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Genetics of Multifactorial Diseases

Guest Editor:

Dr. Yiannis Vasilopoulos

Laboratory of Genetics, Section of Genetics, Cell Biology and Development, Department of Biology, University of Patras, 26504 Patras, Greece

Deadline for manuscript submissions:

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Message from the Guest Editor

Current genetic approaches, with the major example of genome-wide association studies (GWASs), have unveiled numerous associated loci in multifactorial diseases, thus enabling the computation of an individual's predisposition to a complex trait through polygenic risk scores (PRSs). However, existing approaches are limited to the incorporation of identified common genetic variants that explain a small proportion of the estimated genetic variability, thus excluding the effect of rare variants that have been repeatedly shown to explain the 'missing heritability'. The clinical and molecular variability in multifactorial diseases is additionally mediated by multi-layered interactions between the genetic component and environmental factors; these gene–environment interactions are depicted from the epigenetic modulations that orchestrate the expression of respective loci. Deciphering the role of rare genetic variants in a trait's predisposition as well as assessing gene–environment interactions through the functional relevance of the epigenetic modifications.



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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

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

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