



User's Guide for Plant Reactome Database (Gramene database build # 50)

Sushma Naithani and Pankaj Jaiswal
Oregon State University

What is Plant Reactome: The **Plant Reactome** is a free, open-source, curated and peer reviewed pathway database. Our goal is to provide intuitive bioinformatics tools for the visualization, interpretation and analysis of pathway knowledge to support basic research, genome analysis, modeling, systems biology and education.

Accessing Plant Reactome and important Links

From Gramene: <http://www.gramene.org/pathways>

Direct Link: <http://plantreactome.gramene.org>



How many plant species are covered in Plant Reactome database : As of Release # 50, the Plant Reactome contains **gene homology-based pathway projections** for 62 plant species. We regularly update our database for contents and tools. To see current species and associated statistics see http://plantreactome.gramene.org/?page_id=2035.

Use case study #1: Tomato: As a researcher you are working on fruit ripening in tomato, and interested in learning about regulation of ripening associated pathways during fruit development. You also have a few related hypotheses that you would like to test, for which you quickly need to extract relevant genes and pathways.

Q1: Can I identify pathways associated with gene or protein of my interest?

Answer:(Fill)

1. Search for a gene or protein in Plant Reactome and find associated pathways:
Example: 'CORONATINE-INSENSITIVE1' (or COI1), a gene required for the maternal control of seed maturation, jasmonate-signaled defense response and glandular trichome development (reference: Li et al (2004) : Plant Cell, 16:126, PMID:).

Plant Cell 2004 Jan; 16(1): 126-143. doi: 10.1105/pc.017954 PMID: PMC301400

The Tomato Homolog of CORONATINE-INSENSITIVE1 Is Required for the Maternal Control of Seed Maturation, Jasmonate-Signaled Defense Responses, and Glandular Trichome Development^{WJ}

Lei Li,^a Youfu Zhao,^a Bonnie C. McCaig,^a Byron A. Wingerd,^b Jihong Wang,^c Mark E. Whalon,^b Eran Pichersky,^c and Gregg A. Howe^{1,a,d}

Author information ► Article notes ► Copyright and License information ►

This article has been corrected. See *Plant Cell*, 2004 March, 16(3), 703.
This article has been cited by other articles in PMC.

ABSTRACT Go to:

Jasmonic acid (JA) is a fatty acid–derived signaling molecule that regulates a broad range of plant defense responses against herbivores and some microbial pathogens. Molecular genetic studies in Arabidopsis have established that JA also performs a critical role in anther and pollen development but is not essential for other developmental aspects of the plant's life cycle. Here, we describe the phenotypic and molecular characterization of a sterile mutant of tomato (*Jasmonic acid-insensitive1* [*Jai1*]) that is defective in JA signaling. Although the mutant exhibited reduced pollen viability, sterility was caused by a defect in the maternal control of seed maturation, which was associated with the loss of accumulation of JA-regulated proteinase inhibitor proteins in reproductive tissues. *Jai1* plants exhibited several defense-related phenotypes, including the inability to express JA-responsive genes, severely compromised resistance to two-spotted spider mites, and abnormal development of glandular trichomes. We demonstrate that these defects are caused by the loss of function of the tomato homolog of CORONATINE-INSENSITIVE1 (COI1), an F-box protein that is required for JA-signaled processes in Arabidopsis. These findings indicate that the JA/COI1 signaling pathway regulates distinct developmental processes in different plants and suggest a role for JA in the promotion of glandular trichome–based defenses.

INTRODUCTION Go to:

Share
Facebook Twitter Google+

Save Items
Add to Favorites

Similar articles in PubMed

The wound response mutant suppressor of prosystemin-mediated responses5 (spr5) is a weak allele of the *Plant Cell Physiol*. 2006
Virulence systems of *Pseudomonas syringae* pv. tomato promote bacterial speck disease in tomato by targeting the *Plant J*. 2003
The tomato suppressor of prosystemin-mediated responses2 gene encodes a fatty acid desaturase required for *Plant Cell*. 2003
Jasmonate: an oxylipin signal with many roles in plants. *Vitam Horm*. 2005
Jasmonates in flower and seed development. *Biochimie*. 2013
See reviews...
See all...

