

Supporting Information for: Single-Protein Collapse  
Determines Phase Equilibria of a Biological  
Condensate

Han-Yi Chou and Aleksei Aksimentiev\*

Department of Physics, University of Illinois at Urbana-Champaign

1110 W. Green St., Urbana IL, 61801 USA

\*E-mail: aksiment@illinois.edu

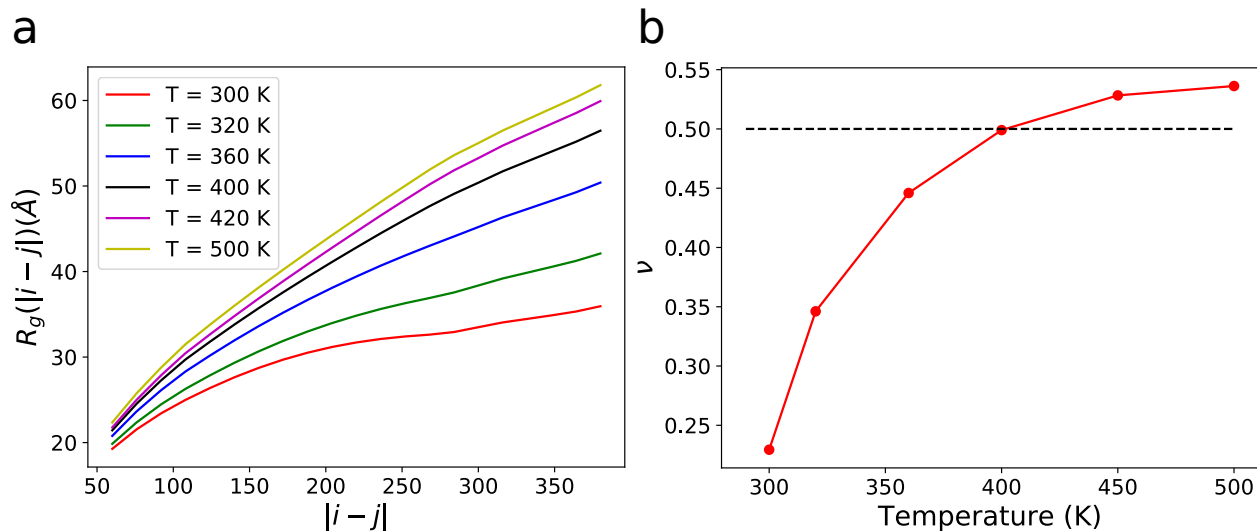


Figure S1: MD simulation of FUS  $\theta$  temperature. (a) Simulated radii of gyration of FUS protein fragments as a function of the fragment length,  $|i - j|$ , where  $i$  and  $j$  indicate the indices of the fragment's terminal beads. Each  $R_g(|i - j|)$  value was obtained by averaging over all  $(i, j)$  pairs of the same index difference. (b) The scaling exponent  $\nu$  that best describes the asymptotic relation  $\langle R_g(i - j) \rangle \sim |i - j|^\nu$  when the difference of the bead indices  $|i - j| \rightarrow \infty$ . The horizontal dashed line indicates the  $\nu = 0.5$  value that corresponds to the  $\theta$  temperature.

