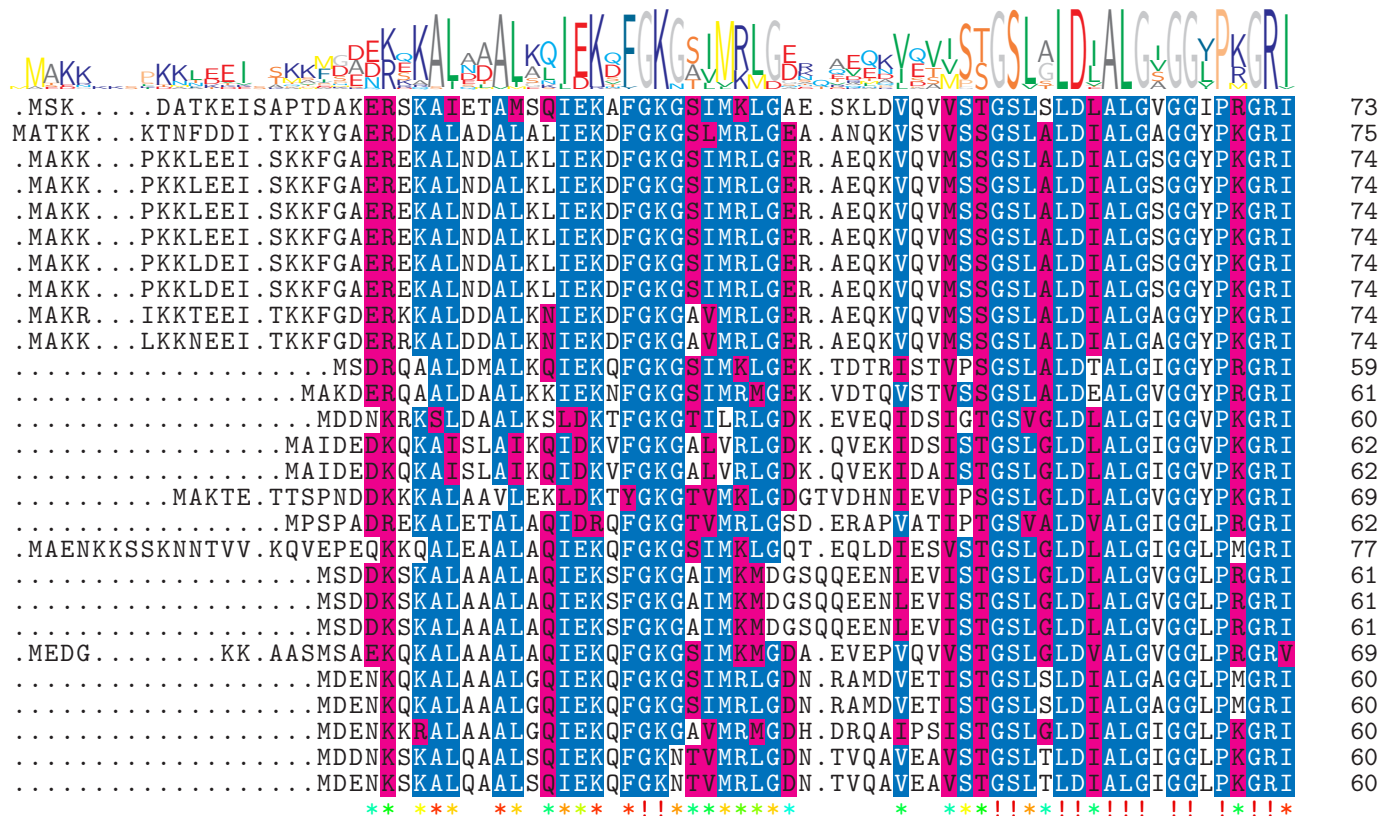


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consensus

