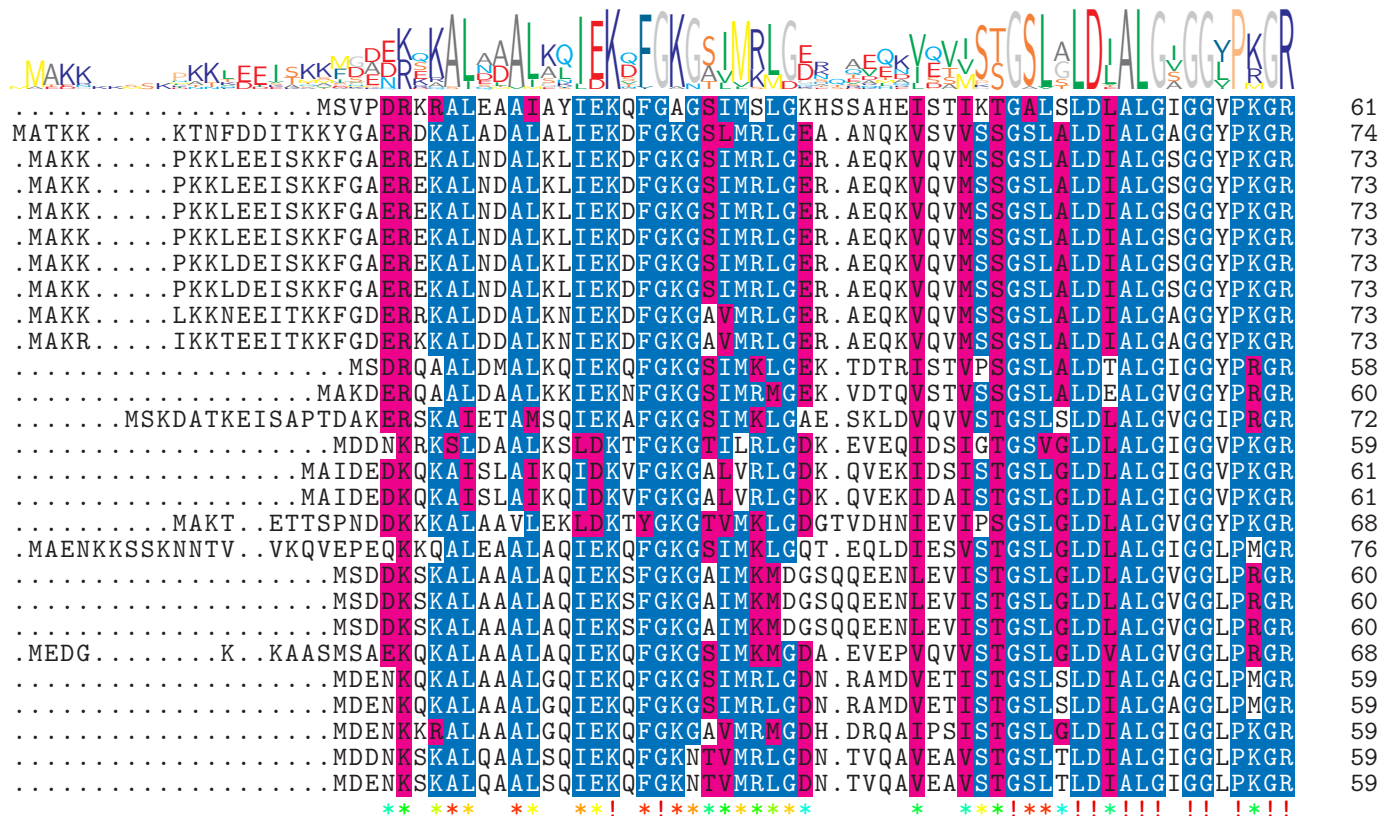


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