

# Resource Summary Report

Generated by T1D on Aug 2, 2026

## PlantTribes

RRID:SCR\_007863

Type: Tool

### Proper Citation

PlantTribes (RRID:SCR\_007863)

### Resource Information

**URL:** <http://fgp.huck.psu.edu/tribedb/index.pl>

**Proper Citation:** PlantTribes (RRID:SCR\_007863)

**Description:** It is an objective classification system for plant proteins based on cluster analyses of the inferred proteomes of the sequenced angiosperms *Arabidopsis thaliana* v. Columbia, *Oryza sativa* v. japonica (Rice), and *Populus trichocarpa* (poplar). Sequence data for *Carica papaya* and *Medicago papaya* are also included in the current version of Tribes. Results for these species are currently masked from view, but will be available when the genomes are publicly released. In addition to the genome-based tribe scaffold, unigenes from more than 200 plant and algal species TIGR Transcript Assemblies have been associated with each tribe (see documentation), resulting in a global classification of about 4 million putative plant protein sequences. PlantTribes 1.0 incorporates an extensive collection of microarray expression data from *Arabidopsis* microarray experiments. Expression data is linked to the individual genes in PlantTribes, and can be accessed through any result including *Arabidopsis* gene sequences. PlantTribes is based on the similarity-based clustering procedure TribeMCL (Enright et al, 2002,2003) to classify protein-coding genes into putative gene families. MCL classifications have been constructed using three clustering stringencies, allowing the user to explore the stability of the protein classification. A second round of MCL clustering identifies SuperTribes that approximate objective superfamilies. PlantTribes also includes information about domains, traditional gene family names, and a unified nomenclature based on common terms.

**Synonyms:** PlantTribes

**Resource Type:** data or information resource, database

**Resource Name:** PlantTribes

**Resource ID:** SCR\_007863

**Alternate IDs:** nif-0000-03312

**Record Creation Time:** 20220129T080244+0000

**Record Last Update:** 20260801T190949+0000

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## Ratings and Alerts

No rating or validation information has been found for PlantTribes.

No alerts have been found for PlantTribes.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 7 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#) .

Winters NP, et al. (2025) Local gene duplications drive extensive NLR copy number variation across multiple genotypes of *Theobroma cacao*. *G3* (Bethesda, Md.), 15(9).

Timilsena PR, et al. (2023) Phylotranscriptomic Analyses of Mycoheterotrophic Monocots Show a Continuum of Convergent Evolutionary Changes in Expressed Nuclear Genes From Three Independent Nonphotosynthetic Lineages. *Genome biology and evolution*, 15(1).

O'Donnell AJ, et al. (2021) Convergent Biochemical Pathways for Xanthine Alkaloid Production in Plants Evolved from Ancestral Enzymes with Different Catalytic Properties. *Molecular biology and evolution*, 38(7), 2704.

Cao S, et al. (2020) Characterization of the AP2/ERF Transcription Factor Family and Expression Profiling of DREB Subfamily under Cold and Osmotic Stresses in *Ammopiptanthus nanus*. *Plants* (Basel, Switzerland), 9(4).

Conze LL, et al. (2017) Transcriptome profiling of tobacco (*Nicotiana tabacum*) pollen and pollen tubes. *BMC genomics*, 18(1), 581.

Goyet V, et al. (2017) Haustorium initiation in the obligate parasitic plant *Phelipanche ramosa* involves a host-exudated cytokinin signal. *Journal of experimental botany*, 68(20), 5539.

McCarthy TW, et al. (2014) Phylogenetic analysis of pectin-related gene families in *Physcomitrella patens* and nine other plant species yields evolutionary insights into cell walls. *BMC plant biology*, 14, 79.