



AraCyc Metabolic Pathway Annotation

AraCyc – An overview

- AraCyc is a metabolic pathway database for *Arabidopsis thaliana*;
- Computational prediction by PathoLogic software using MetaCyc as the reference database (Peter Karp, SRI);
- Predicted pathways were then manually validated; ongoing manual curation.

Recent AraCyc releases


	AraCyc 2.1 Apr 2005	AraCyc 2.5 Oct 2005	AraCyc 2.6 May 2006	AraCyc 3.5 Feb 2007
Total pathways	221	197	228	262
New	-	37	35	51
Updated	-	0	4	37
Deleted	-	61	6	12
Pathways manually reviewed with literature evidence	71 (32%)	170 (86%)	201 (88%)	233 (89%)

Upcoming AraCyc 4.0

- New pathways, updated pathways
- Gene function annotation updated according to TAIR7 genome release
- Significant changes of the assignment of genes to reactions/pathways

Outline

- Search and browse AraCyc
- Arabidopsis Metabolic map
- OmicsViewer


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The Arabidopsis Information Resource

The Arabidopsis Information Resource (TAIR) is a comprehensive biology data for the model high plant. It provides the complete genome sequence, gene annotations, metabolism, gene expression data, protein-protein interactions, markers, publications, and information on gene function. Product function data is updated regularly and community data submissions are accepted. Computational and manual methods are used to annotate genes. TAIR also provides external resources.

The Arabidopsis Biological Resource Project (ABR) preserves and distributes seed and DNA samples for Arabidopsis species. Stock information and ordering details can be found at [www.abr.org](#).

⚙ The 18th Annual Arabidopsis Research Conference

More details can be found at [http://www.arabidopsis.org/conference/](#)

18th International Conference on Arabidopsis Research
Beijing, China June 20-23, 2007

Note: This site has been tested with Netscape 8.1, IE6.X(Win), S

- Tools Overview
- Seqviewer
- Mapviewer
- AraCyc Metabolic Pathways
- BLAST
- WU-BLAST
- FASTA
- Patmatch
- Motif Analysis
- VxInsight
- Java Tree View
- Bulk Data Retrieval
- Chromosome Map Tool
- Gene Hunter
- Restriction Analysis
- Gene Symbol Registry

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BLAST	
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Contributors

Search AraCyc

Browse pathways, enzymes, genes, compounds

AraCyc Tutorials

Paint experiments on the metabolic map

Metabolic Map

'Bird's eye' view of the Arabidopsis metabolic network

Data submission

[Search AraCyc](#) This link allows you to search for compounds, enzymes, etc.

[Introduction](#) You will find here a brief history of the creation of AraCyc and the current status.

[Metabolic Map](#) The Metabolic map provides you with a 'bird's eye' view of *Arabidopsis* metabolism currently stored in AraCyc. (**Note:** This map is not a complete representation of the entire metabolic network. For more info, visit the [Tutorial](#) (contains QuickTime movies).

[Pathway Data Submission Form](#) Your input is invaluable! This preformatted Excel form allows you to send us your suggestions: pathway updates (comments, enzymes...), new pathways or even to point out mistakes.

[Release Notes](#) What's new in the latest AraCyc release? You will find it here along with comprehensive lists of pathways that have been added to and deleted from AraCyc over time.



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AraCyc Tutorial

Searching AraCyc:
Pathways, Reactions,
Genes and Compounds

Understanding the
AraCyc Detail Pages

Browsing AraCyc:
Pathways, Reactions,
Genes and Compounds

Using the Metabolic Map
Overview

Displaying Gene
Expression, Proteomic,
Metabolomic and other
Data in the Omics Viewer

Evidence Codes and
Their Usage in AraCyc

**Demos-Quicktime
Movies**

AraCyc Home

QuickTime Movies

The following movies illustrate some of the features of AraCyc described in this tutorial.

To view the movies you will need to have Quicktime installed on your computer



Tutorial Demo: [Searching and Browsing AraCyc](#)

This Quicktime movie demonstrates how to use the simple search and browse features to query AraCyc.

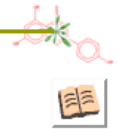
Tutorial Demo: [AraCyc Metabolic Map Overview](#)

This Quicktime movie demonstrates how to browse pathways in AraCyc starting from the metabolic pathway overview diagram.

Tutorial Demo: [Using the Omics Viewer](#)

This Quicktime movie demonstrates how to use the Omics viewer to overlay gene expression data onto the pathway overview.

