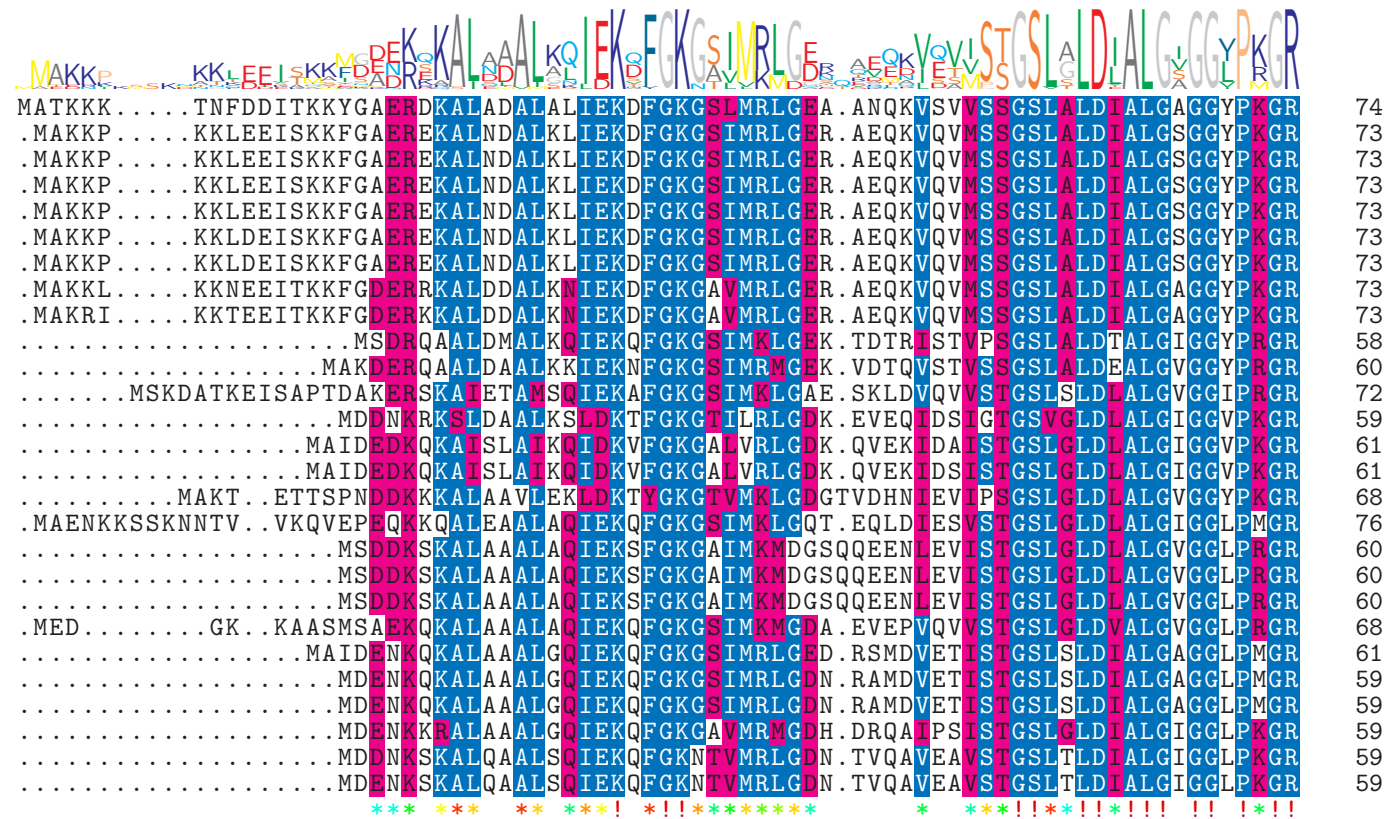


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consensus

