



Epigenome, Epitranscriptome and Single Cell Analysis in Cell Fate Choice

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Message from the Guest Editors

The importance of analyzing these modifications at the single cell level is rapidly emerging as a revolutionary research area. Similarly, understanding the function and mechanisms of the dynamic RNA modifications, which are termed “RNA epigenetics”, represents a new challenge at the frontier between different disciplines. Reversible RNA modifications add a new dimension to the developing picture of post-transcriptional regulation of gene expression. This new dimension awaits integration with transcriptional regulation (i.e., DNA modifications), to decipher the multi-layered information that controls a plethora of biological functions. The epitranscriptome includes all the biochemical modifications of the RNA (the transcriptome) within a cell. Thus, in the era of advanced technologies, the exciting next step is to move from mapping nucleotide modifications to understanding how they contribute to biological processes.

Deadline for manuscript
submissions:

closed (31 December 2019)

- Dynamic DNA and RNA modifications;
- Decoding the function of DNA and RNA modifications;
- DNA and RNA epigenetics in cell and development;
- Epigenomes and epitranscriptomes;
- Single cell analysis





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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.

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