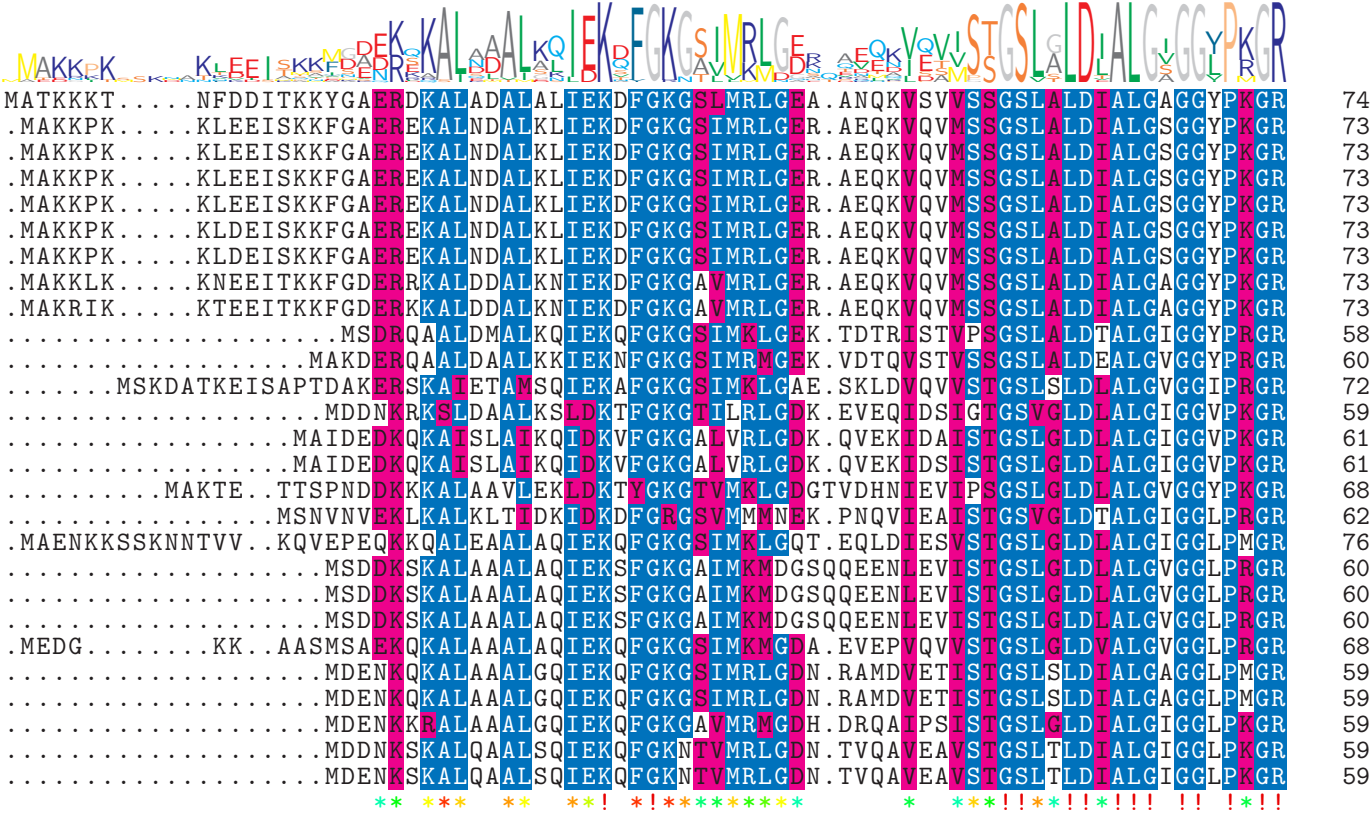


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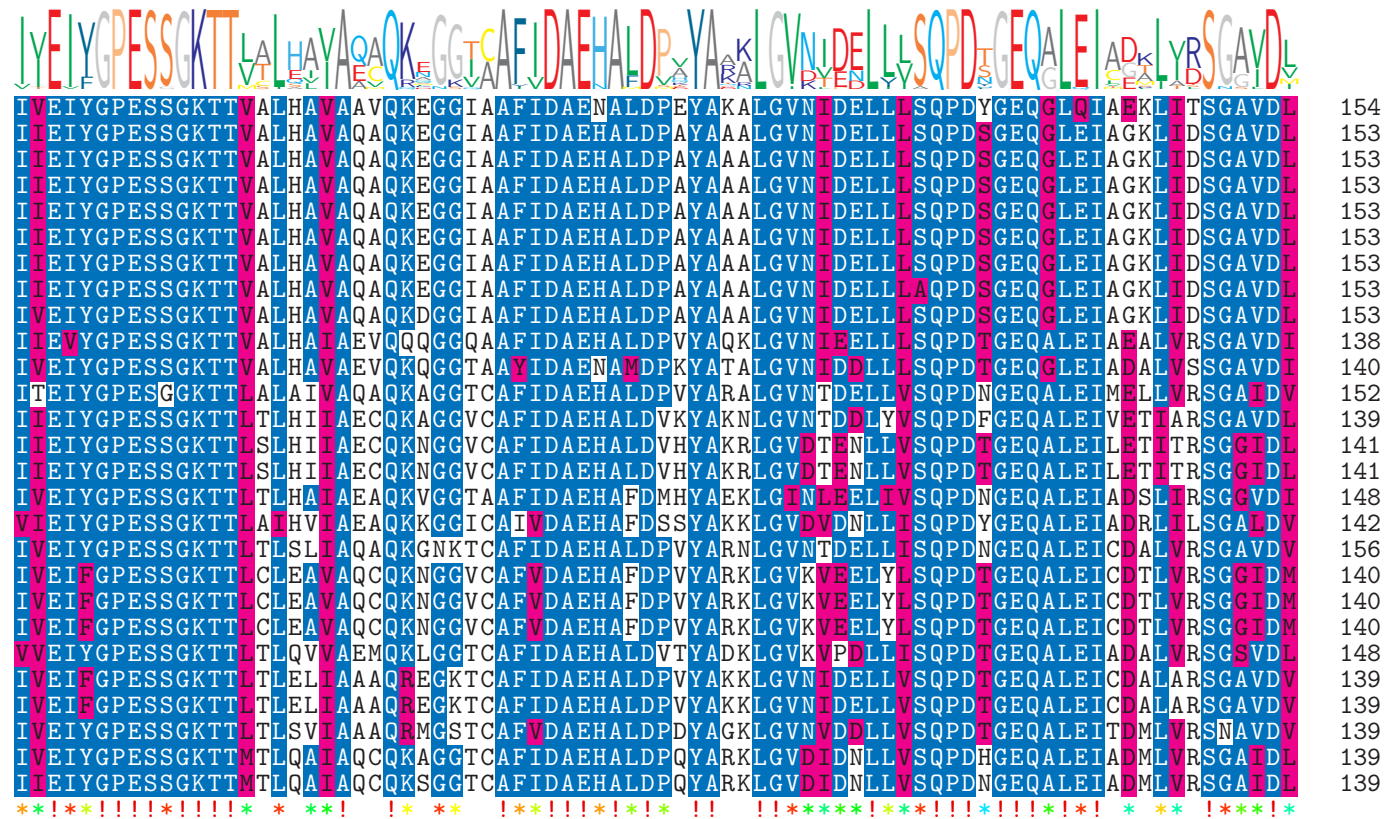
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consensus



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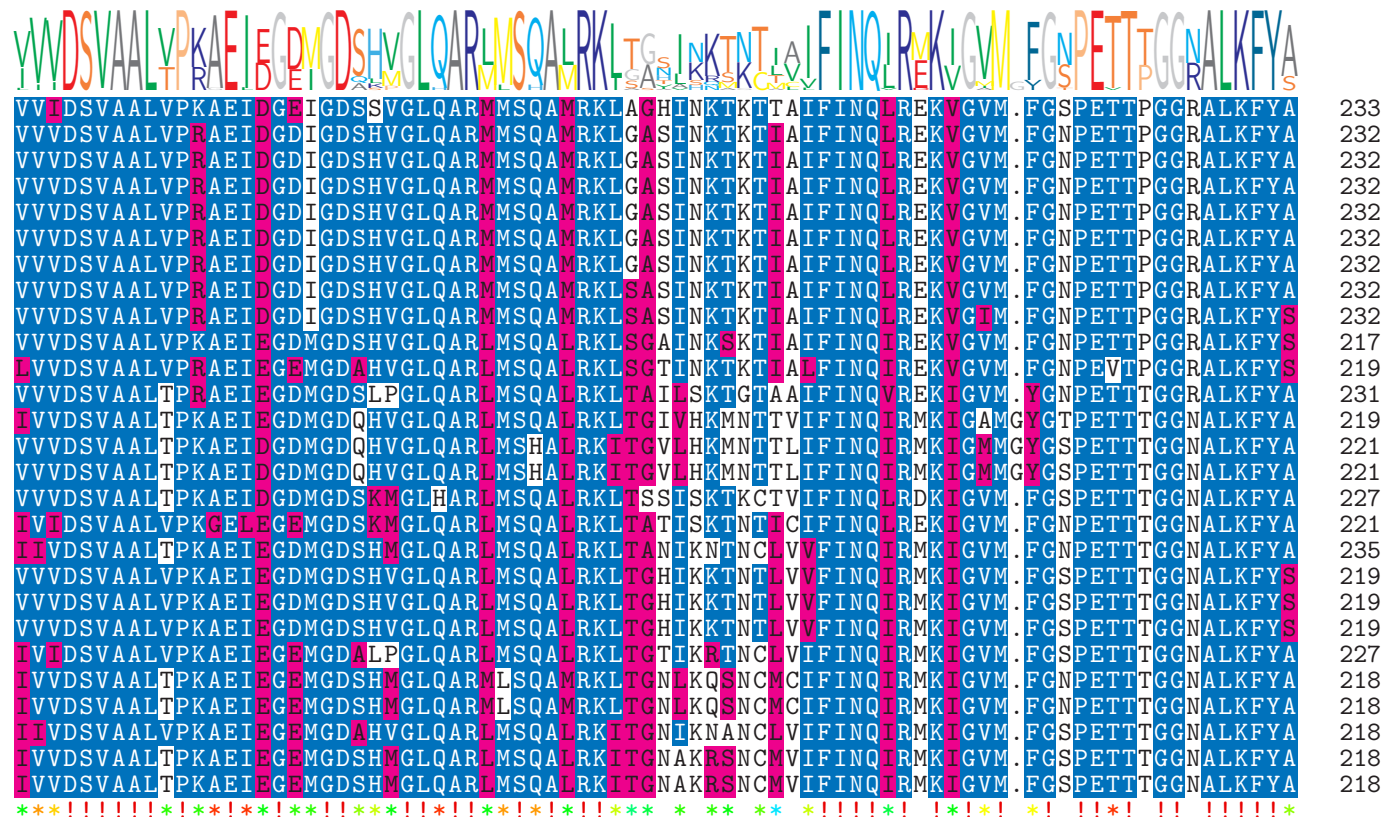
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consensus

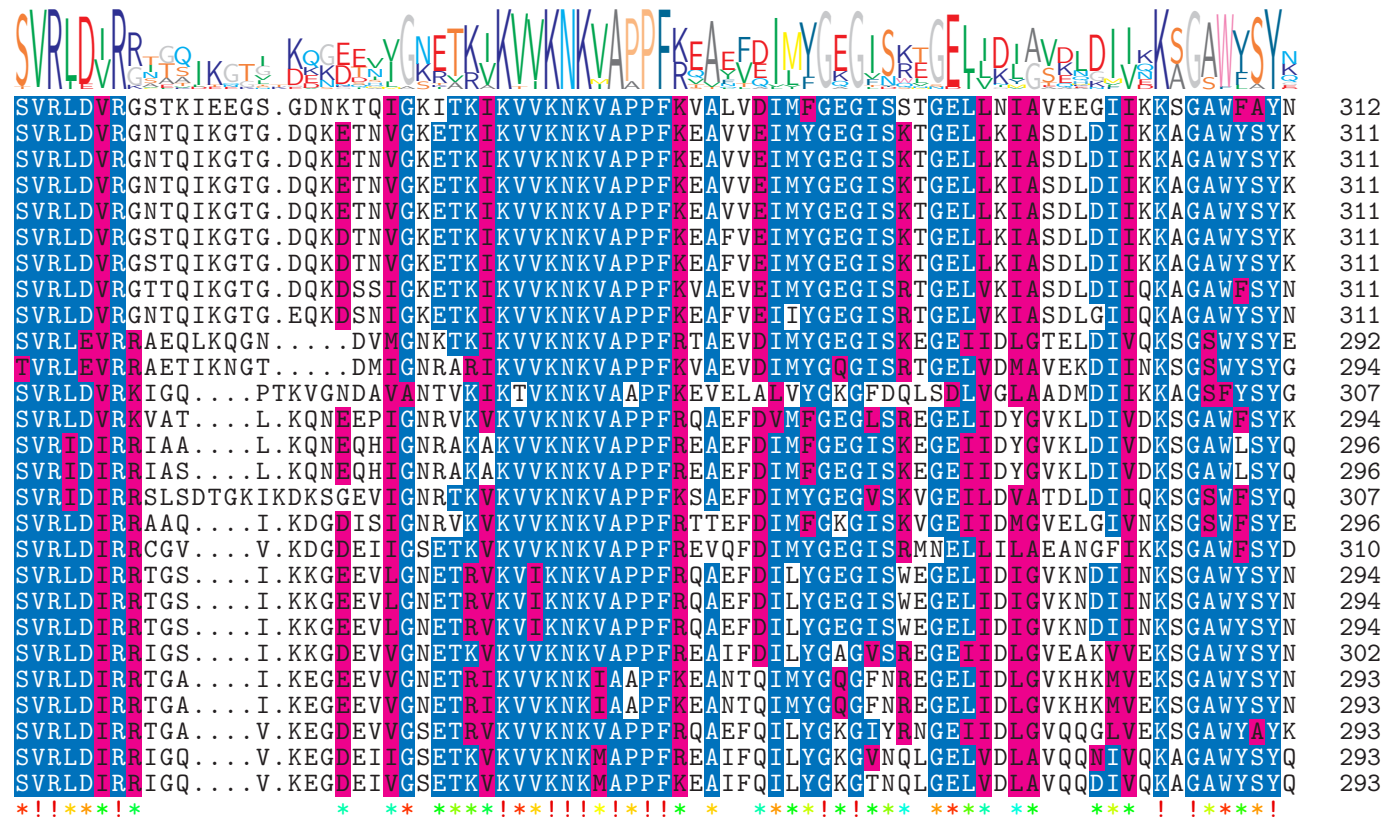
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSE..QDTENKK..DE...PKKEEA..VNEEVPLDLGDE	381
