

Special Issue

Carcinogenesis as an Evolutionary Process

Message from the Guest Editor

In the first phase of carcinogenesis, a cell may acquire a mutation that permits it to proliferate abnormally. In the next phase, other mutations allow for the expansion of cell number and eventually metastasize in distant organs. Analyses of the mutation landscapes and evolutionary trajectories of various tumor tissues have identified a constrained set of driver genes as the key genes whose mutation is most likely to initiate carcinogenesis. And their mutations are subject to positive selection during tumor evolution. Several types of approaches exploit this principle for the identification of genes that drive carcinogenesis. As a result of combined efforts, providing a catalogue of driver mutations that could give rise to cancer has been achieved. However, a rather large fraction of cancer driver genes remain to be identified. Another outstanding problem concerns the existence of tumor essential genes. This Special Issue aims to focus on the toolkit of cancer driver genes and tumor essential genes. The significance of this question is that novel driver genes and tumor essential genes may prove to be valuable targets for cancer therapy.

Guest Editor

Prof. Dr. Laszlo Patthy

Institute of Enzymology, Research Centre for Natural Sciences,
Hungarian Academy of Sciences, H-1117 Budapest, Hungary

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Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland
Tel: +41 61 683 77 34
genes@mdpi.com

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Genes is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving 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. Why not consider *Genes* for your next genetics paper?

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

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