Cited by other articles in PMC

Jasmonate Signalling and Defence Responses in the Model Legume *Medicago truncatula*—A Focus on Responses *Plants*. 1/01
Control of Carbon Assimilation and Partitioning by Jasmonate: An Accounting of Growth-Defense Tradeoffs *Plants*. 1/01
Dynamics of Jasmonate Metabolism upon Flowering and across Leaf Stress Responses in *Arabidopsis thaliana* *Plants*. 1/01
Beyond the Canon: Within-Plant and Population-Level Heterogeneity in Jasmonate Signaling Engaged by F *Plants*. 1/01
Overexpression of SIUPA-like induces cell enlargement, aberrant

Users can type name of a gene in the search box in the Plant reactome home page. Searching for COI1 will give the following result:

(<http://plantreactome.gramene.org/content/query?q=coi1&species=Oryza+sativa&species=Entries+without+species&cluster=true>)

Most Visited Getting Started Miles User account | Internat... Calendar OSU Tutorial: Custom Data ... Millar Lab aracyc Gramene GRIN SRO wheat OSU In

REACTOME

About Content Documentation Tools Community Download Contact

Search results for *coi1*

Showing 24 of 341

Species Set (5 results from a total of 5)

- Entries without species (336)
- Oryza sativa* (5)
- Homo sapiens* (274)
- Aegilops tauschii* (3)
- Brachypodium distachyon* (3)
- Hordeum vulgare* (3)
- More...

Types

- Chemical Compound (244)
- Regulation (82)
- OtherEntity (6)
- Set (5)
- Reaction (3)
- Complex (1)

Compartments

- cytosol (198)
- mitochondrial matrix (41)
- Golgi lumen (8)
- mitochondrial inner membrane (5)
- nucleoplasm (2)
- plastid stroma (2)

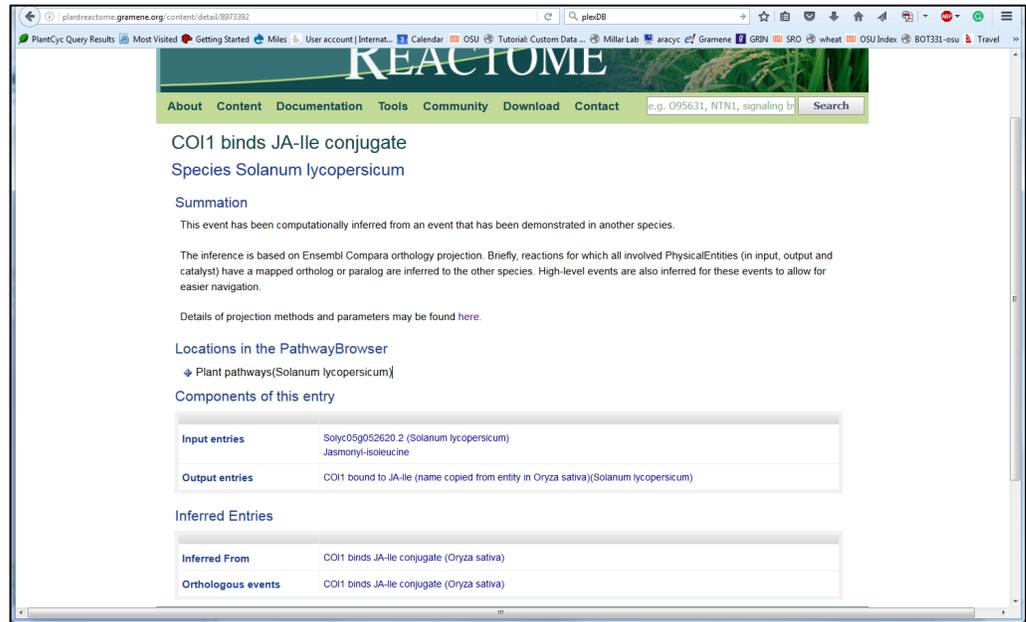
Complex (1 results from a total of 1)

- COI1 bound to JA-Ile (*Oryza sativa*)**
COI1 a Fbox protein act as the JA receptor and binds to JA-Ile conjugate

Reaction (3 results from a total of 3)

- COI1 binds JA-Ile conjugate (*Oryza sativa*)**
COI1 a Fbox protein act as the JA receptor and binds to JA-Ile conjugate
- Ubiquitination and proteosomal degradation of JAZ (*Oryza sativa*)**

By default the database searches are on '*Oryza sativa*'. However, from the Species section, uncheck the *O. sativa* and entries without species and click on the 'more' option to find tomato (*Solanum lycopersicum*). After the selection you will see



