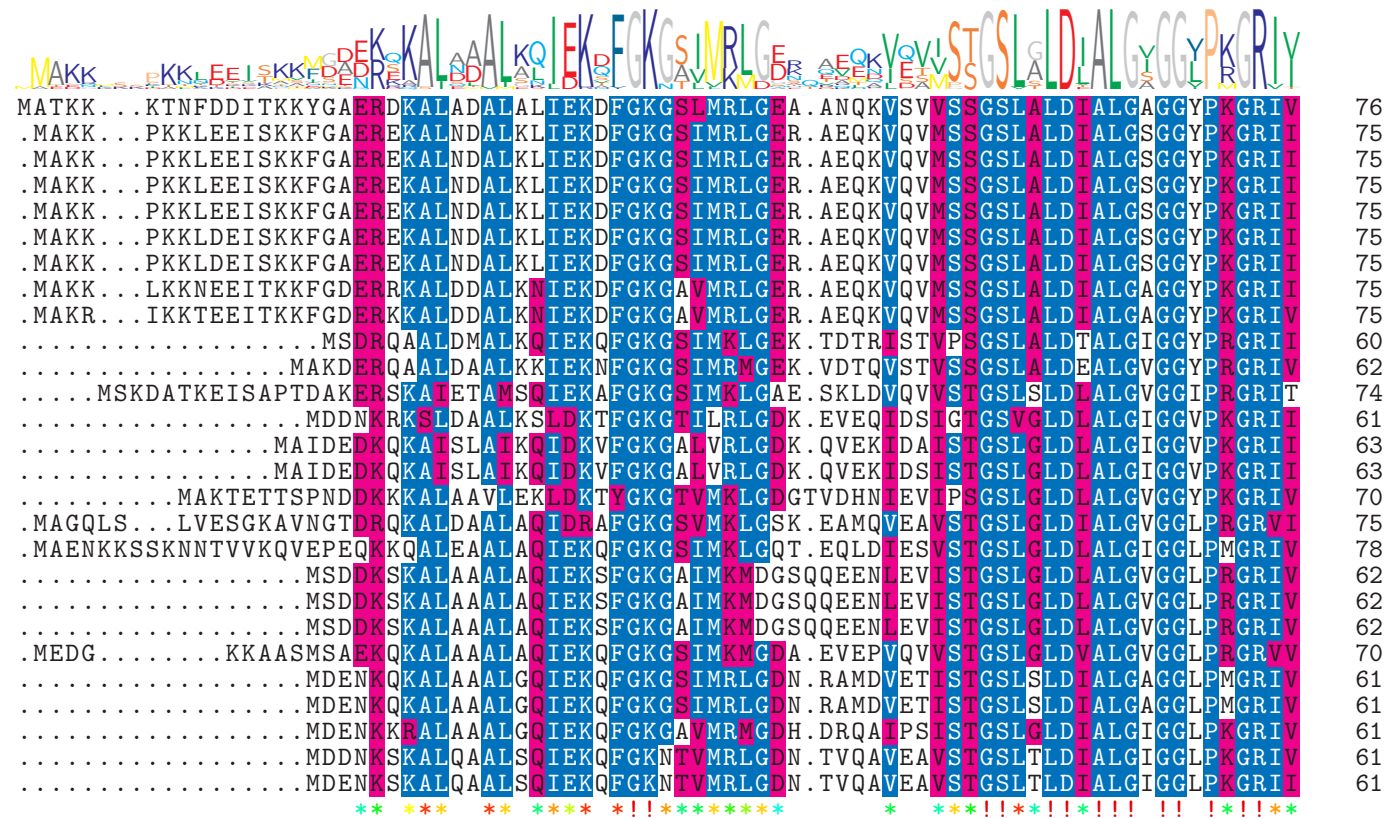


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consensus

