

データベースと ネットワーク解析

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オントロジー

- **オントロジー** (ontology) : 対象となる領域における概念とそれらの関係を形式的に表現
 - 知識を統一的な枠組みで記述するための手法
 - 概念とは、特定の領域で共有される知識を指す
- **統制語** (controlled vocabulary) : 同じ意味をもつ語彙や（それが表す概念）を統一するための標準化された語彙の集合
 - オントロジーで定義された概念を、語彙として具体的に表現したもの → 知識の表現に用いられる語彙の標準化
 - 情報検索で使用する語を限定し、その意味や使用方法を明確に規定 ← 現実には多様な語が用いられる
 - 医学・生命科学 MeSH、情報科学 ACM CCS など
 - 目的: 知識の共有や再利用を可能にし、人間とコンピュータの双方が理解できる形式で記述する

PubMed

- MEDLINE (MEDlars onLINE)
 - NCBI NLM (National Center for Biotechnology Information, National Library of Medicine, 国立医学図書館) が作成する医学・生命科学の文献データベース
 - MEDlars: Medical Literature Analysis and Retrieval System
 - 80カ国で出版された生物医学系ジャーナル5,294誌からの要約、1950年以降の30,966,708件の文献情報を含む (2023年統計)
- PubMed (<https://pubmed.ncbi.nlm.nih.gov/>)
 - MEDLINEにデータを追加し、検索機能をもたせたデータベース
 - 3,900万件以上の文献情報 (現在)、年間36億件の検索 (2023年統計)
 - PubMed Central: 論文のフルテキストのアーカイブ
 - 出版社サイトのフルテキストへのリンク

PubMedの利用 (1)



shimizu.jwu@gmail.c...



SARS-CoV-2

Advanced



Search

「SARS-CoV-2」で検索

PubMed® comprises more than 37 million citations for biomedical literature from MEDLINE, life science journals, and online books. Citations may include links to full text content from PubMed Central and publisher web sites.



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FTP
Batch Citation Matcher



Explore

MeSH Database
Journals

PubMedの利用 (2)



SARS-CoV-2



Search

Advanced Create alert Create RSS

User Guide

Save

Email

Send to

Sort by:

Best match



Display options



MY CUSTOM FILTERS

RESULTS BY YEAR



2003

2025

PUBLICATION DATE

- ☐ 1 year
- ☐ 5 years
- ☐ 10 years
- ☐ Custom Range

TEXT AVAILABILITY

- ☐ Abstract
- ☐ Free full text
- ☐ Full text

245,446 results

Page 1 of 24,545

☐ Mechanisms of SARS-CoV-2 entry into cells.

1 Jackson CB, Farzan M, Chen B, Chen H.
Cite Nat Rev Mol Cell Biol. 2022 Jan;23(1):3-20. doi: 10.1038/s41580-021-00418-x. Epub 2021 Oct 5.
PMID: 34611326 Free PMC article. Review.

Share The unprecedented public health and economic impact of the COVID-19 pandemic caused by infection with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has been met with an equally unprecedented scientific response. Much of this response has focuse ...

☐ Coronavirus biology and replication: implications for SARS-CoV-2.

2 V'kovski P, Kratzel A, Steiner S, Stalder H, Thiel V.
Cite Nat Rev Microbiol. 2021 Mar;19(3):155-170. doi: 10.1038/s41579-020-00468-6. Epub 2020 Oct 28.
PMID: 33116300 Free PMC article. Review.

Share The SARS-CoV-2 pandemic and its unprecedented global societal and economic disruptive impact has marked the third zoonotic introduction of a highly pathogenic coronavirus into the human population. ...The elucidation of similarities and differences between ...

☐ Overview of SARS-CoV-2 genome-encoded proteins.

3 Bai C, Zhong Q, Gao GF.
Cite Sci China Life Sci. 2022 Feb;65(2):280-294. doi: 10.1007/s11427-021-1964-4. Epub 2021 Aug 10.
PMID: 34387838 Free PMC article. Review.

Share Severe acute respiratory syndrome Coronavirus 2 (SARS-CoV-2) has spread rapidly throughout the

デフォルトは「Best match」の順
最初の論文を選択

PubMedの利用 (3)



SARS-CoV-2



Search

Advanced

User Guide

Search results

Save

Email

Send to

Display options



Review > Nat Rev Mol Cell Biol. 2022 Jan;23(1):3-20. doi: 10.1038/s41580-021-00418-x.

Epub 2021 Oct 5.

Mechanisms of SARS-CoV-2 entry into cells

Cody B Jackson^{1 2}, Michael Farzan¹, Bing Chen^{3 4}, Hyeryun Choe⁵

Affiliations + expand

PMID: 34611326 PMCID: PMC8491763 DOI: 10.1038/s41580-021-00418-x

Abstract

アブストラクト(要旨)

The unprecedented public health and economic impact of the COVID-19 pandemic caused by infection with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has been met with an equally unprecedented scientific response. Much of this response has focused, appropriately, on the mechanisms of SARS-CoV-2 entry into host cells, and in particular the binding of the spike (S) protein to its receptor, angiotensin-converting enzyme 2 (ACE2), and subsequent membrane fusion. This Review provides the structural and cellular foundations for understanding the multistep SARS-CoV-2 entry process, including S protein synthesis, S protein structure, conformational transitions necessary for association of the S protein with ACE2, engagement of the receptor-binding domain of the S protein with ACE2, proteolytic activation of the S protein, endocytosis and membrane fusion. We define the roles of furin-like proteases, transmembrane protease, serine 2 (TMPRSS2) and cathepsin L in these processes, and delineate the features of ACE2 orthologues in reservoir animal species and S protein adaptations that facilitate efficient human transmission. We also examine the utility of vaccines, antibodies and other potential therapeutics targeting SARS-CoV-2 entry into host cells.

FULL TEXT LINKS

nature portfolio



ACTIONS

Cite

Collections

NEXT RESULT
2 of 245,446

SHARE



PAGE NAVIGATION

Title & authors

Abstract

Conflict of interest

この下を見てみよう

PubMedの利用 (4)

References

1. Lu R, et al. Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. Lancet. 2020;395:565–574. - [PMC](#) - [PubMed](#)
2. Shang J, et al. Structural basis of receptor recognition by SARS-CoV-2. Nature. 2020;581:221–224. - [PMC](#) - [PubMed](#)
3. Zhou P, et al. A pneumonia outbreak associated with a new coronavirus of probable bat origin. Nature. 2020;579:270–273. - [PMC](#) - [PubMed](#)
4. Walls AC, et al. Structure, function, and antigenicity of the SARS-CoV-2 spike glycoprotein. Cell. 2020 doi: 10.1016/j.cell.2020.02.058. - [DOI](#) - [PMC](#) - [PubMed](#)
5. Lan J, et al. Structure of the SARS-CoV-2 spike receptor-binding domain bound to the ACE2 receptor. Nature. 2020;581:215–220. - [PubMed](#)

Show all 261 references

Publication types

- Research Support, N.I.H., Extramural
- Research Support, Non-U.S. Gov't
- Review

MeSH terms

- Animals
- Evolution, Molecular
- Humans
- Membrane Fusion
- Peptidyl-Dipeptidase A / metabolism
- SARS-CoV-2 / immunology
- SARS-CoV-2 / physiology*
- Viral Proteins / chemistry
- Viral Proteins / metabolism
- Virus Internalization*

Substances

- Viral Proteins
- Peptidyl-Dipeptidase A

MeSH terms

統制語として、論文の主題や内容を体系的に表現

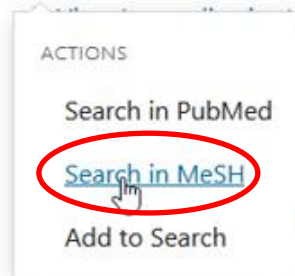
MeSH

- MeSH (Medical Subject Headings)
 - MEDLINEに収録されている論文の主題を表すための生物医学分野の統制語 (control language)、シソーラス (thesaurus)
 - シソーラス: 用語を意味上の関係に基づき整理した辞書・辞典・語彙集
 - 検索の際、自動マッピング機能により、入力した検索語のほか、対応するMeSHの用語も使って自動的に検索

PubMedの利用 (5)

MeSH terms

- > Animals
- > Evolution, Molecular
- > Humans
- > Membrane Fusion
- > Peptidyl-Dipeptidase A / metabolism
- > SARS-CoV-2 / immunology
- > SARS-CoV-2 / physiology*
- > **Viral Proteins / chemistry**
- ▼ Viral Proteins / metabolism



「Viral Proteins / chemistry」を選択

「Search in MeSH」を選択

Related information

PubChem Compound (MeSH Keyword)

「Viral Proteins / chemistry」の「/」の後
は、Subheading (限定語)を表す
→ 例えば、ウイルスタンパク質の化学
的性質、化学的研究側面を表す

「Viral Proteins / physiology」は、ウイル
スタンパク質の生理的機能を表し、
*は、それが論文の主題であることを示す

PubMedの利用 (6)

MeSH

MeSH

Viral Proteins

Search

Create alert Limits Advanced

Help

Summary

Send to:

Search results

Items: 4

☐ [Viral Proteins](#)

1. Proteins found in any species of virus.

☐ [Gene Products_gag](#)

2. Proteins coded by the retroviral gag gene. The products are usually synthesized as protein precursors or POLYPROTEINS, which are then cleaved by viral proteases to yield the final products. Many of the final products are associated with the nucleoprotein core of the virion. gag is short for group-specific antigen.

Year introduced: 1990

☐ [Viral Regulatory and Accessory Proteins](#)

3. A broad category of **viral proteins** that play indirect roles in the biological processes and activities of viruses. Included here are proteins that either regulate the expression of viral genes or are involved in modifying host cell functions. Many of the proteins in this category serve multiple functions.

Year introduced: 2008 (1990)

☐ [Nucleocapsid Proteins](#)

4. **Viral proteins** found in either the NUCLEOCAPSID or the viral core (VIRAL CORE PROTEINS).

Year introduced: 1998

Summary

Send to:

PubMed Search Builder

Add to search builder

AND

Search PubMed

YouTube Tutorial

Find related data

Database: Select

Find items

Search details

"viral proteins"[MeSH Terms] OR
Viral Proteins[Text Word]

Search

See more...

Recent Activity

Turn Off Clear

PubMedの利用 (7)

Full ▾

Send to: ▾

Viral Proteins

Proteins found in any species of virus.

PubMed search builder options

[Subheadings:](#)

- ☐ administration and dosage
- ☐ adverse effects
- ☐ agonists
- ☐ analysis
- ☐ antagonists and inhibitors
- ☐ biosynthesis
- ☐ blood
- ☐ cerebrospinal fluid
- ☐ chemical synthesis
- ☐ chemistry

- ☐ classification
- ☐ drug effects
- ☐ economics
- ☐ genetics
- ☐ history
- ☐ immunology
- ☐ isolation and purification
- ☐ metabolism
- ☐ pharmacokinetics
- ☐ pharmacology

- ☐ physiology
- ☐ poisoning
- ☐ radiation effects
- ☐ standards
- ☐ supply and distribution
- ☐ therapeutic use
- ☐ toxicity
- ☐ ultrastructure
- ☐ urine

☐ Restrict to MeSH Major Topic.

☐ Do not include MeSH terms found below this term in the MeSH hierarchy.

Tree Number(s): D12.776.964

MeSH Unique ID: D014764

Entry Terms:

- Proteins, Viral
- Viral Protein
- Protein, Viral
- Gene Products, Viral
- Viral Gene Products
- Viral Gene Proteins

[All MeSH Categories](#)

[Chemicals and Drugs Category](#)

[Amino Acids, Peptides, and Proteins](#)

[Proteins](#)

[Viral Proteins](#)

[Antigens, Viral](#)

[Adenovirus Early Proteins](#) +

[Antigens, Viral, Tumor](#) +

[Deltaretrovirus Antigens](#) +

[Epstein-Barr Virus Nuclear Antigens](#)

[Hemagglutinins, Viral](#) +

[Hepatitis Antigens](#) +

[HIV Antigens](#) +

subheading: 主要なMeSH用語(heading)
をさらに詳細に分類し、文献の内容をより
細かく記述するための補助的な語句

階層的な概念の整理

Entry Terms: ユーザが使用する検索語が
主要なMeSH用語にマッピングされる

PubMed Search Builder

Add to search builder AND ▾

Search PubMed

[YouTube](#) [Tutorial](#)

Related information

[PubMed](#)

[PubMed - Major Topic](#)

[Clinical Queries](#)

[NLM MeSH Browser](#)

[PubChem Compound](#)

Recent Activity

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[Viral Proteins](#)

MeSH

[Animals](#)

MeSH

"olfactory receptor" AND "homo sapiens"[Organism] AND "pseudogene" Gene

"olfactory receptor" AND "Bos taurus"[Organism] AND "pseudogene" Gene

"olfactory receptor" AND "Bos taurus"[Organism] AND "pseudogene" Gene

[See more...](#)

Web of Science

- Clarivate AnalyticsのWeb of Scienceグループにより提供されているオンラインの学術データベース
- 自然科学、社会科学、人文科学の全分野の文献
- インパクトファクターの計算のもとになっている

The screenshot displays the Web of Science interface. At the top, the Clarivate logo is on the left, and 'English' and 'Products' are on the right. Below the logo, 'Web of Science™' is followed by 'Smart Search', 'Advanced Search', and 'Research Assistant'. On the far right, 'Sign In' and 'Register' buttons are visible. A left-hand menu contains icons for menu, home, history, profile, and notifications. The main content area shows 'Smart Search' results for 'SARS-Cov-2', displaying '419,005 results from 12 selected collections'. Below the search bar, there are buttons for 'Add Keywords' and 'Quick add keywords', followed by a list of keywords: 'sars-cov-2', 'macrodomain', 'info ddc 22 de 614 4', 'info ddc 22 eng 614 4', 'virussequencen', and 'info ddc 22 eng 614 42'. There are also buttons for 'Add collection to search' with 'Preprint Citation Index' and 'Research Commons'. A link 'See how we processed your query' is present. Below this, statistics show '419,005 Documents' and '100 Researchers'. On the right, buttons for 'Analyze Results', 'Citation Report', and 'Create Alert' are shown. The left sidebar has a 'Refine results' section with an 'Export Refine' button and a 'Search within topic...' field. Below this is a 'Quick Filters' section with checkboxes for 'Highly Cited Papers' (5,720), 'Hot Papers' (26), 'Review Article' (49,113), and 'Open Access' (290,905). The main results area shows a list of results, with the first one being 'Characteristics of SARS-CoV-2 and COVID-19' from 'NATURE REVIEWS MICROBIOLOGY', dated 'Mar 2021', with '4,356 Citations' and '165 References'. The interface is clean and professional, with a light blue and white color scheme.

Google Scholar

- Googleが提供する学術向け検索サービスの一つ
- 学術論文、出版物の全文、メタデータのアクセス

≡ プロフィール ★ マイライブラリ 人 Labs



Google Scholar

☐ すべての言語 ☒ 英語 と 日本語のページを検索

新しい検索方法

Scholar Labs を試す

巨人の肩の上に立つ

Google Scholar

Google Scholar

Sars-Cov-2



記事

約 1,600,000 件 (0.07 秒)

プロフィール ★ マイライブラリ

期間指定なし

2026 年以降

2025 年以降

2022 年以降

期間を指定...

関連性で並べ替え

日付順に並べ替え

すべての言語

英語 と 日本語のページを検索

すべての種類

総説論文

☐ 特許を含める

☒ 引用部分を含める

☒ アラートを作成

SARS-CoV-2 pathogenesis

[MM Lamers](#), [BL Haagmans](#) - [Nature reviews microbiology](#), 2022 - [nature.com](#)

... SARS-CoV-2 pathophysiology and discuss potential mechanisms behind SARS-CoV-2-...
We describe how SARS-CoV-2 may infect the lower respiratory tract and cause alveolar ...

☆ 保存 引用 被引用数: 1261 関連記事 全 7 バージョン

[PDF] [nature.com](#)

SARS-CoV-2 vaccines in development

[F Krammer](#) - [Nature](#), 2020 - [nature.com](#)

... Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was first reported in late ...
Here I review the development of vaccines against SARS-CoV-2. Development was initiated ...

☆ 保存 引用 被引用数: 2581 関連記事 全 11 バージョン

[PDF] [nature.com](#)
FullText@日女大

Coronaviruses and sars-cov-2

[M Hasöksüz](#), [S Kilic](#), [F Sarac](#) - [Turkish journal of medical ...](#), 2020 - [journals.tubitak.gov.tr](#)

... severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), and the present outbreak
... Infections with SARS-CoV-2 are now widespread, and as of 10 April 2020, 1,727,602 cases ...

☆ 保存 引用 被引用数: 590 関連記事 全 13 バージョン

[PDF] [tubitak.gov.tr](#)
FullText@日女大

The evolution of SARS-CoV-2

[PV Markov](#), [M Ghafari](#), [M Beer](#), [K Lythgoe](#)... - [Nature Reviews ...](#), 2023 - [nature.com](#)

... generate genetic variation in SARS-CoV-2, underlying the ... reservoir playing a role in
SARS-CoV-2 evolution, and conclude ... the possible future evolutionary trajectories of ...

☆ 保存 引用 被引用数: 1308 関連記事 全 7 バージョン

[PDF] [nature.com](#)

関連キーワード

sars-cov-2 infection

covid-19 sars-cov-2

respiratory syndrome coronavirus

sars-cov-2 severe acute respiratory

sars-cov-2 vaccine

sars-cov-2 variants

Gene Ontology

- **Gene Ontology (GO)** : 遺伝子および遺伝子産物のアノテーションを統一的に行う
- **GO Term**: GOの統制語
- <https://geneontology.org/>

The screenshot shows the Gene Ontology (GO) website homepage. At the top, there is a navigation bar with links: About, Ontology, Annotations, Downloads, and Help. To the right of these links are social media icons for Twitter, Facebook, and GitHub, and the Alliance of Genome Resources logo. Below the navigation bar, a banner displays the current release information: "Current release 2024-11-03: 40,635 GO terms | 8,031,345 annotations | 1,568,326 gene products | 5,435 species (see statistics)". The main heading is "THE GENE ONTOLOGY RESOURCE". Below this, a paragraph states: "The mission of the GO Consortium is to develop a comprehensive, computational model of biological systems, ranging from the molecular to the organism level, across the multiplicity of species in the tree of life." Another paragraph states: "The Gene Ontology (GO) knowledgebase is the world's largest source of information on the functions of genes. This knowledge is both human-readable and machine-readable, and is a foundation for computational analysis of large-scale molecular biology and genetics experiments in biomedical research." A search bar is present with the placeholder text "Search GO term or Gene Product in AmiGO ...". Below the search bar are radio buttons for "Any", "Ontology", and "Gene Product", with "Any" selected. To the right of the search bar is a "GO Enrichment Analysis" section, powered by PANTHER. It includes a text input field for "Your gene IDs here...", a dropdown menu currently showing "biological process", a dropdown for "Homo sapiens", and buttons for "Examples" and "Launch". A hint below these buttons reads: "Hint: can use UniProt ID/AC, Gene Name, Gene Symbols, MOD IDs". At the bottom of the page, there are four small thumbnail images: a network diagram, a diagram showing NEDD4 and Ubiquitin-protein ligase activity, a diagram showing a protein structure, and a DNA double helix.

GENEONTOLOGY
Unifying Biology

About Ontology Annotations Downloads Help

Current release 2024-11-03: 40,635 GO terms | 8,031,345 annotations
1,568,326 gene products | 5,435 species (see statistics)

THE GENE ONTOLOGY RESOURCE

The mission of the GO Consortium is to develop a comprehensive, computational model of biological systems, ranging from the molecular to the organism level, across the multiplicity of species in the tree of life.

The Gene Ontology (GO) knowledgebase is the world's largest source of information on the functions of genes. This knowledge is both human-readable and machine-readable, and is a foundation for computational analysis of large-scale molecular biology and genetics experiments in biomedical research.

Search GO term or Gene Product in AmiGO ...

Any Ontology Gene Product

GO Enrichment Analysis ?

Powered by PANTHER

Your gene IDs here...

biological process

Homo sapiens

Examples Launch >

Hint: can use UniProt ID/AC, Gene Name, Gene Symbols, MOD IDs

GO Termの検索 (1)

 GENE ONTOLOGY
Unifying Biology

AboutOntologyAnnotationsDownloadsHelp



Current release 2024-11-03: 40,635 GO terms | 8,031,345 annotations
1,568,326 gene products | 5,435 species (see statistics)

THE GENE ONTOLOGY RESOURCE

The mission of the GO Consortium is to develop a comprehensive, **computational model of biological systems**, ranging from the molecular to the organism level, across the multiplicity of species in the tree of life.

The Gene Ontology (GO) knowledgebase is the world's largest source of information on the functions of genes. This knowledge is both human-readable and machine-readable, and is a foundation for computational analysis of large-scale molecular biology and genetics experiments in biomedical research.

lipolysis



AnyOntologyGene Product

biological process

Homo sapiens

ExamplesLaunch

Hint: *copy UniProt ID/AC, Gene Name, Gene Symbols, MOD IDs*

「lipolysis」(脂質分解)を入力し、「Search」をクリック



ONTOLOGY

The network of biological classes describing the current best representation



ANNOTATION

Statements, based on specific, traceable scientific evidence, asserting that a specific



GO-CAM

GO Causal Activity Model (GO-CAM) provides a structured framework to link



TOOLS & GUIDES

Tools to curate, browse, search, visualize and download both the ontology and

GO Termの検索 (2)



AmiGO 2

[Home](#)

[Search](#) ▾

[Browse](#)

[Tools & Resources](#)

[Help](#)

[Feedback](#)

[About](#)

lipolysis

[Search](#)



Text search document selection

The following results were found for **lipolysis** using a general search over all text fields.

To narrow your search, select the type of document that you would like to search for and continue narrowing your search from the linked search page.

Ontology

Gene Ontology Term, Synonym, or Definition.

4

Genes and gene products

Genes and gene products associated with GO terms.

23

Annotations

Associations between GO terms and genes or gene products.

176

「Ontology」を選択

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DOI [10.5281/zenodo.10162580](https://doi.org/10.5281/zenodo.10162580)

Last file loaded on 2023-11-17, [see full details](#)

AmiGO 2 version: [2.5.17](#) (amigo-production)

GO Termの検索 (3)



AmiGO 2

Home

Search

Browse

Tools & Resources

Help

Feedback

About

Quick search

Search



Information about **Ontology** search ?

関連するGO Term

Filter results

Total term(s): 3

lipolysis

User filters

+ idspace: GO

+ is_obsolete: false

Your search is pinned to these filters

- document_category: ontology_class

Ontology source

		(79)	biological_process
		(10)	cellular_component
		(7)	molecular_function

Total term(s): 3; showing: 1-3

Results count 10

«First

<Prev

Next>

Last»

Custom DL (up to 100000)

Bookmark

<input type="checkbox"/> Term	Definition	Ontology source	Ontology ID space	Synonyms	Alt ID
<input type="checkbox"/> cytosolic lipolysis	The chemical reactions and pathways resulting in the breakdown of lipid droplets and hydrolysis of s more...	biological_process	GO		
<input type="checkbox"/> discoidal high-density lipoprotein particle	A newly formed high-density lipoprotein particle; consists of a phospholipid bilayer surrounded by t more...	cellular_component	GO	discoidal HDL nascent HDL nascent high-density lipoprotein particle	
<input type="checkbox"/> lipid catabolic process	The chemical reactions and pathways resulting in the breakdown of lipids, compounds soluble in an or more...	biological_process	GO	lipid breakdown lipid catabolism more...	GO:0006724 GO:0044240

例えば、「cytosolic lipolysis」
(細胞内脂肪分解)を選択

GO Termの検索 (4)



AmiGO 2

Home

Search ▾

Browse

Tools & Resources

Help

Feedback

About

Quick search

Search ?

cytosolic lipolysis

GO termの説明

Term Information ?

Accession GO:0061725

Name cytosolic lipolysis

Ontology biological_process

Synonyms None

Alternate IDs None

Definition The chemical reactions and pathways resulting in the breakdown of lipid droplets and hydrolysis of stored triglycerides occurring through the orchestrated activation of cytosolic lipases. *Source:* GOC:autophagy

Comment None

History See term [history](#) for GO:0061725 at QuickGO

Taxon info None

Chem. react. None

Subset None

Related [Link](#) to all **genes and gene products** annotated to cytosolic lipolysis (excluding "regulates").
[Link](#) to all direct and indirect **annotations** to cytosolic lipolysis (excluding "regulates").
[Link](#) to all direct and indirect **annotations download** (limited to first 10,000) for cytosolic lipolysis (excluding "regulates").

