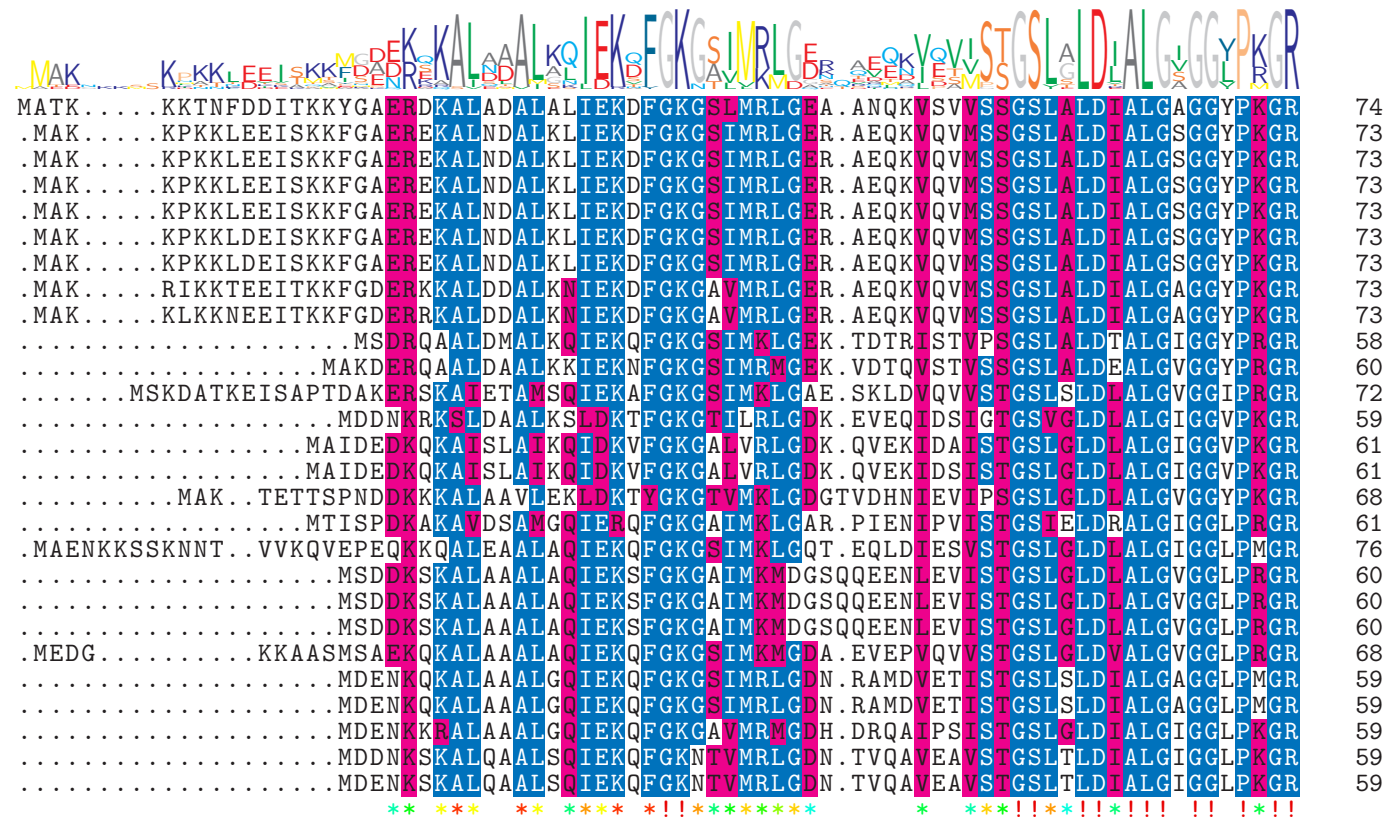


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consensus

