

パスウェイデータベース

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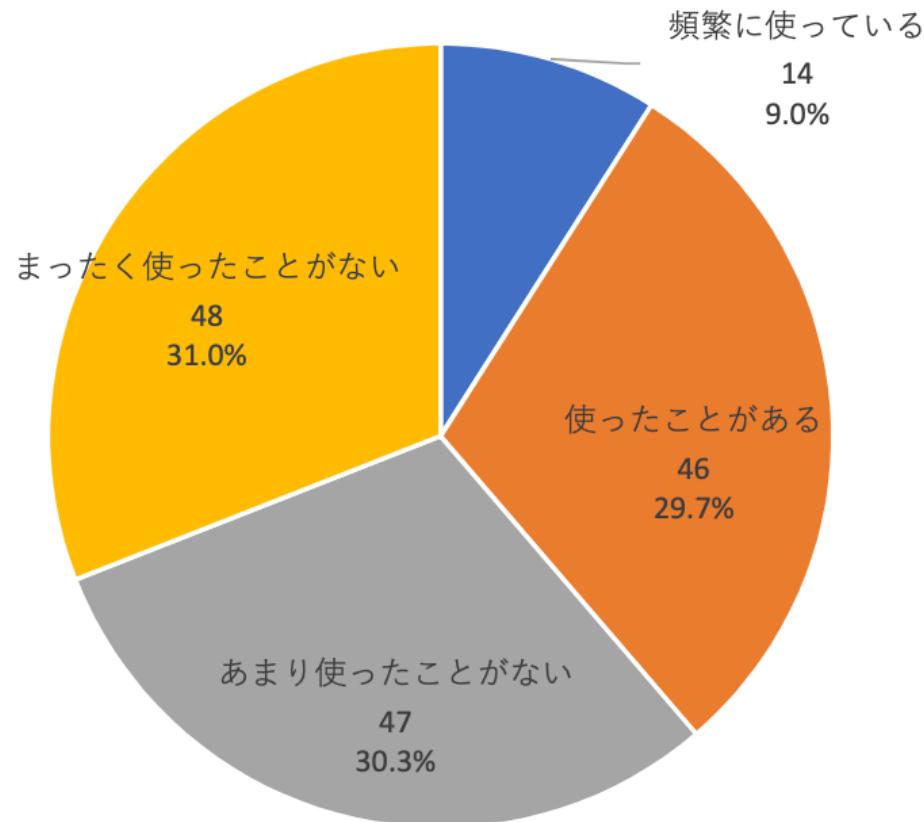
新潟大学大学院医歯学総合研究科

オンライン

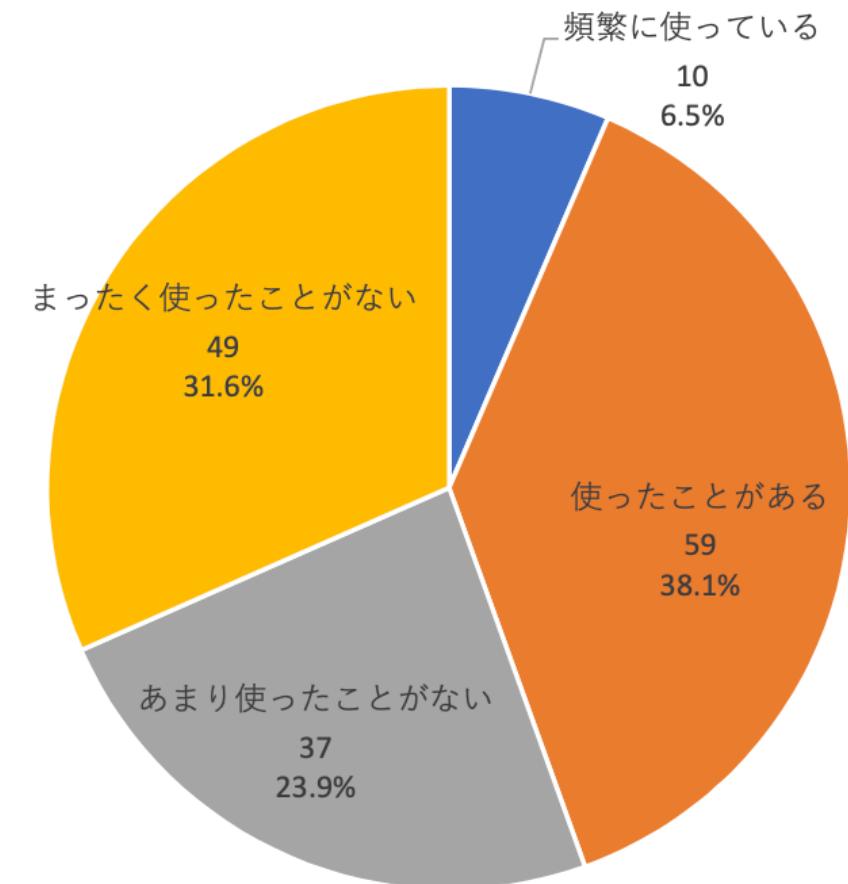
2020年11月11日

事前アンケート

講義3-1. パスウェイ関連のデータベースを使ったことがありますか。

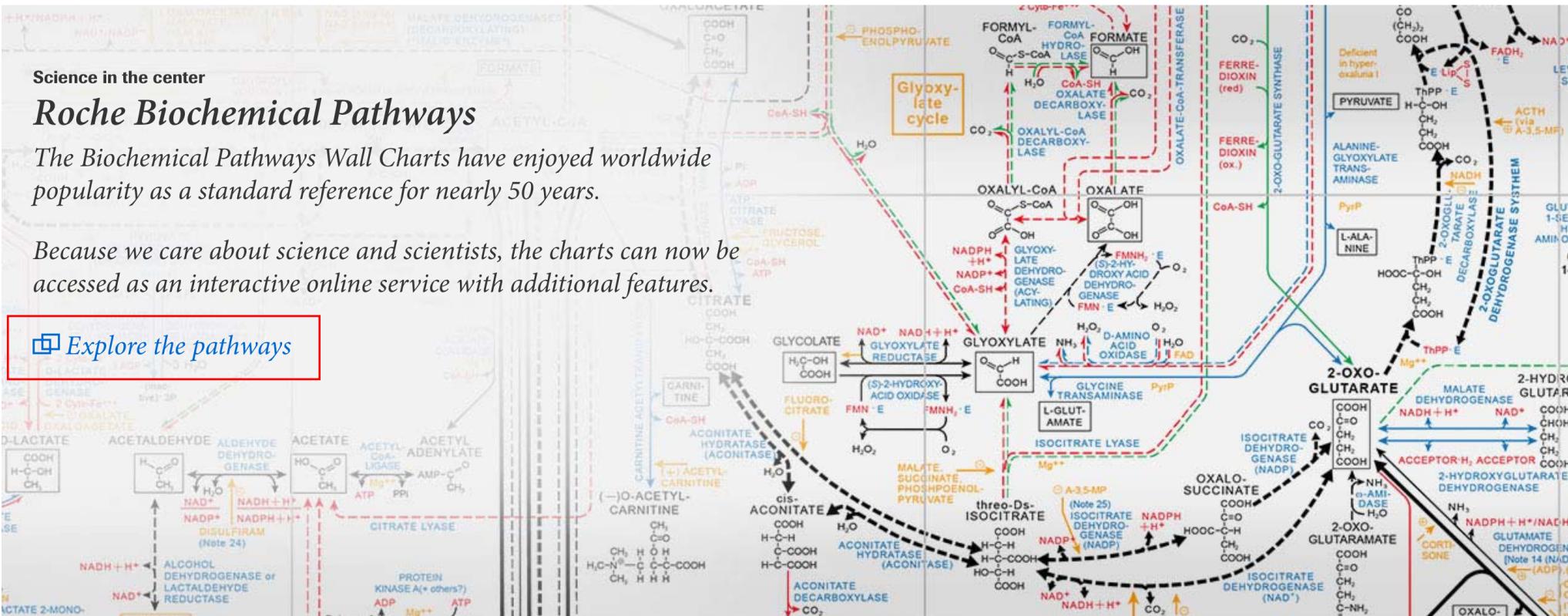


講義3-2. KEGGを使ったことがありますか。



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



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

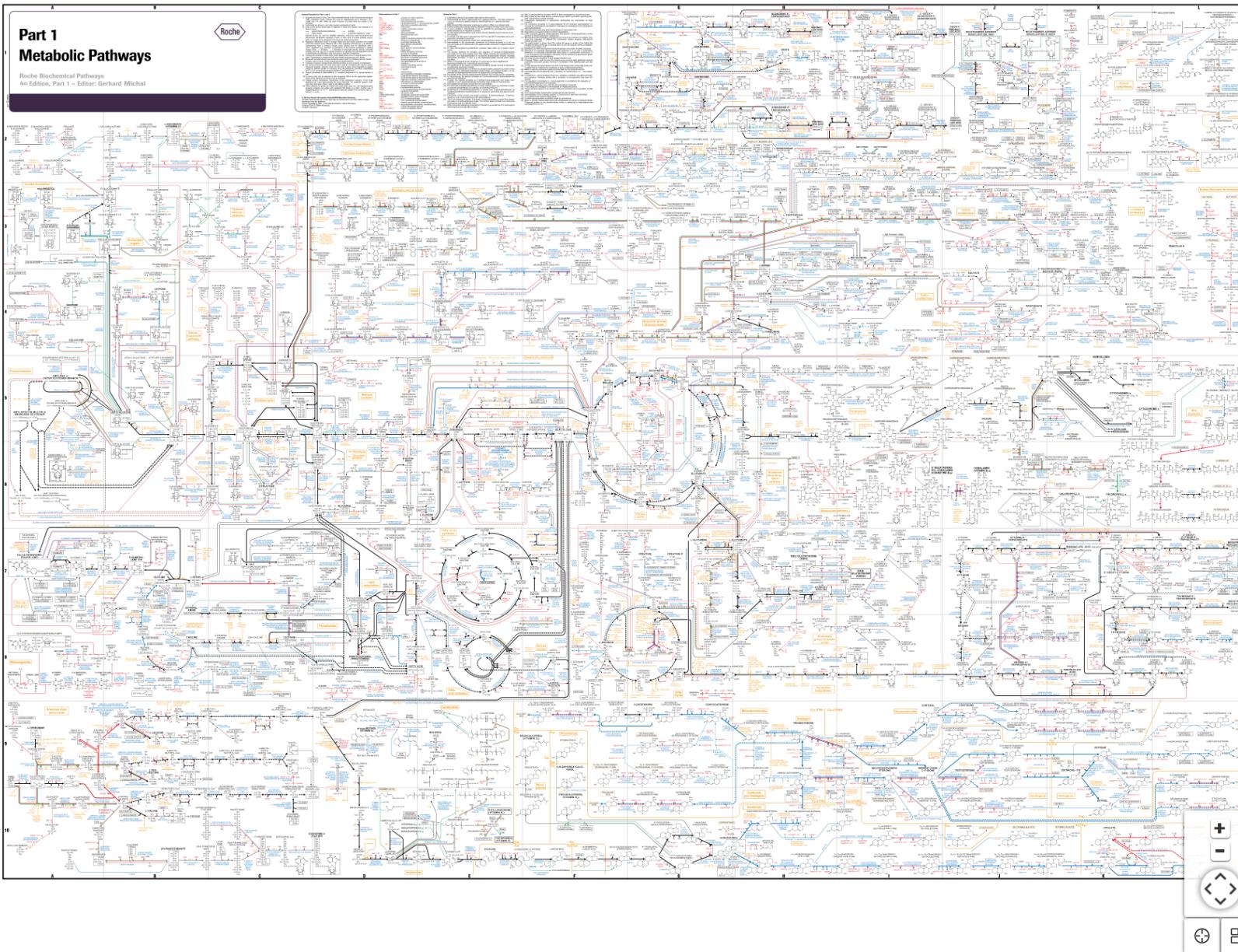
By the numbers

49 years
continuously fine-tuned by the editor himself.

Share Rate

Part 1: Metabolic Pathways Part 2: Cellular and Molecular Processes

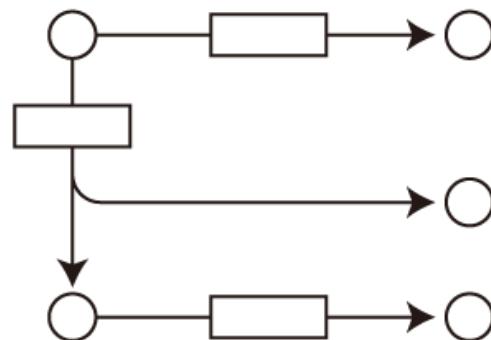
Click here to open the menu



パスウェイデータベースでの表現

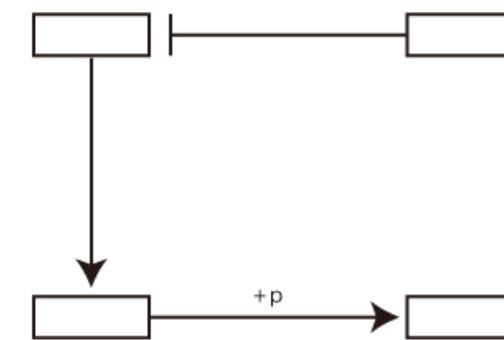
- 見やすくするために、ダイアグラムで表現されていることが多いっています。
- KEGG Pathway での表現例
 - 代謝パスウェイでは代謝産物をノード、酵素反応をエッジとして表現されています
 - 制御系ではタンパク質や遺伝子、その他の小分子をノード、その関係性（活性化、抑制、リン酸化など）がエッジとして表現されています

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いっています。
 - [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

The screenshot shows the BioCyc Database Collection homepage. At the top, there is a navigation bar with links for LOGIN, Why Login?, Create New Account, Sites, Search, Genome, Metabolism, Analysis, SmartTables, and Help. Below the navigation bar, a search bar displays "Searching Escherichia coli K-12 substr. MG1655 (EcoCyc) change organism database". The main content area features a "RouteSearch" section with a diagram illustrating metabolic pathways. The diagram shows three routes: a "Long Route" (orange line), a "Loss of Atoms" route (dashed yellow line), and the "Best Route: Atoms Conserved" (blue line). A chemical structure of a glucose molecule is shown at the start of the best route. To the right of the diagram, text explains "RouteSearch: Search for Paths through the Metabolic Network" and provides instructions for finding lowest-cost paths. Below the diagram, sections include "BioCyc Database Collection", "Getting Started", "Tools", and "BioCyc Databases". The "Tools" section lists various features like Genome browser, metabolic pathways, analysis methods, and comparative analysis tools. The "BioCyc Databases" section discusses the three-tiered database system (Tier 1, Tier 2, Tier 3) and funding sources.

BioCyc

Metabolism -> Cellular Overview



[LOGIN](#) | [Why Login?](#) | [Create New Account](#)

Enter a gene, protein, metabolite or pathway...

