

Supplemental Data

Figure S1. The stereo figure of the OMIT 2fofc map of the bound OliA at the active site. 2fofc map (blue) is contoured at 0.5σ . OliA model was superimposed to the OMIT map.

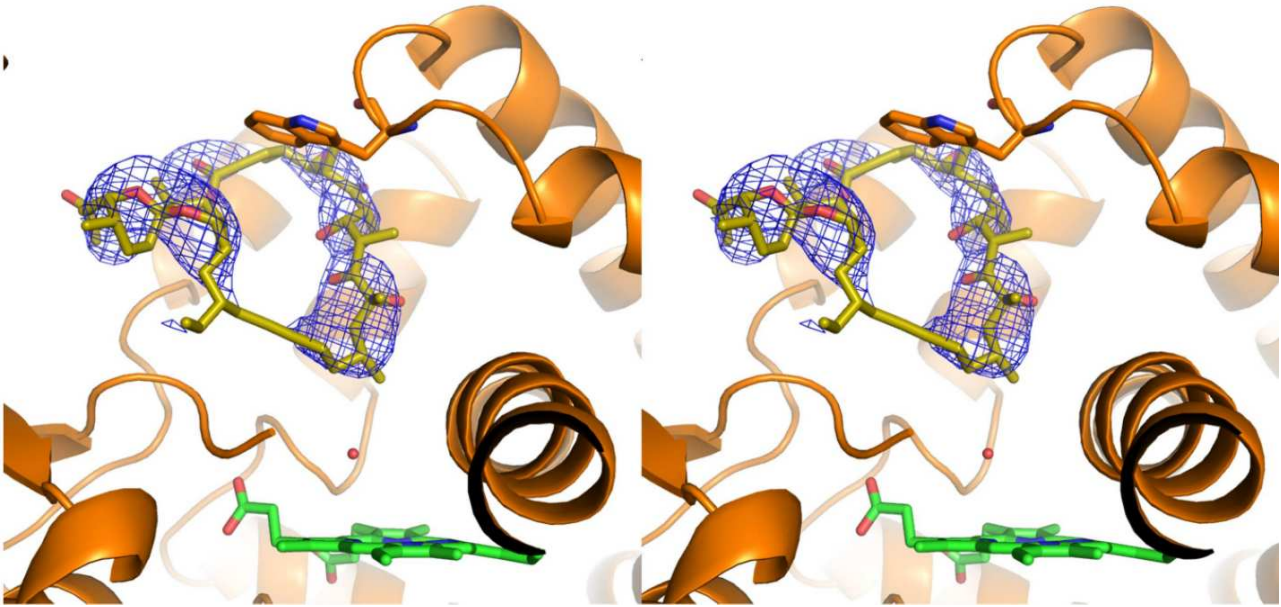


Figure S2. The 2fofc map of the bound Heme in the active site. 2fofc map (blue) is contoured at 1.0 σ . (A) Upside view. (B) Side view.

