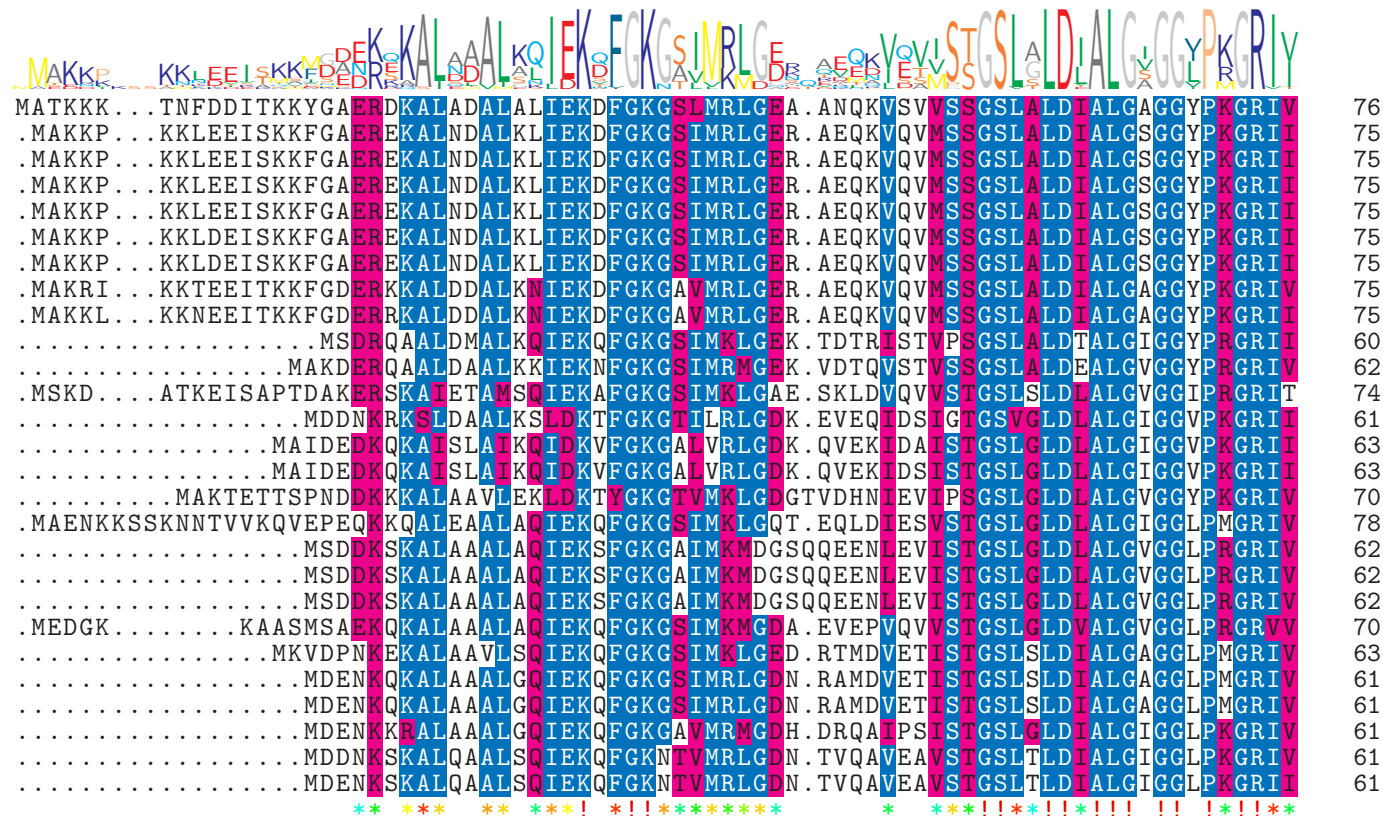


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consensus

