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Protein Dynamics

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Proteins combine properties of solids, liquids, and glasses. Schrödinger anticipated the main features of biomolecules long ago by stating that they had to be solid-like, but able to assume many different conformations. Indeed proteins can assume a gigantic number of conformational substates with the same primary sequence but different conformations. The different substates are described as craters in a very-high-dimensional energy landscape. The energy landscape is organized in a hierarchy of tiers, craters within craters within craters. Protein motions are pictured as transition between substates - jumps from crater to crater. Initially we assumed that these jumps were controlled by internal barriers between substates, but experiments have shown that nature selected a different approach. Proteins are surrounded by one to two layers of water and are embedded in a bulk solvent. Structural motions of the protein are controlled by the alpha fluctuations in the solvent surrounding the protein. Some internal motions most likely involving side chains are controlled electrostatically by beta fluctuations in the hydration shell. The dynamics of proteins is consequently dominated by the environment (H. Frauenfelder et al. PNAS 106, 5129 (2009). One can speculate that this organization permits exchange of information among biomolecules. The energy landscape is not just organized into two tiers, alpha and beta, but cryogenic experiments have revealed more tiers and protein more properties similar to that of glasses. While proteins function at ambient temperatures, cryogenic studies are necessary to understand the physics relevant for biology.