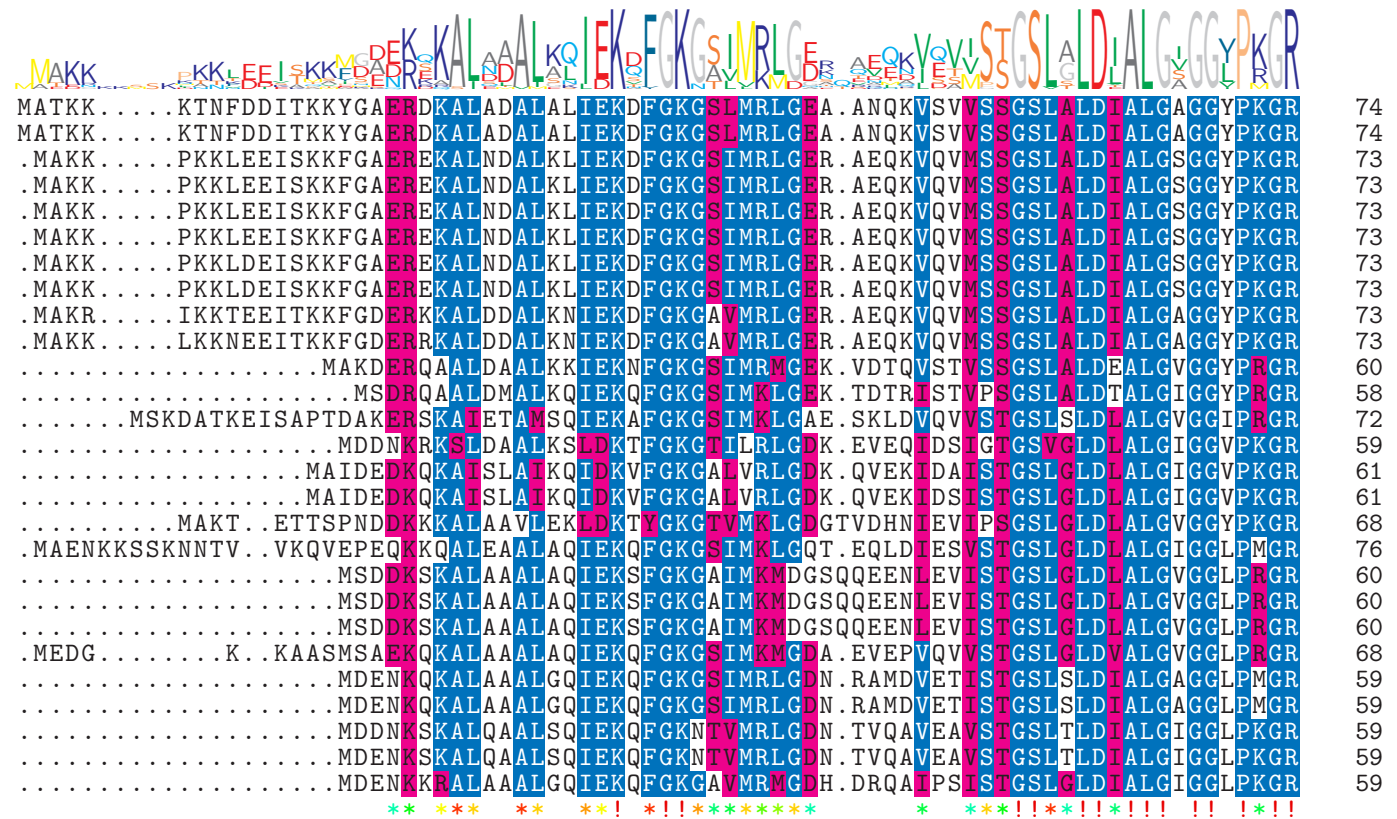


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consensus

