BJ Structure

Biochem. J. (2013) **450**, 417–425 (Printed in Great Britain) doi:10.1042/BJ20121599

SUPPLEMENTARY ONLINE DATA

Structure and mechanism of the PilF DNA transformation ATPase from *Thermus thermophilus*

Richard F. COLLINS, Darin HASSAN, Vijaykumar KARUPPIAH, Angela THISTLETHWAITE and Jeremy P. DERRICK[1]
Faculty of Life Sciences, The University of Manchester, Oxford Road, Manchester M13 9PT, U.K.

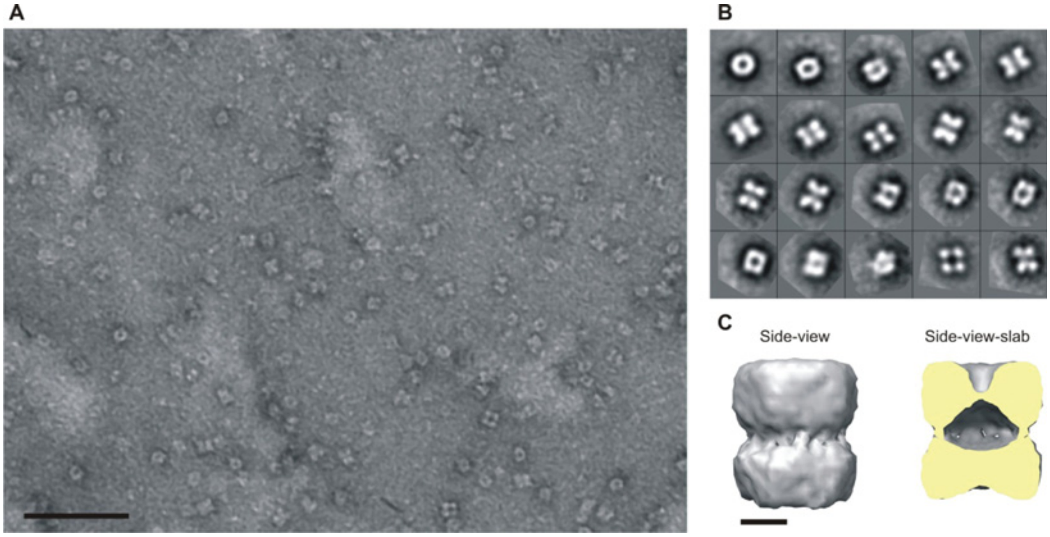

Figure S1 TtPilF raw data and reconstruction from negative stain

Examination of negatively stained TtPilF apoprotein by TEM. (**A**) A sample field of TEM data. Scale bar = 1000 Å. (**B**) Examples of SVD/MSA projection averages produced from the raw data. Box size = 240 Å×240 Å. (**C**) Surface-rendered side views of the TtPilF complex (orthogonal views). The slab view has the foremost 50 % of volume removed to display protein density through the complex. Scale bar = 50 Å.

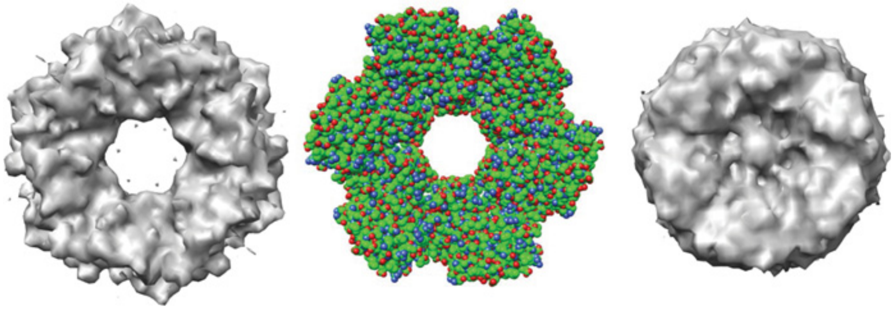

Figure S2 Comparison of top views of the ring (left-hand panel) and disk (right-hand panel) features from the cryoelectron density map with the atomic model of the C-terminal region of TfPilF (centre panel)

The p[NH]ppA-bound forms of the cryoelectron density map are shown. The original model of the C-terminal region of TtPilF is shown, before refinement against the density map.

Received 18 October 2012/19 December 2012; accepted 20 December 2012
Published as BJ Immediate Publication 20 December 2012, doi:10.1042/BJ20121599

---

[1] To whom correspondence should be addressed (email jeremy.derrick@manchester.ac.uk).
The density maps reported in the present paper will appear in the Electron Microscopy Data Bank under accession numbers 2222 and 2223.