A pathway example: sucrose biosynthesis



AraCyc Pathway: sucrose biosynthesis

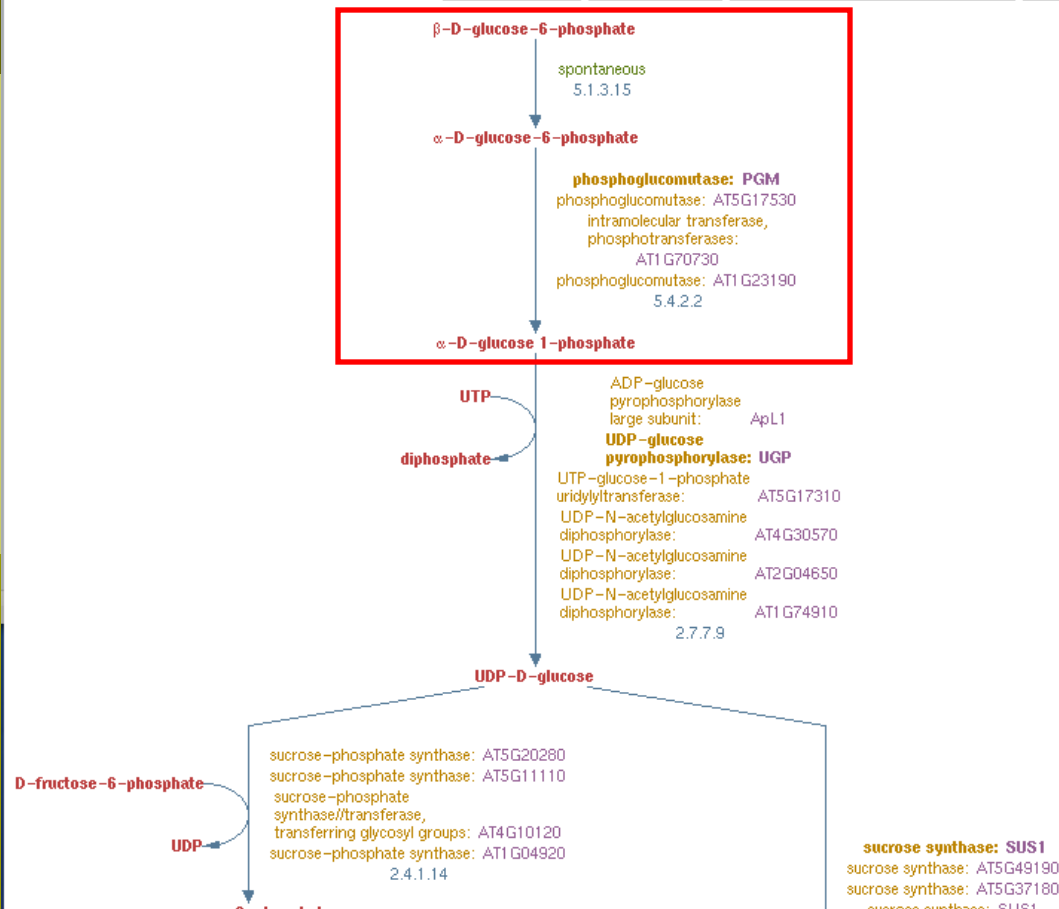
More Detail

Less Detail

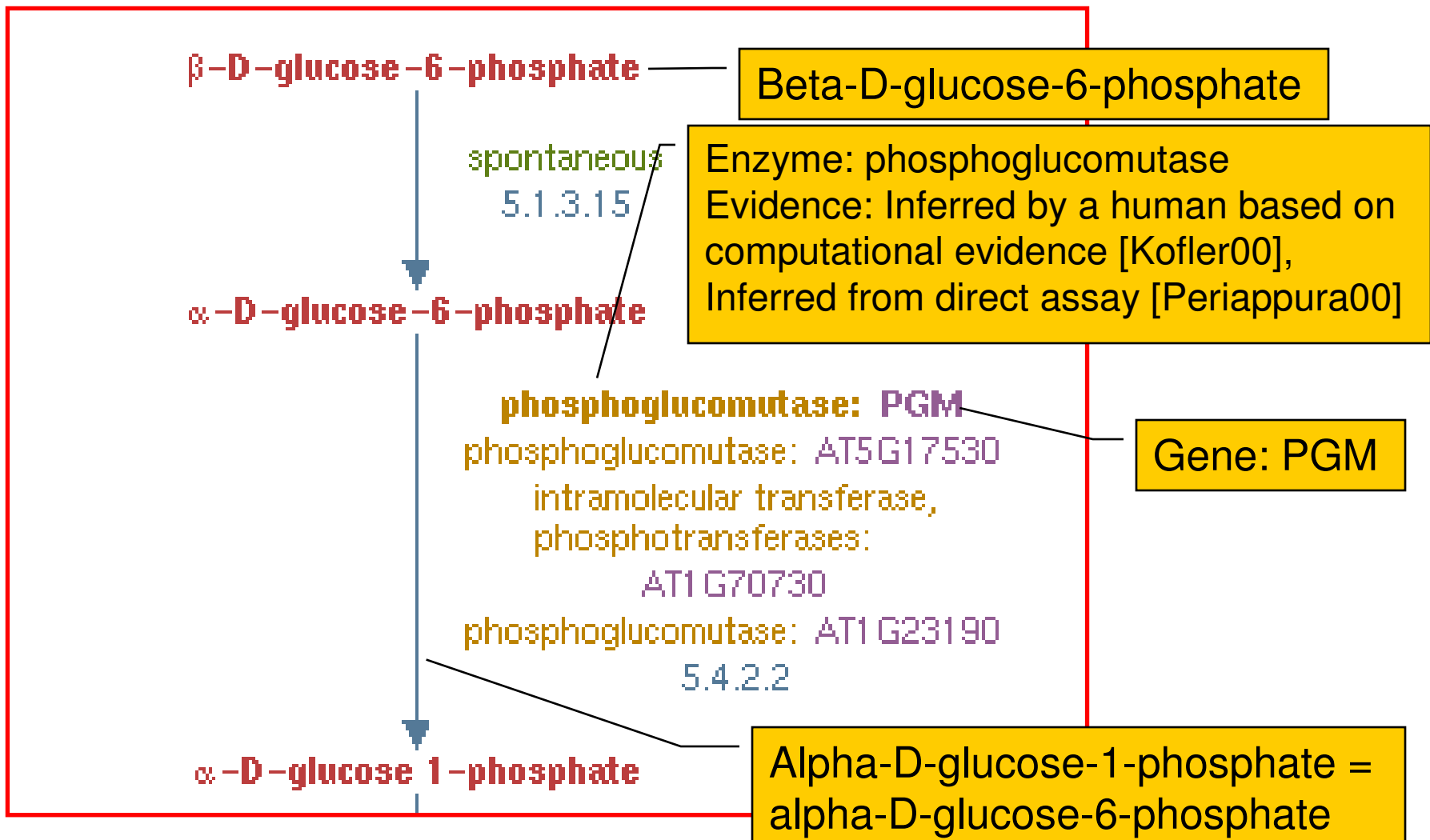
Cross-Species Comparison

Download Genes

BioPAX format



A pathway example: sucrose biosynthesis



Pathway Tools Query Page

This form provides several different mechanisms for querying Pathway/Genome Databases.

Select a dataset:

- **Query** 

To retrieve data, click Submit. EC numbers

All (by name or EC#)

Protein (by name or EC#)

Pathway (by name)

you wish to retrieve, then enter the name of the object. The object will be returned. You may also enter multiple names.

