BioCyc

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- BioCyc is developed by the Bioinformatics Research Group at SRI International, directed by Dr. Peter Karp.

- Director, Bioinformatics Research Group
  Artificial Intelligence Center

- SRI International is an independent, nonprofit research institute conducting client-sponsored research and development for government agencies, commercial businesses, foundations, and other organizations. SRI also brings its innovations to the marketplace by licensing its intellectual property and creating new ventures.

- SRI is well known for its legacy of innovations in communications and networks, computing, economic development and science and technology policy, education, energy and the environment, engineering systems, pharmaceuticals and health sciences, homeland security and national defense, materials and structures, and robotics.

- 网络地址：

  http://biocyc.org/

- BioCyc version 14.5 contains 1004 genomes

News

BioCyc version 14.5 contains 1004 genomes. Read more.

Information

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ABOUT BIOCYC

BioCyc is a collection of 1004 Pathway/Genome Databases. Each database in the BioCyc collection describes the genome and metabolic pathways of a single organism.

New to BioCyc? Typical usage:

- Select a database (genome) to search by clicking "change" at top right
- Enter a gene name or pathway name in the box at top right and click Quick Search

Windows users: We strongly suggest you use Firefox instead of Internet Explorer [more].
To learn more about BioCyc, read the Introduction to BioCyc or watch our instructional videos.

BIOCYC TOOLS

The BioCyc Web site contains many tools for navigating and analyzing these databases, and for analyzing omics data, including the following.

- Genome browser
- Display of individual metabolic pathways, and of full metabolic maps
- Visual analysis of user-supplied omics datasets by painting onto metabolic map, regulatory map, and genome map
- Comparative analysis tools

The downloadable version of BioCyc that includes the Pathway Tools software provides more speed and power than the BioCyc Web site [more]. Multiple database configurations are available for installation with the software including multiple *E. coli* and *Shigella* genomes, multiple *Bacillus* genomes, multiple *Mycobacterium* genomes, and multiple mammalian genomes.

BIOCYC PATHWAY/GENOME DATABASES

The BioCyc databases are divided into three tiers, based on their quality.

BioCyc.org 14.5 Website

- EcoCyc
- MetaCyc
- HumanCyc
- BsubCyc

BioCyc Pathway/Genome Databases

- Tier 1: Intensively Curated Databases
- Tier 2: Computationally-Derived Databases Subject to Moderate Curation
- Tier 3: Computationally-Derived Databases Subject to No Curation

BioCyc Tier 1: Intensively Curated Databases

DATABASE	SCOPE	HIGHLIGHTS	ORGANIZATION
EcoCyc	*Escherichia coli* K-12 MG1655 Model-Organism Database	• Literature curation of complete genome • Information from 20,000 publications • Transcriptional regulatory network • Protein complexes • Enzyme and transporter functions • Gene Ontology assignments	SRI International
MetaCyc	Multiorganism Metabolic Pathway and Enzyme Database	• 1,583 metabolic pathways • Pathways elucidated from 2000 organisms • Extensive commentary • Information from 26,000 publications	SRI International
AraCyc	*Arabidopsis thaliana*	• 423 curated pathways • 1062 enzymes annotated with experimental evidence • Information from 2907 publications	S. Rhee, Department of Plant Biology, Carnegie Institution, USA
YeastCyc	*Saccharomyces cerevisiae*	• 143 curated pathways • Manually curated pathway summaries • Information from 350 publications	SGD Curators, Stanford U., USA

Tier 2 Databases

PGDBs in Tier 2 were generated by the PathoLogic program, which was used to predict their metabolic pathways, their operons (for bacteria only), and their pathway hole fillers (for many of the PGDBs). The resulting PGDBs underwent manual review by a person to remove false-positive pathway predictions that they could detect, and to perform other manual polishing steps such as defining protein complexes. The resulting PGDBs also underwent less than one year of literature-based curation, such as to enter metabolic pathways that had been experimentally elucidated in the organism but that were not inferred by PathoLogic. Most Tier 2 PGDBs have undergone 1-4 months of curation.