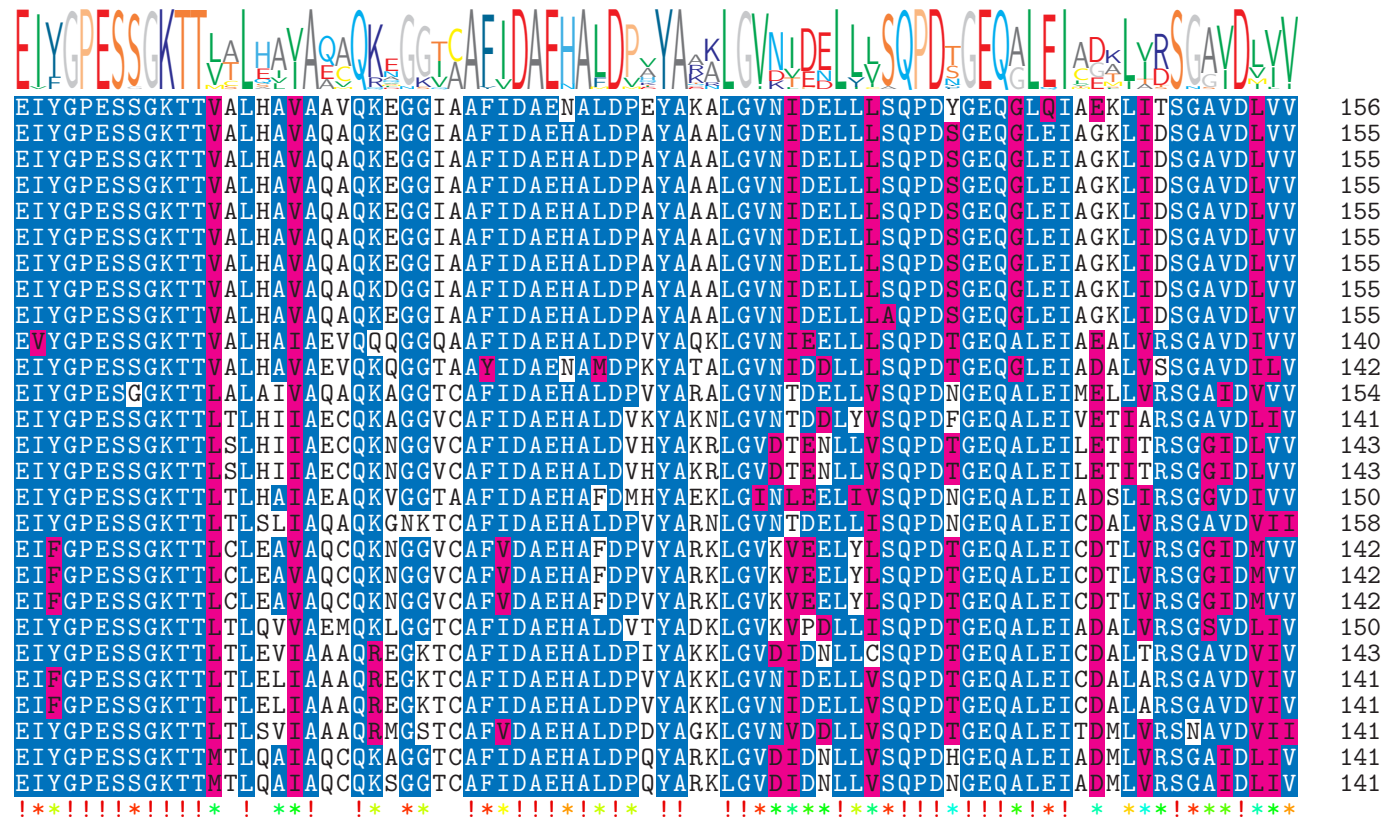
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consensus

