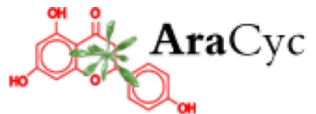


# CARNEGIE INSTITUTION FOR SCIENCE

Department of Plant Biology



PMN  
Plant Metabolic Network





# **Putting the PMN (and TAIR) to work for you:**

## **Tips and Techniques for Accessing Data for Plant Biology Research**



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Carnegie Institution for Science**

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# Overview

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- Introduction to the PMN
- Accessing data in the PMN
- Case study: Putting the PMN and TAIR to work for you



# Welcome to the PMN

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- The Plant Metabolic Network (PMN) maintains a set of metabolic pathway databases for Arabidopsis and other plants (AraCyc, PlantCyc, etc.)
- [www.plantcyc.org](http://www.plantcyc.org)
- Curators and programmers at the PMN:
  - Collect and store metabolic pathway information
  - Provide tools to analyze data
  - Work to generate new metabolic pathway databases for crops and other important plants





# PMN databases

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- Current PMN databases: **PlantCyc, AraCyc, PoplarCyc**
  - Coming soon: databases for wine grape, maize, cassava, Selaginella, and more . . .
- Other plant databases accessible from the PMN:

PGDB	Plant	Source	Status
RiceCyc **	Rice	Gramene	some curation
SorghumCyc	Sorghum	Gramene	no curation
MedicCyc **	Medicago	Noble Foundation	some curation
Lycocyc **	Tomato	Sol Genomics Network	some curation
PotatoCyc	Potato	Sol Genomics Network	no curation
CapCyc	Pepper	Sol Genomics Network	no curation
NicotianaCyc	Tobacco	Sol Genomics Network	no curation
PetuniaCyc	Petunia	Sol Genomics Network	no curation
CoffeaCyc	Coffee	Sol Genomics Network	no curation

\*\* Significant numbers of genes from these databases have been integrated into PlantCyc



# PMN database content statistics

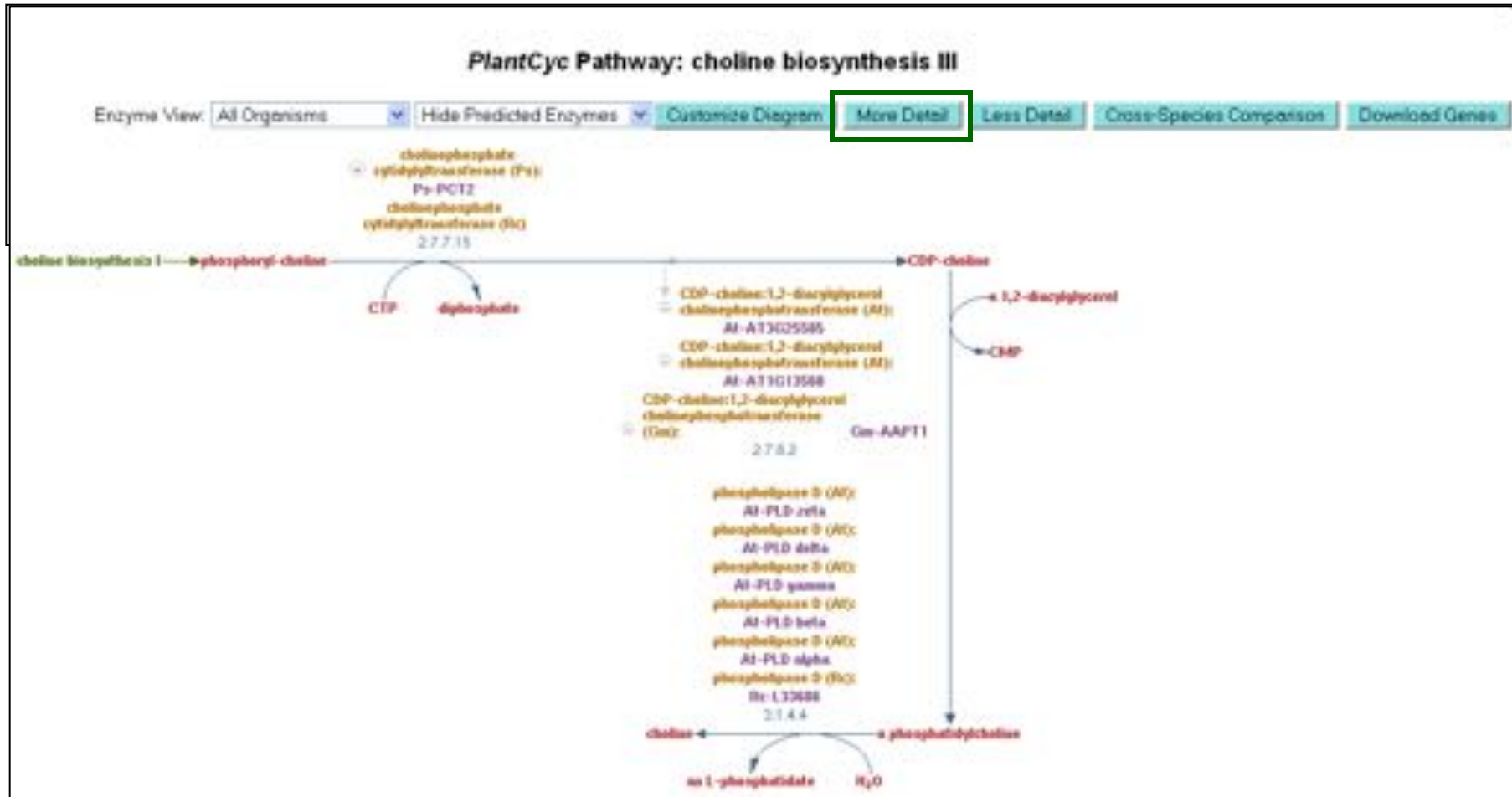
	PlantCyc 4.0
Pathways	685
Enzymes	11058
Reactions	2929
Compounds	2966
Organisms	343

## Species (A - D) [back to top](#)

- *Abies grandis* (yellow fir, white fir, silver fir, lowland fir, grand fir)
- *Acer pseudoplatanus*
- *Adonis aestivale*
- *Adonis annua* (pheasant's-eye, blood-drops)
- *Ajuga reptans*
- *Albizia julibrissin*
- *Alectoria*
- *Alliaceae* (onion family)
- *Allium cepa*
- *Allium sativum*
- *Allium tuberosum*
- *Aloe arborescens*
- *Amanita muscaria*
- *Ammi majus*
- *Amorpha fruticosa*
- *Anabaena variabilis*
- *Anchusa officinalis*
- *Anisodus acutangulus*
- *Antirrhinum majus* (snapdragon)
- *Apium graveolens*
- *Aquilegia vulgaris*
- *Arabisopsis lyrata* (lyrale rockcress)
- *Arabisopsis thaliana*, Col (thale cress, mouse-ear cress)
- *Arabisopsis thaliana*, Ler (thale cress, mouse-ear cress)
- *Arachis hypogaea*
- *Artemisia annua* (sweet Annie)
- *Asclepias syriaca*
- *Atropa belladonna* (deadly nightshade)
- *Avena sativa* (cultivated oat)
- *Berberis beaniana*
- *Berberis stolonifera*
- *Berberis Wilsonae*



