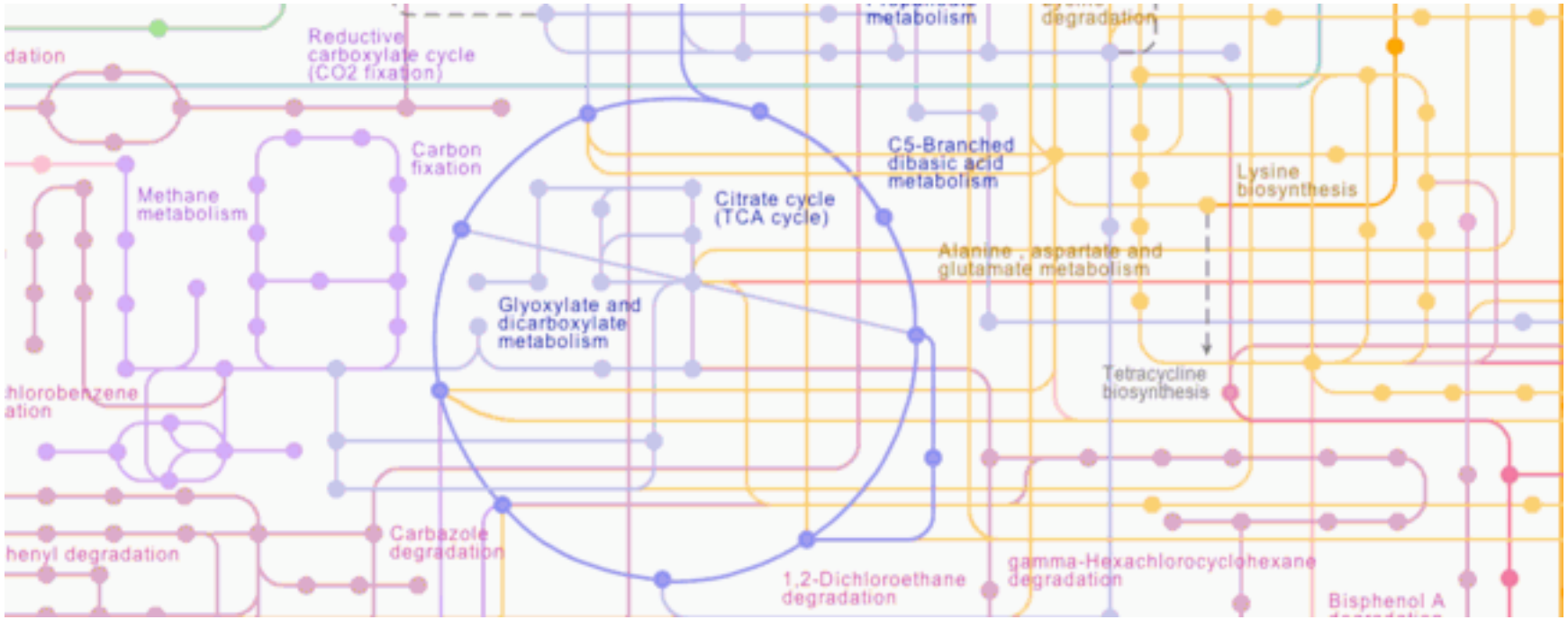


Metabolic network analysis

Masaaki Kotera,

Bioknowledge Systems Laboratory,

Bioinformatics Centre, Institute for Chemical Research,
Kyoto University.

Network

Taken from http://www.bloomsburyhotels.com/images/city/tubemap.gif

Basic knowledge of …

- Network algorithm
  - Depth-first search, Width-first search
  - Connected subgraph
  - Shortest path, Priority-first search
  - Network-flow
- Metabolic network
  - Michaelis-Menten kinetics
  - Differential equation

Wild card search by Google

http://www.google.com/

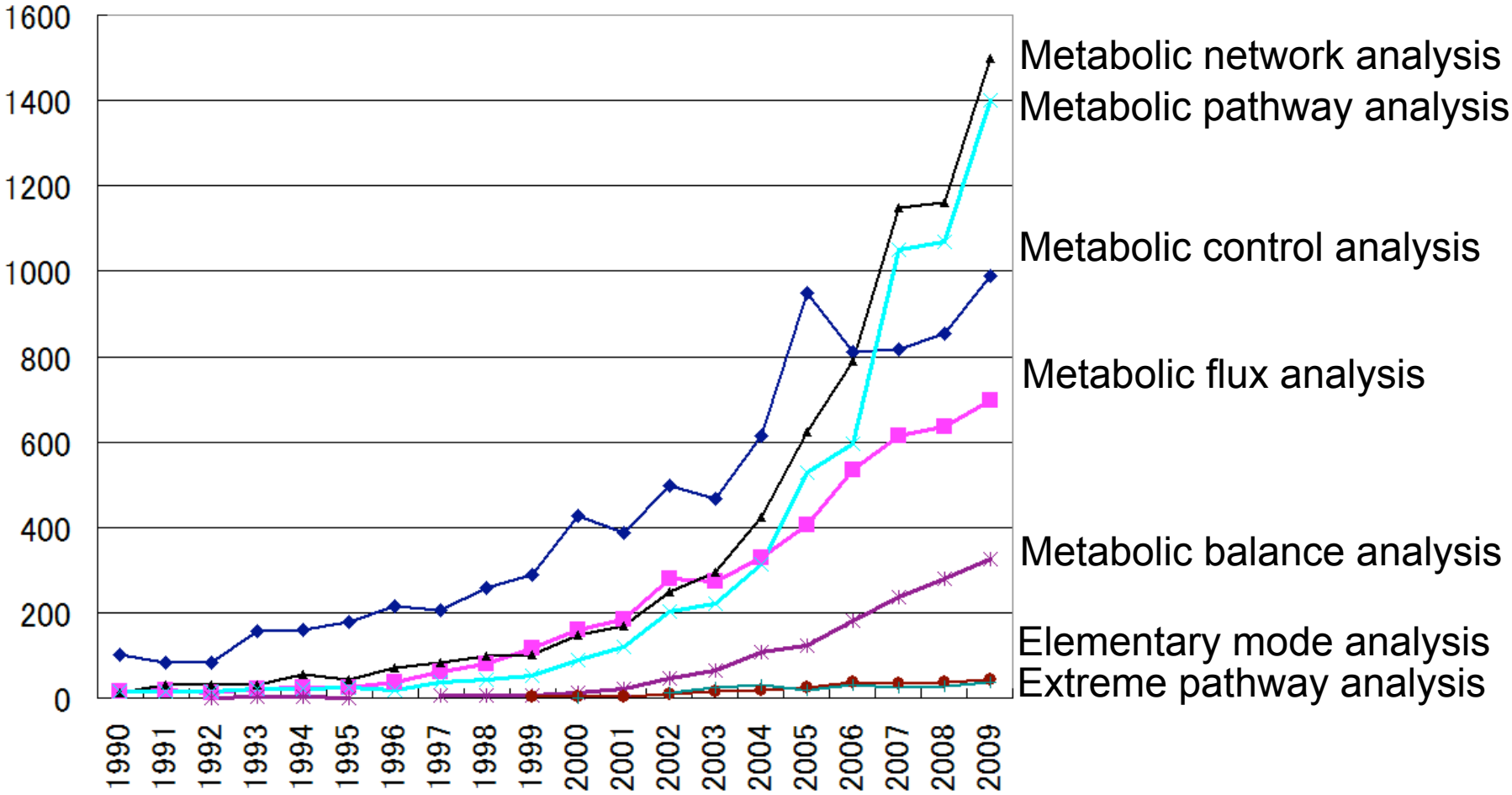
- “Metabolic *”
  - "metabolic pathway” … 500,000 hits
  - "metabolic network“ … 92,100 hits
  - "metabolic map” … 34,800 hits
- “Metabolic * analysis”
  - “metabolic pathway analysis” … 116,000 hits
  - “metabolic network analysis” … 43,500 hits
  - "metabolic map analysis“ … 1 hit
- “Metabolic * reconstruction
  - "metabolic network reconstruction” … 56,800 hits
  - "metabolic pathway reconstruction” … 15,600 hits
  - "metabolic map reconstruction“ … 82 hits

