



RNA-Seq: Data Analysis Methods and Applications

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Message from the Guest Editors

RNA-Seq has become the method of choice in a wide variety of life sciences applications because of the feasibility to combine in a single high-throughput sequencing assay both identification of transcripts and quantification of their expression. Despite the extensive popularity of RNA-seq, several challenges are associated with the followed workflow in data exploration from the initial experimental design, quality control, transcriptome assembly and read alignment/mapping to downstream statistical and bioinformatics data analysis involved in differential transcript/gene expression, and functional analysis or integration of RNA-seq data with data from other multi-omics methodologies.

This Special Issue on "RNA-Seq: Data Analysis Methods and Applications" aims to attract original contributions that address these challenges in the context of different application purposes and provide the latest achievements, advancements or improvements in the state-of-the-art-relevant to this active field of systems biology. Literature reviews as well as innovative studies and protocols on these RNA-Seq topics will be considered for publication.

We look forward to receiving your article.





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Message from the Editor-in-Chief

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