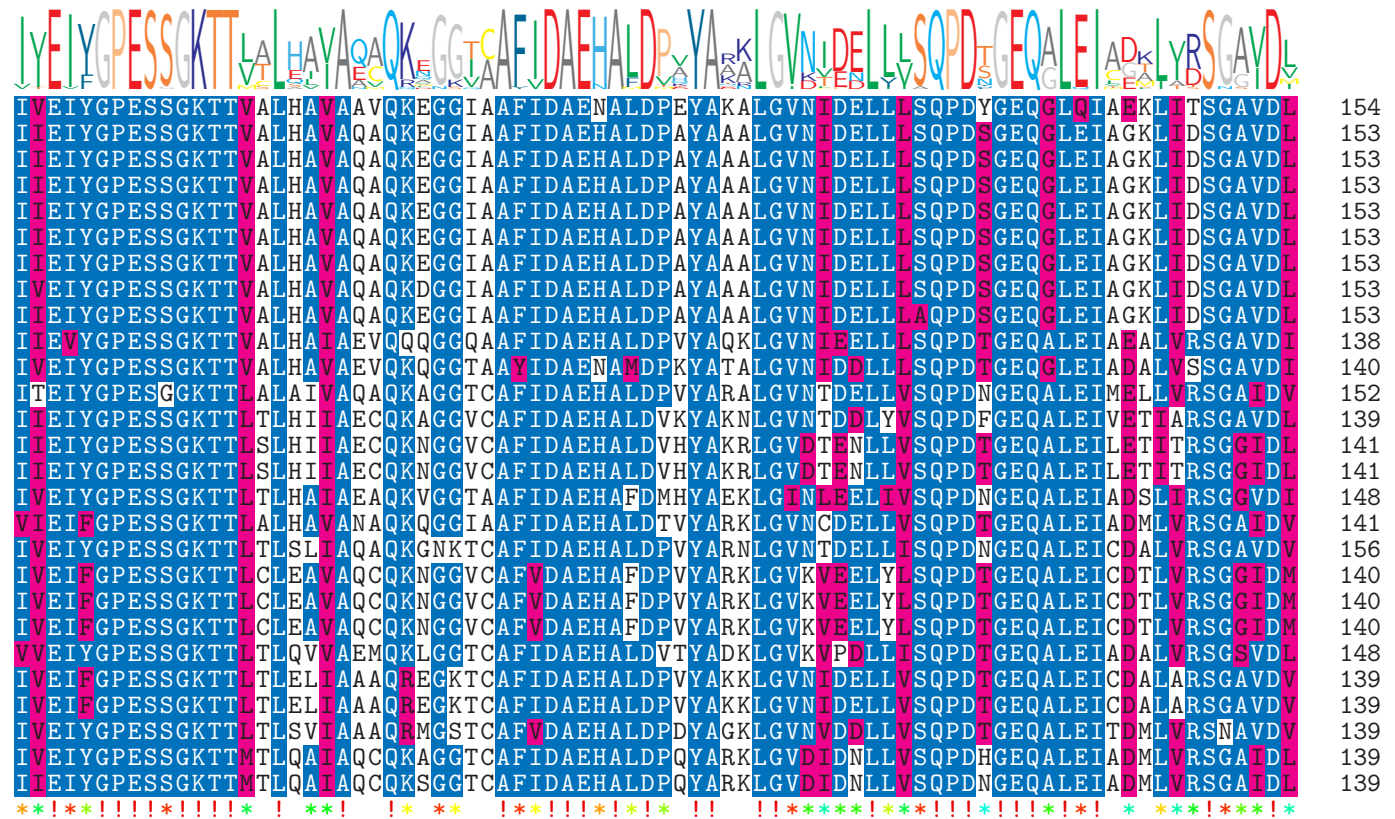
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consensus