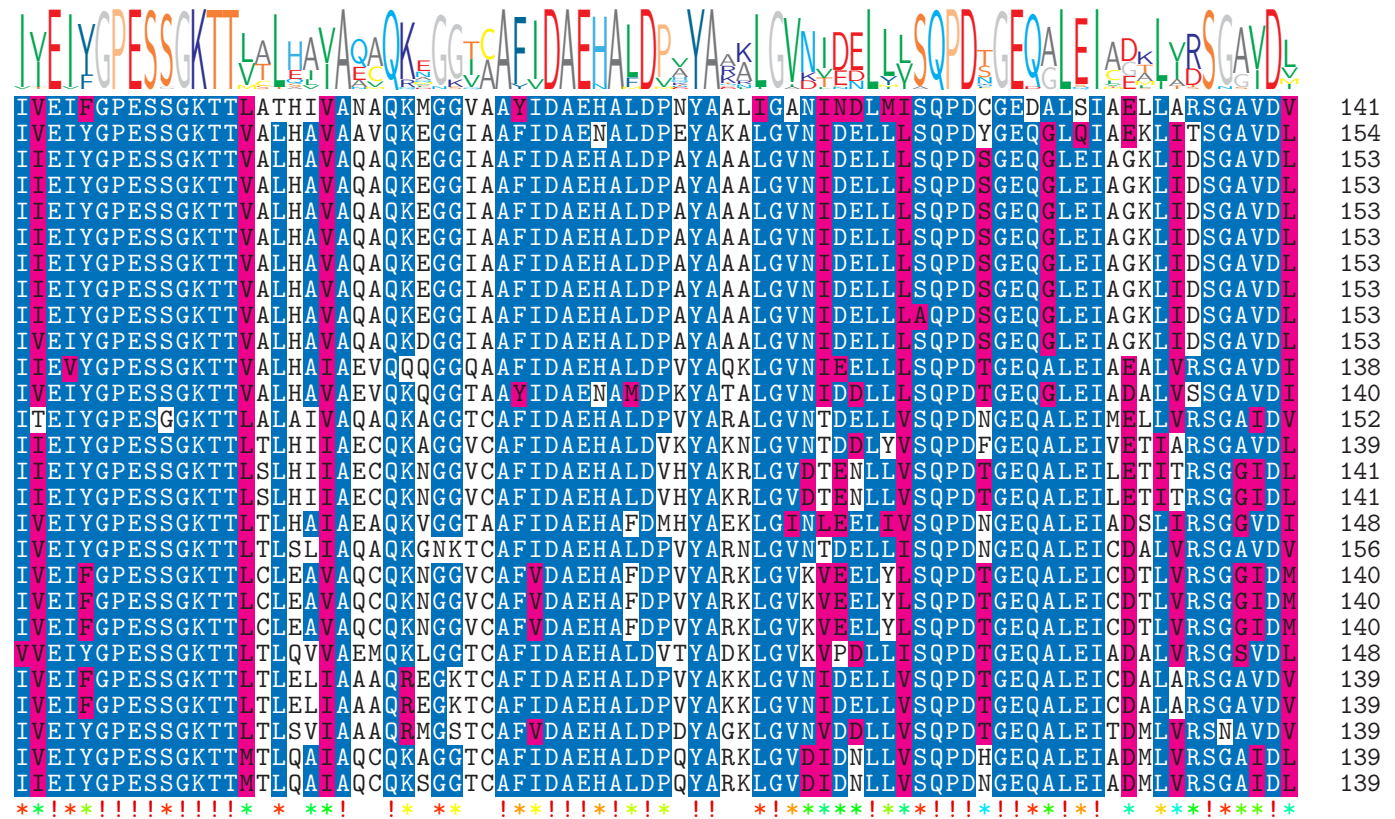
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consensus