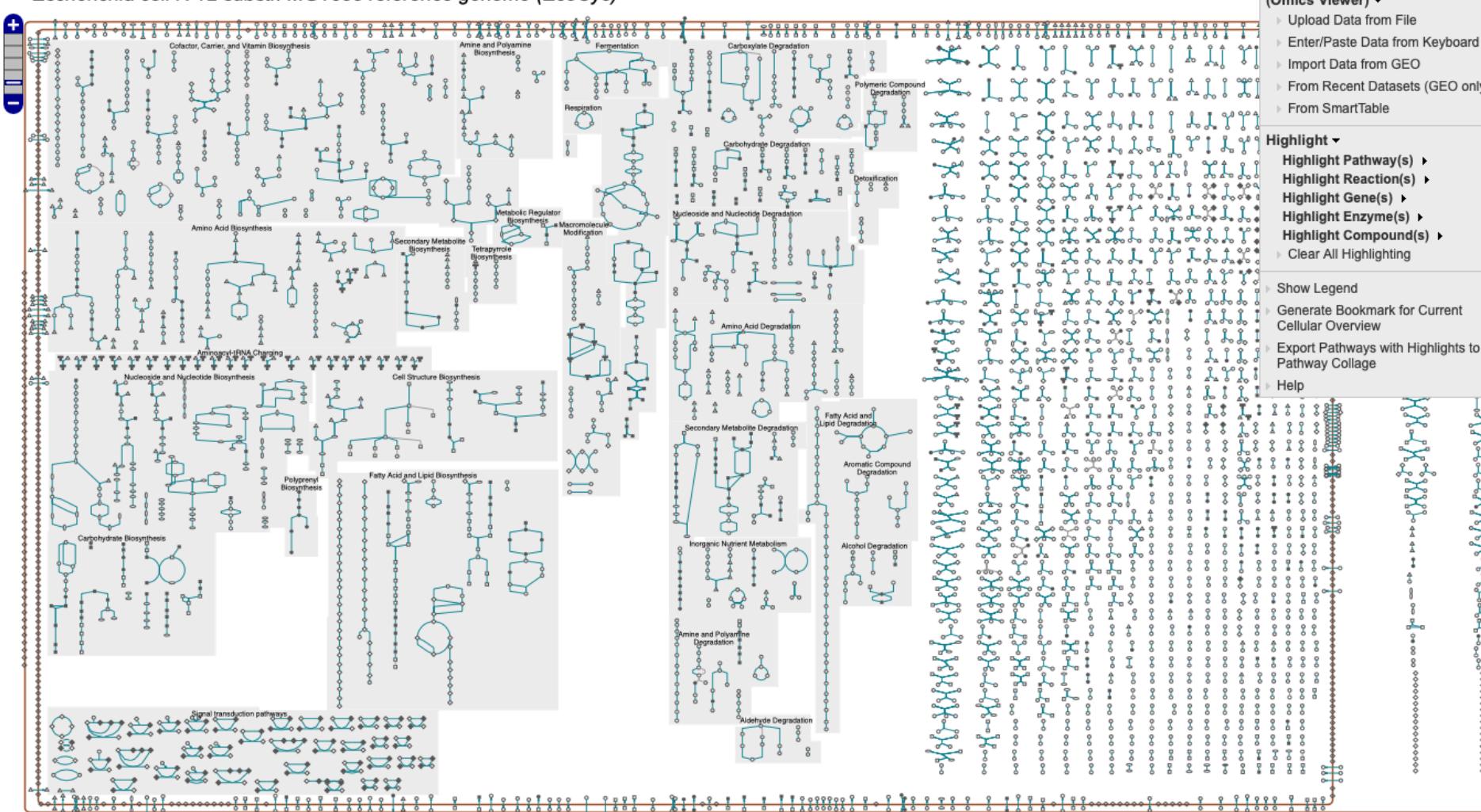
Block Search | Gene Search |

large organism database

[Searching Escherichia coli K-12 substr. MG1655 reference genome \(EcoCyc\)](#) | [change organism database](#)

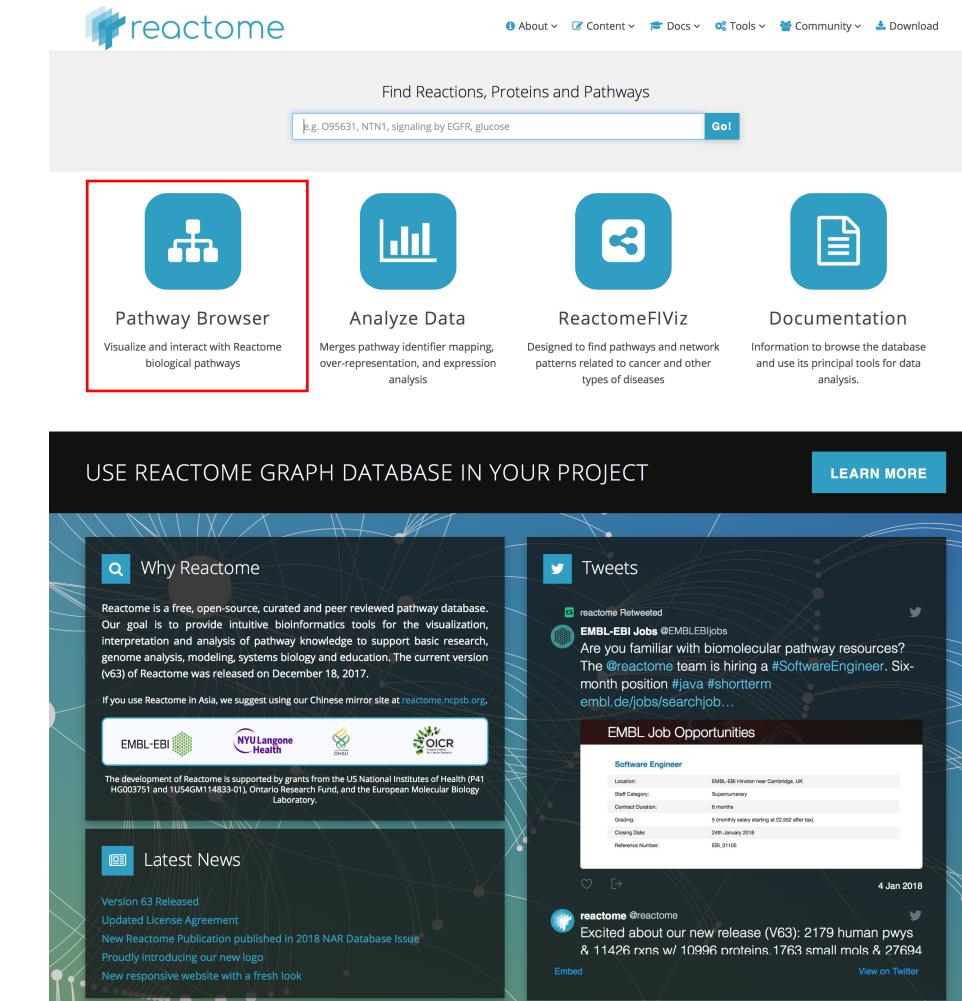
Sites ▾ | Search ▾ | Genome ▾ | Metabolism ▾ | Analysis ▾ | SmartTables ▾ | Help ▾

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



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



Reactome

Pathway Browser

The screenshot shows the Reactome Pathway Browser interface. At the top, there's a navigation bar with the Reactome logo, version 3.7, a search bar for 'Homo sapiens', citation and analysis links, and a tour/toggle layout button. On the left, a sidebar titled 'Event Hierarchy' lists various biological categories with corresponding icons. The main area displays a complex, branching network of pathways in blue, with nodes representing different biological processes like 'Metabolism', 'Signal Transduction', and 'Cell Cycle'. A large central node is labeled 'Metabolism'. Below the main map, there are tabs for 'Description', 'Molecules', 'Structures', 'Expression', 'Analysis', and 'Downloads'. A tooltip at the bottom left explains the 'Description' tab. The bottom right corner features a blue clipboard icon.

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

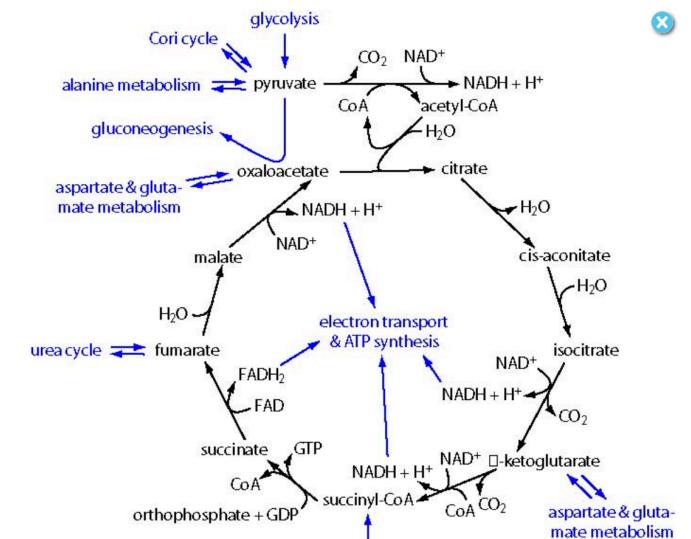
Pathways for: Homo sapiens

Citation: Analysis: Tour: Layout:

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7,000種（>540真核生物、>5,900真正細菌、>330古細菌）、ウイルス 349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。

The screenshot shows the KEGG homepage. At the top is the KEGG logo and a search bar. Below the search bar is a menu bar with links to KEGG Home, Database, Objects, and Software. The main content area features a banner for the Kyoto Encyclopedia of Genes and Genomes (KEGG). It includes a summary of KEGG's purpose, a release note, and an announcement about the KEGG NETWORK release. A red box highlights the "Main entry point to the KEGG web service" link, which points to the KEGG2 page. The KEGG2 page lists various data-oriented entry points such as KEGG PATHWAY, BRITE, MODULE, ORTHOLOGY, GENOME, GENES, SSDB, COMPOUND, GLYCAN, REACTION, ENZYME, NETWORK, DISEASE, DRUG, and MEDICUS.

The screenshot shows the KEGG2 search results page with a table titled "Data-oriented entry points". The table has four columns: Category, Entry Point, Content, and DBGET Search. The categories include Systems information, Genomic information, Chemical information, and Health information. Each category lists specific KEGG entries with their corresponding descriptions and DBGET search terms.

Category	Entry Point	Content	DBGET Search
Systems information	KEGG PATHWAY KEGG BRITE KEGG MODULE	KEGG pathway maps BRITE hierarchies and tables KEGG modules	PATHWAY BRITE MODULE
Genomic information	KO (KEGG Orthology) KEGG GENOME KEGG GENES KEGG SSDB	Functional orthologs KEGG organisms (complete genomes) Genes and proteins GENES sequence similarity	ORTHOLOGY GENOME GENES
Chemical information (KEGG LIGAND)	KEGG COMPOUND KEGG GLYCAN KEGG REACTION KEGG ENZYME	Small molecules Glycans Reactions and reaction classes Enzyme nomenclature	COMPOUND GLYCAN REACTION RCLASS ENZYME
Health information	KEGG NETWORK <small>New!</small> KEGG DISEASE KEGG DRUG KEGG ENVIRON KEGG MEDICUS	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

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

KEGG Cancer	Cancer research
KEGG Pathogen	Pathogen genomes and antimicrobial resistance
KEGG Virus	Virus research
KEGG Plant	Plant research
KEGG Annotation	KO annotation of genes and proteins
KEGG SeqData	KEGG sequence data collection
KEGG RModule	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 Cricetus 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						
Genome information						
T number	T01001					
Org code	hsa					
Aliases	HUMAN, 9606					
Full name	Homo sapiens (human)					
Definition	Homo sapiens (human)					
Category	Reference genome					
Annotation	yes					
Taxonomy	TAX: 9606					
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo					
Data source	RefSeq (Assembly: GCF_000001405.39) BioProject: 168					
Original DB	NCBI , OMIM , HGNC , HPRD , Ensembl , Vega , Pharos					
Statistics	Number of protein genes: 19768 Number of RNA genes: 2641					
Created	2000					
Reference	PMID: 11237011					
Authors	Lander ES, Linton LM, Birren B, Nusbaum C, Zody MC, Baldwin J, Devon K, Dewar K, Doyle M, FitzHugh W, et al.					
Title	Initial sequencing and analysis of the human genome.					
Journal	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: 541 Bacteria: 5955 Archaea: 334

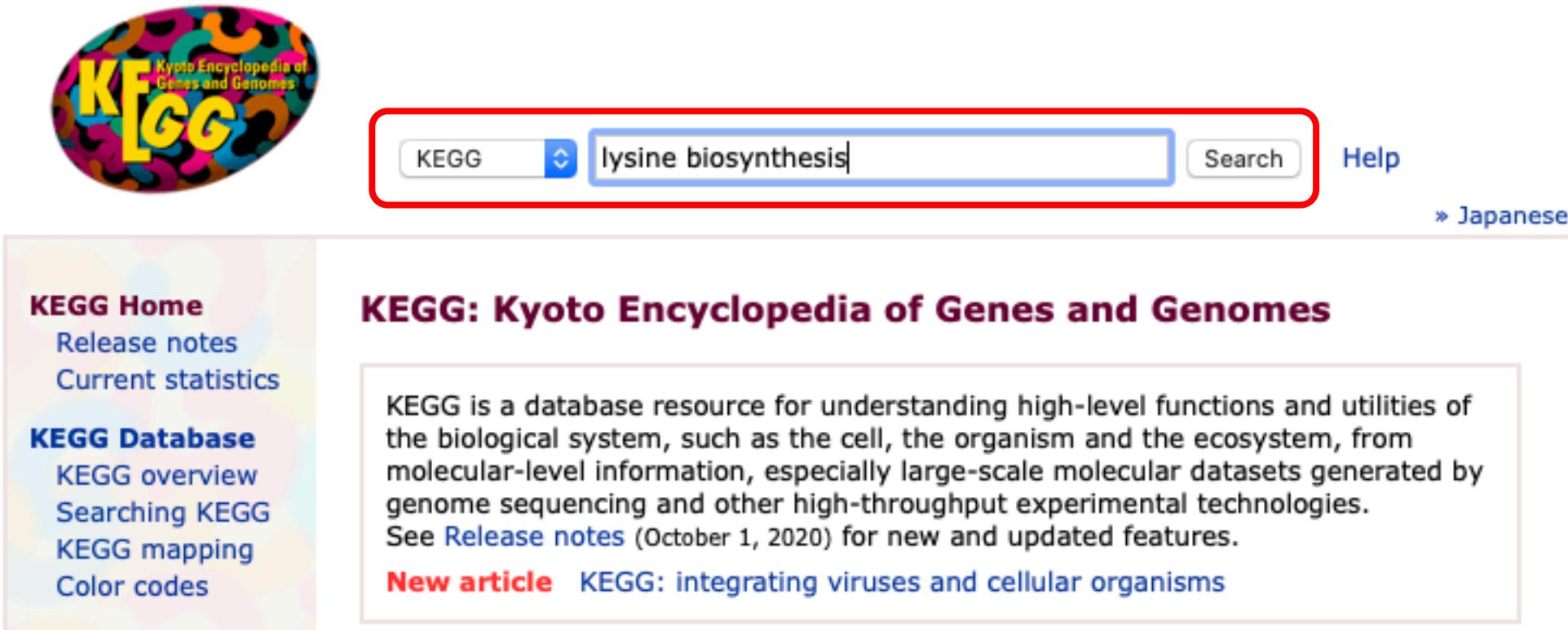
[Genomes | Species | Genus | Viruses | Meta]

Eukaryotes

Category	Organisms		Source
	hsa	Homo sapiens (human)	RefSeq
	ptr	Pan troglodytes (chimpanzee)	RefSeq
	pps	Pan paniscus (bonobo)	RefSeq

