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

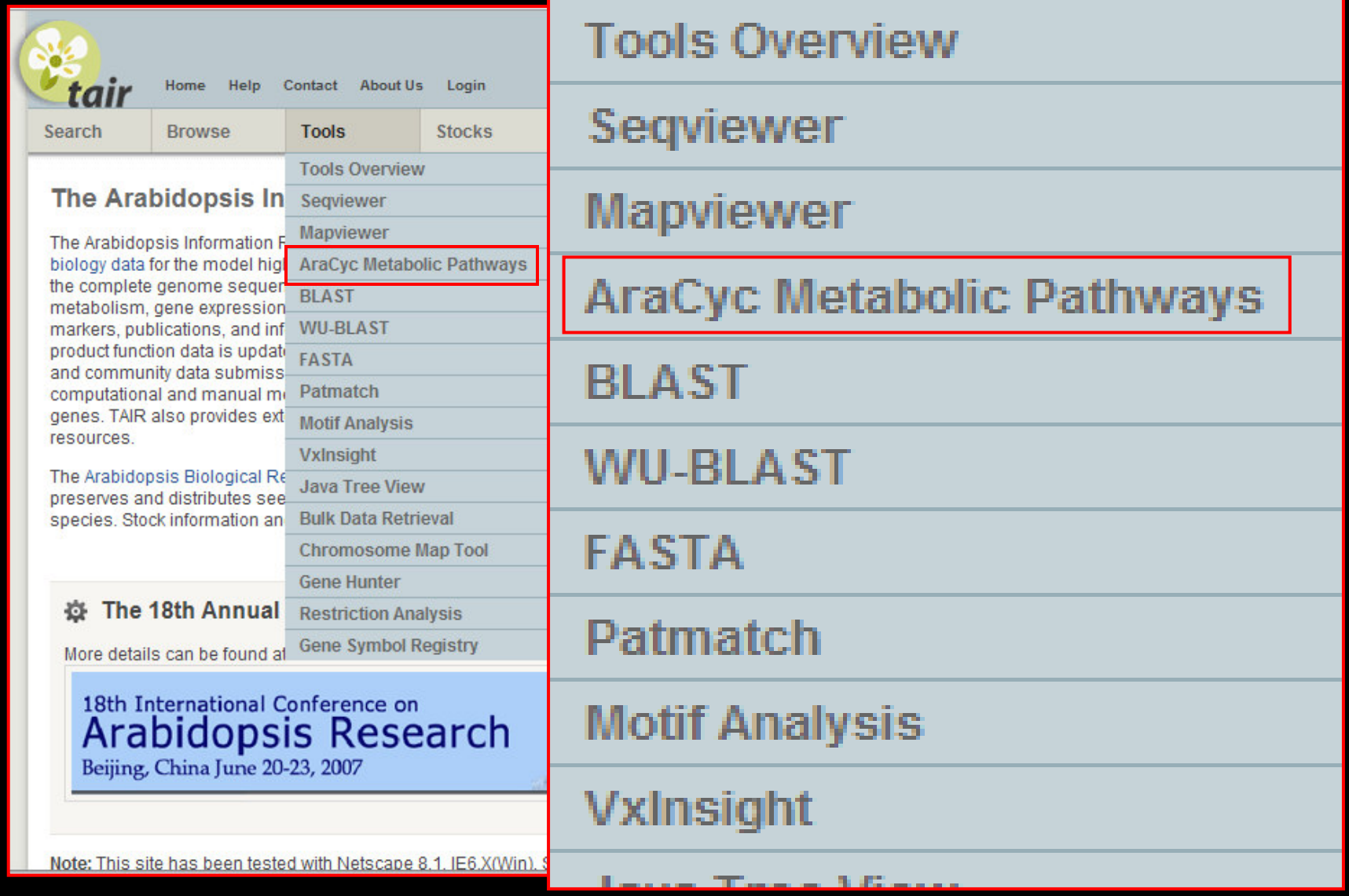
	AraCyc 2.1 Apr 2005	AraCyc 2.5 Oct 2005	AraCyc 2.6 May 2006	AraCyc 3.5 Feb 2007
Total pathways	221	197	228	262
New	-	37	35	51
Updated	-	0	4	37
Deleted	-	61	6	12
Pathways manually reviewed with literature evidence	71 (32%)	170 (86%)	201 (88%)	233 (89%)

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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Stocks
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
The Arabidopsis In
The 18th Annual
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).
Tools
Stocks
Tools Overview
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AraCyc Metabolic Pathways
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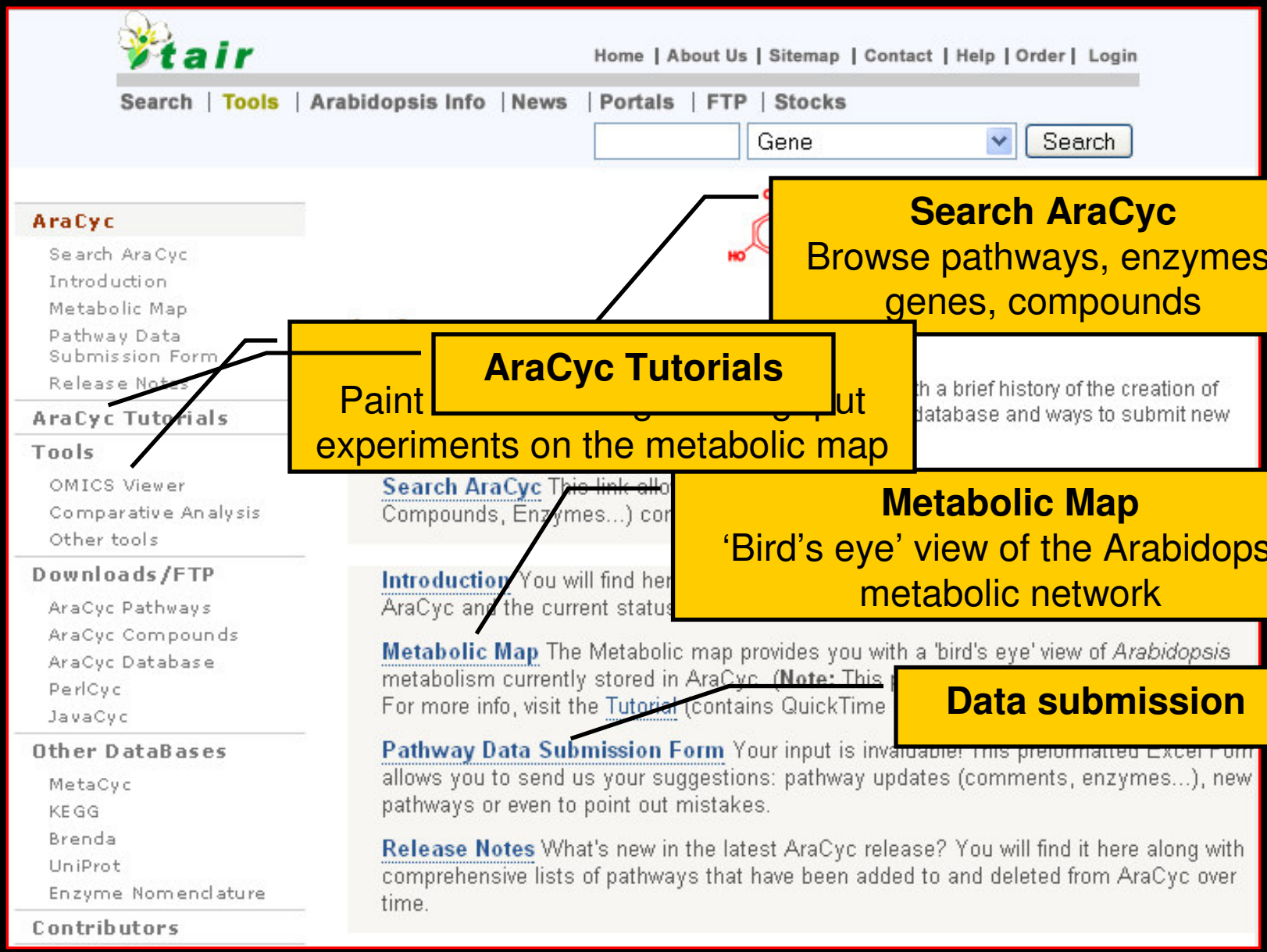
tair
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Enzyme Nomenclature
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Browse pathways, enzymes, genes, compounds
AraCyc Tutorials
Paint
experiments on the metabolic map
Metabolic Map
'Bird's eye' view of the Arabidopsis metabolic network
Data submission
Search AraCyc
Introduction
Metabolic Map The Metabolic map provides you with a 'bird's eye' view of Arabidopsis
Tutorial
Pathway Data Submission 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.

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.

