

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）

The screenshot shows the PubMed homepage with a search bar containing 'SARS-CoV-2'. The search button is highlighted with a red oval and a cursor icon. The NIH logo and a user profile are visible at the top.

NIH National Library of Medicine
National Center for Biotechnology Information

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PubMed®

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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MeSH Database
Journals

PubMedの利用（2）



PubMed

SARS-CoV-2

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

デフォルトは「Best match」の順

Mechanisms of SARS-CoV-2 entry into cells.

1 Jackson CB, Furman M, Chen B, Chou H
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.
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 ...

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

2 V'kovski P, Kratzel A, Steiner S, Stalder H, Thiel V
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.
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
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.
Severe acute respiratory syndrome Coronavirus 2 (SARS-CoV-2) has spread rapidly throughout the

最初の論文を選択

PubMedの利用（3）



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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 Farzan ¹, Bing Chen ^{3 4}, Hyeryun Choe ⁵

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.

この下を見てみよう

FULL TEXT LINKS

nature portfolio

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Full text

NEXT RESULT
2 of 245,446 >

ACTIONS

Cite

Collections

SHARE



PAGE NAVIGATION

< Title & authors

Abstract

Conflict of interest

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

統制語として、論文の主題や内容を体系的に表現

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

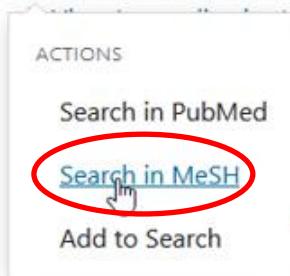
MeSH

- 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）



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MeSH MeSH Viral Proteins Search Help

Summary Send to: PubMed Search Builder

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

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... Turn Off Clear

Recent Activity

Summary Send to:

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

PubMed Search Builder

Add to search builder AND ▾
Search PubMed

YouTube Tutorial

Related information

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Clinical Queries
NLM MeSH Browser
PubChem Compound

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[Viral Proteins](#) Mesh
[Animals](#) Mesh
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["olfactory receptor" AND "Bos taurus"\[Organism\] AND "pseudogene" Gene](#)
["olfactory receptor" AND "Bos taurus"\[Organism\] AND "pseudo" 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 shows the Web of Science search interface. At the top, there are links for Clarivate, English, Products, Sign In, and Register. Below the header, the search term 'SARS-CoV-2' is entered in the Smart Search field, resulting in 419,005 results from 12 selected collections. The search history includes terms like 'sars-cov-2', 'macrodomain', 'info ddc 22 de 614 4', 'virussequencen', and 'info ddc 22 eng 614 42'. There are also filters for 'Add Keywords', 'Preprint Citation Index', and 'Research Commons'. The results summary indicates 419,005 Documents and 100 Researchers. On the left, a 'Refine results' sidebar includes a search bar for 'Search within topic...', 'Quick Filters' for 'Highly Cited Papers', 'Hot Papers', 'Review Article', and 'Open Access', and an 'Export Refine' button. The main results area shows a single entry: 'Characteristics of SARS-CoV-2 and COVID-19' by Hu, B; Guo, H; Shi, ZL, published in Mar 2021 | NATURE REVIEWS MICROBIOLOGY | 19(3), pp.141-154. This entry has 4,356 Citations and 165 References. Navigation controls include 'Preferred Search Results', 'Sort by Relevance', and page navigation for '1 of 2,000'.

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 🔬 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 99 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 99 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 Hasoksuz, 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 99 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 99 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](#)

[sars-cov-2 severe acute respiratory](#)

[covid-19 sars-cov-2](#)

[sars-cov-2 vaccine](#)

[respiratory syndrome coronavirus](#)

[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/>

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

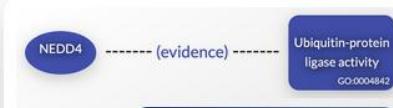
GO Enrichment Analysis 
Powered by PANTHER

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）



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)

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lipolysis

Any Ontology Gene Product



「lipolysis」(脂質分解)を入力し、「Search」をクリック

GO Enrichment Analysis ?

Powered by PANTHER

Your gene IDs here...

biological process

Homo sapiens

Examples

Launch >

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



The network of biological classes
describing the current best representation



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



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



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

GO Termの検索（2）



AmiGO 2

Home

Search ▾

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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

「Ontology」を選択**Genes and gene products**

Genes and gene products associated with GO terms.

23

Annotations

Associations between GO terms and genes or gene products.

176

[Cite this data](#) • [Terms of use](#) • [GO helpdesk](#)

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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

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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

<input type="button" value="+"/> <input type="button" value="-"/> (79)	biological_process
<input type="button" value="+"/> <input type="button" value="-"/> (10)	cellular_component
<input type="button" value="+"/> <input type="button" value="-"/> (7)	molecular_function

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

Results count 10

<First

<Prev

Next>

Last»

Custom DL (up to 100000)

Bookmark

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	GO:0006724 GO:0044240 more...

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	Feedback
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. <i>Source:</i> 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](#).

「Graph Views」をクリック

Annotations **Graph Views** Inferred Tree View Neighborhood Mappings

Total annotations: 6; showing: 1-6 Results count [First](#) [Prev](#) [Next](#) [Last](#) [Download](#)

Filter results

Total annotations: 6

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

User filters

GO Termの検索 (5)



AmiGO 2

Home

Search ▾

Browse

Tools & Resources

Help

Feedback

About

Quick search

Search



cytosolic lipolysis

Term Information

Accession GO:0061725**Feedback** **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](#)

「QuickGO」をクリック

[Graph of GO:0061725 from QuickGO](#)[Additional external viewing options](#)[OLSVs \(interactive\)](#)[Additional internal viewing options](#)

GO Termの検索 (6)

- [Overview](#)
- [Synonyms](#)
- [Ancestor Chart](#)
- [Child Terms](#)
- [Annotation Guidance](#)
- [GO Discussions](#)
- [Taxon Constraints](#)
- [Blacklist](#)
- [Cross-References](#)
- [Cross-Ontology Relations](#)
- [Replaces](#)
- [Replaced By](#)
- [Co-occurring Terms](#)
- [GO Slims](#)
- [Change Log](#)

GO:0061725



JSON

cytosolic lipolysis

Biological Process

Definition (GO:0061725 GONUTS page)

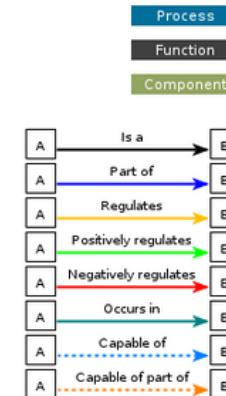
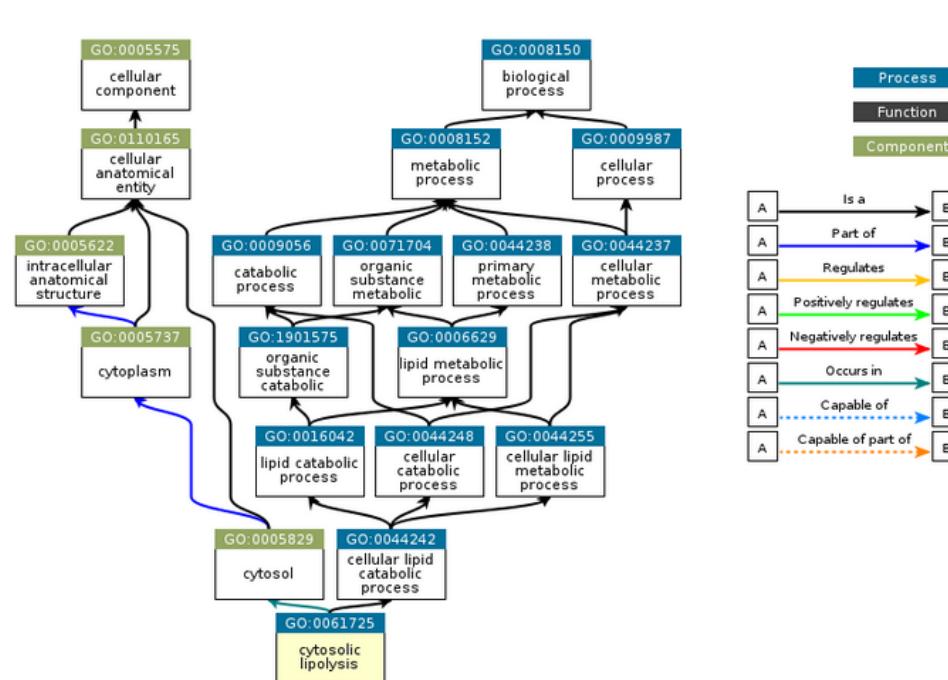
The chemical reactions and pathways resulting in the breakdown of lipid droplets and hydrolysis of stored triglycerides occurring through the orchestrated activation of cytosolic lipases.

7 annotations

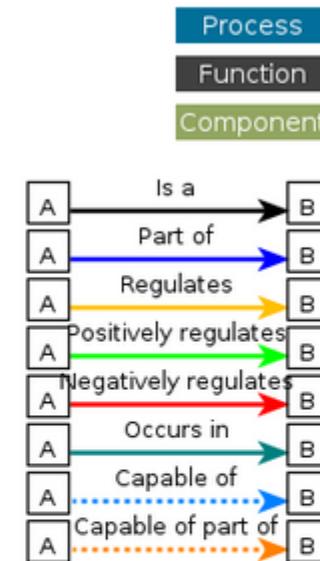
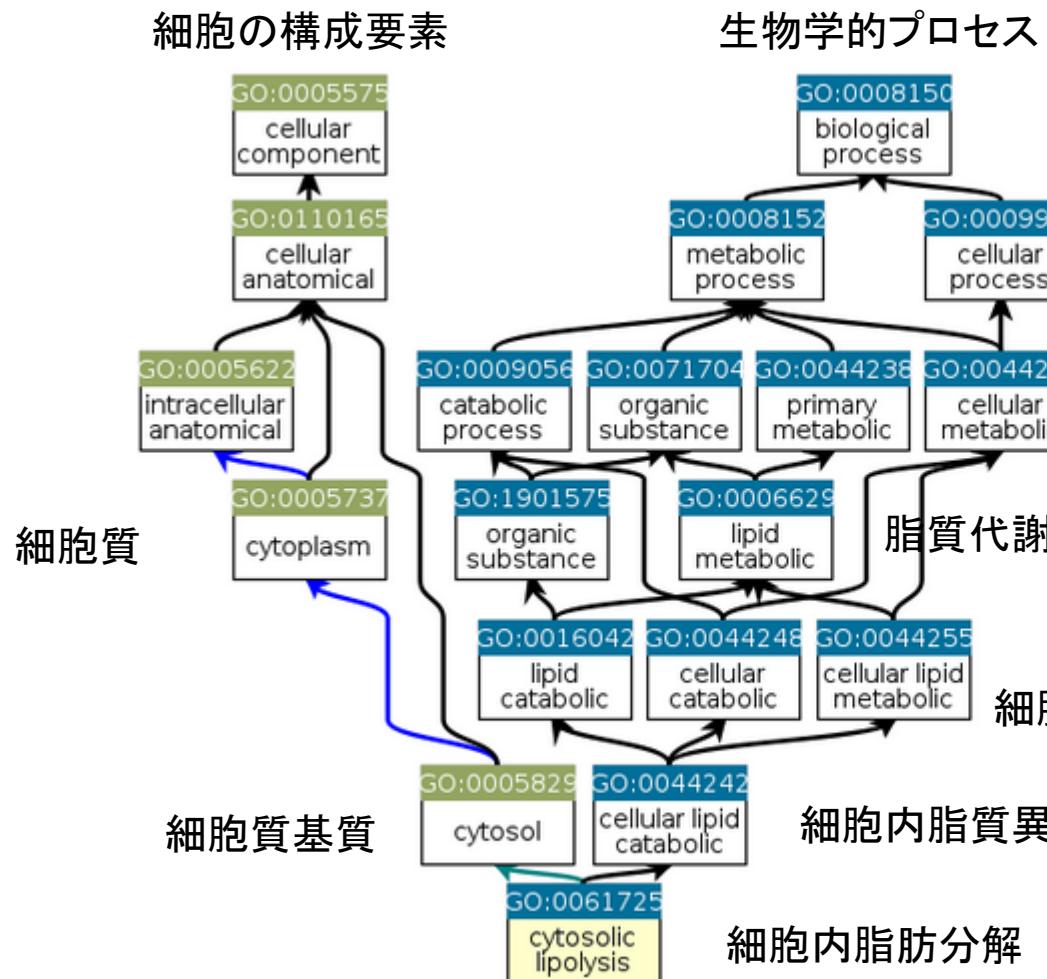
Ancestor Chart

Ancestor chart for GO:0061725

Chart options ▾



GO Termの検索 (7)



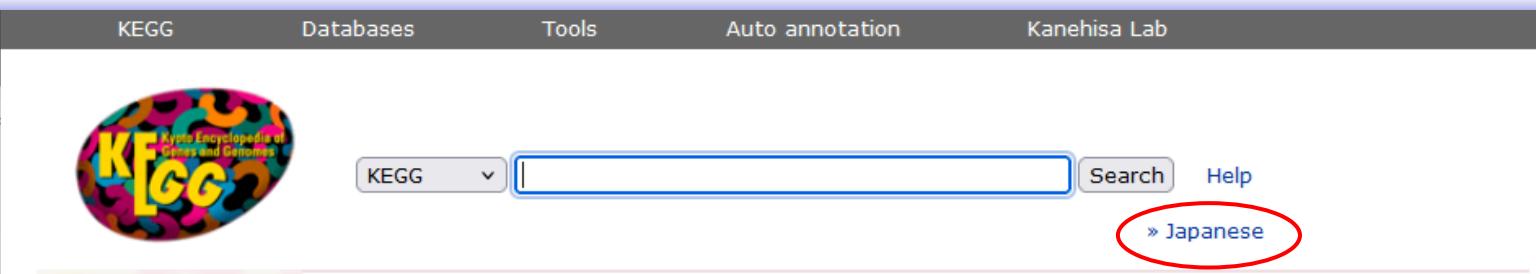
- is_a: 汎化特殊化関係 (A is a B: A is a subtype of B)
- Part of: 部分全体関係 (B is a part of A)

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 (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）



The screenshot shows the KEGG homepage with a navigation bar at the top. The "Japanese" link in the top right corner is circled in red.

KEGG Home
Release notes
Current statistics

KEGG Database
KEGG overview
KEGG mapping
Color codes

KEGG Objects
KEGG Weblinks
Entry format

KEGG Software
KEGG API
KGML

KEGG FTP
Subscription
Background info

GenomeNet

DBGET/LinkDB

Feedback
Copyright request

Kanehisa Labs

KEGG Databases

Tools

Auto annotation

Kanehisa Lab

KEGG

Search

Help

» Japanese

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
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]

Pathway
Brite
Brite table
Module
Network
KO (Function)
Organism
Virus
Compound
Disease (ICD)
Drug (ATC)
Drug (Target)
Antimicrobials

KEGGの利用（2）

KEGG Databases Tools Auto annotation Kanehisa Lab

日本語のページ

KEGG メニュー 検索 ヘルプ

» English

KEGG Home
Release notes
Current statistics

KEGG Database
KEGG の概要
KEGG mapping
Color codes

KEGG Objects
KEGG Weblinks
Entry format

KEGG Software
KEGG API
KGML

KEGG FTP
Subscription
Background info

GenomeNet

DBGET/LinkDB

Feedback
Copyright request

Kanehisa Labs

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ク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	パスウェイ
KEGG BRITE	BRITE 機能階層・テーブル	Brite階層
KEGG MODULE	KEGG モジュール	Briteテーブル
KEGG ORTHOLOGY	KO 機能オーソログ	Module
KEGG GENES	遺伝子・タンパク質 [KEGG Virus]	Network
KEGG GENOME	ゲノム [Taxonomy Synteny]	KO (機能)
KEGG COMPOUND	化合物	生物種
KEGG GLYCAN	糖鎖	Virus
KEGG REACTION	化学反応 [RModule]	化合物
KEGG ENZYME	酵素	疾患 (ICD-11)
KEGG NETWORK	疾患関連のネットワーク多様性	医薬品 (ATC)
KEGG DISEASE	疾患 (日本語)	医薬品 (薬効)
KEGG DRUG	医薬品 (日本語) [日米欧の新薬]	医薬品 (標的)

ネットワーク解析 26

KEGGの利用（3）

KEGG Databases Tools Auto annotation Kanehisa Lab

KEGG Kyoto Encyclopedia of Genes and Genomes Search Help » Japanese

KEGG Home Release notes Current statistics

KEGG Database KEGG overview KEGG mapping Color codes

KEGG Objects KEGG Weblinks Entry format

KEGG Software KEGG API KGML

KEGG FTP Subscription Background info

GenomeNet

DBGET/LinkDB

Feedback Copyright request

Kanehisa Labs

KEGG PATHWAY

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
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 label search

Pathway
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Brite table
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KO (Function)
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Drug (ATC)
Drug (Target)
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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

KEGGの利用（4）

KEGG Databases Tools Auto annotation 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

「Metabolism」→
Pathway Maps 「Global/overview」を選択

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

1. Metabolism
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 geneIDs
vg	viruses pathway generated by converting KOs to geneIDs <i>New!</i>
vx	viruses extended pathway generated by converting KOs to geneIDs

「Metabolic pathways」を選択

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 *New!*

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 *Title and cat*
- 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

