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Genomic Approaches for Disease Diagnosis and Prognosis: From Clinomics to Single-Cell Sequencing and Spatial Transcriptomics

Guest Editor:

Dr. Antonis Giakountis
Department of Biochemistry and Biotechnology, University of Thessaly, Biopolis Mezourlo, 41500 Larisa, Greece

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Message from the Guest Editor

Over the last two decades, next generation sequencing (NGS) has facilitated the transition of biomedical research into the post-genomic era. International consortia, including, but not limited to, the Cancer Genome Atlas (TCGA), the International Cancer Genome Consortium (ICGC) and the Genotype-Tissue Expression Project (gTEX), combined molecular insights (e.g DNA sequence and structure and/or RNA or protein expression) with clinical manifestations, thereby promoting the development of novel diagnostic and prognostic biomarkers or therapeutic targets.

The same efforts highlighted the extensive cellular and molecular heterogeneity that governs complex diseases such as cancer.

This Special Issue welcomes articles that emphasize the role of genomic approaches and/or methodologies in the form of bulk, single-cell or spatial sequencing as novel clinomics strategies designed to convert genomic function into diagnostic, prognostic and therapeutic action against complex human diseases.

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Editor-in-Chief

Prof. Dr. Selvarangan Ponnazhagan
Department of Pathology, The University of Alabama at Birmingham, 1825 University Blvd, SHEL 814, Birmingham, AL 35294-2182, USA

Message from the Editor-in-Chief

Genes are central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fastmoving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised.

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Genes Editorial Office
MDPI, St. Alban-Anlage 66
4052 Basel, Switzerland

Tel: +41 61 683 77 34
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