

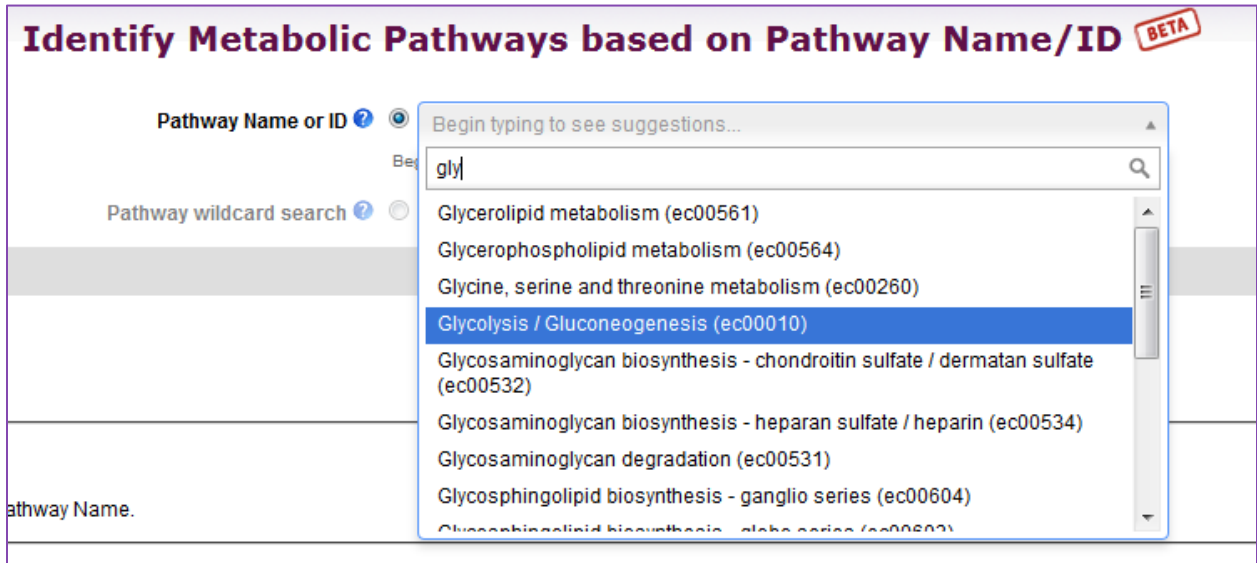
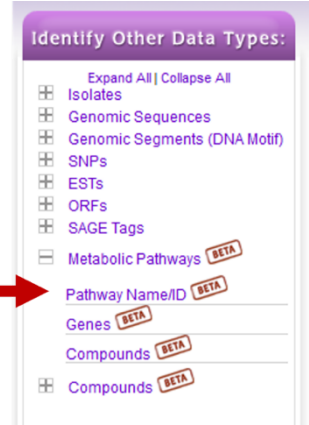
Pathway Exercises

Metabolism and Pathways

1. Find the metabolic pathway for glycolysis.
For this exercise use <http://plasmodb.org>

Navigate to the search page for Identify Metabolic Pathways based on Pathway Name/ID.

- Metabolic pathway and compound searches are available under the “Identify Other Data Types” head on the home page. You can find metabolic pathways based on the pathway name, genes involved in the pathway, or compounds involved in the pathway. Search for the **glycolysis** pathway using the Pathway Name/ID option.
- This search is equipped with a type-ahead function for choosing the metabolic pathway name. Begin typing glycolysis and then choose the pathway name from the list that appears.



- a. Examine the Glycolysis / Gluconeogenesis pathway.
- The search takes you straight to the record page for the Glycolysis / Gluconeogenesis (ec00010) metabolic pathway. The overview section of the record page contains an interactive graphical representation of the pathway. The pathway map and the legend can be repositioned. Located under the map is a table of Metabolic Pathway Reactions.

Metabolic Pathway
ec00010 - Glycolysis / Gluconeogenesis
 Add to Basket Add to Favorites

Overview
 Pathway: ec00010 - Glycolysis / Gluconeogenesis

File Layout Paint Experiment Paint General

Glycolysis / Gluconeogenesis Starch and sucrose metabolism Pentose phosphate pathway

File menu with options for saving images, changing the format/layout and layering data at the nodes.