KEGGパスウェイマップを見る

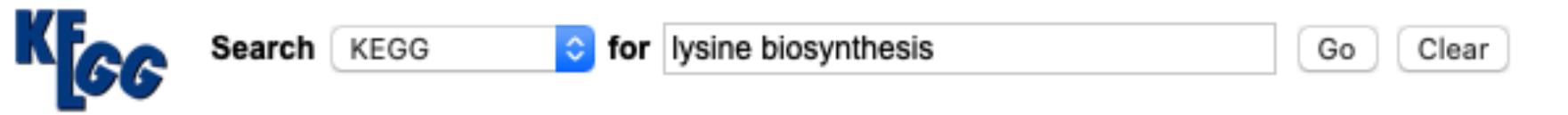
- トップページ (<https://www.kegg.jp>) 上方の検索ボックスで "lysine biosynthesis" や "glycolysis" やなどの生命現象関連の単語を入力し、Search ボタンをクリック



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 buttons for "Search" and "Help", and a link to "» Japanese". Below the search bar, the text "KEGG: Kyoto Encyclopedia of Genes and Genomes" is displayed in bold. A box contains a paragraph about KEGG's purpose and a link to "Release notes". At the bottom of the main content area, there is a red banner with the text "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。



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

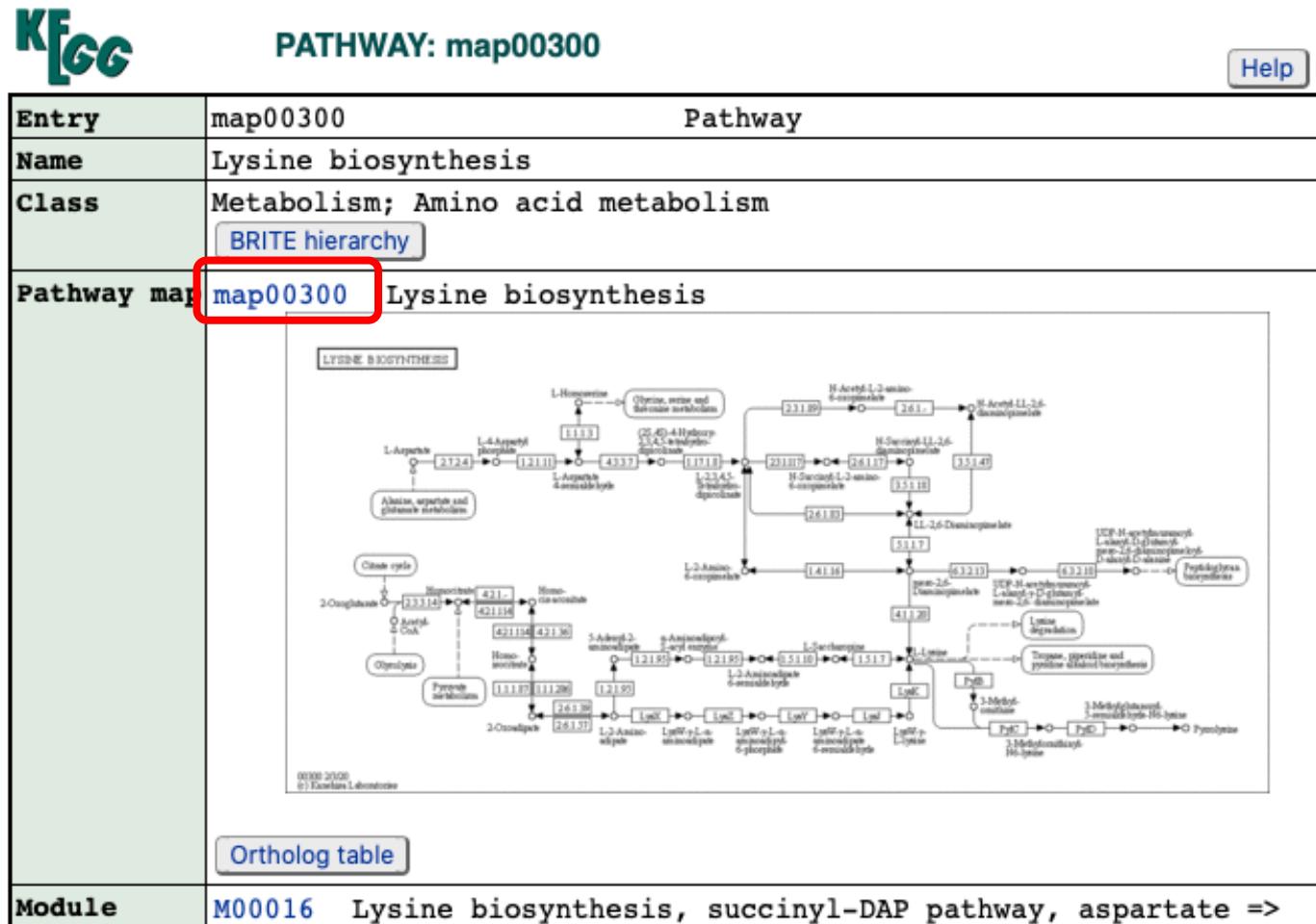
Lysine biosynthesis, mediated by LysW, 2-aminoadipate => lysine

M00433

Lysine biosynthesis, 2-oxoglutarate => 2-oxoadipate

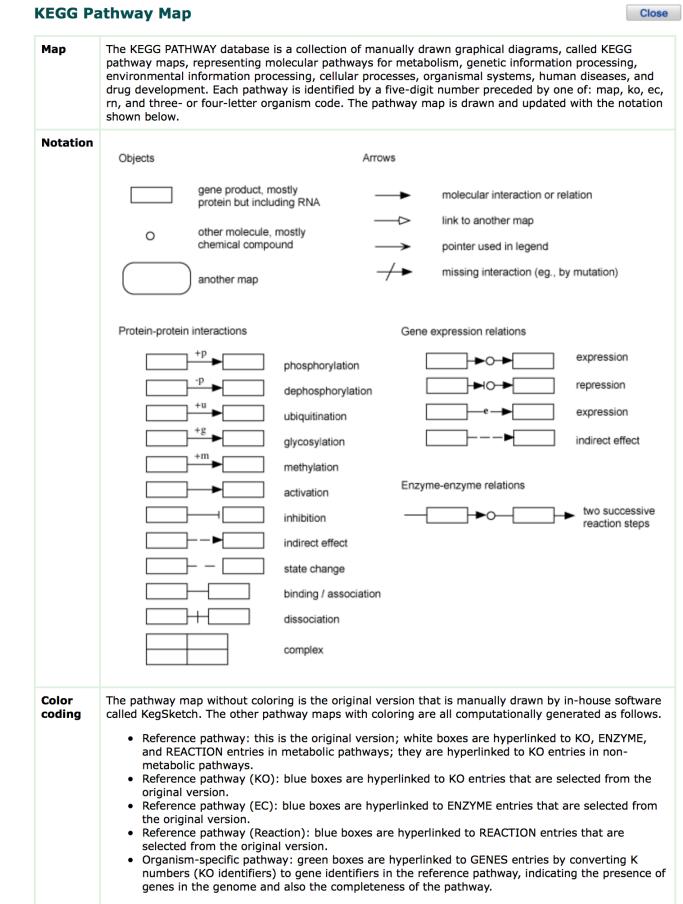
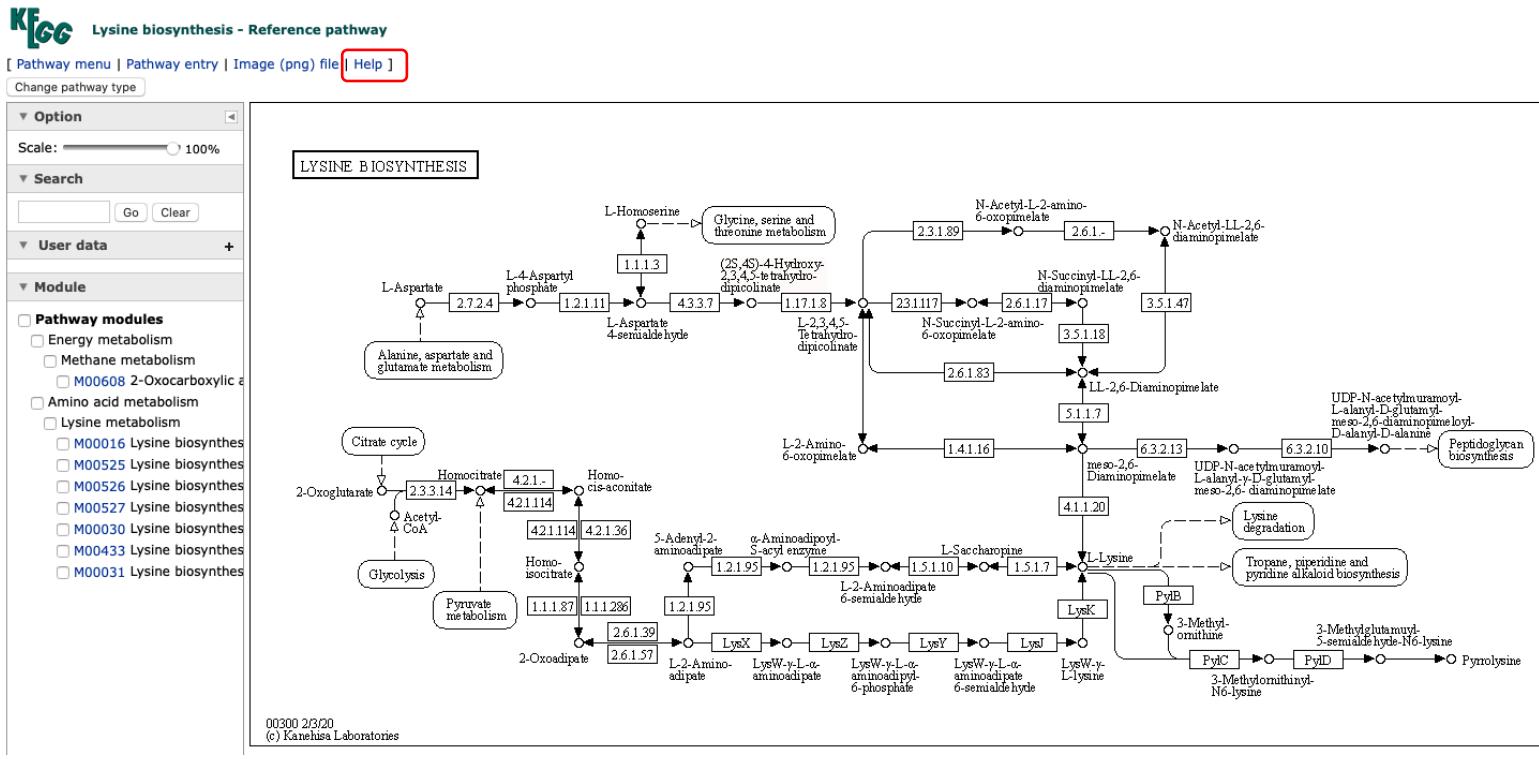
KEGGパスウェイマップ

- 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

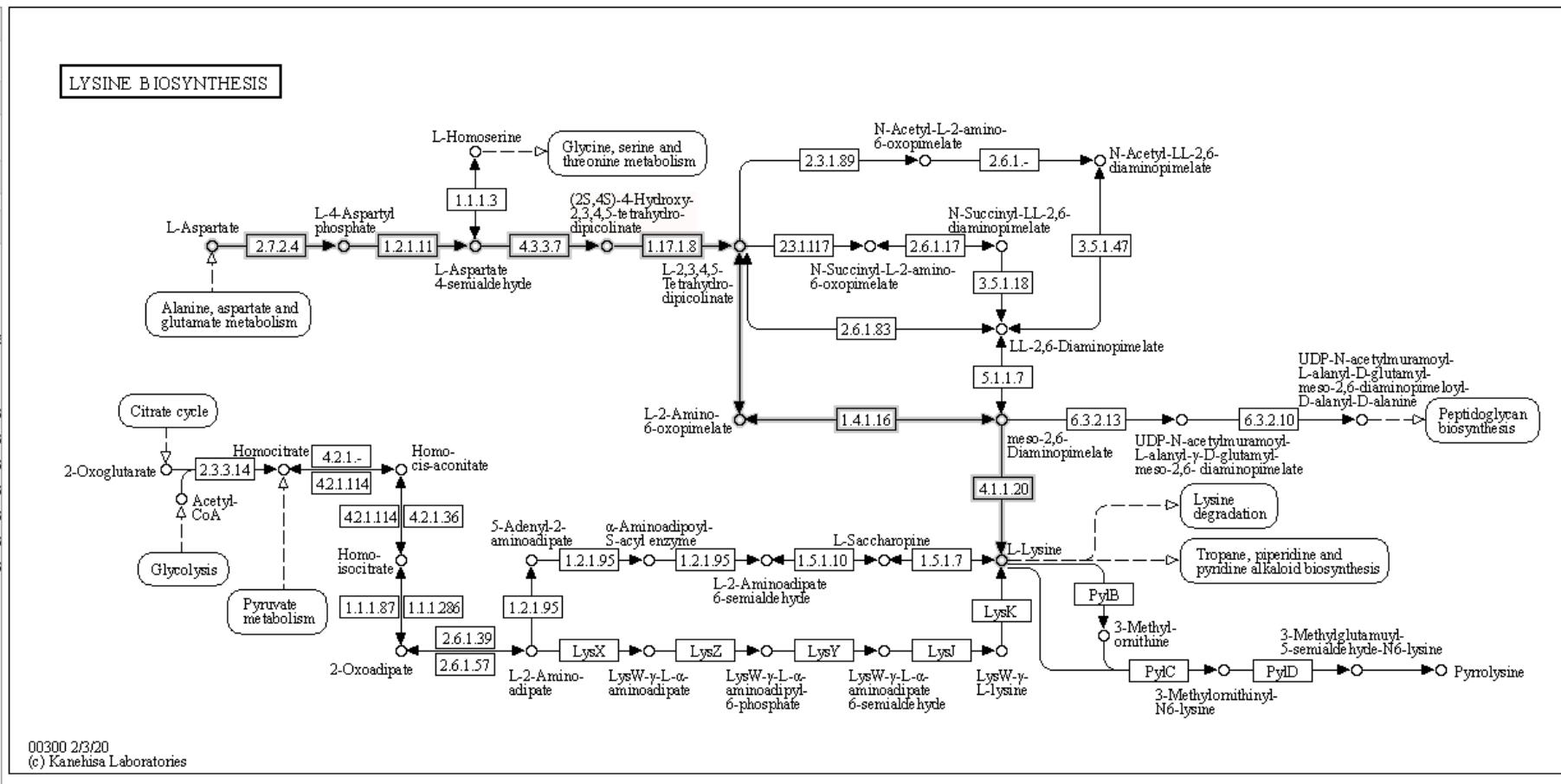
- この色のついていない白いダイアグラムが、専門家が手作業で文献ベースから作成したリファレンスパスウェイになります
 - ボックスが遺伝子やタンパク質などの配列情報、丸が代謝産物、環境物質などの化合物
 - 各図形の説明は右上の Help から見られます



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
 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

