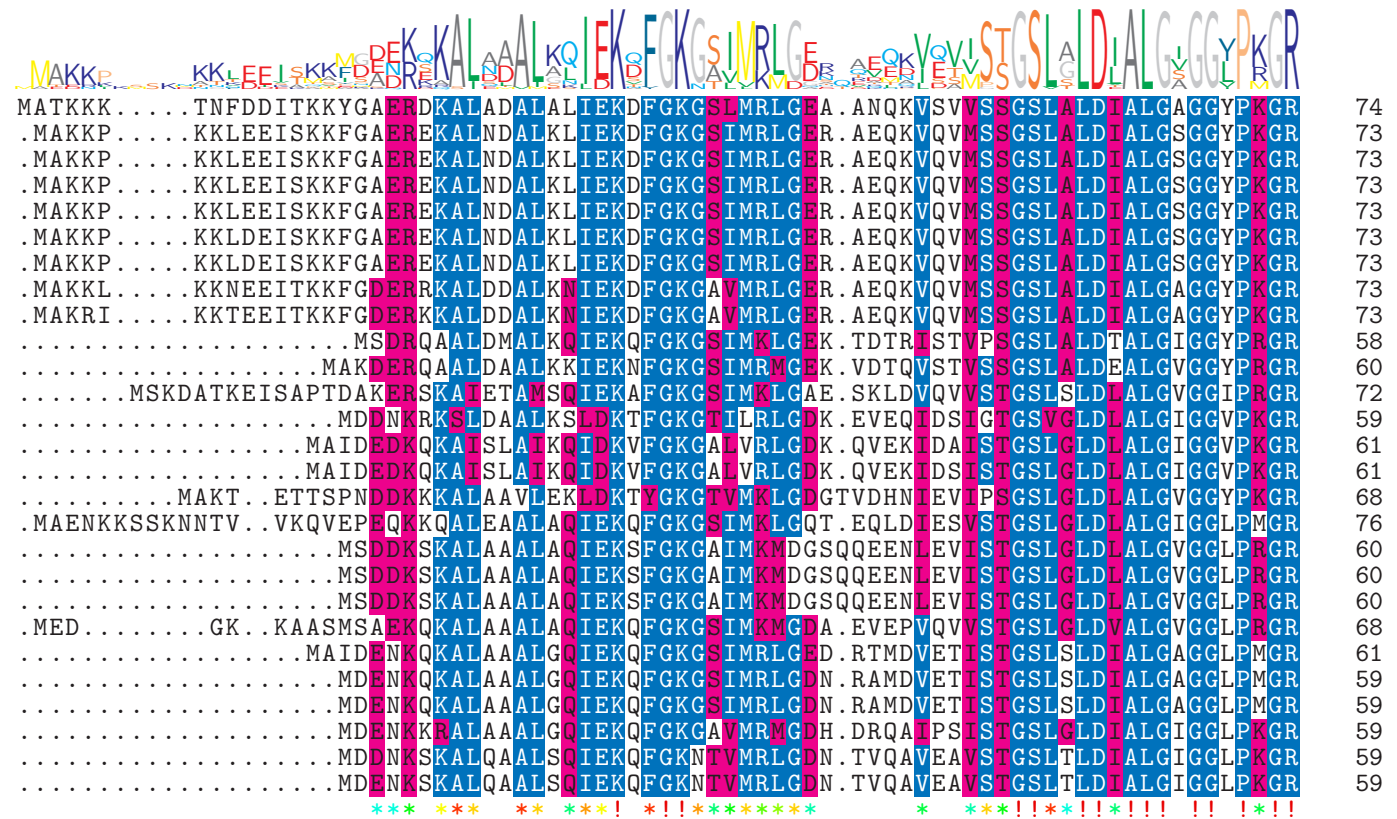


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consensus

