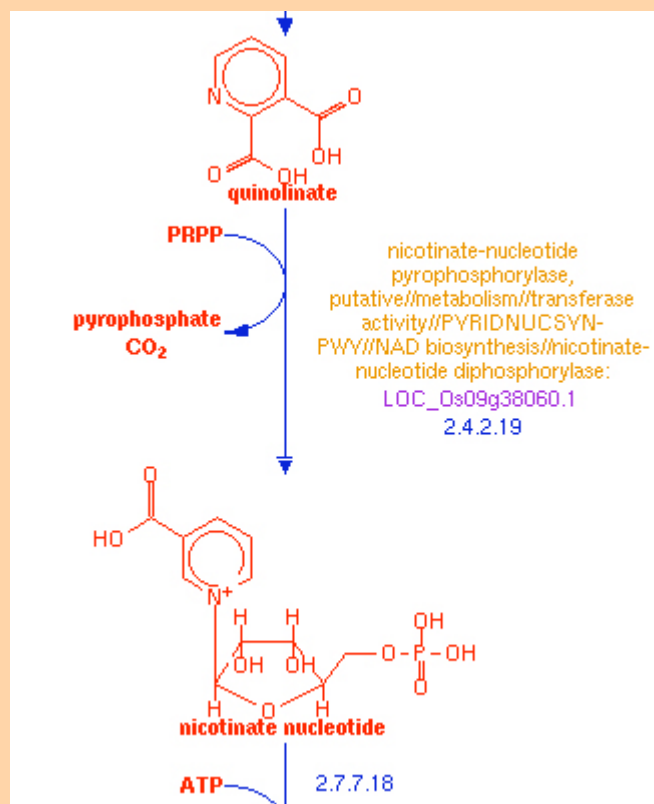


Welcome to Gramene's RiceCyc (Pathways) Tutorial



RiceCyc allows biochemical pathways to be analyzed and visualized.

This tutorial has been developed for first time and casual users of RiceCyc.

These slides relate to Version 1.2 of RiceCyc.



Tutorial Help



If you are viewing this tutorial with Adobe Acrobat Reader, click the "bookmarks" on the left hand side of the Reader for easier navigation.

Introduction

- RiceCyc allows biochemical pathways to be analyzed and visualized.
- Gramene has incorporated the latest TIGR 4 genome into this release to create an *Oryza sativa* specific pathway dataset.
- Data is under development and subject to change. If you do see any errors in the dataset please feel free to contact us through the feedback provided at the top of Gramene webpages.

Gramene Home Page

The screenshot shows the Gramene Home Page with a green header and a light green sidebar. A blue callout bubble points to the 'Pathways' link in the sidebar menu.

GRAMENE *A Resource for Comparative Grass Genomics* V24 (March 2007)

Search | Genomes | Species | Download | Resources | About | Help | [Feedback](#)

Quick Search

Search a single module or all available modules plus online documentation.
Diversity, Pathways, BLAST and Mart not available in this search.

Have Questions...?

- Gramene now has [tutorials](#) for every module, also recommended for experienced users.
- Ask questions through [Feedback](#) or [Email](#).
- See [FAQ](#) for questions and answers.

Gramene Tip:

Map details can be [downloaded](#) in a tab-delimited

Quick Start

enced genomes for [Rice](#), [Maize](#) & [Arabidopsis](#); Look for [rice/maize synteny](#); Narrow your Search for sequence alignment with [BLAST](#); search by [Gene Ontology](#).

Pathways

Click here to open the Pathways module

Featured News

- [NEW](#) March 2007, V 24 [release notes](#).
- [NEW](#) [Gramene Jan/Feb Newsletter](#)
- [Rice News Worldwide](#) from IRRI

Visit with us at

- March 15-18, 2007. [CSHL Plant Genome meeting](#)
- March 22-25, 2007. [Maize Genetics Meeting](#)
- April 16-20, 2007. [ITMI](#)
- May 8-12, 2007. [Biology of Genomes](#)
- July 7-11, 2007. [ASPB](#)

[View Previous Gramene Presentations Calendar](#)

TRAITS: Search the [Genes](#) or [QTL](#) database for important phenotype-related loci such as [Rice Genes](#), [Rice QTL](#), [Maize QTL](#). Don't forget to explore [traits in Ontologies](#).

GENETIC DIVERSITY: Search for SNP and SSR allelic variation on loci of [rice](#), [maize](#), and [wheat](#) germplasms.

BIOCHEMICAL PATHWAYS: Search for ALL the rice pathways on [starch biosynthesis](#) or get an overview of the [metabolic network](#). Compare [rice and Arabidopsis](#) pathway datasets.

LITERATURE: Search the literature for your friends and topics of interest.

SUBMISSION: Submit a [Rice Gene](#) or [Ontology Term](#) to Gramene.

Most current
release notes

Pathways Home Page

Click here to
begin your
search

RiceCyc home and Biochemical pathways

Click here to SEARCH and BROWSE the pathways

A short summary
of RiceCyc

RiceCyc
navigation

Quick links to rice
pathways

Lists available
species

About
Pathway
Tools

External
links

[Tutorial](#) | [FAQ](#) | [Help](#) | [Release notes](#)

About pathway tools

The Pathway Tools is a web-based tool for viewing gene annotations mapped to various biochemical pathways in rice (*Oryza sativa*) and Arabidopsis (*Arabidopsis thaliana*) and Escherichia coli (*Escherichia coli*).

The Pathway Tools is developed by Gramene. The current version of RiceCyc is based on release 4 of the Rice Genome Annotation Project (RGAP) and the Arabidopsis Genome Initiative (AGI) genome sequences.

Your favorite rice pathways

[Auxin metabolism](#)
[Brassinosteroid metabolism](#)
[Cytokinin metabolism](#)
[Photosynthesis](#)
[Respiration](#)
[TCA cycle](#)
[Secondary metabolic pathways](#)
[Starch biosynthesis](#)
[Pentose phosphate pathways](#)
[ALL pathways](#)




In order to promote exciting new discoveries on biochemical pathways in rice, the current version of RiceCyc has undergone a round of curation that has removed data unlikely to be relevant to Rice. We maintain a [list of pathways](#) that have been deleted.

Since the functions of many of the rice genes are either provided by homology and HMM based predictions or unknown, many of the pathways might be incomplete or may contain errors. The manual curation of pathways is an ongoing process at Gramene and we welcome feedback from the research community.

If you notice problems or errors on the pathways, please send a message to [Gramene](#) or by clicking the 'Feedback' button at the bottom of the pathway page.

Pathway Tools is a bioinformatics software system for pathway analysis of Pathway/Genome Databases (PGDBs). It was developed by workers at the [Bioinformatics Research Group](#) at SRI International. The pathways were created using the Pathway Tools' PathoLogic module. This tool generates an initial set of pathways by comparing annotations of genes and gene

Pathways in Gramene

Species	Source	Overview#	Summary	Pathway comparison
RICE <i>Oryza sativa japonica</i> cv. Nipponbare	Gramene, RiceCyc 1.2		view	Arabidopsis E. coli
ARABIDOPSIS* <i>Arabidopsis thaliana</i> strain Columbia	TAIR, AraCyc 3.5		view	Rice E. coli
E. COLI* <i>Escherichia coli</i> strain K-12 MG1655	SRI, EcoCyc 10.5			

* Not curated by Gramene. # click on icons to visit the overview

Useful links to pathway tools

Compare data sets from the three species for reactions, pathways, compounds and proteins	Compare
Map your microarray expression, proteomics, metabolomics and other datasets on Pathway overview diagrams	Omics viewer
Details on pathway visualization [Help document]	Help
Learn how to use the tool	Tutorial
Still have questions, consult the frequently asked questions section	FAQs
RiceCyc? Download from our ftp archive. If you have any questions or pathways please visit AraCyc and EcoCyc project sites.	Download

Useful external links

[KEGG pathways](#)
[IUBMB Enzyme nomenclature](#)
[Brenda enzyme database](#)

Search Options

Select a dataset (*see slide 8*)

GRAMENE

Pathway Tools Query Page

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

Select a dataset:

• **Query**

To retrieve objects by name, first select the type of object you wish to retrieve, then enter the names of the objects. The results will be returned. You may also enter multiple names or EC numbers, separating them with commas.