- **Browse** 

Each dataset contains compounds

Pathways

Pathways

EC Hierarchy

Compounds

Genes

Pathways

Biosynthesis

Degradation/Utilization/Assimilation

Generation of precursor metabolites and energy

Super-Pathways

- **Choose**
- **Links**
 - [Summary page for dataset](#)
 - [Cellular Overview Diagram/Omics Viewer](#) (not available for MetaCyc)
 - [History of updates to this dataset](#)
 - [PathoLogic Pathway Analysis](#) (not available for *E. coli* or MetaCyc)

- **[Comparative Analysis](#)**

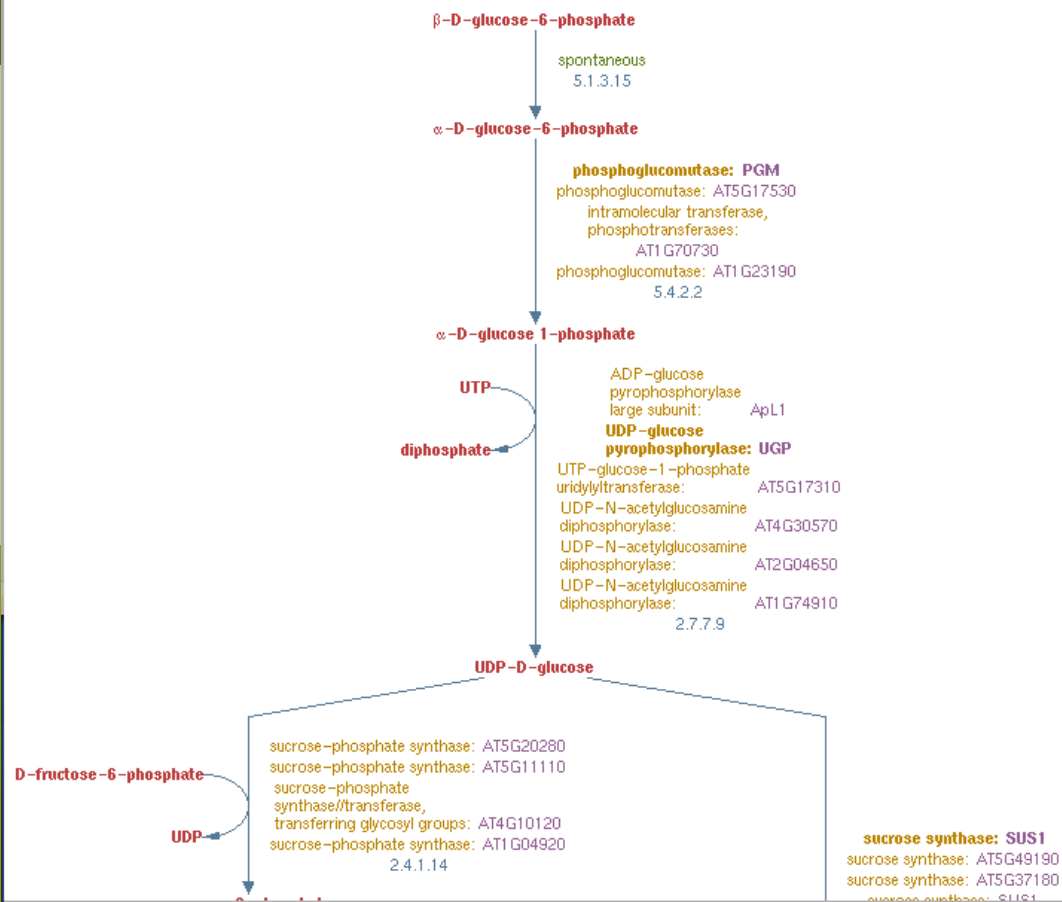
Generate summary tables that compare various properties across one or more selected organisms.

Evidence codes



AraCyc Pathway: sucrose biosynthesis

[More Detail](#)
[Less Detail](#)
[Cross-Species Comparison](#)
[Download Genes](#)
[BioPAX format](#)



Evidence codes



Experimental evidence



Computational evidence



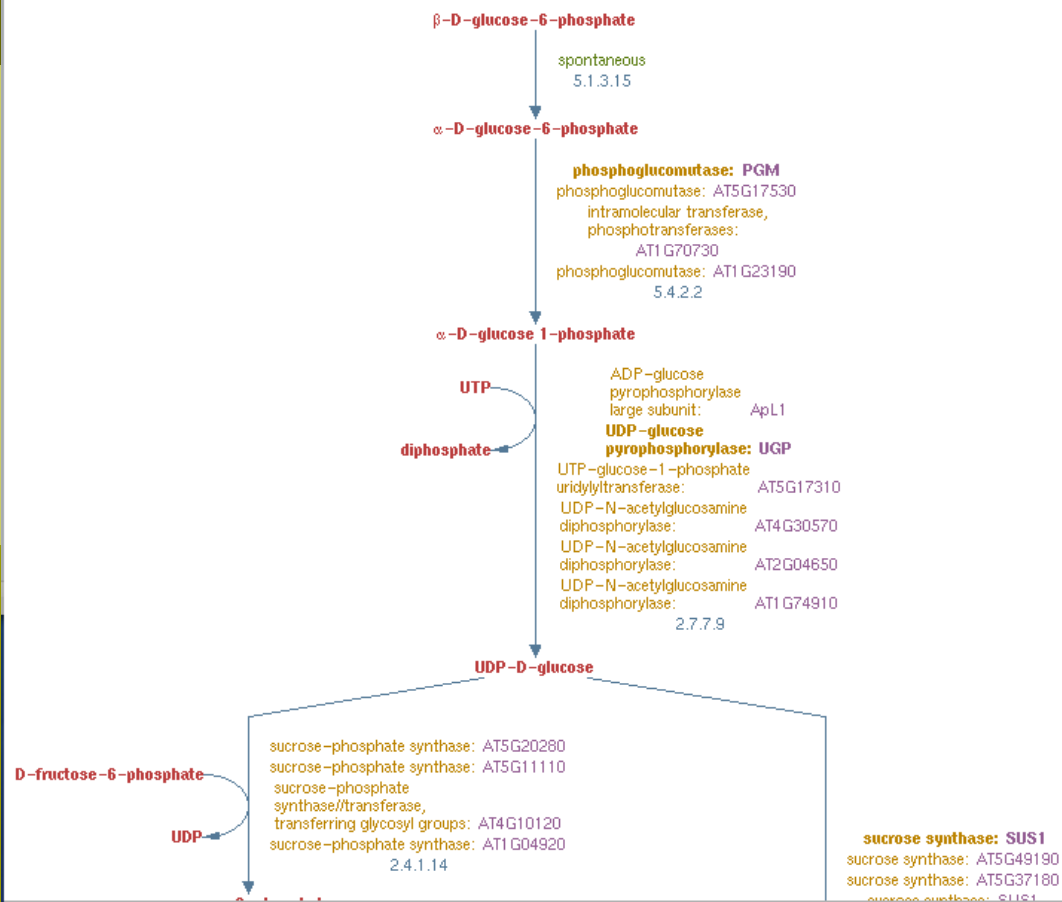
Evidence based on an Author Statement

Evidence in pathways



AraCyc Pathway: sucrose biosynthesis

More Detail Less Detail Cross-Species Comparison Download Genes BioPAX format



Evidence for enzymatic activities

Enzymatic reaction of: phosphoglucomutase



β -D-glucose-6-phosphate

Evidence: Inferred by a human based on computational evidence
[Kofler00]
[Click for more details...]