Wild card search by Google scholar beta

http://scholar.google.com/

- “Metabolic *”
  - "metabolic pathway” … 160,000 hits
  - "metabolic network“ … 12,600 hits
  - "metabolic map” … 1,840 hits
- “Metabolic * analysis”
  - “metabolic pathway analysis” … 1,200 hits
  - “metabolic network analysis” … 984 hits
  - "metabolic map analysis“ … 0 hit
- “Metabolic * reconstruction
  - "metabolic network reconstruction” … 384 hits
  - "metabolic pathway reconstruction” … 161 hits
  - "metabolic map reconstruction“ … 7 hits

Words in fashion



1995-1997

A metabolic network stoichiometry analysis of microbial growth and product formation
WM Van Gulik, JJ Heijnen - Biotechnology and ..., 1995 - interscience.wiley.com
... Other work on **metabolic network analysis** using linear op- timization techniques has been performed on hybridoma cell Esehenchiu coli metabolism,3' .32 and acetate overflow in E. c01i.""~ Following the approach to solve underdetermined metabolic networks by conducting ...
引用元 131 - 関連記事 - 全 6 バージョン

The complete genome sequence of the gastric pathogen Helicobacter pylori
JF Tomb, O White, AR Kerlavage, RA Clayton, GG ... - Nature, 1997 - nature.com
... Top of page Metabolism. **Metabolic pathway analysis** of the H. pylori genome suggests the following features. H. pylori uses glucose as the only source of carbohydrate and the main source for substrate-level phosphorylation. ...
引用元 2319 - 関連記事 - 全 14 バージョン

Metabolic correlates of pallidal neuronal activity in Parkinson's disease
D Eidelberg, JR Moeller, K Kazumata, A Antonini, D ... - Brain, 1997 - Oxford Univ Press
... Because different individuals express these relationships to greater or lesser degrees, **Metabolic network analysis** To determine whether the expression of Parkinson's disease- ... **Metabolic network analysis** In the scaled subprofile model analysis of the Group B 0.35, P 0.1). ...
引用元 91 - 関連記事 - 全 4 バージョン

An on-line physiological state recognition system for the lysine fermentation process based on a metabolic reaction model
N Takiguchi, H Shimizu, S ... - Biotechnology and ..., 1997 - interscience.wiley.com
... As an alternative approach INTRODUCTION to **metabolic pathway analysis**, metabolic control analy- sis (MCA) was developed, in which the sensitivity of Metabolic engineering, generally defined as "engi- the enzyme reaction for metabolic flux is analyzed and ...
引用元 61 - 関連記事 - 全 7 バージョン

1998-1999

Complete genome sequence of Treponema pallidum, the syphilis spirochete
CM Fraser, SJ Norris, GM Weinstock, O White, GG … - Science, 1998 - sciencemag.org
... compounds. **Metabolic pathway analysis** reveals that genes encoding all of the enzymes of the glycolytic pathway are present in T. pallidum, including hexokinase, which phosphorylates glucose and other hexose sugars (Fig. **...**
引用元 673 - 関連記事 - 全 9 バージョン

Metabolic pathway analysis: basic concepts and scientific applications in the post-genomic era
CH Schilling, S Schuster, BO Palsson, … - Biotechnology …, 1999 - interscience.wiley.com
This article reviews the relatively short history of **metabolic pathway analysis**. Computer-aided algorithms for the synthesis of metabolic pathways are discussed. Important algebraic concepts used in pathway analysis, such as null space and convex cone, are explained. It is **...**
引用元 220 - 関連記事 - 全 17 バージョン

