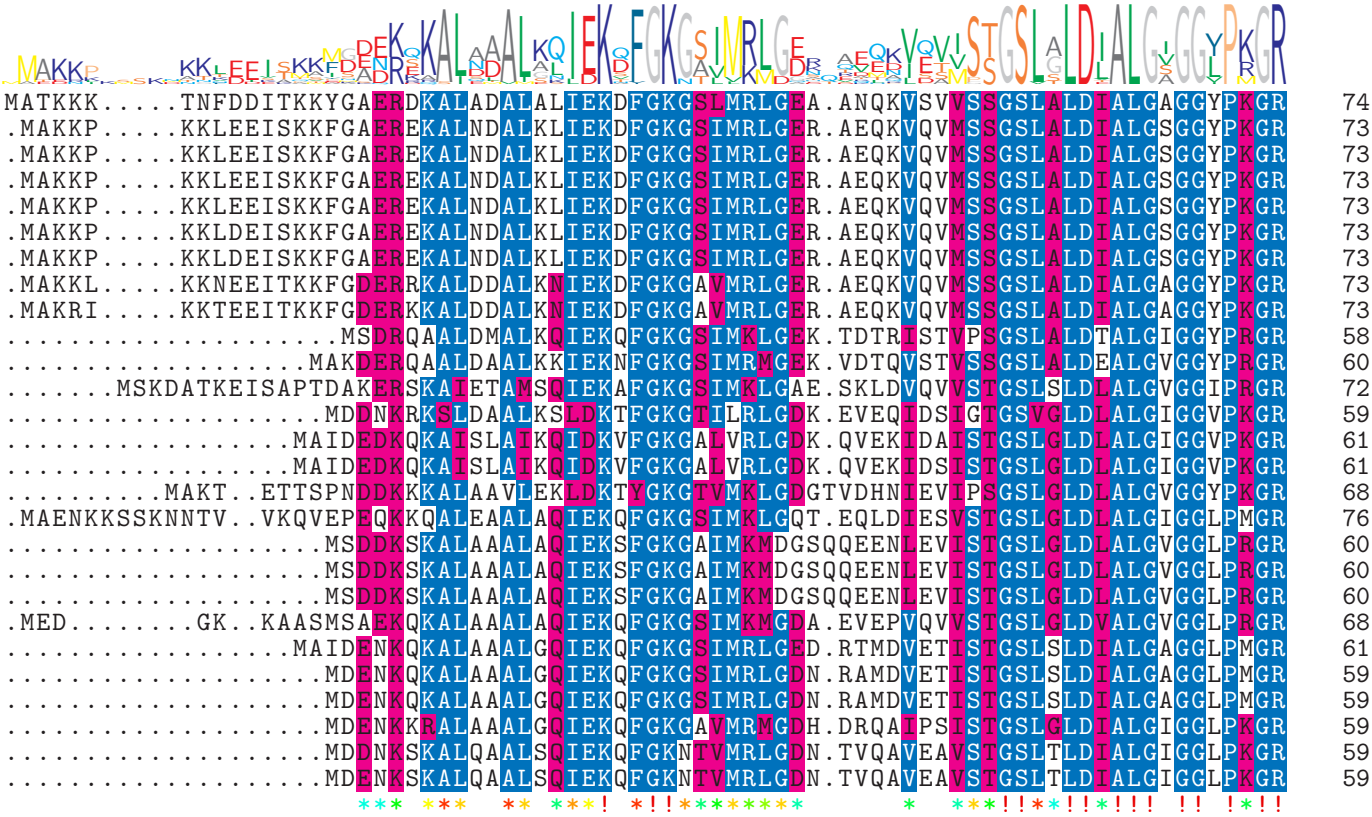


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NTDB id 159 SP RS09750 WP 001085462.1
NTDB id 527 SMSK321 RS11065 WP 001085454.1
NTDB id 499 SM12261 RS08315 WP 078228268.1
NTDB id 453 Spy49 1753c ACI62003.1
NTDB id 408 SMU RS09530 WP 002262392.1
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
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consensus

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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQD TENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQD TENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQD TENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAHNPEVFAEIDHQVRVQFLIDGEEAAE . . . SKKDE . . . VAQVDS . VNEEVTLDLGDELEIE	381
DEKIGQGSENAKKYLAHNPEIFDEIDHQVRVQFLIDGEEIAE . . . SKKDE . . . AAQVDS . VNEEVTLDLGDELEIE	381
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESSEESAMAVASE E TDDLALDLNGIEIE	377
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK ETDEK . . ADKNLVLELDDTIELE	382
EERLGGGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEETQEEL . EFE . E	348
SERIGGGRENAKNYLADHEDVEDEVRLKVRAAAYGISDVPEEDLPTTEDE . QI . NILPDDST EE	355
DERIGGKEKTIAYIAERPMEQETIDRVMAAIRAGNAGEAPALAPAPAA . PEAEEA	363
DKKLGGGRENASKAFLKENPEIADEITKAIQNSMGTIEGMISGSEDDE . . GE . E	343
DKKLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIMPLPDEP . . LE . EME	347
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GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEGTQDE . . TD GERPEE	348
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEGTQDE . . TD GERPEE	348
GERIGGGRDNCREFLRENAELAREIENKVRHGLVTPMGAVTLAAE . . VE . ED	352
GDKIGGQKANAITWLKENPAAAEIEKKVRELLNNQDAKPD . . FV . . VD . GNDAAETE QDF	352
GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPNMQLI . . AE TSSAADDFEFGAVPEEF	354
GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPNMQLI . . AE TSSAADDFEFGAVPEEF	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