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The Contribution of Proteomics to Chromatin Biology and Epigenetic Research

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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.

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Special Issue



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