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Computational Analysis for Protein Structure and Interaction

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Message from the Guest Editor

Dear Colleagues,

Protein structure analysis is a hot topic and key issue in organic chemistry and molecular biology research. Several essential protein molecules were rebuilt with Cryo-EM (Cryo-Electron Microscopy) and their structures were published in *Nature* and *Science*. Computational structure analysis and prediction is a key process for the 3D structure reconstruction. Machine learning techniques have been employed for protein secondary and tertiary structure prediction for a long time, and it seemed to have reached a bottleneck. However, the development of the Cryo-EM technique brings new challenges and requirements to computer science. Additionally, deep learning in machine learning also seems to be powerful. Therefore, there is considerable and increasing interest in developing computational methods for protein structure analysis and prediction. Moreover, new techniques on structure could also facilitate protein–protein interaction research.

Prof. Dr. Quan Zou
Guest Editor

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Message from the Editor-in-Chief

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