Interactive pathway map that will display information about the gene or compound node that click.

Repositioning: Drag the entire pathway map, individual nodes, or the legend to reposition.

Interactive legend that will display information about the last node you clicked on.

Click on nodes for more info. Nodes highlighted in red are EC numbers that we have mapped to at least one gene. The nodes, as well as this info box, can be repositioned by dragging.

- Use the Tool Box to move (drag) the map and individual nodes. Zoom in and out to help explore the map.
- What do the circles represent?
- What do the rectangles with numbers like 2.7.1.11 represent?
- Click on the pathway nodes.
- What is the difference between the rectangular nodes that are outlined in red and those that are outlined in black?
- Do you see new information appear in the legend? Try some of the new links in the legend.
- Notice the gray dropdown menus above the map.
 - File: Zoom around and reposition some of the nodes; then use the file menu to save an image or xml file of the map.



- Layout: change the look of the map to something more familiar to you – a tree view perhaps.
- Paint Experiment: change the EC number in the nodes to a graph representing that gene's expression in RNA Seq or microarray experiments. We will explore this function later.
- Paint Genera: change the EC number in the nodes to a graph representing the presence of orthologs in other genera.

- Find the node representing 6-phosphofructokinase (EC number = 2.7.1.11). You may need to zoom and reposition the map to find the node.
- Click on the 2.7.1.11 node to populate the legend with information about genes that are annotated with the EC number 2.7.1.11.
- What genomes contain genes that are annotated with the EC number 2.7.1.11?

2.7.1.11 2.7.1.146

EC Number: 2.7.1.11

Enzyme Name or Description: 6-phosphofructokinase

Organism(s):
P. falciparum 3D7
P. yoelii yoelii 17X

Organism(s) inferred from OrthoMCL:
P. berghei ANKA
P. chabaudi chabaudi
P. cynomolgi strain B
P. falciparum 3D7
P. falciparum IT
P. knowlesi strain H
P. vivax Sal-1
P. yoelii yoelii 17X
P. yoelii yoelii 17XNL
P. yoelii yoelii YM

[Search for Gene\(s\) By EC Number](#)

- What organisms have orthologs of these genes?
- Try the link 'Search for Gene(s) by EC Number'. Where did you end up? What do the 22 genes in the result list represent? Is 6-phosphofructokinase unique to *P. falciparum*?

My Strategies: [New](#) [Opened \(1\)](#) [All \(4\)](#) [Basket](#) [Public Strategies \(16\)](#) [Help](#)

(Genes) Strategy: EC Number * Rename Duplicate Save As Share Delete

EC Number 22 Genes Add Step

Step 1

22 Genes from Step 1 Strategy: EC Number [Add 22 Genes to Basket](#) | [Download 22 Genes](#)

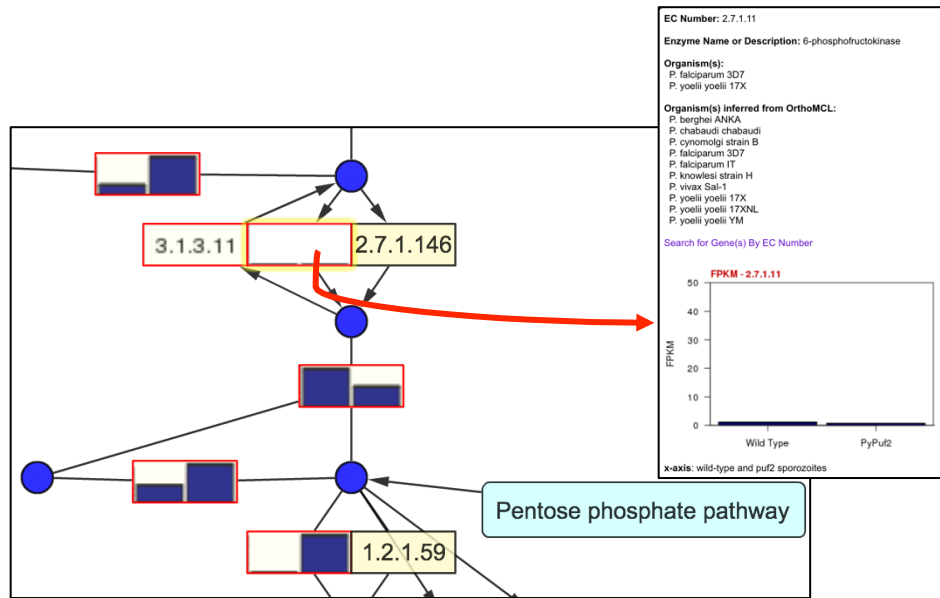
Click on a number in this table to limit/filter your results

