Special Issue

The Contribution of Proteomics to Chromatin Biology and Epigenetic Research

Message from the Guest Editors

Epigenetic features, including histones, which allow DNA wrapping and compaction into chromatin, exist in several variants and are modified by a number of reversible post-translational modifications. Histone modifications and variants contribute to the regulation of gene expression by affecting chromatin compaction and by recruiting downstream effectors, which translate the epigenetic information into biological outcomes. Aberrations in this complex machinery can lead to diseased states, and can be targeted to restore physiological conditions.

Thanks to its unbiased nature, comprehensiveness, and quantitative accuracy, mass spectrometry (MS)-based proteomics have emerged as a versatile and powerful tool to study epigenetic mechanisms, from histone post-translational modifications and variants, to chromatin-associated factors. In this Special Issue, we seek contributions (original research articles and methods) that exploit MS-based proteomics technologies to investigate epigenetic mechanisms. Perspectives and reviews on this subject are also welcome.

Guest Editors

Prof. Dr. Tiziana Bonaldi

1. Department of Oncology and Haemato-Oncology, university of Milan, Milan, Italy
2. Department of Experimental Oncology, European Institute of Oncology (IEO), Milan, Italy

Dr. Roberta Noberini

Department of Experimental Oncology, IEO, European Institute of Oncology IRCCS, 20139 Milan, Italy

Deadline for manuscript submissions

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Cells
Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland
Tel: +41 61 683 77 34
cells@mdpi.com

mdpi.com/journal/cells

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Message from the Editorial Board

Cells has become a solid international scientific journal that is now indexed on SCIE and in other databases. We have successfully introduced a special issues format so that these issues serve as mini-forums in specific areas of cell science. *Cells* encourages researchers to suggest new special issues, serve as special issues editors, and volunteer to be reviewers. Our main focus will remain on cell anatomy and physiology, the structure and function of organelles, cell adhesion and motility, and the regulation of intracellular signaling, growth, differentiation, and aging. We are open to both original research papers and reviews.

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Dental Basic Sciences, University of Minnesota, 308 Harvard St. SE, Minneapolis, MN 55455, USA

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