Include "regulates"

For more information, please see the [ontology relation documentation](#).

Feedback ♥

Annotations

Graph Views

Inferred Tree View

Neighborhood

Mappings

「Graph Views」をクリック

Filter results

Total annotations: 6

User filters

Total annotations: 6; showing: 1-6

Results count 10 ▾

«First

<Prev

Next>

Last»

Download

	Gene/product name	Annotation qualifier	GO class (direct)	Annotation extension	Contributor	Organism	Evidence	Evidence with	PANTHER family	Type
<input type="checkbox"/>	Gene/product									
<input type="checkbox"/>	Ces1d	carboxylesterase	cytosolic		RGD	Rattus	ISO	MGI:2148202	carboxylesterase	gene

GO Termの検索 (5)



AmiGO 2

[Home](#)

[Search](#) ▾

[Browse](#)

[Tools & Resources](#)

[Help](#)

[Feedback](#)

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Quick search

[Search](#) ?

cytosolic lipolysis

Term Information ?

Accession GO:0061725

Name cytosolic lipolysis

Ontology biological_process

Synonyms None

Alternate IDs None

Definition The chemical reactions and pathways resulting in the breakdown of lipid droplets and hydrolysis of stored triglycerides occurring through the orchestrated activation of cytosolic lipases. *Source:* GOC:autophagy

Comment None

History See term [history](#) for GO:0061725 at QuickGO

Taxon info None

Chem. react. None

Subset None

Related [Link](#) to all **genes and gene products** annotated to cytosolic lipolysis (excluding "regulates").
[Link](#) to all direct and indirect **annotations** to cytosolic lipolysis (excluding "regulates").
[Link](#) to all direct and indirect **annotations download** (limited to first 10,000) for cytosolic lipolysis (excluding "regulates").

[Include "regulates"](#)

For more information, please see the [ontology relation documentation](#).

[Annotations](#)

[Graph Views](#)

[Inferred Tree View](#)

[Neighborhood](#)

[Mappings](#)

View this term in [QuickGO](#).

Graph of GO:0061725 from QuickGO

Additional external viewing options

[OLSVis \(interactive\)](#)

Additional internal viewing options

「QuickGO」をクリック

GO Termの検索 (6)

Overview

Synonyms

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Child Terms

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Cross-Ontology Relations

Replaces

Replaced By

Co-occurring Terms

GO Slims

Change Log

GO:0061725   

cytosolic lipolysis

Biological Process

Definition ([GO:0061725 GONUTS page](#))

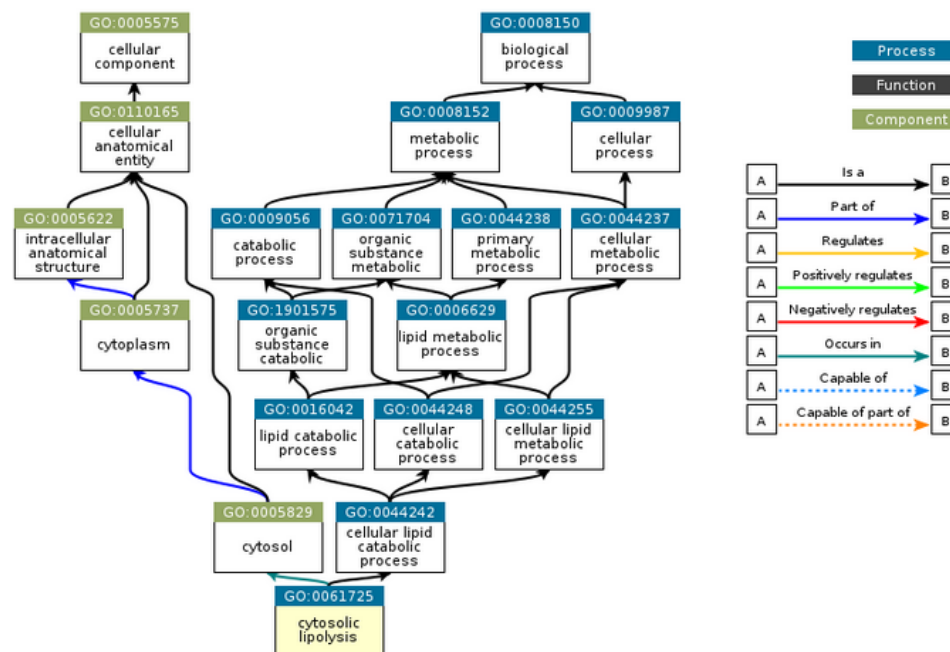
The chemical reactions and pathways resulting in the breakdown of lipid droplets and hydrolysis of stored triglycerides occurring through the orchestrated activation of cytosolic lipases.

7 annotations

Ancestor Chart 

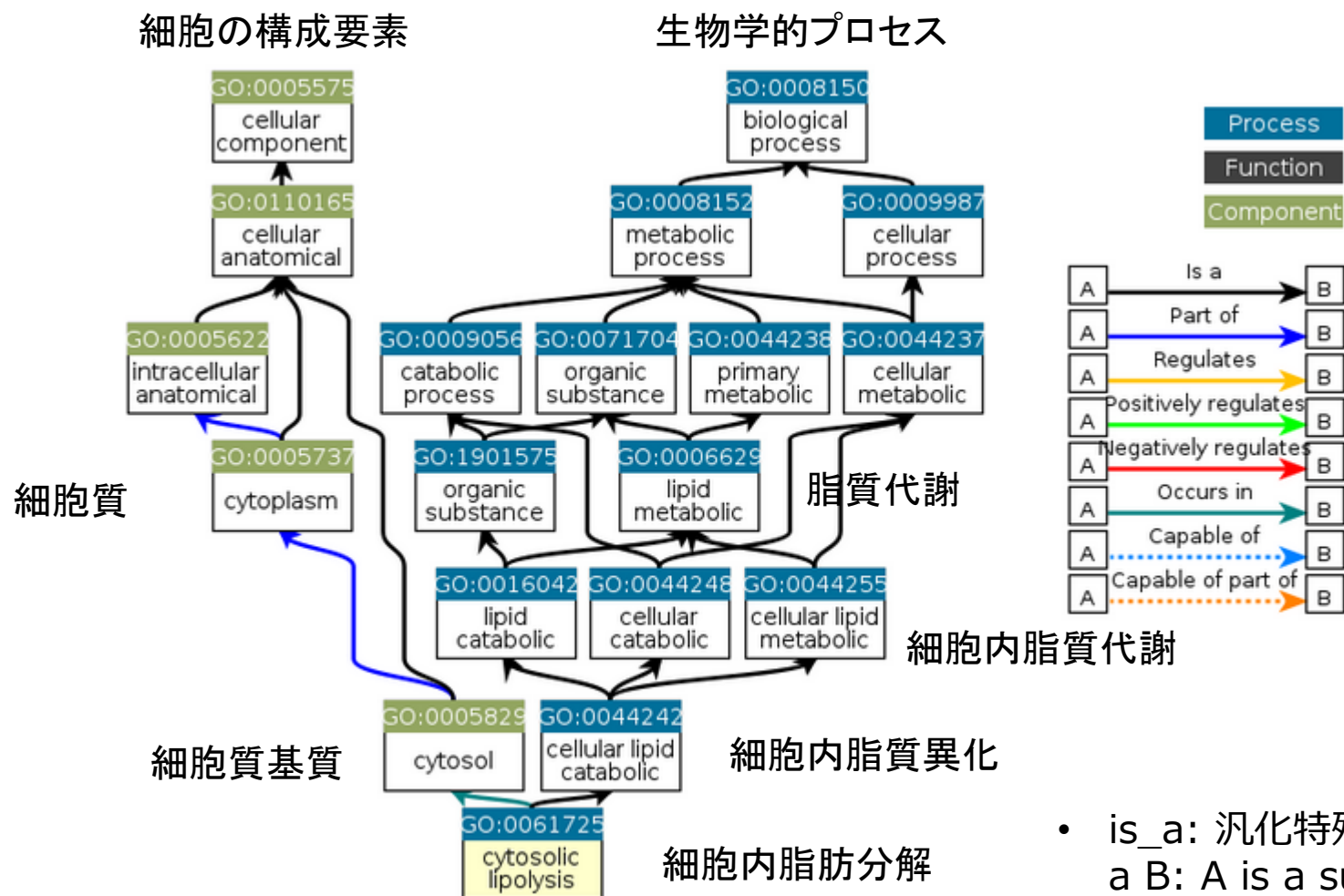
Ancestor chart for GO:0061725

Chart options ▾



QuickGO - <https://www.ebi.ac.uk/QuickGO>

GO Termの検索 (7)



QuickGO - <https://www.ebi.ac.uk/QuickGO>

- is_a: 汎化特殊化関係 (A is a B: A is a subtype of B)
- Part of: 部分全体関係 (B is a part of A)

Gene Ontologyの構成

- GO Termのカテゴリー
 - Biological process (生物学的プロセス)
 - 生理的プロセスやシグナル伝達など、一連の分子機能によって起きる細胞内イベント
 - Cellular component (細胞の構成要素)
 - 細胞中の存在場所
 - Molecular function (分子機能)
 - 触媒活性や結合活性など
- アノテーションのevidence (根拠、裏付け)
 - 実験、系統学的推定、計算手法による推定など

KEGG

- KEGG (Kyoto Encyclopedia of Genes and Genomes)
- 遺伝子の機能情報を登録した統合的なデータベース
 - PATHWAY: 遺伝子、タンパク質、化合物の相互情報をネットワークの形でデータベース化
 - BRITE: さまざまな機能の情報を階層的に分類
 - KEGG ORTHOLOGY: PATHWAYとBRITEをまとめて、すべての生物種に適用できるようにしたもの
- 文献などをもとに人手によって登録
- <https://www.genome.jp/kegg/>

KEGGの利用 (1)

KEGG

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[KGML](#)

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GenomeNet

DBGET/LinkDB

Feedback

Copyright request

Kanehisa Labs

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, 2025) for new and updated features.

Announcement: [Updated procedure to generate organism-specific pathways](#)

New article: [KEGG: biological systems database as a model of the real world](#)

Main entry point to the KEGG web service

KEGG2

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[KEGG pathway maps](#)

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[BRITE hierarchies and tables](#)

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KEGG ORTHOLOGY

[KO functional orthologs](#)

KEGG GENES

[Genes and proteins](#) [[KEGG Virus](#)]

KEGG GENOME

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[Small molecules](#)

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[Glycans](#)

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[Disease-related network variations](#)

KEGG DISEASE

[Human diseases](#)

KEGG DRUG

[Drugs](#) [[New drug approvals](#)]

KEGG MEDICUS

[Health information resource](#) [[Drug labels search](#)]

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KEGGの利用 (2)

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KEGG



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KEGG: Kyoto Encyclopedia of Genes and Genomes

KEGG は分子レベルの情報から細胞、個体、エコシステムといった高次生命システムレベルの機能や有用性を理解するためのリソースです。とくにゲノムをはじめとしたハイスループットデータの生物学的意味解釈に広く利用されています。また KEGG MEDICUS では医薬品添付文書など社会的ニーズの高いデータとの統合も行われています。

新規・更新等の内容は英文の [Release notes](#) (January 1, 2025) をご覧ください。

Announcement: [Updated procedure to generate organism-specific pathways](#)

New article: [KEGG: biological systems database as a model of the real world](#)

KEGG の主要エントリーポイント

KEGG2

[KEGG の目次のページ](#) [[Update notes](#) | [Release history](#)]

データタイプごとのエントリーポイント

KEGG PATHWAY

[KEGG パスウェイマップ](#)

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[BRITE 機能階層・テーブル](#)

KEGG MODULE

[KEGG モジュール](#)

KEGG ORTHOLOGY

[KO 機能オーソログ](#)

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[遺伝子・タンパク質](#) [[KEGG Virus](#)]

KEGG GENOME

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KEGG COMPOUND

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KEGG DISEASE

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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, 2025) for new and updated features.

Announcement: Updated procedure to generate organism-specific pathways

New article: KEGG: biological systems database as a model of the real world

「KEGG PATHWAY」を選択

● Main entry point to the KEGG web service

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● Data-oriented entry points

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KEGGの利用 (4)

KEGG

Databases

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Kanehisa Lab



KEGG PATHWAY Database

Wiring diagrams of molecular interactions, reactions and relations

KEGG2 PATHWAY BRITE MODULE KO GENES COMPOUND NETWORK DISEASE DRUG

Select prefix

map

Organism

Enter keywords

Go

Help

「Metabolic pathways」を選択

Pathway Maps

「Metabolism」→
「Global/overview」を選択

KEGG PATHWAY is a collection of manually drawn pathway maps representing reaction and relation networks for:

1. Metabolism

Global/overview Carbohydrate Energy Lipid Nucleotide Amino acid
Cofactor/vitamin Terpenoid/PK Other secondary metabolite Xenobiot

2. Genetic Information Processing

3. Environmental Information Processing

4. Cellular Processes

5. Organismal Systems

6. Human Diseases

7. Drug Development

The pathway map viewer linked from this page is a part of KEGG Web Apps and

Pathway Identifiers

Each pathway map is identified by the combination of 2-4 letter prefix code and has the following meaning:

map	manually drawn reference pathway identifiers
ko	reference pathway highlighting KOs
ec	reference metabolic pathway highlighting EC numbers
rn	reference metabolic pathway highlighting reactions
<org>	organism-specific pathway generated by converting KOs to gene IDs
vg	viruses pathway generated by converting KOs to gene IDs <i>New!</i>
vx	viruses extended pathway generated by converting KOs to gene IDs

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
01232 M R	Nucleotide metabolism
01250 M R	Biosynthesis of nucleotide sugars
01240 M R	Biosynthesis of cofactors
01220 M R	Degradation of aromatic compounds
01310 M T	Nitrogen cycle <i>New!</i>

1.1 Carbohydrate metabolism

00010 M N	Glycolysis / Gluconeogenesis
00020 M N	Citrate cycle (TCA cycle)
00030 M	Pentose phosphate pathway
00040 M	Pentose and glucuronate interconversions
00051 M	Fructose and mannose metabolism
00052 M N	Galactose metabolism
00053 M	Ascorbate and aldarate metabolism
00500 M N	Starch and sucrose metabolism
00520 M N	Amino sugar and nucleotide sugar metabolism
00541 M	Biosynthesis of various nucleotide sugars <i>Title and cat</i>
00620 M N	Pyruvate metabolism
00630 M	Glyoxylate and dicarboxylate metabolism
00640 M	Propanoate metabolism
00650 M	Butanoate metabolism
00660 M	C5-Branched dibasic acid metabolism
00562 M	Inositol phosphate metabolism

1.2 Energy metabolism

KEGGの利用 (5)

KEGG Metabolic pathways - Reference pathway

[Pathway menu | Pathway entry | Download | Help]

Change pathway type

「Scale」で調整できる

Option

Scale: 30%

Link: Normal

Search

Go

ID search

Go

Color

Module

☐ Pathway modules

☐ Carbohydrate metabolism

☐ Central carbohydrate metabo

☐ M00001 Glycolysis (Embde

☐ M00002 Glycolysis, core m

☐ M00003 Gluconeogenesis

☐ M00307 Pyruvate oxidator

☐ M00009 Citrate cycle (TCA

☐ M00010 Citrate cycle, first

☐ M00011 Citrate cycle, seco

☐ M00004 Pentose phosphat

☐ M00006 Pentose phosphat

☐ M00007 Pentose phosphat

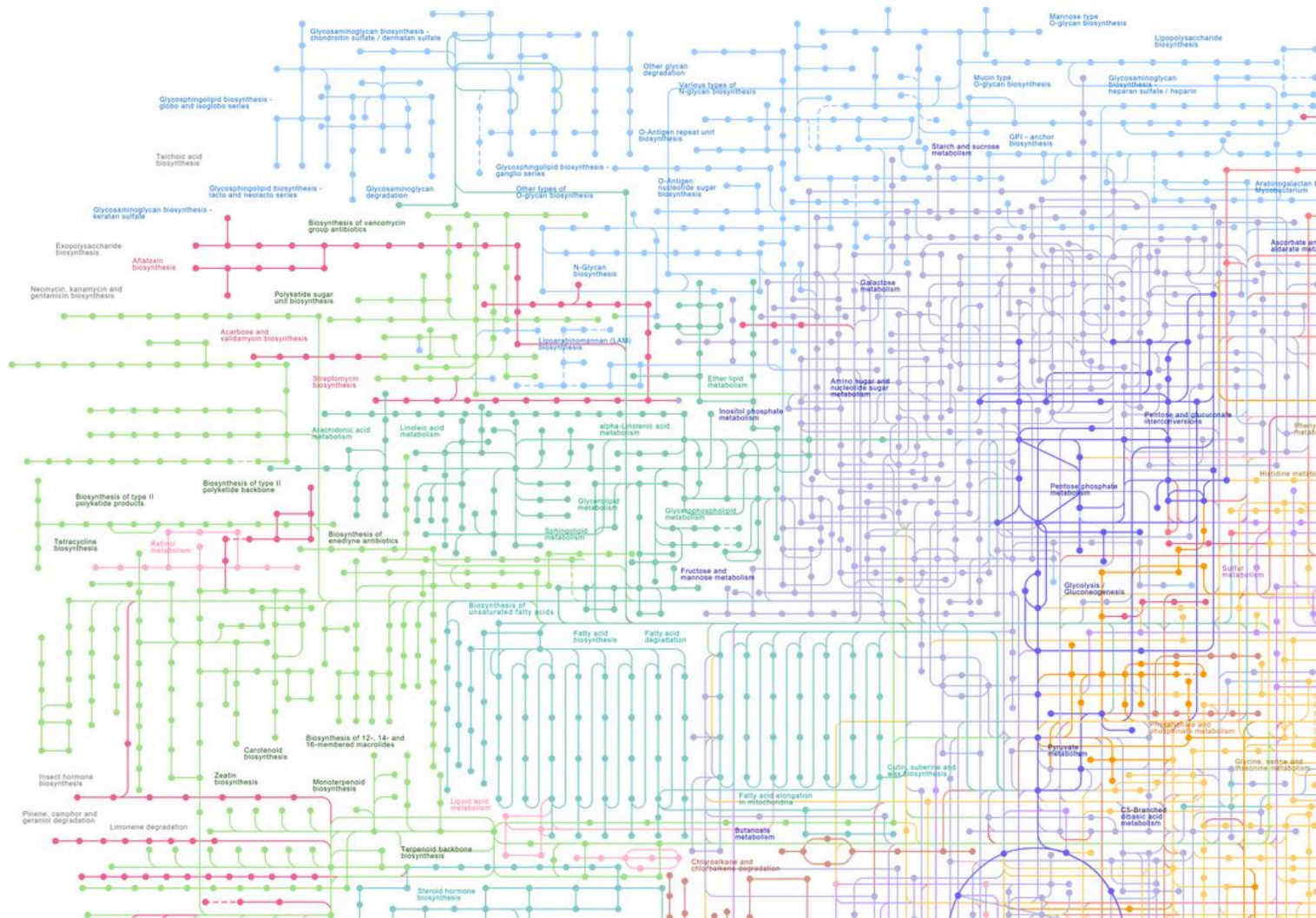
☐ M00580 Pentose phosphat

☐ M00005 PRPP biosynthesis

☐ M00008 Entner-Doudoroff

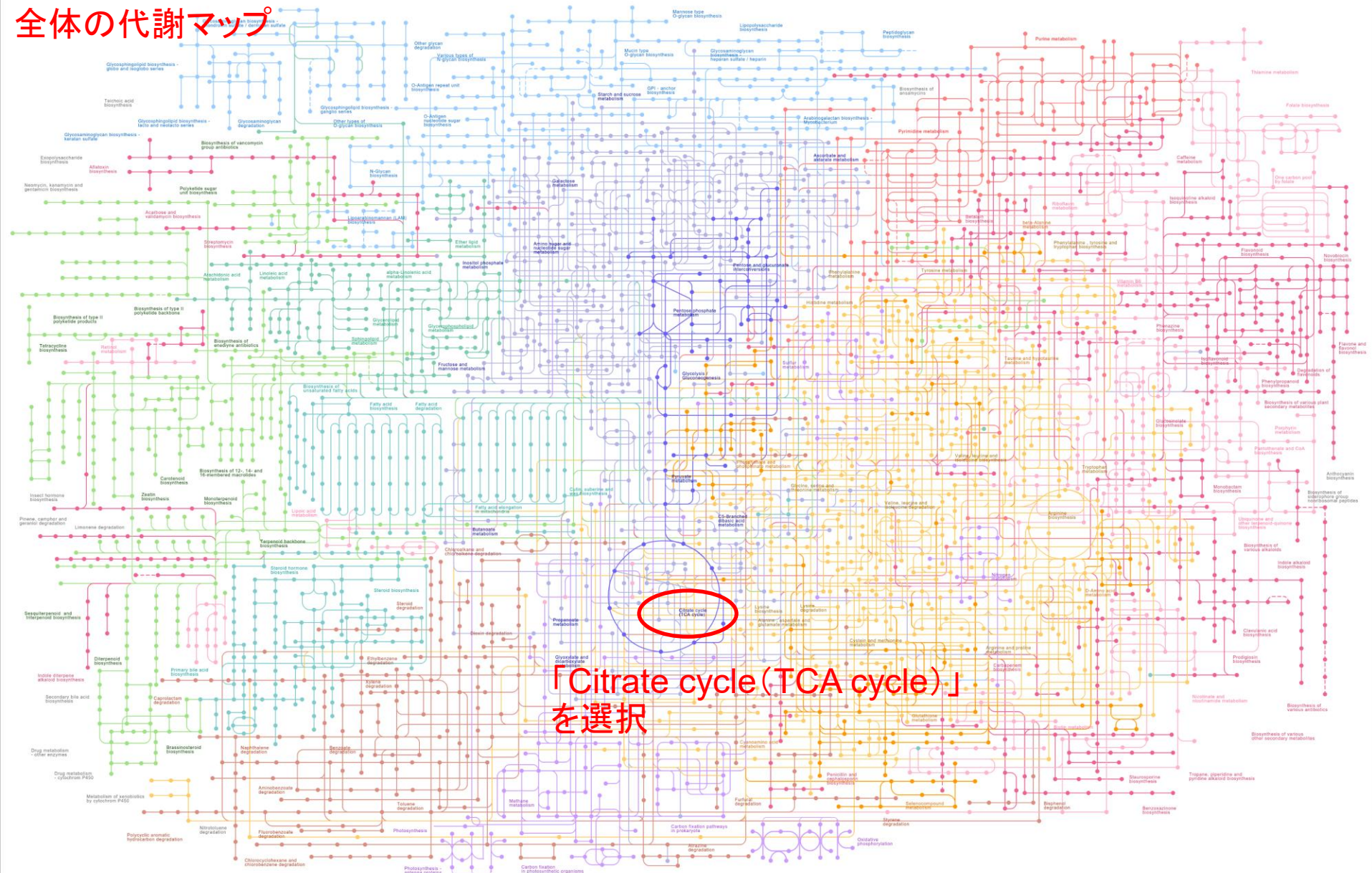
☐ M00308 Semi-phosphoryla

☐ M00633 Semi-phosphoryla



KEGGの利用 (6)

全体の代謝マップ



KEGGの利用 (7)



Citrate cycle (TCA cycle) - Reference pathway

[Pathway menu | Organism group | Pathway entry | Show description | Download | Help]

