



BIOLOGICAL
CRYSTALLOGRAPHY

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2 **Volume 71 (2015)**

3 **Supporting information for article:**

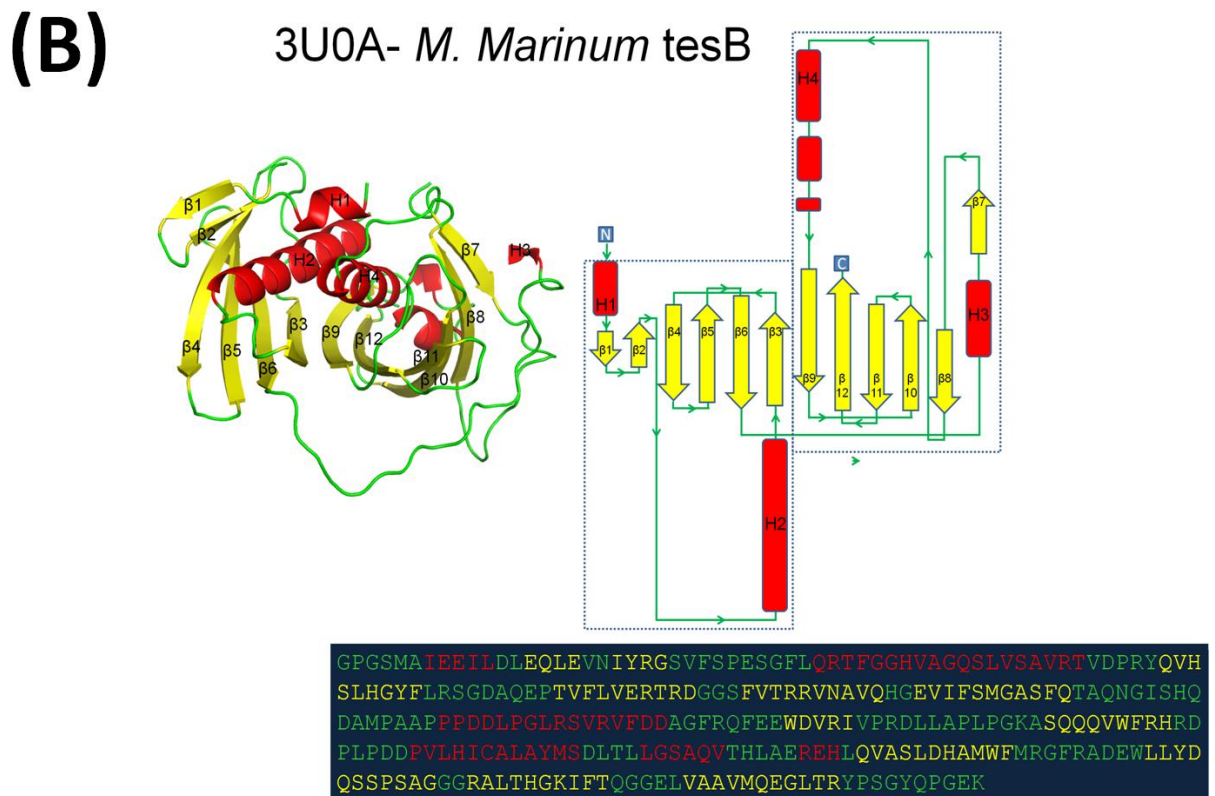