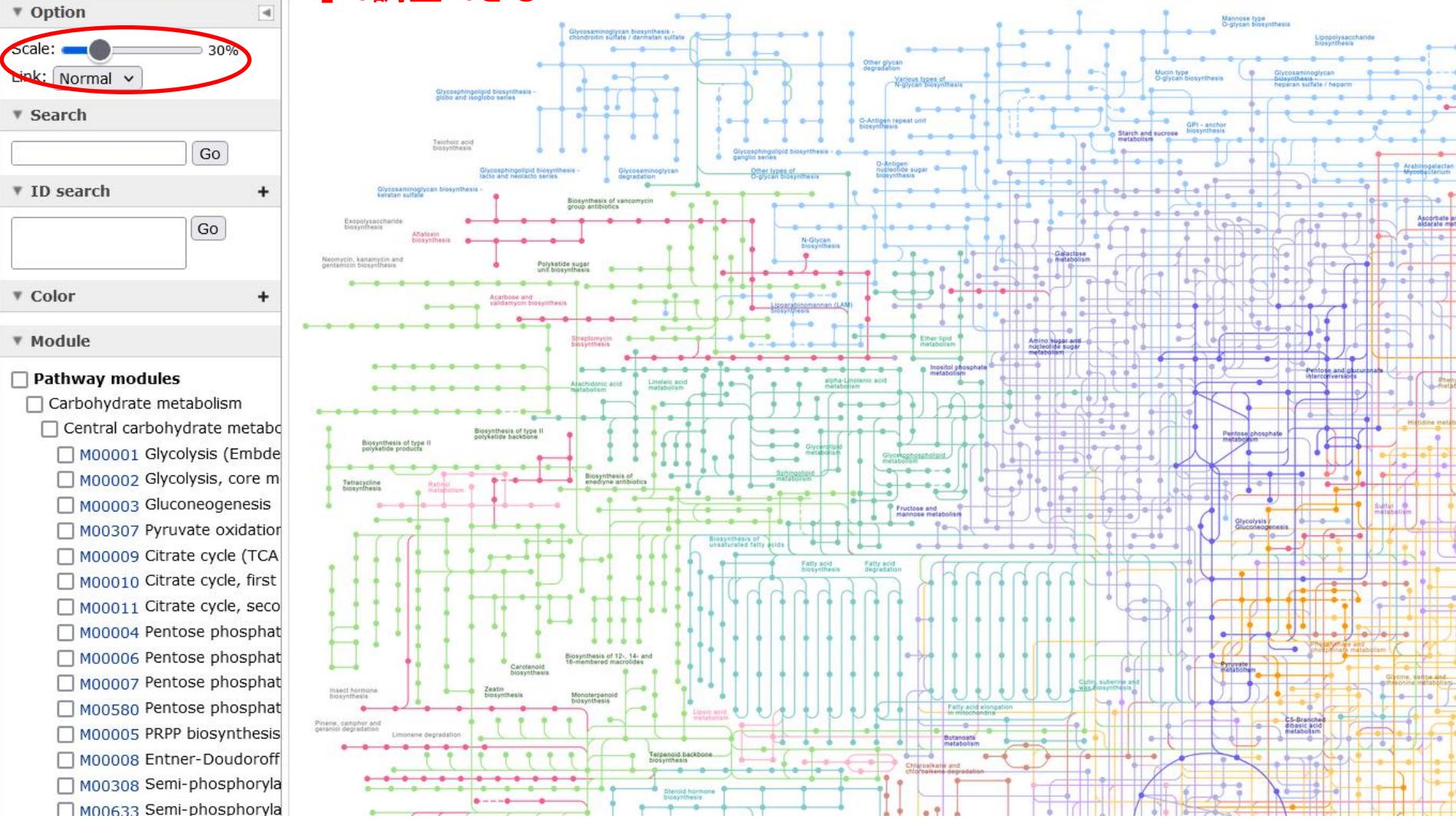
KEGGの利用 (5)

KEGG Metabolic pathways - Reference pathway

[Pathway menu | Pathway entry | Download | Help]

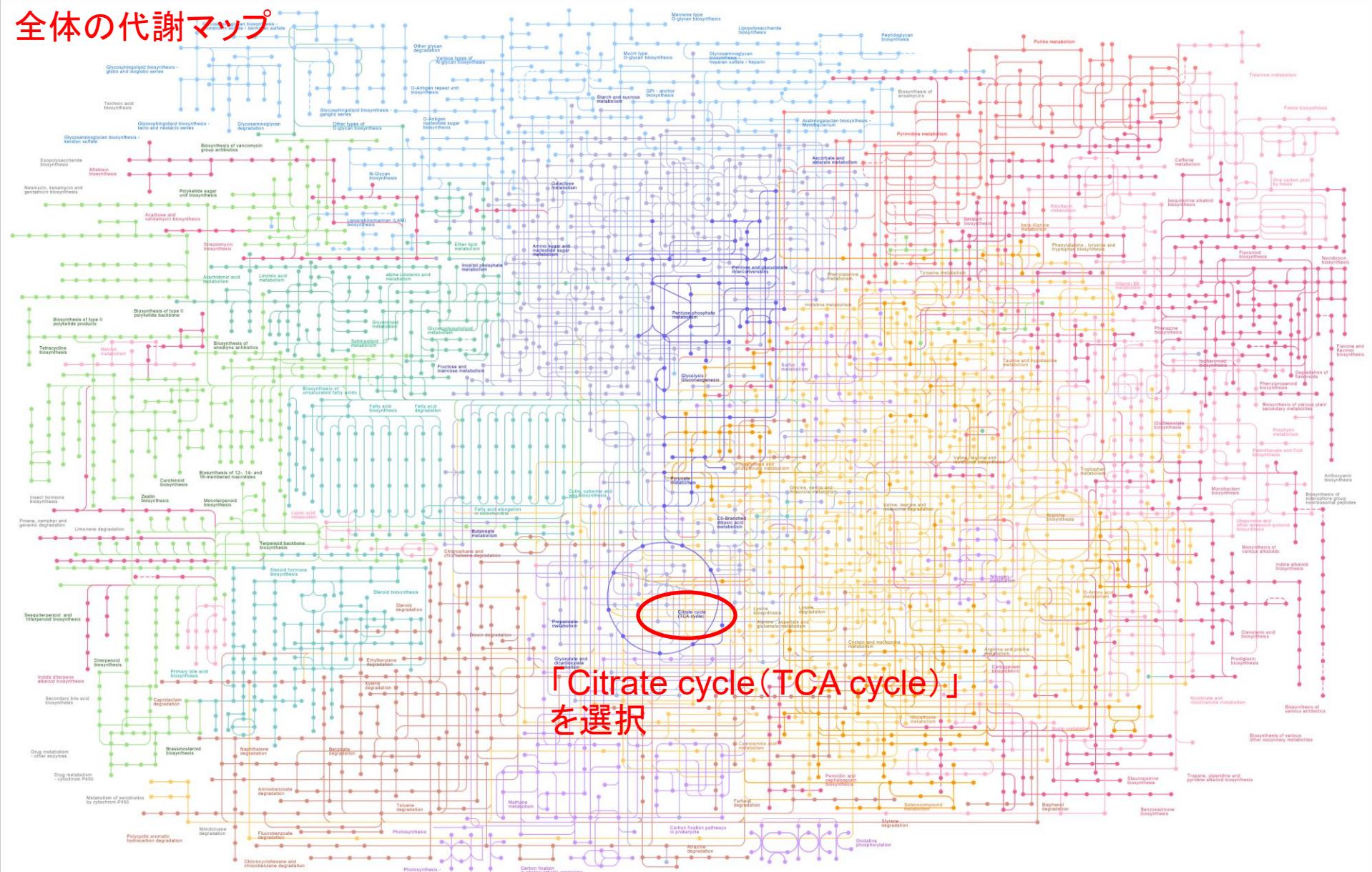
[Change pathway type](#)

「Scale」で調整できる



KEGGの利用 (6)

全体の代謝マップ



「Citrate cycle (TCA cycle)」を選択

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

Go

ID search

Go

Color

Module

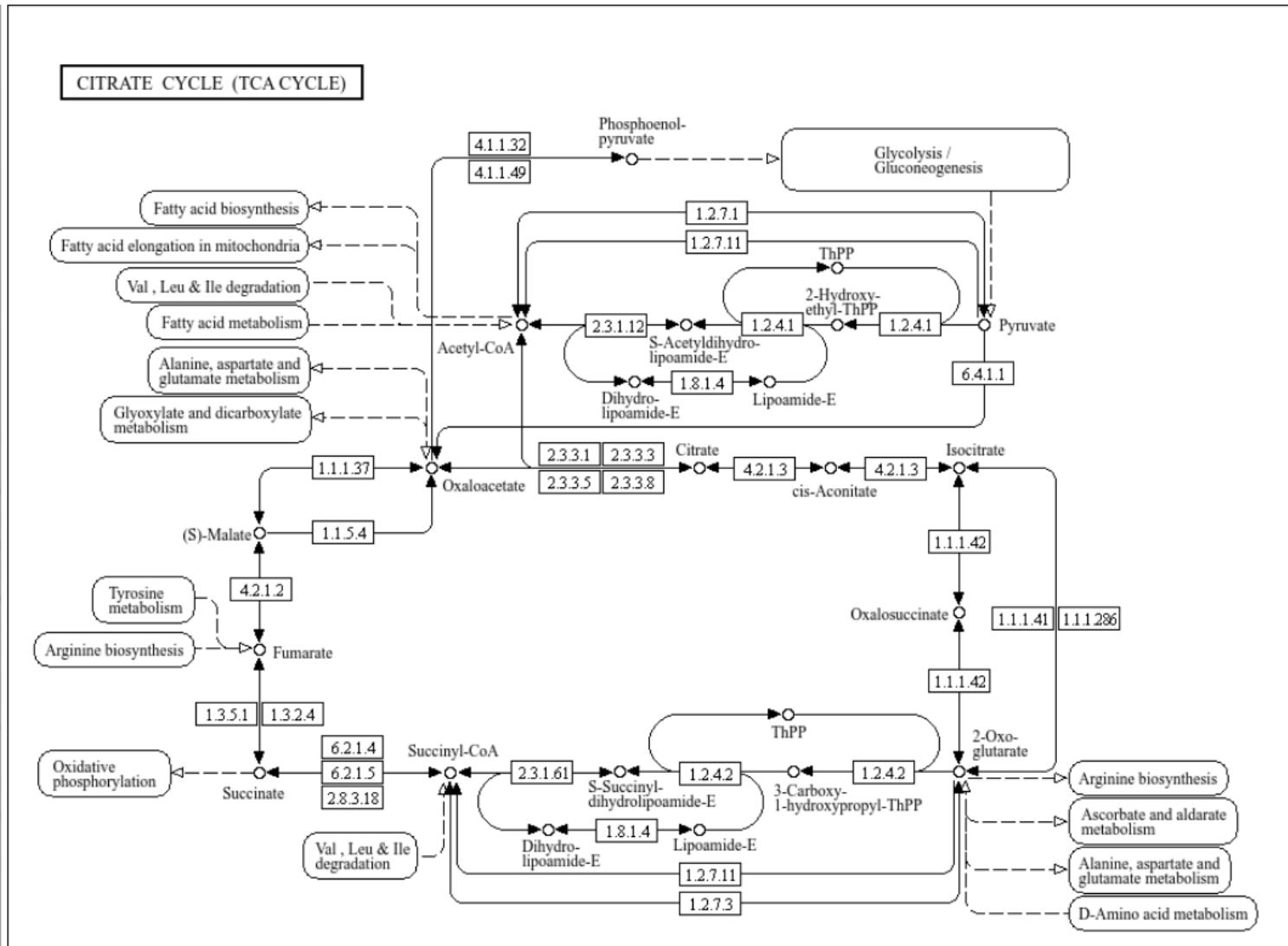
Pathway modules

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

Network

nt06031 Citrate cycle and pyruvate oxidation

- N01603 Pyruvate oxidation
- N01609 Citrate cycle, second
- N01616 Dihydrolipoamide dehydrogenase
- N01604 Citrate cycle, first carbon
- N01617 Citrate cycle, second carbon
- N01605 Gluconeogenesis



KEGGの利用（8）

KEGG 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 (TC)
 - M00010 Citrate cycle, first
 - M00011 Citrate cycle, second
- Other carbohydrate metabolism
 - M00740 Methylaspartate
 - M00982 Methylcitrate cycle

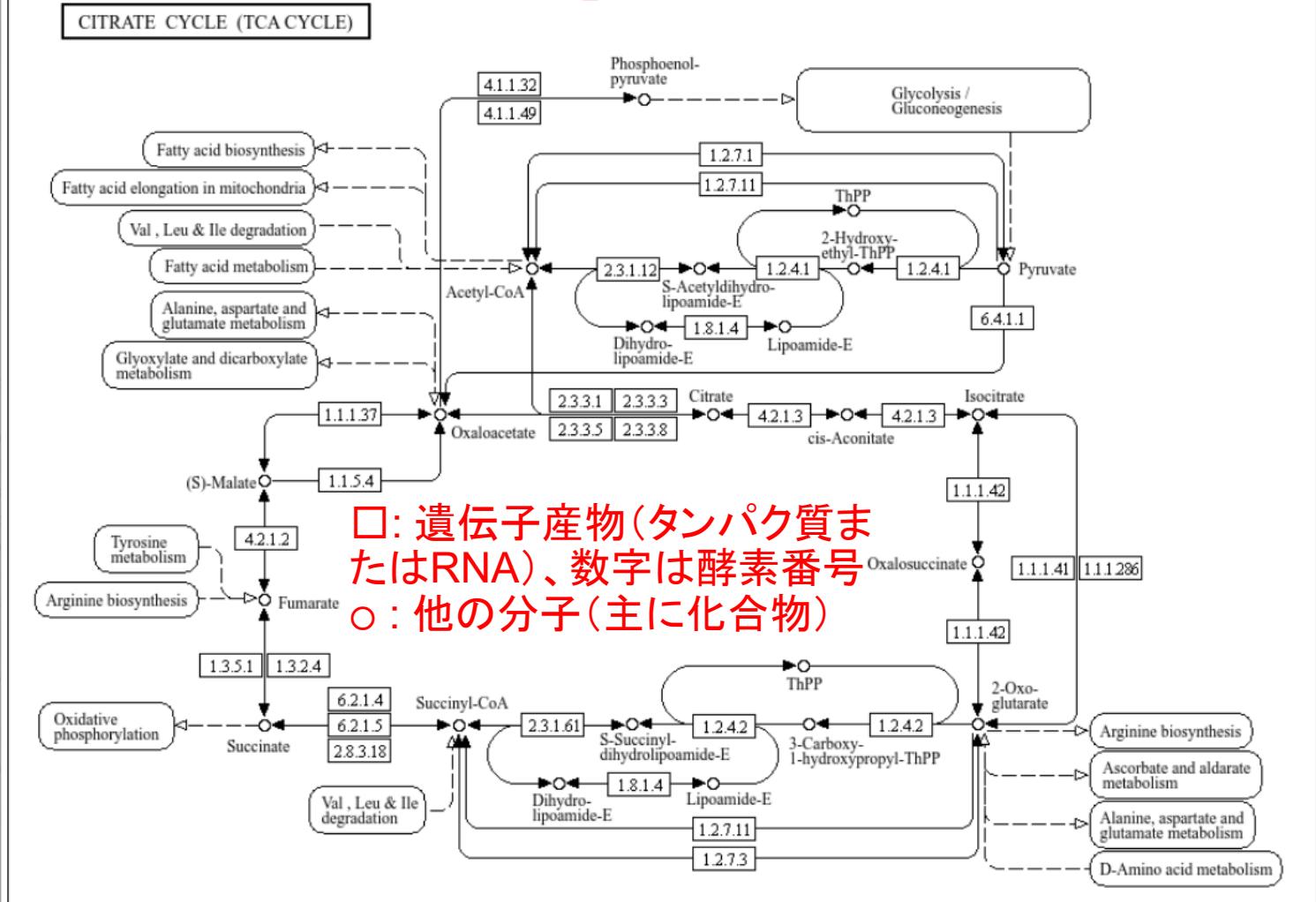
▼ Network

nt06031 Citrate cycle and pyruvate oxidation

- N01603 Pyruvate oxidation
- N01609 Citrate cycle, second
- N01616 Dihydrolipoamide dehydrogenase
- N01604 Citrate cycle, first carbon
- N01617 Citrate cycle, second carbon
- 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



KEGGの利用 (9)

KEGG

Citrate cycle (TCA cycle) - Reference pathway

[Pathway menu | Organism group | Pa

▼ 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 (TC)
 - M00010 Citrate cycle, first carbon
 - M00011 Citrate cycle, second carbon
- Other carbohydrate metabolism
 - M00740 Methylaspartate
 - M00982 Methylcitrate cycle

▼ Network

- nt06031 Citrate cycle and pyruvate metabolism
 - N01603 Pyruvate oxidation
 - N01609 Citrate cycle, second carbon
 - N01616 Dihydrolipoamide dehydrogenase
 - N01604 Citrate cycle, first carbon
 - N01617 Citrate cycle, second carbon
 - 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

