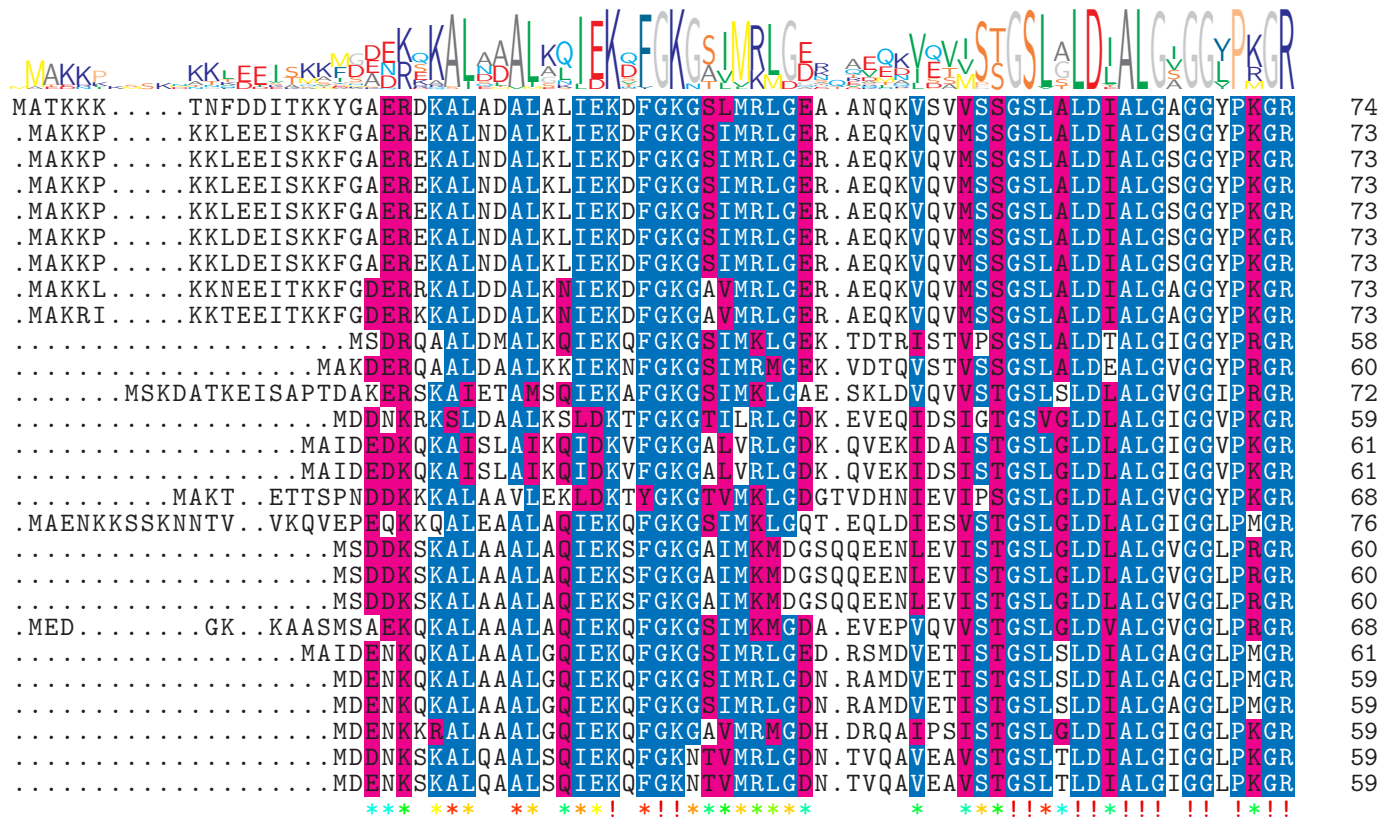


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NTDB id 159 SP RS09750 WP 001085462.1
NTDB id 499 SM12261 RS08315 WP 078228268.1
NTDB id 527 SMSK321 RS11065 WP 001085454.1
NTDB id 453 Spy49 1753c ACI62003.1
NTDB id 408 SMU RS09530 WP 002262392.1
NTDB id 115 BSU 16940 NP 389576.2
NTDB id 625 LCA 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
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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
DEKIGGGAEKAKNYLKEHQDVFEIDHKVRAAHGLDDSEVAETEEETTASKTAKAKKKEKAVETEEIELELED....	387
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAHNPEIFDEIDHQRVVFGLIDGEEIAES...KKDE...AAQVDS..VNEEVTLDLGDELEIE	381
DEKIGQGSENAKKYLAHNPEVFAEIDHQRVVFGLIDGEEAAES...KKDE...VAQVDS..VNEEVTLDLGDELEIE	381
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EERLGQGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEETQEEL.EFE.E.....	348
SERIGQGRENAKNYLADHEDVEDEVRLKVRAAAYGISDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGQGEKTIATYIAERPMEQEIRDRVMMAAIRAGNAGEAPALAPAPAAPEAA...EA.....	363
DKKLGQGRNSKAFLENPEIADEITKATINSMGTIEGM.....ISGSEDDEG.....EE.....	343
DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEE....IMPLPDEPL.....EEME.....	347
DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEE....IMPLPDEPL.....EEME.....	347
DTKLGQGRDTPVKELIKDNPELAELEAKIREKLQAK.....	343
GTKIGQGKNNAVKWLKENPEIADKLEQIRNTLASNPN....SVLKATASDSN...DES.DVEEFSEEL	372
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMH....ITEG.....T...QDETGDGERPEE	348
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMH....ITEG.....T...QDETGDGERPEE	348
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMH....ITEG.....T...QDETGDGERPEE	348
GERIGQGRDNCREFLRENAELAREIENKVRHGLVTPM.....GAVTLAEE.VE...ED.....	352
GEKIGQGANATAWLKDNPETAKIEKKVRELLNSNP....STPDFSV..D..DSEGVATNEDF	353
GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPN....MQLIAETSSAA..DDVEFGAVPEEF	354
GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPN....MQLIAETSSAA..DDVEFGAVPEEF	354
GSKIGGQKANAAKYLEENPEIGQIEEQIRAKLLVTSA....NTKATPVAEDL..ADADI.....	347
GNKIGGQKNNVIRYLEENPQISTEIEAVIREQLLTKAS....DQTAA.HDETE...EEDPLLLES	349
GNKIGGQKNNVIRIFYENNQIAEIERNIREFQLLTGT....NGAVQ.I.EDE...EEDPLLLES	349

logo

		IEE	
NTDB id 600 KW2 RS01765 WP 011675413.1	...		387
NTDB id 269 KZH43 RS08665 WP 001085462.1	IEE		388
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NTDB id 159 SP RS09750 WP 001085462.1	IEE		388
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NTDB id 1022 ACIAD RS06390 WP 004925639.1	...		349
NTDB id 1074 ABD1 RS10195 WP 000344167.1	...		349
consensus			

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