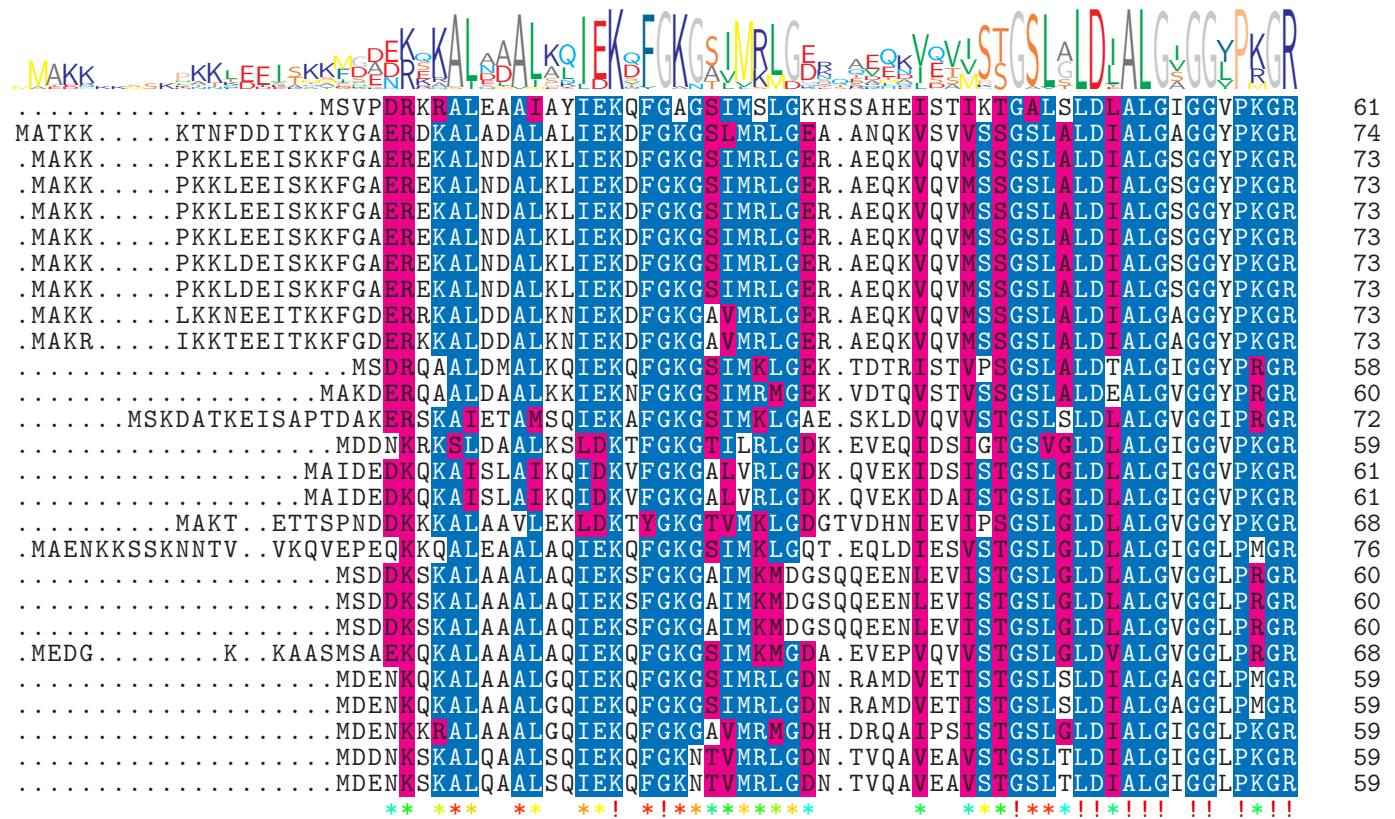


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consensus

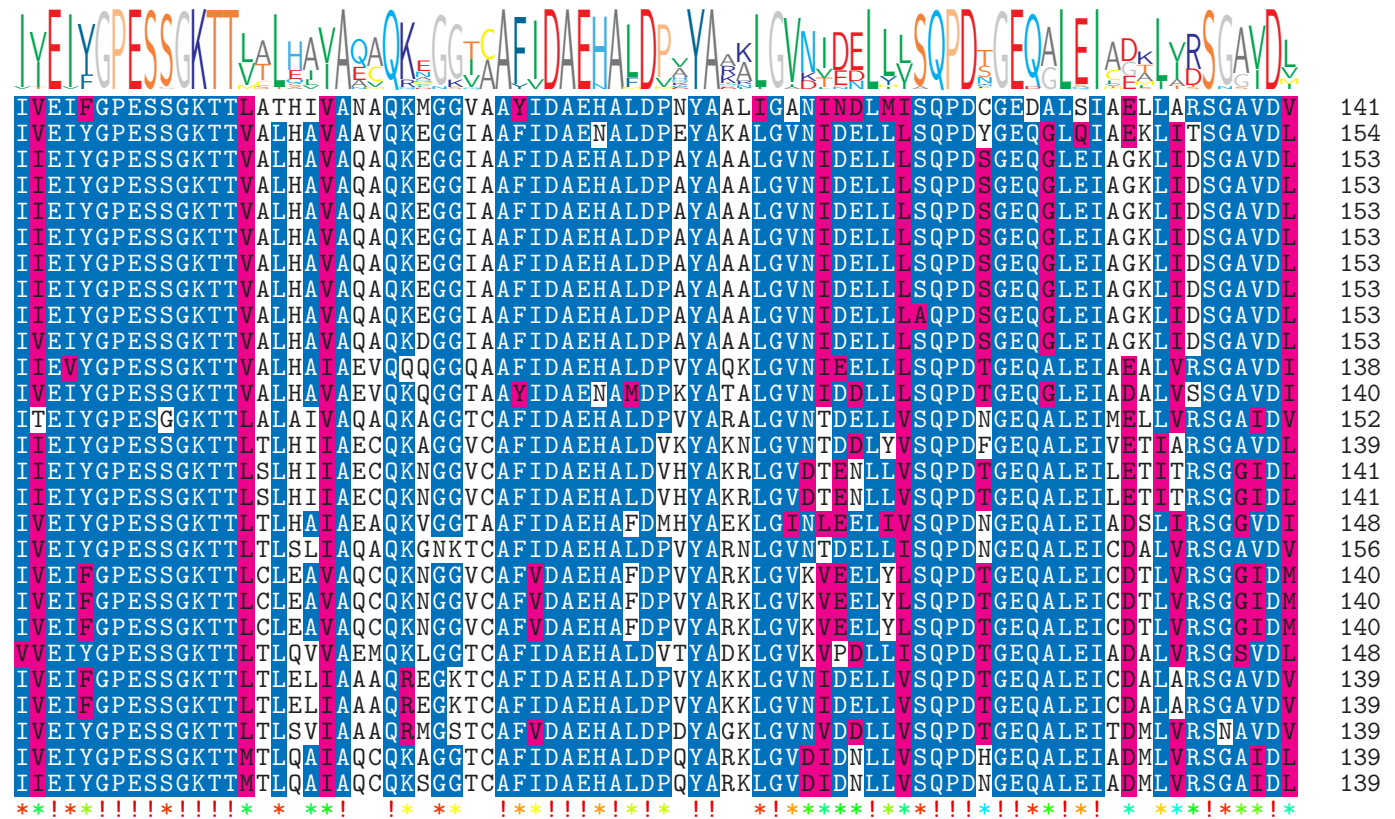
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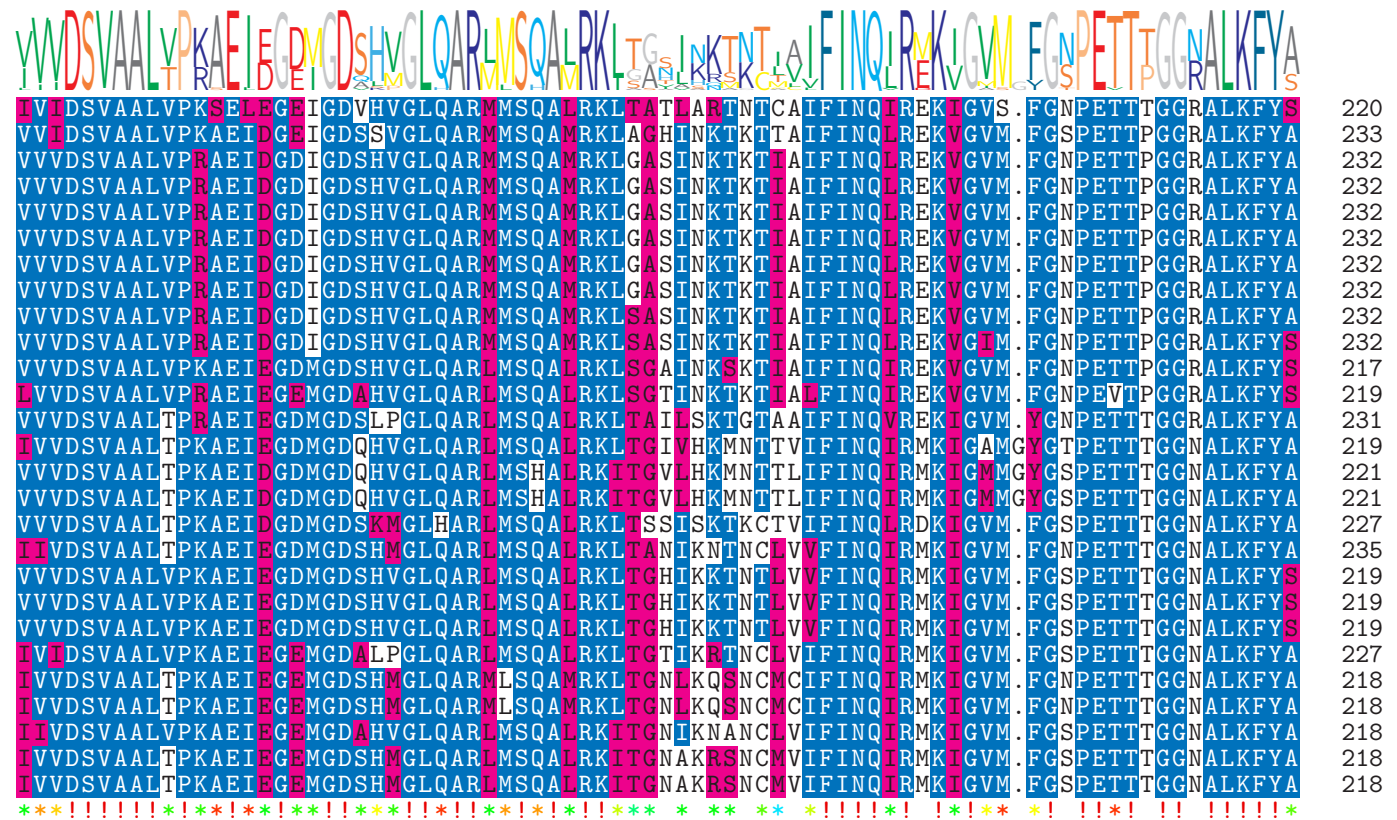
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consensus

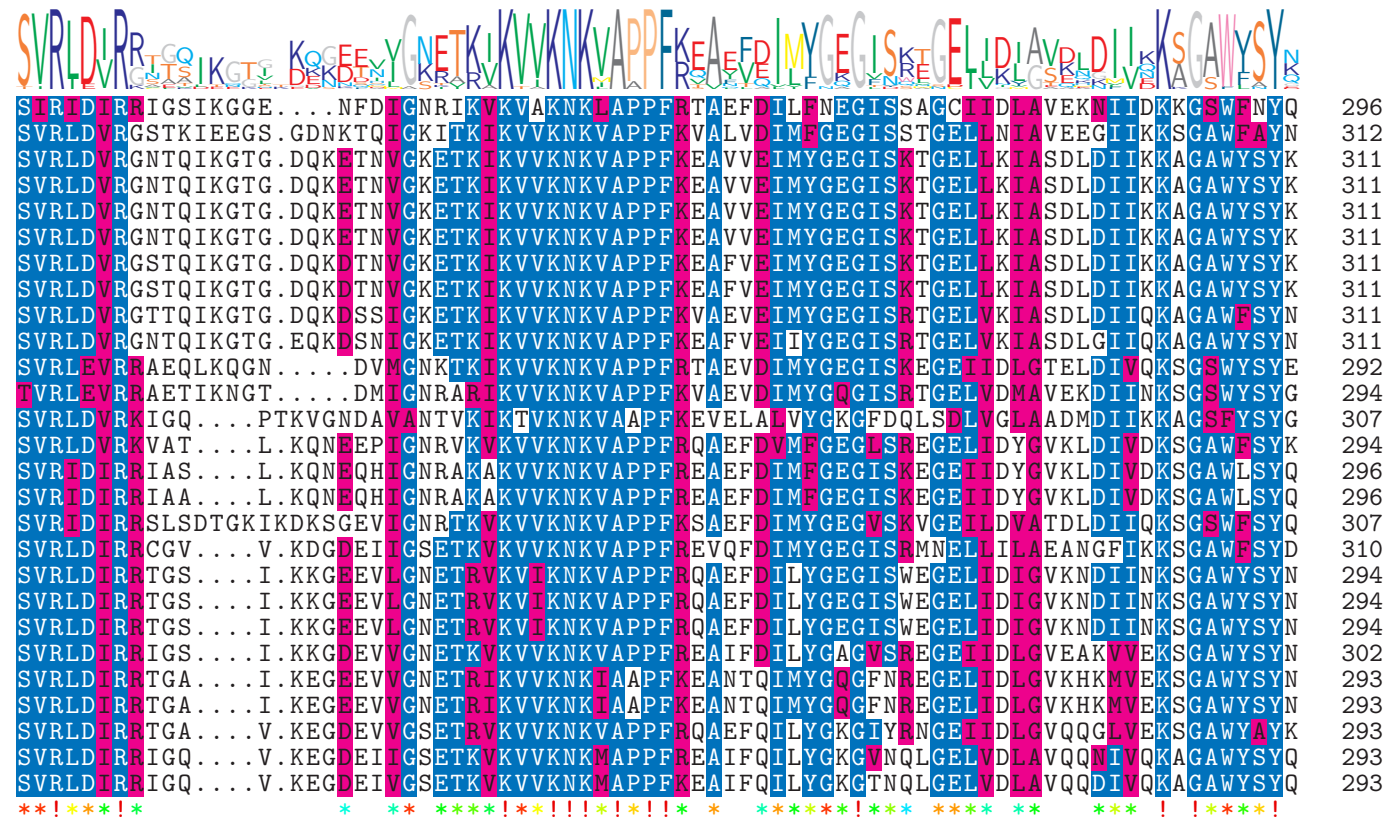
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
