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Role of miRNAs in Cancer—Analysis of Their Targetome

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Message from the Guest Editor

Dear Colleague,

MicroRNAs (miRNAs) are the best studied noncoding RNA sequences of our genome. Since the discovery of the second miRNA sequence, let-7a, in 2000, the identification of new miRNAs has increased considerably. The first evidence that miRNAs were related to cancer also came from let-7a, which was described as a tumor suppressor in 2002. Since then, it has become clear that miRNA expression is dysregulated in human cancers. In order to identify the functions of the dysregulated miRNAs, it is necessary to decipher their target genes.

More efforts are still needed to decipher the critical targets—both coding and noncoding RNAs—of the miRNAs involved in cancer and to identify their contribution to malignant transformation and metastasis. The present issue will focus on the identification of the functions of tumorigenic miRNAs through the study of their targetome in both tumor and nontumor cells, where they are transported through exosomes. The large-scale identification of miRNA targets will allow a greater understanding of the complex networks regulated by miRNAs.

- microRNAs
- targetome
- AGO-CLIP
- deep sequencing
- exosomes
- extracellular vesicles

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Message from the Editor-in-Chief

Cancers (ISSN 2072-6694) is an international, online journal addressing both clinical and basic science issues related to cancer research. The journal will continue its open access format, which will certainly evolve to ensure that the journal takes full advantage of the rapidly changing world of information and knowledge dissemination. It publishes high-quality clinical, translational, and basic science research on cancer prevention, initiation, progression, and treatment, as well as other related topics, particularly to capture the most seminal studies in the rapidly growing area of immunology, immunotherapy, and tumor microenvironment.

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