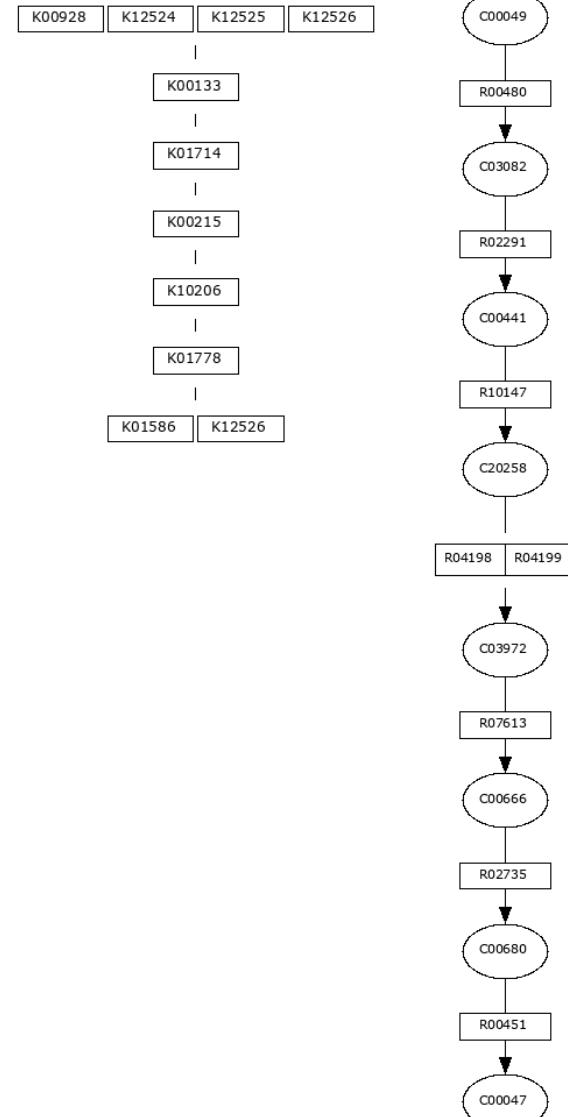
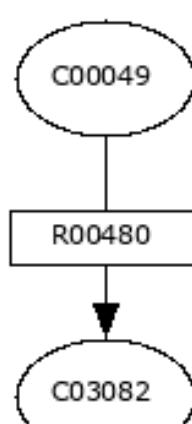
R02735 C00666 -> C00680

R00451 C00680 -> C00047

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

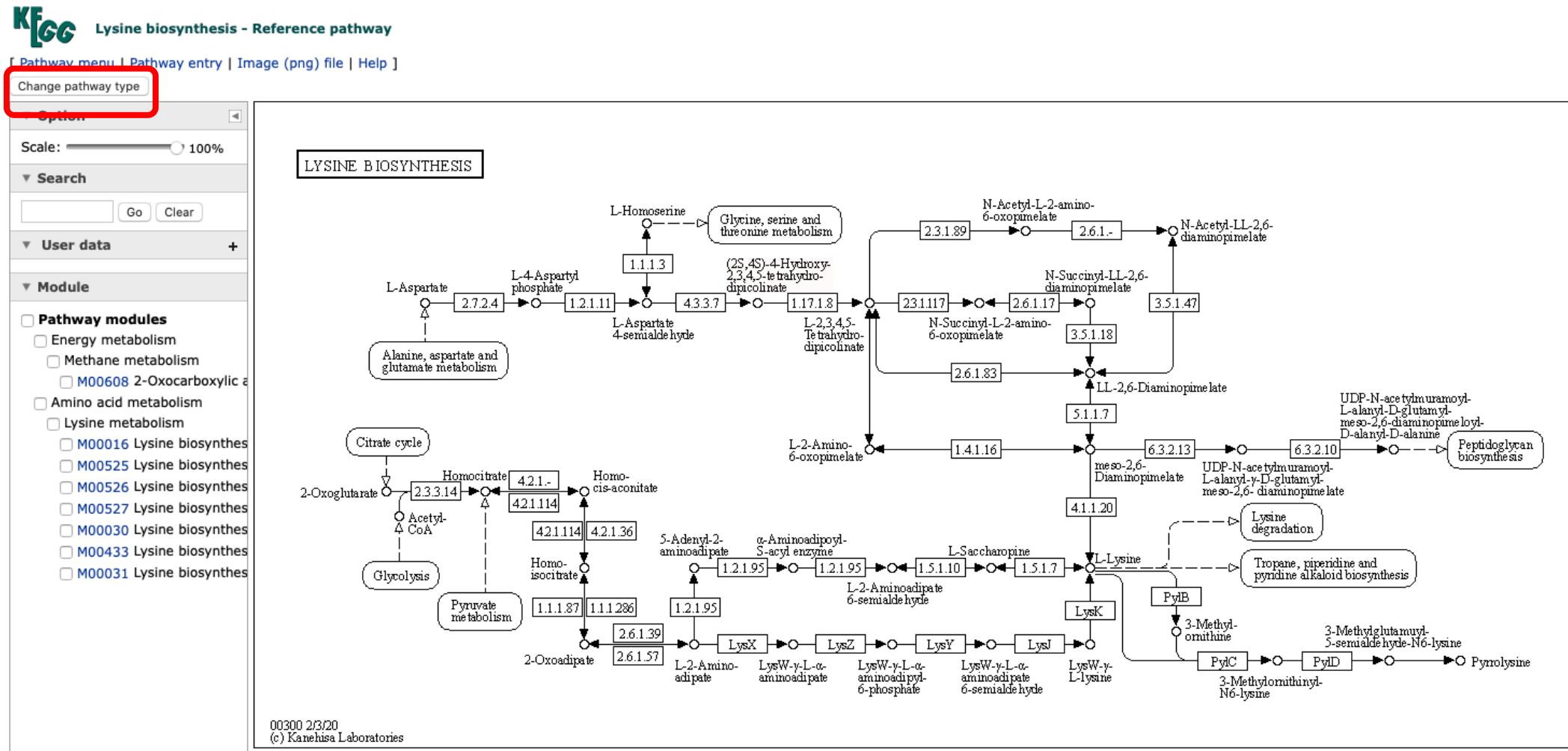
|
K00133
|

|
K01714
|



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

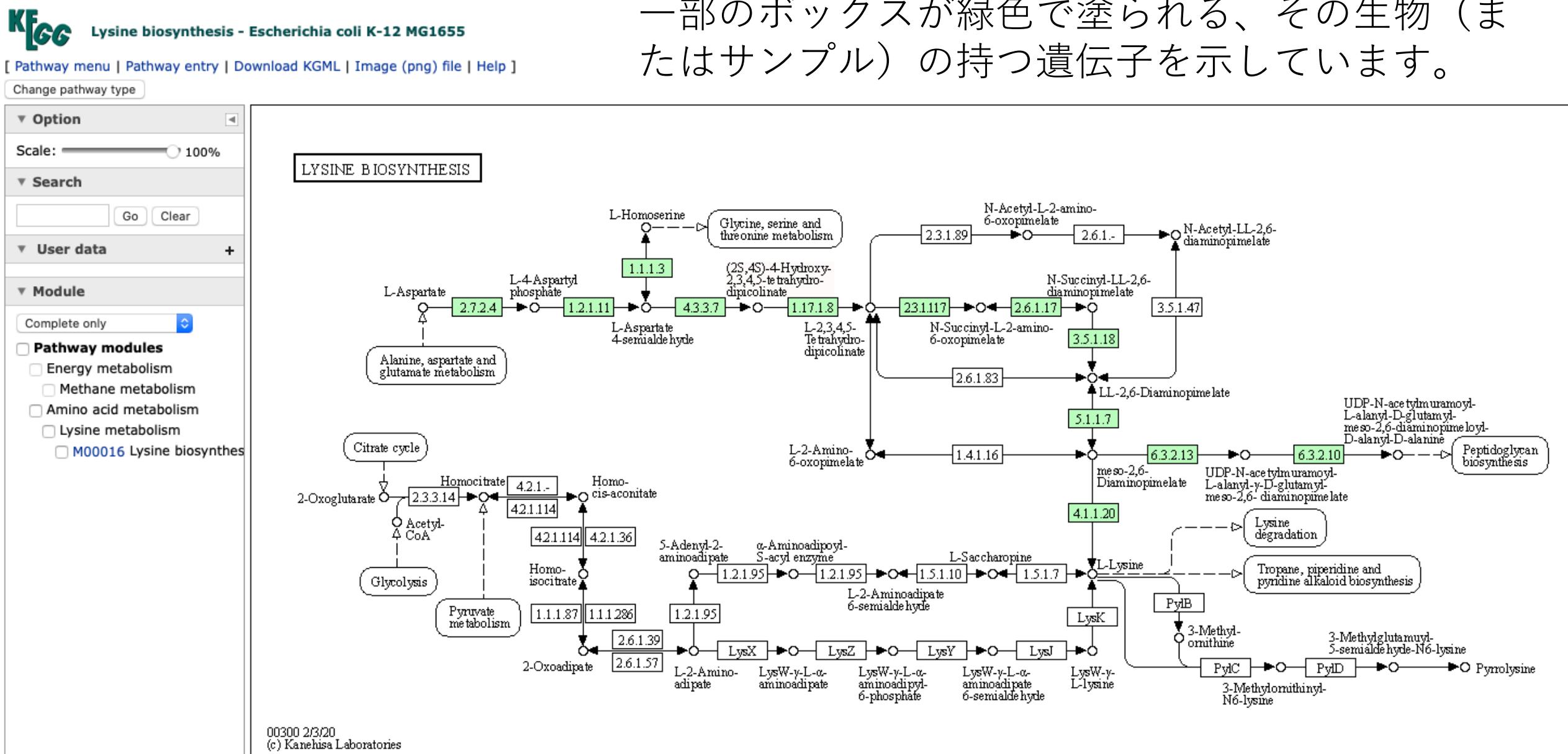
Select pathway typeのパネルがポップアップ

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

一部のボックスが緑色で塗られる、その生物（またはサンプル）の持つ遺伝子を示しています。



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

Prokaryotes

Category

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)
	eo Escherichia coli O111:H- 11128 (EHEC)

Pathway map

Genome info Pathway map Brite hierarchy Module Genome map Blast Taxonomy

Search genes: Go Clear

Genome information

T number	T00007
Org code	eco
Aliases	ECOLI, 511145
Full name	Escherichia coli K-12 MG1655
Definition	Escherichia coli K-12 MG1655
Category	Reference genome
Annotation	yes
Taxonomy	TAX: 511145

