

Proteomic Biomarkers in Human Diseases

Guest Editors:

Prof. Dr. Stephen Pennington

Department of Pathology,
University College Dublin, Dublin,
Ireland

Prof. Dr. Jennifer Van Eyk

Advanced Clinical Biosystems
Research Institute, Cedars-Sinai
Medical Center, Los Angeles, CA,
USA

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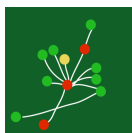
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Message from the Guest Editors

The latest methods for protein identification and quantification offer the opportunity to systematically study disease mechanisms as well as identify biomarkers and measure markers for the diagnosis and prognosis of disease and those that might predict or monitor a patient's response to treatment. Notably, advances in mass spectrometry instrumentation and other proteomic methods are leading to advances in the field of clinical proteomics towards the multiplexed analysis of large numbers of patient samples.

This Special Issue will cover applications of various biomarker panels for cancer, cardiovascular, and neurological diseases, as well as the role of proteomics in other pathological processes. We welcome manuscripts describing all aspects of the current challenges in applying proteomic technologies to the development of disease biomarkers for clinical utility, i.e., the need for analytical rigor, reproducibility between laboratories, standardization of sample collection, storage and processing, proteomics workflows, data analysis and reporting.





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Editors-in-Chief

Dr. Matthew P. Padula

School of Life Sciences and
Proteomics Core Facility, Faculty
of Science, The University of
Technology Sydney, Ultimo 2007,
Australia

Prof. Dr. Jens R. Coorsen

1. Department of Biological
Sciences, Faculty of Mathematics
and Science, Brock University, St.
Catharines, ON L2S 3A1, Canada
2. Institute for Globally
Distributed Open Research and
Education (IGDORE), Catharines,
ON L2S 3A1, Canada

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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Proteomes Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland

Tel: +41 61 683 77 34
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