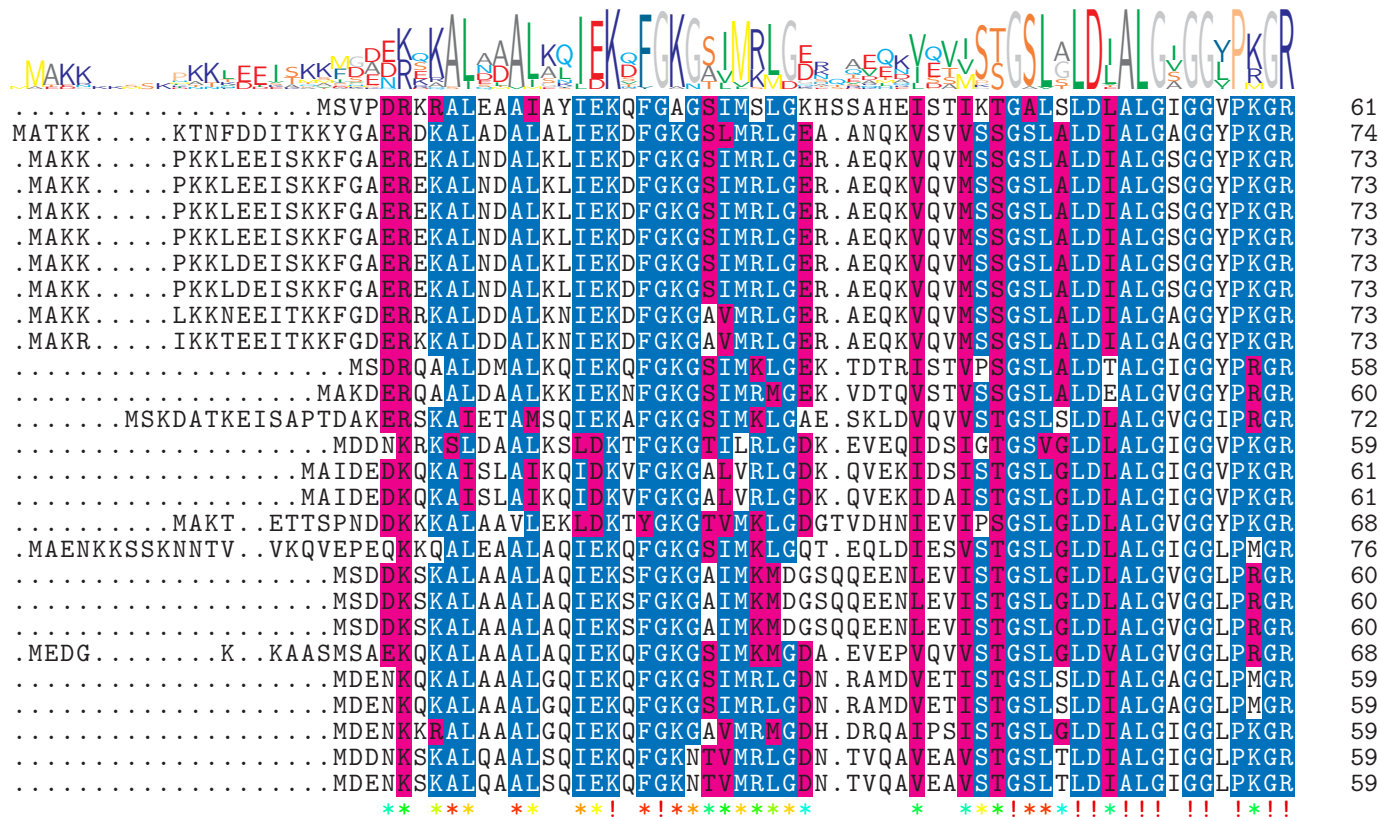


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consensus

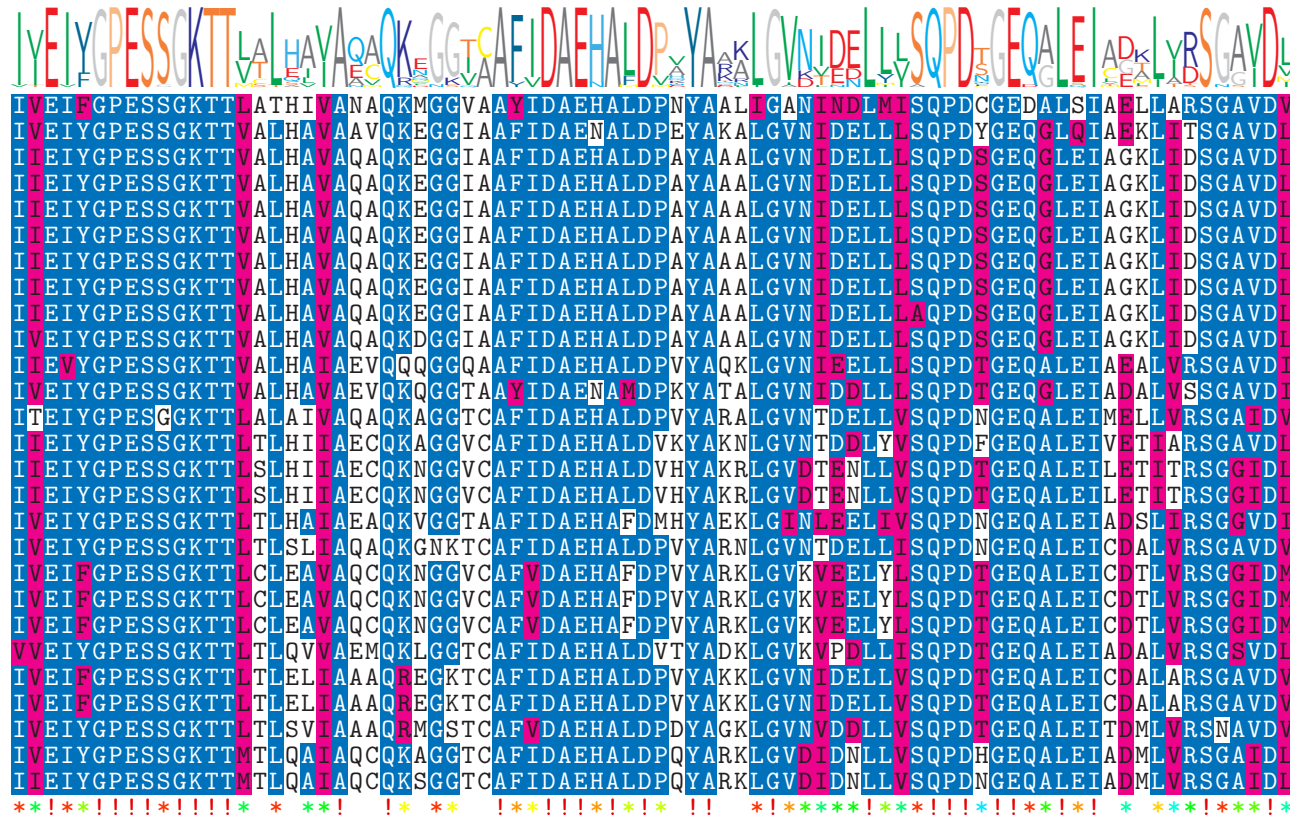
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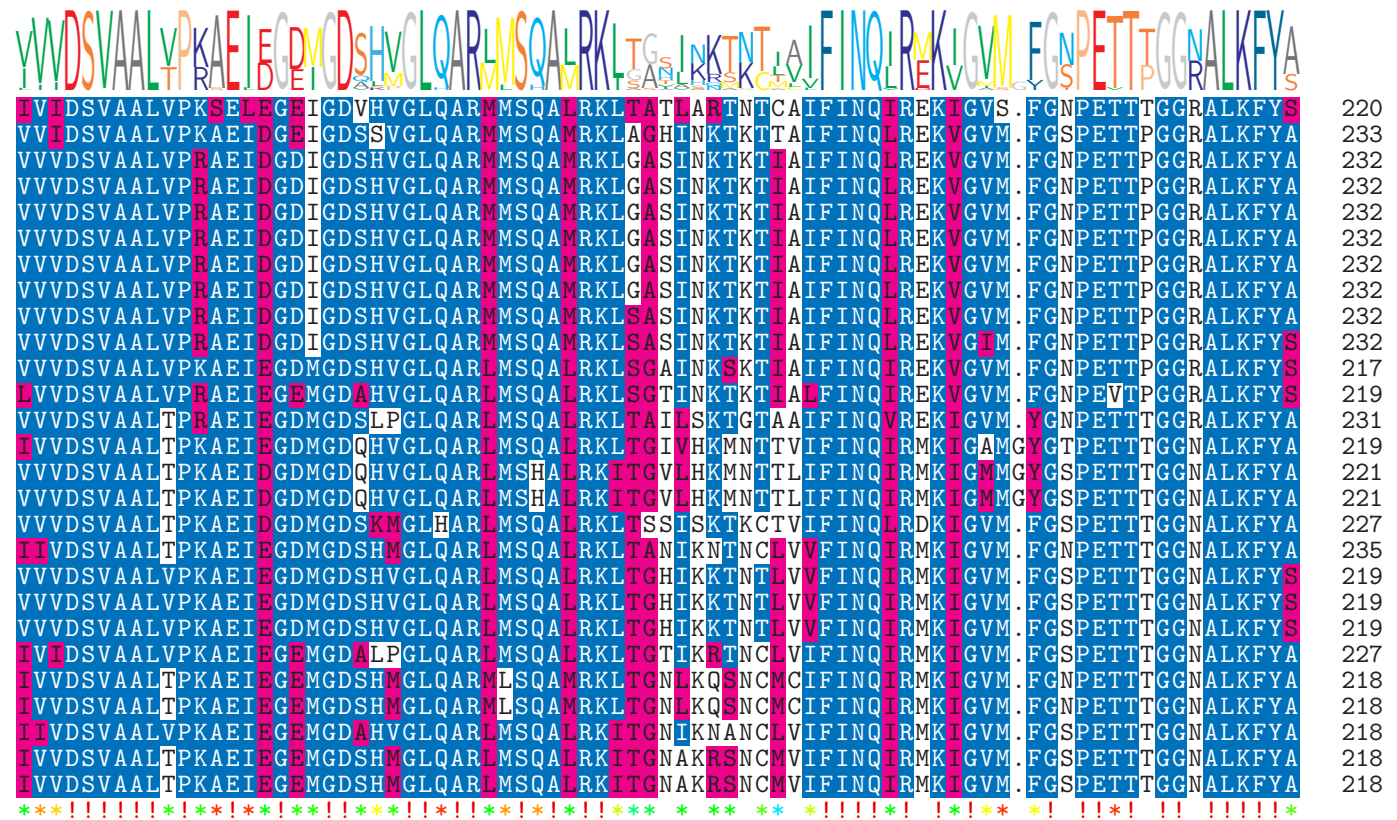
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

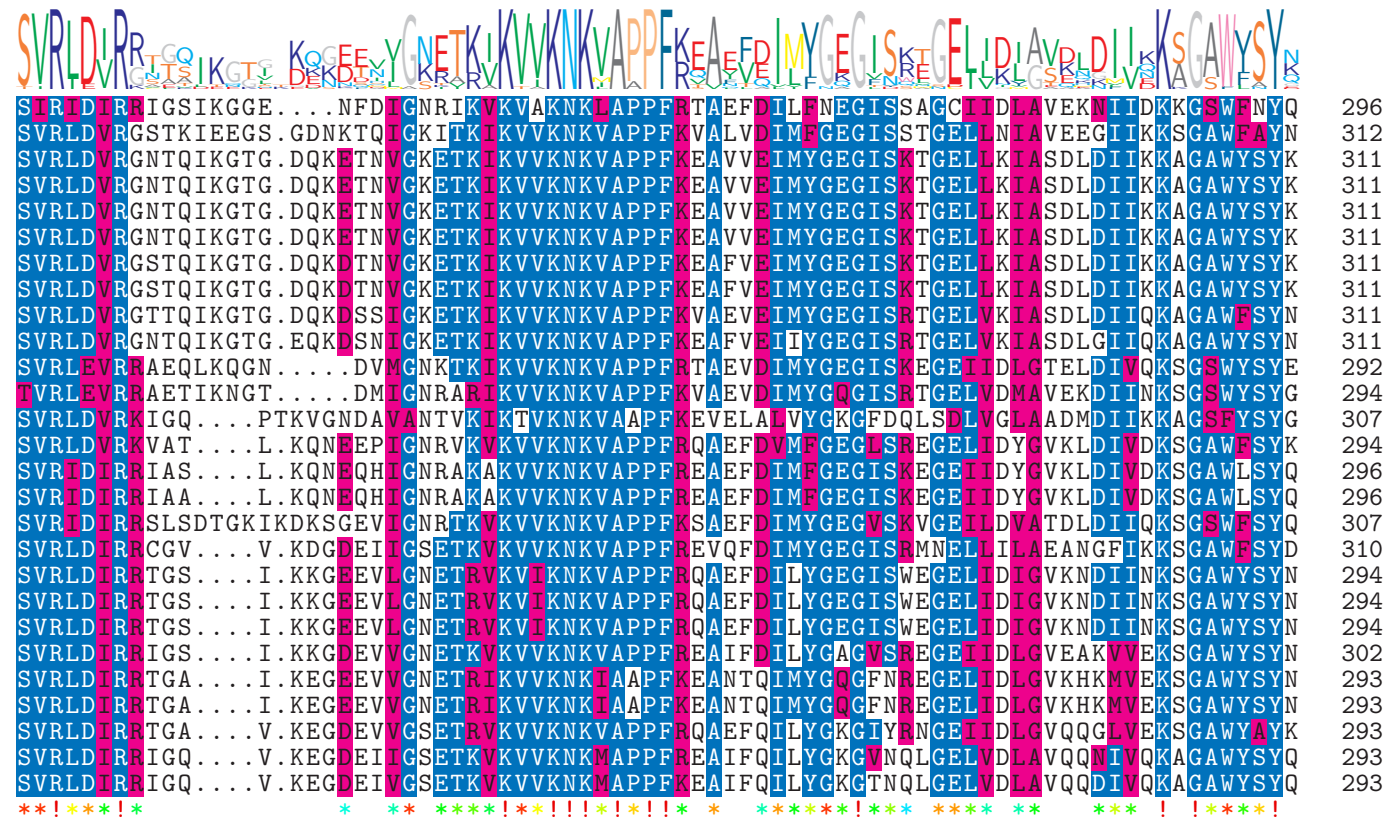
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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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
