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.

Guest Editors

Prof. Dr. Jeroen Krijgsveld

Division of Proteomics of Stem Cells and Cancer, DKFZ Heidelberg, 69120 Heidelberg, Germany

Dr. Tiziana Bonaldi

Department of Experimental Oncology, European Institute of Oncology (IEO), Milan, Italy

Deadline for manuscript submissions

closed (31 March 2020)



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

mdpi.com/journal/proteomes





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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.

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. Coorssen

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

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