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Computational Biology of Epigenomics and Transcriptomics

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submissions:

closed (31 August 2018)

Message from the Guest Editors

In the last few years, the genomics field has witnessed a data revolution through the implementation of next-generation sequencing technologies. In this framework, Computational Biology plays a central role in the analysis and integration of the unaffordable amount of data generated in the field and in the development of sensitive, specific and efficient computational tools.

This Special Issue will be focused on the computational analysis of chromatin modifications, gene expression and RNA processing data, as well as in the development of computational tools to analyze epigenomics and transcriptomics high-throughput data. In addition to invited reviews, we welcome research and/or methods manuscripts of exceptional interest on the following topics:

- Chromatin modifications and gene expression
- Epigenetic marks and RNA processing
- Epigenomics along dynamic processes such as differentiation, reprogramming and development
- Chromatin segmentation
- Three-dimensional chromatin structure

Dr. Roderic Guigó
Dr. Sílvia Pérez-Lluch
Guest Editors



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Special Issue



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Message from the Editor-in-Chief

In the past years the growth of the epigenetic field has been outstanding, from here the need of a journal where to centralize all new information on the subject. The term epigenetics is now broadly used to indicate changes in gene functions that do not depend on changes in the sequence of DNA. *Epigenomes* covers all areas of DNA modification from single cell level to multicellular organism as well as the epigenetics on human pathologies and behavior.

Epigenomes (ISSN 2075-4655) is a fully peer-reviewed publication outlet with a rapid and economical route to open access publication. All articles are peer-reviewed and the editorial focus is on determining that the work is scientifically sound rather than trying to predict its future impact.

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