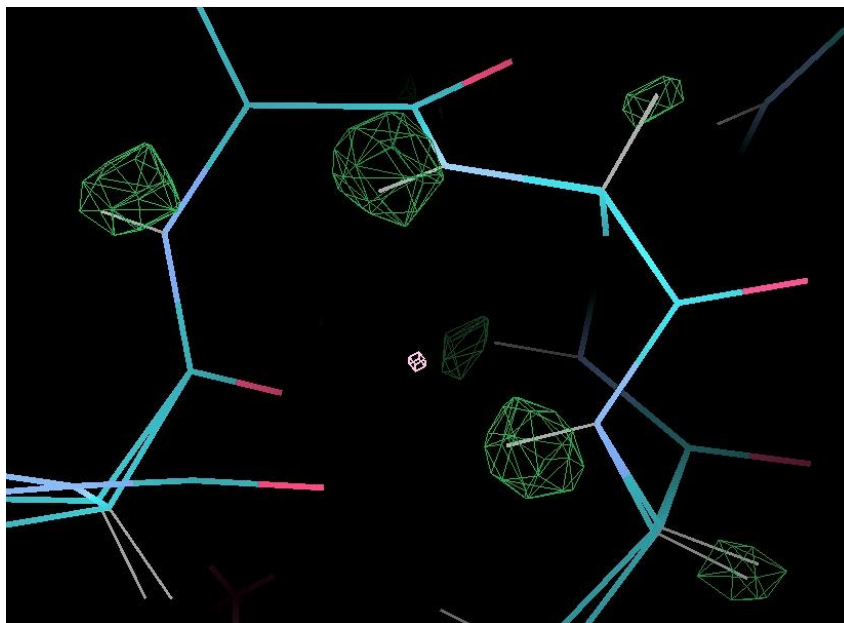


Supplementary Figures

The 1.2 Å resolution crystal structure of TcpG, the *Vibrio cholerae* DsbA disulfide-forming protein required for pilus and cholera-toxin production

Walden *et al.* (2012)

Supplementary Figure S1. Difference electron density of TcpG. The difference electron density map ($F_o - F_c$, 3σ) using F_c from an early refinement of TcpG without hydrogens (green, positive difference, red negative difference), is shown superimposed on the final refined TcpG coordinates that included hydrogens. The difference density suggests that hydrogens are observable in the electron density.



Supplementary Figure S2. Sequence alignment of VcDsbB and EcDsbB. Sequence alignment was performed using *ClustalW* (Altschul *et al.*, 1990). The active site cysteines of both proteins are highlighted in blue and the transmembrane helices are highlighted in yellow. The PSPFATCD sequence element that is identical in EcDsbB and VcDsbB, is boxed. The sequence identity for VcDsbB and EcDsbB is 47%.

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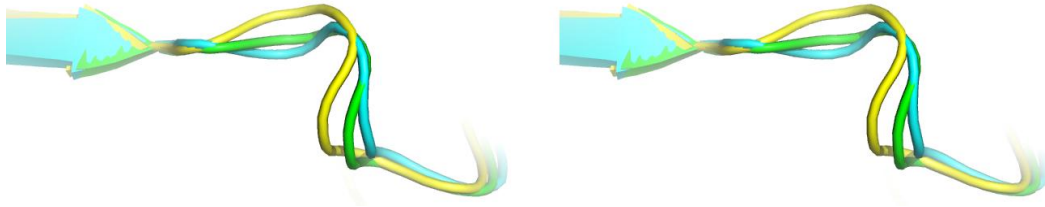
VcDsbB  MRILSSLKTFQSRLSWLLLLAFVVFVFTLCAMYFQHVMLLAPCVMCIYERIAMLGIGVAA  60
EcDsbB  --MLRFLNQASQGRGAWLLMAFTALALELTALWFQHVMLLKPCVLCIYERVALFGVLGAA  58

VcDsbB  LIGAIAPQNPVVRWLGFAAWGASSYKGLMLAIEHVNYQFNPSPFATCDLEFVTFPAWAPLN 120
EcDsbB  LIGAIAPKTP-LRYVAMVIWLYSAFRGVQLTYEHTMLQLYPSPFATCDFMVRFPEWLPLD 117

VcDsbB  QWAPNLFEAYGDCSKVWVQFLTSLMPQWLVVIFAANLLALAIFFVVAQLAKTSR----- 173
EcDsbB  KWVPQVFBASGDCAERQWDFLGLEMPQWLLGIFIAYLIVAVLVVISQPFKAKKRDLFGRRS 178

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Supplementary Figure S3. Comparison of $\beta 5$ - $\alpha 7$ loop. Superimposition of the $\beta 5$ - $\alpha 7$ loops from structures 1bed (cyan), 1bed_final (green) and 4dvc (yellow) show that the newly refined 1bed_final has a similar conformation to that of 1bed (both refined against the same data).



Reference

Altschul, S. F., Gish, W., Miller, W., Myers, E. W. & Lipman, D. J. (1990) *J. Mol. Biol.* **215**, 403-410