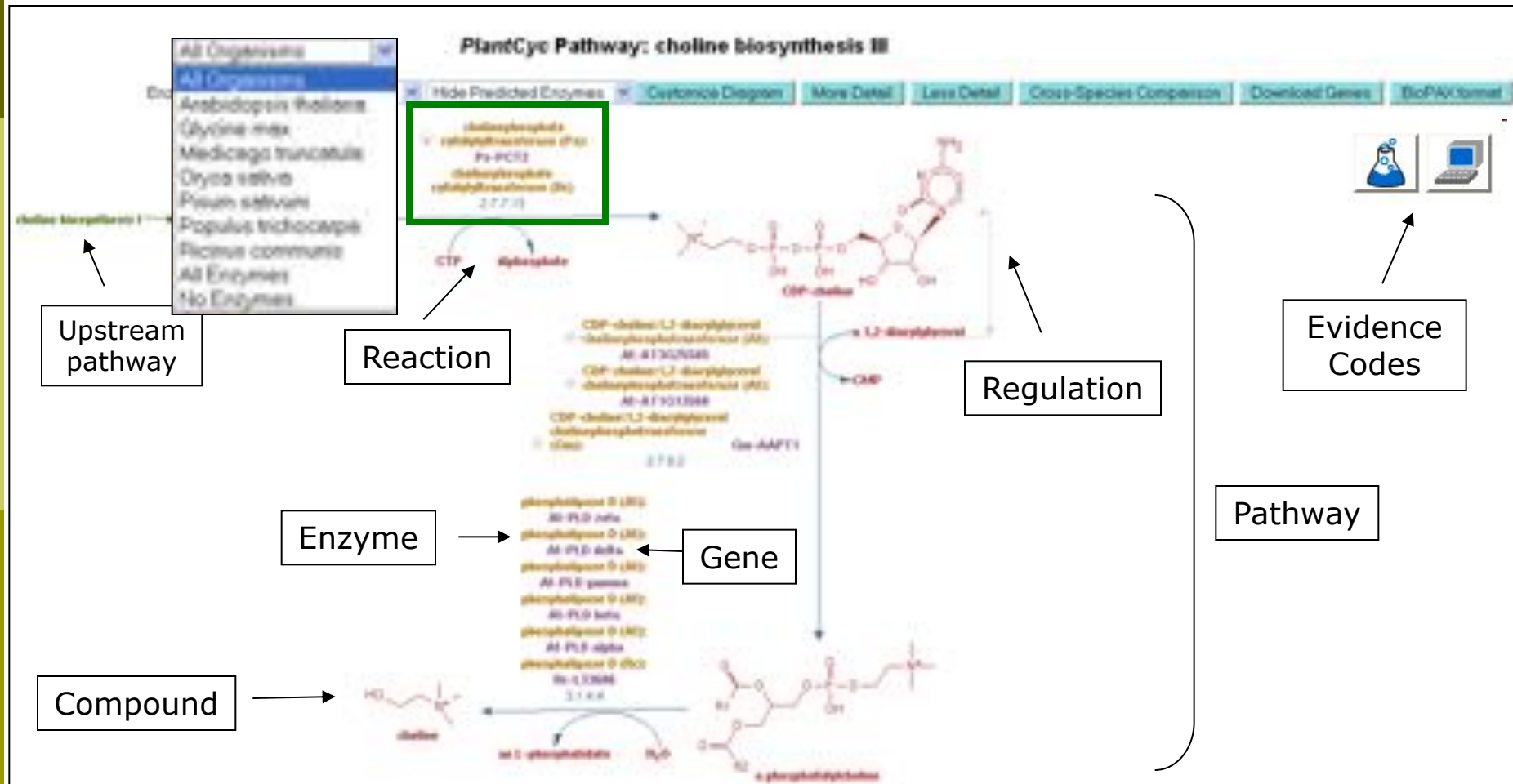
# Getting information from PMN pathway pages



- Better . . . but what about compound structures?
  - Keep clicking on “More Detail” – sometimes several times



# Getting information from PMN pathway pages





# Getting information from PMN pathway pages

Superclasses: [Biosynthesis -> Fatty Acids and Lipids Biosynthesis -> Choline Biosynthesis](#)

Species Data Available for: [Arabidopsis thaliana cel.](#), [Glycine max.](#), [Medicago truncatula](#), [Oryza sativa-Japonica Group](#), [Pisum sativum](#), [Populus trichocarpa](#), [Ricinus communis](#)

## Summary:

**General information:** Choline is a fundamental metabolite in plants because of its contribution to the synthesis of the membrane phospholipid phosphatidylcholine, which accounts for 40 to 60% of lipids in non-plastid plant membranes [ [Mou02](#) ]. Choline is also a precursor for the formation of glycine betaine ( [glycine betaine biosynthesis](#) ) in certain plants such as spinach, where this osmoprotectant is accumulated and confers also tolerance to salinity, drought, and other environmental stresses. In addition choline has been recognized as an essential nutrient for humans [ [McNeil01](#) ].

The choline biosynthetic pathway enables plants to decouple choline synthesis from lipid metabolism (Kennedy pathway - [triacylglycerol biosynthesis](#) ) and provides them with the metabolic flexibility to adapt to environmental conditions where large and variable amounts of choline are beneficial for survival [ [Rontgen01](#) ].

**Pathway information:** The first step in choline biosynthesis is the direct decarboxylation of serine to ethanolamine [ [Rontgen01](#) ], which is catalyzed by a serine decarboxylase unique to plants [ [Rontgen03](#) ]. Ethanolamine is widely recognized as the entrance compound to choline biosynthesis.

## References

[Curator09](#): Curator (2009). "Following the initial computational build of PoplarCyc in 2009, pathways were validated by PMN curators based on a preliminary literature search. For pathways that lacked direct experimental support, curators considered a number of factors to judge the validity of the predicted pathways including: 1) critical compound(s) in the pathway are found in a *Populus* species; 2) a *Populus trichocarpa* gene is predicted to catalyze a critical or unique reaction of the pathway; or 3) the pathway is expected to exist in all plants."

[Datko88](#): Datko AH, Mudd SH. (1988) "Enzymes of phosphatidylcholine synthesis in Lemna, soybean, and carrot." *Plant Physiol.* (1988), 88, 1338-1348.

[Datko88a](#): Datko AH, Mudd SH. (1988) "Phosphatidylcholine synthesis: Differing patterns in soybean and carrot." *Plant Physiol.* (1988), 88, 854-861.

[Hitz81](#): Hitz WD, Rhodes D, Hanson AD. (1981) "Radiotracer evidence implicating phosphoryl and phosphatidyl bases as intermediates in betaine synthesis by water-stressed barley leaves." *Plant Physiol.* (1981), 68, 814-822.

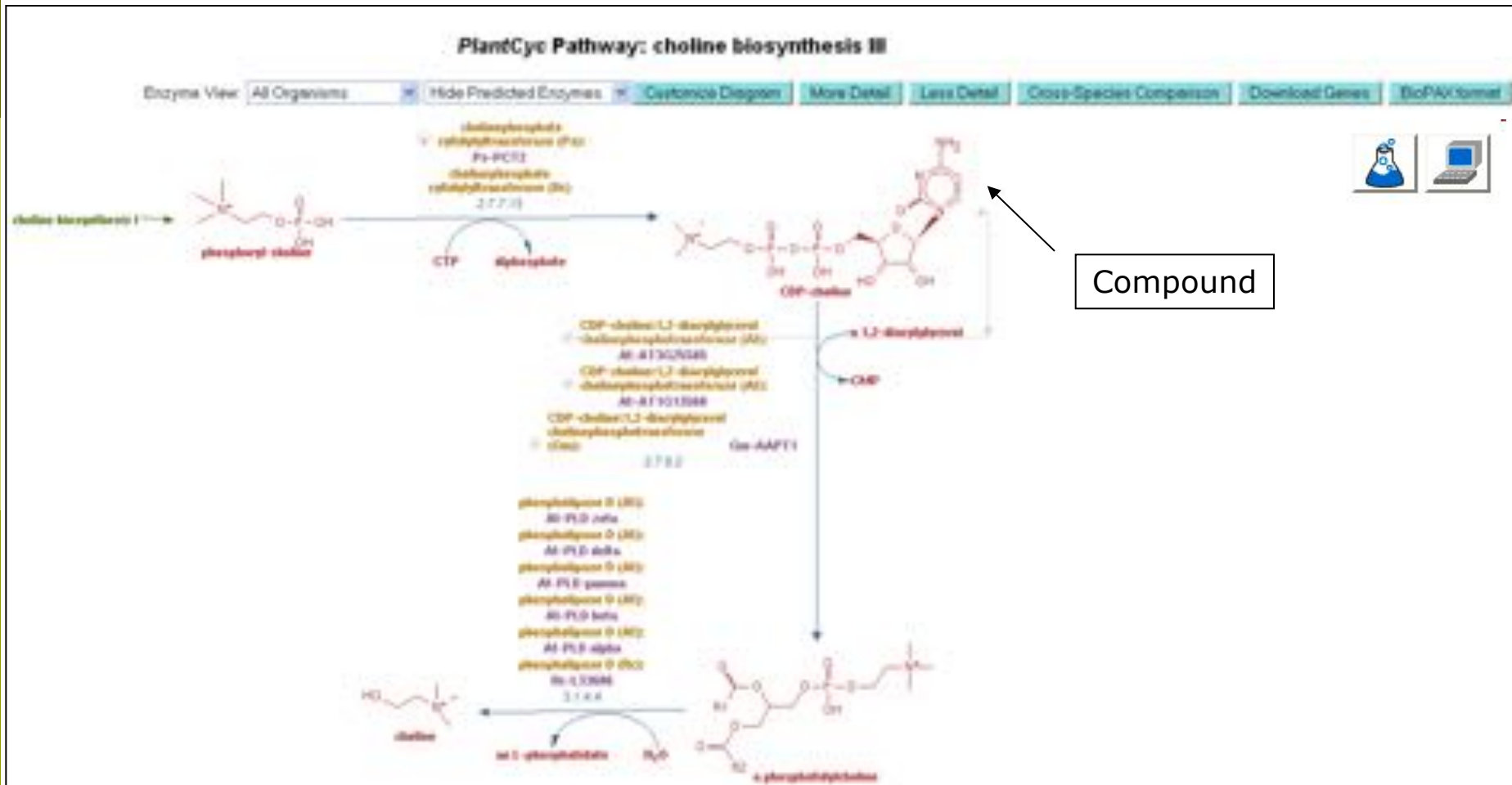
[Kinney93](#): Kinney AJ. (1993) "Phospholipid head groups." In: Moore, TS Jr. (ed.) *Lipid metabolism in plants*. CRC Press Boca Raton Ann Arbor London Tokyo (1993), 259-264.

