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Genome-Wide Identifications: Recent Trends in Genomic Studies

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Deadline for manuscript submissions:

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Message from the Guest Editors

The field of genome-wide identification is rapidly evolving with regard to the identification of genes playing a role in economic, evolutionary, and medicinal traits. To obtain fruitful results in this field, it is necessary to expand our understanding of genome localization, gene identification, motif structures, phylogenetic relationships, protein interactions, biochemical pathways, and gene expression. These studies also involve testing genetic variants in the whole genome of various plants, mutation mapping, histone modifications, microorganisms, and animals to identify genotypic and phenotypic associations. Such studies facilitate and lay the foundation for functional identification of important genes in different processes such as plant development, disease resistance in plants and animals, fruit protection, molecular mechanisms of gene expression, production of active metabolites, and coupling biotic and abiotic stresses. In this Special Issue of *Genes*, we invite researchers to submit research articles, review papers, editorials, and opinions revealing the functions and dynamics of specific genes and entire genomes.



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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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