Fig. S1. (A) Fluorescence decay curve of cytochrome cbs52 in 6.9 M GuHCl (gray) and its fitting curves based on wormlike chain model (red), freely joint chain model (blue), Gaussian chain model (green), and model independent with maximum entropy method (black). (B) Residual of the fitting curve of wormlike chain model. (C) Residual of the fitting curve of freely joint chain model. (D) Residual of the fitting curve of Gaussian chain model. (E) Residual of the fitting curve of maximum entropy method.
Fig. S2. Distance distributions of the unfolded cytochrome cβ562. Distributions are calculated based on wormlike chain model (red line), freely joint chain model (blue line), Gaussian chain model (green line), and model independent with maximum entropy method (black bar) as shown in Fig. S1.
Fig. S3. Folding kinetics of cyt cb562. Original and logarithmically smoothed data points are shown in black and red, respectively. (A) Integrated Trp-59 fluorescence intensity as a function of folding time. The solid line is a fit to a single exponential function with a rate constant of $2.6 \times 10^2$ s$^{-1}$. (B) Mean center-to-center distance between tryptophan and heme ($M_1$) as a function of folding time. The solid line is a fit to a single exponential function: rate constant of $2.6 \times 10^2$ s$^{-1}$. (C) Time course of the second moment ($M_2$). The solid line is a fit of a single exponential function: rate constant of $2.4 \times 10^2$ s$^{-1}$. (D) Time course of the variance ($v$). The solid line is a fit of a double exponential function: rate constants of $5.1 \times 10^2$ and $2.6 \times 10^2$ s$^{-1}$.

Other Supporting Information Files

SI Appendix