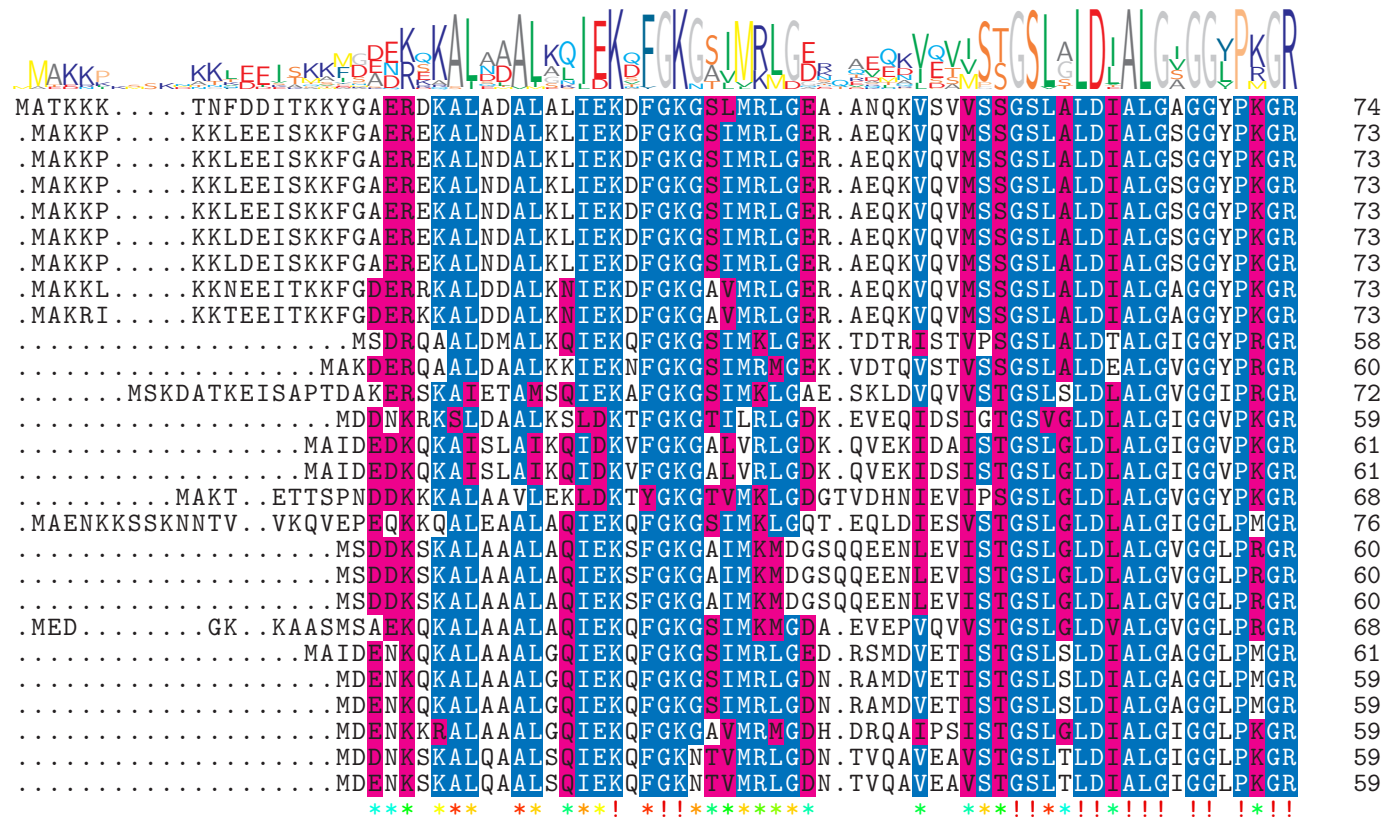


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NTDB id 159 SP RS09750 WP 001085462.1
NTDB id 499 SM12261 RS08315 WP 078228268.1
NTDB id 527 SMSK321 RS11065 WP 001085454.1
NTDB id 453 Spy49 1753c ACI62003.1
NTDB id 408 SMU RS09530 WP 002262392.1
NTDB id 115 BSU 16940 NP 389576.2
NTDB id 625 LCA 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..VNEEVTLDLGDLEIE	381
DEKIGQGSENAKKYLAHNPEVFAEIDHQRVVFGLIDGEEAAES...KKDE...VAQVDS..VNEEVTLDLGDLEIE	381
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EERLGQGGRENAKQFLKENKDIMLMIQEQIREHYGLDNGGVVQQAEETQEEL.EFE.E.....	348
SERIGQGGRENAKNYLADHEDVEDEVRLKVRVAAAYGISDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGQGEKTTIAYIAERPMEQEIRDRVMMAAIRAGNAGEAPALAPAPAAPEAA...EA.....	363
DKKLGGGRENKAFLENPEIADEITKATINSMGTIEGM.....ISGSEDDEG.....EE.....	343
DKKLGGGRENKALLKEDKALADEITLKIKESIGSNEE.....IMPLPDEPL.....EEME.....	347
DKKLGGGRENKALLKEDKALADEITLKIKESIGSNEE.....IMPLPDEPL.....EEME.....	347
DTKLGGGRDTPVKELIKDNPELAELEAKIREKLQAK.....	343
GTKIGQGGKNNNAVKWLKENPEIADKLEQIRNTLASNPN....SVLKATASDSN...DES.DVEEFSEEL	372
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMH....ITEG.....T...QDETGDGERPEE	348
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMH....ITEG.....T...QDETGDGERPEE	348
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMH....ITEG.....T...QDETGDGERPEE	348
GERIGQGRDNCREFLRENAELAREIENKVRHGLVTPM.....GAVTLAEE.VE...ED.....	352
GEKIGQGGKANATAWLKDNPETAKIEKKVRELLNSNP....STPDFSV..D..DSEGVATNEDF	353
GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPN....MQLIAETSSAA...DDVEFGAVPEEF	354
GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPN....MQLIAETSSAA...DDVEFGAVPEEF	354
GSKIGGQKANAAKYLEENPEIGQIEEQIRAKLLVTSA....NTKATPVAEDL..ADADI.....	347
GNKIGGQKNNVIRYLEENPQISTEIEAVIREQLLTKAS....DQTAA.HDETE...EEDPLLLES	349
GNKIGGQKNNVIRYFENNQIAEIERNIEREQLLTGT....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 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