Lysine biosynthesis マップ

00250 Pyrimidine metabolism

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

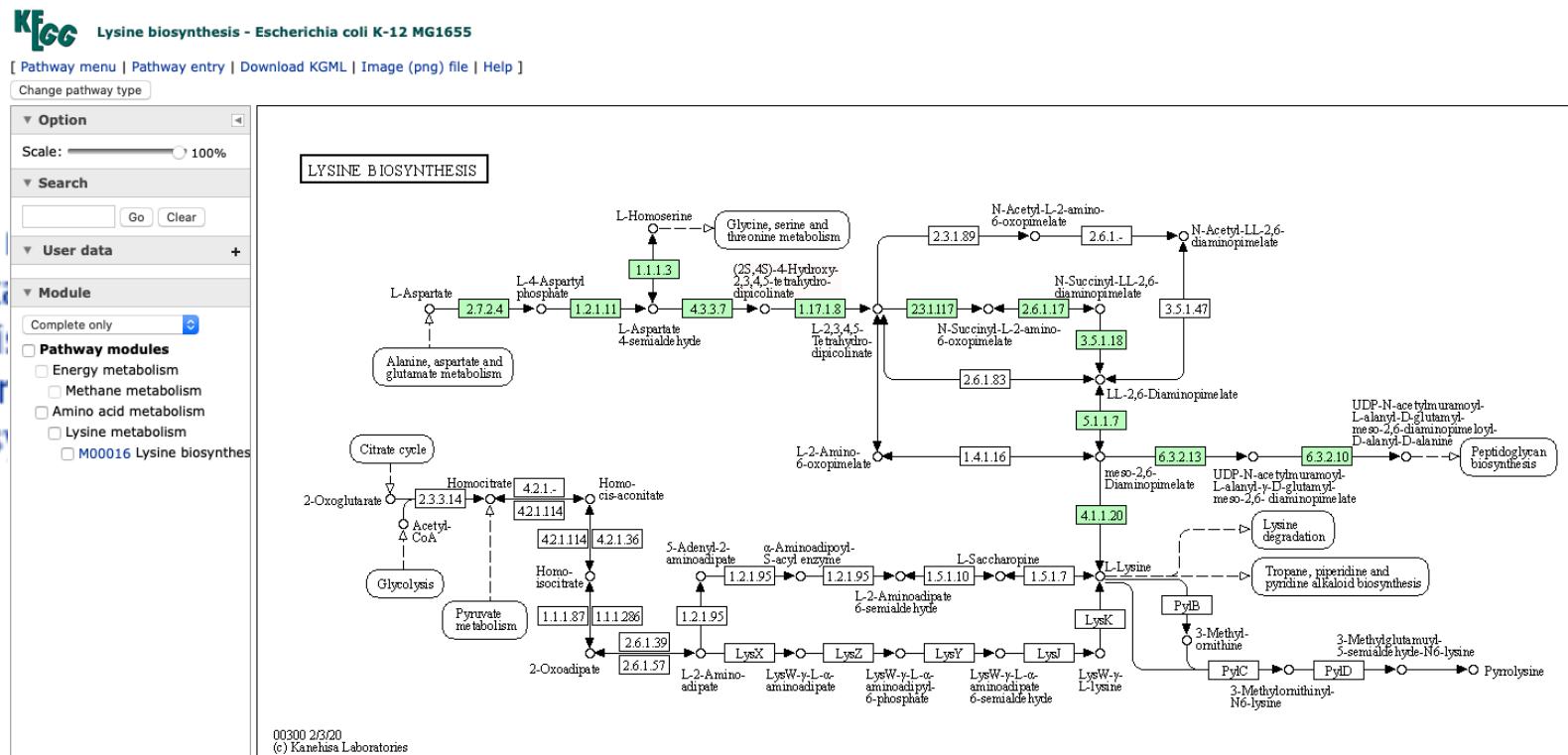
00380 Tryptophan metabolism

00400 Phenylalanine, tyrosine and tryptophan biosynthesis

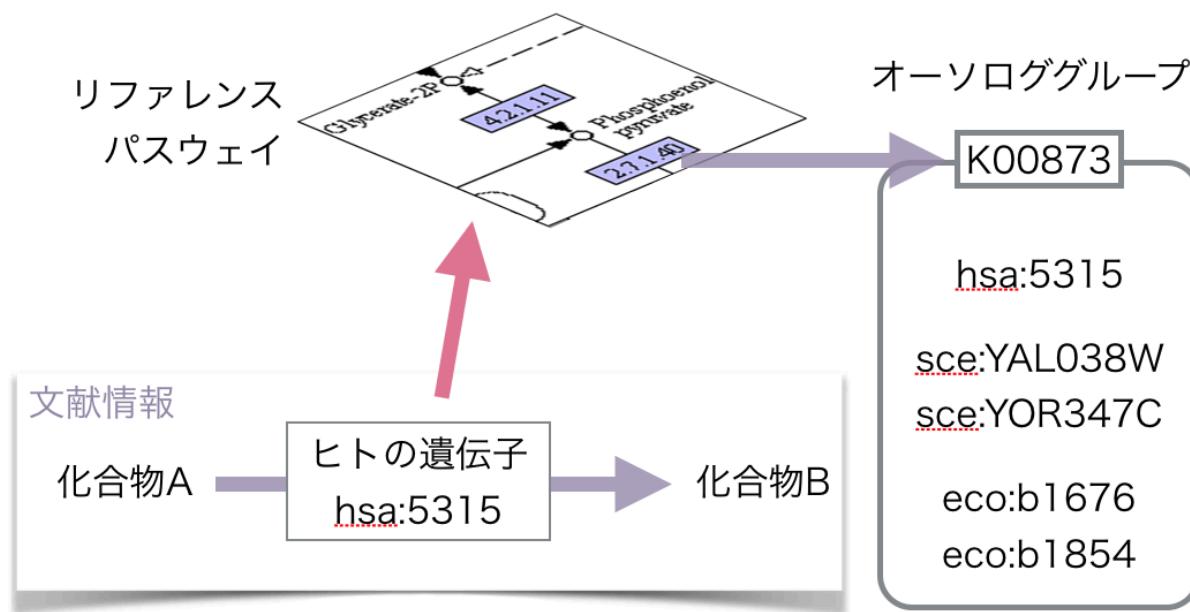
Metabolism of other amino acids

00410 beta-Alanine metabolism

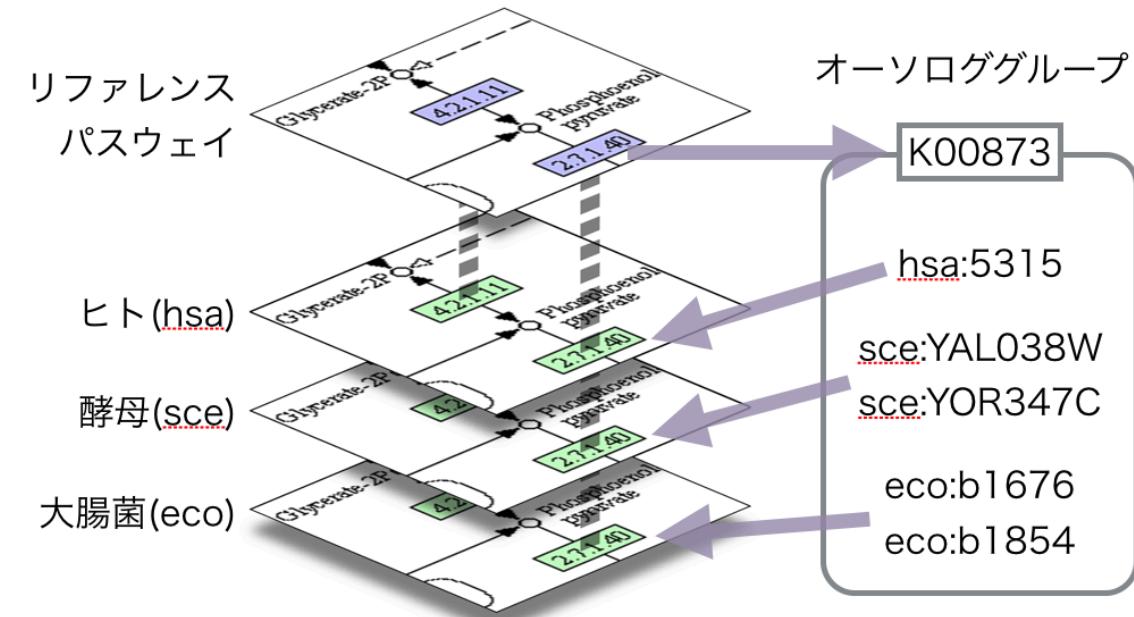
00430 Taurine and hypotaurine metabolism



リファレンスパスウェイと種毎のパスウェイの関係



文献情報からリファレンスパスウェイが作成される



KOと化合物のネットワークであるリファレンスパスウェイを基に、生物種毎のパスウェイが作られる

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](#)

▼ Option

Scale:  30%

Link: Normal

Search

10

1

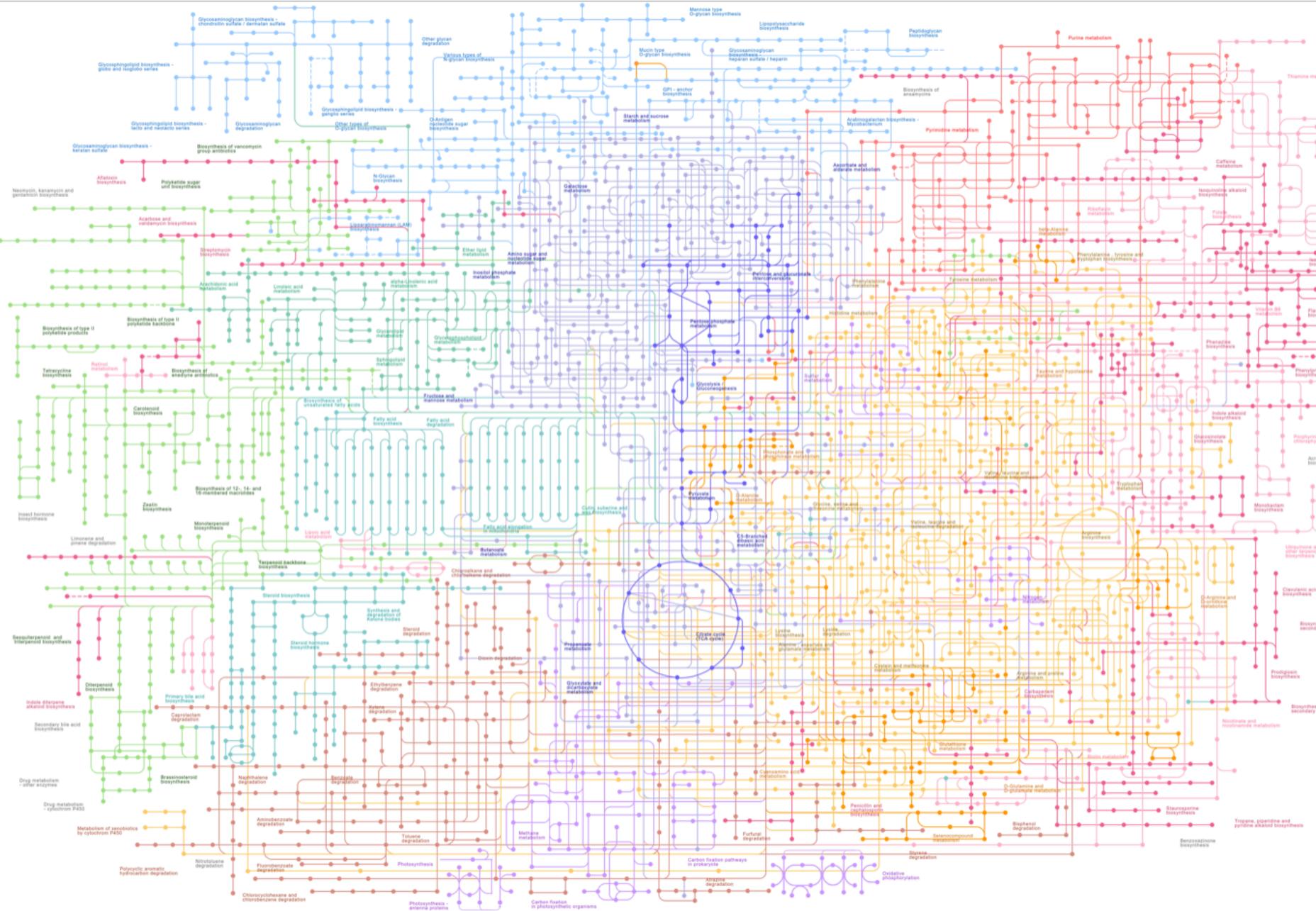
▼ User data

Page 1

▼ Module

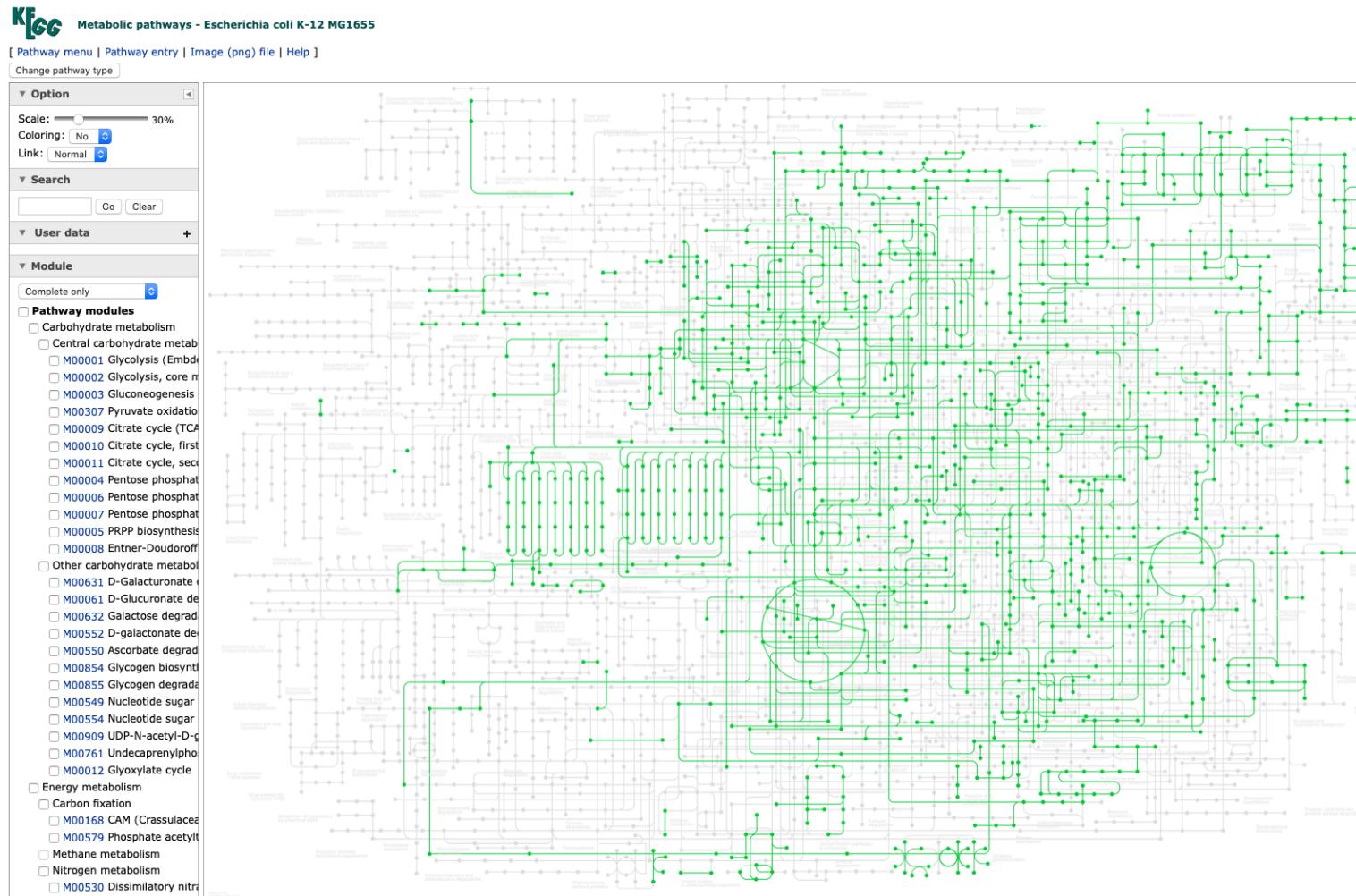
Pathway modules

- Carbohydrate metabolism
 - Central carbohydrate metab
 - M00001 Glycolysis (Embden-Meyerhof-Parnet pathway)
 - M00002 Glycolysis, core part
 - M00003 Gluconeogenesis
 - M00307 Pyruvate oxidation
 - M00009 Citrate cycle (TCA cycle)
 - M00010 Citrate cycle, first step
 - M00011 Citrate cycle, second step
 - M00004 Pentose phosphate pathway
 - M00006 Pentose phosphate pathway
 - M00007 Pentose phosphate pathway
 - M00580 Pentose phosphate pathway
 - M00005 PRPP biosynthesis
 - M00008 Entner-Doudoroff pathway
 - M00308 Semi-phosphorylated glucose-6-phosphate
 - M00633 Semi-phosphorylated glucose-6-phosphate
 - M00309 Non-phosphorylated glucose-6-phosphate
 - Other carbohydrate metabolism
 - M00014 Glucuronate pathway
 - M00630 D-Galacturonate degradation
 - M00631 D-Galacturonate biosynthesis
 - M00061 D-Glucuronate degradation
 - M00081 Pectin degradation
 - M00632 Galactose degradation
 - M00552 D-galactonate degradation
 - M00129 Ascorbate biosynthesis
 - M00114 Ascorbate biosynthesis
 - M00550 Ascorbate degradation
 - M00854 Glycogen biosynthesis
 - M00855 Glycogen degradation
 - M00565 Trehalose biosynthesis
 - M00549 Nucleotide sugar nucleotidyl transferase
 - M00554 Nucleotide sugar nucleotidyl transferase
 - M00892 UDP-N-acetyl-D-glucosamine
 - M00909 UDP-N-acetyl-D-glucosamine
 - M00761 UDP-N-acetyl-D-glucosamine



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

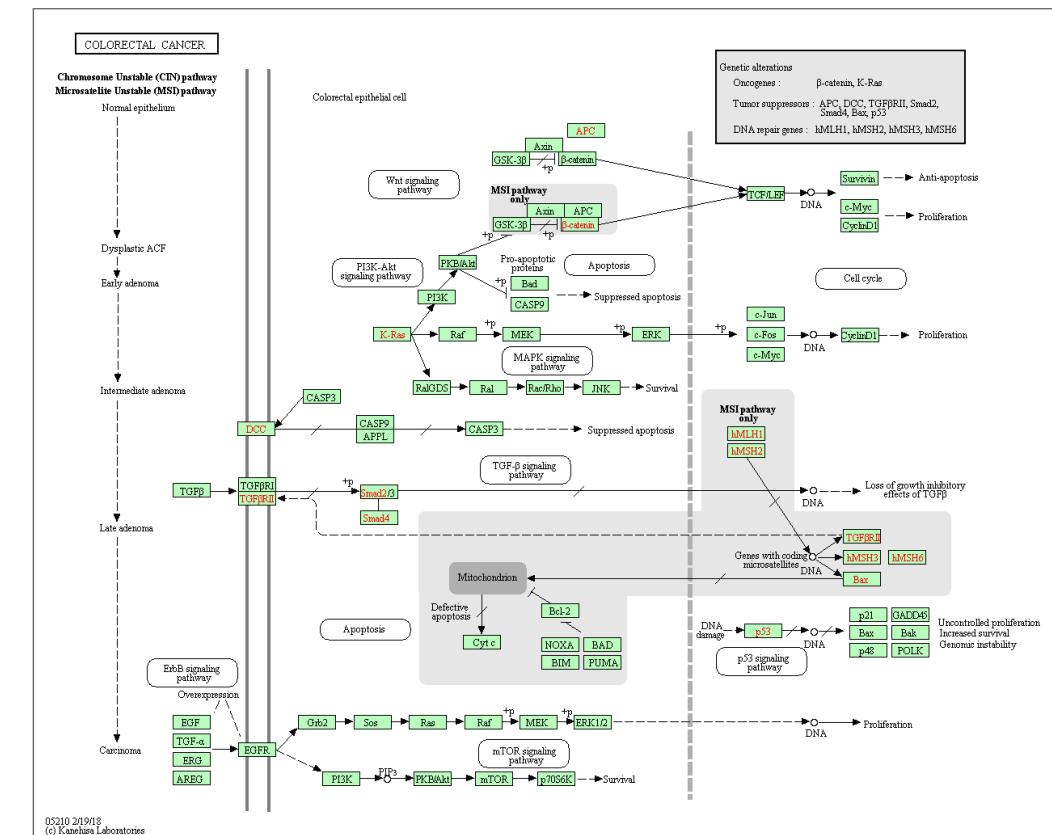
- <https://www.kegg.jp/kegg/pathway.html#disease>
- がん、免疫系疾患、神経変性疾患など多因子性の疾患
- 好きな疾患パスウェイをクリック（例：[大腸がん](#)）
 - 赤字の遺伝子が疾患の病因遺伝子を示しています。