Many of the Tier 2 DBs are available for adoption [more] for curation and updating by interested scientists.

Click on the name of a database to navigate to the home page for that database for more information, such as the database authors, and statistics on the database content.

Database
Agrobacterium tumefaciens C58
Aurantimonas manganoxydans SI85-9A1
Bacillus anthracis Ames
Bacillus subtilis subtilis 168
Bos taurus
Caulobacter crescentus CB15
Chlamydomonas reinhardtii
Cryptosporidium hominis TU502
Cryptosporidium parvum Iowa
Drosophila melanogaster
Escherichia coli CFT073
Escherichia coli O157:H7 EDL933
Francisella tularensis tularensis SCHU S4
Helicobacter pylori 26695
Homo sapiens
Leishmania major Friedlin
Mus musculus
Mycobacterium tuberculosis CDC1551
Mycobacterium tuberculosis H37Rv
Penicillium chrysogenum Wisconsin 54-1255
Plasmodium berghei ANKA
Plasmodium chabaudi
Plasmodium falciparum 3D7
Plasmodium vivax SaI-1
Plasmodium yoelii yoelii 17XNL
Schistosoma mansoni
Shigella flexneri 2a str. 2457T
Streptomyces coelicolor A3(2)
Synechococcus elongatus PCC 7942(2)
Toxoplasma gondii ME49
Trypanosoma brucei
Vibrio cholerae O1 biovar El Tor str. N16961

Tier 3 Databases

The 968 PGDBs in Tier 3 were generated by the PathoLogic program, which was used to predict their metabolic pathways and their operons (for bacteria only). The pathway hole filler was not used for the current release because of its computational cost. The resulting PGDBs did not undergo manual review of the pathway predictions, nor subsequent literature curation. Therefore, the pathway predictions should be treated with due caution. PathoLogic is tuned to err on the side of over-predicting pathways to bring them to scientists' attention, rather than under-predicting pathways. PGDBs in Tier 3 were produced as a collaboration between the group of Peter D. Karp at SRI International and the group of Christos Ouzounis at the European Bioinformatics Institute.

The Tier 3 DBs are available for adoption [more] by interested scientists, to undergo curation and updating.

Click on the name of a database to navigate to the home page for that database for more information, such as the database authors, and statistics on the database content.

Database
Acaryochloris marina MBIC11017
Acholeplasma laidlawii PG-8A
Acidiphilium cryptum JF-5
Acidithiobacillus ferrooxidans ATCC 23270
Acidothermus cellulolyticus 11B
Acidovorax citrulli AAC00-1
Acidovorax sp. JS42
Acinetobacter sp. ADP1
Actinobacillus pleuropneumoniae L20
Actinobacillus pleuropneumoniae serovar 3 str. JL03
Actinomyces oris MG1
Aeromonas hydrophila dhakensis
Aeromonas salmonicida salmonicida A449

- 以MetaCyc为重点讲解

  6-phosphofructokinase

  Glycolysis

About MetaCyc

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METACYC OVERVIEW

MetaCyc is a database of nonredundant, experimentally elucidated metabolic pathways. MetaCyc contains more than 1500 pathways from more than 2000 different organisms [more], and is curated from the scientific experimental literature. [more]

MetaCyc contains pathways involved in both primary [def] and secondary [def] metabolism, as well as associated compounds, enzymes, and genes. [more]

Motivations

The goal of MetaCyc is to catalog the universe of metabolism by storing a representative sample of each experimentally elucidated pathway. [MetaCyc mission]

MetaCyc is used in a variety of scientific applications, such as providing a reference data set for computationally predicting the metabolic pathways of organisms from their sequenced genomes, supporting metabolic engineering, helping to compare biochemical networks, and serving as an encyclopedia of metabolism. [scientific applications]

Recent Publication

- The MetaCyc Database of metabolic pathways and enzymes and the BioCyc collection of Pathway/Genome Databases, *Nucleic Acids Research* 38:D473-D479 2010.