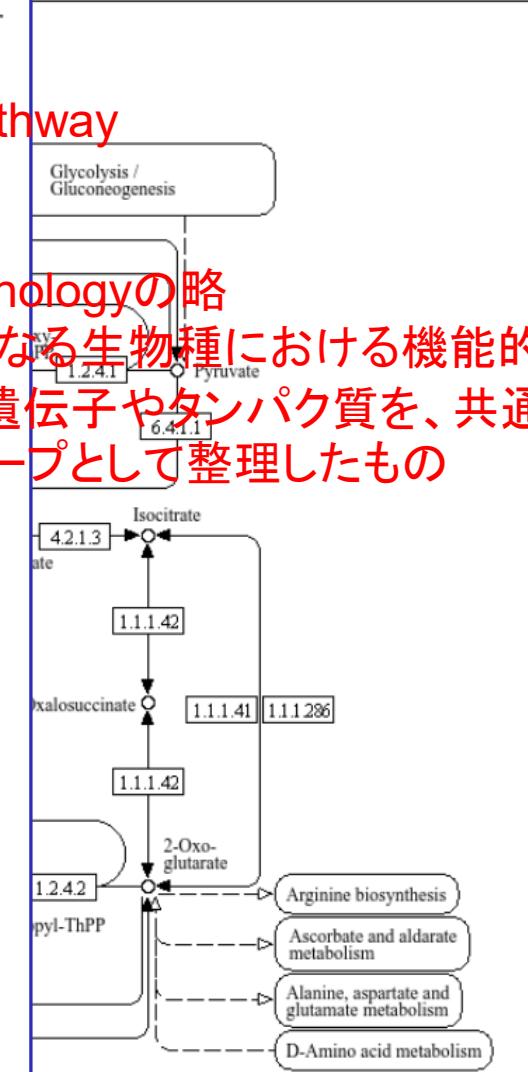
Animals

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)	22/33
pon	Pongo abelii (sumatran orangutan)	22/33
ppyg	Pongo pygmaeus (Bornean orangutan)	22/33
nle	Nomascus leucogenys (northern white-cheeked gibbon)	22/33
hmh	Hylobates moloch (silvery gibbon)	22/33
ssyn	Sympalangus 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 macaque)	22/33
mni	Macaca nemestrina (pig-tailed macaque)	22/33
csab	Chlorocebus sabaeus (green monkey)	22/33
caty	Cercopithecus 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	Piliocolobus 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



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

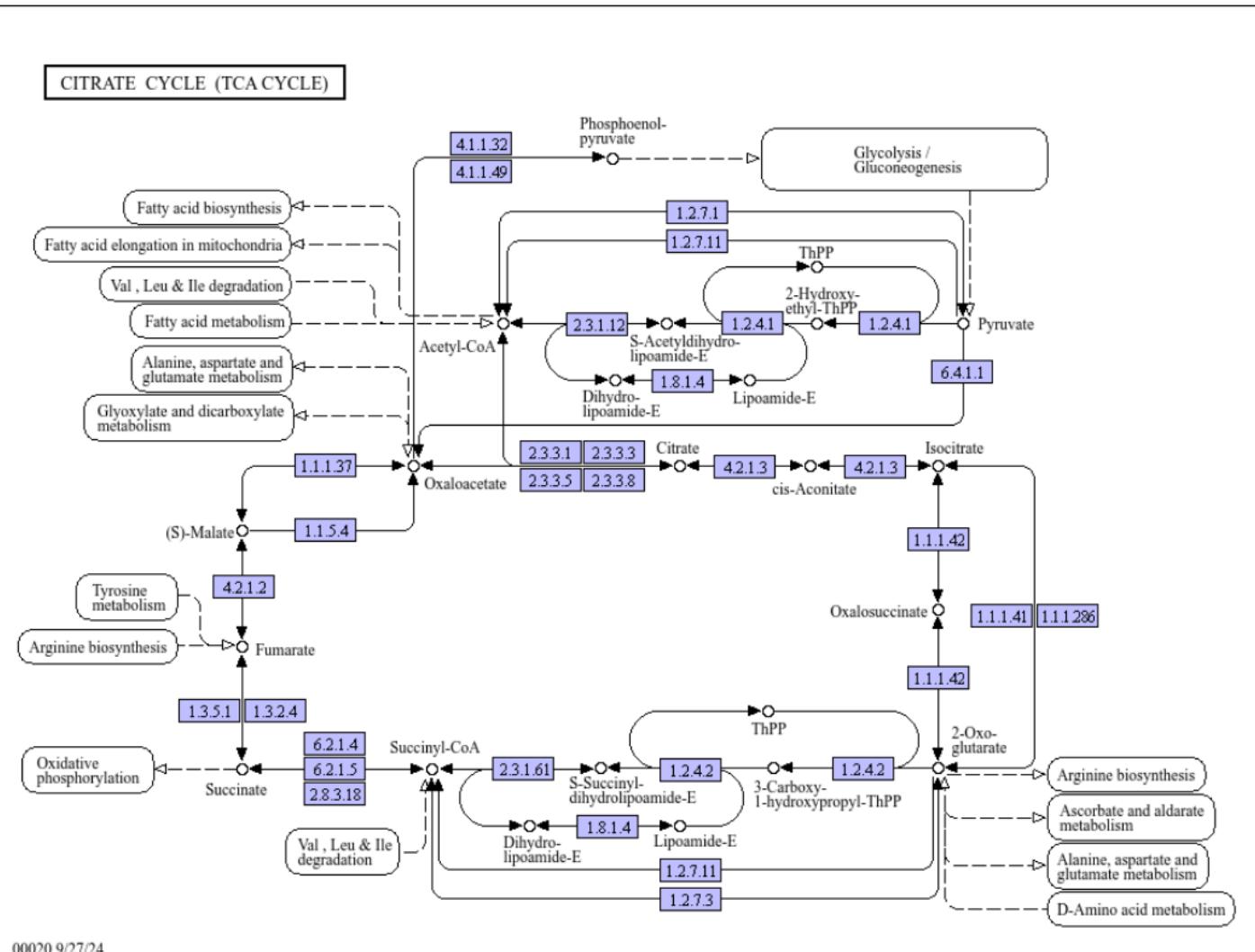
Pathway modules

- Carbohydrate metabolism
- Central carbohydrate metab
- M00003 Gluconeogenesis
- M00307 Pyruvate oxidatio
- M00009 Citrate cycle (TC
- M00010 Citrate cycle, firs
- M00011 Citrate cycle, sec

Other carbohydrate metab

- M00740 Methylaspartate
- M00982 Methylcitrate cyc

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

「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

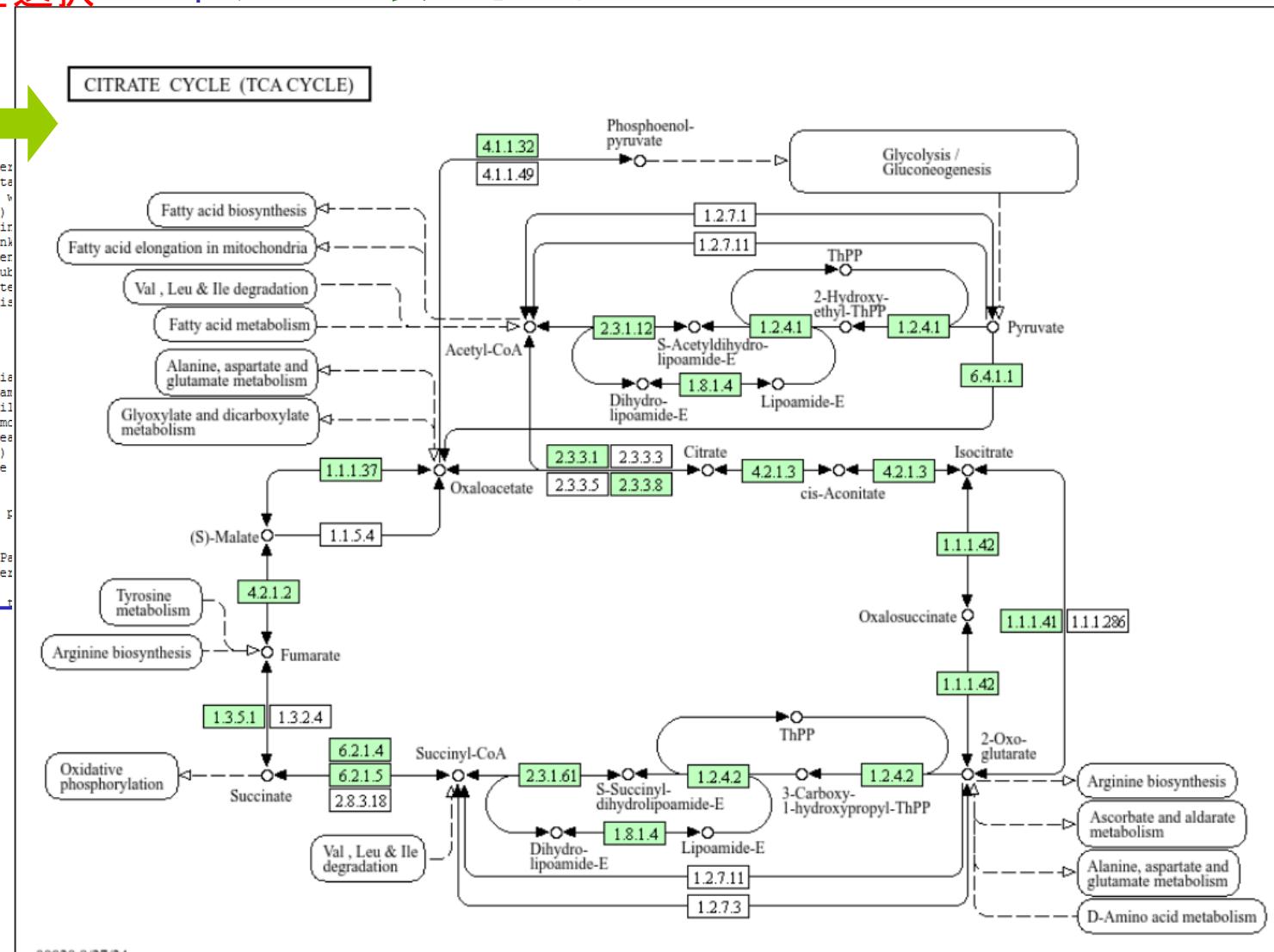
▼ Reference

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

▼ Organism specific

▼ Animals

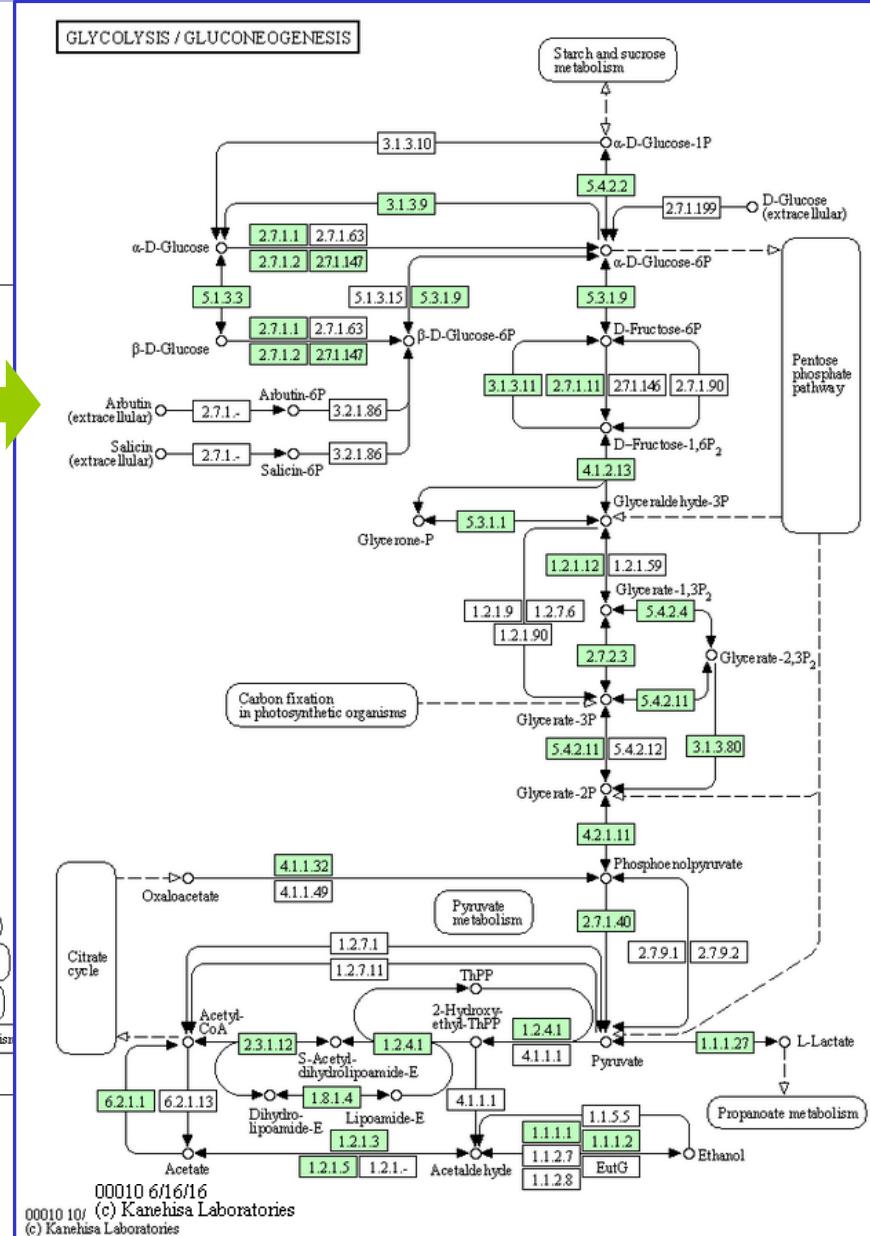
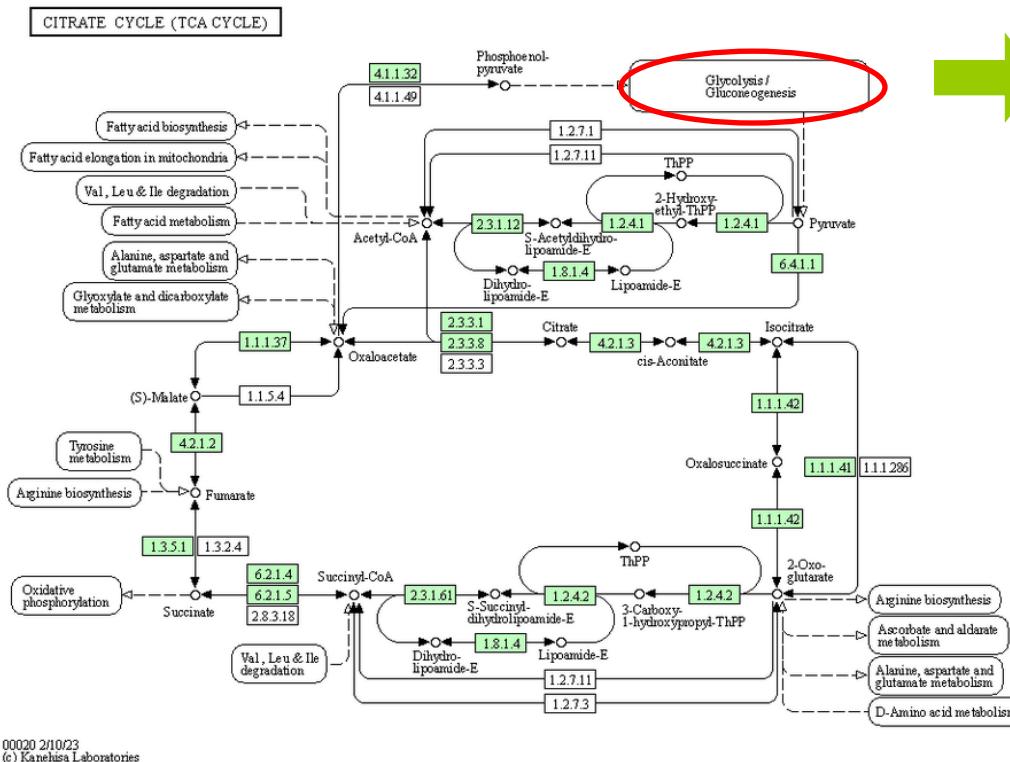
Mammals
hsa Homo sapiens (human)
pan Pan troglodytes (chimpanzee)
ppa Pan paniscus (bonobo)
ggo Gorilla gorilla gorilla (western gorilla)
pon Pongo abelii (Sumatran orangutan)
nle Nomascus leucogenys (northern white-cheeked gibbon)
mcc Macaca mulatta (rhesus monkey)
mcf Macaca fascicularis (crab-eating macaque)
csab Chlorocebus sabaeus (green monkey)
rro Rhinopithecus roxellana (golden snub-nosed monkey)
rbp Rhinopithecus bieti (black snub-nosed monkey)
cjo Callithrix jacchus (white-tufted marmoset)
sbq Saimiri boliviensis boliviensis (bolivian squirrel monkey)
mmu Mus musculus (mouse)
mcau Mus caroli (Ryukyu mouse)
mpah Mus pahari (shrew mouse)
rno Rattus norvegicus (rat)
mun Meriones unguiculatus (Mongolian gerbil)
cge Cricetus griseus (Chinese hamster)
ngi Nanopipistrellus galili (Upper Galilee pipistrelle)
hgl Heterocephalus glaber (naked mole rat)
ccan Castor canadensis (American beaver)
ocu Oryctolagus cuniculus (rabbit)
tup Tupai chaniensis (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 (Polar bear)
elk Enhydra lutris kenyoni (northern sea otter)
fca Felis catus (domestic cat)
png Panthera tigris altaica (Amur tiger)



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



KEGGの利用（13）

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

ガンに関する遺伝子のネットワークを調べる

[KEGG](#)[Search](#)[Help](#)[» Japanese](#)[KEGG Home](#)[Release notes](#)[Current statistics](#)[KEGG Database](#)[KEGG overview](#)[KEGG mapping](#)[Color codes](#)[KEGG Objects](#)[KEGG Weblinks](#)[Entry format](#)[KEGG Software](#)[KEGG API](#)[KGML](#)[KEGG FTP](#)[Subscription](#)[Background info](#)[GenomeNet](#)[DBGET/LinkDB](#)[Feedback](#)[Copyright request](#)[Kanehisa Labs](#)

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[KEGG PATHWAY](#) KEGG pathway maps

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[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]

Pathway
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Brite table
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Organism
Virus
Compound
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Drug (ATC)
Drug (Target)
Antimicrobials

「KEGG DISEASE」を選択

Organism-specific entry points

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
 検索

DISEASE を KEGG MEDICUS で検索
 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。

The diagram illustrates the complex interactions that lead to disease. On the left, various factors are listed: 'ゆらぎ' (perturbation), 'ヒトゲノム (先天性・後天性の変異, など)' (Human genome (congenital, acquired mutations, etc.)), '病原体ゲノム (ウイルス, 細菌, 真菌, など)' (Pathogen genome (viruses, bacteria, fungi, etc.)), '常在菌叢メタゲノム (腸内細菌叢, など)' (Normal gut microbiome metagenome (intestinal microbiome, etc.)), and '環境要因' (Environmental factors). Arrows point from these factors to a central box labeled '生体システム (分子ネットワーク)' (Biological system (molecular network)). From this central box, arrows point to 'ゲノムバイオマーカー' (Genomic biomarkers), '治療薬' (Therapeutic drugs), '診断マーカー' (Diagnostic markers), and 'ワクチン' (Vaccines). A blue arrow also points from the environment back up to the central system.

