

Resource Summary Report

Generated by [RRID](#) on Aug 4, 2026

Plant Ontology

RRID:SCR_006494

Type: Tool

Proper Citation

Plant Ontology (RRID:SCR_006494)

Resource Information

URL: <http://www.plantontology.org>

Proper Citation: Plant Ontology (RRID:SCR_006494)

Description: Ontology and database that links plant anatomy, morphology and growth and development to plant genomics data. Plant Ontology Consortium develops, curates and shares controlled vocabularies (ontologies) that describe plant structures and growth and developmental stages, providing semantic framework for meaningful cross species queries across databases. PO is under active development to expand to encompass terms and annotations from all plants.

Abbreviations: PO

Synonyms: Plant Ontology Browser, PO Browser, Plant Ontology Consortium Database, PO Database, Plant Ontology Database, POC Database

Resource Type: ontology, database, data or information resource, controlled vocabulary

Defining Citation: [PMID:18628842](#), [PMID:18194960](#)

Keywords: obo, gene, development, anatomy, morphology, growth, genomics, database

Funding: NSF 0822201;
NSF 0321685

Resource Name: Plant Ontology

Resource ID: SCR_006494

Alternate IDs: SCR_006844, nlx_55564

License: Creative Commons Attribution-NoDerivs License v3

Record Creation Time: 20220129T080236+0000

Ratings and Alerts

No rating or validation information has been found for Plant Ontology.

No alerts have been found for Plant Ontology.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 31 mentions in open access literature.

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

Freschet GT, et al. (2021) A starting guide to root ecology: strengthening ecological concepts and standardising root classification, sampling, processing and trait measurements. *The New phytologist*, 232(3), 973.

Plackett ARG, et al. (2021) Conditional stomatal closure in a fern shares molecular features with flowering plant active stomatal responses. *Current biology : CB*, 31(20), 4560.

Roitsch T, et al. (2019) Review: New sensors and data-driven approaches-A path to next generation phenomics. *Plant science : an international journal of experimental plant biology*, 282, 2.

Ochoterena H, et al. (2019) The Search for Common Origin: Homology Revisited. *Systematic biology*, 68(5), 767.

Neveu P, et al. (2019) Dealing with multi-source and multi-scale information in plant phenomics: the ontology-driven Phenotyping Hybrid Information System. *The New phytologist*, 221(1), 588.

Gao W, et al. (2017) Margin based ontology sparse vector learning algorithm and applied in biology science. *Saudi journal of biological sciences*, 24(1), 132.

Hassani-Pak K, et al. (2017) Knowledge Discovery in Biological Databases for Revealing Candidate Genes Linked to Complex Phenotypes. *Journal of integrative bioinformatics*, 14(1).

Li J, et al. (2016) LegumeIP 2.0--a platform for the study of gene function and genome evolution in legumes. *Nucleic acids research*, 44(D1), D1189.

Reiser L, et al. (2016) Sustainable funding for biocuration: The Arabidopsis Information Resource (TAIR) as a case study of a subscription-based funding model. *Database : the journal of biological databases and curation*, 2016.

Moretto M, et al. (2016) VESPUCCI: Exploring Patterns of Gene Expression in Grapevine. *Frontiers in plant science*, 7, 633.

Kang YJ, et al. (2016) Translational genomics for plant breeding with the genome sequence explosion. *Plant biotechnology journal*, 14(4), 1057.

Thessen AE, et al. (2015) Emerging semantics to link phenotype and environment. *PeerJ*, 3, e1470.

Akiyama K, et al. (2014) RARGE II: an integrated phenotype database of Arabidopsis mutant traits using a controlled vocabulary. *Plant & cell physiology*, 55(1), e4.

Debat HJ, et al. (2014) Exploring the genes of yerba mate (*Ilex paraguariensis* A. St.-Hil.) by NGS and de novo transcriptome assembly. *PloS one*, 9(10), e109835.

Cooper L, et al. (2013) The plant ontology as a tool for comparative plant anatomy and genomic analyses. *Plant & cell physiology*, 54(2), e1.

Li D, et al. (2012) Building an efficient curation workflow for the Arabidopsis literature corpus. *Database : the journal of biological databases and curation*, 2012, bas047.

Ningthoujam SS, et al. (2012) Challenges in developing medicinal plant databases for sharing ethnopharmacological knowledge. *Journal of ethnopharmacology*, 141(1), 9.

Shrestha R, et al. (2012) Bridging the phenotypic and genetic data useful for integrated breeding through a data annotation using the Crop Ontology developed by the crop communities of practice. *Frontiers in physiology*, 3, 326.

Ferry-Dumazet H, et al. (2011) MeRy-B: a web knowledgebase for the storage, visualization, analysis and annotation of plant NMR metabolomic profiles. *BMC plant biology*, 11, 104.

Harnsomburana J, et al. (2011) Computable visually observed phenotype ontological framework for plants. *BMC bioinformatics*, 12, 260.