



STRUCTURAL BIOLOGY
COMMUNICATIONS

Volume 75 (2019)

Supporting information for article:

Novel T9 loop conformation of filamenting temperature-sensitive mutant Z from *Mycobacterium tuberculosis*

E. O. Lazo, J. Jakoncic, S. RoyChowdhury, D. Awasthi and I. Ojima

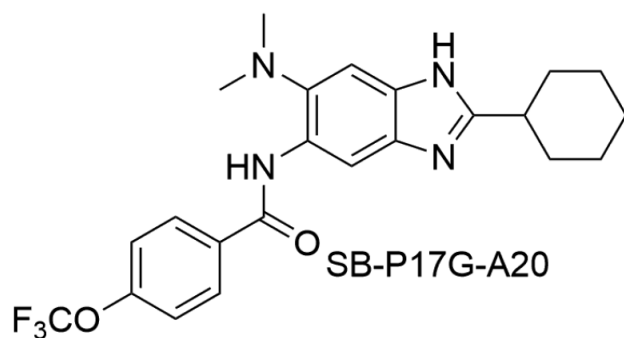


Figure S1 Structure of SB-P17G-A2-. The anti-TB drug (MIC 0.16 μ g/mL) that was incubated (0.5mM) with MtbFtsZ.

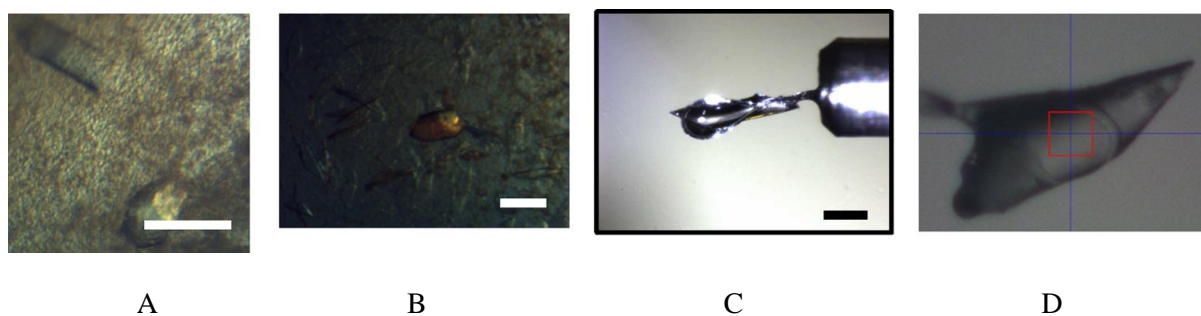


Figure S2 Crystals of MtbFtsZ. All crystals grew in 0.1M NaCitrate pH 5.6, 0.3M NH₄OAc, 15% PEG 4000 with minor differences. The same protein batch was used (no His tag) and the protein concentration was 3mg/ml. Protein with His tag produced poorly diffracting crystals. A) Protein was incubated in 5mM SB-P17-A20. B) Protein from crystal B was incubated in 0.1mM SB-P17-A20. C) Protein from crystal C was incubated in 0.5mM SB-P17G-C2. D) Protein from crystal D was incubated with 0.5mM SB-P17G-A20, which is the crystal used to solve this structure we present here. Scale bar for A and B represent 100 μ m, C 150 μ m. The red box is 100 μ m in D.

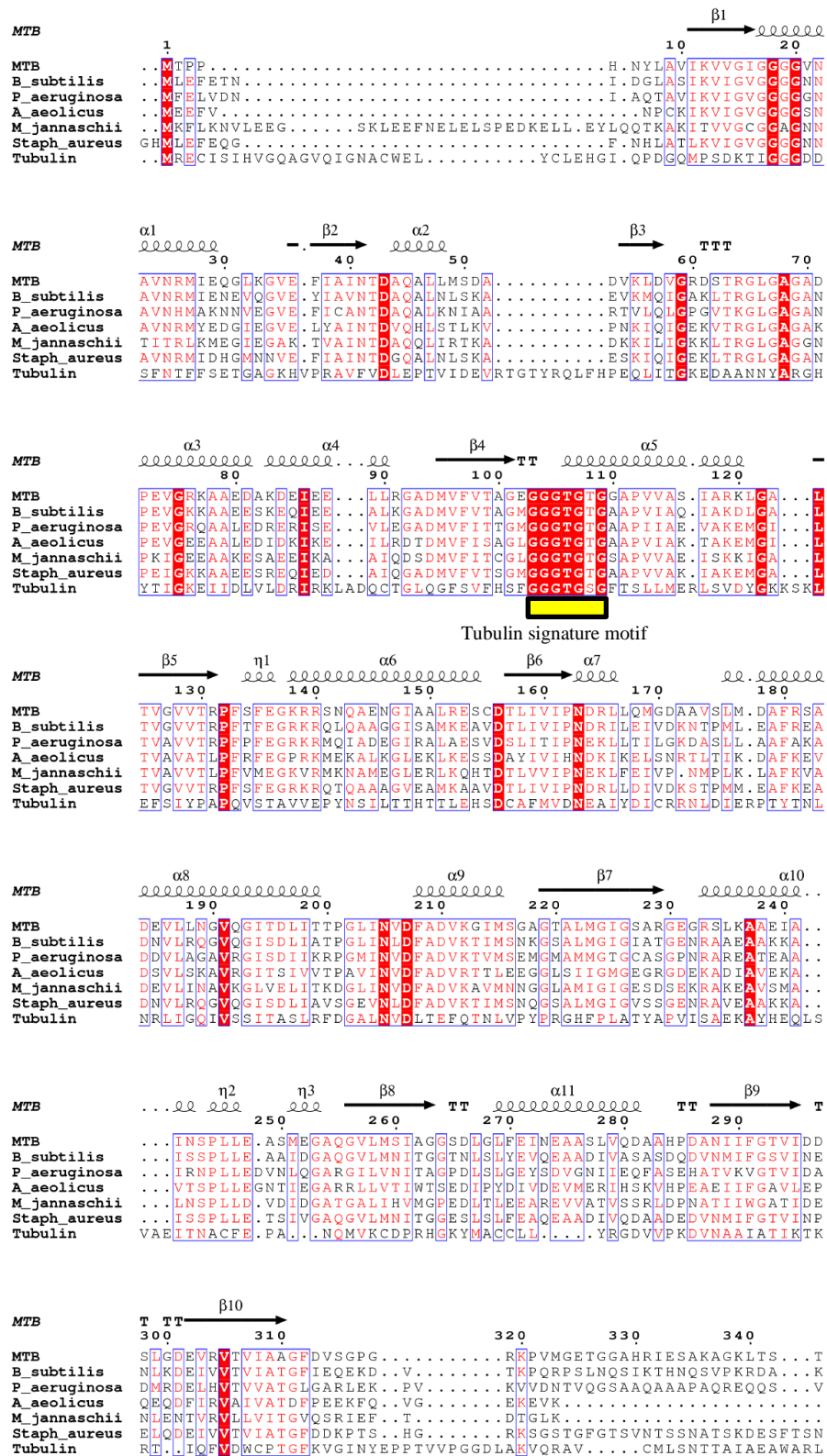


Figure S3 Sequence alignment of Ftsz from different organism and tubulin. Note that the tubulin signature motif is conserved (underlined by a yellow bar).