DRIVING FORCES OF GYRASE RECOGNITION BY THE ADDICTION TOXIN CcdB

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SUPPLEMENTAL MATERIALS

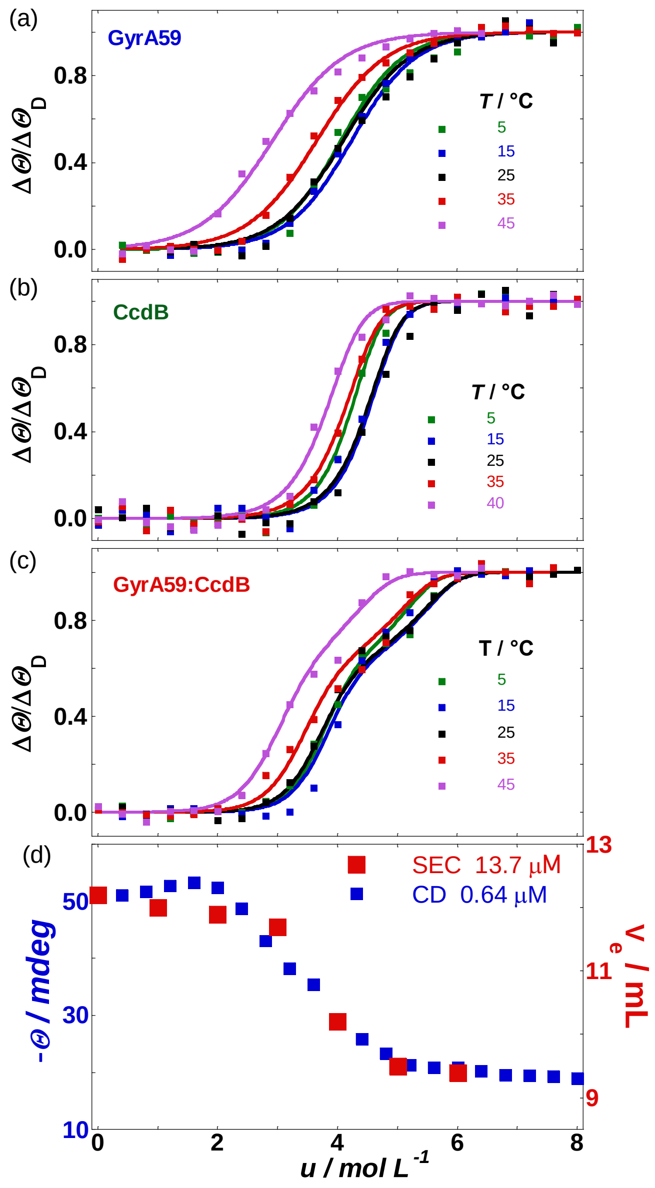

Figure 1-SM. Modeling urea induced denaturation profiles (second dataset). Ellipticity measured as a function of urea concentration expressed as normalized ellipticity (eq. 3 - main text) for GyrA59 **(a)** and CcdB **(b)** and GyrA59**:** CcdB complex **(c)**. The presented set of experimental data was obtained at the same protein concentrations as the dataset presented in Fig. 3 – main text. Lines represent the best global fits of the denaturation models (eq. 3 - main text) to the experimental data. Comparison of GyrA59 denaturation curves measured by CD - spectroscopy and size exclusion cromatography (SEC) at 25 °C at significantly different protein concentrations is presented in panel **(d)**. The observed concentration independence of denaturation curves indicates that GyrA59 denaturation can be considered as a monomolecular process.