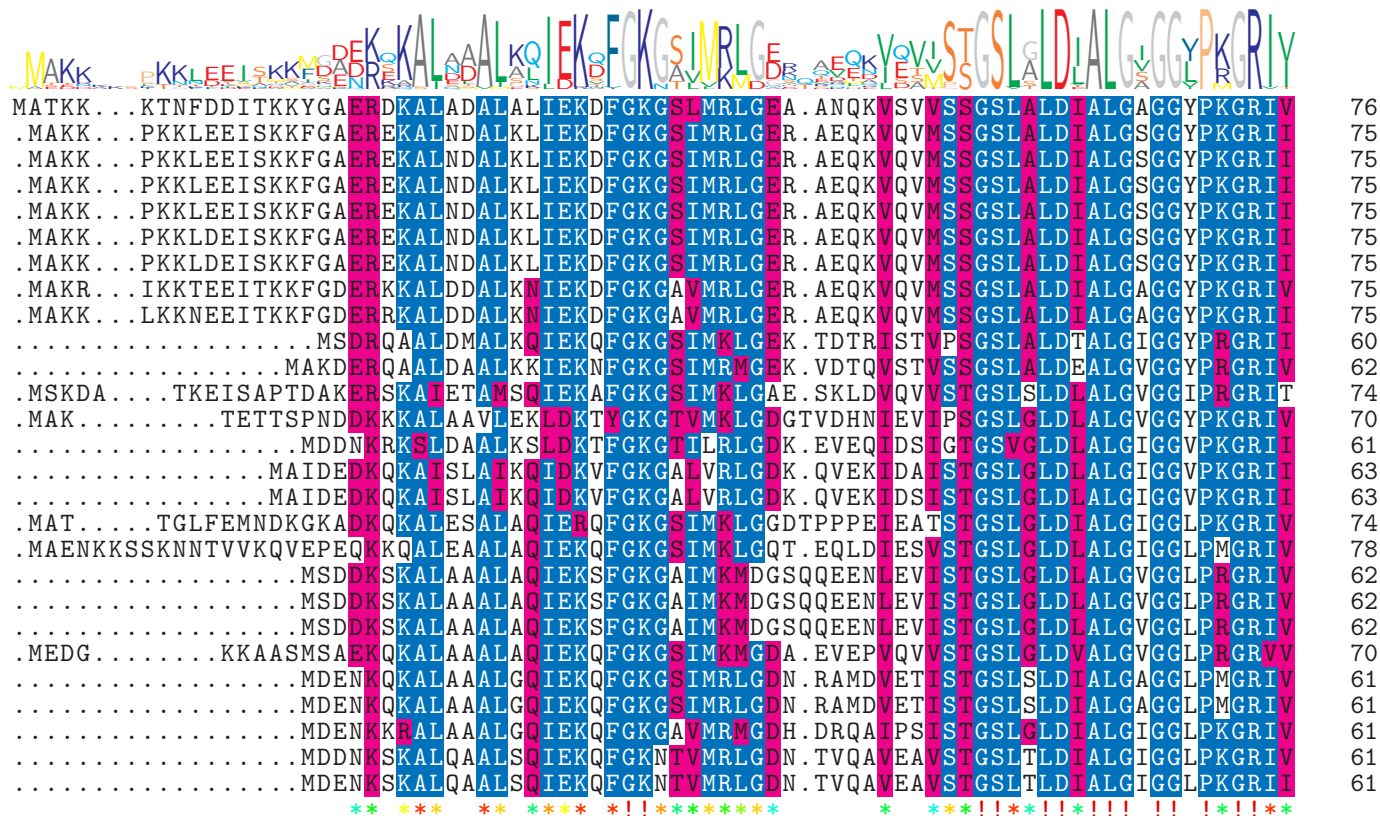


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consensus

