

Supplementary data

Solution structure of Domains IVa and V of the τ subunit of *Escherichia coli* DNA
polymerase III and interaction with the α subunit

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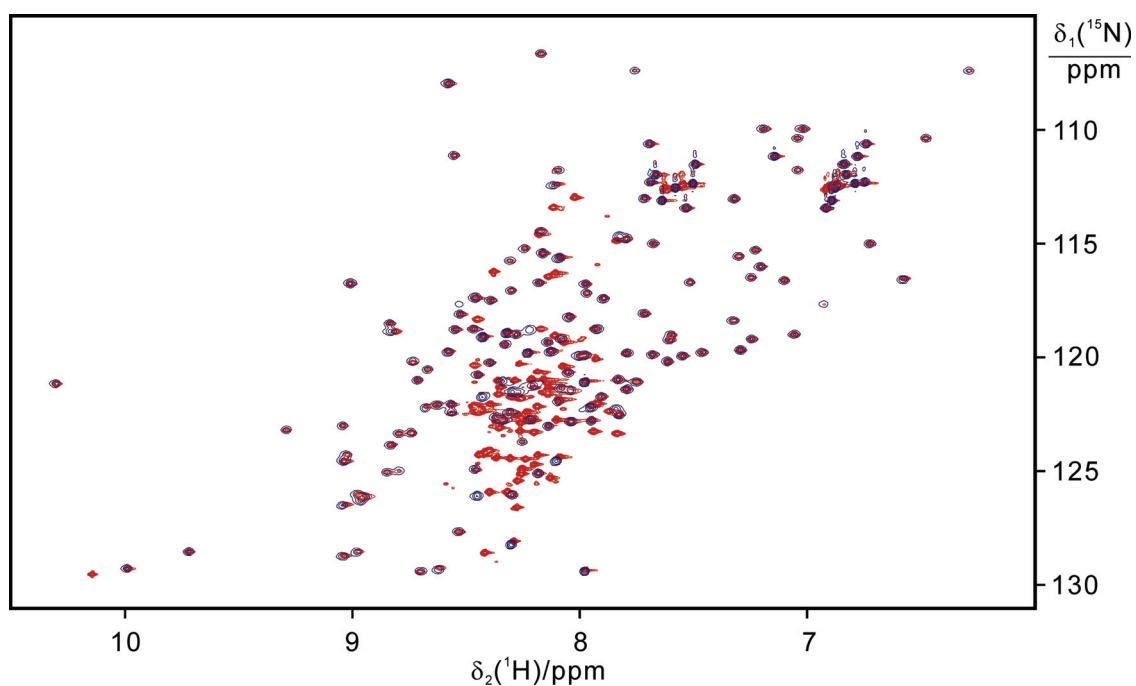


Figure S1. Superposition of ^{15}N -HSQC spectra of ^{15}N -labeled $\tau_{\text{C}22}$ (red) and $\tau_{\text{C}14}$ (blue). The spectra were recorded in 10 mM sodium phosphate (pH 6.8) containing 100 mM NaCl, 1 mM dithiothreitol, 0.1 mM NaN_3 and 90% $\text{H}_2\text{O}/10\%$ D_2O on a Bruker Avance 800 NMR spectrometer. The sample concentrations were 0.4 mM for $\tau_{\text{C}22}$ and 0.2 mM for $\tau_{\text{C}14}$. The additional cross-peaks observed for $\tau_{\text{C}22}$ display a narrow ^1H chemical shift dispersion around about 8.2 ppm which is characteristic of random coil chemical shifts. The cross-peaks of $\tau_{\text{C}14}$ superimpose closely with corresponding cross-peaks of $\tau_{\text{C}22}$, indicating that the globular structure of $\tau_{\text{C}14}$ is unperturbed by the additional residues present in $\tau_{\text{C}22}$.

