Title:	The Dynamism of Intrinsically Disordered Proteins: Binding-Induced Folding, Amyloid Formation, and Phase Separation
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Abstract:	Intrinsically disordered proteins (IDPs) or natively unfolded proteins do not undergo autonomous folding into a well-defined 3-D structure and challenge the conventional structure–function paradigm. They are involved in a multitude of critical physiological functions by adopting various structural states via order-to-disorder transitions or by maintaining their disordered characteristics in functional complexes. In recent times, there has been a burgeoning interest in the investigation of intriguing behavior of IDPs using highly multidisciplinary and complementary approaches due to the pivotal role of this unique class of protein chameleons in physiology and disease. Over the past decade or so, our laboratory has been actively investigating the unique physicochemical properties of this class of highly dynamic, flexible, rapidly interconverting proteins. We have utilized a diverse array of existing and emerging tools involving steady-state and time-resolved fluorescence, Raman spectroscopy, circular dichroism, light scattering, fluorescence microscopy, and atomic force microscopy coupled with site-directed mutagenesis and other biochemical and biophysical tools to study a variety of interesting and important aspects of IDPs. In this Feature Article, I describe our work on the conformational characteristics, solvation dynamics, binding-induced folding, amyloid formation, and liquid–liquid phase separation of a number of amyloidogenic IDPs. A series of these studies described here captures the role of conformational plasticity and dynamics in directing binding, folding, assembly, aggregation, and phase transitions implicated in physiology and pathology.
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