Special Issue

Clinical, Functional and Fitness Consequences of Genetic Variants

Message from the Guest Editor

A major bottleneck in interpreting genetic data is estimating the impact of each single variant. Genome-wide association studies (GWASs) and family segregation studies (FSSs) may associate diseases with single variants or with genes. Experimental studies may associate variants with the loss or gain of protein function and indicate alterations in specific biological processes. Computational studies may use evolutionary and structural information to suggest variant effects on fitness and mechanistic insights, respectively. These studies improve our understanding of variant consequences and help in interpreting variants that are currently described as variants of unknown significance (VUS). In this Special Issue, we welcome the submission of reviews, original articles, and short reports that cover any aspects of variant consequences. These may include works focused on specific genes, biological functions, phenotypes, or samples.

Guest Editor

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Deadline for manuscript submissions

closed (20 April 2024)

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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

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