

## SUPPLEMENTS

### INTRACELLULAR ION CONCENTRATIONS AND CATION-DEPENDENT REMODELLING OF BACTERIAL MREB ASSEMBLIES

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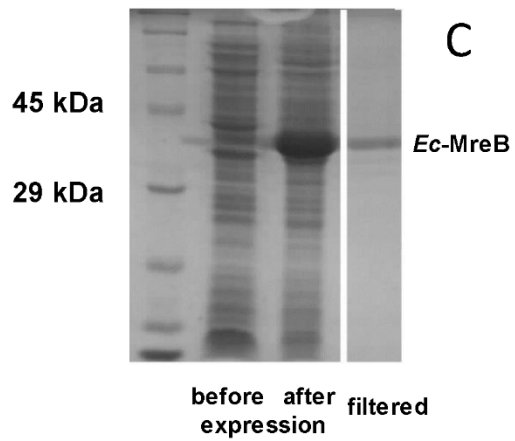
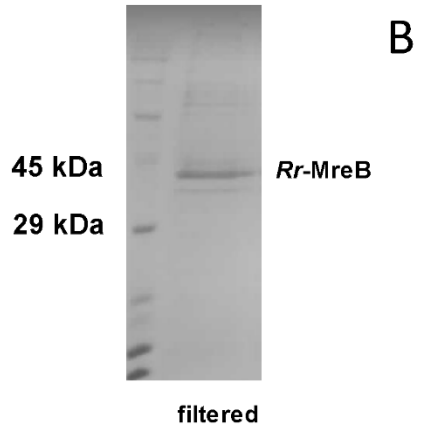
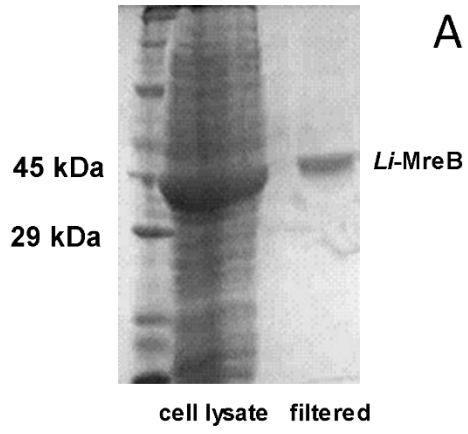
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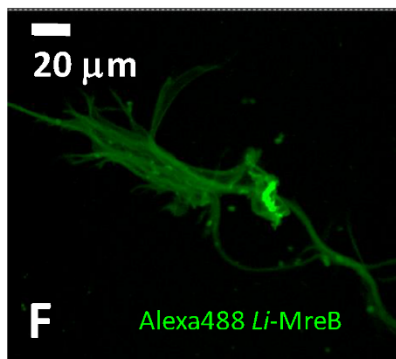
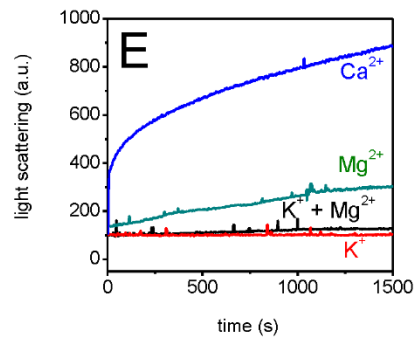
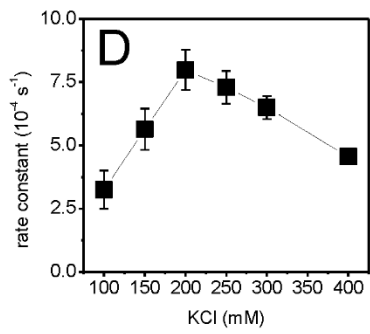
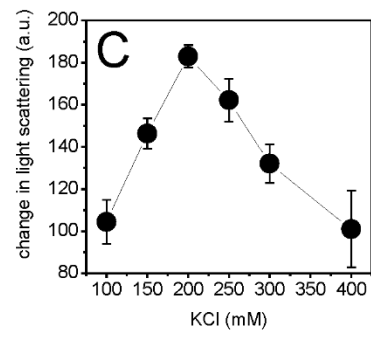
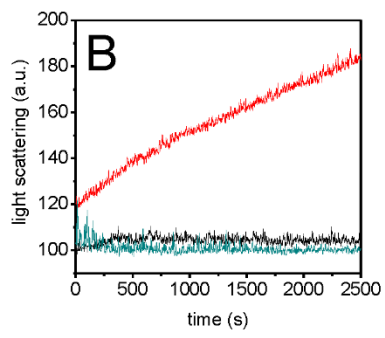
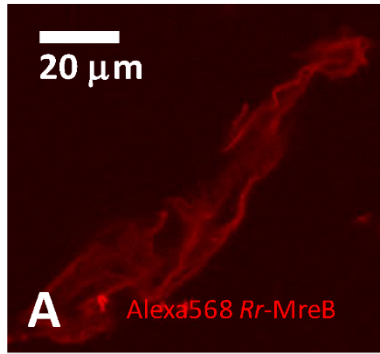
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**Keywords:** *prokaryotic cell, ionic strength, protein conformations, supramolecular assembly, cytoskeleton, bacteria, fluorescence, spectroscopy.*