Change pathway type

Option

Scale: 100%

Search

ID search

Color

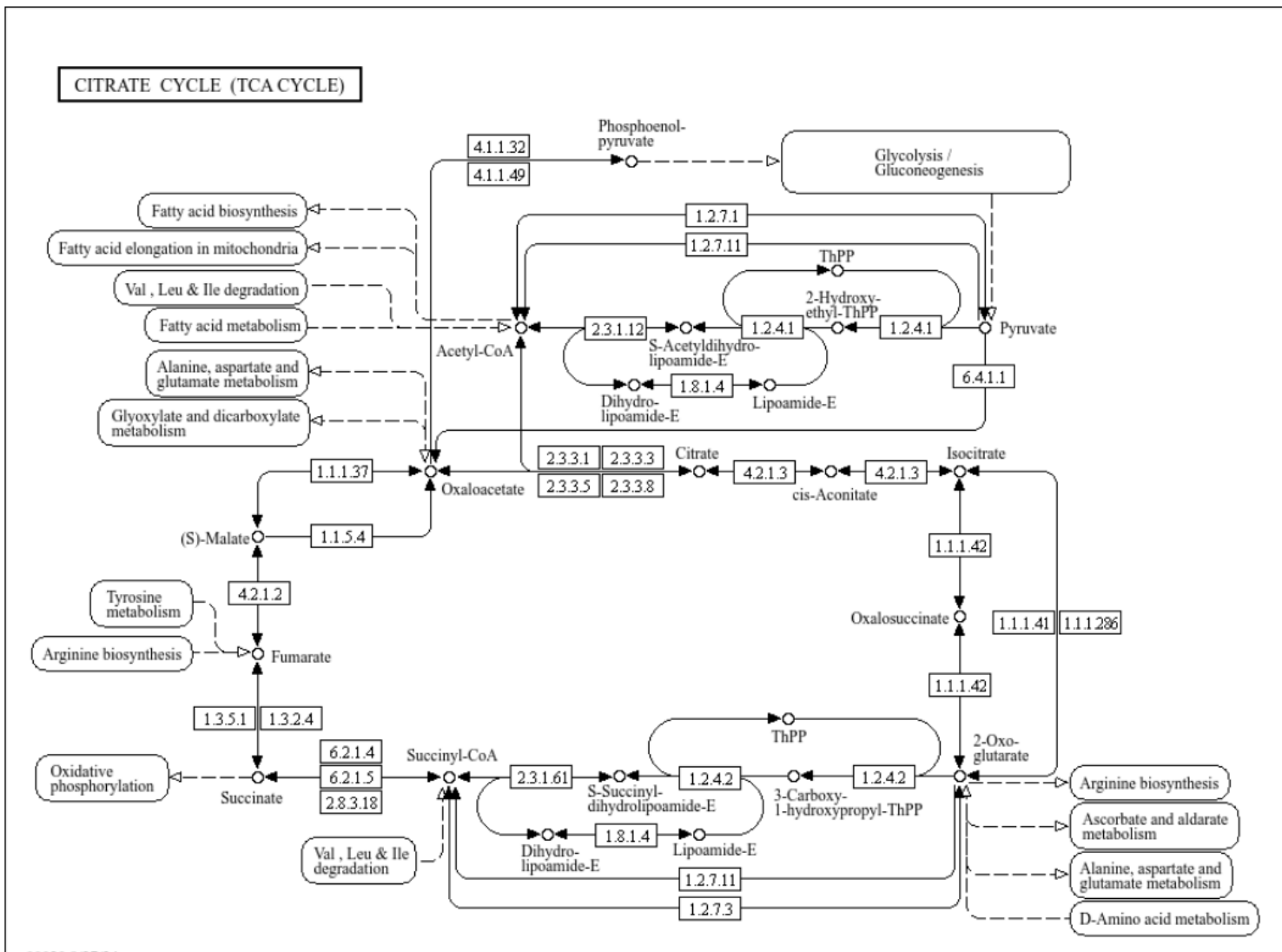
Module

☐ **Pathway modules**

- ☐ Carbohydrate metabolism
 - ☐ Central carbohydrate metabolism
 - ☐ M00003 Gluconeogenesis
 - ☐ M00307 Pyruvate oxidation
 - ☐ M00009 Citrate cycle (TCA cycle)
 - ☐ M00010 Citrate cycle, first half
 - ☐ M00011 Citrate cycle, second half
 - ☐ Other carbohydrate metabolism
 - ☐ M00740 Methylaspartate
 - ☐ M00982 Methylcitrate cycle

Network

- ☐ nt06031 Citrate cycle and pyruvate metabolism
 - ☐ N01603 Pyruvate oxidation
 - ☐ N01609 Citrate cycle, second half
 - ☐ N01616 Dihydrolipoamide dehydrogenase
 - ☐ N01604 Citrate cycle, first half
 - ☐ N01617 Citrate cycle, second half
 - ☐ N01605 Gluconeogenesis



00030 0/27/04

KEGGの利用 (8)



Citrate cycle (TCA cycle) - Reference pathway

[Pathway menu | Organism group | Pathway entry | Show description | Download | Help]

Change pathway type

Option

Scale: 100%

Search

Go

ID search

Go

Color

Module

Pathway modules

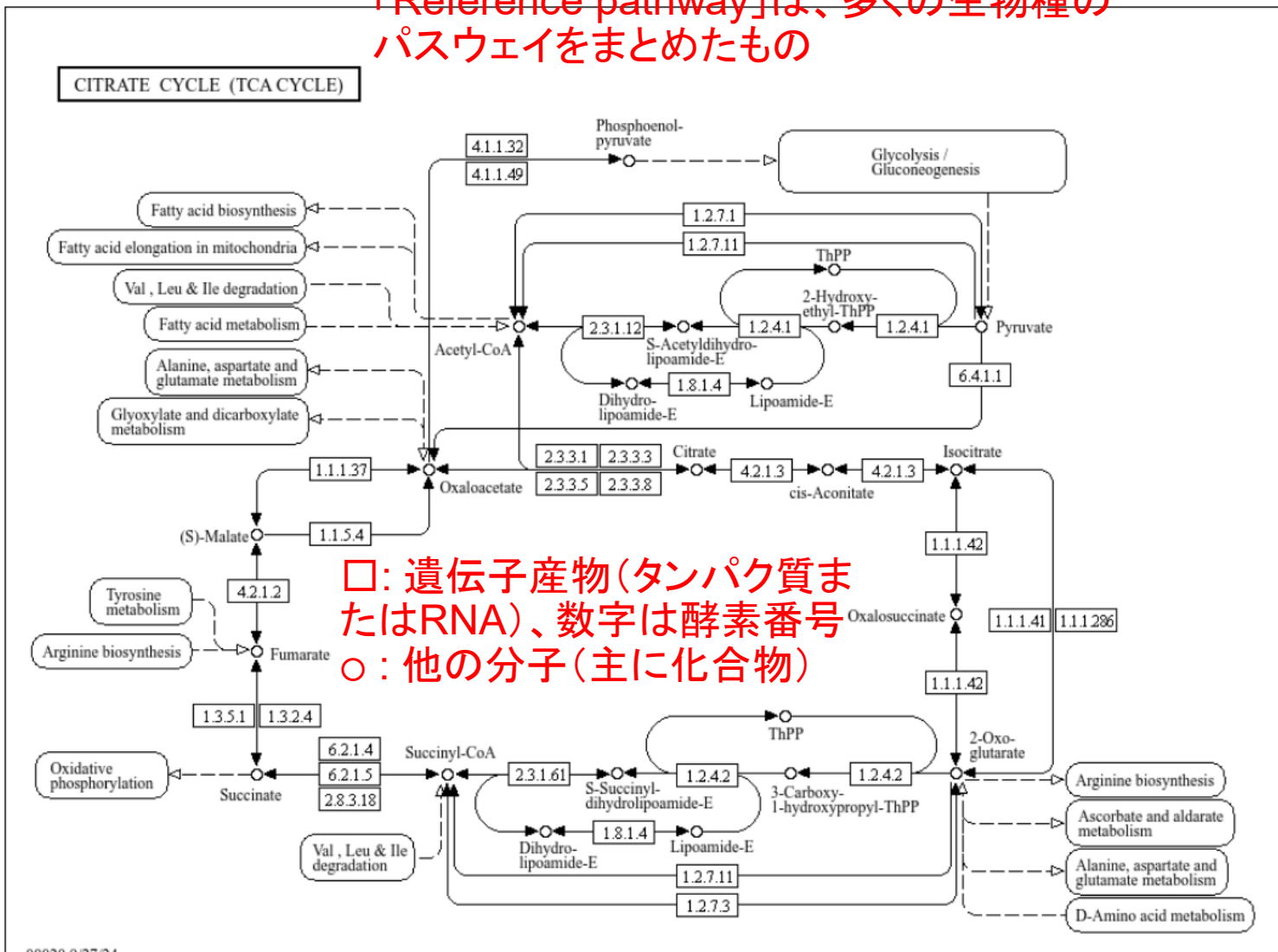
- ☐ Carbohydrate metabolism
 - ☐ Central carbohydrate metabolism
 - ☐ M00003 Gluconeogenesis
 - ☐ M00307 Pyruvate oxidation
 - ☐ M00009 Citrate cycle (TCA cycle)
 - ☐ M00010 Citrate cycle, first half
 - ☐ M00011 Citrate cycle, second half
 - ☐ Other carbohydrate metabolism
 - ☐ M00740 Methylaspartate
 - ☐ M00982 Methylcitrate cycle

Network

- ☐ nt06031 Citrate cycle and pyruvate
- ☐ N01603 Pyruvate oxidation
- ☐ N01609 Citrate cycle, second half
- ☐ N01616 Dihydrolipoamide dehydrogenase
- ☐ N01604 Citrate cycle, first half
- ☐ N01617 Citrate cycle, second half
- ☐ N01605 Gluconeogenesis

参照パスウェイ(Reference pathway)が表示される

「Reference pathway」は、多くの生物種のパスウェイをまとめたもの



□: 遺伝子産物(タンパク質またはRNA)、数字は酵素番号
○: 他の分子(主に化合物)

00030 0/27/04

KEGGの利用 (9)



Citrate cycle (TCA cycle) - Reference pathway

[Pathway menu | Organism group | Pathway search]

Change pathway type

▼ Option

Scale: 100%

▼ Search

Go

▼ ID search

Go

▼ Color

+

▼ Module

☐ Pathway modules

- ☐ Carbohydrate metabolism
- ☐ Central carbohydrate metabolism
- ☐ M00003 Gluconeogenesis
- ☐ M00307 Pyruvate oxidation
- ☐ M00009 Citrate cycle (TCA cycle)
- ☐ M00010 Citrate cycle, first half
- ☐ M00011 Citrate cycle, second half
- ☐ Other carbohydrate metabolism
- ☐ M00740 Methylaspartate
- ☐ M00982 Methylcitrate cycle

▼ Network

- ☐ nt06031 Citrate cycle and pyruvate
- ☐ N01603 Pyruvate oxidation
- ☐ N01609 Citrate cycle, second half
- ☐ N01616 Dihydropyrimidine dehydrogenase
- ☐ N01604 Citrate cycle, first half
- ☐ N01617 Citrate cycle, second half
- ☐ N01605 Gluconeogenesis

Select pathway type for 00020

▼ ▼ ▼ ▼ Org code(s): Exec C

Reference

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

Organism specific

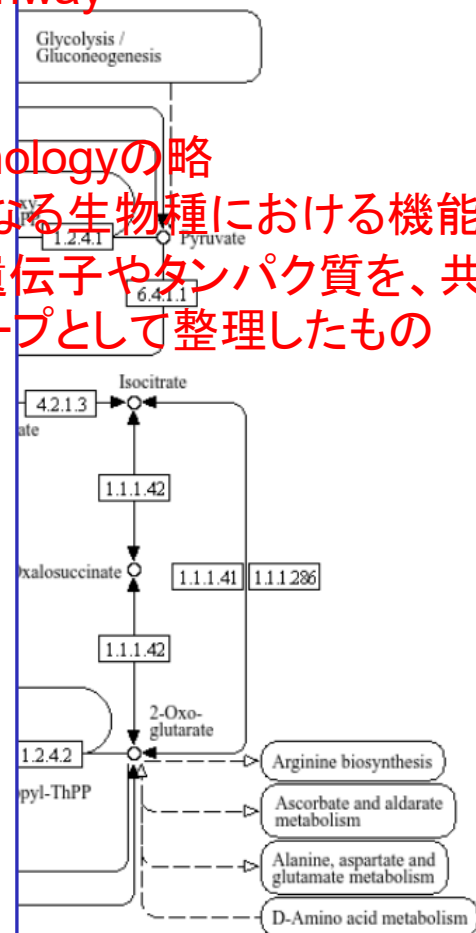
▼ Animals

▼ Mammals

hsa	Homo sapiens (human)	22/33
ptr	Pan troglodytes (chimpanzee)	22/33
pps	Pan paniscus (bonobo)	22/33
ggo	Gorilla gorilla gorilla (western lowland gibbon)	22/33
pon	Pongo abelii (Sumatran orangutan)	22/33
ppyg	Pongo pygmaeus (Bornean orangutan)	22/33
nle	Nomascus leucogenys (northern white-cheeked lemur)	22/33
hnh	Hylobates moloch (silvery gibbon)	22/33
ssyn	Symphalangus syndactylus (siamang)	22/33
mcc	Macaca mulatta (rhesus monkey)	22/33
mcf	Macaca fascicularis (crab-eating macaque)	22/33
mthb	Macaca thibetana thibetana (Pere David's monkey)	22/33
mni	Macaca nemestrina (pig-tailed macaque)	22/33
csab	Chlorocebus sabaeus (green monkey)	22/33
caty	Cercocebus atys (sooty mangabey)	22/33
panu	Papio anubis (olive baboon)	22/33
tge	Theropithecus gelada (gelada)	22/33
mleu	Mandrillus leucophaeus (drill)	22/33
rro	Rhinopithecus roxellana (golden snub-nosed monkey)	22/33
rbb	Rhinopithecus bieti (black snub-nosed monkey)	22/33
tfn	Trachypithecus francoisi (Francois's langur)	22/33
pteh	Ptilocobus tephrosceles (Ugandan red colobus)	22/33
cang	Colobus angolensis palliatus (Angola colobus)	22/33
cjc	Callithrix jacchus (white-tufted-ear marmoset)	22/33
sbq	Saimiri boliviensis boliviensis (Bolivian squirrel monkey)	22/33

「ko Reference pathway (KO Only)」を選択

KOは、KEGG Orthologyの略
Orthologyとは、異なる生物種における機能的に同じ役割をもつ遺伝子やタンパク質を、共通のオーソロググループとして整理したもの



00020 0/27/24

KEGGの利用 (10)

KEGG Citrate cycle (TCA cycle)

[Pathway menu | Organism group | Pathway entry | Show description | Download | Help]

Change pathway type

▼ Option

Scale: 100%

▼ Search

Go

▼ ID search

Go

▼ Color

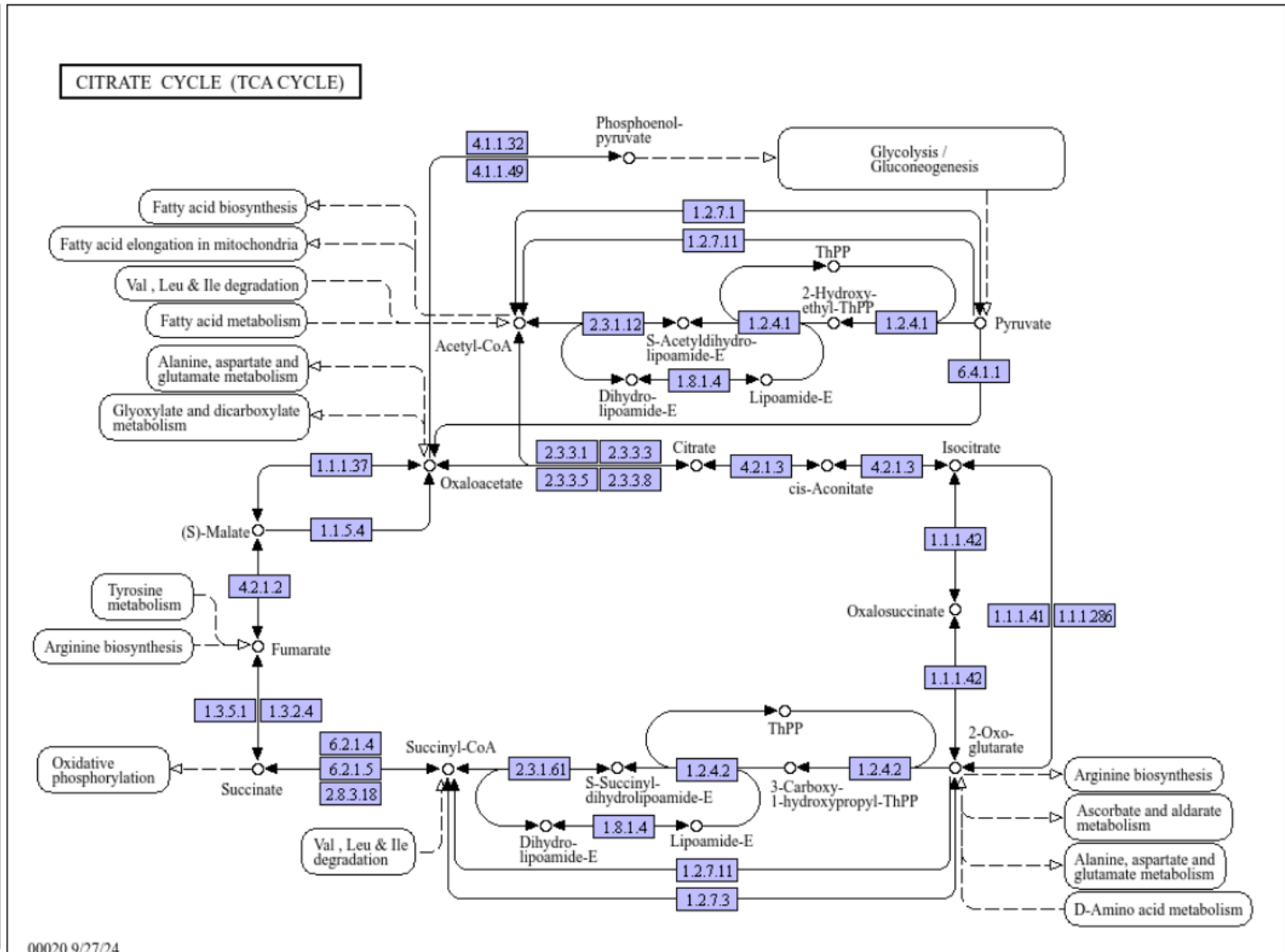
+

▼ Module

☐ Pathway modules

- ☐ Carbohydrate metabolism
 - ☐ Central carbohydrate metabolism
 - ☐ M00003 Gluconeogenesis
 - ☐ M00307 Pyruvate oxidation
 - ☐ M00009 Citrate cycle (TCA cycle)
 - ☐ M00010 Citrate cycle, first half
 - ☐ M00011 Citrate cycle, second half
 - ☐ Other carbohydrate metabolism
 - ☐ M00740 Methylaspartate metabolism
 - ☐ M00982 Methylcitrate cycle

多くの生物種で保存されている遺伝子が
紫色で表示される



KEGGの利用 (11)

Select pathway type for 00020

▼ ▼ ▼ ▼

▼ Reference

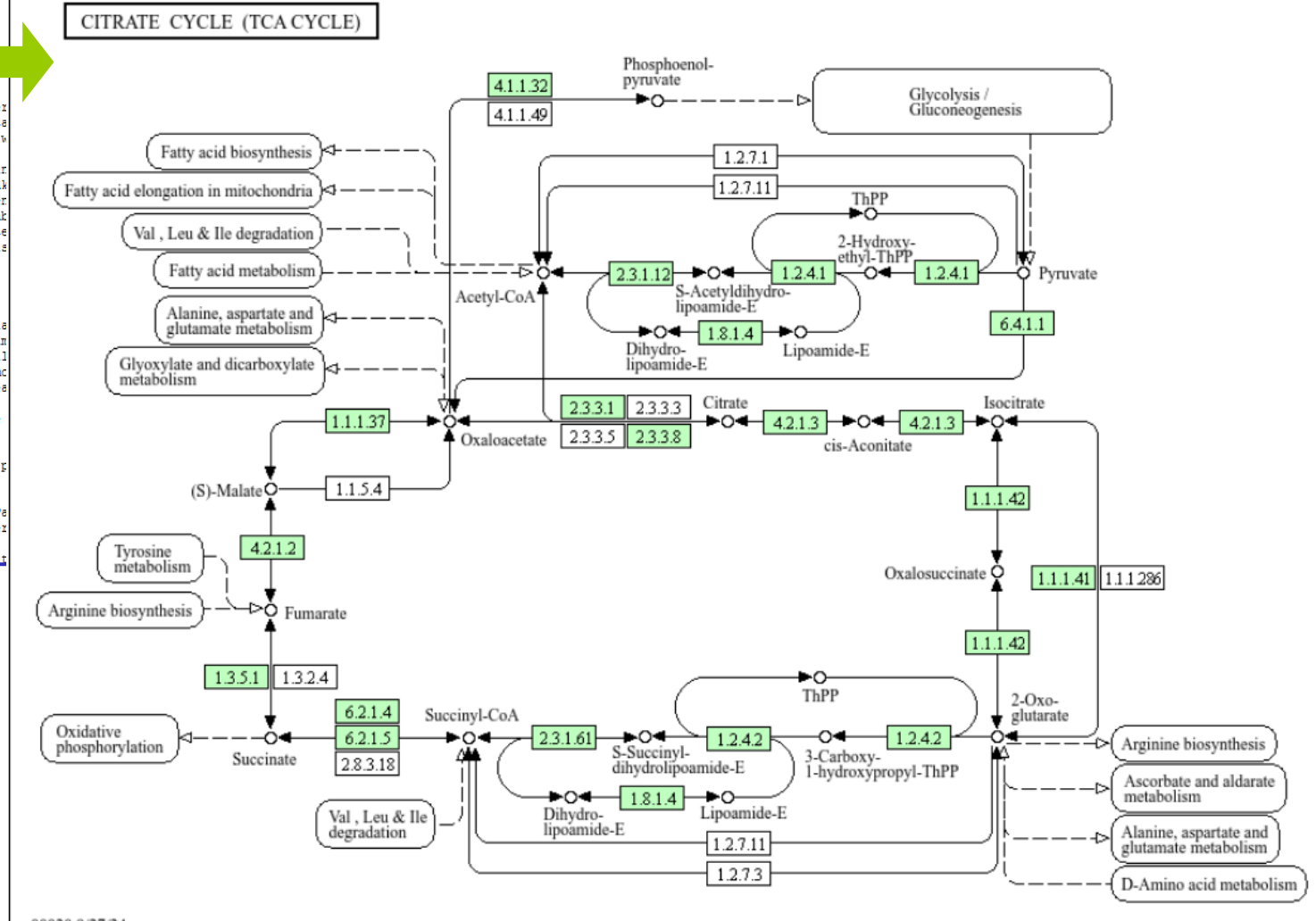
map Reference pathway (map only)
ko Reference pathway (KO only)
ec Reference pathway (EC only)
rn Reference pathway (Reaction only)

▼ Organism specific

▼ Animals
▼ Mammals
hsa Homo sapiens (human)
gor Pan troglodytes (chimpanzee)
pps Pan paniscus (bonobo)
ggo Gorilla gorilla gorilla (western lowland gorilla)
pon Pongo abelii (Sumatran orangutan)
nle Nomascus leucogenys (northern white-cheeked lemur)
mcc Macaca mulatta (rhesus monkey)
mcf Macaca fascicularis (crab-eating macaque)
csab Chlorocebus sabaeus (green monkey)
rrh Rhinopithecus roxellana (golden snub-nosed monkey)
rbb Rhinopithecus bieti (black snub-nosed monkey)
cjc Callithrix jacchus (white-tufted-ear marmoset)
sbq Saimiri boliviensis boliviensis (brown capuchin monkey)
mmu Mus musculus (mouse)
mcal Mus caroli (Ryukyu mouse)
mpah Mus pahari (shrew mouse)
rno Rattus norvegicus (rat)
mun Meriones unguiculatus (Mongolian gerbil)
cge Cricetus griseus (Chinese hamster)
ngi Nannospalax galili (Upper Galilee blind mole rat)
hgl Heterocephalus glaber (naked mole-rat)
ccan Castor canadensis (American beaver)
ocu Oryctolagus cuniculus (rabbit)
tup Tupaia chinensis (Chinese tree shrew)
cfa Canis lupus familiaris (dog)
vvp Vulpes vulpes (red fox)
aml Ailuropoda melanoleuca (giant panda)
umr Ursus maritimus (polar bear)
uah Ursus arctos horribilis (brown bear)
oro Odobenus rosmarus divergens (walrus)
elk Enhydra lutris kenyoni (northern fur seal)
foa Felis catus (domestic cat)
ptg Panthera tigris altaica (Amur tiger)