6.1 Cancer: overview

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

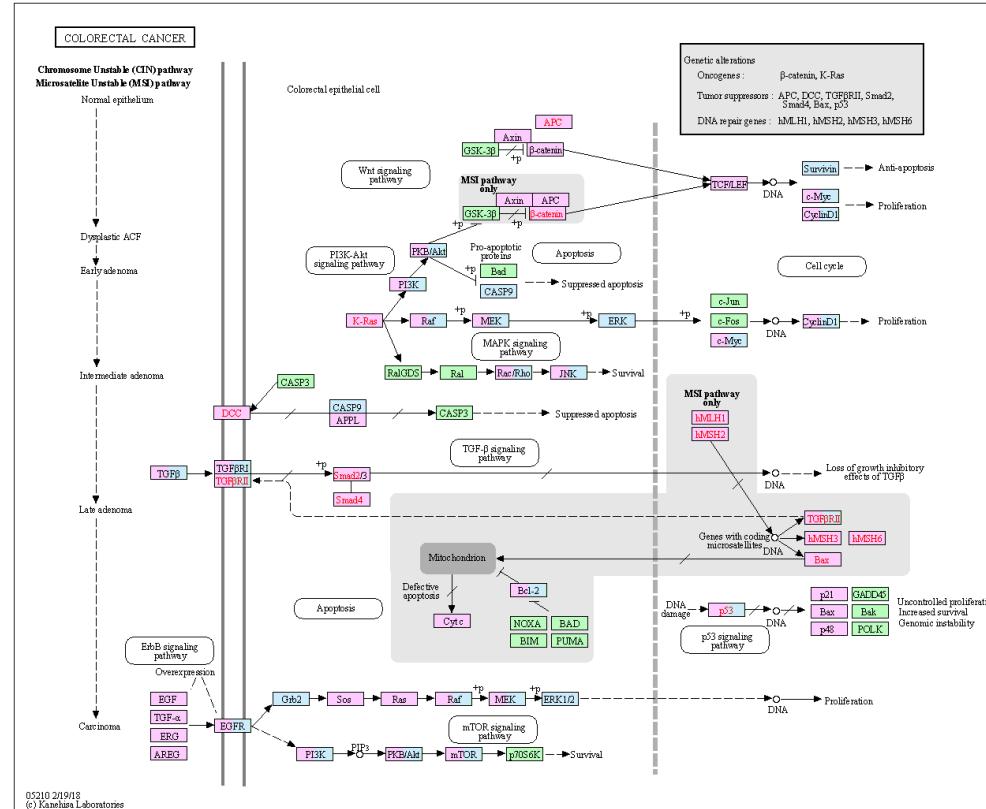
6.2 Cancer: specific types

- 05210 N Colorectal cancer
- 05212 N Pancreatic cancer
- 05225 N Hepatocellular carcinoma
- 05226 N Gastric cancer
- 05214 N Glioma
- 05216 N Thyroid cancer
- 05231 N Acute myeloid leukemia



ヒトの疾患パスウェイ

- Change pathway typeで Homo sapiens (human) + Disease/drug 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



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

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)

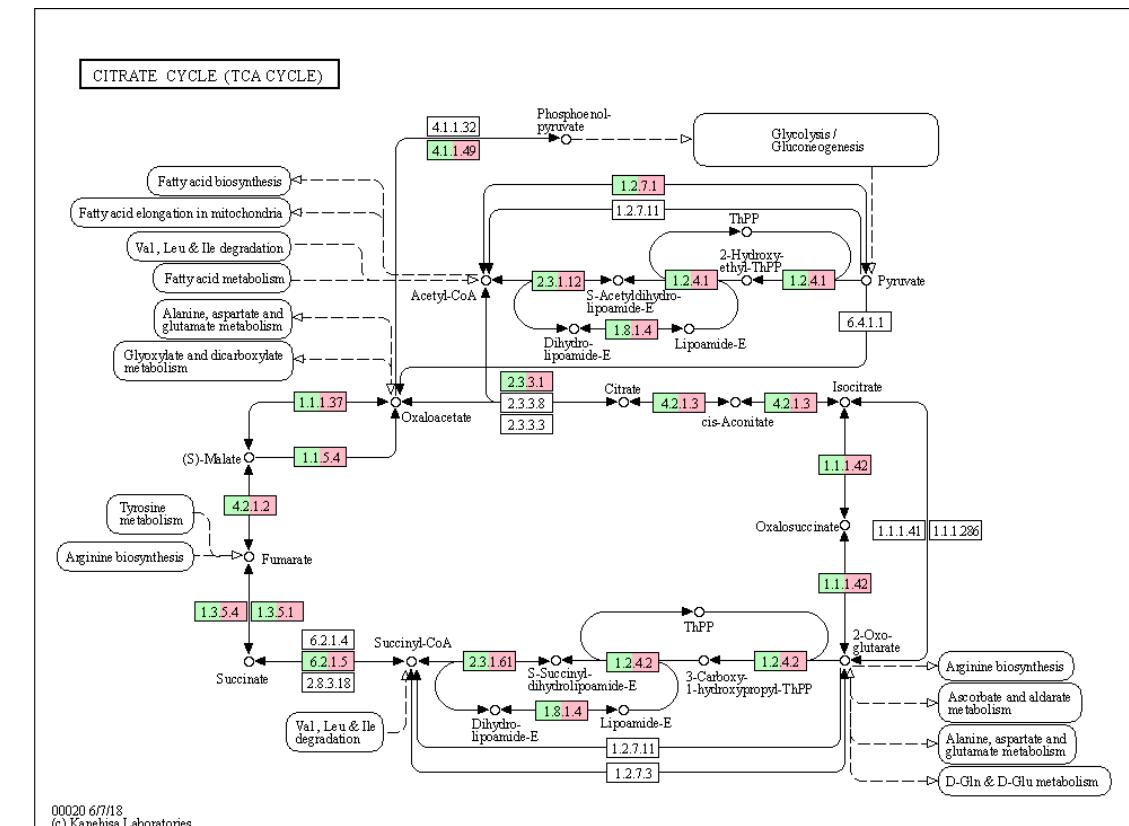
[hsa+T30003](#) Homo sapiens (human) + gut microbiome
such as [Global metabolism map](#)
where green for human, red for gut microbiome, and blue for both

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

KEGG Organism group: eco ecs

Category info	Pathway map	Brite hierarchy	Taxonomy
Search genes:	<input type="text"/> 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

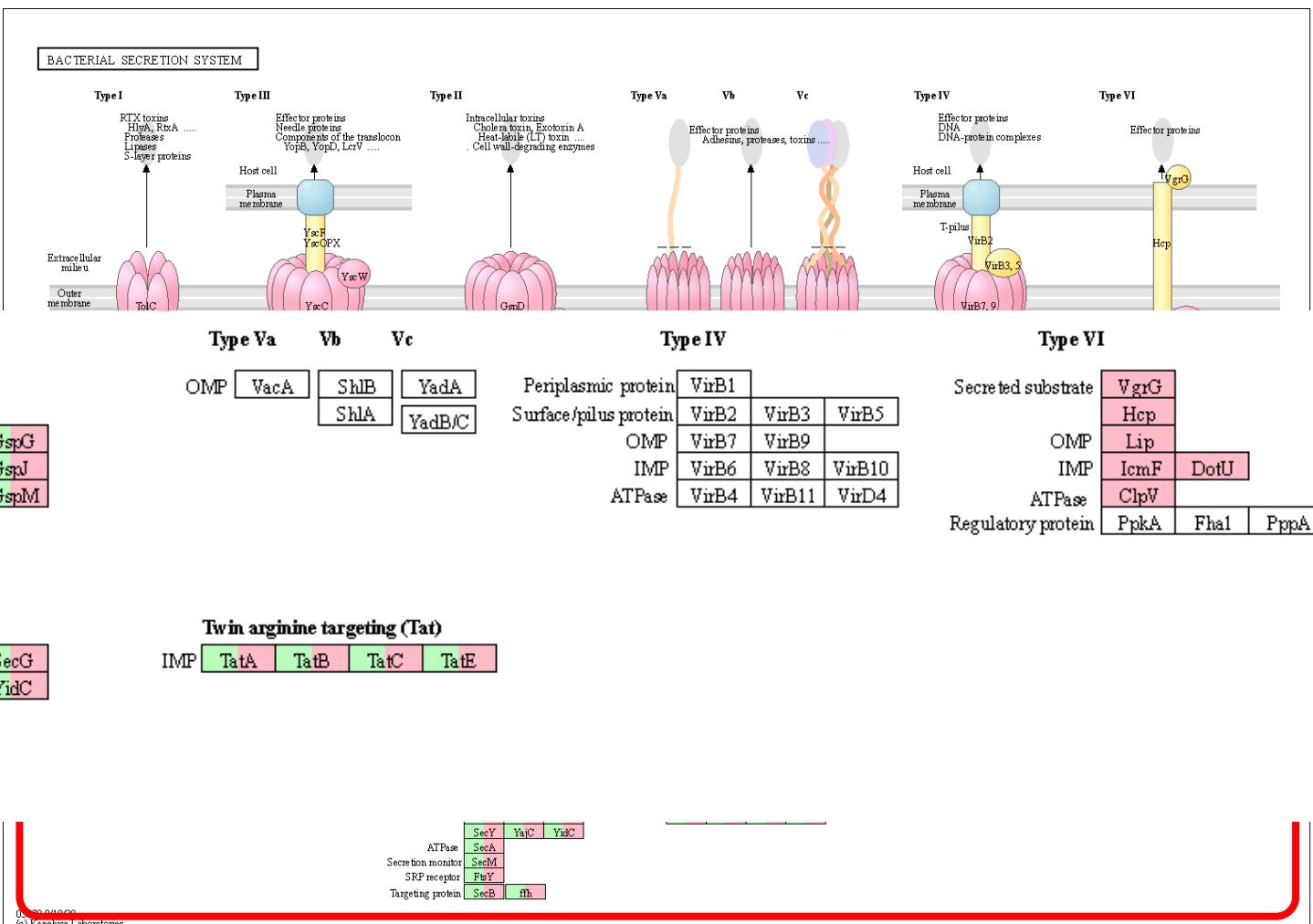
02010 ABC transporters

02060 Phosphotransferase system (PTS)

	Type I	Type III
Outer membrane protein (OMP)	TolC	YscF
Membrane fusion protein	HlyD	YscO YscP YscX
ABC transporter	HlyB	
Inner membrane protein (IMP)	YscC	
	YscW	
ATPase	YscJ YscR YscS	
	YscT YscU YscV	
ATPase-associated protein	YscN	YscL
	YscQ	

	Type II
Secretin	GspD
OMP	GspS
IMP	GspC GspF GspG
	GspH GspI GspJ
	GspK GspL GspM
ATPase	GspE
Leaderpeptidase	GspO

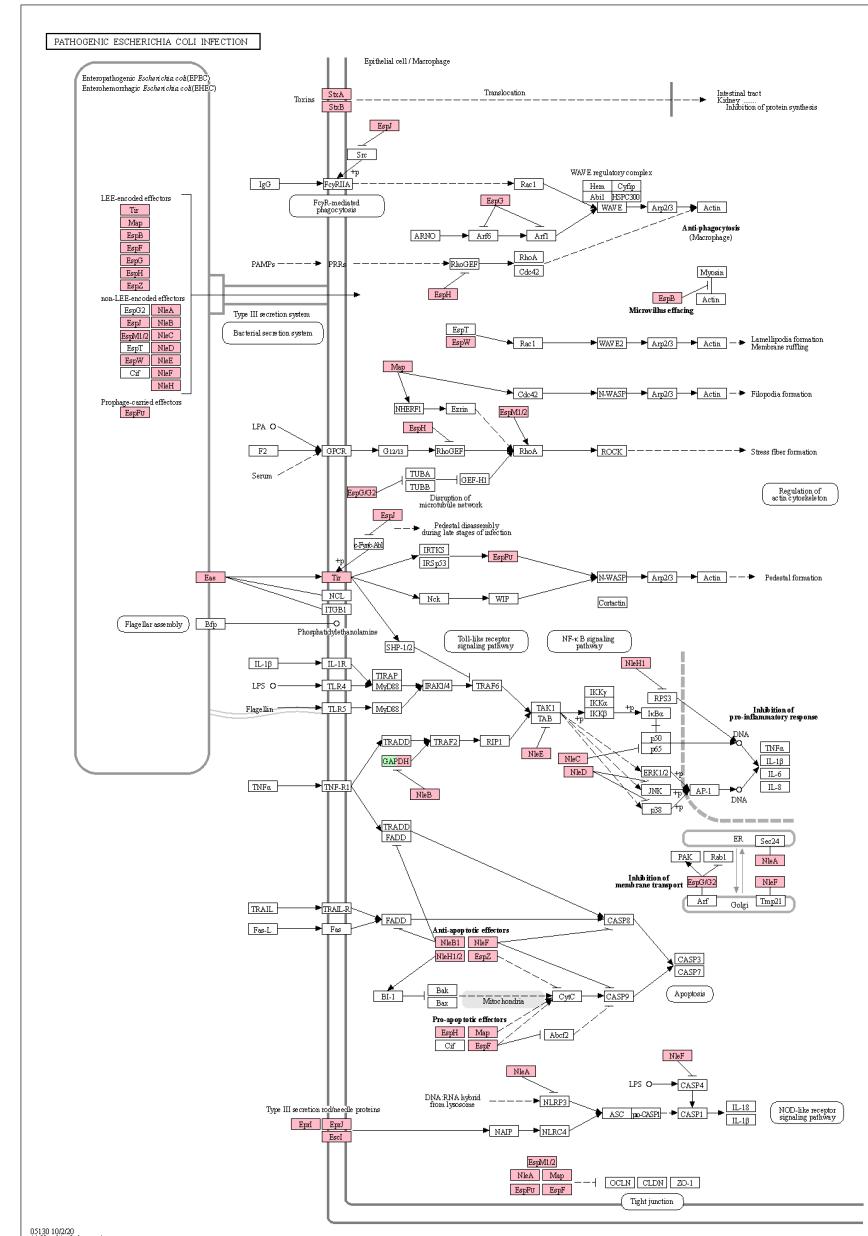
	Sec-SRP	Twin arginine targeting (Tat)
IMP	SecD/F SecE SecG	TatA TatB TatC TatE
	SecY YajC YidC	
ATPase	SecA	
Secretion monitor	SecM	
SRP receptor	FtsY	
Targeting protein	SecB ffh	



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 *Salmonella* infection
 - 05131 Shigellosis
 - 05135 *Yersinia* infection
 - 05133 Pertussis
 - 05134 Legionellosis
 - 05150 *Staphylococcus aureus* infection
 - 05152 Tuberculosis
 - 05100 Bacterial invasion of epithelial cells

