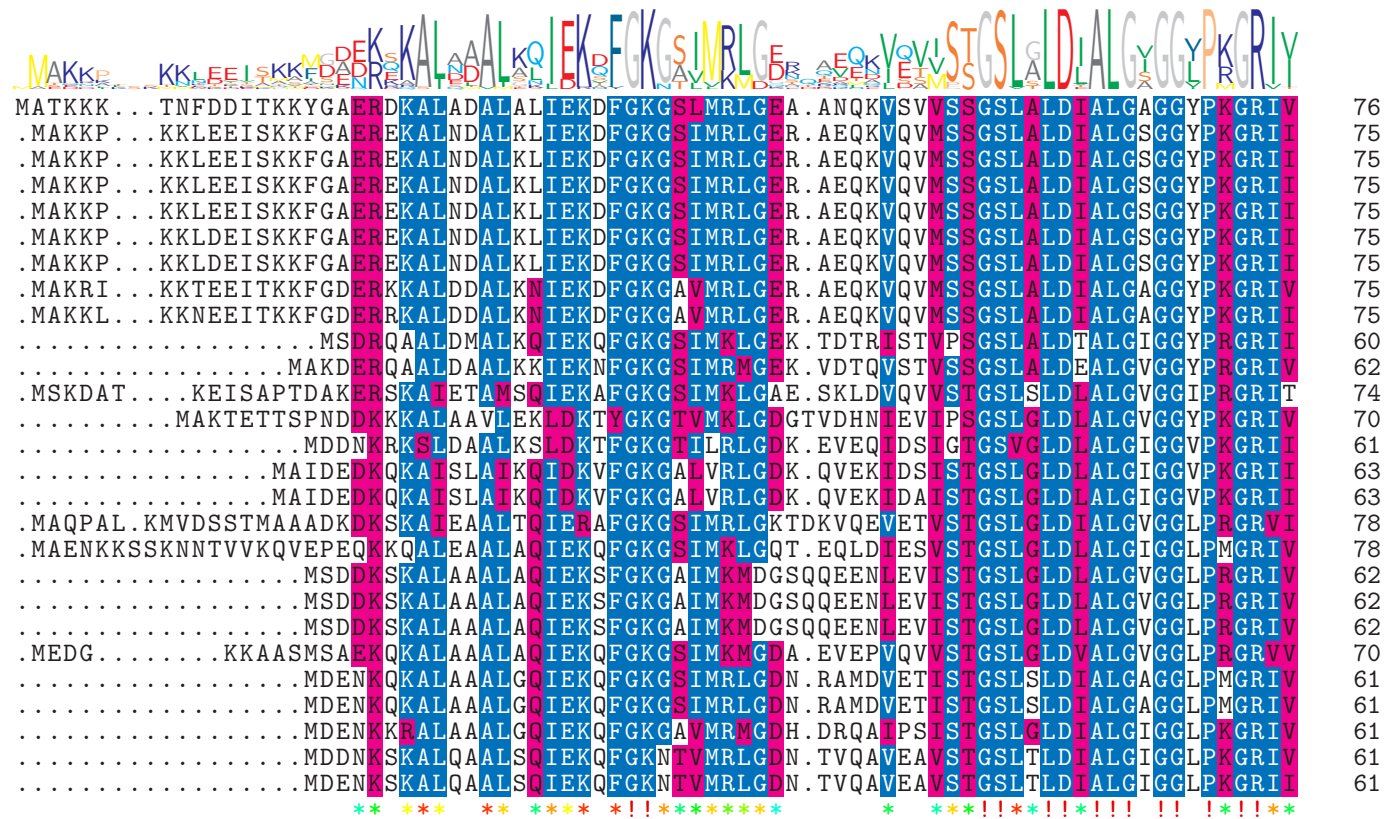


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consensus

