Determining the Structure of a Protein When it Doesn't Have One

George N. Phillips Jr.

Rice University, Houston, TX, USA, 77005, georgep@rice.edu

Whether macromolecular structures are determined X-ray crystallography, cryo-EM or NMR, they require averaging over many copies of the protein. Compelling narratives about how these structures map to biological function is one of the triumphs of molecular biology. However, these individual molecules are all different at some level of detail and the extent of variability depends on the particular system. On one pole, we have highly ordered proteins, whose average structure can be determined with sub-atomic precision as confirmed using multiple methods. The other pole would be a protein with an extremely broad distribution of states, sometimes referred to as intrinsically disordered. And then there is everything in between. The talk will review this range of order through the lens of energy landscapes and the Boltzmann distribution of states and methods we use to study order and disorder.