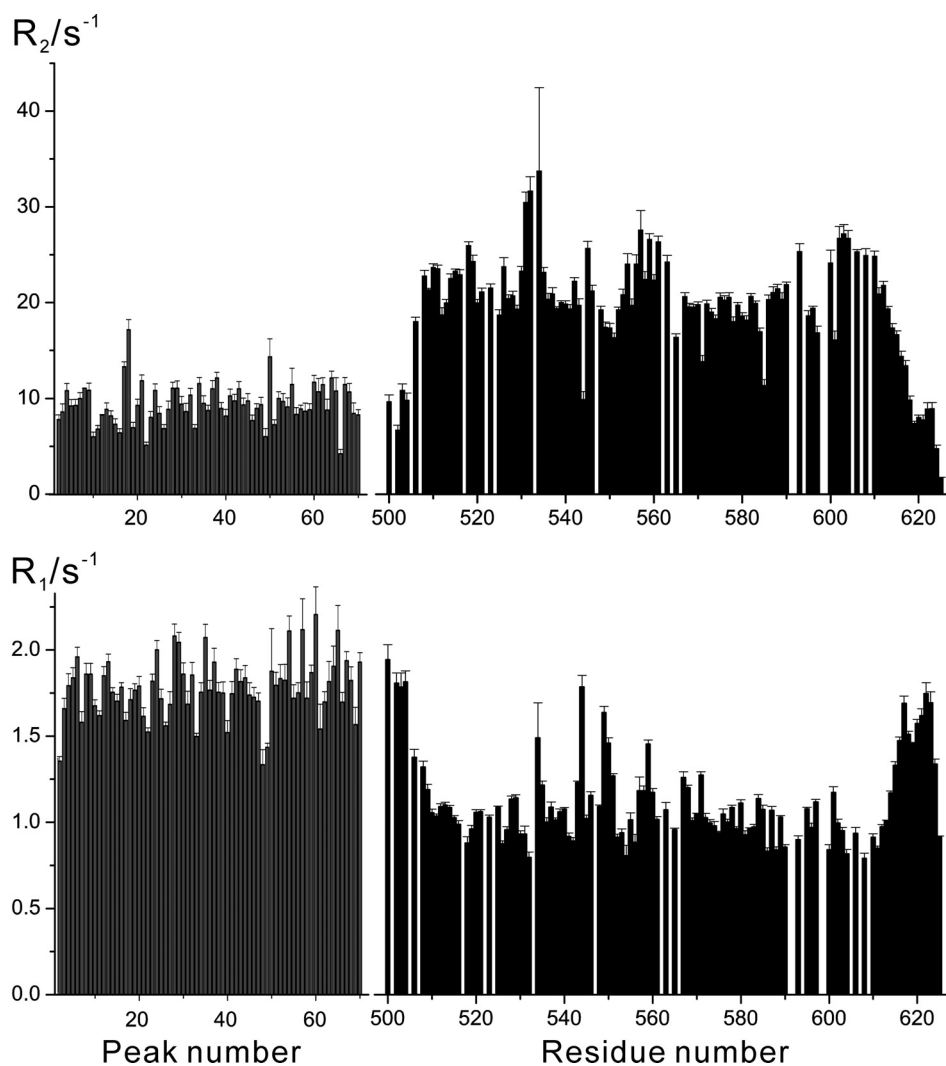


Figure S2. ^{15}N -relaxation rates of $\tau_{\text{C}22}$ recorded under the conditions of Figure S1. Sequence specific resonance assignments were obtained only for Domain V and the additional cross-peaks present in the ^{15}N -HSQC spectrum of $\tau_{\text{C}22}$ were arbitrarily numbered from 1 to 69. Their relaxation data are shown on the left. The R_1 relaxation rates (lower panel) were derived from nine spectra recorded with relaxation delays of 3, 30, 100, 200, 350, 600, 900, and 1300 ms. The R_2 relaxation rates (upper panel) were derived from eight spectra recorded with relaxation delays of 9, 17, 26, 43, 60, 78, 95, and 112 ms. The uniformly large R_1 and small R_2 values of the additional 69 residues present in $\tau_{\text{C}22}$ are characteristic of highly mobile random coil conformation.