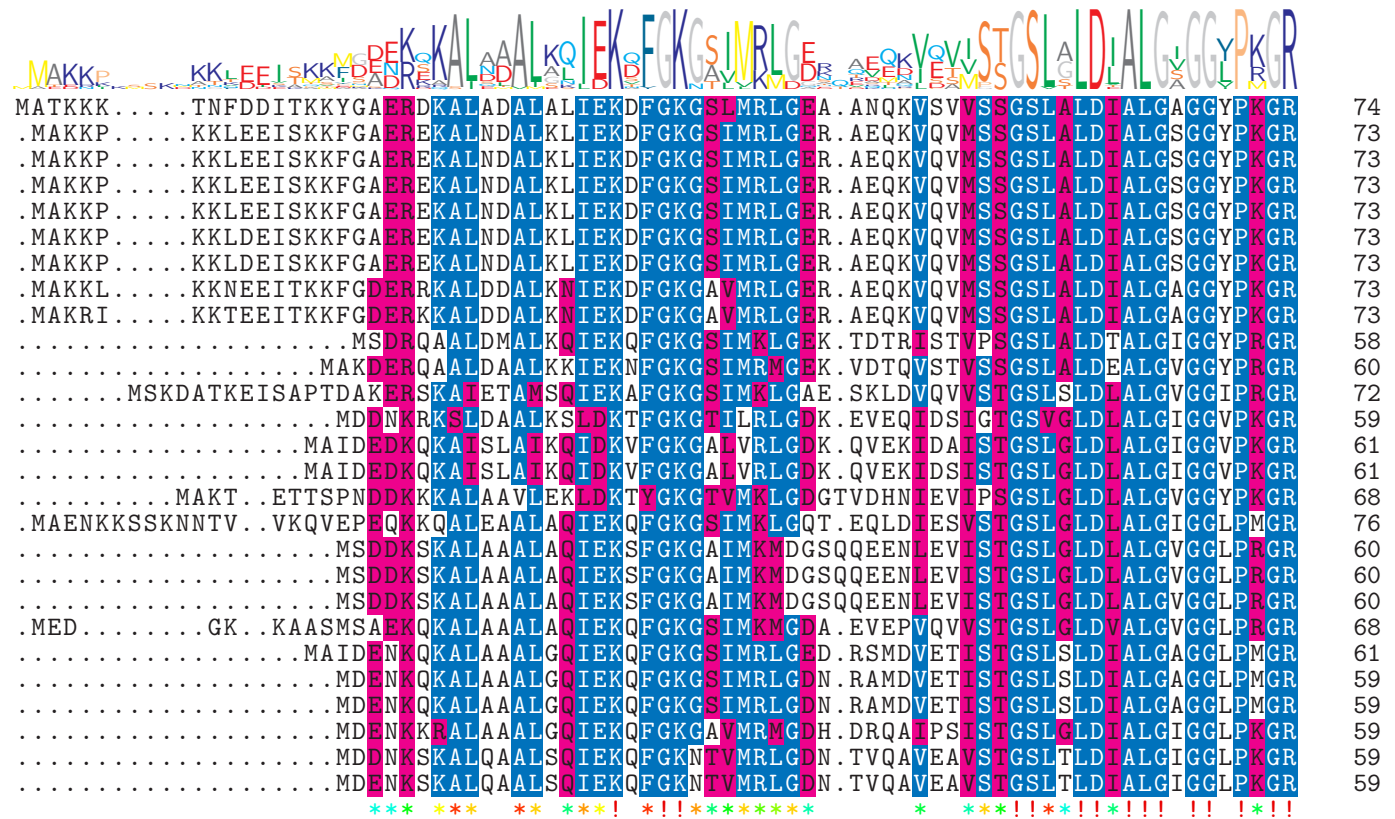


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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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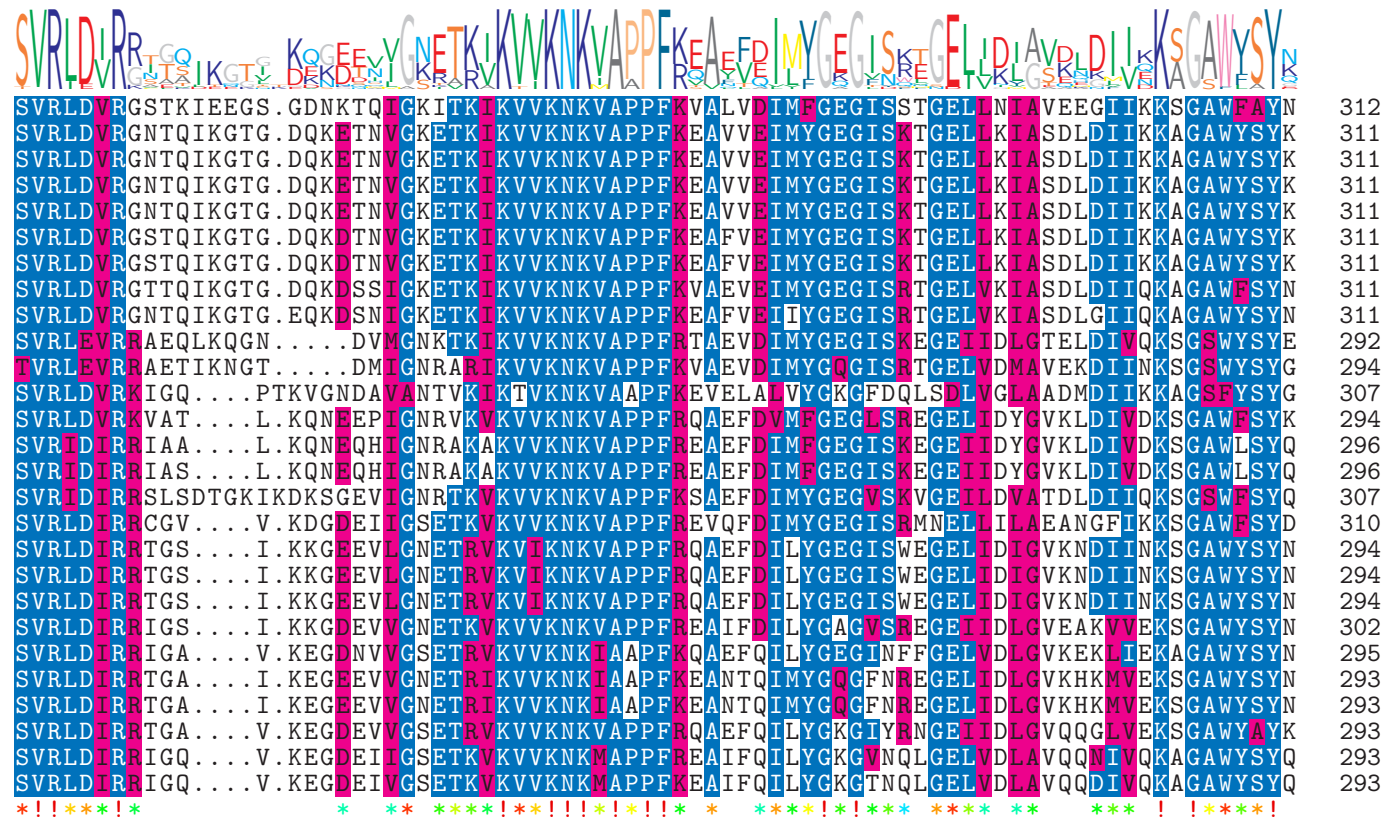
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consensus

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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAADNPEVFAEIDHQVRVQFGLIDGEEAAE...SKKDE...VAQVDS..VNEEVTLDLGDLEIE	381
DEKIGQGSENAKKYLAADNPEIFDEIDHQVRVQFGLIDGEEIAE...SKKDE...AAQVDS..VNEEVTLDLGDLEIE	381
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE...E.....TDDLALDLNGIEIE	377
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EERLGQGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEETQEEL.EFE.E.....	348
SERIGQGRENAKNYLADHEDVEDEVRLKVRAAYGISDVPPEEDLPTTEDE.QI.NILPDDST....EE.....	355
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DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEE.....IMPLPDEP.....LEEM..E.....	347
DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEE.....IMPLPDEP.....LEEM..E.....	347
