



## Computational Studies in Analysis and Prediction of Protein Properties

Guest Editor:

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### Message from the Guest Editor

Proteins are macromolecules essential for biological life. They play many critical roles in countless biological processes, for instance, they are involved in DNA replication, catalysis and regulation of biochemical reactions and networks, and so on. Protein function and properties can be understood in terms of its three-dimensional structure. Establishing a protein structure–function relationship is crucial for understanding its biological function. Experimental techniques (e.g., X-Ray, NMR, SAXS, and Cryo-EM) have been employed for protein structure prediction in solution and crystal state and to understand the mechanisms defining the function of proteins; however, the determination of the structure and dynamics of large protein complexes and other biomolecular assemblies remains a major challenge in structural biology and biochemistry. Computational structural biology has made enormous progress over the last three decades. These methods include molecular modeling and refinement of 3D structures, de novo design of proteins, protein folding and stability, macromolecular function and protein design and prediction of macromolecular interactions and so on.





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## Editor-in-Chief

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## Message from the Editor-in-Chief

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