[Kirk99](#): Kirk Pappan, Xuemin Wang "Molecular and biochemical properties and physiological roles of plant phospholipase D." *Biochimica Biophysica Acta* (1999) 1439, 151-166.

[McNeil00](#): McNeil SD, Nuccio ML, Rhodes D, Shachar-Hill Y, Hanson AD (2000). "Radiotracer and computer modeling evidence that phospho-base methylation is the main route of choline synthesis in tobacco." *Plant Physiol* 123(1):371-80. PMID: 10806254



## Getting information from PMN pathway pages





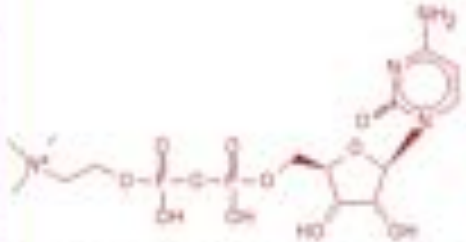
# PMN compound pages

Compound:  
CDP-choline

Synonyms: [cibcoline](#) , [cibcholine](#) , [cibiles](#) , [cylcholine](#) , [cytidine 5'-diphosphocholine](#) , [cytidine diphosphate choline](#) ← **Synonyms**

Superclasses: [a nucleic acid component](#) -> [a base derivative](#)  
[a nucleic acid component](#) -> [a pyrimidine-related compound](#) ← **Classification(s)**

Empirical Formula:  $C_{14}H_{27}N_4O_{11}P_2$   
Molecular Weight: 489.34 daltons ← **Molecular Weight / Formula**



Smiles: C(=O)OP(=O)(=O)OP(=O)(=O)OCC(N+)(C(C)C)C1=OC(C(=O)O)C(=O)N(C)C2

Unification Links: CAS:967-78-0

Gibbs Energy of Formation (kcal/mol, estimated): -116.7

In Pathway Reactions as a Reactant:

[phospholipid biosynthesis](#):  
[a 1,2-diacylglycerol](#) + **CDP-choline** = [a phosphatidylcholine](#) + [CMP](#) ← **Appears as Reactant**

[choline biosynthesis III](#):  
[a 1,2-diacylglycerol](#) + **CDP-choline** = [a phosphatidylcholine](#) + [CMP](#)

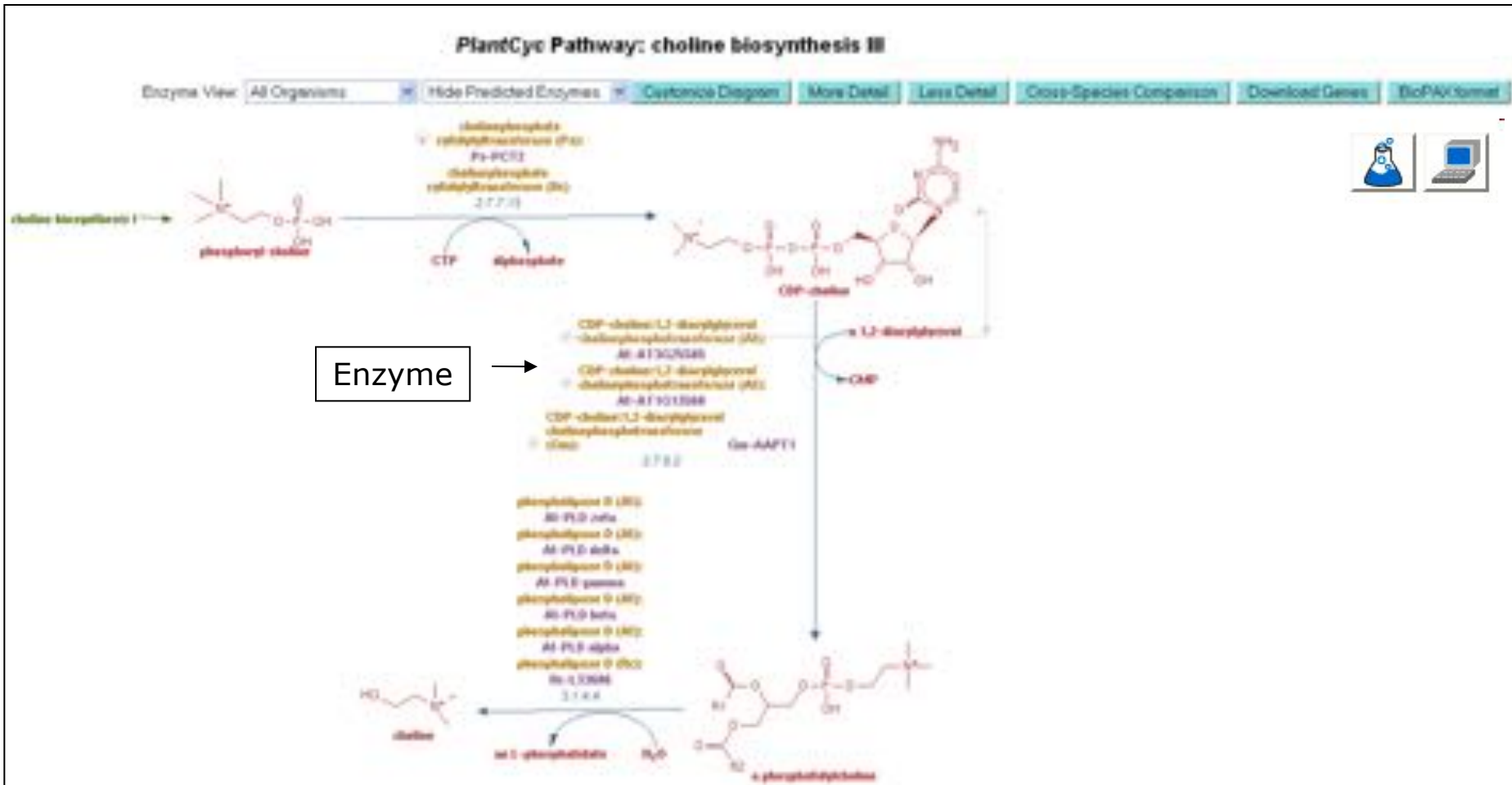
In Pathway Reactions as a Product:

[phospholipid biosynthesis](#):  
[phosphorylcholine](#) + [CTP](#) = **CDP-choline** + [diphosphate](#) ← **Appears as Product**

[choline biosynthesis III](#):  
[phosphorylcholine](#) + [CTP](#) = **CDP-choline** + [diphosphate](#)



## Getting information from PMN pathway pages





# PMN enzyme pages

## *Arabidopsis* Enzyme: phosphatidyltransferase

Synonyms: aminolipidphosphotransferase

Gene: [AT1G13880](#)

Sequence Length: 1196 AAs

Unification Links: [Entrez: AAC61750](#)

Gene-Reaction Schematic: 



Enzymatic reaction of: cholinephosphotransferase (phosphatidyltran

[1,3-diacylglycerol + CDP-choline <=> 1-phosphatidylcholine + CMP](#)

Enzymatic reaction of: ethanolaminephosphotransferase (phosphatidyltransferase)

[1,3-diacylglycerol + CDP-ethanolamine <=> sn-1'-phosphatidyl-ethanolamine + CMP](#)

Pathway Tools evidence ontology click on:  
<http://bioinformatics.wri.com/evidence-ontology/>

 **Experimental Evidence:**

Evidence code: EV-EXP-IDA-UNPURIFIED-PROTEIN  
Source: [Goad99](#)  
Definition: Direct assay of unpurified protein. Presence of a protein activity is indicated by an assay. However, the precise identity of the protein with that activity is not established by this experiment (protein has not been purified).