α -D-glucose-6-phosphate

phosphoglucomutase
phosphoglucomutase
intramolecular
phosphorylation

α -D-glucose 1-phosphate

system.

Reversibility of this reaction is unspecified.

In Pathways: [sucrose degradation to ethanol and lactate \(anaerobic\)](#), [starch biosynthesis](#), [UDP-glucose conversion](#), [sucrose biosynthesis](#), [starch degradation](#), [sucrose degradation](#)

References

Kofler00: Kofler H, Hausler RE, Schulz B, Groner F, Flugge UI, Weber A (2000). "Molecular characterisation of a new mutant allele of the plastid phosphoglucomutase in Arabidopsis, and complementation of the mutant with the wild-type cDNA." *Mol Cell Biochem* 200: 1-10.

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[pathways](#) or even to point out mistakes.

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[Troubleshooting](#)

PH

with a brief history of the creation of the database and ways to submit new

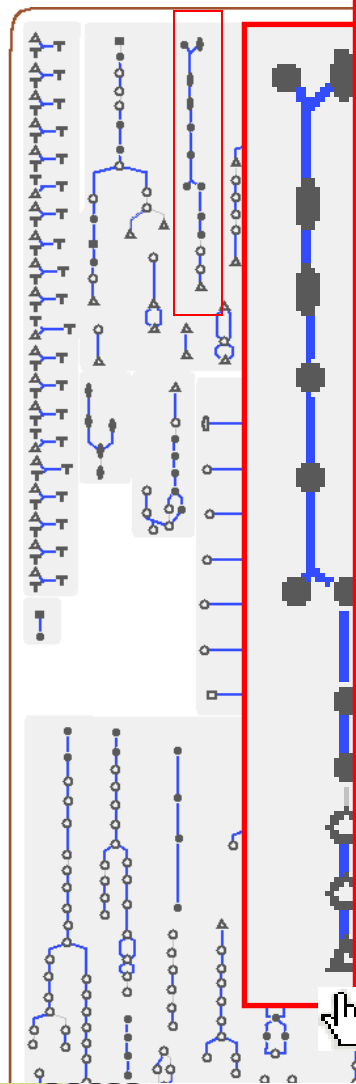
browse the information (Pathways, database).

you need concerning the creation of recommended short read!

with a 'bird's eye' view of *Arabidopsis* (page may take a moment to load). demo).

valuable! This preformatted Excel Form updates (comments, enzymes...), new

AraCyc: Metabolic Map

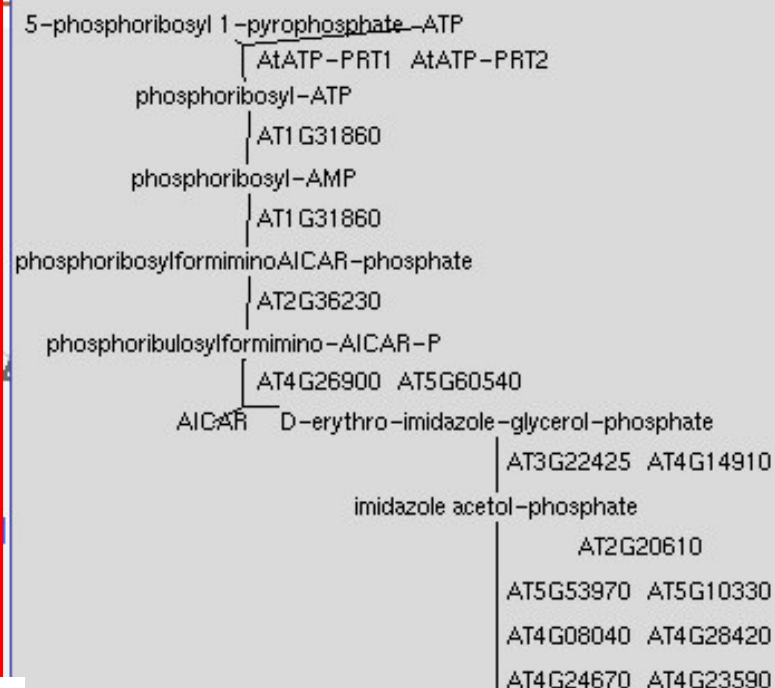


Navigate to...

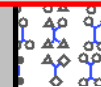
Close

Pathway: [histidine biosynthesis](#)

Compound: [L-histidinol-phosphate](#)