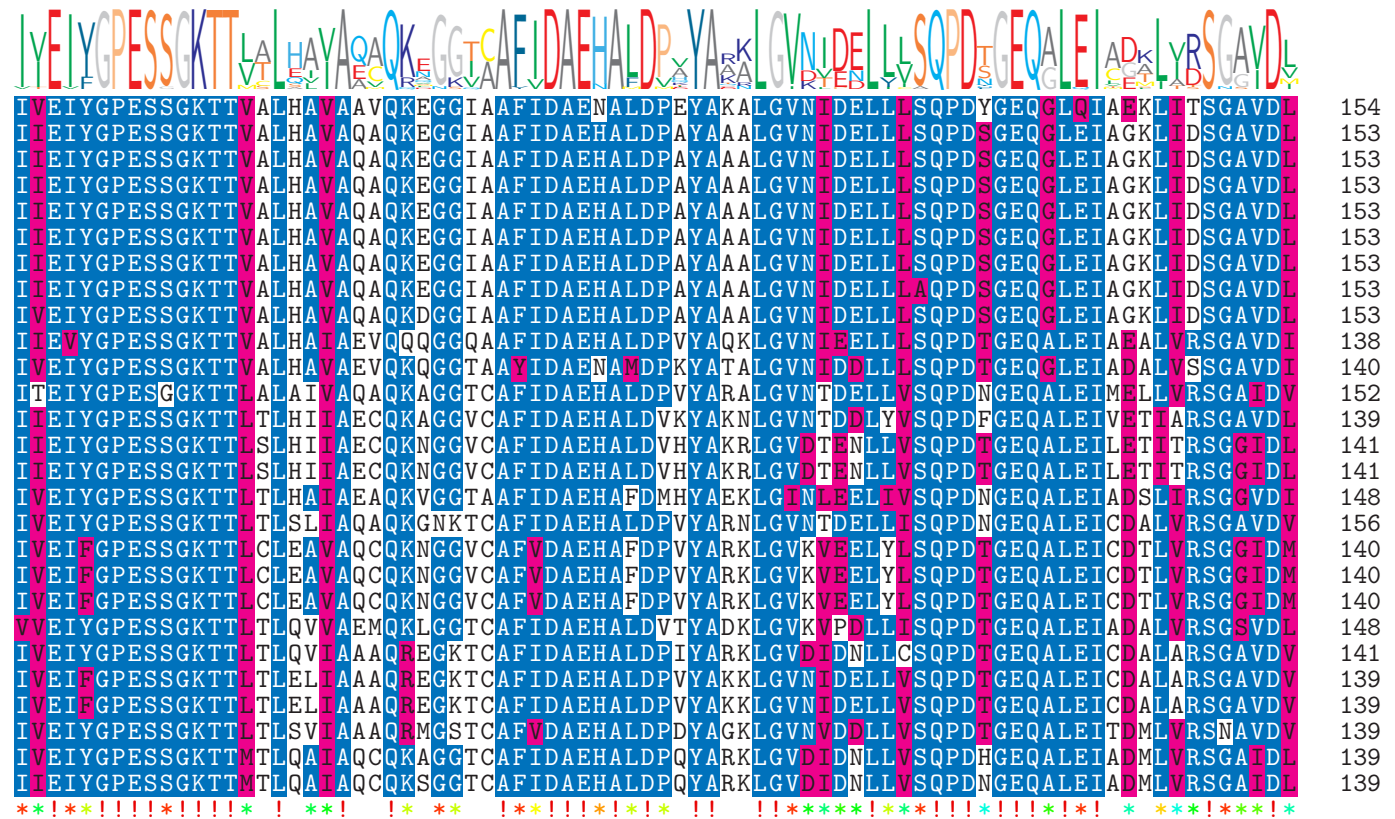
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consensus

