



genes



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Genes Networking Analysis Applied to Immune Response in Lung Cancer

Guest Editor:

Dr. Fortunato Bianconi

Department of Experimental
Medicine, University of Perugia,
06128 Perugia, Italy

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submissions:

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Message from the Guest Editor

Lung cancer is the most frequent cause of cancer death worldwide, representing one of the most significant challenges in oncology. In recent years, immunotherapy, specifically therapy with immune checkpoint inhibitors (ICIs), has revolutionized the therapeutic paradigm, demonstrating durable antitumor effects in different types of cancers, including lung cancer. To date, the mechanism of action of these new therapies is still under study, since only a fraction of patients benefit from ICIs, and the only known predictive biomarker, PD-L1, is insufficient to predict immunotherapy response. Thus, identifying new potential biomarkers and understanding the tumor and immune system interactions are crucial aspects for improving patients outcomes. Advanced sequencing technologies integrated with systems biology approaches are giving rise to large-scale study and can help toward the discovery of specific gene expression signatures associated with immune response in patients.

For this Special Issue, we are soliciting state-of-the-art work in genes networking analysis applied to immune response in lung cancer, in order to collect the most recent advances in this field all in one place.



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Special Issue



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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

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