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る形で作成されています。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や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応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、ヒト遺伝子バリアント、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)のどの影響を与え、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)



「がんのパスウェイ」を選択

KEGG パスウェイマップ

Option

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

Search

ID search

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 ウィルス発がん

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 膝癌

05225 肝細胞癌

05226 胃癌

05214 神経膠腫

05216 甲状腺癌

05221 急性骨髓性白血病

05220 慢性骨髓性白血病

05217 基底細胞癌

05218 悪性黒色腫

05211 腎細胞癌

05219 膀胱癌

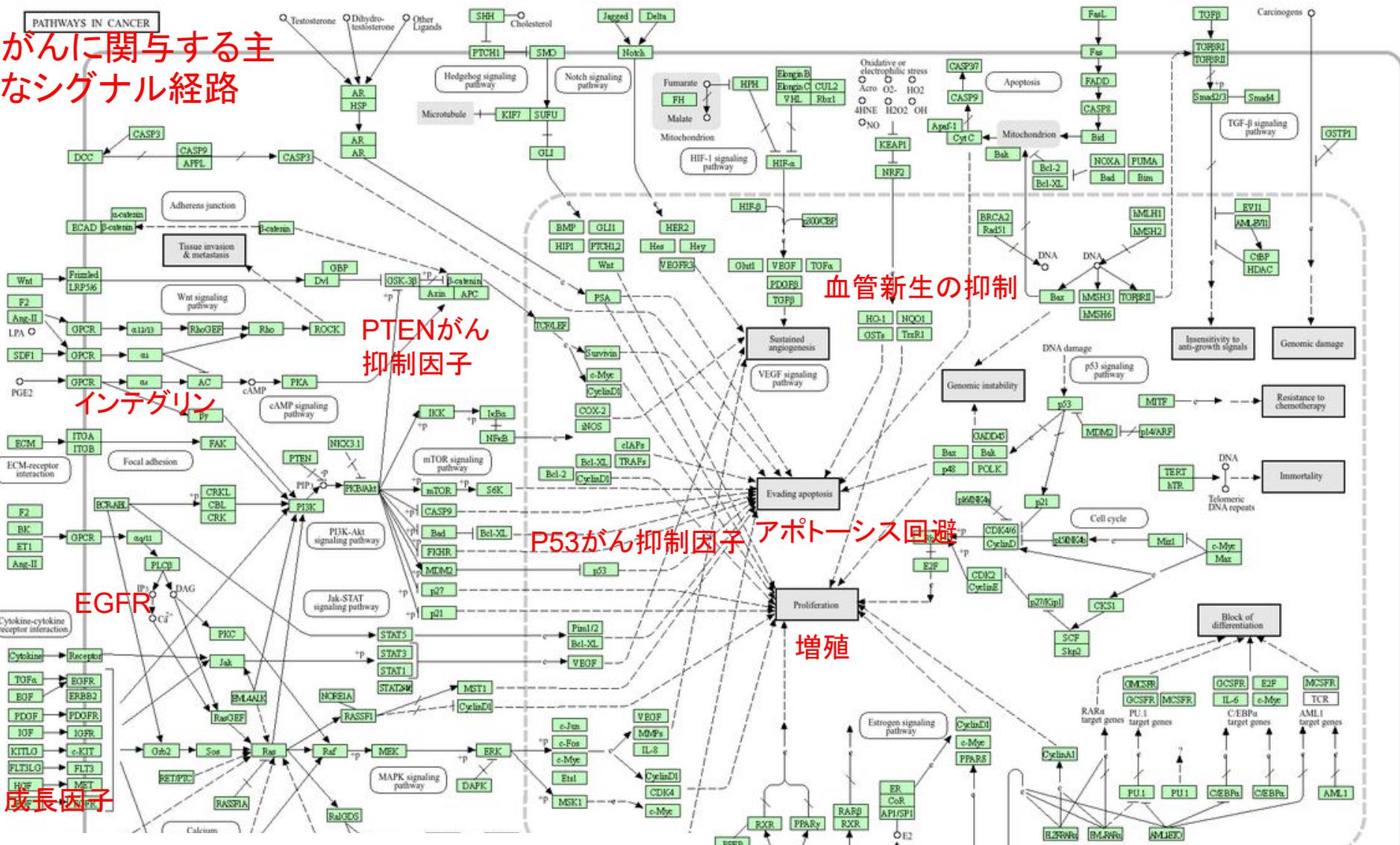
05215 前立腺癌

05213 子宮内膜癌

05224 乳癌

KEGGの利用 (17)

がんに関与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

Kyoto Encyclopedia of Genes and Genomes

KEGG caffeine Search Help » Japanese

「caffeine」と入力

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
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]

Pathway
Brite
Brite table
Module
Network
KO (Function)
Organism
Virus
Compound
Disease (ICD)
Drug (ATC)
Drug (Target)
Antimicrobials

Organism-specific entry points

代謝経路の探索（2）

KEGG Search KEGG for caffeine Go Clear

Database: KEGG - Search term: caffeine

KEGG PATHWAY

map00232 (Caffeine metabolism) を選択

map00232
Caffeine metabolism

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
cfel:113374615
no KO assigned | (RefSeq) caffeine-induced protein 16-like
hrf: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 map	map00232 Caffeine metabolism	
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

代謝経路の探索（4）

KFC

Caffeine metabolism - Reference pathway

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

Change pathway type

▼ Option

Scale: 100%

▼ Search

▼ ID search

▼ Color

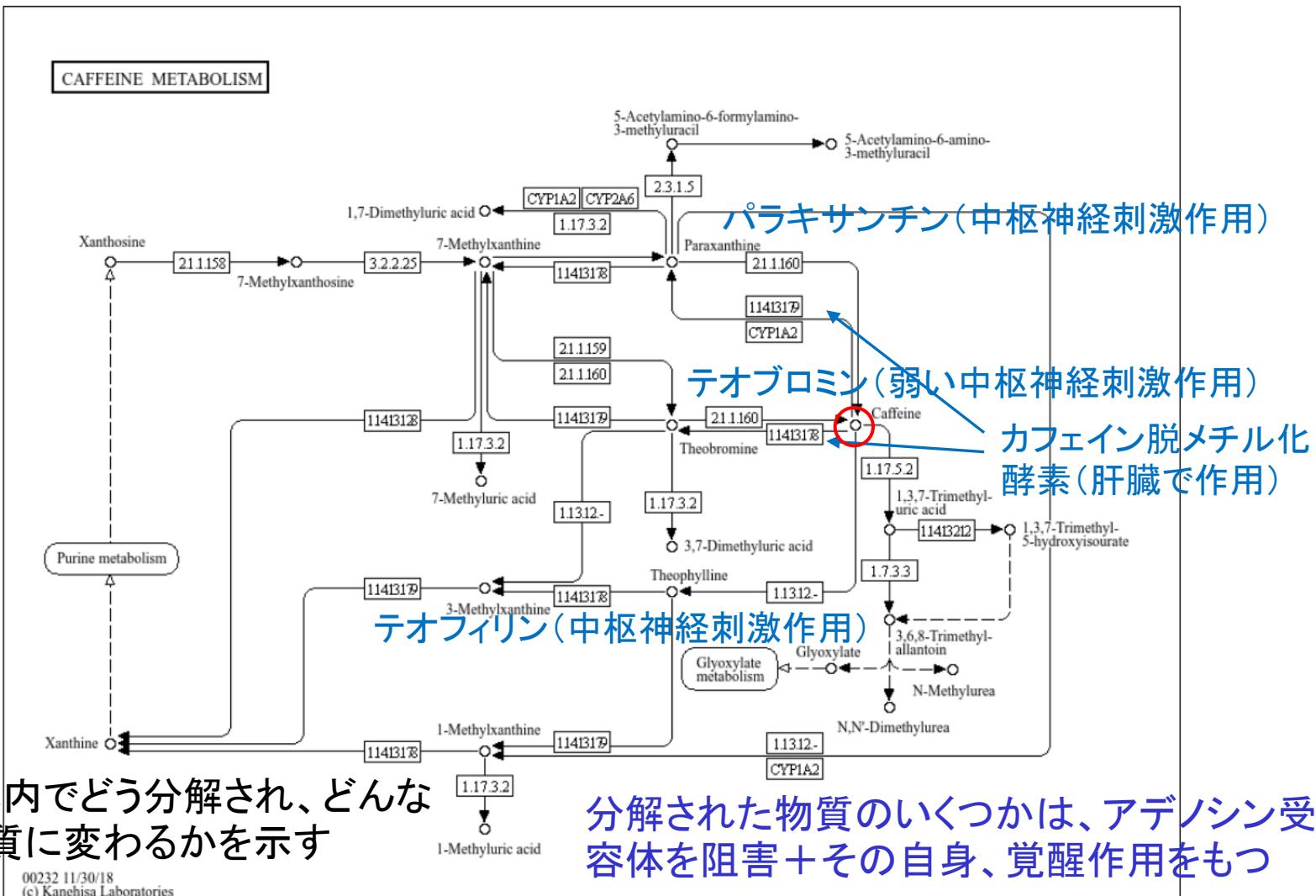
▼ Module

Pathway modules

Xenobiotics biodegradation

Aromatics degradation

M00915 Caffeine degradat



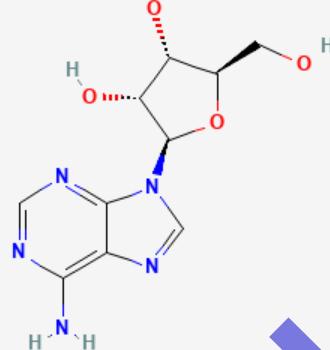
カフェインが体内でどう分解され、どんな作用をもつ物質に変わるかを示す

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

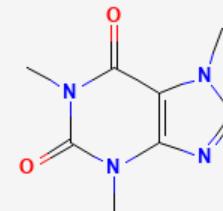
代謝経路の探索（5）

アデノシンとカフェインは構造が似ている

アデノシン

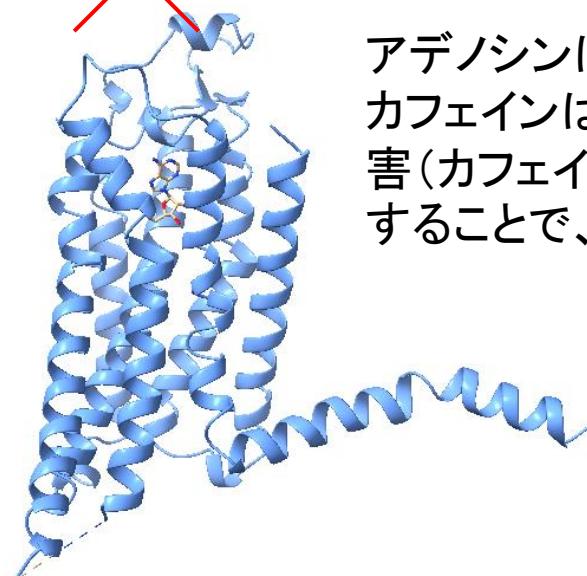


カフェイン



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

KEGG Database
[KEGG の概要](#)
[KEGG mapping](#)
[Color codes](#)

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

KEGG Software
[KEGG API](#)
[KGML](#)
[KEGG FTP](#)
[Subscription](#)
[Background info](#)

[GenomeNet](#)
[DBGET/LinkDB](#)
[Feedback](#)
[Copyright request](#)

Kanehisa Labs

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ク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
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]

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

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) Go hsa hsa eco

解析ツール

[KEGG Mapper](#)

[KEGG Web Apps](#)

「KEGG Mapper」を選択

PATHWAY/BRITE/MODULE 等へのマッピングツール群

Pathway viewer の色付け機能など

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」を選択

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

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
K02284
K02285
K02286
K02287

Examples: Select

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

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

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）

KFCC Photosynthesis - Reference pathway

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

[Change pathway type](#)

▼ Option

Scale: 100%

▼ Search

▼ ID search

▼ Color

KEGG Mapper

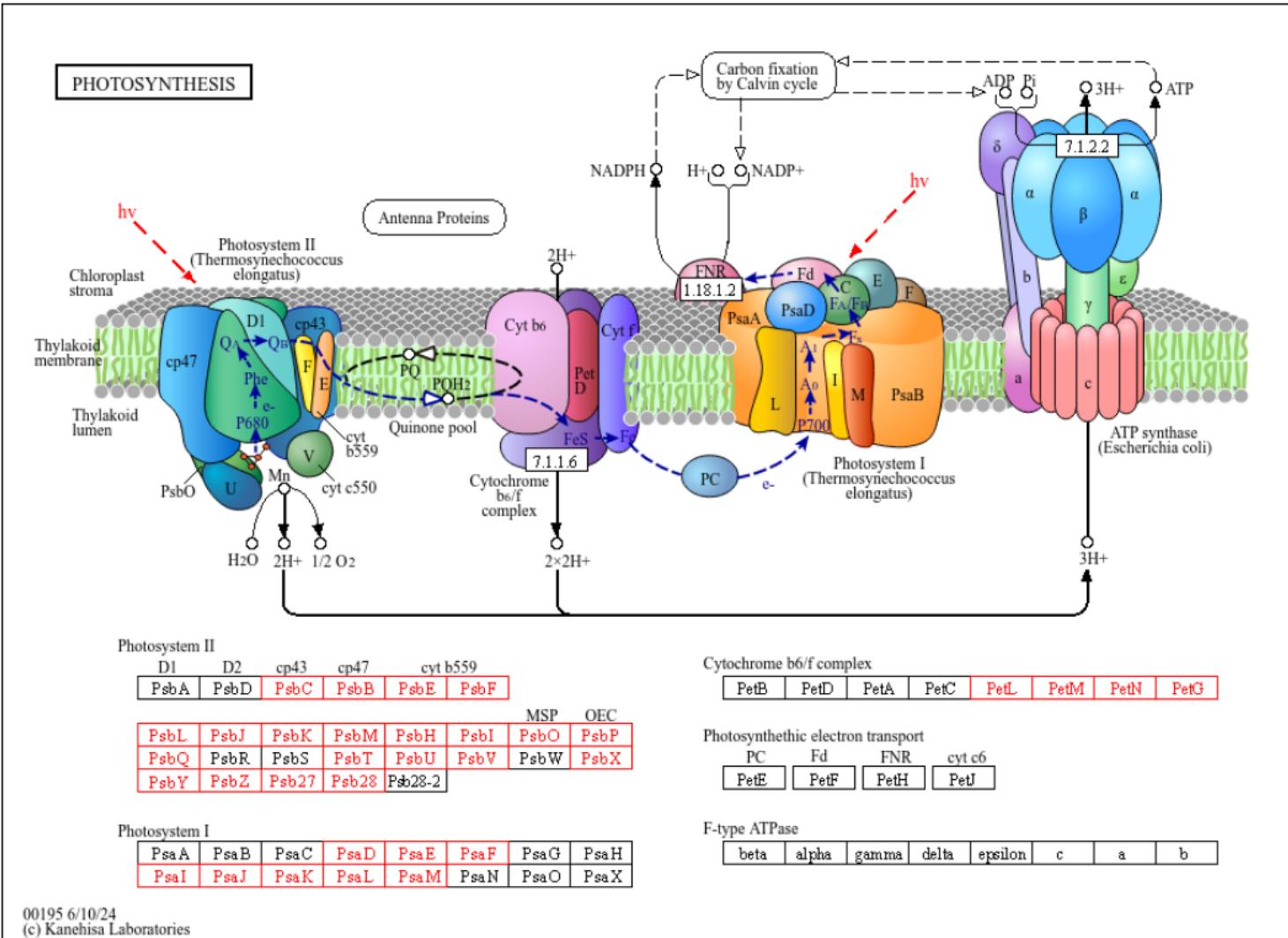
▼ Module

Pathway modules

- Energy metabolism
- Photosynthesis
 - M00161 Photosystem II
 - M00163 Photosystem I
- ATP synthesis
 - M00162 Cytochrome b6f
 - 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/>

The screenshot shows the homepage of the Microbial Genome Database for Comparative Analysis (MBGD). The header features the MBGD logo and the text "Microbial Genome Database for Comparative Analysis". The left sidebar contains a navigation menu with sections like "About MBGD", "Documents", "Ortholog Classification", "Ortholog Table", "Searching MBGD", "Downloads & Programs", and various API links. The main content area includes a "Welcome to MBGD" section with a brief description of the database's purpose and references to a 2019 paper in Nucleic Acids Res. It also displays genome statistics: 34,079 genomes (6,316 species, 1,812 genera) including 33,249 Bacteria, 414 Archaea, and 416 Eukaryota. Below this are links for "Data Sources" and "Taxonomy Browser". Further down are sections for "Ortholog table summary viewer" and "Keyword Search", each with input fields and "Search" buttons.

