

# パスウェイデータベースを使って ゲノムを理解する

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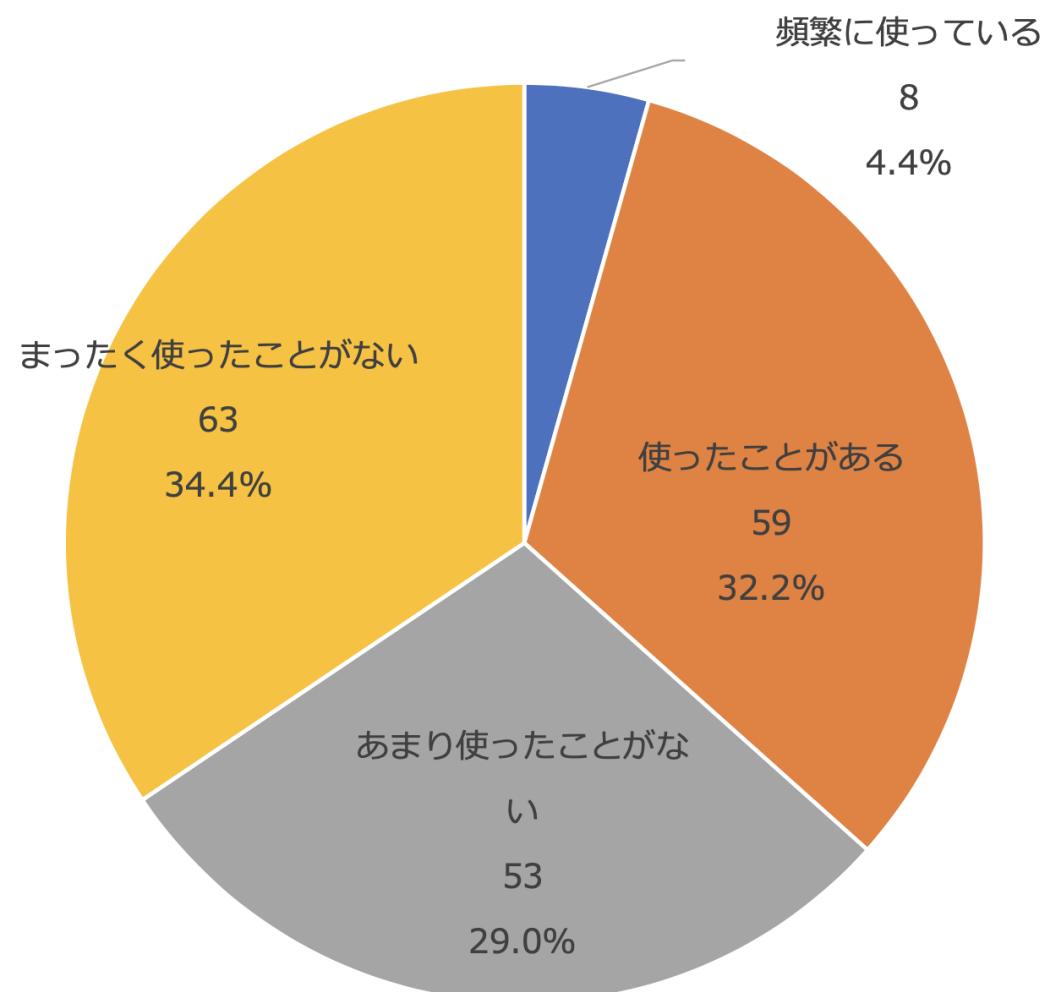
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オンライン

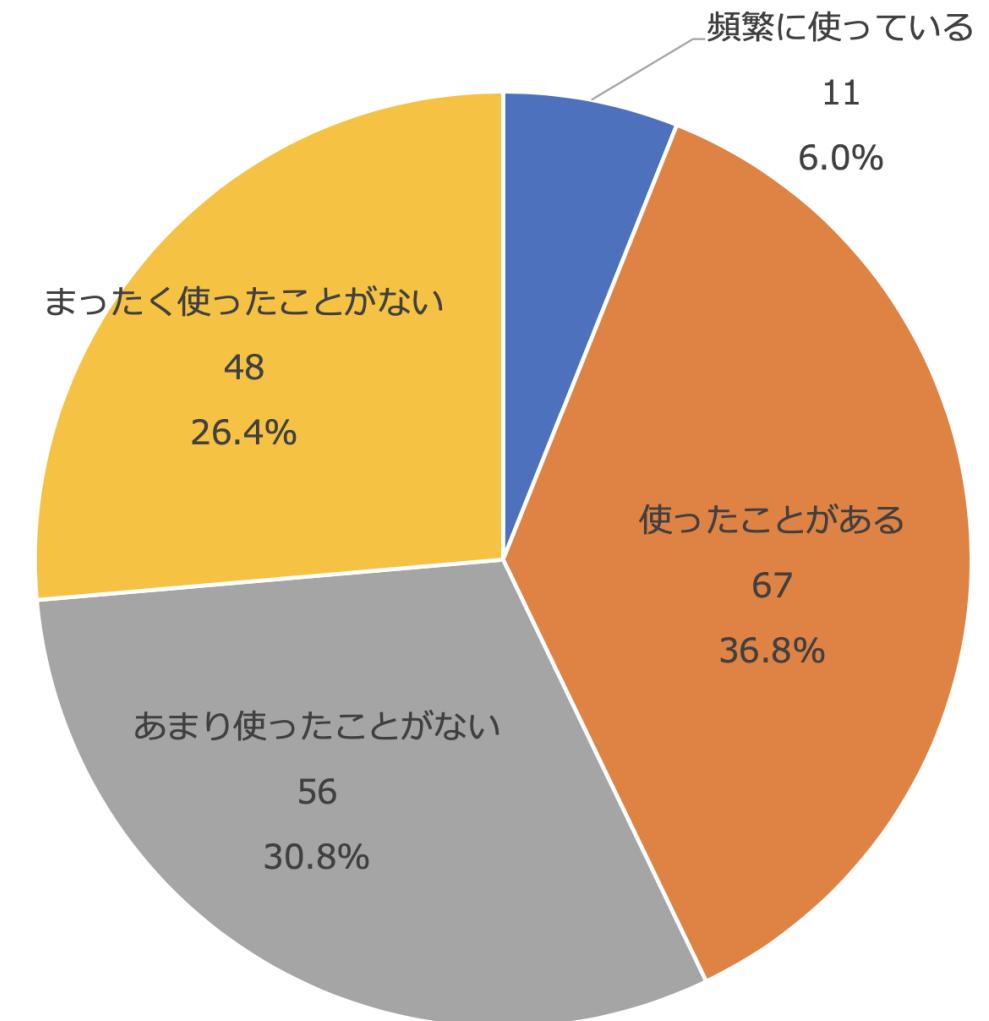
2022年8月25日

# 事前アンケート

【講義1-1】パスウェイデータベースを使ったことがありますか？

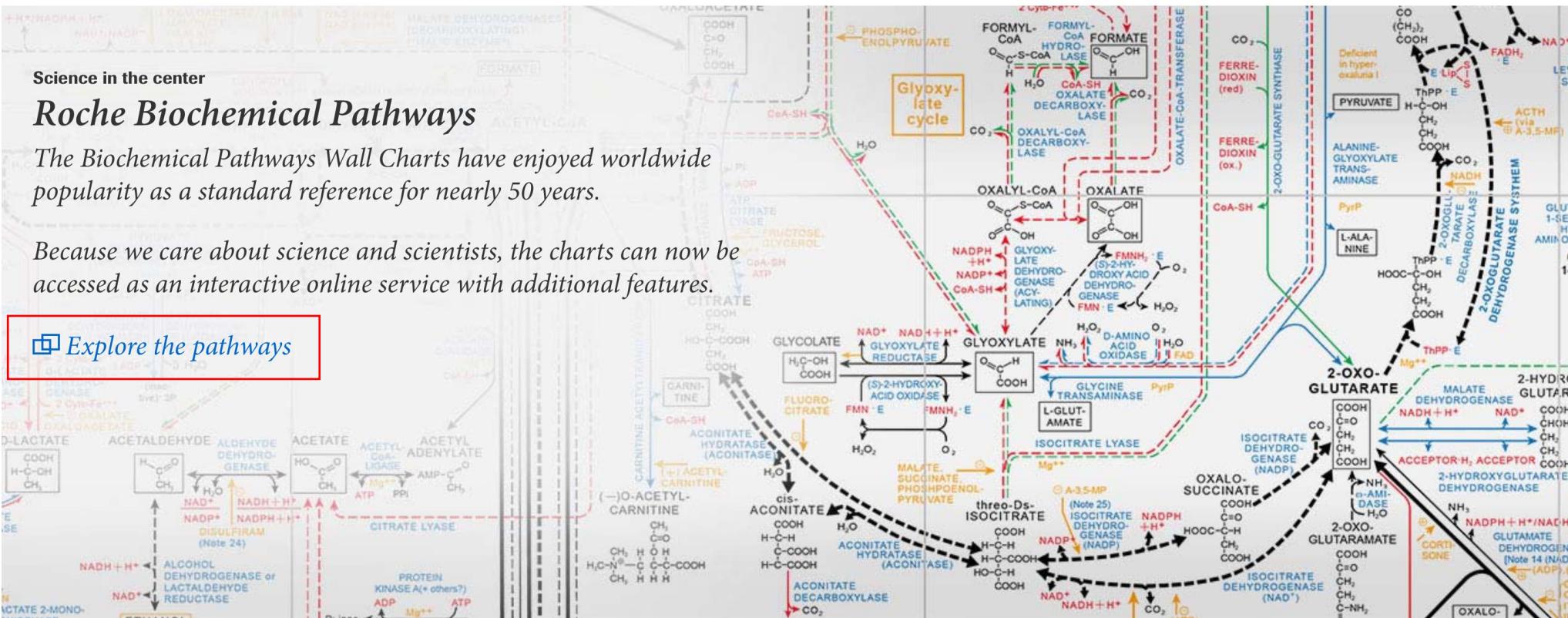


【講義1-2】KEGGデータベースを使ったことがありますか？



# パスウェイデータベースとは

- パスウェイとは、生体内での遺伝子やタンパク質、その他の化合物等の分子間相互作用を "経路" として表現したものです。相互作用の知識を集積して可視化、電子化したものがパスウェイデータベースと呼ばれています。歴史的には、代謝経路の表現から始まりました
  - ベーリングガーマンハイム社（現ロシュ社）の代謝マップ (1965~)
  - 最初は紙媒体での出版。のちに電子化されています
- 計算機上で表現することで、様々な可視化が行えるようになり、パスウェイ全体を俯瞰したり、一部の相互作用に注目したり、生命現象の理解が行い易くなります。また、データベース化することで網羅的に扱えるようになり、コンピューターでの利用が可能になります
  - ゲノムアノテーションや種間比較、進化解析
  - 遺伝子発現などのエンリッチメント解析
  - モデル化、シミュレーション、予測


 [Share](#)
 [Rate](#)

### Mapping the paths of life

Biochemical Pathways provide an overview of the chemical reactions of cells in various species and organs. Dr. Michal first compiled the Pathways Chart in 1965 and has been fine-tuning it ever since. Today, and with the collaboration of Roche, the two enormous posters can be found hanging in just about every research institute from Argentina to New Zealand.

“ You have to be someone with tenacity and patience. And love for science

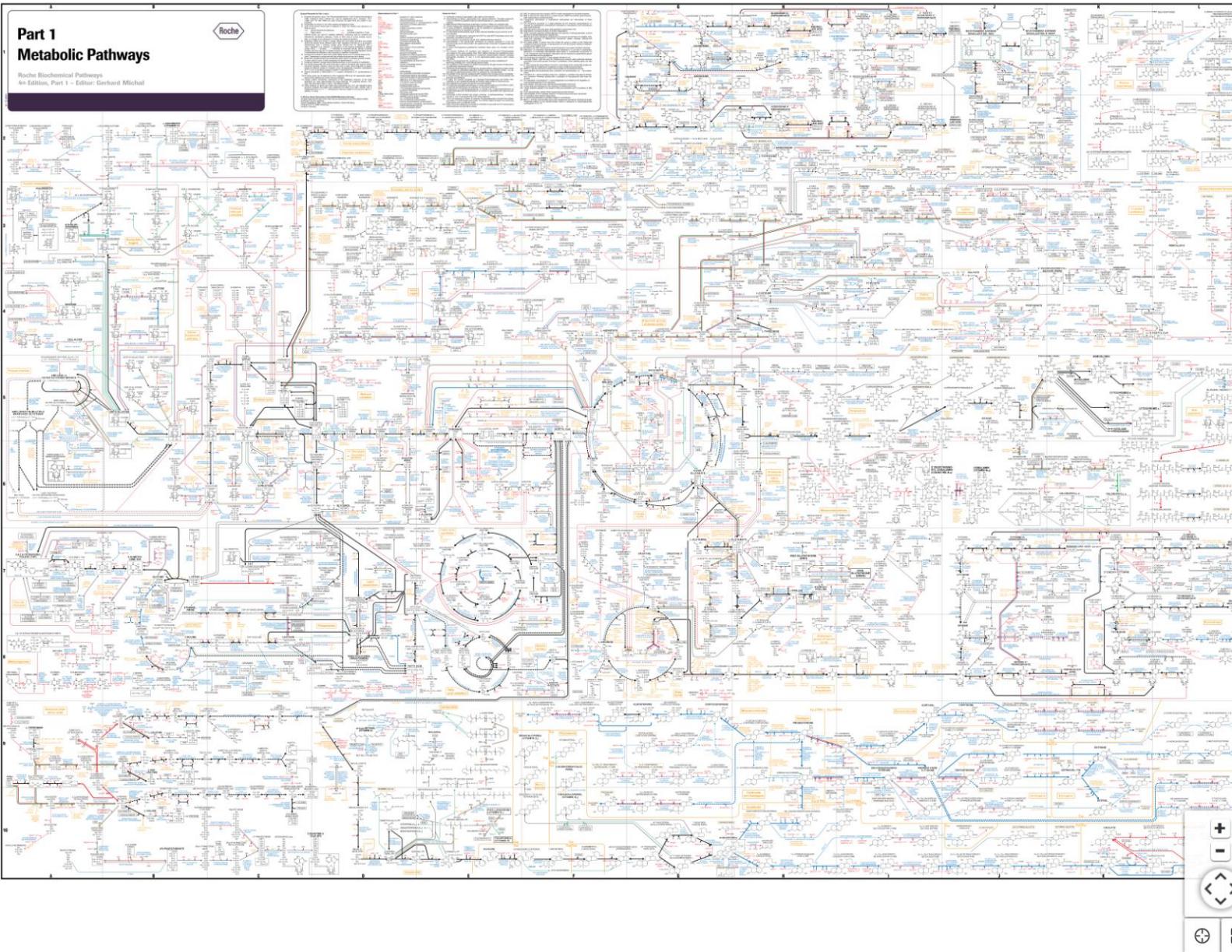
**Dr Gerhard Michal**  
Editor of the Roche Biochemical Pathways

検索 : Roche pathway

### By the numbers

**49 years**  
continuously fine-tuned by the editor himself.

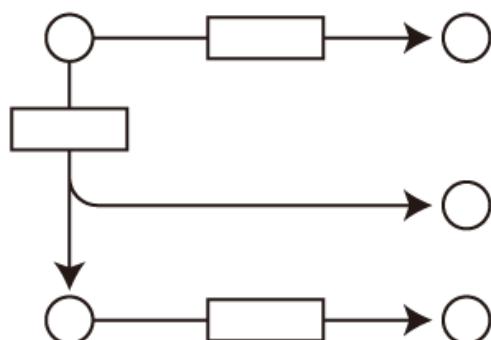
Click here to open the menu



# パスウェイデータベースでの表現

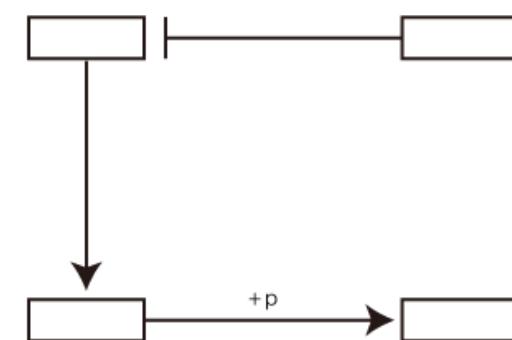
- 見やすくするために、ダイアグラムで表現されていることが多いっています。
- KEGG Pathway での表現例
  - 代謝パスウェイでは代謝産物をノード、酵素反応をエッジとして表現されています
  - 制御系ではタンパク質や遺伝子、その他の小分子をノード、その関係性（活性化、抑制、リン酸化など）がエッジとして表現されています

代謝系



代謝産物(○)と酵素(□)の関係

制御系



タンパク質や遺伝子(□)間の関係

# パスウェイデータベースのデータ形式

- 計算機での取り扱いを目的として XML (Extensible Markup Language) で記述されていることが多くなっています。
  - [KGML](#) (KEGG Markup Language) は分子間の関係とダイアグラムのレイアウトを取り扱うための KEGG 独自のフォーマット
  - [SBML](#) (Systems Biology Markup Language)、[CellML](#)、[CSML](#) (Cell System Markup Language) はパスウェイのシミュレーションやモデリングを行うためのフォーマット
  - [PSI-MI](#) (Proteomics Standards Initiative Molecular Interaction XML Format) はタンパク質間相互作用を記述するためのフォーマット
  - [BioPAX](#) (Biological Pathways Exchange) は様々なパスウェイデータを統合したり、データ交換を行うことを目的として策定された標準化を目指したフォーマット
- これらのデータ形式を扱うことのできるネットワーク可視化ソフトウェアには [Cytoscape](#) や [VisANT](#) などがあります。
  - [AJACS58 : Cytoscapeを使ったデータの可視化](#)
- どのパスウェイデータベースを研究に使えば良いかは、対象生物や対象パスウェイ、目的によって異なってきます。
- 今回は 主にKEGG PATHWAY のブラウザ上での使い方を紹介します。

# BioCyc

- ウェブサイト：<https://biocyc.org/>
- 開発：SRIインターナショナル  
(Stanford Research Institute)
- 対象：大腸菌からヒトまで、異株を含めて 18,000 種以上
  - 専門家が手作業で作成した文献ベースのデータ + 自動解析ツール
  - 代謝パスウェイ、制御系
- 利用：アカデミックフリー
- データ形式：BioPAX

LOGIN | Why Login? | Create New Account

Enter a gene, protein, metabolite or pathway... Quick Search | Gene Search

Searching Escherichia coli K-12 substr. MG1655 (EcoCyc) change organism database

**BIOCYC Database Collection**

Sites | Search | Genome | Metabolism | Analysis | SmartTables | Help |

**BioCyc Database Collection**

Subscriptions are now required to access BioCyc. For more information on obtaining a subscription, click here. Why the transition to subscriptions? You do not need to purchase a subscription if your institution's name is displayed on the top right corner of this page or appears here.