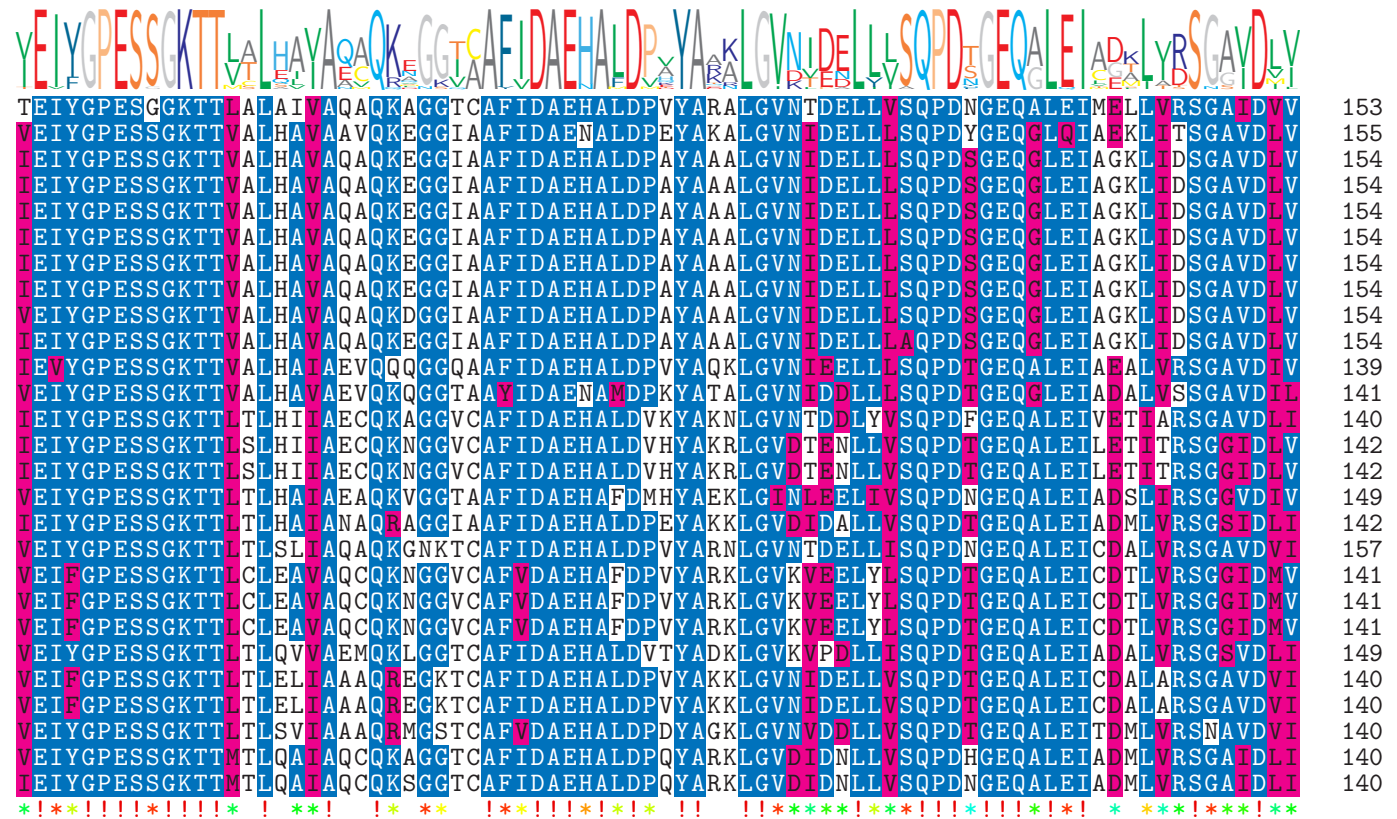
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

