Supplementary Materials and Methods

Data collection, structure determination and refinement

The model produced by PHASER showed a number of characteristics which suggested correctness: firstly that the tetrameric ring-like structure of drRecR (Lee et al., 2004) was reconstructed from one monomer of drRecR and secondly that the molecular ratio 2:1 drRecR to drRecO estimated from biochemical characterisation was maintained in a plausible manner (Leiros et al., 2005). The tetrameric structure of drRecR was generated from the dimer by a crystallographic twofold symmetry axis of the C2 space group. Initial results and further refinement resulted in a three-dimensional structure possessing both expected and unexpected features. Biochemical characterisation of wild-type and mutated complex proteins further verified the crystal structure. In addition to conventional 2mFo-DFc and mFo-DFc sigmaA-weighted electron density maps, SFCHECK-generated omit maps were also calculated and used in the rebuilding.

Native gel electrophoresis

2 µg of drRecR, drRecO and drRecOR alone and in the presence of 0.5 and 2.5 µM 3’-OH2 DNA were run on a 5% TBE pH 8.3 native gel at 4°C for 90 minutes at 100V. The gel was subsequently transferred to a nitrocellulose membrane and analysed by Western blotting using anti-drRecO (1:10,000) and anti-drRecR (1:25,000) in 5% milk. The bands were revealed using a second anti-rabbit antibody conjugated to alkaline phosphatase and a colorimetric substrate (Promega).