**References**

[Goad99](#): Goad JH, Dewey RE, (1999) "Characterization of aminolipidphosphotransferases from *Arabidopsis thaliana* and soybean." *Plant Physiol. Biochem.* (1999), 37(5), 485-497.

Home Help Contact [CMAA/PMN LMR](#)  



# PMN enzyme pages

## *Arabidopsis* Enzyme: phosphatidyltransferase

### Enzymatic reaction of: cholinephosphotransferase (phosphatidyltransferase)



$1,2\text{-diacylglycerol} + \text{CDP-choline} \rightleftharpoons \text{a phosphatidylcholine} + \text{CMP}$

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

Reversibility of this reaction is unspecified.

In Pathways: [choline biosynthesis II](#), [phospholipid biosynthesis](#)

Pathway(s)

#### Summary:

Two cDNA's from *Arabidopsis thaliana* (AtAAPT1, AtAAPT2) have been isolated from an *Arabidopsis* cDNA library using the AAPT cDNA from soybean as a heterologous hybridization probe. Both cDNA's encode aminoalcoholphosphotransferases involved in the nucleotide pathway of the biosynthesis of phosphatidylethanolamine (PE) and phosphatidylcholine (PC) as demonstrated by gene expression in yeast mutants lacking these enzyme activities. It has been demonstrated that both AtAAPT1 and AtAAPT2 convert CDP-ethanolamine and CDP-choline into the corresponding phosphatidylethanolamines although with slight differences regarding the substrate preference. AtAAPT2 showed a higher preference for CDP-choline over CDP-ethanolamine in comparison to AtAAPT1 and was also inhibited to a lesser degree by  $\text{Ca}^{2+}$  and Cytidine monophosphate (CMP) than AtAAPT1 [Goode99]. Both enzymes (AtAAPT1, AtAAPT2) were able to catalyze the reverse reaction supporting the proposal that diacylglycerol, involved as substrate in both PC and triacylglycerol biosynthesis [triacylglycerol biosynthesis], is in equilibrium with PC and maintains this equilibrium via the reversibility of the cholinephosphotransferase reaction [Slack85]. AtAAPT1 and AtAAPT2 seem to represent the only aminoalcoholphosphotransferases in *Arabidopsis* as concluded from the Southern blotting patterns. Both polypeptides contain seven membrane spanning regions as shown by their hydropathy files. This finding is in agreement with other AAPT's isolated so far and confirms their localization in membranes [Goode99].

Inhibitors (Allosteric): [CMP](#) [Goode99]

Inhibitors (Unknown): [Ca<sup>2+</sup>](#) [Goode99]

Primary Physiological Regulators of Enzyme Activity: [CMP](#)

Inhibitors, Kinetic Parameters, etc.

Summary

#### References

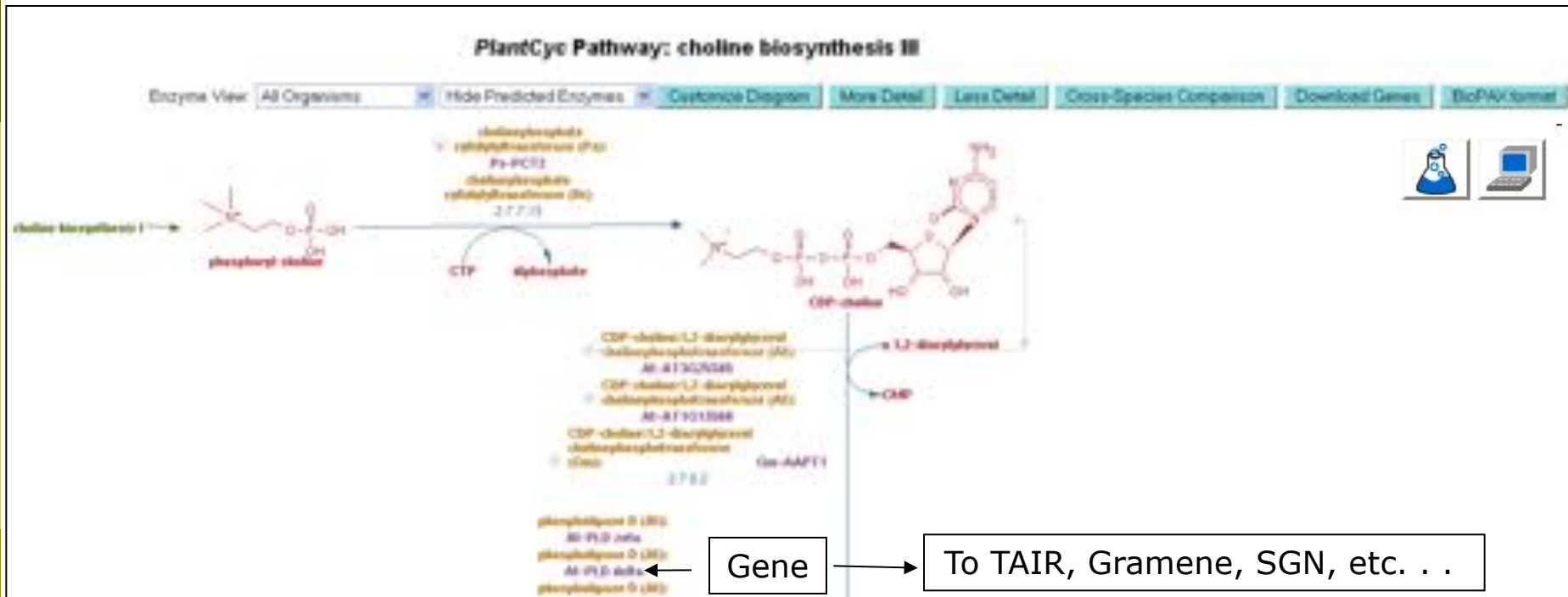
Goode99. Goode JH, Dewar SE, (1999) "Characterization of aminoalcoholphosphotransferases from *Arabidopsis thaliana* and soybean." *Plant Physiol. Biochem.* (1999), 37(5), 445-457.

Slack85. Slack CR, Broughan PG, Brown JA, Gardner SE, (1985) "Some properties of cholinephosphotransferase from developing safflower cotyledons." *Biochim. Biophys. Acta* (1985), 833, 439-446.

References



## Getting information from PMN pathway pages



Locus: AT4G15790

Date last modified: 2018-05-01

11/10/14 10:00 AM 11/10/14 10:00 AM

**Fingerprint Evidence**

Current Blinded 67

Other names: ARABIDOPSIS THALYIAA PHOSPHOLIPASE D DELTA, ATP10DELTA, F4B14.30, F4B14.30, PLDDELTA

**Enzymes** Encodes a protein with phospholipase D activity involved in phospholipid metabolism. Mutants are affected in tail-toen necrosis mediated cell death.



# Searching in the PMN databases

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## □ PMN quick search bar



The image shows a screenshot of the PMN (Plant Metabolic Network) quick search bar. The search bar is a horizontal input field with a light blue background. Inside the bar, the word "choline" is entered. To the right of the input field is a dropdown menu currently set to "PlantOyc" with a small downward arrow. Further right is a "search" button. Below the search bar is a dark blue navigation bar with white text links: "About PMN", "Search", "Tools", "Downloads", "Useful Sites", "Submit Data", and "Feedback". A dropdown menu is open below the "PlantOyc" selection, showing four options: "PlantOyc", "AraOyc", "PoplarOyc", and "Google PMN".