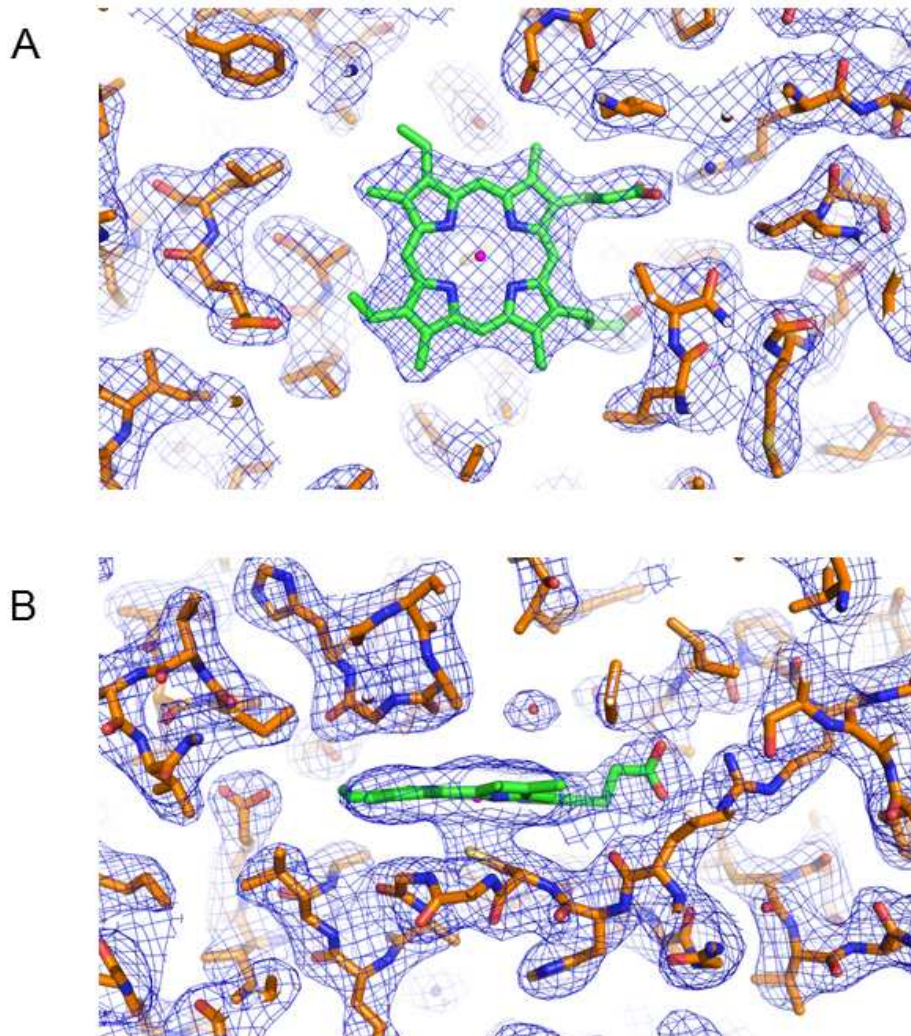


Figure S3. CO-binding spectra of purified W178G mutant enzyme of CYP107W1. (A) Whole cell level. (B) Final purified P450 enzyme.

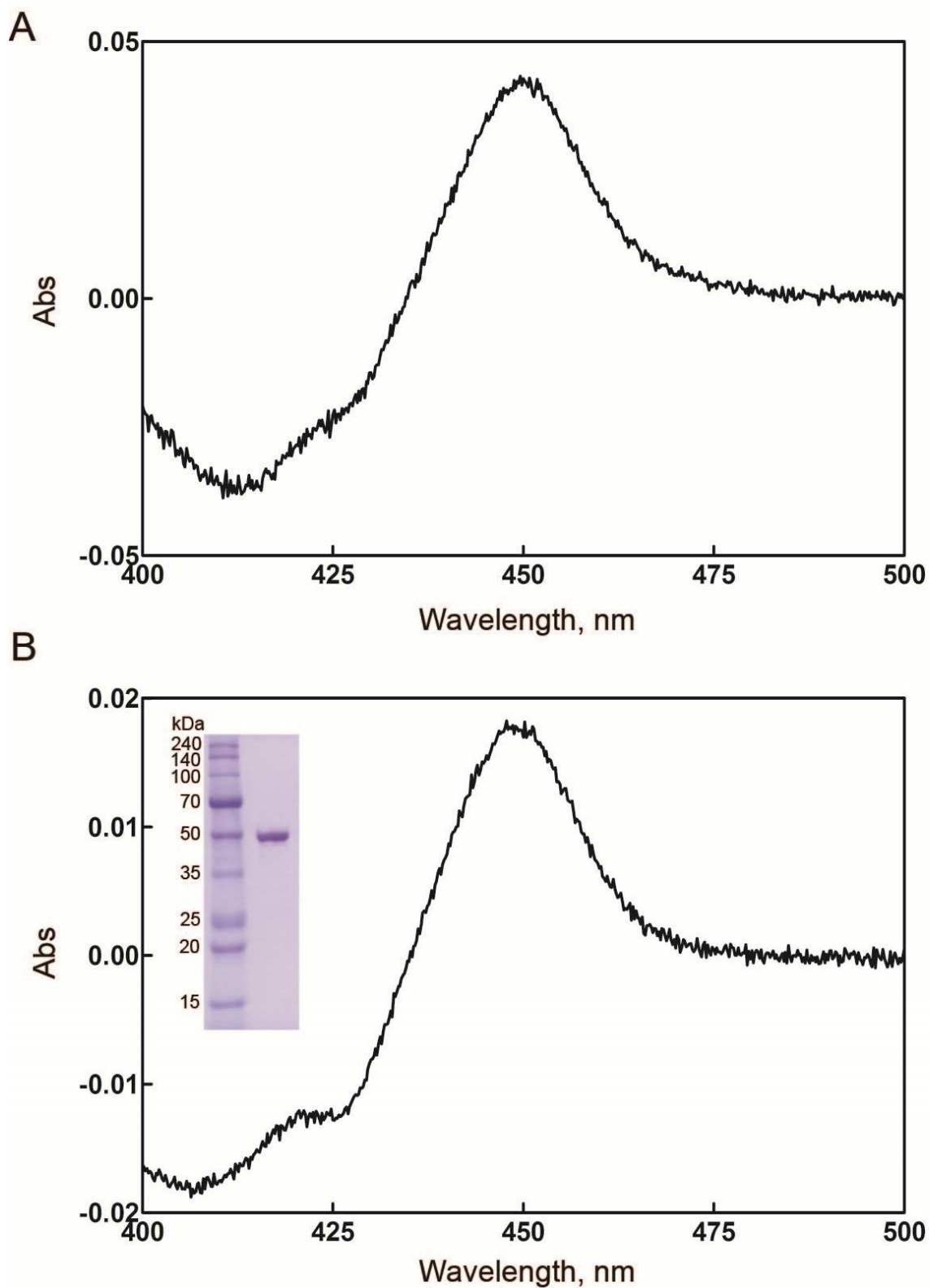


Figure S4. Substrate binding modes of P450 structures in complex with macrolides. The root-mean-square deviation (RMSD) of the CYP107W1-oligomycin A structure (purple) with the CYP105P1 structure (dark green) was 1.296 Å for 1,859 C α atoms and with MycG (salmon), 1.090 Å for 1,958 C α atoms.