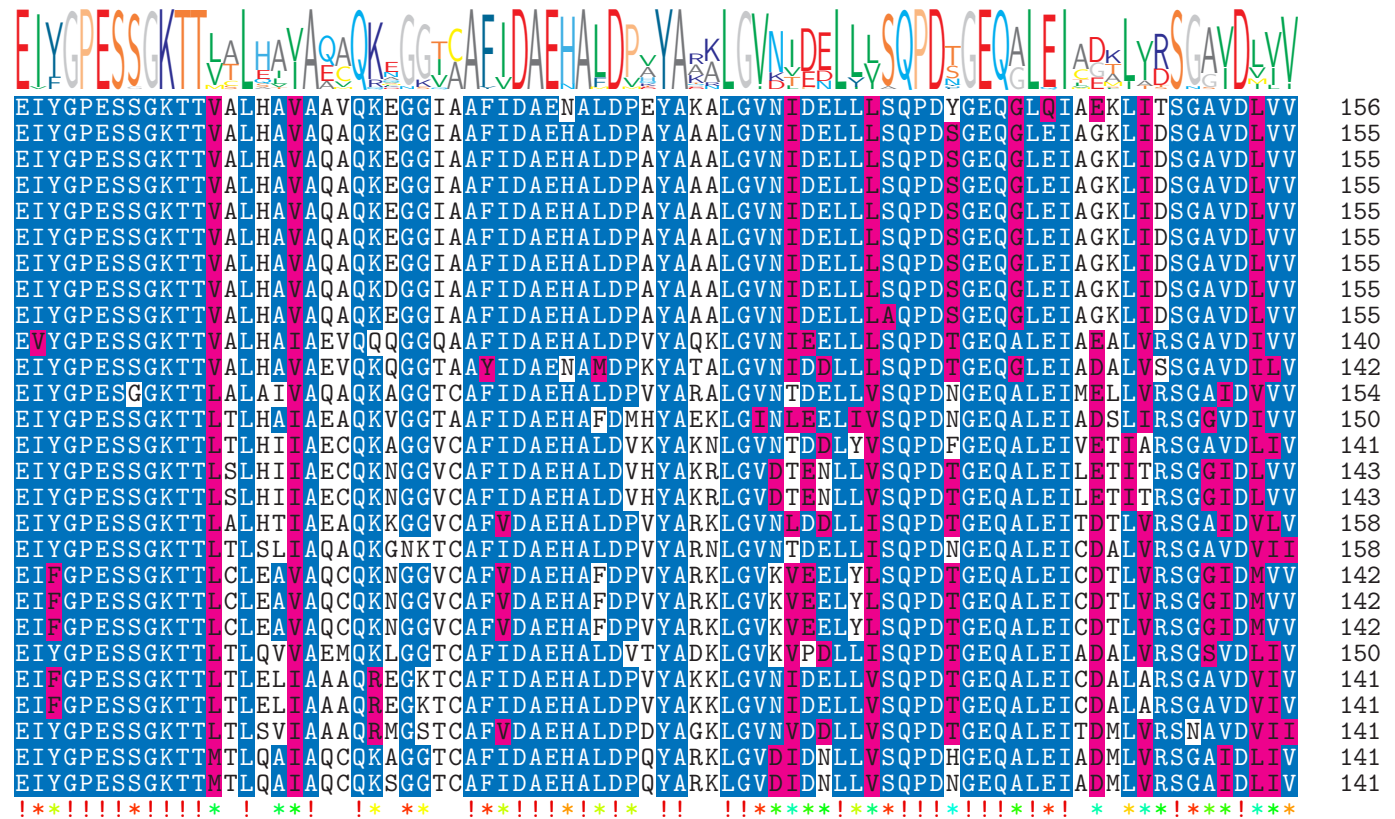
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consensus

