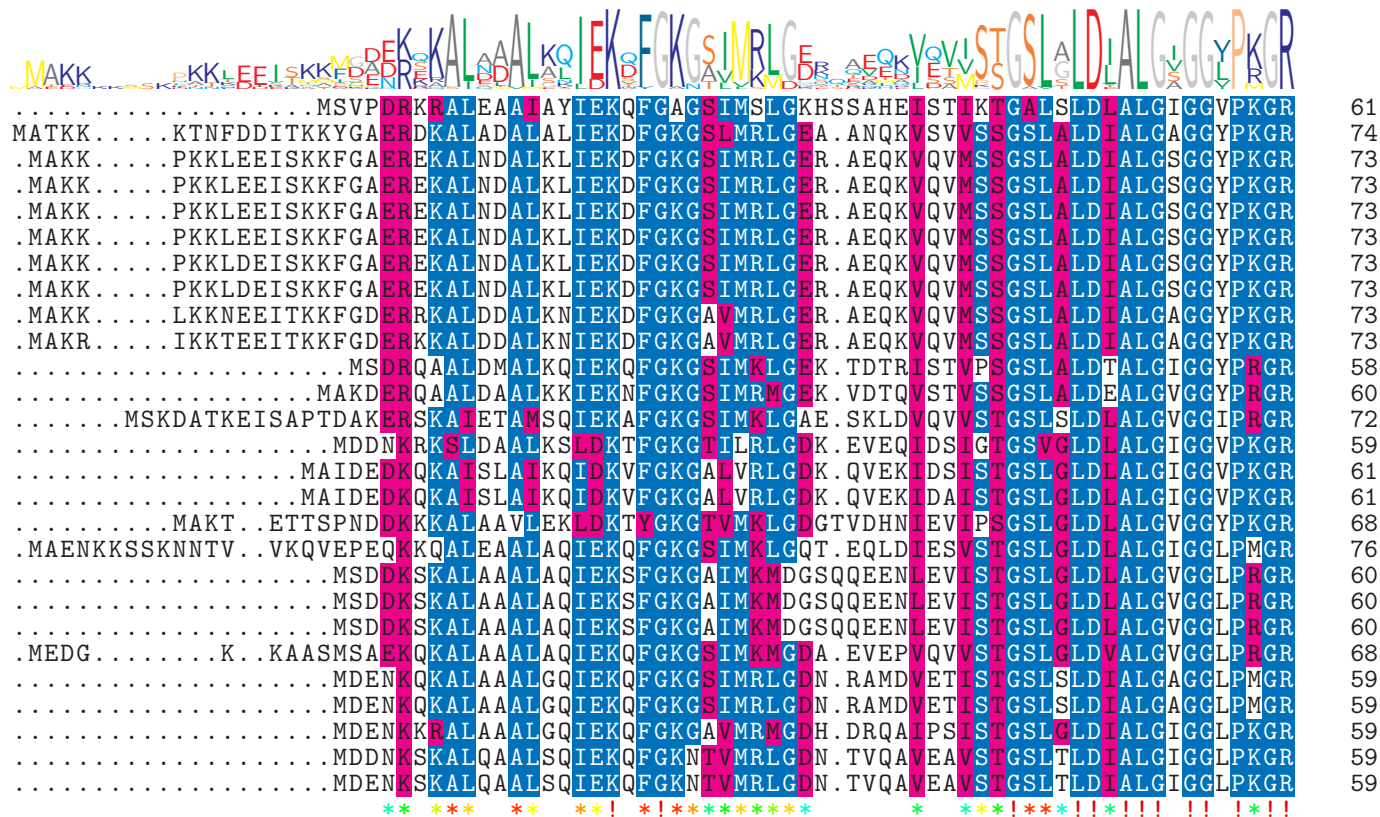


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NTDB id 527 SMSK321 RS11065 WP 001085454.1
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NTDB id 625 LCA RS02525 WP 011374196.1
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consensus

