Special Issue

Next Generation Sequencing for Cancer Diagnostics

Message from the Guest Editor

Cancer is a leading cause of death worldwide, and accounted for ~10 million cancer deaths in 2020. The introduction of next-generation sequencing (NGS) technologies in clinical oncology laboratories has allowed the detection of somatic alterations, including single nucleotide variants, small indels, copy number variants and structural variants, on a genome-wide scale. Large-scale sequencing studies have illustrated the genomic landscapes of different cancers, thus leading to the identification of novel driver mutations, prognostic markers and a large number of therapeutic targets. Recent progress in genomic analysis using NGS technology has enabled the comprehensive detection of mutations, as well as the tumor mutation burden (TMB), in patient tumors, a biomarker for immunotherapy. NGS-based techniques have also been applied at the transcriptomic and epigenomic levels in order to accelerate our understanding of cancer biology and clinical trials for novel therapeutics In this issue of *Cancers*, we would like to present a review of the currently available data on the utility of NGS-based applications for cancer diagnostics.

Guest Editor

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Message from the Editor-in-Chief

Cancers is an international online journal addressing both clinical and basic science issues related to cancer research. The journal is publishing in 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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