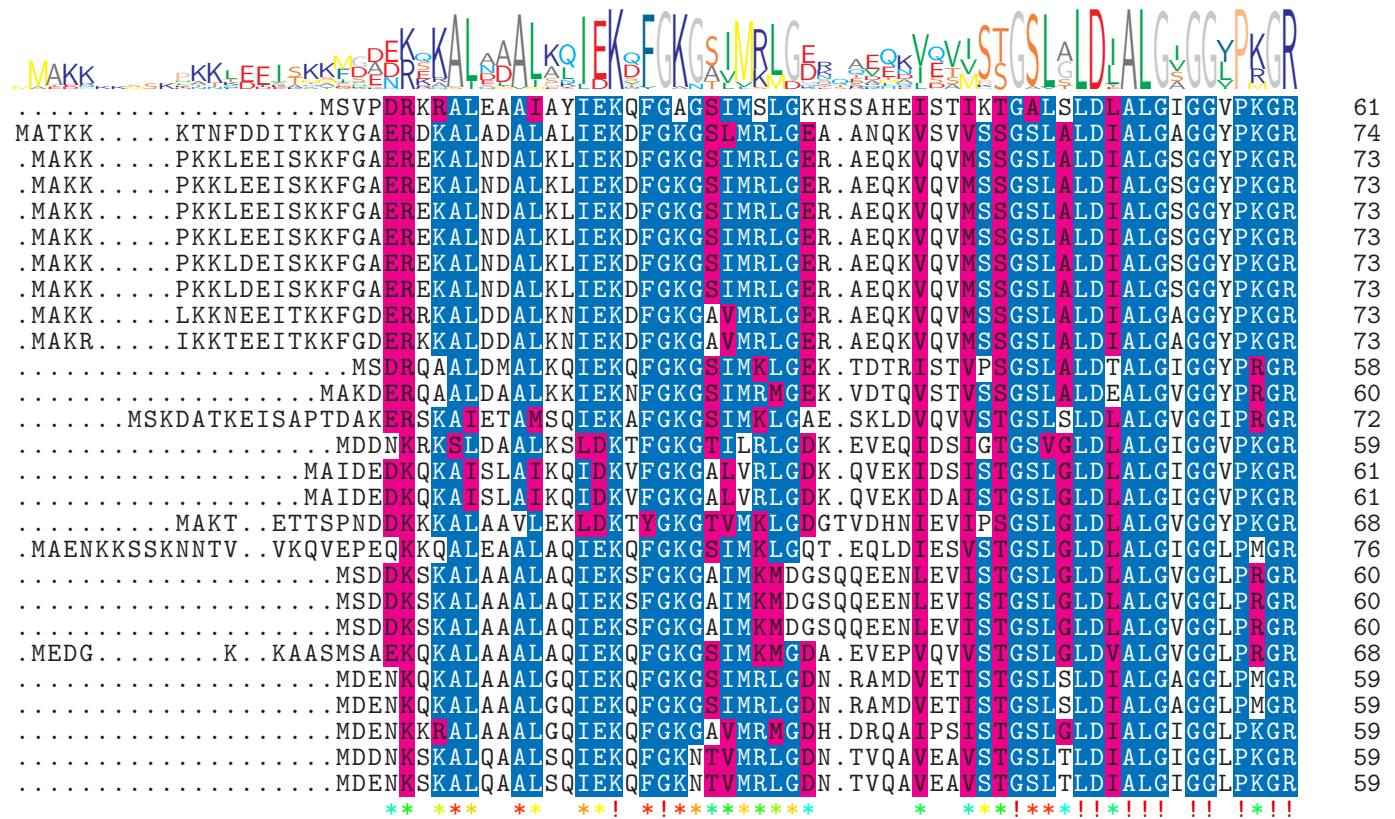


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consensus