BioCyc is a collection of 10980 Pathway/Genome Databases (PGDBs), plus software tools for understanding their data.

**Getting Started**

New to BioCyc? Typical usage is:

- Select one or more databases (genomes) to search. To do so, click "change organism database" in the box in the top right of every page. By default, BioCyc searches *Escherichia coli* K-12 substr. MG1655.
- Search for a gene or pathway using the Quick Search, or see the Search menu for more options.

New User Guide >>

**Tools**

BioCyc provides tools for navigating, visualizing, and analyzing the underlying databases, and for analyzing omics data:

- Genome browser
- Display of individual metabolic pathways, and of full metabolic maps
- Multiple analysis methods for user-supplied omics and multi-omics datasets including painting onto metabolic maps, regulatory maps, and genome maps
- Store groups of genes and pathways in your account as SmartTables; share, analyze, transform those groups
- Comparative analysis tools

**RouteSearch**

RouteSearch: Search for Paths through the Metabolic Network

Search for lowest-cost paths through the metabolic network of the selected organism. Or, design lowest-cost pathways to novel compounds by adding reactions from MetaCyc.

Learn More

1 2 3 4 5 6 7 8 9 10

**BioCyc Databases**

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

Tier 1 databases have received at least one person-year of literature-based curation, and are the most accurate. EcoCyc and MetaCyc have each received more than 20 person-years of curation.

Tier 2 and Tier 3 databases contain computationally predicted metabolic pathways, predictions as to which genes code for missing enzymes in metabolic pathways, and predicted operons.

**Funding Sources**

The development of BioCyc is funded by NIH grant GM080746 from the NIH National Institute of General Medical Sciences.

## Metabolism -> Cellular Overview

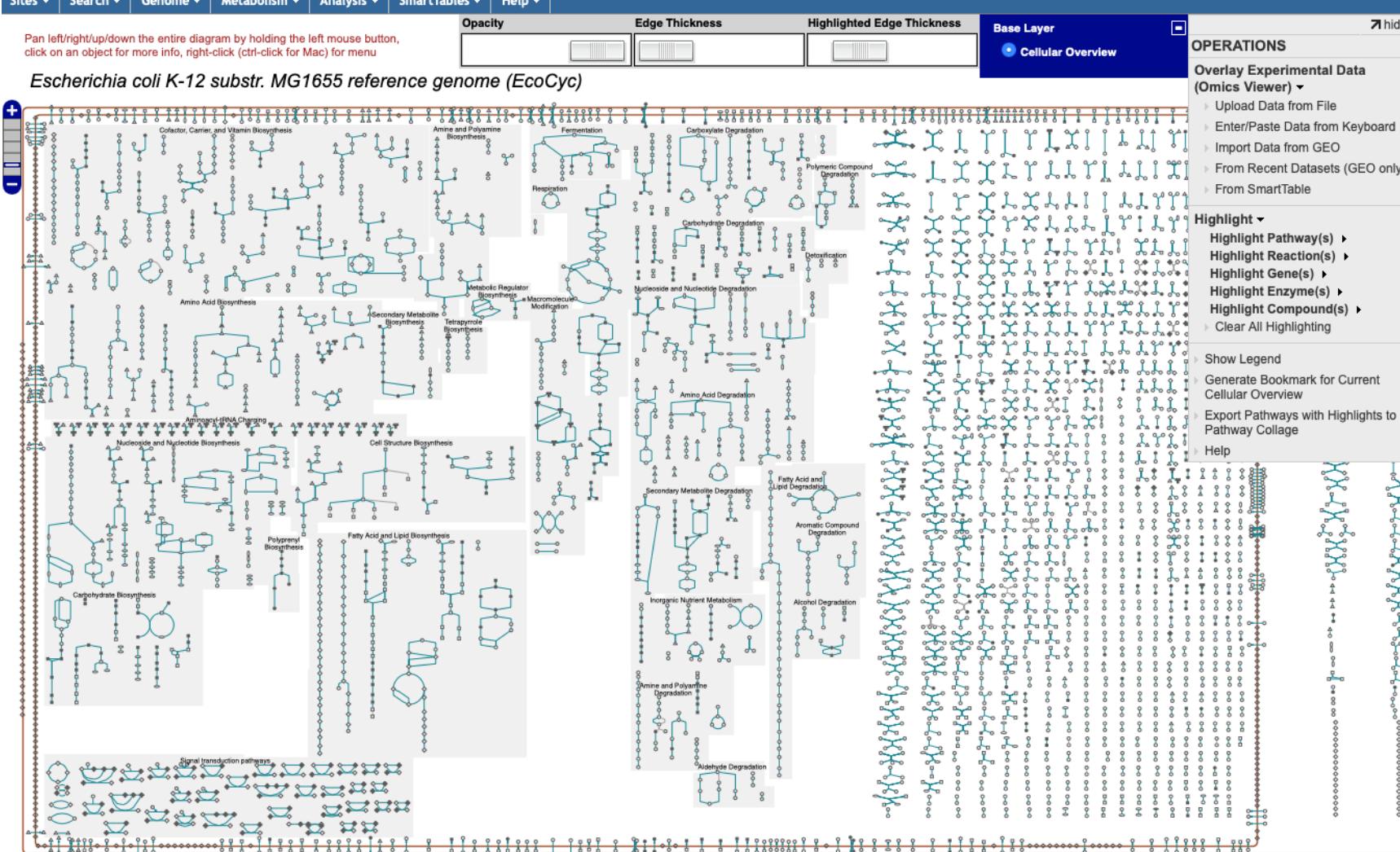


Sites ▾ | Search ▾ | Genome ▾ | Metabolism ▾ | Analysis ▾ | SmartTables ▾ | Help ▾

Pan left/right/up/down the entire diagram by holding the left mouse button, click on an object for more info, right-click (ctrl-click for Mac) for menu

*Escherichia coli K-12 substr. MG1655 reference genome (EcoCyc)*

LOGIN | Why Login? | Create New Account  
Enter a gene, protein, metabolite or pathway... Quick Search Gene Search  
Searching *Escherichia coli K-12 substr. MG1655 reference genome (EcoCyc)* change organism database



# Reactome

- ウェブサイト：<https://www.reactome.org/>
- 開発：EMBLE-EBI 他
- 対象：ヒトを中心に脊椎動物、酵母、植物、16種
  - ヒト：専門家が手作業で作成した文献ベースのデータ
  - その他：計算機での推定（<https://reactome.org/documentation/inferred-events>）
  - 代謝パスウェイ、シグナル伝達系、他
- 利用：フリー
- データ形式：BioPAX, SBML

The image shows two screenshots of the Reactome website. The top screenshot is the homepage, featuring the Reactome logo, a search bar, and four main navigation icons: Pathway Browser (highlighted with a red border), Analyze Data, ReactomeFiViz, and Documentation. Below these are brief descriptions and small icons. The bottom screenshot is a news or project section titled 'USE REACTOME GRAPH DATABASE IN YOUR PROJECT' with a 'LEARN MORE' button. It includes sections for 'Why Reactome', 'Tweets' from the @reactome account, 'EMBL Job Opportunities' for a Software Engineer position, and 'Latest News' about version 63.

# Reactome

## Pathway Browser

The screenshot shows the Reactome Pathway Browser interface. At the top, there is a navigation bar with the Reactome logo, version 9.7, and a search bar for "Homo sapiens". Below the search bar are buttons for Citation, Analysis, Tour, and Layout. On the left, a sidebar titled "Event Hierarchy" lists various biological processes. The main area displays a complex network of pathways, with "Metabolism" at the center, branching into glycolysis, gluconeogenesis, and the citric acid cycle. Other major branches include "Signal Transduction", "DNA Replication", "Cell Cycle", and "Programmed Cell Death". A legend at the bottom explains the icons used in the pathway map.

Event Hierarchy:

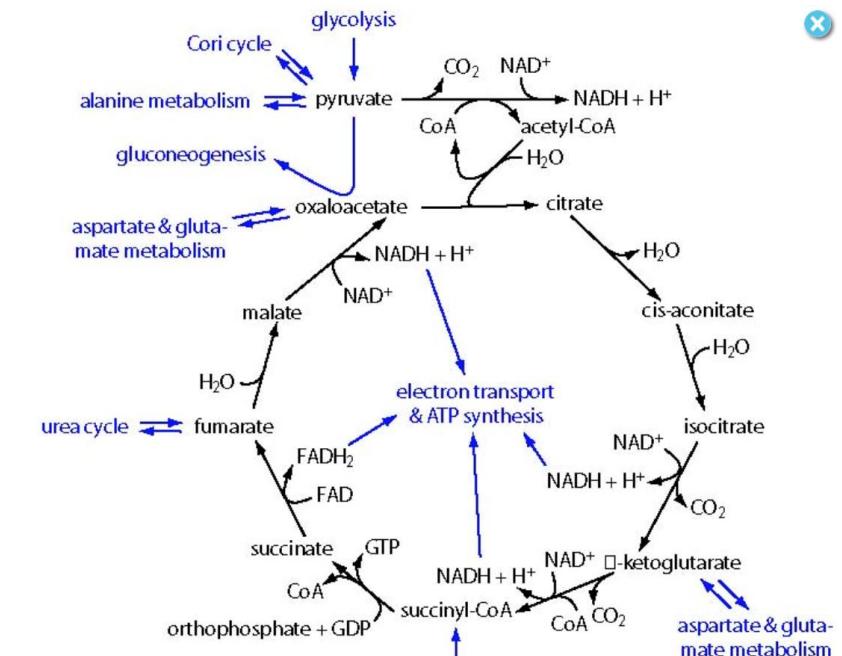
- Autophagy
- Cell Cycle
- Cell-Cell communication
- Cellular responses to external stimuli
- Chromatin organization
- Circadian Clock
- Developmental Biology
- Digestion and absorption
- Disease
- DNA Repair
- DNA Replication
- Extracellular matrix organization
- Gene expression (Transcription)
- Hemostasis
- Immune System
- Metabolism
- Metabolism of proteins
- Metabolism of RNA
- Muscle contraction
- Neuronal System
- Organelle biogenesis and maintenance
- Programmed Cell Death
- Protein localization
- Reproduction
- Signal Transduction
- Transport of small molecules
- Vesicle-mediated transport

Pathways for: Homo sapiens

Search for a term, e.g. pten ...

Description Molecules Structures Expression Analysis Downloads

Displays details when you select an item in the Pathway Browser. For example, when a reaction is selected, shows details including the input and output molecules, summary and references containing supporting evidence. When relevant, shows details of the catalyst, regulators, preceding and following events.



# KEGG PATHWAY

- ウェブサイト：<https://www.kegg.jp/>
- 開発：京都大学
- 対象：ゲノムの決まった全生物種（異株を含む）約8,000種（>780真核生物、>7,100真正細菌、>390古細菌）、ウイルス 359ゲノム、環境メタゲノム 477サンプル、生体メタゲノム 712サンプル
  - 専門家が手作業で作成した文献ベースのデータ + 自動ツール
    - リファレンスパスウェイ：専門家が手作業で文献ベースから作成
    - 生物種パスウェイ
      - 自動ツールでリファレンスパスウェイから作成し、手作業でキュレーション
      - 自動ツールで作成（自動ツールにも段階があります）
  - 代謝パスウェイ、シグナル伝達系、他
- 利用：アカデミックフリー
- データ形式：KGML
  - [KCPAVS KEGG-XML converter](#) などで代謝パスウェイ、シグナル伝達などの多くのパスウェイを標準形式に変換可能
  - [KEGGscape] (<http://apps.cytoscape.org/apps/keggscape>) でネットワーク可視化ソフト Cytoscape に読み込み可能

# KEGGはデータベースの集合

- KEGG2をクリック
- KEGG PATHWAY を含むシステム情報データベースの他に、遺伝情報、化学情報、健康情報などのデータベースがリンクしています。

KEGG Home  
Release notes  
Current statistics  
Plea from KEGG

KEGG Database  
KEGG overview  
Searching KEGG  
KEGG mapping  
Color codes

KEGG Objects  
Pathway maps  
Brite hierarchies  
KEGG DB links

KEGG Software  
Keg Tools  
KEGG API  
KGML

KEGG FTP  
Subscription

GenomeNet

**KEGG: Kyoto Encyclopedia of Genes and Genomes**

KEGG is a database resource for understanding high-level functions and utilities of the biological system, such as the cell, the organism and the ecosystem, from molecular-level information, especially large-scale molecular datasets generated by genome sequencing and other high-throughput experimental technologies. See [Release notes](#) (January 1, 2018) for new and updated features.

**Announcement:** KEGG NETWORK released

**Main entry point to the KEGG web service**

**KEGG2** KEGG Table of Contents [Update notes | Release history]

**Data-oriented entry points**

<b>KEGG PATHWAY</b>	KEGG pathway maps
<b>KEGG BRITE</b>	BRITE hierarchies and tables
<b>KEGG MODULE</b>	KEGG modules
<b>KEGG ORTHOLOGY</b>	KO functional orthologs [Annotation]
<b>KEGG GENOME</b>	Genomes [Pathogen   Virus   Plant]
<b>KEGG GENES</b>	Genes and proteins [SeqData]
<b>KEGG COMPOUND</b>	Small molecules
<b>KEGG GLYCAN</b>	Glycans

**Classification**

Pathway
Brite
Brite table
Module
KO (Function)
Organism
Compound
Network
Disease (ICD)

Menu PATHWAY BRITE MODULE KO GENES LIGAND NETWORK DISEASE DRUG DBGET

Search KEGG for Go

**Data-oriented entry points**

Category	Entry Point	Content	DBGET Search
Systems information	<b>KEGG PATHWAY</b> <b>KEGG BRITE</b> <b>KEGG MODULE</b>	KEGG pathway maps BRITE hierarchies and tables KEGG modules	PATHWAY BRITE MODULE
Genomic information	<b>KO (KEGG Orthology)</b>	Functional orthologs	ORTHOLOGY
	<b>KEGG GENOME</b> <b>KEGG GENES</b> <b>KEGG SSDB</b>	KEGG organisms (complete genomes) Genes and proteins GENES sequence similarity	GENOME GENES
Chemical information	<b>KEGG COMPOUND</b> <b>KEGG GLYCAN</b> <b>KEGG REACTION</b> <b>KEGG ENZYME</b>	Small molecules Glycans Reactions and reaction classes Enzyme nomenclature	COMPOUND GLYCAN REACTION ENZYME
Health information	<b>KEGG NETWORK</b> <i>New!</i> <b>KEGG DISEASE</b> <b>KEGG DRUG</b> <b>KEGG ENVIRON</b> <b>KEGG MEDICUS</b>	Disease-related network elements Human diseases Drugs and drug groups Health related substances Japanese drug labels (JAPIC) FDA drug labels (DailyMed)	NETWORK VARIANT DISEASE DRUG DGROUP ENVIRON

KEGG is developed by Kansai Biosciences. See [Kanehisa et al. \(2017\)](#) for updates of KEGG

# 対象生物種を見る

- データベースのテーブルの下、KEGG organisms をクリック

## Subject-oriented entry points

<a href="#">KEGG Cancer</a>	Cancer research
<a href="#">KEGG Pathogen</a>	Pathogen genomes and antimicrobial resistance
<a href="#">KEGG Virus</a>	Virus research
<a href="#">KEGG Plant</a>	Plant research
<a href="#">KEGG Annotation</a>	KO annotation of genes and proteins
<a href="#">KEGG SeqData</a>	KEGG sequence data collection
<a href="#">KEGG RModule</a>	Architecture of metabolic networks

## Organism-specific entry points

### [KEGG organisms](#)

the list of currently available organisms

Select     (examples) hsa mmu sce eco bsu syn

Organism group		Pangenome		Genome
Eukaryotes	Animals Plants Fungi Protists	Genus level pangenomes	Species level pangenomes	KEGG organisms
Prokaryotes	Bacteria Archaea			

See [KEGG GENOME](#) for more details.