• **Browse Ontology:**

Each dataset contains classification hierarchies for pathways, for reactions (the enzyme nomenclature system), for compounds, and for other objects.

• **Choose from a list of all**

• **Links to summary information about the selected organism:**

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

• **Comparative Analysis** NEW

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

Pathway Tools version 9.5

1) Term search (*slides 9-19*)

2) Browse by RiceCyc ontology (*slides 20-21*)

3) Find a Pathway (*slide 22*)

Note: the RiceCyc ontology is separate from the other Gramene ontologies in the Ontologies Database.

Search Page Navigation



Pathway Tools Query Page

This form provides several different mechanisms for querying Pathway Tools.

Select a dataset:

• **Query**

To retrieve objects by name, first select the type of object you wish to query, then enter the name of the object and click Submit. All objects matching the name will be returned. You may also enter multiple names or EC numbers, separating them with commas.

• **Browse Ontology:**

Each dataset contains classification hierarchies for pathways, for reactions (the enzyme nomenclature system), for compounds, and for other objects.

• **Choose from a list of all**

• **Links to summary information about the selected organism:**

- [Summary page for dataset](#)
- [Cellular Overview Diagram/Omics Viewer](#)
- [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.

Click to follow links
(Slides 23-32)

Click to return to
Pathways home

Click to compare
available species (slides
33-36)

Click to access
Help docs.

Submit a question or
give feedback

Select your organism

It is important that you choose the right dataset before starting your work. Rice is the default.

Select a dataset:

Oryza sativa japonica Nipponbare

Arabis thaliana COL

Escherichia coli K-12

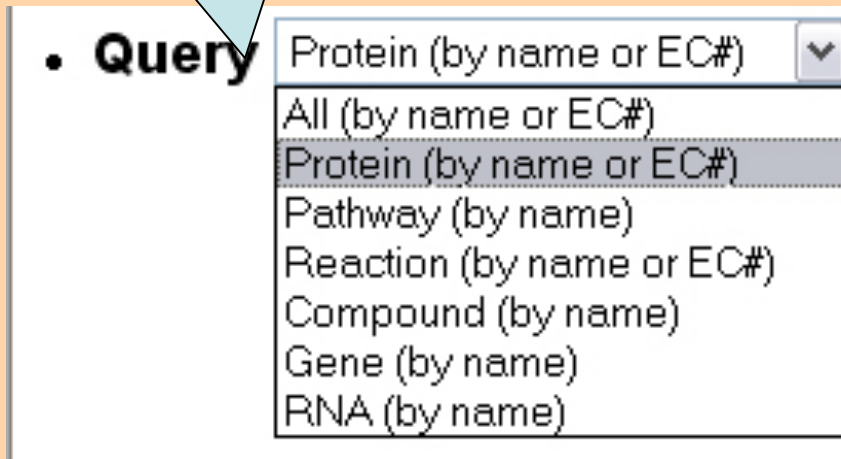
Oryza sativa japonica Nipponbare

Submit

?

1. Searches in RiceCyc

RiceCyc can be searched by several parameters



1. Protein (slide 10-11)
2. Pathway (slide 12 - 14)
3. Reaction (slide 15)
4. Compound (slide 16-17)
5. Gene (slide 18 - 19)
6. RNA (Currently not available)

Protein Search

Select "Protein"

• Query Submit

☐ All (by name or EC#)
☒ Protein (by name or EC#)
☐ Pathway (by name)
☐ Reaction (by name or EC#)
☐ Compound (by name)
☐ Gene (by name)
☐ RNA (by name)

Enter protein name or EC#

Click Submit

Results

[[Pathway Home](#)]

RiceCyc Query Results

The query **aldehyde dehydrogenase** matched 51 proteins:

- [Aldehyde oxidase and xanthine dehydrogenase, molybdopterin binding domain containing protein, expressed /aldehyde oxidase activity](#)
- [aldehyde dehydrogenase activity](#)
- [aldehyde dehydrogenase family protein, expressed \(polypeptide\) -LOC_Os02g43194.1](#)
- [aldehyde dehydrogenase family protein, expressed \(polypeptide\)-LOC_Os02g43280.1](#)
- [aldehyde dehydrogenase family protein, expressed \(polypeptide\)-LOC_Os11g08300.1](#)
- [aldehyde dehydrogenase family protein, expressed \(polypeptide\)-LOC_Os12g07810.1](#)
- [aldehyde dehydrogenase family protein, expressed /1-pyrroline-5-carboxylate dehydrogenase \(polypeptide\)-LOC_Os04g45720.1](#)
- [aldehyde dehydrogenase family protein, expressed /1-pyrroline-5-carboxylate dehydrogenase \(polypeptide\)-LOC_Os07g48920.1](#)
- [Aldehyde dehydrogenase, mitochondrial precursor, putative, expressed](#)
- [Aldehyde dehydrogenase, mitochondrial precursor, putative, expressed /1-pyrroline-5-carboxylate dehydrogenase \(polypeptide\)-LOC_Os01g40870.1](#)
- [Aldehyde dehydrogenase, mitochondrial precursor, putative, expressed /1-pyrroline-5-carboxylate dehydrogenase \(polypeptide\)-LOC_Os06g15990.1](#)
- [aldehyde dehydrogenase, putative, expressed /1-pyrroline-5-carboxylate dehydrogenase](#)
- [aspartate-semialdehyde dehydrogenase \(polypeptide\)-LOC_Os03g42110.1](#)
- [aspartate-semialdehyde dehydrogenase \(polypeptide\)-LOC_Os03g55280.1](#)
- [Betaine-aldehyde dehydrogenase, chloroplast precursor, putative, expressed](#)
- [betaine-aldehyde dehydrogenase, putative](#)
- [formaldehyde dehydrogenase \(glutathione\)](#)
- [formaldehyde dehydrogenase \(glutathione\) activity \(polypeptide\)-LOC_Os02g42520.1](#)
- [formaldehyde dehydrogenase \(glutathione\) activity \(polypeptide\)-LOC_Os08g01760.1](#)
- [formaldehyde dehydrogenase \(glutathione\) activity \(polypeptide\)-LOC_Os11g10480.1](#)

Click on the appropriate selection

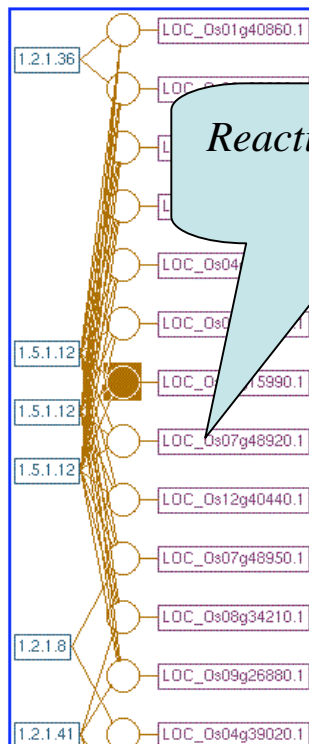
Protein

***O. sativa japonica* Enzyme: Aldehyde dehydrogenase, mitochondrial precursor, putative, expressed / 1 pyrroline-5-carboxylate dehydrogenase**

Gene: [LOC_Os06g15990.1](#)

Sequence Length: 5525/3 AAs

Gene-Reaction Schematic: [?](#)



Reaction schematic of the gene

Gene associated with protein

Protein name and synonyms

Enzymatic reaction of: 1-pyrroline-5-carboxylate dehydrogenase



The reaction direction shown, that is, $\text{A} + \text{B} \rightleftharpoons \text{C} + \text{D}$ versus $\text{C} + \text{D} \rightleftharpoons \text{A} + \text{B}$, is in accordance with the Enzyme Commission system.

Reversibility of this reaction is unspecified.