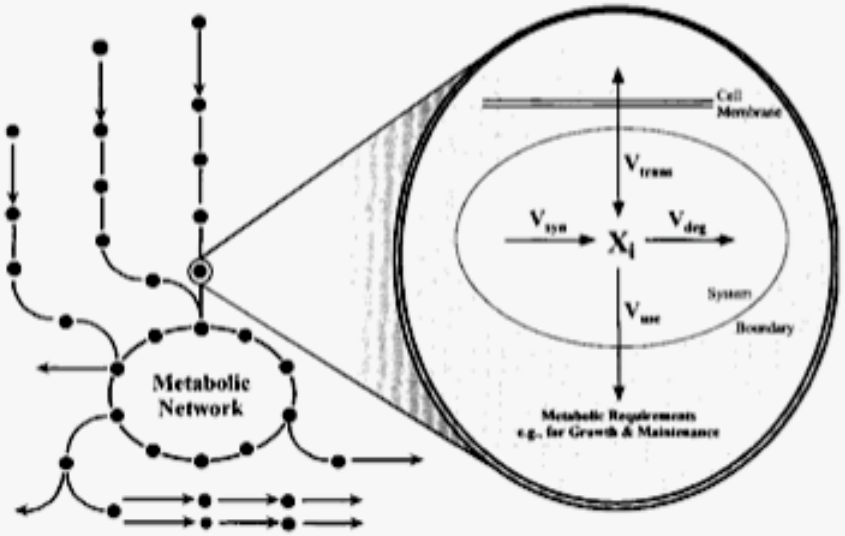
Toward metabolic phenomics: analysis of genomic data using flux balances
CH Schilling, JS Edwards, BO … - Biotechnology progress, 1999 - Wiley Online Library
... This approach of **metabolic pathway analysis** accompanied with FBA techniques can allow one to assess the basic structural capabilities and fitness of an organism as a result of the pathways that are theoretically present within the cell. **...**
引用元 116 - 関連記事 - 全 9 バージョン

Toward metabolic phenomics: analysis of genomic data using flux balances

CH Schilling, JS Edwards, BO … - Biotechnology progress, 1999 - Wiley Online Library

Fundamentals of Flux Balance Analysis

The fundamental principle underlying FBA is the conservation of mass. A flux balance can be written for each metabolite(X_i) within a metabolic system to yield the dynamic mass balance equations that interconnect the various metabolites.



Dynamic Flux Balances

$$\frac{d\mathbf{X}}{dt} = \mathbf{S} \bullet \mathbf{v} - \mathbf{b}$$

$$\mathbf{v} = fn(\mathbf{X}, \ldots)$$

X = Metabolite Concentrations
S = Stoichiometric Matrix
v = Metabolic Reaction Fluxes (V_{syn}, V_{deg})
b = Net Transport out of Network (V_{use}- V_{trans})

Steady State Analysis

$$\mathbf{S} \bullet \mathbf{v} = \mathbf{b}$$

Solve for Unknown Metabolic Fluxes **v**

A steady state assumption is made which produces the system of linear equations in the lower box, which simply states that the formation fluxes are balanced by degradation fluxes. This situation is analogous to Kirchhoff's current law used in electrical circuit analysis, where the sum of the currents coming in and out of a node must sum to zero.

Typically there are more fluxes in the system than metabolites. Thus, the system of equations is underdetermined and can therefore be formulated as a linear programming (LP) problem, in which one finds the optimal flux distribution that minimizes or maximizes a particular objective. Various objective function can be used such as those listed below:

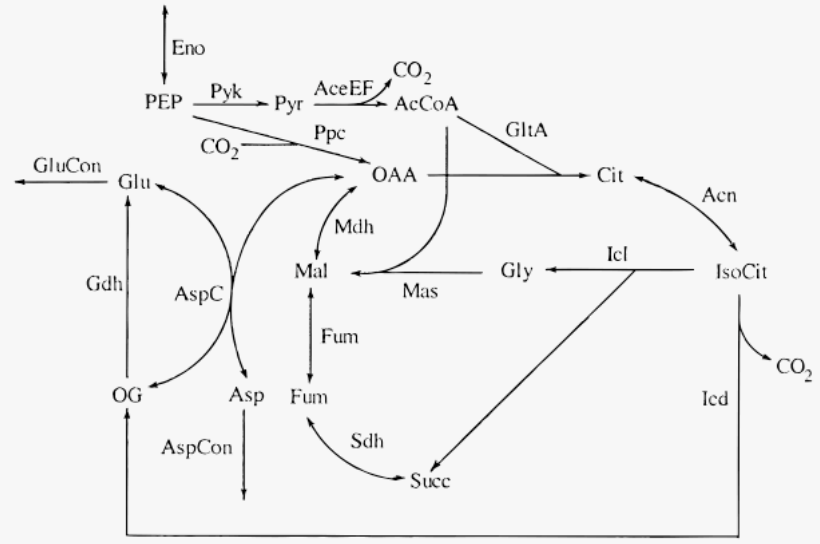
- *Minimize ATP production*
- *Minimize nutrient uptake*
- *Minimize redox production*
- *Maximize metabolite production*
- *Maximize biomass production (i.e growth)*
- *Minimize the Euclidean norm of the flux vector*

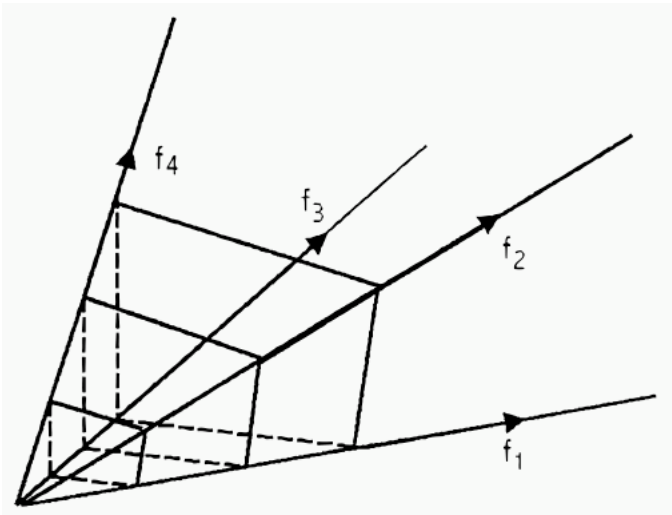
Metabolic pathway analysis: basic concepts and scientific applications in the post-genomic era

CH Schilling, S Schuster, BO Palsson, ... - Biotechnology ..., 1999 - interscience.wiley.com

This article reviews the relatively short history of **metabolic pathway analysis**. Computer-aided algorithms for the synthesis of metabolic pathways are discussed. Important algebraic concepts used in pathway analysis, such as null space and convex cone, are explained. It is **...**

引用元 220 - 関連記事 - 全 17 バージョン





2000

[HTML] The Escherichia coli MG1655 in silico metabolic genotype: its definition, characteristics, and capabilities

JS Edwards, BO Palsson - ⋯ of Sciences of the United States …, 2000 - National Acad Sciences

