Special Issue

Recent Research of Protein Structure Prediction and Design

Message from the Guest Editor

Proteins support the majority of biological functions. Having access to partial or complete 3D structural information of proteins is therefore of major interest from basic research to pharmacological developments. Recent research in the field of protein structure prediction and design has focused on developing more accurate and efficient computational methods for predicting protein structures, i.e., proposing structural models. This Special Issue highlights recent breakthroughs in protein structure prediction and design. Advances in deep learning have enhanced these breakthroughs. Key achievements include AlphaFold, ESMFold and RoseTTAfold, which have significantly increased the number of proteins available for prediction, thereby expanding the structural proteome. This Special Issue is supervised by Dr Alexandre G. de Brevern, assisted by our 's assistant editor Dr. Joseph Rebehmed (Department of Computer Science and Mathematics, Lebanese American University).

Guest Editor

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Message from the Editor-in-Chief

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