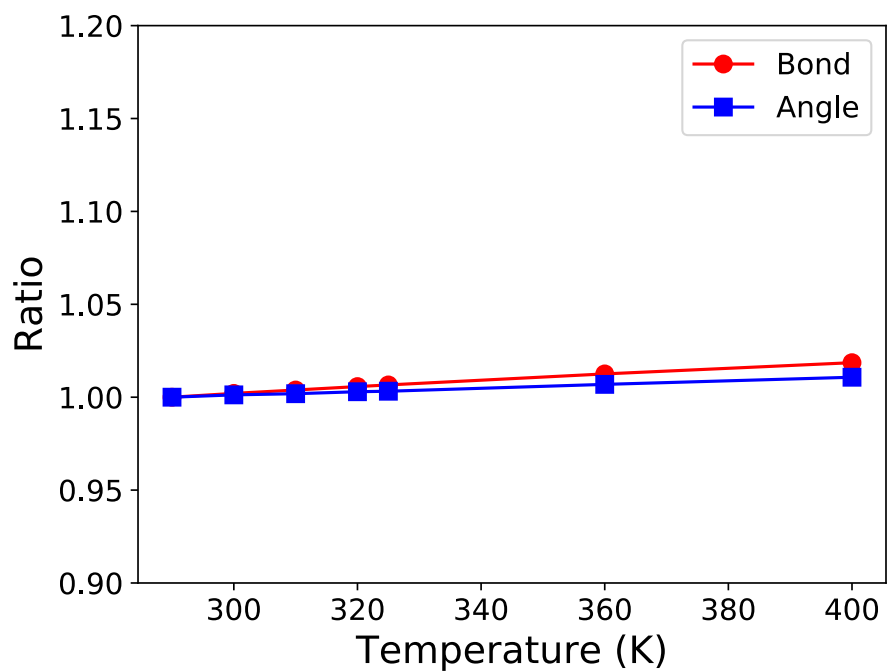


Figure S2: The ratio of the averaged bond length,  $l_0$  and averaged the bond angle,  $\psi$  at different temperatures to the values at 290 K. Each data point was extracted from the last 3  $\mu\text{s}$  fragment of a 5  $\mu\text{s}$  MD trajectory of a single FUS protein.

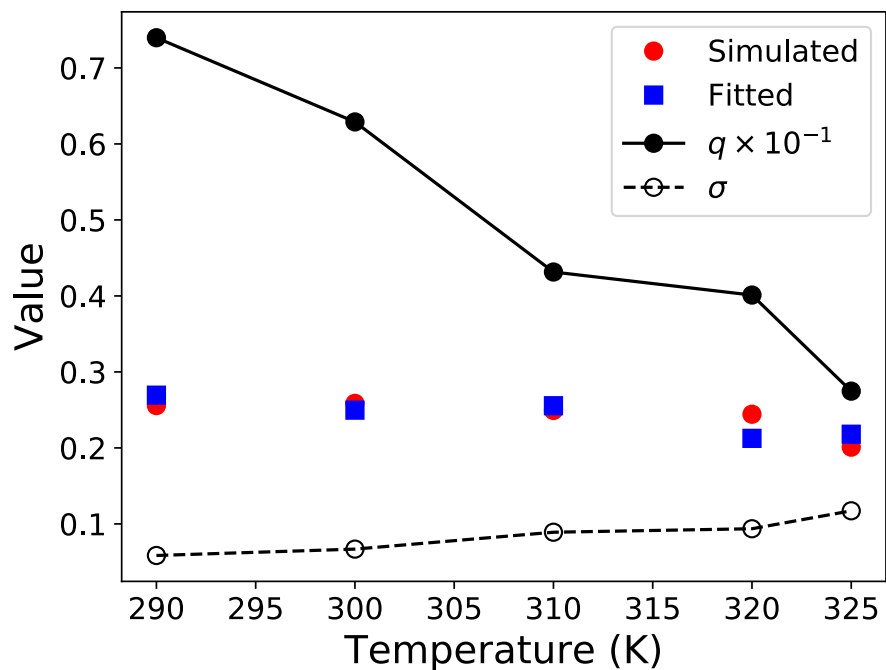
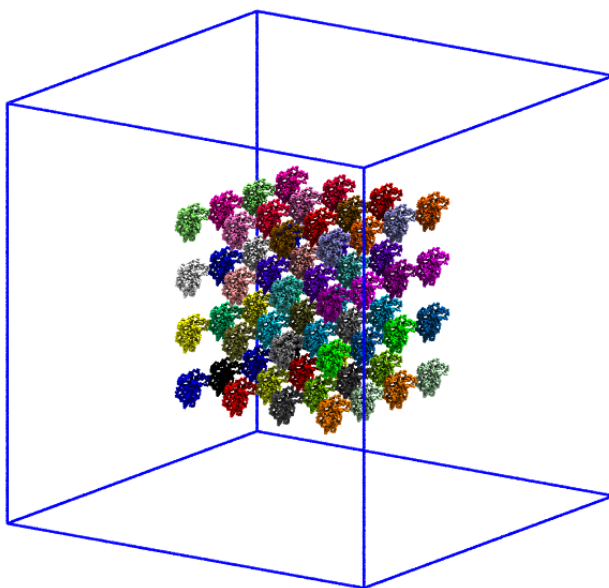
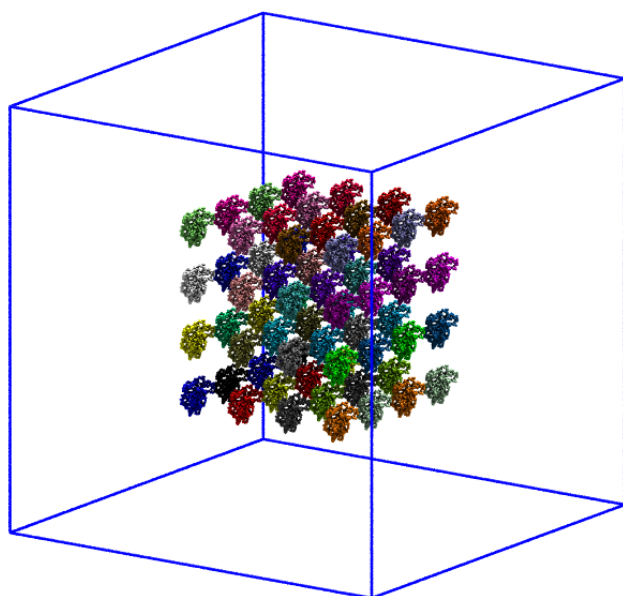