# KEGG Organisms

- KEGG では 3-4 文字の独自の生物種コードを使用している

## Eukaryotes

Category	Organisms	Source
	hsa Homo sapiens (human)	RefSeq
	ptr Pan troglodytes (chimpanzee)	RefSeq
	pps Pan paniscus (bonobo)	RefSeq
	ggo Gorilla gorilla gorilla (western lowland gorilla)	RefSeq
	pon Pongo abelii (Sumatran orangutan)	RefSeq
	nle Nomascus leucogenys (northern white-cheeked gibbon)	RefSeq
	mcc Macaca mulatta (rhesus monkey)	RefSeq
	mcf Macaca fascicularis (crab-eating macaque)	RefSeq
	csab Chlorocebus sabaeus (green monkey)	RefSeq
	rro Rhinopithecus roxellana (golden snub-nosed monkey)	RefSeq
	rbb Rhinopithecus bieti (black snub-nosed monkey)	RefSeq
	cjc Callithrix jacchus (white-tufted-ear marmoset)	RefSeq
	sbq Saimiri boliviensis boliviensis (Bolivian squirrel monkey)	RefSeq
	mmu Mus musculus (mouse)	RefSeq
	rno Rattus norvegicus (rat)	RefSeq
	cge Cricetulus griseus (Chinese hamster)	RefSeq
	ngi Nannospalax galili (Upper Galilee mountains blind mole rat)	RefSeq
	hgl Heterocephalus glaber (naked mole rat)	RefSeq
	ccan Castor canadensis (American beaver)	RefSeq
	ocu Oryctolagus cuniculus (rabbit)	RefSeq
	tup Tupaia chinensis (Chinese tree shrew)	RefSeq

# KEGG Organisms

- 生物種コードのリンクをクリックすると、種の情報が表示されます

**KEGG Homo sapiens (human)**

Genome info	Pathway map	Brite hierarchy	Module	Genome map	Blast	Taxonomy
Search genes: <input type="text"/> Go Clear						
<b>Genome information</b>						
<b>T number</b>	T01001					
<b>Org code</b>	hsa					
<b>Aliases</b>	HUMAN, 9606					
<b>Full name</b>	Homo sapiens (human)					
<b>Definition</b>	Homo sapiens (human)					
<b>Category</b>	Reference genome					
<b>Annotation</b>	yes					
<b>Taxonomy</b>	TAX: 9606					
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo					
<b>Data source</b>	RefSeq (Assembly: GCF_000001405.39) BioProject: 168					
<b>Original DB</b>	NCBI, OMIM, HGNC, HPRD, Ensembl, Vega, Pharos					
<b>Statistics</b>	Number of protein genes: 19768 Number of RNA genes: 2641					
<b>Created</b>	2000					
<b>Reference</b>	PMID: 11237011					
<b>Authors</b>	Lander ES, Linton LM, Birren B, Nusbaum C, Zody MC, Baldwin J, Devon K, Dewar K, Doyle M, FitzHugh W, et al.					
<b>Title</b>	Initial sequencing and analysis of the human genome.					
<b>Journal</b>	Nature 409:860-921 (2001) DOI: 10.1038/35057062					

# データベースリスト

- Genomes : 主に NCBI Refseq、GenBank に登録された生物種
- Species : 異株を一つにまとめたデータベース
- Genus : Genus レベルでまとめたデータベース
- Virus : ウイルスゲノム
- Meta : メタゲノム



## KEGG Organisms: Complete Genomes

Eukaryotes: 782 Bacteria: 7141 Archaea: 395

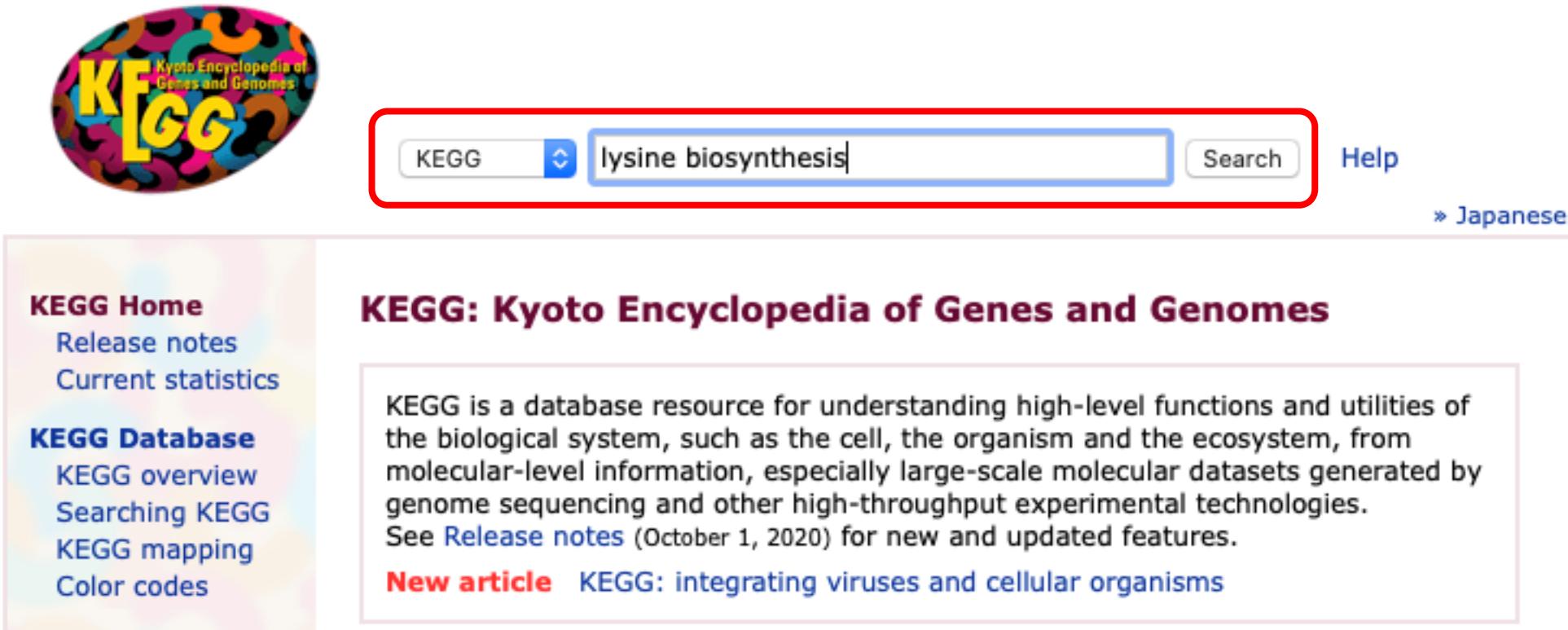
[ Genomes | Species | Genus | Viruses | Meta ]

### Eukaryotes

Category	Organisms			Source
	hsa	KGB	Homo sapiens (human)	RefSeq
	ptr	KGB	Pan troglodytes (chimpanzee)	RefSeq
	pps	KGB	Pan paniscus (bonobo)	RefSeq
	gor	KGB	Gorilla gorilla gorilla (western lowland gorilla)	RefSeq

# KEGGパスウェイマップを見る

- トップページ (<https://www.kegg.jp>) 上方の検索ボックスで "lysine biosynthesis" や "glycolysis" やなどの生命現象関連の単語を入力し、Search ボタンをクリック



The screenshot shows the KEGG homepage. On the left, there is a sidebar with links to "KEGG Home", "Release notes", "Current statistics", "KEGG Database", "KEGG overview", "Searching KEGG", "KEGG mapping", and "Color codes". The main content area features the KEGG logo at the top left. To its right is a search bar with the text "lysine biosynthesis" entered. A red rectangle highlights this search term. To the right of the search bar are "Search" and "Help" buttons, and a link to "» Japanese". Below the search bar, the text "KEGG: Kyoto Encyclopedia of Genes and Genomes" is displayed in large, bold, maroon letters. A pink-bordered box contains a paragraph about KEGG's purpose and a link to "Release notes". At the bottom of this box, the text "New article KEGG: integrating viruses and cellular organisms" is shown in red.

lysine biosynthesis

KEGG

lysine biosynthesis

Search

Help

» Japanese

KEGG Home

Release notes

Current statistics

KEGG Database

KEGG overview

Searching KEGG

KEGG mapping

Color codes

KEGG: Kyoto Encyclopedia of Genes and Genomes

KEGG is a database resource for understanding high-level functions and utilities of the biological system, such as the cell, the organism and the ecosystem, from molecular-level information, especially large-scale molecular datasets generated by genome sequencing and other high-throughput experimental technologies. See [Release notes](#) (October 1, 2020) for new and updated features.

New article KEGG: integrating viruses and cellular organisms

# KEGGパスウェイマップ

- KEGG データベース全体でヒットしたエントリーが全てリストアップされ、KEGG PATHWAY にヒットがあれば、一番上に表示されます。

 Search KEGG for lysine biosynthesis Go Clear

Database: KEGG - Search term: lysine biosynthesis

**KEGG PATHWAY**

map00300  
Lysine biosynthesis

map01064  
Biosynthesis of alkaloids derived from ornithine, lysine and nicotinic acid

**KEGG MODULE**

M00016  
Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine

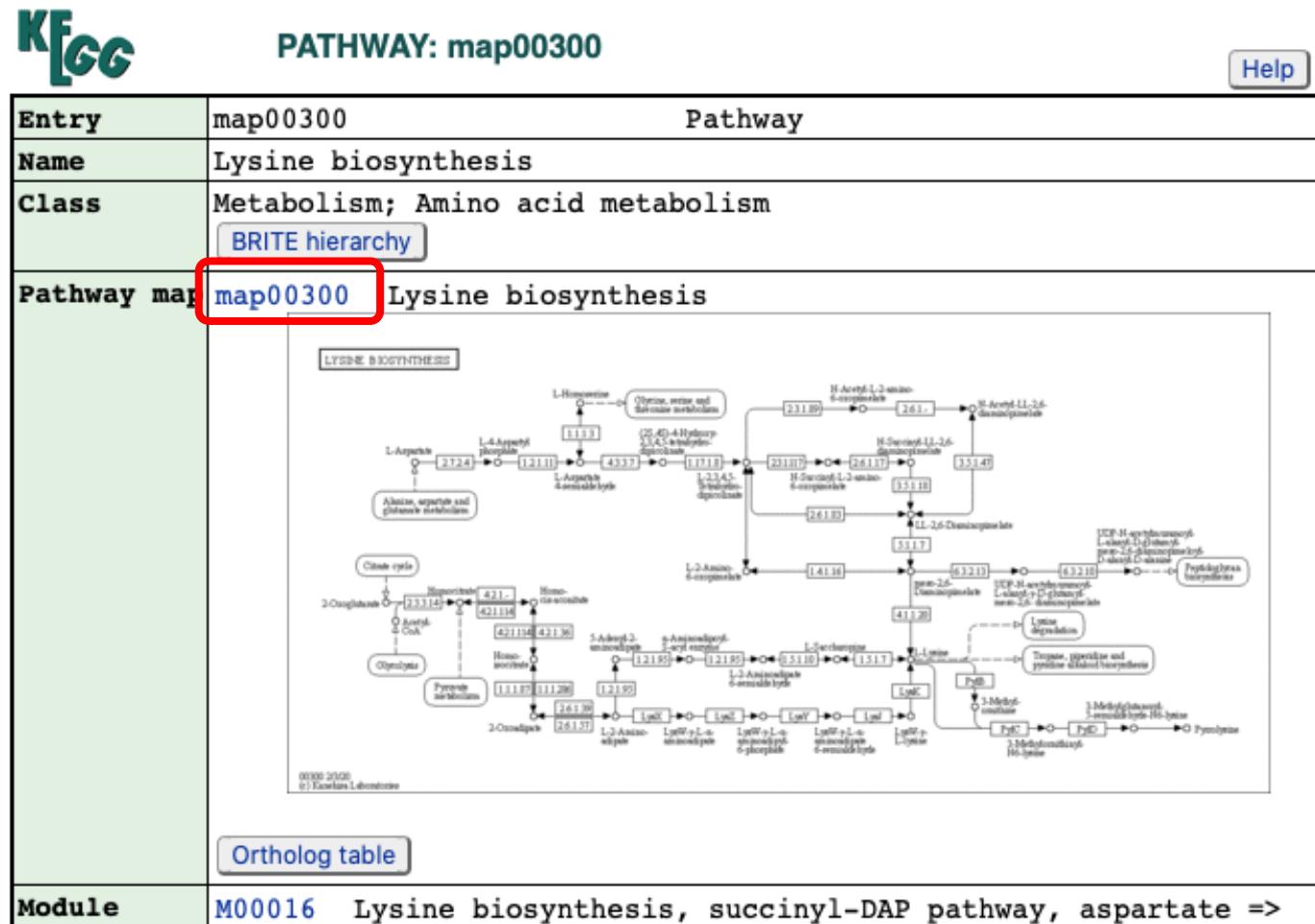
M00030  
Lysine biosynthesis, AAA pathway, 2-oxoglutarate => 2-aminoadipate => lysine

M00031  
Lysine biosynthesis, mediated by LysW, 2-aminoadipate => lysine

M00433  
Lysine biosynthesis, 2-oxoglutarate => 2-oxoadipate

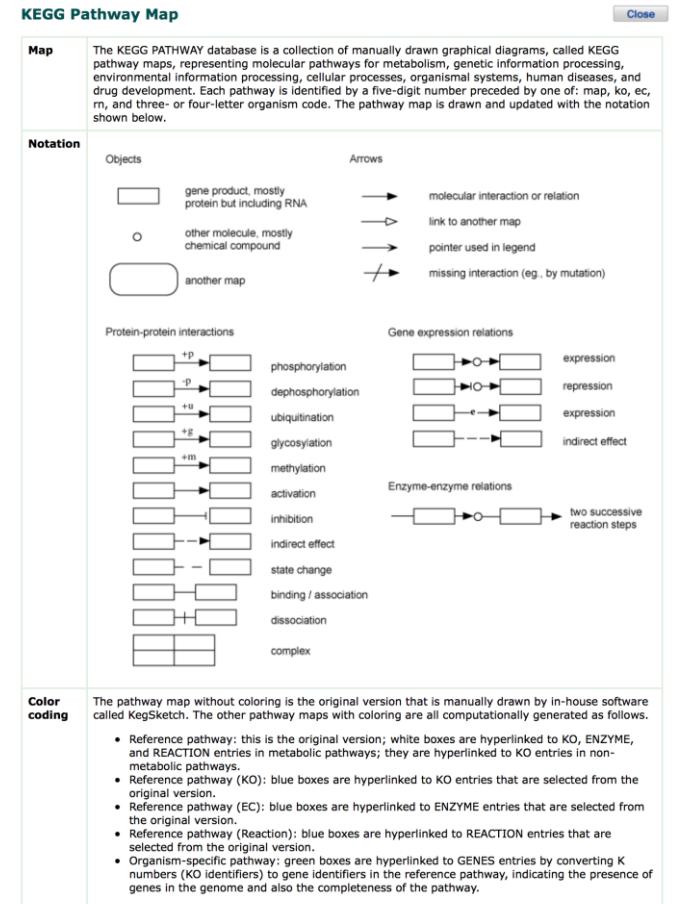
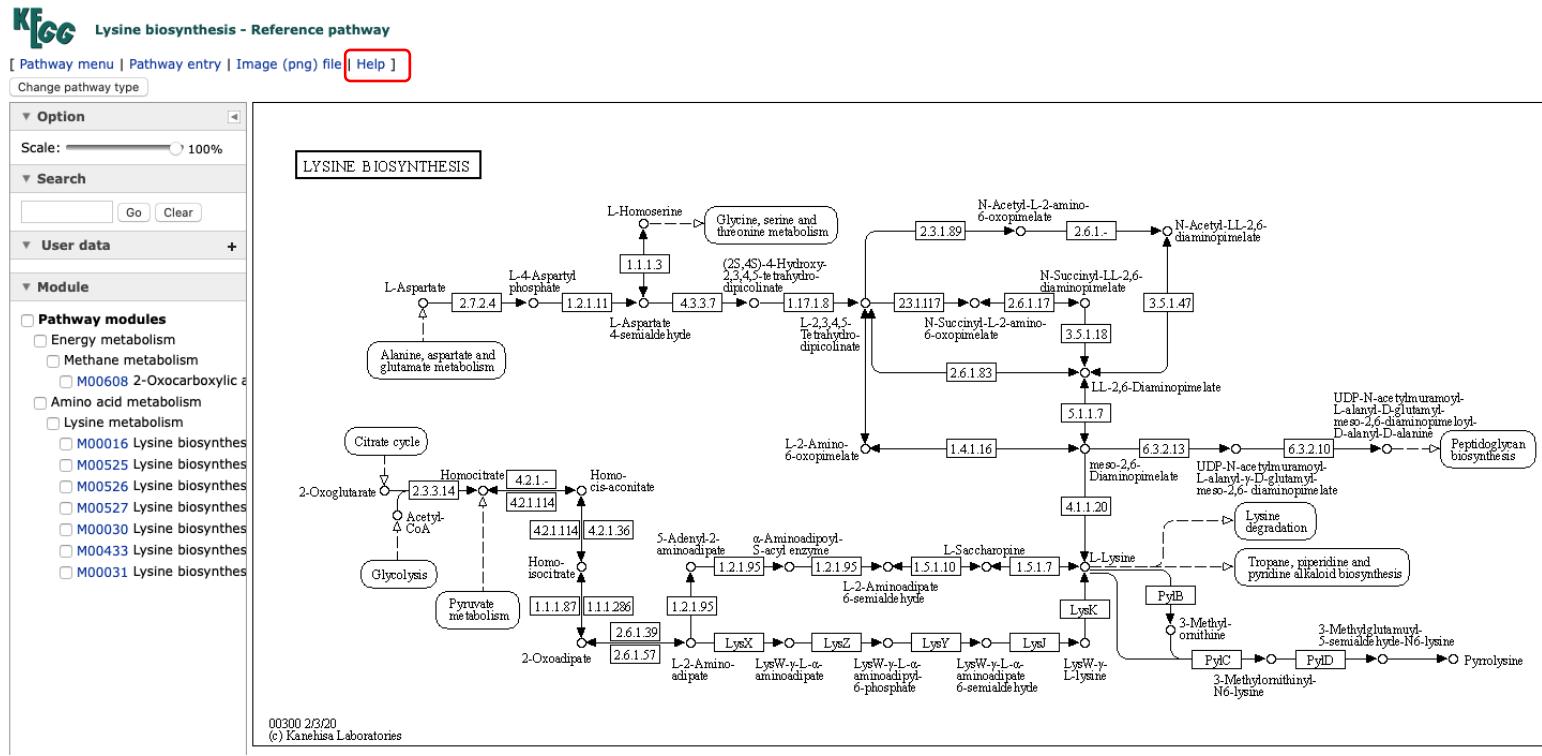
# KEGGパスウェイマップ