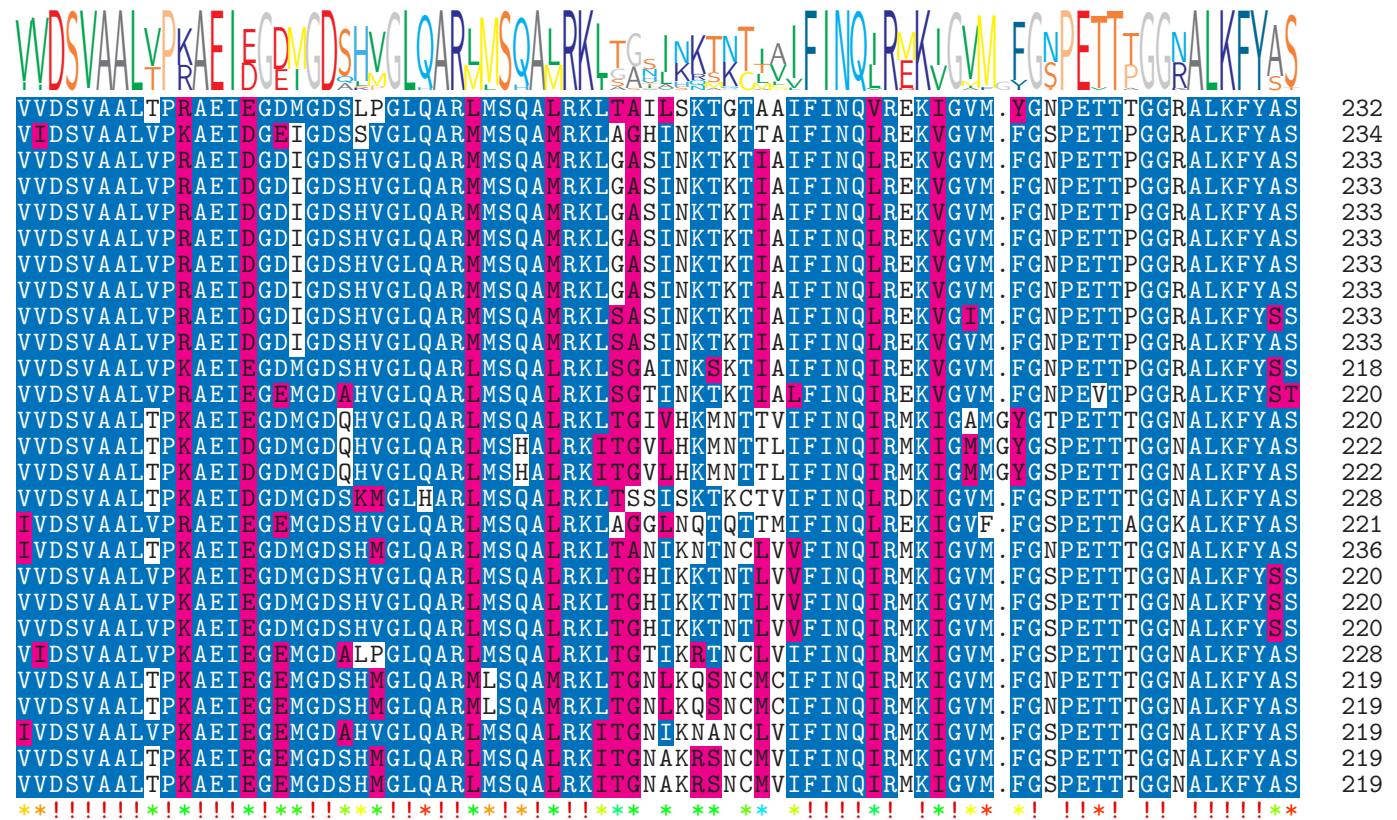
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