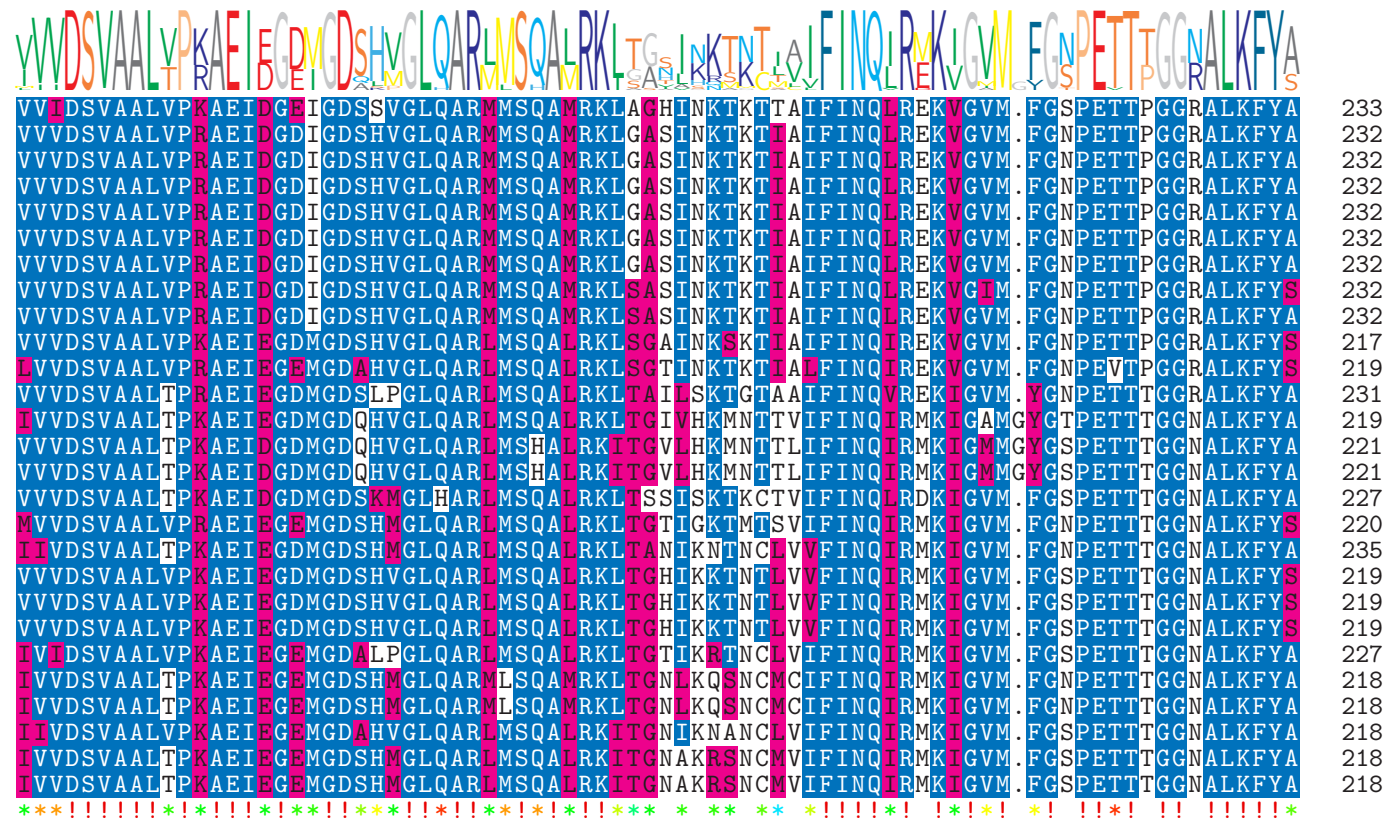
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