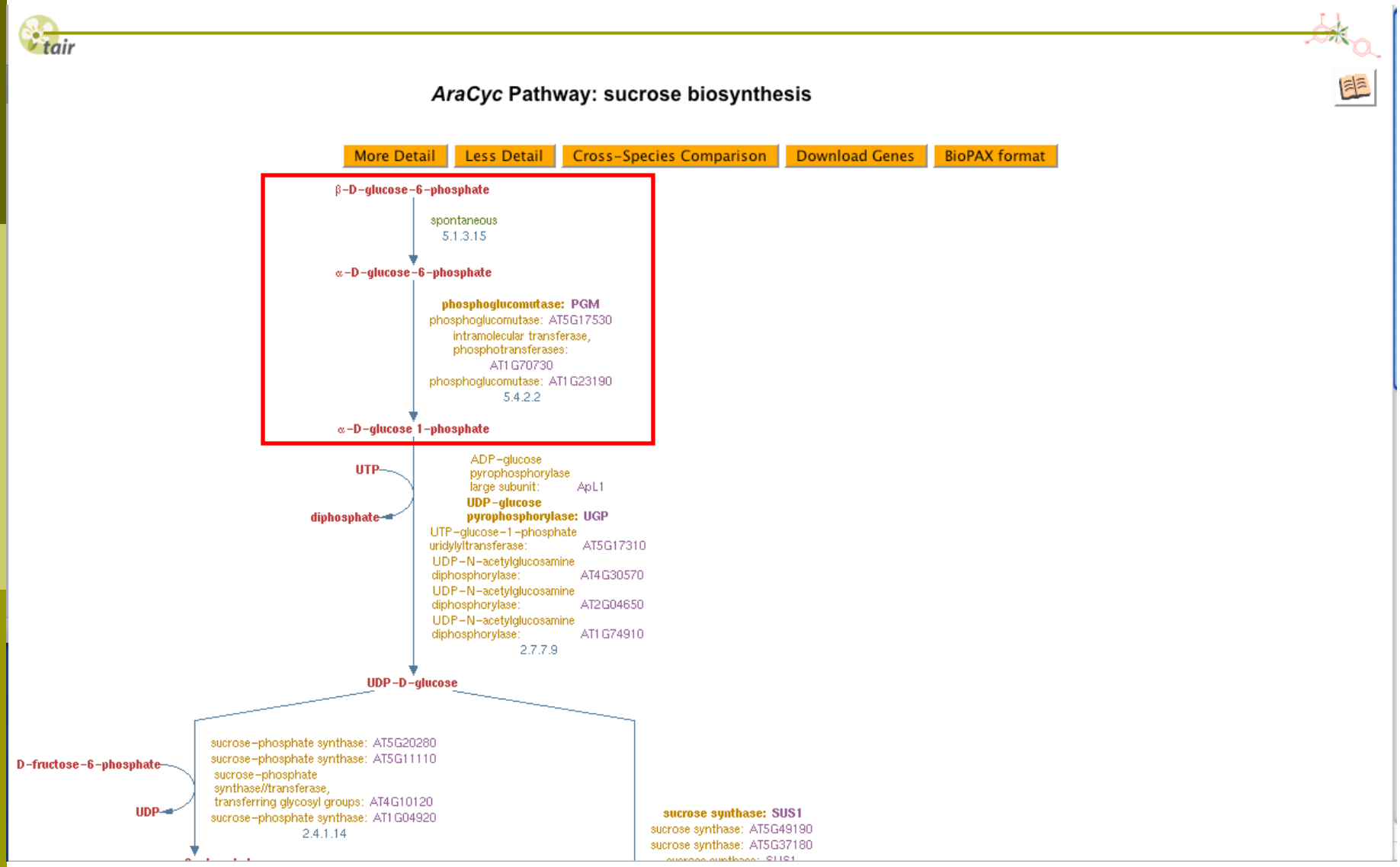
Tutorial Demo: AraCyc Metabolic Map Overview