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: 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

About MBGD

Documents

Ortholog Classification

Ortholog Table (オーソログテーブルを指定)

Create ortholog table

My MBGD Mode

Cluster Tables

Searching MBGD

Advanced Search

Sequence Search

Profile Search

Genomaple

Function Categories

Downloads & Programs

MBGD API

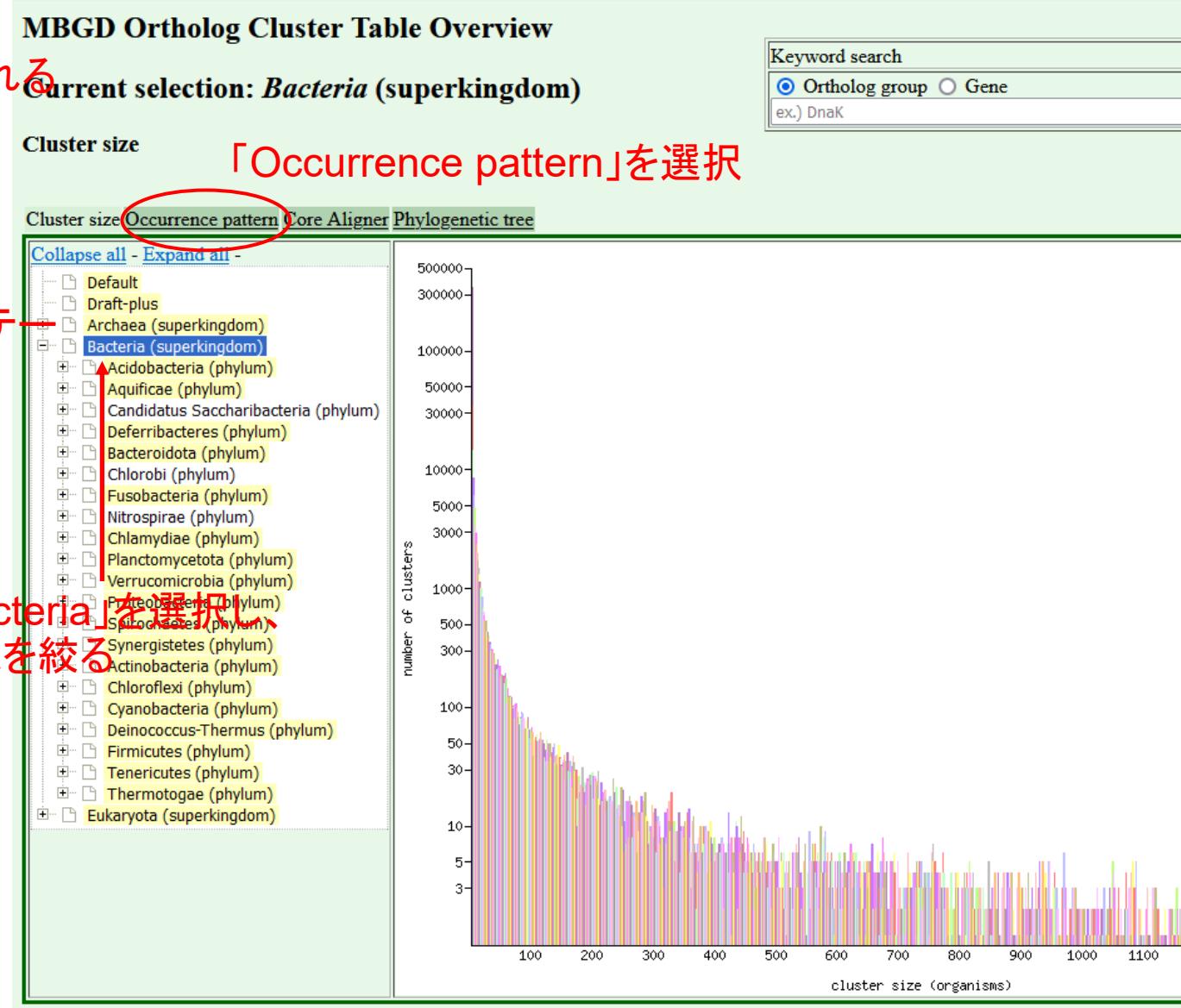
Data Archive

SPARQL interface

DomClust

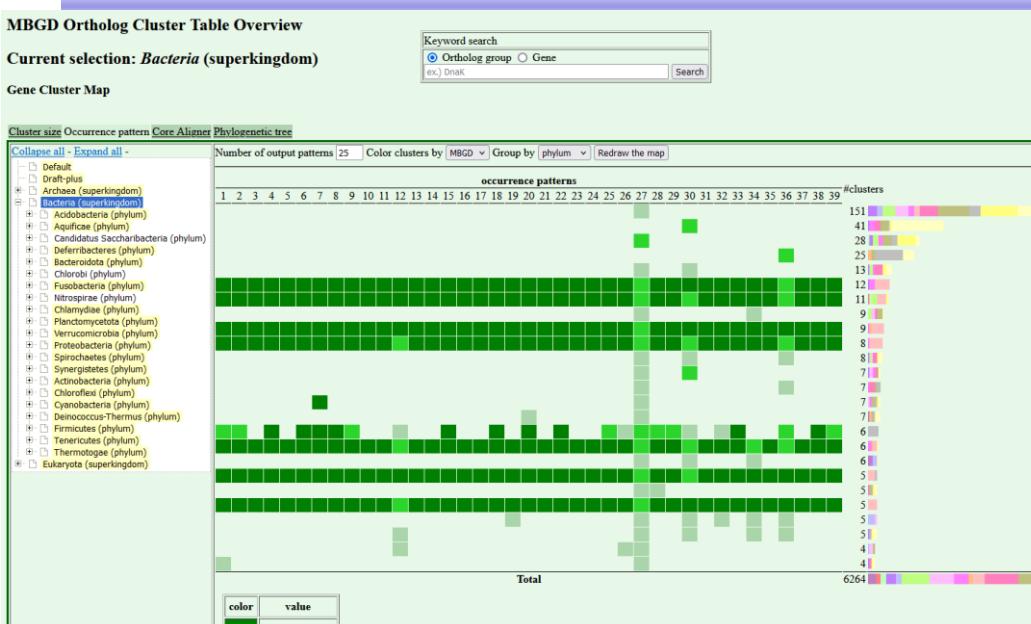
DomRefine

CGAT



「Bacteria」を選択し、
対象を絞る

MBGDの利用 (2)



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) Save Summary Table

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)

Table format

「Redraw the Map」を選択

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 checked="" 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

MBGDの利用 (3)

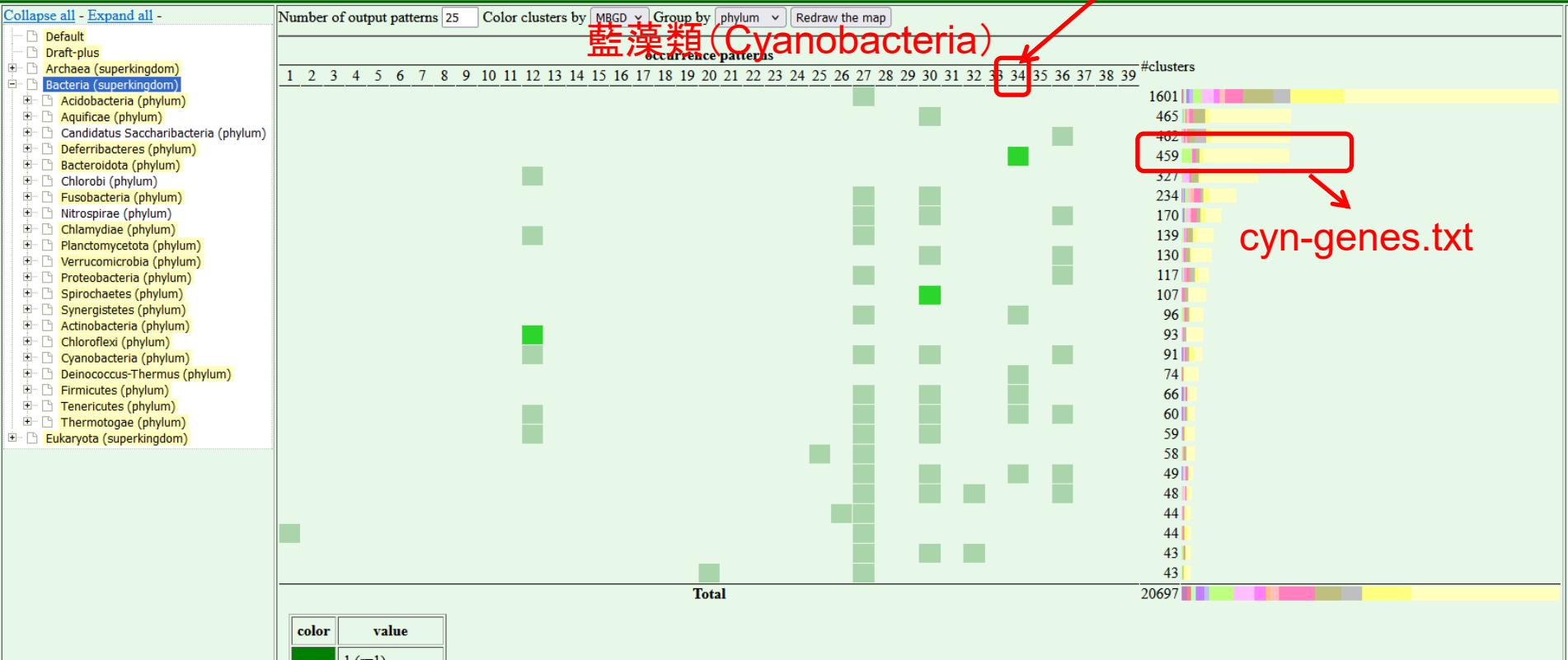
藍藻類(Cyanobacteria)に特徴的な遺伝子を集める

MBGD Ortholog Cluster Table Overview

Current selection: **Bacteria** (superkingdom)

Gene Cluster Map

Cluster size Occurrence pattern Core Aligner Phylogenetic tree



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

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

生物種

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

GENEONTOLOGY Unifying Biology About Ontology Annotations Downloads Help ALLIANCE OF GENOME RESOURCES FOUNDING MEMBER

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

「biological process」を選択(デフォルト)

「Oryza sativa」(イネ)を選択

「Launch」を押す

GO Enrichment Analysis ?
Powered by PANTHER

ycf36
ycf4
ycf51
ycf54
ycf58
ycf65
ycf66

biological process

Oryza sativa Examples Launch >

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

TOOLS & GUIDES

ONTOGONY

(evidence)

NEDD4

Ubiquitin-protein ligase activity
GO:0004842

ANNOTATION

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

GO-CAM

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.

search keyword

Home About Data Version Tools API/Services Publications Workspace Downloads FAQ/Help/Tutorial Login Register Contact us

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

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

Analyzed List: [upload](#)

Reference List: Oryza

Annotation Data Set: [GO biological pr](#)

Test Type: Fisher's Exact Bino

Correction: Calculate False Discove

Results [?](#)

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

Unmapped IDs: [0](#)

Multiple mapping information: [0](#)

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

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）とともに収集したデータベース
 - <https://thebiogrid.org/>

The screenshot shows the BioGRID 4.4 homepage. At the top, there's a navigation bar with links for home, help, wiki, projects, tools, contribute, stats, downloads, partners, and about us. A Twitter icon is also present. Below the navigation, a banner reads "Welcome to our Database of Protein, Genetic and Chemical Interactions". It highlights version 4.4.241, 86,161 publications, 2,826,897 protein and genetic interactions, 31,144 chemical interactions, and 1,128,339 post translational modifications. It also mentions that all data is freely provided via search index and available for download in many standardized formats. Two buttons at the bottom of this section are "BioGRID Statistics" and "Latest Downloads". To the right, a large search interface titled "Search BioGRID:" includes a dropdown for "By Protein/Gene", a text input for "Search by Protein/Gene Identifiers ...", a dropdown for "All Organisms", and a "Submit Identifier Search" button. Below the search are links for "Advanced Search", "Helpful Search Tips", and "Featured Datasets". A yellow banner at the bottom promotes the "BioGRID COVID-19 Coronavirus Curation Project" and links to "SARS-CoV-2 Protein Interactions" and "Download SARS-CoV-2 and Coronavirus-Related Interactions". At the very bottom, there are sections for "Related Resources" (linking to BioGRID ORCS) and "Partners" (listing NIH, ORIP, and SickKids).

BioGRID 4.4

home help wiki projects tools contribute stats downloads partners about us

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

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.

Learn more

Partners

NIH

ORIP OFFICE OF RESEARCH INFRASTRUCTURE PROGRAMS

SickKids THE HOSPITAL FOR

BioGRIDの利用

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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.

「Homo sapiens」を選択

BioGRID Statistics 

Latest Downloads 

Q Search BioGRID:

By Protein/Gene

INS

Homo sapiens

Submit Identifier Search 

Advanced Search  Helpful Search Tips  Featured Datasets 

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

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。



THE HOSPITAL FOR
SICK CHILDREN



PRINCETON
UNIVERSITY

BioGRIDの利用

BioGRID^{4.4}

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Result Summary

INS
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

insulin

Homo sapiens

 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

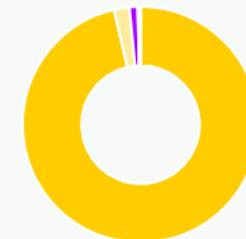
526

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					
Interactor	Organism / Chemical Type	Aliases	Description	Evidence	
M-Cresol	Small Molecule	-	-	3	View
HSPA5	H. sapiens	BIP, MIF2, GRP78, HEL-S-80n	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	2 1	View

BioGRIDの利用

BioGRID^{4.4}

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BioGRID Downloads

|INS

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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BioGRIDの利用

BioGRID 4.4

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BioGRID Downloads

INS

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

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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.

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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

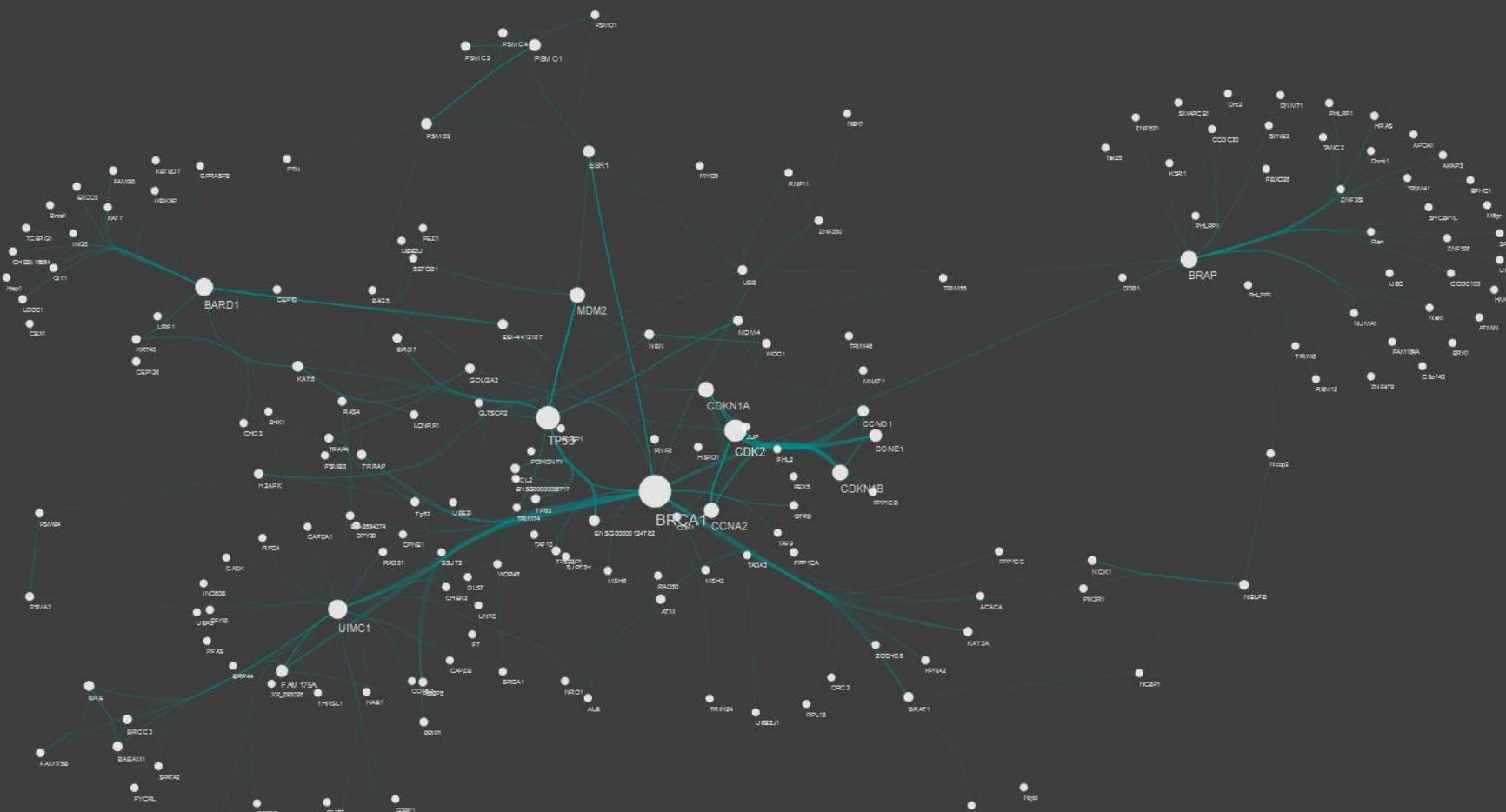
Cytoscape

- 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





「Sample visualizations」の例



Cytoscapeの利用



Cytoscapeの利用

WikiPathways: WP5447 - GLP-1 in pancreatic islet cells - Hom...