Search Results for fructose kinase
using database *MetaCyc* what is this?

Alternative searches:
- Full text search for **fructose kinase** on all pages in this database using Google

Proteins (5) | Gene Ontology Terms (3) | Reactions (2)

Proteins Gene/Gene Product pages contain: chromosomal location of gene; depiction of its operon; link to genome browser; detailed summaries and citations; subunit structure (for protein complexes); cofactors, activators, and inhibitors (for enzymes), depiction of regulon (for transcriptional regulators), protein features.

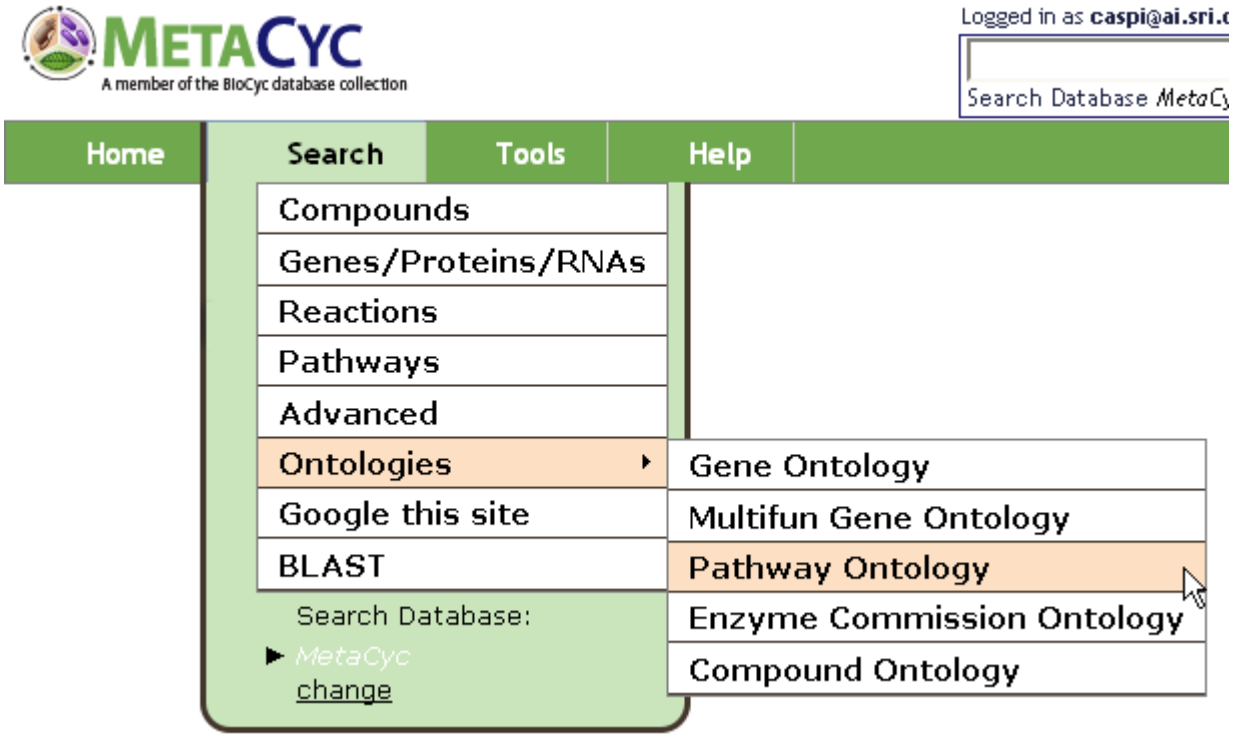
- 1-phosphofructokinase *(**fructose**-1-phosphate **kinase**) - Escherichia coli*
- 6-phosphofructokinase *(**fructose**-6-p-1-**kinase**) - Escherichia coli* (protein complex)
- 6-phosphofructokinase *(**fructose**-6-p-1-**kinase**) - Escherichia coli* (protein complex)
- **fructose kinase** - *Solanum lycopersicum*
- **fructose**lysine 6-**kinase** - *Escherichia coli*

Gene Ontology Terms GO term pages contain: Parent and child terms, and lists of matching gene products. Note that only those terms that have one or more associated genes in the selected organism (or that have children with one or more associated genes) are listed.