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

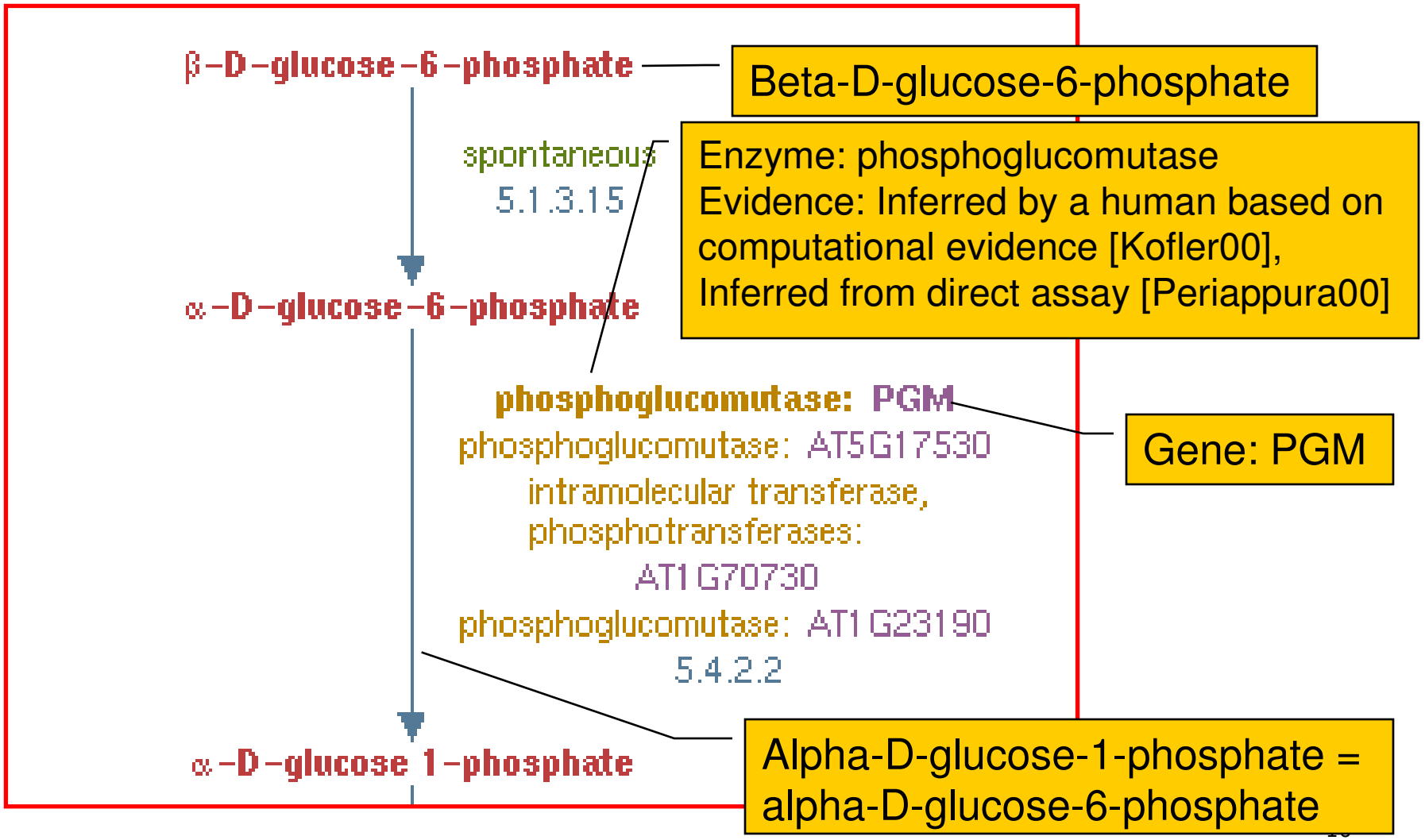
Tutorial Demo: Using the Omics Viewer

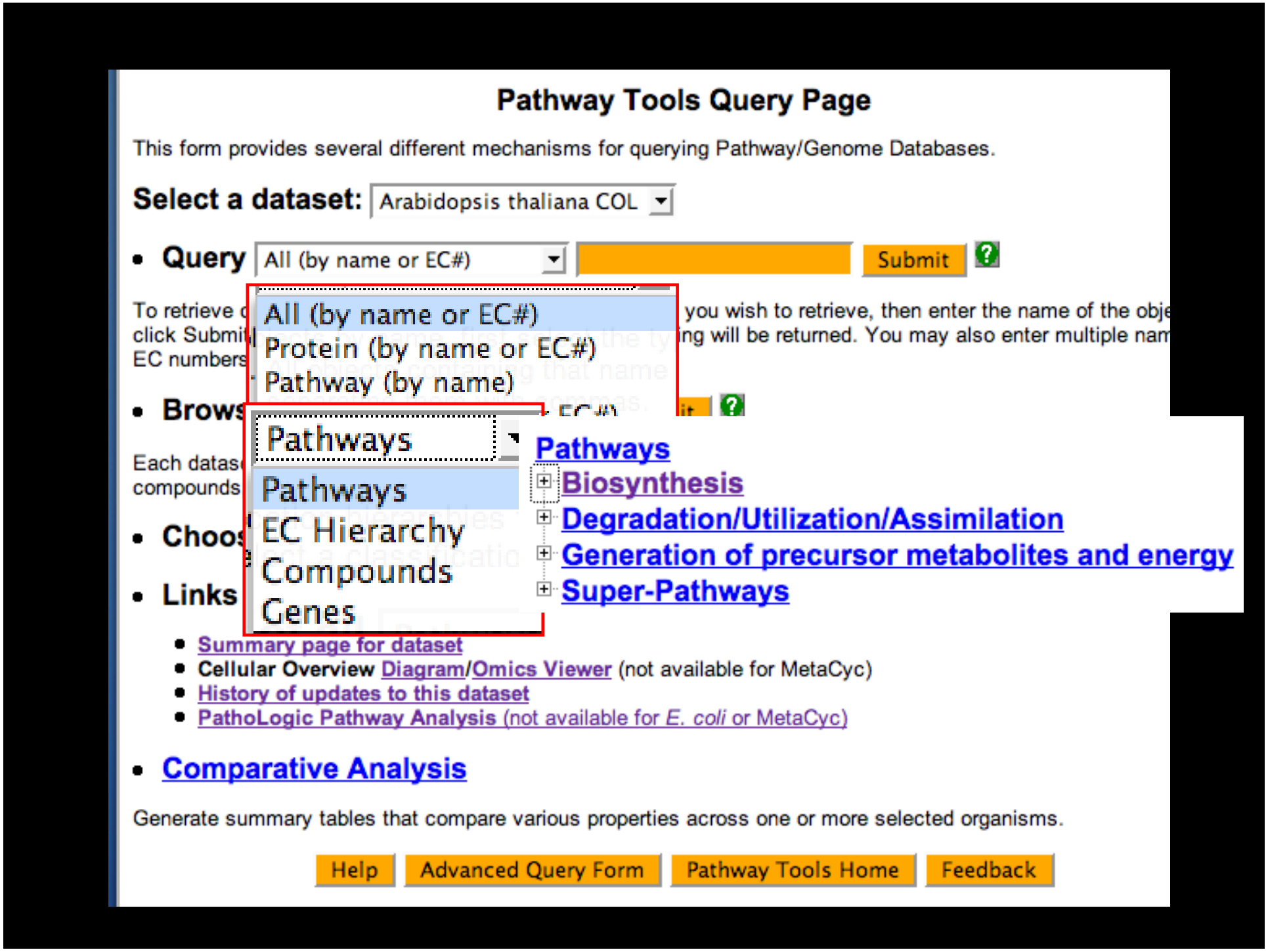
This Quicktime movie demonstrates how to use the Omics viewer to overlay gene expression data onto the pathway overview.

A pathway example: sucrose biosynthesis

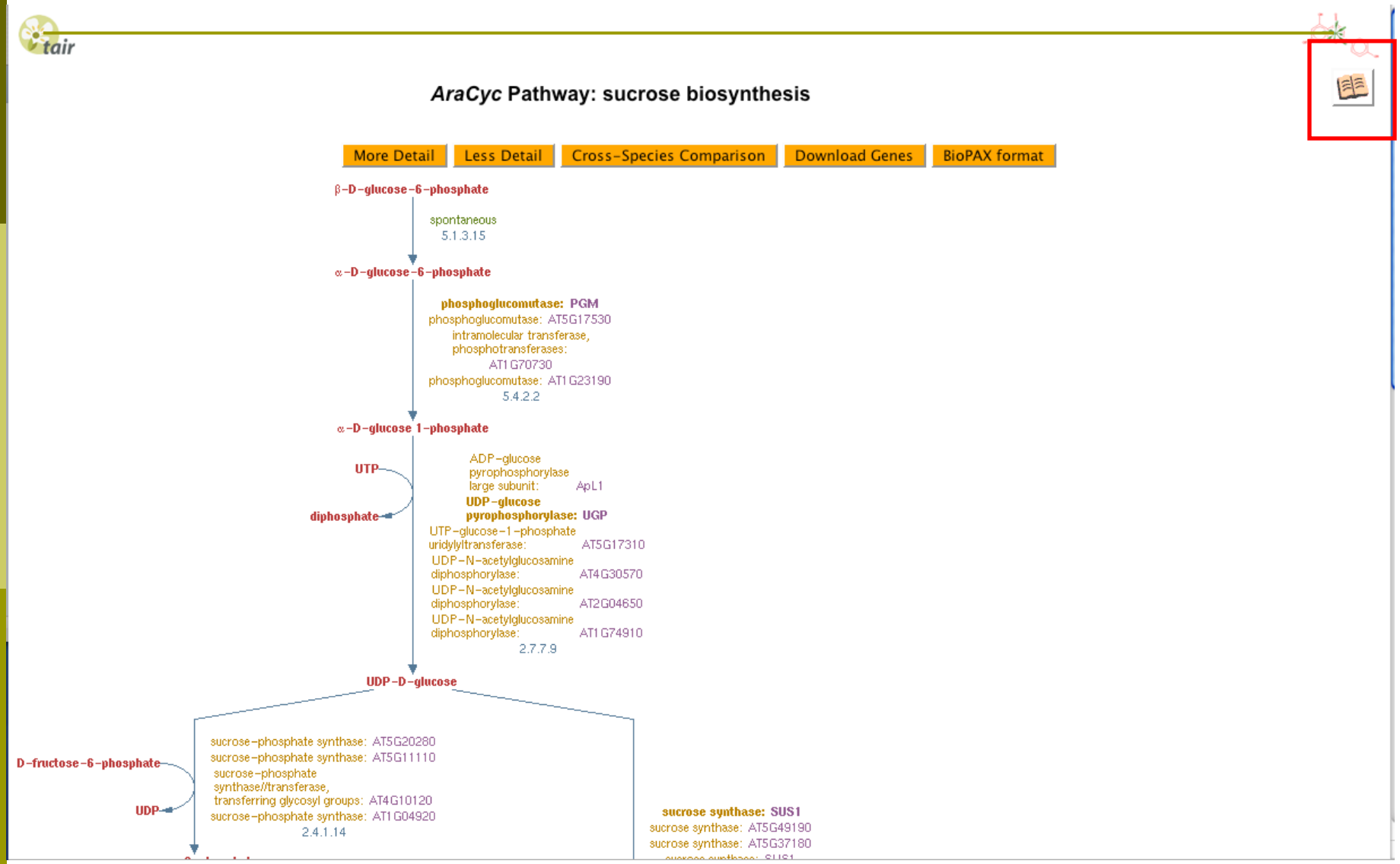


A pathway example: sucrose biosynthesis




Pathway Tools Query Page
This form provides several different mechanisms for querying Pathway/Genome Databases.
Select a dataset:
Arabidopsis thaliana COL
Query
All (by name or EC#)
Submit
All (by name or EC#)
Protein (by name or EC#)
Pathway (by name)
you wish to retrieve, then enter the name of the obje
ng will be returned. You may also enter multiple nam
Pathways
Pathways
EC Hierarchy
Compounds
Genes
Pathways
Biosynthesis
Degradation/Utilization/Assimilation
Generation of precursor metabolites and energy
Super-Pathways
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.
Help
Advanced Query Form
Pathway Tools Home
Feedback

