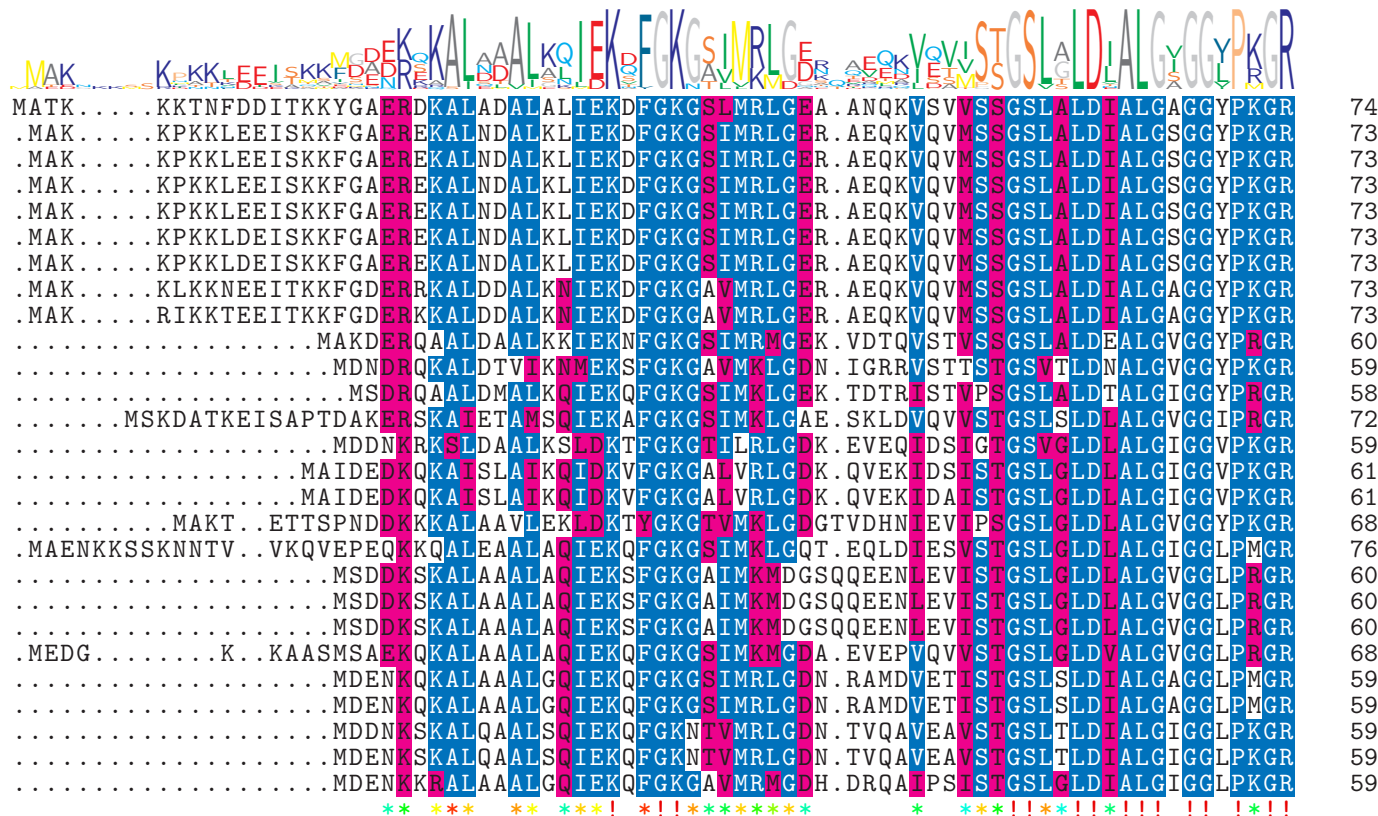


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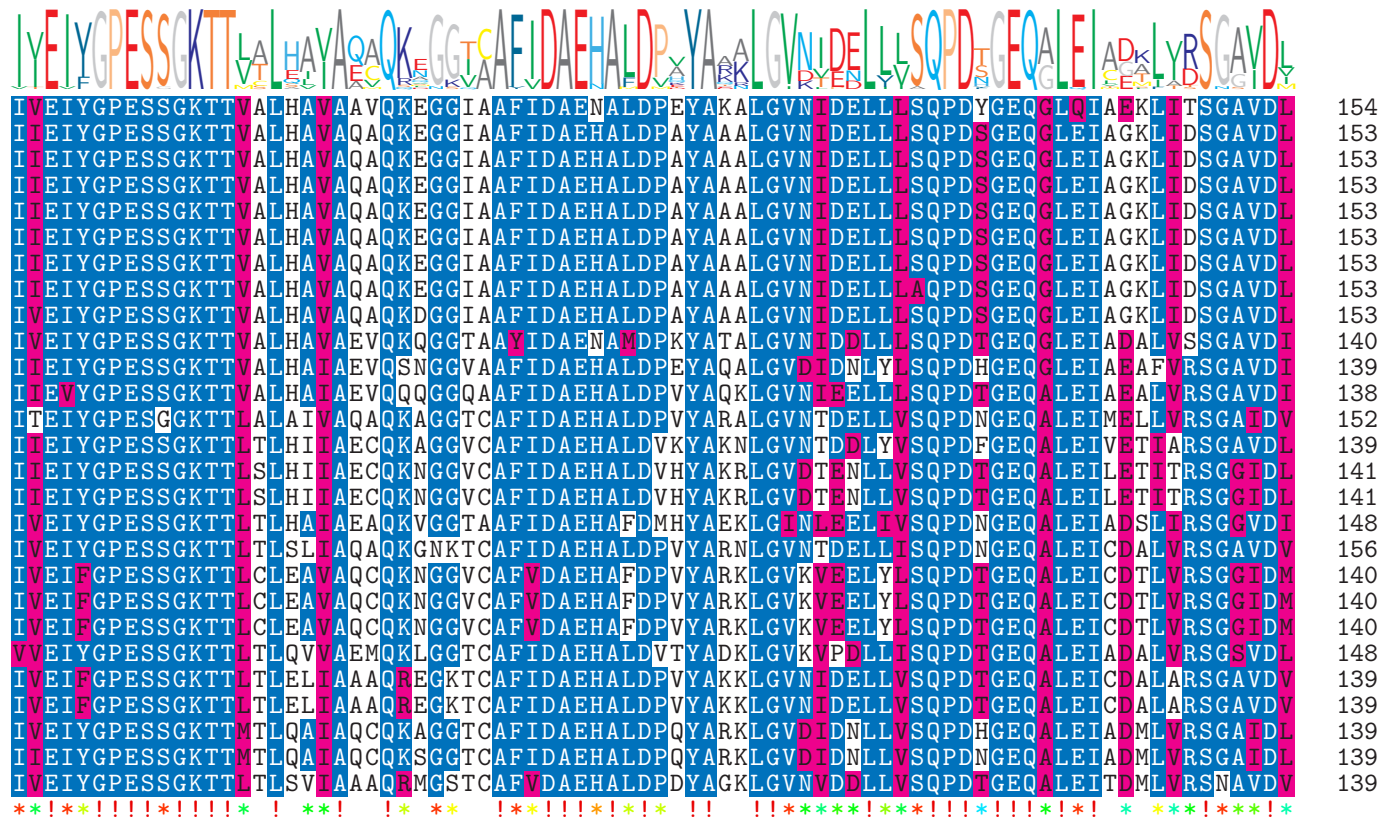
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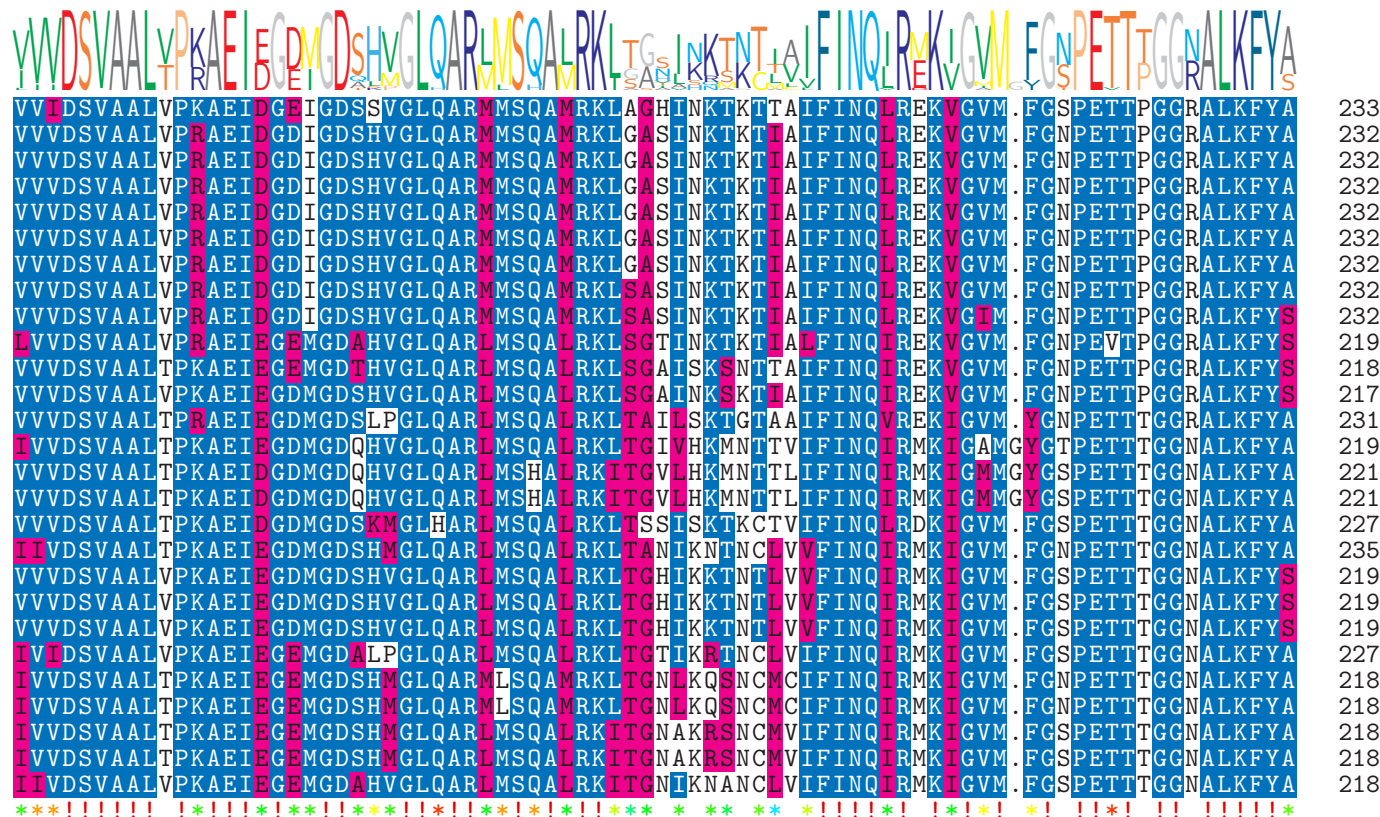
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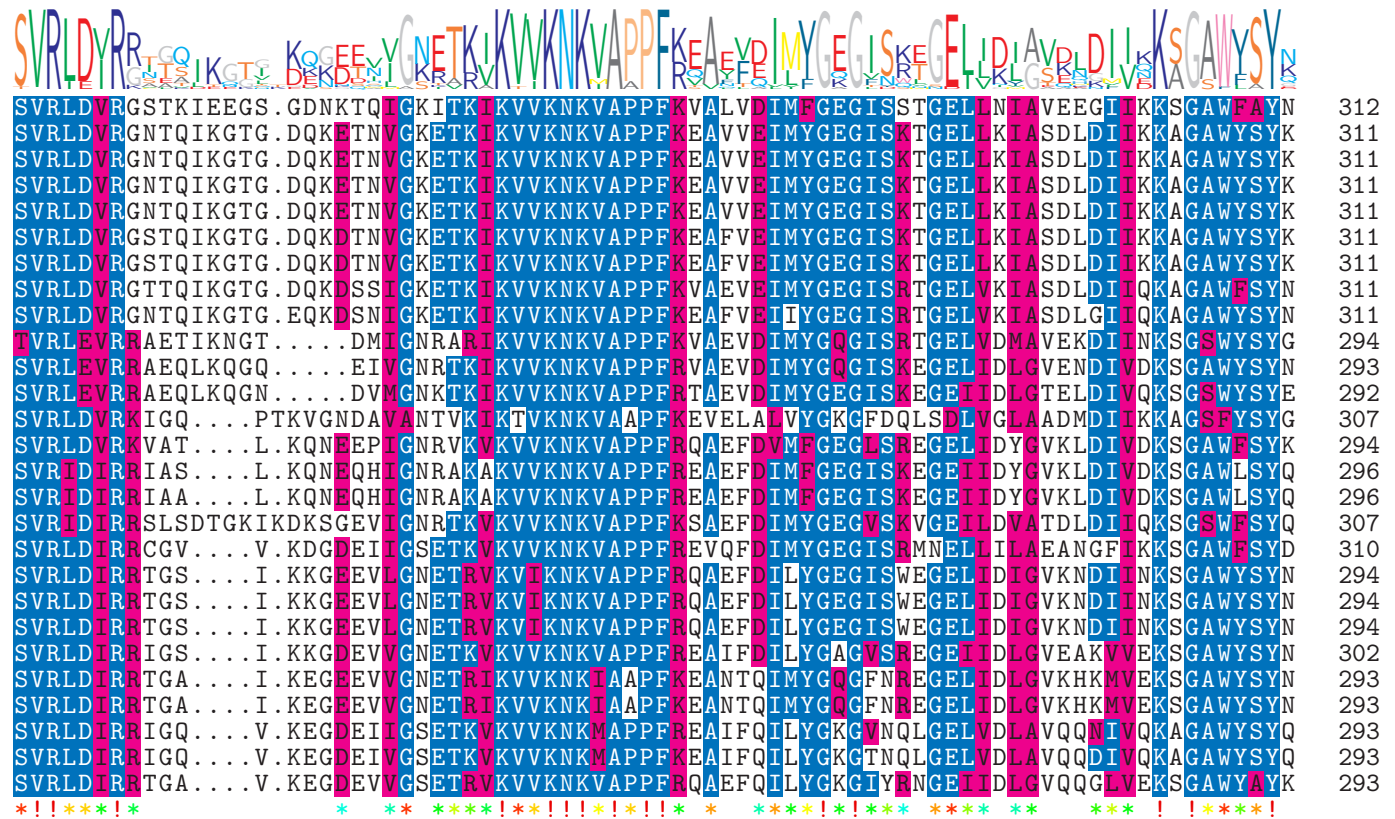
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consensus

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Sequence	Score
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DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
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DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
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DEKIGQGS ENAKKYLAADNPEVFAEIDHQVRVQFGLIDGEEIAES . . . KKDE . . . VAQVDS . VNEEVTLDLGDELEIE	381
GEKIGQGS ENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE E TDDLALDLNGIEIE	377
GEKIGQGS ENAKKFLADNPEIFDDIDHKVVRVQGLIEEDNTEEKQSSKEK ETDEK . ADKNLVLELDDTIELE	382
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GSKIGQGANAAKYYLENPEIQEIEQQIRAKLLVTSAN TKATPVAEDLADAD . I	347

logo

NTDB id 600 KW2 RS01765 WP 011675413.1	... 387
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consensus	

-  non conserved
-  similar
-  ≥ 50% conserved