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consensus

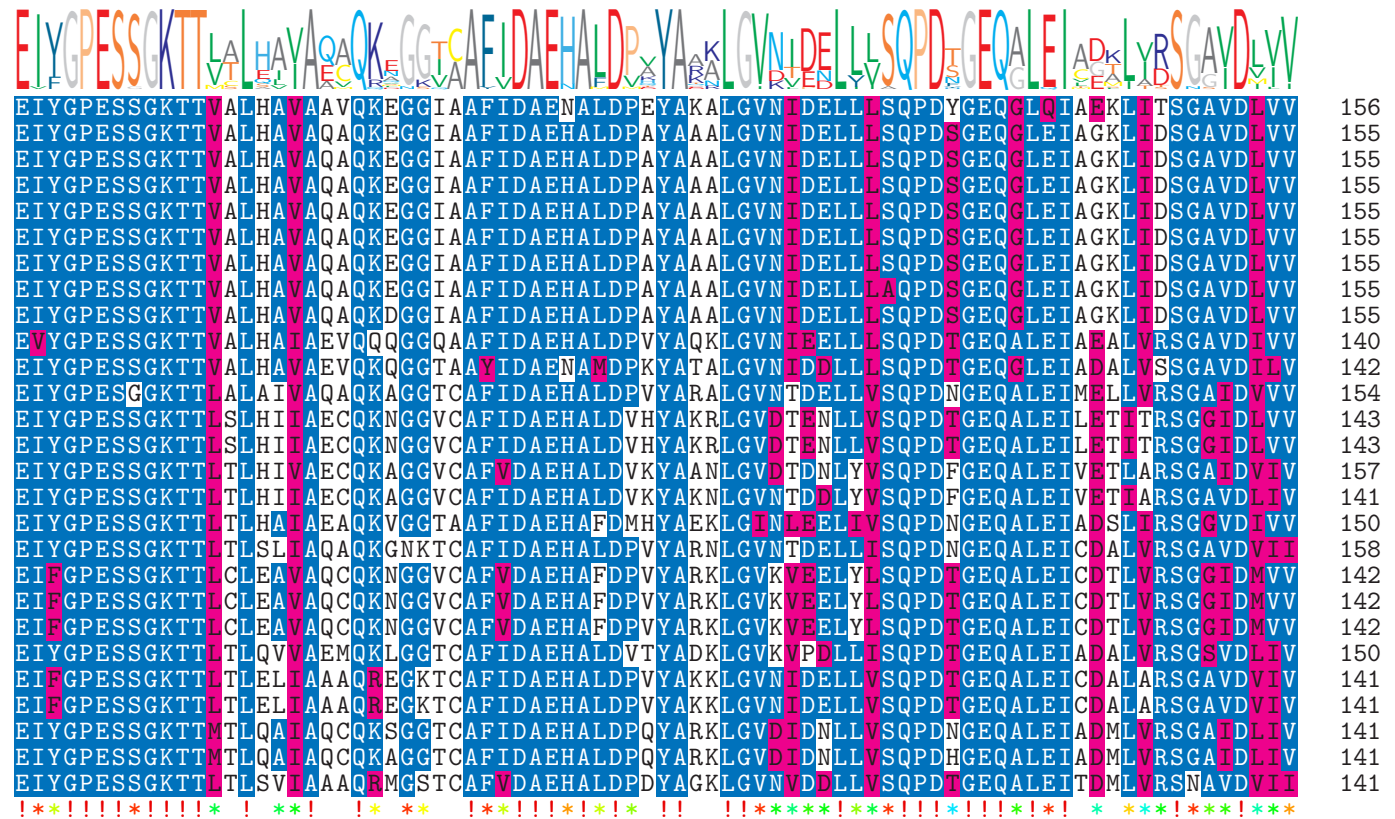
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consensus

