Special Issue

Algorithms and Tools in Computational Proteomics

Message from the Guest Editor

Computational proteomics is focused on statistical methods, algorithms, databases and other computational approaches to process, analyze and interpret proteomic data. The high-throughput nature of proteomic data, as well as the specific nuances of the data introduced by measurement via mass spectrometry, generate unique challenges that require novel methods for data handling, data processing, statistical analyses, as well as modeling and interpretation of the results. This Special Issue focuses on state-of-the-art approaches to handling proteomics data from the initial steps of data generation through the final steps of visualization and interpretation, as well as the essential functions of quality control and statistics that happen in-between.

Guest Editor

Dr. Bobbie-Jo Webb-Robertson
Pacific Northwest National Laboratory

Deadline for manuscript submissions

closed (30 November 2018)

MDPI

About the Journal

Message from the Editor-in-Chief

Editor-in-Chief

Prof. Dr. Massimo Negrini
Department of Morphology, Surgery and Experimental Medicine,
University of Ferrara, Ferrara, Italy

Author Benefits

Rapid Publication:
first decisions in 19 days; acceptance to publication in 8 days (median values for MDPI journals in the second half of 2025).

Recognition of Reviewers:
reviewers who provide timely, thorough peer-review reports receive vouchers entitling them to a discount on the APC of their next publication in any MDPI journal, in appreciation of the work done.

MDPI