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DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLADNPFIQFDEIDHKQVRVQFGLIDGEEIAES...KKDE...AAQVDS..VNEEVTLDLGDLEIE	381
DEKIGQGSSENAKKYLADNPVFAEIDHKQVRVQFGLIDGEEAAES...KKDE...VAQVDS..VNEEVTLDLGDLEIE	381
GEKIGQGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE...E...TDDLALDLNGIEIE	377
GEKIGQGSSENAKKFLADNPFIQFDDIDHKQVRVQYGLIEEDNTEEKQSSKEK...ETDEK..ADKNLVLELDDTIELE	382
EERLGQGGRENAKQFLKENKDIMLMIQEIRHYGLDNNGVVQQAAETQEEL.EFE.E	348
SERIGQGRENAKNYLADHEDVEVLKVRVRAAYGISDVPPEEDLPTTEDE.QI.NILPDST...EE	355
DERIGQGEKTIAYIAERPEMEQEIRDRVMAAIRAGNAGEAPALAPAAPEAAE..A	363
DKKLGQGGRENSKAFLENPEIADAITKAIQNSMGIEGMI...SGSEDDE..GE..E	343
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GERIGQGRDNCREFLENALARIEIENKVRHLGVTPMG...AV.TLAEVEVE..D	352
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GDKIGQGKANACKYLNKENPEIAKTLDDKLREMLLNPNEM...QLIAETSSAAD..DVEFGAVPEEF	354
GSKIGQGKANAAKYLEENPEIGQIEEQIRAKLLVTSAN...TKATPVAEDLA..DADI	347
GNKIGQGKNNVIRYLEENPQISTEIEAVIREQLLTKASD...QTAA.HDETEE..EPDLL..ES	349
GNKIGQGKNNVIRIFYENNQIAEIERNIQREQLLTGTN...GAVQ.I.EDEE..EPDLL..LES	349

logo

		IEE	
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consensus			

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