... These methods include approaches such as metabolic control analysis (3, 4), flux balance analysis (FBA) (5–7), **metabolic pathway analysis** (8–11, 69), cybernetic modeling (12), biochemical systems theory (13), temporal decomposition (14), and so on. **...**

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A general definition of metabolic pathways useful for systematic organization and analysis of complex metabolic networks

S Schuster, DA Fell, T Dandekar - Nature biotechnology, 2000 - nature.com

... Trends Biotechnol. 17, 53–60(1999). | Article | PubMed | ISI | ChemPort |; Schilling, CH, Schuster, S., Palsson, BO & Heinrich R. **Metabolic pathway analysis**: basic concepts and scientific applications in the post-genomic era. Biotechnol. Prog. 15, 296–303 (1999). **...**

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The small world of metabolism

DA Fell, A Wagner - Nature Biotechnology, 2000 - nature.com

... propositions. Top of page References. Schilling, CH, Schuster, S., Palsson, BO & Heinrich, R. **Metabolic pathway analysis**: basic concepts and scientific applications in the post-genomic era. Biotechnol. Prog. 15, 296–303 (1999). **...**

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[PDF] The challenges of in silico biology

B Palsson - Nature biotechnology, 2000 - complex.upf.es

... 10. McAdams, HH & Shapiro, L. Circuit simulation of genetic networks. Science 269, 651–656 (1995). 11. Schilling, CH et al. **Metabolic pathway analysis**: basic concepts and scientific applications in the post- genomic era. Biotechnol. Prog. 15, 296–303 (1999). 12. **...**

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Combining pathway analysis with flux balance analysis for the comprehensive study of metabolic systems

… JS Edwards, D Letscher, BØ Palsson - Biotechnology and …, 2000 - interscience.wiley.com

Abstract: The elucidation of organism-scale metabolic networks necessitates the development of integrative methods to analyze and interpret the systemic properties of cellular metabolism. A shift in emphasis from single metabolic reactions to systemically defined ...

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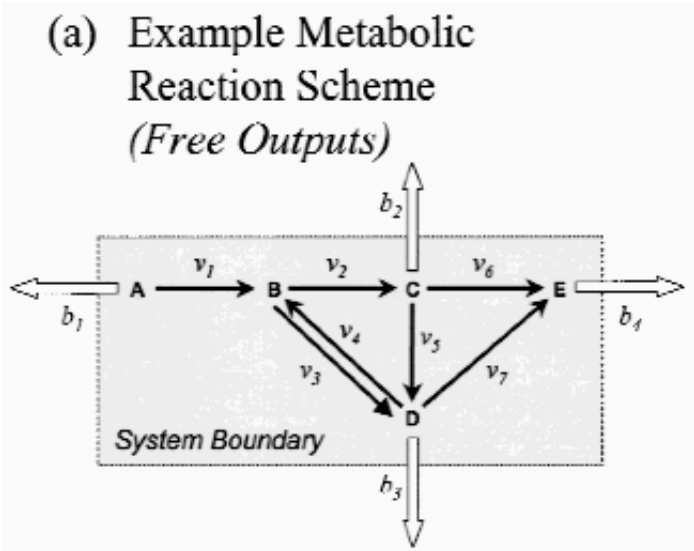


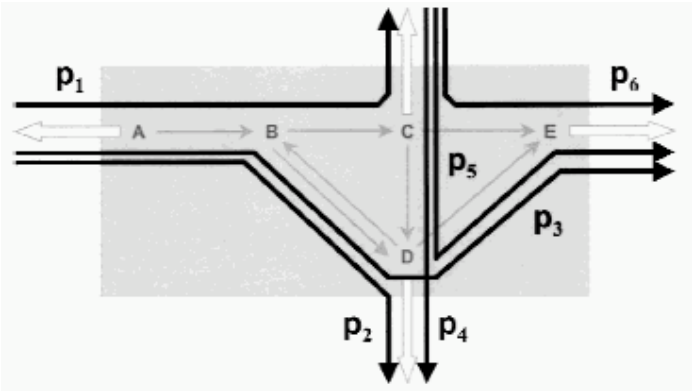


Table I. The eight extreme pathway vectors for the example network with free outputs.[a]

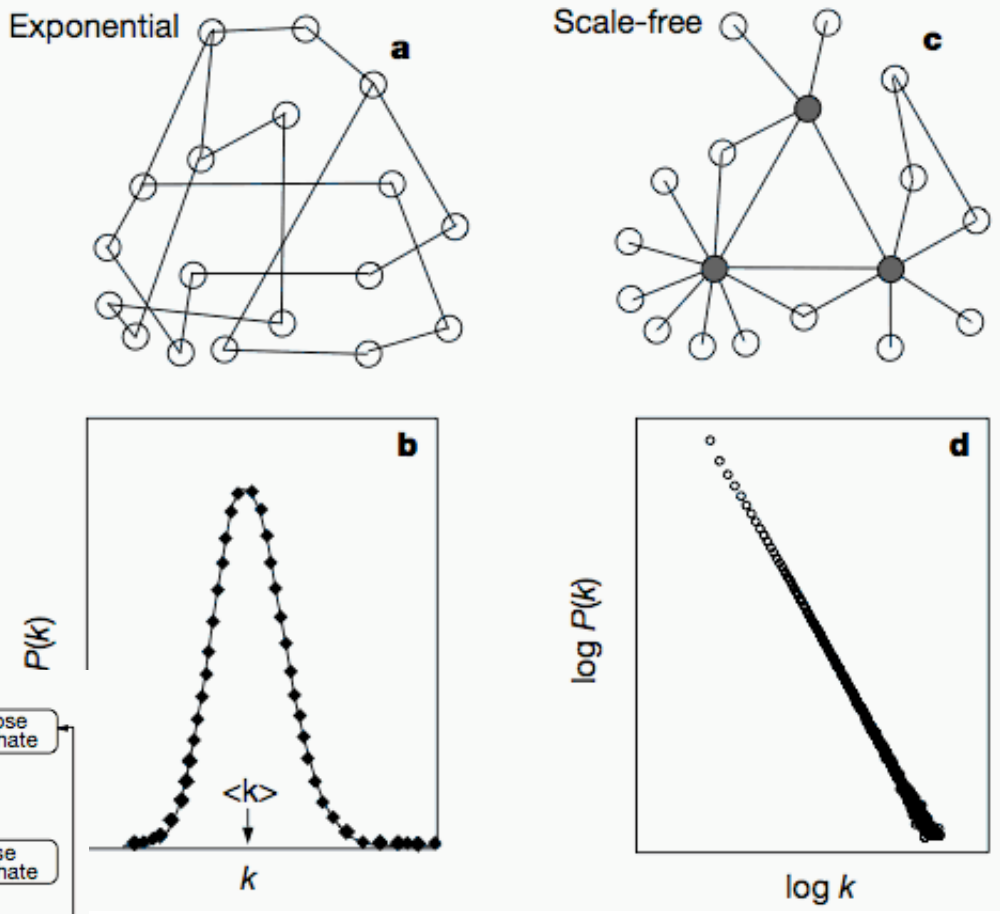
Pathway number	Internal fluxes							Exchange fluxes			
	v_1	v_2	v_3	v_4	v_5	v_6	v_7	b_1	b_2	b_3	b_4
$\mathbf{p}_1$	1	1	0	0	0	0	0	−1	1	0	0
$\mathbf{p}_2$	1	0	1	0	0	0	0	−1	0	1	0
$\mathbf{p}_3$	2	0	2	0	0	0	1	−2	0	0	1
$\mathbf{p}_4$	0	0	0	0	1	0	0	0	−1	1	0
$\mathbf{p}_5$	0	0	0	0	2	0	1	0	−2	0	1
$\mathbf{p}_6$	0	0	0	0	0	1	0	0	−1	0	1
$\mathbf{p}_7$	0	0	1	1	0	0	0	0	0	0	0
$\mathbf{p}_8$	0	1	0	1	1	0	0	0	0	0	0

