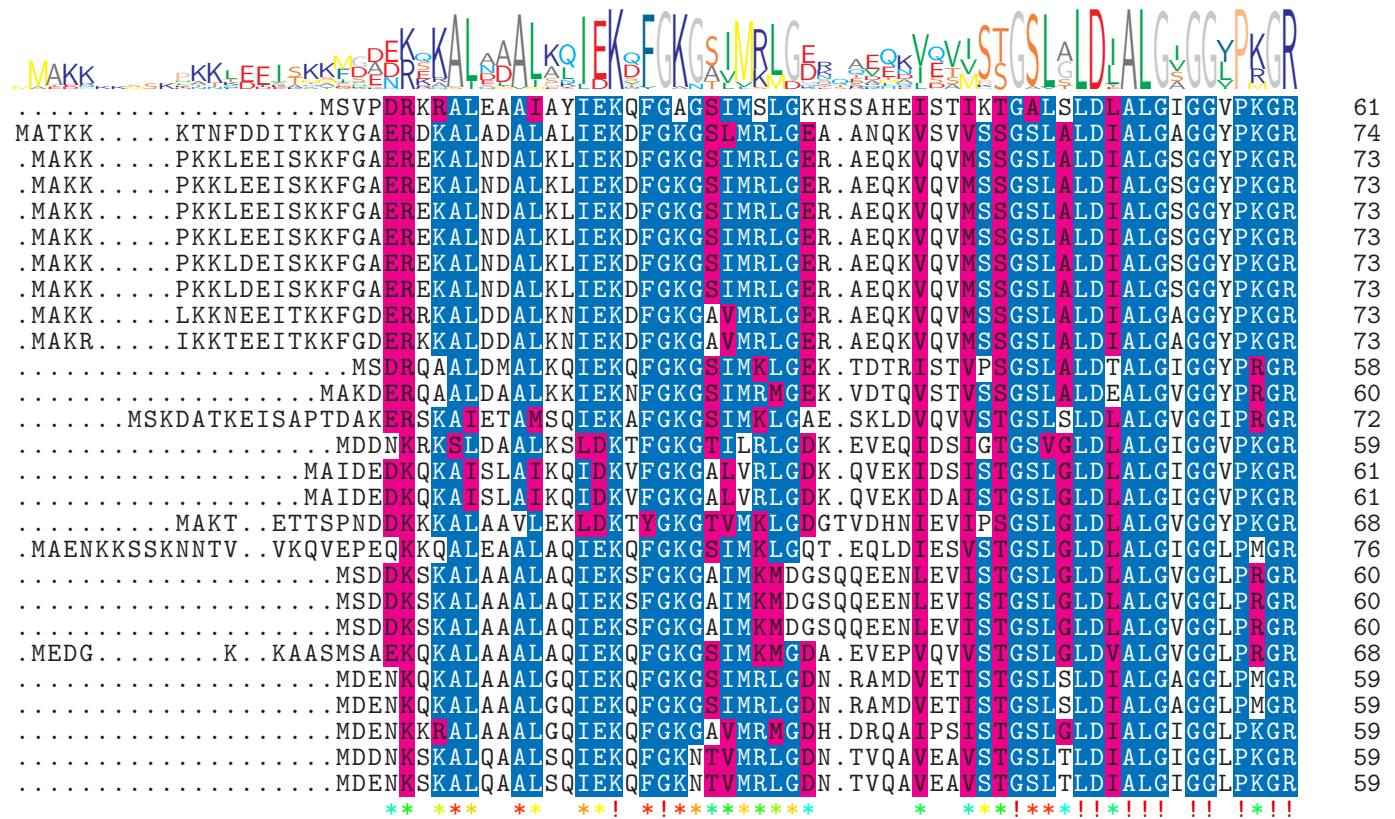


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consensus

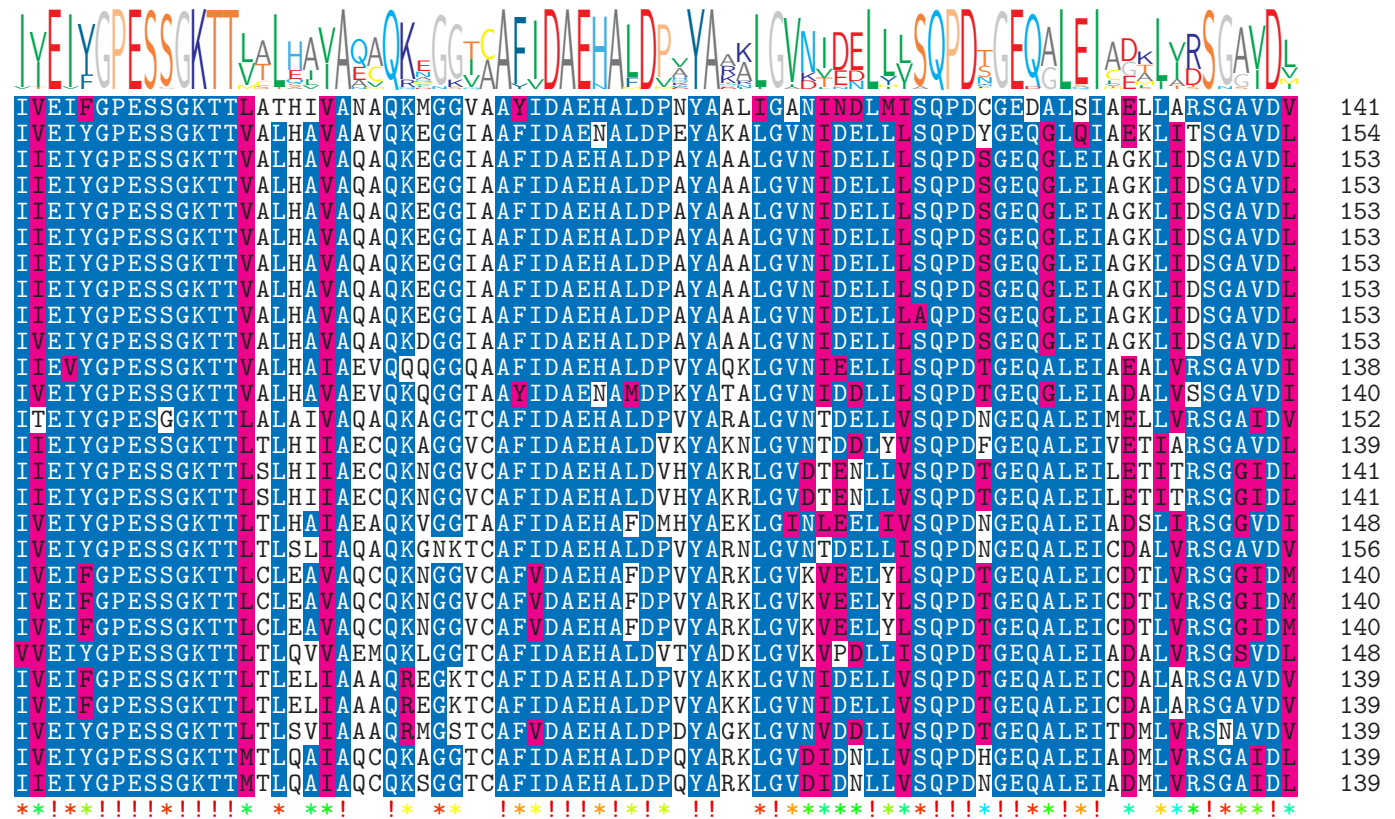
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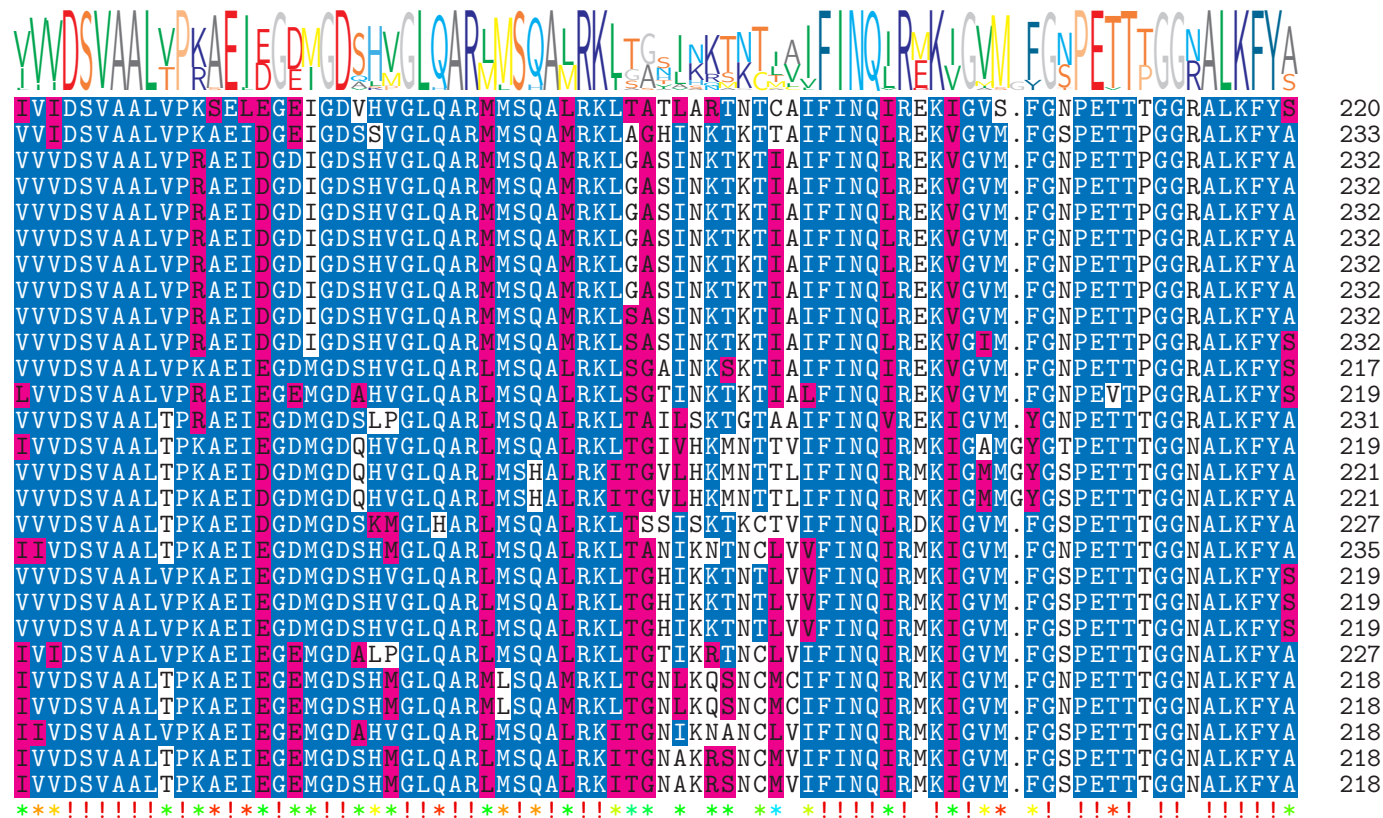
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

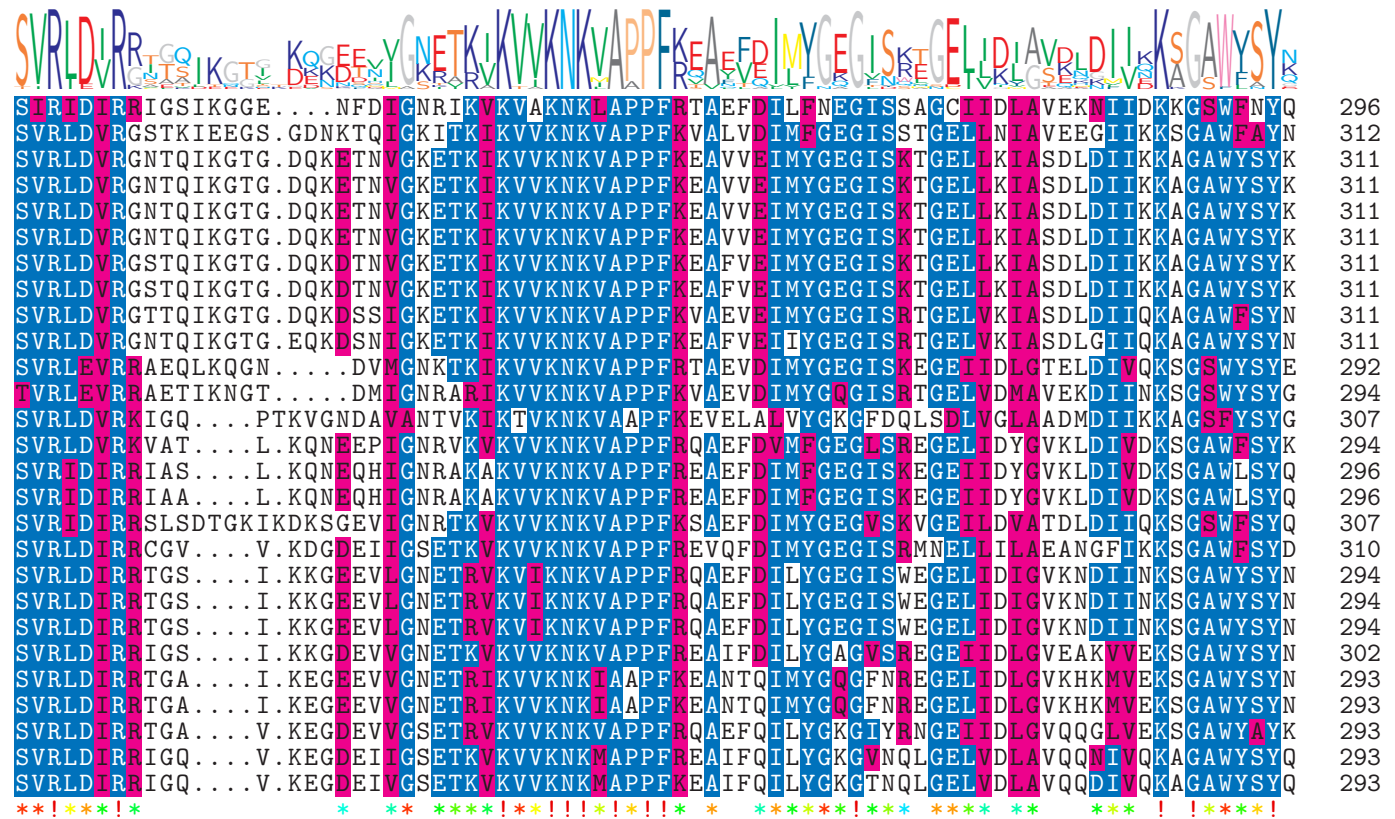
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consensus

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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