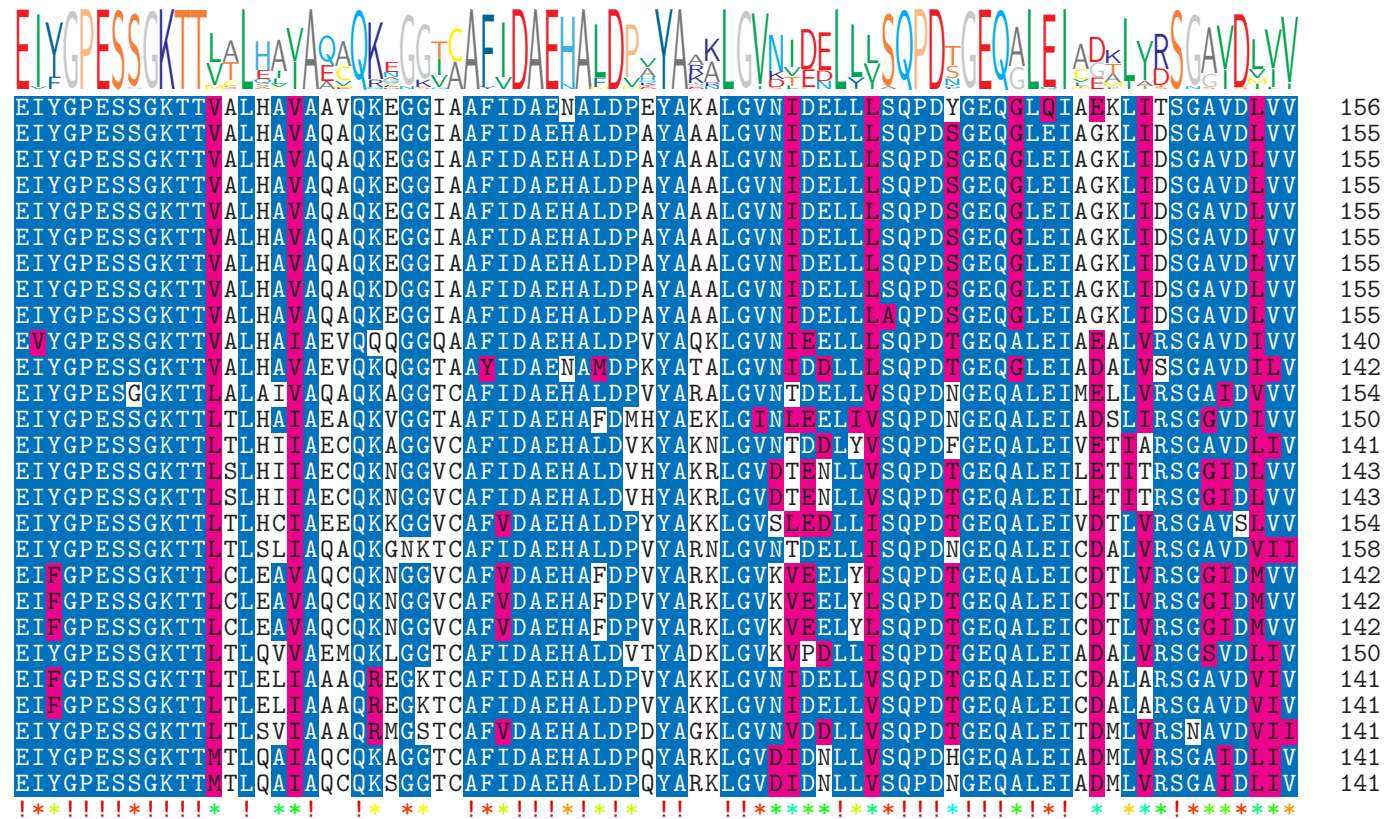
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consensus

