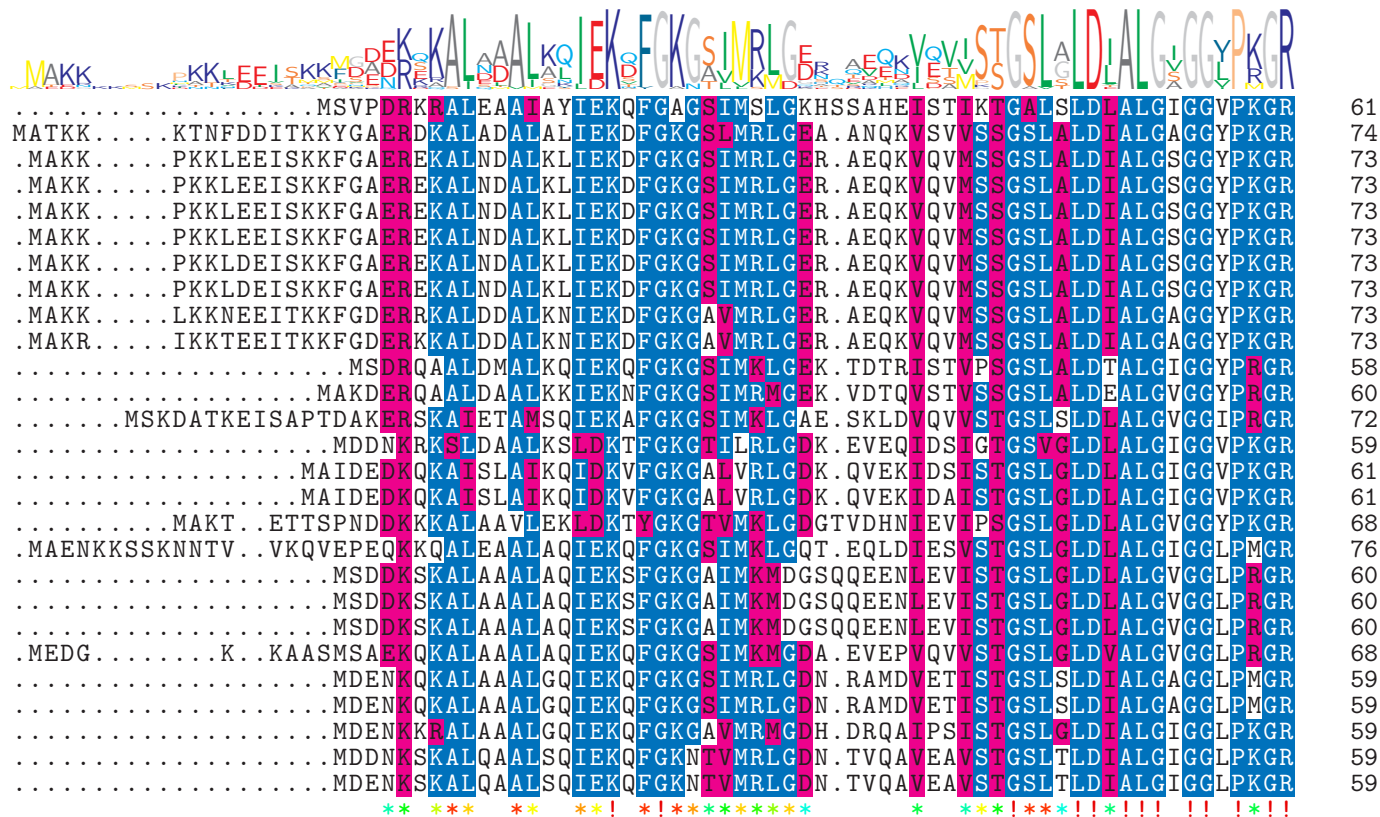


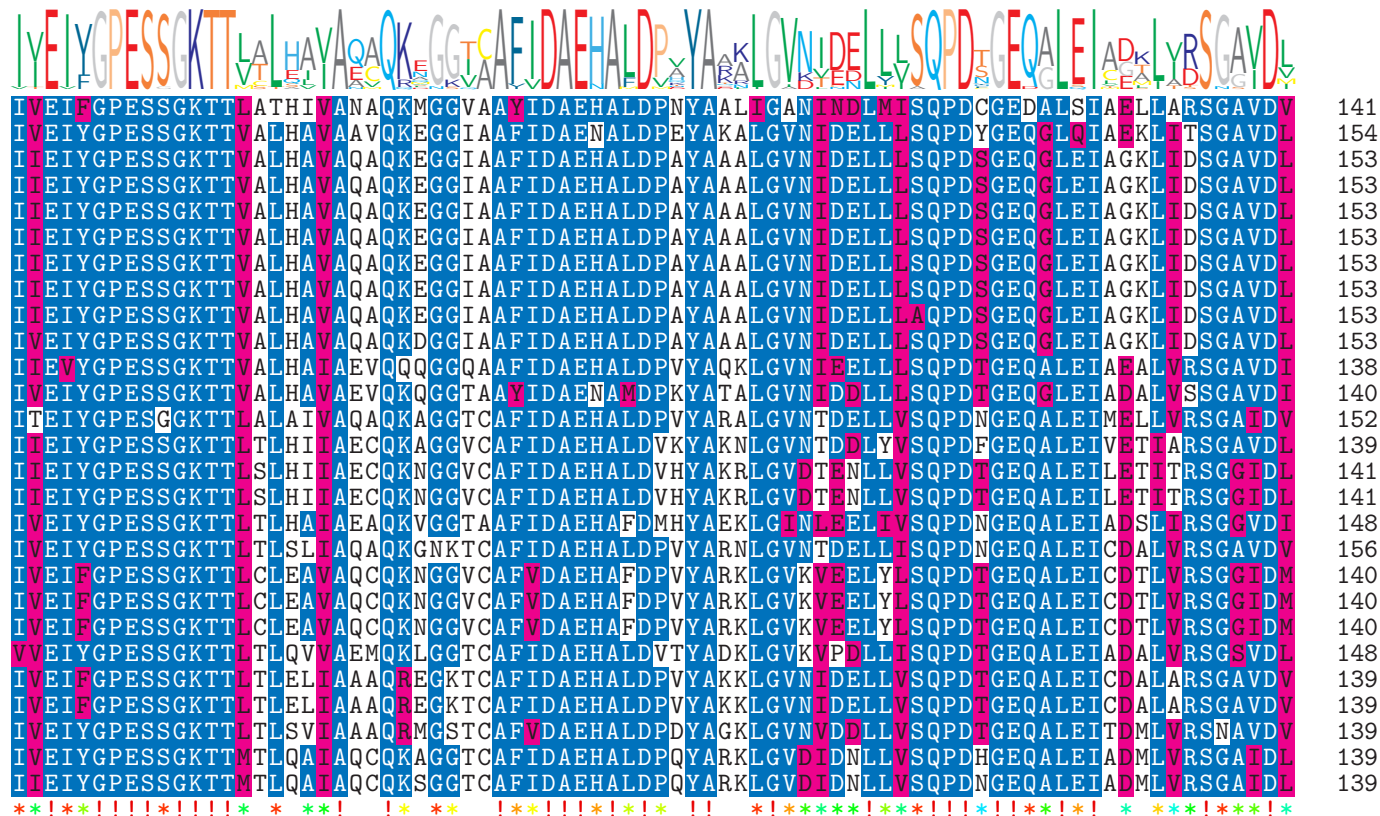
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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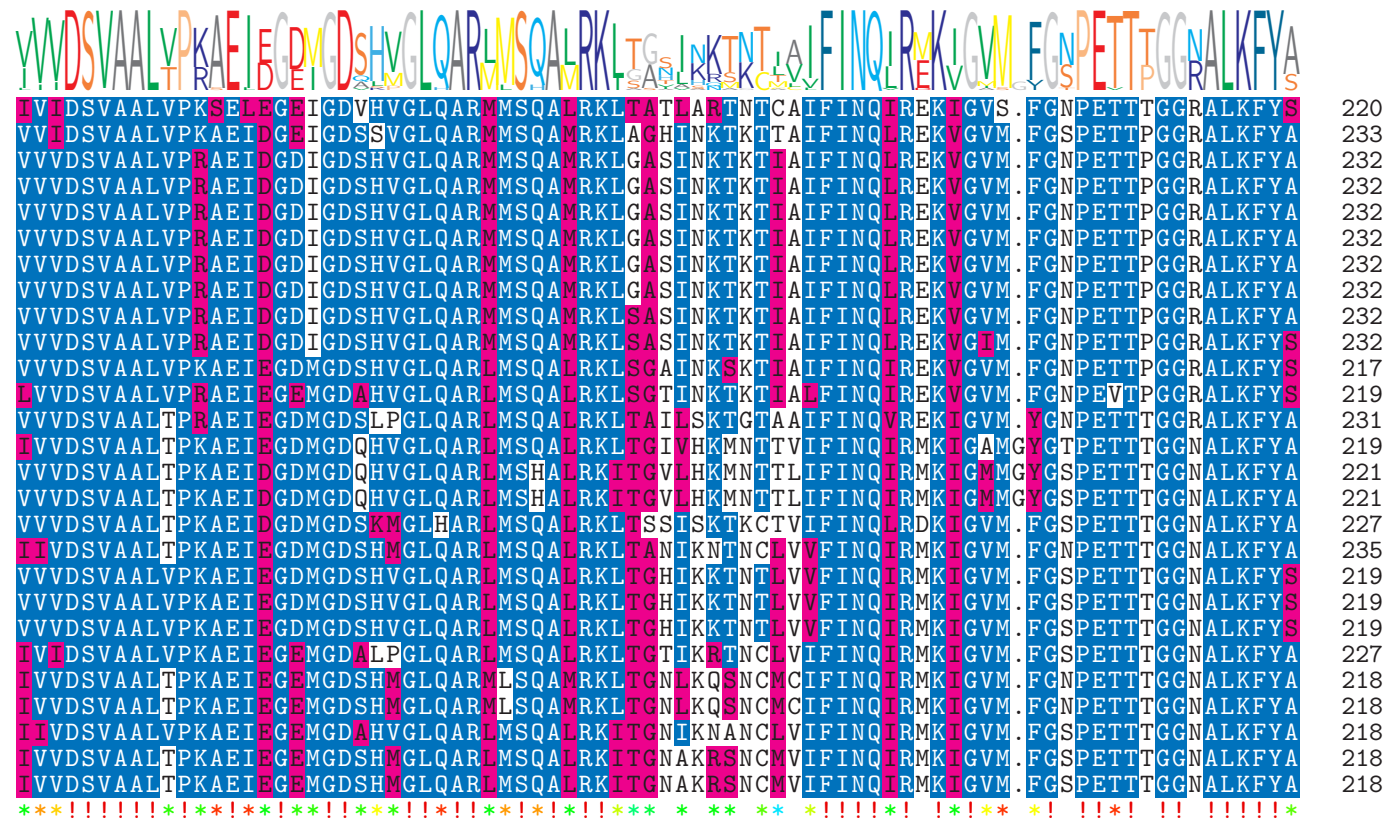
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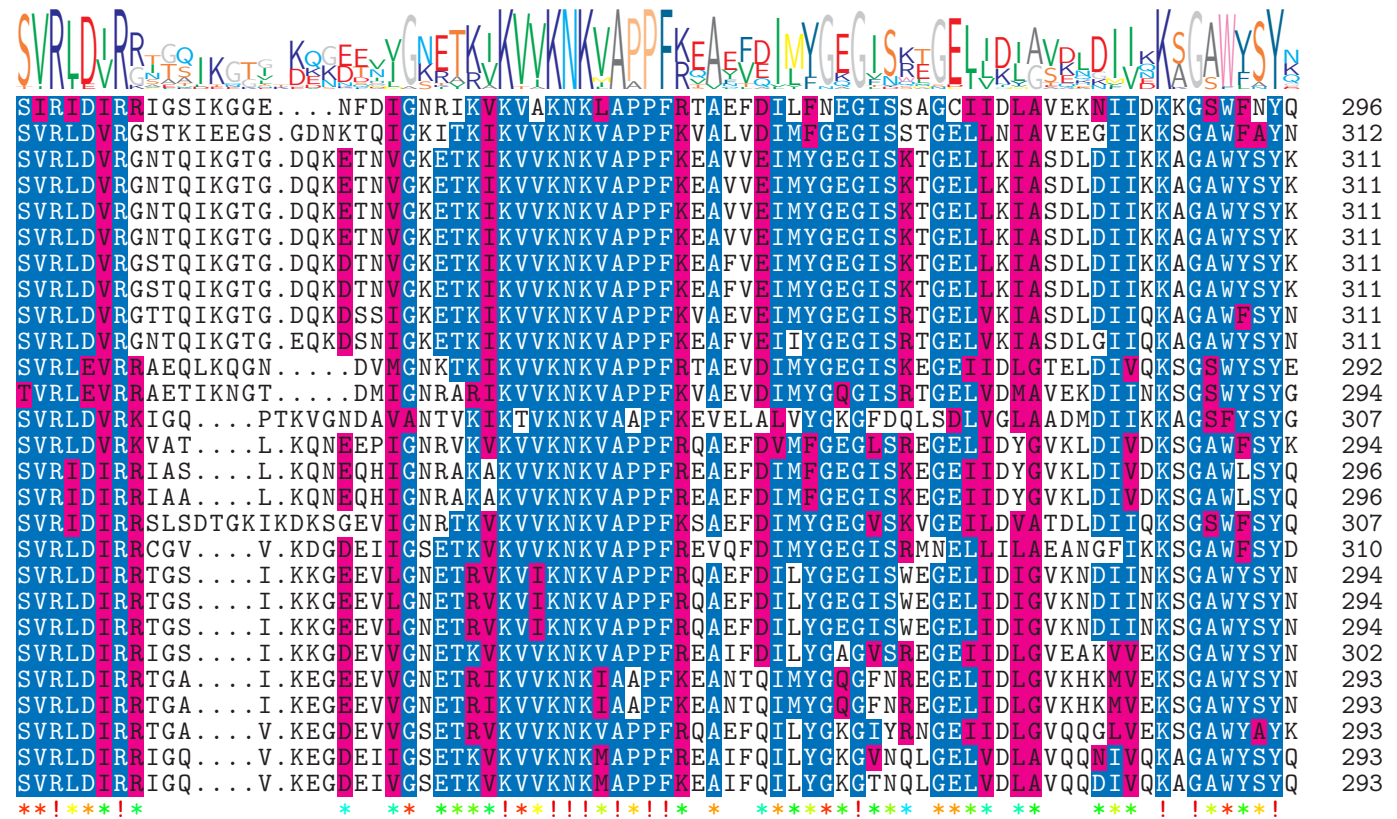
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

Sequence	Score
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DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