Search Term	Database	Search Button
choline	PlantOyc	search

Navigation Links: About PMN | Search | Tools | Downloads | Useful Sites | Submit Data | Feedback

Database Selection: PlantOyc, AraOyc, PoplarOyc, Google PMN



## Searching in PMN databases

The query `choline` matched the following

## Pathways

Pathway pages cover  
pathway, of chromo-  
somes, and of regu-

- **choline biosynthesis I**
- **choline biosynthesis II**
- **choline biosynthesis II**
- **phosphatidylcholine biosynthesis I**
- **phosphatidylcholine biosynthesis II**
- **phosphatidylcholine biosynthesis III**
- **phosphatidylcholine biosynthesis IV**
- **supernatural pathway of phosphatidylcholine biosynthesis**
- **supernatural pathway of choline biosynthesis**

## Genes

Gene pages contain:  
depiction of its operon  
product information  
corresponding protein

- [choline monoxygenase](#)

## Proteins

Protein pages contain: Detailed comments and citations; subunit structure; cofactors, activators, and inhibitors (for enzymes), depiction of regulon (for transcription factors).

- [choline kinase \(pchl\)](#)
- [choline kinase \(pchl\)](#)
- [choline kinase \(pchl\)](#)
- [choline kinase \(pchl\)](#)
- [choline kinase \(pchl\)](#)
- [choline kinase \(pchl\)](#)
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- [choline kinase \(pchl\)](#)
- [choline kinase \(pchl\)](#)
- [choline kinase \(pchl\)](#)
- [CHOLINE MONOOXY](#)
- [choline monooxygenase](#)
- [choline monooxygenase](#)
- [choline monooxygenase](#)
- [expressed](#)
- [choline-phosphate r](#)
- [AT2G32260](#)
- [choline-phosphate r](#)
- [AT4G15130](#)
- [choline-phosphate r](#)
- [LOC\\_Os02g07720.1](#)
- [cholinephosphate o](#)

### Compounds

Compound pages contain: compound structural information, and links to all reactions and pathways in which the compound participates.

- 18:0-18:1-PC (1-18)
- 18:0-18:2-PC (1-18)
- 18:0-18:3-PC (1-18)
- 18:1-18:1-PC (1-18)
- 3-phosphocholine
- 18:1-18:2-PC (1-18)
- 18:1-18:3-PC (1-18)
- 18:2-18:1-PC (1-18)
- 18:2-18:2-PC (1-18)
- 3-phosphocholine
- 18:2-18:3-PC (1-18)
- 18:3-18:1-PC (1-18)
- 18:3-18:2-PC (1-18)
- 18:3-18:3-PC (1-18)
- **choline**
- **Q-sinagoylcholine**
- **Sn-3-glycerophosp**
- **a-1-acyl-2-lyso-gly**
- **a-1-alkyl-2-acetyl-a**
- **a-1-alkyl-sn-glycen**
- **a-1-lyso-2-acyl-sn-**
- **a-1-oryanyl-2-acyl-**
- **a-2-lyso-phosphatid**




### Reactions

Reaction pages contain: reaction equation with chemical structures, links to all enzymes that catalyze the reaction, and all pathways in which the reaction participates.

- $1\text{-O-sinapoyl-}\beta\text{-D-glucose} + \text{choline} \rightarrow \text{O-sinapoylcholine} + \beta\text{-D-glucose}$
- $\text{choline} + \text{ATP} \rightarrow \text{phosphorylcholine} + \text{ADP}$
- $\alpha\text{-1,2-diacylglycerol} + \text{CDP-choline} \rightarrow \alpha\text{-phosphatidylcholine} + \text{CMP}$
- $\alpha\text{-phosphatidylcholine} + \text{H}_2\text{O} \rightarrow \alpha\text{-1-acyl-2-lyso-glycerophosphocholine} + \alpha\text{-carboxylate}$
- $\alpha\text{-phosphatidylcholine} + \text{H}_2\text{O} \rightarrow \alpha\text{-L-phosphatidate} + \text{choline}$
- $\text{phosphorylcholine} + \text{CTP} \rightarrow \text{CDP-choline} + \text{diphosphate}$



# Specific search pages



Search Database *PlantCyc* [change](#)

About PMN

**Search**

Tools

Downloads

Useful Sites

Submit Data

Help

Feedback

Databases Overview

**Compounds**

## PlantCyc Compound Search

▼ Search for compound by name or ID

Enter a compound name, or a database identifier from this database or from an external database such as ChEBI, LIGAND, PubChem or CkS. This database may not contain mappings to all of these other databases. Partial names will generate a substring search on compound names only (not on database identifiers).  
Examples: "tryptophan", "C00036"

▶ Search/Filter by ontology (inactive)

▶ Search/Filter by molecular weight (inactive)

▶ Search/Filter by chemical formula (partial or full) (inactive)

▶ Search by InChI string (inactive)



# Additional search options



The screenshot displays the PMN (Plant Metabolic Network) website interface. At the top left is the PMN logo, which includes a stylized plant icon. To the right of the logo is a chemical reaction diagram showing a substrate being converted to a product by an enzyme. Further right is a search bar with the text "Search Database PlantCyc" and a "Quick Search" button. Below the search bar is a navigation menu with the following items: "About PMN", "Search", "Tools", "Downloads", "Useful Sites", "Submit Data", "Help", and "Feedback". The "Search" item is highlighted with a yellow box. A dropdown menu is visible below the "Search" item, listing the following options: "Databases Overview", "Compounds", "Genes/Proteins", "Reactions", "Pathways", "Advanced Query", "Browse/Ontologies", "Google the PMN", "BLAST", and "Species in the PMN". The "Advanced Query", "Browse/Ontologies", and "BLAST" items are highlighted with yellow boxes. At the bottom of the dropdown menu, there is a "Search Database:" section with a link to "PlantCyc" and a "change" link.

PMN

Search Database *PlantCyc* [change](#) Quick Search

About PMN Search Tools Downloads Useful Sites Submit Data Help Feedback

Databases Overview  
Compounds  
Genes/Proteins  
Reactions  
Pathways  
Advanced Query  
Browse/Ontologies  
Google the PMN  
BLAST  
Species in the PMN

Search Database:  
► *PlantCyc*  
[change](#)



## PMN BLAST 2.2.8

Please note that this form uses NCBI BLAST2 2.8

### Blast

BLAST™ program BLASTP: AA query, AA db

#### Datasets:

PlantCyc Enzymes

Input  
query sequence

Reference Enzymes

PlantCyc Enzymes

AraCyc Enzymes

PoplarCyc Enzymes

GIVQ  
ALF

QDYHGLPAFKDAMAKFMGKIRENKVKFDTNKMVLTAGSTS  
ANETLMFCLANPGDAFLIPAPYYPGFDRDLKWRTGVEIVPI

Upload a file

Browse...

Raw, FASTA, GCG and RSB formats accepted.

☒ Filter query

### Advanced BLAST™ Parameter Options

expand

### Results Return Options

Output Title: optional, will be added to output for your use

E-mail address:

Return Results: To your web browser

Result Format: HTML hypertext

Please be patient. Replies directly to your browser may take a minute or two.  
Selecting an e-mail reply allows you to immediately request more searches.

