

Special Issue

How Are Predicted Protein Structures Advancing the Development of New Drugs?

Message from the Guest Editor

Structural drug development has relied on having access to the three-dimensional structure of the protein or nucleic acid targets. This approach has been effective at enabling computational screening of molecular libraries containing as many as a billion small molecules and prioritizing those that can be utilized in experimental validation. However, given the available DNA and amino acid sequence data sets, the number of known high-resolution target structures is limited. There have been significant advances in the ability to predict the three-dimensional structure of proteins from their amino acid sequence. This Special Issue is soliciting articles that address:

- How accurate is structure-based drug design in producing drugs that go on to be approved for clinical use?
- Are there new generalizable approaches/methods that are proving to be more effective?
- What is the effectiveness of using the newly predicted protein structures, i.e., are they accurate enough to supply the critically needed targets and lead to new drugs?

Guest Editor

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Message from the Editor-in-Chief

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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