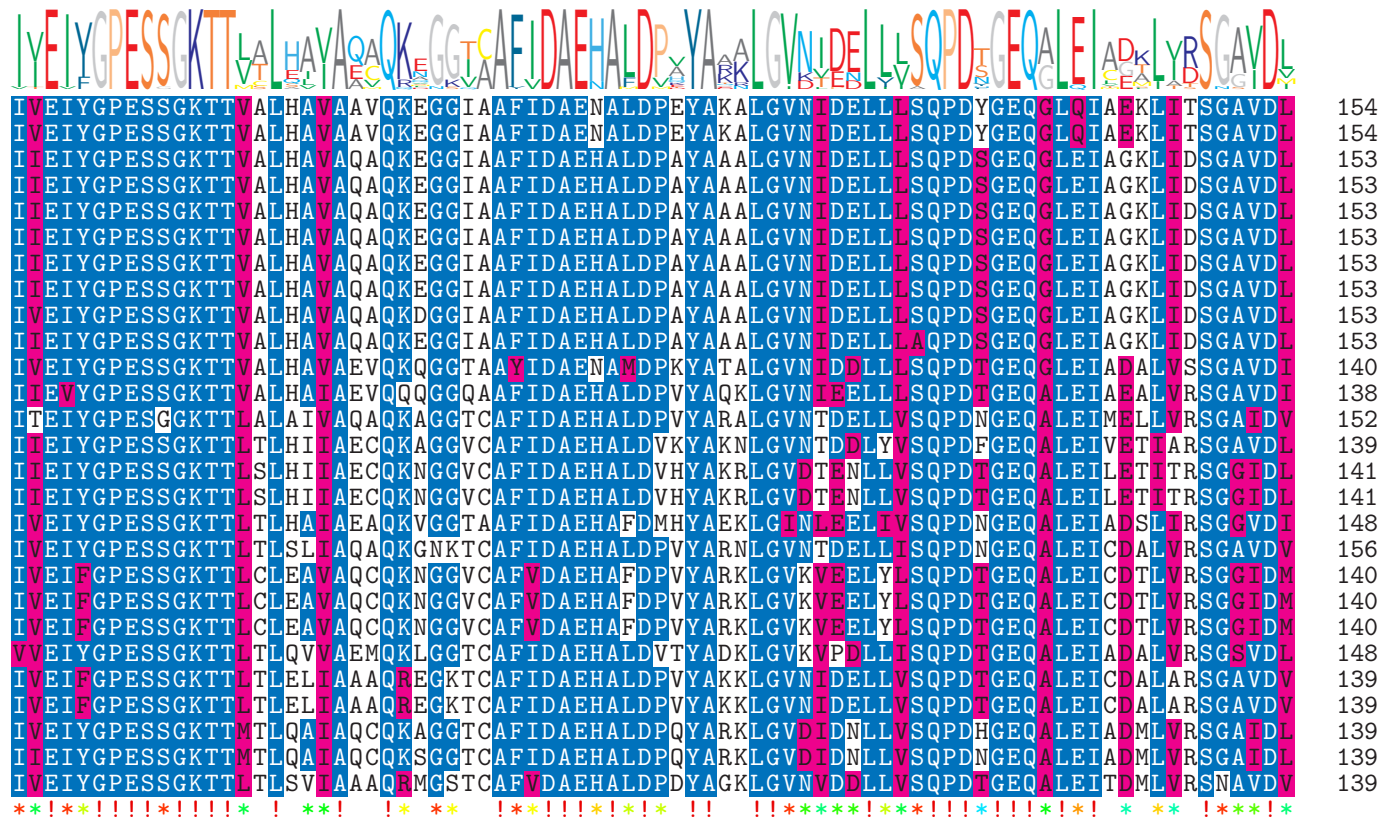
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