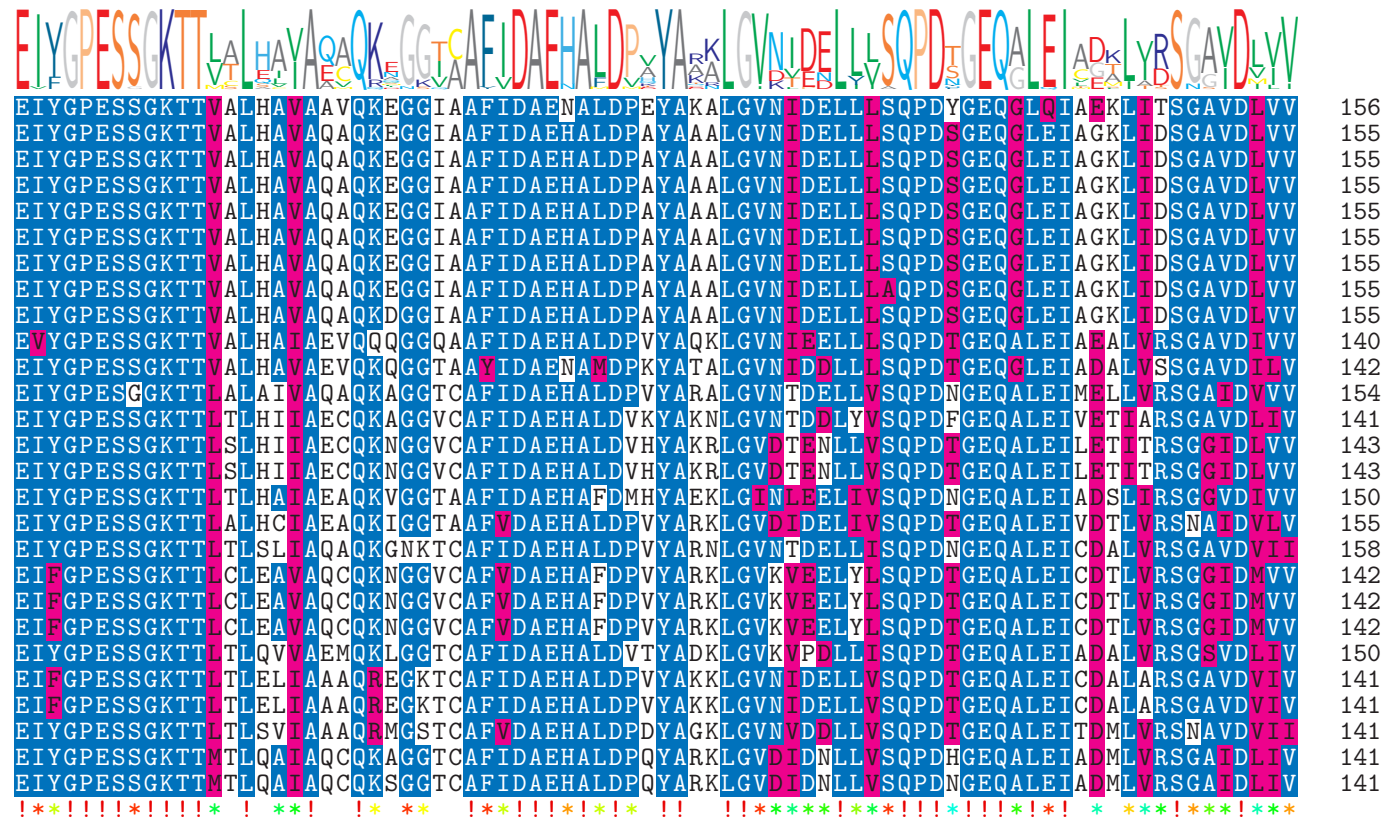
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