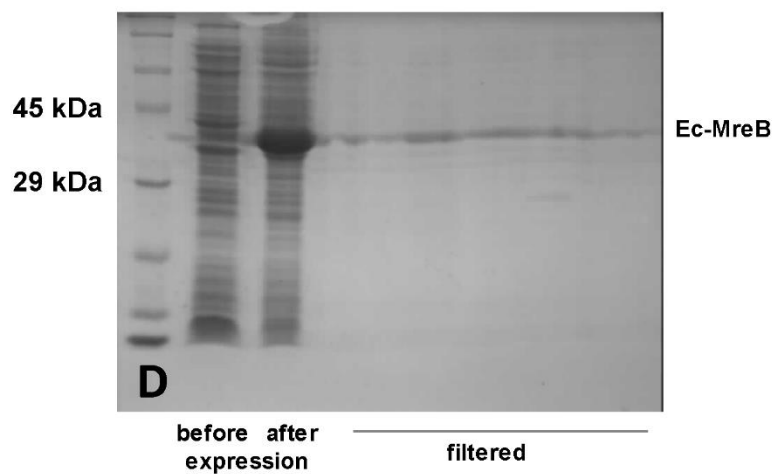
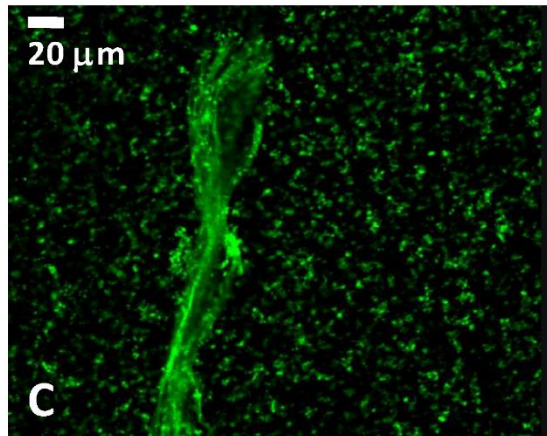
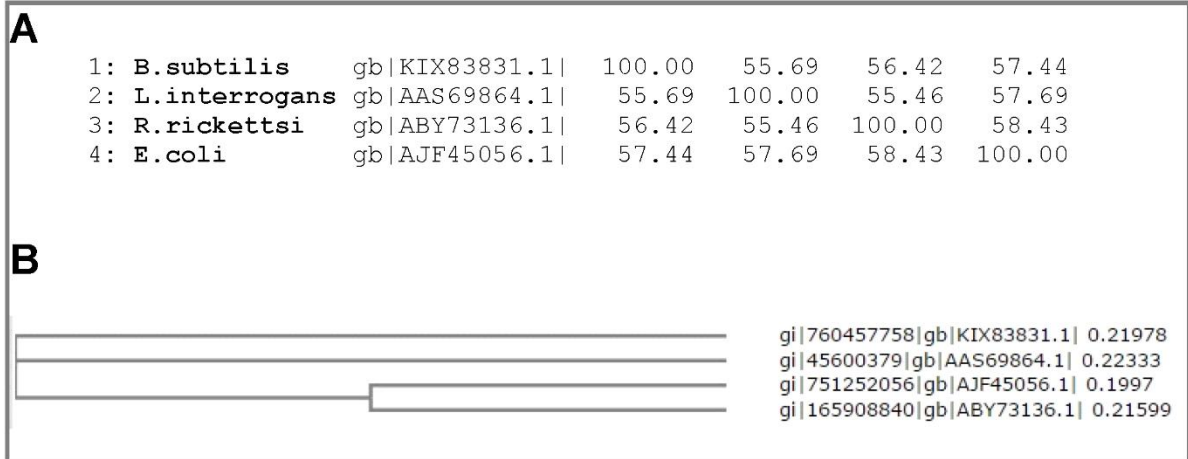
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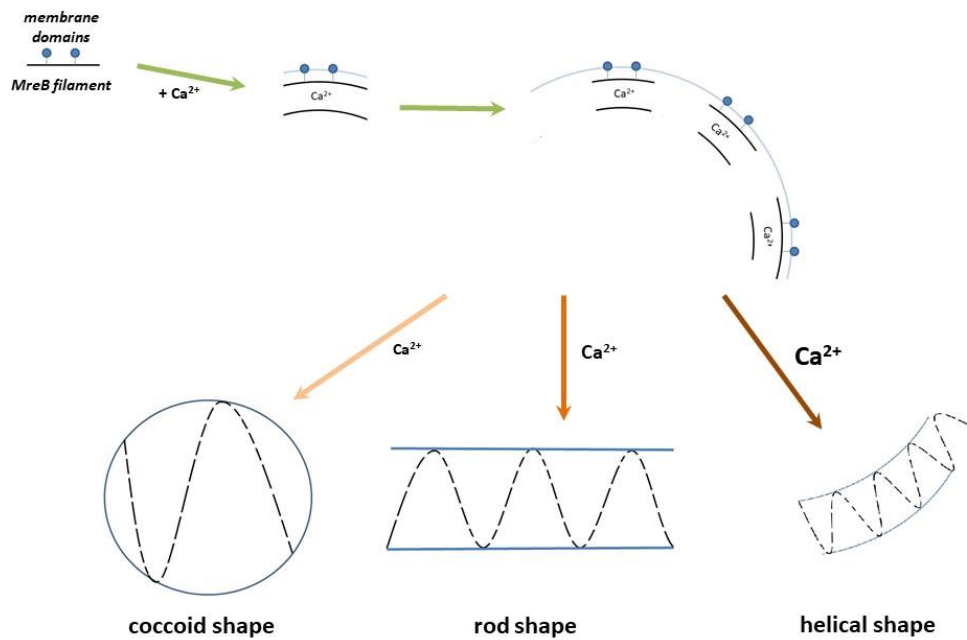
**Supplement 1. SDS-PAGE gels of MreB filaments prepared by the PF protocol. (A)** MreB from *Leptospira interrogans*; **(B)** MreB from *Rickettsia rickettsii*; **(C)** MreB from *Escherichia coli* (including a cropped image from *Supp.3D*).



