

Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

PO

RRID:SCR_006844

Type: Tool

Proper Citation

PO (RRID:SCR_006844)

Resource Information

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

Proper Citation: PO (RRID:SCR_006844)

Description: Ontology and database that links plant anatomy, morphology and growth and development to plant genomics data. The 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, Plant Ontology, PO Database, Plant Ontology Database, POC Database

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

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

Funding: NSF 0822201;
NSF 0321685

Availability: The community can contribute to this resource

Resource Name: PO

Resource ID: SCR_006844

Alternate IDs: nlx_55564

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Record Creation Time: 20220129T080238+0000

Record Last Update: 20260903T234857+0000

Ratings and Alerts

No rating or validation information has been found for PO.

No alerts have been found for PO.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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.

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.

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.

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).

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.

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.

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