



Computational Intelligence in Structure and Function Prediction and Modeling of Proteins—2nd Edition

Guest Editors:

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submissions:

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Message from the Guest Editors

Dear Colleagues,

Exploring the functions and structures of proteins is paramount for understanding the molecular mechanisms of life. The analyses and predictions of protein functional residues contribute to the research of protein function. The traditional approaches used to extract information regarding protein structures and functions all rely on biophysical or biochemical-associated technologies. These technologies need expensive experimental instruments, complex experimental procedures, and elaborate human resources. They benefit from the development of bioinformatics, which uses intelligent computing methods to accurately predict protein structure information and functional residues.

This Special Issue of Biomolecules is dedicated to computational methods and analyses focusing on the identification, elucidation, and analysis of protein function-related factors. We welcome both original articles and surveys that cover state-of-the-art advances in this rapidly developing area. We also encourage the submission of experimental studies that are coupled with computational analysis.

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Message from the Editorial Board

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