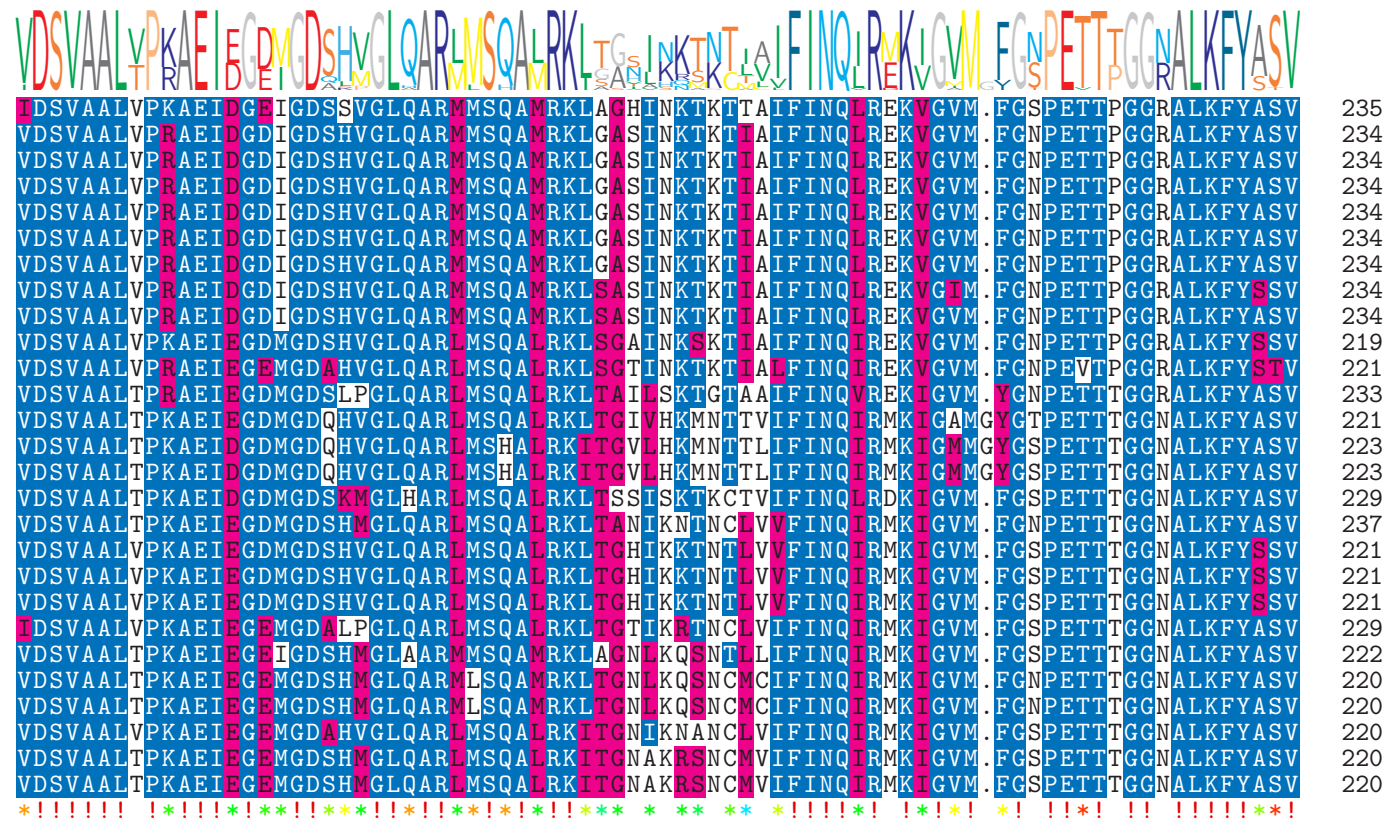
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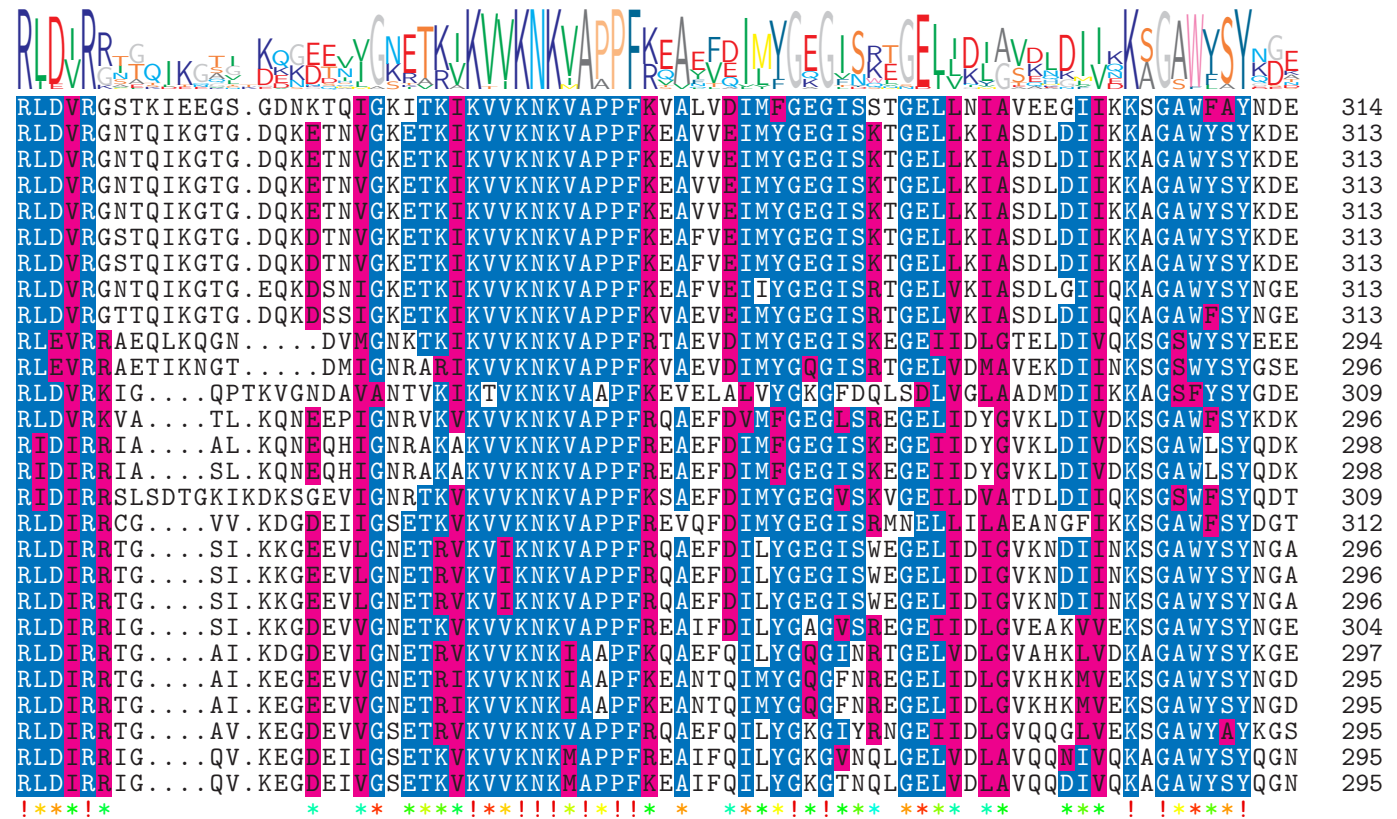
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consensus

