Special Issue

Harnessing the Power of Genome and Transcriptome Assemblies

Message from the Guest Editor

The availability of high-quality genome and transcriptome assemblies is crucial for numerous studies of specific plant functions. Long-read sequencing technologies boost the contiguity of genome assemblies and open up novel opportunities in plant transcriptomics. Transcriptome assemblies are a cost-effective way to access the genes of plant species with large and complex genomes. Direct RNA sequencing allows the identification of modifications on these transcripts. Deep sequencing with long reads enables detailed investigations of splicing processes, leading to a huge variety of transcript isoforms. This Special Issue is open to all research articles providing new insights into the biology of plants based on genome or transcriptome assemblies.

Guest Editor

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