

Special Issue

Feature Papers in Protein and Proteomics

Message from the Guest Editors

With the application of deep learning in protein and proteomics studies, the 3D structure of protein can be accurately predicted based only on sequence information, allowing biomarkers for various diseases to be discovered via proteomics. Proteomics is focused on proteins, which are directly responsible for the biological or pathological changes, in contrast to genomic, epigenetic or transcriptomic data. Changes in proteins are closest to determining phenotypes. To investigate the molecular mechanisms of phenotypes, we must incorporate protein and proteomics perspectives. We encourage submissions from researchers in biology, medicine, computer science and mathematics.

Potential topics of interest include but are not limited to: Protein Structure Prediction/ Protein Function Prediction Protein–Protein Interaction Prediction Protein Network Analysis Protein–Phenotype/Disease Association Mass Spectrometry Data Analysis Software Development Proteomics Biomarker Discovery Post-Translational Modification Study Multi-omics Integrative Analysis/ Proteogenomics Study Single Cell Proteomics/ Spatial Proteomics

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Life (ISSN 2075-1729) is an international, peer-reviewed open access journal that publishes scientific studies related to fundamental themes in life sciences. Some papers are published individually, while others are submitted for inclusion in special issues with guest editors. You are invited to contribute a research article, essay, or a review to be considered for publication.

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