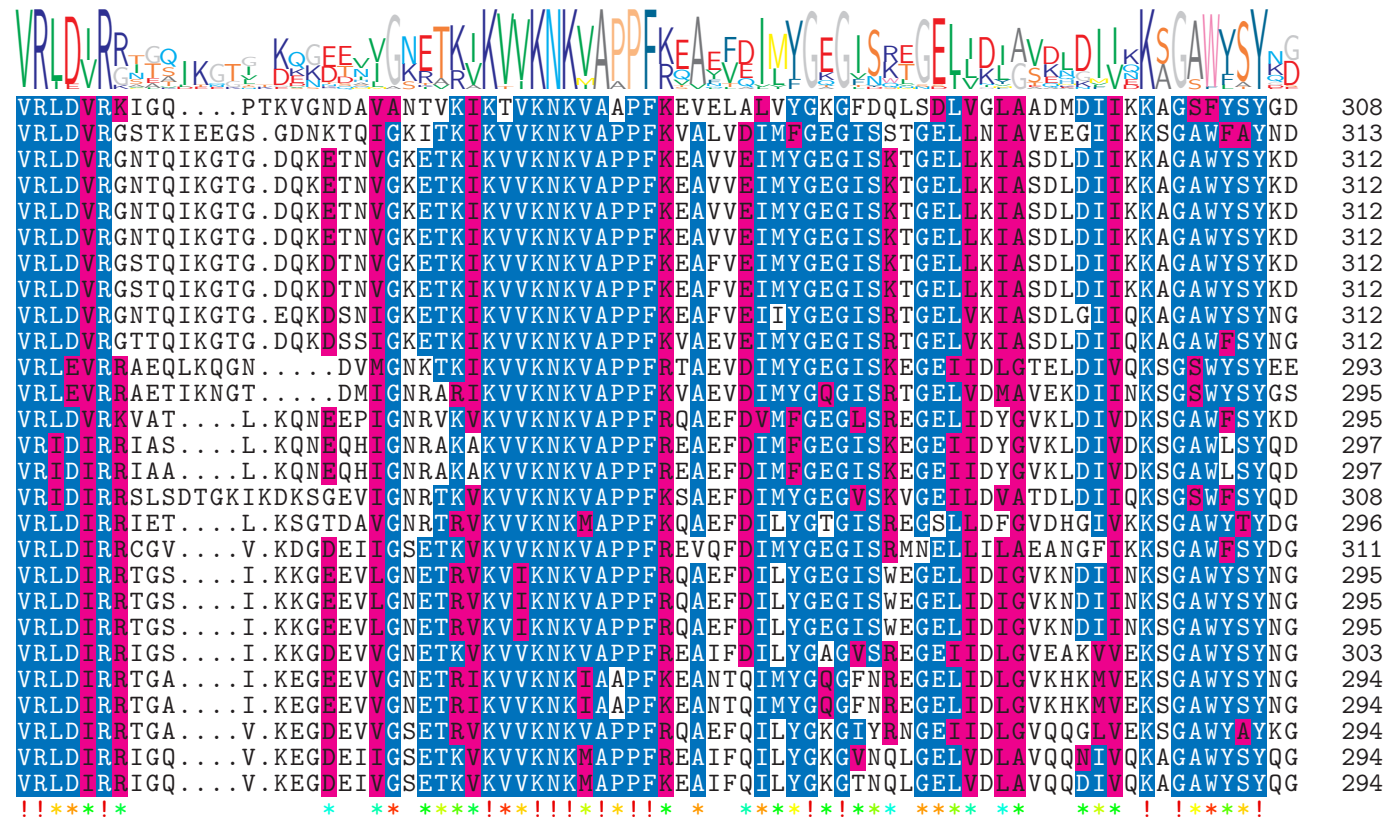
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

Sequence	Score
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EKIGQGAEAKAKNYLKEHQDVFEIDHKVRAAHGLDDSEVAETEETTASKTKAKAKKEEKAVETEEIELELED.....	387
EKIGQGSENAKKYLAEHPFEIDDKQVRSKFGLDIGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIEI	386
EKIGQGSSENAKKYLAHPFEIDDKQVRSKFGLDIGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIEI	386
EKIGQGSSENAKKYLAHPFEIDDKQVRSKFGLDIGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIEI	386
EKIGQGSSENAKKYLAHPFEIDDKQVRSKFGLDIGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIEI	386
EKIGQGSSENAKKYLADNPVFAEIDHQVRVQFGLIDGEAAE...SKKDE...VAQVDS..VNEEVTLDLGDELEIEI	382
EKIGQGSSENAKKYLADNPFEIDHQVRVQFGLIDGEAIEA...SKKDE...AAQVDS..VNEEVTLDLGDELEIEI	382
EKIGQGSSENAKKFLADNPFEIDDKVVRVQGLIEEDNTEEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELED	383
EKIGQGSSENAKKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIED	378
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TKLGGGRDRTVKELIKDNPELAEELEAKIREKLQAK.....	343
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DKIGQGKANACKYLLKENPEIAKTLDDKKLREMLLNPNMQLIAETSSAADV.EFGAVPE.....EF.....	354
DKIGQGKANACKYLLKENPEIAKTLDDKKLREMLLNPNMQLIAETSSAADV.EFGAVPE.....EF.....	354
SKIGQGKANAAKYLEENPEIGQIEQQIRAKLLVTSANTKATPVAEDLADA.DI.....	347
NKIGQGKNNVIRYLEENPQISTEIEAVIREQLLTKASDQTA.HDETEEEP.DLL..ES.....	349
NKIGQGKNNVIRYFENNQIAEIERNIREQLLTGTNGAVQ.I.EDEEEP.DLL..LE.....S.....	349

logo

NTDB id 1313 DR RS12030 WP 010888966.1	..	363
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NTDB id 269 KZH43 RS08665 WP 001085462.1	EE	388
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NTDB id 1074 ABD1 RS10195 WP 000344167.1	..	349

consensus

 non conserved
 similar
 ≥ 50% conserved