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Single-Nucleotide Polymorphisms: Association, Molecular Function, Application, and Progress

Guest Editor:

Dr. Zsolt Ronai
Institute of Biochemistry and Molecular Biology, Department of Molecular Biology, Semmelweis University, P.O. Box 2, H-1428 Budapest, Hungary

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Message from the Guest Editor

Single nucleotide variation: a tiny change in the 3 billion base pair long sequence of the human genome. Alter less than 5 × 10–8% of the genetic information, and the consequence can be fateful. Or it can be nothing. Or an alteration in regulation, signal transduction, enzyme activity. There are more than 1 billion entries related to Homo sapiens in the dbSNP database of NCBI.

It has been less than two decades since the Human Genome Project was completed. During this time, incredible progress has been achieved in the investigation of DNA sequencing. It is challenging to understand the function of the identified sequence variations. It is, however, of significant importance, as the SNPs can shed light on molecular dysfunctions related to diseases, offering the definition of novel, biologically more relevant diagnostic categories, not to mention prevention as well as the elaboration of targeted therapeutical approaches.

Studies on the molecular function as well as clinical consequences of SNPs (including positive and negative results) will be collected in the form of original research publications, as well as systematic review articles in this 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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Contact Us

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

Tel: +41 61 683 77 34
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