

Release Notes Archive

PhyloGenes 4.0

May 11, 2022. We are pleased to announce the **PhyloGenes version 4.0** release. The gene families and gene trees are from the [PANTHER 17.0 release](#). In PhyloGenes only genes from [plant genomes and selected non-plant model organisms](#) were included. 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 on 2022-01-13). Phylogenetic inferred gene function annotations were extracted from the [GO PAINT project](#) (downloaded on 2022-03-22, based on the [2022-01-13 GO release](#) which uses PANTHER 15 tree information).

Improved user interface and user experience: We have split out functionality for Downloads from Tools into two separate menus to make these actions clearer and more easily accessible. We have also introduced wording to suggest pruning a tree to a subset of species when accessing trees that contain more than 500 sequences. The pruned view will give each user a customized view of their gene family and a faster page load time.

PhyloGenes 3.2

September 21, 2021. We are pleased to announce the **PhyloGenes version 3.2** release. The gene families and gene trees are not changed in this release. They are still based on the [PANTHER 16.0 release](#). As always in PhyloGenes, only genes from [plant genomes and selected non-plant model organisms](#) were included and genes from other genomes in the PANTHER build have been removed (pruned). [More stats](#)

Updated GO annotations: Experimental gene function data was extracted from the Gene Ontology Consortium (files created on 2021-07-19). Phylogenetically-inferred gene function data was extracted from the [PAINT project](#) (files created on 2021-07-19).

Improved user interface and user experience: This release features enhanced technology behind our gene family pages. Page loading and scrolling are now faster and smoother for large gene trees that also have extensive number of GO annotations to the family members. For an even better site experience, we recommend that users [use the on-the-fly tree pruning and gene table customization options](#). Customization not only speeds up the page loading time but also allows you to focus on the species of interest and the GO functional aspects most relevant to your study.

New! Publications now available!: Extensive publication lists for individual family members can now be accessed via hyperlinks from the gene information table. The publication counts are retrieved from [UniProt](#) via their API and will be updated on a quarterly basis.

PhyloGenes 3.1

May 18, 2021. We are pleased to announce the **PhyloGenes version 3.1** release. The gene families and gene trees are from the [PANTHER 16.0 release](#). In PhyloGenes only genes from [plant genomes and selected non-plant model organisms](#) were included. Genes from other genomes in the PANTHER build have been removed (pruned). [More stats](#)

Experimental gene function annotations were extracted from the Gene Ontology Consortium (files created on 2021-04-01). Phylogenetic inferred gene function annotations were extracted from the [GO PAINT project](#) (files created on 2021-04-01).

External gene links were added:

- maizeGDB (for maize genes)
- SoyBase (for soybean genes)
- SGN (for tomato genes)
- GrainGenes (for wheat and barley genes)
- TAIR (for Arabidopsis genes)

More external links will be added over time.

PhyloGenes 3.0

February 11, 2021. We are pleased to announce the **PhyloGenes version 3.0** release. In this release the gene families and gene trees were updated from the [PANTHER 15.0 release](#) to [PANTHER 16.0 release](#). In PhyloGenes only genes from [plant genomes and selected non-plant model organisms](#) were included. Genes from other genomes in the PANTHER build have been removed (pruned). [More stats](#)

Experimental gene function data was extracted from the Gene Ontology Consortium (files created on 2020-12-07). Phylogenetic inferred gene function data was extracted from the [GO PAINT project](#) (files created on 2021-01-04).

PhyloGenes 2.2

December 4, 2020. We are pleased to announce the PhyloGenes version 2.2 release. The gene families and gene trees are from the [PANTHER 15.0 release](#). In PhyloGenes only genes from [plant genomes and selected non-plant model organisms](#) were included. Genes from other genomes in the PANTHER build have been removed (pruned). [More stats](#)

Experimental gene function data was extracted from the Gene Ontology Consortium (files created on 2020-04-28). Phylogenetic inferred gene function data was extracted from the [PAINT project](#) (files created on 2020-05-21).

