

Special Issue

Crop Genome Sequencing and Analysis

Message from the Guest Editor

Dear colleagues, With the reduction in sequencing prices brought about by new technologies, tasks like genome-wide sequencing or resequencing and subsequent whole genome analysis have become routine. At the same time, with more fully annotated and ordered reference genome sequences in place, researchers and breeders can now easily access or generate high-quality sequence-level information to precisely define the necessary changes in the genomes for breeding programs. This Special Issue of *Plants* will highlight contributions in which high-throughput genomic methods are used to drive information on aspects such as, but not limited to, crop sequencing and assembly, crop genome and transcriptome analyses, gene expression, high-throughput marker identification, genomics-aided breeding, genomic selection, and targeted breeding technologies, including genome editing. Priority will be given to crops. Manuscripts on orphan crops are welcome. I hope you may find this Special Issue of interest for submitting your manuscripts.

Guest Editor

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Deadline for manuscript submissions

closed (30 November 2025)



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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.

Editor-in-Chief

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