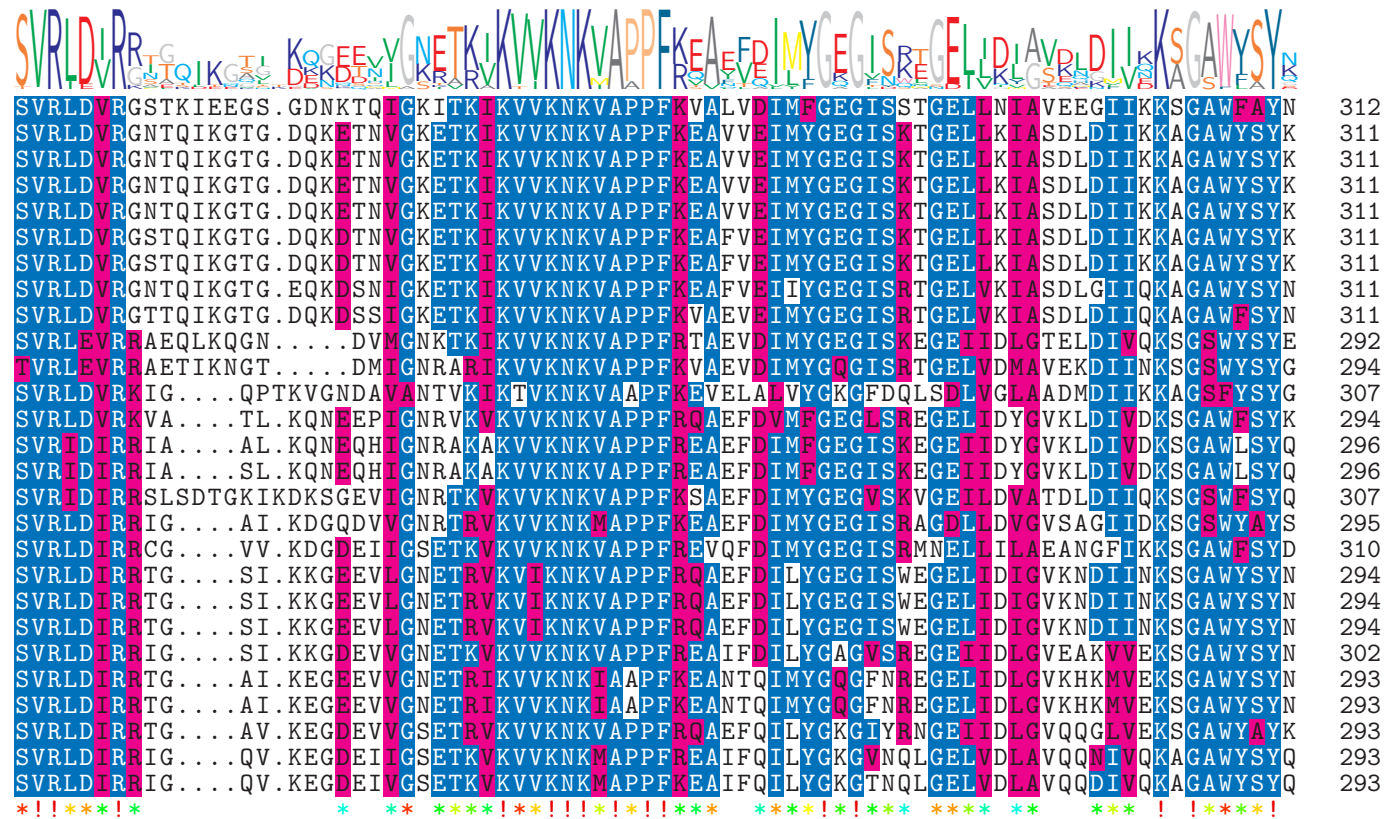
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consensus

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consensus

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Sequence	Score
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DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAADNPEVFAEIDHQVRVQFLIDGEEAAE...SKKDE...VAQVDS..VNEEVPLDLGDELEIE	381
DEKIGQGSSENAKKYLAADNPEIFDEIDHQVRVQFLIDGEEIAE...SKKDE...AAQVDS..VNEEVPLDLGDELEIE	381
GEKIGQGSSENAKKFLADNPEIFDDIDHKVRVQGLIEEDNTEEEKSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
GEKIGQGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNNGIEIE	377
EERLGQGRENAKQFLKENKDIMLMIQEQIREHYGLDNGGVVQQAEETQEEL.EFE.E.....	348
SERIGQGRENAKNYLADHEDVEDEVRLKVRAAAYGISDVPPEEDLPTTEDE.QI.NILPDST.....EE.....	355
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DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEE....IMPLPDEPL..E..EME.....	347
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GAKIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMH....ITEGT.....Q..DETDGERPEE.....	348
GERIGQGRDNCREFLRNAAELAREIENKVRHLGVTPM....GAV.TLAEVEEV..D.....	352
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GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPN.....MQLIAETSSAAD..DVEFGAVPEEF.....	354
GSKIGGQKANAAKYLEENPEIGQIEEQIRAKLLVTSA....NTKATPVAEDLA..DADI.....	347
GNIKIGGQKNNVIRYLEENPQISTEIEAVIREQLLTKAS....DQTAA.HDETEE..EPDLL..ES.....	349
GNKIGGQKNNVIRIFYENNQIAEIERNIQREQLLTGT....NGAVQ.I.EDEE..EPDLL..LES.....	349

logo

		IEE	
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NTDB id 194 SPR RS08825 WP 001085462.1	IEE		388
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NTDB id 1074 ABD1 RS10195 WP 000344167.1	...		349
consensus			

-  non conserved
-  similar
-  ≥ 50% conserved