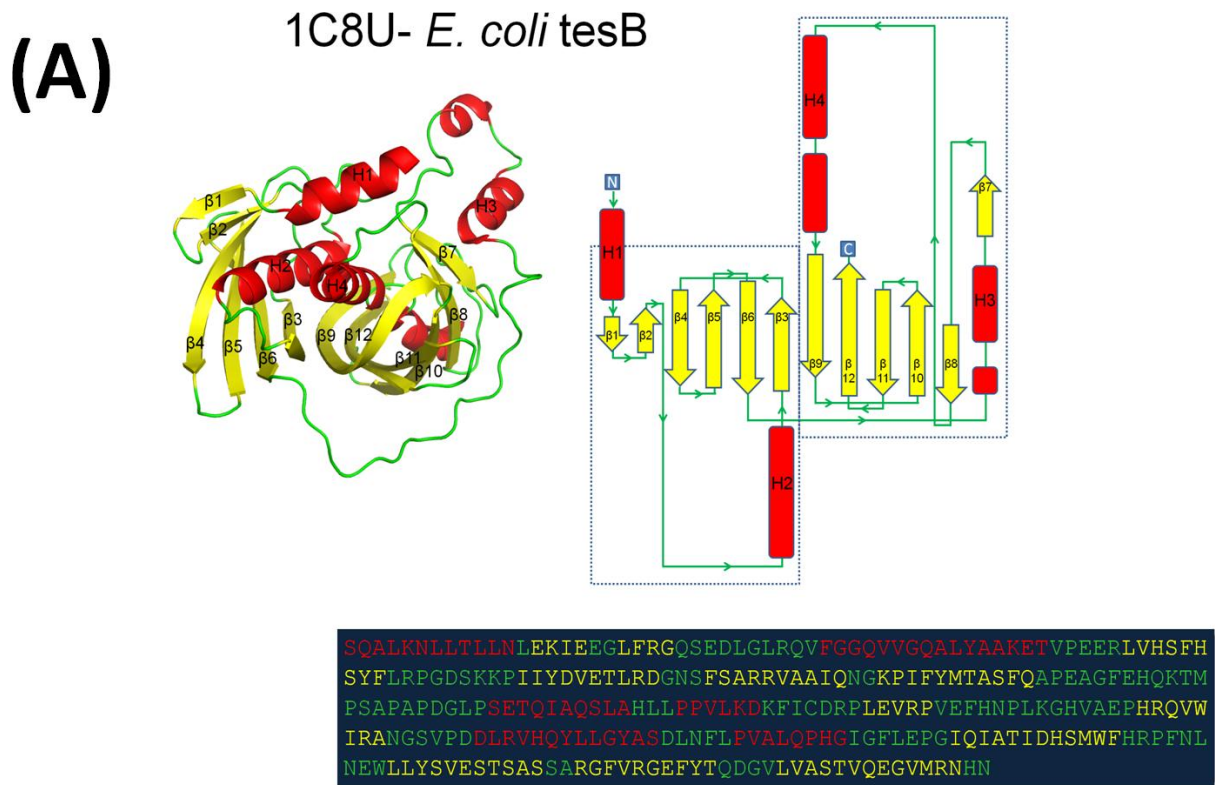
4 **Structural and functional characterization of TesB from *Yersinia***
5 ***pestis* reveals a unique octameric arrangement of hotdog domains**