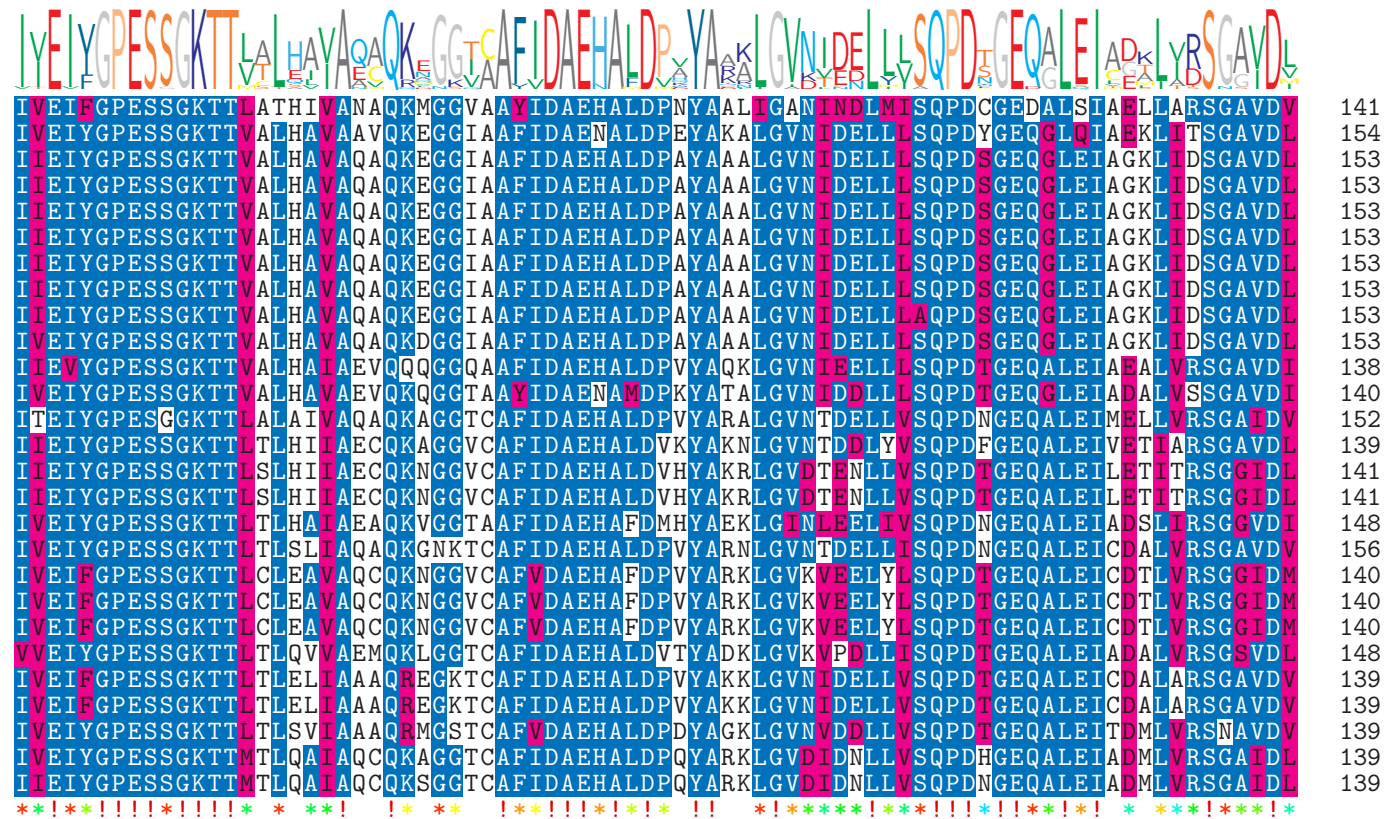
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