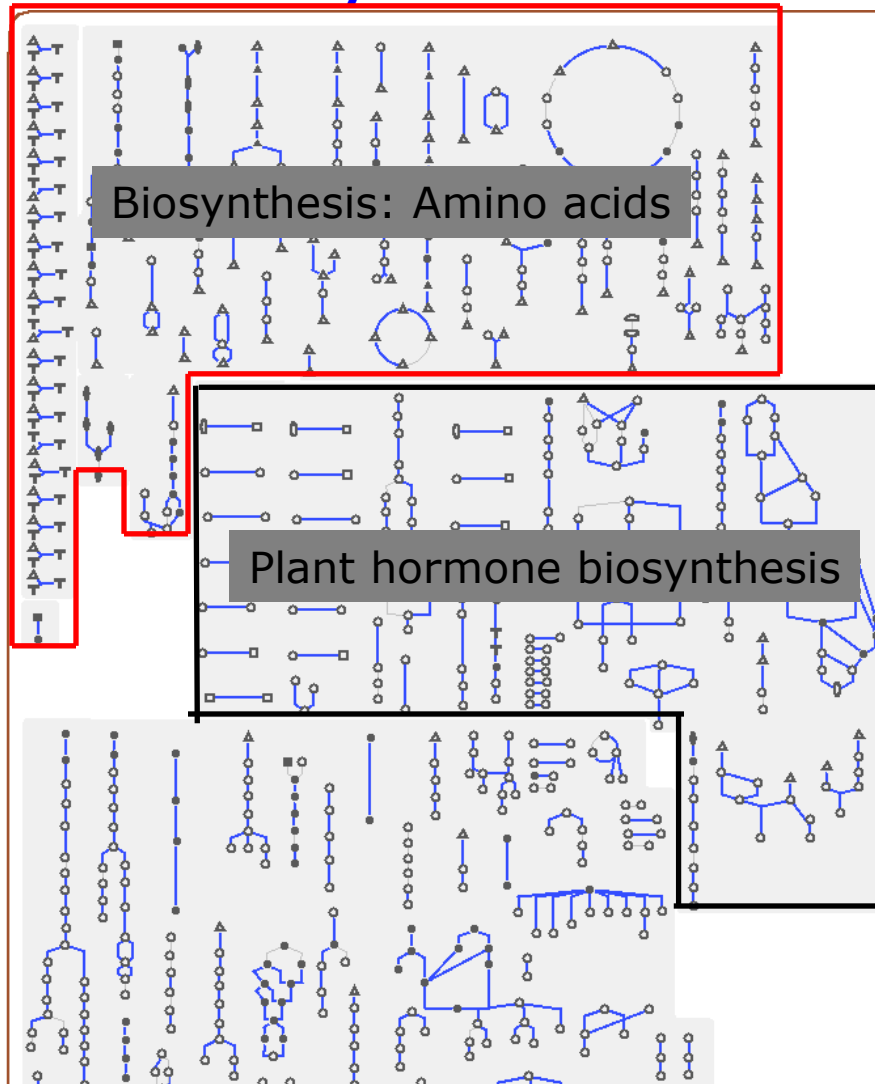


Pathway: histidine biosynthesis

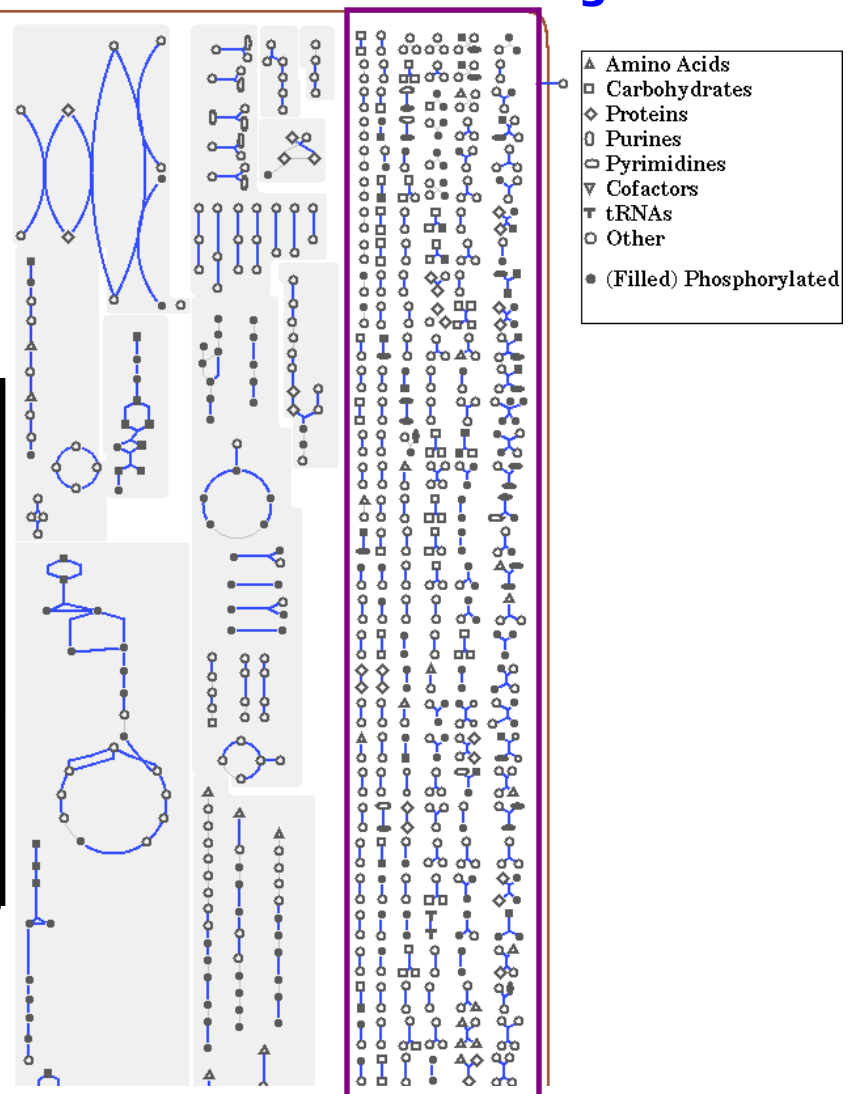


AraCyc: Metabolic Map

Biosynthetic

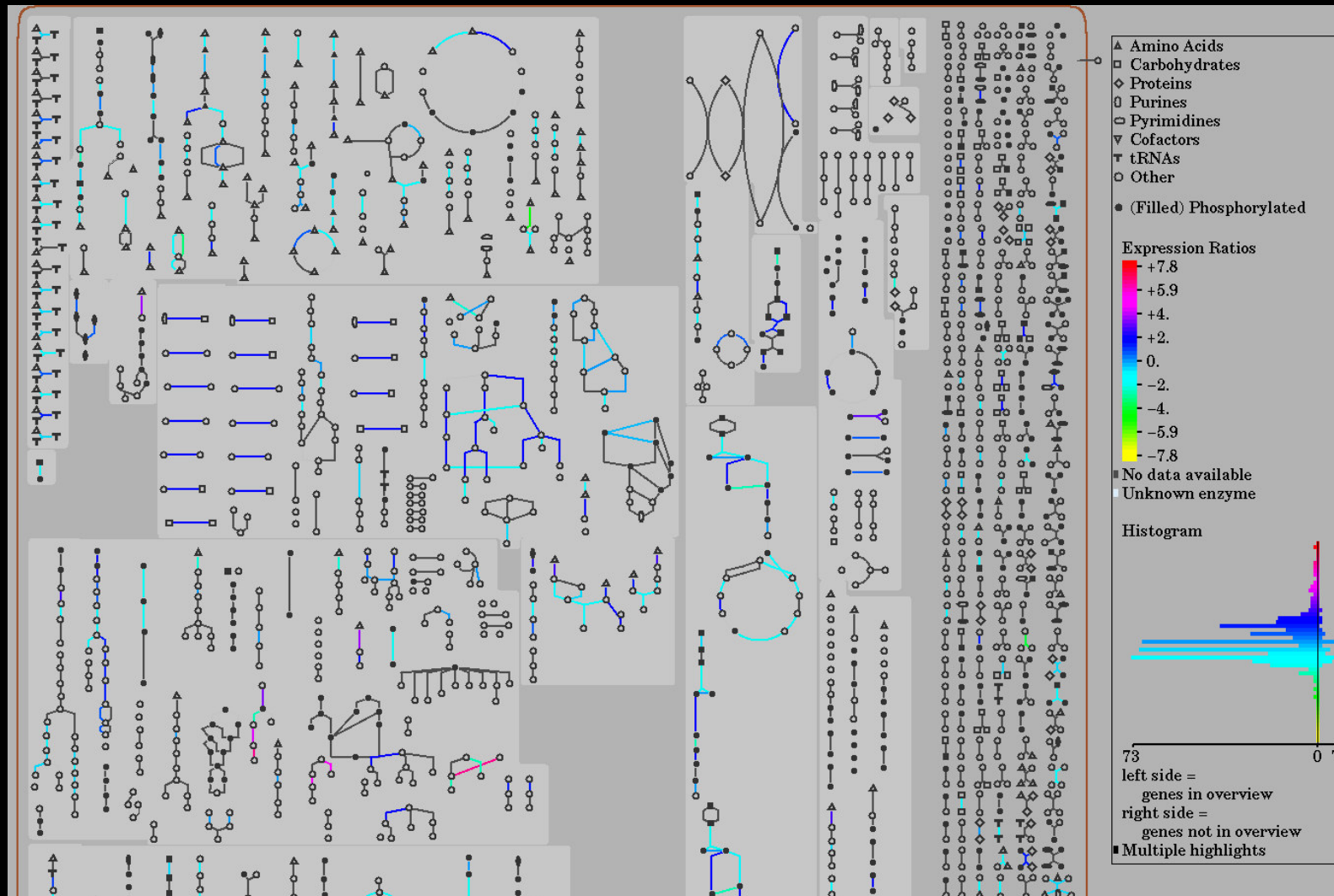