Run BLAST

reset

### ■ PlantCyc, AraCyc, PoplarCyc Enzymes:

- include enzymes with available sequence information from each database

### ■ Reference Enzymes:

- includes enzymes with experimental support from both plant and non-plant species



# Finding enzymes through BLAST

Sequences produced	Score	E
<a href="#">Q959U6</a>   PlantCyc		
<a href="#">SGN-U565890</a>   PlantCyc		
<a href="#">Q9T065</a>   PlantCyc		
<a href="#">Q56Y32</a>   PlantCyc		
<a href="#">SGN-U565891</a>   PlantCyc		
<a href="#">Q9H2Y8</a>   PlantCyc		
<a href="#">SGN-U565888</a>   PlantCyc		
<a href="#">Q37001</a>   PlantCyc		
<a href="#">Q0MP12</a>   PlantCyc		
<a href="#">LOC_0803051740</a>   PlantCyc		
<a href="#">SGN-U565889</a>   PlantCyc		
<a href="#">Q43309</a>   PlantCyc		
<a href="#">LOC_0804048850</a>   PlantCyc		
<a href="#">Q95TR4</a>   PlantCyc		
<a href="#">Q95AR0</a>   PlantCyc		
<a href="#">SGN-U583843</a>   PlantCyc		
<a href="#">SGN-U567978</a>   PlantCyc		
<a href="#">SGN-U583839</a>   PlantCyc		
<a href="#">Q06402</a>   PlantCyc		
<a href="#">SGN-U583842</a>   PlantCyc		
<a href="#">LOC_0805010780</a>   PlantCyc		
<a href="#">LOC_0805025490</a>   PlantCyc		
<a href="#">LOC_0801009700</a>   PlantCyc		
<a href="#">LOC_0806003990</a>   PlantCyc		
<a href="#">Q8GYY0</a>   PlantCyc		
<a href="#">Q570P9</a>   PlantCyc		

## PlantCyc Enzyme: 1-aminocyclopropane-1-carboxylate synthase

Species: [Arabidopsis thaliana col](#)

Summary:  
When recombinantly expressed in *E. coli*, this enzyme was shown to have ACS activity [ [Yamagami03](#) ]

Gene: [ACS11](#)

Sequence Length: 1825/3 AAs

Unification Links: [Phytozome Plant Orthologs AT4G08040.1](#)

Gene-Reaction Schematic: 

 [4.4.1.14](#)  [4.4.1.14](#)  [4.4.1.14](#)  [4.4.1.14](#)  [4.4.1.14](#)  [4.4.1.14](#)  [4.4.1.14](#)  [4.4.1.14](#)  [4.4.1.14](#)  [4.4.1.14](#)  [4.4.1.14](#)  [4.4.1.14](#)  [4.4.1.14](#)  [4.4.1.14](#)  [4.4.1.14](#)  [4.4.1.14](#)  [4.4.1.14](#)  [4.4.1.14](#)  [4.4.1.14](#)  [4.4.1.14](#)  [4.4.1.14](#)  [4.4.1.14](#)  [4.4.1](#)



# Compa

## ■ Use

This page allow  
Pathway/Geno  
you have choos

[Click here](#) to g

Note: In additio  
data availability

Select which

- ☐ Rea
- ☒ Patl
- ☐ Cen
- ☐ Prot  
activator
- ☐ Orth
- ☐ Trait
- ☐ Trait

Select one c

☐ Arabidopsi

Organism	Evidence Glyph	Enzymes and Genes for choline biosynthesis III	
<a href="#">AraCyc.col</a>		EC#2.7.7.15	choline-phosphate cytidyltransferase: <a href="#">AT4G15130</a> choline-phosphate cytidyltransferase: <a href="#">AT2G32260</a>
		EC#2.7.8.2	phosphatidyltransferase: <a href="#">AT3G25585</a> phosphatidyltransferase: <a href="#">AT1G13560</a>
		EC#3.1.4.4	phospholipase D: <a href="#">AT1G52570</a> phospholipase D: <a href="#">AT1G55180</a> phospholipase D: <a href="#">AT3G05630</a> phospholipase D: <a href="#">AT4G00240</a> phospholipase D: <a href="#">AT4G11830</a> phospholipase D: <a href="#">AT4G11840</a> phospholipase D: <a href="#">AT5G25370</a> phospholipase D: <a href="#">PLD alpha</a> phospholipase D: <a href="#">PLD beta</a> phospholipase D: <a href="#">PLD gamma</a> phospholipase D: <a href="#">PLD delta</a> phospholipase D: <a href="#">PLD zeta</a>
<a href="#">P. trichocarpa</a>		EC#2.7.7.15	None
		EC#2.7.8.2	diacylglycerol cholinephosphotransferase: <a href="#">JGI-225724</a> diacylglycerol cholinephosphotransferase: <a href="#">JGI-720905</a>
		EC#3.1.4.4	phospholipase D: <a href="#">JGI-811801</a> phospholipase D: <a href="#">JGI-781949</a> phospholipase D: <a href="#">JGI-810176</a> phospholipase D: <a href="#">JGI-593768</a> phospholipase D: <a href="#">JGI-827396</a> phospholipase D: <a href="#">JGI-578949</a> phospholipase D: <a href="#">JGI-730956</a> phospholipase D: <a href="#">JGI-240457</a> phospholipase D: <a href="#">JGI-833366</a> phospholipase D: <a href="#">JGI-417354</a> phospholipase D: <a href="#">JGI-763496</a> phospholipase D: <a href="#">JGI-559891</a> phospholipase D: <a href="#">JGI-415367</a> phospholipase D: <a href="#">JGI-550827</a> phospholipase D: <a href="#">JGI-755219</a> phospholipase D: <a href="#">JGI-180605</a> phospholipase D: <a href="#">JGI-829577</a>

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# Visualizing OMICs data

- Overlay “pre-cleaned” quantitative data sets on a metabolic map
  - Gene transcription data
  - Proteomic data
  - Metabolomic data
- Only available for single-species databases, not PlantCyc
- Demonstrations available from 3:30 – 5:30 PM!





