

Special Issue

Applications of Bioinformatics in Plant Resources and Omics

Message from the Guest Editors

The advances in sequencing technologies and genome assembly methods that do not require genetic maps to generate chromosome-scale genome references are generating a plethora of genome sequences in plants, especially for non-model species. Today, projects to sequence thousands of plant transcriptomes and genomes are in progress, and many bioinformatics tools have been developed and applied for omics plant research. These advances are allowing us to access a great number of useful resources and bioinformatics tools to study plants, in some cases in species which had few or even no omics data before. This Special Issue of *Plants* aims to highlight omics resources produced for plants, such as genomes, transcriptomes, gene expression data, gene or genome annotations, metabolomes, proteomes, epigenomes, and metagenomes of microorganisms interacting with plants, and bioinformatics tools used or developed to generate these resources, such as analysis tools, automated pipelines, databases or web tools.

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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, and 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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