**Supplement 2.** (A) *Rr*-MreB monomers purified under denaturing conditions, polymerized and labeled with Alexa568-maleimide. (B) Light scattering assay following the polymerization of 50  $\mu$ M *Rr*-MreB initiated by the addition of 2 mM MgCl<sub>2</sub> and various concentrations of KCl (black line: 100 mM, red: 200 mM, cyan: 400 mM), in the presence of 0.1 mM CaCl<sub>2</sub>. (C) The relative change in the light scattering signal as the function of the KCl concentration. (D) The rates of polymerization obtained by using single exponential fits ( $I = s_{\max} e^{t/T}$ , I is the scattered light intensity,  $s_{\max}$  is the amplitude, t is elapsed time, T is the rate constant). (E) Light scattering change of 50  $\mu$ M *Rr*-MreB monomers under 100 mM KCl, 2 mM MgCl<sub>2</sub> (black line). In 100 mM KCl, in the absence of magnesium (red line). In 4 mM MgCl<sub>2</sub>, in the absence of potassium (cyan line), and in 4 mM CaCl<sub>2</sub> in the absence of potassium and magnesium (blue line). (F) Alexa488-*Li*-MreB forms similar purified assemblies in 300 mM NaCl compared to 300 mM KCl (compare with *Fig. 2A*). Error bars refer to mean  $\pm$ SD of three independent measurements.