The screenshot shows the REACTOME website interface. The search bar contains 'e.g. O95631, NTN1, signaling b'. The search results display the reaction 'COI1 binds JA-Ile conjugate' for the species 'Solanum lycopersicum'. The 'Summation' section states: 'This event has been computationally inferred from an event that has been demonstrated in another species. The inference is based on Ensembl Compara orthology projection. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped ortholog or paralog are inferred to the other species. High-level events are also inferred for these events to allow for easier navigation. Details of projection methods and parameters may be found here.' The 'Locations in the PathwayBrowser' section shows 'Plant pathways(Solanum lycopersicum)'. The 'Components of this entry' section includes a table with 'Input entries' (Soyc05g052620.2 (Solanum lycopersicum) Jasmonyl-isoleucine) and 'Output entries' (COI1 bound to JA-Ile (name copied from entity in Oryza sativa)(Solanum lycopersicum)). The 'Inferred Entries' section shows 'Inferred From' (COI1 binds JA-Ile conjugate (Oryza sativa)) and 'Orthologous events' (COI1 binds JA-Ile conjugate (Oryza sativa)).

<http://plantreactome.gramene.org/content/query?q=coi1&species=Solanum+lycopersicum&cluster=true>



The screenshot shows the REACTOME website search results for 'coi1'. The search bar contains 'coi1' and the search button is labeled 'Search'. The search results are displayed under the heading 'Search results for coi1'. The 'Showing 2 of 2' text is visible. The 'Species' section shows a list of species with checkboxes: Solanum lycopersicum (2), Entries without species (336), Homo sapiens (274), Oryza sativa (5), Aegilops tauschii (3), and Brachypodium distachyon (3). The 'Types' section is partially visible. The 'Reaction' section shows 1 result from a total of 1: 'COI1 binds JA-Ile conjugate (Solanum lycopersicum)'. The 'Complex' section shows 1 result from a total of 1: 'COI1 bound to JA-Ile (name copied from entity in Oryza sativa) (Solanum lycopersicum)'. The text below the complex result states: 'This complex/polymer has been computationally inferred (based on Ensembl Compara orthology projection)'.

The results also suggest that the COI1 gene product participates in a reaction where it binds Jasmonate-Ile and forms a complex. Now click on the Reaction Link for 'COI1



binds JA-Ile conjugate (Solanum lycopersicum)'. It will take you to the Reaction detail page which tells you about how the reaction was curated/projected, inputs and outputs of the reactions and the pathway this reaction is associated with.

Click on the '+' sign next to the 'Plant Patwhays (Solanum lycopersicum).

The hierarchy chart opens up telling about the pathways this reaction is associated with. In this case the Jasmoic acid signaling.

<http://plantreactome.gramene.org/content/detail/8973392>

Click on the hyperlinked reaction name and it will lead you to the **Pathway Browser** highlighting the selected reaction

<http://plantreactome.gramene.org/PathwayBrowser/#SPECIES=8969285&DIAGRAM=8>

The screenshot shows the REACTOME website interface. At the top, there is a navigation bar with links for About, Content, Documentation, Tools, Community, Download, and Contact. A search bar is located on the right side of the navigation bar. Below the navigation bar, the main content area displays the reaction name "COI1 binds JA-Ile conjugate" and the species "Solanum lycopersicum". Underneath, there is a section titled "Summation" which contains text explaining that the event has been computationally inferred from an event demonstrated in another species. The text further details the inference process based on Ensembl Compara orthology projection. Below the summation, there is a section titled "Locations in the PathwayBrowser" which shows a hierarchical tree structure of pathways. The tree starts with "Plant pathways(Solanum lycopersicum)" and branches down to "COI1 binds JA-Ile conjugate(Solanum lycopersicum)".

In the browser you see the reaction and pathways highlighted to suggest its placement in the data structure.

Zoom-in/out functions for pathway viewer are in the red-box

Download the pathway in different formats (click the download button in grey box)

See list of molecules participating in the reaction (click the molecules button in cyan box).

You will see the highlighted genes products and inputs/outputs. Click on the + sign next to chemical compounds of genes based on your interest to see a full list.

Depending on your selection in the left hand tree, if it is for pathway you will see a larger list. Also there is a download data option in this tab.

We chose to use gene products section to look for the tomato gene that was mapped to this reaction. **It turns out there is one tomato gene, Solyc05g052620.2** was mapped to COI1 function in this pathway.

The screenshot displays the Gramene Pathway Browser interface for *Solanum lycopersicum*. The left sidebar shows the 'Event Hierarchy' with 'Jasmonic acid signaling' selected. The main area shows a metabolic pathway diagram where the reaction 'COI1 binds JA-Ile conjugate' is highlighted in yellow. A blue box labeled 'Solyc05g052620.2' is connected to this reaction, indicating it is a homolog of JAR1. Below the diagram, the 'Molecules (2/42)' and 'Proteins (1/36)' sections are visible, listing 'Solyc05g052620.2' as the protein associated with the reaction.

