

## Special Issue

# Chromatin Proteomes

### Message from the Guest Editors

Chromatin is a nucleoprotein complex composed of a large diversity of proteins that dynamically interact with DNA to control its compaction and to regulate gene expression. This includes histones that can be modified in multiple ways to adjust DNA folding and to regulate association with transcription factors and epigenetic factors, and extends to the transcriptional machinery itself. In addition, chromatin integrates many upstream cellular signaling pathways, to convert this into a transcriptional response. Collectively, chromatin factors are key determinants of many cellular processes. For this Special Issue of *Proteomes*, we invite manuscript submissions that shed light on proteomic aspects of chromatin in the widest sense. This may include (but is not restricted to) analysis of post-translational modifications, characterization of protein interactions (with DNA, RNA, or with other proteins) in a chromatin context, or deciphering the role of chromatin proteins in any aspect of cellular signaling.

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### Guest Editors

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### Deadline for manuscript submissions

closed (31 March 2020)



## Proteomes

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Impact Factor 3.6  
CiteScore 7.2  
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## About the Journal

### 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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### Editors-in-Chief

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