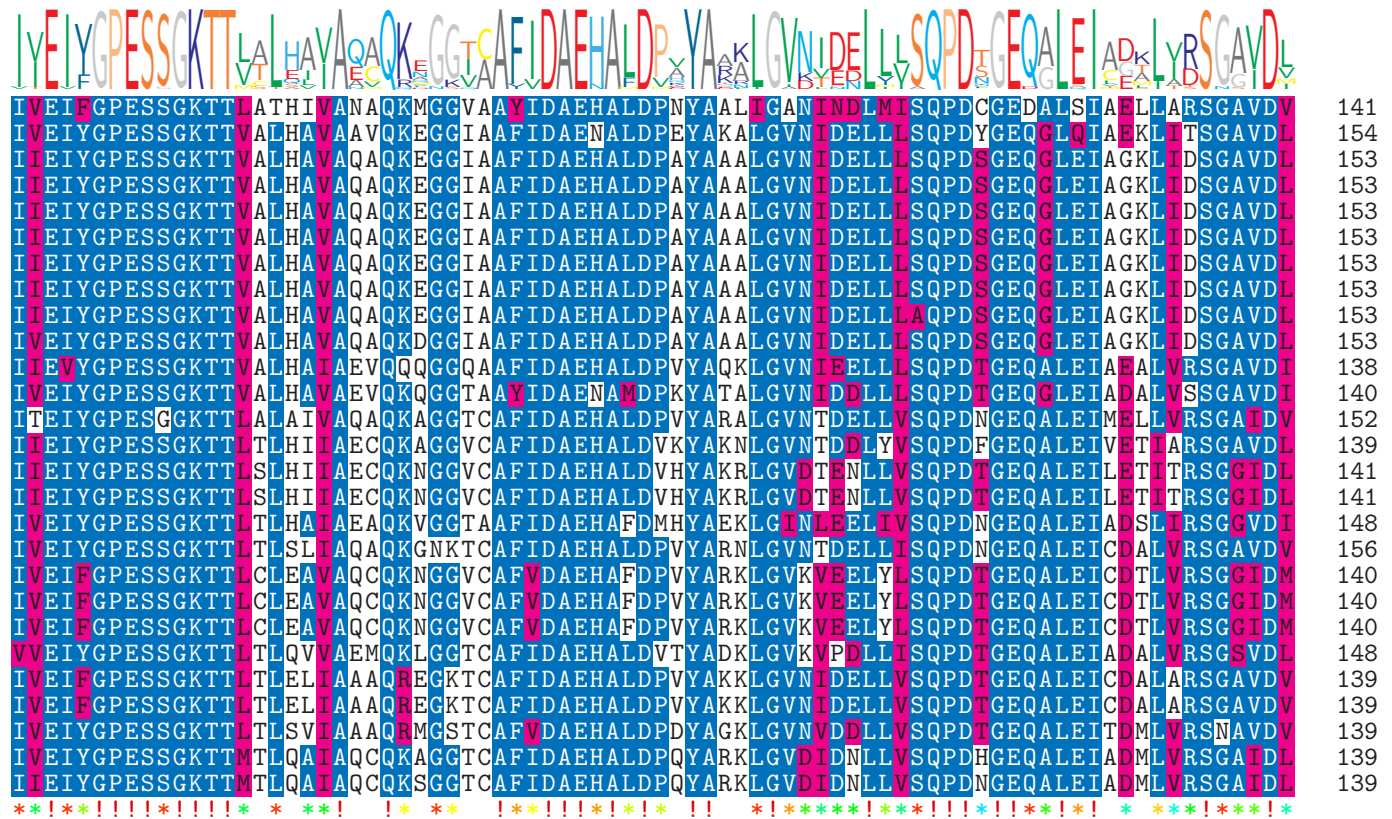
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consensus

