

Structure and Function of Protein

Smita Mohanty*

Department of Chemistry and Biochemistry, Auburn University, Auburn, AL, USA

A host of micro and macromolecules are responsible for the proper functioning of a living cell/s. Among them, proteins are the most important and versatile macromolecules and carry out essentially all biological functions in the cells of living systems. Proteins present in the nasal fluid of vertebrates or in the sensillum lymph of insect antenna can smell, proteins present in mouth can taste, and proteins present in the eye lens can see. Proteins generate energy, transport and store different molecules, and in the immune system protect organism against diseases. Proteins provide mechanical support and generate movement, transmit nerve impulses, and control growth and differentiation in the living system. These are only a few of the wide variety of functions carried out by proteins which define the very existence of life. Understanding the structures, functions and interactions of proteins is critical for the advancement in the diagnosis and treatment of many diseases and disorders. Identification of particular structural features of a protein and correlating it to specific functions can provide insight into the mechanistic relationships, help to create working models of the complex biological systems and ultimately pave the way for the design of drug candidates through the discovery processes.

This special issue of the journal Biochemistry and Physiology will focus on structure and function of proteins studied using biochemical, biophysical and/or computational tools. Through the use of biochemical tools, Wower and colleagues provide insight into the role of protein S1 in the binding of tRNA and stalled ribosome. Biochemical tools such as manipulation of a gene along with biophysical techniques especially solution-state NMR provides fine details of the role of a single amino acid residue or a group of residues that form a motif or a domain or a module. In this special issue the articles by Mcfeeters and colleagues and Xue and colleagues illustrate the use of biochemical and biophysical tools for the investigation of protein structure and function providing both mechanistic insight and a framework for the designing of anti-HIV inhibitors.

Protein dynamics is intimately associated with protein structure and function since these biomolecules are not static. Proteins are dynamic molecules exhibiting either subtle or dramatic movements while in action. These motions are critical for the proper functioning of proteins. The mini-review article by Petit brings out the importance of protein side chain motion and its effect on conformational entropy, allostery and function.

In silico calculation is a very important tool for understanding the structural and functional relationship of proteins. Such computational methods have been increasingly used to understand the structural elements responsible for proper functioning of proteins. The effect of Leigh Syndrome mutations on the human mitochondrial complex-I Q described by Jaokar and colleagues and the interaction studies of lectin, rCAL (*Cicer arietinum*) to hemin and spermine by Wakankar and colleagues have been performed through computational methods.

Smita Mohanty was awarded a MS and a PhD in Chemistry from University of Delhi, India. She performed her postdoctoral studies in structural biology at the University of Washington, Seattle and also in New York. In 1999, she joined the faculty of State University of New York at Stony Brook (Stony Brook University). In 2005, she joined the faculty of Auburn University. Her research interests encompass molecular biology, protein chemistry, structural biology, biophysics and computational chemistry. She takes a multidisciplinary approach to characterizing the structure, and function of both globular and membrane associated proteins involved in various diseases and disorders with the overall objective of understanding the molecular basis of function with a goal for exploiting these as new therapeutic targets to address the underlying diseases.

*Corresponding author: Smita Mohanty, Department of Chemistry and Biochemistry, Auburn University, Auburn, AL 36849, USA, E-mail: mohansm@auburn.edu

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