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DEKIGQGSSENAKKYLAADNPEVFAEIDHQVRVQFGLIDGEEIAES...KKDE...VAQVDS..VNEEVTLDLGDLEIE	381
GEKIGQGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....ETDEK..ADKNLVLELDDTIELE	377
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EERLGQGSRENAKQFLKENKDIIMLMIQEQIREHYGLDNGGVVQQAAETQEEL.EFE.E.....	348
SERIGQGSRENAKNYLADHEDVEURLKVRVRAAYGISDVPEEDLPTTEDE.QI.NILPDST.....EE.....	355
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DKKLGQGSRENAKALLKEDKALADEITLKIKESIGSNEEI...MPLPDEP..LE..EME.....	347
DKKLGQGSRENAKALLKEDKALADEITLKIKESIGSNEEI...MPLPDEP..LE..EME.....	347
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GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI...TEGT.....Q..DETDERPEE.....	348
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GERIGQGRDNCREFLRNAAELARENENKVRHGLVTPMG...AV.TLAEVEVE..D.....	352
GDKIGQGGKANACKYFLKENPEIAKTLDKKLREMLLNPNEM...QLIAETSSAAD..DVEFGAVPEEF..	354
GDKIGQGGKANACKYFLKENPEIAKTLDKKLREMLLNPNEM...QLIAETSSAAD..DVEFGAVPEEF..	354
GSKIGQGGKANAAKYLEENPEIGQIEEQIRAKLLVTSAN...TKATPVAEDLA..DADI.....	347
GNKIGQGGKNNVIRYLEENPQISTEIEAVIREQLLTKASD...QTA..HDETEE..EPDLL..ES.....	349
GNKIGQGGKNNVIRIFYENNQIAEIERNIREQLLTGTN...GAVQ.I.EDEE..EPDLL..LES.....	349

logo

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

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