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Genome-Wide Identification: Recent Trends in Genomic Studies, Volume II

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Deadline for manuscript submissions:
closed (20 May 2024)

Message from the Guest Editors

Dear Colleagues,

With the advances in high-throughput sequencing in recent years, rich sources of genotype and phenotype data have been produced, providing unprecedented opportunities for genome-wide identification of complex traits and disease-related biomarkers in humans, animals, and even plants and posing statistical and computational challenges to the paradigm of traditional GWAS. New methodological research continues to emerge at an impressive pace, breaking through the limitations of classical association mapping theory and expanding the scope of more sophisticated genomic applications. We invite you to contribute original articles, new methods, and thought-provoking reviews addressing recent trends in genome-wide identification to this Special Issue. If you would like more information about this Special Issue, or have any other questions, please feel free to contact us.

Dr. Xiaowei Wu
Dr. Hailan Liu
Dr. Lide Han
Guest Editors

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Special Issue

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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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