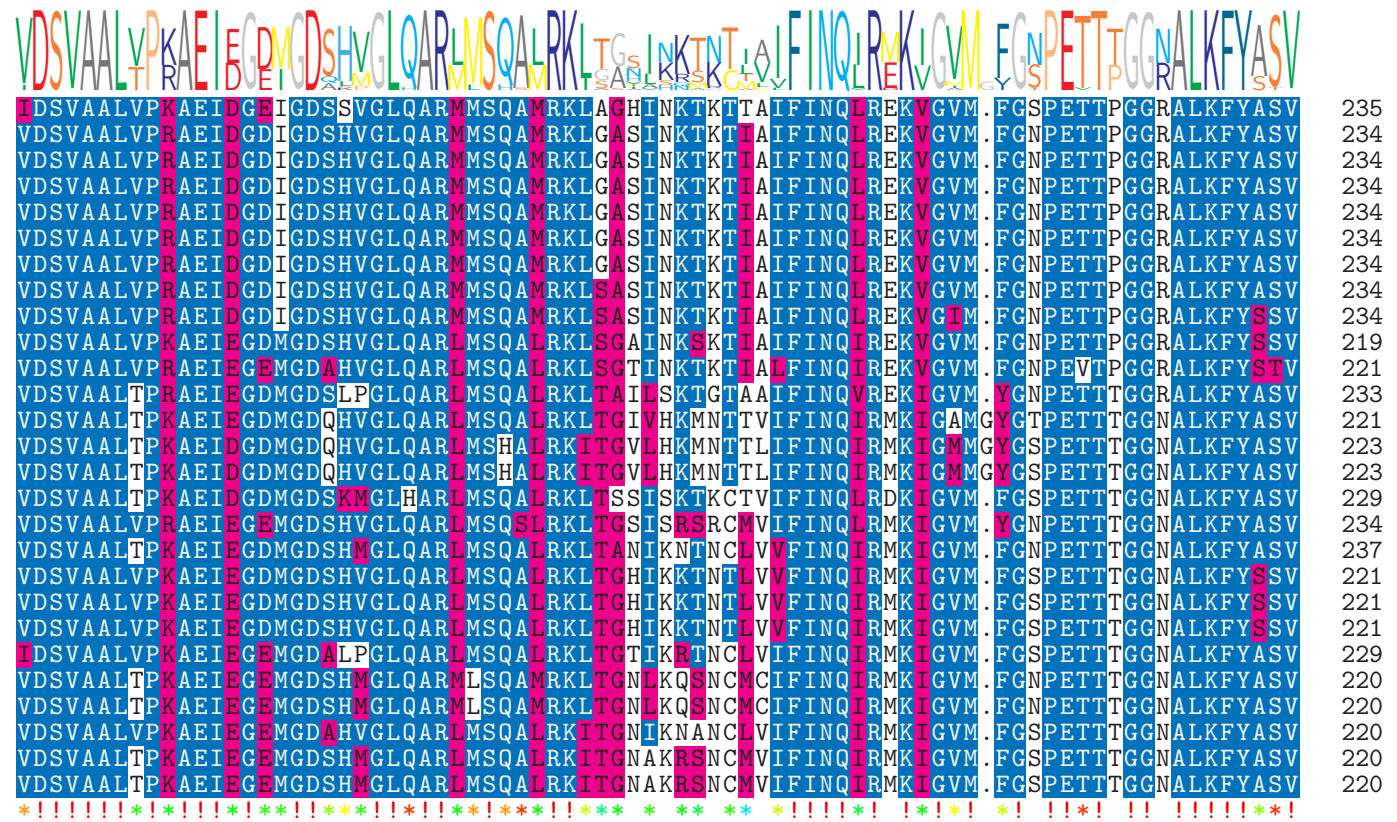
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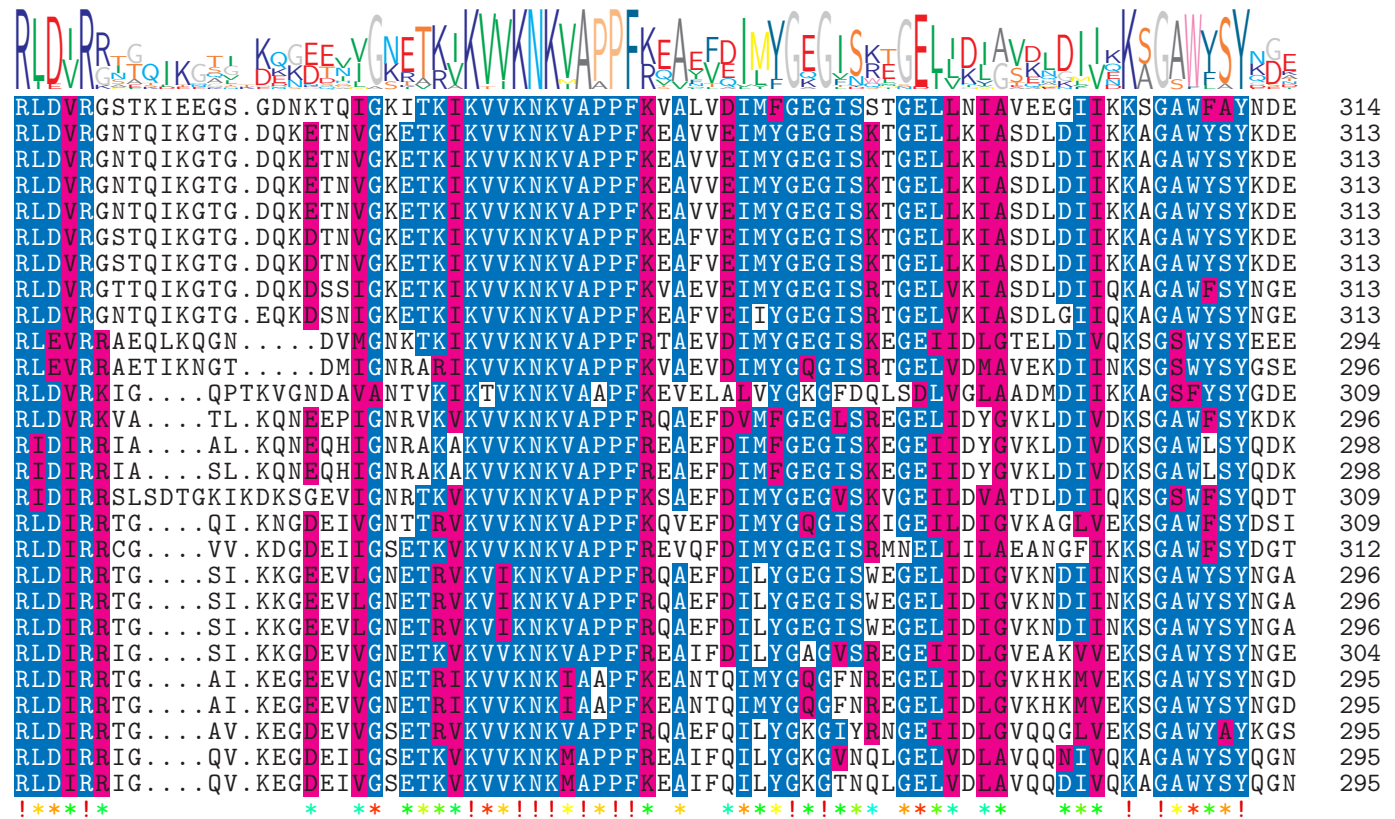
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

