Special Issue

New Advance on Functional Genomics and Genome Editing in Plant

Message from the Guest Editors

Exponential growth in whole-genome sequence data availability in plants, including model and fruit crops, has accelerated functional genomic research.The genome-wide analysis of several important genes and transcription factors at the DNA, RNA, and protein levels conclude a few important genes for trait improvements. The potential genes, promoter, long noncoding, and miRNA need to validate their functional role. For this, various genetic engineering tools, such as overexpression and RNAi, and genome editing tools, such as ZNF, TALENS, and CRISPR/Cas, have been utilized in various plants. However, the development of CRISPR/Cas technology and its variants has become a powerful, efficient, and versatile tool for gene editing, transcriptional activation, suppression, etc. Functional genomics and genome editing technology is widely used in various plants to improve key traits in plant systems, such as high levels of desirable secondary metabolites, higher yield, disease resistance, good storage stability, improved nutritional and medicinal value. In the present Special Issue, reviews and research articles related to functional genomics and genome editing in plants are welcomed.

Guest Editors

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Deadline for manuscript submissions

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Message from the Editor-in-Chief

The International Journal of Molecular Sciences (*IJMS*, ISSN 1422-0067) is an open access journal, which was established in 2000. The journal aims to provide a forum for scholarly research on a range of topics, including biochemistry, molecular and cell biology, molecular biophysics, molecular medicine, and all aspects of molecular research in chemistry. *IJMS* publishes both original research and review articles, and regularly publishes special issues to highlight advances at the cutting edge of research. We invite you to read recent articles published in *IJMS* and consider publishing your next paper with us.

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