Evidence codes



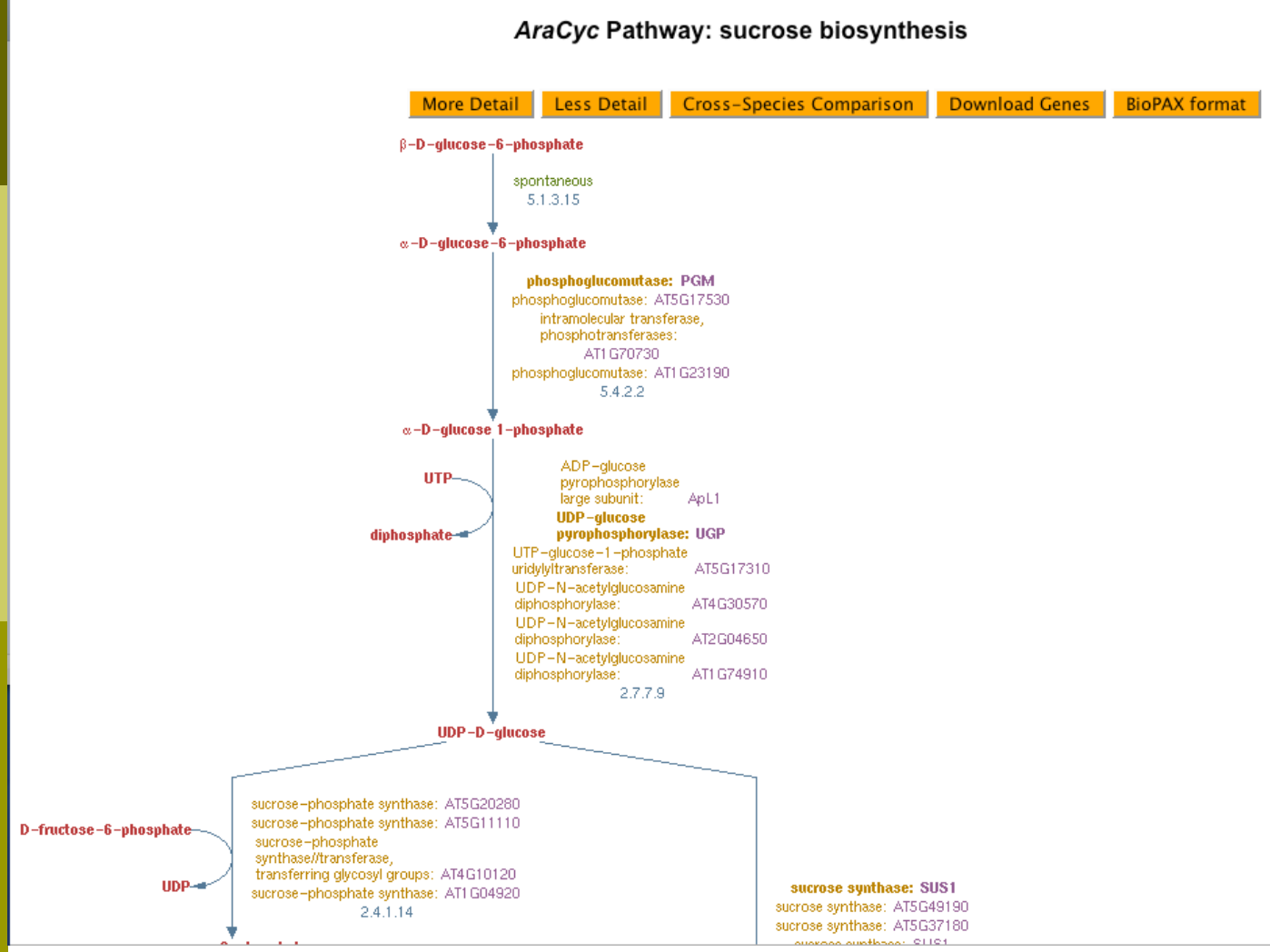
Evidence codes

Experimental evidence

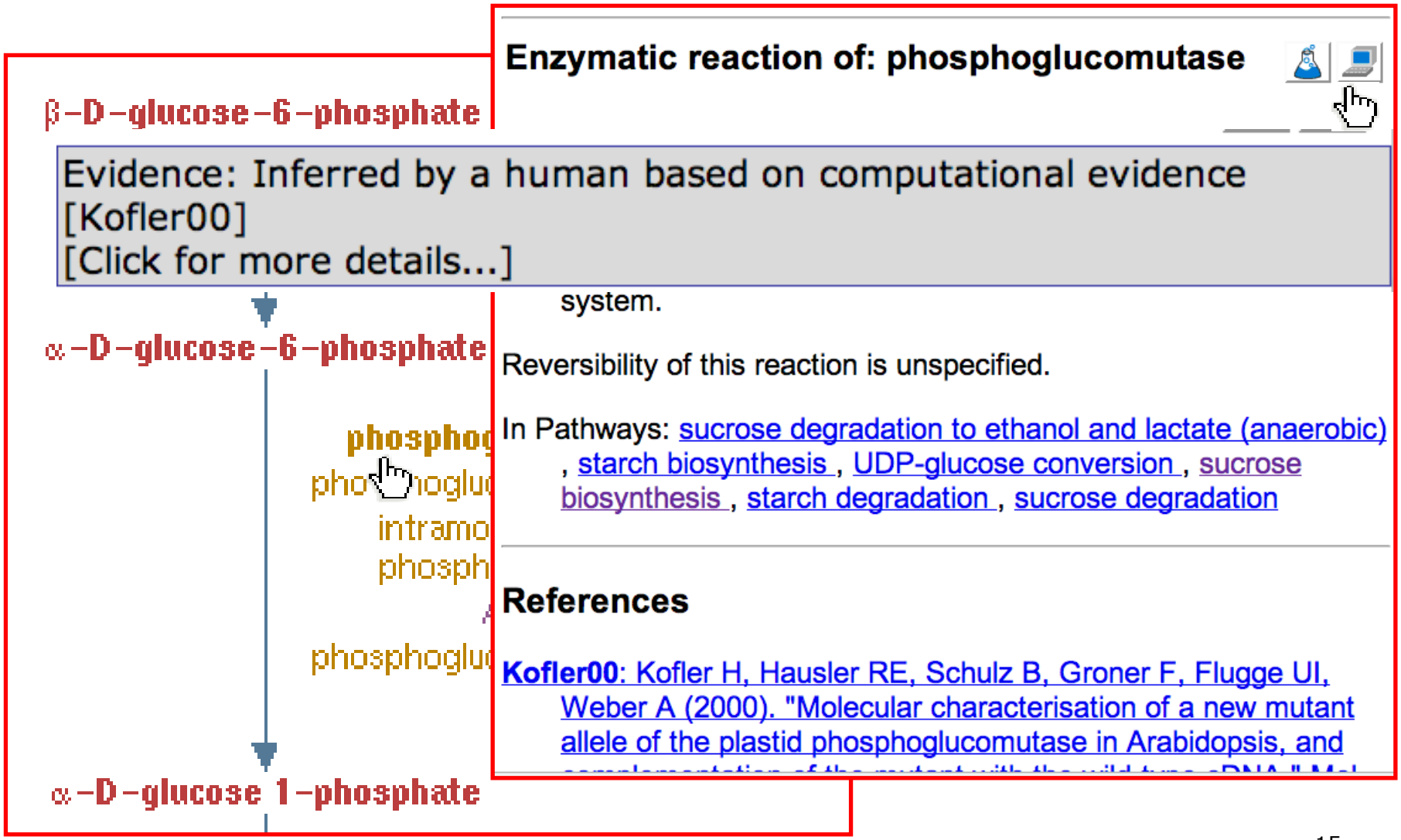
Computational evidence

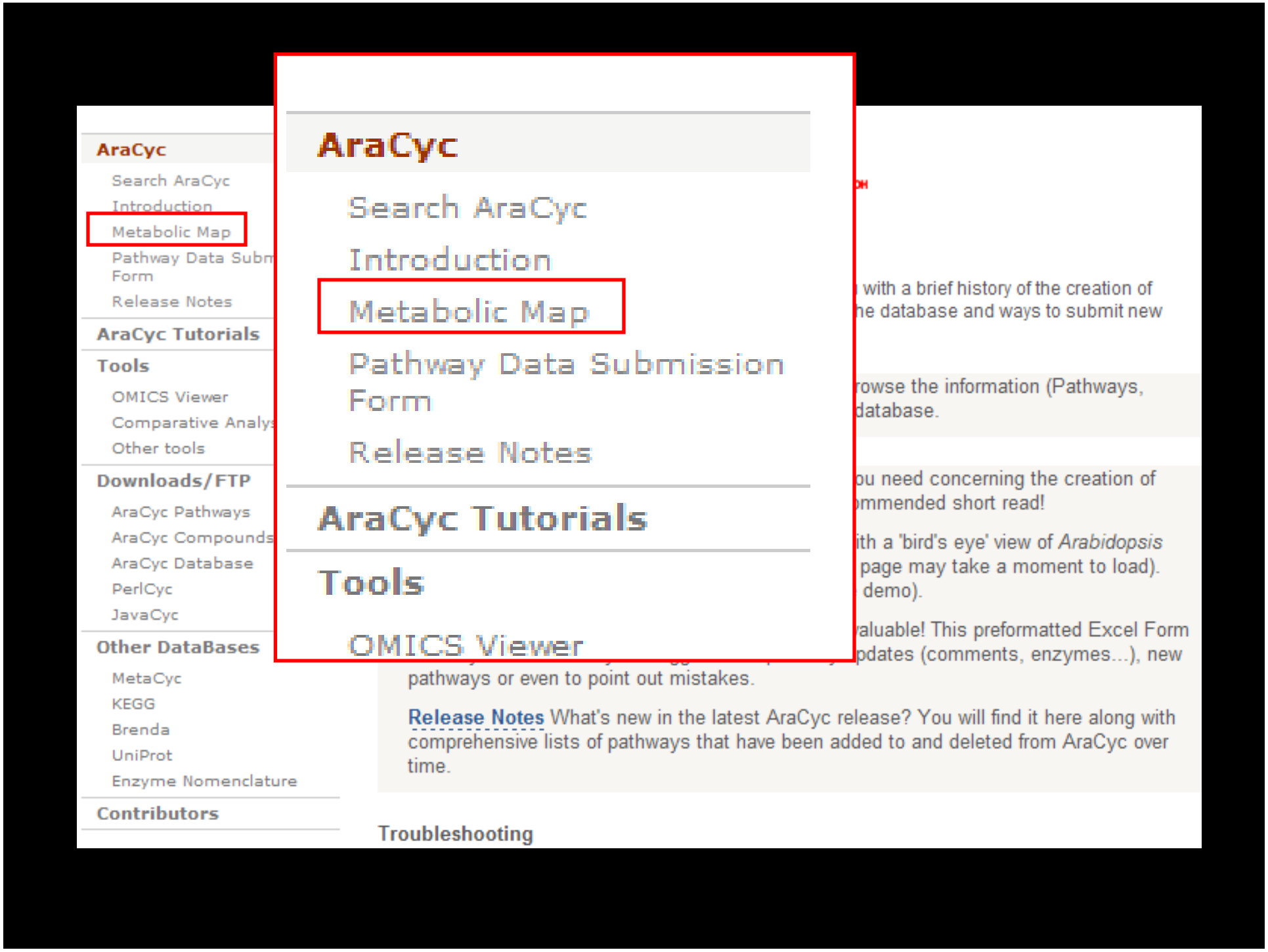
Evidence based on an Author Statement

Evidence in pathways



Evidence for enzymatic activities

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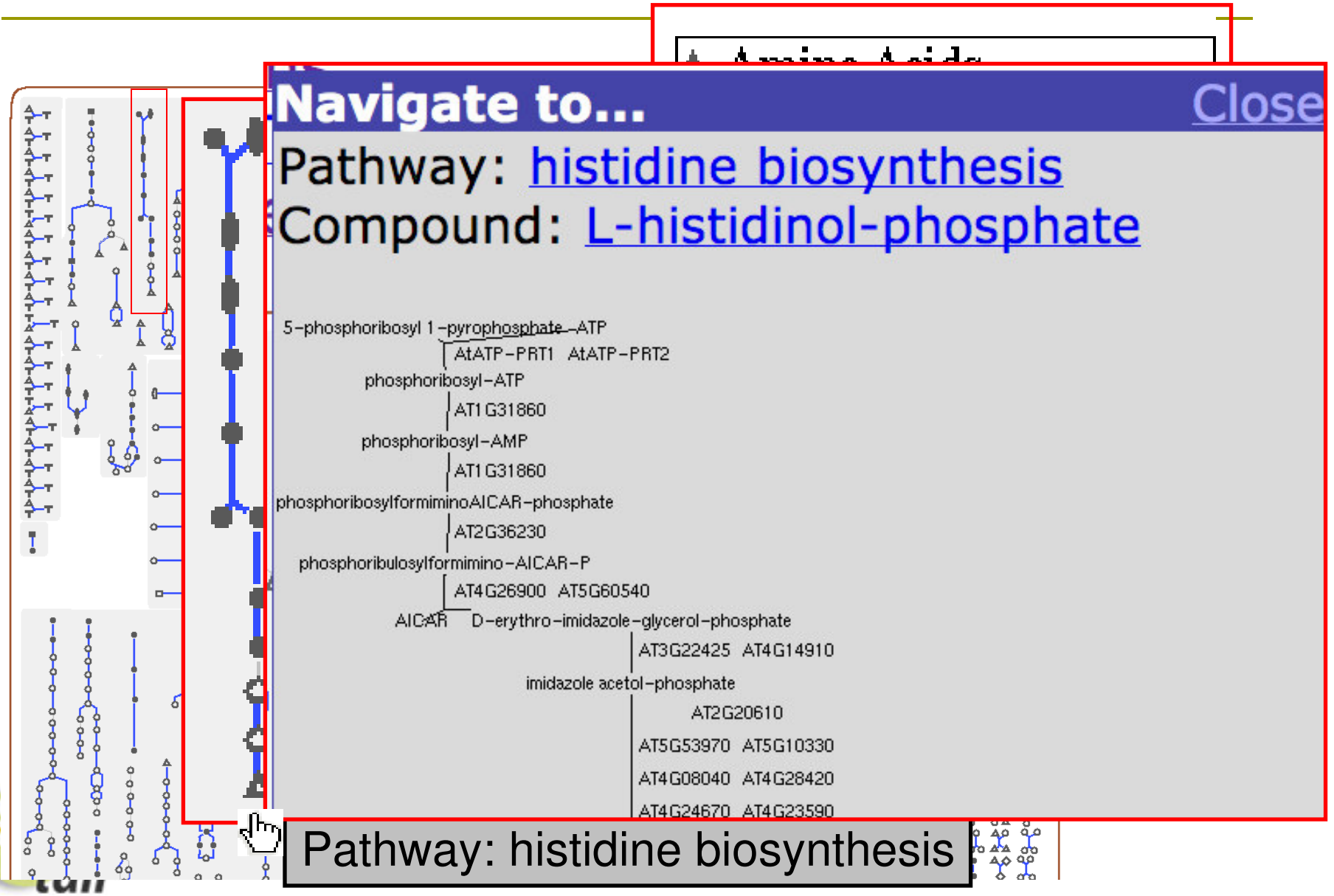
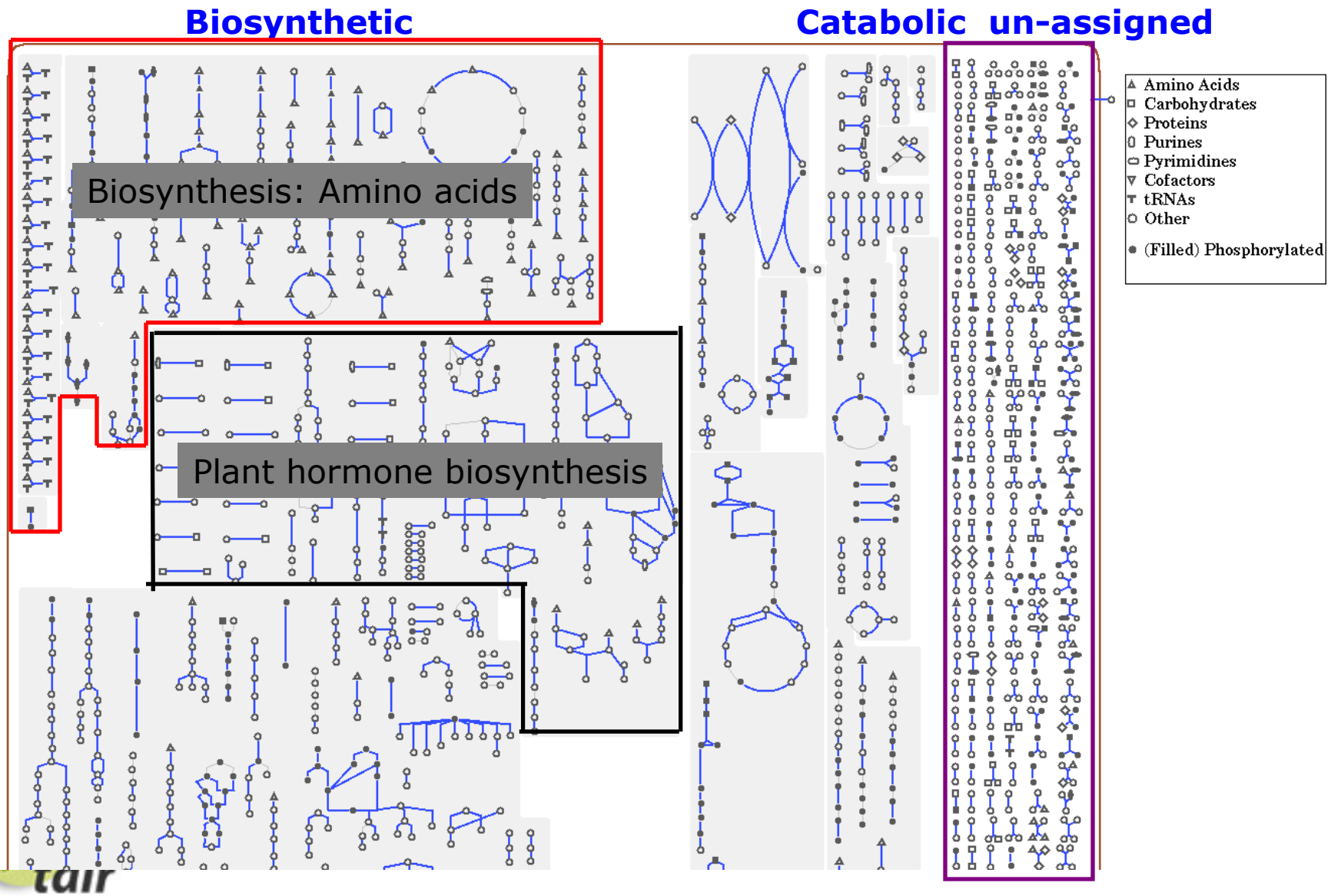
AraCyc Database
PerlCyc
JavaCyc
Other DataBases
MetaCyc
KEGG
Brenda
UniProt
Enzyme Nomenclature
Contributors
with a brief history of the creation of
he database and ways to submit new
rowse the information (Pathways,
database.
ou need concerning the creation of
mmended short read!
ith a 'bird's eye' view of Arabidopsis
page may take a moment to load).
demo).
valuable! This preformatted Excel Form
pdates (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.
Troubleshooting

