

Figure S1

Structure of *S. aureus* gyrase (green) complex with ciprofloxacin (grey) and DNA (red/magenta), viewed from the protein-protein interface. For clarity, only one half of the dimer is shown. Figures were adapted using Jmol (protein data base 2XCT, <http://molvis.sdsc.edu/fgij/fg.htm?mol=2XCT>). The structure was determined by Bax *et al.* (Nature 2010;466:935-940).

A) Fusion protein consisting of the C-terminal region of GyrB and the N-terminal region of GyrA (GyrB27–A56) is shown. Residues of interest are highlighted in yellow.

Corresponding amino acids in the native GyrA, GyrB, ParC, and ParE proteins are presented in parentheses. 1: Ser1084 (GyrA Ser-84, ParC Ser-80); 2: Glu1088 (GyrA Glu-88, ParC Glu-84); 3: Asp-437 (ParE Asp-432); 4: Arg-458 (ParE Arg-455); 5: Ala-588 (ParE Pro-585). B) Rotated, detailed view of figure A. 6: location of the Mg^{2+} ion that is thought to stabilize the fluoroquinolone-GyrA interaction.