What's new:

- You can download the multiple sequence alignment of a gene family. This feature is accessed from the Operations menu icon above a gene tree.
- Click on a gene, a leaf node on a gene tree, you will be able to download a list of its plant orthologs. [More...](#)

PhyloGenes 2.1

August 14, 2020. We are pleased to announce the PhyloGenes version 2.1 release. The gene families and gene trees are from the [PANTHER 15.0 release](#). In PhyloGenes only genes from [plant genomes and selected non-plant model organisms](#) were included. Genes from other genomes in the PANTHER build have been removed (pruned). [More stats](#)

Experimental gene function data was extracted from the Gene Ontology Consortium (files created on 2020-04-28). Phylogenetic inferred gene function data was extracted from the [PAINT project](#) (files created on 2020-05-21).

What's new:

- We added experimentally validated gene function annotations from GO Biological Process
- We added phylogenetic inferred gene functions (GO Biological Process and Molecular Function)
- Added feature to customize Gene information display to show/hide selected data and reorder columns. [More details](#)

PhyloGenes 2.0

March 4, 2020. We are pleased to announce the PhyloGenes version 2.0. A total of 8512 gene families are included in this release. The gene families and gene trees are pruned versions of [PANTHER 15.0 release](#). They contain only genes from [plant genomes and selected non-plant model organisms](#). Genes from other genomes in the PANTHER build have been removed (pruned). Experimental gene function data are extracted from the files available from the [Gene Ontology Annotations \(GOA\)](#) project at the EBI (file generated on 2020-02-07). [More stats](#)

What's new:

- 10 more plant genomes were added to gene families including potato, cassava, oilseed rape (see complete species list [here](#))
- You can select an organism to have its genes highlighted in a tree
- Easier tree browsing using mouse wheel or trackpad for scrolling
- Better alignment between a tree and its gene information table
- Compact UI showing more data on a family page
- Safari and Firefox browsers are now supported

PhyloGenes 1.2

We are pleased to announce the PhyloGenes version 1.2 release (released on November 8, 2019). The gene family build has not changed in this release. The gene families and gene trees are pruned versions of [PANTHER 14.1 release](#). They contain only genes from [selected plant genomes and 10 non-plant model organisms](#). Genes from other genomes in the PANTHER build have been removed (pruned). [More stats](#)

What's new

- Experimental gene function data have been updated. They were extracted using the QuickGO REST API (<https://www.ebi.ac.uk/QuickGO/api/index.html>) on 2019-10-25.
- Toggle to see multiple sequence alignment (MSA) of a gene family ([more](#))
- Graft your sequence to an existing PhyloGenes gene family tree (for species not included in PhyloGenes) ([more](#))

We enhanced the alignment between trees and their adjacent gene information tables. Leaf nodes in a tree now stay aligned with their corresponding gene rows in the gene table when resizing to a narrow browser window. We also fixed a rare data bug where some members were missing from the DUF641 gene family tree. If you notice anything else wrong [please let us know!](#)

PhyloGenes 1.1

We are pleased to announce the PhyloGenes version 1.1 release (released on August 1, 2019). A total of 8171 gene families are included in this release. The gene families and gene trees are pruned versions of [PANTHER 14.1 release](#). They contain only genes from [selected plant genomes and 10 non-plant model organisms](#). Genes from other genomes in the PANTHER build have been removed (pruned). Experimental gene function data are extracted from the files available from the [Gene Ontology Annotations \(GOA\)](#) project at the EBI (file generated on 2019-07-01). [More stats](#)

Highlights of new features of PhyloGenes gene tree display:

- Toggle between a compact view and a fully expanded view
- Remove (prune) selected organisms from a gene tree
- Tree images can be downloaded as PNG or SVG files
- Gene trees can be downloaded in PhyloXML format
- Gene data tables can be downloaded as csv files

PhyloGenes 1.0

We are pleased to announce the initial launch of [Phylogenies.org](#) and the PhyloGenes version 1.0 release (released on April 2, 2019). A total of 8173 gene families are included in this release. The gene families and gene trees are pruned versions of [PANTHER 14.0 release](#). They contain only genes from [selected plant genomes and 10 non-plant model organisms](#). Genes from other genomes in the PANTHER build have been removed (pruned). Experimental gene function data are extracted from the files available from the [Gene Ontology Annotations \(GOA\)](#) project at the EBI (file generated on 2018-12-03). [More stats](#)