Locus Page-Homologs Section

Homologs in TAIR

To facilitate comparison of protein function between Arabidopsis and other species, the TAIR locus pages includes resources and data to make it easier for you to find homologs and analyze gene families.

The gene family information is found just below the Protein Data band on the locus page and consists of the following feature bands:

- Gene Families
- Tree Viewer (PhyloGenes)
- Panther Plant Homologs

Gene Families

Each locus page also contains links to external Gene Family resources where you can access datasets of pre-computed gene families and ortholog sets that contain the locus of interest. Clicking on a link will either retrieve the corresponding locus entry in the external database or initiate a search of that resource with the Arabidopsis locus as the query term. Between those databases there is a lot of overlap but each has unique datasets so you may need to look at more than one to find out if your organism is represented. For example, Phytozome and PLAZA are specifically for finding plant orthologs, including close relatives of *Arabidopsis thaliana* , and contain many more plant genomes than PANTHER. PANTHER includes well curated genomes from many taxa that have been manually assigned functions which is useful when when using orthology for inferring functions of unknown genes.

PhyloGenes Tree Viewer

Clicking on the PhyloGenes icon will open a new tab that displays the PhyloGenes TreeViewer for the family containing the Arabidopsis locus of interest. PhyloGenes trees are based on the PANTHER families but contain only plant species and 10 representative non plant model organisms. If the locus is not part of a PANTHER family, this band will not display.

The PhyloGenes tool can be used to visualize gene families alongside functional annotation data. Some of the things you can do with the PhyloGenes Tree Viewer include:

- Expand and collapse nodes to show/hide families and subfamilies
- View duplications, gene transfer and gene loss events
- Toggle between annotation display and multiple sequence alignment display
- Prune species to remove from tree or highlight species in tree
- Download data such as the entire tree in PhyloXML format or annotation data in csv format

For more information on how to use Phylogenes please see the user guide and tutorials .

Plant Homologs on Locus Page

On each locus page we have incorporated homologs from the PANTHER project. PANTHER (Protein ANalysis THrough Evolutionary Relationships) is a high quality curated data resource for protein family classification. For a current list of genomes included in each PANTHER build see their genome statistics .

PANTHER includes only the most well annotated species from the UniProt reference genome set. PANTHER families are rigorously curated including phylo genetic inference of gene function.Please see the PANTHER website for more information and publications about this resource.

Arabidopsis Paralogs

This section displays links to Arabidopsis paralogs and links to download sequences or gene lists. If there are no paralogs, this band is not displayed.

Functions available in this section include:

- Links to TAIR locus pages. By default only the first few paralog IDS are show. Clicking on the ellipsis (...) will display a popup window containing the entire list of paralogs. Clicking on the locus name will open the corresponding TAIR locus page.
- Download Sequences. Clicking on this button will send the set of Arabidopsis paralog locus IDS to the bulk sequence download tool where you can retrieve the corresponding sequences of your choosing.
- Download AGI IDs. Clicking on this button will retrive a tab delimited text file containing the AGI Locus Identifiers and Primary Gene Symbol for the paralogs

Plant Orthologs

This section displays lists of plant orthologs from the PANTHER gene families. The orthologs are organized according to broad taxonomic groups. The number of orthologs per species is shown. If there are no orthologs, this band does not display.

Download Orthologs: Clicking this button will retrieve a tab delimited text file containing the list of orthologs from the PANTHER families. The file includes Organism, UniProt ID, Gene ID, Ortholog Type