| All Results | Ortholog Groups | <i>Plasmodium</i> | | | | | | | | | | | |
|-------------|-----------------|-------------------|------------------|-------------------|----------------------------------|----|---------------------|------------------|--------------------|---------------|------------------------------|------------|-----------|
| | | <i>Pberghei</i> | <i>Pchabaudi</i> | <i>Pcynomolgi</i> | <i>Pfalciparum</i> (nr Genes: 2) | | <i>Pgallinaceum</i> | <i>Pknowlesi</i> | <i>Preichenowi</i> | <i>Pvivax</i> | <i>Pyoelii</i> (nr Genes: 2) | | |
| | | ANKA | chabaudi | strain B | 3D7 | IT | 8A | strain H | CDC | Sal-1 | yoelii 17XNL | yoelii 17X | yoelii YM |
| 22 | 2 | 2 | 2 | 2 | 2 | 2 | 0 | 2 | 2 | 2 | 2 | 2 | 2 |

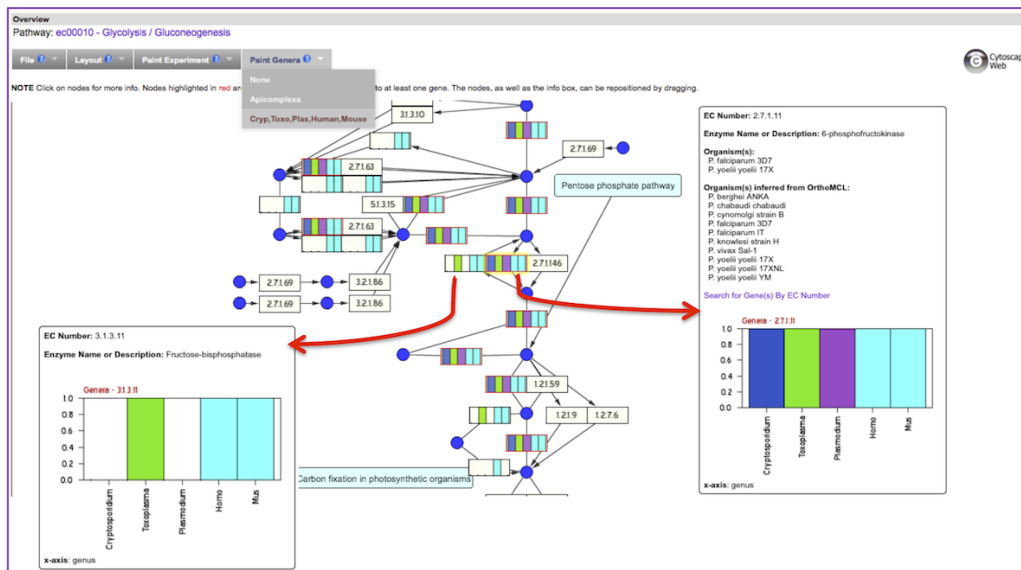
Gene Results Genome View Analyze Results BETA [Add Columns](#)

| Gene ID | Genomic Location | Product Description | EC Numbers | EC Numbers inferred from OrthoMCL |
|---------|---------------------------------|---|------------|-----------------------------------|
| PY01321 | AABL01000347: 3,716 - 7,645 (-) | pyrophosphate-dependent phosphofructokinase | N/A | 2.7.1.11 (6-phosphofructokinase) |
| PY05918 | AABL01001942: 2,396 - 6,022 (-) | 63231-59202 | N/A | 2.7.1.11 (6-phosphofructokinase) |

- Use your Browser's back button to return to the Glycolysis pathway record page and open the Paint Experiment menu. Choose the experiment "Salivary gland sporozoite transcriptomes: wild type vs Pfu2 knockout". Be patient while the graphs appear in place of the EC numbers.
- Does 6-phosphofructokinase appear to be expressed in salivary gland sporozoites? What enzymes in this pathway are affected in knockouts of Pfu2?



