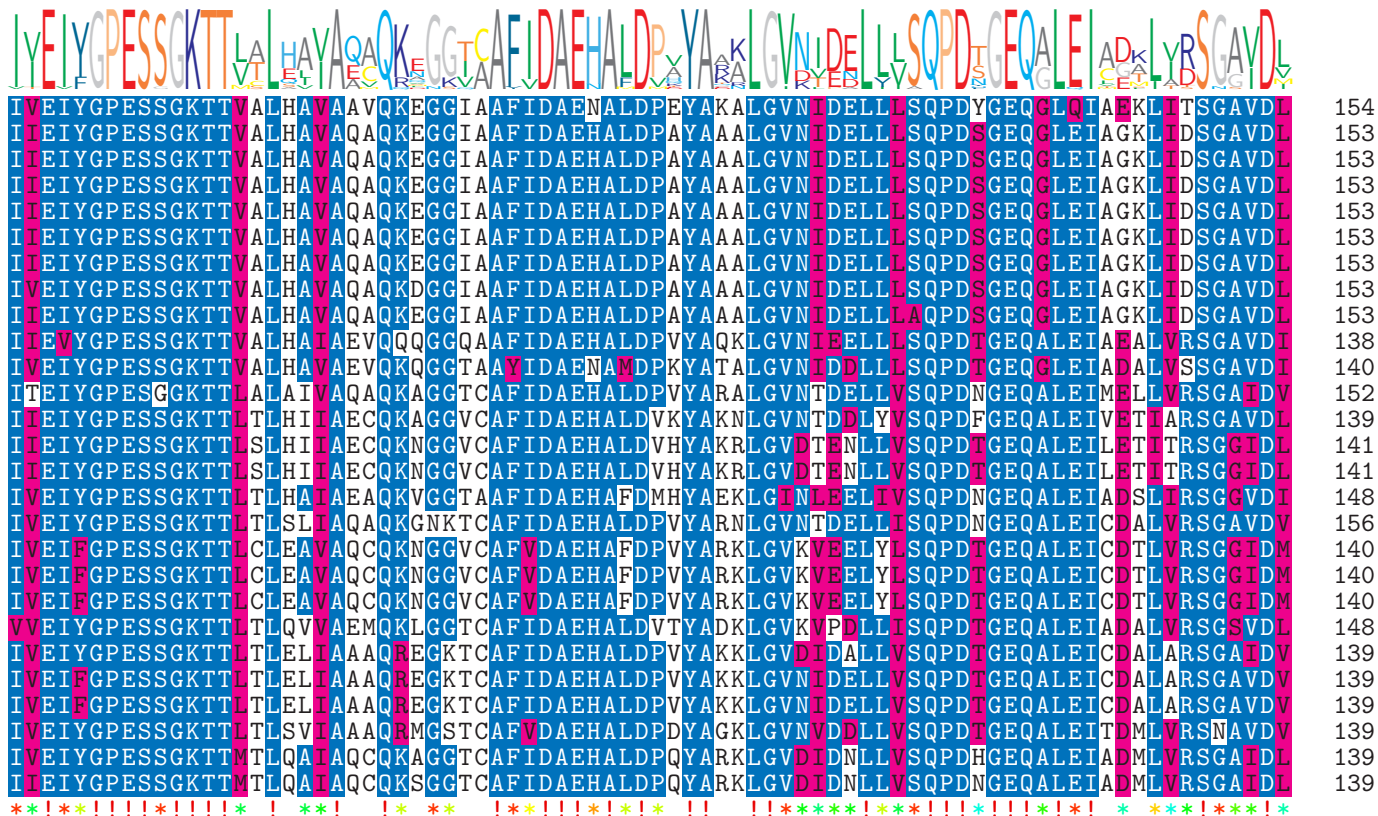
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consensus