「hsa Homo sapiens (human)」を選択

ヒトがもつ要素がグリーンで表示される

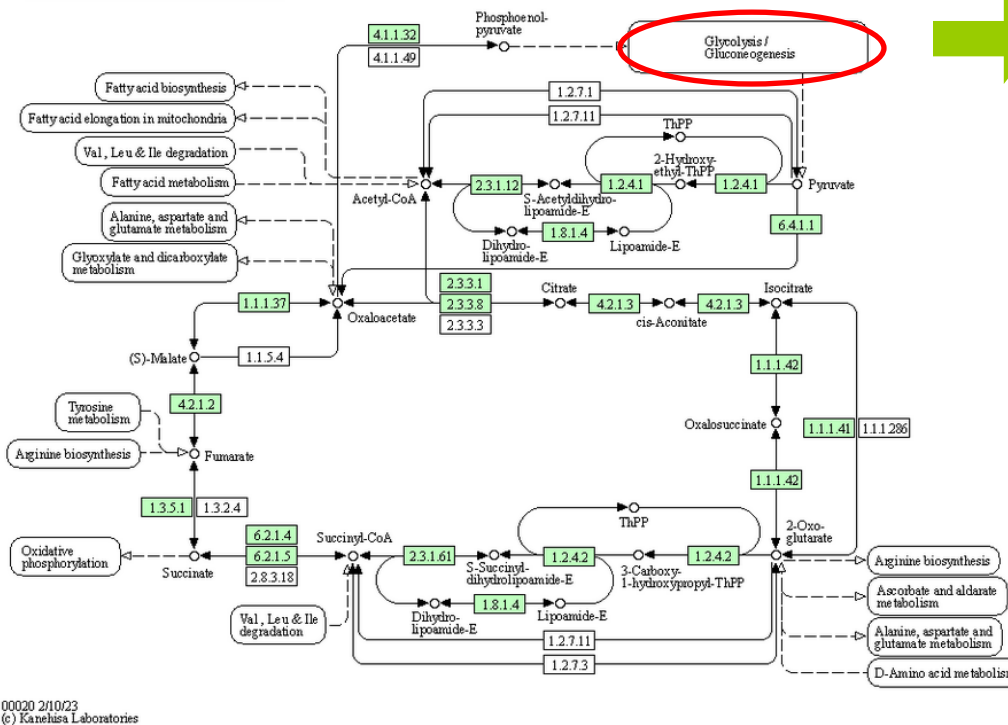


KEGGの利用 (12)

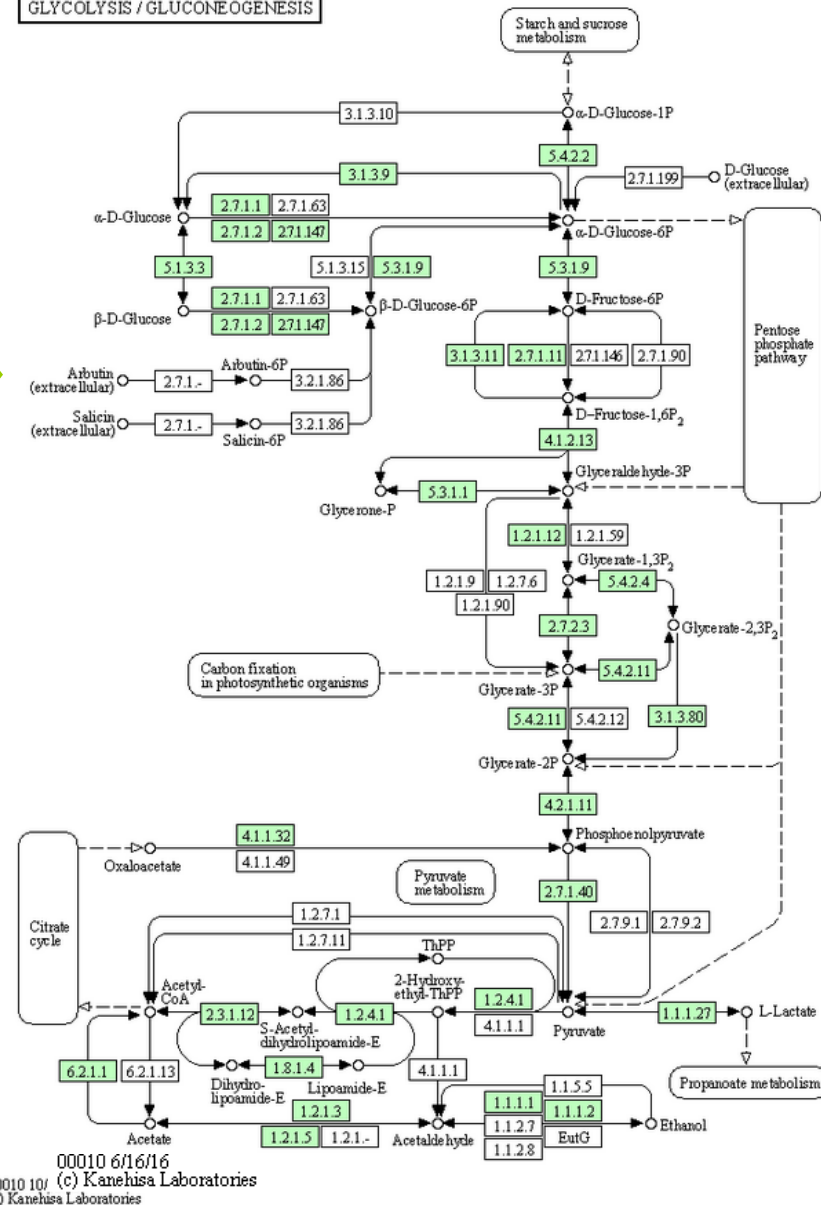
解糖系／糖新生系をクリック

グルコースを分解してピルビン酸を生成→ミトコンドリア内に取り込まれ、アセチルCoAに変換→TCAサイクルで利用される

CITRATE CYCLE (TCA CYCLE)



GLYCOLYSIS / GLUCONEOGENESIS



KEGGの利用 (13)

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KEGG: Kyoto Encyclopedia of Genes and Genomes

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- [KEGG Weblinks](#)
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KEGG Software

- [KEGG API](#)
- [KGML](#)

KEGG FTP

- [Subscription](#)
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[Kanehisa Labs](#)

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, 2025) for new and updated features.

Announcement: Updated procedure to generate organism-specific pathways

New article: KEGG: biological systems database as a model of the real world

- Main entry point to the KEGG web service**
 - KEGG2** [KEGG Table of Contents](#) [[Update notes](#) | [Release history](#)]
- Data-oriented entry points**

KEGG PATHWAY	KEGG pathway maps	Pathway Brite Brite table Module Network KO (Function) Organism Virus Compound Disease (ICD) Drug (ATC) Drug (Target) Antimicrobials
KEGG BRITE	BRITE hierarchies and tables	
KEGG MODULE	KEGG modules	
KEGG ORTHOLOGY	KO functional orthologs	
KEGG GENES	Genes and proteins [KEGG Virus]	
KEGG GENOME	Genomes [Taxonomy Synteny]	
KEGG COMPOUND	Small molecules	
KEGG GLYCAN	Glycans	
KEGG REACTION	Biochemical reactions [RModule]	
KEGG ENZYME	Enzyme nomenclature	
KEGG NETWORK	Disease-related network variations	
KEGG DISEASE	Human diseases	
KEGG DRUG	Drugs [New drug approvals]	
KEGG MEDICUS	Health information resource [Drug labels search]	
- Organism-specific entry points**

「KEGG DISEASE」を選択

KEGGの利用 (14)

[KEGG](#)[Databases](#)[Tools](#)[Auto annotation](#)[Kanehisa Lab](#)

KEGG DISEASE Database

分子ネットワークのゆらぎ状態としての疾患情報リソース

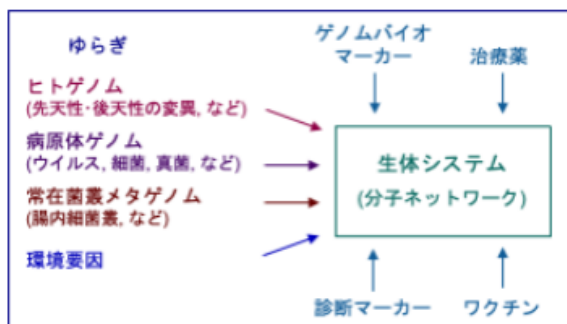
[» English](#)[KEGG2](#)[PATHWAY](#)[BRITE](#)[MODULE](#)[KO](#)[NETWORK](#)[DISEASE](#)[DRUG](#)[MEDICUS](#)

DISEASE を H番号、名称、概要、カテゴリ、パスウェイ、病因遺伝子で検索

DISEASE を KEGG MEDICUS で検索

背景

KEGG では、疾患とは生体システムを司る分子ネットワークがゆらいだ状態であるとみなしています。疾患の遺伝要因と環境要因、それに医薬品は分子ネットワークへのゆらぎ物質です。単一遺伝子疾患、多因子性疾患、感染症疾患など様々な疾患は、ゆらぎ物質とその相互作用を蓄積することで統一的に扱うことができます。



現在のデータ数 (2024/12/25)

疾患(KEGG DISEASE H番号エントリ)の数	2,832
病因遺伝子を含む疾患数	2,292
病因遺伝子の数	5,003
ネットワークバリエーションマップにある疾患数	851
ネットワークバリエーションマップの数	118
疾患パスウェイマップがある疾患数	75
疾患パスウェイマップの数	70

ゆらいだ分子ネットワークに関する知識は疾患パスウェイマップとして表現され、KEGG PATHWAY データベースの一部として提供されてきましたが、特定の疾患に限定されていました。現在は KEGG NETWORK データベースのネットワークバリエーションマップとして、幅広い疾患に対し幅広いゆらぎを蓄積する試みがなされています。

下を見ると

KEGG DISEASE データベース

KEGGの利用 (15)

KEGG DISEASE データベース

KEGG DISEASE は、疾患の要因となるゆらぎ物質として上の概念図の中で、とくにヒト疾患遺伝子と病原体をリスト化したデータベースです。ゆらぎ物質が分子ネットワークにどのような影響を与えるかの詳細は KEGG NETWORK データベースのネットワークバリエーションマップで表現され、両者は密接につながりながら作成されています。環境因子については、当初は KEGG DISEASE に含まれていましたが、現在は分子ネットワークのつながりが明確なものに限定して、KEGG NETWORK にのみ含まれています。各疾患エントリは H 番号で識別され、ネットワークバリエーションマップへのリンクでゆらいだ分子ネットワークが分かる形になっています(例えば、脊髄性筋萎縮症の疾患エントリ [H00455](#))。治療薬については日本語版では日本の、英語版では米国の医薬品添付文書に適合と記載された医薬品が治療薬フィールドに入っています。

疾患は以下の BRITE 階層ファイルで分類されています。

- ICD-11 による疾患分類
- パスウェイに基づく疾患分類
- ゲノムに基づく感染症分類

また日本の法令で定められた疾患との対応づけも行われています。

- 感染症法による感染症分類
- 感染症法における特定病原体等
- 指定難病

ネットワークバリエーションマップ

KEGG NETWORK データベースのネットワークバリエーションマップは上の図で表現した概念を実現したもので、ヒト遺伝子バリエーション、ウイルスその他病原体のタンパク質、環境因子など様々なゆらぎ物質が、レファレンスとなる分子ネットワーク (緑色で表現されています) のどこに影響を与え、それがどの疾患と関連しているかを示しています。

- KEGG network variation maps

疾患パスウェイマップ

KEGG PATHWAY データベースの「ヒト疾患」カテゴリには、疾患パスウェイマップが蓄積されています。

- KEGG パスウェイマップ: ヒト疾患

疾患パスウェイマップは、がん、免疫系疾患、神経変性疾患、循環器疾患、代謝疾患などの多因子性疾患が中心で、病因遺伝子は赤字で示されています。また感染症疾患では、病原体の分子ネットワークとヒトの分子ネットワークの相関が表現されています。

KEGGの利用 (16)

▼ Option

☐ One-click mode
☐ Row border ☐ shading
☒ Pruning neighbor

▼ Search

Go

▼ ID search

Go

▼ Join

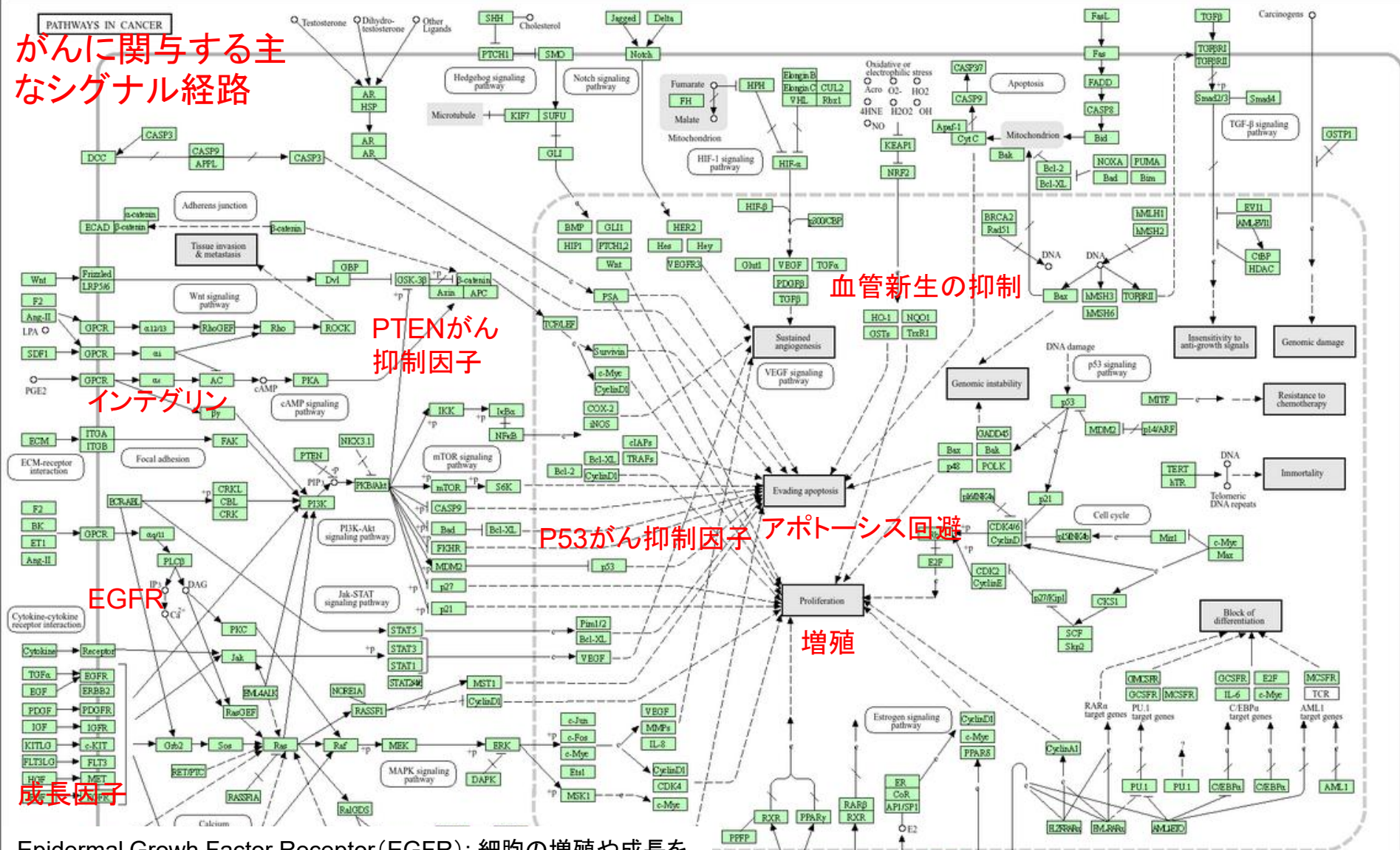
▼ ▼ ▼

- ▶ 代謝
- ▶ 遺伝情報処理
- ▶ 環境情報処理
- ▶ 細胞プロセス
- ▶ 生体システム
- ▼ ヒト疾患
 - ▼ がん：全体像
 - 05200 がんのパスウェイ**
 - 05202 がんにおける転写調節不全
 - 05206 microRNA とがん
 - 05205 プロテオグリカンとがん
 - 05204 化学発がん - DNA付加体
 - 05207 化学発がん - 受容体活性化
 - 05208 化学発がん - 活性酸素種
 - 05203 ウイルス発がん
 - 05230 がんにおける中心炭素代謝
 - 05231 がんにおけるコリン代謝
 - 05235 がんにおける PD-L1 の発現と PD-1 チェックポイントパスウェイ
 - ▼ がん：個別のタイプ
 - 05210 大腸癌
 - 05212 肺癌
 - 05225 肝細胞癌
 - 05226 胃癌
 - 05214 神経膠腫
 - 05216 甲状腺癌
 - 05221 急性骨髄性白血病
 - 05220 慢性骨髄性白血病
 - 05217 基底細胞癌
 - 05218 悪性黒色腫
 - 05211 腎細胞癌
 - 05219 膀胱癌
 - 05215 前立腺癌
 - 05213 子宮内膜癌
 - 05224 乳癌

「がんのパスウェイ」を選択

KEGGの利用 (17)

がんに関する主
なシグナル経路




Epidermal Growth Factor Receptor(EGFR): 細胞の増殖や成長を制御する上皮成長因子(EGF)を認識し、シグナル伝達を行う受容体
P53: DNA損傷の修復やアポトーシス誘導を担う(異常細胞が死なずに分裂変異が蓄積)

インテグリン: 細胞表面の細胞接着タンパク質、細胞の移動や浸潤を助け、がん細胞が周囲の組織へ広がるのを促進
PTEN: 細胞内増殖因子PIP3の脱リン酸化によりシグナル伝達を抑制

代謝経路の探索 (1)

[KEGG](#) [Databases](#) [Tools](#) [Auto annotation](#) [Kanehisa Lab](#)



KEGG ▼

caffeine

Search

Help

[» Japanese](#)

「caffeine」と入力

KEGG Home

- [Release notes](#)
- [Current statistics](#)

KEGG Database

- [KEGG overview](#)
- [KEGG mapping](#)
- [Color codes](#)

KEGG Objects

- [KEGG Weblinks](#)
- [Entry format](#)

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KEGG FTP

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- [Feedback](#)
- [Copyright request](#)
- [Kanehisa Labs](#)

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Announcement: [Updated procedure to generate organism-specific pathways](#)

New article: [KEGG: biological systems database as a model of the real world](#)

- Main entry point to the KEGG web service**
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KEGG GENOME	Genomes [Taxonomy Synteny]	
KEGG COMPOUND	Small molecules	
KEGG GLYCAN	Glycans	
KEGG REACTION	Biochemical reactions [RModule]	
KEGG ENZYME	Enzyme nomenclature	
KEGG NETWORK	Disease-related network variations	
KEGG DISEASE	Human diseases	
KEGG DRUG	Drugs [New drug approvals]	
KEGG MEDICUS	Health information resource [Drug labels search]	
- Organism-specific entry points**

代謝経路の探索 (2)



Search for

Database: KEGG - Search term: caffeine

KEGG PATHWAY

[map00232](#)

Caffeine metabolism

「map00232 (Caffeine metabolism)」を選択

KEGG MODULE

M00915

Caffeine degradation, caffeine => xanthine

KEGG ORTHOLOGY

K12731

DXMT; caffeine synthase [EC:2.1.1.160]

K21673

cdhA; caffeine dehydrogenase subunit alpha [EC:1.17.5.2]

K21674

cdhB; caffeine dehydrogenase subunit beta [EC:1.17.5.2]

K21675

cdhC; caffeine dehydrogenase subunit gamma [EC:1.17.5.2]

KEGG GENES

dme:Dmel_CG14980

K27045 vacuolar fusion protein CCZ1, animal type | (RefSeq) Ccz1; Caffeine, calcium, zinc sensitivity 1

cfe:113374615

no KO assigned | (RefSeq) caffeine-induced protein 16-like

hfr:124148568

no KO assigned | (RefSeq) probable caffeine synthase 4

epa:110240480

no KO assigned | (RefSeq) caffeine synthase 1

epa:110240476

no KO assigned | (RefSeq) probable caffeine synthase 2 isoform X1

... » display all

KEGG MGENES


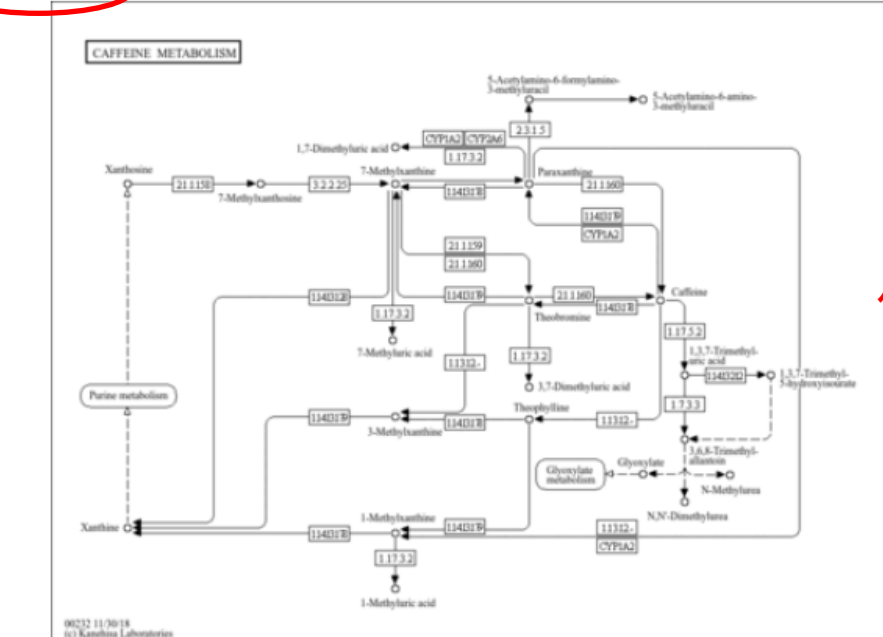
T30176:19157

K08158 MFS transporter, DHA1 family, multidrug resistance protein | caf5; caffeine resistance protein 5

T30231:3551

K08158 MFS transporter, DHA1 family, multidrug resistance protein | caf5; caffeine resistance protein 5

代謝経路の探索 (3)

	PATHWAY: map00232		Help
Entry	map00232 Pathway		
Name	Caffeine metabolism		
Class	Metabolism; Biosynthesis of other secondary metabolites BRITE hierarchy		
Pathway	map00232 Caffeine metabolism		
	 <p>000232 11/30/18 (c) Kanehisa Laboratories</p> <p>Ortholog table</p>		
Module	M00915 Caffeine degradation, caffeine => xanthine [PATH:map00232]		
Other DBs	UMBBD: caf caf2		
Reference	PMID:9705852		
Authors	Madyastha KM, Sridhar GR.		
Title	A novel pathway for the metabolism of caffeine by a mixed culture consortium.		

