



Computational Biology of Epigenomics and Transcriptomics

Guest Editors:

Dr. Roderic Guigó

Centre for Genomic Regulation
(CRG), The Barcelona Institute for
Science and Technology, Dr.
Aiguader 88, 08003 Barcelona,
Spain

Dr. Sílvia Pérez-Lluch

Centre for Genomic Regulation
(CRG), Barcelona, Spain

Deadline for manuscript
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





an Open Access Journal by MDPI

Editor-in-Chief

Prof. Dr. Ernesto Guccione

Icahn School of Medicine at
Mount Sinai, Hess Center for
Science and Medicine, New York,
NY 10029, USA

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.

Author Benefits

Open Access: free for readers, with [article processing charges \(APC\)](#) paid by authors or their institutions.

High Visibility: indexed within [Scopus](#), [ESCI \(Web of Science\)](#), [PMC](#), [PubMed](#), [Embase](#), [PubAg](#), [CAPus / SciFinder](#), and [other databases](#).

Journal Rank: CiteScore - Q2 (*Biochemistry, Genetics and Molecular Biology (miscellaneous)*)

Contact Us

Epigenomes Editorial Office
MDPI, St. Alban-Anlage 66
4052 Basel, Switzerland

Tel: +41 61 683 77 34
www.mdpi.com

mdpi.com/journal/epigenomes
epigenomes@mdpi.com
[X@Epigenomes](#)