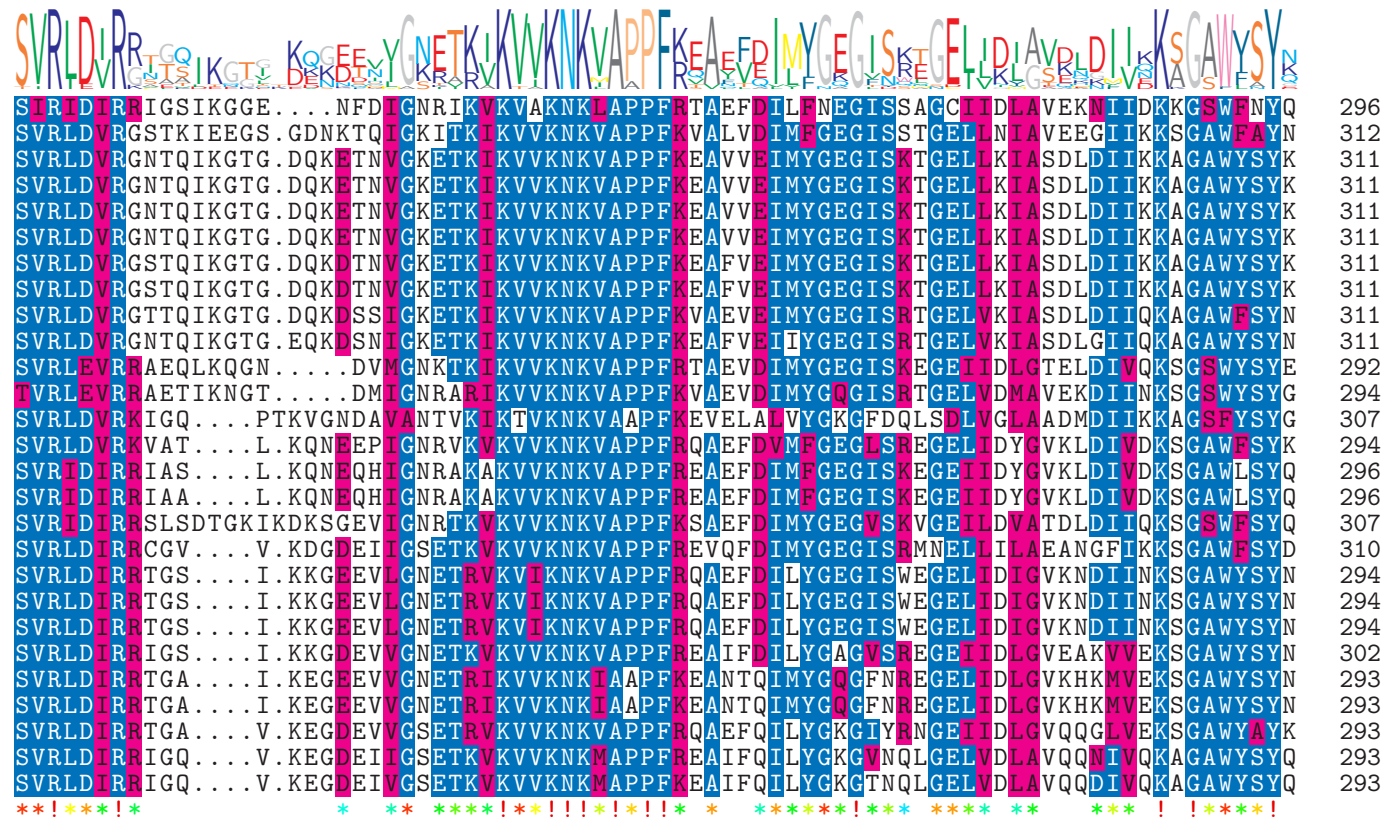
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consensus

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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
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DEKIGQGGAEKAKNYLKEHQDVDFEIDHKVRAAHGLDDSEVAETEETETASKTAKAKKEEKAVETEIELELED	387
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLADNPEIFDEIDHKVVRVQFGLIDGEEIAES...KKDE...AAQVDS..VNEEVTLDLGDLEIE	381
DEKIGQGSSENAKKYLADNPEVFAEIDHKVVRVQFGLIDGEEAAES...KKDE...VAQVDS..VNEEVTLDLGDLEIE	381
GEKIGQGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE...E...TDDLALDLNGIEIE	377
GEKIGQGSSENAKKFLADNPEIFDDIDHKVVRVQYGLIEEDNTEEKQSSKEK...ETDEK..ADKNLVLELDDTIELE	382
EERLGQGGRENAKQFLKENKDIMLMIQEIREHYGLDNNGVVQQAAETQEEL.EFE.E	348
SERIGQGRENAKNYLADHEDVEVLKVRVRAAYGISDVPPEEDLPTTEDE.QI.NILPDST...EE	355
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DKKLGQGGRENSKAFLENPEIADBITKAIQNSMGIEGMI...SGSEDDE..GE..E	343
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DKKLGQGGRENAKALLKEDKALADEITLKIKESIGSNEEI...MPLPDEP..LE..EME	347
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GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI...TEGT...Q..DETDERPEE	348
GERIGQGRDNCREFLENALARIEIENKVREHLGVTPMG...AV.TLAEVEVE..D	352
GDKIGQGGKANACKYLNKENPEIAKTLDKKLREMLLNPNEM...QLIAETSSAAD..DVEFGAVPEEF	354
GDKIGQGGKANACKYLNKENPEIAKTLDKKLREMLLNPNEM...QLIAETSSAAD..DVEFGAVPEEF	354
GSKIGQGGKANAAKYLEENPEIGQIEEQIRAKLLVTSAN...TKATPVAEDLA..DADI	347
GNKIGQGGKNNVIRYLEENPQISTEIEAVIREQLLTKASD...QTAA.HDETEE..EPDLL..ES	349
GNKIGQGGKNNVIRIFYENNQIAEIERNIREQLLTTGTN...GAVQ.I.EDEE..EPDLL..LES	349

logo

		IEE	
NTDB id 61252 KW39 RS03510 WP 009872817.1	...	352	
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NTDB id 1074 ABD1 RS10195 WP 000344167.1	...	349	
consensus			

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