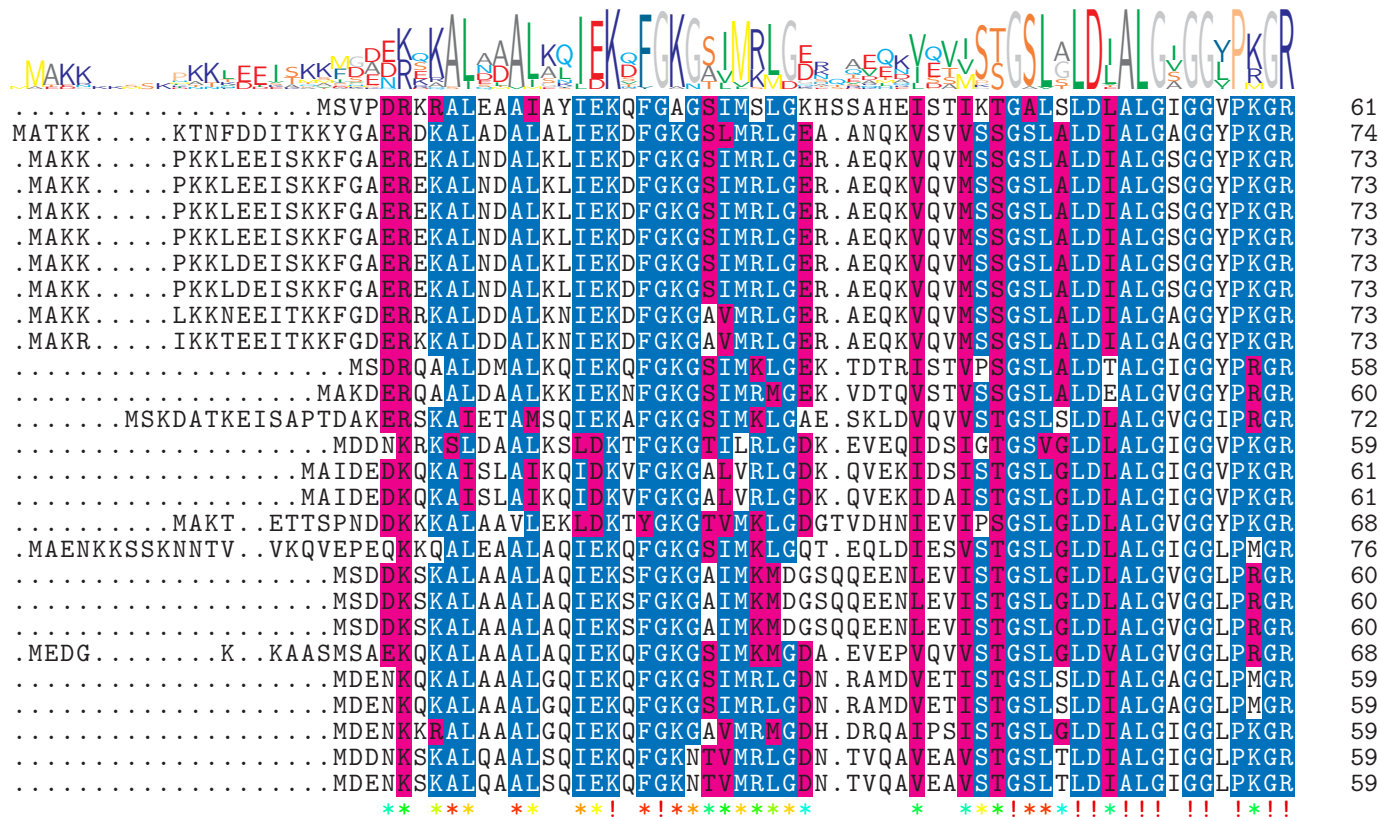


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consensus

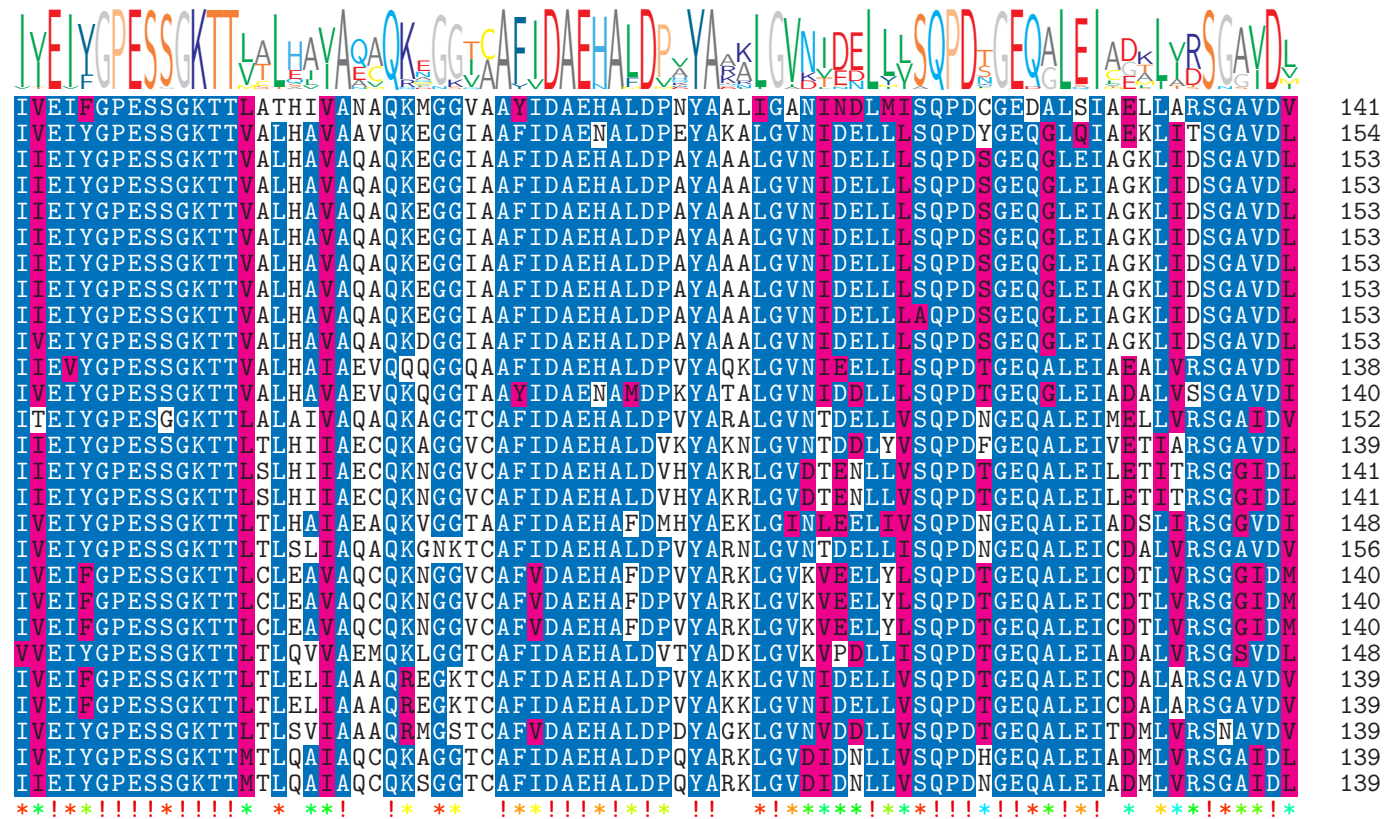
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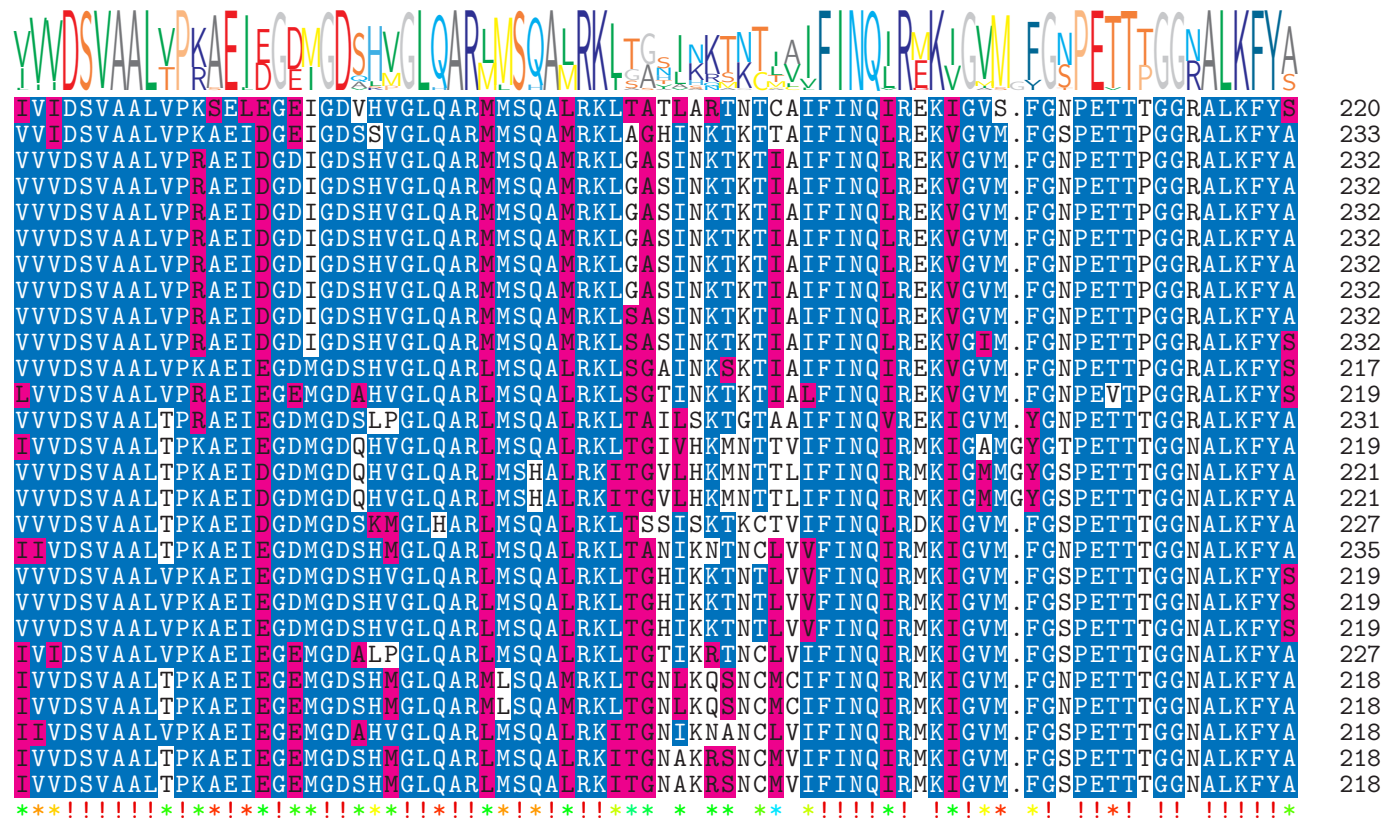
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

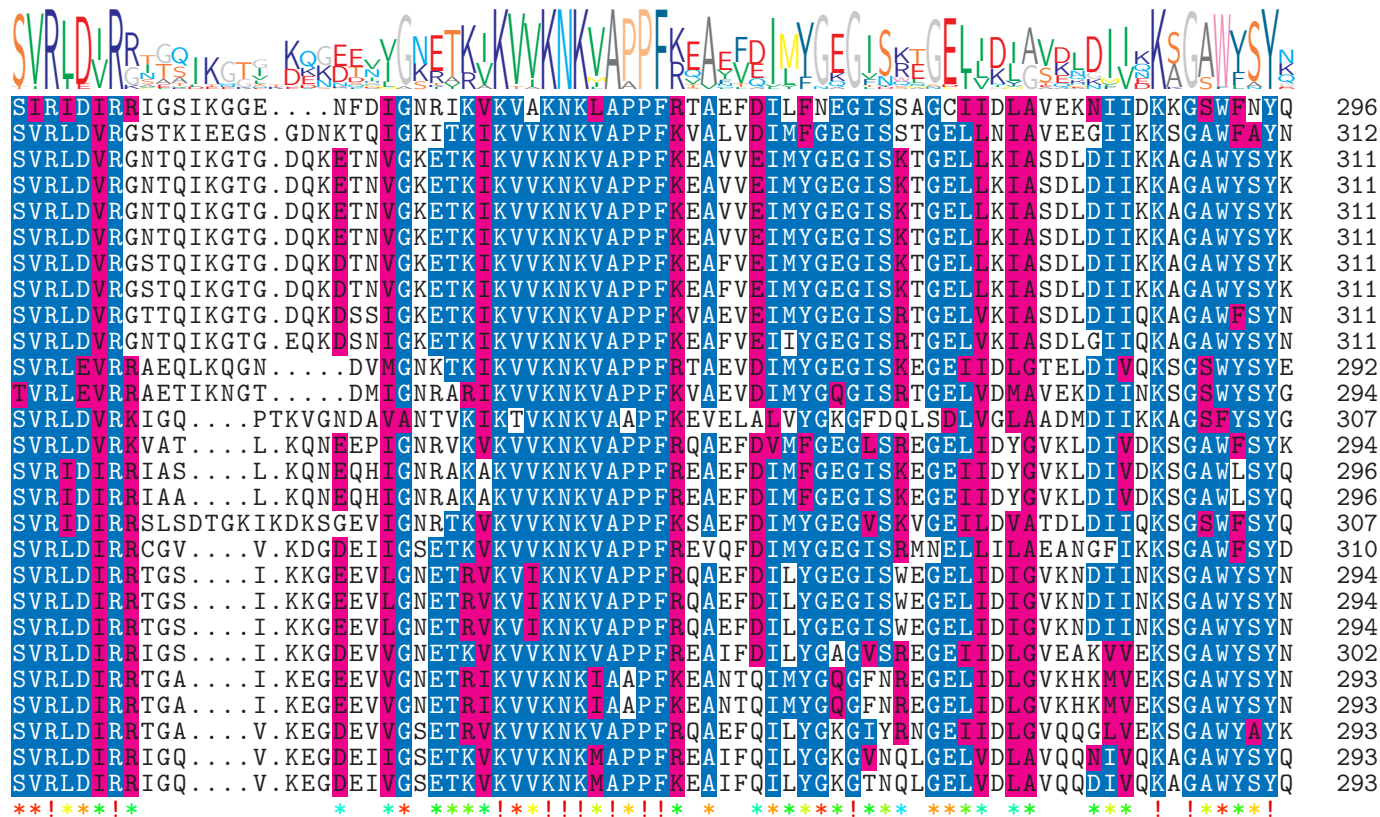
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consensus

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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