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GTKIGQGGKNNAVKWLKENPEIADKLEQEIINTLASNP.....SVLKATASDSNDESDFEF..SEEL.....	372
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GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMH.....ITEGT.....QDETGDGER..PEE.....	348
GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMH.....ITEGT.....QDETGDGER..PEE.....	348
GERIGQGRDNCREFLRENAELAREIENKVRHGLVTPM.....GAVTLAE.EVEED.....	352
GDKIGQGGKANAIISWLKNPAAAEIEKKVRELLNNQD.....STPDFAVD.....GNDAAEET..EQDF.....	352
GDKIGQGGKANACKYLKENPEIAKTLDDKKLREMLLPEN.....MQLIAETSSAADDVEFGAV..PEEF.....	354
GDKIGQGGKANACKYLKENPEIAKTLDDKKLREMLLPEN.....MQLIAETSSAADDVEFGAV..PEEF.....	354
GSKIGQGGKANAAKYLEENPEIGQETIEQQIRAKLLVTS.....NTKATPVAEDLADADI.....	347
GNKIGQGGKNNVIRYLEENPQISTEIEEAVIREQLLTKAS.....DQTA..HDETEEEPDLLES.....	349
GNKIGQGGKNNVIRYFENNQIAEIEERNIREQLLTTGT.....NGAVQ..I.EDEEEPDLLE..S.....	349

logo

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

- X non conserved
- X similar
- X ≥ 50% conserved