Q2. Can I find a similar event in Potato? And find COI1 gene homologs.

A. Fill in your answer.....

Navigating Projected pathways in another plant species:

On the Pathway Browse page, select '*Solanum tuberosum*' from the species drop down list (see red box)

Pathways for: **Solanum lycopersicum**

Event Hierarchy:

- Plant pathways
 - Metabolism and regulation
 - COI1 binds JA-ile conjugate

Find Reaction/Entity: Highlight All X

Protein Small molecule Complex

Overview Molecules (2/42) Expression Analysis Processes Downloads

COI1 binds JA-ile conjugate Species: **Solanum lycopersicum** Download Info

Proteins (1/36)

Gene ID	Ensembl ID	Count
Soly05g052620.2	Ensembl:Soly05g052620.2 (2x)	2
Soly01g006650.1	Ensembl:Soly01g006650.1 (1x)	1
Soly01g014480.2	Ensembl:Soly01g014480.2 (1x)	1
Soly01g095580.2	Ensembl:Soly01g095580.2 (1x)	1

As soon as you select the potato species, the browser view will refresh.

<http://plantreactome.gramene.org/PathwayBrowser/#SPECIES=8973856&DIAGRAM=8978286&PAT=8978105,8978104,8978117&>

Pathways for: **Solanum tuberosum**

Event Hierarchy:

- Plant pathways
 - Metabolism and regulation
 - Jasmonic acid signaling

Find Reaction/Entity: Highlight All X

Protein Small molecule Complex

Overview Molecules (36) Expression Analysis Processes Downloads

Jasmonic acid signaling Species: **Solanum tuberosum** Download Info

Result: You will see that this reaction was not projected for potato, as JA-Ile to JAZ connection is missing in potato.

There are following possible reasons for this difference.

The potato gene homolog was not identified that's why we do not see the mapped gene and the missing reaction from potato.

Absence of potato gene could be due to

- Annotated gene was not identified by the potato genome project. Therefore missing
- The gene was there but it didn't meet the homolog calling criteria, thus missing from the gene family cluster
- This may be case of either true biology or evolutionary effects or the genotype that was sequenced to produce reference potato genome.
- These are all good observations, that become research questions that can be discussed in the Genome exercise.

Projections in other species:

Let's try another species 'Glycine max', strawberry and peanut. We see the reaction being projected in all three species.

Link for 'Glycine Max':

<http://plantreactome.gramene.org/PathwayBrowser/#SPECIES=8962006&DIAGRAM=8969281&ID=8968635&PATH=8969100,8969099,8969112&DTAB=MT>

The screenshot shows the Gramene Pathway Browser interface for the species 'Glycine max'. The main pathway diagram illustrates the conversion of JA-Ile to JAZ. Key components include:

- Enzymes:** Jasmonyl-isoleucine synthetase (green box) and COI1 bound to JA-Ile (yellow box).
- Reactants:** ATP, L-Ile, and Jasmonyl-isoleucine synthetase.
- Products:** Jasmonyl-isoleucine, PPI, and AMP.
- Annotations:** 'Homologues of OS1g0853400' is noted near the Jasmonyl-isoleucine product.
- Event Hierarchy (Left Panel):**
 - Cofactor biosyntheses
 - Hormone biosynthesis and signaling
 - IAA biosynthesis I
 - IAA biosynthesis II
 - IAA biosynthesis VI (via indole-3-acetamide)
 - Polar Auxin transport
 - IAA conjugate biosynthesis I
 - brassinosteroid biosynthesis II
 - trans-zeatin biosynthesis
 - jasmonic acid biosynthesis
 - Jasmonic acid signaling
 - Jasmonate conjugation
 - COI1 binds JA-Ile conjugate
 - Nuclear uptake of JAZ
 - Ubiquitination and proteasomal degradation
 - JAZ binds MYC like
 - JAZ/MYC binds NINJA
 - MYC induced transcription of JA inducible genes

Link for peanut (*Arachis ipaensis*):

<http://plantreactome.gramene.org/PathwayBrowser/#SPECIES=8928096&DIAGRAM=8932127&ID=8931817&PATH=8931939,8931938,8931951&DTAB=MT>

Link for strawberry (*Fragaria vesca*)