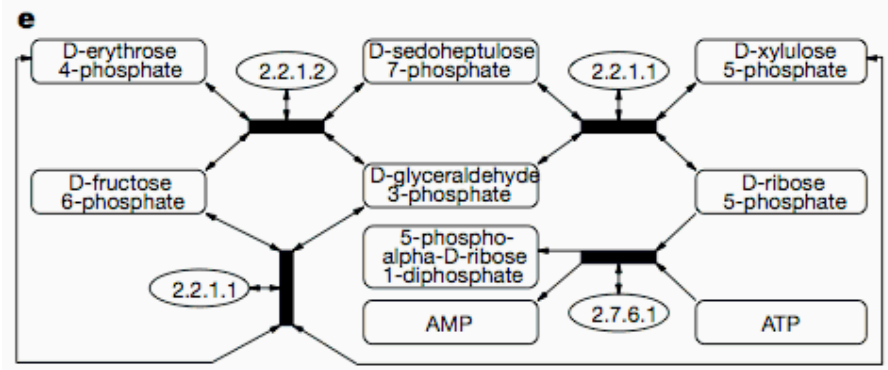
The large-scale organization of metabolic networks

H Jeong, B Tombor, R Albert, ZN Oltvai, AL Barabási - Nature, 2000 - nature.com

In a cell or microorganism, the processes that generate mass, energy, information transfer and cell-fate specification are seamlessly integrated through a complex network of cellular constituents and reactions 1 . However, despite the key role of these networks in sustaining cellular ...

引用元 2343 - 関連記事 - 全 66 バージョン





2001

[The small world inside large metabolic networks]
A Wagner, DA Fell - ⋯ of the Royal Society of London …, 2001 - rspb.royalsocietypublishing.org
Page 1. doi: 10.1098/rspb.2001.1711 , 1803-1810 268 2001 Proc. R. Soc. Lond. B Andreas Wagner and David A. Fell The small world inside large metabolic networks References http://rspb.royalsocietypublishing.org/content/268/1478/1803#related-urls Article cited in: ...
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[In silico predictions of Escherichia coli metabolic capabilities are consistent with experimental data]
JS Edwards, RU Ibarra, BO Palsson - Nature biotechnology, 2001 - nature.com
... J. Theor. Biol. 203, 249–83 (2000). | Article | PubMed | ISI | ChemPort |; Schilling, CH, Schuster, S., Palsson, BO & Heinrich, R. **Metabolic pathway analysis**: basic concepts and scientific applications in the post-genomic era. Biotechnol. Prog. 15, 296–303 (1999). ...
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[13C metabolic flux analysis]
W Wiechert - Metabolic Engineering, 2001 - Elsevier
... 6. B. Christensen and J. Nielsen, **Metabolic network analysis**, a powerful tool in metabolic engineering. Adv. Biochem. Eng. ... 209–231. 7. B. Christensen and J. Nielsen, **Metabolic network analysis** of Penicillium chrysogenum using 13 C-labeled glucose. Biotechnol. Bioeng. ...
引用元 267 - 関連記事 - 全 6 バージョン

[Combining genomics, metabolome analysis, and biochemical modelling to understand metabolic networks]
O Fiehn - Comparative and Functional Genomics, 2001 - Wiley Online Library
... Metabolomics. The obvious next step in **metabolic network analysis** is to try to determine metabolic snapshots in a broad and comprehensive way. ... 13 Christensen B, Nielsen J. **Metabolic network analysis**: a powerful tool in metabolic engineering. ...
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2002

[PDF] Co-clustering of biological networks and gene expression data
D Hanisch, A Zien, R Zimmer, T Lengauer - Bioinformatics, 2002 - Oxford Univ Press
Page 1. BIOINFORMATICS Vol. 18 Suppl. 1 2002 Pages S145–S154 Co-clustering of biological networks and gene expression data Daniel Hanisch 1 , Alexander Zien 1 , Ralf Zimmer 2 and Thomas Lengauer 3 1 Institute for ...
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Exploring the pathway structure of metabolism: decomposition into subnetworks and application to Mycoplasma pneumoniae
S Schuster, T Pfeiffer, F Moldenhauer, I Koch, T ... - ⋯, 2002 - Oxford Univ Press
Page 1. BIOINFORMATICS Vol. 18 no. 2 2002 Pages 351–361 Exploring the pathway structure of metabolism: decomposition into subnetworks and application to Mycoplasma pneumoniae S. Schuster 1 , T. Pfeiffer 2 , F. Moldenhauer 1 , I. Koch 3 and T. Dandekar 4, 5 ...
引用元 130 - 関連記事 - 全 11 バージョン

