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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Deadline for manuscript submissions

20 September 2025

International Journal of Molecular Sciences

an Open Access Journal by MDPI

Impact Factor 4.9
CiteScore 9.0
Indexed in PubMed

mdpi.com/si/216206

International Journal of Molecular Sciences
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The International Journal of Molecular Sciences (*IJMS*, ISSN 1422-0067) is an open access journal, which was established in 2000. The journal aims to provide a forum for scholarly research on a range of topics, including biochemistry, molecular and cell biology, molecular biophysics, molecular medicine, and all aspects of molecular research in chemistry. *IJMS* publishes both original research and review articles, and regularly publishes special issues to highlight advances at the cutting edge of research. We invite you to read recent articles published in *IJMS* and consider publishing your next paper with us.

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