



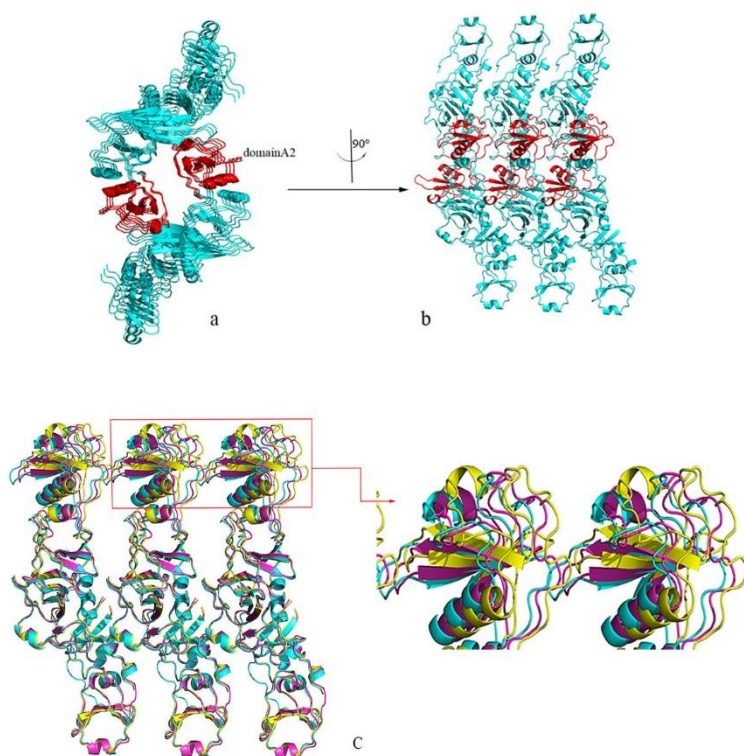
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**Supporting information for article:**

**Crystallographic observations of the movements of the membrane-distal domain of T7SS core component EccB1 from *Mycobacterium tuberculosis***

**Xiao-Qian Xie, Xiao-Li Zhang, Chao Qi, De-Feng Li, Joy Fleming, Da-Cheng Wang and Li-Jun Bi**



**Figure S1** Crystal packing of EccB1 in states II, III and IV. (a) and (b) Crystal packing of EccB1 in State II shows that domain A2 is mainly packed against itself in the crystal and has limited interactions with domain B. (c) Comparison of crystal packing in States II, III and IV suggests that the domain movement of A2 only causes movement of the packing interface of A2 and thus does not affect crystal packing.

**Table S1** The r.m.s.d. of different conformations of the overall structure (residues 72-451), the assembly of domains A1, B, C1 and C2 (residues 72-242 and 342-451), and domain A2 (residues 265-323).

<b>RMSD (Å)</b>	<b>STATE I</b>	<b>STATE II</b>	<b>STATE III</b>	<b>STATE IV</b>
<b>(72-450 )</b>				
<b>STATE I</b>		1.71	1.78	2.17
<b>STATE II</b>			0.92	1.91
<b>STATE III</b>				1.59
<b>STATE IV</b>				
<b>RMSD (72-242 &amp; 342-451)</b>				
<b>STATE I</b>		0.74	0.89	0.98
<b>STATE II</b>			0.59	0.59
<b>STATE III</b>				0.73
<b>STATE IV</b>				
<b>RMSD (265-323)</b>				
<b>STATE I</b>		0.42	0.42	0.40
<b>STATE II</b>			0.51	0.50
<b>STATE III</b>				0.46
<b>STATE IV</b>				