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Genetics and Genomics of Lung Cancer May Contribute to the Development of Precision Medicine

Guest Editor:

Dr. Vienna Ludovini
Department of Medical Oncology, Molecular biology laboratory, S. Maria Della Misericordia Hospital, 06132 Perugia, Italy

Deadline for manuscript submissions:
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Message from the Guest Editor

Lung cancer results from multiple changes in the genome of susceptible pulmonary cells caused by exposure to carcinogens found in tobacco smoke, the environment, or the workplace. Recent studies suggest that histologically apparent lung cancer is due to the sequential accumulation of specific genetic and morphologic changes to the normal epithelial cells of the lung. The new knowledge of the human genome coupled with global methods of detecting genetic abnormalities and profiling gene expression in tumor cells may enable us to understand the signaling pathways of lung cancer cells.

This Special Issue will provide a comprehensive update on the latest findings on lung cancer-associated genes, with a focus on the clinical application of some mutation genes as biomarkers for cancer diagnosis and prognosis, and treatment prediction, as well as mutation-based therapeutic strategies, may contribute to the development of precision medicine. Original papers and review articles that describe advances in detection methodology, bioinformatics approaches, and statistical analysis with an impact on the clinical application of mutation genes as cancer biomarkers are welcome.

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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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Contact Us

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

Tel: +41 61 683 77 34
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𝕏@Genes_MDPI