

# The Arabidopsis Information Resource

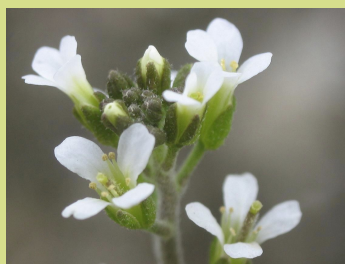


The Arabidopsis Information Resource (TAIR) is an online database of genetic and genomic information for the model plant *Arabidopsis thaliana*. Established in 1999, TAIR provides the most comprehensive and current set of plant gene function data. Although the development of TAIR was funded by the National Science Foundation, TAIR now operates under a non-profit subscription support model administered by Phoenix Bioinformatics.

Contact us at [subscriptions@arabidopsis.org](mailto:subscriptions@arabidopsis.org)

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## *Arabidopsis thaliana*



Because of its physical size, short life, and small genome, *Arabidopsis thaliana* is the preferred model organism for the study of gene function in higher plants. Many fundamental research questions in plant biology are studied in Arabidopsis, such as how plants grow, reproduce, sense their environment, and adapt to their surroundings. Approximately 4,000 research articles are published on Arabidopsis every year.

## TAIR is considered an indispensable resource by tens of thousands of researchers around the world.

TAIR is used by plant biologists worldwide because of the extensive experimental information available for Arabidopsis gene function and genome organization. The research results from *Arabidopsis thaliana* are often directly transferrable to other plant species, including crops and plants of special ecological or evolutionary interest.

“TAIR is *the* resource for plant scientists like me involved in both experimental and computational work... **The most important positive about TAIR is its curator team.** They are very involved in this work, are very quick to respond to a question, do not mind going back-and-forth on an issue, and are most willing to cater to very personalized requests. Rarely does a day go by when I don't use TAIR. It is a clear model for a web resource.”

–Dr. Arjun Krishnan, Princeton University, USA

“My research interests are plant miRNAs and other small RNAs. **The huge datasets provided by TAIR really helped us** doing bioinformatics analysis of small RNAs in Arabidopsis.”

–Yijun Meng, Dept. of Bioinformatics, Zhejiang University, China

“**TAIR saved me three months of map-based cloning work** due to its morphological phenotype database.”

–Dr. Christopher DeFraia, The Ohio State University, USA

“**The world's most valued plant database.**” –Nature 462, 258-259 (2008)

# Features

## Gene Ontology (GO) Annotations

GO-based functional annotation allows for powerful query and genome-wide data analysis.

## Alleles and Phenotypes

Details on mutagen, mutation location, and phenotypes linked to sources including publications and stock center observations.

## Locus Pages

Arabidopsis gene function, mutant phenotypes, expression pattern, new publications and related data are updated weekly from the latest research literature.

## SeqViewer

Find Arabidopsis sequence and annotation. View results on the whole genome, closeup, or nucleotide level. Tracks include genes, cDNA and ESTs, insertion mutants, SNPs, markers, and BACs.



# TAIR Tools

## Search, Browse, and Display

### Comprehensive Search

- Search for genes, loci, proteins, DNA, seed stocks, and much more with our comprehensive search

### Textpresso Full Text

- Partnership with Wormbase/Caltech
- Extracts and processes information for biological literature
- Searches over 40,000 full-text plant biology research articles in TAIR

### Other Data Types:

- Polymorphisms, germplasms, ecotypes, proteins, and more!

## Data Visualization

### Map Viewer

- View and compare genetic, physical, and sequence maps

### GBrowse

- Search or browse a map of the Arabidopsis genome
- Upload your own annotation track

### WU-Blast

- Visualize matching segments on your nucleotide or protein query sequence

### Chromosome Map Tool

- Maps your favorite genes and relates them to the five Arabidopsis chromosomes in a graphic format

## Data Analysis

### GO Term Enrichment

- Uses the PANTHER term enrichment service to find over- or underrepresented GO terms in sets of genes
- Can be used for any plant species in the PANTHER genome set

### BLAST

- Compares your sequences with specialized datasets developed by TAIR for the community

### Pattern Matching

- Searches TAIR datasets for short nucleotide and peptide sequences or degenerate patterns

### Motif Analysis

- Finds overrepresented 6-mer oligonucleotides in upstream regions of Arabidopsis genes

### Bulk Data Retrieval

- Retrieve gene summaries, GO annotations, sequences, proteins, locus history, and microarray elements for list of genes

# Subscriptions

Academic researchers have relied on TAIR for decades. We aim to keep TAIR sustainable as long as there is a need for this resource.