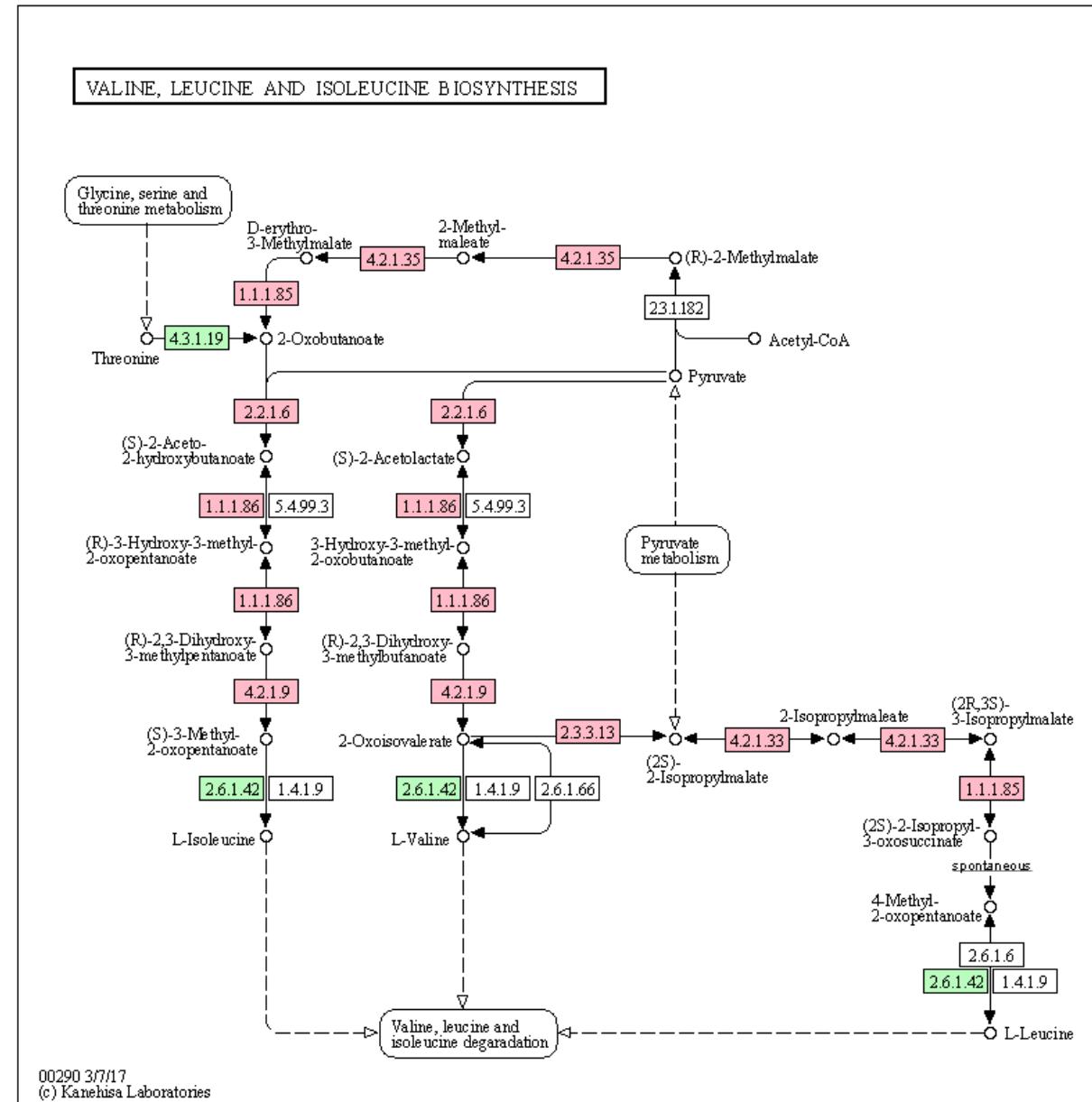


アブラムシとブフネラで種間比較

- 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 [Search&Color Pathway](#) をクリック
 - Search against : データベースコード
 - Primary ID : ID 種類 (KEGG ID, NCBI-GeneID, NCBI-ProteinID, UniProt)
 - 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-GeneID, 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](#): most popular KEGG pathway mapping, as well as BRITE mapping and MODULE mapping. In this new release, fourteen existing tools were reorganized into just five tools. Three of them, "Reconstruct Pathway", "Search Pathway" and "Search&Color Pathway" allow multiple mapping operations to be done at the same time. The result is shown in multiple tabs in the result page. The other two are specialized tools, "Color Pathway" and "Join Brite", for mapping against a single pathway map or a single brite hierarchy/table file.

Reference: Kanehisa, M. and Sato, Y. (2020) KEGG Mapper for inferring cellular functions from protein sequences. *Protein Sci.* 29, 28-35. [[pubmed](#)] [[pdf](#)]

General mapping tools against multiple databases

There are three general mapping tools with the name of "Pathway" but applicable to other target databases as well (see table below).

Reconstruct Pathway is the basic mapping tool used for processing of KO annotation (K number assignment) data both internally for KEGG GENES and in the outside services of [BlastKOALA](#) and other annotation servers.

Search Pathway and **Search&Color Pathway** are traditional tools present from the beginning of the KEGG project, although the target databases have been expanded. These tools match objects as they appear in both reference and organism-specific pathways, etc. Mapped objects are marked in red in Search Pathway, while they can be marked in any background and foreground colors in Search&Color Pathway.



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 – Search&Color Pathway

Target databases: Pathway, Brite hierarchy, Module

Search mode: Reference
 Organism-specific **hsa** Enter:
Optional use of outside ID:

Enter objects one per line followed by bgcolor, fgcolor:

7167 red,blue
C00118 pink

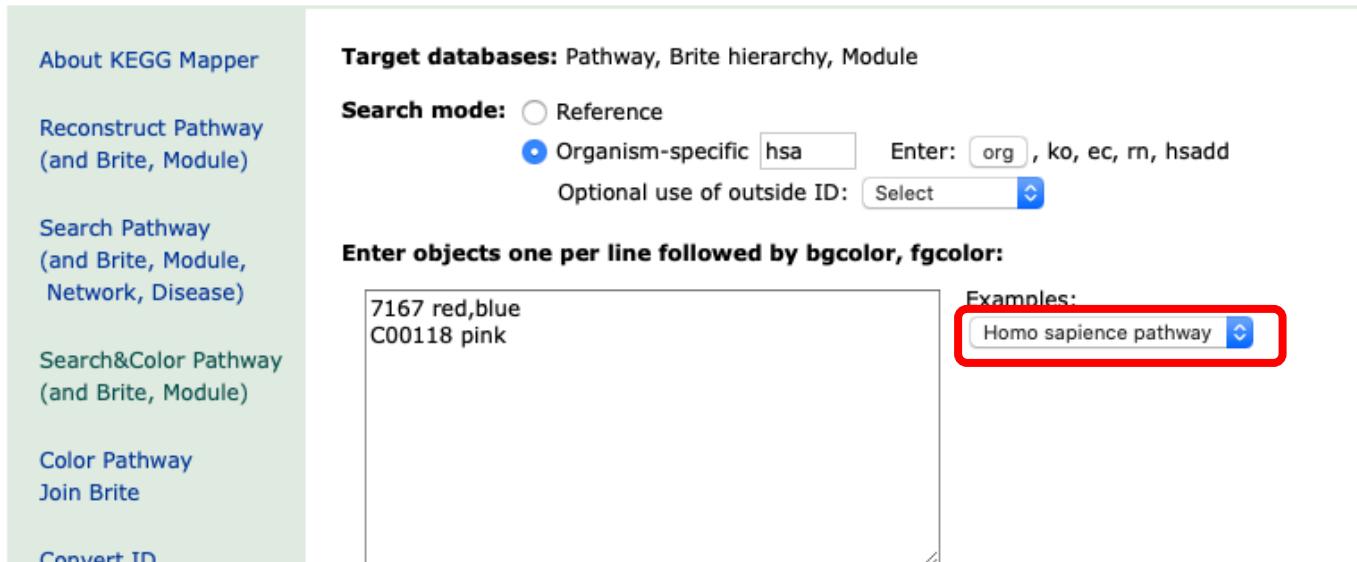
Examples:

Or upload file:
 ファイル未選択

If necessary, change default bgcolor:

Include aliases

Use uncolored diagrams



KEGG Mapper Search Result

[Pathway \(11\)](#)
[Brite \(3\)](#)
[Module \(13\)](#)
[Sort by the pathway list](#)
[Show matched objects](#)

[hsa01200](#) Carbon metabolism - Homo sapiens (human) (2)

[hsa01100](#) Metabolic pathways - Homo sapiens (human) (2)

[hsa01230](#) Biosynthesis of amino acids - Homo sapiens (human) (2)

[hsa00051](#) Fructose and mannose metabolism - Homo sapiens (human) (2)

[hsa00562](#) Inositol phosphate metabolism - Homo sapiens (human) (2)

[hsa00010](#) Glycolysis / Gluconeogenesis - Homo sapiens (human) (2)

[hsa00030](#) Pentose phosphate pathway - Homo sapiens (human) (1)

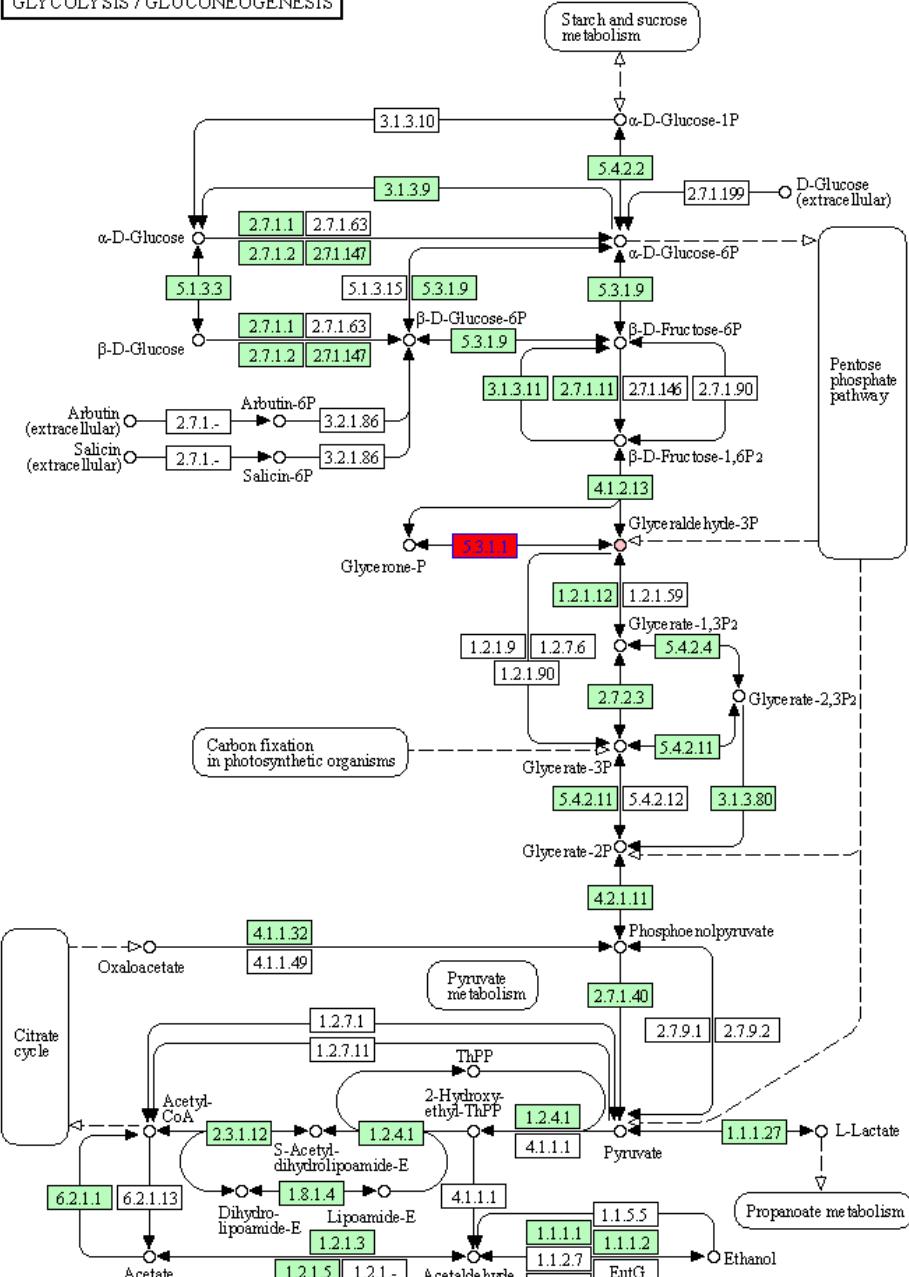
[hsa00052](#) Galactose metabolism - Homo sapiens (human) (1)

[hsa00900](#) Terpenoid backbone biosynthesis - Homo sapiens (human) (1)

[hsa00730](#) Thiamine metabolism - Homo sapiens (human) (1)

[hsa00750](#) Vitamin B6 metabolism - Homo sapiens (human) (1)

GLYCOLYSIS / GLUCONEOGENESIS



数値データをマッピング

- [Color Pathway](https://www.kegg.jp/kegg/tool/map_pathway3.html) (https://www.kegg.jp/kegg/tool/map_pathway3.html) をクリック
- 右のサンプル Numerical values to colorを選択
 - 中身は配列 ID と数値の対応リスト
- Select KEGG pathway map: でパスウェイを指定 (hsa05200)
- Option: で Numerical values converted to color gradationを選択
- Exec ボタンをクリック

KEGG Mapper – Color Pathway

About KEGG Mapper
Reconstruct Pathway (and Brite, Module)
Search Pathway (and Brite, Module, Network, Disease)
Search&Color Pathway (and Brite, Module)
Color Pathway Join Brite
Convert ID Annotate Sequence
BlastKOALA Map Taxonomy KEGG

Target data: Single pathway map
Select KEGG pathway map: hsa05200 (such as hsa05200)
Enter data:
#hsa COSMIC
hsa:25 678
hsa:861 26
hsa:867 13
hsa:1029 44
hsa:1050 4
hsa:1436 3
hsa:2146 9
hsa:2322 7
hsa:2623 2

Examples:
Numerical values to color

Or upload file:
ファイルを選択 ファイル未選択

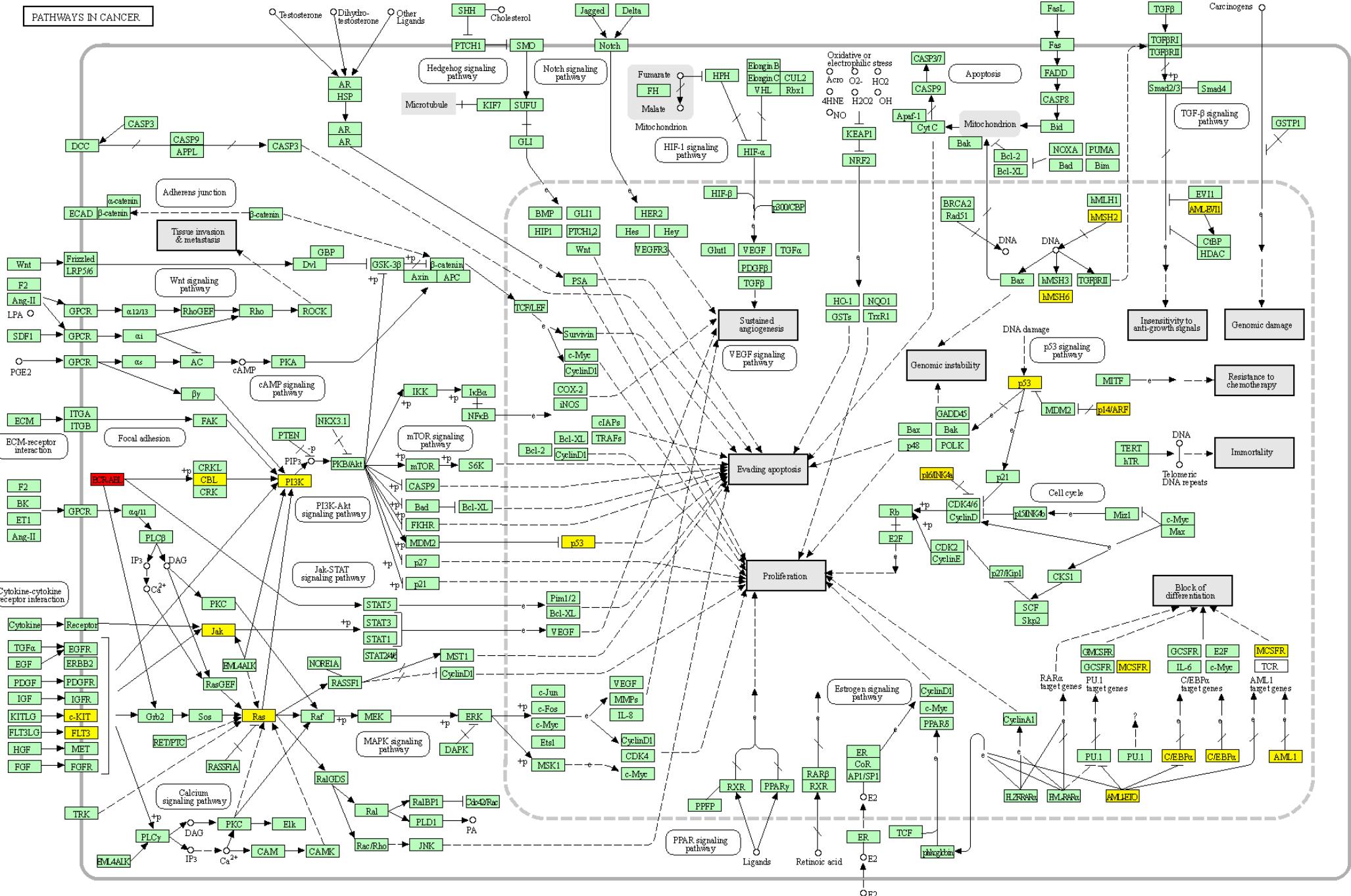
Option:
 Color specification
 Numerical values converted to color gradation
 Numerical values converted to 3D bar graph