In Pathways: [proline degradation II](#), [arginine degradation VII](#), [proline degradation](#)

Reactions catalyzed by the enzyme

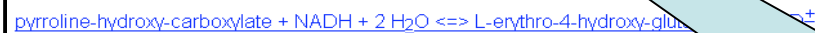
Enzymatic reaction of: 1-pyrroline-5-carboxylate dehydrogenase



The reaction direction shown, that is, $\text{A} + \text{B} \rightleftharpoons \text{C} + \text{D}$ versus $\text{C} + \text{D} \rightleftharpoons \text{A} + \text{B}$, is in accordance with the Enzyme Commission system.

Reversibility of this reaction is unspecified.

Enzymatic reaction of: 1-pyrroline-5-carboxylate dehydrogenase



The reaction direction shown, that is, $\text{A} + \text{B} \rightleftharpoons \text{C} + \text{D}$ versus $\text{C} + \text{D} \rightleftharpoons \text{A} + \text{B}$, is in accordance with the Enzyme Commission system.

Reversibility of this reaction is unspecified.

In Pathways: [4-hydroxyproline degradation](#)

Pathways containing the enzyme. Click to access pathway

[Query Page](#) [Advanced Query Page](#) [Report Errors or Provide Feedback](#)

Pathway Search

Select
“pathway”

All (by name or EC#)
Protein (by name or EC#)
Pathway (by name)
Reaction (by name or EC#)
Compound (by name)
Gene (by name)
RNA (by name)

Enter pathway
name (or partial
name)

Level 1

Compound (red text). Click for
more info (slide 17)

Click for more
detail (next
slide)

D. sativa japonica Pathway: 4-hydroxyproline degradation

More Detail

Cross-Species Comparison

Download Genes

BioPAX format

L-4-hydroxy-proline → D-4-hydroxy-2-keto-glutarate → pyruvate
glyoxylate

Locations of Mapped Genes:



Reaction (blue line) Click to go to
reaction page (Slide 15)

Superclasses: [Degradation/Utilization/Assimilation](#) -> [Amino Acids](#) -> [4-hydroxyproline degradation](#)

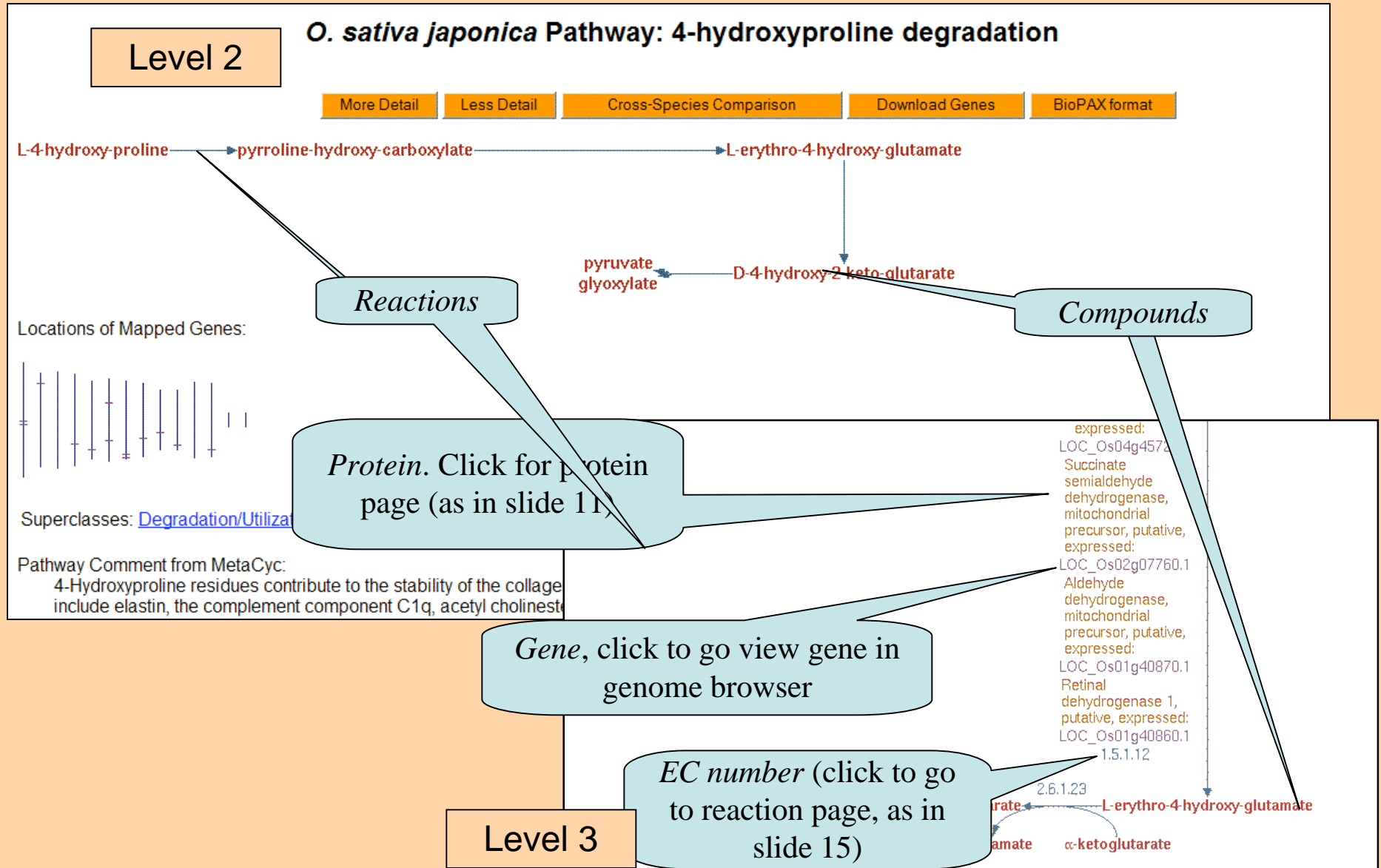
Pathway Comment from MetaCyc:

4-Hydroxyproline residues contribute to the stability of the collagen triple helix. Collagen is a major constituent of animal protein. Other animal proteins containing 4-hydroxyproline include elastin, the complement component C1q, acetyl cholinesterase. 4-Hydroxyproline is also found in some proteins of higher plants and algae. Most of the 4-hydroxyproline in animals is biosynthesized by post-translational modification of appropriate proline residues by proline hydroxylase during the biosynthesis and maturation of collagen. 4-Hydroxyproline released during collagen degradation cannot be reutilized, and is degraded.

This major mammalian pathway for 4-hydroxyproline degradation has been demonstrated in liver and kidney mitochondria. The first two reactions of the pathway are those of proline degradation (see MetaCyc pathway [proline degradation 1](#)). However the first enzyme, hydroxyproline oxidase, is distinct from proline oxidase based on the accumulation of free hydroxyproline, but not proline, in the plasma and urine of individuals with a deficiency of this enzyme, while those deficient in proline oxidase show elevated 4-hydroxyproline levels. The two enzyme activities can also be differentially destroyed by chemical, physical, or enzymatic treatment (reviewed in [[Adams60](#)]).

The second enzyme pyrroline-5-carboxylate dehydrogenase appears to be shared by the two pathways [[Valle79](#), [Adams60](#)]. The substrate for the second enzyme, 4-hydroxy-2-keto-glutarate, can also exist in an open chain form (4-hydroxy-glutamic-4-semialdehyde) [[Takayama03](#)], but evidence suggests that this enzyme uses the ring form (4-hydroxy-2-keto-glutarate) [[Adams60](#)].

Pathway Levels 2 & 3



Pathway Levels 4 & 5

Level 4

dehydrogenase,
mitochondrial
precursor, putative,
expressed:
LOC_Os02g07760.1
Aldehyde
dehydrogenase,
mitochondrial
precursor, putative,
expressed:

Move between levels with
“more detail” and “less detail” buttons.

