



Lung Cancer Proteogenomics: New Era, New Insights

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Message from the Guest Editor

Lung cancer remains a major public health concern, constituting the second most prevalent malignancy and the leading cause of cancer-related mortality worldwide. Lung cancer incidence and outcomes vary depending on factors such as age, sex, ethnicity, smoking habits, environment, and socioeconomic status.

Integration of high-throughput molecular data originating from mass spectrometry (proteomics) to those of next-generation sequencing (genomics, transcriptomics) are currently paving the way towards designating molecular causes of cancer tumorigenesis. Proteogenomics is increasingly becoming a valuable instrument for biomedical research.

For this Special Issue, we invite authors to contribute original research articles, as well as review articles that address recent achievements in proteogenomics associated with lung cancer research.

Potential topics include but are not limited to the following:

- Methods of genomic, transcriptomic, and proteomic data integration;
- Bioinformatic tools towards metagenomics and metaproteomics;
- Clinical lung cancer proteogenomics towards precision medicine;
- Lung cancer multi-omics.





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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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