Layout



Legend
Show

全身状態(炎症・高血糖・肥満)が
IL-6経路を通じてα細胞側に影響

Pancreatic islet

Metabolic stress
Exercise
Systematic inflammation
Hyperglycemia
Obesity
Diabetes

Glucose → SLC2A1

IL6

IL6R

GCG

Alpha cell
α細胞

GLP-1

インスリンの分泌

Insulin

Glucose

グルコースの取り込み

ランゲルハンス島内
のハブの位置づけ

GLP-1受容体刺激

Proliferation

INS

SLC2A2

GLP1R

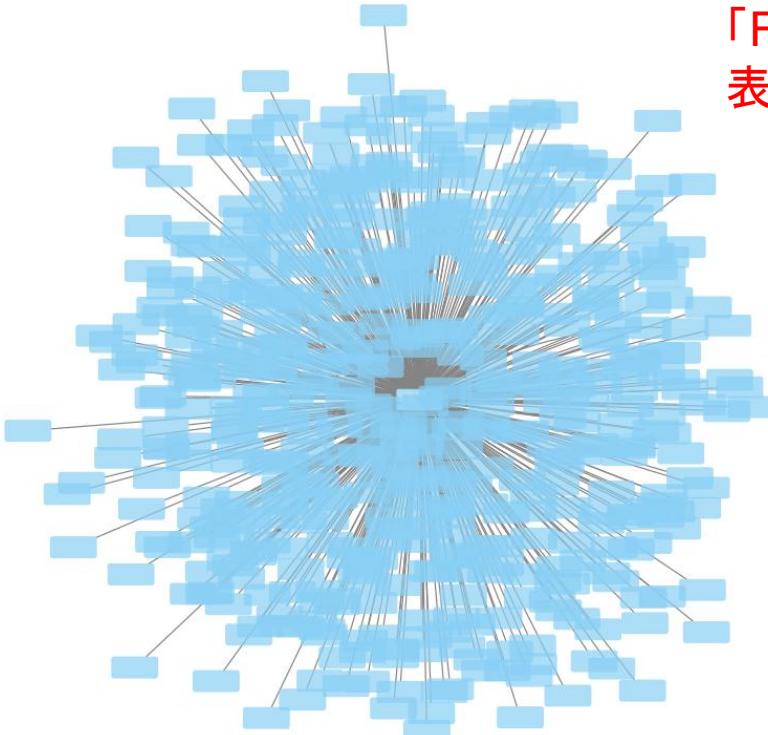
?

β細胞自身の増殖・維持

Beta cell
β細胞

Cytoscapeの利用

Cytoscapeのダウンロード版に、「BIOGRID-GENE-109842-4.4.228.tab3.txt」を入力して表示したINSとのインタラクションの図
「File」→「import」→「Network from file」を選択
表示するカラムで、ソースとデスティネーションを指定

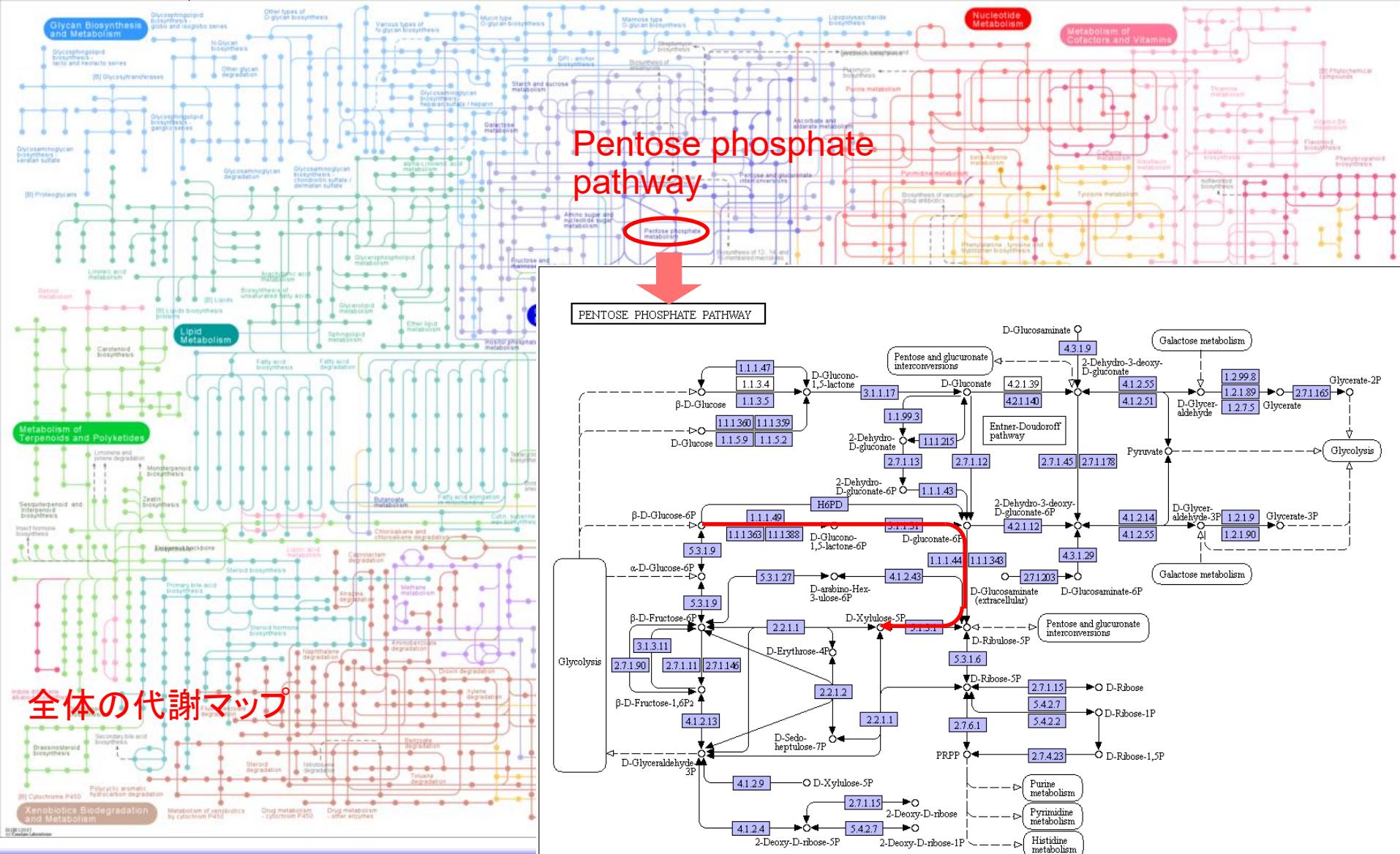


拡大するとラベルが表示される



代謝ネットワークの表現の例

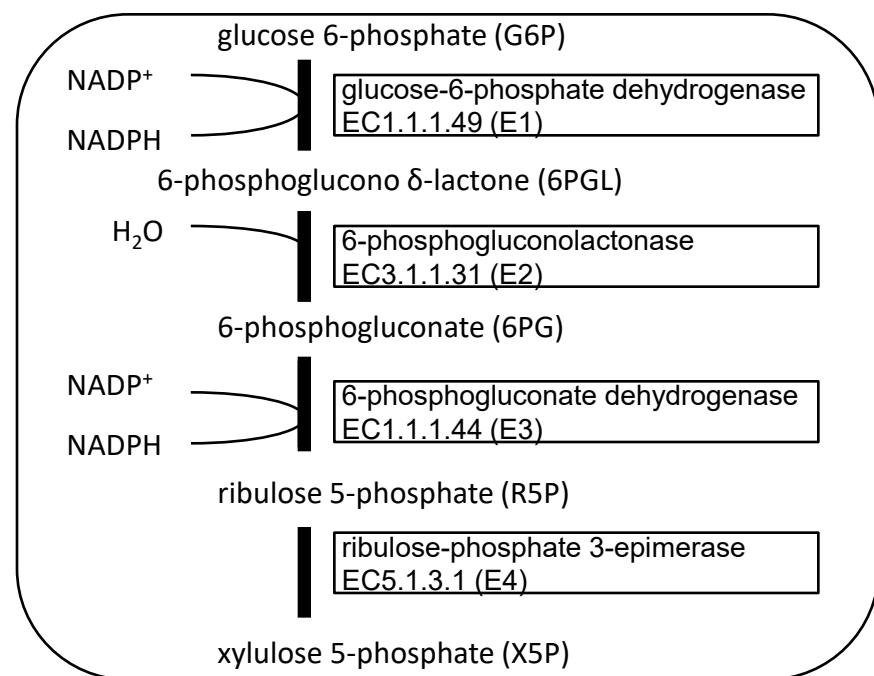
KEGGの表示



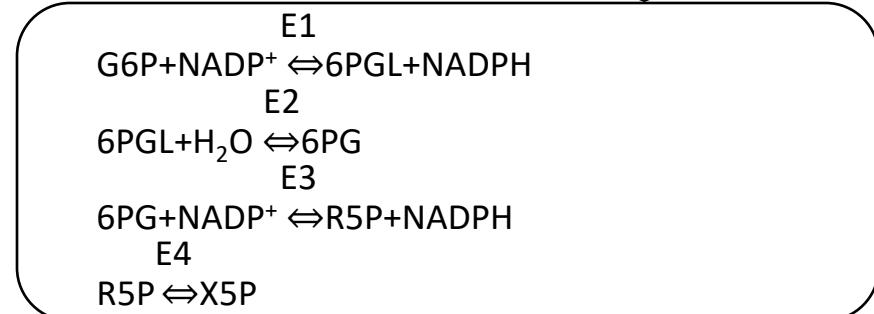
ネットワーク解析

代謝ネットワークの表現の例

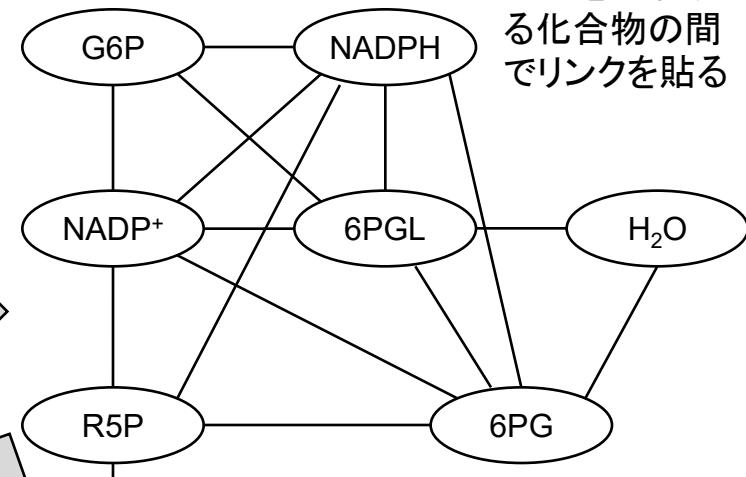
代謝ネットワーク



反応式の列

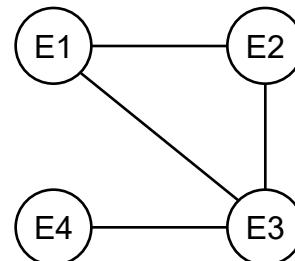


化合物グラフ



反応を共有する化合物の間でリンクを貼る

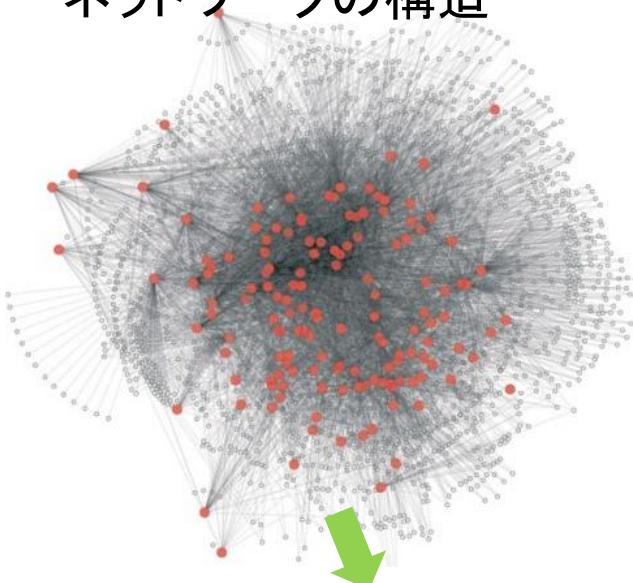
反応グラフ



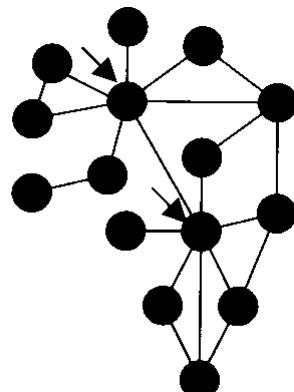
化合物を共有する酵素の間でリンクを貼る

ネットワーク構造の解析の例

ネットワークの構造



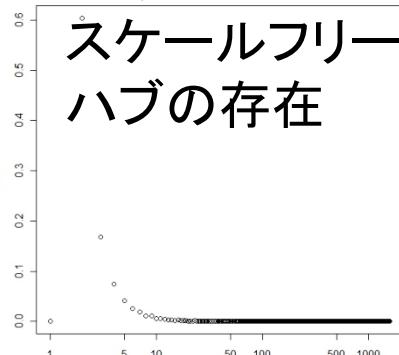
ネットワークの特性解析



スモールワールド性

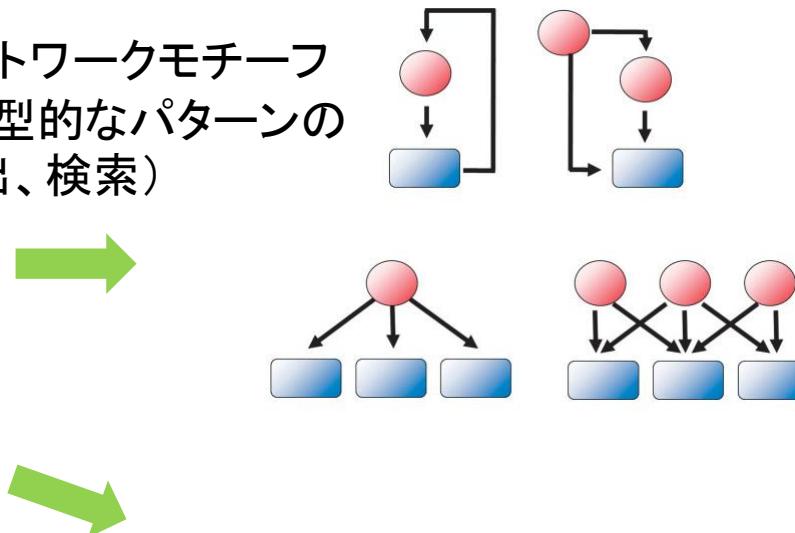
次数 k の分布の解析

スケールフリー性 $P(k) = Ck^{-\gamma}$
ハブの存在

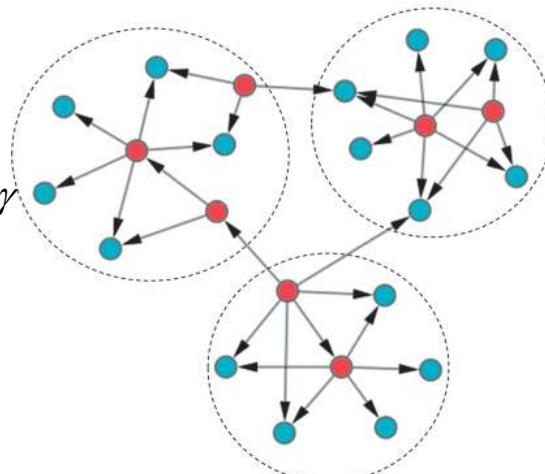


ハブ: 枝の数がと
くに多い頂点

ネットワークモチーフ
(典型的なパターンの
抽出、検索)