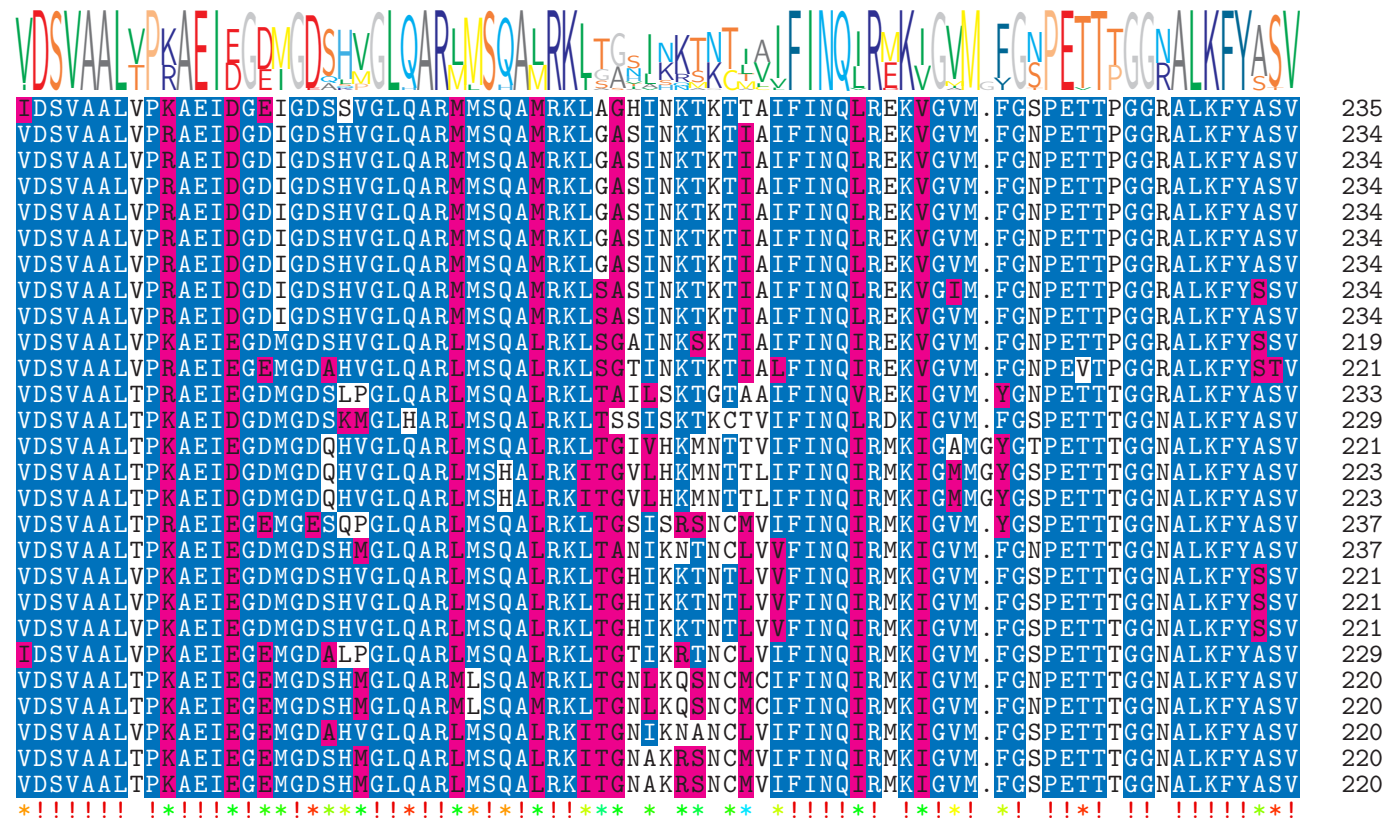
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consensus