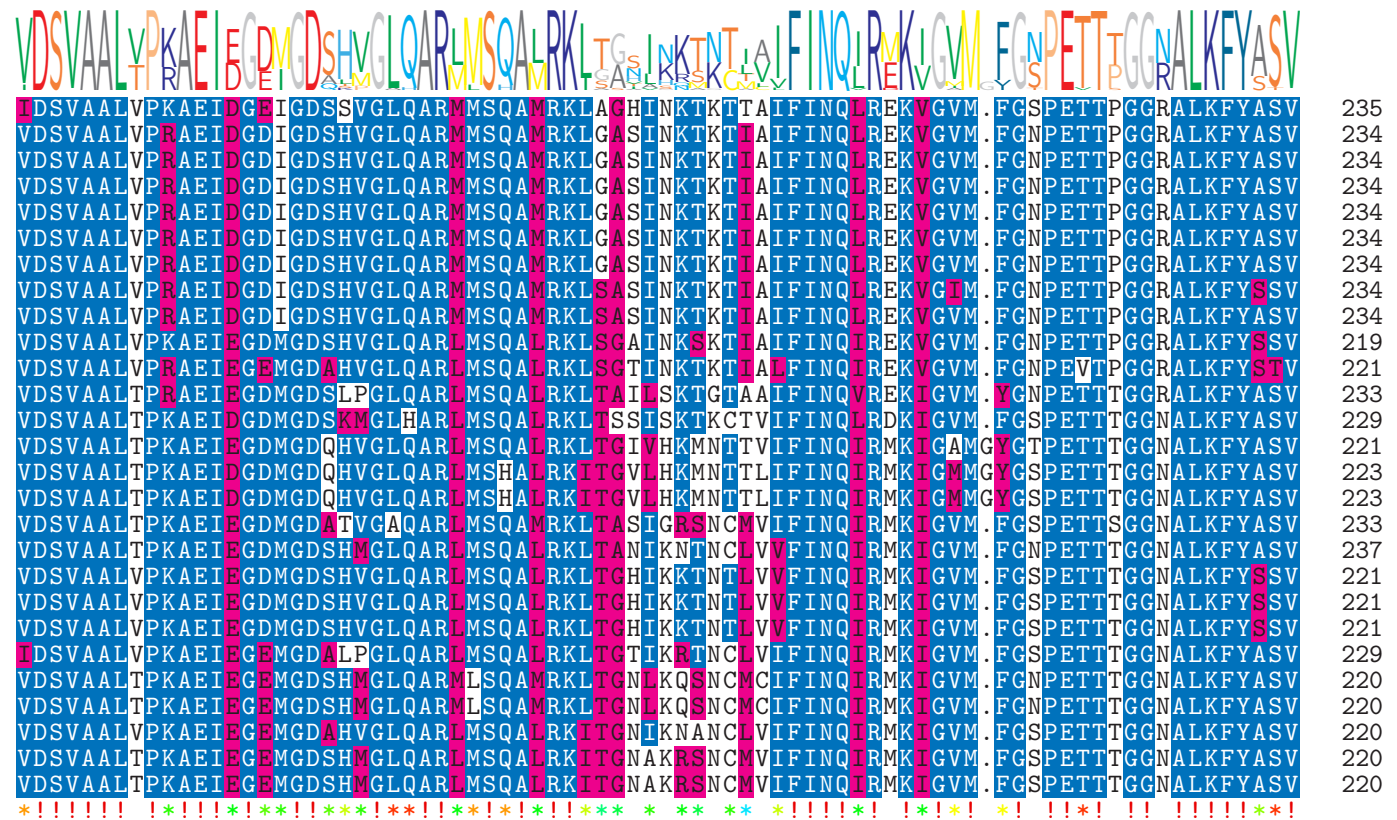
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consensus