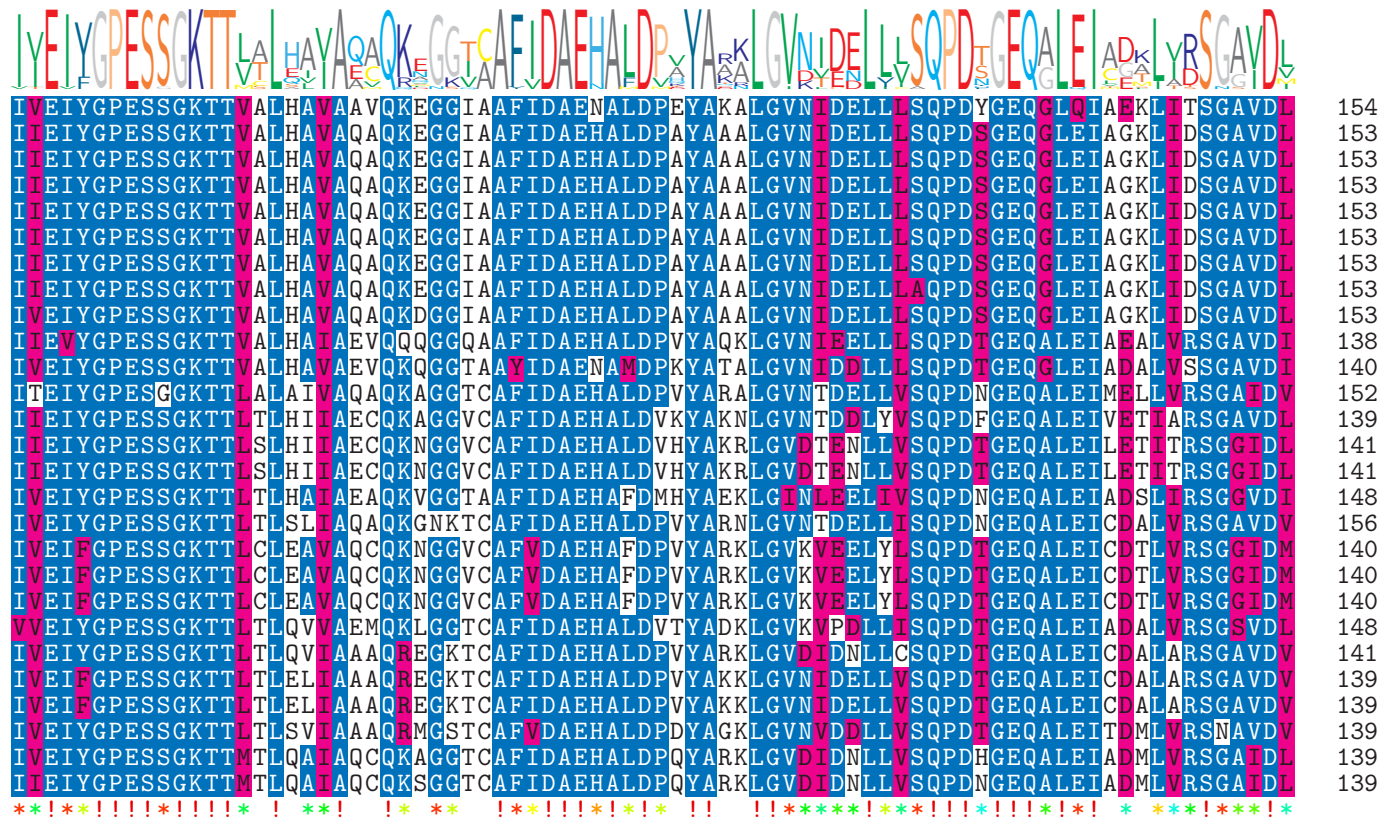
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consensus

