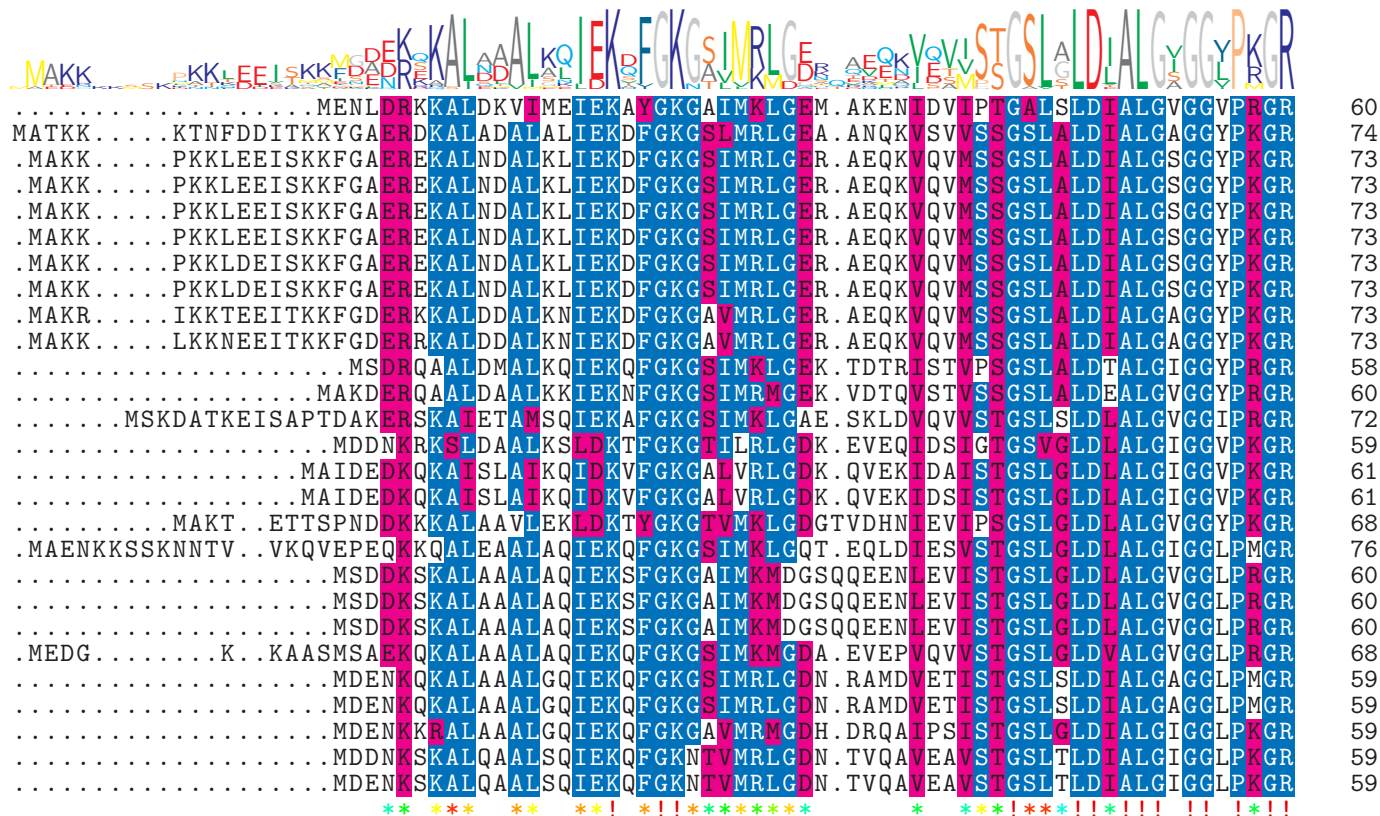


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consensus

