Resource Summary Report

Generated by NIF on May 16, 2025

Ensembl Plants

RRID:SCR_008680

Type: Tool

Proper Citation

Ensembl Plants (RRID:SCR_008680)

Resource Information

URL: http://plants.ensembl.org/index.html

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Description: The Ensembl Genomes project produces genome databases for important species from across the taxonomic range, using the Ensembl software system. Five sites are now available, one of which is Ensembl Plants, which houses plant species. Sponsors: EnsembPlants is a project run by EMBL - EBI to maintain annotation on selected genomes, based on the software developed in the Ensembl project developed jointly by the EBI and the Wellcome Trust Sanger Institute.

Synonyms: EnsemblPlants

Resource Type: data or information resource, database

Keywords: database, genome, plant, software, specie, taxonomic, FASEB list

Funding:

Resource Name: Ensembl Plants

Resource ID: SCR_008680

Alternate IDs: nif-0000-33715

Record Creation Time: 20220129T080248+0000

Record Last Update: 20250507T060632+0000

Ratings and Alerts

No rating or validation information has been found for Ensembl Plants.

No alerts have been found for Ensembl Plants.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1100 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Mangini G, et al. (2025) Genome-wide association study identifies QTL and candidate genes for grain size and weight in a Triticum turgidum collection. The plant genome, 18(1), e20562.

Murithi A, et al. (2025) Global Transcriptomic Analysis of Inbred Lines Reveal Candidate Genes for Response to Maize Lethal Necrosis. Plants (Basel, Switzerland), 14(2).

Zhang Y, et al. (2025) Wheat TaPYL9-involved signalling pathway impacts plant drought response through regulating distinct osmotic stress-associated physiological indices. Plant biotechnology journal, 23(2), 352.

Jiang X, et al. (2025) The whole-genome dissection of root system architecture provides new insights for the genetic improvement of alfalfa (Medicago sativa L.). Horticulture research, 12(1), uhae271.

Rizwan HM, et al. (2025) The members of zinc finger-homeodomain (ZF-HD) transcription factors are associated with abiotic stresses in soybean: insights from genomics and expression analysis. BMC plant biology, 25(1), 56.

Wang X, et al. (2025) Genome-wide identification and functional roles relating to anthocyanin biosynthesis analysis in maize. BMC plant biology, 25(1), 57.

Sertse D, et al. (2025) Genome scans capture key adaptation and historical hybridization signatures in tetraploid wheat. The plant genome, 18(1), e20410.

Peters Haugrud AR, et al. (2025) Future of durum wheat research and breeding: Insights from early career researchers. The plant genome, 18(1), e20453.

Wang HW, et al. (2025) Identification, characterization, and expression of Oryza sativa tryptophan decarboxylase genes associated with fluroxypyr-meptyl metabolism. The plant genome, 18(1), e20547.

Krishnan M, et al. (2025) A novel mutation in SoIAA20 confers cross-resistance to 2,4-Dichlorophenoxyacetic acid and other auxinic herbicides in Sonchus oleraceus. Pest

management science, 81(1), 141.

Huang X, et al. (2025) Mutation spectra and genotype?phenotype analysis of congenital hypothyroidism in a neonatal population. Biomedical reports, 22(2), 30.

Liang X, et al. (2025) Genome-Wide Identification of GmPIF Family and Regulatory Pathway Analysis of GmPIF3g in Different Temperature Environments. International journal of molecular sciences, 26(2).

Zhao Y, et al. (2025) Genome-Wide Identification of CONSTANS-like (COL) Gene Family and the Potential Function of ApCOL08 Under Salt Stress in Andrographis paniculata. International journal of molecular sciences, 26(2).

Yang T, et al. (2025) Genome-Wide Study of Plant-Specific PLATZ Transcription Factors and Functional Analysis of OsPLATZ1 in Regulating Caryopsis Development of Rice (Oryza sativa L.). Plants (Basel, Switzerland), 14(2).

Zhou W, et al. (2025) Genome-wide identification of CAMTA gene family in teak (Tectona grandis) and functional characterization of TgCAMTA1 and TgCAMTA3 in cold tolerance. BMC plant biology, 25(1), 35.

Steele K, et al. (2025) Thousands of trait-specific KASP markers designed for diverse breeding applications in rice (Oryza sativa). G3 (Bethesda, Md.), 15(1).

Kumar M, et al. (2025) Identification of resistance sources and genomic regions regulating Septoria tritici blotch resistance in South Asian bread wheat germplasm. The plant genome, 18(1), e20531.

Cui J, et al. (2025) Genome-wide identification and expression analysis of CBF/DREB1 gene family in Medicago sativa L. and functional verification of MsCBF9 affecting flowering time. BMC plant biology, 25(1), 87.

Zhang J, et al. (2025) Genome- and Transcriptome-Wide Characterization and Expression Analyses of bHLH Transcription Factor Family Reveal Their Relevance to Salt Stress Response in Tomato. Plants (Basel, Switzerland), 14(2).

Fang H, et al. (2025) Unveiling the Role of GhP5CS1 in Cotton Salt Stress Tolerance: A Comprehensive Genomic and Functional Analysis of P5CS Genes. Plants (Basel, Switzerland), 14(2).