# Special Issue

## New Insight into Protein Bioinformatics

### Message from the Guest Editor

This special issue highlights recent advancements in protein bioinformatics and covers various computational tasks, from phylogeny to structural predictions. In addition, we would like to welcome contributions from the peptide structure and function prediction field. One of the side goals of this special issue is also to combat the reproducibility crisis that deeply permeates our field. New initiatives (e.g., Elofsson et al., 2019 or Walsh et al., 2021) clarify prerequisites for the reproducibility of bioinformatics tools. To help enforce this standard, all authors should refer their submitted manuscripts to a set of reproducibility guidelines appropriate to their field and point out how their software or analysis fulfills them. Elofsson, A. et al. Ten simple rules on how to create open access and reproducible molecular simulations of biological systems. PLOS Computational Biology 15, e1006649 (2019). Walsh, I. et al. DOME: recommendations for supervised machine learning validation in biology. Nat Methods 18, 1122–1127 (2021).

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### Guest Editor

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### Deadline for manuscript submissions

closed (16 April 2024)

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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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