# Visualizing OMICs data

---

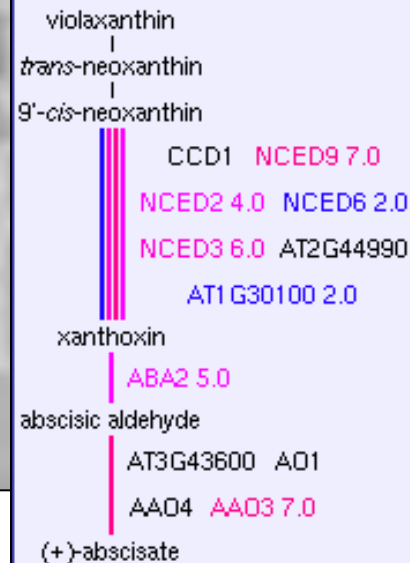




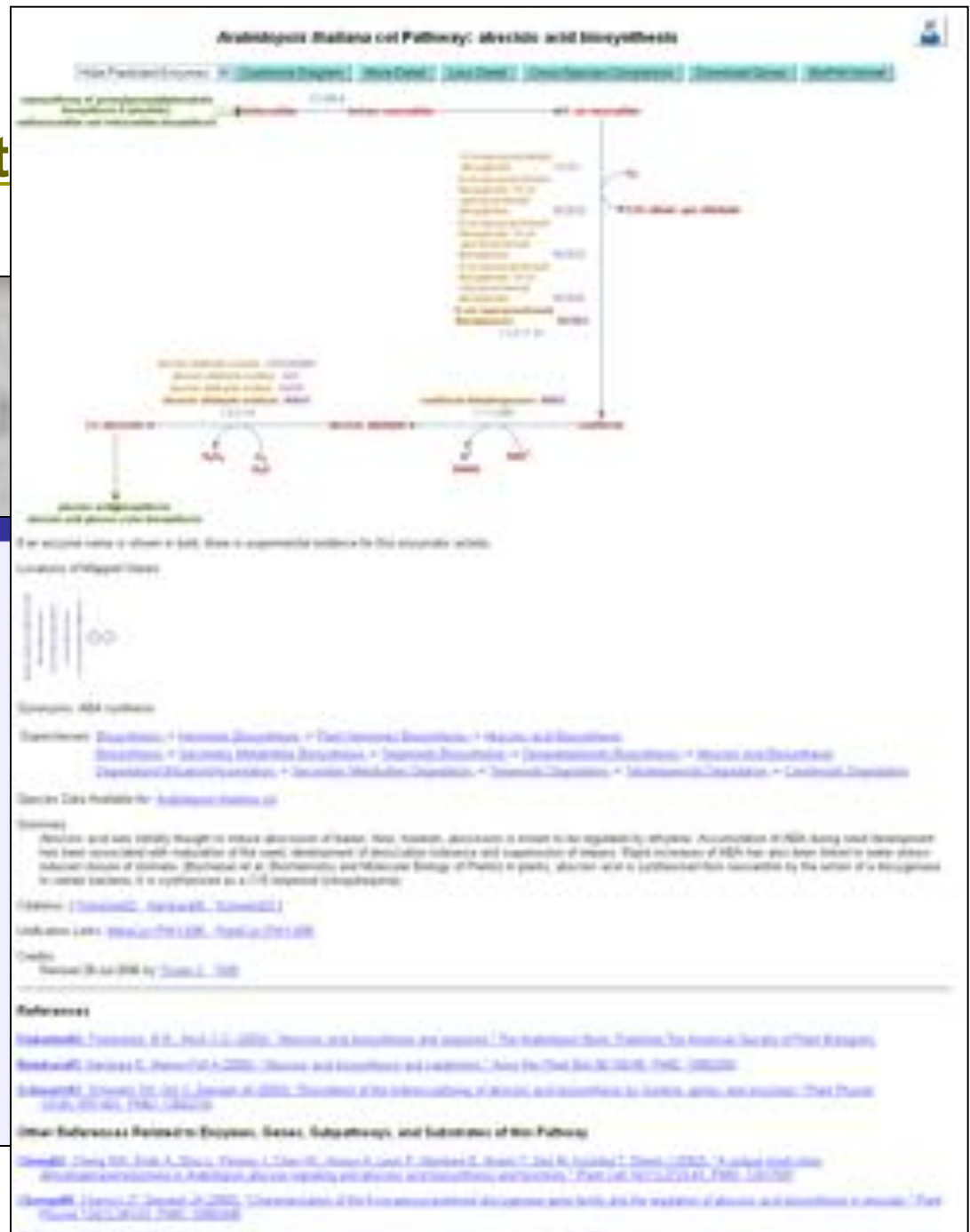
## Visualizing OMICs data



Compound: violaxanthin



[Printable version of this pathway diagram](#)





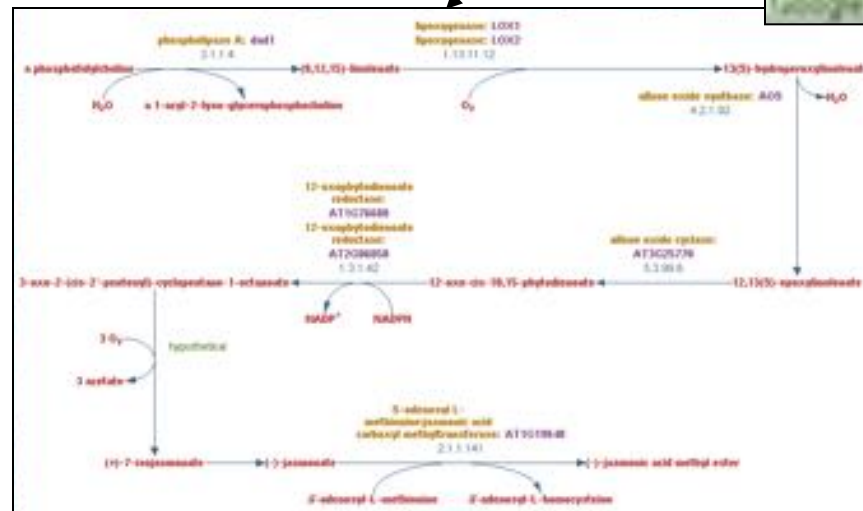
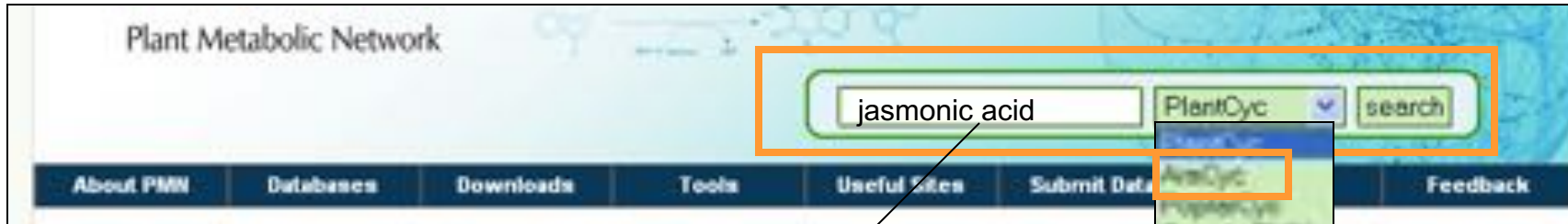
## Case study: Jasmonic acid biosynthesis

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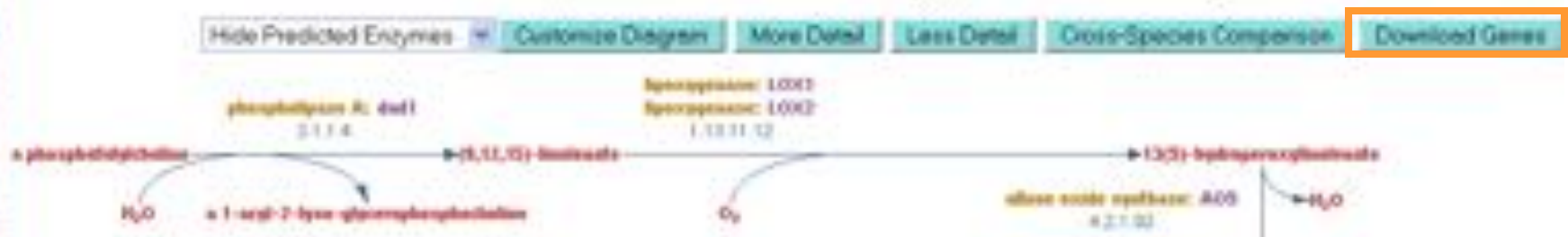
- You are studying jasmonic acid biosynthesis in your favorite plant
- You want to identify potential orthologs for all of the Arabidopsis enzymes associated with the pathway



## Case study: Jasmonic acid biosynthesis



**Arabidopsis thaliana col Pathway: jasmonic acid biosynthesis**





# Case study: Jasmonic acid biosynthesis

Plant Metabolic Network

PlantCyc

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jasmonic acid biosynthesis

Gene ID	Gene name	Reaction ID	Reaction EC	Enzymatic activity	Evidence
AT1G031480	AT1G031480	R2M-1501	3.1.1.4	phospholipase A1	EV-COMP
AT2G44810	Gad1	R2M-1501	3.1.1.4	phospholipase A	EV-EXP
AT3G22400	AT3G22400	R2M-1321	1.13.11.12	lipoxygenase	EV-COMP
AT1G072510	AT1G072510	R2M-1321	1.13.11.12	lipoxygenase	EV-COMP
AT1G067560	AT1G067560	R2M-1321	1.13.11.12	lipoxygenase	EV-COMP
AT1G017410	AT1G017410	R2M-1321	1.13.11.12	lipoxygenase	EV-COMP
AT1G080010	LOX2	R2M-1321	1.13.11.12	lipoxygenase	EV-EXP
AT3G45140	LOX2	R2M-1321	1.13.11.12	lipoxygenase	EV-EXP
AT5G42630	AOS	R2M1F-19	4.2.1.92	allene oxide synthase	EV-EXP
AT1G039460	AT1G039460	R2M1F-19	2.1.1.141	O-acetylserine 1-methyltransferase	EV-EXP
AT1G076690	AT1G076690	12-OXOPHYTODIENOATE-REDUCTASE-R2M	1.3.1.42	12-oxophytodienoate reductase	EV-COMP
AT1G076680	AT1G076680	12-OXOPHYTODIENOATE-REDUCTASE-R2M	1.3.1.42	12-oxophytodienoate reductase	EV-EXP
AT2G06050	AT2G06050	12-OXOPHYTODIENOATE-REDUCTASE-R2M	1.3.1.42	12-oxophytodienoate reductase	EV-EXP
AT3G25770	AT3G25770	ALLENE-OXIDE-CYCLASE-R2M	5.3.99.6	allene oxide cyclase	EV-EXP
AT3G25760	AT3G25760	ALLENE-OXIDE-CYCLASE-R2M	5.3.99.6	allene oxide cyclase	EV-COMP
AT3G25760	AT3G25760	ALLENE-OXIDE-CYCLASE-R2M	5.3.99.6	allene oxide cyclase	EV-COMP
AT1G033280	AT1G033280	ALLENE-OXIDE-CYCLASE-R2M	5.3.99.6	allene oxide cyclase	EV-COMP

Take this gene list to TAIR to get sequences



## Case study: Jasmonic acid biosynthesis

- Obtain protein sequences for all of the enzymes

The Arabidopsis Information Resource (TAIR) maintains a database of genetic and genomic data for the model higher plant *Arabidopsis thaliana*. Data available from the complete genome sequence along with gene structure, gene product information, metabolites, gene expression, DNA and seed stocks, genome maps, genetic markers, publications, and information about the Arabidopsis research community product function data is updated every two weeks from the latest published review and community data submissions. Gene structures are updated 1-2 times per year. Computational and manual methods as well as community submissions of new genes. TAIR also provides various other resources.

