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Failure of the Zimm model: Thermal unfolding of Ribonuclease A

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Disordered regions as found in intrinsically disordered proteins (IDP) or during protein folding define response time to stimuli and protein folding times. Neutron Spinecho Spectroscopy is a powerful tool to access directly collective motions of the unfolded chain to observe conformational relaxations. During thermal unfolding of native Ribonuclease A we examine structure and dynamics of the disordered state within a two-state transition model using polymer models including internal friction. The presence of 4 disulfide bonds alters the disordered configuration to a more compact configuration compared to a Gaussian chain that is defined by the additional links. The dynamics of the disordered chain is described by ZIMM dynamics with internal friction between neighboring amino acids. The mode structure is not changed by the additional links, but relaxation times are dominated by mode independent internal friction. Internal friction relaxation times show an Arrhenius like behavior. The dominating internal friction suppresses the characteristics of the ZIMM dynamics and suggest that the characteristic motions correspond to elastic overdamped modes similar to motions observed for folded proteins.

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