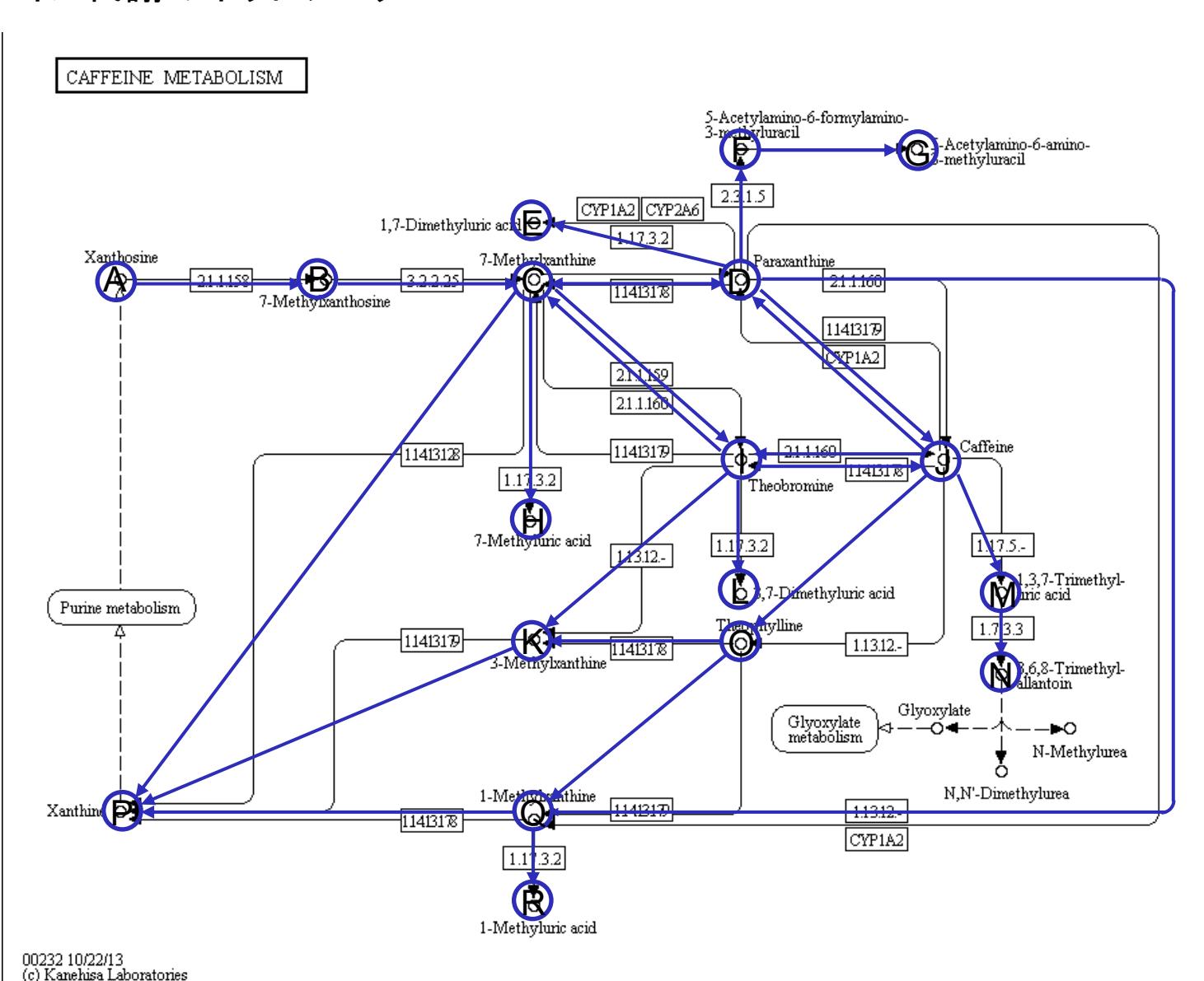


モジュール構造の同定



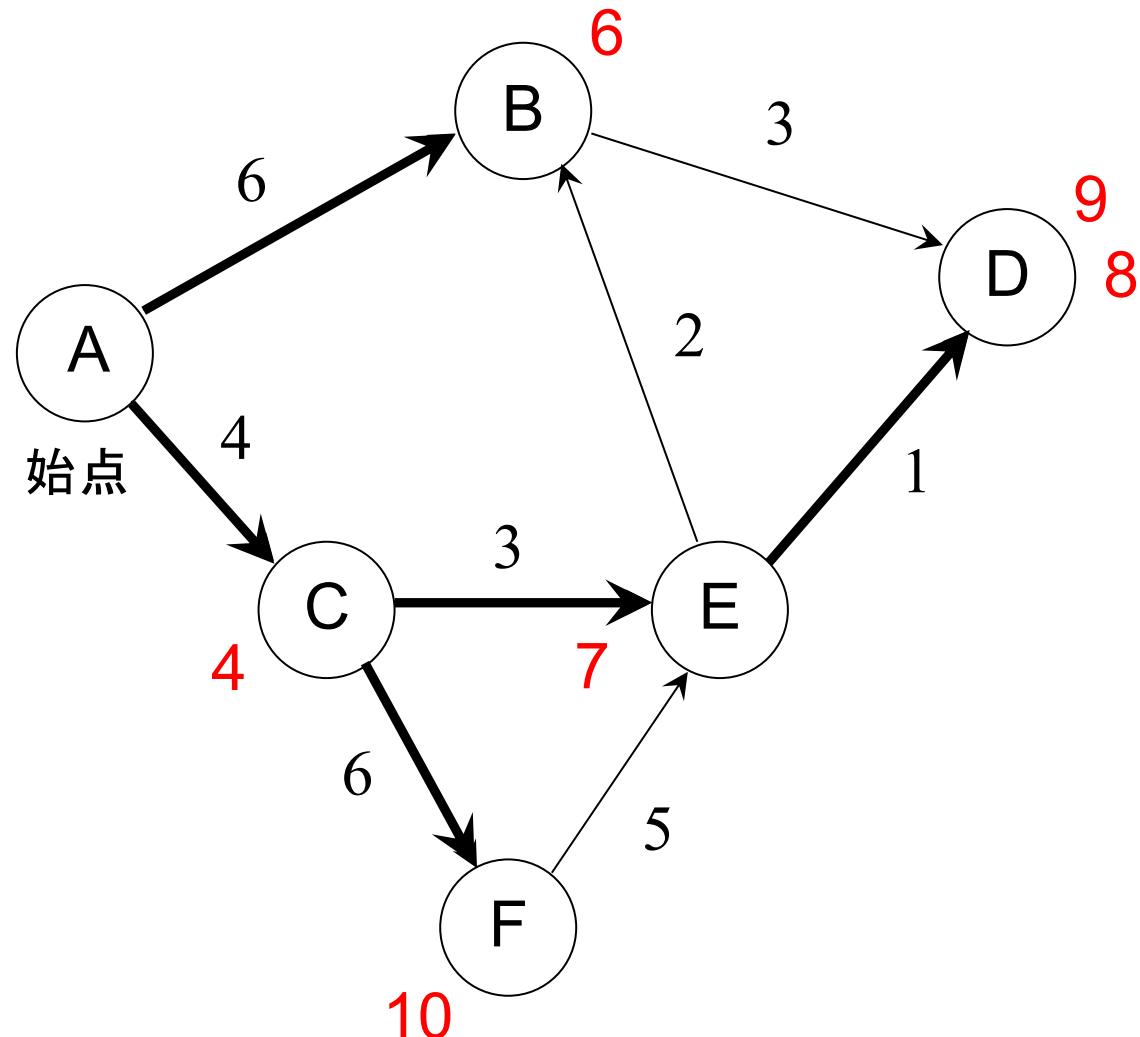
グラフの例

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

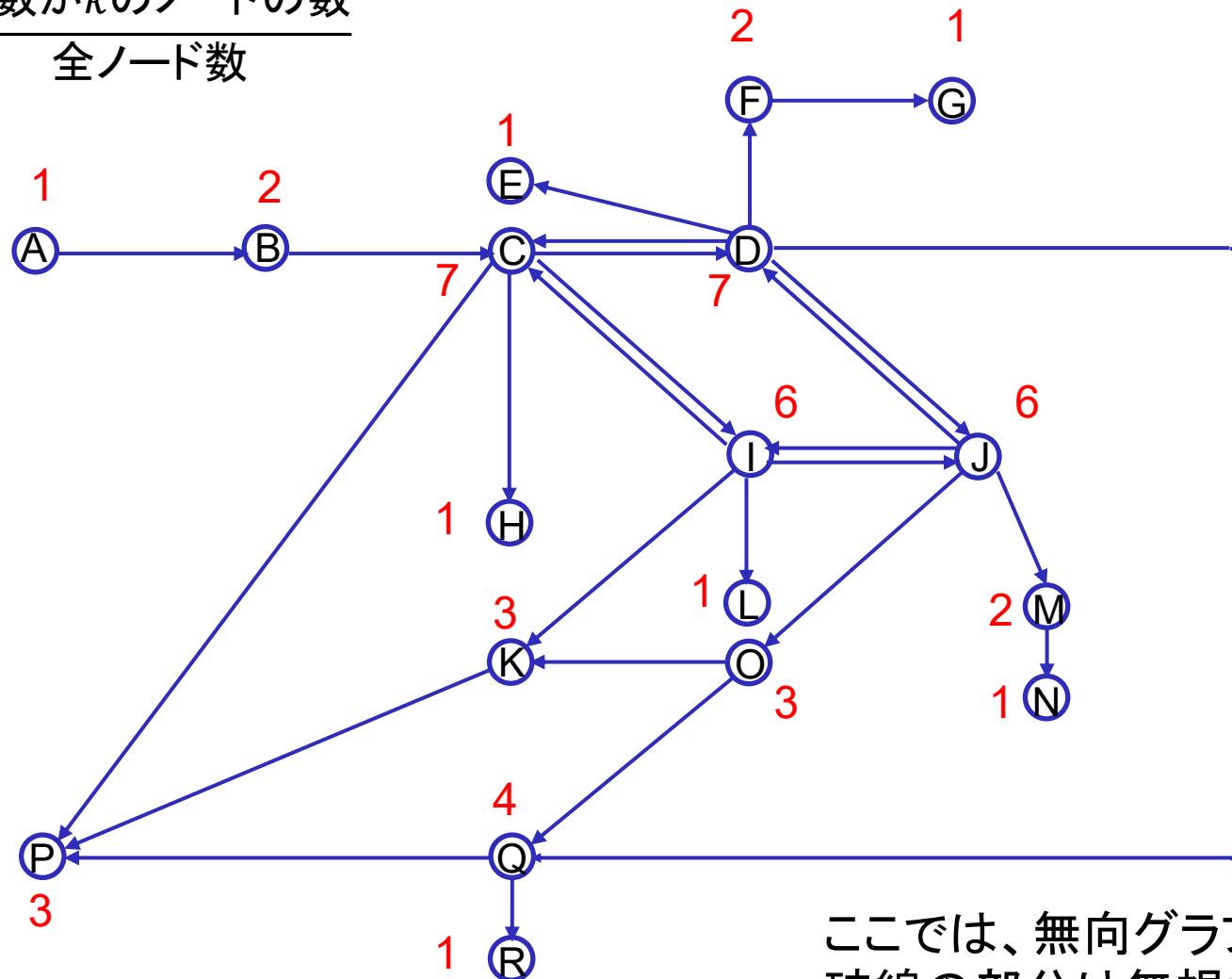
- 各辺に重み（頂点間の距離）が定義される
- 経路上の重みの和が最小になるのが最短経路
- 始点から各頂点への最短経路を、始点に近いところから1つずつ確定していく



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)

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

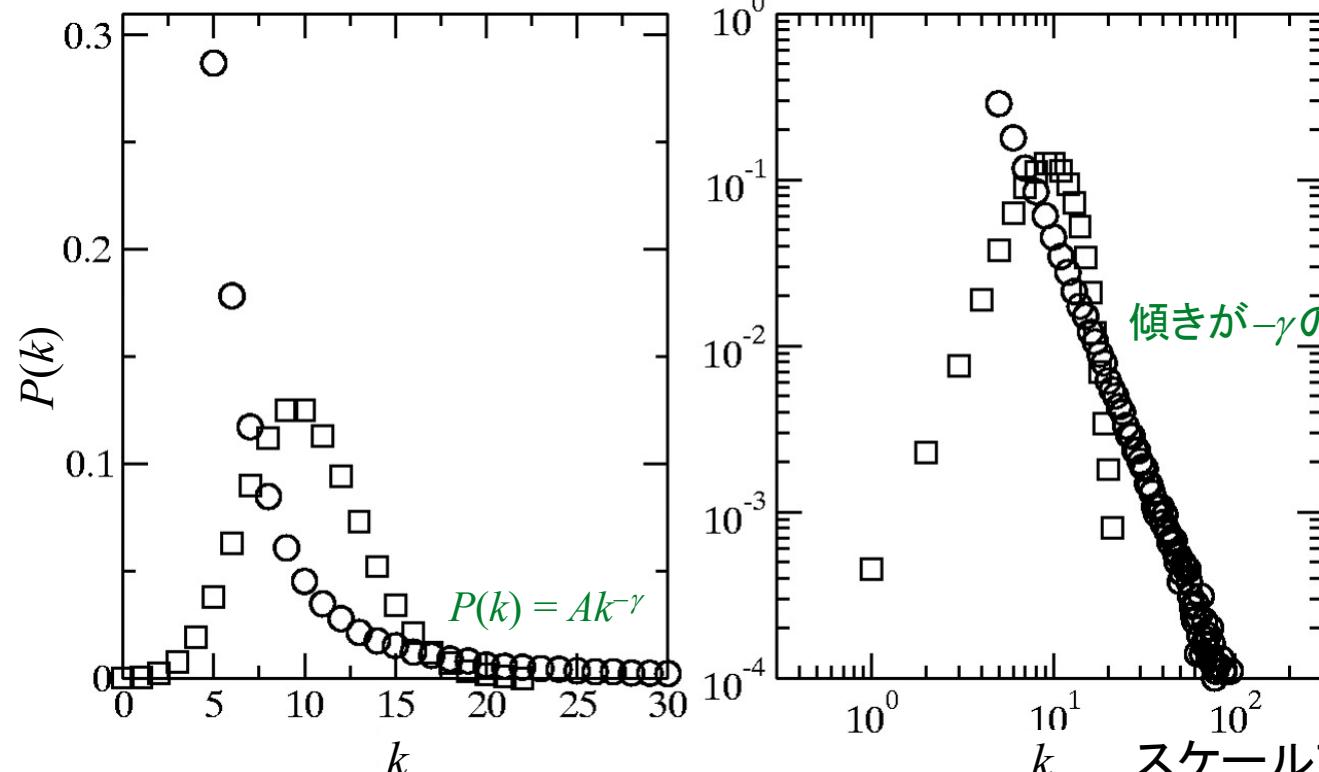


$$\begin{aligned}P(1) &= 7/18 \\P(2) &= 3/18 \\P(3) &= 3/18 \\P(4) &= 1/18 \\P(5) &= 0/18 \\P(6) &= 2/18 \\P(7) &= 2/18\end{aligned}$$

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: $P(k) \propto k^{-\gamma}$

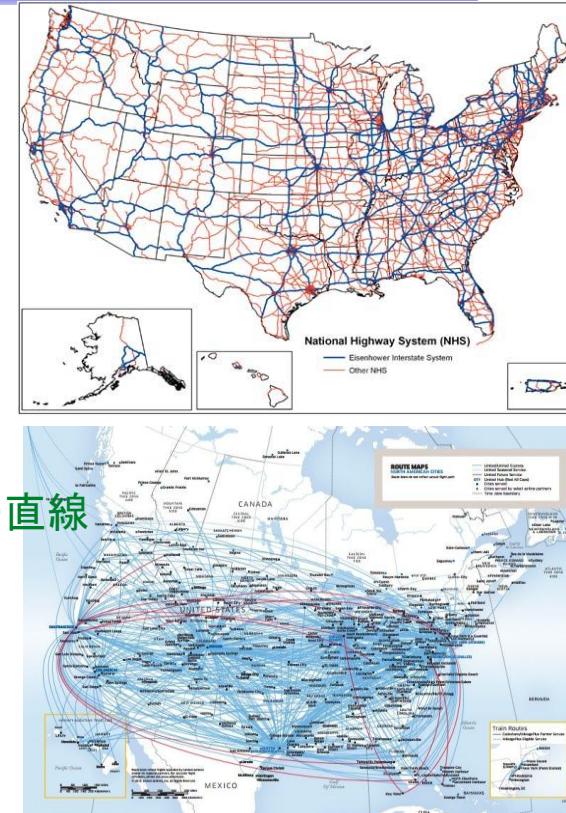


n 個の頂点だけからなるグラフで、各頂点の対に対して、ランダムに確率 p で辺を引いてできるグラフ

次数が小さい場合、次数分布はポアソン分布に従う

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

$$P(k) = \frac{\mu^k e^{-\mu}}{k!}$$



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つの辺を通過することを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

$L = \frac{2}{n(n-1)} \sum_{\text{ペア}} \text{距離}$

 - 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

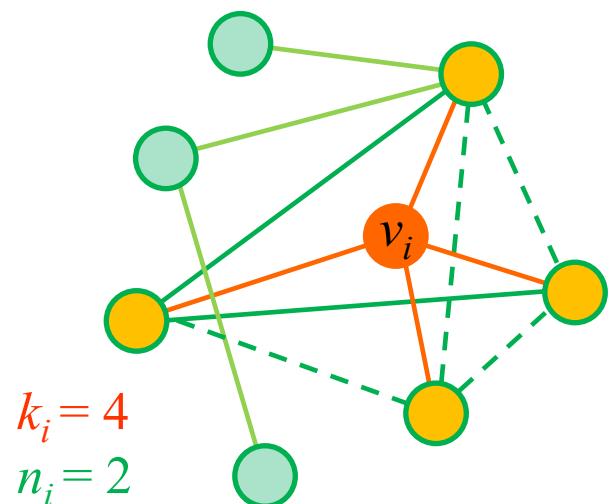
- クラスター係数
 - ある頂点に接続されている頂点のすべての組み合わせのうち、実際に辺（枝）で接続されている割合
 - 頂点 v_i の次数を k_i とするとき、その頂点 v_i に接続されている頂点のすべての組み合わせの数は
 $k_i(k_i - 1)/2$
 - 実際に辺で接続されている個数を n_i とすると、 n_i は v_i を含む三角形の数となり、クラスター係数 C_i は、