6 **C. M. D. Swarbrick, M. E. Perugini, N. Cowieson and J. K. Forwood**

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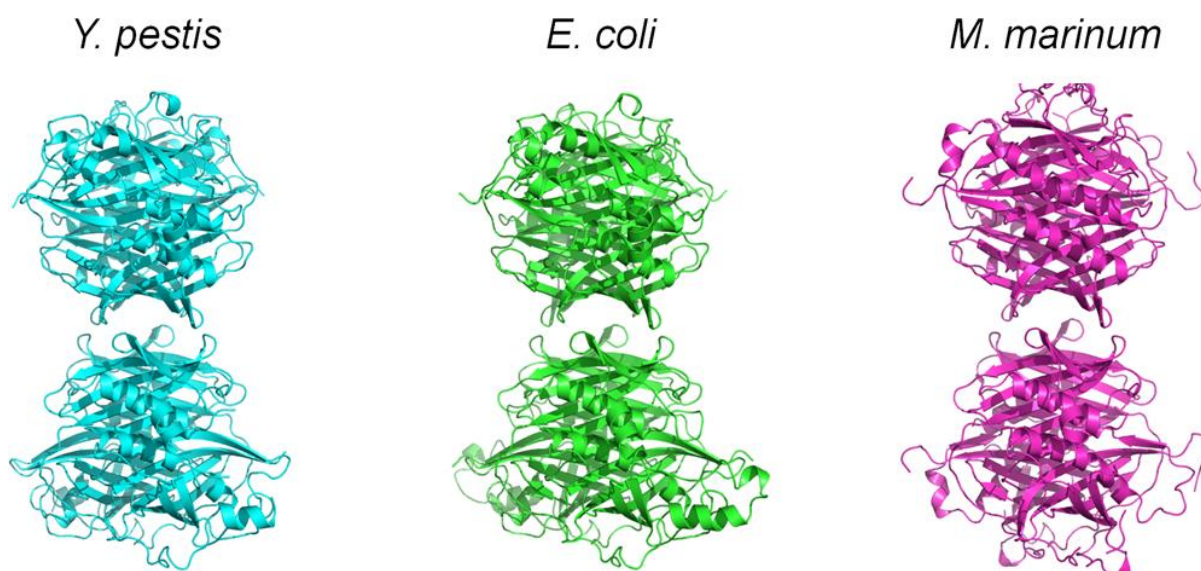
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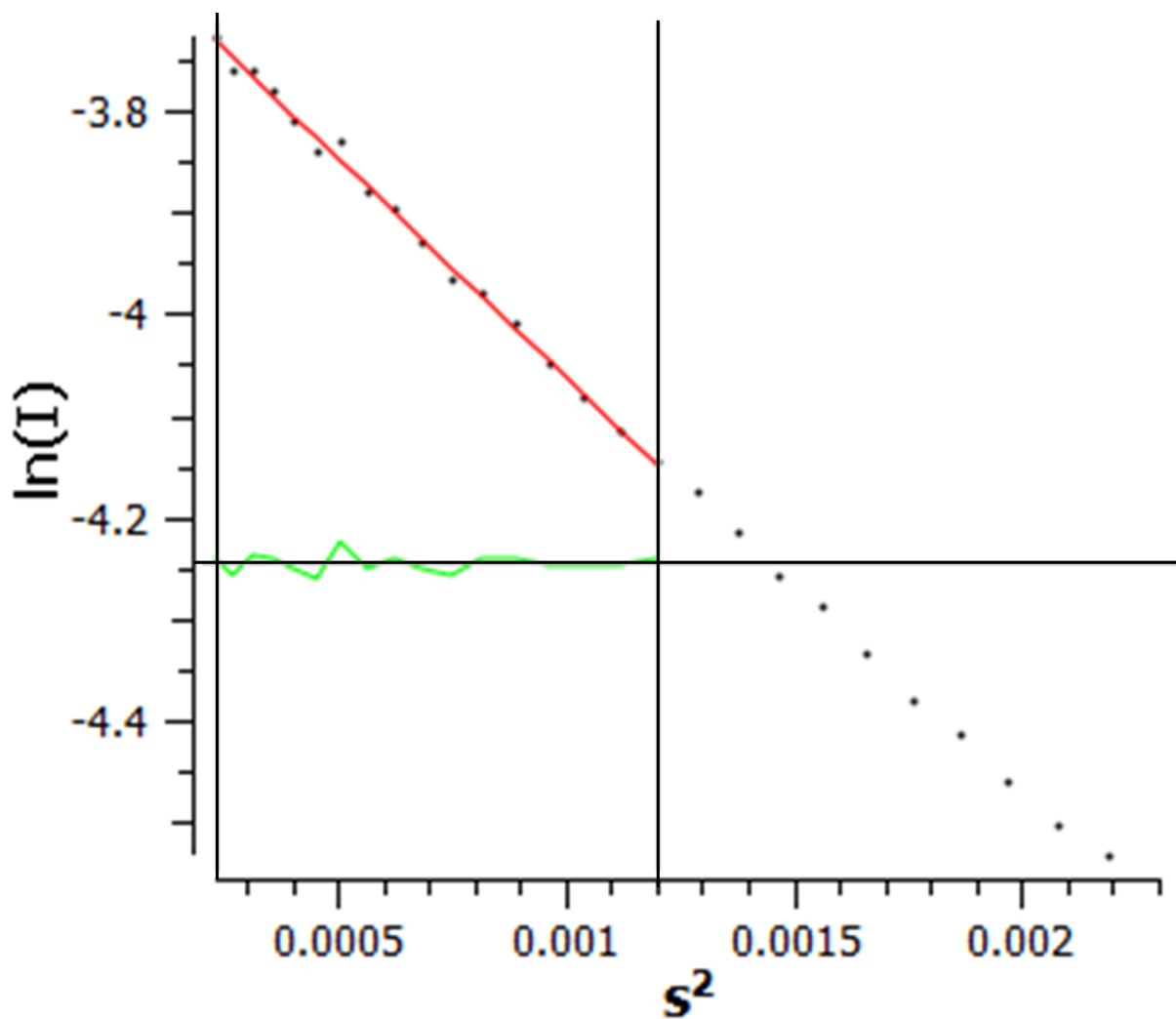


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3 **Figure S1** The primary, secondary and tertiary structure of (A) *EctesB* and (B) *MptesB* with α -
4 helices coloured red, β -stands in yellow, and loops in green.

