non-coding RNA

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Bioinformatics Tools for Studying the Regulatory Functions of Non-Coding RNAs

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Deadline for manuscript submissions:
closed (25 June 2019)

Message from the Guest Editors

In higher organisms, the majority of the genome is transcribed into non-coding RNAs (ncRNAs). Examples include microRNAs of ~22 nucleotides (nts), small bacterial RNAs of 50–250 nts, lncRNAs and circRNAs of thousands of nts. ncRNAs have been shown to have diverse regulatory functions. ncRNAs are involved in gene editing, transcription and translation. They regulate diverse developmental, physiological and pathological processes. Dysregulation of many ncRNAs can cause cancer and are associated with other human diseases. However, the regulatory functions for a majority of ncRNA are not yet known. Bioinformatic tools are valuable for guiding experimental discoveries. This Special Issue of *Non-Coding RNAs* will focus on a collection of current bioinformatic software and database tools for functional studies of non-coding RNAs. Topics of interest will include, but are not limited to, microRNAs, sRNAs, lncRNAs, circRNAs, RNA modification, viral ncRNAs, RNA structure prediction and analysis, RNA–RNA interaction modeling, guide RNAs directed gene editing, and piwi-interacting RNAs.

For more information, please visit the *Special Issue website*.

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Special Issue

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Editor-in-Chief

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Message from the Editor-in-Chief

This field finally has a dedicated journal where its broad community can communicate and exchange its latest findings in one centralized place. This field was built stone by stone from the many scientific contributions from extremely diverse horizons, studying gene silencing in plants, position effect variegation in drosophila or quelling in fungi. This field has achieved maturity, but a lot remains to be discovered! Our aim is to publish manuscripts from all horizons that will have a high impact on the development of the field. Let’s have fun and wish *Non-Coding RNA* a long and rewarding life!

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