Special Issue

Progress in Genetics of Autism

Message from the Guest Editors

Detailed phenotyping coupled with the sequencing of patient cohorts with autism spectrum disorder (ASD) have dramatically accelerated the deciphering of genetic architecture and discovery of risk genes.

With an increasing sample size and application of whole-genome sequencing approaches, we now have the opportunity to identify ASD-associated rare coding and non-coding variants with high and moderate effect sizes and to decipher individual-level genetic architecture.

This issue will focus on new progress in the following directions: (i) identification of ASD-associated rare non-coding variants; (ii) identification of new genes/variants with a moderate effect size; (iii) better understanding of the prevalence, inheritance, and genotype–phenotype correlations of known and new ASD high-risk genes, (iv) investigation of the genetic architecture (e.g., combination pattern of rare risk variants) at the individual level, and (v) comparison of the mutation pattern and genetic architecture of ASD between different populations.

Guest Editors

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Deadline for manuscript submissions

closed (25 July 2022)

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Message from the Editor-in-Chief

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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