<http://plantreactome.gramene.org/PathwayBrowser/#SPECIES=8900291&DIAGRAM=8904569&ID=8904260&PATH=8904377,8904376,8904389&DTAB=MT>

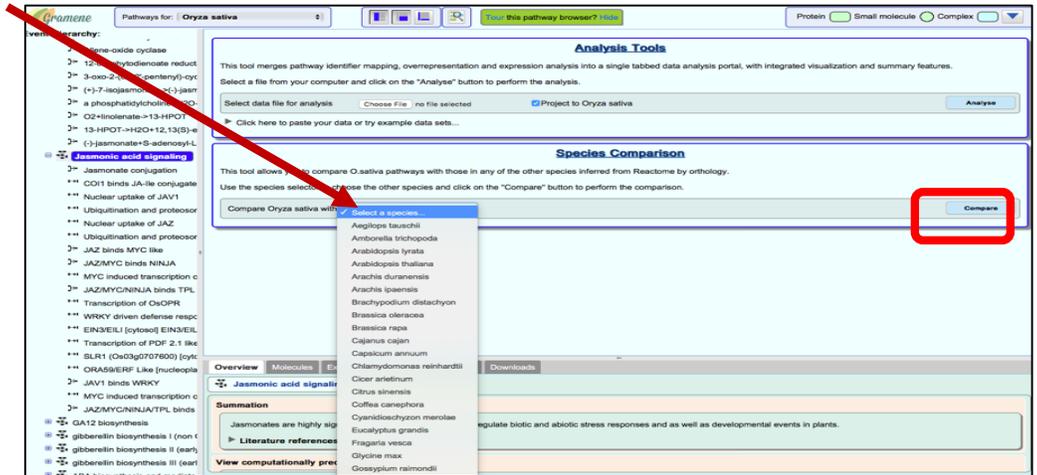
Q3. Can I compare a pathway between reference species rice and anyone of the 62 plant species for which pathway projection are available?

Example: jasmonic acid

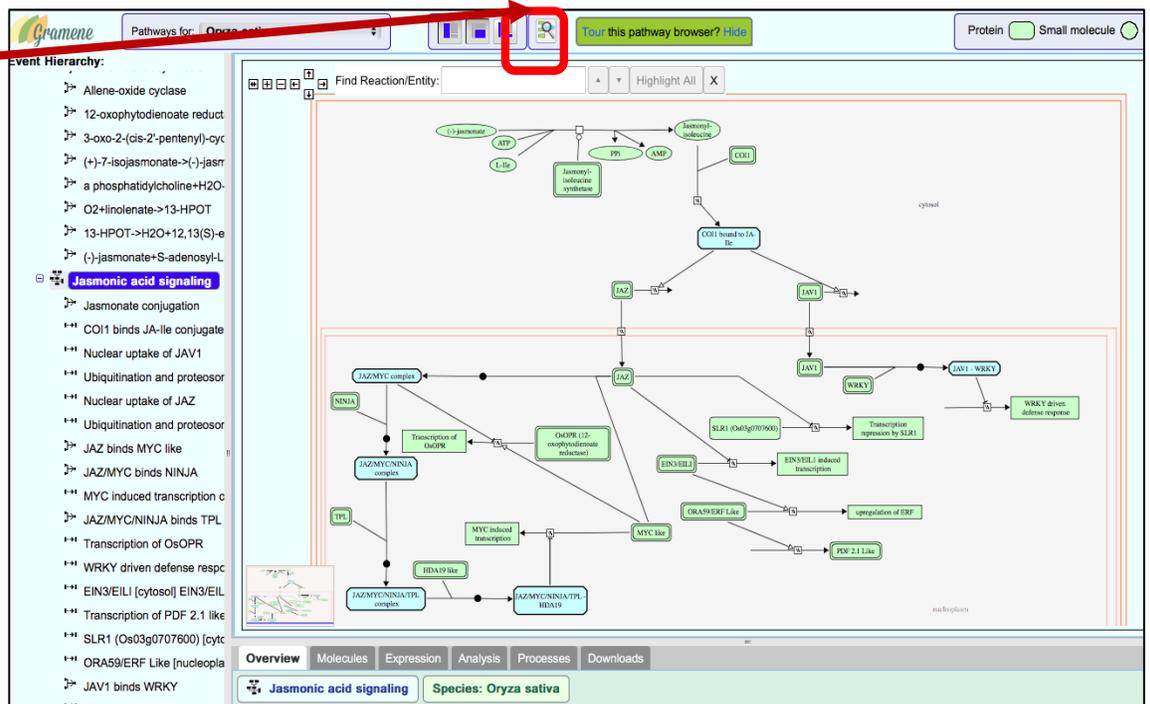
signaling pathway comparisons between tomato and rice

Step 1: navigate and open Jasmonic acid signaling pathways in reference species rice (*Oryza Sativa*). Link:

<http://plantreactome.gramene.org/PathwayBrowser/#DIAGRAM=6787011&PATH=2894885,2744345,2744341&DTAB=AN&ANALYSIS=MjAxNjA1MTcxNDMzMTRfNDE%2525253D>



Step2: Click on the Tools (boxed in the figure). A new window with Tools menu opens as following.