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DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTEENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTEENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
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DEKIGQGSSENAKKYLAENPEIFDEIDHKQVRVQFGLIDGEEIAES...KKDE...AAQVDS..VNEEVTLDLGDLEIE	381
DEKIGQGSSENAKKYLAENPEVFAEIDHKQVRVQFGLIDGEEAAES...KKDE...VAQVDS..VNEEVTLDLGDLEIE	381
GEKIGQGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGSSENAKKFLADNPEIFDDIDHKQVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EERLGQGGRENAKQFLKENKDIMLMIQEIREHYGLDNNGVVQQAAETQEEL.EFE.E.....	348
SERIGQGGRENAKNYLADHEDVEVLKVRVRAAYGISDVPEEDLPTTEDE.QI.NILPDST.....EE.....	355
DERIGQGGKEKTIAYIAERPEMEQEIRDRVMAAIRAGNAGEAPALAPAAPEAAE..A.....	363
DKKLGQGGRENSKAFLENPEIADAITKAIQNSMGIEGMI....SGSEDDE..GE..E.....	343
DKKLGQGGRENAKALLKEDKALADEITLKIKESIGSNEEI....MPLPDEP..LE..EME.....	347
DKKLGQGGRENAKALLKEDKALADEITLKIKESIGSNEEI....MPLPDEP..LE..EME.....	347
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GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI....TEGT.....Q..DETDERPEE.....	348
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GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI....TEGT.....Q..DETDERPEE.....	348
GERIGQGGKDNCRFLRENAELAREIENKVRHLGVTPMG....AV.TLAEVEVE..D.....	352
GDKIGQGGKANACKYFLKENPEIAKTLDDKRLREMLLNPNEM....QLIAETSSAAD..DVEFGAVPEEF.....	354
GDKIGQGGKANACKYFLKENPEIAKTLDDKRLREMLLNPNEM....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