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

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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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Special Issue



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Message from the Editor-in-Chief

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