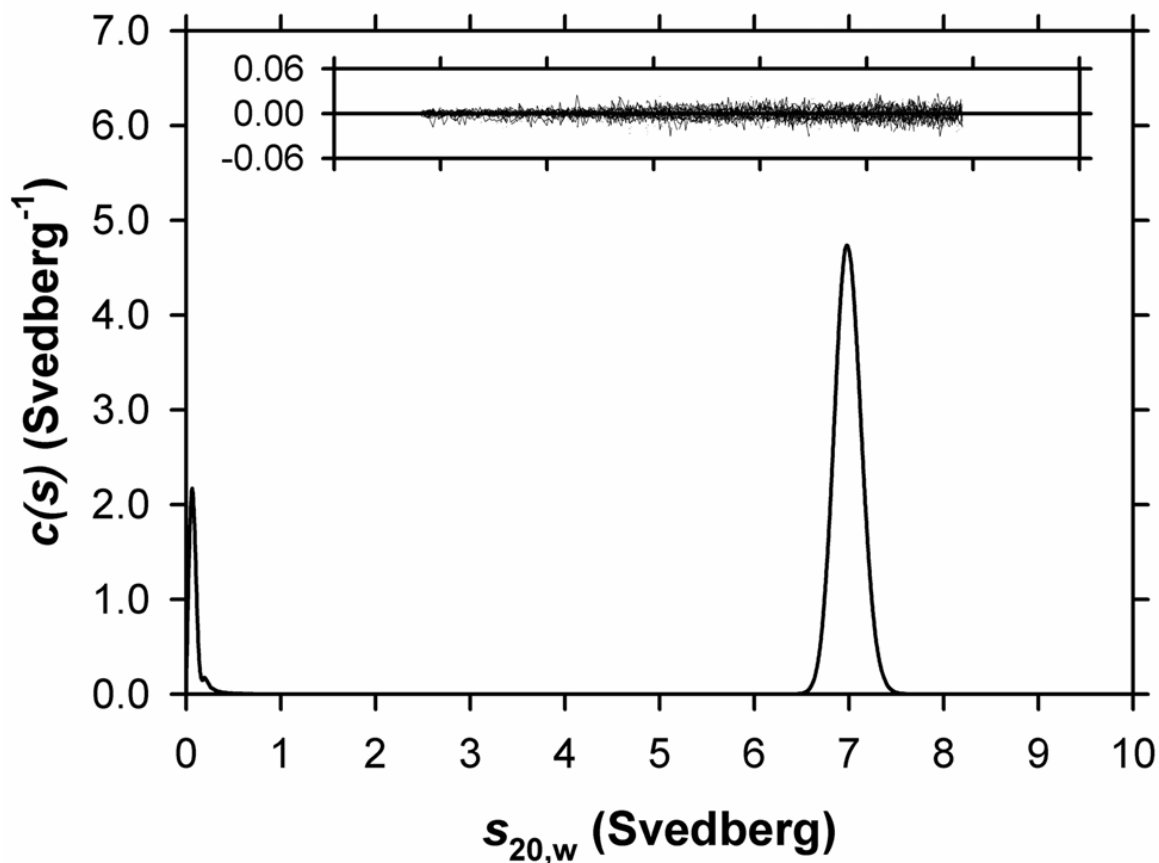


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2 **Figure S2** Alternate view of the *Y. pestis*, *E. coli* and *M. marinum* structures.

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4 **Figure S3** Guinier plot of $\ln(I)$ vs S^2 demonstrating the protein sample from which SAXS data was
5 derived is free of aggregation.



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3 **Figure S4** Sedimentation velocity analysis of TesB. The continuous sedimentation coefficient [c(s)]

4 distribution is plotted as a function of standardized sedimentation (Svedberg) for TesB (2.4 mg/ml).

5 The sedimentation coefficient at the ordinate maximum of the peak shown corresponds to 7.0 S.

6 The c(s) distribution was calculated using 200 sedimentation coefficients from 0 to 10 S at a P-value

7 of 0.95, which resulted in a RMSD of 0.00686, Runs test $Z = 7.39$ and yielded a frictional ratio of

8 1.28. Inset - Residuals for the c(s) best fit plotted as a function of radial position.

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