- 各パスウェイの情報が表示されます。
  - KEGGにおけるパスウェイの最小単位で、ダイアグラム画像を“マップ”と呼んでいます。



# KEGGパスウェイマップ

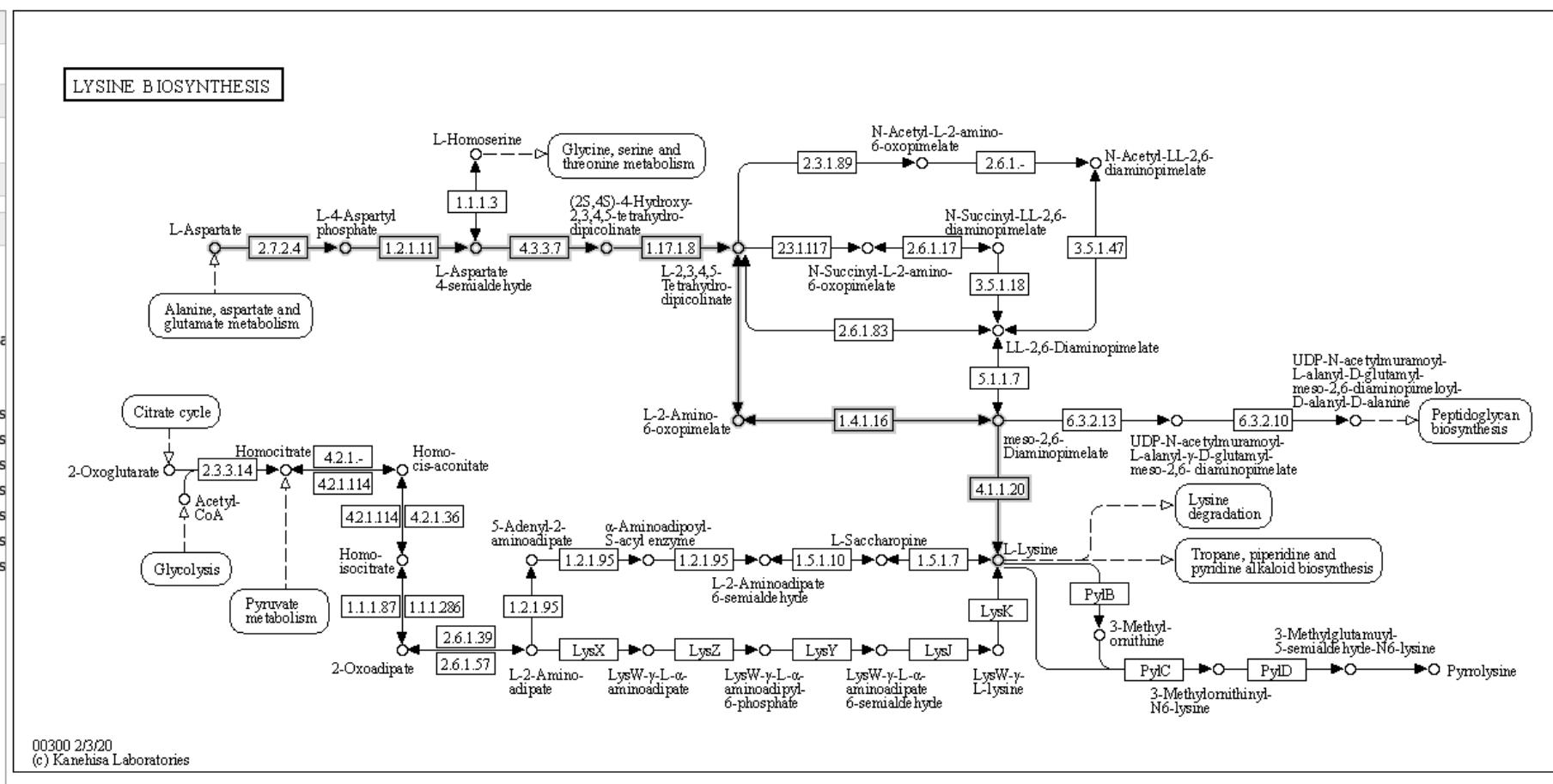
- この色のついていない白いダイアグラムが、専門家が手作業で文献ベースから作成したリファレンスパスウェイになります
  - ボックスが遺伝子やタンパク質などの配列情報、丸が代謝産物、環境物質などの化合物
  - 各図形の説明は右上の Help から見られます



# KEGGパスウェイマップ

**KEGG** Lysine biosynthesis - Reference pathway  
[ Pathway menu | Pathway entry | Image (png) file | Help ]  
Change pathway type

▼ Option  
Scale: 100%  
▼ Search  
Go Clear  
▼ User data +  
▼ Module  
 Pathway modules  
 Energy metabolism  
 Methane metabolism  
 M00608 2-Oxocarboxylic acid metabolism  
 Amino acid metabolism  
 Lysine metabolism  
 M00016 Lysine biosyntheses  
 M00525 Lysine biosyntheses  
 M00526 Lysine biosyntheses  
 M00527 Lysine biosyntheses  
 M00030 Lysine biosyntheses  
 M00433 Lysine biosyntheses  
 M00031 Lysine biosyntheses



# KEGG MODULE



## Lysine biosynthesis, DAP aminotransferase pathway, aspartate => lysine

[ [Module menu](#) | [Module entry](#) | [KO/Compound list](#) | [Help](#) ]

[Change module type](#)

Entry M00527

Name Lysine biosynthesis, DAP aminotransferase pathway, aspartate => lysine

Definition ([K00928](#),[K12524](#),[K12525](#),[K12526](#)) [K00133](#) [K01714](#) [K00215](#) [K10206](#) [K01778](#) ([K01586](#),[K12526](#))

[Ortholog table](#)

[Taxonomy](#)

[Module table](#)

Type Pathway module

Pathway [map00300](#) [map01230](#) [map01100](#) [map01110](#)

Reaction [R00480](#) [C00049](#) -> [C03082](#)

[R02291](#) [C03082](#) -> [C00441](#)

[R10147](#) [C00441](#) -> [C20258](#)

[R04198](#),[R04199](#) [C20258](#) -> [C03972](#)

[R07613](#) [C03972](#) -> [C00666](#)

[R02735](#) [C00666](#) -> [C00680](#)

[R00451](#) [C00680](#) -> [C00047](#)

[K00928](#) [K12524](#) [K12525](#) [K12526](#)

|

[K00133](#)

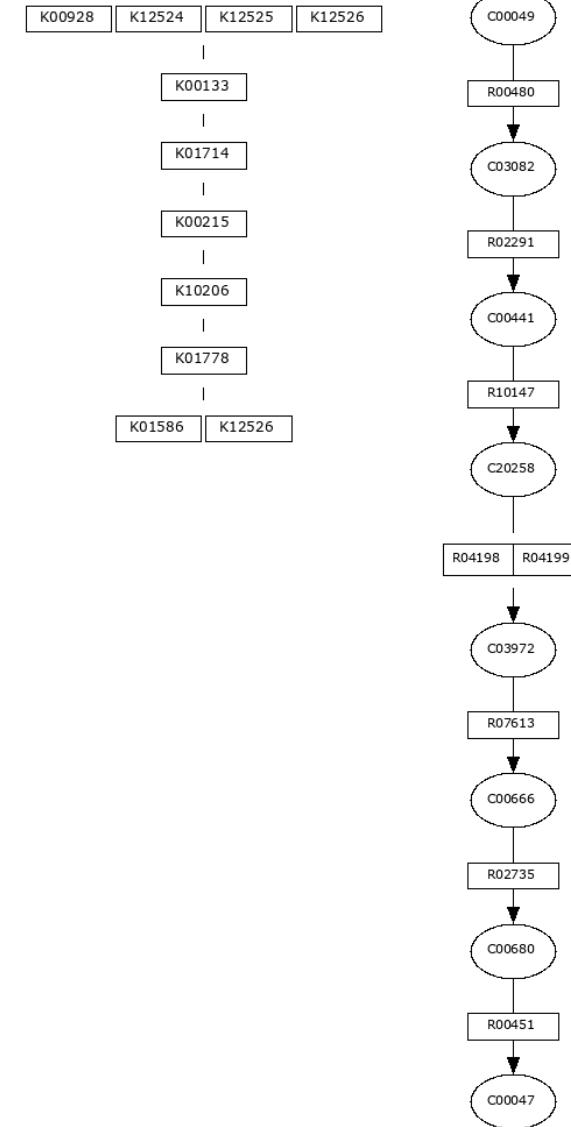
|

[K01714](#)

C00049

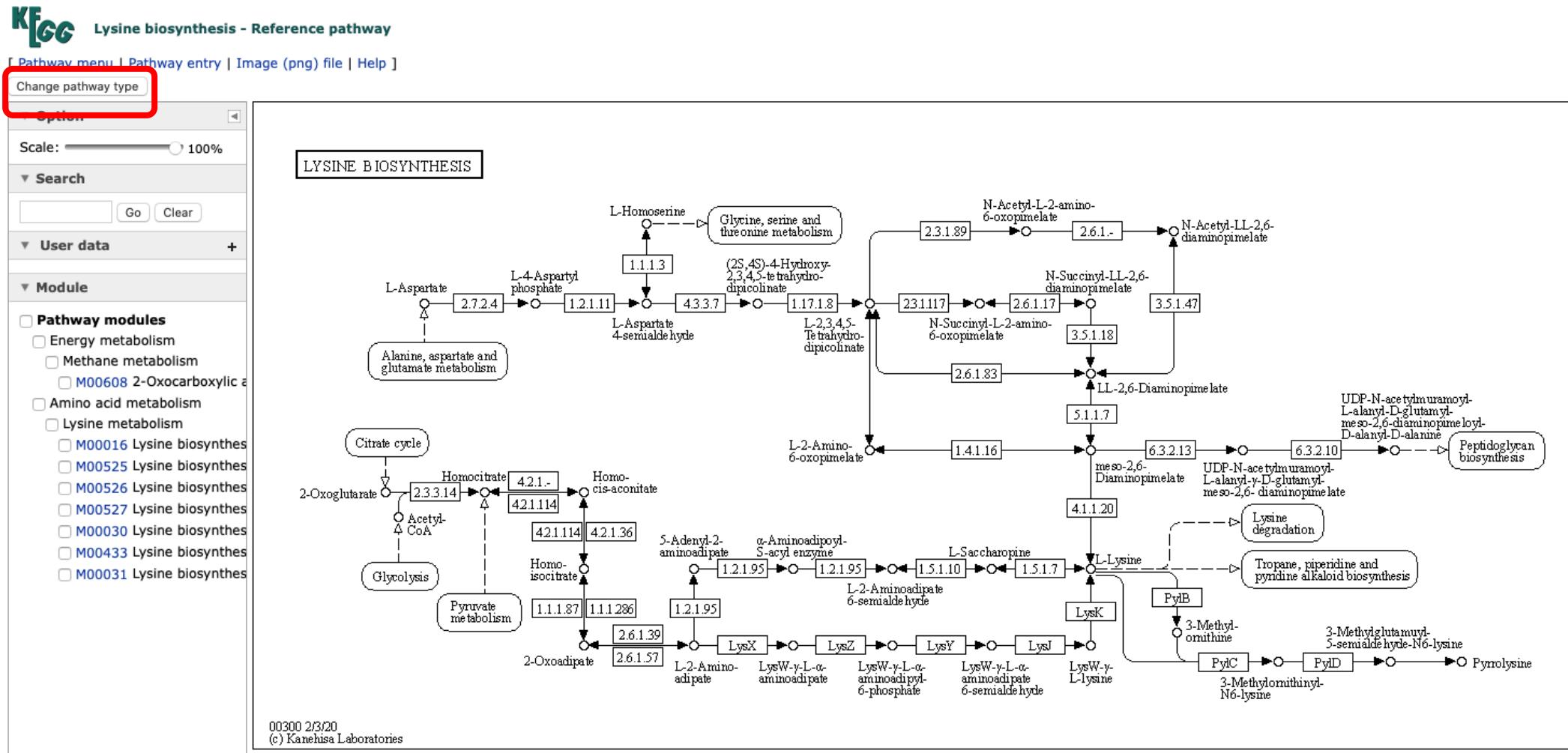
R00480

C03082



# 好きな生物のパスウェイを見る

- Change pathway type をクリック



# 好きな生物のパスウェイを見る

Select pathway type for 00300

▼ ▼ ▼ ▼

▼ Reference

map Reference pathway  
ko Reference pathway (KO only)  
ec Reference pathway (EC only)  
rn Reference pathway (Reaction only)

▼ Organism specific

▼ Animals		
▼ Mammals		
chx	Capra hircus (goat)	2/39
pcad	Physeter catodon (sperm whale)	2/39
▼ Lancelets		
bfo	Branchiostoma floridae (Florida lancelet)	2/39
▼ Insects		
mpha	Monomorium pharaonis (pharaoh ant)	2/39
fcd	Folsomia candida	2/39
▼ Crustaceans		
dpx	Daphnia pulex (common water flea)	2/39
pvm	Penaeus vannamei (Pacific white shrimp)	3/39
▼ Mollusks		
lgi	Lottia gigantea (owl limpet)	2/39
pcan	Pomacea canaliculata (golden apple snail)	3/39
crg	Crassostrea gigas (Pacific oyster)	2/39
myi	Mizuhopecten yessoensis (Yesso scallop)	2/39
▼ Brachiopods		
lak	Lingula anatina	2/39
▼ Cnidarians		
nve	Nematostella vectensis (starlet sea anemone)	2/39
spis	Stylophora pistillata	2/39
▼ Plants		
▼ Eudicots		
ath	Arabidopsis thaliana (thale cress)	8/39
aly	Arabidopsis lyrata (lyrate rockcress)	8/39
crb	Capsella rubella	8/39
csat	Camelina sativa (false flax)	8/39
eus	Eutrema salsugineum	8/39
brp	Brassica rapa (field mustard)	8/39
bna	Brassica napus (rape)	8/39
boe	Brassica oleracea (wild cabbage)	8/39
rsz	Raphanus sativus (radish)	8/39
thj	Tarenaya hassleriana (spider flower)	8/39
cpap	Carica papaya (papaya)	8/39
cit	Citrus sinensis (Valencia orange)	8/39
cic	Citrus clementina (mandarin orange)	8/39
tsc	Theobroma cacao (cacao)	8/39

Select pathway typeのパネルがポップアップ

見たい生物種の名前で検索（例えば、Escherichia coli）  
ecoをクリック

ngr	Naegleria gruberi	2/39
▼ Bacteria		
▼ Gammaproteobacteria - Enterobacteri		
eco	Escherichia coli K-12 MG1655	12/39
ecj	Escherichia coli K-12 W3110	12/39
ecd	Escherichia coli K-12 DH10B	12/39
ebw	Escherichia coli K-12 BW2952	12/39
ecok	Escherichia coli K-12 MDS42	12/39
ece	Escherichia coli O157:H7 EDL933 (EHEC)	12/39
ecs	Escherichia coli O157:H7 Sakai (EHEC)	12/39
ecf	Escherichia coli O157:H7 EC4115 (EHEC)	12/39
etw	Escherichia coli O157:H7 TW14359 (EHEC)	12/39
elx	Escherichia coli O157:H7 Xuzhou21 (EHEC)	12/39
eo1	Escherichia coli O111:H- 11128 (EHEC)	12/39
eoj	Escherichia coli O26:H11 11368 (EHEC)	12/39
eoh	Escherichia coli O103:H2 12009 (EHEC)	12/39
ecoo	Escherichia coli O145:H28 RM13514 (EHEC)	12/39
ecoh	Escherichia coli O145:H28 RM13516 (EHEC)	12/39
esl	Escherichia coli O104:H4 2011C-3493 (EAEC)	12/39
eso	Escherichia coli O104:H4 2009EL-2071 (EAEC)	12/39
esm	Escherichia coli O104:H4 2009EL-2050 (EAEC)	12/39
eck	Escherichia coli 55989 (EAEC)	12/39
ecg	Escherichia coli O127:H6 E2348/69 (EPEC)	12/39
eok	Escherichia coli O55:H7 CB9615 (EPEC)	12/39
elr	Escherichia coli O55:H7 RM12579 (EPEC)	12/39
elh	Escherichia coli O78:H11:K80 H10407 (ETEC)	12/39

# Escherichia coli K-12 MG1655ゲノムでマッピング

KEGG Lysine biosynthesis - Escherichia coli K-12 MG1655

[ Pathway menu | Pathway entry | Download KGML | Image (png) file | Help ]