Dynamic flux balance analysis of diauxic growth in Escherichia coli
R Mahadevan, JS Edwards, FJ Doyle III - Biophysical Journal, 2002 - Elsevier
... shown in Fig. 1. From a **metabolic pathway analysis** with glucose, acetate, and oxygen as the input and biomass and acetate as the output, a set of 300 extreme pathways were identified (Schilling et al., 2000a). The biomass ...
引用元 128 - 関連記事 - 全 15 バージョン

The genome-scale metabolic extreme pathway structure in Haemophilus influenzae shows significant network redundancy
JA Papin, ND Price, JS Edwards, BØ ... - Journal of theoretical ..., 2002 - Elsevier
... 229–248. Abstract | PDF (428 K) | View Record in Scopus | Cited By in Scopus (198). 19. CH SCHILLING, S. SCHUSTER, BO PALSSON and R. HEINRICH, **Metabolic pathway analysis**: basic concepts and scientific applications in the post-genomic era. Biotechnol. Prog. ...
引用元 80 - 関連記事 - 全 7 バージョン

2003

Reconstruction of metabolic networks from genome data and analysis of their global structure for various organisms
H Ma, AP Zeng - Bioinformatics, 2003 - Oxford Univ Press
... It is one of the main tasks of **metabolic network analysis** to find possible conversion pathways between two metabolites. There may be many different pathways between two metabolites, among them the shortest pathway is of particular interest for network analysis. ...
引用元 251 - 関連記事 - 全 22 バージョン

Metabolic pathways in the post-genome era
JA Papin, ND Price, SJ Wiback, DA Fell, BO ... - Trends in Biochemical ..., 2003 - Elsevier
... All possible flux distributions of a metabolic network lie within the 'cone' circumscribed by the pathways. View Within Article. 1. History of network-based metabolic pathway analyses. Network-based **metabolic pathway analysis** has a relatively short history. ...
引用元 211 - 関連記事 - 全 23 バージョン

Metabolic flux profiling of Escherichia coli mutants in central carbon metabolism using GC-MS
E Fischer, U Sauer - European Journal of Biochemistry, 2003 - Wiley Online Library
... U- 13 C]glucose experiments. This methodology is used for **metabolic network analysis** in Escherichia coli strains with knockout mutations in all major pathways of central carbon metabolism. The analyses presented here provide ...
引用元 188 - 関連記事 - 全 9 バージョン

Two approaches for **metabolic pathway analysis**?
S Klamt, J Stelling - TRENDS in Biotechnology, 2003 - Elsevier
Metabolic pathway analysis is becoming increasingly important for assessing inherent network properties in (reconstructed) biochemical reaction networks. Of the two most promising concepts for pathway analysis, one relies on elementary flux modes and the other on extreme ...
引用元 120 - 関連記事 - 全 11 バージョン

2004

Comparison of network-based pathway analysis methods
JA Papin, J Stelling, ND Price, S Klamt, S ... - TRENDS in ..., 2004 - Elsevier
... Recent network-based **metabolic pathway analysis** has focused on two approaches, those of elementary modes [4] and extreme pathways [5]. Both of these methods use convex analysis [6], a branch of mathematics that enables the analysis of inequalities and systems of linear ...
引用元 181 - 関連記事 - 全 8 バージョン

The challenges of modeling mammalian biocomplexity
JK Nicholson, E Holmes, JC Lindon, ID Wilson - Nature Biotechnology, 2004 - nature.com
... For simple systems, the way in which intracellular biochemistry can be modeled is now becoming mature, especially for single-celled organisms such as Saccharomyces cerevisiae, and a clear approach that combines conventional **metabolic pathway analysis** at the metabolite ...
引用元 175 - 関連記事 - 全 9 バージョン

Metabolic network analysis of the causes and evolution of enzyme dispensability in yeast
B Papp, C Pál, LD Hurst - Nature, 2004 - nature.com
Under laboratory conditions 80% of yeast genes seem not to be essential for viability 1 . This raises the question of what the mechanistic basis for dispensability is, and whether it is the result of selection for buffering or an incidental side product. Here we analyse these issues ...
引用元 172 - 関連記事 - 全 9 バージョン

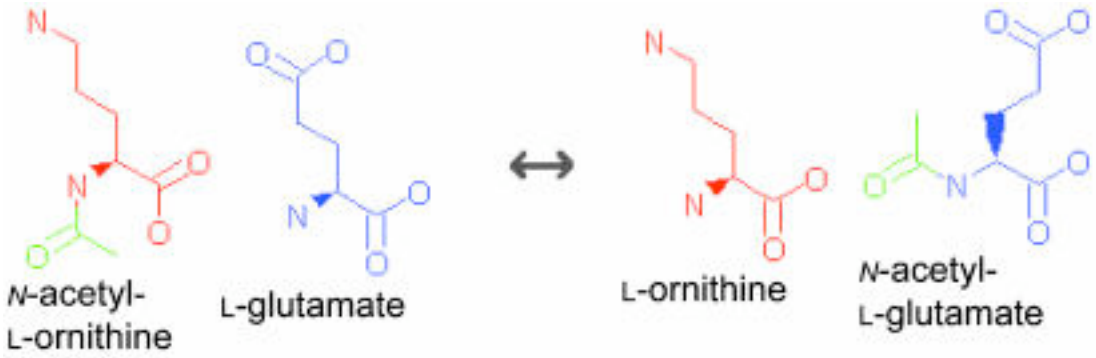
High-throughput phenomics: experimental methods for mapping fluxomes
U Sauer - Current opinion in Biotechnology, 2004 - Elsevier
... From its early days when material fluxes were balanced within assumed reaction networks [7.], **metabolic network analysis** [6. and 8.] has matured to actually identify the topology of active reactions and pathways and to quantify the molecular flux through them on a variety of ...
引用元 158 - 関連記事 - 全 8 バージョン