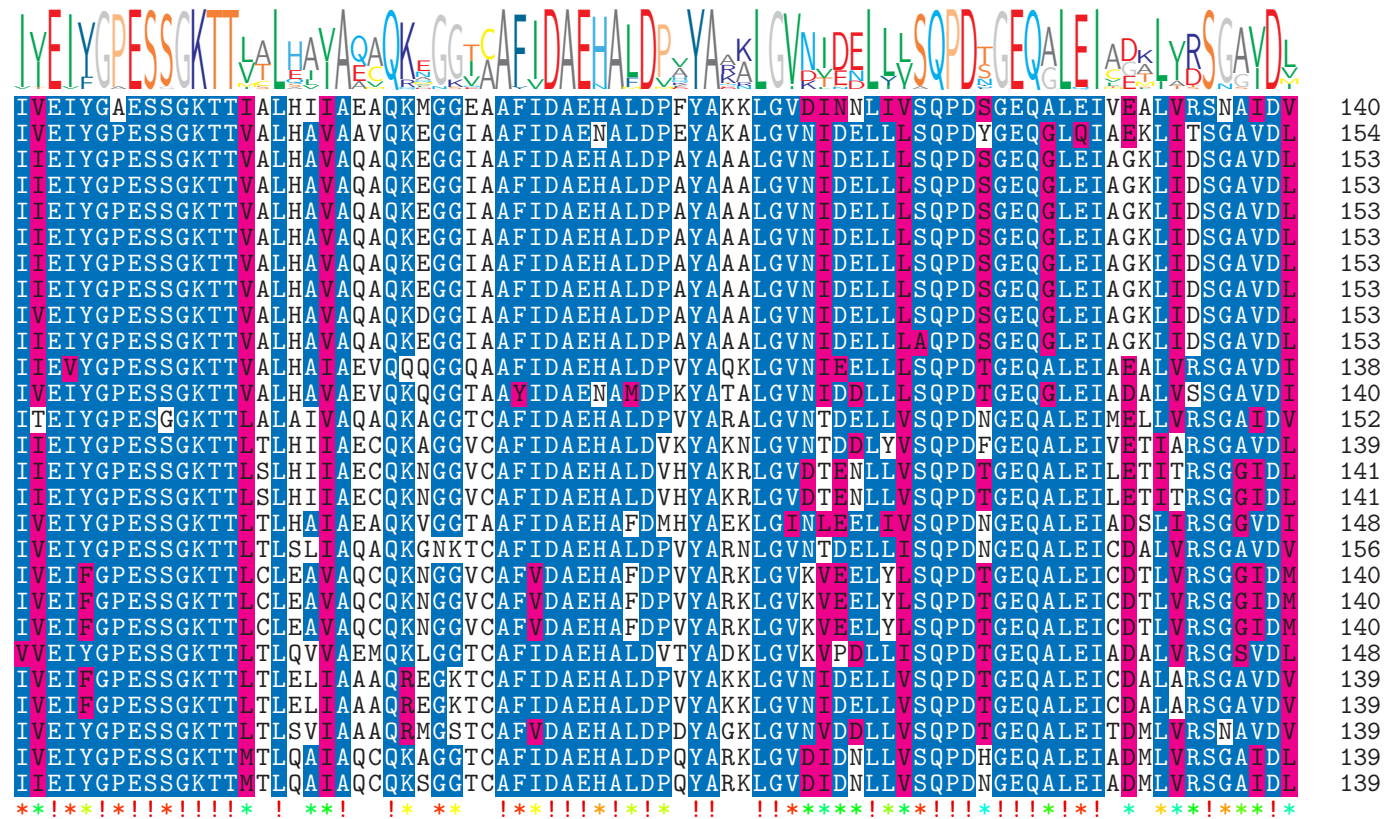
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consensus