**Supplement 3.** (A) Percent Identity matrix created by Clustal2.1. (B) Phylogenetic neighbor-joining tree created by Clustal Omega. (ncbi.nlm.nih.gov) (KIX83831.1:0.227374,(AAS69864.1:0.225,(AJF45056.1:0.219653,ABY73136.1:0.219653):0.00534682):0.00237389) (C) *Li*-MreB expressing *E. coli* after lysis in high salt contained buffer (2 mM TRIS.HCl, 300 mM KCl, 2 mM MgCl<sub>2</sub>, 0.1 mM CaCl<sub>2</sub>, 0.2 mM ATP, 1 mM DTT, pH 8.0) and DNase I with lysozyme treatment, before filtering. All cysteines in the sample were labeled with Alexa488-maleimide. (D) SDS-PAGE of *Ec*-MreB filaments prepared by the PF protocol.



**Supplement 4.** A hypothetical model to explain how calcium-bound MreB may play a role in cell shape determination.

	<i>E.coli</i>	<i>L.interrogans</i>	<i>B.subtilis</i>
[Na <sup>+</sup> ]/[total cation]	0.845	0.978	0.808
[K <sup>+</sup> ]/[total cation]	0.145	0.018	0.182
[Ca <sup>2+</sup> ]/[total cation]	0.0009	0.003	0.003
[Mg <sup>2+</sup> ]/[total cation]	0.009	0.001	0.007
[Cl <sup>-</sup> ]/[total cation]	0.797	0.542	0.7

**Table 1.** Ratios for each ion as a total of cation concentrations.

**Movie 1.** The initial large *Li*-MreB assemblies (green), appeared to shorten and become less flexible after ten minutes on the addition of 2 mM CaCl<sub>2</sub>.

**Supplemental Movie 1.** Movie generated by ImageJ (NIH/Fiji) from 3D reconstruction of confocal images of *Li*-MreB-Alexa488 assemblies purified by PF method in high salt contained buffer (2 mM TRIS.HCl, 300 mM KCl, 2 mM MgCl<sub>2</sub>, 0.1 mM CaCl<sub>2</sub>, 0.2 mM ATP, 1 mM DTT, pH 8.0). Superstructures are based on the interlacement of curved ribbon-like sheets.

**Supplemental Movie 2.** Movie generated by ImageJ (NIH/Fiji) from 3D reconstruction of confocal images of *Li*-MreB-Alexa488 assemblies purified by PF method in high salt containing buffer (2 mM TRIS.HCl, 300 mM KCl, 2 mM MgCl<sub>2</sub>, 0.1 mM CaCl<sub>2</sub>, 0.2 mM ATP, 1 mM DTT, pH 8.0) then treated with 3 mM EGTA. In the absence of calcium, MreB superstructures disassembled and reformed a continuous sheet.