All links

Pathway (1)
 KEGG MODULE (1)
 Chemical substance (22)
 KEGG COMPOUND (22)
 Chemical reaction (55)
 KEGG ENZYME (13)
 KEGG REACTION (42)
 Gene (11047)
 KEGG ORTHOLOGY (16)
 RefGene (11031)
 Literature (5)
 PubMed (5)
 All databases (11130)

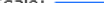
[Download RDF](#)

代謝経路の画像をクリック

KF **GC** Caffeine metabolism - Reference pathway

Change pathway type

▼ Option

Scale:  100%

▼ Search

▼ ID search

▼ Color

▼ Module

□ Pathway modules

☐ Xenobiotics biodegradation

☐ Aromatics degradation

☐ M00915 Caffeine degrada



テオブロミン(弱い中枢神経刺激作用)

カフェイン脱メチル化
酵素(肝臓で作用)

3-Methylxanthine
テオフィリン(中枢神経刺激作用)

カフェインが体内でどう分解され、どんな作用をもつ物質に変わるかを示す

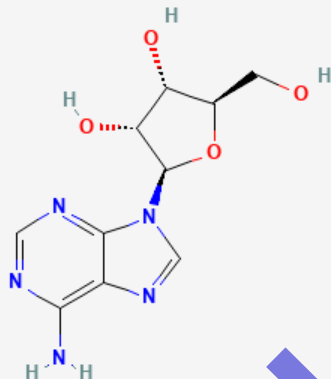
分解された物質のいくつかは、アデノシン受容体を阻害+その自身、覚醒作用をもつ

00232 11/30/18
(c) Kanehisa Laboratories

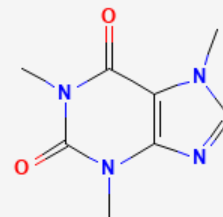
代謝経路の探索 (5)

アデノシンとカフェインは構造が似ている

アデノシン

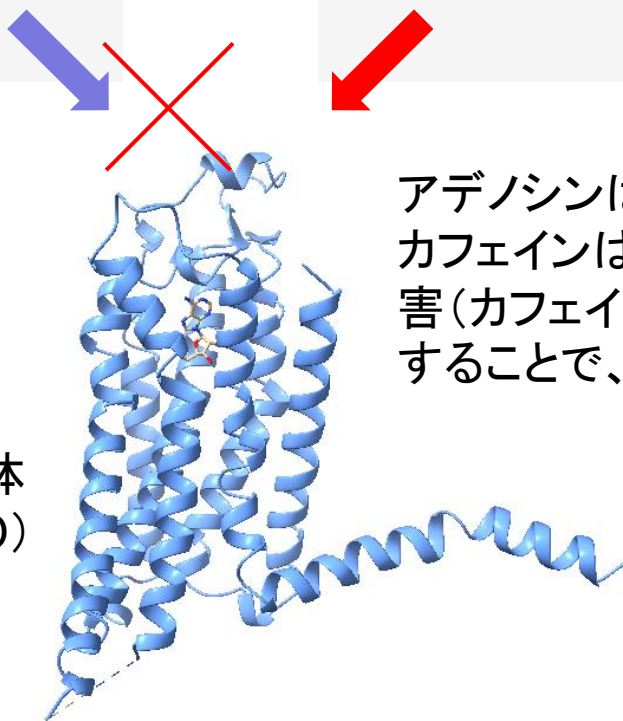


カフェイン



ストレスやエネルギー不足
で興奮するが、アデノシンは、
心拍数を抑え、興奮を抑制する

アデノシン受容体
(PDB ID: 2YDO)



アデノシンは脳内で眠気を誘発するが、
カフェインはアデノシン受容体を競合阻
害(カフェインがアデノシン受容体に結合
することで、アデノシンの効果を阻害)

遺伝子からの代謝経路の探索 (1)

KEGG: Kyoto Encyclopedia of Genes and Genomes



KEGG は分子レベルの情報から細胞、個体、エコシステムといった高次生命システムレベルの機能や有用性を理解するためのリソースです。とくにゲノムをはじめとしたハイスループットデータの生物学的意味解釈に広く利用されています。また **KEGG MEDICUS** では医薬品添付文書など社会的ニーズの高いデータとの統合も行われています。
新規・更新等の内容は英文の [Release notes](#) (January 1, 2025) をご覧ください。

Announcement: Updated procedure to generate organism-specific pathways

New article: KEGG: biological systems database as a model of the real world

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KEGG の主要エントリーポイント

KEGG2

[KEGG の目次のページ](#) [[Update notes](#) | [Release history](#)]

データタイプごとのエントリーポイント

KEGG PATHWAY

[KEGG パスウェイマップ](#)

KEGG BRITE

[BRITE 機能階層・テーブル](#)

KEGG MODULE

[KEGG モジュール](#)

KEGG ORTHOLOGY

[KO 機能オーソログ](#)

KEGG GENES

[遺伝子・タンパク質](#) [[KEGG Virus](#)]

KEGG GENOME

[ゲノム](#) [[Taxonomy](#) | [Synteny](#)]

KEGG COMPOUND

[化合物](#)

KEGG GLYCAN

[糖鎖](#)

KEGG REACTION

[化学反応](#) [[RModule](#)]

KEGG ENZYME

[酵素](#)

KEGG NETWORK

[疾患関連のネットワーク多様性](#)

KEGG DISEASE

[疾患 \(日本語\)](#)

KEGG DRUG

[医薬品 \(日本語\)](#) [[日米欧の新薬](#)]

KEGG MEDICUS

[疾患・医薬品の統合リソース \(日本語\)](#) [[添付文書検索](#)]

生物種ごとのエントリーポイント

KEGG 生物種

[生物種コード\(複数可\)](#) [hsa](#) [hsa eco](#)

解析ツール

KEGG Mapper

[PATHWAY/BRITE/MODULE 等へのマッピングツール群](#)

KEGG Web Apps

[Pathway viewer の色付け機能など](#)

[パスウェイ](#)
[Brite階層](#)
[Briteテーブル](#)
[Module](#)
[Network](#)
[KO \(機能\)](#)
[生物種](#)
[Virus](#)
[化合物](#)
[疾患 \(ICD-11\)](#)
[医薬品 \(ATC\)](#)
[医薬品 \(薬効\)](#)
[医薬品 \(標的\)](#)
[抗微生物薬](#)

「KEGG Mapper」を選択

遺伝子からの代謝経路の探索 (2)



KEGG Mapper

A suite of KEGG mapping tools

KEGG Mapper

[Reconstruct](#)

[Search](#)

[Color](#)

[Join](#)

[MWsearch](#)

[Convert ID](#)

KEGG Web Apps

[Map coloring GUI](#)

[Map coloring URL](#)

KEGG Syntax

[Taxonomy mapping](#)

[Genome alignment](#)

[Synteny analysis](#)

KEGG Annotation

[KO assignment](#)

[BlastKOALA](#)

[GhostKOALA](#)

[KEGG2](#)

[KEGG](#)

[[Reconstruct](#) | [Search](#) | [Color](#) | [Join](#) | [MWsearch](#)]

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, two basic tools of "Search Pathway" (currently, [Search](#)) and "Search&Color Pathway" (currently, [Color](#)) were introduced at the beginning of the KEGG project. As the KEGG database contents expanded, so did the mapping tools [1,2].

The current version 5 of KEGG Mapper released in July 2021 consists of four main tools: [Reconstruct](#), [Search](#), [Color](#) and [Join](#). Since October 2023 these tools are tightly integrated with KEGG pathway map viewer and Brite hierarchy viewer, so that the final steps of mapping are processed on the client side.

See also: [Map coloring GUI](#) and [Map coloring URL](#) in KEGG Web Apps.

KEGG Mapper tools

There are five KEGG Mapper tools as summarized below.

Reconstruct 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 is the traditional tool for searching mapped objects in the user's dataset and mark them in red.

Color is another traditional tool for searching mapped objects in the user's dataset and mark them in any combination of background and foreground colors. This tool now applies only to KEGG pathway maps. Use the [Join](#) tool for coloring of Brite hierarchies.

Join is a tool to combine a Brite hierarchy file and a binary relation file, effectively adding a new column to the hierarchy file.

MWsearch is a variant of the [Search](#) tool performing conversion of mass spectrometry data, either as a set of molecular masses or molecular formulas, to a set of numbers.

[Query data](#)

遺伝子からの代謝経路の探索 (3)



KEGG Mapper – Search

KEGG Mapper
Reconstruct
Search
Color
Join
MWsearch
Convert ID

KEGG Web Apps
Map coloring GUI
Map coloring URL

KEGG Syntax
Taxonomy mapping
Genome alignment
Synteny analysis

KEGG Annotation
KO assignment
BlastKOALA
GhostKOALA

KEGG2
KEGG

Search tool

The Search tool searches various KEGG objects, including genes, KOs, EC numbers, metabolites and drugs, against KEGG pathway maps and other network entities. Found objects are marked in red.

Search mode: ☒ Reference ☐ hsa ☐ other org

Enter query KEGG identifiers

K02092
K02093
K02094
K02095
K02096
K02284
K02285
K02286
K02287

ファイルcyn-gene-k.txt
の遺伝子群を入力

Or upload file: ファイルが選択されていません。

Filter1 Filter2 (to extract K/C/G/D/R/RC numbers)

☐ Include "same as" objects

☐ Include aliases (for hsa and other org modes)

「Exec」を押す

Examples:

▼

hsa mode
[diseasegene.txt](#) (human disease genes)
[drugtarget.txt](#) (drug targets)
[mabtarget.txt](#) (drug targets, MAB only)

..

遺伝子からの代謝経路の探索（４）

KEGG Mapper Search Result

Pathway (30)

Brite (11)

Brite Table(0)

Module (7)

Sort by the pathway list

Show matched objects

map01100 Metabolic pathways (51)

map00195 Photosynthesis (33)

map00196 Photosynthesis - antenna proteins (11)

map01110 Biosynthesis of secondary metabolites (2)

map00130 Ubiquinone and other terpenoid-quinone biosynthesis (1)

map05208 Chemical carcinogenesis - reactive oxygen species (1)

map05207 Chemical carcinogenesis - receptor activation (1)

map05225 Hepatocellular carcinoma (1)

map01240 Biosynthesis of cofactors (1)

map02020 Two-component system (1)

map00982 Drug metabolism - cytochrome P450 (1)

map01120 Microbial metabolism in diverse environments (1)

map01524 Platinum drug resistance (1)

map00520 Amino sugar and nucleotide sugar metabolism (1)

map00910 Nitrogen metabolism (1)

map00480 Glutathione metabolism (1)

map00190 oxidative phosphorylation (1)

全体の代謝マップ

光合成系の代謝マップ

遺伝子からの代謝経路の探索 (5)



Photosynthesis - Reference pathway

[Pathway menu | Organism group | Pathway entry | Show description | Download | Help]

Change pathway type

Option

Scale: 100%

Search

Go

ID search

Go

Color

☒ KEGG Mapper

Module

☐ Pathway modules

☐ Energy metabolism

☐ Photosynthesis

☐ M00161 Photosystem II

☐ M00163 Photosystem I

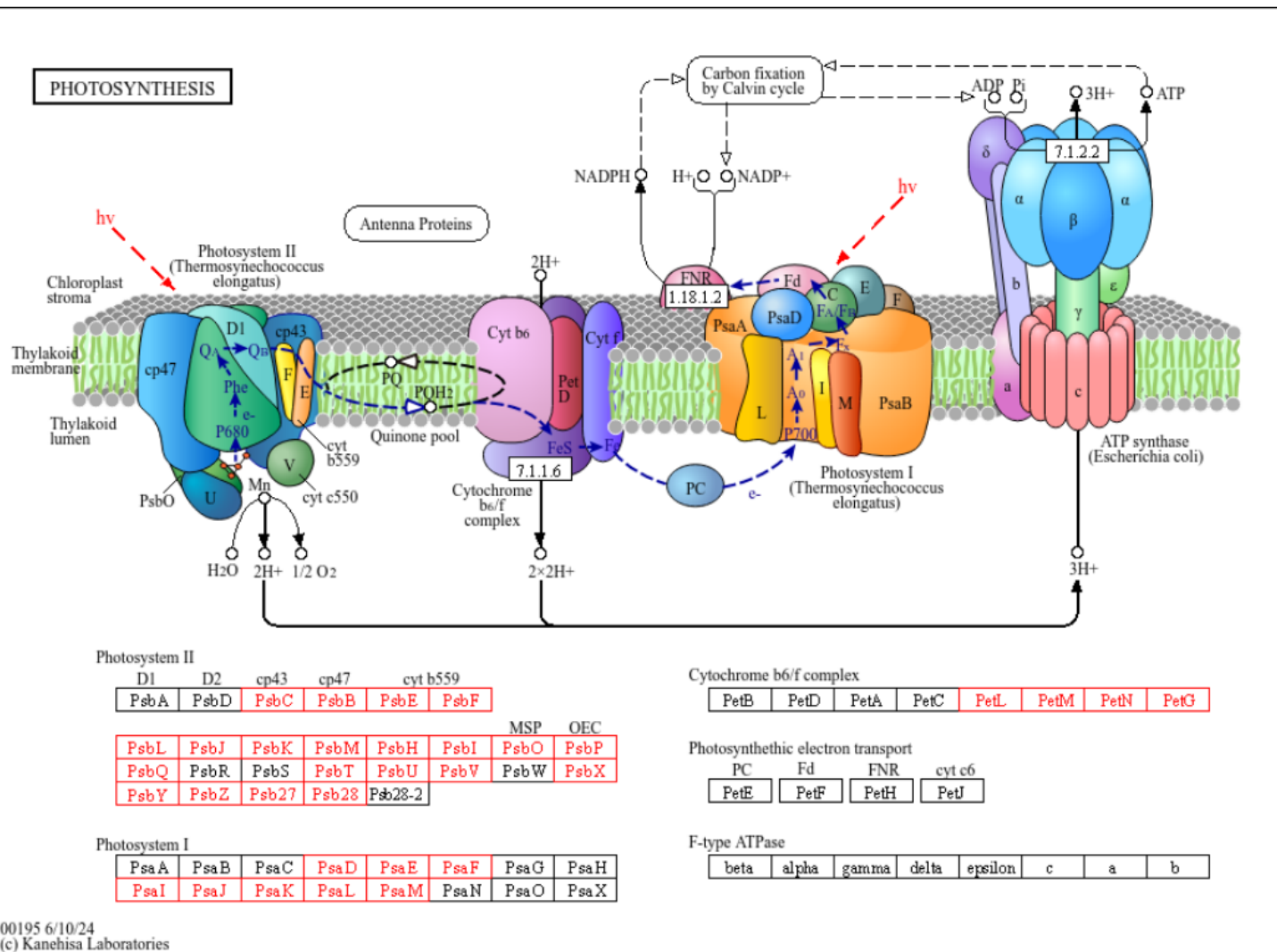
☐ ATP synthesis

☐ M00162 Cytochrome b6/f

☐ M00157 F-type ATPase, p


Related Brite

00194 Photosynthesis proteins



MBGD

- 微生物ゲノム比較解析データベース (Microbial Genome Database for Comparative Analysis)
- 真正細菌33249、古細菌414、真核生物416のゲノムを登録 (2024年10月4日更新)
- オーソログのグルーピング
 - デフォルトの生物種、利用者が指定した生物種
- 生物種間の比較ゲノム解析
- <https://mbgd.nib.ac.jp/>



MICROBIAL GENOME DATABASE

Microbial Genome Database for Comparative Analysis

About MBGD

Documents

Ortholog Classification

Ortholog Table

Create ortholog table

My MBGD Mode

Cluster Tables

Searching MBGD

Advanced Search

Sequence Search

Profile Search

Genomape

Function Categories

Downloads & Programs

MBGD API

Data Archive

SPARQL interface

DomClust

DomRefine

CGAT

CoreAligner

Welcome to MBGD

MBGD is a database for comparative analysis of completely sequenced microbial genomes, the number of which is now growing rapidly. The aim of **MBGD** is to facilitate comparative genomics from various points of view such as ortholog identification, paralog clustering, motif analysis and gene order comparison.
References: *Nucleic Acids Res.* **47:D382-D389 (2019)**

Complete genome and Draft sequences

Complete: Total 34079 genomes (6,316 species, 1,812 genera) including 33,249 Bacteria, 414 Archaea and 416 Eukaryota.
Draft-plus: Total 36156 genomes (8,338 species, 3,834 genera) including 35,326 Bacteria, 414 Archaea and 416 Eukaryota.
(Last update 2024/10/4).

Data Sources

Taxonomy Browser

Ortholog table summary viewer

Go

Keyword Search

Ortholog group

ex.) DnaK

Search

Gene

ex.) species="Escherichia coli" DnaK

Search

Species/Taxon

ex.) Escherichia

Search

MBGDの利用 (1)

藍藻類に特異的な遺伝子をどのように取得したか？

クラスタの統計が表示される

MBGD Ortholog Cluster Table Overview

Current selection: *Bacteria* (superkingdom)

Cluster size

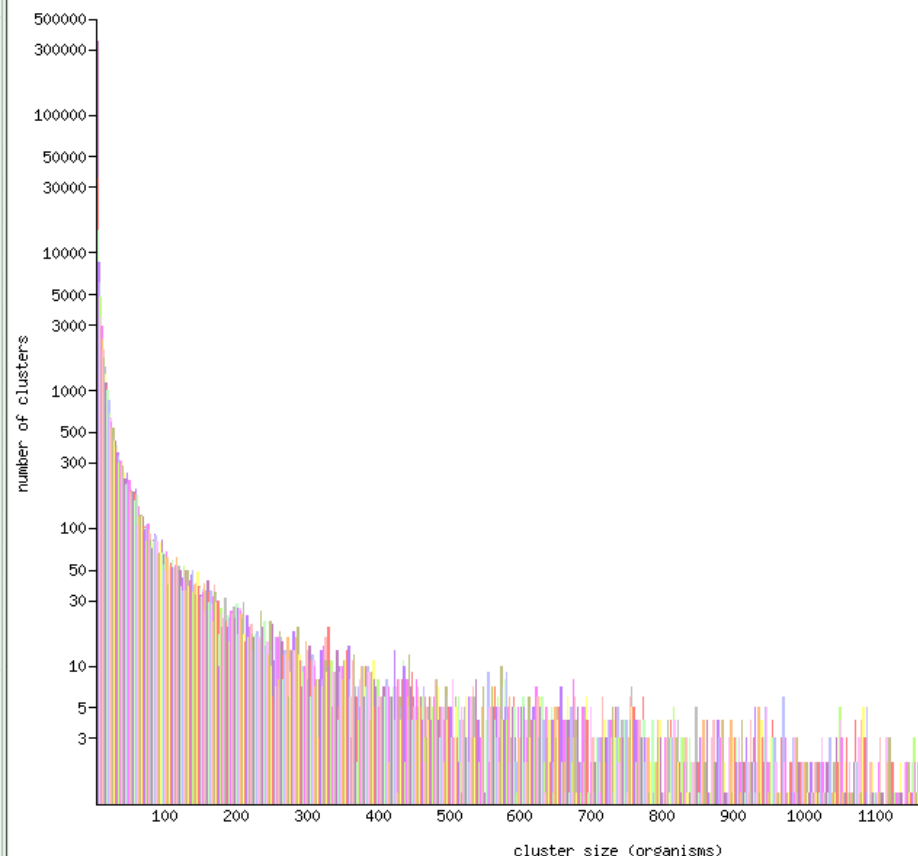
「Occurrence pattern」を選択

Cluster size Occurrence pattern Core Aligner Phylogenetic tree

[Collapse all](#) - [Expand all](#) -

- Default
- Draft-plus
- Archaea (superkingdom)
- Bacteria (superkingdom)**
- Acidobacteria (phylum)
- Aquificae (phylum)
- Candidatus Saccharibacteria (phylum)
- Deferribacteres (phylum)
- Bacteroidota (phylum)
- Chlorobi (phylum)
- Fusobacteria (phylum)
- Nitrospirae (phylum)
- Chlamydiae (phylum)
- Planctomycetota (phylum)
- Verrucomicrobia (phylum)
- Proteobacteria (phylum)
- Spirochaetes (phylum)
- Synergistetes (phylum)
- Actinobacteria (phylum)
- Chloroflexi (phylum)
- Cyanobacteria (phylum)
- Deinococcus-Thermus (phylum)
- Firmicutes (phylum)
- Tenericutes (phylum)
- Thermotogae (phylum)
- Eukaryota (superkingdom)

「Bacteria」を選択し、対象を絞る



Keyword search

☒ Ortholog group ☐ Gene

ex.) DnaK

About MBGD

Documents

Ortholog
Classification

Ortholog Table

Create ortholog table

My MBGD Mode

Cluster Tables

Searching MBGD

Advanced Search

Sequence Search

Profile Search

Genomaple

Function Categories

Downloads &
Programs

MBGD API

Data Archive

SPARQL interface

DomClust

DomRefine

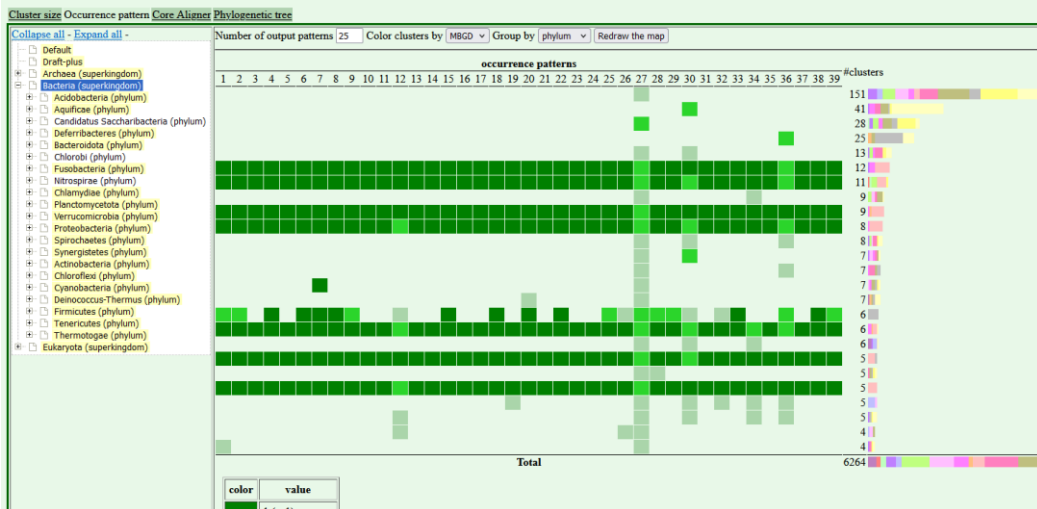
CGAT

MBGDの利用 (2)

MBGD Ortholog Cluster Table Overview

Current selection: *Bacteria* (superkingdom)

Gene Cluster Map



このページの下の方

Filter

Minimum cluster size # min organisms: 147 # max organisms:

リセット Show cluster table Redraw the map Save Selected Table Save Complete Table (Format tab (List) Save my table)

Table format

Additional information:

Annotation from None

☐ Motifs found in 50 % or more of the clustered sequences

Display options:

Parameter	Value
Color genes	<input type="radio"/> off <input type="radio"/> function category
Display cluster members as	<input type="radio"/> Phylogenetic pattern <input type="radio"/> ORF IDs <input checked="" type="radio"/> gene names <input type="radio"/> counts of members
Maximum outputs / page	100

クラスタリングの対象生物種はデフォルトのものを使用、
ただし、クラスタを形成する最小の生物種数をデフォルトの値 (Bacteriaを選択したとき「147」になっているので、「25」に減らす)

「Redraw the Map」を選択

MBGDの利用 (3)

藍藻類 (Cyanobacteria) に特徴的な遺伝子を集める

MBGD Ortholog Cluster Table Overview

Current selection: *Bacteria* (superkingdom)

Gene Cluster Map

Cluster size Occurrence pattern Core Aligner Phylogenetic tree

Collapse all - Expand all -

- Default
- Draft-plus
- Archaea (superkingdom)
- Bacteria (superkingdom)**
- Acidobacteria (phylum)
- Aquificae (phylum)
- Candidatus Saccharibacteria (phylum)
- Deferribacteres (phylum)
- Bacteroidota (phylum)
- Chlorobi (phylum)
- Fusobacteria (phylum)
- Nitrospirae (phylum)
- Chlamydiae (phylum)
- Planctomycetota (phylum)
- Verrucomicrobia (phylum)
- Proteobacteria (phylum)
- Spirochaetes (phylum)
- Synergistetes (phylum)
- Actinobacteria (phylum)
- Chloroflexi (phylum)
- Cyanobacteria (phylum)
- Deinococcus-Thermus (phylum)
- Firmicutes (phylum)
- Tenericutes (phylum)
- Thermotogae (phylum)
- Eukaryota (superkingdom)