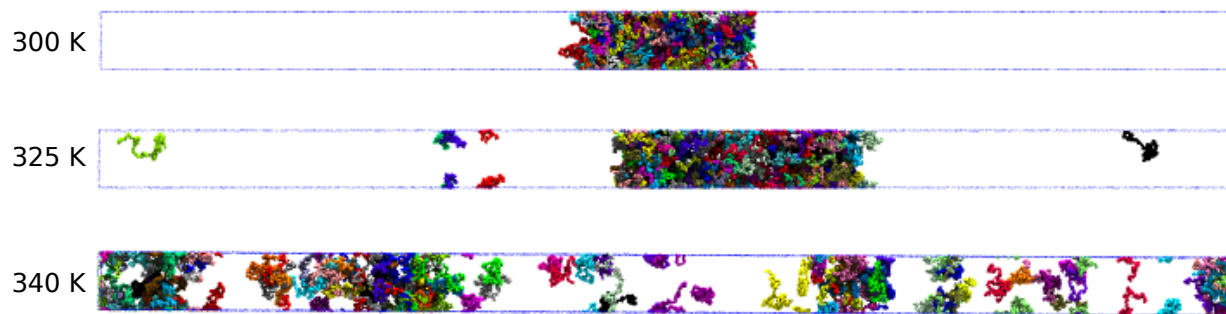
Figure S3: Determination of virial coefficient parameters. Open and solid symbols show the values of  $\sigma$  and  $q$ , respectively, obtained directly from MD simulations of individual FUS proteins at specified temperature. Red circles plot the right-hand side of Eq. (5) evaluated using the  $\sigma$  and  $q$  obtained from the MD simulations. Blue squares show the values of the left-hand side of Eq. (5) evaluated using the best fit values for  $B$  and  $K$ . The residue of the fitting, *i.e.*, the difference between the right-hand side and the left-hand side of Eq. (5), is 0.04, which corresponds to a relative error of  $\sim 7\%$ .



Movie 1: Animation illustrating a CG MD simulation of 64 WT FUS proteins at 292 K, forming a liquid-like droplet after  $\sim 1\mu\text{s}$ .



Movie 2: Animation illustrating a CG MD simulation of 64 (R→ K) FUS mutants at 292 K, remaining disperse state after  $\sim 1\mu\text{s}$ .



Movie 3: Animation illustrating three CG MD simulations of a slab FUS system performed at different temperatures. Each system contains 125 FUS proteins.