The Arabidopsis Genome Project presents and distributes species stock information.

**The Arabidopsis Information Resource**

**Download / Upload**  
**Genes**  
**GO (and other) Annotations**  
**Maps**  
**Pathways**  
**Proteins**  
**Protocols**  
**Miscellaneous Data**  
**Sequences**

**Home > Tools > Bulk Data Retrieval**

**Bulk Data Retrieval and Analysis**

**Gene Descriptions**  
 Download gene descriptions using locus identifiers (ARL codes) or gene names.

**GO Annotations**  
 Search and download GO annotations using locus identifiers. Functionally classify Arabidopsis genes and view the results as tables or pie charts.

**Sequences**  
 Download nucleotide and protein sequences using locus identifiers. Send FASTA formatted sequences to ClustalW multiple sequence alignment program at the European Bioinformatics Institute.



# Case study: Jasmonic acid biosynthesis

- Obtain protein sequences for all of the enzymes

**Sequences**

Locus/Gene Model Identifiers or Sequences:

- AT1G031400
- AT2G44810
- AT3G22400
- AT1G72520
- AT1G67540
- AT1G51740
- AT1G55020
- AT3G45140

Upload file:

Dataset: AGI transcripts

Search Against:

- ☒ Get one sequence per locus (representative gene model/splice form only)
- ☐ Get sequences for all gene models/splice forms
- ☐ Get sequences for only the gene model/splice form matching my query

Output Options:

Select output format:

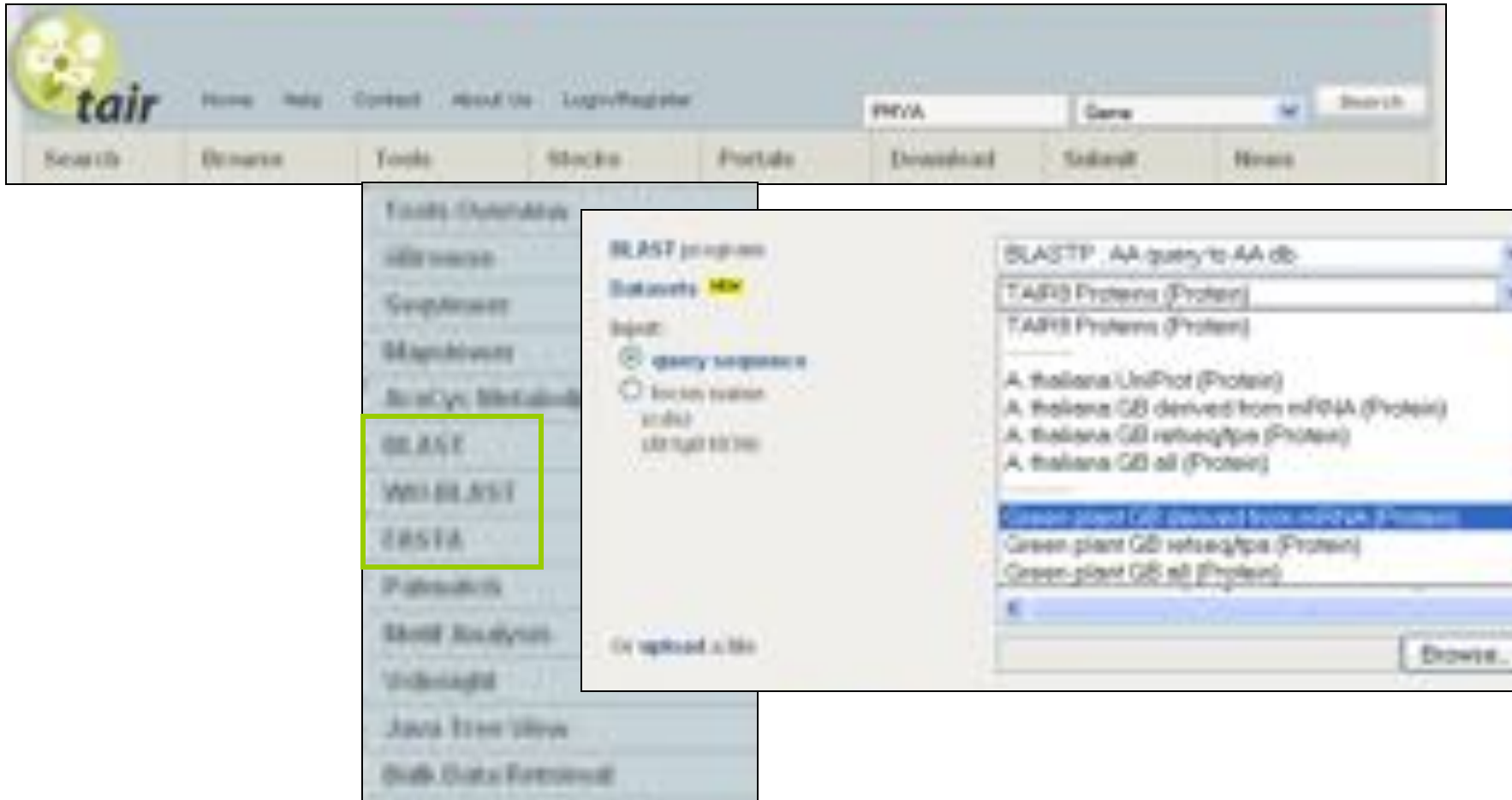
- ☒ Fasta
- ☐ Tab-delimited text (format: id tab description tab sequence)

AGI transcripts  
AGI coding sequences  
AGI genomic locus sequences  
**AGI protein sequences**  
Upstream Sequences - 500bp  
Upstream Sequences - 1000bp  
Upstream Sequences - 3000bp  
Downstream Sequences - 500bp  
Downstream Sequences - 1000bp  
Downstream Sequences - 3000bp  
Intergenic Sequences  
Intron Sequences  
AGI 5' UTRs  
AGI 3' UTRs



## Case study: Jasmonic acid biosynthesis

- Blast enzymes against all Genbank Plant proteins in TAIR



- Or use UniProt, Genbank, your species-specific database, etc.



# Putting the PMN and TAIR to work for you

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- Use the PMN to learn more about metabolic pathways
- Use TAIR to find detailed information for specific genes / proteins
- Use TAIR and the PMN to enhance your plant biology research
- If you're having trouble getting any information you want . . .



# We are here to help!





# We appreciate YOUR help!

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# PMN and TAIR Acknowledgements

Sue Rhee (*PI - PMN*)

Eva Huala (*PI-TAIR*)

Peifen Zhang (*Director-PMN*)

## Current Curators:

- Tanya Berardini (*lead curator*)
- Philippe Lamesch (*lead curator*)
- Donghui Li (*curator*)
- Dave Swarbreck (*former lead curator*)
  
- Debbie Alexander (*curator*)
- A. S. Karthikeyan (*curator*)
- Marga Garcia (*curator*)
- Leonore Reiser

## PMN Collaborators:

- Peter Karp (SRI)
- Ron Caspi (SRI)
- Suzanne Paley (SRI)
- SRI Tech Team
- Lukas Mueller (SGN)
- Anuradha Pujar (SGN)
- Gramene and MedicCyc

## Current Tech Team Members:

- Bob Muller (*Manager*)
- Larry Ploetz (*Sys. Administrator*)
- Anjo Chi
- Raymond Chetty
- Cynthia Lee
- Shanker Singh
- Chris Wilks

## PMN project post-doc

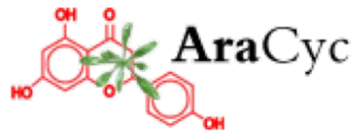
- Lee Chae



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INSTITUTION FOR  
SCIENCE



# We are here to help!



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