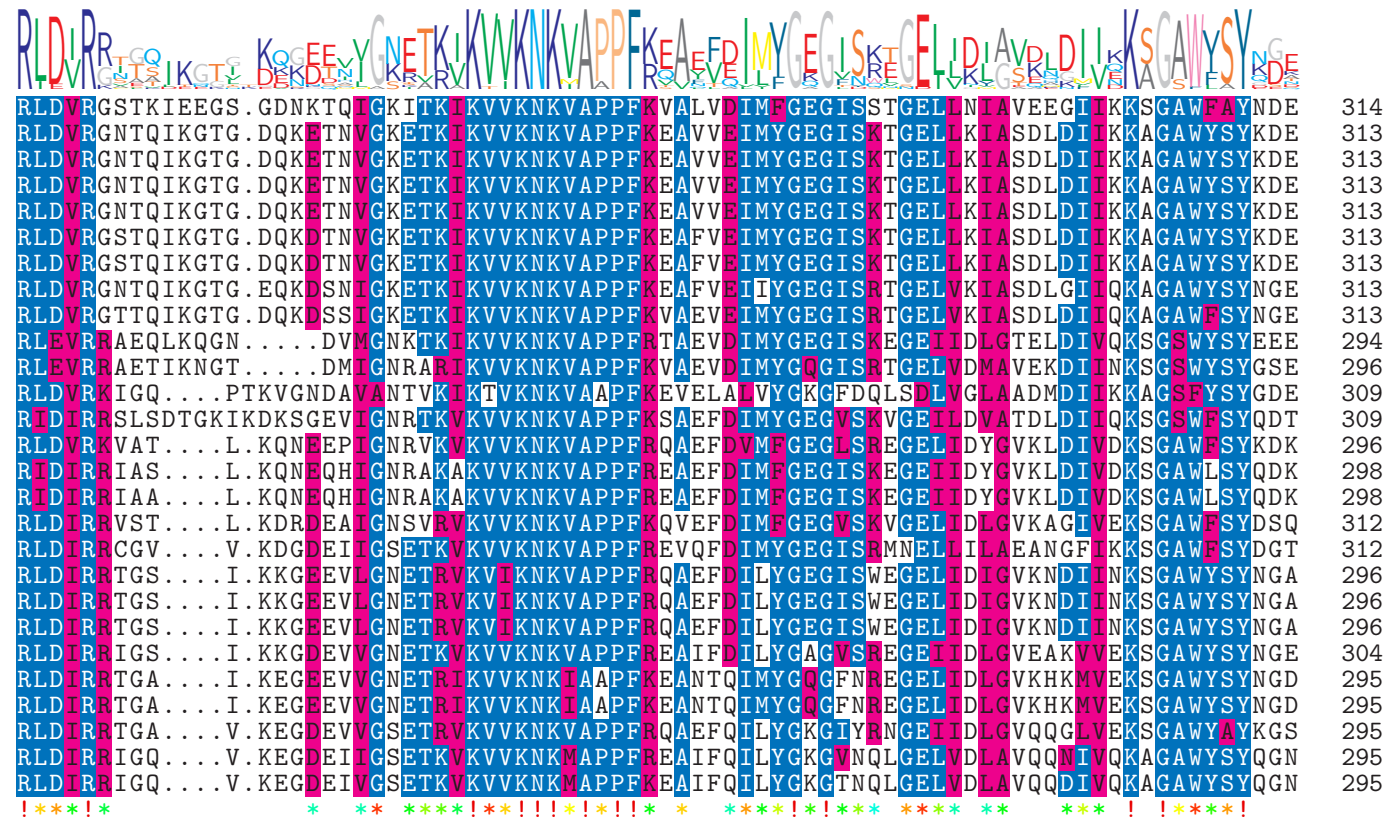
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consensus

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Sequence	Score
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KIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQD TENKKDE...PKKEEA..VNEEVPLDLGDELEIEIE	387
KIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQD TENKKDE...PKKEEA..VNEEVPLDLGDELEIEIE	387
KIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQD TENKKDE...PKKEEA..VNEEVPLDLGDELEIEIE	387
KIGQGSSENAKKYLADNPEIFDEIDHQVRVQFLIDGEEIAES...KKDE...AAQVDS..VNEEVPLDLGDELEIEIE	383
KIGQGSSENAKKYLADNPEVFAEIDHQVRVQFLIDGEEIAES...KKDE...VAQVDS..VNEEVPLDLGDELEIEIE	383
KIGQGSSENAKKFLADNPEIFDDIDHKVRVQGLIEEDNTEEEKSSKEK.....ETDEK..ADKNLVLELDDTIELED	383
KIGQGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIED.	378
RLGQGRENAKQFLKENKDIMLMIQEQIREHYGLDNGGVVQQAEETQEEL.EFE.E.....	348
RIGQGRENAKKNYLADHEDVEDEVRLKVRAAAYGISDVPPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
RIGQGKEKTIAYIAERPMEQEIRDRVMAAIRAGNAGEAPAL.APAPAAPEAAAA.....	363
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KLGGGRENSKAFLENKENPEIADEITKAIQNSMGIEGMISGSED..DEGEE.....	343
KLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIMPLPD..EPLEEME.....	347
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KIGQGGKNNVIRYFENNQIAEIERNIREQLLTGTNGAVQ.I.EDEEEPDL.....LES.....	349

logo

NTDB id 600 KW2 RS01765 WP 011675413.1	.	387
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consensus

 non conserved
 similar
 ≥ 50% conserved