



Mass Spectrometric Proteomics II

Guest Editors:

Prof. Dr. Pierluigi Luigi Mauri

Istituto di Tecnologie
Biomediche, Consiglio Nazionale
delle Ricerche (ITB-CNR), 20090
Segrate (MI), Italy

**Prof. Dr. Martina Marchetti-
Deschmann**

Institute of Chemical
Technologies and Analytics, TU
Wien, Wien, Austria

Dr. Diana Canetti

Centre for Amyloidosis & Acute
Phase Proteins, Division of
Medicine, University College
London, Rowland Hill Street,
London NW3 2PF, UK

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Message from the Guest Editors

The investigation of genome, including transcriptome, has been widely applied and has permitted us to improve our understanding of it; however, at the same time, it has increased the demand to characterize other -omes sectors.

In addition, the improvements of both proteomics applications and related hyphenated techniques, have permitted us to develop the so-called mass spectrometry-based proteomics. Today, the MS-based approach has become the gold standard for proteomics study.

This Special Issue on “Mass Spectrometric Proteomics” will cover several topics, including but not limited to:

- Proteome analysis;
- Study of protein–protein interactions;
- Clinical proteomics;
- Proteomics for biomarker discovery;
- Proteomics for amyloid investigations;
- Quantitative proteomics by label-free or label-based approaches;
- Mass spectrometry analysis for the identification and the characterization of post-translational modifications (PTMs);
- Study of protein structure by mass spectrometry;
- MS-based proteomics imaging;
- Development of new analytical MS-based methods.

We warmly invite our colleagues to submit their original contributions to this Special Issue.





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Editor-in-Chief

Prof. Dr. Thomas J. Schmidt

Institute of Pharmaceutical
Biology and Phytochemistry,
University of Münster,
Corrensstrasse 48, D-48149
Münster, Germany

Message from the Editor-in-Chief

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Molecules Editorial Office
MDPI, St. Alban-Anlage 66
4052 Basel, Switzerland

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