Supporting Information

Capturing the Impact of Protein Unfolding on the Dynamic Assembly of Protein Networks

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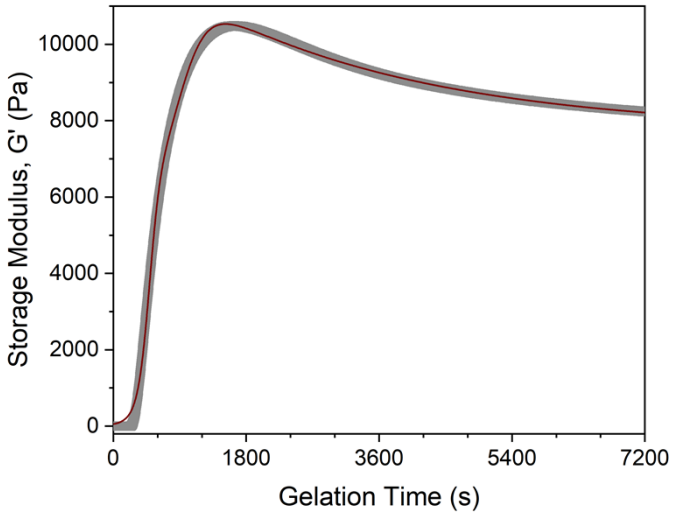

Figure S1: Dual sigmoid formation with post formation relaxation effectively fits rheology gelation curves of force labile BSA hydrogels. Example fitted gelation curve of force-labile BSA hydrogels (final concentrations: 100 mg/mL BSA, 50 mM NaPS, 100 µM $Ru(BiPy)_3$, 3mM DTT). Where the grey squares are the rheology data of a single BSA hydrogel repeat and the dark red line shows equation 1 fitted to the data.

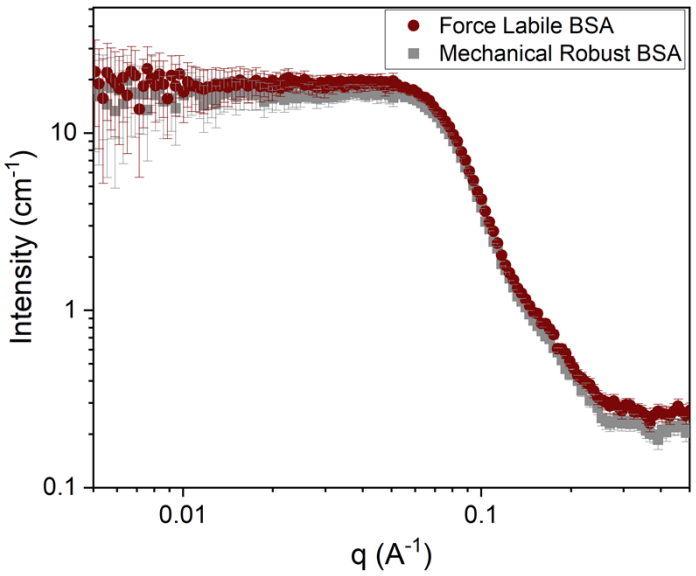

Figure S2: The addition of dithiothreitol (DTT) to BSA at 100mg/ml does not lead to a significant change in monomer shape detectable via SAXS. SAXS curves of BSA pre-gel solutions (final concentrations: 100 mg/mL BSA, 50 mM NaPS, 100 µM $Ru(BiPy)_3$), in the presence (force labile) and absence (mechanically robust) of 3mM DTT.

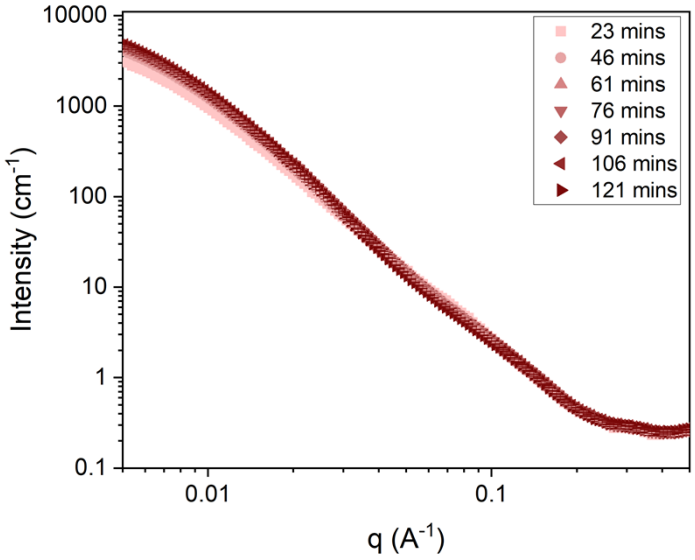

Figure S3: Time-resolved SAXS tracks the full gelation of force-labile over 2 hours. Additional SAXS curves of force-labile BSA (final concentrations: 100 mg/mL BSA, 50 mM NaPS, 100 µM $Ru(BiPy)_3$, 3mM DTT) as a function of gelation time, for gelation times from 23 mins up to 121 mins, in 15 mins intervals