O. sativa japonica Pathway: 4-hydroxyproline degradation

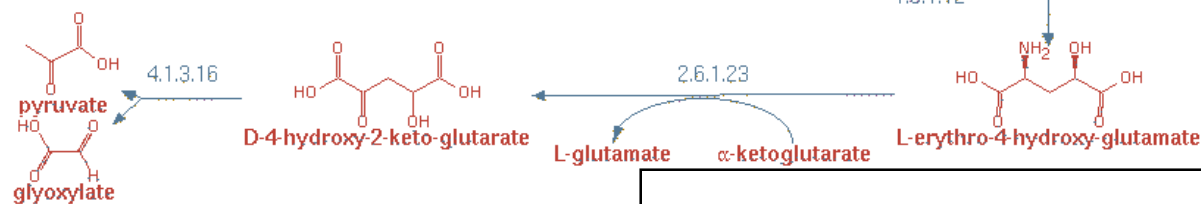
More Detail

Less Detail

Cross-Species Comparison

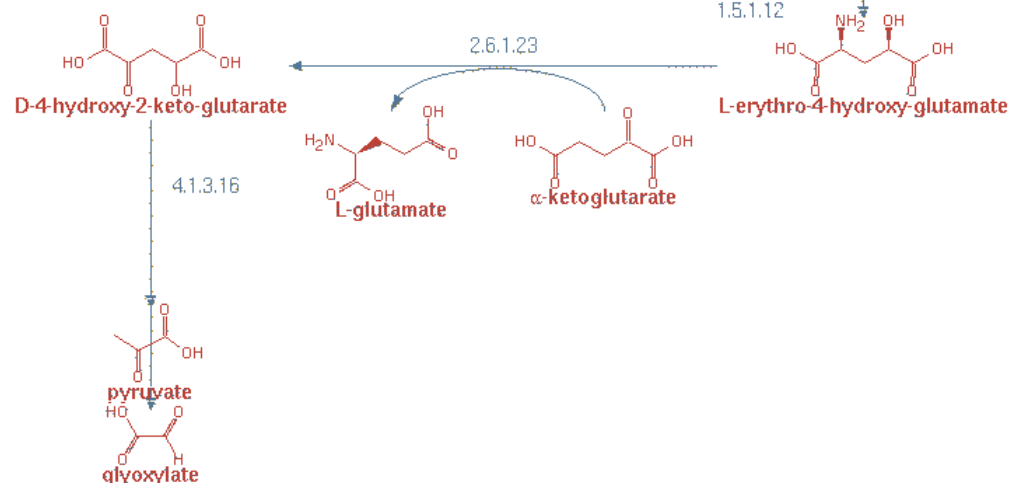
Download Genes

BioPAX format



Level 5

dehydrogenase,
mitochondrial
precursor, putative,
expressed:
LOC_Os01g40870.1
Retinal
dehydrogenase 1,
putative, expressed:
LOC_Os01g40860.1
1.5.1.12



Reaction Search

Select
"Reaction"

Search by name or EC#

2.4.2.3

Submit

☐ All (by name or EC#)
☐ Protein (by name or EC#)
☐ Pathway (by name)
☒ Reaction (by name or EC#)
☐ Compound (by name)
☐ Gene (by name)
☐ RNA (by name)

Click Submit

Enter reaction
name or EC#

Results

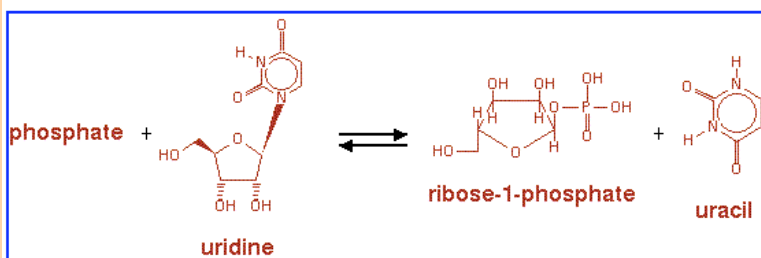
[\[Pathway Home \]](#)

O. sativa japonica Reaction: 2.4.2.3

Cross-Species Comparison

Superclasses: [Reactions-Classified-By-Conversion-Type](#) -> [Simple-Reactions](#) -> [Chemical-Reactions](#) -> [EC-Reactions](#) -> [2 -- Transferases](#) -> [2.4 -- Glycosyltransferases](#) -> [Pentosyltransferases](#)
[Reactions-Classified-By-Substrate](#) -> [Small-Molecule-Reactions](#)

In Pathway: [salvage pathways of pyrimidine ribonucleotides](#), [\(deoxy\)ribose phosphate degradation](#)



The reaction direction shown, that is, $A + B \rightleftharpoons C + D$ versus $C + D \rightleftharpoons A + B$, is in accordance with the Enzyme Commission

Unification Links: [ENZYME:2.4.2.3](#)

Click to go to ExPaSy
for more gene products
that catalyze the
reaction.

[Query Page](#)

[Advanced Query Page](#)

[Report Errors or Provide Feedback](#)

Compound Search

Select
"Compound"

Click Submit

Enter protein
name or EC#

Results

Query Results

The query **uridine** matched 16 compounds:

- ♦ [uridine](#)
- ♦ [deoxyuridine](#)
- ♦ [dUDP \(2'-deoxyuridine-5'-diphosphate\)](#)
- ♦ [dUMP \(2'-deoxyuridine-5'-monophosphate\)](#)
- ♦ [dUTP \(2'-deoxyuridine-5'-triphosphate\)](#)
- ♦ [pseudouridine 5'-phosphate](#)
- ♦ [spermine \(neuridine\)](#)
- ♦ [UDP \(uridine-diphosphate\)](#)
- ♦ [UDP-N-acetyl-D-glucosamine \(uridine diphosphate N-acetylglucosamine\)](#)
- ♦ [UDP-N-acetyl-D-mannosamine \(uridine diphosphate N-acetylmannosamine\)](#)
- ♦ [UDP-N-acetylmuramate \(uridine diphosphate N-acetylmuramic acid\)](#)
- ♦ [UDP-D-glucuronate \(uridine diphosphate glucuronate\)](#)
- ♦ [UDP-galactose \(uridine diphosphate galactose\)](#)
- ♦ [UDP-N-acetylgalactosamine \(uridine diphosphate N-acetylgalactosamine\)](#)
- ♦ [UMP \(uridine-5'-monophosphate\)](#)
- ♦ [UTP \(uridine-triphosphate\)](#)

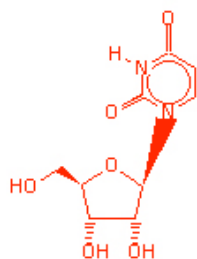
Compounds

O. sativa japonica Compound: uridine

Superclasses: [Nucleic acid components](#) -> [a nucleoside](#) -> [a ribonucleoside](#)
[Nucleic acid components](#) -> [Pyrimidine-Related](#) -> [a pyrimidine nucleoside](#)

Empirical Formula: C₉H₁₂N₂O₆

Molecular Weight: 244.2



Smiles: c1(n(c(=O)[nH]c(c1)=O)C2(C(O)C(O)C(O2)CO))

Unification Links: CAS:58-96-8 , [LIGAND:C00299](#)

In Pathway Reactions as a Reactant:

[salvage pathways of purine and pyrimidine nucleotides:](#)
[uridine + ATP = UMP + ADP](#)

[salvage pathways of pyrimidine ribonucleotides:](#)
[phosphate + uridine = ribose-1-phosphate + uracil](#),
[uridine + GTP = UMP + GDP](#)

Gene Search

Select "Gene"

All (by name or EC#)
Protein (by name or EC#)
Pathway (by name)
Reaction (by name or EC#)
Compound (by name)
Gene (by name)
RNA (by name)

Os09g36270

Submit

Click Submit

Enter gene name

Results

O. sativa japonica Gene: [LOC_Os09g36270.1](#)

Superclasses: [UNCLASSIFIED](#)

Chromosome: Chromosome 9

Map Position: 20,928,304 -> 20,937,524 (nucleotides) 90.948 (centisomes) [click for genome browser]

Sequence Length: 9221 bp / 9218/3 AAs

Products: [Pantothenate kinase 2, putative, expressed / pantothenate kinase](#)