DEKIGQGSENAKKYLAADNPEIFDEIDHQVRVQFGLIDGEEIAE..S...KK..DE...AAQVDS..VNEEVTLDLGD	377
DEKIGQGSENAKKYLAADNPEIFDEIDHQVRVQFGLIDGEEIAE..S...KK..DE...VAQVDS..VNEEVTLDLGD	377
GEKIGQGSENAKRYLADHPQLFEIDRKVRVKFGLLEESEES..E.....TDDLALDLNG	373
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEE..KQSSKEK.....ETDEK..ADKNLVLELDDT	378
EERLGGQRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQ..QAEETQE..EL.EFE.E.....	348
SERIGQGRENAKNYLADHEDVEDEVRLKVRAAAYGISDVPEEDL..PTTEDE..QI.NILPDDST.....EE.....	355
DERIGQGKEKTIAIYIAERPMEQIEIDRVMMAAIRAGNAGEAPALAPAPAAPEAAEA.....	363
DKKLGGQRENSKAFLENPEIADEITKAIQNSMGIEGMISGS..E...DDEGEE.....	343
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DKKLGGQRENAKALLKEDKALADEITLKIKESIGSNEEIMPL..P...DEPLEEME.....	347
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GAKIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEG..T.....QDETGERPEE.....	348
GERIGQGRDNCREFLENARAEIENKVRHGLVTPMGAV..TLAEVEED	352
GDKIGQGGKANACKYLKENPEIAKTLDDKLREMLLNPNMQLI..AETSSAADDVEFGAVPEEF	354
GDKIGQGGKANACKYLKENPEIAKTLDDKLREMLLNPNMQLI..AETSSAADDVEFGAVPEEF	354
GSKIGQGGKANAAKYLEENPEIGQIEEQIRAKLLVTSANTKA..TPVAEDLADADI.....	347
GNKIGQGGKNNVIRYLEENPQISTEIEAVIREQLLTAKASDQTA..A.HDETEEEPDL..ES.....	349
GNKIGQGGKNNVIRIYFENNQIAEIEIRNIREQLLTGTNGAV..Q.I.EDEEEDPDL..LES.....	349

logo

		LEIELEE	
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consensus			

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