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DEKIGGGSENAKKYLAEHPFIDFIDDKQVRSKFGIDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGSENAKKYLAEHPFIDFIDDKQVRSKFGIDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGSENAKKYLAEHPFIDFIDDKQVRSKFGIDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGSENAKKYLADNPEIFDEIDHQVRVQFGLIDGEEIAES....KKDE....AAQVDS..VNEEVTLDLGDELEIE	381
DEKIGGGSENAKKYLADNPEVFAEIDHQVRVQFGLIDGEEAAES....KKDE....VAQVDS..VNEEVTLDLGDELEIE	381
GEKIGGGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEEEESAMAVASE.....E.....TDDLALDLNNGIEIE	377
GEKIGGGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EERLGQGRENAKQLFLENKDIMLMIQEQIREHYCLDNNGVVQQQAETQEEL.EFE.E.....	348
SERIGQGRENAKNYLADHEDVEDVIRLKVRAAYGISDVPEEDLPTTEDE.QI.NILPDST.....EE.....	355
DERIGQGKEKTIAYIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAAE..A.....	363
DKKLGQGRENSKAFLENKEPIADEITKAIQNSMCTEGMI....SGSEDDE..GE..E.....	343
DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEEI....MPLPDEP..LE..EME.....	347
DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEEI....MPLPDEP..LE..EME.....	347
DTKLGGGRDTPVKELIKDNPELAELEAKIREKLQAK.....	343
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GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHI....TEGT.....Q..DETGDGERPEE.....	348
GIRIGGGRDNCREFLKENAEELAREIENKVRHLGVTPMG....AV.TLAEVEVE..D.....	352
GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPNEM....QLIAETSSAAD..DVEFGAVPEEF.....	354
GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPNEM....QLIAETSSAAD..DVEFGAVPEEF.....	354
GSKIGGQKANAAYLEENPEIQQEIEQQIRAKLLVTSAN....TKATPVAEDLA..DADI.....	347
GNKIGGQKNNVIRYLEENPEIISTEIEAVIREQLLTKASD....QTAA.HDETEE..EPDLL..ES.....	349
GNKIGGQKNNVIRYFEENQIAEIEERNIREQLLTTGTN....GAVQ.I.EDEE..EPDLL..LES.....	349

logo

		IEE	
NTDB id 64464 C17 RS0103590 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