Catabolic un-assigned

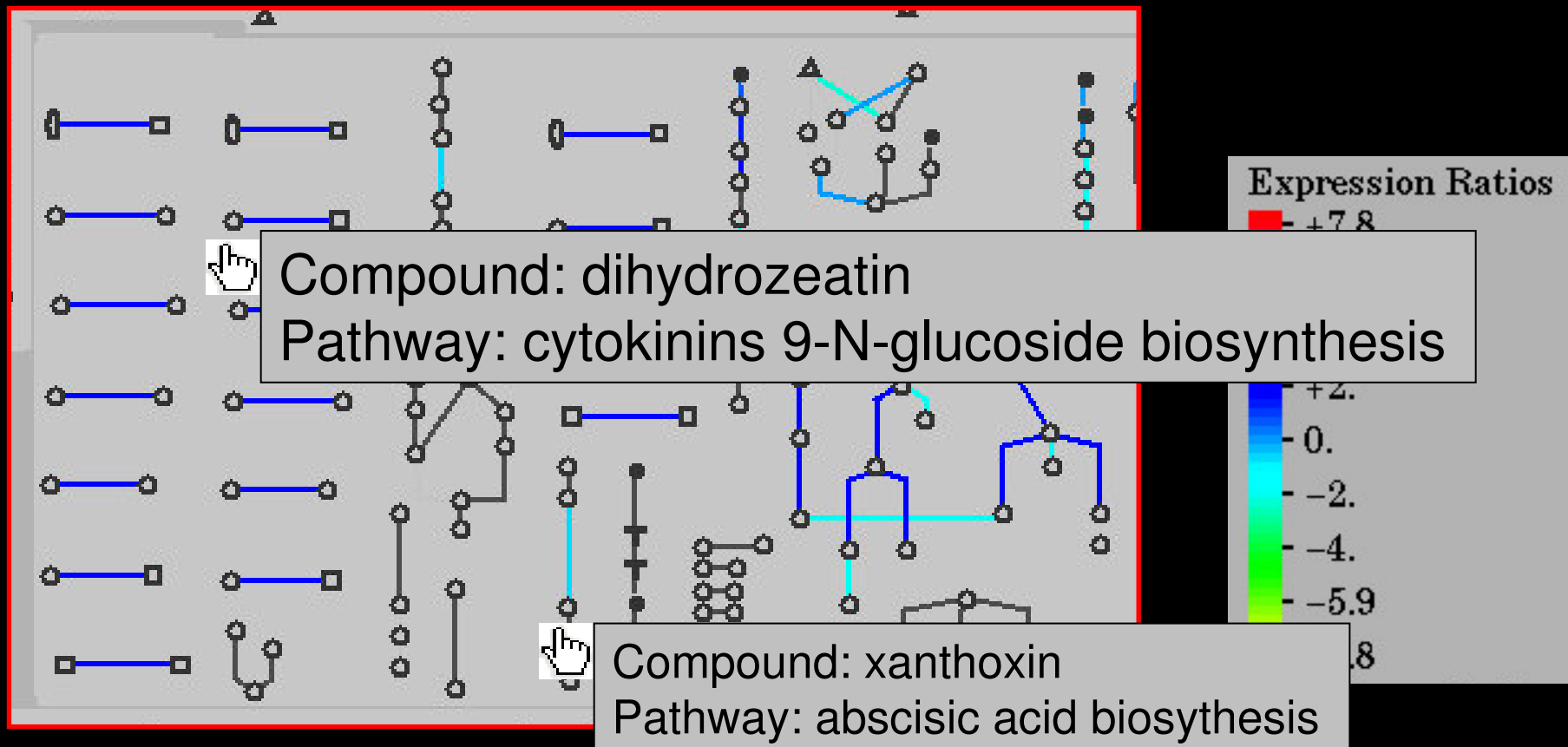


- ▲ Amino Acids
- Carbohydrates
- ◇ Proteins
- Purines
- Pyrimidines
- ▽ Cofactors
- ⌣ tRNAs
- Other
- (Filled) Phosphorylated