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DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAENPEIFDEIDHKVVRVQFGLIDGEEIAES...KKDE...AAQVDS..VNEEVTLDLGDLEIE	381
DEKIGQGSSENAKKYLAENPEVFAEIDHKVVRVQFGLIDGEEAAES...KKDE...VAQVDS..VNEEVTLDLGDLEIE	381
GEKIGQGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE...E...TDDLALDLNGIEIE	377
GEKIGQGSSENAKKFLADNPEIFDDIDHKVVRVQYGLIEEDNTEEKQSSKEK...ETDEK..ADKNLVLELDDTIELE	382
EERLGGGRENAKQFLKENKDIMLMIQEIREHYGLDNNGVVQQAAETQEEL.EFE.E	348
SERIGQGRENAKNYLADHEDVEURLKVRVRAAYGISDVPPEEDLPTTEDE.QI.NILPDST...EE	355
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DKKLGQGRENSKAFLENPEIADAITKAIQNSMGIEGMI...SGSEDDE..GE..E	343
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GERIGQGRDNCREFLENALARIEIENKVRHLGVTPMG...AV.TLAEVEVE..D	352
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GDKIGQGGKANACKYLNKENPEIAKTLDKKLREMLLNPNEM...QLIAETSSAAD..DVEFGAVPEEF	354
GSKIGQGGKANAAKYLEENPEIGQIEEQIRAKLLVTSAN...TKATPVAEDLA..DADI	347
GNKIGQGGKNNVIRYLEENPQISTEIEAVIREQLLTKASD...QTAA.HDETEE..EPDLL..ES	349
GNKIGQGGKNNVIRIFYENNQIAEIERNIREQLLTTGTN...GAVQ.I.EDEE..EPDLL..LES	349

logo

		IEE	
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NTDB id 1022 ACIAD RS06390 WP 004925639.1	...	349	
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consensus			

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