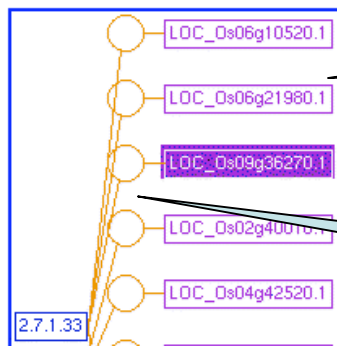
Reactions Catalyzed by Enzymes:

[pantothenate + ATP = D-4'-phosphopantothenate + ADP](#)

Pathways Involving Enzymes: [coenzyme A biosynthesis](#)

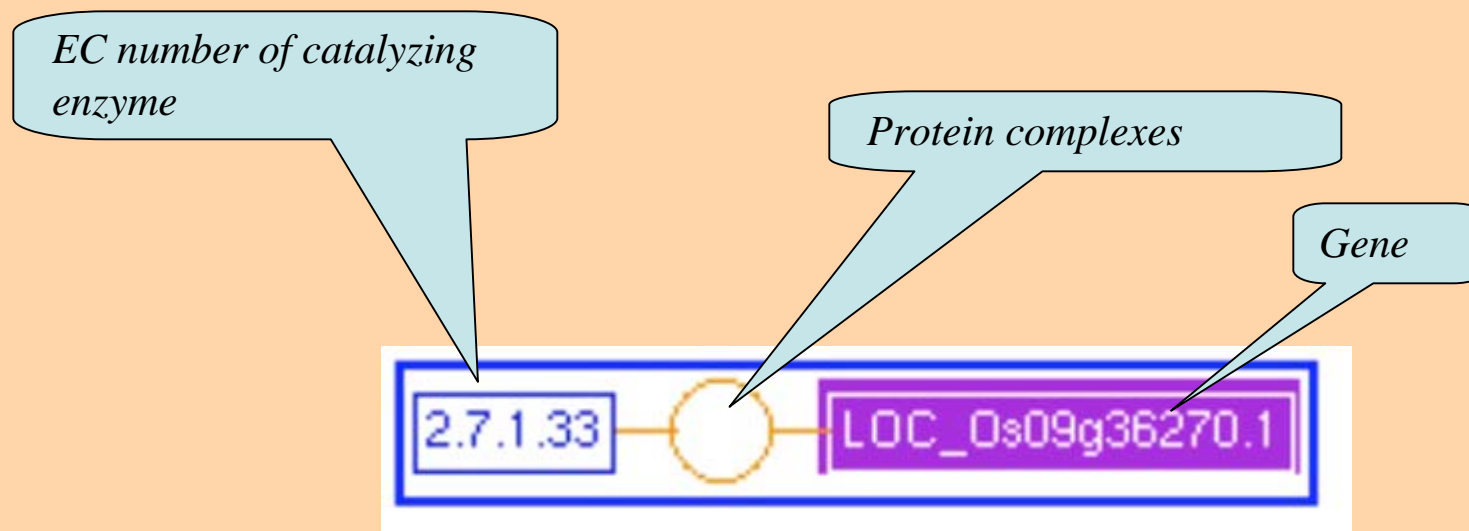
Gene-Reaction Schematic: ?

Click to go to
Gramene Ensembl
page



Gene Schematic, see slide
19.

Gene Schematic




A line from a gene to a circle - the gene codes for the protein

Two circles linked together - a gene product is a subunit of a protein complex

Circle connected to reaction - reaction is catalyzed by enzyme.

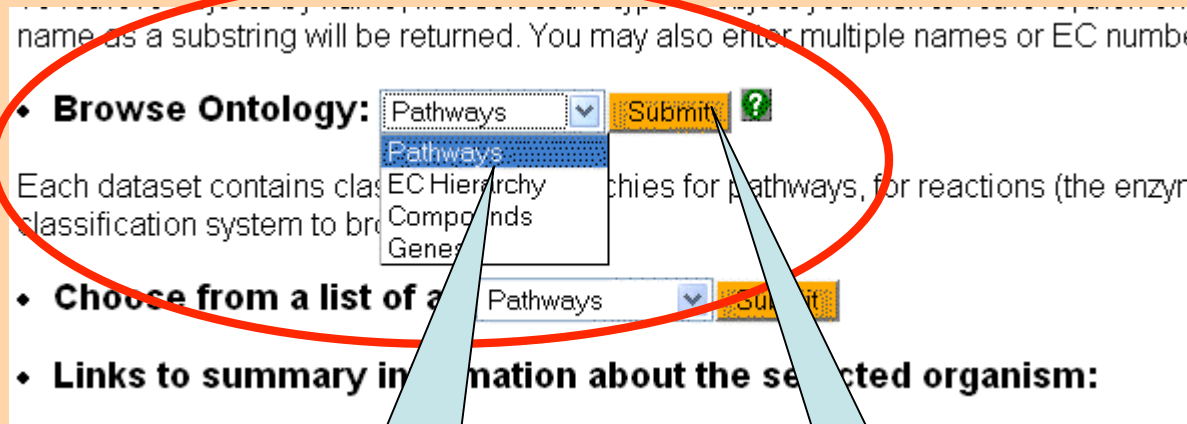
2. Browse RiceCyc Ontology

name as a substring will be returned. You may also enter multiple names or EC number

- **Browse Ontology:** Pathways 

Each dataset contains classification system to browse

- **Choose from a list of a** Pathways
- **Links to summary information about the selected organism:**



Select your ontology

Click "submit"

Browse RiceCyc Ontologies

The screenshot shows the RiceCyc ontology browser interface. At the top, there are two buttons: "Expand All" and "Collapse All". Below them is a tree view of the ontology. The tree is currently expanded to show the "Biosynthesis" category, which includes sub-terms like "Amines and Polyamines", "Betaine biosynthesis", "Amino acids", "Amino acid families", and "Individual amino acids". A red arrow points from the "Biosynthesis" term in the tree to a detailed view of the "O. sativa japonica Class: Biosynthesis". This detailed view includes a comment, parent classes, and child classes. Callouts provide instructions on how to use the interface: one points to the minus sign icon indicating a term is expanded, another points to the plus sign icon indicating a term is collapsed, and a third points to the "Biosynthesis" term in the tree, explaining that clicking it leads to more information on other relationships. A fourth callout points to the end of the tree, explaining that clicking terms at the end of the tree leads to the pathway (as in slides 12-14).

Expand All Collapse All

Pathways

- Biosynthesis** (minus icon)
 - Amines and Polyamines** (minus icon)
 - Betaine biosynthesis (minus icon)
 - betaine biosynthesis (plants)
 - betaine biosynthesis I
 - betaine biosynthesis II
 - betaine biosynthesis III
 - betaine biosynthesis IV
 - betaine biosynthesis V
 - UDP-N-acetyl-D-glucosamine biosynthesis
 - ureide biosynthesis
 - Amino acids** (minus icon)
 - Amino acid families** (minus icon)
 - chorismate biosynthesis
 - homoserine biosynthesis
 - methionine and S-adenosylmethionine synthesis
 - superpathway of aspartate and asparagine biosynthesis
 - superpathway of isoleucine and valine biosynthesis
 - superpathway of isoleucine biosynthesis
 - superpathway of leucine, valine, and isoleucine biosynthesis
 - superpathway of lysine, threonine and methionine biosynthesis
 - superpathway of methionine, threonine and methionine biosynthesis
 - valalanine and tyrosine biosynthesis
 - valalanine, tyrosine and methionine biosynthesis
 - valalanine, tyrosine, and methionine biosynthesis
 - valalanine, tyrosine, and glycine biosynthesis
 - valalanine and glycine biosynthesis II
 - superpathway of sulfur amino acid biosynthesis
 - Individual amino acids** (minus icon)
 - Aminoacyl-tRNAs** (plus icon)

O. sativa japonica Class: Biosynthesis

Comment:
This class contains pathways that constitute a cell's complete spectrum of biosynthetic capacities, including the routes of synthesis of small molecules, macromolecules and organelles.

