Special Issue

Computational Biology: Protein Structure Prediction

Message from the Guest Editor

This Special Issue aims to gather cutting-edge research that explores novel computational methods and algorithms to predict protein structures more accurately. Our goal is to highlight advancements that can enhance our understanding of protein folding, stability, and interactions, which are crucial for developing targeted therapies and understanding cellular functions. This Special Issue aims to advance the current limitations of protein structure prediction by incorporating contributions from a wide range of fields, including machine learning, molecular dynamics, and quantum mechanics. The knowledge gained from these studies will enrich academic understanding while also offering practical applications in fields such as drug discovery, enzyme technology, and beyond.

Guest Editor

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Biomolecules is a multidisciplinary open-access journal that reports on all aspects of research related to biogenic substances, from small molecules to complex polymers. We invite manuscripts of high scientific quality that pertain to the diverse aspects relevant to organic molecules, irrespective of the biological question or methodology. We aim for a competent, fair peer review and rapid publication. Please look at some of the exciting work that has been published in *Biomolecules* so far. We would be delighted to welcome you as one of our authors.

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