Keyword search

☒ Ortholog group ☐ Gene

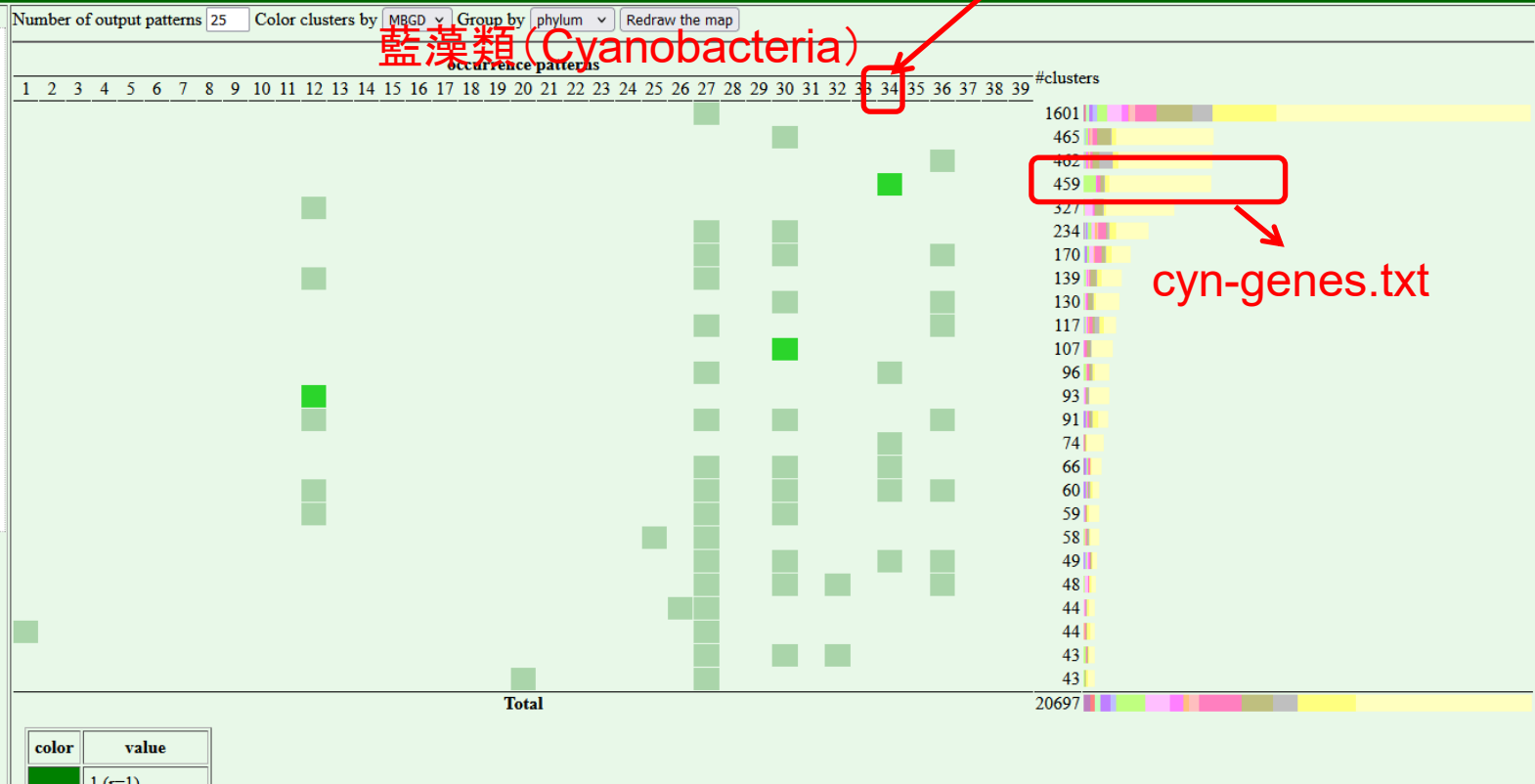
ex.) DnaK

[Cyanobacteria(38)]

Search

カーソルを置くと、その番号の生物の分類(門, phylum)が表示される

藍藻類 (Cyanobacteria)



MBGDの利用 (4)

MBGD Ortholog Cluster Table Overview

- A Multiple sequence alignment (☒ Clustal Omega ☐ MAP ☐ MAFFT)
- M Multiple genome map comparison
- H Find homologous clusters
- P Similar phylogenetic pattern search (☐ Correlation coefficient ☐ Hamming distance ☐ Mutual information)

Analyze the checked clusters

生物種

ClusterID	Name	abas	aca	aba	acm	tsa	gm32244	sus	ctm	gm28578	abac	aae	hth	hya	tal	ttk	pmx	sul	dte	tam	bana	mox	ceg	gm04998	din	cpo	cni	ddf	fsi	dap	gtl	gm28987	dth	emi	epo	rmr	sru
<input type="checkbox"/> O19641	A M H P																																				
<input type="checkbox"/> O20344	A M H P																																				
<input type="checkbox"/> O20342	A M H P																																				
<input type="checkbox"/> O12443	A M H P																																				
<input type="checkbox"/> O12455	A M H P																																				
<input type="checkbox"/> O12454	A M H P																																				
<input type="checkbox"/> O28398	A M H P																																				
<input type="checkbox"/> O12445	A M H P																																				
<input type="checkbox"/> O12438	A M H P																																				
<input type="checkbox"/> O12458	A M H P																																				
<input type="checkbox"/> O12452	A M H P																																				

遺伝子名

エンリッチメント解析

• エンリッチメント解析

- 遺伝子のリストを入力し、それらがもつ機能や特性を解析すること
- 例えば、ある生物のグループに特徴的に見られる遺伝子、特定の条件で特異的に発現した遺伝子あるいは発現変動が大きい遺伝子など

• KEGGエンリッチメント解析

- 関連性の認められた遺伝子を代謝経路上にマップ

• GOエンリッチメント解析

- GO termでヒットした機能や特性が有意性ととともに表示される
 - 生物学的プロセス、細胞の構成要素、分子機能ごと
- GOのサイトではPANTHER (Gene List Analysis) が利用される

GOエンリッチメント解析の例

The screenshot shows the Gene Ontology website. At the top, there's a navigation bar with links: About, Ontology, Annotations, Downloads, Help. On the right, there are social media icons and the ALLIANCE of GENOME RESOURCES logo. Below the navigation bar, a banner displays the current release date and statistics: "Current release 2024-11-03: 40,635 GO terms | 8,031,345 annotations | 1,568,326 gene products | 5,435 species (see statistics)". The main heading is "THE GENE ONTOLOGY RESOURCE". Below this, two paragraphs describe the mission and the knowledgebase. A search bar is present with the text "Search GO term or Gene Product in AmiGO ...". To the right, the "GO Enrichment Analysis" section is highlighted with a red box. It includes a list of gene IDs (ycf36, ycf4, ycf51, ycf54, ycf58, ycf65, ycf66) with a red box around them and a red annotation "cyn-gene.txtの内容をペースト". Below the list, the term "biological process" is selected in the dropdown menu, with a red box around it and a red annotation "「biological process」を選択(デフォルト)". The species "Oryza sativa" is selected in the dropdown menu, with a red box around it and a red annotation "「Oryza sativa」(イネ)を選択". The "Launch" button is circled in red with a red annotation "「Launch」を押す". A hint at the bottom of the section reads: "Hint: can use UniProt ID/AC, Gene Name, Gene Symbols, MOD IDs".

GENE ONTOLOGY
Unifying Biology

About Ontology Annotations Downloads Help

Current release 2024-11-03: 40,635 GO terms | 8,031,345 annotations
1,568,326 gene products | 5,435 species (see statistics)

THE GENE ONTOLOGY RESOURCE

The mission of the GO Consortium is to develop a comprehensive, **computational model of biological systems**, ranging from the molecular to the organism level, across the multiplicity of species in the tree of life.

The Gene Ontology (GO) knowledgebase is the world's largest source of information on the functions of genes. This knowledge is both human-readable and machine-readable, and is a foundation for computational analysis of large-scale molecular biology and genetics experiments in biomedical research.

Search GO term or Gene Product in AmiGO ...

Any Ontology Gene Product

GO Enrichment Analysis ?

Powered by PANTHER

ycf36
ycf4
ycf51
ycf54
ycf58
ycf65
ycf66

cyn-gene.txtの内容をペースト

biological process

Oryza sativa

Examples Launch >

Hint: can use UniProt ID/AC, Gene Name, Gene Symbols, MOD IDs

「biological process」を選択(デフォルト)

「Oryza sativa」(イネ)を選択

「Launch」を押す



The network of biological classes describing the current best representation of the "universe" of biology: the molecular



Statements, based on specific, traceable scientific evidence, asserting that a specific gene product is a real exemplar of a particular



GO Causal Activity Model (GO-CAM) provides a structured framework to link standard GO annotations into a more



Tools to curate, browse, search, visualize and download both the ontology and annotations. Includes bioinformatic guides

GOエンリッチメント解析の例



The mission of the PANTHER knowledgebase is to support biomedical and other research by providing **comprehensive information about the evolution of protein-coding gene families**, particularly protein phylogeny, function and genetic variation impacting that function. [Learn more](#)

PANTHER19.0 Released. [Click](#) for more details.

AI Go

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Current Release: **PANTHER 19.0** | **15,683** family phylogenetic trees | **144** species | [News](#)
[Whole genome function views](#)

Analysis Summary: Please report in publication [?](#)

Analysis Type: PANTHER Overrepresentation Test (Released 20240807)

Annotation Version and Release Date

Analyzed List: upload

Reference List: Oryza

Annotation Data Set: ☒ GO biological process

Test Type: ☒ Fisher's Exact ☐ Binomial

Correction: ☒ Calculate False Discovery Rate

Displaying only results for FDR P < 0.05, [click here to display all results](#)

	Oryza sativa (REF)	upload_1 (Hierarchy NEW! ?)					
GO biological process complete	#	#	expected	Fold Enrichment	+/-	raw P value	FDR
photosynthetic electron transport in photosystem II	8	4	.01	> 100	+	6.66E-11	2.72E-08
↳ photosynthetic electron transport chain	32	8	.02	> 100	+	7.17E-19	6.45E-16
↳ electron transport chain	190	11	.12	90.27	+	2.97E-19	3.34E-16
↳ generation of precursor metabolites and energy	326	13	.21	62.18	+	9.90E-21	1.48E-17
↳ cellular metabolic process	6607	25	4.24	5.90	+	6.70E-18	5.02E-15
↳ metabolic process	9567	27	6.14	4.40	+	3.60E-17	2.31E-14
↳ cellular process	10813	25	6.93	3.61	+	1.04E-12	5.84E-10
↳ photosynthesis, light reaction	77	10	.05	> 100	+	7.32E-21	1.64E-17
↳ photosynthesis	179	24	.11	> 100	+	5.06E-53	2.27E-49
Unclassified	27815	1	17.84	.06	-	2.40E-11	1.20E-08

Results [?](#)

Uniquely Mapped IDs: [43658](#) out of 4

Unmapped IDs: [0](#)

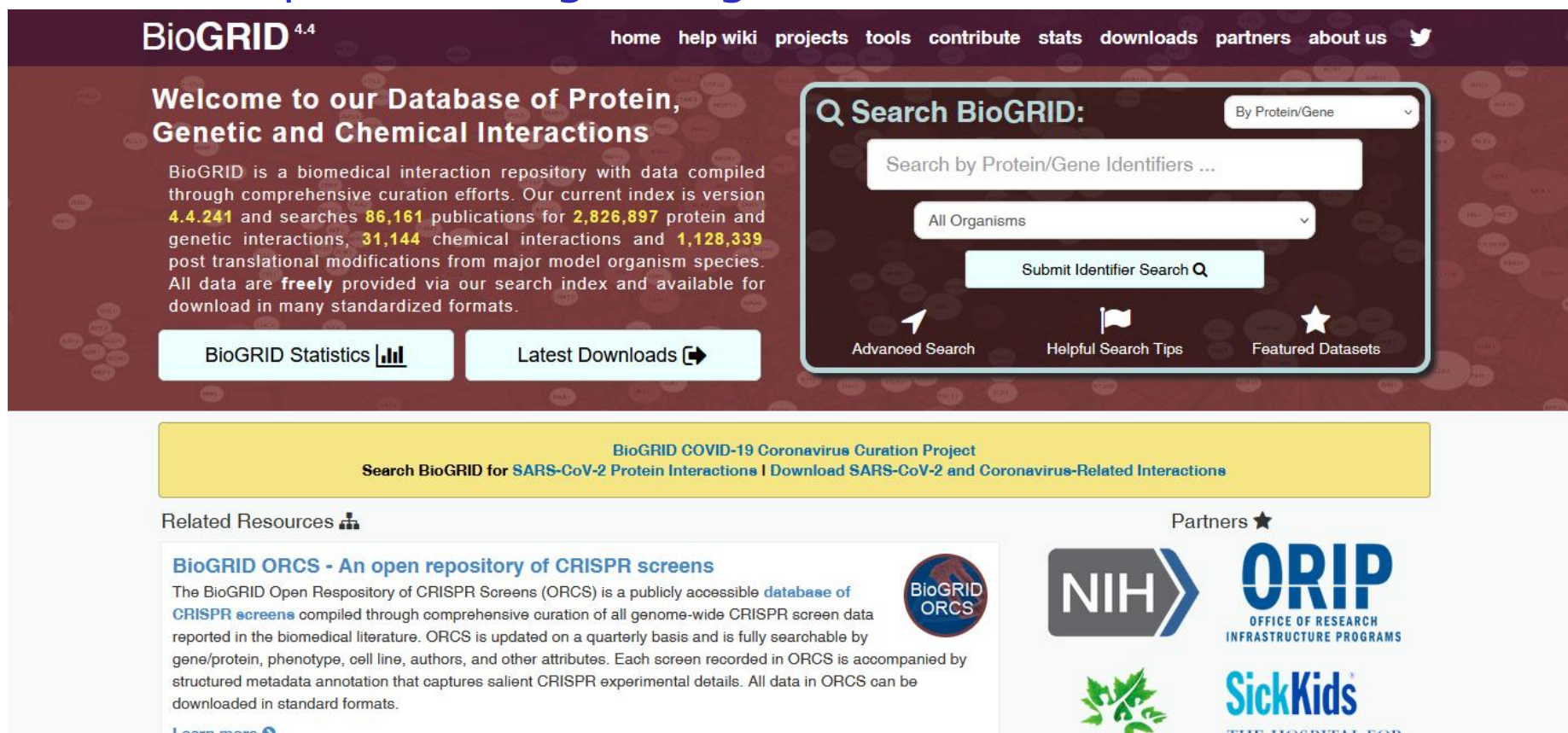
Multiple mapping information: [0](#)

Export [Table](#) [XML with user input ids](#)

タンパク質間相互作用ネットワーク

- BioGRID

- 主要なモデル生物種のタンパク質および遺伝子の相互作用、化学的相互作用、翻訳後修飾を、文献情報（実験結果）をもとに収集したデータベース
- <https://thebiogrid.org/>



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Welcome to our Database of Protein, Genetic and Chemical Interactions

BioGRID is a biomedical interaction repository with data compiled through comprehensive curation efforts. Our current index is version **4.4.241** and searches **86,161** publications for **2,826,897** protein and genetic interactions, **31,144** chemical interactions and **1,128,339** post translational modifications from major model organism species. All data are **freely** provided via our search index and available for download in many standardized formats.

BioGRID Statistics **Latest Downloads**

Q Search BioGRID: By Protein/Gene

Search by Protein/Gene Identifiers ...

All Organisms

Submit Identifier Search Q

Advanced Search Helpful Search Tips Featured Datasets

BioGRID COVID-19 Coronavirus Curation Project
Search BioGRID for SARS-CoV-2 Protein Interactions | Download SARS-CoV-2 and Coronavirus-Related Interactions

Related Resources

BioGRID ORCS - An open repository of CRISPR screens
The BioGRID Open Repository of CRISPR Screens (ORCS) is a publicly accessible database of CRISPR screens compiled through comprehensive curation of all genome-wide CRISPR screen data reported in the biomedical literature. ORCS is updated on a quarterly basis and is fully searchable by gene/protein, phenotype, cell line, authors, and other attributes. Each screen recorded in ORCS is accompanied by structured metadata annotation that captures salient CRISPR experimental details. All data in ORCS can be downloaded in standard formats.

Partners

NIH **ORIP** **SickKids**


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Welcome to our Database of Protein, Genetic and Chemical Interactions

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[BioGRID Statistics](#) 

[Latest Downloads](#) 

Q Search BioGRID: By Protein/Gene

[Advanced Search](#) [Helpful Search Tips](#) [Featured Datasets](#)

「Homo sapiens」を選択

インスリンの遺伝子「INS」を入力して、
「Submit Identifier Search」を押す

BioGRID COVID-19 Coronavirus Curation Project
Search BioGRID for SARS-CoV-2 Protein Interactions | Download SARS-CoV-2 and Coronavirus-Related Interactions

Related Resources

BioGRID ORCS - An open repository of CRISPR screens

The BioGRID Open Repository of CRISPR Screens (ORCS) is a publicly accessible **database of CRISPR screens** compiled through comprehensive curation of all genome-wide CRISPR screen data reported in the biomedical literature. ORCS is updated on a quarterly basis and is fully searchable by gene/protein, phenotype, cell line, authors, and other attributes. Each screen recorded in ORCS is accompanied by structured metadata annotation that captures salient CRISPR experimental details. All data in ORCS can be downloaded in standard formats.

[Learn more](#) 

BioGRID Themed Curation Projects

BioGRID themed curation projects focus on specific biological processes with disease relevance. Core genes/proteins central to the process are assembled with expert input and relevant publications curated for biological interactions. Themed curation projects are updated monthly and additional projects are generated on a regular basis.

See [current projects](#) on [Autism spectrum disorder](#), [Alzheimer's Disease](#), [COVID-19 Coronavirus](#), [Fanconi Anemia](#), [Glioblastoma](#), [the Yeast Kinome](#), [the Ubiquitin-Proteasome System](#) and [Autophagy](#). If you would like to suggest or participate in a new themed project, please contact support@thebiogrid.org


Partners



インスリンは血糖調節に関わるホルモンであり、特定のインスリン受容体と結合する。その相互作用は特化しており、多数のタンパク質と結合するわけではない。

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Result Summary

Homo sapiens

GO


BioGRID COVID-19 Coronavirus Curation Project
Search BioGRID for [SARS-CoV-2 Protein Interactions](#) | [Download SARS-CoV-2 and Coronavirus-Related Interactions](#)

INS

IDDM, IDDM1, IDDM2, ILPR, IRDN, MODY10

Homo sapiens

insulin


 Alzheimer's Disease Project

GO Process (60)

GO Function (6)

GO Component (6)

[CRISPR Database](#) [VEGA](#) [HGNC](#) [Alliance of Genome Resources](#) [OMIM](#)
[Entrez Gene](#) [RefSeq](#) [UniprotKB](#) [Ensembl](#) [HPRD](#)

 Download Curated Data for this Protein

「Download Curated Data for this protein」を押す

Interactor Statistics

Proteins/Genes

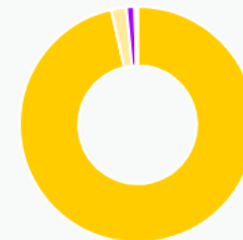
520





Chemicals

2

Publications

22



-  Interactors w/ Physical (HTP) Evidence (509)
-  Interactors w/ Physical (LTP) Evidence (11)
-  Interactors w/ More than One Evidence Type (6)
-  Chemical Interactors (2)

Switch View: **Interactors 528** Interactions 538 Chemical Interactions 4 Network

Showing 1 to 300 of 528 unique interactors

Filter Interactions...




ADV 

Interactor	Organism / Chemical Type	Aliases	Description	Evidence
M-Cresol	Small Molecule	-	-	3 View
HSPA5	H. sapiens	BIP, MIF2, GRP78, HEL-S-89n	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	2 1 View

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BioGRID Downloads

Homo sapiens

GO

BioGRID COVID-19 Coronavirus Curation Project

Search BioGRID for [SARS-CoV-2 Protein Interactions](#) | [Download SARS-CoV-2 and Coronavirus-Related Interactions](#)

Download Data for INS

You've chosen to download a BioGRID dataset for INS. To create your dataset, choose your output format below and click **Download**. If you're unsure which interaction download format to choose, you can view our [BioGRID Download Format](#) documentation. The BioGRID download tool is a queue-based system, so downloads may take several minutes to complete.



Select interaction download format:

BioGRID TAB 3.0 Format

DOWNLOAD ✓

「DOWNLOAD」を押す

CITATION: BioGRID data are 100% freely available to both commercial and academic users under the [MIT License](#) and are provided **WITHOUT ANY WARRANTY**. Publications that make use of this data are requested to please cite the contributing authors and : [Stark C, Breitkreutz BJ, Reguly T, Boucher L, Breitkreutz A, Tyers M. Biogrid: A General Repository for Interaction Datasets. Nucleic Acids Res. Jan1; 34:D535-9](#) where applicable.


Did you know that the BioGRID also provides large pre-compiled datasets of all of our interaction data in all of the major formats supported by our site? You can download these, and many others via our [interaction download page](#). Be sure to check back regularly as each set is updated every month...

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INS

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例えば、「BIOGRID-GENE-109842-4.4.241.DOWNLOADS.zip」といった名前の圧縮ファイルがダウンロードされる
これを解凍すると、2つのファイルが得られる
そのうち、「BIOGRID-GENE-109842-4.4.241.tab3.txt」という名前のファイルがINSと相互作用する相手の遺伝子の表になっている

Cytoscape

- Cytoscape

- 生物学的ネットワークの視覚化、解析のためのオープンソースプラットフォーム
- タンパク質間の相互作用、遺伝的相互作用、パスウェイなどを直感的にマッピングし表現するのに用いられる
- ダウンロードして利用する
 - Webでの利用は、遺伝子を入力して、既知のネットワークを検索

ENHANCED BY Goc

Cytoscape

Network Data Integration, Analysis, and Visualization in a Box

[Introduction](#) [Download 3.10.3](#)

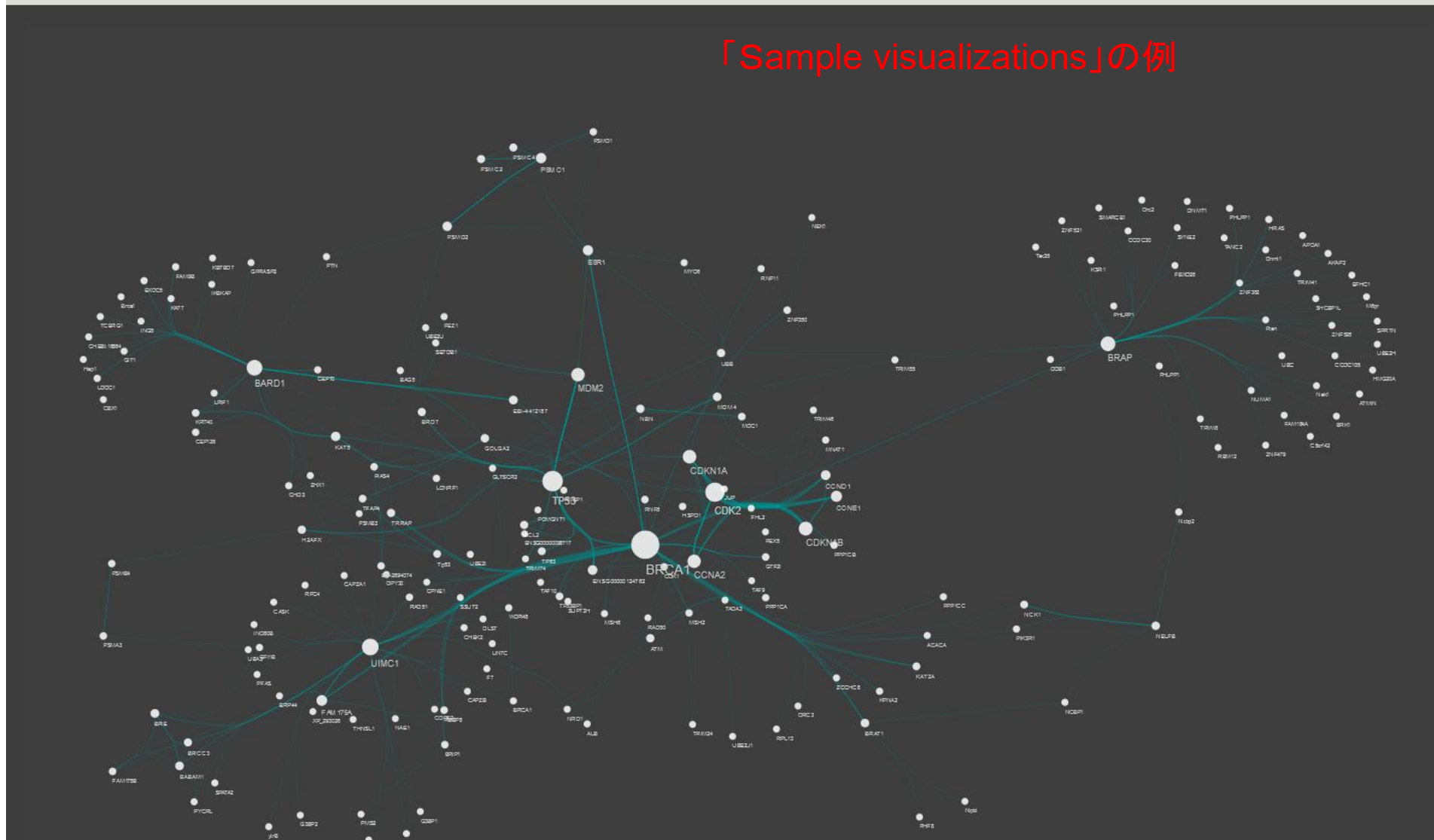
Analyze Your Genes With NDEx iQuery

Type or paste your list of genes here...