OmicsViewer: evaluating data in metabolic context



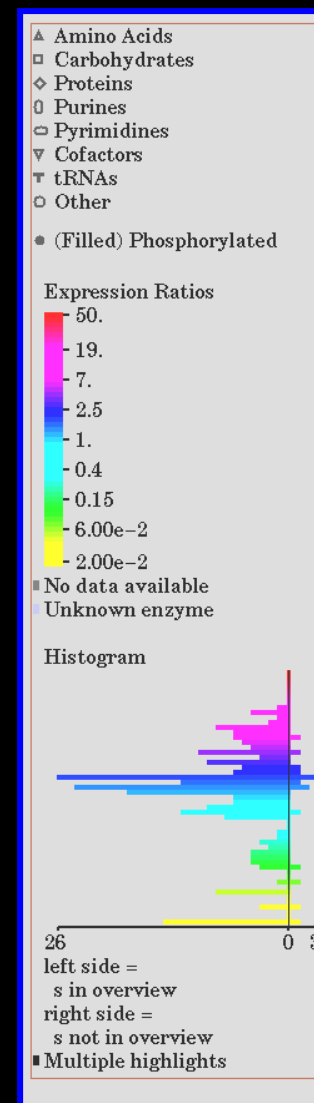
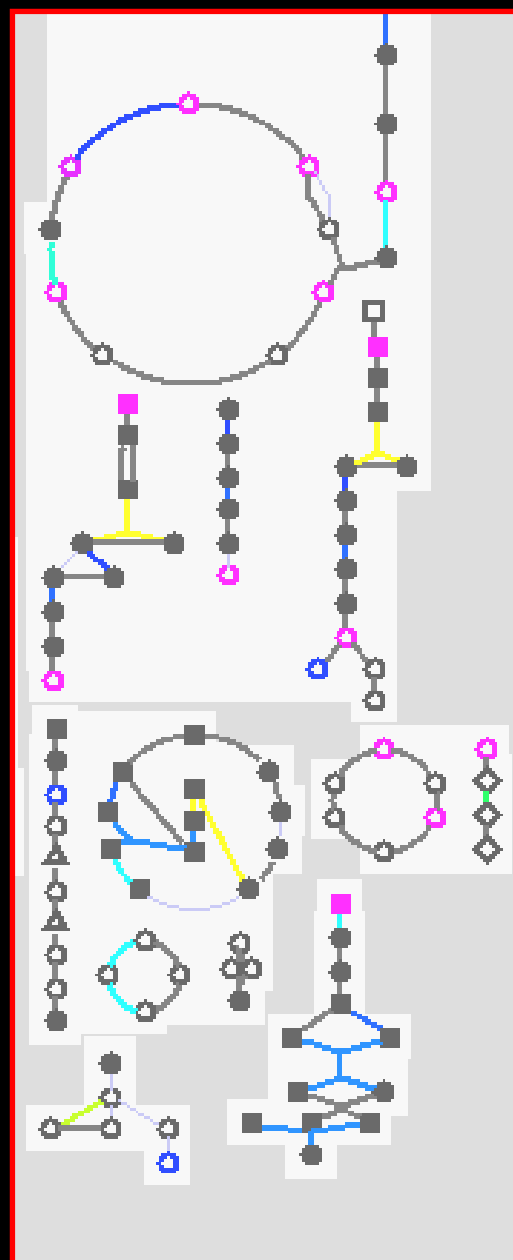
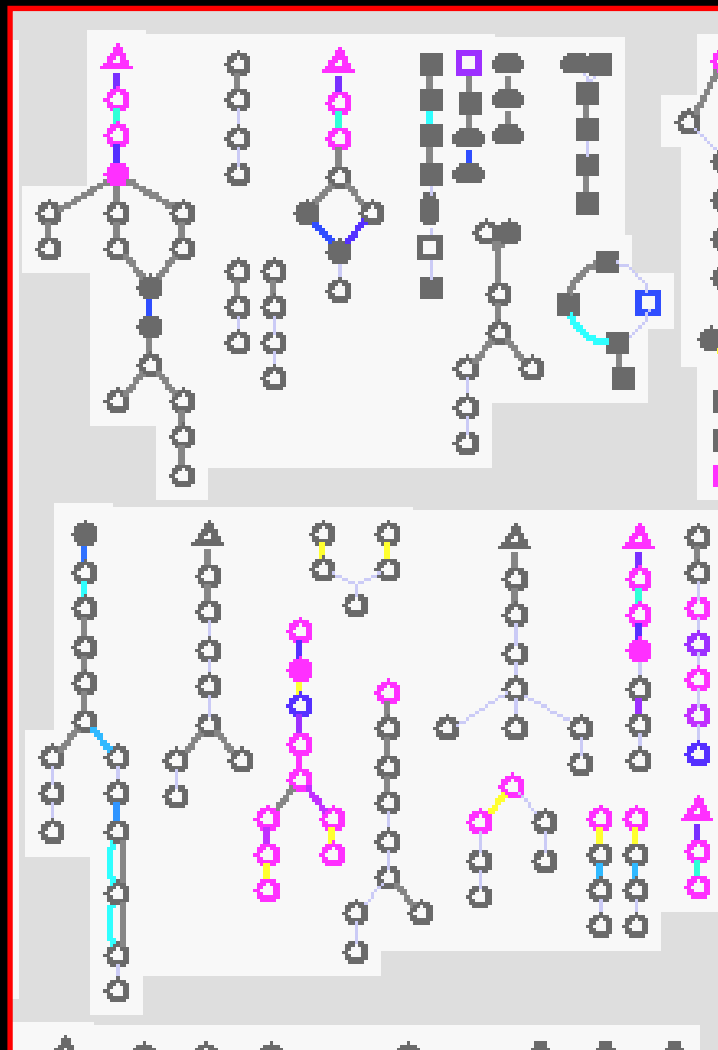
Microarray expression data: low temperature regulatory circuits and gene regulons in higher plants (Michael Tomashow group).



OMICS Viewer

Data types accepted by OmicsViewer

Experiment/ Data	Value assigned to	OmicsViewer output
Microarray Expression	Genes (enzymes)	Colored reaction lines
Proteomics	Proteins (enzymes)	Colored reaction lines
Metabolomics	Metabolites (compounds)	Colored compounds



Access Omics Viewer

The screenshot displays the AraCyc website interface. On the left is a vertical navigation menu with the following sections: AraCyc, AraCyc Tutorials, Tools, Downloads/FTP, Other DataBases, and Contributors. The 'Tools' section is expanded, and the 'OMICS Viewer' link is highlighted with a red rectangular box. The main content area on the right mirrors the menu structure, with links for Search AraCyc, Introduction, Metabolic Map, Pathway Data Submission Form, and Release Notes under the AraCyc header. Below these are links for AraCyc Tutorials and Tools. The 'Tools' section also has a red box around the 'OMICS Viewer' link. At the bottom of the main content area, there is a 'Troubleshooting' link. The background of the main content area features a light gray sidebar with text about the creation of the database and ways to submit new information.