- Use the Paint Genera option to determine whether 6-phosphofructokinase has orthologs in *Toxoplasma*.



- What about the enzyme that catalyzes the reverse reaction (Fructose-bisphosphatase)? Does it have orthologs in *Toxoplasma*?

2. Find the compound record page for phosphoenolpyruvate (PEP).

Compound records are accessed by running a compound search available under the “Identify Other Data Types” heading on the home page. For example, compounds may be retrieved by ID, text, metabolic pathway, molecular formula, molecular weight and metabolite levels. Compound records can also be accessed from the metabolic pathway legend after clicking on a compound (blue circle) in the map.

Identify Other Data Types:

Expand All | Collapse All

- Isolates
- Genomic Sequences
- Genomic Segments (DNA Motif)
- SNPs
- ESTs
- ORFs
- SAGE Tags
- Metabolic Pathways **BETA**
- Compounds** **BETA**
 - Compound ID **BETA**
 - Text (synonym, InChI, etc.) **BETA**
 - Enzymes **BETA**
 - Metabolic Pathway **BETA**
 - Molecular Formula **BETA**
 - Molecular Weight **BETA**
 - Metabolite Levels **BETA**

Identify Compounds based on Text (synonym, InChI, etc.) **BETA**

Text term (use * as wildcard)

Fields **BETA**

- Name, Property (InChI, IUPAC Name, SMILES, Molecular Weight)
- Synonym
- Substance Properties
- Reaction/Pathway/Enzyme

[select all](#) | [clear all](#)

Advanced Parameters

- Choose one of these searches and retrieve the PEP record page.

- Alternatively, you can reach the PEP record page via a metabolic pathway where it is present as a substrate or a product of an enzymatic reaction (ie. glycolysis). Click on the blue circle representing

- Examine the PEP record page.

- What data sections do you see?

- Under which conditions is PEP present at highest concentrations? (Hint: open the “Mass Profiles for Compounds” data section)

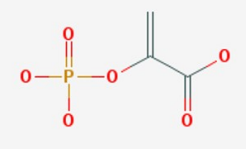
Compound ID: C00074

Name: Phosphoenolpyruvate

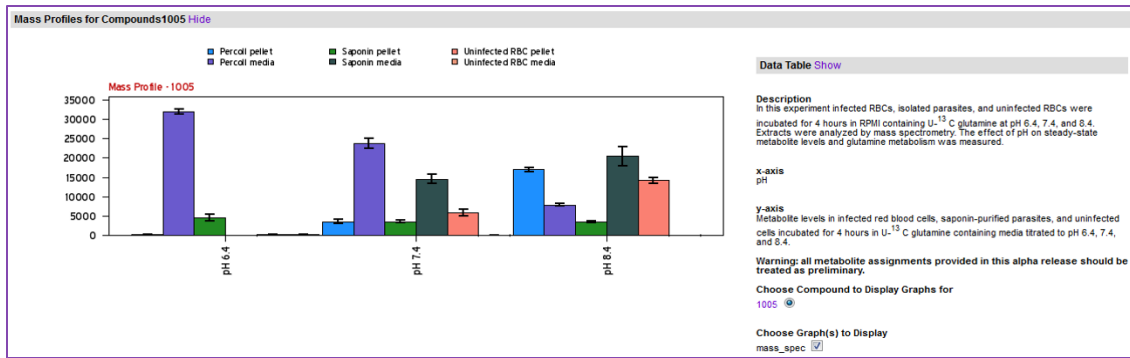
[View on this site](#) **BETA**

[View in KEGG](#)

[View in PubChem](#)



Metabolic pathway diagram showing PEP as a substrate for enzyme 4.2.1.11 and a product of enzyme 2.7.1.40. A blue circle highlights the PEP node in the pathway.