Step 3: From the species comparison drop down option select your favorite species and then hit compare.

As a result, a new pathway browsing window, showing the projection of Tomato pathway over the reference pathway from rice will open as shown here.

In this pathway diagram, complete blue boxes represent rice enzyme and genes for which no corresponding orthologs were found in tomato. The filled yellow box represents the enzyme for which tomato ortholog(s) have been found. The box filled with yellow and blue represent the difference in the number of genes mapped to this particular enzyme in reference species rice and the projected species tomato. Users can click on a given enzyme to see for which rice genes homologs have been identified in the tomato (rice gene highlighted in yellow color) and for which gene orthologs were not found in tomato (genes highlighted with blue color).

Q4. How to link to other external DBLinks for accessing Genome Browser, gene expression, etc. from Plant Reactome

We currently provide external links for Arabidopsis, rice and Maize only. We are working on tomato and other species.

Q5. How one can we analyze transcriptomic data using Plant Reactome?

A note about web browsers: At present the Firefox, Netscape and Safari are having problems with projection of expression data on plant pathways. Although Safari, allows the display of the expression data mapped to pathways in tabulated format. We suggest users currently use Chrome.

Here is the case study for analysis of transcriptomic data analysis of a publicly available data from published study.

Study: [Transcriptome analysis of various tissues in tomato cultivar Heinz](#)

Reference: PMID: 22660326 ([Nature](#), 2012 May 30;485(7400):635-41. doi: 10.1038/nature11119). **The tomato genome sequence provides insights into fleshy fruit evolution.**

Data: <http://ted.bti.cornell.edu/cgi-bin/TFGD/digital/experiment.cgi?ID=D004>

File: <https://www.dropbox.com/s/0i3b1jqoroxb9gz/tomato-baseline-ted-bti-D004-3-log2fold.txt?dl=0>

Experiment description: Illumina RNA-seq analysis of leaves, roots, flower buds, fully opened flowers, and 1 cm, 2 cm, 3 cm, mature green, breaker, and breaker+10 fruits of tomato cultivar Heinz, and leaves, immature green, breaker, and breaker+5 fruits of *Solanum pimpinellifolium*

