

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).

Guest Editor

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