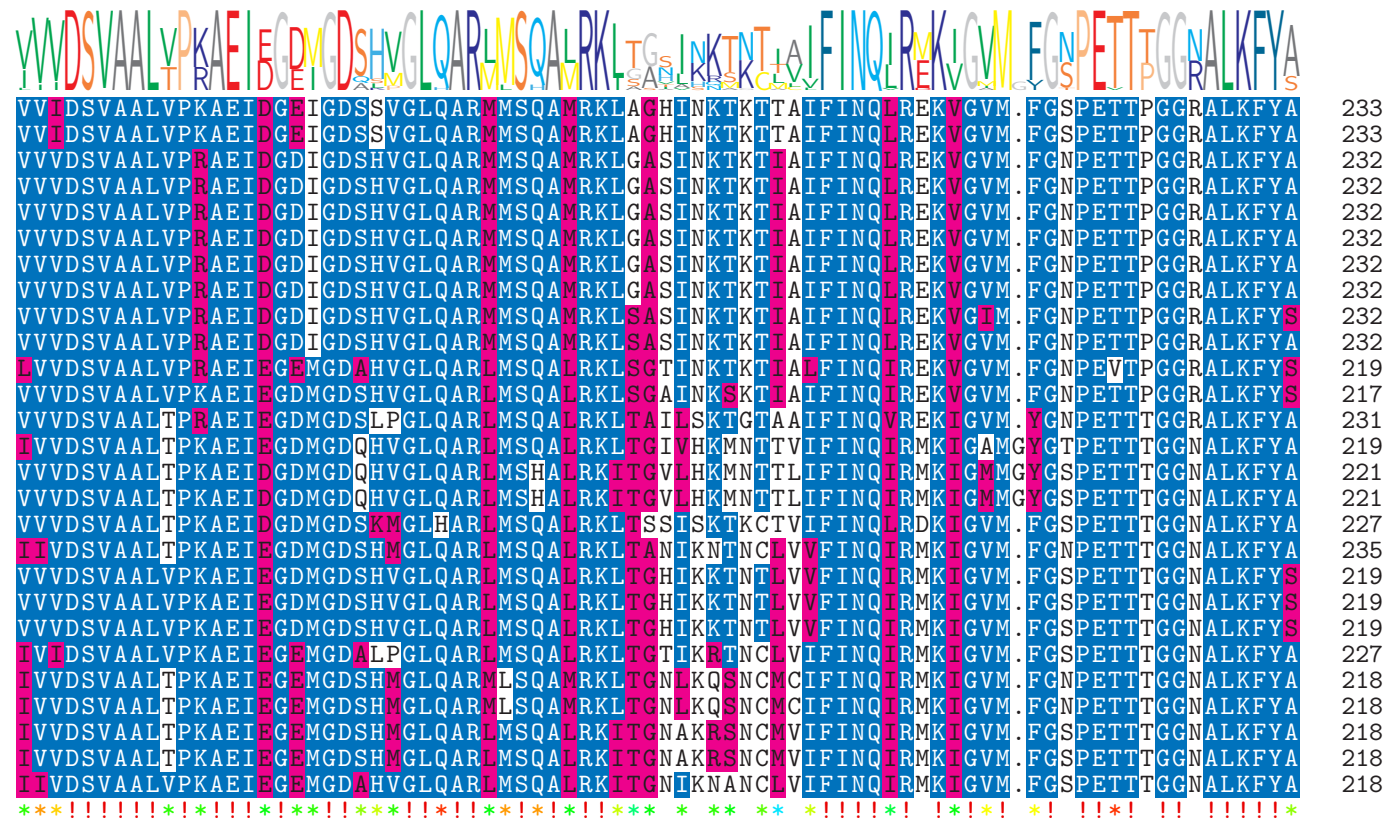
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consensus