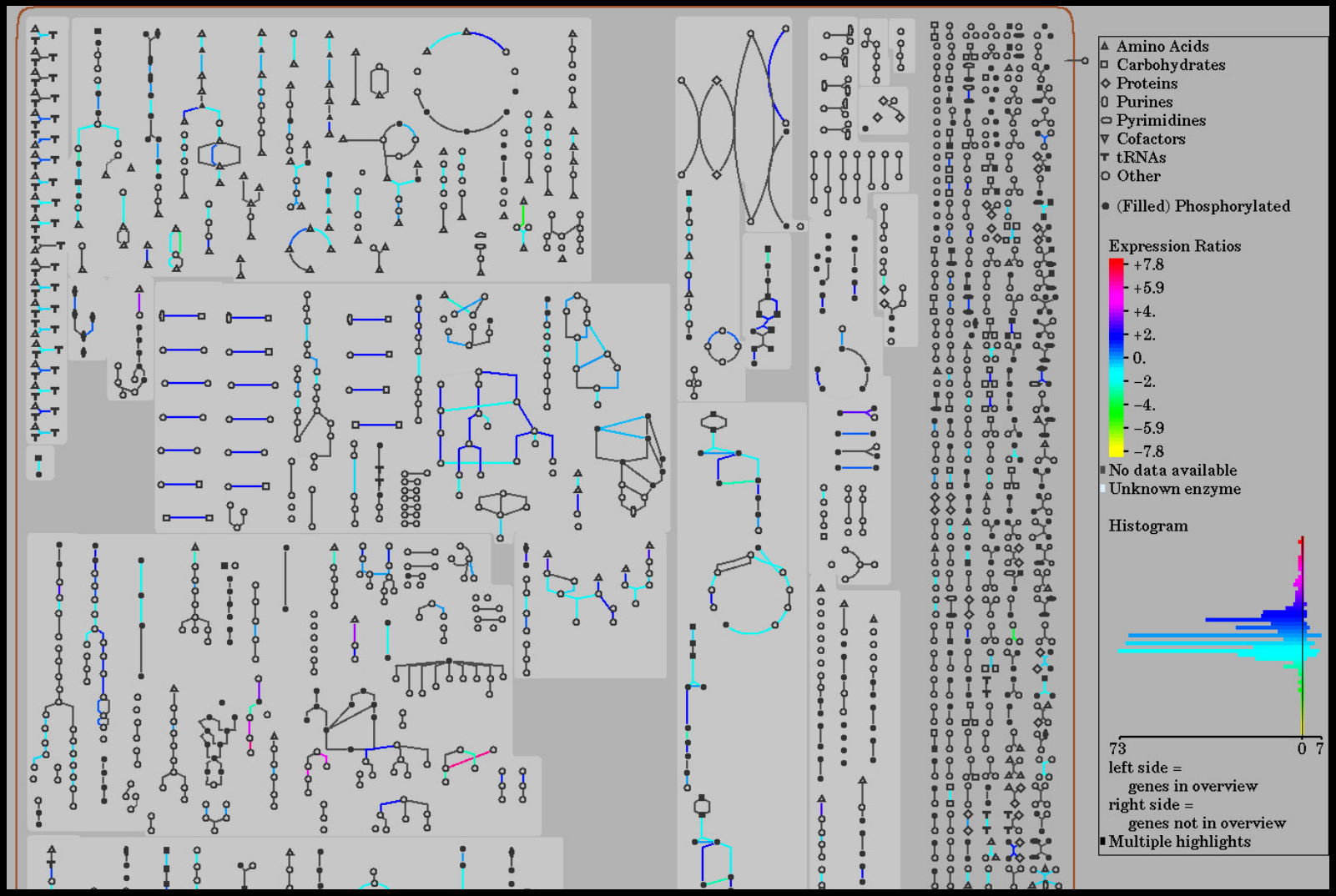
AraCyc: Metabolic Map



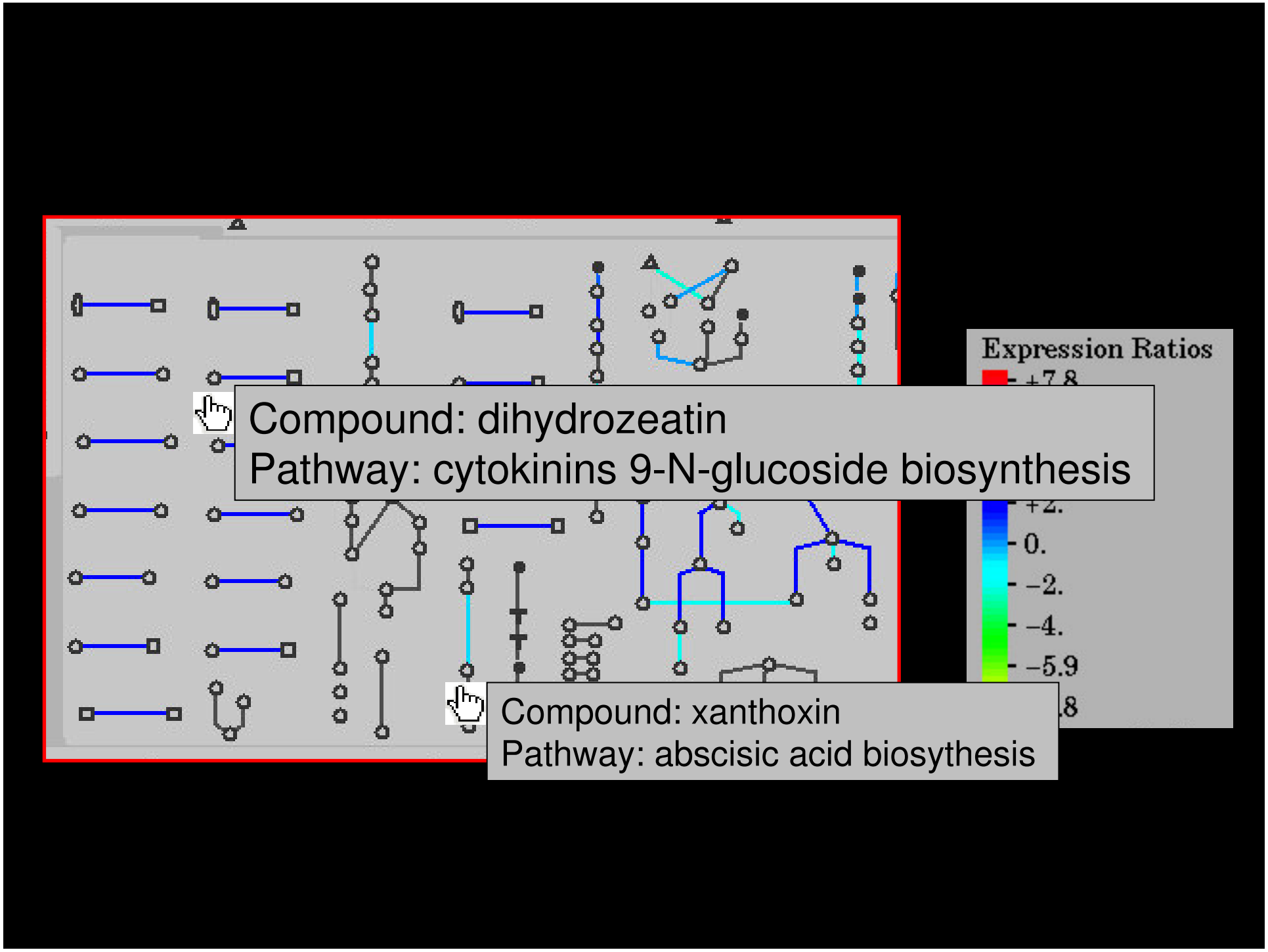
AraCyc: Metabolic Map



OmicsViewer: evaluating data in metabolic context



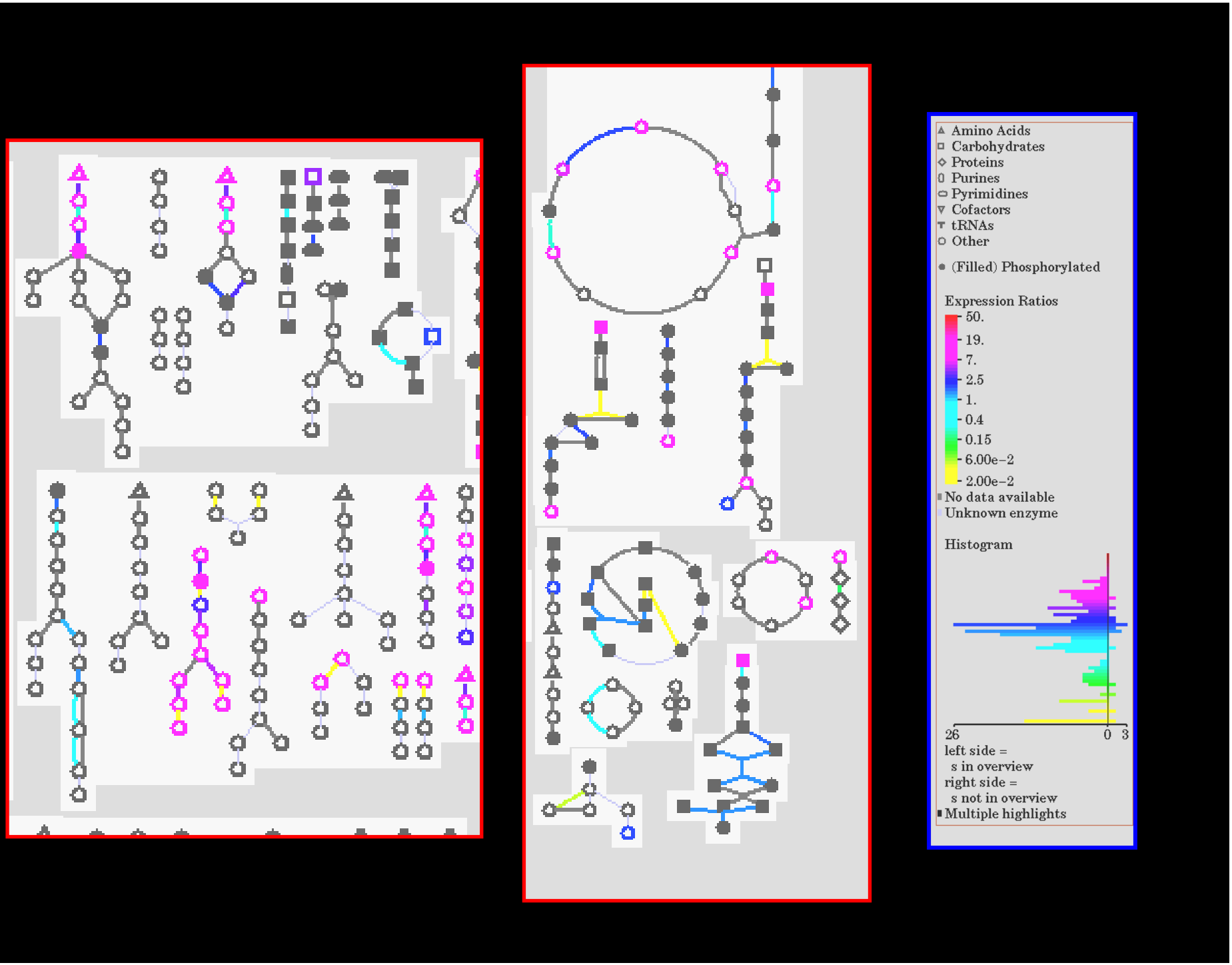
Microarray expression data: low temperature regulatory circuits and gene regulons in higher plants (Michael Tomashow group).


Expression Ratios
+7.8
+2.
0.
−2.
−4.
−5.9
Compound: dihydrozeatin
Pathway: cytokinins 9-N-glucoside biosynthesis