Molecular Function
- Class: GO:0003872 - 6-phosphofructokinase activity
- Class: GO:0008662 - 1-phosphofructokinase activity
- Class: GO:0008865 - fructokinase activity

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.

- ATP + fructose-1-phosphate -> ADP + fructose-1,6-bisphosphate + 2 H^+ *(**Fructose** 1-phosphate **kinase**)*
- D-fructose-6-phosphate + diphosphate = phosphate + fructose-1,6-bisphosphate + H^+ *(Diphosphate-dependent 6-phosphofructose-1-**kinase**)*


METACYC
A member of the BioCyc database collection
Logged in as caspi@ai.sri.
Search Database MetaCy
Home
Search
Tools
Help
Compounds
Genes/Proteins/RNAs
Reactions
Pathways
Advanced
Ontologies
Google this site
BLAST
Search Database:
MetaCyc
change
Gene Ontology
Multifun Gene Ontology
Pathway Ontology
Enzyme Commission Ontology
Compound Ontology

MetaCyc Pathways

How to Navigate: A class hierarchy (ontology) allows you to retrieve information according to categories of interest. In the class hierarchy that follows, each line names a single class of biological objects. The levels of indentation indicate a subclass relationship to the class above. The numbers in parentheses indicate the number of instances of that class. Clicking on a class will display a page containing its instances (the biological objects that are direct children of that class). A class page also lists the parent classes and child classes, allowing you to navigate up and down in the hierarchy.

Summary: This class is the root of a classification hierarchy for metabolic pathways. Its subclasses divide pathways into groups based on their biological functions, and based on the classes of metabolites that they produce and/or consume.

- Pathways
  - Biosynthesis (1023 instances)
  - Degradation/Utilization/Assimilation (717 instances)
  - Detoxification (24 instances)
  - Generation of precursor metabolites and energy (134 instances)
  - Signal transduction pathways (0 instances)
  - Superpathways (263 instances)
  - Transport (22 instances)
  - tRNA processing pathway

MetaCyc Pathways

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- Pathways
  - Biosynthesis (1023 instances)
  - Degradation/Utilization/Assimilation (717 instances)
  - Detoxification (24 instances)
  - Generation of precursor metabolites and energy (134 instances)
    - Chemoautotrophic Energy Metabolism (15 instances)
    - Electron Transfer (12 instances)
    - Fermentation (39 instances)
    - Glycolysis (6 instances)
    - Methanogenesis (12 instances)
    - Other (5 instances)
    - Pentose Phosphate Pathways (4 instances)
    - Photosynthesis (6 instances)
    - Respiration (27 instances)
    - TCA cycle (8 instances)

MetaCyc Pathways Class: Glycolysis

Parent Classes:

Generation of precursor metabolites and energy

Note: This class is a variant class, i.e. its purpose is to group together a set of variant pathways. Variant pathways are those that accomplish roughly the same biological function, such as degradation of a given starting material, or biosynthesis of an end product. The variant pathways may or may not share any common reactions.

Instances:

glycolysis I ,
glycolysis II ,
glycolysis III ,
glycolysis IV (plant cytosol) ,
glycolysis V (Pyrococcus) ,
superpathway of glycolysis, pyruvate dehydrogenase, TCA, and glyoxylate bypass

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MetaCyc Pathway: glycolysis I

More Detail Less Detail