Sequence	Score
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KIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDT..ENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
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KIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDT..ENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
KIGQGSSENAKKYLAADNPEVFAEIDHQVVRVQFGLIDGEEAAE.....SKKDE...VAQVDS..VNEEVTLDLGDLEIE	381
KIGQGSSENAKKYLAADNPEIFDEIDHQVVRVQFGLIDGEEIAE.....SKKDE...AAQVDS..VNEEVTLDLGDLEIE	381
KIGQGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMA..VASE.....E.....TDDLALDLNGIEIE	377
KIGQGSSENAKKFLADNPEIFDDIDHKVVRVQYGLIEEDNTEEEKQS..SKEK.....ETDEK..ADKNLVLELDDTIELE	382
RLGQGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQQAE..ETQEEL.EFE.E.....	348
RIGQGRENAKNYLADHEDVEDEVRLKVRAAAYGISDVPPEEDLPTT..EDE.QI.NILPDDST....EE.....	355
RIGQGKEKTIAYIAERPEMEQETIDRVMMAAIRAGNAGEAPALAPAPAAPEAA.EA.....	363
KLGGGRENKAFLEKENPEIADEITKAIQNSMGIEGMISG..SED..DEGEF.....	343
KLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIMP..LPD..EPLEEM.E.....	347
KLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIMP..LPD..EPLEEM.E.....	347
KLGGGRDRTVKELIKDNPELAELEAKIREKLQAK.....	343
RIGQGRENAKTFLKENPELMGRLEAAIRGRTDVAEEMM..AGPDDDVGGDA.I.....	360
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KIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHITE..GT.....QDE.TDGER.....PEE.....	348
KIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHITE..GT.....QDE.TDGER.....PEE.....	348
RIGQGRDNCREFLENAREIENKLVREHLGVTPMGAV...TLAEVEVED.....	352
KIGQGKANACKYLKENPEIAKTLDDKKLREMLLNPNMQL..IAETSSAADV.EFGAV.....PEEF.....	354
KIGQGKANACKYLKENPEIAKTLDDKKLREMLLNPNMQL..IAETSSAADV.EFGAV.....PEEF.....	354
KIGQGKANAAKYLEENPEIGQIEEQQIRAKLLVTSANTK..ATPVAEDLADA.DI.....	347
KIGQGKNNVIRYLEENPQISTEIEAVIREQLLTKASDQT..AA.HDETEEEP.DLL.....ES.....	349
KIGQGKNNVIRYFENNQIAEIERNIIREQLLTGTNGA..VQ.I.EDEEEP.DLL.....LES.....	349

logo

		IEE	
NTDB id 600 KW2 RS01765 WP 011675413.1	...	387	
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NTDB id 1022 ACIAD RS06390 WP 004925639.1	...	349	
NTDB id 1074 ABD1 RS10195 WP 000344167.1	...	349	
consensus			

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