



Regulatory Non-Coding RNAs in Oncogenesis and Tumor Inhibition

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Message from the Guest Editors

Current analyses of the human transcriptome indicate that a mere 2% of the genome corresponds to protein coding transcripts, yet it is estimated that ~70–90% of the genome is transcribed. Essentially, the majority of RNA transcribed is non-coding.

Many of these ncRNAs play a variety of important cellular roles. Critically, aberrant expression of many ncRNAs is associated with cancer. Some, such as miRNAs, can affect the regulation of critical tumor suppressors through competitive endogenous RNA (ceRNA)-mediated effects. Others, such as circRNAs, can act as “molecular sponges” to limit miRNA availability and affect growth. Many ncRNAs also act to regulate processes such as epithelial-mesenchymal transition (EMT), a key element in oncogenesis.

The purpose of this Special Issue is to bring together a series of articles (both reviews and original research) related to these important non-coding RNAs with respect to their roles in cancer formation and development.

For more information, please visit the [*Special Issue website*](#).





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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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