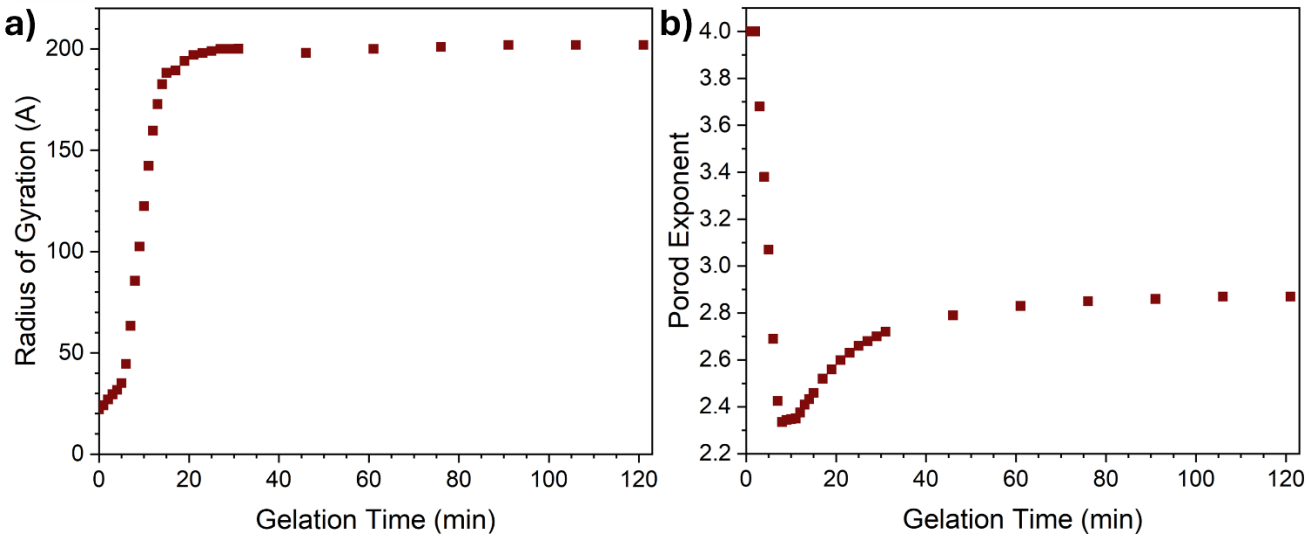

Figure S4: Model independent SAXS analysis, of force labile BSA hydrogels, shows similar temporal trends observed in the extracted parameters from fractal model analysis. The model-independent fit parameters, radius of gyration, R_g (**a)**) and Porod exponent (**b)**), extracted from the SAXS curves in figure 4a as a function of gelation time for force labile BSA protein hydrogel.

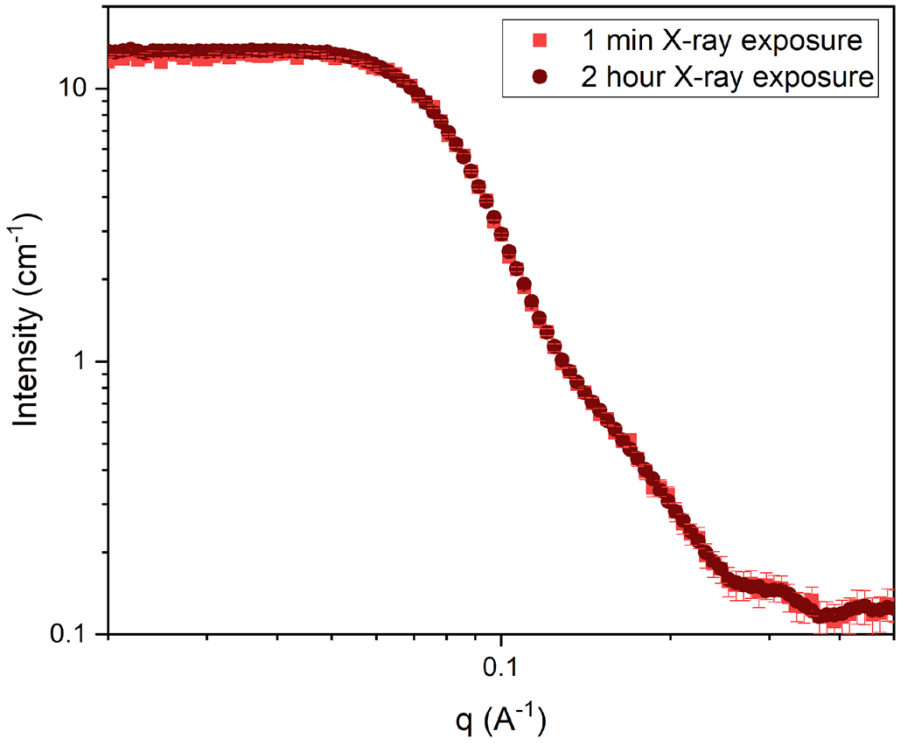

Figure S5: The exposure to x-rays during the experiment are not sufficient to cause radiation damage or significant crosslinking which leads to structural changes. SAXS curves of BSA pre-gel solutions (final concentrations: 100 mg/mL BSA, 50 mM NaPS, 100 µM $Ru(BiPy)_3$) exposed to 1min of X-rays (light red) and 2 hours X-rays (dark red).