The metabolic world of Escherichia coli is not small

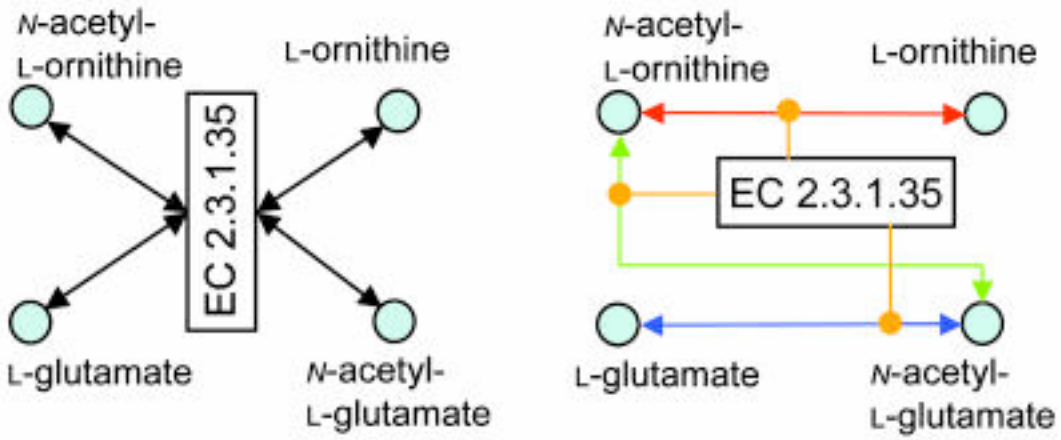
M Arita - Proceedings of the National Academy of …, 2004 - National Acad Sciences

To elucidate the organizational and evolutionary principles of the metabolism of living organisms, recent studies have addressed the graph-theoretic analysis of large biochemical networks responsible for the synthesis and degradation of cellular building blocks [Jeong, ...

引用元 188 - 関連記事 - 全 20 バージョン



EC 2.3.1.35 *N*-acetyl- L-ornithine:L-glutamate *N*-acetyltransferase



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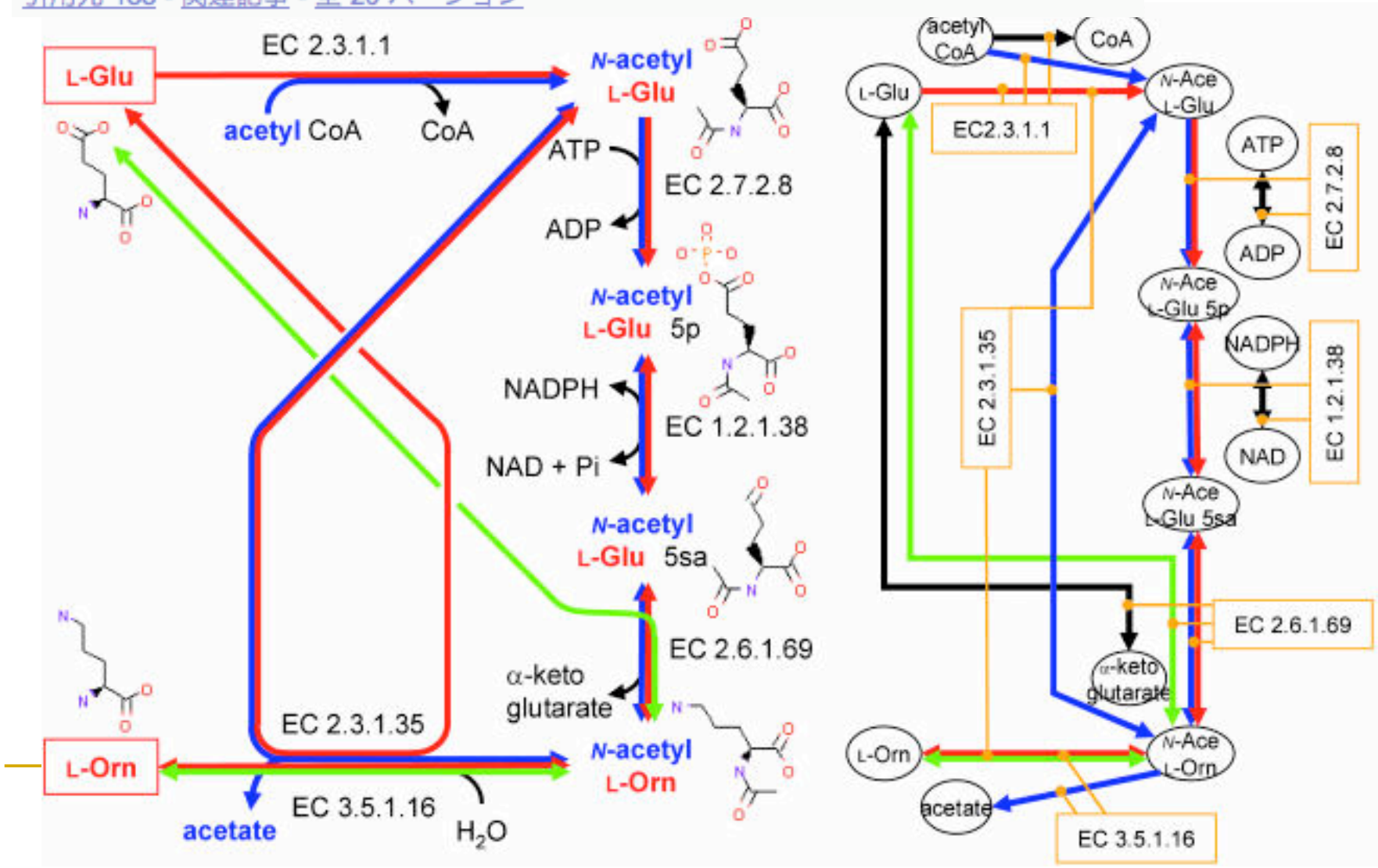
引用元 188 - 関連記事 - 全 20 バージョン



2005

The efficiency of multi-target drugs: the network approach might help drug design
P Csermely, V Agoston, S Pongor - Trends in pharmacological sciences, 2005 - Elsevier
... 6111–6121. Full Text via CrossRef | View Record in Scopus | Cited By in Scopus (53). 8 B. Papp et al., **Metabolic network analysis** of the causes and evolution of enzyme dispensability in yeast, Nature 429 (2004), pp. 661–664. Full Text via CrossRef | View Record in Scopus |.
引用元 138 - 関連記事 - 全 9 バージョン