Cytoscape

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「Sample visualizations」の例



Cytoscapeの利用

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Cytoscape

Network Data Integration, Analysis, and Visualization in a Box

[Introduction](#) [Download 3.10.3](#)

Analyze Your Genes With NDEx iQuery

INS

[Run Analysis](#)

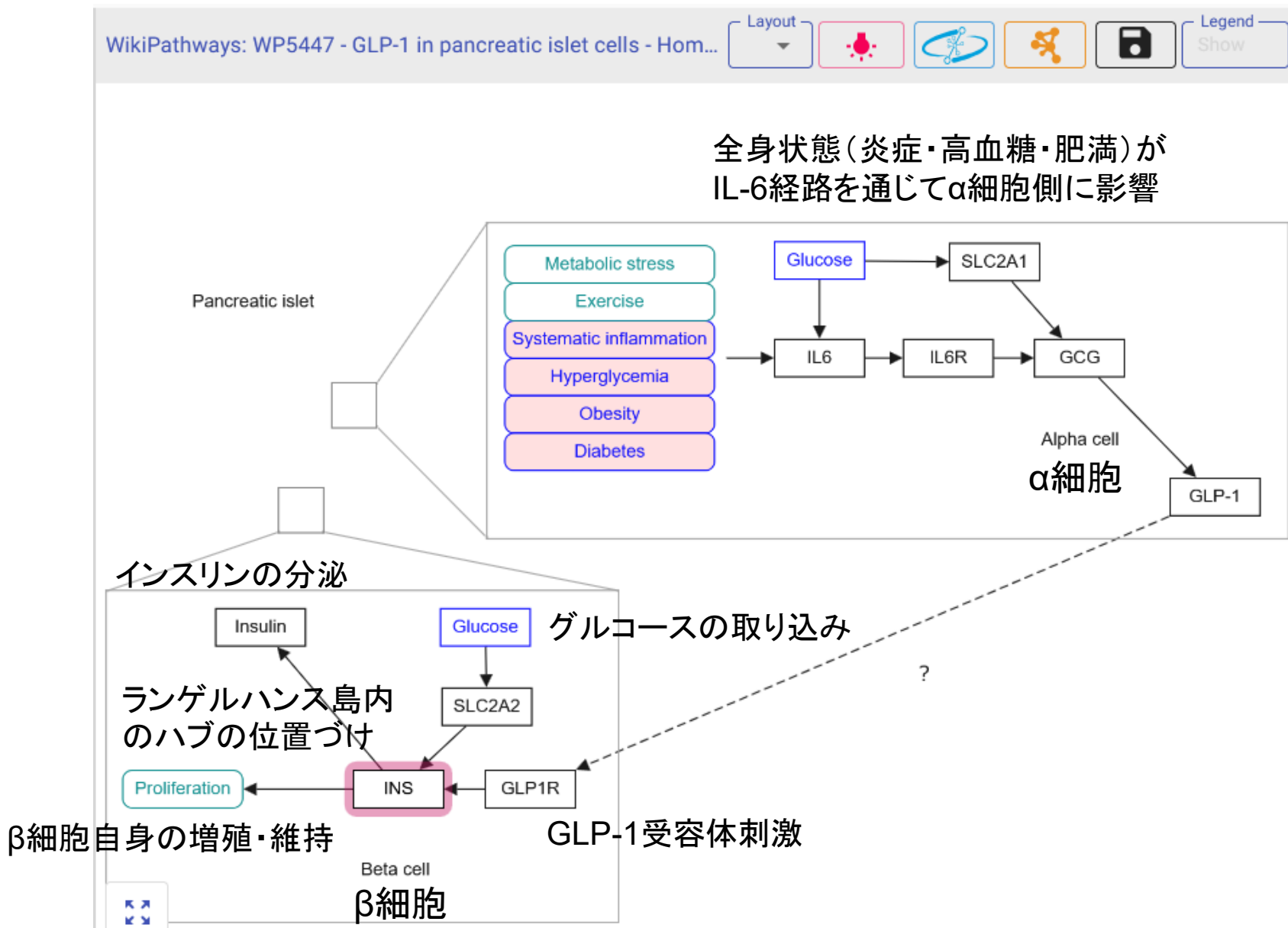
インスリンの遺伝子「INS」を入力して、「Run Analysis」を押す

Cytoscape is an [open source](#) software platform for visualizing complex networks and integrating these with any type of attribute data. A lot of [Apps](#) are available for various kinds of problem domains, including bioinformatics, social network analysis, and semantic web.

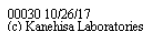
[Release Notes](#)

[Sample Visualizations](#)

Cytoscapeの利用

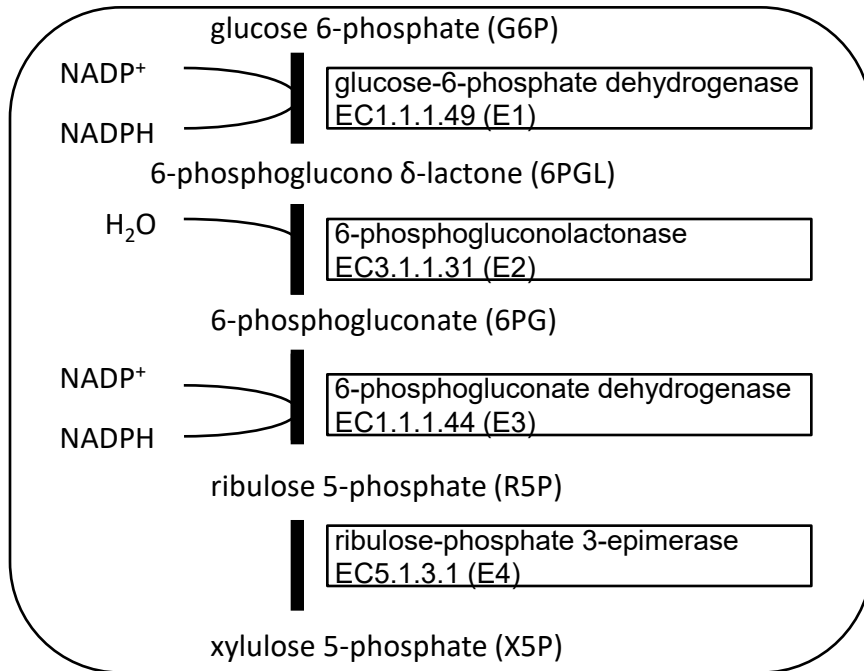


KEGGの表示

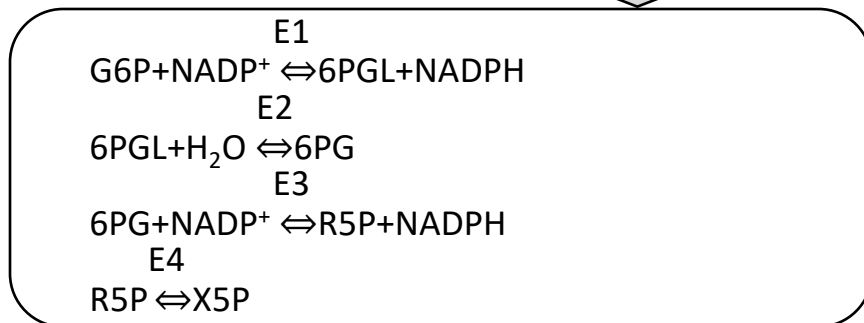


代謝ネットワークの表現の例

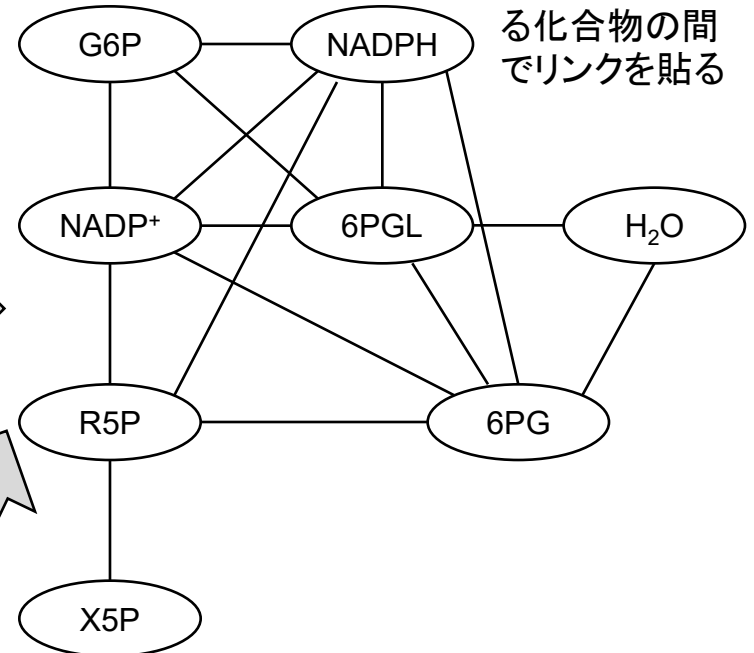
代謝ネットワーク



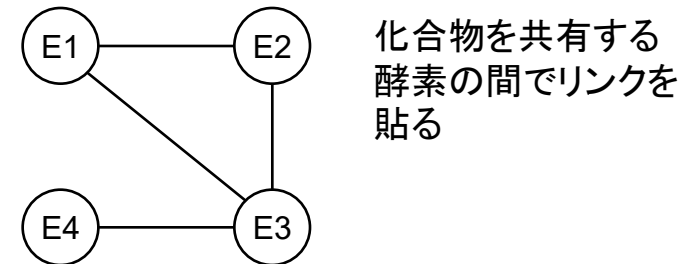
反応式の列



化合物グラフ

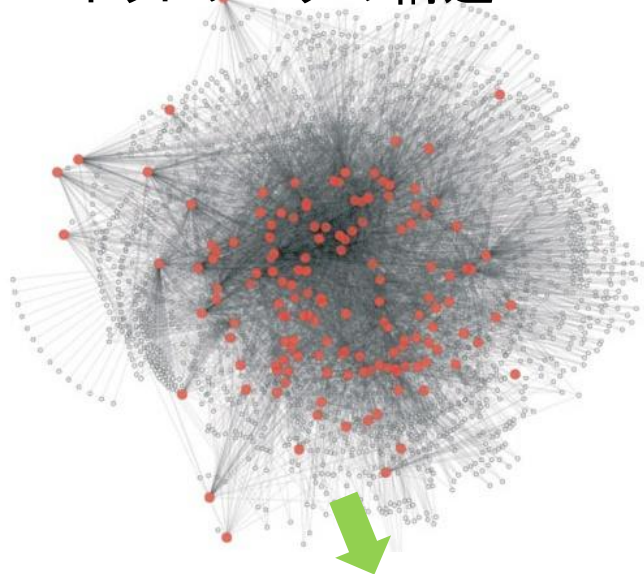


反応グラフ

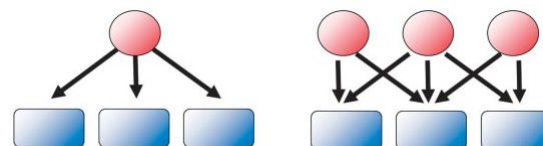
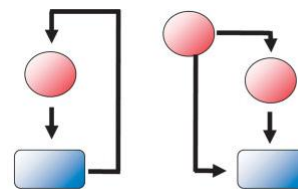


ネットワーク構造の解析の例

ネットワークの構造

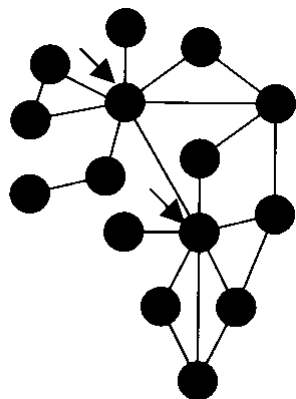


ネットワークモチーフ
(典型的なパターンの
抽出、検索)



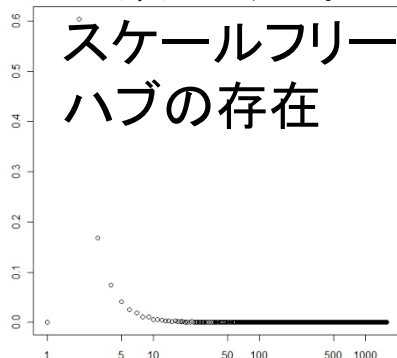
ネットワークの特性解析

スモールワールド性

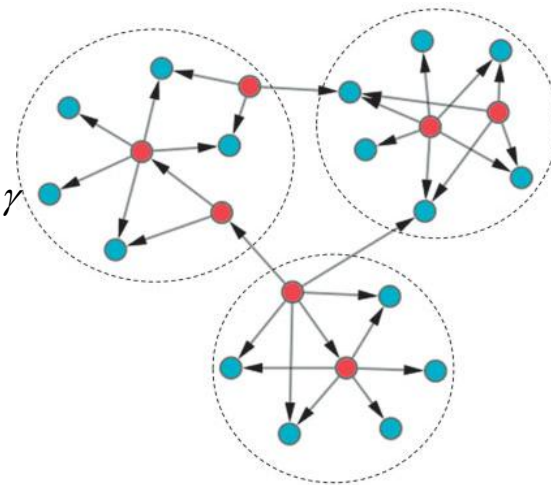


次数 k の分布の解析

スケールフリー性 $P(k) = Ck^{-\gamma}$
ハブの存在



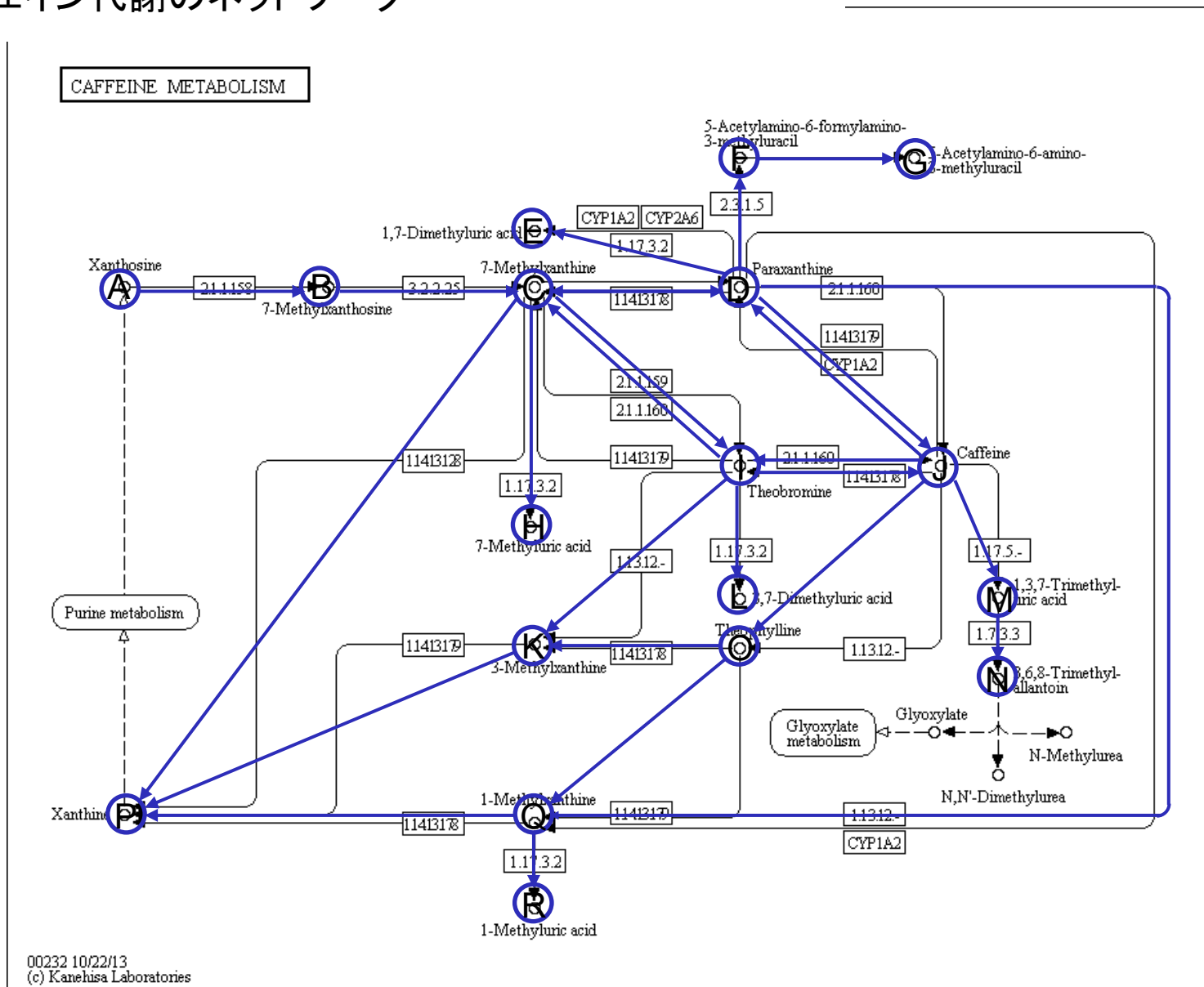
モジュール構造の同定



ハブ: 枝の数がとくに多い頂点

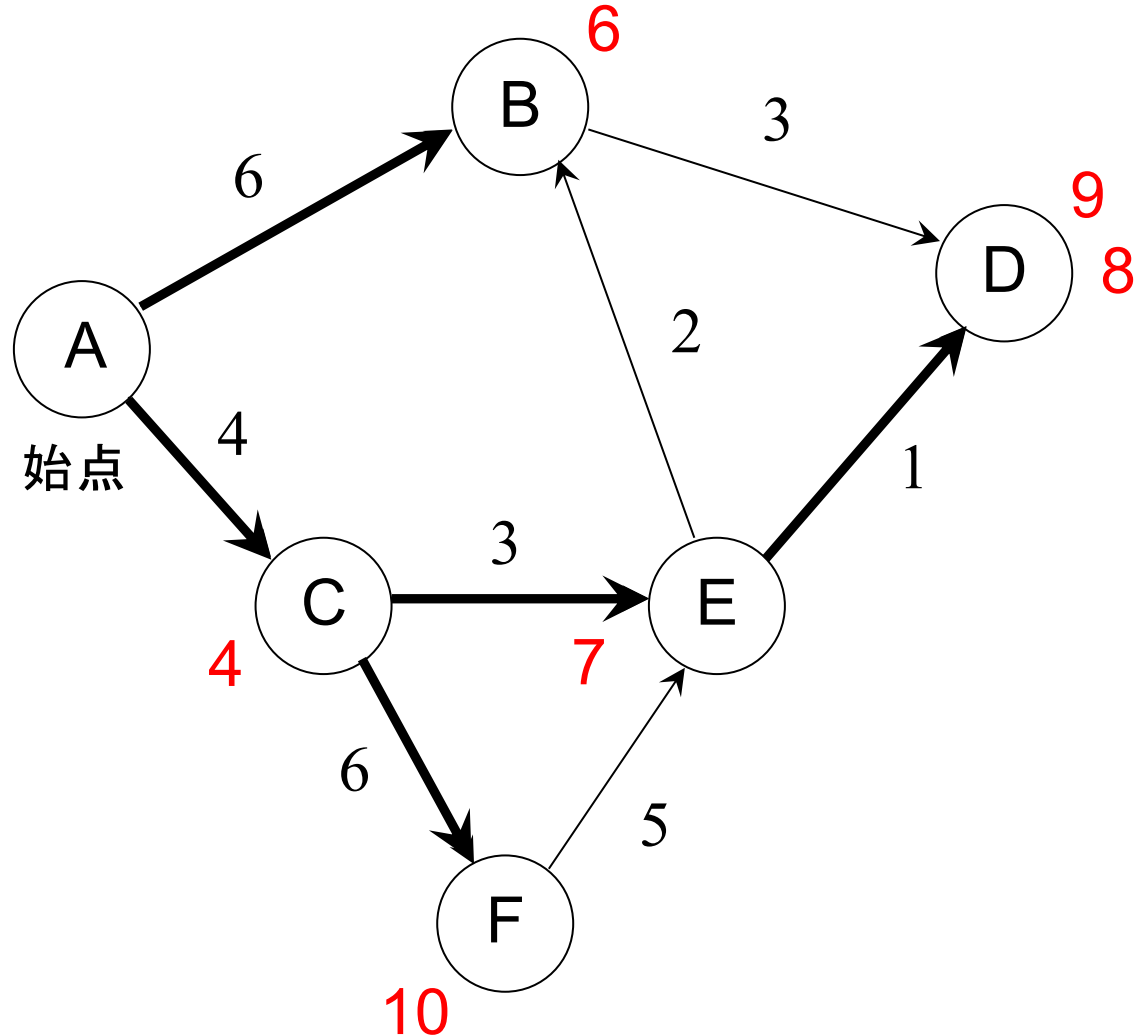
グラフの例

カフェイン代謝のネットワーク



最短経路を求めるアルゴリズム

- 各辺に重み（頂点間の距離）が定義される
- 経路上の重みの和が最小になるのが最短経路
- 始点から各頂点への最短経路を、始点に近いところから1つずつ確定していく



次数分布

$P(k)$: 次数分布 (次数 k の頂点がネットワーク内に存在する頻度)