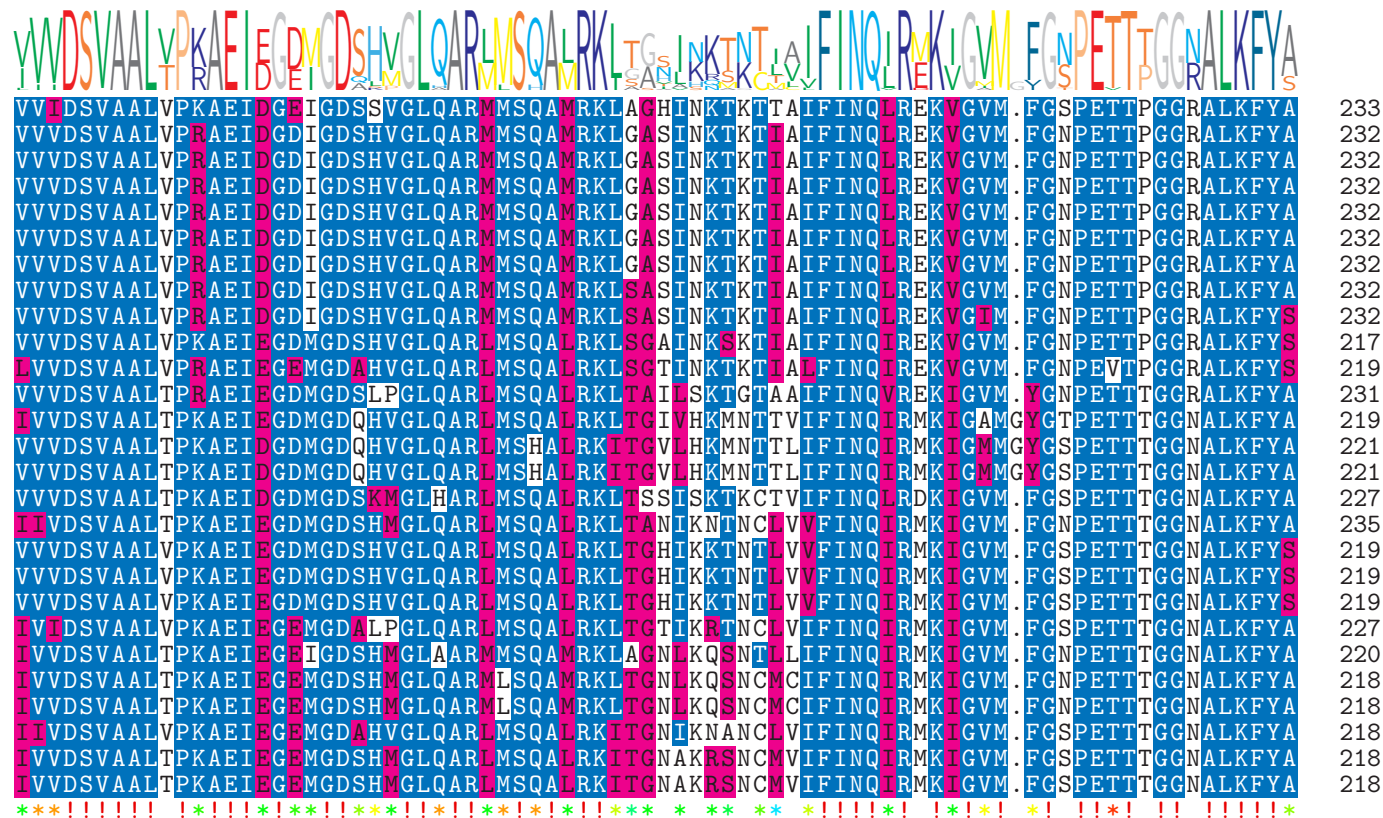
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consensus