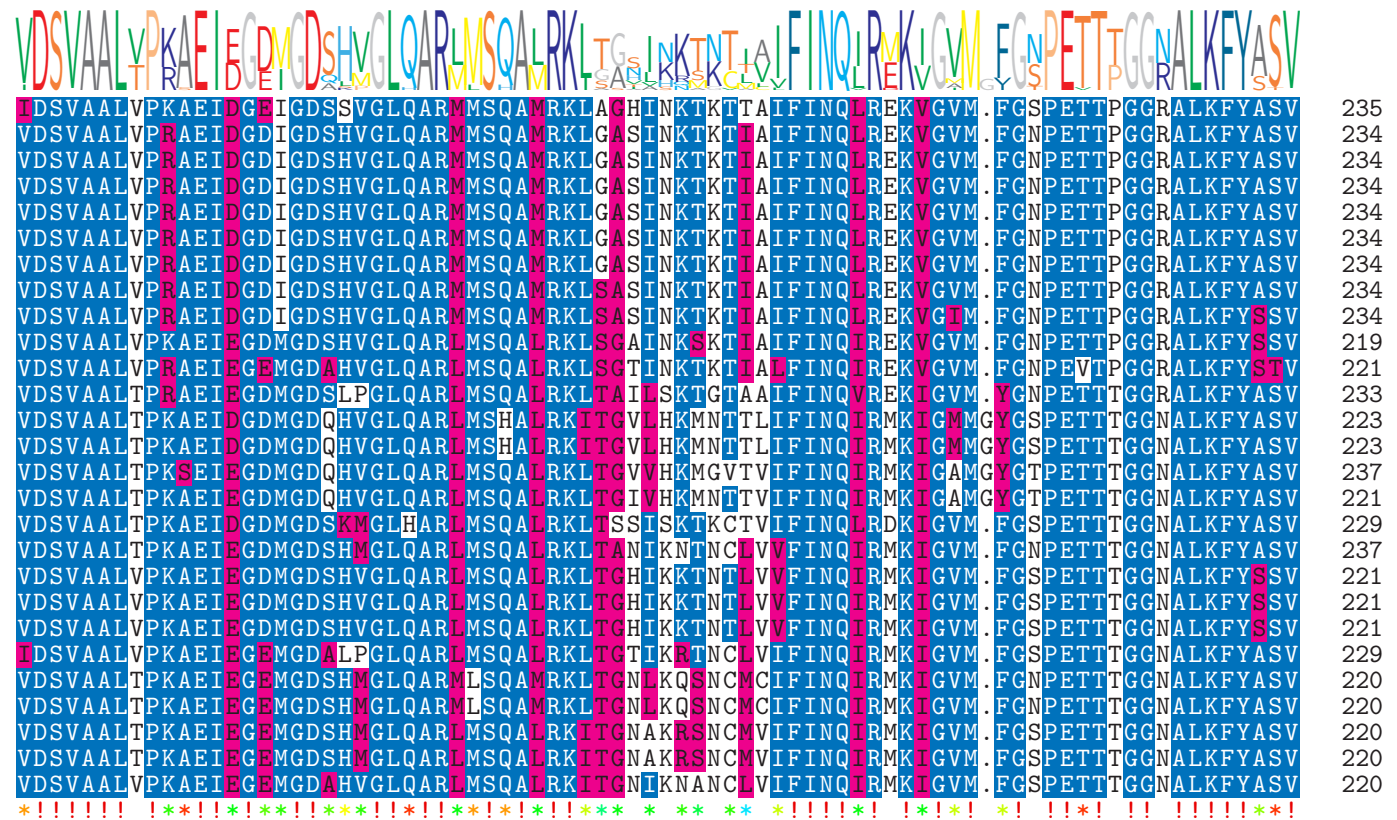
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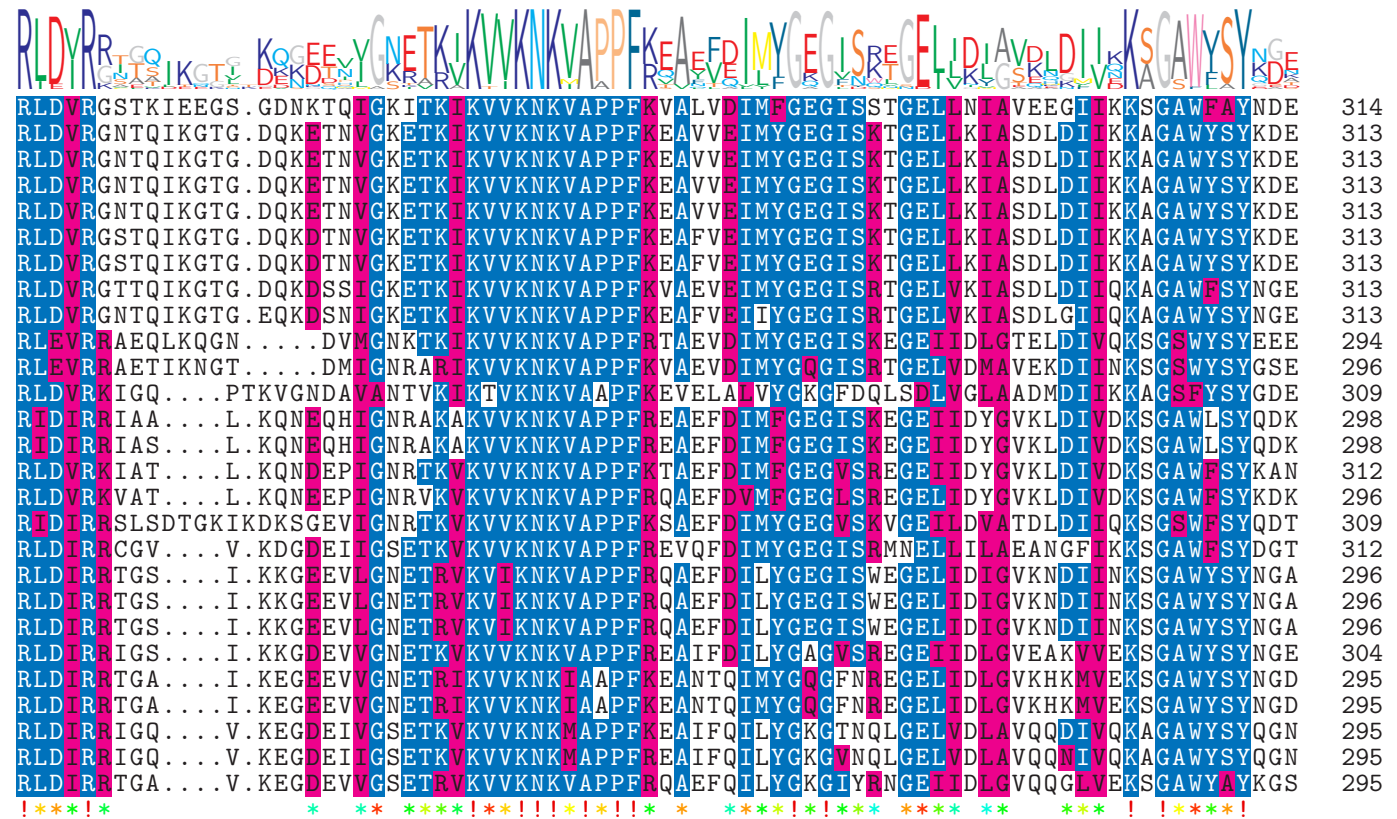
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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Sequence	Score
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KIGGQSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIEIE	387
KIGGQSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIEIE	387
KIGGQSENAKKYLAADNPVFDEIDHQRVVFQLIDGEEIAES....KKDE....AAQVDS..VNEEVPLDLGDELEIEIE	383
KIGGQSENAKKYLAADNPVFDEIDHQRVVFQLIDGEEIAES....KKDE....VAQVDS..VNEEVPLDLGDELEIEIE	383
KIGGQSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIED.	378
KIGGQSENAKKFLADNPVFDEIDHQRVVFQLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELED.	383
RLGGQRENAKQFLKENKDIMLMIQEQIREHYGLDNNGVVQQQAETQEEL.EFE.E.....	348
RIGGQRENAKNYLADHEDVEDEVRLKVRVAYGTSVPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
RIGGQKEKTIAYIAERPEMEQETDRVMAAIRAGNAGEAPALAPAPAAPE.....AAEA.....	363
KLGGQRENAKALLKEDKALADEITLKIKESIGSNEEIMPLP...DEPLEE.....ME.....	347
KLGGQRENAKALLKEDKALADEITLKIKESIGSNEEIMPLP...DEPLEE.....ME.....	347
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KLGGQRENSKAFLENPEIADEITKAIQNSMCTEGMISGSE...DDEGEE.....	343
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KIGGQKANACKYLKENPEIAKTLDKKLREMLLNPNMQLIA..ETSSAAD.....DVEFGAVPEEF.....	354
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KIGGQKANAAKYLENPEIGQEIEQQIRAKLLVTSANTKAT..PVAEDLA.....DAD..I.....	347

logo

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NTDB id 228 SPD RS09265 WP 001085462.1	E	388
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consensus

 non conserved
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 ≥ 50% conserved