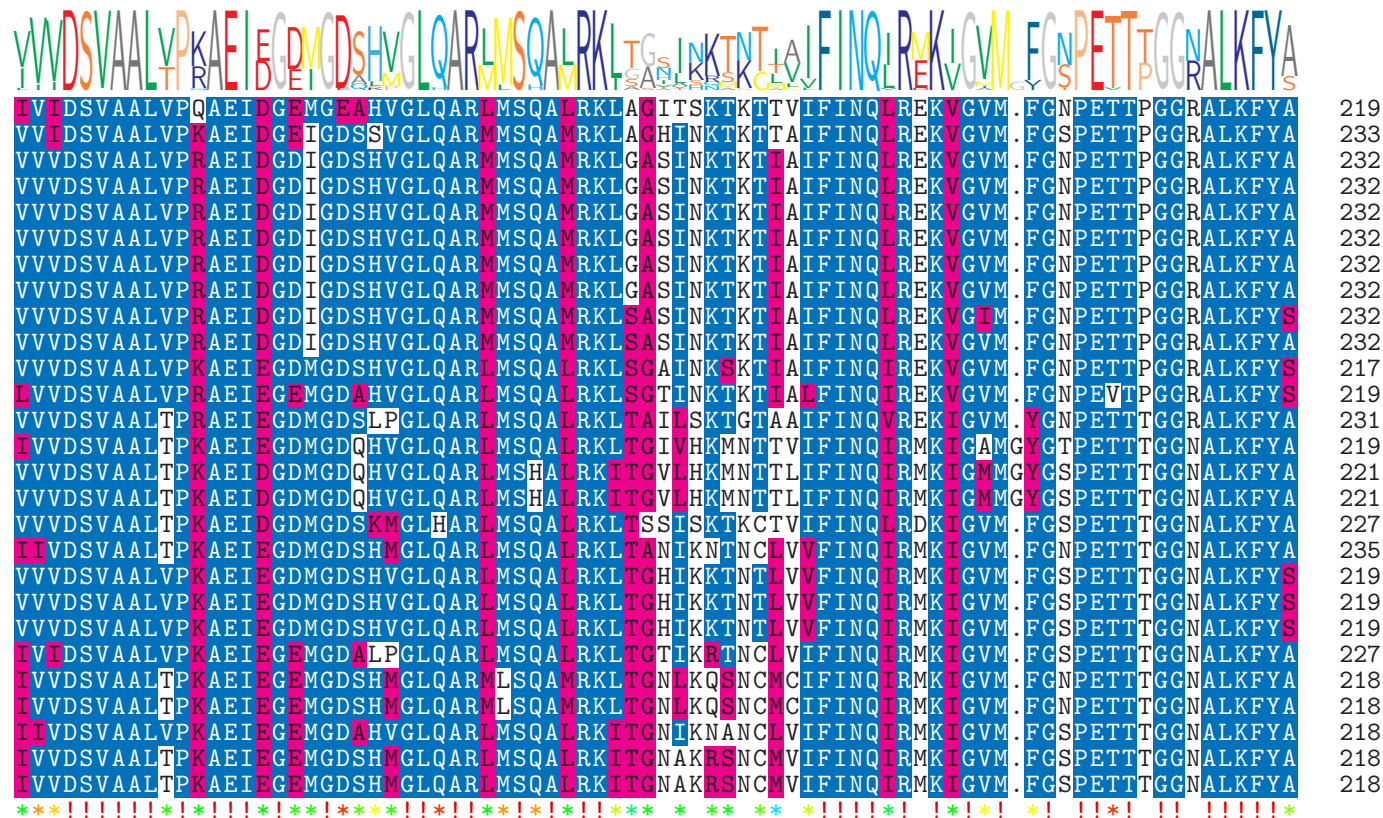
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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NTDB id 600 KW2 RS01765 WP 011675413.1	SVRLDVRGSTKIEEGS.GDNKTQ	IGKITIKVVKKNKVAPPFKVALVDIMFGEGISSTGELLNIAVEEGTIKKSGAWFAYN	312
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NTDB id 453 Spy49 1753c ACI62003.1	SVRLDVRGTTQIKGTG.DQKDS	IGKETKIKVVKKNKVAPPFKVAEVEIMYEGEGISRTGELVKIASDLDIQKAGAWFSYN	311
NTDB id 115 BSU 16940 NP 389576.2	SVRLDVRRAEQLKQGN.....DVMGNKTKIKVVKKNKVAPPFRTAEVDIMYEGEGISKEGEIIDLGTELDI	VQKSGSWYSYE	292
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Sequence	Score
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DEKIGQGSNAKKYLADNPEVFAEIDHQVRVQFGLIDGEEAAES...KK...DE....VAQVDS..VNEEVTLDLGDE	377
GEKIGQGSNAKKFLADNPEIFDDIDHKVVRVQGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDT	378
GEKIGQGSNAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNG	373
EERLGGGRENAAKQFLKENKDIIMLMIQEIQIREHYGLDNGGVVQQQAETQE...EL.EFE.E.....	348
SERIGQGRENAAKYLADHEDVEVRLKVRAAAGISDVPEEDLPTTEDE.....QI.NILPDDST.....EE	355
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DKKLGGGRENAAKALLKEDKALADEITLKIKESIGSNEEI....MPLPDEP..LEEME.....	347
DKKLGGGRENAAKALLKEDKALADEITLKIKESIGSNEEI....MPLPDEP..LEEME.....	347
DTKLGGGRDITVKELIKDNPELAEELEAKIREKLQAK.....	343
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GAKIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI.....TEGT.....QDET DGERPE.....E.....	348
GAKIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI.....TEGT.....QDET DGERPE.....E.....	348
GERIGQGRDNCREFLENALAREIENKVRHLGVTPMG....AV.TLAEVEED.....	352
GDKIGGQKANACKYLKENPEIAKTLDDKKLREMLLNPNEM....QLIAETSSAAD DVEFGAVPE.....EF.....	354
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GSKIGGQKANAACKYLEENPEIGQETIEQQIRAKLLVTSAN....TKATPVAEDLADADI.....	347
GNKIGQGKNNVIRYLEENPQISTEIEAVIREQLLTKASD....QTAH.HDETEEPDLL..ES.....	349
GNKIGQGKNNVIRYFENNQIAEIERNIHQREQLLTGTN....GAVQ.I.EDEEIPDLL..LE.....S.....	349

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consensus			

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