

Supporting Information Text S3:  
MukB supplementary figures

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          10      20      30      40      50      60
-----+-----+-----+-----+-----+-----+
UniProt: MIERGKFRSLTLINWNGFFARTFDLDELVTTLGGNGAGKSTTMAAFVTALIPDLTLLHF
PDB seq:  --RKGFRSLTLINWNGFFARTFDLDELVTTLGGNGAGKSTTMAAFVTALIPDLTLI--

          70      80      90     100     110     120
-----+-----+-----+-----+-----+-----+
RNTTEAGATSGSRDKGLHGKLGKAGVCYSMLDTINSRRHORVVVGVRLQOVAGRDRKVDIKP
-----LHGKLGKAGVCYSMLDTINSRRHORVVVGVRLQOVAGRDRKVDIKP

          130     140     150     160     170     180
-----+-----+-----+-----+-----+-----+
FAIOGLPMSVQPTOLVTETLNERQARVLPNELKDKLEAMEGVQFKQFNSTITDYHSLMFD
FAIOGLPMSVQPTOLVTETLNERQARVLPNELKDKLEAMEGVQFKQFNSTITDYHSLMFD

          190     200     210     220
-----+-----+-----+-----+
LGI IARRLSASDRSKFYRLIEASLYGGISSAITRSLRDYLLPEN
LGI IARRLSASDRSKFYRLIEASLYGGISSAITRSLRDYLLPEN

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Figure 1: MukB protein: partitions indicated on the sequence.

Blue, green and red amino-acids correspond to MukB partitions obtained by running BIS (on blocks) over 200 sequences for  $d = 0$  and  $d = 1$  (with  $\Delta = 0.05$ ) and highlighted in Fig. 3 in the main text. The pdb sequence (1qh1:A) is aligned against the UniProt sequence P22523 (*Escherichia coli* MukB).



