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The protein dance: when moves matter.

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Pavillon Charles-Eugène Marchand, salle Hydro-Québec (1210)

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Abstract:

Proteins are dynamic systems and our understanding of the interplay between protein motions and function is still nascent. By discussing 3 different protein systems, I will expose how protein motions are vast, both in their amplitude and by the speed (or timescales) at which they occur. I will first discuss how motions are relevant to enzyme function and an important consideration for protein engineering applications in a model system constituted by the beta-lactamases TEM-1, PSE-4, and evolutionary intermediates. I will next discuss how protein motions can be exploited to design antifungal drugs using the immunosuppressive agent FK506 as a scaffold to increase its selectivity for the fungal target and reduce its immunosuppressive potency. Finally, I will illustrate how large domain movements are required for receptor and antibody binding to the SARS-CoV-2 spike (S) protein, and how the structure and antigenicity of the S protein have been altered by the mutations that have arisen in the variants we have seen so far. Together, these studies pave the way for investigations exploring the role of conformational dynamics in protein-protein interactions.

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