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Sequence	Score
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KIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIEIE	387
KIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIEIE	387
KIGQGSSENAKKYLAENPEVFAEIDHQVRVQFLIDGEEAAE...SKKDE...VAQVDS..VNEEVPLDLGDELEIEIE	383
KIGQGSSENAKKYLAENPEIFDEIDHQVRVQFLIDGEEIAE...SKKDE...AAQVDS..VNEEVTLDLGDELEIEIE	383
KIGQGSSENAKKFLADNPEIFDDIDHKVRVQGLIEEDNTEEQSSKEK.....ETDEK..ADKNLVLELDDTIELED	383
KIGQGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIED.	378
RLGQGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEETQEEL.EFE.E.....	348
RIGQGRENAKNYLADHEDVEDEVRLKVRAAAYGISDVPPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
RIGQGKEKTIAYIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPA.APEAA..EA.....	363
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KIGQGGKNVVRVWLKENPEISDEIDAKIRALNGVEMHITEGTQ.....DE.....TDGERPEE.....	348
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RIGQGGRDNCREFLRENAELAREIENKVRHGLVTPMGAVTLAAEEVEE.D.....	352
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KIGQGGKANACKYLKENPEIAKTLDDKKLREMLLNPNENMQL..IAETS...SAAD..DV.....EFGAVPEEF.....	354
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KIGQGGKANAAKYLEENPEIGQIEEQQIRAKLLVTSANTK..ATPVAE.DLADA..DI.....	347
KIGQGGKNNVIRYLEENPQISTEIEAVIREQLLTKASDQT..AA.HDE.TEEEP..DL.....LES.....	349
KIGQGGKNNVIRYFENNQIAEIERNIREQLLTGTNGA..VQ.I.E.DEEP..DL.....LLES.....	349

logo

NTDB id 600 KW2 RS01765 WP 011675413.1	.	387
NTDB id 269 KZH43 RS08665 WP 001085462.1	E	388
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consensus

 non conserved
 similar
 ≥ 50% conserved