Parent Classes:
[Pathways](#)

Child Classes:
[Amines and Polyamines \(13\)](#),
[Amino acids \(61\)](#),
[Carriers \(37\)](#),
[Fatty Acids and Lipids \(20\)](#),
[Hormones \(12\)](#),
[Metabolic Regulators \(1\)](#),
[Nucleosides and Nucleotides \(9\)](#),
[Other \(2\)](#),
[Secondary Metabolism \(0\)](#).

- Indicates term is expanded. Click to collapse.

+ indicates term is collapsed, Click to expand ontology tree.

Click parent term for more information on other relationships

Click terms at end of tree to go to Pathway (as in slides 12-14)

3. Browse Pathways

- Choose from a list of all
- Links to summary information
 - [Summary page for data](#)

Pathways
Proteins
Compounds
Genes
Pseudogenes

Submit

the select

Select your
pathway type

Click "submit"

The query "Pathways" matched 313 objects:

[β-alanine betaine biosynthesis](#)
[β-alanine biosynthesis I](#)
[β-alanine biosynthesis III](#)
[β-D-glucuronide degradation](#)
[γ-glutamyl cycle](#)
[\(deoxy\)ribose phosphate degradation](#)
[\(S\)-reticuline biosynthesis](#)
[4-hydroxyproline degradation](#)
[cis-zeatin biosynthesis](#)
[m-cresol degradation](#)
[myo-inositol biosynthesis](#)
[p-cymene degradation](#)
[trans-zeatin biosynthesis](#)
[acetate utilization](#)
[acetyl-CoA assimilation](#)
[acrylonitrile degradation](#)
[aerobic respiration](#)
[aerobic respiration -- electron donors reaction list](#)
[alanine biosynthesis II](#)
[alanine biosynthesis III](#)
[alanine degradation II](#)
[alanine degradation III](#)
[aldoxime degradation](#)
[allantoin degradation I](#)
[ammonia assimilation cycle](#)
[ammonia assimilation cycle II](#)
[anthocyanin biosynthesis](#)
[arginine biosynthesis II \(acetyl cycle\)](#)

Click term to
open pathway
(as in slides 12-
14)

4. Summary Information

(Image from
search page,
Slide 7)

- **Links to summary information about the selected organism:**

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

Summary for
RiceCyc in table
form (*Slide 24*)

Metabolic Map
(*Slides 25-27*)

Omics Viewer
(*Slides 28-32*)

Pathway
summary

Release info

Summary of *Oryza sativa japonica*, version 1.2

Summarize Pathway Evidence

Replicon	Total Genes	Protein Genes	RNA Genes	Pseudogenes	Size (bp)
Chromosome 1	5255	5255	0	0	43,596,771
Chromosome 2	4255	4255	0	0	35,925,388
Chromosome 3	4468	4468	0	0	36,345,490
Chromosome 4	4147	4147	0	0	35,244,269
Chromosome 5	3553	3553	0	0	29,874,162
Chromosome 6	3584	3584	0	0	31,246,789
Chromosome 7	3380	3380	0	0	29,688,601
Chromosome 8	3115	3115	0	0	28,309,179
Chromosome 9	2550	2550	0	0	23,011,239
Chromosome 10	2594	2594	0	0	22,876,596
Chromosome 11	3005	3005	0	0	28,462,103
Chromosome 12	3001	3001	0	0	27,497,214
mitochondrion	71	71	0	0	490,520
chloroplast	137	137	0	0	134,525
Total:	43115	43115	0	0	372,702,846

Pathways:	279
Enzymatic Reactions:	1687
Transport Reactions:	5
Polypeptides:	43172
Protein Complexes:	4
Enzymes:	10387
Transporters:	62
Compounds:	1265
Transcription Units:	0
tRNAs:	0