$$P(k) = \frac{\text{次数が} k \text{ のノードの数}}{\text{全ノード数}}$$

$$P(1) = 7/18$$

$$P(2) = 3/18$$

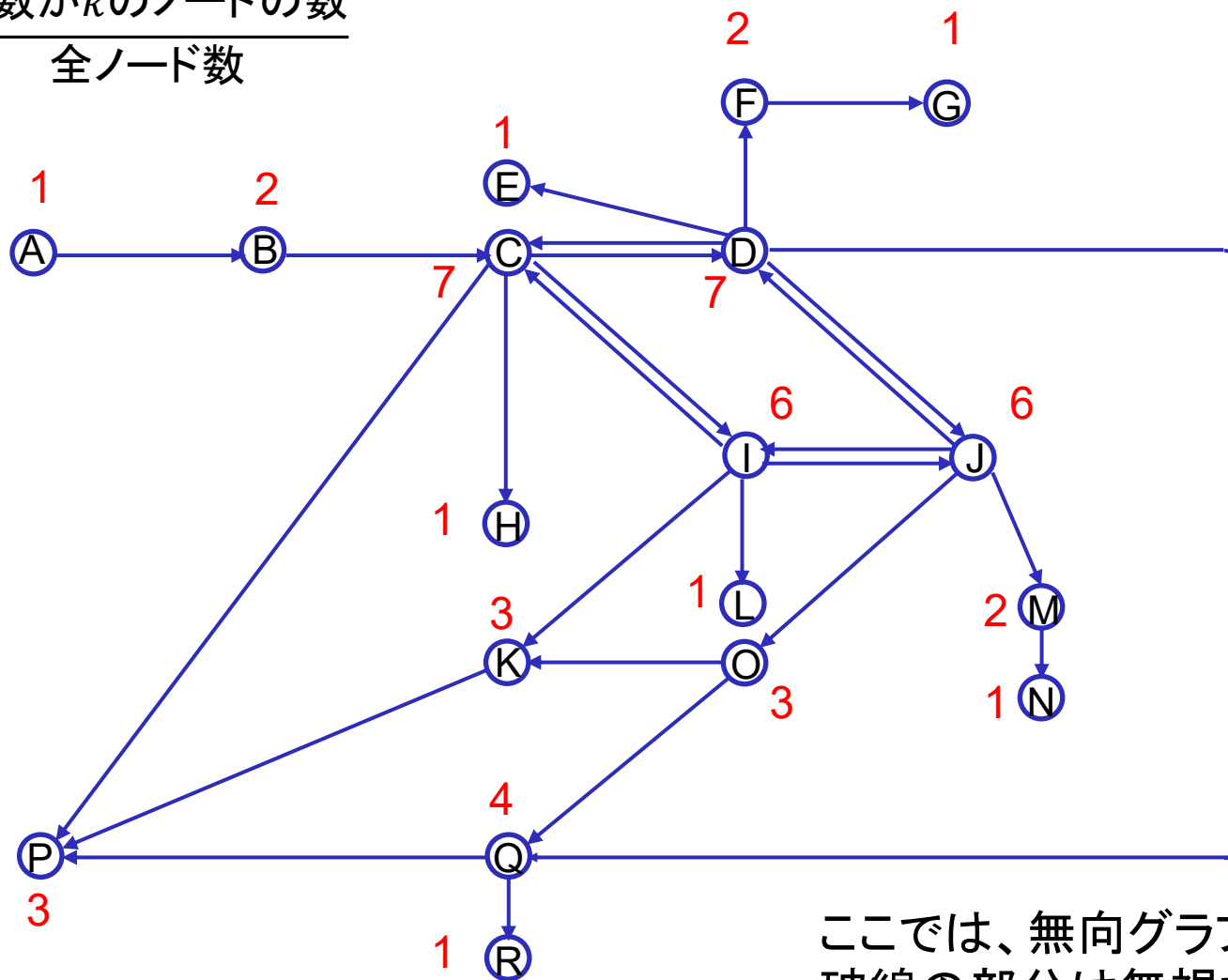
$$P(3) = 3/18$$

$$P(4) = 1/18$$

$$P(5) = 0/18$$

$$P(6) = 2/18$$

$$P(7) = 2/18$$

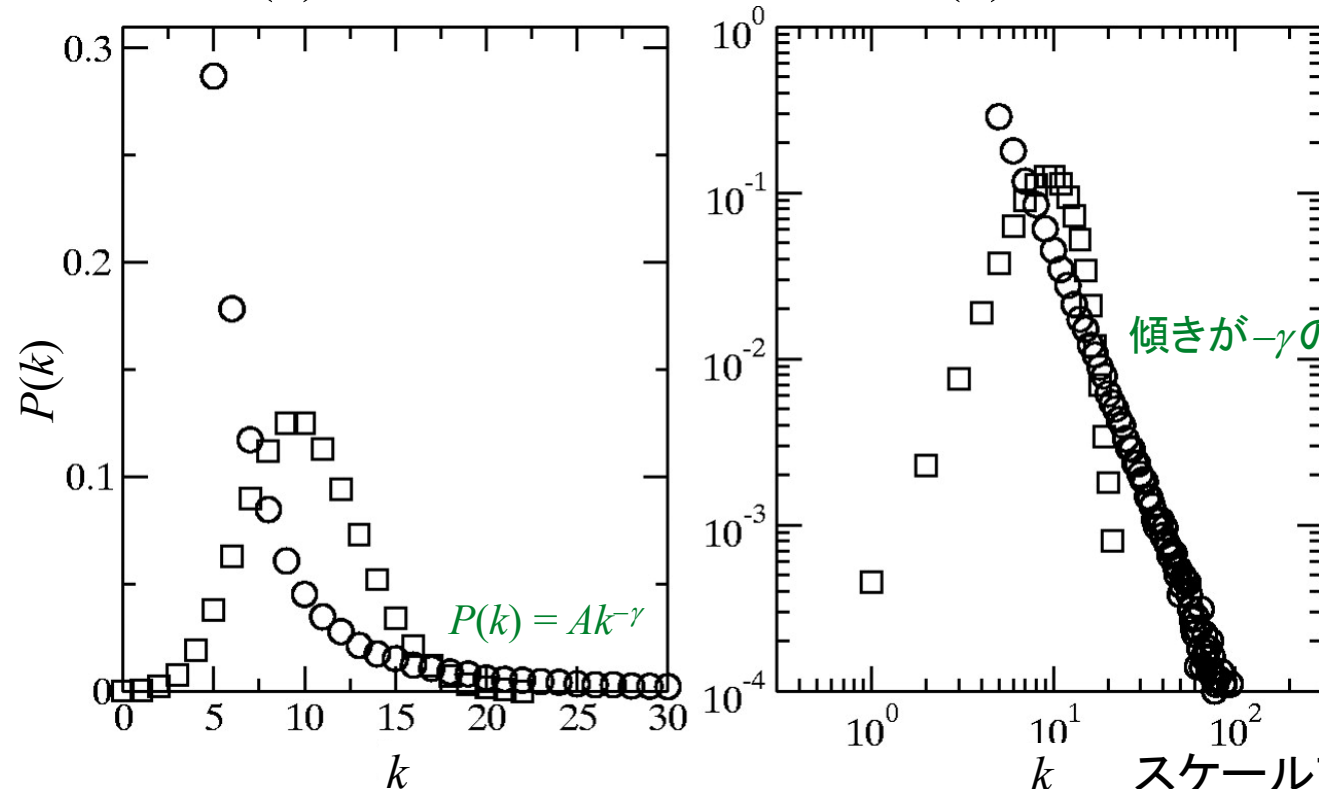


ここでは、無向グラフとして扱い、
破線の部分は無視するものとする

ネットワークの特性解析

- スケールフリーネットワーク

- $P(k)$ がべき乗則に従う: $P(k) \propto k^{-\gamma}$



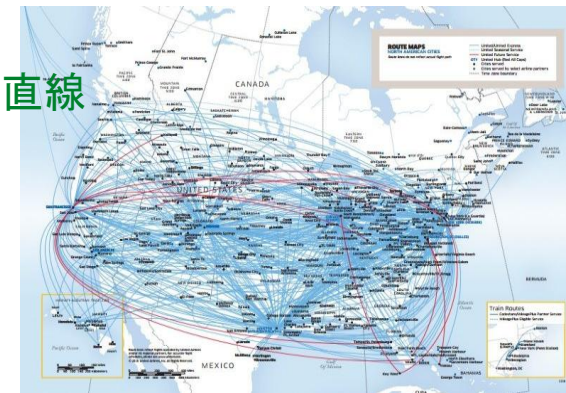
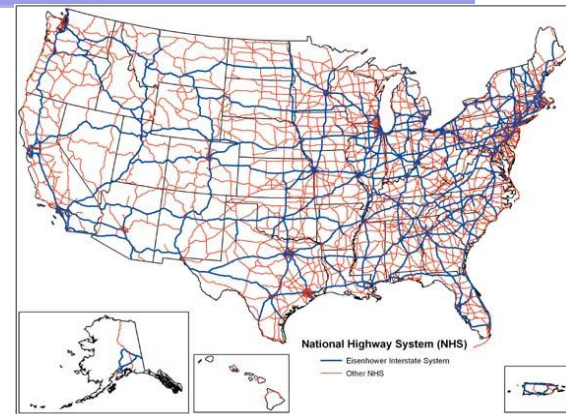
□ ランダムグラフ (Erdős-Rényi モデル)

○ スケールフリーネットワーク

n 個の頂点だけからなるグラフで、各頂点の対に対して、ランダムに確率 p で辺を引いてできるグラフ

スケールフリーネットワークの方が、ランダムグラフに比べ、次数の増加に対してなだらかに減少 → 次数の大きな頂点 (ハブ) がある程度存在

次数が小さい場合、次数分布はポアソン分布に従う $P(k) = \frac{\mu^k e^{-k}}{k!}$



ネットワークの特性解析

- 頂点間の経路
 - 2つの頂点をつなぐ辺（枝）の列
- 経路の長さ
 - 経路中の辺の個数
 - 1つの辺を通ることを1ステップとするとき、何ステップで到達できるかを示す
- 頂点間距離
 - 最短の経路の長さ（経路中の辺の数の最小値）
 - 有向グラフ、無向グラフに対して定義できる
 - 有向グラフの場合は、辺の方向でつながりが決まる
- 頂点数 n のネットワークの平均頂点間距離 L
 - $L = 2$ 点間距離の $n(n-1)/2$ ペア全体の平均
 - ネットワーク直径（network diameter）と呼ぶこともある

ネットワークの特性解析

• クラスター係数

- ある頂点に接続されている頂点のすべての組み合わせのうち、実際に辺（枝）で接続されている割合
- 頂点 v_i の次数を k_i とすると、その頂点 v_i に接続されている頂点のすべての組み合わせの数は

$$k_i(k_i - 1)/2$$

- 実際に辺で接続されている個数を n_i とすると、 n_i は v_i を含む三角形の数となり、クラスター係数 C_i は、

$$C_i = \frac{n_i}{k_i(k_i - 1)/2}$$

- 頂点がかたまっている度合いを表す
 - 頂点の周りのモジュール性

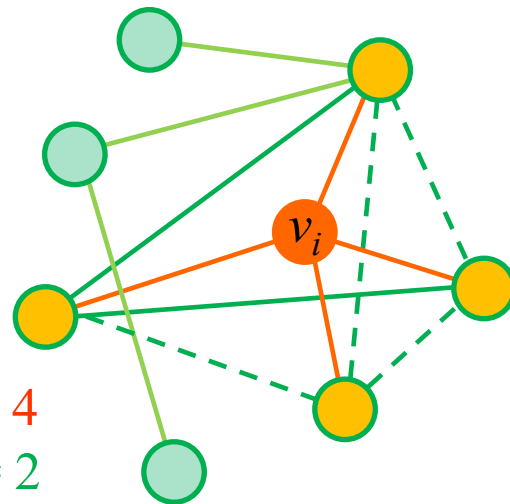
• ネットワーク全体のクラスター係数

$$C = \frac{1}{n} \sum_{i=1}^n C_i$$

- n はネットワークの頂点の数
- すべてのノードのクラスター係数の平均

$$k_i = 4$$

$$n_i = 2$$

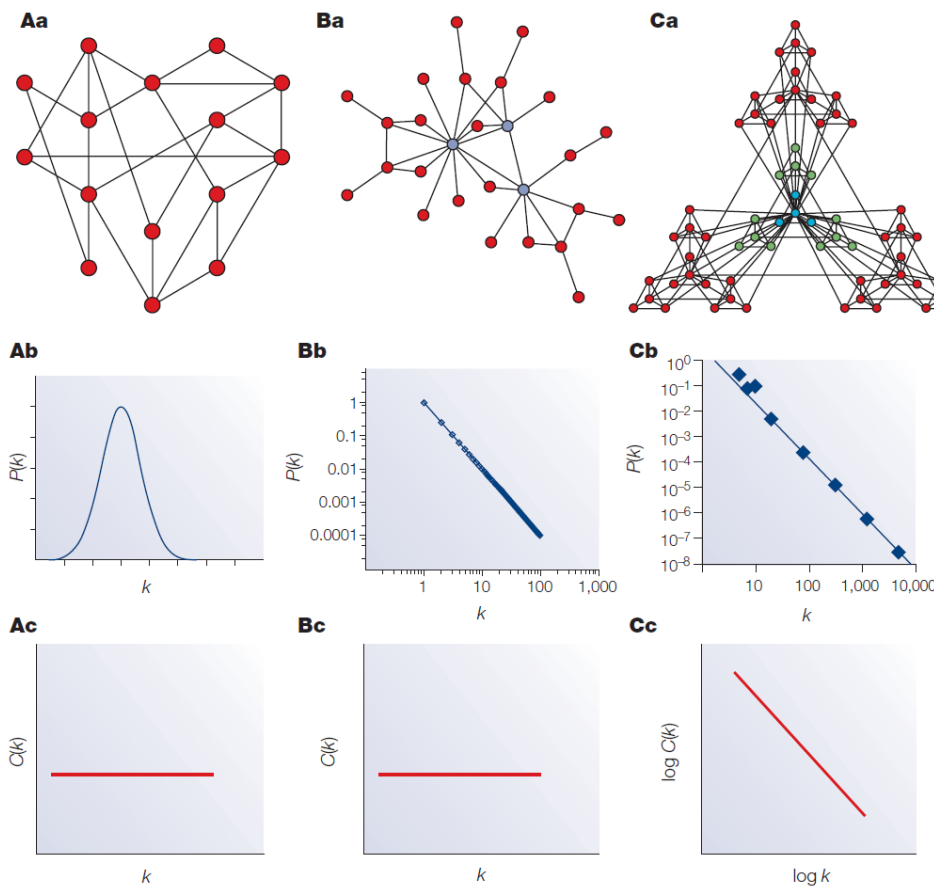


スモールワールド性

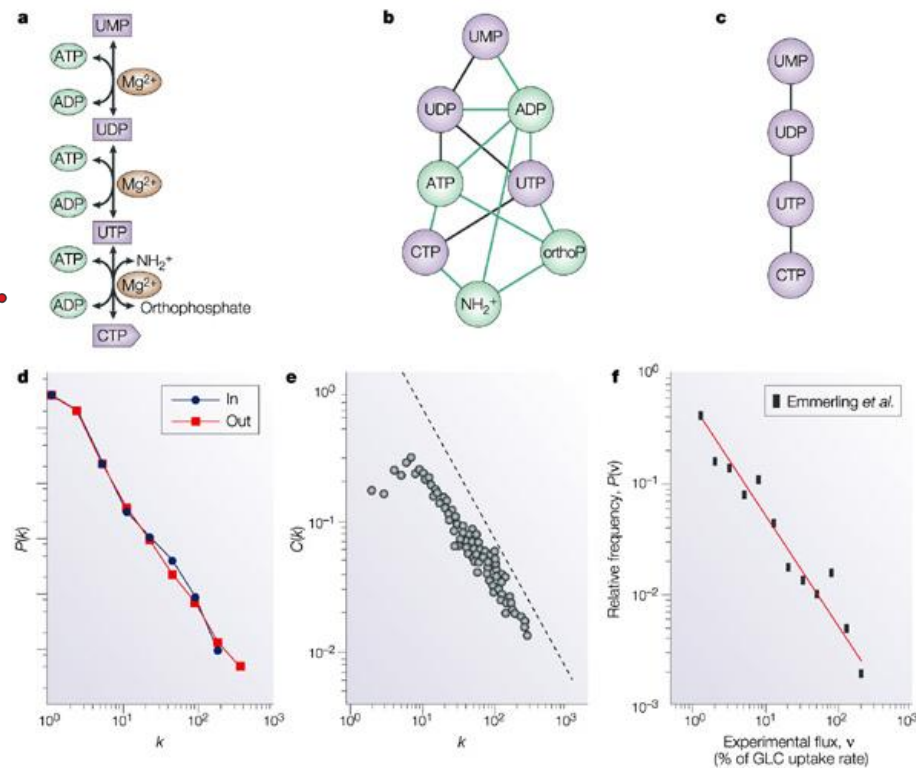
- スモールワールドネットワーク: 平均頂点間距離 L が小さく ($O(\log n)$ 以下)、かつクラスター係数 C の平均値が大きいグラフ
 - 次数の分布は比較的均等
- 単純な格子からなる (クラスターのある) 構造に、ランダムな辺を少数導入することで平均頂点間距離が小さくなる
 - D. J. Watts and S. H. Strogatz: "Collective dynamics of 'small-world' networks", Nature, 393, 440-442 (1998).

代謝ネットワークの例

参考



現実の代謝ネットワークでは生化学的にまとまった機能的モジュールが存在
実際の代謝ネットワークの形状はCの階層的ネットワークに近い



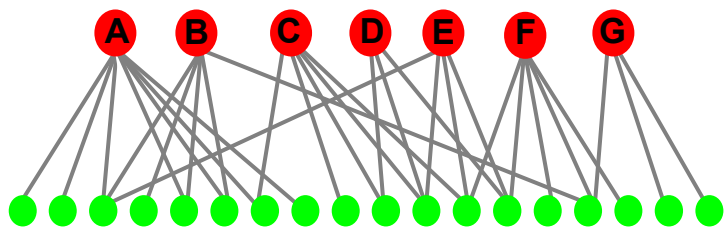
Mg^{2+} に関する 酵素によって触媒 される反応 通常グラフ表現
すべての代謝物を 頂点にしたグラフ
主要な生成物 (ATP などの共通因子を無視) を 頂点にしたグラフ

E. Ravasz, et al. Network biology: understanding the cell's functional organization., Nature Review Genetics, 5, 101-13. (2004).

酵母の転写制御ネットワーク

参考

Transcriptional regulatory network

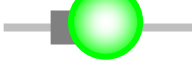


酵母の転写制御因子とそれらのターゲットの遺伝子の関係からなるネットワーク

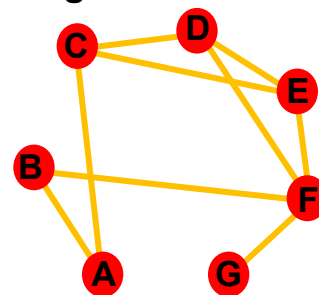
Transcription factor



Target gene



Co-regulation network



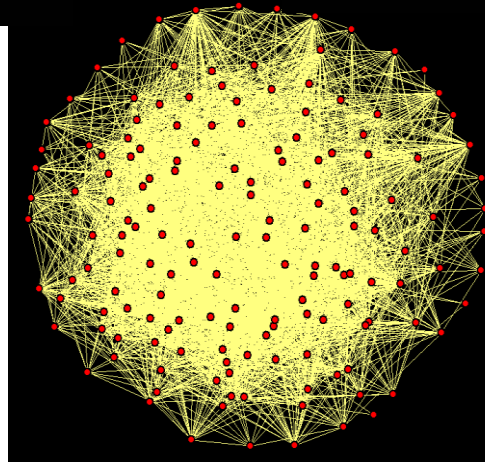
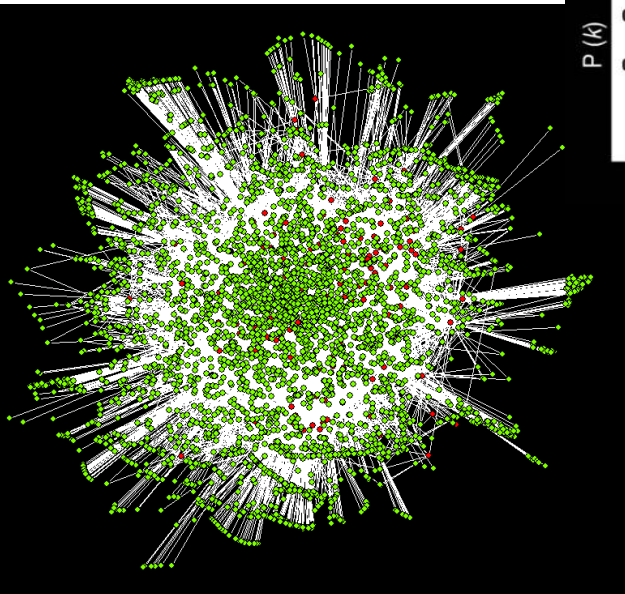
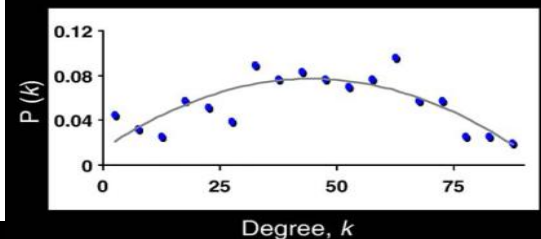
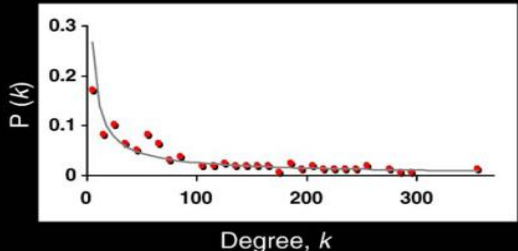
Transcription factor



Transcription factor



共発現の関係を示すネットワーク



- Transcription factors (157)
- Target genes (4410)
- Regulatory interactions (12,873)

On average 82 targets

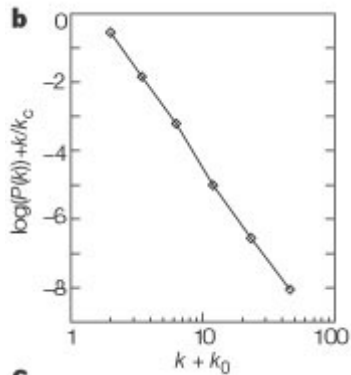
- Transcription factors (157)
- Co-regulatory association (3,459)

On average 44 co-regulatory partners

タンパク質間相互作用ネットワークの例

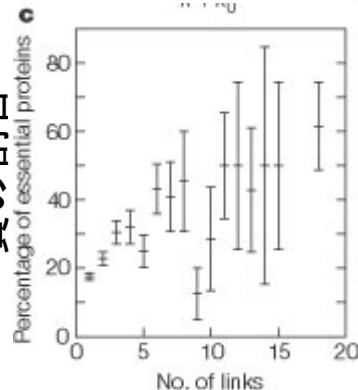
- Y2Hによる出芽酵母のタンパク質間相互作用ネットワーク
(全タンパク質の約78%を含む最大のクラスター)
- 多数の頂点に結合している頂点（ハブ）が少数存在
- 対応するタンパク質を除いたときの表現型として表れる効果

– 赤色: 致死、橙色: 低成長、
緑色: 非致死、黄色: 不明

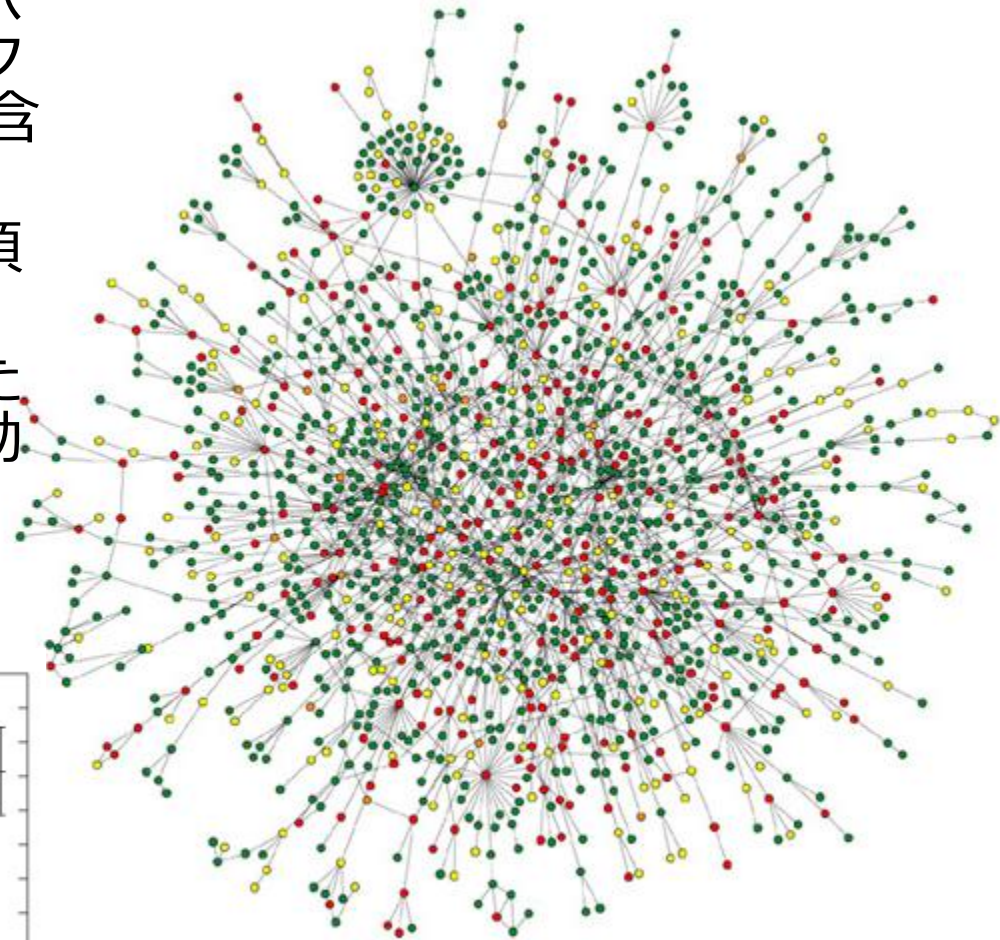


次数分布

削除すると致死のタンパク質の割合



各タンパク質のリンク数



Nature Reviews | Genetics

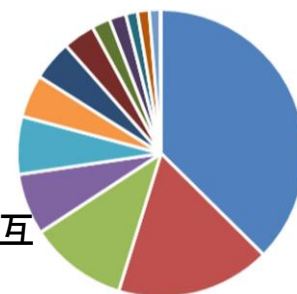
H. Jeong, et al. Lethality and centrality in protein networks, Nature, 411, 41-2 (2001).

タンパク質間相互作用ネットワークの例

参考

インフルエンザAウイルス(IAV)と宿主のヒトのタンパク質間相互作用

829個のノード(タンパク質)のうち14個がウイルスタンパク質、815個がヒトタンパク質
平均次数 2.4 → 相互作用は比較的疎
ネットワーク直径 6
クラスタ係数 0.001



IAVタンパク質の相互作用数の内訳



Basal cell carcinoma

Synaptic vesicle cycle

Collecting duct acid secretion

Cocaine addiction

Ferroptosis

Cortisol synthesis and secretion

Cytosolic DNA-sensing pathway

TNF signaling pathway

Notch signaling pathway

RNA polymerase

IAVと相互作用する宿主側のタンパク質(遺伝子)のKEGGエンリッチメント解析

A systems biology-driven approach to construct a comprehensive protein interaction network of influenza A virus with its host, BMC Infectious Diseases 20: 480 (2020).

NS : Nonstructural protein

NP : Nucleoprotein

PB : Polymerase basic protein

M: Matrix protein

PA: Polymerase acidic protein

NA: Neuraminidase

HA : Hemagglutinin

Cytoscapeによる

ネットワーク解析