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Recent Development of Bioinformatics Tools of RNA

Guest Editor:

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Message from the Guest Editor

Dear Colleagues,

Recent studies have shown that there are many noncoding RNAs (ncRNAs) that are not translated into proteins but play important roles in various cellular functions. On the other hand, various types of RNA-related omics data such as transcriptome (e.g., RNA-seq), epi-transcriptome (e.g., m6A-seq, m1A-seq), structurome (e.g., DMS-seq, SHAPE-seq), and interactome (e.g., CLIP-seq) are accumulating. Integrating these omics data with bioinformatic approaches has also become important in RNA biology. In addition to natural RNAs, artificial RNAs such as RNA aptamers are also attracting attention from researchers as a new generation of target molecules for drug discovery; the computational design of RNA sequences (e.g., RNA aptamer design, RNA inverse folding) is an important problem in this field. This Special Issue covers all aspects of RNA informatics. We welcome papers on both fundamental computational methods for analyzing RNAs and omics data analysis of RNAs.

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Special Issue