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Editorial

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Recent Advances in Biophysical Chemistry

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Editorial

A branch of the multidisciplinary study of biophysics is biophysical chemistry. The discipline is dedicated to the quantitative study of the use of experimental, theoretical and analytical methods in biological systems. Biophysical chemistry focuses on the molecular level, in contrast to a physics-centered approach to biophysics that addresses forces and scaling rules, or a biology-centered view that addresses the phenotype of the studied system. Biophysical chemistry is aimed at the processing and analysis of quantitative data to provide predictive physical models explaining biological phenomena occurring at the molecular level, unlike biochemistry, which mostly focuses on chemical reactions driving biological systems. The goal of biophysical chemistry is to bridge physical and biological disciplines: physical forces and interactions in biological systems are mediated by molecules, which ultimately decide the phenotype. In unravelling several basic molecular structures that control biological processes, the experimental and theoretical methods of biophysical chemistry have demonstrated considerable progress. Some of the relevant contemporary areas and issues currently studied in the field of biophysical chemistry are highlighted here. Since molecules are at the heart of this research the focus of our discussion is on three groups of molecules that are important to all living organisms: proteins, nucleic acids, and lipids.

Proteins are molecular machines that enable life to mediate or perform practically all biological processes. Proteins are polymers made up of amino acids, which perform a wide range of functions necessary for the cell to function properly. These include catalysis, signaling, control of transcription, transport, and proteolysis. In determining the secondary structure of the protein (local structural elements) and the three-dimensional structure of the protein (tertiary structure, the overall fold of the protein), the amino acid sequence of the protein (often referred to as the primary structure) along with the composition of the surrounding solution are critical. The protein structure is difficult to predict, despite its apparent deterministic existence, due to the insurmountable number of possible amino acid chain configurations. A single well-defined structure in an ocean of other possible structures is the native, or functioning, state. In the Levinthal paradox, decades earlier, the impossibility of spontaneously hitting the native state from an extended polymer in a finite time was pointed out.

Proteins need to interact with other biomolecules, including other proteins, nucleic acids, peptides, sugars and small molecules, in order to function correctly. Indeed in the cellular sense, where all the other binding partners and co-factors are present, protein function is also better understood. Methods such as fluorescence, circular dichroism, NMR spectroscopy, stopped-flow kinetics, micro calorimetry, and surface-Plasmon resonance, allow accurate activity quantification, binding affinity, stoichiometry and thermodynamics, and protein interaction kinetics. Although most of these experimental methods are focused on average protein measurements, other techniques research protein interactions. The behaviour of single molecules was revealed by single-molecule methods including optical trapping, fluorescence energy transfer and force microscopy based measurements. Importantly, these behaviours not only demonstrate the average that is often seen by ensemble measurements, but also expose the dynamics that occur away from balance, single molecules in excited states that lead to biological function dynamics.

In determining the structure of proteins and mediating their interactions, the cellular environment plays an important role, as both processes are regulated by the same non-covalent interactions. Details on the molecular structure of the protein may be elucidated by disrupting the solution (e.g. increasing osmotic stress, levels of macromolecular crowding, temperature, or composition of the solute). Conformational changes in the folded state of the protein ('Mis-folding') are often caused by environmental factors or protein sequence mutations and can trigger pathogenic protein aggregation or malfunction that eventually leads to disease. In pathologies such as Alzheimer's and Parkinson's diseases and cancer, studies of protein folding and interactions have included misfolded proteins. For these sequences, principles from polymer physics and amino acid composition research have revealed complex transient structure and interaction capabilities.

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