Supporting Information, Fragments of Alkyl Hydroperoxide Reductase AhpF, Poole et al.

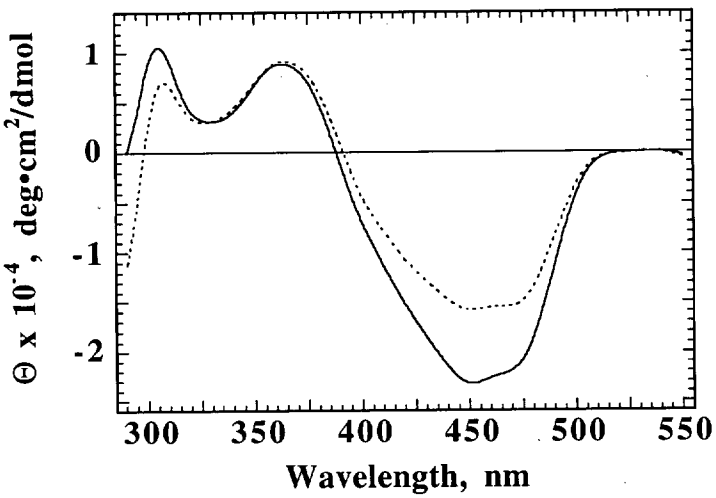

Figure S1. Comparison of visible CD spectra for F[208-521] and intact AhpF. Spectra were obtained at room temperature for 60 μM of F[208-521] (dotted line) or intact AhpF (solid line) in 25 mM potassium phosphate buffer at pH 7.0 (without EDTA). Measurements were taken in 1 nm increments from 550 to 290 nm in a 1.0 cm path length cuvette; each spectrum is the average of nine scans, and data were smoothed once using the default parameters within the Jasco J-720 software.

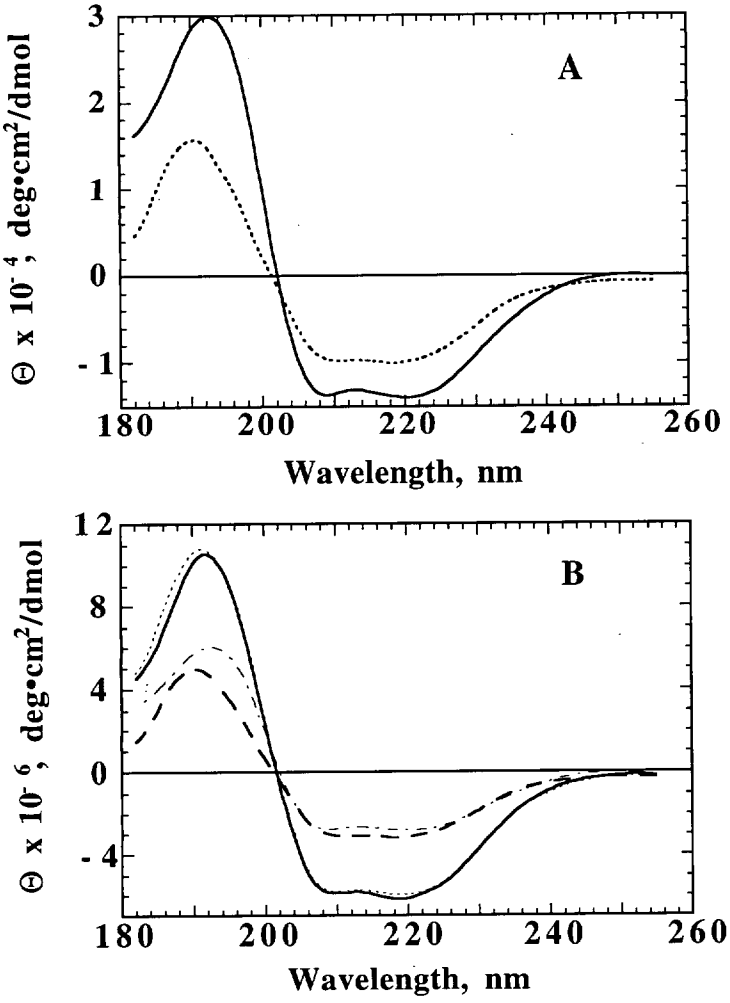

Figure S2. Far UV circular dichroism (CD) spectroscopy of F[1-202] and F[208-521] compared with intact AhpF. Panel A depicts spectra obtained for 0.3 and 0.4 mg/mL, respectively, of F[1-202] (solid line) and F[208-521] (dotted line), expressed per mean residue. Conditions for data acquisition were the same as those described in Figure S1, except that measurements were taken in 0.5 nm increments from 255 to 182 nm in a 0.05 cm path length cuvette and four scans were averaged for each spectrum. Panel B shows the same data from A, expressed per polypeptide, for F[1-202] (dash-dotted line) and F[208-521] (dashed line), as well as the sum of the two (dotted line) and the corresponding CD spectrum for 0.4 mg/mL of intact AhpF (solid line).

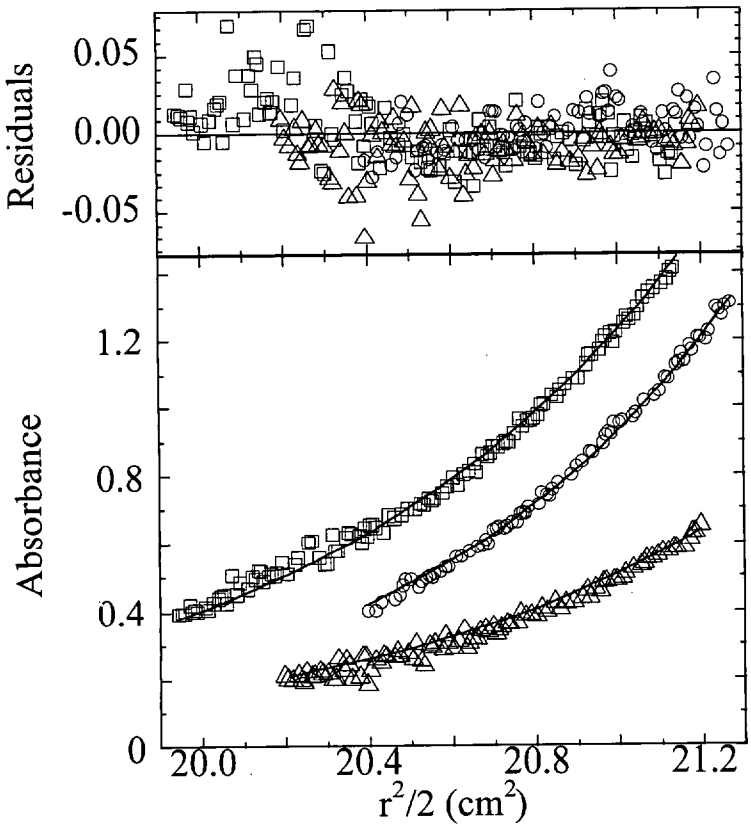

Figure S3. Sedimentation equilibrium analyses of AhpF protein and fragments to determine molecular weight. Shown are single data sets for intact AhpF (circles), F[208-521] (squares) and F[1-202] (triangles) equilibrated to 20 °C at 10,400, 14,300 and 22,000 rpm, respectively. Solid lines represent global fits to a single ideal species model of 9 to 15 data sets for each protein at 279 or 280 nm. M_w values obtained by this method are shown in Table 3 of the manuscript. The upper panel depicts the deviations between experimental and calculated data (residuals) for each data set.