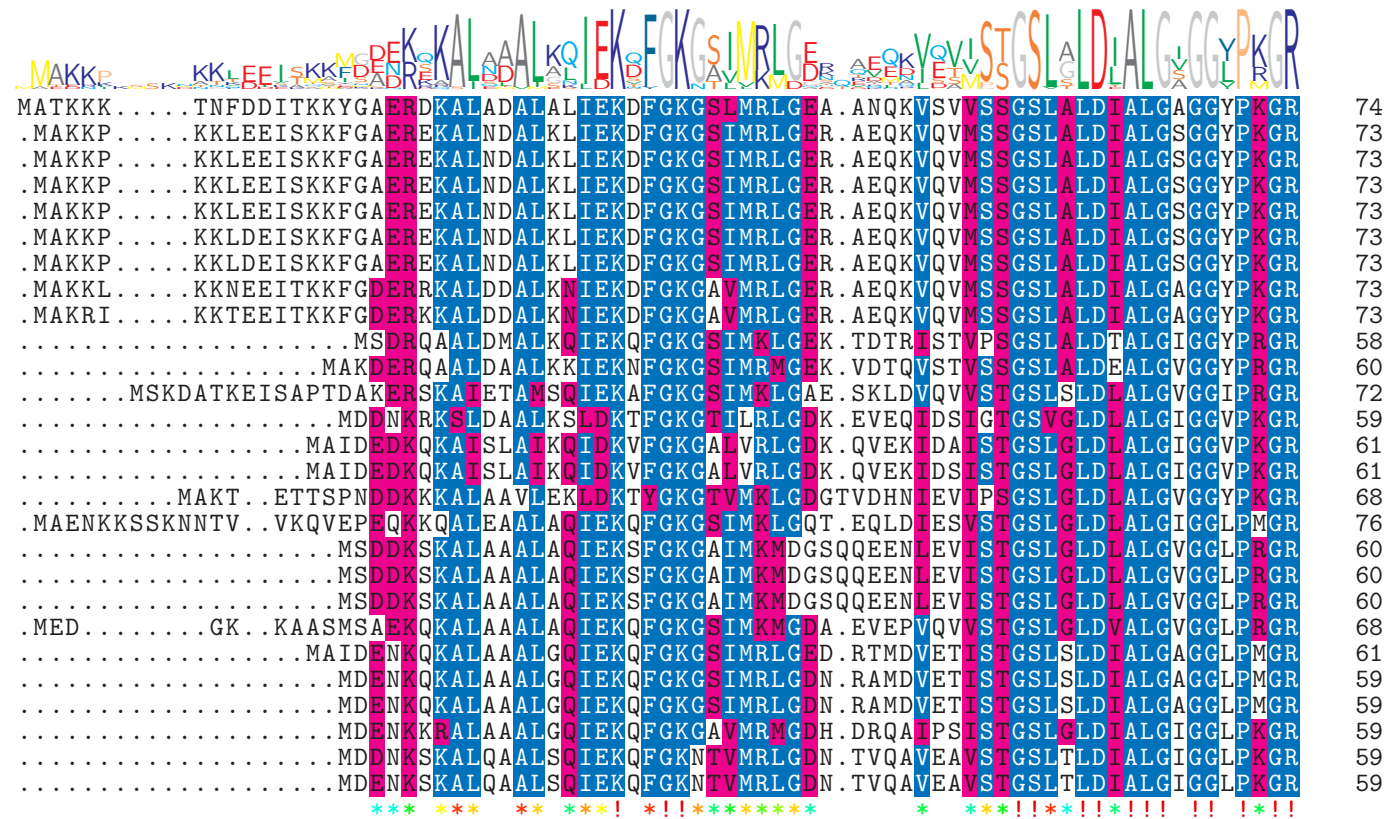


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NTDB id 159 SP RS09750 WP 001085462.1
NTDB id 527 SMSK321 RS11065 WP 001085454.1
NTDB id 499 SM12261 RS08315 WP 078228268.1
NTDB id 453 Spy49 1753c ACI62003.1
NTDB id 408 SMU RS09530 WP 002262392.1
NTDB id 115 BSU 16940 NP 389576.2
NTDB id 625 LCA RS02525 WP 011374196.1
NTDB id 1313 DR RS12030 WP 010888966.1
NTDB id 1245 Cj1673c YP 002345041.1
NTDB id 1214 NCTC11637 00359 SQJ03206.1
NTDB id 1211 C694 RS00795 WP 000963128.1
NTDB id 1334 RAOC RS04870 WP 004918236.1
NTDB id 1389 A4U84 RS07560 WP 021112712.1
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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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
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAHNPEVFAEIDHQVRVQFLIDGEEAAE . . . SKKDE . . . VAQVDS . VNEEVTLDLGDLEIE	381
DEKIGQGSENAKKYLAHNPEIFDEIDHQVRVQFLIDGEEIAE . . . SKKDE . . . AAQVDS . VNEEVTLDLGDLEIE	381
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE E TDDLALDLNGIEIE	377
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK ETDEK . . ADKNLVLELDDTIELE	382
EERLGQGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEETQEEL . EFE . E	348
SERIGQGRENAKNYLADHEDVEDEVRLKVRAAAYGISDVPEEDLPTTEDE . QI . NILPDDST EE	355
DERIGQKEKTIAYIAERPMEQETIDRVMAAIRAGNAGEAPALAPAPAA . PEAEEA	363
DKKLGGGRENKSAFLKENPEIADEITKAIQNSMGTIEGMISGSEDDE . . GE . E	343
DKKLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIMPLPDEP . . LE . EME	347
DKKLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIMPLPDEP . . LE . EME	347
DTKLGGGRDTPVKELIKDNPELAELEAKIREKLQAK	343
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GAKIGQKKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEGTQDE . . TD GERPEE	348
GAKIGQKKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEGTQDE . . TD GERPEE	348
GERIGQGRDNCREFLRENAELAREIENKVRHGLVTPMGAVTLAAE . . VE . ED	352
GDKIGQKKANAITWLKENPAAAEIEKKVRELLNNQDAKPD . . FV . . VD . GNDAAETEEDQDF	352
GDKIGQKKANACKYLKENPEIAKTLDDKKLREMLLNPNEMQLI . . AE TSSAADDVEFGAVPEEF	354
GDKIGQKKANACKYLKENPEIAKTLDDKKLREMLLNPNEMQLI . . AE TSSAADDVEFGAVPEEF	354
GSKIGQKKANAACKYLEENPEIGQIEEQIRAKLLVTSANTKA . . TP . . VA . EDLADADI	347
GNKIGQKKNNVIRYLEENPQISTEIEAVIREQLLTAKASQTA . . A . . HD . ETEEEPDLLES	349
GNKIGQKKNNVIRYFENNQIAEIERNIREQLLTGTNGAV . . Q . . I . . EDEEEPDLLES	349

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		IEE	
NTDB id 600 KW2 RS01765 WP 011675413.1	...		387
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NTDB id 194 SPR RS08825 WP 001085462.1	IEE		388
NTDB id 159 SP RS09750 WP 001085462.1	IEE		388
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NTDB id 1074 ABD1 RS10195 WP 000344167.1	...		349
consensus			

-  non conserved
-  similar
-  ≥ 50% conserved