Feature Papers in Protein and Proteomics

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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

Special Issue

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Message from the Editor-in-Chief

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