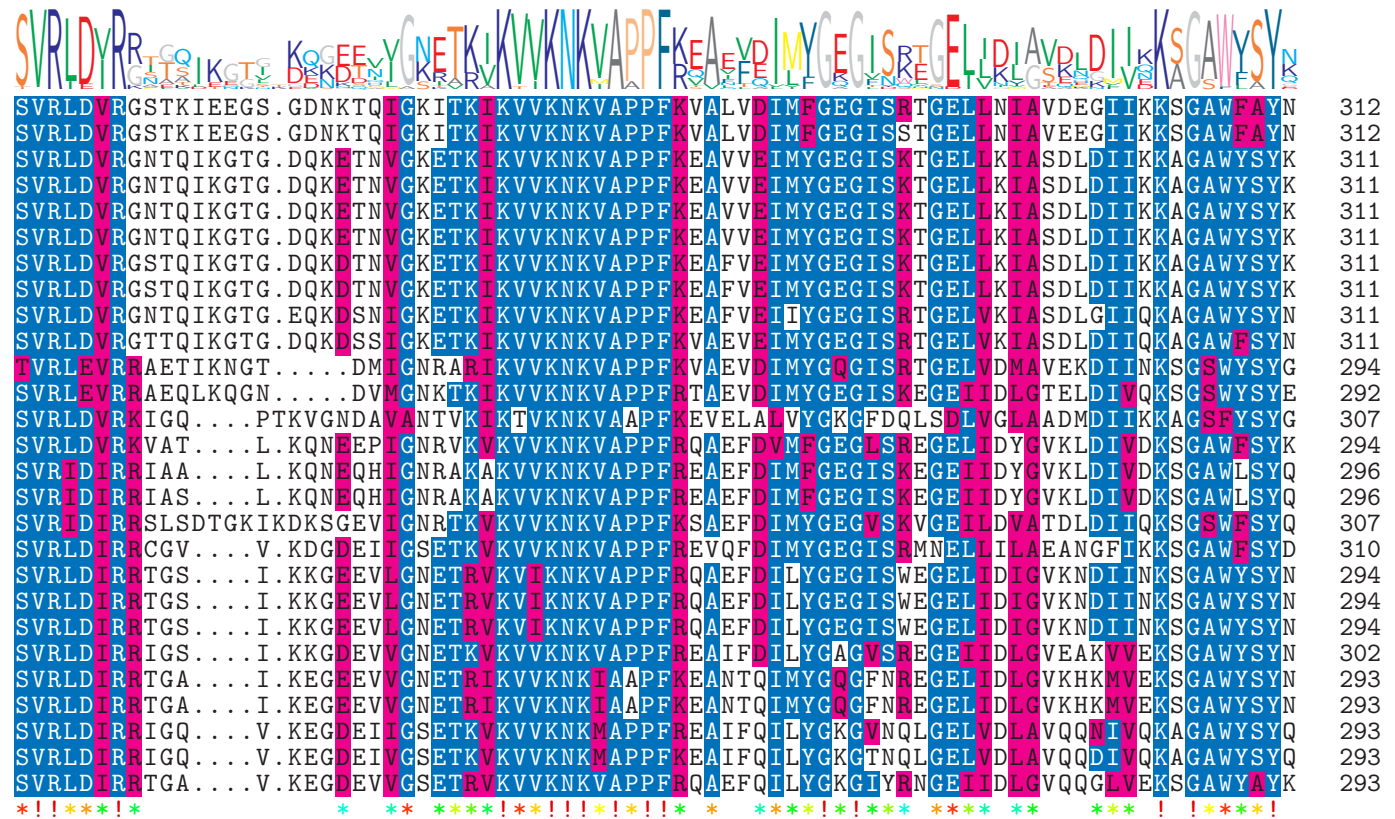
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consensus

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consensus

Sequence	Score
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DEKIGGGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDNTENKKDEPK...KEEAV...NEEVPLDLGDELEIE	385
DEKIGGGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDNTENKKDEPK...KEEAV...NEEVPLDLGDELEIE	385
DEKIGGGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDNTENKKDEPK...KEEAV...NEEVPLDLGDELEIE	385
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GEKIGGGSENAKKFLADNPEIFDDIDHKVVRVQGLIEEDNTEEKQSSKEK...E...TDEKA...DKNLVLELDDTIELE	382
GEKIGGGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE...E...TDDLALDLNGIEIE	377
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GNKIGGQKNNVIRYLEENPQISTEIEAVIREQLLTKASD...QTAA.HDETE...EEDPLL...ES...	349
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logo

NTDB id 47556 CVCAS RS01790 WP 003131629.1 ... 387
NTDB id 600 KW2 RS01765 WP 011675413.1 ... 387
NTDB id 269 KZH43 RS08665 WP 001085462.1 IEE 388
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consensus

 non conserved
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