

Resource Summary Report

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[PlantGSEA](#)

RRID:SCR_016866

Type: Tool

Proper Citation

PlantGSEA (RRID:SCR_016866)

Resource Information

URL: <http://structuralbiology.cau.edu.cn/PlantGSEA/>

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Description: Webserver for gene set enrichment analysis of plants. Used for interpreting biological meaning of a list of genes by computing the overlaps with various previously defined gene sets.

Abbreviations: PlantGSEA

Synonyms: The Plant GeneSet Enrichment Analysis Toolkit, Plant GeneSet Enrichment Analysis, Gene Set Enrichment Analysis (GSEA)

Resource Type: service resource, production service resource, analysis service resource, data analysis service

Defining Citation: [DOI:10.1093/nar/gkt281](https://doi.org/10.1093/nar/gkt281)

Keywords: gene, set, enrichment, analysis, plant

Funding: Ministry of Science and Technology of China ;
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Resource Name: PlantGSEA

Resource ID: SCR_016866

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260731T043006+0000

Ratings and Alerts

No rating or validation information has been found for PlantGSEA.

No alerts have been found for PlantGSEA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Yuan X, et al. (2025) The SUMO-conjugating enzyme OsSCE1a from wild rice regulates the functional stay-green trait in rice. *Plant biotechnology journal*, 23(2), 615.

Zhang N, et al. (2025) Deciphering the molecular logic of WOX5 function in the root stem cell organizer. *The EMBO journal*, 44(1), 281.

Hu Y, et al. (2025) An auxin response factor regulates tiller angle and shoot gravitropism by directly activating related gene expression in rice. *Journal of advanced research*, 78, 147.

Cao Y, et al. (2024) Nuclear lamina component KAKU4 regulates chromatin states and transcriptional regulation in the Arabidopsis genome. *BMC biology*, 22(1), 80.

Liu C, et al. (2022) eQTLs play critical roles in regulating gene expression and identifying key regulators in rice. *Plant biotechnology journal*, 20(12), 2357.

Li M, et al. (2022) The Transcriptional Responses of Ectomycorrhizal Fungus, *Cenococcum geophilum*, to Drought Stress. *Journal of fungi (Basel, Switzerland)*, 9(1).

You C, et al. (2021) Proteomic Analysis of Generative and Vegetative Nuclei Reveals Molecular Characteristics of Pollen Cell Differentiation in Lily. *Frontiers in plant science*, 12, 641517.

Wu X, et al. (2021) Enhancing rice grain production by manipulating the naturally evolved cis-regulatory element-containing inverted repeat sequence of OsREM20. *Molecular plant*, 14(6), 997.

Rajavel A, et al. (2021) Unravelling the Complex Interplay of Transcription Factors Orchestrating Seed Oil Content in *Brassica napus* L. *International journal of molecular sciences*, 22(3).

Zhang F, et al. (2021) The landscape of gene-CDS-haplotype diversity in rice: Properties, population organization, footprints of domestication and breeding, and implications for genetic improvement. *Molecular plant*, 14(5), 787.

Wu TY, et al. (2020) Genome Wide Analysis of the Transcriptional Profiles in Different Regions of the Developing Rice Grains. *Rice* (New York, N.Y.), 13(1), 62.

Liu P, et al. (2020) Integrating transcriptome and metabolome reveals molecular networks involved in genetic and environmental variation in tobacco. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 27(2).

Alvarez JM, et al. (2020) Transient genome-wide interactions of the master transcription factor NLP7 initiate a rapid nitrogen-response cascade. *Nature communications*, 11(1), 1157.

Yan J, et al. (2020) SR4R: An Integrative SNP Resource for Genomic Breeding and Population Research in Rice. *Genomics, proteomics & bioinformatics*, 18(2), 173.

Da L, et al. (2019) AppleMDO: A Multi-Dimensional Omics Database for Apple Co-Expression Networks and Chromatin States. *Frontiers in plant science*, 10, 1333.

Zhang Y, et al. (2019) Comprehensive analysis of dynamic gene expression and investigation of the roles of hydrogen peroxide during adventitious rooting in poplar. *BMC plant biology*, 19(1), 99.

Bei X, et al. (2019) Re-sequencing and transcriptome analysis reveal rich DNA variations and differential expressions of fertility-related genes in neo-tetraploid rice. *PloS one*, 14(4), e0214953.