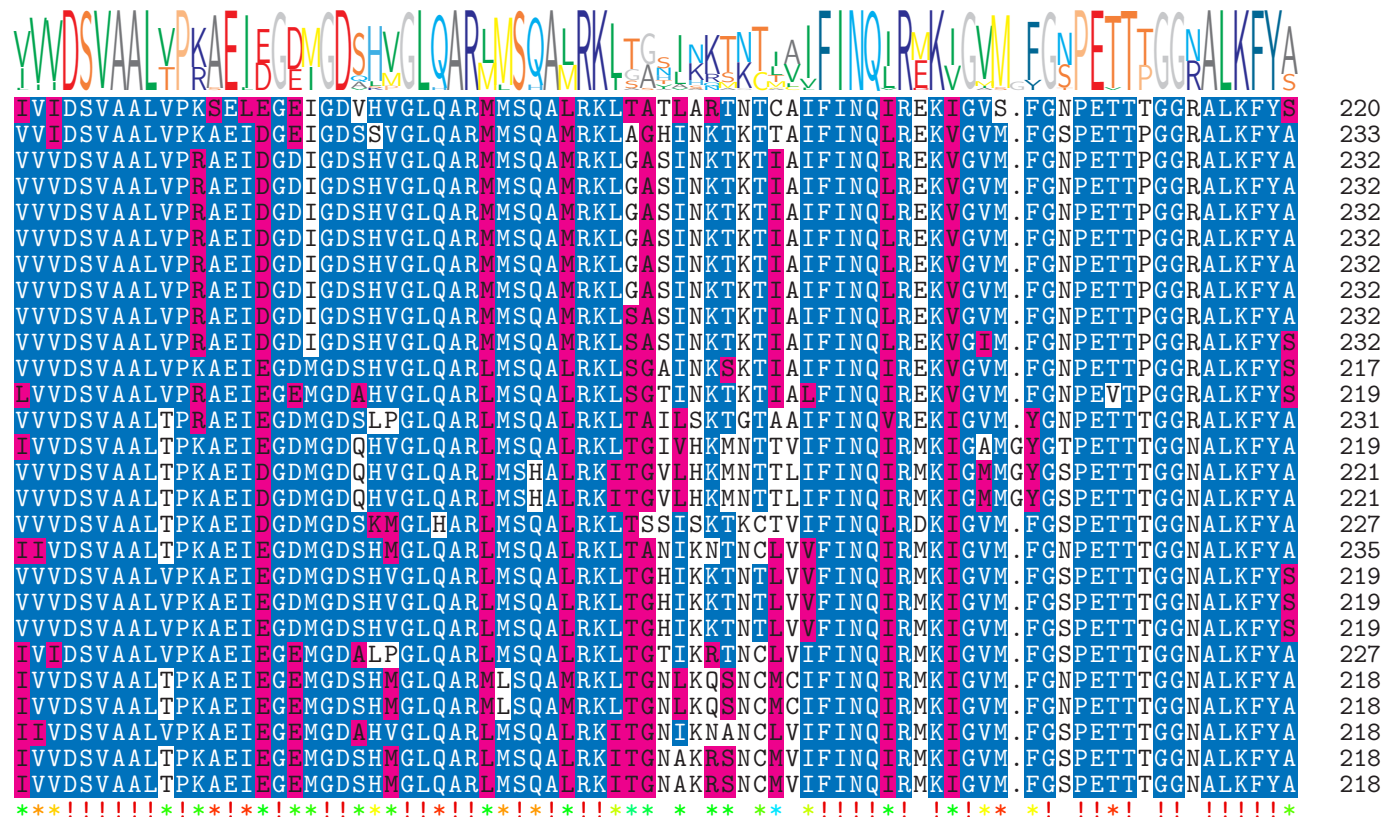
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consensus