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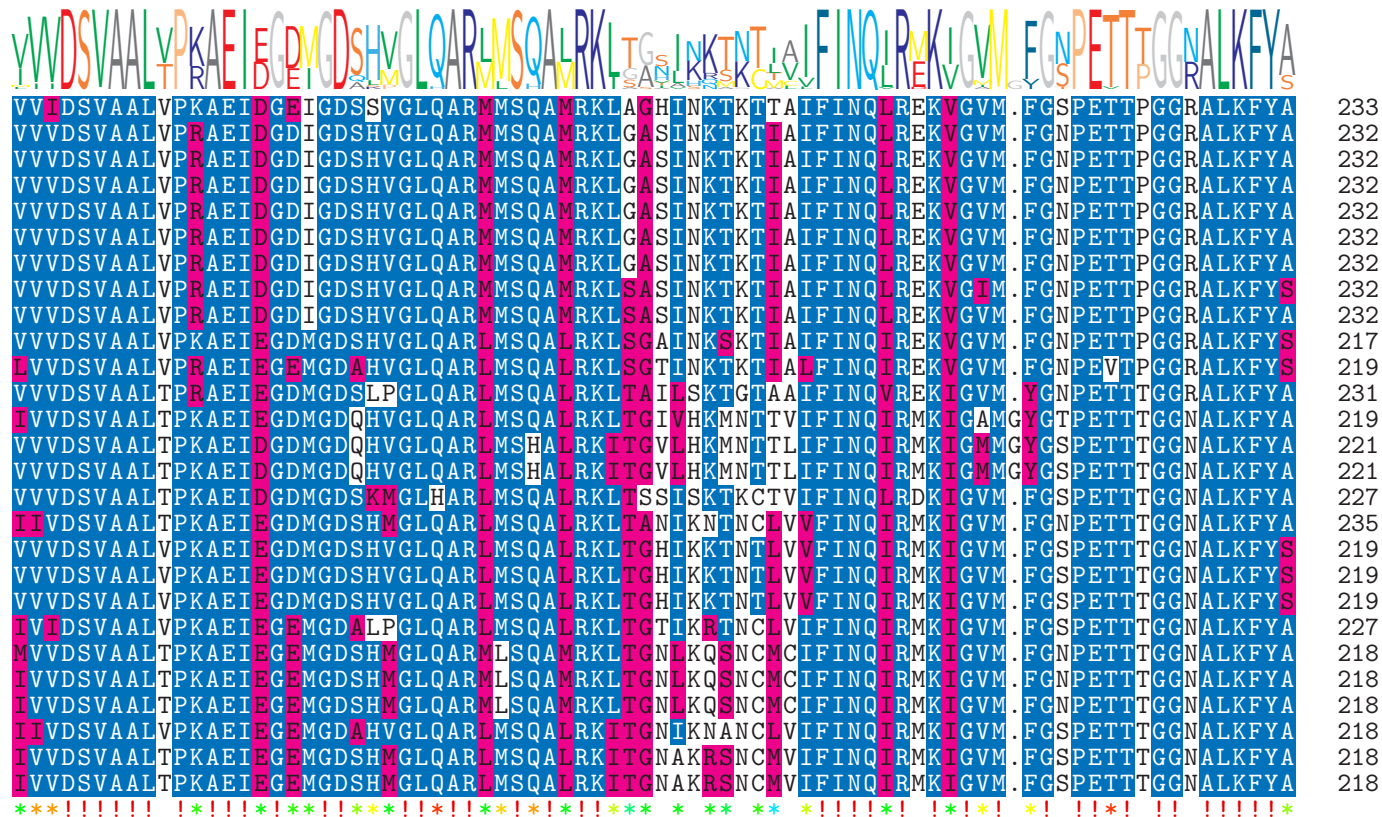
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

