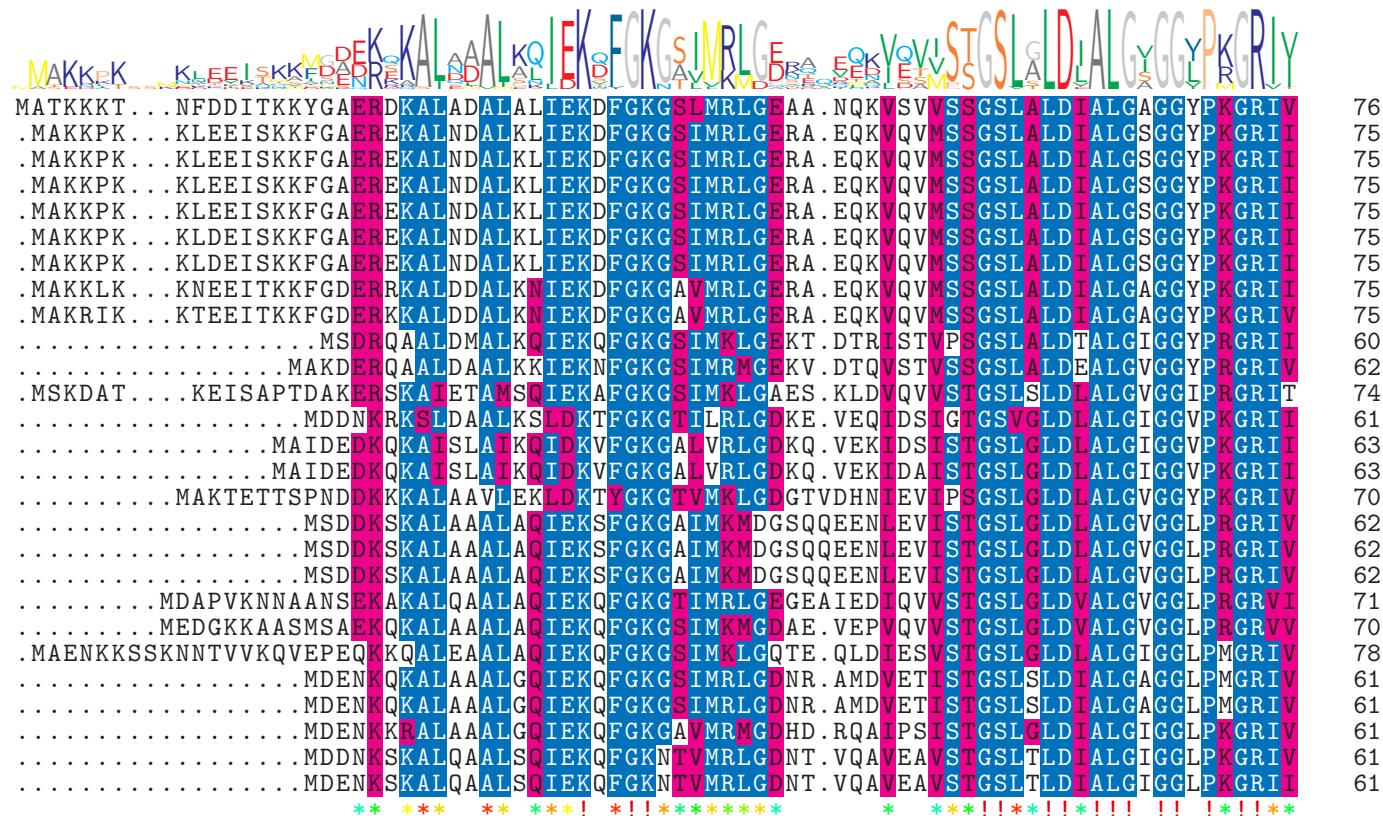


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consensus

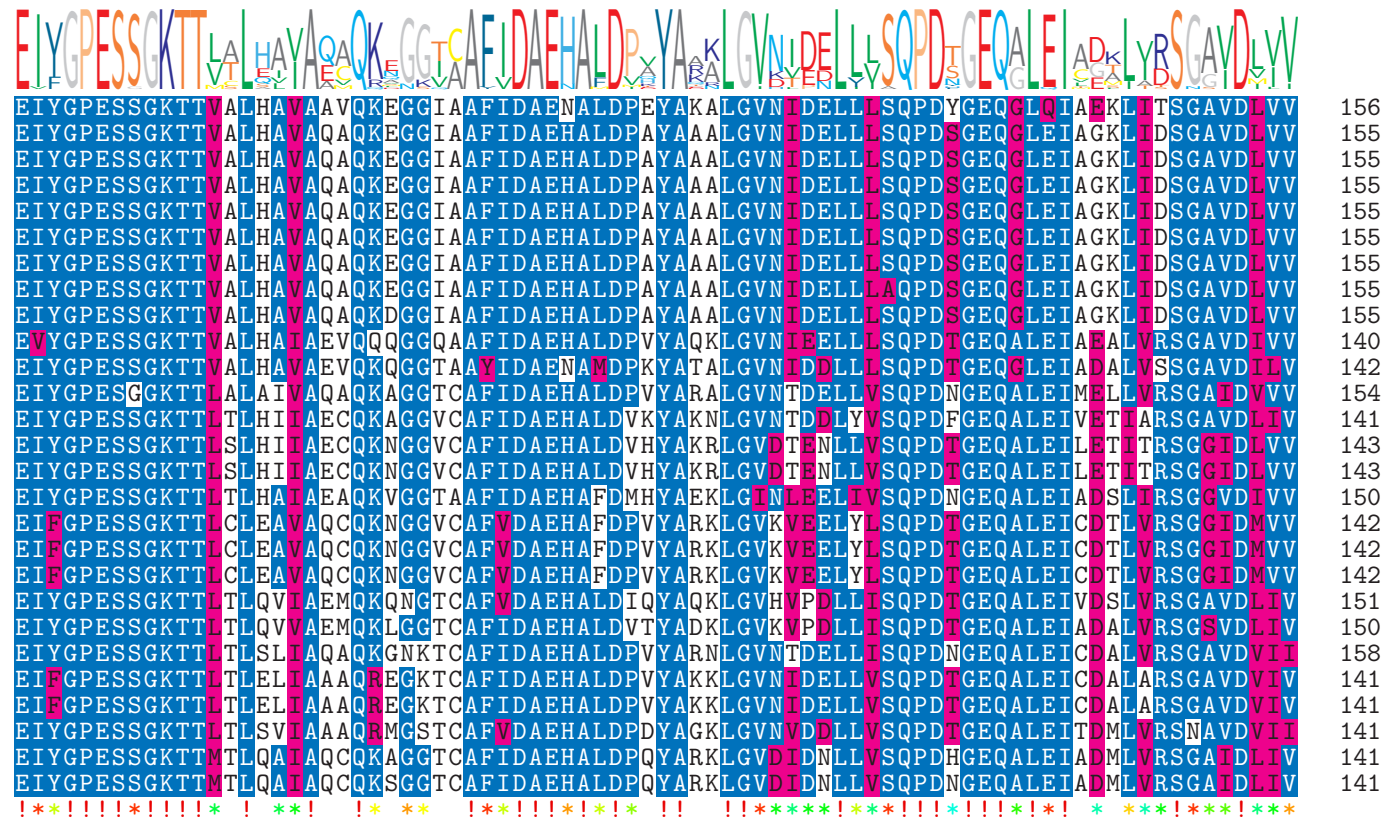
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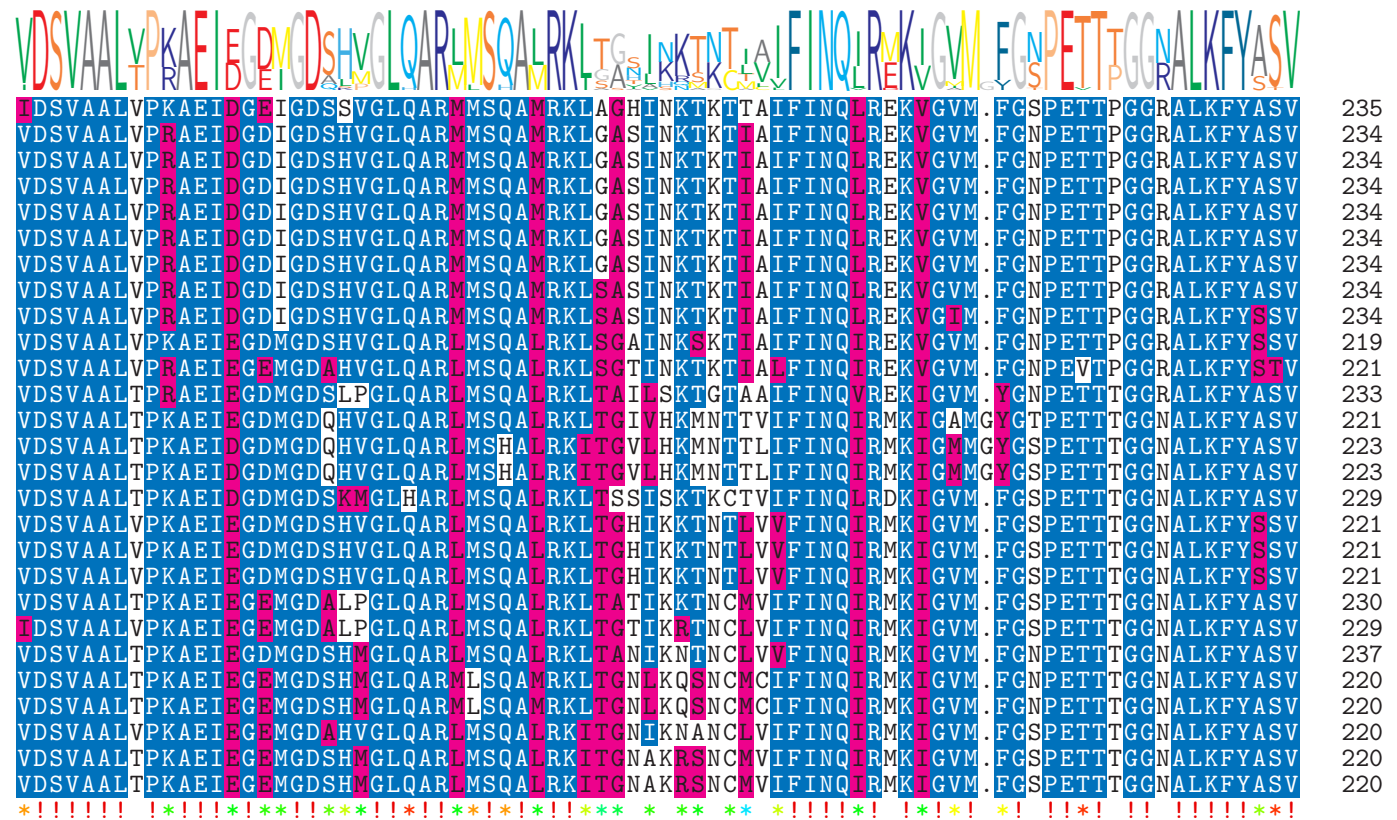
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consensus

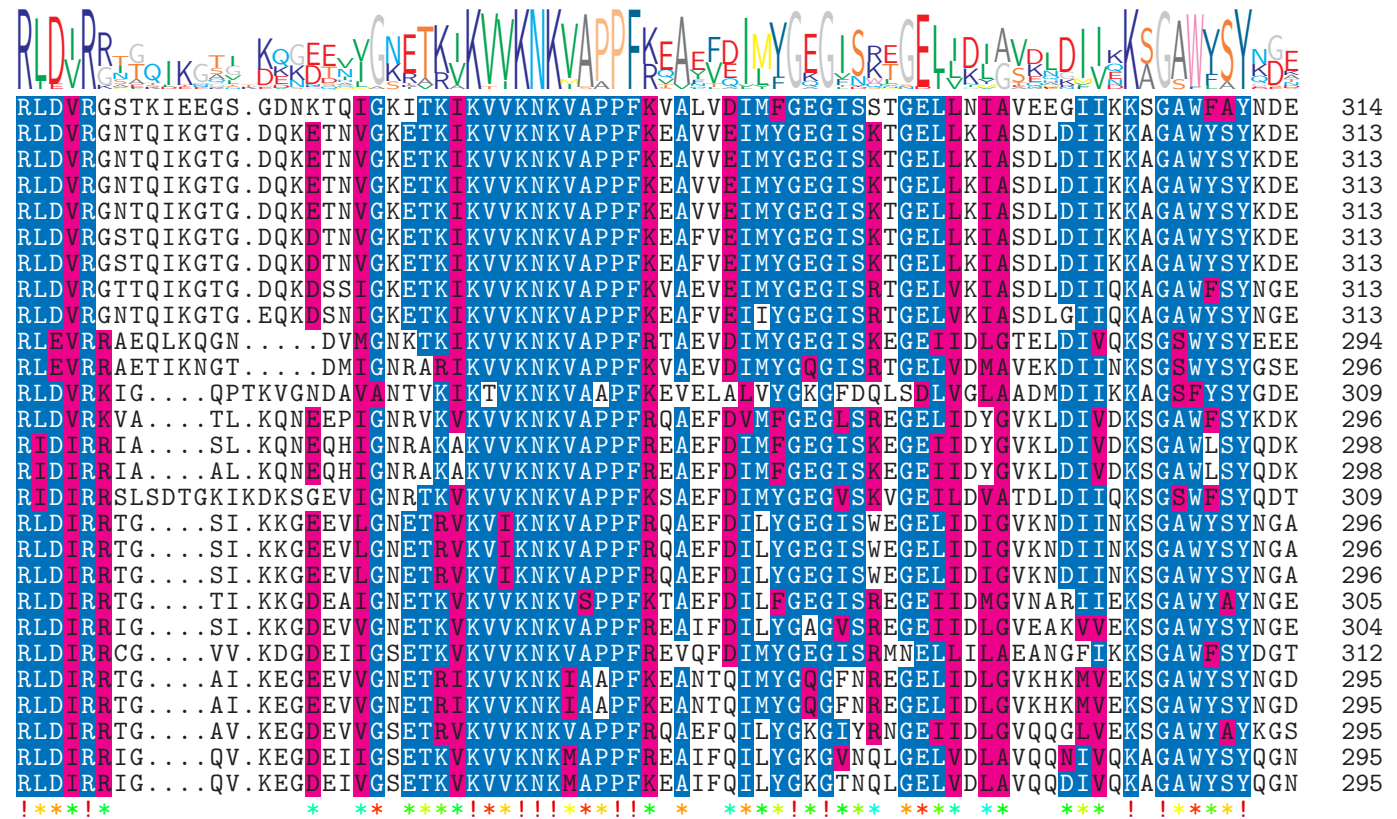
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consensus

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Sequence	Score
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KIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKD.E...PKKEEA..VNEEVPLDLGDELEIEI	386
KIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKD.E...PKKEEA..VNEEVPLDLGDELEIEI	386
KIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKD.E...PKKEEA..VNEEVPLDLGDELEIEI	386
KIGQGSSENAKKYLAHNPEIFDEIDHQRVVFGLIDGEEIAES...KKD.E...AAQVDS..VNEEVTLDLGDELEIEI	382
KIGQGSSENAKKYLAHNPEVFAEIDHQRVVFGLIDGEEIAES...KKD.E...VAQVDS..VNEEVTLDLGDELEIEI	382
KIGQGSSENAKRYLADHPQLFDEIDRKRVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIED	378
KIGQGSSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELED	383
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logo

NTDB id 600 KW2 RS01765 WP 011675413.1	..	387
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consensus

 non conserved
 similar
 ≥ 50% conserved