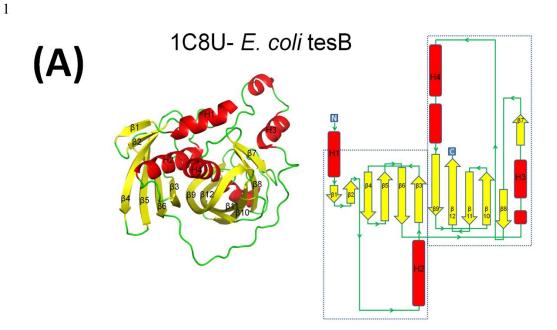


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- 3 Supporting information for article:
- 4 Structural and functional characterization of TesB from Yersinia
- 5 pestis reveals a unique octameric arrangement of hotdog domains
- 6 C. M. D. Swarbrick, M. E. Perugini, N. Cowieson and J. K. Forwood



SQALKNLLTLLNLEKIEEGLFRGQSEDLGLRQVFGGQVVGQALYAAKETVPEERLVHSFH SYFLRPGDSKKPIIYDVETLRDGNSFSARRVAAIQNGKPIFYMTASFQAPEAGFEHQKTM PSAPAPDGLPSETQIAQSLAHLLPPVLKDKFICDRPLEVRPVEFHNPLKGHVAEPHRQVW IRANGSVPDDLRVHQYLLGYASDLNFLPVALQPHGIGFLEPGIQIATIDHSMWFHRPFNL NEWLLYSVESTSASSARGFVRGEFYTQDGVLVASTVQEGVMRNHN

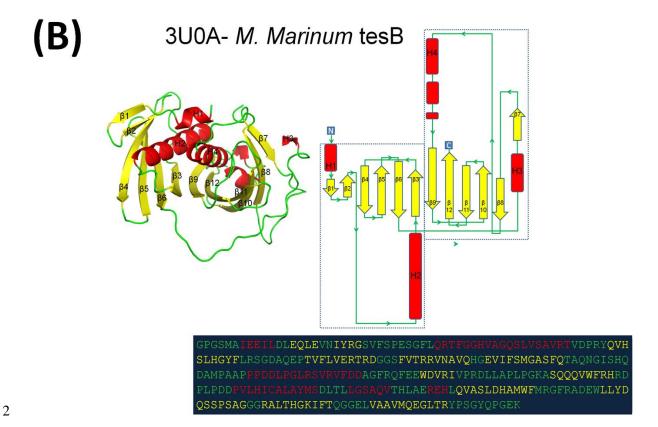
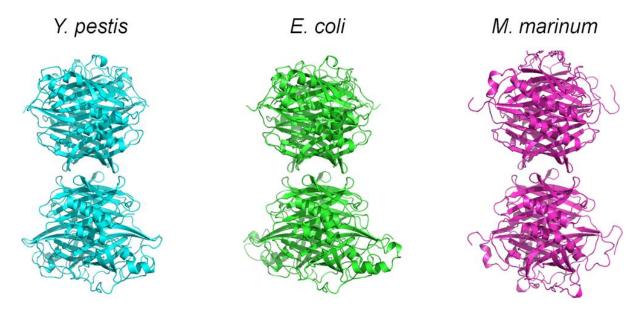


Figure S1 The primary, secondary and tertiary structure of (A) EctesB and (B) MmtesB with α-

4 helices coloured red, β-stands in yellow, and loops in green.



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

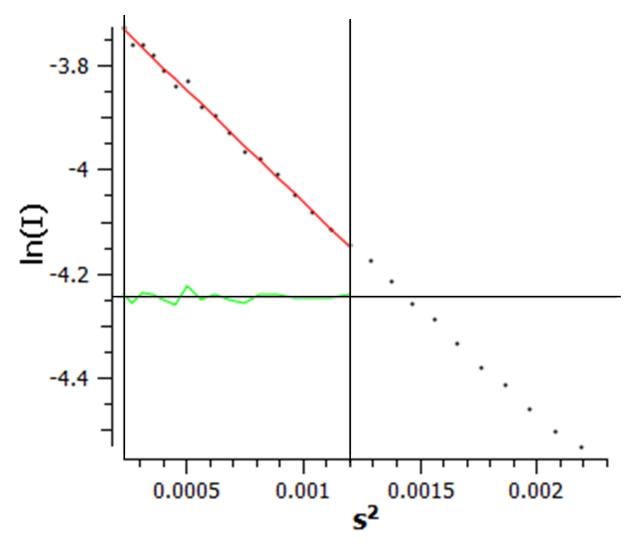


Figure S3 Guinier plot of ln(I) vs S² demonstrating the protein sample from which SAXS data was

5 derived is free of aggregation.

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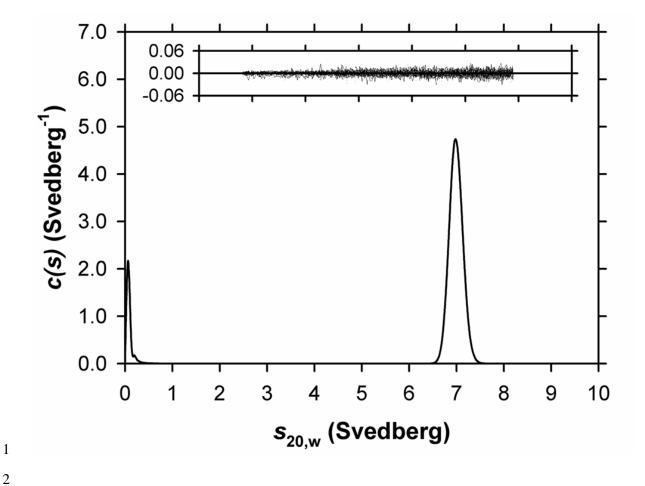


Figure S4 Sedimentation velocity analysis of TesB. The continuous sedimentation coefficient [c(s)] distribution is plotted as a function of standardized sedimentation (Svedberg) for TesB (2.4 mg/ml). The sedimentation coefficient at the ordinate maximum of the peak shown corresponds to 7.0 S. The c(s) distribution was calculated using 200 sedimentation coefficients from 0 to 10 S at a P-value of 0.95, which resulted in a RMSD of 0.00686, Runs test Z = 7.39 and yielded a frictional ratio of 1.28. Inset - Residuals for the c(s) best fit plotted as a function of radial position.