Change pathway type

▼ Option  
Scale: 100%

▼ Search  
Go Clear

▼ User data +  
Complete only

Pathway modules

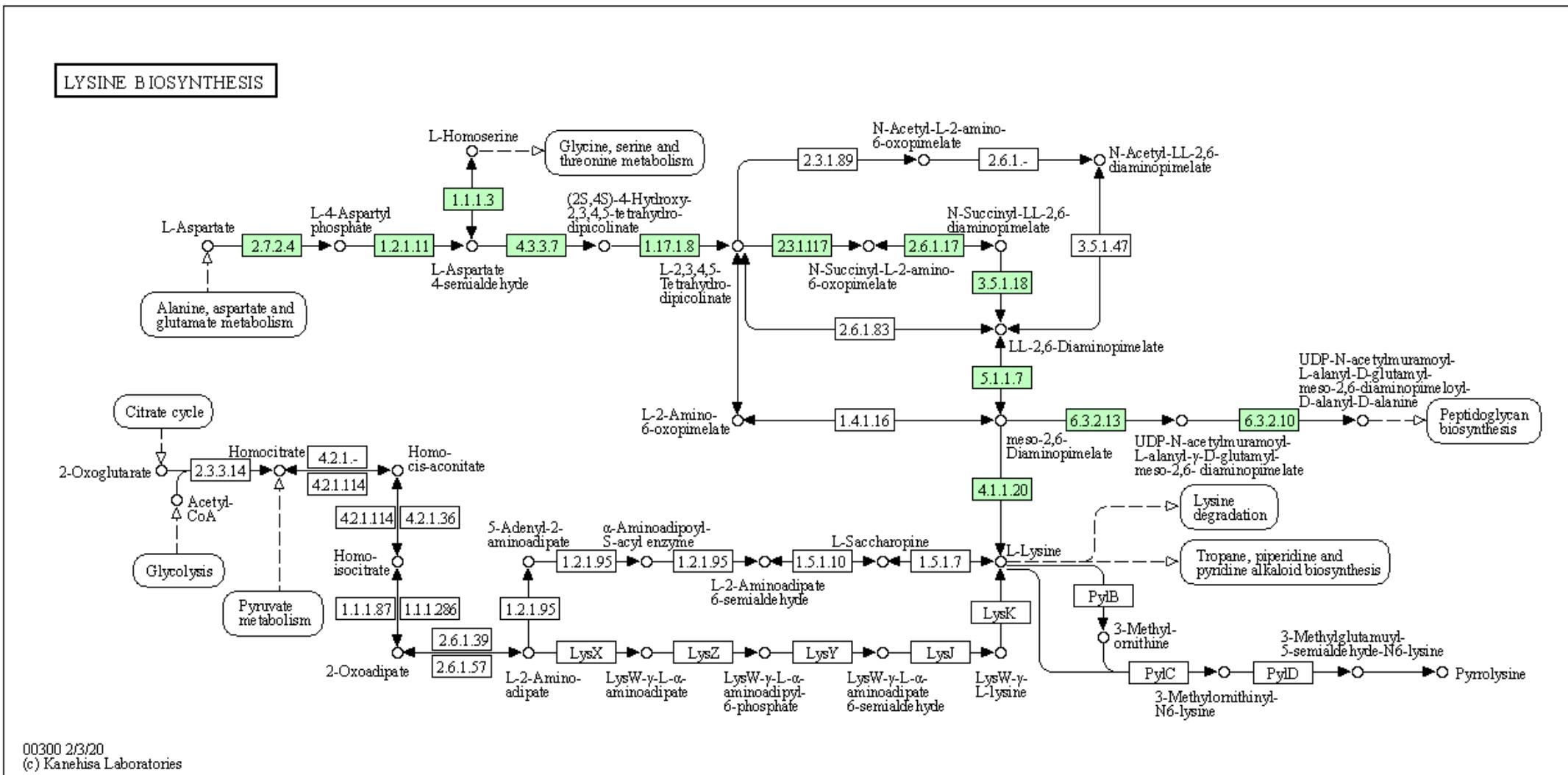
Energy metabolism

Methane metabolism

Amino acid metabolism

Lysine metabolism

M00016 Lysine biosynthes



# 別のアプローチ

- 種、属でまとめたパスウェイ、ドラフトゲノム、メタゲノムの  
パスウェイはここからは選べないので、生物種リストのページ  
から、種のページ、パスウェイリストへ移動する必要があります。

KEGG Escherichia coli K-12 MG1655

Genome info Pathway map Brite hierarchy Module Genome map Blast Taxonomy

Search genes:  Go Clear

Prokaryotes

Category	Organism
	eco Escherichia coli K-12 MG1655
	ecj Escherichia coli K-12 W3110
	ecd Escherichia coli K-12 DH10B
	ebw Escherichia coli BW2952
	ecok Escherichia coli K-12 MDS42
	ece Escherichia coli O157:H7 EDL933 (EHEC)
	ecs Escherichia coli O157:H7 Sakai (EHEC)
	ecf Escherichia coli O157:H7 EC4115 (EHEC)
	etw Escherichia coli O157:H7 TW14359 (EHEC)
	elx Escherichia coli O157:H7 Xuzhou21 (EHEC)
	ej Escherichia coli O26:H11 11368 (EHEC)
	eoi Escherichia coli O111:H- 11128 (EHEC)

The 'Pathway map' tab is highlighted with a red box.

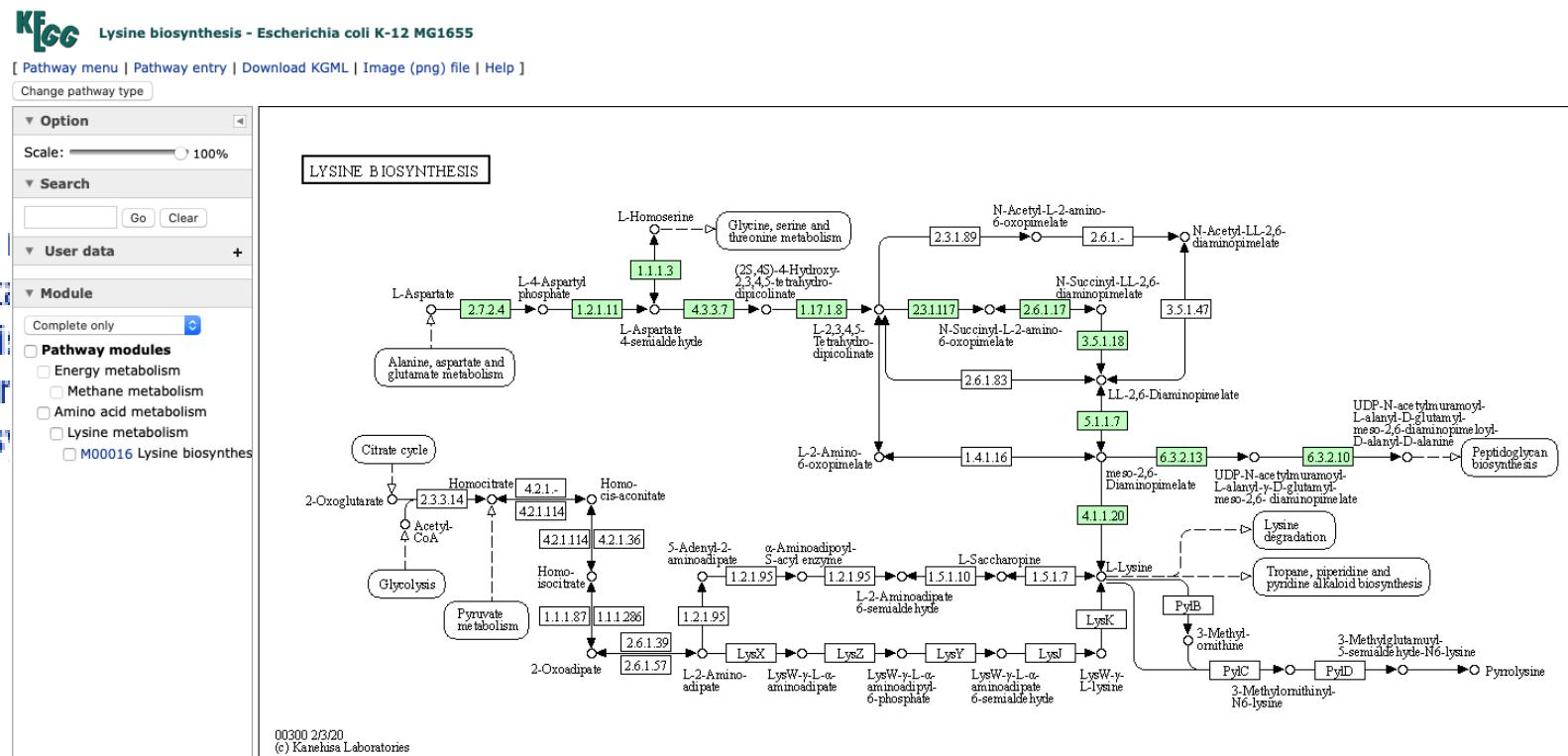
[https://www.kegg.jp/kegg/catalog/org\\_list.html](https://www.kegg.jp/kegg/catalog/org_list.html)

# Lysine biosynthesis マップ

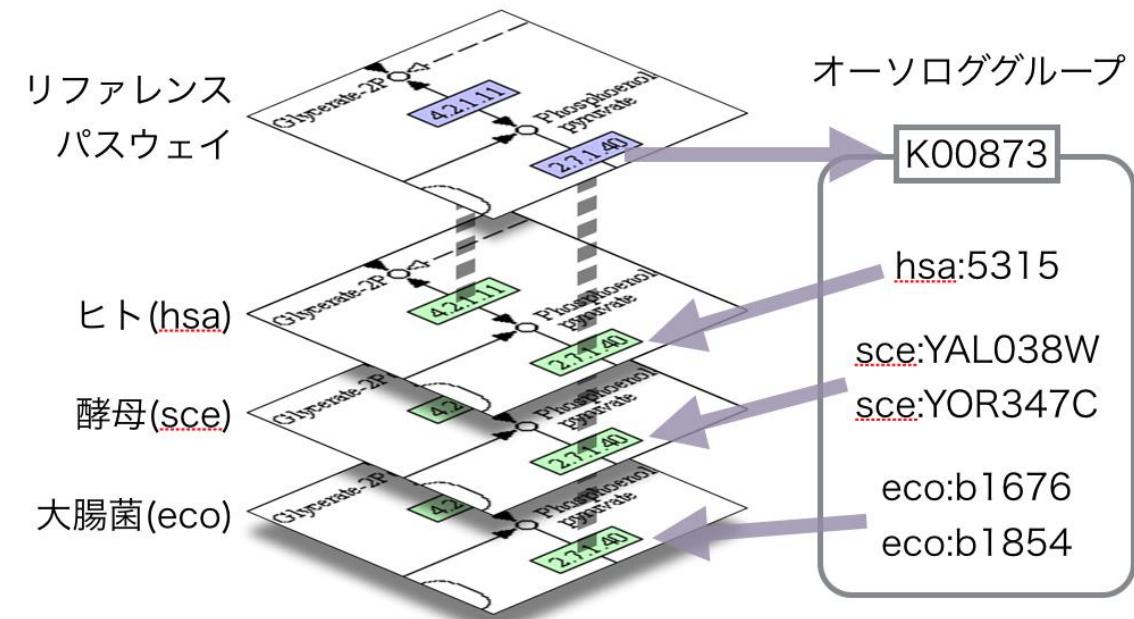
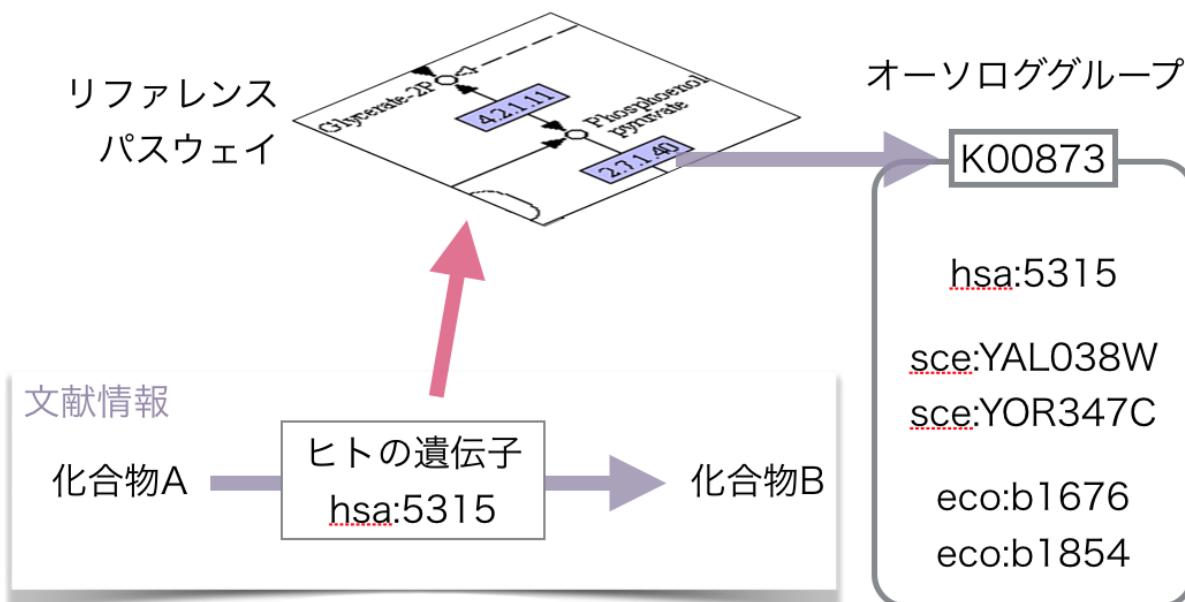
## 00240 Pyrimidine metabolism

### Amino acid metabolism

- 00250 Alanine, aspartate and glutamate metabolism
- 00260 Glycine, serine and threonine metabolism
- 00270 Cysteine and methionine metabolism
- 00280 Valine, leucine and isoleucine degradation
- 00290 Valine, leucine and isoleucine biosynthesis
- 00300 Lysine biosynthesis**
- 00310 Lysine degradation
- 00220 Arginine biosynthesis
- 00330 Arginine and proline metabolism
- 00340 Histidine metabolism
- 00350 Tyrosine metabolism
- 00360 Phenylalanine metabolism
- 00380 Tryptophan metabolism
- 00400 Phenylalanine, tyrosine and tryptophan biosynthesis
- Metabolism of other amino acids
- 00410 beta-Alanine metabolism
- 00430 Taurine and hypotaurine metabolism



# リファレンスパスウェイと種毎のパスウェイの関係



# Overviewマップを見る

- <https://www.kegg.jp/kegg/pathway.html>
- 1.0 Global and overview maps の [Metabolic pathways](#) をクリック
- 左にモジュールのリスト（KEGG におけるパスウェイの小さい機能単位）、右にマップが表示
- 機能単位毎にパスウェイを強調表示できる

## 1. Metabolism

### 1.0 Global and overview maps

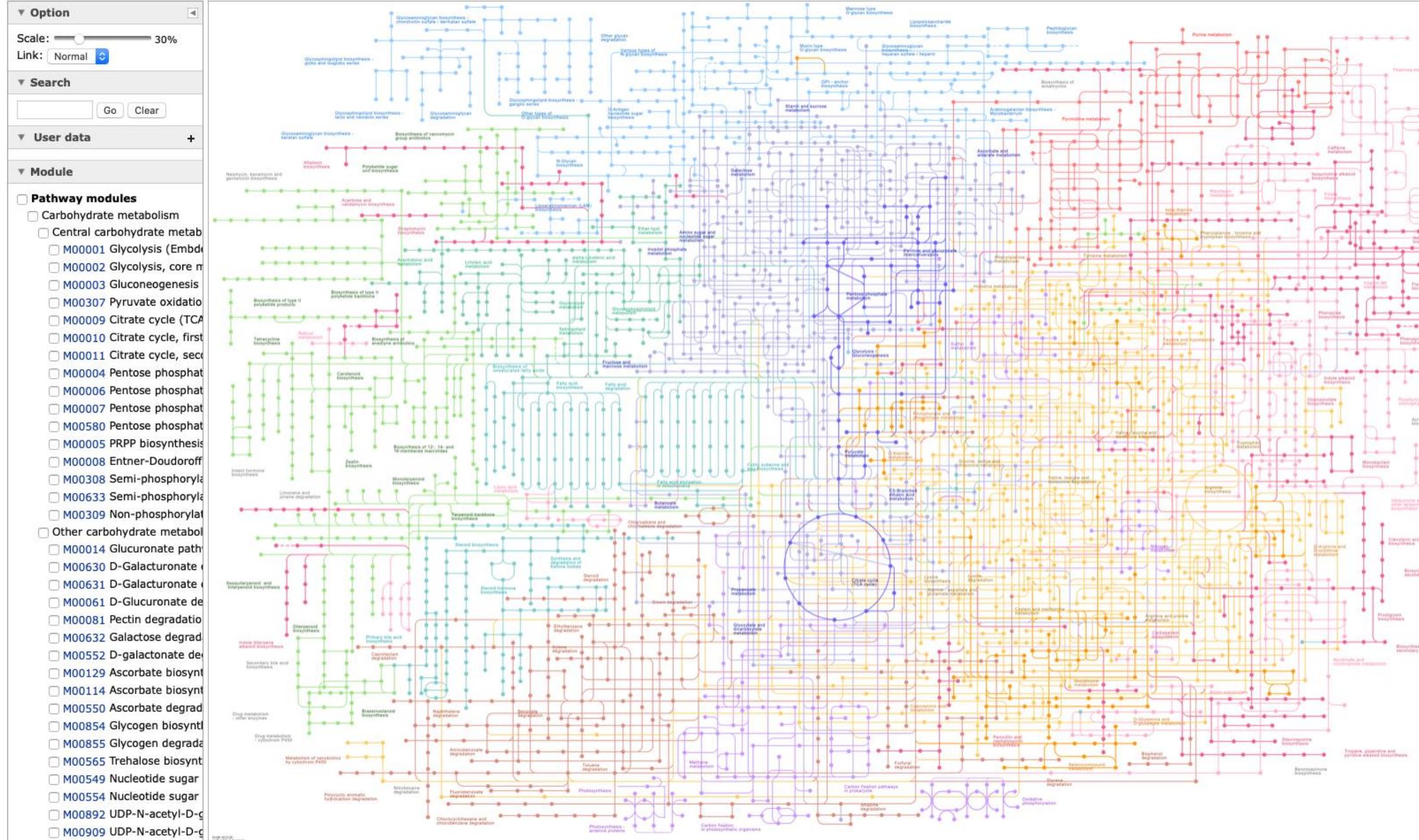
- 01100 M [Metabolic pathways](#)
- 01110 M [Biosynthesis of secondary metabolites](#)
- 01120 M [Microbial metabolism in diverse environments](#)
- 01200 M R [Carbon metabolism](#)
- 01210 M R [2-Oxocarboxylic acid metabolism](#)
- 01212 M R [Fatty acid metabolism](#)
- 01230 M R [Biosynthesis of amino acids](#)
- 01220 M R [Degradation of aromatic compounds](#)

### 1.1 Carbohydrate metabolism

- 00010 M N [Glycolysis / Gluconeogenesis](#)

