

About PhyloGenes

PhyloGenes is a web resource that displays pre-computed phylogenetic trees of gene families alongside experimental gene function data to facilitate inference of unknown gene function in plants.

PhyloGenes is maintained by the nonprofit [Phoenix Bioinformatics Corporation](#). It is co-developed by Phoenix Bioinformatics and the [PANTHER](#) project at University of Southern California. Its initial development was supported by funding provided by the National Science Foundation ([Grant No. DBI-1661543](#)).

Citing PhyloGenes:

[PhyloGenes: An online phylogenetics and functional genomics resource for plant gene function inference](#)

Zhang P, Berardini TZ, Ebert D, Li Q, Mi H, Muruganujan A, Prithvi T, Reiser L, Sawant S, Thomas PD, Huala E

Plant Direct. 2020 Dec;4(12):e00293

Current release (version 4.1)

November 15, 2022. We are pleased to announce the **PhyloGenes version 4.1** release. ***This release updates only the GO annotation data and the publications counts for the gene family members.*** The gene families and gene trees are the same as for the PhyloGenes 4.0 release and are still from the [PANTHER 17.0 release](#). Genes from other genomes in the PANTHER build have been removed (pruned). [More stats](#)

Updated GO annotations: Experimental gene function annotations were extracted from the Gene Ontology Consortium ([files created by PANTHER](#) on 2022-10-27, based on the 2022-07-01 GO release). Phylogenetic inferred gene function annotations were extracted from the [GO PAINT project](#) (generated on [2022-09-26](#), based on the [2022-07-01 GO release](#) which uses PANTHER 15 tree information, downloaded by the PhyloGenes team on 2022-10-20).

Please [take a few minutes](#) to share with us your experience of using the PhyloGenes resource.