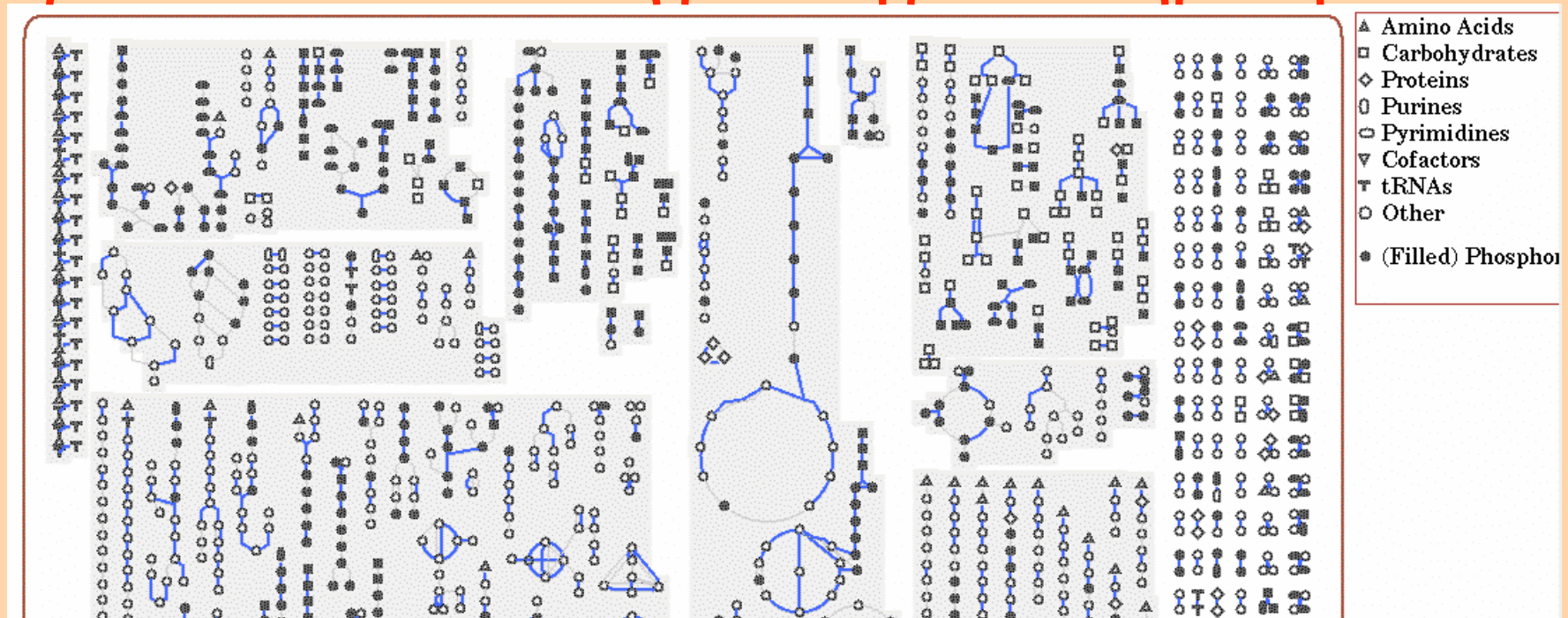
5a. Metabolic Map Overview

Biosynthetic pathways

TCA Cycle

Catabolic

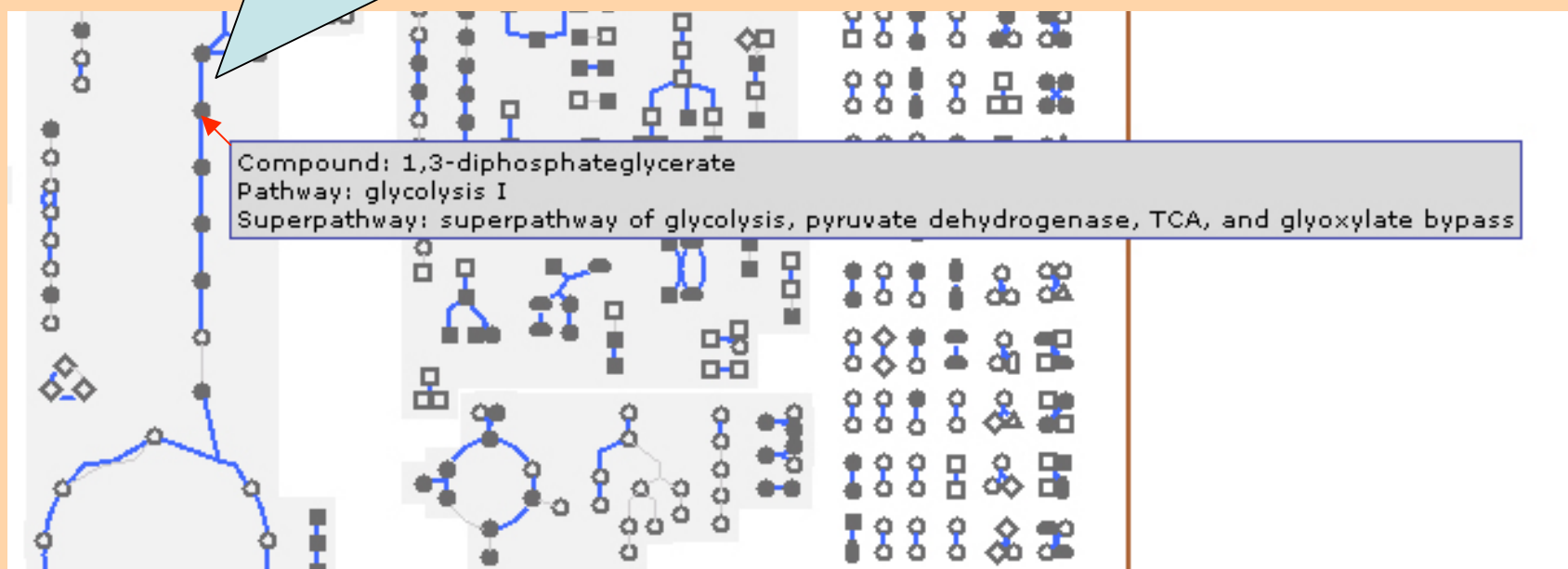
Orphan



The flow of the pathway is from the top of the page to the bottom

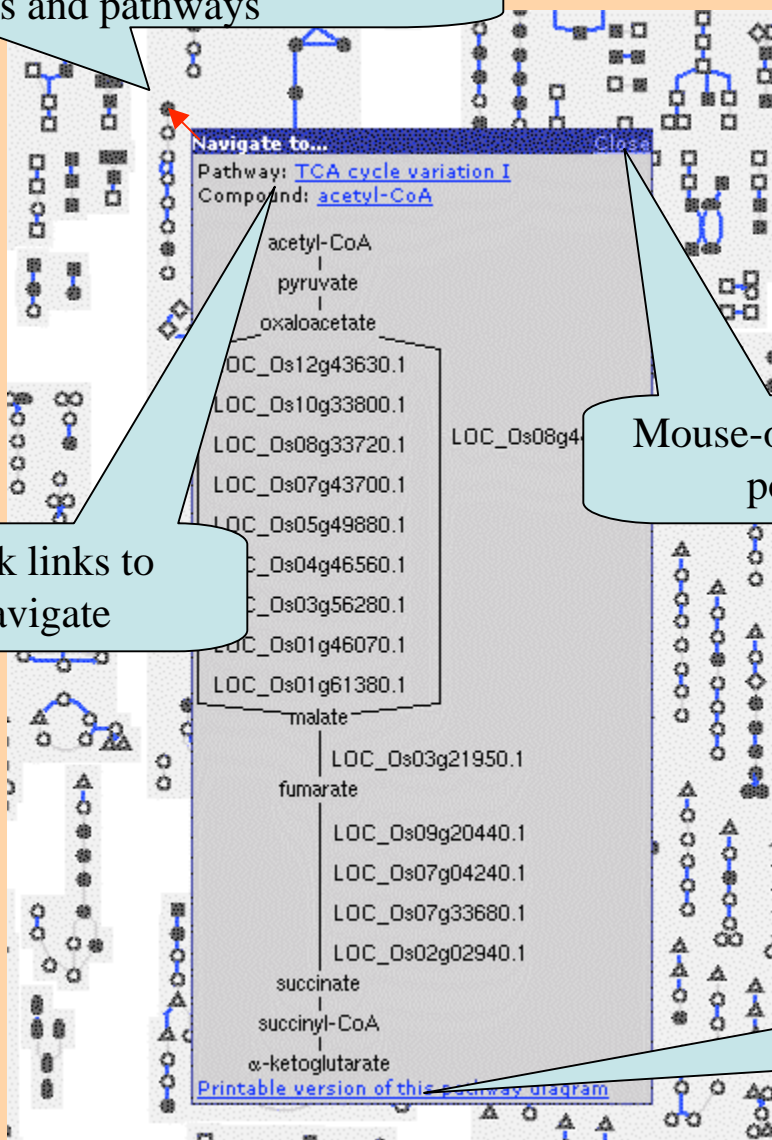
Metabolic Map Overview

Mouse over compound to see
compound name and pathway.
(requires javascript browser)



Metabolic Map Overview

Click a compound to access details and pathways



Click links to navigate

Mouse-over to close pop-up

Click to print out a diagram of pathway

5b. Omics viewer data selection

Visualize your Microarray Expression data, Proteomics data, Metabolomics data, Reaction Flux data, or other experimental data on the Metabolic Overview diagram.

[[Pathway Home](#)]

Pathway Tools Omics Viewer

The Pathway Tools Omics Viewer (formerly the Pathway Tools Expression Viewer) paints data values from the user's high-throughput and other experiments onto the Metabolic Overview diagram for an organism.

The Omics Viewer can be used for:

- **Microarray Expression Data:** Reaction lines (and protein icons, where present) are color-coded according to the relative or absolute expression level of the gene that codes for the enzyme that catalyzes that reaction step. The Omics Viewer allows a scientist to interpret the results of gene-expression experiments in a pathway context.
- **Proteomics Data:** Reaction lines (and protein icons, where present) are color-coded according to the concentration of the enzyme that catalyzes that reaction step.
- **Metabolomics Data:** Compound icons are color-coded according to the concentration of the compound.
- **Reaction Flux Data:** Reaction lines are color-coded according to reaction flux values.
- **Other Experimental Data:** Any experiment, high-throughput or otherwise, in which data values are assigned to genes, proteins, reactions or metabolites can be viewed in a pathway context using the Omics Viewer.

[More information about the Omics Viewer, including sample datafiles and displays.](#)

Select a dataset:

Oryza sativa japonica Nipponbare

File containing experimental data (NOT a URL):

Browse...

Do you want to display absolute or relative data values?

Relative

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)

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 names may be ambiguous if it is not known if they refer to genes, proteins or metabolites. In addition, data values from different kinds of experiments may not be directly comparable, so the resulting diagram may be misleading in some important ways.

Select dataset

Select data to upload

Identify terms

Select values

Omics viewer display selection

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:

Enter column numbers

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:

Select color scheme

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)

Select display type

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

Click "submit"

Omics Viewer display



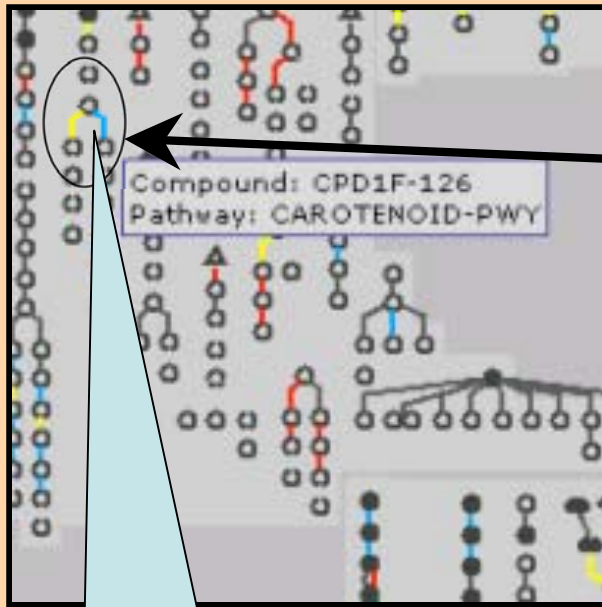
Red lines represent upregulated processes.