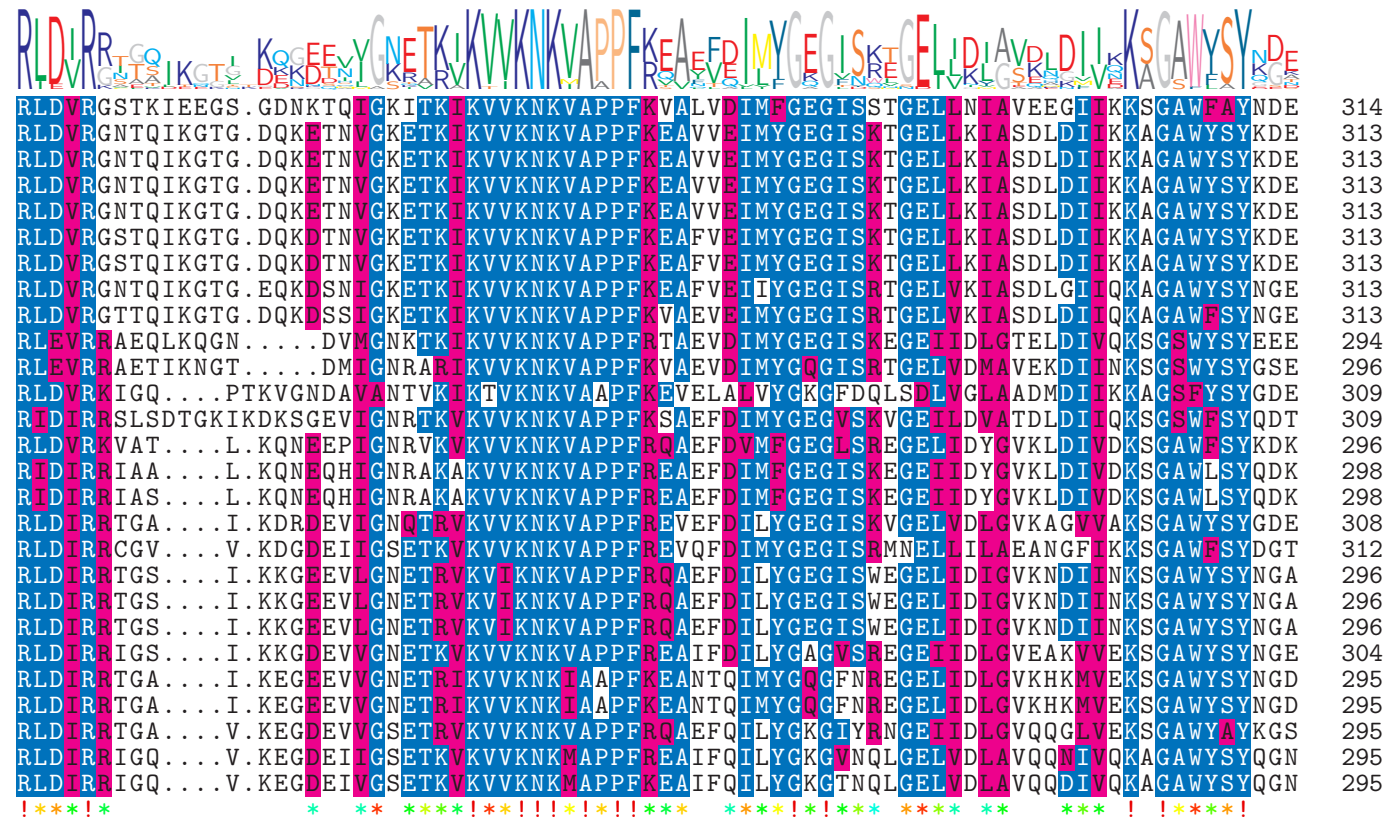
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consensus

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Sequence	Score
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KIGGQSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE....PKKEEA..VNEEVPLDLGDELEIEIE	387
KIGGQSENAKKYLAADNPEVFAEIDHQVVRVQFLIDGEEAAE....SKKDE....VAQVDS..VNEEVTLDLGDELEIEIE	383
KIGGQSENAKKYLAADNPEIFDEIDHQVVRVQFLIDGEEIAE....SKKDE....AAQVDS..VNEEVTLDLGDELEIEIE	383
KIGGQSENAKKFLADNPEIFDDIDHKVVRVQCLIEEDNTEEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELED.	383
KIGGQSENAKRYLADHPQLFDEIDRKVVRVKFLLEESEEEESAMAVASE.....E.....TDDLALDLNNGIEIED.	378
RLGGQRENAKQFLKENKDIMLMIQEQIREHYCLDNNGVVQQQAEETQEEL.EFE.E.....	348
RIGGQRENAKNYLADHEDVEDVRLKVRVAAAYCISDVPEEDLPTTEDE.QI.NILPD DST.....EE.....	355
RIGGQKEKTIAYIAERPEMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAAE..A.....	363
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KLGGQRENAKALLKEDKALADEITLKIKESIGSNEEI....MPLPDEPL..E..EME.....	347
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KIGGQKNNVIRYLEENPEIISTEIEAVIREQLLTKASD....QTAA.HDETEE..EPDLL..ES.....	349
KIGGQKNNVIRYFEENQIAEIEIRNIREQLLTTGTN....GAVQ.I.EDEE..EPDLL..LES.....	349

logo

NTDB id 600 KW2 RS01765 WP 011675413.1	.	387
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consensus

 non conserved
 similar
 ≥ 50% conserved