Abstract Submitted
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Coupled folding and binding kinetics in the intrinsically disordered peptide IA_3[1] RANJANI NARAYANAN, Department of Physics, University of Florida, OMJOY GANESH, ARTHUR EDISON, Department of Biochemistry and Molecular Biology, University of Florida, STEPHEN HAGEN, Department of Physics, University of Florida — IA_3 is an intrinsically disordered 68 residue peptide and is an endogenous inhibitor of yeast proteinase A (YPrA). X-ray crystallography of the IA_3·YPrA complex [Li et al, Nat. Struct. Biol. (7), 113-117 (2000)] indicates that the N-terminus of IA_3 adopts an alpha-helical fold when it is bound to the YPrA active site. We have used equilibrium circular dichroism and multi-wavelength, nanosecond time-resolved laser temperature-jump spectroscopy to study the coupled folding and binding interaction of IA_3 with YPrA. Our initial measurements of the rate of helix formation in free IA_3 indicate mono-exponential folding kinetics that extrapolate to $k_F \sim 10^5$/s at room temperature in aqueous solutions. By comparing this rate to the kinetics we observe for IA_3 interacting with YPrA, we can assess possible mechanisms for the coupled folding and binding of IA_3.

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