

Special Issue

Computational Analysis of Cancer Clonal Evolution: Signatures, Determinants and Dynamics

Message from the Guest Editor

With breakthroughs in immune cell therapy, cancer vaccines, and gene editing, there is an urgent need for computational frameworks that can quantitatively characterize the origins, trajectories, and clinical consequences of cancer clonality. This Special Issue is therefore dedicated to the computational analysis of the determinants and dynamics of clonal evolution in cancers. By integrating multimodal, high-throughput data with innovative analytical approaches, we aim to resolve and reconstruct clonal evolution in diverse tumor types and to reveal new hallmarks of cancer that encode quantifiable laws governing tumorigenesis, progression, and treatment response. Ultimately, this Special Issue seeks to bridge the gap between single-gene driver research and a holistic, evolution-based understanding of cancer biology and precision oncology.

Guest Editor

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About the Journal

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.

Editor-in-Chief

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