

Special Issue

Plant Responses to Environmental Stresses

Message from the Guest Editors

Datasets in genomics/metagenomics, transcriptomics/meta-transcriptomics, proteomics/meta-proteomics, metabolomics, epigenomics, ionomics, phenomics—just to mention the most popular platforms—are piling up elsewhere intending to gain insights on the molecular mechanisms behind plant interaction with biotic and abiotic stresses. Multi-Omics Integration (MOI) uses conceptual integration and element- (correlation, clustering, and multivariate analysis), pathway- (pathway mapping, co-expression analysis), or mathematical- (differential analysis, genome-scale analysis) based approaches to integrate omics datasets. MOI is facilitating the hypothesis generation leading to a further understanding of biological, molecular, and ecological functions and mechanisms, in addition to performing associations and correlations studies. Groups applying MOI strategies to study plant responses to biotic (virus, bacteria, fungi, nematodes, insects and so on—alone or in combination) or abiotic (cold, heat, salinity, drought, heavy metals and so on—alone or in combination), or even the combination of both types of stresses, are welcome to submit the results of their studies.

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Deadline for manuscript submissions

closed (31 July 2023)



Plants

an Open Access Journal
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Impact Factor 4.1
CiteScore 7.6
Indexed in PubMed



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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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