Compound: xanthoxin
Pathway: abscisic acid biosythesis

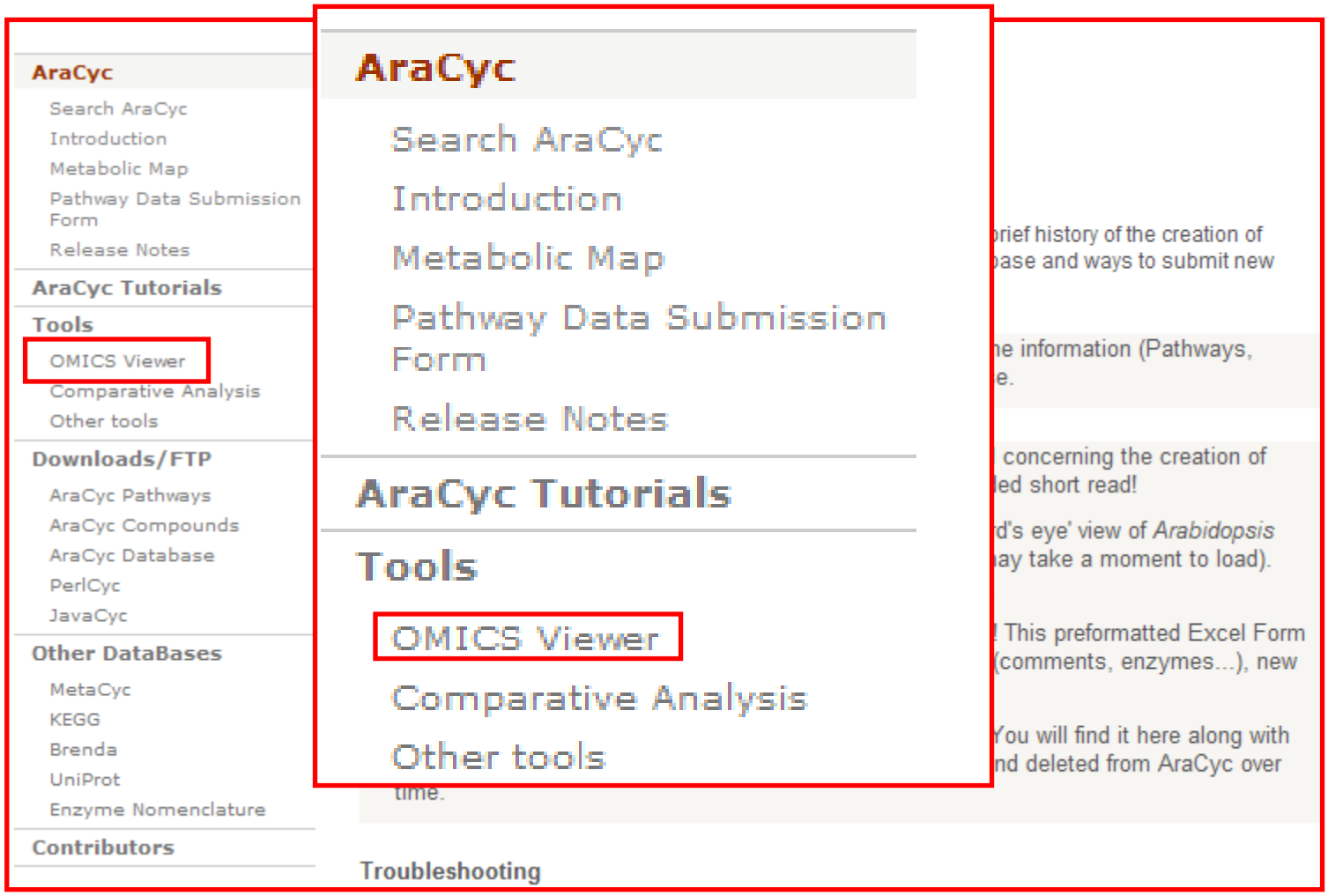
OMICS Viewer

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


Amino Acids
Carbohydrates
Proteins
Purines
Pyrimidines
Cofactors
tRNAs
Other
(Filled) Phosphorylated
Expression Ratios
50.
19.
7.
2.5
1.
0.4
0.15
6.00e−2
2.00e−2
No data available
Unknown enzyme
Histogram
26
0
3
left side =
s in overview
right side =
s not in overview
Multiple highlights

