



Application of Multi-Omics Analysis in Cancer Diagnosis, Treatment and Prognosis

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Deadline for manuscript
submissions:

closed (15 November 2023)

Message from the Guest Editors

Dear Colleagues,

Cancer is currently viewed as a disease of evolving genomic instability and abnormal epigenomic modifications. Pioneering work had discovered and chromosomally mapped the genomic locations of oncogenes and tumor suppressor genes that are responsible for cancer initiation, progression, and metastasis. As such, we are witnessing mutation signatures, gene copy number alterations and aberrant gene expression profiles in specific types of cancer.

This Special Issue will highlight recent developments in computational biology and cancer biology, a major focus is on the integration of multi-omics data such as WGS, WES, scRNAseq, and spatial transcriptomics and proteomics to better understand the basis of the initiation of cancer, its evolution, and drug tolerant persist cancer state and full therapy resistance. Unbiased, systematic analyses using multi-omics data could advance our knowledge to further improve cancer treatment. This Special Issue accepts all types of papers, including reviews, perspectives, or original research articles, from a wide range of types of cancers.

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Guest Editors





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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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