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## Deciphering Plant Molecular Data Using Computational Methods

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### **Message from the Guest Editor**

High-throughput sequencing technologies continue to generate vast amounts of plant molecular data, advancing the frontier of plant biology research and making significant contributions to the understanding of plants. Computational analysis has become an indispensable tool in unraveling complex plant molecular networks.

This Special Issue aims to provide a platform for researchers to share the latest findings and advancements in the use of computational methods for unraveling the mysteries of plant molecular networks. We welcome original research articles, critical review papers and perspectives that delve into various aspects of this field, including the genomics, transcriptomics, proteomics, metabolomics and epigenomics of plants. Additionally, we encourage contributions on data processing, analysis and visualization techniques that pave the way for novel insights into plant molecular mechanisms.



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# Special Issue



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## Editor-in-Chief

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## Message from the Editor-in-Chief

*Plants* is an open access journal which provides an advanced forum for research findings in areas related to plant function, its physiology, biology, taxonomy, stresses, and its interactions with other organisms. It publishes original research articles, reviews, reports, conference proceedings (peer reviewed full articles) and communications. In original research papers, it is important that full experimental details are provided. We also encourage timely reviews and commentaries on topics of interest to the plant research community.

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