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Clinical Proteomics: Fourth Edition

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Deadline for manuscript submissions:
closed (30 May 2025)

Message from the Guest Editor

Computational and technological advances have ushered in a new era in the field of proteomics, leading to the analysis of large numbers of samples in record time. There has also been a remarkable shift in protein quantification approaches, led primarily by the development of label-free quantification methods using either DDA- or DIA-based approaches. This is further complemented by the now-popular use of chemical labeling techniques, such as TMT, and/or targeted quantification techniques, such as MRM/SRM and, most importantly, PRM. These developments offer unprecedented opportunities to discover novel biomarker signatures and to systematically study disease mechanisms. For this Special Issue, we look forward to receiving original clinical proteomics studies and review articles focused on (1) the underlying mechanisms of disease progression using human tissues or representative cell lines, (2) biomarker discovery studies using quantitative proteomics, and (3) mass spectrometry-based biomarker validation studies, as well as (4) the use of proteomics to discover modes of action of new and existing drugs.

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Editors-in-Chief

Message from the Editorial Board

Proteomes is an international, peer-reviewed, open access journal that was first published in 2013 by MDPI. *Proteomes* addresses all aspects of proteome analysis with a special focus on the quantification and characterisation of the proteome at the level of proteoforms. We encourage submission of articles that accurately quantify and characterise the proteome, as well as new and updated methods and technologies that enhance the accurate quantification and characterisation of the proteome and thereby provide evidence directly facilitating the understanding of biological mechanisms. Articles emphasising a multi/ transdisciplinary approach combining different omics techniques are welcomed.

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