1. Go to the pathway browser page of your favorite species, for example, tomato

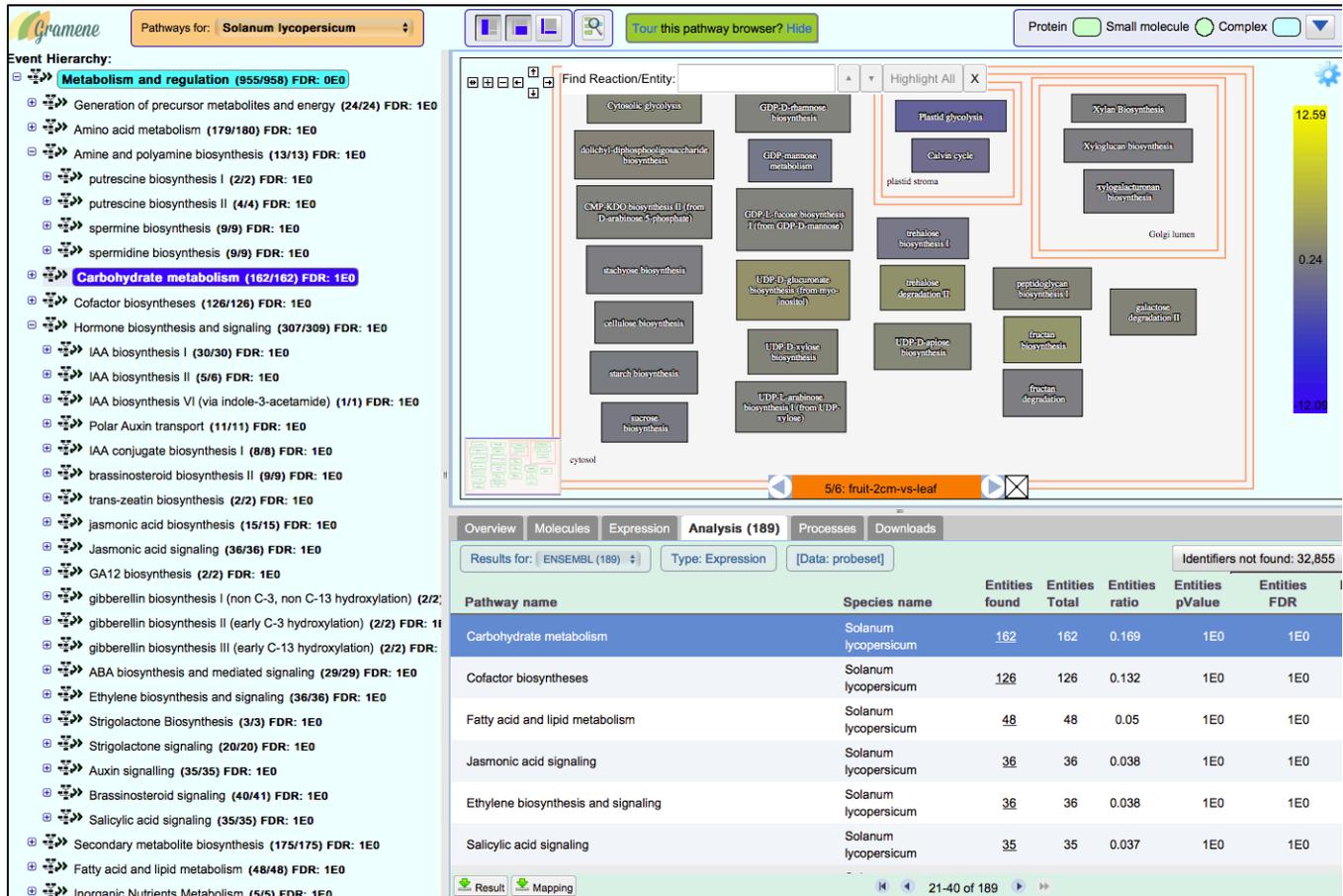
<http://plantreactome.gramene.org/PathwayBrowser/#SPECIES=8969285&DIAGRAM=8973667&PATH=8973668>

2. Click on Tools→ Choose a data file to upload (under Analysis Tools) window or enter your data into the text box (as shown in the following figure)

The screenshot shows the Plant Reactome Analysis Tools interface. On the left, there is a sidebar with a tree view of 'Plant pathways' and 'Metabolism and regulation'. The main area is titled 'Analysis Tools' and contains a text box for pasting data, a table of example data sets, and buttons for 'Uniprot accession list', 'Gene identifier list', 'Microarray data', and 'Metabolomics data'. The 'Metabolism and regulation' pathway is selected, and the 'Species: Solanum lycopersicum' is set.