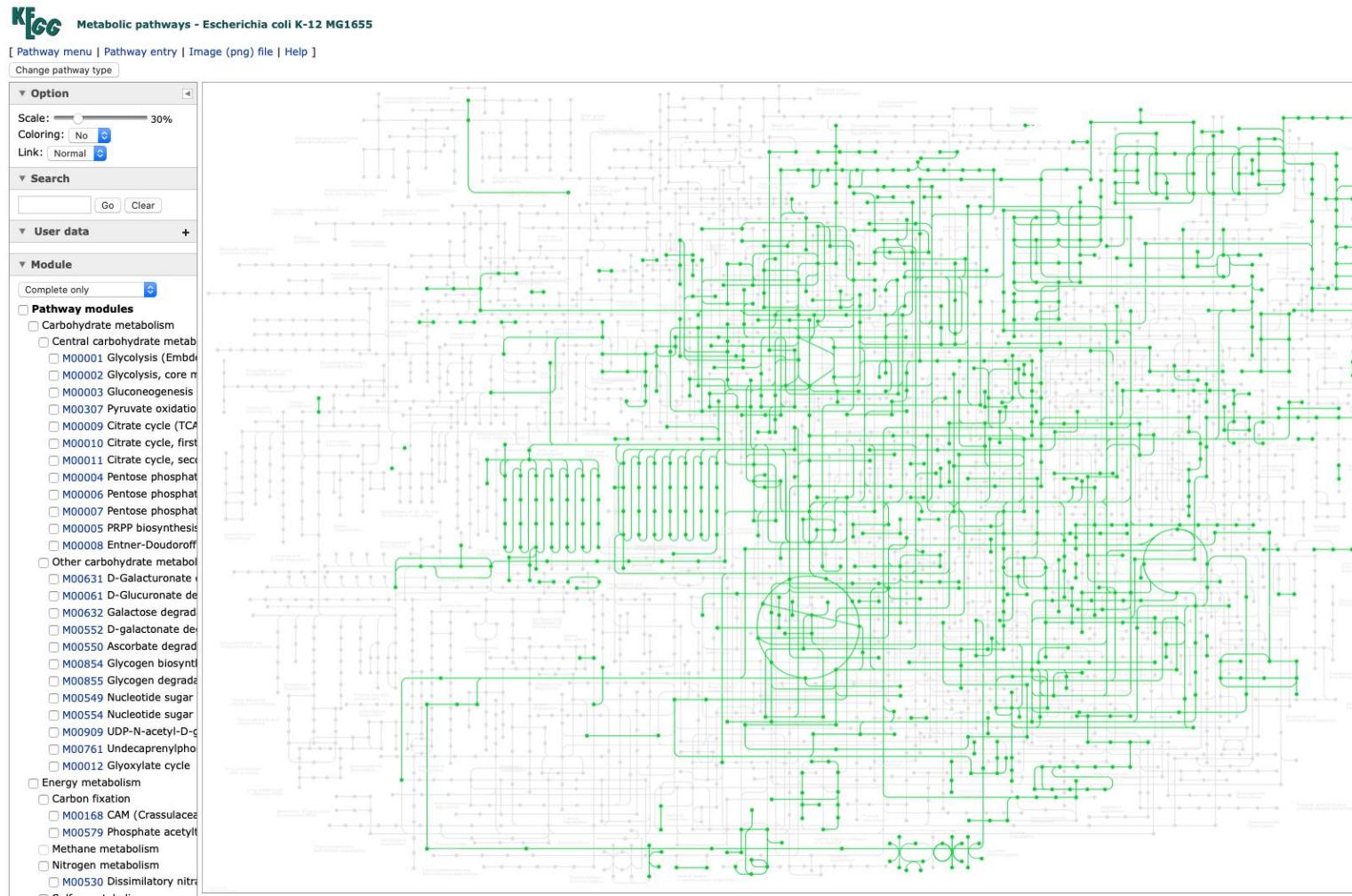
[ Pathway menu | Pathway entry | Image (png) file | Help ]

Change pathway type



# 生物種毎のOverviewマップを見る

- Change pathway type から生物コードをクリック
- 生物の持っていない経路は灰色になる (ecoの例)



# ヒトの疾患パスウェイを見る

- <https://www.kegg.jp/kegg/disease/>
- がん、免疫系疾患、神経変性疾患など多因子性の疾患
- 好きな疾患パスウェイをクリック（例：[大腸がん](#)）
  - 赤字の遺伝子が疾患の病因遺伝子を示しています。

## Disease Pathway Maps

The Human Diseases category of the KEGG PATHWAY database

- KEGG Pathway Maps: Human Diseases

It contains multifactorial diseases such as cancers, neurodegenerative diseases, and metabolic diseases where known disease-associated pathways and interacting molecular networks of both pathogens

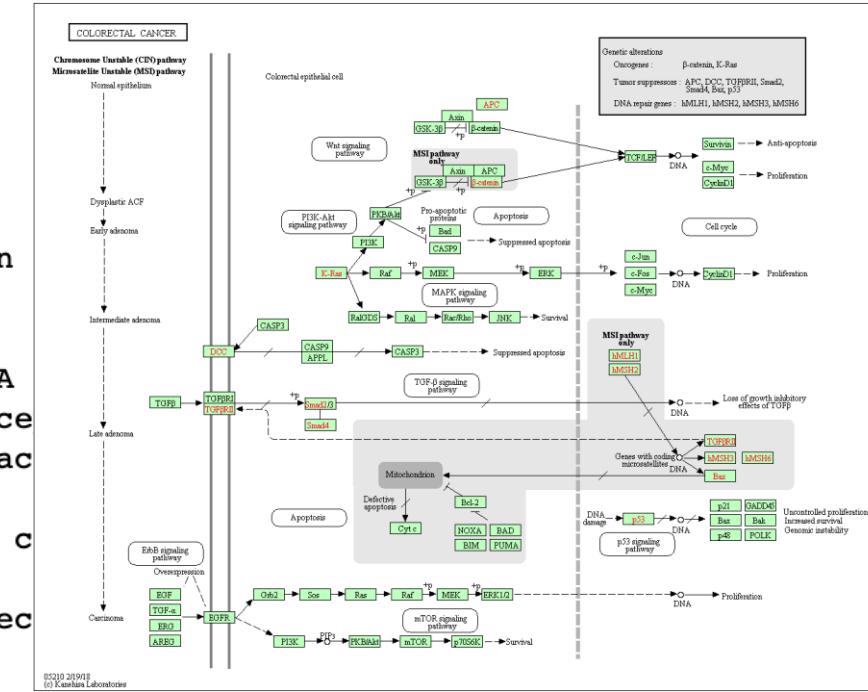
### ▼ Human Diseases

#### ▼ Cancer: overview

- 05200 Pathways in cancer
- 05202 Transcriptional misregulation
- 05206 MicroRNAs in cancer
- 05205 Proteoglycans in cancer
- 05204 Chemical carcinogenesis - DNA
- 05207 Chemical carcinogenesis - receptor
- 05208 Chemical carcinogenesis - reaction
- 05203 Viral carcinogenesis
- 05230 Central carbon metabolism in cancer
- 05231 Choline metabolism in cancer
- 05235 PD-L1 expression and PD-1 checkpoint

#### ▼ Cancer: specific types

- 05210 Colorectal cancer
- 05212 Pancreatic cancer
- 05225 Hepatocellular carcinoma



# ヒトの疾患パスウェイ

- Disease genes and drug targets in KEGG pathwaysから「Colorectal cancer」を選択
  - ピンクのボックスは何らかの疾患で病因遺伝子となっている遺伝子を示しています
  - ライトブルーのボックスは何らかの疾患で医薬品のターゲットとなっている遺伝子を示しています
- このように、KEGGでは正常な状態のパスウェイの他に、病原因子や医薬品、そのターゲットなどの情報もパスウェイとして表現されています

## Disease Mapping

The Search Disease tool in KEGG Mapper is a mapping tool against disease genes accumulated in KEGG DISEASE entries, together with related KEGG pathway maps. The user may upload a set of human genes or KOs to check if any diseases may be associated with the dataset.

[KEGG Mapper - Search Disease](#)

## Pathway/Brite mapping of disease genes and drug targets

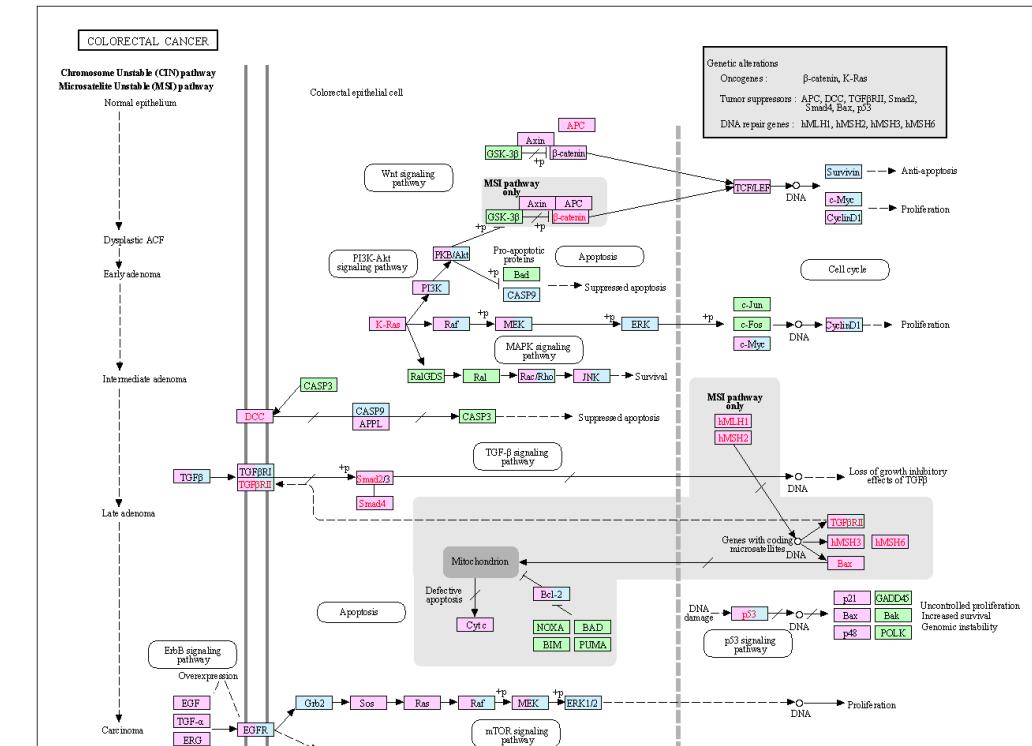
Disease genes accumulated in the KEGG DISEASE database and drug targets stored in the KEGG DRUG database are often represented in the KEGG PATHWAY and BRITE databases as well. The pathway maps and BRITE hierarchy files with mapping of disease genes and drug targets are identified by the five-letter organism code "hsadd" and the extension code "\_dd", respectively.

For example, hsadd04620 represents disease/drug mapped toll-like receptor signaling pathway with the coloring convention as follows:

- When the gene is associated with a disease, it is marked in pink.
- When the gene (product) is a drug target, it is marked in light blue.
- When the gene is both a disease gene and a drug target, its coloring is split into pink and light blue.

The disease/drug mapped version is precomputed in the daily KEGG database update procedure, and each map or BRITE hierarchy can be selected from the organisms selection menu. For the disease/drug pathway maps the following list may also be used.

[Disease genes and drug targets in KEGG pathways](#)



# 種間比較をする

- <https://www.kegg.jp/kegg/kegg2.html>
- KEGG GENOMEのリンクをクリック
- KEGG Mapping for Genome Comparison and Combination のテキストボックスに "eco ecs" と入力して Go をクリック
  - eco : 非病原性大腸菌 k-12
  - ecs : 病原性大腸菌 O157

## Data-oriented entry points

Category	Entry Point	Content	DBGET Search
Systems information	<a href="#">KEGG PATHWAY</a>	KEGG pathway maps	PATHWAY
	<a href="#">KEGG BRITE</a>	BRITE hierarchies and tables	BRITE
	<a href="#">KEGG MODULE</a>	KEGG modules	MODULE
Genomic information	<a href="#">KO (KEGG Orthology)</a>	Functional orthologs	ORTHOLOGY
	<a href="#">KEGG GENOME</a>	KEGG organisms (complete genomes)	GENOME
	<a href="#">KEGG GENES</a>	Genes and proteins	GENES
Chemical information (KEGG LIGAND)	<a href="#">KEGG SSDB</a>	GENES sequence similarity	
	<a href="#">KEGG COMPOUND</a>	Small molecules	COMPOUND
	<a href="#">KEGG GLYCAN</a>	Glycans	GLYCAN
	<a href="#">KEGG REACTION</a>	Reactions and reaction classes	REACTION
Health information	<a href="#">KEGG ENZYME</a>	Enzyme nomenclature	RCLASS ENZYME
	<a href="#">KEGG NETWORK</a>	Disease-related network elements	NETWORK
	<a href="#">KEGG DISEASE</a>	Human diseases	VARIANT DISEASE
	<a href="#">KEGG DRUG</a>	Drugs and drug groups	DRUG
	<a href="#">KEGG ENVIRON</a>	Health related substances	DGROUP ENVIRON
	<a href="#">KEGG MEDICUS</a>	Japanese drug labels (JAPIC)	
		FDA drug labels (DailyMed)	

## KEGG Mapping for Genome Comparison and Combination

An organism group may be defined to compare or combine KEGG organisms, other organisms and environmental samples, enabling the analysis of combined pathway maps for the group.

Define organism group (enter organism codes or T numbers):

(Genome comparison)

[hsa eco](#) Homo sapiens (human) vs. Escherichia coli K-12 strain  
such as [Terpenoid backbone biosynthesis](#)  
where green for human, red for E.coli, and split for both

(Host-microbiome relationship)

[hsa+T30003](#) Homo sapiens (human) + gut microbiome  
such as [Global metabolism map](#)  
where green for human, red for gut microbiome, and blue for both

# 種間比較

- 上のメニューの Pathway map をクリック
- 好きなパスウェイをクリック
  - 前者の遺伝子が緑、後者の遺伝子がピンクで表示
  - Overview パスウェイの場合、両者が持っている遺伝子はライトブルーで表示

00020 Citrate cycle (TCA cycle)

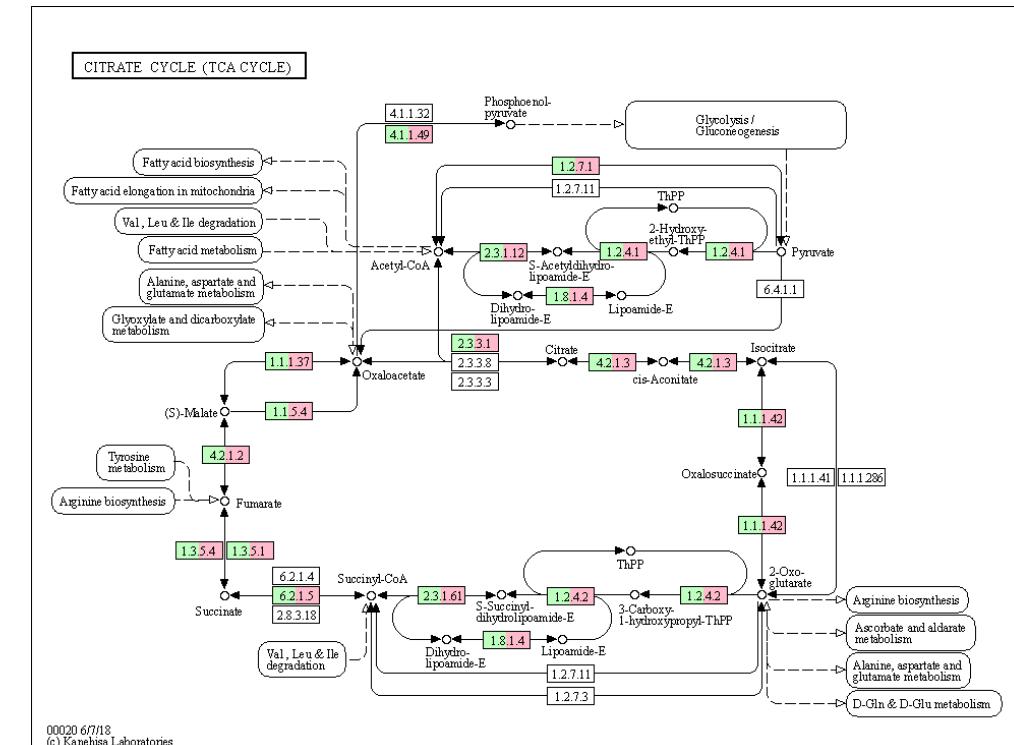
KEGG Organism group: eco ecs

Category info Pathway map Brite hierarchy Taxonomy

Search genes:  Go Clear

eco ecs

T00007	eco	Escherichia coli K-12 MG1655
T00048	ecs	Escherichia coli O157:H7 Sakai (EHEC)



# Bacterial secretion system マップ

- 03070 : Bacterial secretion system パスウェイでは病原性に関わる III型、VI型分泌装置が O157 側だけが持っているのがわかる

