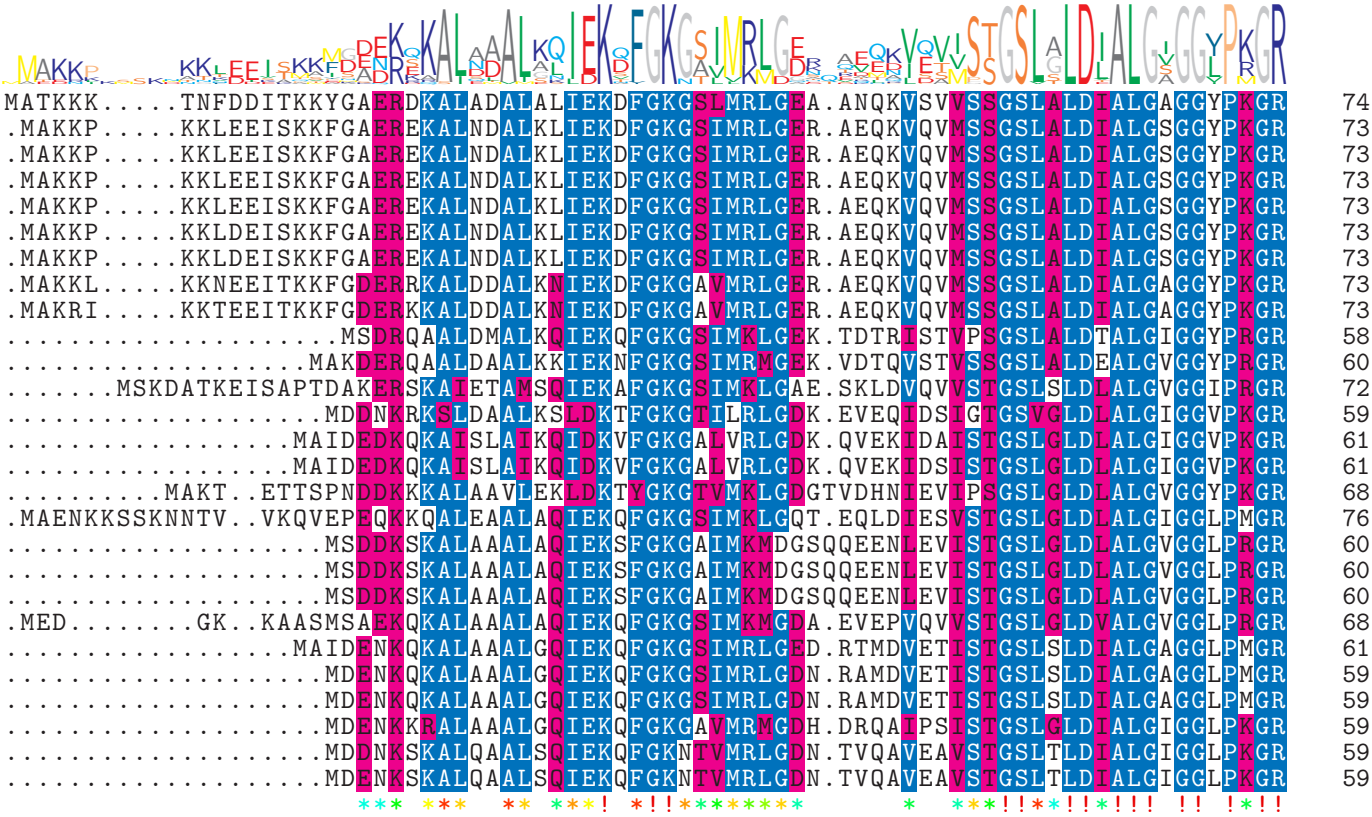


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NTDB id 159 SP RS09750 WP 001085462.1
NTDB id 527 SMSK321 RS11065 WP 001085454.1
NTDB id 499 SM12261 RS08315 WP 078228268.1
NTDB id 453 Spy49 1753c ACI62003.1
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus



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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . . VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . . VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAHNPEVFAEIDHQVRVQFLIDGEEAAE . . . SKKDE . . . VAQVDS . . VNEEVTLDLGDLEIE	381
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GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE E TDDLALDLNGIEIE	377
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK ETDEK . . ADKNLVLELDDTIELE	382
EERLGQGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEETQEEL . EFE . E	348
SERIGQGRENAKNYLADHEDVEDEVRLKVRAAAYGISDVPEEDLPTTEDE . QI . NILPDDST EE	355
DERIGQKEKTIAYIAERPMEQETIDRVMAAIRAGNAGEAPALAPAPAA . PEAEEA	363
DKKLGQGRNSKAFLKENPEIADEITKAIQNSMGTIEGMISGSEDDE . . GE . E	343
DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEEIMPLPDEP . . LE . EME	347
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GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEGTQDE . . TD GERPEE	348
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GERIGQGRDNCREFLRENAELAREIENKVRHGLVTPMGAVTLAAEE . . VE . ED	352
GDKIGQGKANAITWLKENPAAAEIEKKVRELLNNQDAKPD . . FV . . VD . GNDAAETEEDQDF	352
GDKIGGQKANACKYLKENPEIAKTLDDKKLREMLLNPNEMQLI . . AE TSSAADDVEFGAVPEEF	354
GDKIGGQKANACKYLKENPEIAKTLDDKKLREMLLNPNEMQLI . . AE TSSAADDVEFGAVPEEF	354
GSKIGGQKANAAKYLEENPEIGQIEEQIRAKLLVTSANTKA . . TP . . VA . EDLADADI	347
GNKIGGQKNNVIRYLEENPQISTEIEAVIREQLLTAKASQTA . . A . . HD . ETEEEPDLLES	349
GNKIGGQKNNVIRYFENNQIAEIERNIREQLLTGTNGAV . . Q . . I . . EDEEEPDLLES	349

logo

NTDB id 600 KW2 RS01765 WP 011675413.1	...	387
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consensus

 non conserved
 similar
 ≥ 50% conserved