Blue lines represent unchanged processes.

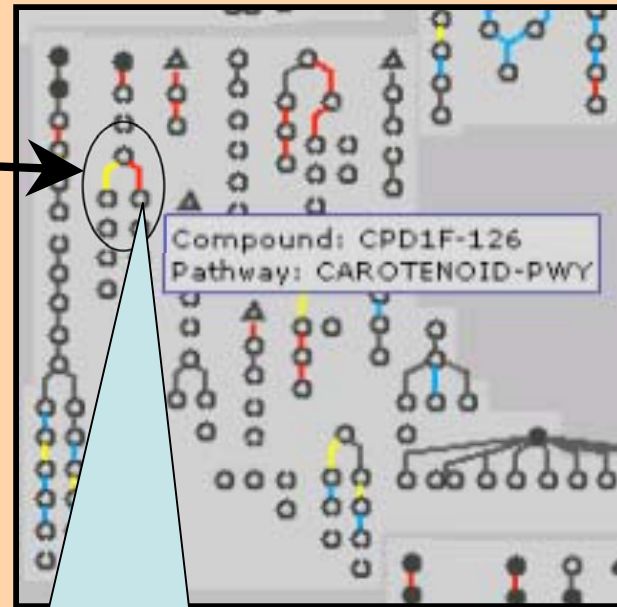
Yellow lines represent downregulated processes.

Caution: Requires 5-30 minutes to process!

Omics viewer pathway regulation



Hovering over a reaction will tell you the name of the compound affected and the influenced pathway.



Regulation of a pathway can be followed over a timecourse. In this example the carotenoid pathway becomes switched on over time.

Omics Viewer Table



Pathway display

Details of differentially regulated genes in pathway

Gene names

AT5G42740
AT4G25220
PGH1
AT1G30560
AT5G56630
AT5G61580
AT5G47810
AT5G03300
AT4G04040
AT4G29220
AT4G32840
AT4G26270
AT2G41850
AT2G22480
AT1G12000
AT1G20950
AT1G59810
AT1G76550
AT5G03690
AT4G38970
AT4G26530
AT4G26520
AT5G52930
AT2G16940
AT2G36460
AT2G01140
AT2G21330
AT1G18270
AT1G12800
AT3G55440
AT2G21170
AT4G09205
AT4G05632
AT3G42806
AT3G53780
AT3G04120
AT3G26650

5. Comparative Analysis

GRAMENE

Comparative Analysis

This page allows you to generate summary tables comparing the metabolic network across a set of organisms which may take several minutes.

Note: In addition to reflecting differences in biology among different organisms, these statistics and data will also reflect differences in biology among different organisms.

Select which set(s) of comparative-analysis tables you wish to generate:

- ☐ **Reactions:** breakdowns by type of substrate, by EC Number, by number of isozymes, etc.
- ☒ **Pathways:** breakdown by pathway class, information on pathway holes.
- ☐ **Compounds:** small molecules that act as substrates, enzyme activators/inhibitors/cofactors.
- ☐ **Proteins:** proteins shared among organisms or unique to an organism, breakdown of protein complexes, activators/inhibitors/cofactors, multifunctional enzymes.
- ☐ **Transcription Units:** number of genes per transcription unit, number of operons per pathway.

Select one or more organisms:

☒ Arabidopsis thaliana COL ☐ Escherichia coli K-12 ☒ Oryza sativa japonica Nipponbare

Select analysis to make

Select organisms to compare

Click "submit"

Comparative Analysis Table 1

Table 1: Breakdown of Pathways by Pathway Class

This table presents statistics on the number of pathways present in each pathway class. The two largest top-level classes, Biosynthesis and Degradation/Utilization/Assimilation, are broken down further to show the distribution of pathways among their next-level subclasses. The vast majority of pathways are assigned to only a single class. However, a small number may be assigned to more than one. If you expand this table, you will see all pathways, organized by class, and which organisms each are present in. If you expand a class, you will see only those pathways in that are members of that class.

<u>Pathway Class</u>	<u>AraCyc</u>	<u>Cyc</u>
<u>Biosynthesis</u>	189	189
- <u>Amines and Polyamines</u>	<u>6</u>	<u>9</u>
- <u>Amino acids</u>	<u>36</u>	<u>44</u>
- <u>Aminoacyl-tRNAs</u>	<u>1</u>	<u>1</u>
- <u>Aromatic Compounds</u>	<u>1</u>	<u>1</u>
- <u>Cell structures</u>	<u>11</u>	<u>10</u>
- <u>Cofactors, Prosthetic Groups, Electron Carriers</u>	<u>29</u>	<u>36</u>
- <u>Fatty Acids and Lipids</u>	<u>26</u>	<u>17</u>
- <u>Hormones</u>	<u>21</u>	<u>16</u>
- <u>Metabolic Regulators</u>	<u>1</u>	<u>1</u>
- <u>Nucleosides and Nucleotides</u>	<u>5</u>	<u>9</u>
- <u>Other</u>	<u>1</u>	<u>1</u>
- <u>Polysaccharides</u>	<u>0</u>	<u>2</u>
- <u>Secondary Metabolites</u>	<u>50</u>	<u>23</u>
- <u>Siderophores</u>	<u>0</u>	<u>0</u>
- <u>Sugars</u>	<u>26</u>	<u>16</u>
<u>Degradation/Utilization/Assimilation</u>	72	102
- <u>Alcohols</u>	<u>1</u>	<u>2</u>

Click on a pathway class to get more detail (*see next slide*)

Table 2 at bottom of page (*see slide 36*)

Comparative Analysis Amino Acids

[[Pathway Home](#)]

Note: In addition to reflecting differences in biology among different organisms, these statistics and data will also reflect differences in the level of curation and data availability and completeness among different organisms.

Pathway Class: - Amino acids	AraCyc COL	O. sativa japonica Nipponbare
β-alanine biosynthesis I	X	X
β-alanine biosynthesis II	X	
β-alanine biosynthesis III	X	X
adenosylmethionine biosynthesis	X	X
alanine biosynthesis	X	X
alanine biosynthesis III		X
arginine biosynthesis I	X	
arginine biosynthesis II (acetyl cycle)	X	X
arginine biosynthesis III		
arginine degradation I		
arginine degradation II	X	
asparagine biosynthesis	X	
asparagine biosynthesis II		
aspartate biosynthesis and degradation	X	X
chorismate biosynthesis	X	X
cysteine biosynthesis	X	X
cysteine biosynthesis II		X
glutamate biosynthesis I	X	
glutamate biosynthesis I		X
glutamate biosynthesis II	X	X
glutamate biosynthesis II		X

“X” indicates this pathway is present in this organism. Click to see Pathway (as in slides 12-14.)

Comparative Analysis Table 2

Table 2: Pathway Holes

A pathway hole is a reaction in a pathway for which no corresponding gene has been identified. Pathway holes may exist for a number of possible reasons: They may represent true enzymatic functions for which the gene has not yet been found, or they could represent false positive pathway predictions. This table compares the pathway in this organism differs slightly from the reference pathway in MetaCyc. This table compares each organism, and classifies pathways based on their number of pathway holes.

Clicking on the first row (Number of Pathway Holes) will show all reactions that are holes in any selected organism, plus the corresponding genes in other organisms.

Information on pathway holes.

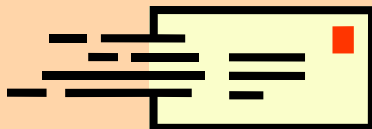
Pathway Holes	AraCyc COL	O. sativa japonica Nipponbare
Number of Pathway Holes	389	529
Pathway Holes as a percentage of total reactions in pathways	32%	45%
Pathways with No Holes	125	97
Pathways with 1 Hole	48	56
Pathways with 2 Holes	34	27
Pathways with 3 Holes	14	39
Pathways with 4 Holes	13	14
Pathways with 5 Holes	6	15
Pathways with > 5 Holes	22	31
Total Pathways with Holes	137	182

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or



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