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Computational Analysis of RNA Structure and Function

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Message from the Guest Editor

RNA is being intensively studied across all living organisms in numerous ways, ranging from analysis of its structure and folding properties to high-throughput sequencing (HTS) and its applications. Many trait and disease related mutations in higher eukaryotes are in non-coding regions of the genome and since most of the genome is transcribed into RNA, the mutations hold the potential impact structure and thereby function of the RNA molecules. In this Special Issue, we welcome work on computational strategies for analysis of RNA structure and function covering both algorithmic aspects, as well as bioinformatic analysis large-scale related data sets, as well as work on prediction of RNA structure and RNA interactions of single sequences.



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Special Issue



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Message from the Editor-in-Chief

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