## Environmental Information Processing

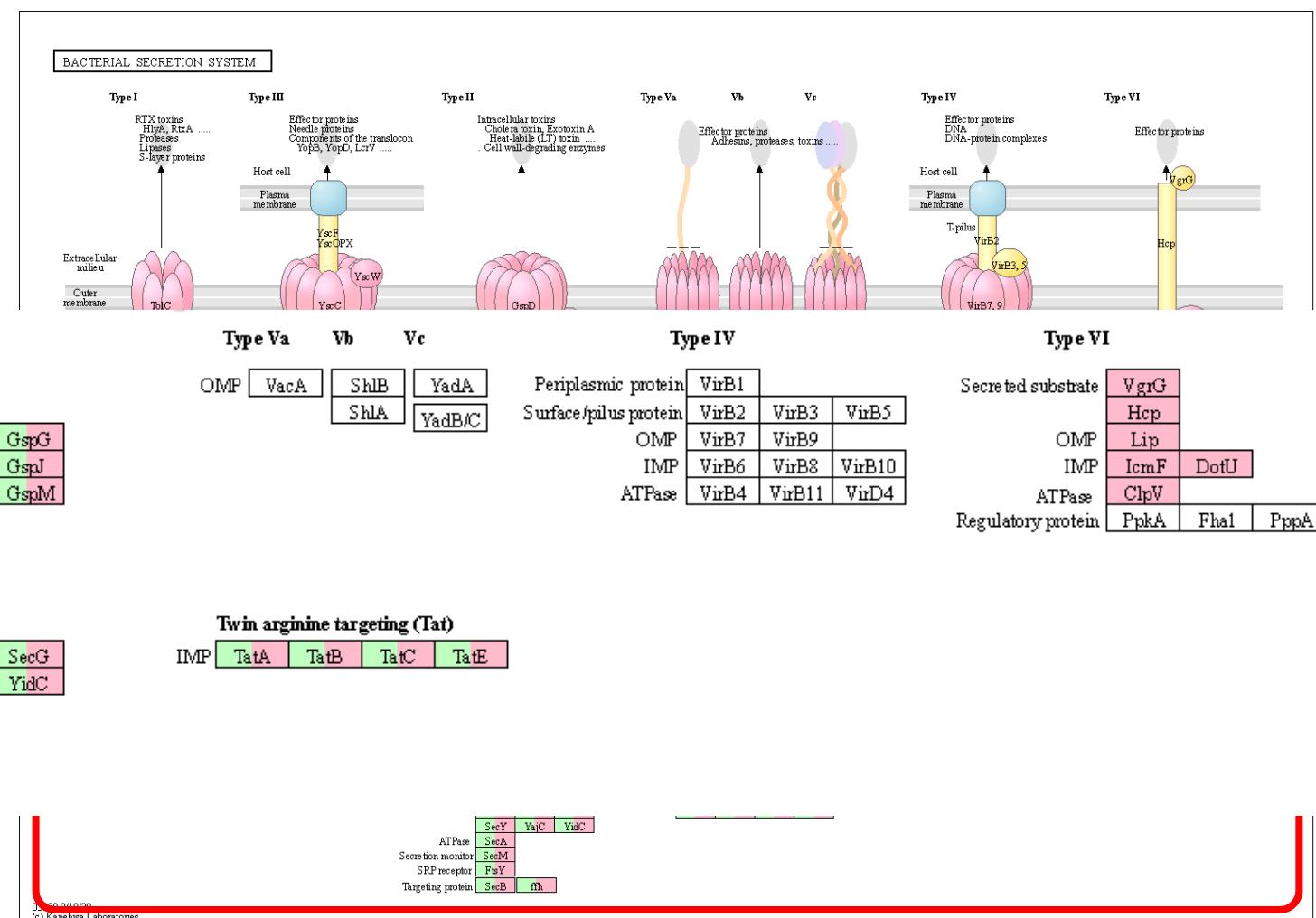
### Membrane transport

#### 02010 ABC transporters

#### 02060 Phosphotransferase system (PTS)

Type I	Type III	Type II
Outer membrane protein (OMP) TolC	Needle YscF	Secretin GspD
Membrane fusion protein HlyD	YscO YscP YscX	OMP GspS
ABC transporter HlyB		IMP GspC GspF GspG
	Secretin YscC	IMP GspH GspI GspJ
	OMP YscW	GspK GspL GspM
Inner membrane protein (IMP) YscJ YscR YscS		ATPase GspE
YscT YscU YscV		Leaderpeptidase GspO
ATPase YscN		
ATPase-associated protein YscQ YscL		

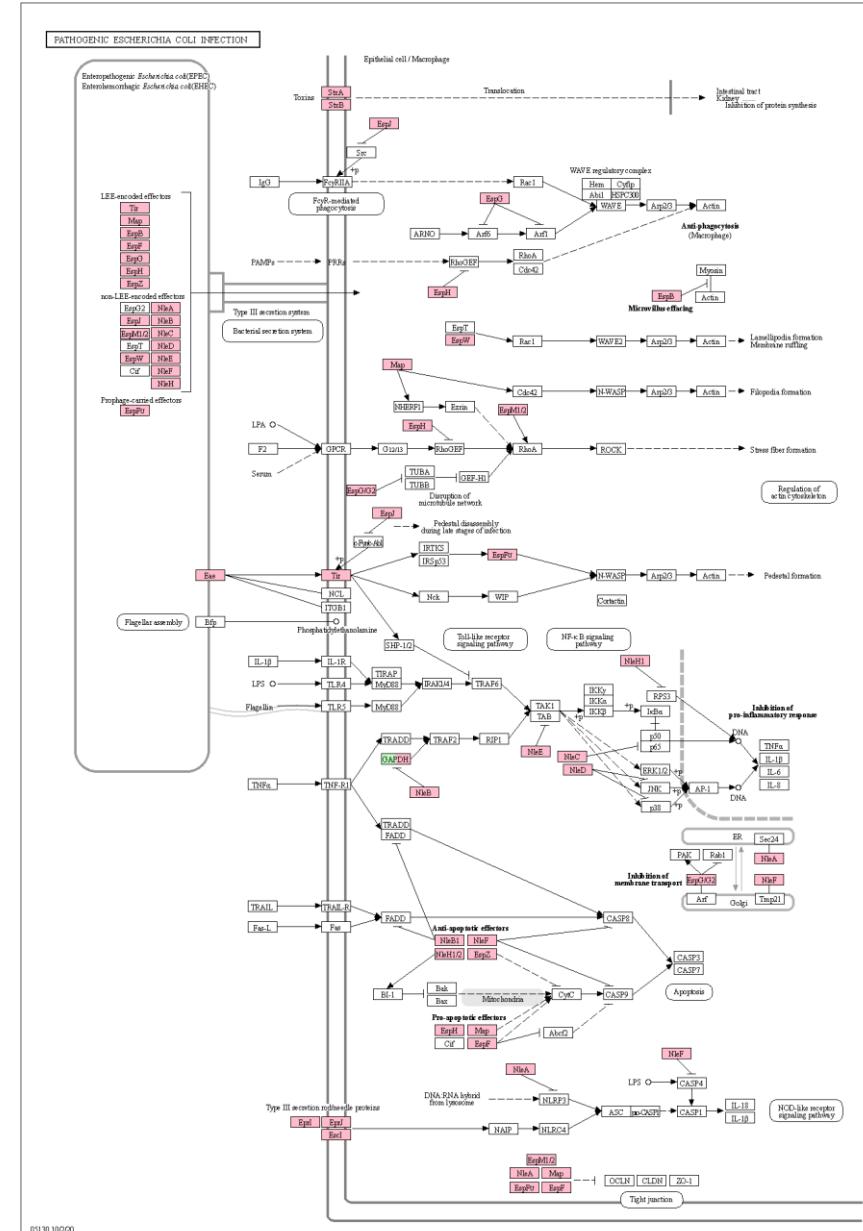
Sec-SRP	Twin arginine targeting (Tat)
IMP SecD/F SecE SecG	IMP TatA TatB TatC TatE
SecY YajC YidC	
ATPase SecA	
Secretion monitor SecM	
SRP receptor FtsY	
Targeting protein SecB ffh	



# Pathogenic Escherichia coli infection

Infectious disease: bacterial

- 05110 Vibrio cholerae infection
- 05120 Epithelial cell signaling in Helicobacter pylori infection
- 05130 Pathogenic Escherichia coli infection**
- 05132 Salmoneilla infection
- 05131 Shigellosis
- 05135 Yersinia infection
- 05133 Pertussis
- 05134 Legionellosis
- 05150 Staphylococcus aureus infection
- 05152 Tuberculosis
- 05100 Bacterial invasion of epithelial cells

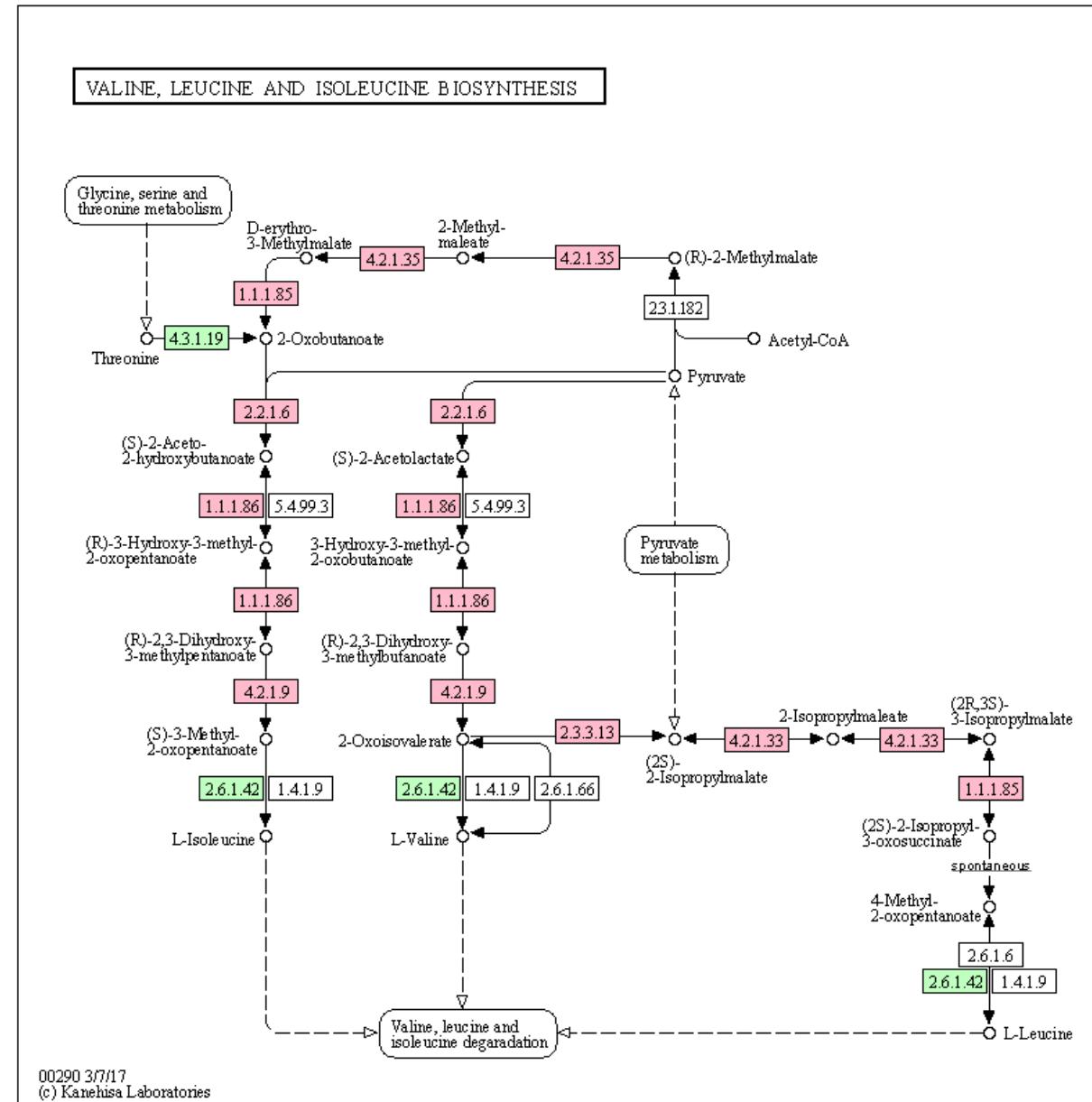


# アブラムシとブフネラで種間比較

- 00290 : Valine, leucine and isoleucine biosynthesis マップ
  - アブラムシ : api (緑)
  - ブフネラ : buc (ピンク)
- 共生生物間のパスウェイ補完によってアミノ酸合成が可能になっていることがわかる

## Amino acid metabolism

- 00250 Alanine, aspartate and glutamate metabolism
- 00260 Glycine, serine and threonine metabolism
- 00270 Cysteine and methionine metabolism
- 00280 Valine, leucine and isoleucine degradation
- 00290 Valine, leucine and isoleucine biosynthesis
- 00300 Lysine biosynthesis
- 00310 Lysine degradation
- 00220 Arginine biosynthesis
- 00330 Arginine and proline metabolism
- 00340 Histidine metabolism
- 00350 Tyrosine metabolism
- 00360 Phenylalanine metabolism
- 00380 Tryptophan metabolism
- 00400 Phenylalanine, tyrosine and tryptophan biosynthesis



# サンプルデータのマッピング

- KEGGには遺伝子リストからパスウェイをマッピングするツールが組み込まれています。
  - [KEGG Mapper](https://www.kegg.jp/kegg/mapper.html)  
(<https://www.kegg.jp/kegg/mapper.html>)
  - Pathway mapping tool の3番目の[Color](#)をクリック
    - Search mode : データベースコード
    - テキストエリア : 要素のリスト（遺伝子、タンパク質、化合物）
      - [配列 ID or 代謝産物 ID] 塗りつぶし色[,線の色]
        - 配列 ID は KEGG gene ID, NCBI-GenID, NCBI-ProteinID, UniProt ID
        - 代謝産物 ID は KEGG Compound ID (C番号) のみ
        - 線の色はオプション
        - 色は16進数表記か基本的なカラーネームで記述

**KEGG Mapper**  
A suite of KEGG mapping tools

**About KEGG Mapper**

KEGG Mapper is a collection of tools for KEGG mapping including popular KEGG pathway mapping, JOIN BRITE operations and MODULE completeness checks. Historically, "Search Pathway" and "Search&Color Pathway" tools were introduced at the beginning of the KEGG project. As the KEGG database contents expanded, so did the mapping tools. In the last version released in July 2019 [1], fourteen existing tools were reorganized into just five tools, allowing multiple mapping operations to be done at the same time and the result page shown in multiple tabs. This new version 5 of KEGG Mapper [2] has a further simplified architecture together with the enhancement of the join tool.

See new article: [KEGG mapping tools for uncovering hidden features in biological data](#)

**KEGG mapping tools**

There are four KEGG mapping tools as summarized below.

**Reconstruct** (used to be called Reconstruct Pathway) is the basic mapping tool used for linking KO annotation (K number assignment) data to KEGG pathway maps, BRITE hierarchies and tables, and KEGG modules.

**Search** (used to be called Search Pathway) is the traditional tool for searching mapped objects in the user's dataset and mark them in red.

**Color** (used to be called Search&Color Pathway) is another traditional tool for searching mapped objects in the user's dataset and mark them in red. It also allows users to change the background and foreground colors. This tool now applies only to KEGG pathway maps. Use the Join tool for coloring of Brite hierarchies.

**Join** (used to be called Join Brite) is a tool to combine a Brite hierarchy file and a binary relation file, effectively adding a new column to the hierarchy file. This tool has been significantly expanded in this release.

# KEGG Mapper

- テキストエリア右の Example を選択して Exec ボタンをクリックすると、ヒットしたパスウェイのリストが表示されます（カッコの中はヒットした要素の数）

 KEGG Mapper – Color

KEGG2 About Reconstruct Search Color Join Convert ID Assign KO Taxonomy

**Color tool**

The Color tool searches various KEGG objects, including genes, KOs, EC numbers, metabolites and drugs, against KEGG pathway maps. Found objects may be marked in any combination of background and foreground colors.  
See new article: KEGG mapping tools for uncovering hidden features in biological data

Search mode:  Reference  hsa  other org  Get org code

Enter KEGG identifiers followed by color specification

Examples:

C00079	red
C00423	red
C00811	red
C00223	red
C06561	red
C00509	red
K00487	yellow
K00660	pink
K01859	cyan

Or upload file:  ファイルを選択 | ファイル未選択

Default bgcolor:

Use uncolored diagrams

Include aliases (for hsa and other org modes)

# KEGG Mapper Search Result

Pathway (34)