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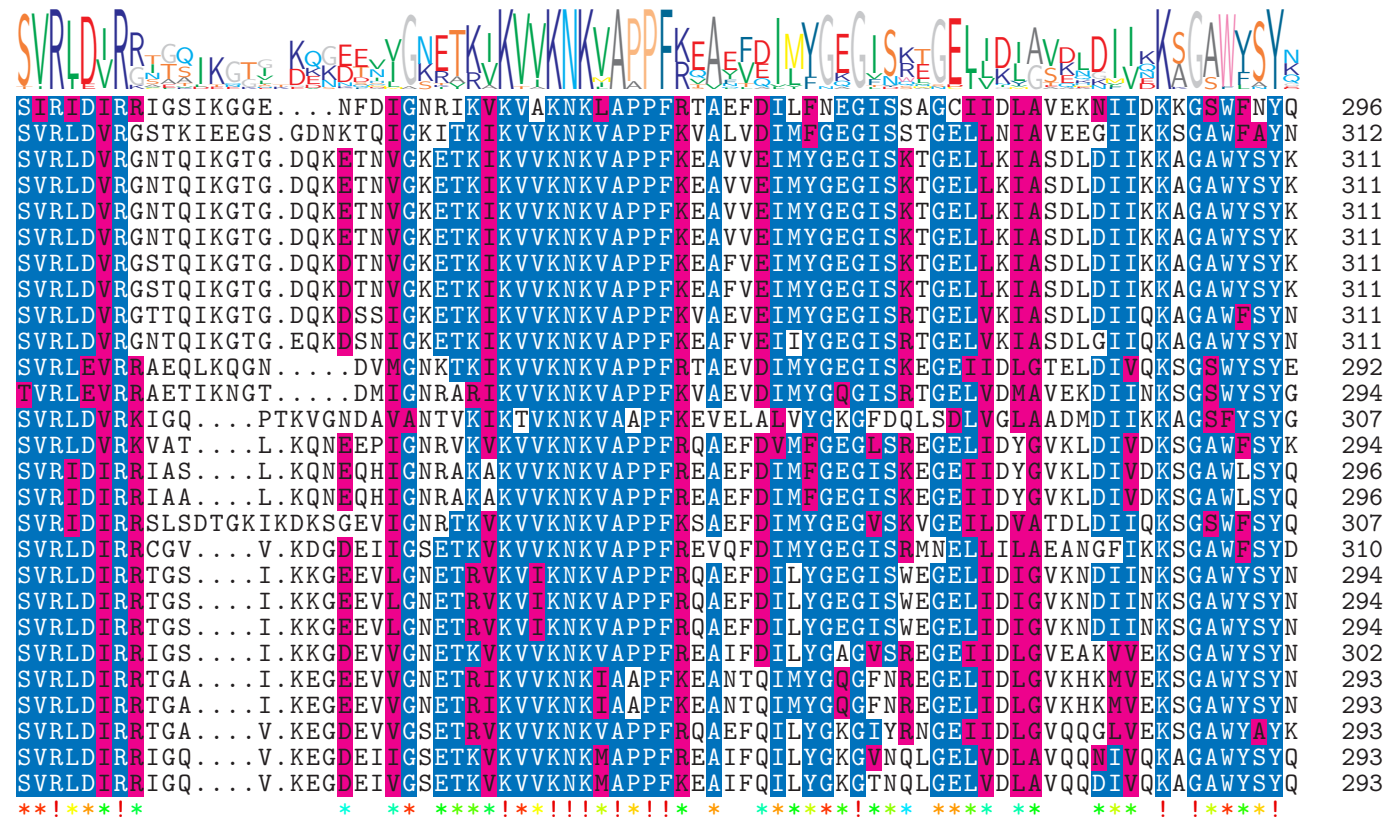
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consensus

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Sequence	Score
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GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI...TEGT...Q..DET DGERPEE	348
GERIGQGGKNCREFLRNAAELAR E IENKVR EHLGVTPMG...AV.TLAE E VEE..D	352
GDKIGQGGKANACKY LKENPEIAKTLDKKLREMLLNPNEM...QLIAETSSAAD..DVEFGAVPEEF	354
GDKIGQGGKANACKY LKENPEIAKTLDKKLREMLLNPNEM...QLIAETSSAAD..DVEFGAVPEEF	354
GSKIGQGGKANAAKYLEENPEIGQEIEQQIRAKLLVTSAN...TKATPVAEDLA..DADI	347
GNKIGQGGKNNVIRYLEENPQISTEIEAVIREQLLTKASD...QTAA.HDETEE..EPDLL..ES	349
GNKIGQGGKNNVIRIFYENNQIAEIEIRNIREQLLTGTN...GAVQ.I.EDEE..EPDLL..LES	349

logo

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NTDB id 1165	A1552VC	RS01565	WP 000344154.1	...	354
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consensus					

-  non conserved
-  similar
-  ≥ 50% conserved