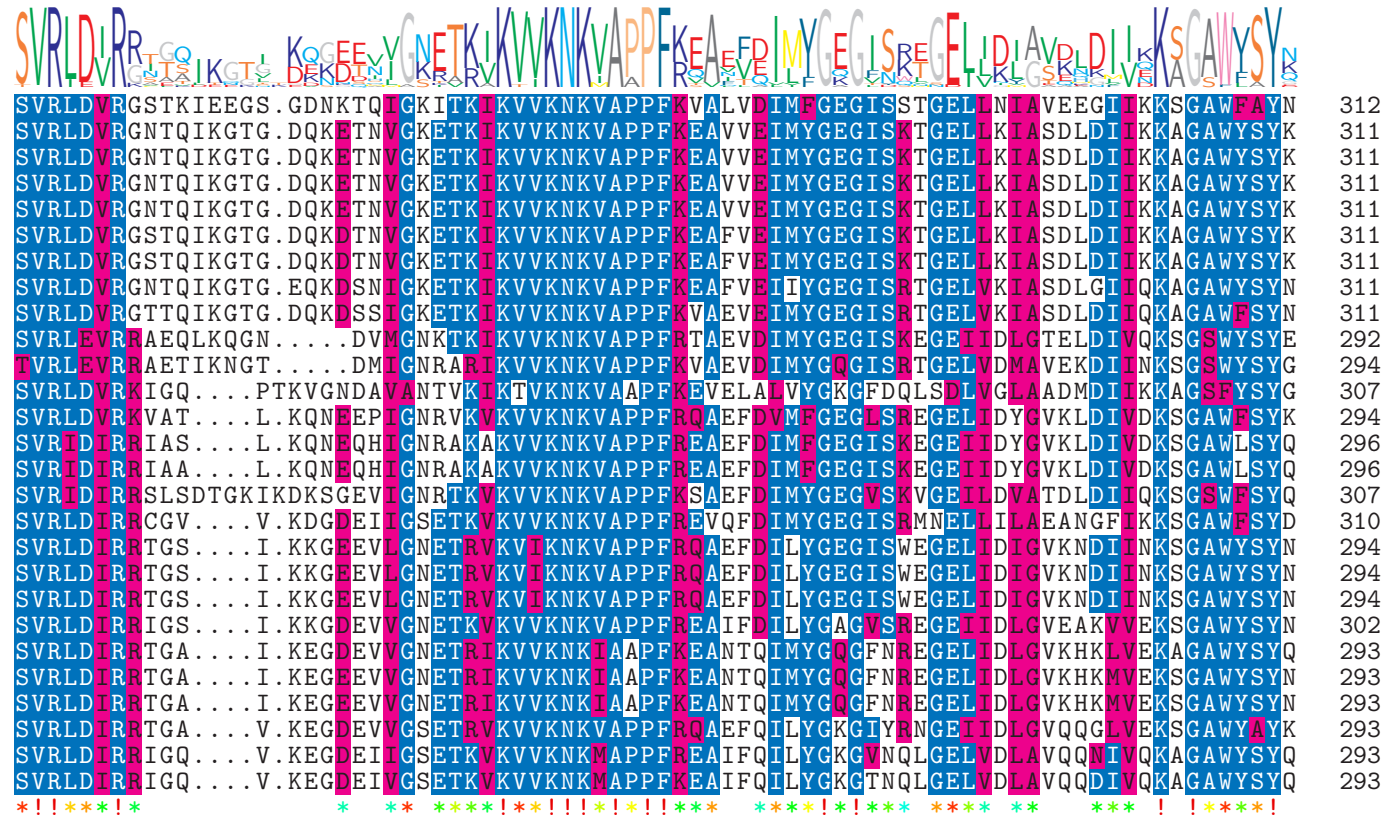
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consensus

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consensus

Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGLEDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGLEDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLADNPEIFDEIDHQRVVRVQFGLIDGEEIAES....KKDE....AAQVDS..VNEEVPLDLGDELEIE	381
DEKIGQGSENAKKYLADNPEVFAEIDHQRVVRVQFGLIDGEEAAES....KKDE....VAQVDS..VNEEVPLDLGDELEIE	381
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEDNTTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIEIE	382
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEEEESAMAVASE.....E.....TDDLALDLNNGIEIE	377
EERLGQGRENAKQFLKENKDIMLMIQEQUIREHYGLDNNGVVQQQAETQEEL.EFE.E.....	348
SERIGQGRENAKNYLADHEDVEDEVRLKVRVAAAGISDVPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
DERIGQGKEKTIAYIAERPMEQEIRDRVMAAATAGNAGEAPALAPAAPEAAEA.....	363
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DKKLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIM....PLPD.....EPLLEE..ME..	347
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GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHIT....E.....GTQDETGE..RPEE.....	348
GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHIT....E.....GTQDETGE..RPEE.....	348
GERIGQGRDNCREFLRENAELAREIENKVRREHLGVTPMGA....VTL.AEEVEED.....	352
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GDKIGQGGKANACKYLKENPEIAKTLDDKKLREMLLNPNEMQ....LIAETSSAADDVEFGA..VPEEF.....	354
GSKIGQGGKANAAYLEENPEIQQEIEQQIRAKLLVTSANT....KATPVAEDLADADI.....	347
GNKIGQGGKNNVIRYLEENPQISTEIEAVIREQLLTKASDQ....TAA.HDETEEEEPDL....LES.....	349
GNKIGQGGKNNVIRYFEENNQIAEEIERNIREQLLTGTNG....AVQ.I.EDEEEEPDL....LLES.....	349

logo

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

- non conserved
- similar
- ≥ 50% conserved