Sort by the pathway list

Show matched objects

map01110 Biosynthesis of secondary metabolites (9)

map01100 Metabolic pathways (9)

map00941 Flavonoid biosynthesis (6)

map00940 Phenylpropanoid biosynthesis (5)

map01061 Biosynthesis of phenylpropanoids (5)

map00130 Ubiquinone and other terpenoid-quinone biosynthesis

map01220 Degradation of aromatic compounds (4)

map00996 Biosynthesis of various alkaloids (3)

map00999 Biosynthesis of various plant secondary metabolites

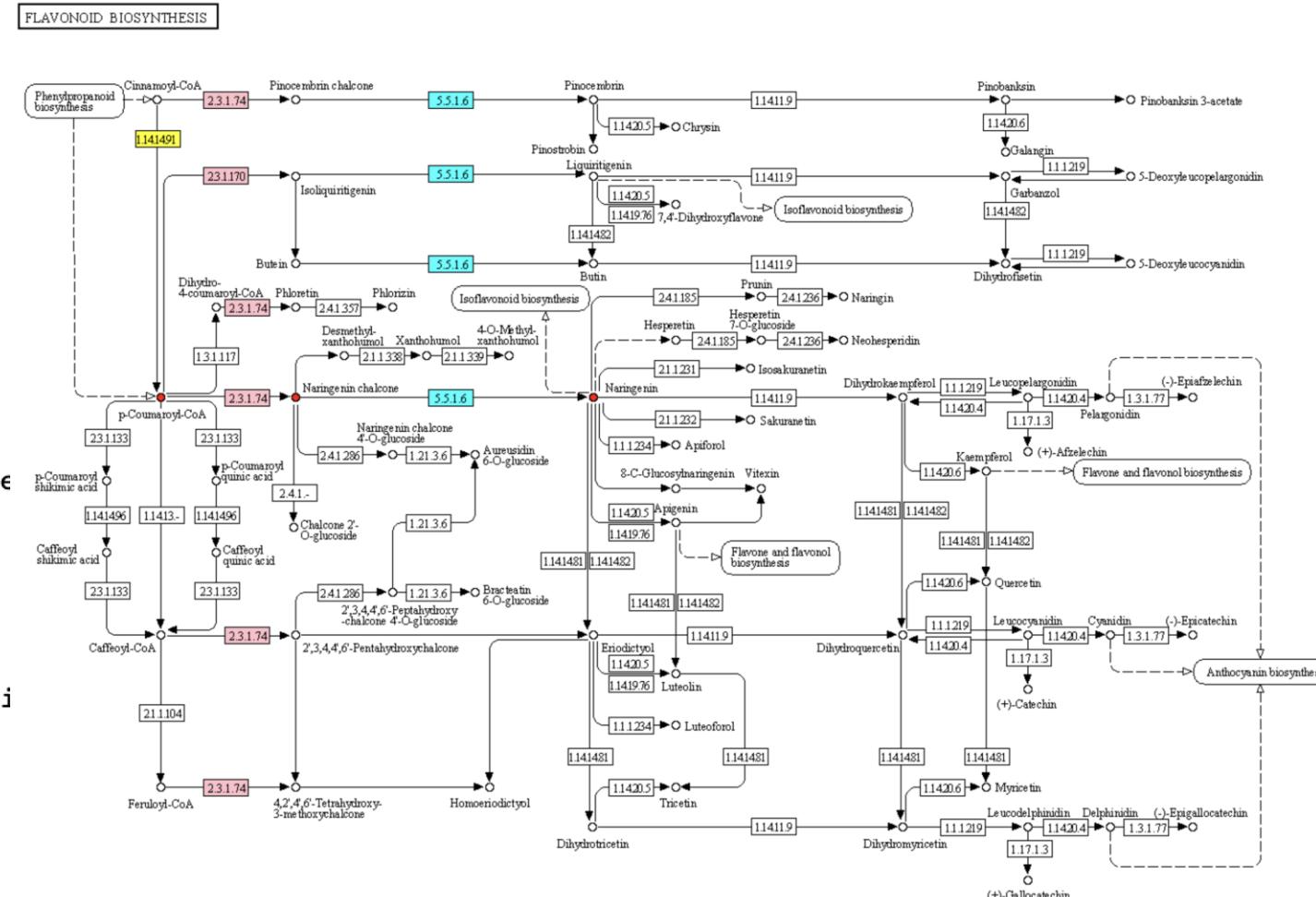
map01060 Biosynthesis of plant secondary metabolites (2)

map00360 Phenylalanine metabolism (2)

map00960 Tropane, piperidine and pyridine alkaloid biosynthesis (2)

map01070 Biosynthesis of plant hormones (2)

map00945 Stilbenoid, diarylheptanoid and gingerol biosynthesis (2)



# KEGGデータベースにはない遺伝子のマッピング

- KEGGに登録されている配列データと類似性を計算し、自動で遺伝子機能を推定、パスウェイへのマッピングを行う。
- KAAS (<https://www.genome.jp/tools/kaas/>)
- BlastKOALA, GhostKOALA



**KAAS - KEGG Automatic Annotation Server**  
for ortholog assignment and pathway mapping

**Request**

**About KAAS**

KAAS (KEGG Automatic Annotation Server) provides functional annotation of genes by BLAST or GHOST comparisons against the manually curated KEGG GENES database. The result contains KO (KEGG Orthology) assignments and automatically generated KEGG pathways.

- KAAS Help

**Complete or Draft Genome**

KAAS works best when a complete set of genes in a genome is known. Prepare query amino acid sequences and use the BBH (bi-directional best hit) method to assign orthologs.

- KAAS job request (BBH method)

**Partial Genome**

KAAS can also be used for a limited number of genes. Prepare query amino acid sequences and use the SBH (single-directional best hit) method to assign orthologs.

- KAAS job request (SBH method)  
- KAAS interactive

**Metagenomes**

When the query consists of large numbers of sequences and / or sequences from mixture of species such as those from metagenome sequencing project, we recommend the GHOSTX search and SBH method.

- KAAS job request (SBH method for amino acid sequence query)

**Example of Results**

**KO assignment**

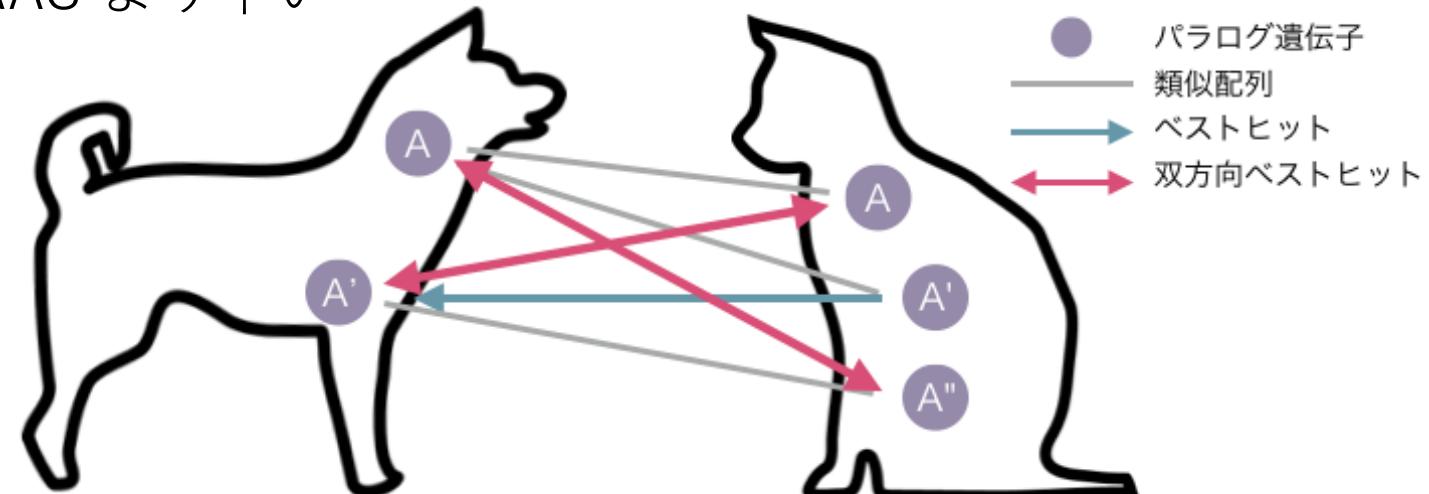
Query gene : KO assignment
Intf70411 query_0001 query_0002 400003 query_0003 400072 query_0004 401373 query_0005 query_0006 query_0007 403310 query_0008 403316 query_0009 403331 query_0010 407324 query_0011 query_0012 query_0013 query_0014 404043 query_0015 403308 query_0016

**KEGG pathway mapping**

The diagram illustrates the KEGG pathway mapping for GLYCOLYSIS. It shows the flow of metabolites through various enzymes and pathways, including Glyceraldehyde-3-phosphate dehydrogenase, Phosphoglycerate kinase, and Pyruvate kinase. Pathways like Glycolysis/Gluconeogenesis and Pentose and glucuronate interconversions are depicted with their respective KEGG IDs (e.g., 30010, 30020, 30030).

# 配列相同意検索

- [KAAS](https://www.genome.jp/tools/kaas/) (<https://www.genome.jp/tools/kaas/>)
  - 配列類似性の計算は [BLAST](#), [GhostX](#), [GhostZ](#) ベースの 3 つ
    - GhostX は BLAST より精度は劣るが 100 倍早い
    - GhostZ は GhostX より精度は劣るが 2 倍早い
  - 種間で両方向ベストヒットを利用して遺伝子機能を推定（片方向も可能）
- [BlastKOALA](#), [GhostKOALA](#)
  - 配列類似性の計算は BLAST, GhostX ベース
  - クエリーからデータベースへの片方向の計算なのと、データベースを圧縮しているぶん KAAS より早い



# BlastKOALAを使ったパスウェイマッピング

- **KEGG Mapper – Assign KO**

([https://www.kegg.jp/kegg/mapper/assign\\_ko.html](https://www.kegg.jp/kegg/mapper/assign_ko.html))

- Example: の sequence.txt をコピー & ペースト、もしくはダウンロードしてファイルを選択
- Family/Genus ボタンをクリック
  - サンプルが Buchnera の仲間なので、KEGG の Buchnera データを使う
  - 新たに開いたウィンドウで、Buchnera を探し、Taxonomy番号をクリック

KEGG Mapper – Assign KO

KEGG2 About Reconstruct Search Color Join Convert ID **Assign KO** Taxonomy

Assign KO tool

The Assign KO tool is an interface to the BlastKOALA server in the interactive mode. BlastKOALA assigns KO identifiers (numbers) to a given set of sequence data for subsequent analysis with the Reconstruct tool. This tool may also be used converting users' sequence IDs to K numbers for use in the Seach and Color tools.

Upload query amino acid sequences in FASTA format

Enter FASTA sequences

```
YLINFFYKTLKIKGTPIQIQFKDNENPYVKNKN  
>Icl|NZ_ACFK0100001.1_prot_WP_009874555.1_575 [gene=C5S_RS0103170]  
[protein=/inference=EXISTENCE: similar to AA sequence:SwissProt:P57663.1]  
[protein_id=WP_009874555.1] [location=complement(641210..641791)]  
MLNISKKNIIFFLIISLILFNWKYFSLVNKENLESLKYEKIIKKKSKNLYEVENVIVQ  
NTSI  
YGTLTALSLLAKKYVECNNDLKAOLNNSLKYTKNEENLNKLLKINIAKIOIOKNNENNKKAMNL
```

Example:  
Query data: **sequence.txt**  
Select Buchnera (32199)

Erwinia	551	Erwinia amylovora
		Erwinia billingiae
		Erwinia sp. Ejp617
		Erwinia gerundensis
Buchnera	32199	Buchnera aphidicola
Wigglesworthia	51228	Wigglesworthia glossinidia
		Pantoea ananatis
		Pantoea vagans
		Pantoea sp. At-Ah

# 計算中

- Exec ボタンをクリック
- 数分待つ



## BlastKOALA Job Request

### Request accepted

Your job ID is 196cfba9f578d1b20d2aae154e896c678f5d9866

Started at Tue Nov 3 12:54:38 JST 2020

This page reloads automatically every 5 seconds

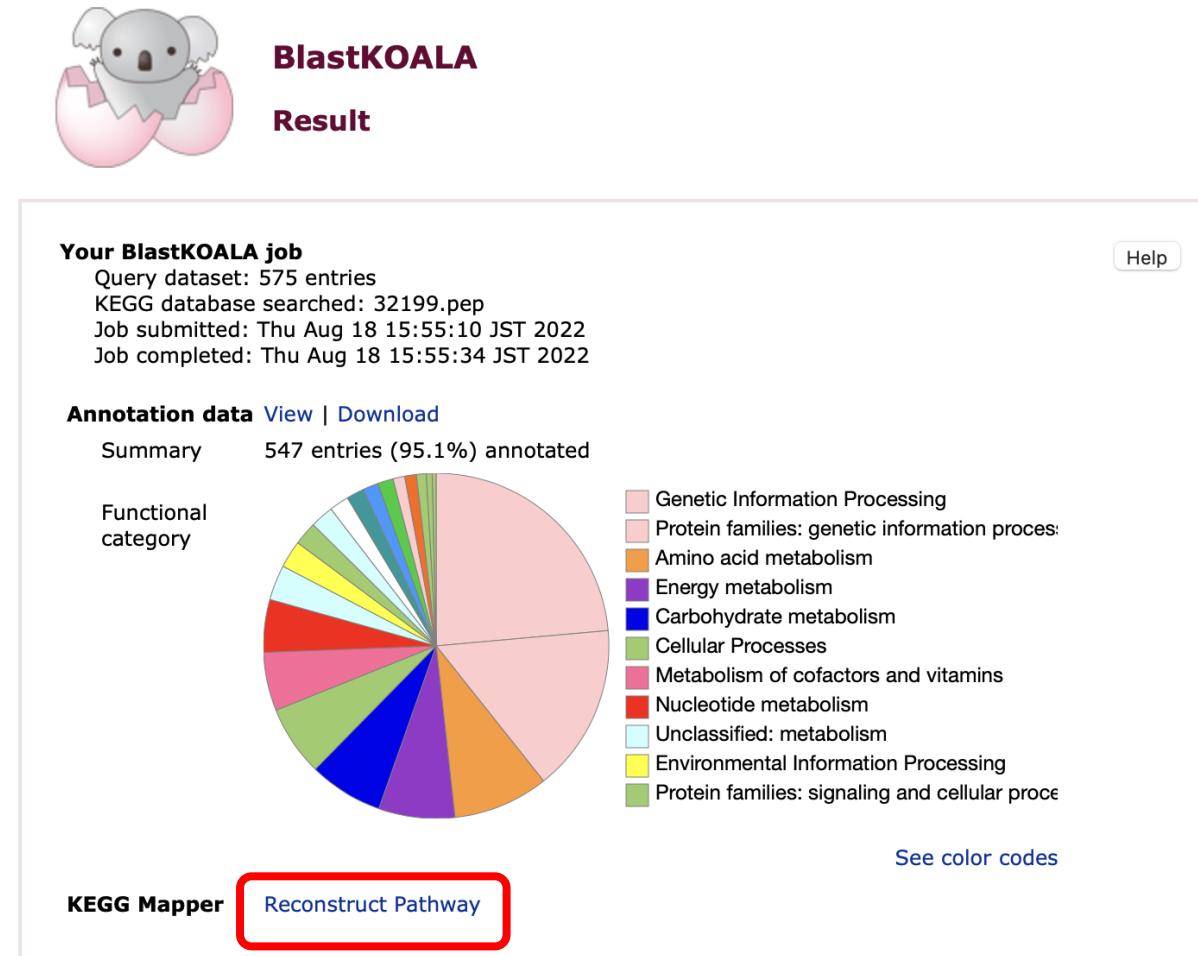
Your result will be displayed in the following page

[https://www.kegg.jp/kegg-bin/blastkoala\\_result?](https://www.kegg.jp/kegg-bin/blastkoala_result?)

[id=196cfba9f578d1b20d2aae154e896c678f5d9866&passwd=cMFA3A&mode=mapper](https://www.kegg.jp/kegg-bin/blastkoala_result?id=196cfba9f578d1b20d2aae154e896c678f5d9866&passwd=cMFA3A&mode=mapper)

# 計算結果

- Reconstruct Pathway から遺伝子がマッピングされたパスウェイを見ることができる



# Overviewマップの再構築結果

KEGG Mapper Reconstruction Result

Pathway (144) Brite (32) Brite Table (5) Metabolism

Show matched objects

**Metabolism**

Global and overview maps  
01100 Metabolic pathways (207) **01110 Biosynthesis of secondary metabolites (105)**

01120 Microbial metabolism in diverse environments (52)  
01200 Carbon metabolism (30)  
01210 2-Oxocarboxylic acid metabolism (10)  
01212 Fatty acid metabolism (5)  
01230 Biosynthesis of amino acids (62)

Carbohydrate metabolism  
00010 Glycolysis / Gluconeogenesis (14)  
00020 Citrate cycle (TCA cycle) (5)  
00030 Pentose phosphate pathway (12)  
00040 Pentose and glucuronate interconversions (1)  
00051 Fructose and mannose metabolism (5)  
00052 Galactose metabolism (1)  
00500 Starch and sucrose metabolism (2)  
00520 Amino sugar and nucleotide sugar metabolism (8)  
00620 Pyruvate metabolism (6)  
00630 Glyoxylate and dicarboxylate metabolism (2)  
00640 Propanoate metabolism (3)  
00650 Butanoate metabolism (2)  
00660 C5-Branched dibasic acid metabolism (2)  
00562 Inositol phosphate metabolism (2)

Energy metabolism  
00190 Oxidative phosphorylation (27)  
00195 Photosynthesis (8)  
00710 Carbon fixation in photosynthetic organisms (7)  
00720 Carbon fixation pathways in prokaryotes (4)  
00680 Methane metabolism (8)  
00920 Sulfur metabolism (9)

Lipid metabolism  
00061 Fatty acid biosynthesis (5)  
00564 Glycerophospholipid metabolism (1)  
01040 Biosynthesis of unsaturated fatty acids (1)

Nucleotide metabolism  
00230 Purine metabolism (18)  
00240 Pyrimidine metabolism (18)

Amino acid metabolism

KEGG Metabolic Pathways - Reference pathway

[ Pathway menu | Pathway entry | Image (png) file | Help ]

Change pathway type

▼ Option  
Scale: 30% Link: Normal

▼ Search

▼ Module  
Complete only

Pathway modules  
 Carbohydrate metabolism  
 Central carbohydrate metab...  
 M0002 Glycolysis, core m...  
 M00307 Pyruvate oxidatio...  
 M0004 Pentose phosphat...  
 M0006 Pentose phosphat...  
 M0007 Pentose phosphat...  
 M0005 PRPP biosynthesi...  
 Other carbohydrate metab...  
 Energy metabolism  
 Carbon fixation  
 M00579 Phosphate acetyl...  
 Methane metabolism  
 Nitrogen metabolism  
 Sulfur metabolism  
 M00176 Assimilatory sulfa...  
 Lipid metabolism  
 Fatty acid metabolism  
 M00083 Fatty acid biosynt...  
 Sterol biosynthesis  
 Lipid metabolism  
 Nucleotide metabolism  
 Purine metabolism  
 M00049 Adenine ribonucle...  
 Pyrimidine metabolism  
 M00051 Uridine monophos...  
 Amino acid metabolism  
 Serine and threonine metab...  
 M00018 Threonine biosynt...  
 Cysteine and methionine me...  
 M00021 Cysteine biosynth...  
 Branched-chain amino acid ...  
 Lysine metabolism  
 M00016 Lysine biosynthes...  
 Arginine and proline metab...  
 M00028 Ornithine biosynt...  
 M00844 Arginine biosynth...  
 Polyamine biosynthesis  
 Histidine metabolism

ご清聴ありがとうございました。