AraCyc

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- Pathway Data Submission Form
- Release Notes

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- OMICS Viewer**
- Comparative Analysis
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Troubleshooting

Select a dataset:

Arabidopsis thaliana COL 

File containing
experimental data (NOT
a URL):

C:\Documents and Settings\...

Browse...

Do you want to
absolute or relative
values?

If displaying relative
values, use

Data values use

Arabidopsis locus id	time_point_1	time_point_2	time_point_3	time_point_4
At1g77760	1.15	2.3	3.2	2.15
At2g13360	0.7	-0.53	0	-0.73
At3g10230	-1.1	-0.05	1.05	1.15
At3g10230	-0.65	-0.58	1.13	1.23
At3g01120	-1.08	-0.15	-1.2	-1.15
At3g01500	0.07	-0.72	-0.68	1.4
At3g02470	0.03	-0.53	0.58	1.28
At3g02470	0.55	-0.12	0.62	0.65
At3g02580	0.6	-0.55	0.08	0.55
At3g02580	1.15	0.7	0.03	-0.6
At3g02780	-1.15	0.05	0.1	-0.08
At3g04120	-0.15	-1.55	0.12	-0.3
At3g04120	-0.15	-1.5	0.05	-0.32

0

1

2

3

4

Do you want to display absolute or relative data values?

Absolute ▼

If displaying relative data values, use

- ☒ a single data column
- ☐ the ratio of two data columns

Data values use a:

- ☒ 0-centered scale (e.g. log scale)
- ☐ 1-centered scale (negative values will be discarded)

Data value

The items in the first (zeroth) column of your datafile are

Genes ▼

Note: By selecting *Any of the above*, you can combine, for example, gene expression and metabolomics data into a single display. There are some dangers inherent in this approach, however. Some narrow data values from different kinds of experiments may not be directly comparable. The resulting diagram may be misleading in some important ways.

Genes
Proteins
Compounds
Reactions
Any of the above

Arabidopsis locus id	time_point_1	time_point_2	time_point_3	time_point_4
-------------------------	--------------	--------------	--------------	--------------

At1g77760	1.15	2.3	3.2	2.15
At2g13360	0.7	-0.53	0	-0.73
At3g10230	-1.1	-0.05	1.05	1.15

0

1

2

3

4

Single Experiment Time Step or Animated Time Series

To display a single experiment time step, enter a single column number in one or both of the column number fields below.

To display an animated time series, enter a list of column numbers (with each column number corresponding to a single timepoint), one per line, in the first column number field below. If you wish to include a denominator column for a ratio calculation, you can enter either a single column number (in which case the same data column will be used as the denominator for all timepoints), or one column number for each numerator column number. Note that zoomed views of individual pathways are not available with animations.

Data column (numerator in ratios):

If using two columns, denominator data column:

Note: For column numbering purposes, the first column, which contains the gene name, is column number 0. The first potential data column is column number 1.

Arabidopsis <u>locus id</u>	time_point_1	time_point_2	time_point_3	time_point_4
At1g77760	1.15	2.3	3.2	2.15
At2g13360	0.7	-0.53	0	-0.73
At3g10230	-1.1	-0.05	1.05	1.15
At3g10230	-0.65	-0.58	1.13	1.23
0	1	2	3	4

Data column (numerator in ratios):

2

If using two columns, denominator data column:

Note: For column numbering purposes, the first column, which contains the gene name, is column number 0. The first potential data column is column number 1.

Result A: single page for a single time point

Arabidopsis locus id	time_point_1	time_point_2	time_point_3	time_point_4	
At1g77760	1.15	2.3	3.2	2.15	
At2g13360	0.7	-0.53	0	-0.73	
At3g10230	-1.1	-0.05	1.05	1.15	
At3g10230	-0.65	-0.58	1.13	1.23	
	0	1	2	3	4

Data column (numerator in ratios):

2
3

If using two columns, denominator data column:

Note: For column numbering purposes, the first column, which contains the gene name, is column number 0. The first potential data column is column number 1.

Result B: animation (two time points)

Arabidopsis locus id	time_point_1	time_point_2	time_point_3	time_point_4	
At1g77760	1.15	2.3	3.2	2.15	
At2g13360	0.7	-0.53	0	-0.73	
At3g10230	-1.1	-0.05	1.05	1.15	
At3g10230	-0.65	-0.58	1.13	1.23	
	0	1	2	3	4

Data column (numerator in ratios):

2

If using two columns, denominator data column:

3

Note: For column numbering purposes, the first column, which contains the gene name, is column number 0. The first potential data column is column number 1.

Result C: single page (ratio of two time points: **2** / **3**)

Arabidopsis locus id	time_point_1	time_point_2	time_point_3	time_point_4
At1g77760	1.15	2.3	3.2	2.15
At2g13360	0.7	-0.53	0	-0.73
At3g10230	-1.1	-0.05	1.05	1.15
At3g10230	-0.65	-0.58	1.13	1.23
0	1	2	3	4

Data column (numerator in ratios):

2
3
4

If using two columns, denominator data column:

1
1
2

Note: For column numbering purposes, the first column, which contains the gene name, is column number 0. The first potential data column is column number 1.

Result D: animation (three pages: : **2 / 1, 3 / 1, 4 / 2**)

Choose a color scheme:

- ☒ Full color spectrum, computed from data provided (default)
- ☐ Full color spectrum with a maximum cutoff:
- ☐ Three color display with specified threshold:

Display Type

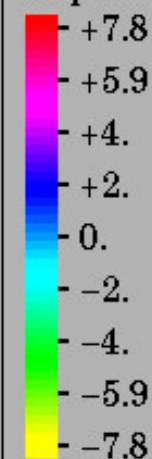
By default, data values are painted on the cellular overview chart. However an alternative display is to generate a table containing all individual pathways which have one or more data values that exceed some threshold (or are less than the inverse of that threshold). To select this alternative display, choose the corresponding option below and specify the threshold.

- ☒ Paint data on overview chart (default)
- ☐ Generate a table of individual pathways exceeding threshold:
- ☐ Combine both displays (not yet implemented for animations)

Submit

Note that this request will take several minutes to complete (possibly longer for large datasets).

Expression Ratios



- No data available
- Unknown enzyme

