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RNA Epigenetics: RNA Modification and Epitranscriptome Analysis

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Deadline for manuscript submissions:

closed (15 April 2023)

Message from the Guest Editors

Dear Colleagues,

We would like to invite you to participate in this Special Issue, entitled *RNA Epigenetics: RNA Modification and Epitranscriptome Analysis*.

In this Special Issue, we aim to gather articles from epitranscriptomics studies on every aspect of RNA epigenetics to decipher the regulation and function of RNA epigenetics on any form of life. We will consider studies on topics including, but not limited to new experimental results, interesting discoveries, new biomolecular mechanisms, novel computational/experimental approaches, bioinformatics and epigenetics analyses, new software tools for the analysis of epigenetics data, RNA modifications databases, as well as review articles related to post-transcriptional RNA modification and epitranscriptome for publication.

However, simple biomarker (or signature) prediction and analysis based on mining public biological databases such as TCGA or ENCODE without in-depth experimental validation will NOT be considered.

Dr. Jia Meng
Dr. Kunqi Chen
Guest Editors



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Special Issue



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Editor-in-Chief

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Message from the Editor-in-Chief

Genes are central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fastmoving 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.

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