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Genetics of Multifactorial Diseases

Guest Editor:

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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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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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