Range:
 minimum-maximum negative-zero-positive
minimum #ffff00 黄色 maximum #ff0000 赤色 Check

Use uncolored diagram
Exec **Clear**

Option: Color specification
 Numerical values converted to color gradation
Range: minimum-maximum negative-zero-positive
minimum #ffff00 黄色 maximum #ff0000 赤色 Check

Numerical values converted to 3D bar graph



3Dグラフマッピング

- 右のサンプルから「Numerical values to color」
- 下のオプションから「Numerical values converted to 3D graph」を選択する

Enter data:

```
#hsa COSMIC
hsa:25 678
hsa:861 26
hsa:867 13
hsa:1029 44
hsa:1050 4
hsa:1436 3
hsa:2146 9
hsa:2322 7
hsa:2623 2
```

Examples:

Numerical values to graph

Or upload file:

ファイル未選択

Option: Color specification

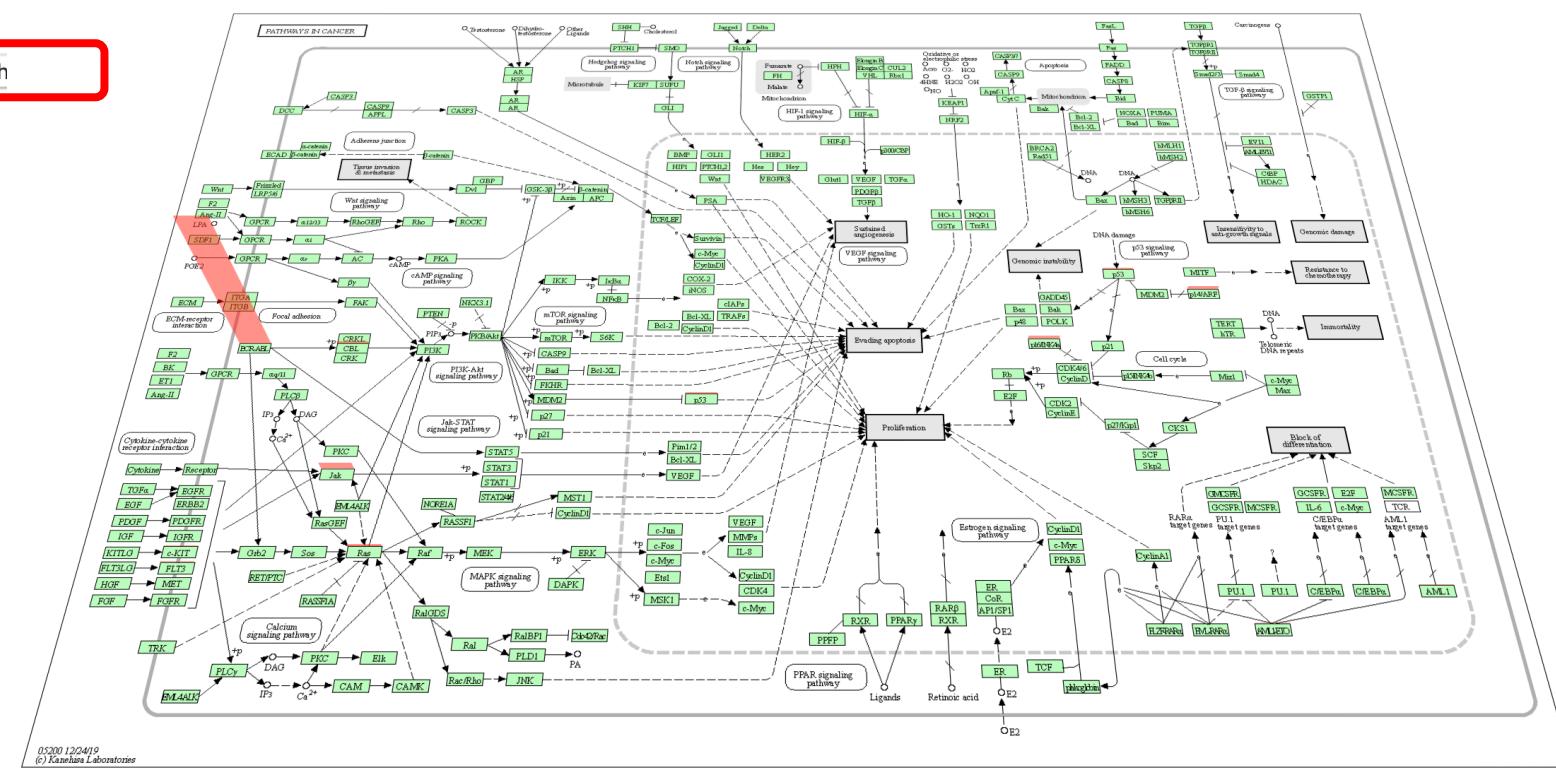
Numerical values converted to color gradation

Range: minimum-maximum negative-zero-positive

minimum maximum

Check

Numerical values converted to 3D bar graph



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)

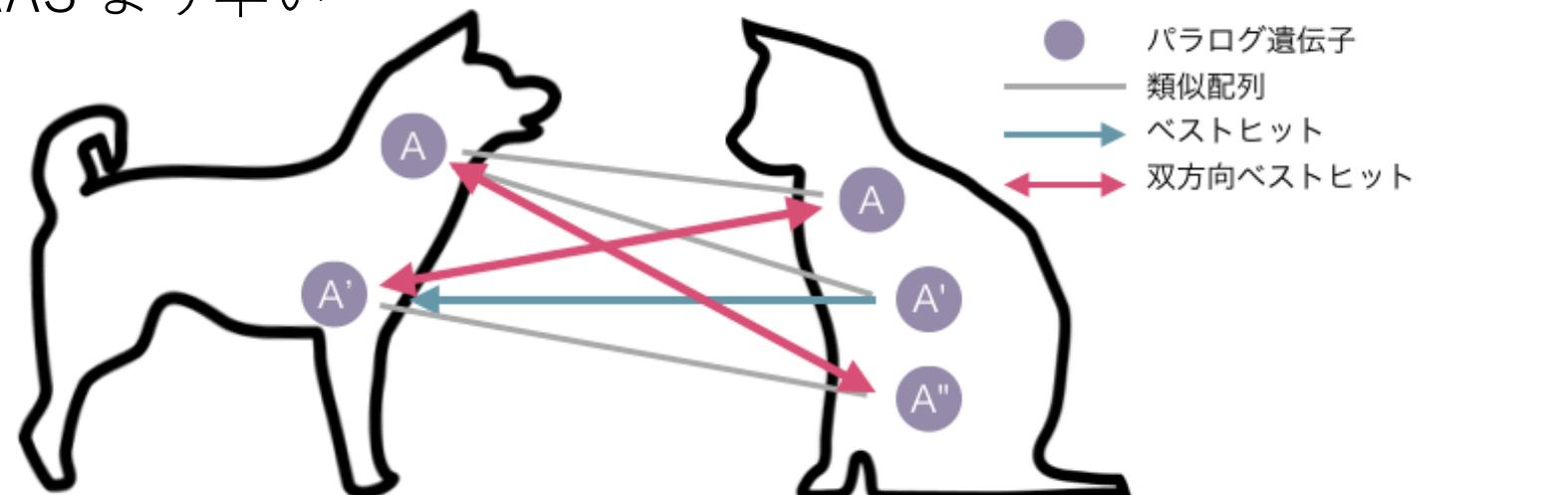
Example of Results

KO assignment

KEGG pathway mapping

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

- [Annotate Sequence by BlastKOALA](#)
(https://www.kegg.jp/kegg/tool/annotate_sequence.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 – Annotate Sequence by BlastKOALA

About KEGG Mapper
Reconstruct Pathway (and Brite, Module)
Search Pathway (and Brite, Module, Network, Disease)
Search&Color Pathway (and Brite, Module)
Color Pathway
Join Brite
Convert ID
Annotate Sequence

Upload query amino acid sequences in FASTA format

Enter FASTA sequences

```
YLINFFYKTLKIKGTPIQFQFDNENPYVKKN  
>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)]  
MLNISKNNIFFLFLIISLILFNWKYFSLVNKENLESLKYEKIKKINKKSKNLYEVENVIVQ  
NTSI  
YGTLTALSLAKKYVECNNLDKALLQLNNSLKYTKNEENLNLLKINIAKIQIQQNNKAMNL  
ETIQNH  
WKNIEHMKGDIFININNNKKEAIKSWKSLFIEDSNASKEINMKLNELKEQN
```

Or upload file:

Select GENES family/genus dataset to be searched

Example:
Query data: [sequence.txt](#)
Select [Buchnera \(32199\)](#)

Select Family/Genus

Exec Clear

Erwinia	551	Erwinia amylovora
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

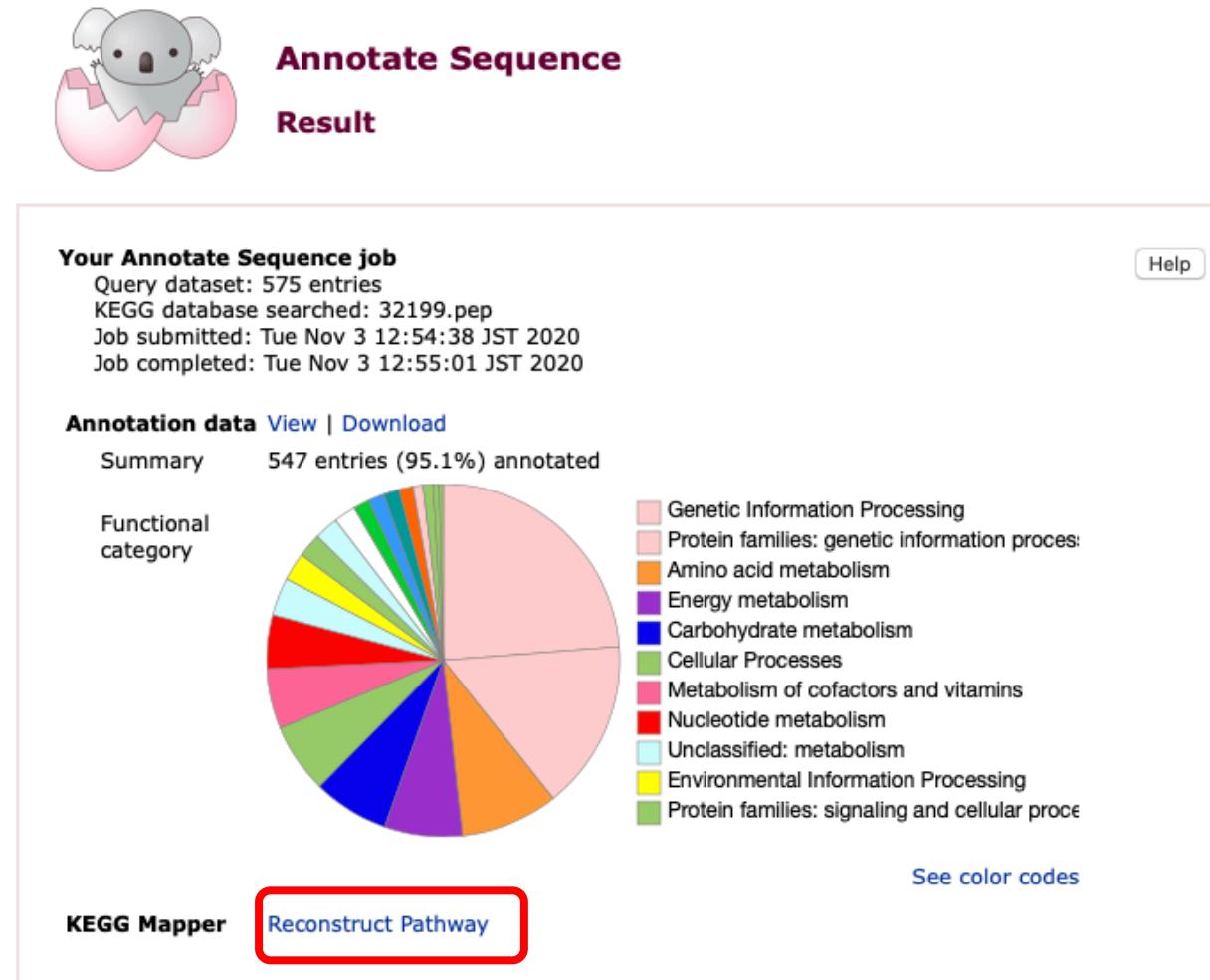
Your result will be displayed in the following page

https://www.kegg.jp/kegg-bin/blastkoala_result?

[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) Metabolic pathways - Reference pathway

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 Mapper Reconstruction Result

Pathway menu | Pathway entry | Image (png) file | Help | Change pathway type

Option: Scale: 30%, Link: Normal

Search: Go, Clear

Module: Complete only

Pathway modules:

- Carbohydrate metabolism
 - M0002 Glycolysis, core
 - M0030 Pyruvate oxidatio
 - M0004 Pentose phosphat
 - M0006 Pentose phosphat
 - M0007 Pentose phosphat
 - M0005 PRPP biosynthes
 - Other carbohydrate metab
- Energy metabolism
 - Carbon fixation
 - M00579 Phosphate acetyl
 - Methane metabolism
 - Nitrogen metabolism
 - Sulfur metabolism
 - M00176 Assimilatory sulf
- Lipid metabolism
 - Fatty acid metabolism
 - M00083 Fatty acid biosynt
 - Sterol biosynthesis
 - Lipid metabolism
- Nucleotide metabolism
 - Purine metabolism
 - M00049 Adenine ribonucle
 - M00051 Uridine monophos
 - Pyrimidine metabolism
- Amino acid metabolism
 - Serine and threonine metab
 - M00018 Threonine biosyn
 - Cysteine and methionine me
 - M00021 Cysteine biosynth
 - Branched-chain amino acid i
 - 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。
