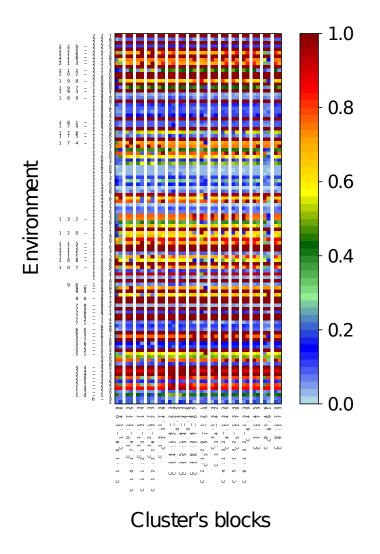
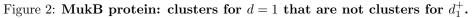
Supporting Information Text S3: MukB supplementary figures

	10	20	30	40	50	60
	+	+	+	+	+	+
UniProt:	MIE R GKFR S LTLIN	WNGFFARTFD	LDELVTTLSG	GNGAGKSTT	AAFVTALIPD	LTLLHF
PDB seq:	RGKFRSLTLIN	WNGFFARTFD	LDELVTTLSG	GNGAGKSTIN	AAFVTALIPD	LTLL
	70	80	90	100	110	120
	+	+	+	+	+	+
	RNTTEAGATSGS RD	KGLHGKLKAG	VCYSMLDTIN	SRHORVVVGV	RLQQVAGRDR	KVDIKP
		LHGKLKAG	VCYSMLDTIN	SRHQRVVVGV	RLQQVAGRDR	KVDIKP
	130	140	150	160	170	180
	+	+	+	+	+	+
	FAIQGLPMSVQPTQ	LVTETLNERO	ARVLPLNELK	DKLEAMEGVO	FKQFNSITDY	HSLMFD
	FAIQGLPMSVQPTQ	LVTETLNERO	ARVLPLNELK	DKLEAMEGVO	FKQFNSITDY	HSLMFD
	190	200	210	220		
	+	+	+	+	-	
	LGIIARRLRSASDR	SKFYRLIEAS	LYGGISSAIT	RSLRDYLLPE	N	
	LGIIARRLRSASDR	SKFYRLIEAS	LYGGISSAIT	RSLRDYLLPE	N	

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 (1qhl:A) is aligned against the UniProt sequence P22523 (*Escherichia coli* MukB).





Clusters of the MukB score matrix that are detected by CLAG for d = 1 but that are not detected for d_1^+ (that is, $d \le 1$). (Notice that not all clusters for d = 1 are reported.) This is due to the environment (that is, the set of blocks) for d = 1 that differs from the one for $d \le 1$. Recall that the environment for $d \le 1$ contains all blocks for d = 0 and all blocks for d = 1.

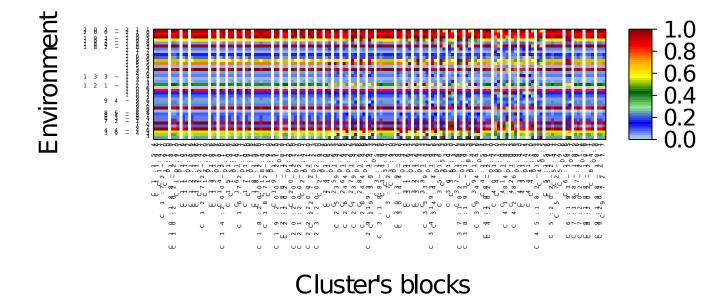


Figure 3: MukB protein: clusters for d_1^+ that are not clusters for d = 1. See legend in Fig. 2-Text S3.