

Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

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: 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: EnsemblPlants 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

Availability: Free, Freely available,

Resource Name: Ensembl Plants

Resource ID: SCR_008680

Alternate IDs: nif-0000-33715, r3d100011199

Alternate URLs: <https://doi.org/10.17616/R3CD1Q>

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260912T200201+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 2191 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Esposito S, et al. (2026) Reverse BSA-QTLseq: A new genotype-driven bioinformatics approach for simultaneous trait mapping. *Plant communications*, 7(1), 101588.

Darvishzadeh R, et al. (2026) Genome-wide assessment of genetic diversity and selective signatures in sunflower (*Helianthus annuus* L.) using a 10??K SNP array. *Scientific reports*, 16(1).

Sokhtanlo S, et al. (2026) Wheat transcriptome changes in response to the black stem rust pathogen (*Puccinia graminis* f. sp. *tritici*). *BMC biotechnology*, 26(1).

Zanotto S, et al. (2026) Characterization of Genetic Diversity and Genomic Prediction of Secondary Metabolites in Pea Genetic Resources. *Plants (Basel, Switzerland)*, 15(3).

Chen J, et al. (2026) Analysis of the TGA gene family and the role of SITGA03 in tomato resistance to *Meloidogyne enterolobii*. *BMC genomics*, 27(1).

Li J, et al. (2026) The FBXL Gene Family in Tobacco (*Nicotiana tabacum* L.): Identification and Expression Response to TMV and Abiotic Stresses. *Antioxidants (Basel, Switzerland)*, 15(2).

Wang Z, et al. (2026) Methionine Synthase Positively Regulates Plant Defence to Both RNA and DNA Viruses and Is Useful for Developing Broad-Spectrum Antiviral Resistance in Crops. *Plant biotechnology journal*, 24(6), 3821.

Sun Y, et al. (2026) Systematic analysis of the Diacylglycerol acyltransferase (DGAT) genes in oat and functional characterization of AsDGAT2-1 involved in oil accumulation and cold stress tolerance. *BMC plant biology*, 26(1).

Sabouri H, et al. (2026) Uncovering the potential MTAs, candidate genes and microRNAs regulatory networks involved in salinity stress tolerance triggered in Iranian *Aegilops tauschii*. *Scientific reports*, 16(1), 6877.

Liang J, et al. (2026) Evolutionary analysis of ascorbate-glutathione cycle genes across green plants with lineage-specific profiling in grapevine (*Vitis vinifera* L.). *Horticulture research*, 13(1), uhaf247.

Wang R, et al. (2026) Genome-Wide Identification and Analysis of Plant Cysteine Oxidase (PCO) Family Genes and Expression Pattern Under Abiotic Stresses in *Medicago sativa*. *International journal of molecular sciences*, 27(5).

Wang G, et al. (2026) Genome-Wide Identification of Ovarian Tumor Proteases Gene Family and Knockout of TaOTU6 Increases Grain Width and Weight in Wheat. *Plants (Basel, Switzerland)*, 15(5).

Xu Z, et al. (2026) Analysis of the TIL gene family in Brassicaceae species and functional study of BrTIL1 in cold tolerance. *Frontiers in plant science*, 17, 1794987.

Zhou H, et al. (2026) Genome-wide analysis of the GPAT gene family in wheat and the potential roles of TaGPAT58 and its homologs in male reproductive development. *Frontiers in plant science*, 17, 1779919.

Ebeed HT, et al. (2026) Integrative gene duplication and genome-wide analysis characterize Peroxin11 gene family in wheat. *BMC genomics*, 27(1).

Niu R, et al. (2026) Maize ZmGBSS1 Promotes Early Flowering and Enhances Drought Tolerance in *Arabidopsis*. *Plants (Basel, Switzerland)*, 15(7).

Liu D, et al. (2026) Genome-wide Identification and expression analysis of TOR signaling pathway components in apple in response to low nitrogen. *The plant genome*, 19(1), e70215.

Zhang Y, et al. (2026) Computational prediction-combined proteogenomics unveils widespread non-AUG translation initiation events in plants. *Nucleic acids research*, 54(7).

Kurt F, et al. (2026) A Phase-Dependent Model of Sorghum (*Sorghum bicolor*) Cold Acclimation: Integrating Multi-Layered Networks and Alternative Splicing Signatures. *Biology*, 15(7).

Hu K, et al. (2026) Functional analyses of homoeologous pericentromeric cohesion protective genes TaSGO1s during meiosis in *Triticum aestivum*. *BMC plant biology*, 26(1).