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Bioinformatics of RNA Modifications and Epitranscriptome

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Message from the Guest Editors

We would like to invite you to participate to this Special Issue, titled “Bioinformatics of RNA modifications and Epitranscriptome”.

To date, more than 170 types of post-transcriptional RNA modifications which occur on all types of RNA and regulate nearly every stage of RNA life have been discovered. Increasing evidence has suggested that RNA modifications regulate many molecular functions and biological processes, including (but not limited to) gene expression regulation, translation, embryo development, and mRNA stability. With the accumulation of a large number of high-throughput datasets, bioinformatics approaches have become increasingly critical for unraveling the epitranscriptome.

In this Special Issue, we aim to gather articles from every aspect of the emerging topics in epitranscriptome bioinformatics. We will consider, among other things, new results from computational and experimental combined analysis, novel bioinformatics approaches/pipelines, bioinformatics and epigenetics analysis, new/updated epitranscriptome databases, and new software tools for analysis epigenetics data, as well as review articles for publication.



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Special Issue



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Message from the Editor-in-Chief

Genes is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised. Why not consider *Genes* for your next genetics paper?

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