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Genome-Wide Association Studies (GWAS) to Understand Disease

Guest Editor:

Dr. Tim Beck
Department of Genetics and Genome Biology, University of Leicester, Leicester LE1 7RH, UK

Deadline for manuscript submissions:
closed (25 March 2021)

Message from the Guest Editor

Genome-wide association studies (GWAS) - where genetic variants across the genomes of samples from populations are tested for associations to disease traits - have caused a seismic shift in our understanding of disease aetiology. Over the years, improvements in genotyping technologies available at competitive cost, have allowed more variants to be tested over larger population samples, with this trend set to continue with whole-genome and whole-exome sequencing becoming more accessible. In parallel, bioinformatics advances have kept pace to identify actionable genetic variants on a single-study basis, and also to gather, compare and analyse summary data from across published GWAS.

We would like to invite submissions of original research or review articles on any topic related to “Genome-wide Association Studies (GWAS) to Understand Disease”. This Special Issue addresses all kinds of research related to our current knowledge on GWAS, from novel health related GWAS findings to methodology and bioinformatics perspectives, as well as critical perspectives on the challenges facing this area.

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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

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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Contact Us

Genes Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland

Tel: +41 61 683 77 34
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mdpi.com/journal/genes
genes@mdpi.com
𝕏@Genes_MDPI