



Application of Computational Studies for Elucidation of Protein Structure and Function

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Message from the Guest Editor

Dear Colleagues,

Nowadays, computational techniques are widely applied to various problems including biological systems. In particular, many computer simulation techniques are applied to protein dynamics and folding. Bioinformatics techniques are also applied to extract various information from amino acid sequences and evolutionary results. Artificial intelligence techniques have been developed in the field of protein structure prediction. Thus, we are planning this Special Issue regarding new applications of various computational techniques to solve problems related to protein structures and functions. It should be noted that pure theoretical works are important to solve protein problems. We are also interested in very complicated protein systems and drug discovery.

Dr. Takeshi Kikuchi
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Message from the Editor-in-Chief

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