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

- 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

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

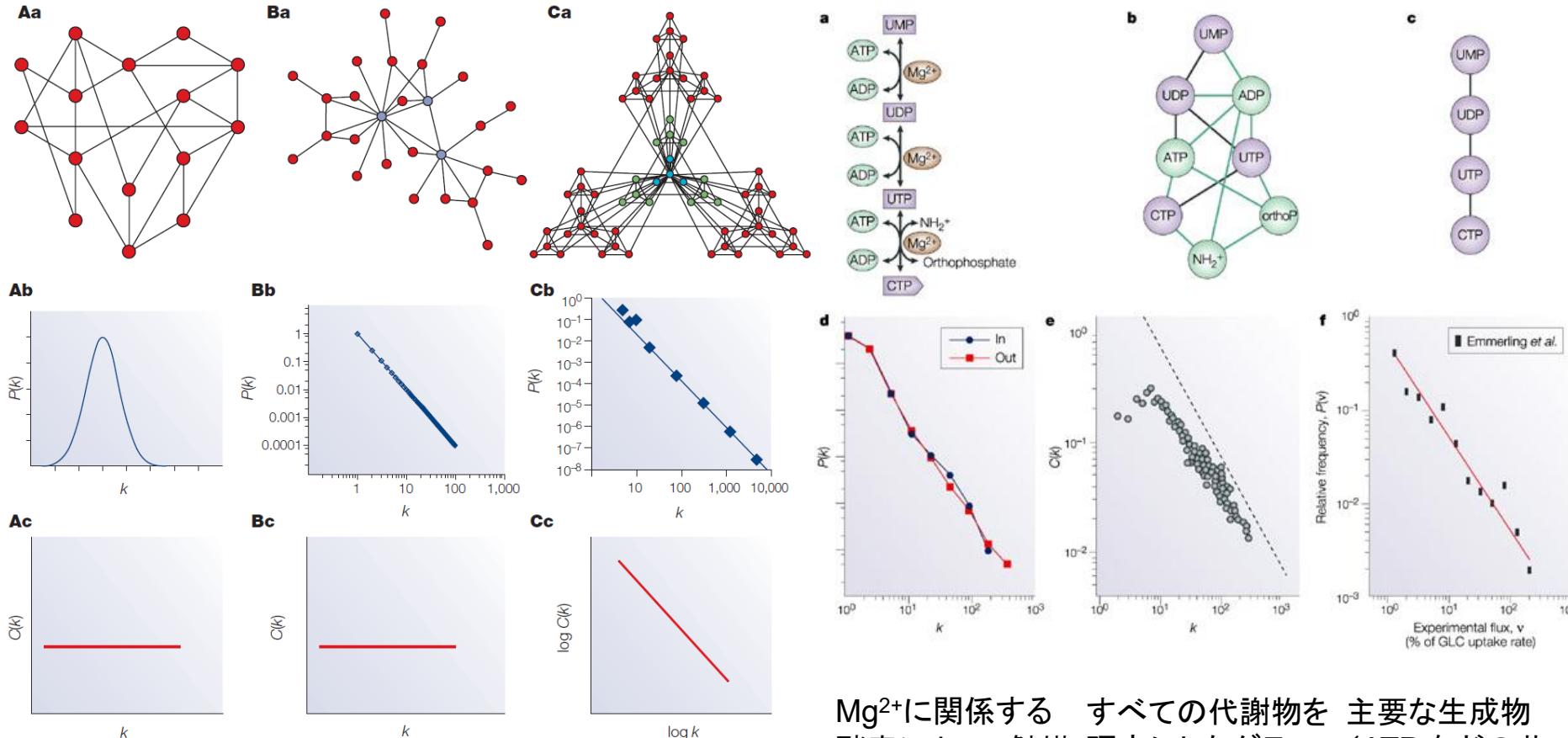
- n はネットワークの頂点の数
- すべてのノードのクラスター係数の平均



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



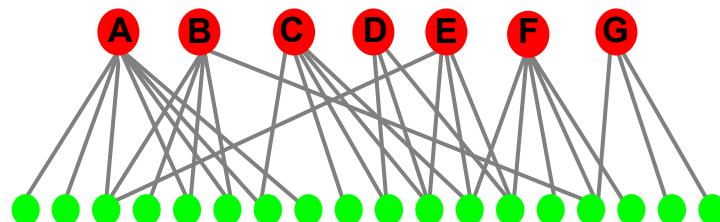
現実の代謝ネットワークでは生化学的にまとめた機能的モジュールが存在
実際の代謝ネットワークの形状はCの階層的ネットワークに近い

Mg²⁺に関するすべての代謝物を主要な生成物（ATPなどの共通因子を無視）を頂点にしたグラフ
酵素によって触媒される反応
通常のグラフ表現

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

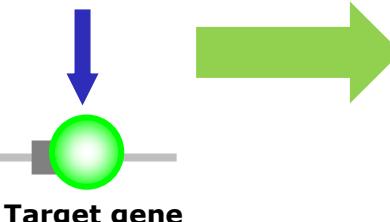
酵母の転写制御ネットワーク

Transcriptional regulatory network

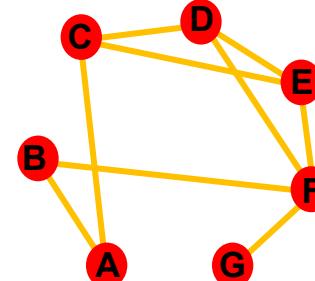


酵母の転写制御因子とそれらのターゲットの遺伝子の関係からなるネットワーク

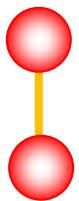
Transcription factor



Co-regulation network

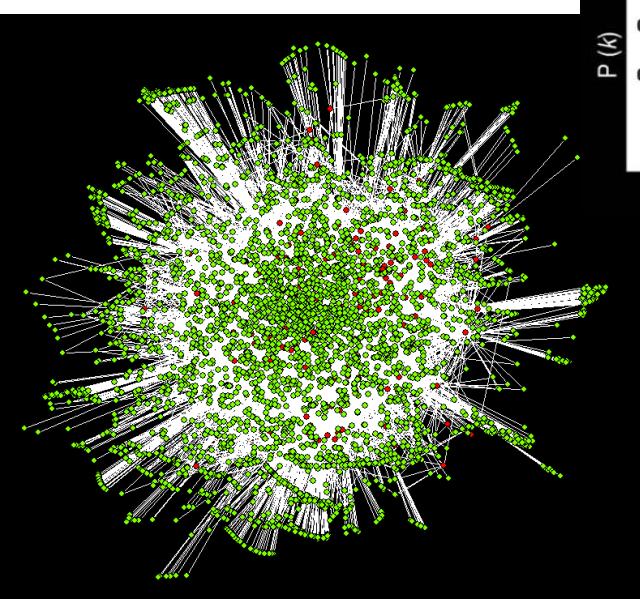
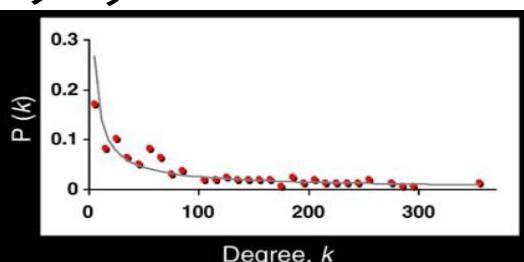


Transcription factor

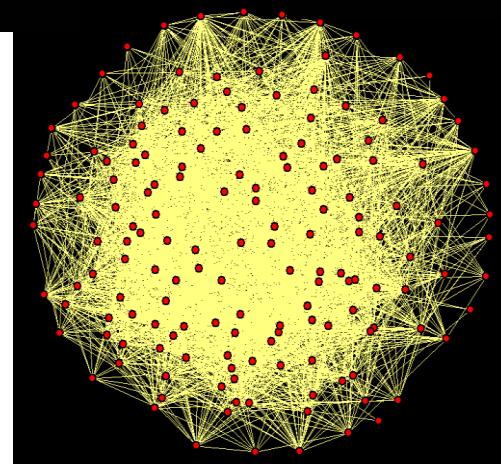


Transcription factor

共発現の関係を示すネットワーク



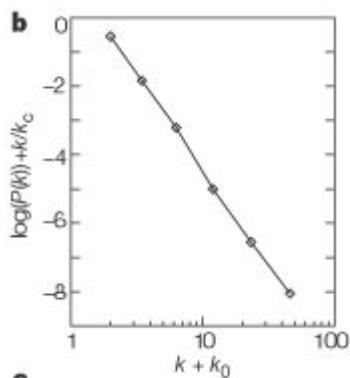
- Transcription factors (157)
 - Target genes (4410)
 - Regulatory interactions (12,873)
- On average 82 targets



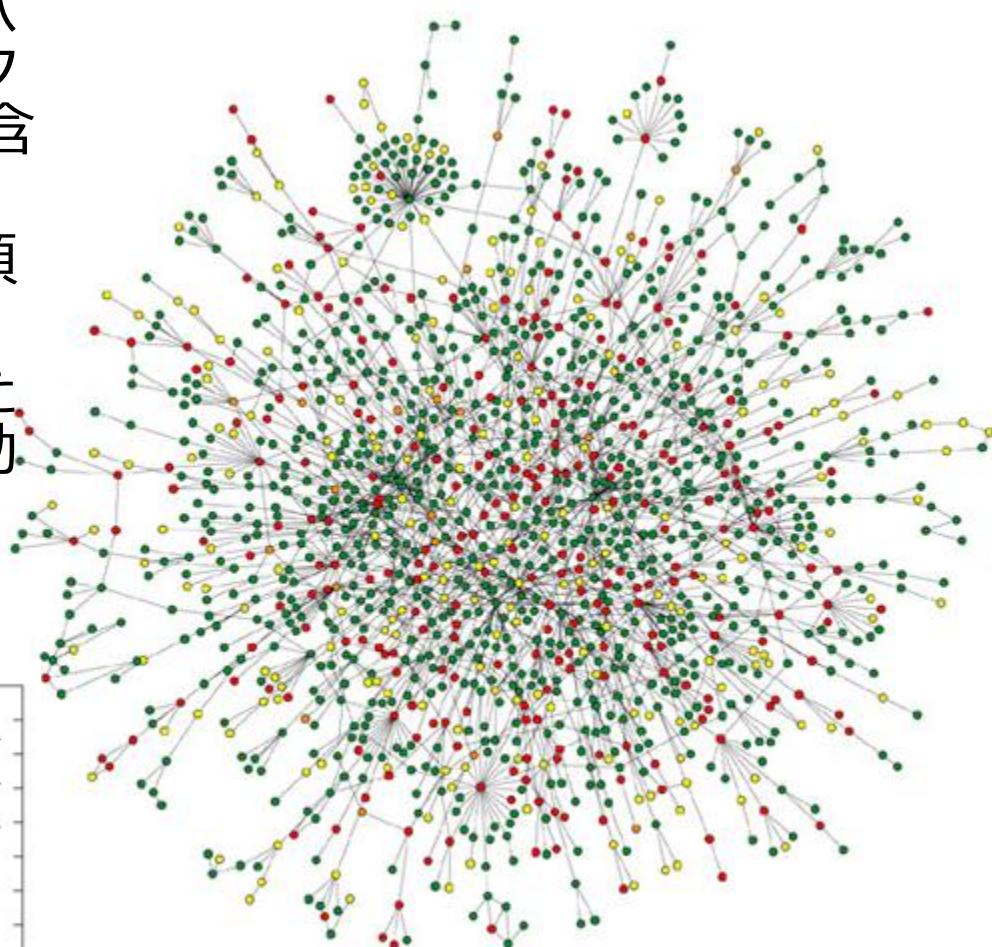
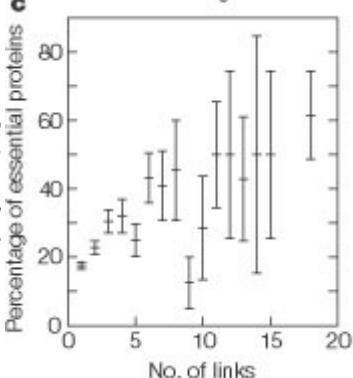
- Transcription factors (157)
 - Co-regulatory association (3,459)
- On average 44 co-regulatory partners

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



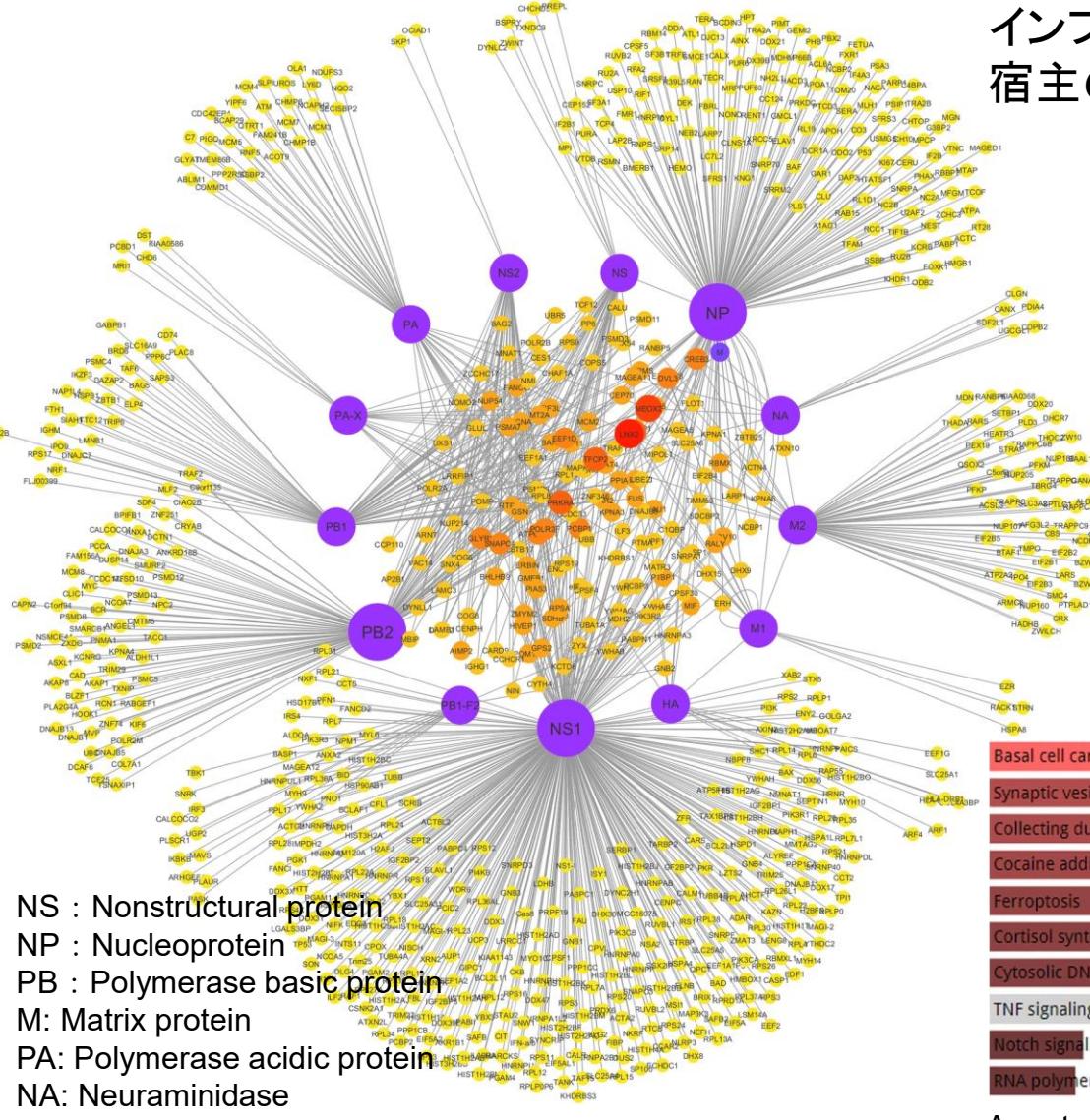
削除すると致死のタンパク質の割合



Nature Reviews | Genetics

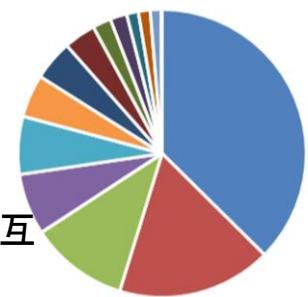
H. Jeong, et al. Lethality and centrality in protein networks, Nature, 411, 41-2 (2001).

タンパク質間相互作用ネットワークの例

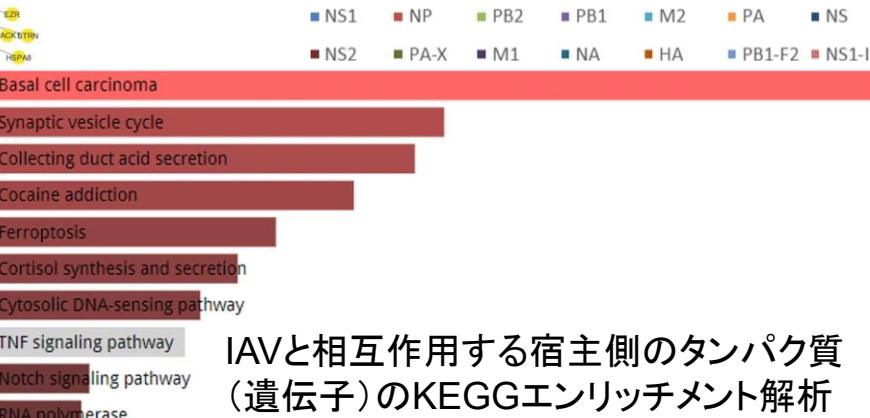


インフルエンザAウイルス(IAV)と宿主のヒトのタンパク質間相互作用

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



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).