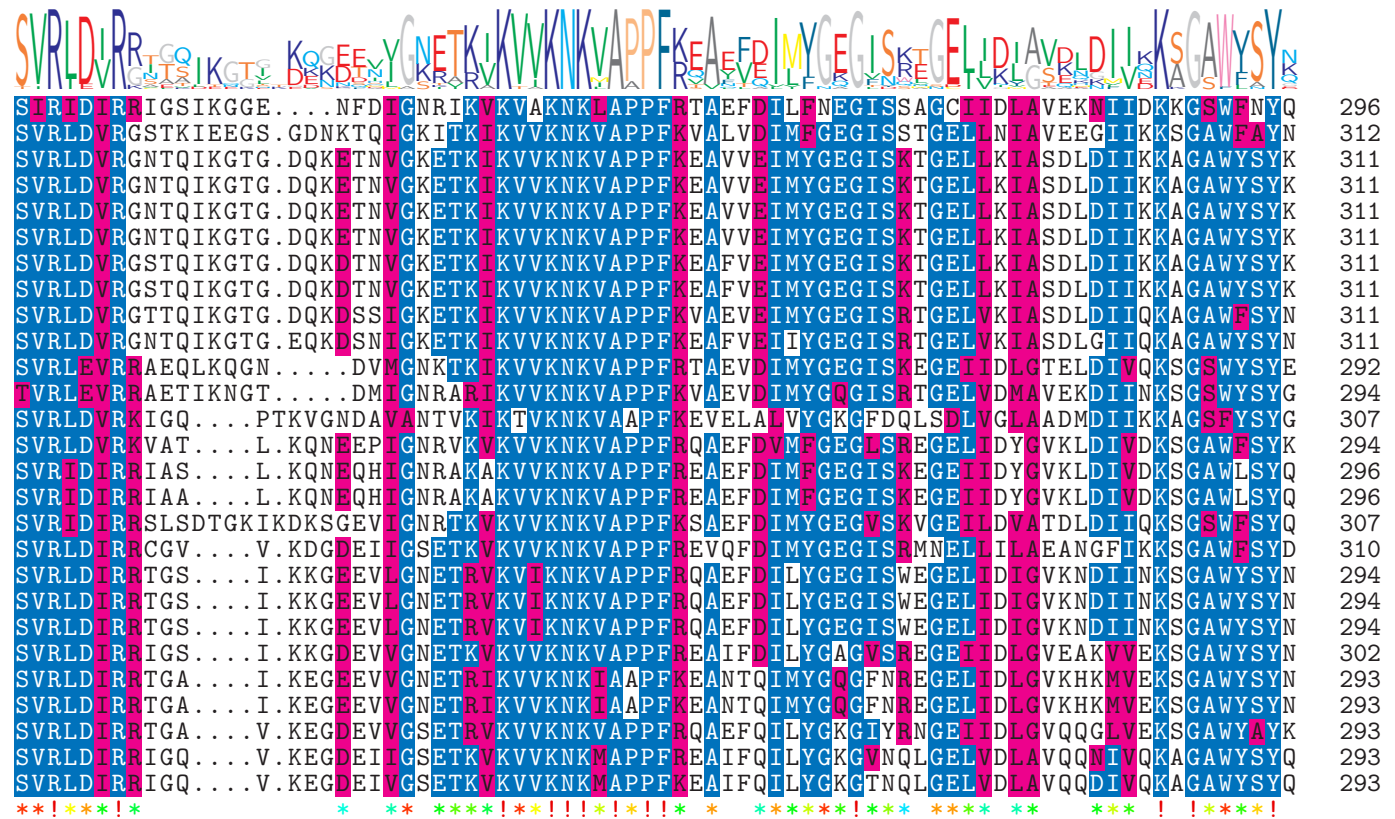
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
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DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAADNPEIFDEIDHQVRVQFGLIDGEEIAES...KKDE...AAQVDS..VNEEVTLDLGDLEIE	381
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GEKIGQGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....ETDEK..ADKNLVLELDDTIELE	377
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GERIGQGRDNCREFLRNALARAIENKVRHGLVTPMG...AV.TLAEVEVE..D.....	352
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GDKIGQGGKANACKYLKENPEIAKTLDKKLREMLLNPNEM...QLIAETSSAAD..DVEFGAVPEEF..	354
GSKIGQGGKANAAKYLEENPEIGQIEEQIRAKLLVTSAN...TKATPVAEDLA..DADI.....	347
GNKIGQGGKNNVIRYLEENPQISTEIEAVIREQLLTKASD...QTAA.HDETEE..EPDLL..ES.....	349
GNKIGQGGKNNVIRIFYENNQIAEIERNIREQLLTGTN...GAVQ.I.EDEE..EPDLL..LES.....	349

logo

NTDB id 64495 IB85 RS0100100 WP 009872817.1 ... 352
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NTDB id 269 KZH43 RS08665 WP 001085462.1 IEE 388
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consensus

 non conserved
 similar
 ≥ 50% conserved