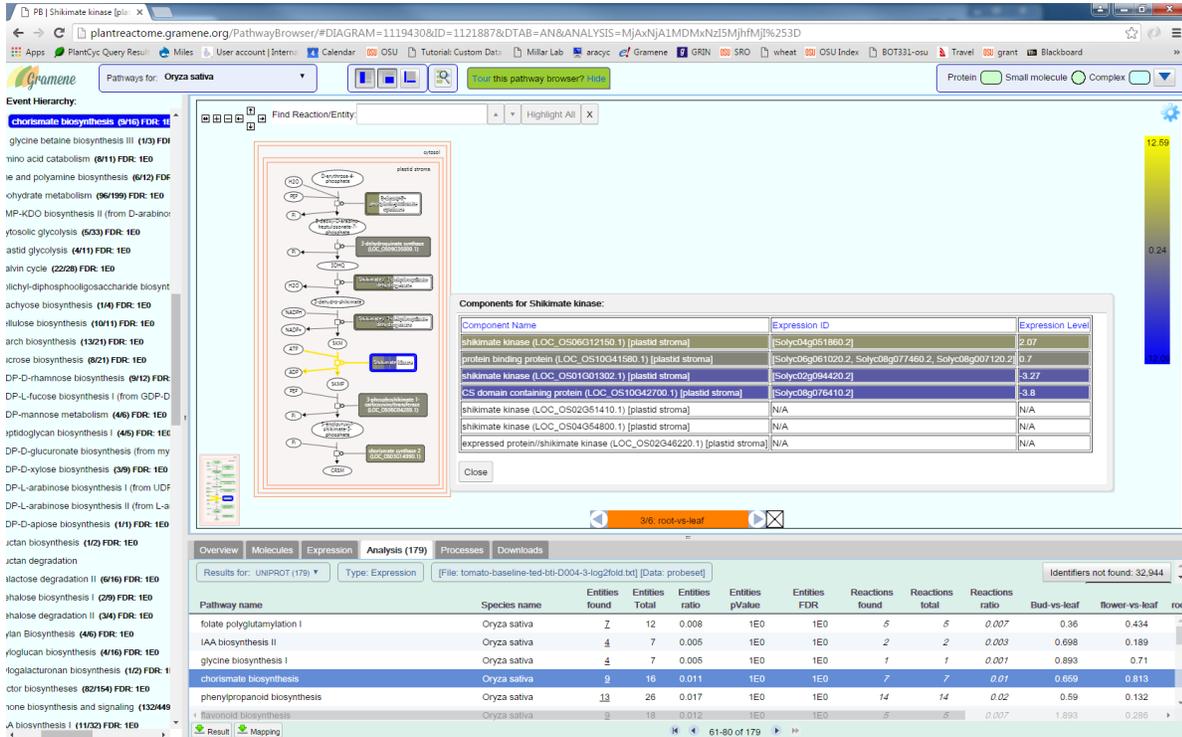
Gene	Bud vs leaf	Flower vs leaf	Root vs leaf	Fruit 1cm vs leaf	Fruit 2cm vs leaf	Fruit 3cm vs leaf
Soly01g005000.2	0.703795167	0.340956266	-0.80066477	0.261373419	0.938566143	0.891020559
Soly01g005010.2	-0.590218226	-0.503374966	-0.053439259	0.053439259	0.186413124	-0.569309236
Soly01g005020.2	0.165728967	0.445918619	1.453483167	0.86025259	1.346238002	1.548916343
Soly01g005030.2	0.134899519	-0.008441774	0.742677915	0.128753844	0.283372048	0.90969379
Soly01g005040.2	1.150559677	0.948925815	-1.039528364	-1.02621542	1.150559677	0.781188611
Soly01g005050.2	6.201241771	5.406332578	0.201633861	0	0.23878686	0.189033824
Soly01g005060.2	0.696721962	0.820321341	1.142856758	3.017988119	1.82789456	0.820321341
Soly01g005070.2	2.25534041	4.045666898	0.004859186	0.992979572	0.379588663	0.054666459
Soly01g005080.2	0.789439758	2.037050976	1.080336207	0.579918107	0.097646092	-0.587324864
Soly01g005090.2	0	0	4.434294618	0.070389228	0	0
Soly01g005100.2	-0.938083808	0.821696743	-0.184612125	-0.600170735	-0.735590944	-0.819265963
Soly01g005110.2	1.814761393	1.180538272	1.046597589	0.741348231	-0.254512035	0.083039585
Soly01g005120.2	2.46889493	1.837998877	3.131703679	1.109733823	1.168745867	0.280107919
Soly01g005130.2	-1.91136013	-1.469202287	0.43980529	-1.2340836	-1.556824744	-0.011502971

- After uploading/ pasting the data, click on analyze to map gene expression data on Tomato. Users also have an option to project Tomato expression data on the reference rice pathways by checking the small icon “Project to *Oryza sativa*”. Users can browse pathways belonging to a category (e.g. Carbohydrate metabolism) or individual pathways or sub-pathways by selecting the options from left-hand side window that list pathways



- The Figure above shows all the pathways involved in the carbohydrate metabolism that show differential expression between fruit and leaf tissue. The Bottom right-hand side bottom panel lists the pathways and associated data.
- Users can browse this list or the left-hand side panel to select an individual pathway, such as Chorismate biosynthesis pathway to see the expression of genes mapped to a pathway. At present we are having problem to do that directly on the tomato and some of the projected species. So users can select reference species rice and can project the tomato expression data on rice pathways.

- By clicking on a given enzyme, users can open a pop-up window showing the rice genes and their tomato orthologs with expression data. As shown in the figure.



- The expression data mapped to the various pathways in plant Reactome can also be downloaded.

Q6. Can I download Plant Reactome database for conducting analysis in my local desktop.

Plant Reactome is a complex platform and currently we do not provide this option.

Q7. How can I send my feedback to Plant Reactome group:

If you have questions or comments about Plant Reactome data, our website, or the downloads that we provide, we would be pleased to hear from you!

You can email us at reactome-curator@gramene.org