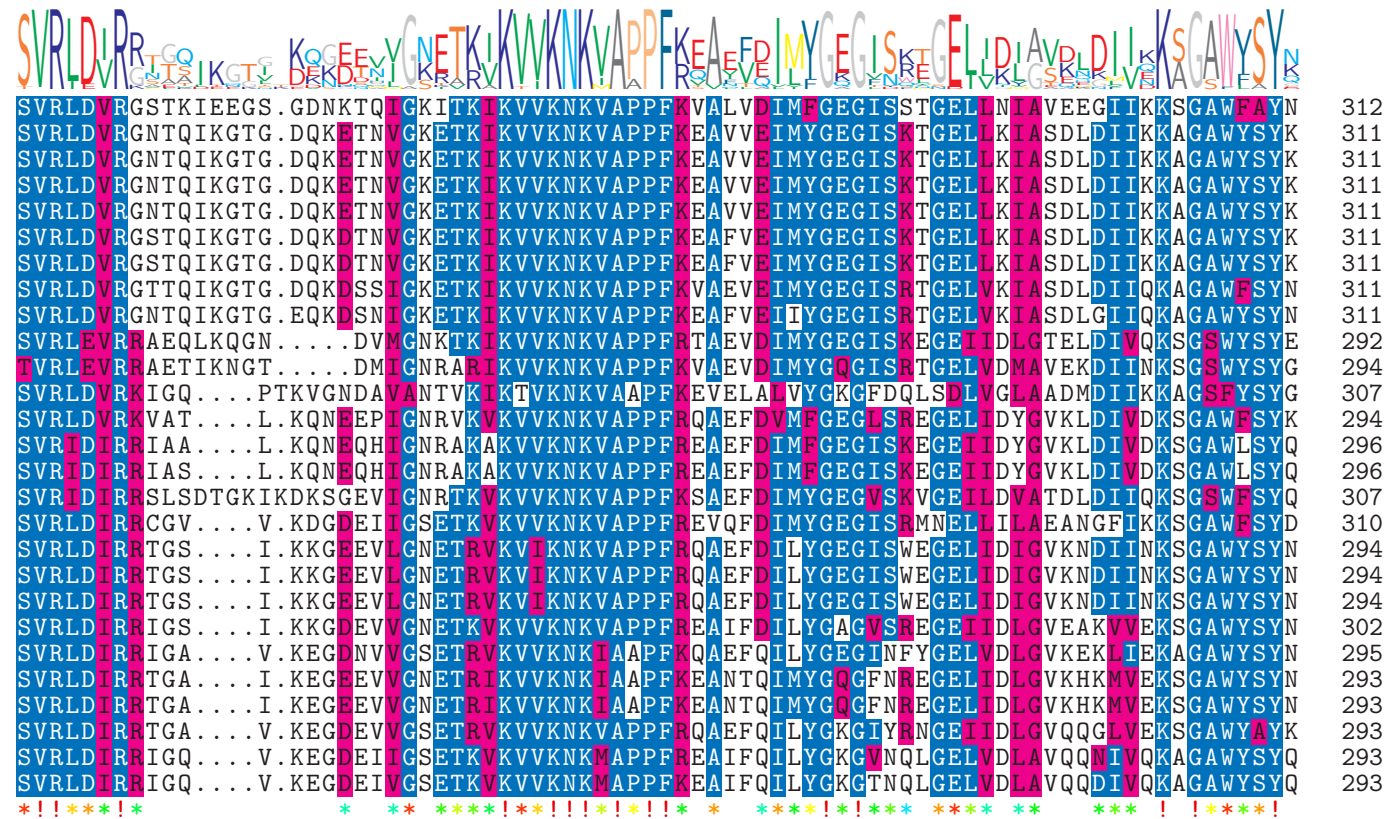
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consensus

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consensus

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Sequence	Score
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GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE E TDDLALDLNGIEIE	377
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK ETDEK . . ADKNLVLELDDTIELE	382
EERLGQGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEETQEEL . EFE . E	348
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DKKLGGGRENKSAFLKENPEIADEITKAIQNSMGTIEGMISGSEDDE . . GE . E	343
DKKLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIMPLPDEP . . LE . EME	347
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GERIGQGRDNCREFLRENAELAREIENKVRHGLVTPMGAVTLAAE . . VE . ED	352
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GNKIGQKKNNVIRYFENNQIAEIERNIREQLLTGTNGAV . . Q . . I . . EDEEEPDLLES	349

logo

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NTDB id 1074 ABD1 RS10195 WP 000344167.1	...	349	
consensus			

-  non conserved
-  similar
-  ≥ 50% conserved