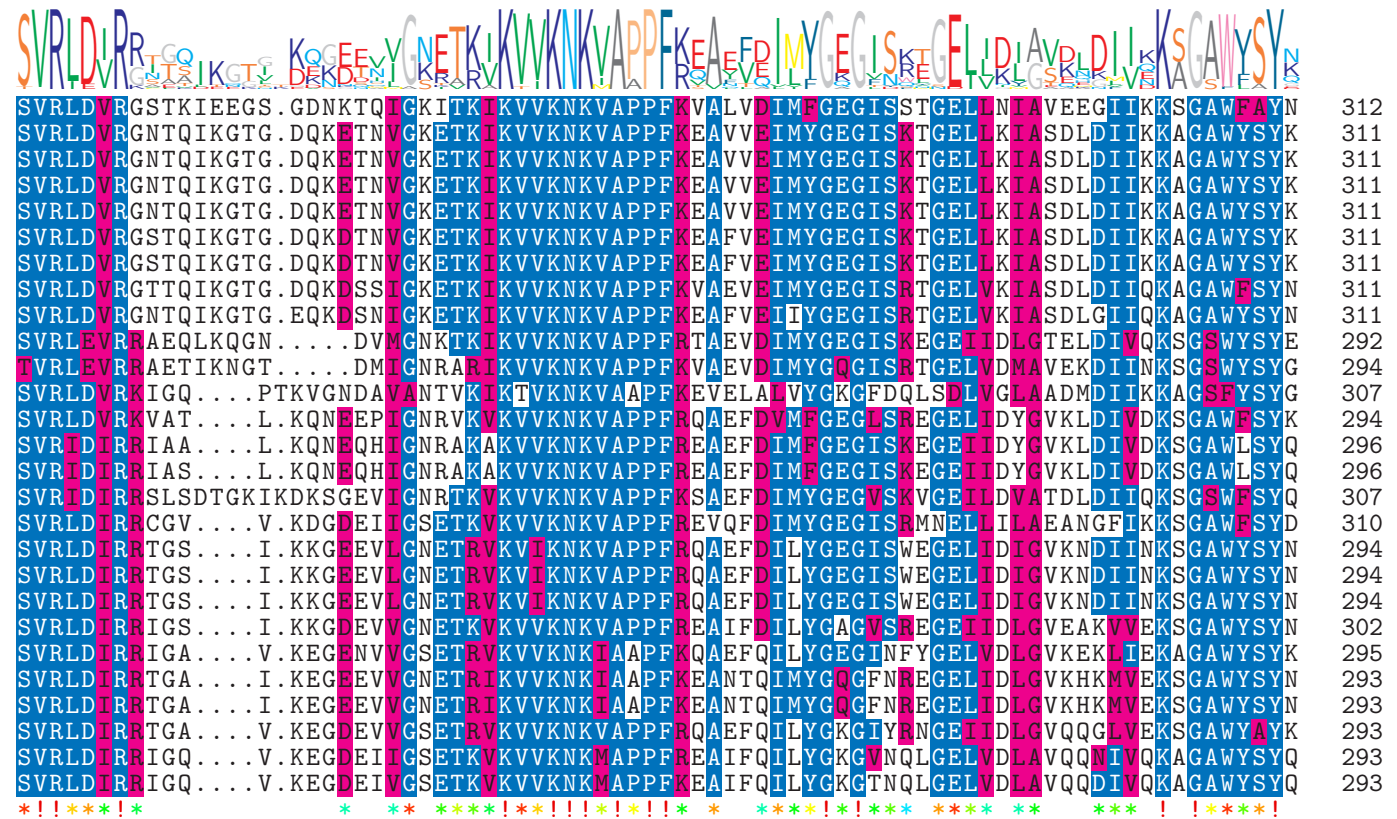
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consensus

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consensus

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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
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DEKIGQGSENAKKYLAHNPEVFAEIDHQRVVFGLIDGEEAAES...KKDE...VAQVDS..VNEEVTLDLGDELEIE	381
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EERLGQGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEETQEEL.EFE.E.....	348
SERIGQGRENAKNYLADHEDVEDEVRLKVRVAAAYGISDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGQGEKTIATYIAERPMEQEIRDRVMMAAIRAGNAGEAPALAPAPAAPEAA...EA.....	363
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DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEE....IMPLPDEPL.....EEME.....	347
DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEE....IMPLPDEPL.....EEME.....	347
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GSKIGGQKANAAKYLEENPEIGQIEEQIRAKLLVTSA....NTKATPVAEDL...ADADI.....	347
GNKIGGQKNNVIRYLEENPQISTEIEAVIREQLLTKAS....DQTAA.HDETE...EEDPLLLES	349
GNKIGGQKNNVIRYFENNQIAEIERNIEREQLLTGT....NGAVQ.I.EDE...EEDPLLLES	349

logo

NTDB id 600 KW2 RS01765 WP 011675413.1	...	387
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NTDB id 1074 ABD1 RS10195 WP 000344167.1	...	349

consensus

 non conserved
 similar
 ≥ 50% conserved