- Data in TAIR is updated weekly.
- Subscriptions are required for unlimited access to all data and analysis tools.

**TAIR runs on a usage-based, tiered pricing system.**

- Every subscription provides the same access to the same database.
- The pricing tier for each institution is based on usage history, not institution size.
- Subscriptions can be ordered for any timeframe between six months and five years.

## Single Year Subscriptions

Tier	2023 Price (USD)
Tier 1	\$9,350
Tier 2	\$6,600
Tier 3	\$3,575
Tier 4	\$1,400

## Multi-Year Subscriptions

### Paid Annually

- Cap your price increase for future years
- Billed automatically every year

### Prepaid Subscriptions

- Keep fee locked in for future years
- Pay full amount upfront

Subscriptions can be purchased on a multi-year basis (either Prepaid or Paid Annually) for 2, 3, 4, or 5 years.

## Other Options

### Consortium Subscriptions

- We offer a 10% discounted rate when two or more institutions sign up in a multi-institution consortium
- If you are interested in this option, please contact us and the librarians at other interested institutions

### Trial Subscriptions

- Because we offer metered access, we don't offer trials, but your institution can subscribe for a shorter time period than a year, such as six months

Still can't find an option that works for you?

- Contact us at [subscriptions@arabidopsis.org](mailto:subscriptions@arabidopsis.org) and we'd be happy to help

# How the Subscription Process Works

# 1

## Metered Access

- Non-subscribers automatically get a limited numbers of free page views per month.
- Phoenix uses Google Analytics to track the number of visits to the data pages from each institution.

# 2

## Contact Phoenix Bioinformatics For a Quote

- Individual users contact their librarians to request a TAIR subscription.
- Librarians contact Phoenix Bioinformatics ([subscriptions@arabidopsis.org](mailto:subscriptions@arabidopsis.org)) to request a price quote for a TAIR subscription.

# 3

## Usage-Based Institutional Pricing

- The total number of visits from an institution over the previous year (September 1 - August 31) is used to set the subscription price for the following year.
- Phoenix uses this data to decide a particular institution's price tier, calculate a quote, and develop a licensing agreement

# 4

## Agreement and Full Access

- Phoenix quickly activates the institution's subscription. Enjoy your access to the most comprehensive plant genome database!

# What makes TAIR different

## ...from bibliographic databases

TAIR is a continuously curated genome database specifically focused on Arabidopsis.

Plant biologists with graduate or postdoctoral training curate and integrate experimental results about Arabidopsis gene function from the primary literature.

The information is presented in a highly integrated and standardized format for efficient querying and use in large scale data analyses.

Searches within TAIR are not bibliographic searches; a search in TAIR is a search through the accumulated and interconnected knowledge about Arabidopsis, including specialized annotations, keywords, and categories, with citations and links to the articles from which the information was gathered.

## ...from other databases

TAIR produces gene function annotation data through an in-house curation effort and by working directly with authors via scholarly collaboration.

TAIR shares data for public reuse after it has been in the TAIR system for one year-- which means that the TAIR data on other sites is at least a year out of date.

TAIR continuously updates its database, including gene function information, gene symbols, alleles, mutant phenotypes, publications, and gene expression patterns.

In addition, TAIR's expert biocurators are within easy reach via the TAIR Helpdesk, which provides personalized datasets to subscribers upon request.

## Community Services



### Arabidopsis Gene Symbol Registry

Register a class gene symbol



### TAIR Online Annotation Submission Tool (TOAST)

Web-based tool for community members to submit gene function annotations and interactions from literature.



### User Support

Extensive user support services including a help desk staffed by trained biocurators, response time, online video tutorials, help documentation, and more...