- Identify metabolites (compounds) that are 20-fold enriched at pH7.4 in saponin lysed infected red blood cell (iRBCs) pellets compared the pH7.4

Identify Other Data Types:

Expand All | Collapse All

- Isolates
- Genomic Sequences
- Genomic Segments (DNA Motif)
- SNPs
- SNPs (from Chips)
- ESTs
- ORFs
- SAGE Tags
- Metabolic Pathways BETA
- Compounds BETA
- Compound ID BETA
- Text (synonym, InChI, etc.) BETA
- Enzymes BETA
- Metabolic Pathway BETA
- Molecular Formula BETA
- Molecular Weight BETA
- Metabolite levels BETA

Identify Compounds based on Metabolite levels BETA

Experiment Effect of pH on metabolite levels (Lewis, Baska and Llinas)

Reference Samples

Comparison Samples

Fold change >=

Direction

Advanced Parameters

percoll pellet.

This requires running a metabolite levels search (20-fold enriched in saponin pellet compared to the percoll pellet as the reference).

- How many compounds did you get?
- How many of these compounds (metabolites) are NOT enriched by 20-fold in the pH7.4 saponin media fraction compared to the percoll media as reference?

My Strategies: **New** **Opened (5)** All (5) Basket Public Strategies (8) Help

(Compounds) Strategy: *fold change* *
 Rename Duplicate Save As Share Delete

fold change
12 Compounds
Step 1

Add Step

Run a new Search for
 Add contents of Basket
 Add existing Strategy
 Transform to Genes
 Transform to Pathways

Compounds

Compound ID **BETA**
 Text (synonym, InChI, etc.) **BETA**
 Enzymes **BETA**
 Metabolic Pathway **BETA**
 Molecular Formula **BETA**
 Molecular Weight **BETA**
 Metabolite levels **BETA**

Add Step 2 : Metabolite levels

Experiment Effect of pH on metabolite levels (Lewis, Baska and Linas)
 Reference Samples Percoll pH 7.4 pellet
 Comparison Samples Saponin pH 7.4 media
 Fold change >= 20
 Direction up-regulated

Advanced Parameters

Combine Compounds in Step 1 with Compounds in Step 2:

1 Intersect 2 1 Minus 2
 1 Union 2 2 Minus 1

Run Step

(Compounds)

fold change
2 Compounds

fold change
12 Compounds
Step 1

11 Compounds
Step 2

Add Step

To which metabolic pathways do these compounds belong? Click Add Step and transform the results to metabolic pathways.

Add Step

Run a new Search for
 Add contents of Basket
 Add existing Strategy
 Transform to Genes
 Transform to Pathways

Compounds

Compound ID **BETA**
 Text (synonym, InChI, etc.) **BETA**
 Enzymes **BETA**
 Metabolic Pathway **BETA**
 Molecular Formula **BETA**
 Molecular Weight **BETA**
 Metabolite levels **BETA**

Close

My Strategies: **New** **Opened (5)** All (5) Basket Public Strategies (8) Help

(Pathways) Strategy: *fold change* *
 Rename Duplicate Save As Share Delete

fold change
12 Compounds
Step 1

fold change
2 Compounds
Step 2

11 Compounds
Step 2

cpd->pthwy
15 Pathways
Step 3

Add Step

15 Metabolic Pathways from Step 3
 Strategy: *fold change* [Add 15 Metabolic Pathways to Basket](#) | [Download 15 Metabolic Pathways](#)

Metabolic Pathway Results

Advanced Paging [Add Columns](#)

| Pathway Id | Pathway | Source | No. of Compounds | Total Pathway Enzymes | Total Pathway Compounds | Map - Painted With Transformed Compounds (new window) |
|------------|---|---------|------------------|-----------------------|-------------------------|---|
| ec00230 | Purine metabolism | ec00230 | 2 | 174 | 100 | Pathway Map |
| ec00030 | Pentose phosphate pathway | ec00030 | 1 | 42 | 34 | Pathway Map |
| ec00052 | Galactose metabolism | ec00052 | 1 | 49 | 43 | Pathway Map |
| ec00053 | Ascorbate and aldarate metabolism | ec00053 | 1 | 55 | 45 | Pathway Map |
| ec00270 | Cysteine and methionine metabolism | ec00270 | 1 | 82 | 58 | Pathway Map |
| ec00290 | Valine, leucine and isoleucine biosynthesis | ec00290 | 1 | 31 | 27 | Pathway Map |