COLLECTIVE MORPHOLOGIES OF THE ASSEMBLIES OF THE INTRINSICALLY DISORDERED PROTEINS OF THE NUCLEAR PORE COMPLEX

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Nuclear Pore Complex (NPC) is a key cellular transporter that controls nucleocytoplasmic transport in eukaryotic cells, and is involved in large number of regulatory processes. It is a remarkable device that combines high selectivity with robustness and speed. Its unique transport mechanism is still not fully understood. Recently, the Nuclear Pore Complex transport mechanism inspired creation of artificial selective nano-channels that mimic its structure and function for nano-technology applications.

The centerpiece of NPC transport is the assembly of intrinsically disordered polypeptides, known as FG nucleoporins, lining its passageway, which serve as a template for binding of the cargo-carrying transport proteins. Their conformations and collective dynamics during transport are difficult to assess in vivo. In vitro investigations provide partially conflicting results, lending support to different models of transport, which invoke various conformational transitions of the FG nucleoporins induced by the cargo-carrying transport proteins.

I will present a theoretical and computational framework that provides rigorous biophysical underpinnings for the mechanism of transport through the Nuclear Pore Complex, and its detailed comparison with experimental results It shows that the spatial organization of FG nucleoporin assemblies with the transport proteins can be understood within a first principles biophysical model with a minimal number of key physical variables, such as the average protein interaction strengths and spatial densities. These results reconcile some of the outstanding controversies and suggest strategies for creation of artificial selective nanomaterials.