Access Omics Viewer



Select a dataset: Arabidopsis thaliana COL

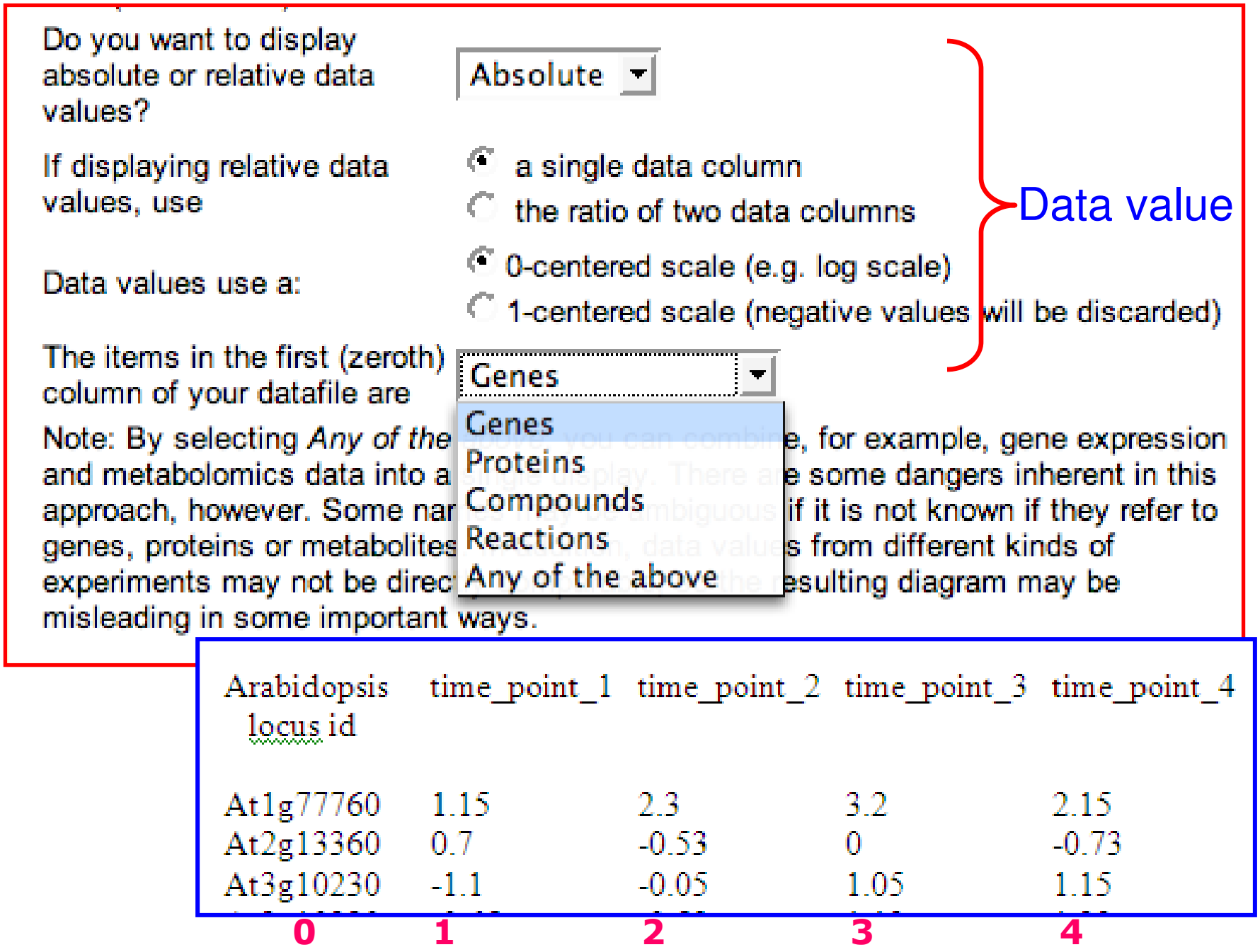
File containing experimental data (NOT a URL): C:\Documents and Setti Browse...

Do you want to absolute or rela values?

If displaying rel values, use

Data values us

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
Genes
Proteins
Compounds
Reactions
Any of the above
Note: By selecting Any of the
e, for example, gene expression
and metabolomics data into a
e some dangers inherent in this
approach, however. Some nar
if it is not known if they refer to
genes, proteins or metabolites
s from different kinds of
experiments may not be direc
esulting diagram may be
misleading in some important ways.
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 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:

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:

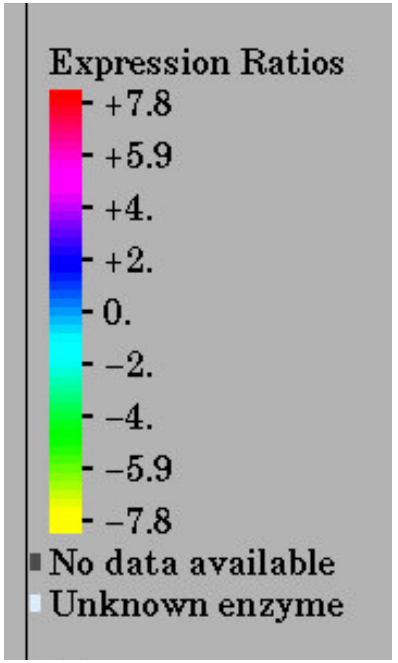
- (•) Full color spectrum, computed from data provided (default)
- ( ) Full color spectrum with a maximum cutoff:
- ( ) Three color display with specified threshhold:

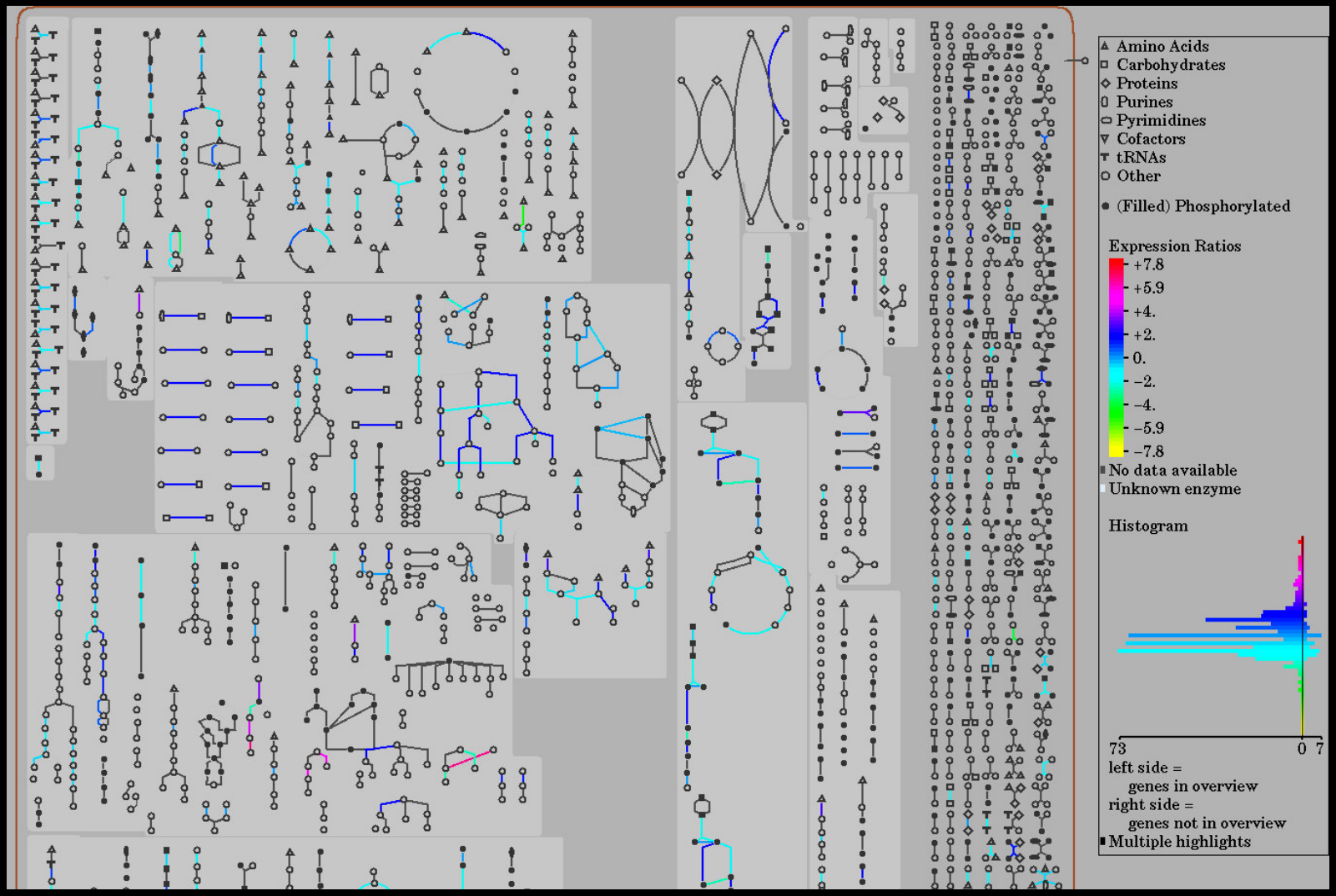
Display Type

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 threshhold (or are less than the inverse of that threshhold). To select this alternative display, choose the corresponding option below and specify the threshhold.

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

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




Amino Acids
Carbohydrates
Proteins
Purines
Pyrimidines
Cofactors
tRNAs
Other
(Filled) Phosphorylated
Expression Ratios
+7.8
+5.9
+4.
+2.
0.
−2.
−4.
−5.9
−7.8
No data available
Unknown enzyme
Histogram
73
0 7
left side =
genes in overview
right side =
genes not in overview
Multiple highlights