Adaptive evolution of bacterial metabolic networks by horizontal gene transfer
C Pál, B Papp, MJ Lercher - Nature Genetics, 2005 - nature.com
... were present. Gene families with more than one member in E. coli K-12 were excluded from the analysis. **Metabolic network analysis**. We examined the reconstructed metabolic network (iJR904 GSM/GPR) of E. coli K-12. We ...
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[HTML] Genome-scale reconstruction of the metabolic network in Staphylococcus aureus N 315: an initial draft to the two-dimensional annotation
SA Becker, BØ Palsson - BMC microbiology, 2005 - biomedcentral.com
... J Biol Chem 2004, 279:39532-39540. PubMed Abstract | Publisher Full Text OpenURL. Papp B, Pal C, Hurst LD: **Metabolic network analysis** of the causes and evolution of enzyme dispensability in yeast. Nature 2004, 429:661-664. ...
引用元 112 - 関連記事 - キャッシュ - 全 11 バージョン

[HTML] Large-scale 13C-flux analysis reveals mechanistic principles of metabolic network robustness to null mutations in yeast
LM Blank, L Kuepfer, U Sauer - Genome Biology, 2005 - biomedcentral.com
genomebiology.com/article. Bottom,Top. ...
引用元 108 - 関連記事 - キャッシュ - 全 14 バージョン

2006

Towards multidimensional genome annotation
JL Reed, I Famili, I Thiele, BO Palsson - Nature Reviews Genetics, 2006 - nature.com
... production of lactic acid. Biotechnol. Bioeng. 91, 743–748 (2005). Article. Carlson, R., Fell, D. & Srienc, F. **Metabolic pathway analysis** of a recombinant yeast for rational strain development. Biotechnol. Bioeng. 79, 121–134 (2002). ...
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Metabolic networks in motion: 13C-based flux analysis
U Sauer - Molecular systems biology, 2006 - nature.com
... Curr Opin Biotechnol 16: 350–355 | Article | PubMed | ISI | ChemPort |; Borodina I, Schöller C, Eliasson A, Nielsen J (2005) **Metabolic network analysis** of Streptomyces tenebrarius, a Streptomyces species with an active Entner–Doudoroff pathway. ...
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The effect of oxygen on biochemical networks and the evolution of complex life
J Raymond, D Segre - Science, 2006 - sciencemag.org
... is a collection of data from across known genomes, these metabol- ic networks correspond not to the reactions tenable within any one organism but to the meta- bolic potential of the collective (and currently characterized) biosphere that can be thought of as a **meta-metabolome**. ...
引用元 113 - 関連記事 - 全 12 バージョン

Integrated analysis of regulatory and metabolic networks reveals novel regulatory mechanisms in Saccharomyces cerevisiae
MJ Herrgård, BS Lee, V Portnoy, BØ ... - Genome research, 2006 - genome.cshlp.org
... biomass composition). The integration of the **metabolic network analysis** and the transcriptional regulatory network model described above is accomplished using the regulated flux balance analysis approach (Covert et al. 2001). In ...
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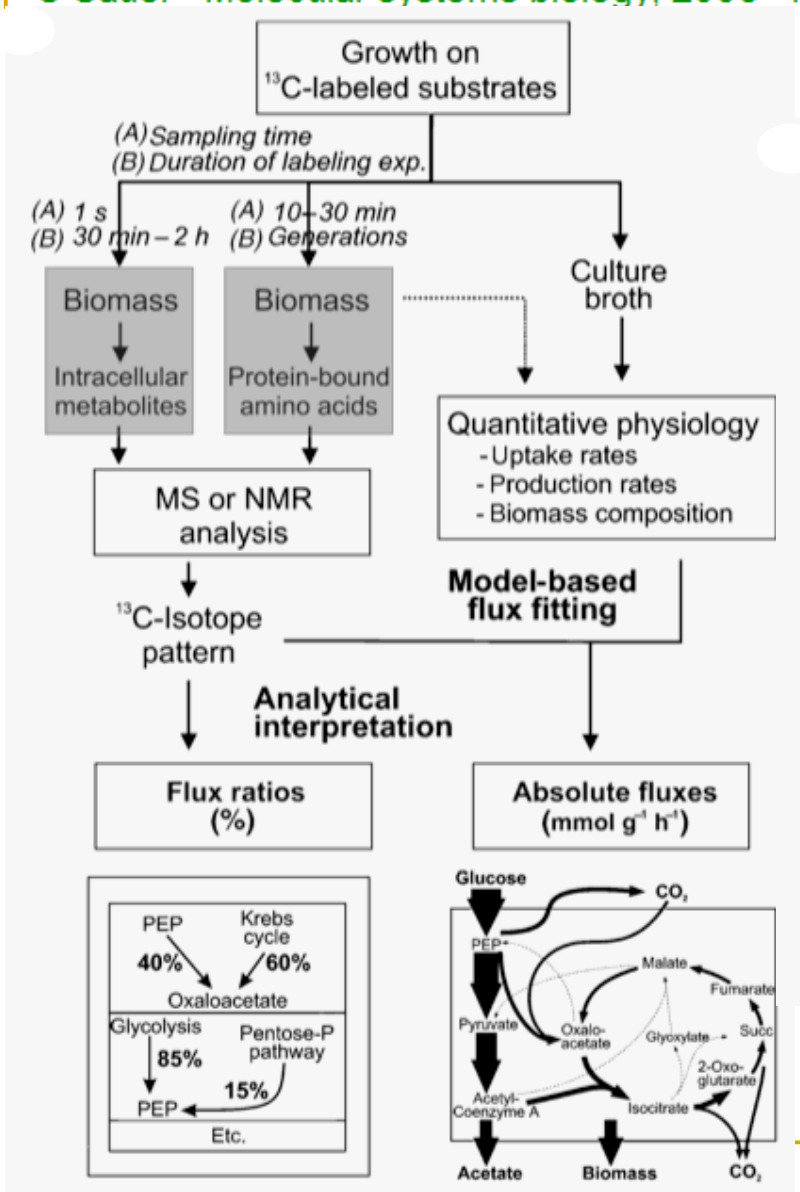
Metabolic networks in motion: 13C-based flux analysis

U Sauer - Molecular systems biology, 2006 - nature.com

Schöller

rarius,



- Linear
- Convergent
- Few connections
- Typically one or few paths are simultaneously active
- One-way flux
- Organism specific

Nutrient transport/catabolism

Common intermediates

Central (core) metabolism

Precursors cofactors

- Many cycles
- Many connections
- Redundant
- Flux direction variable
- Ubiquitous

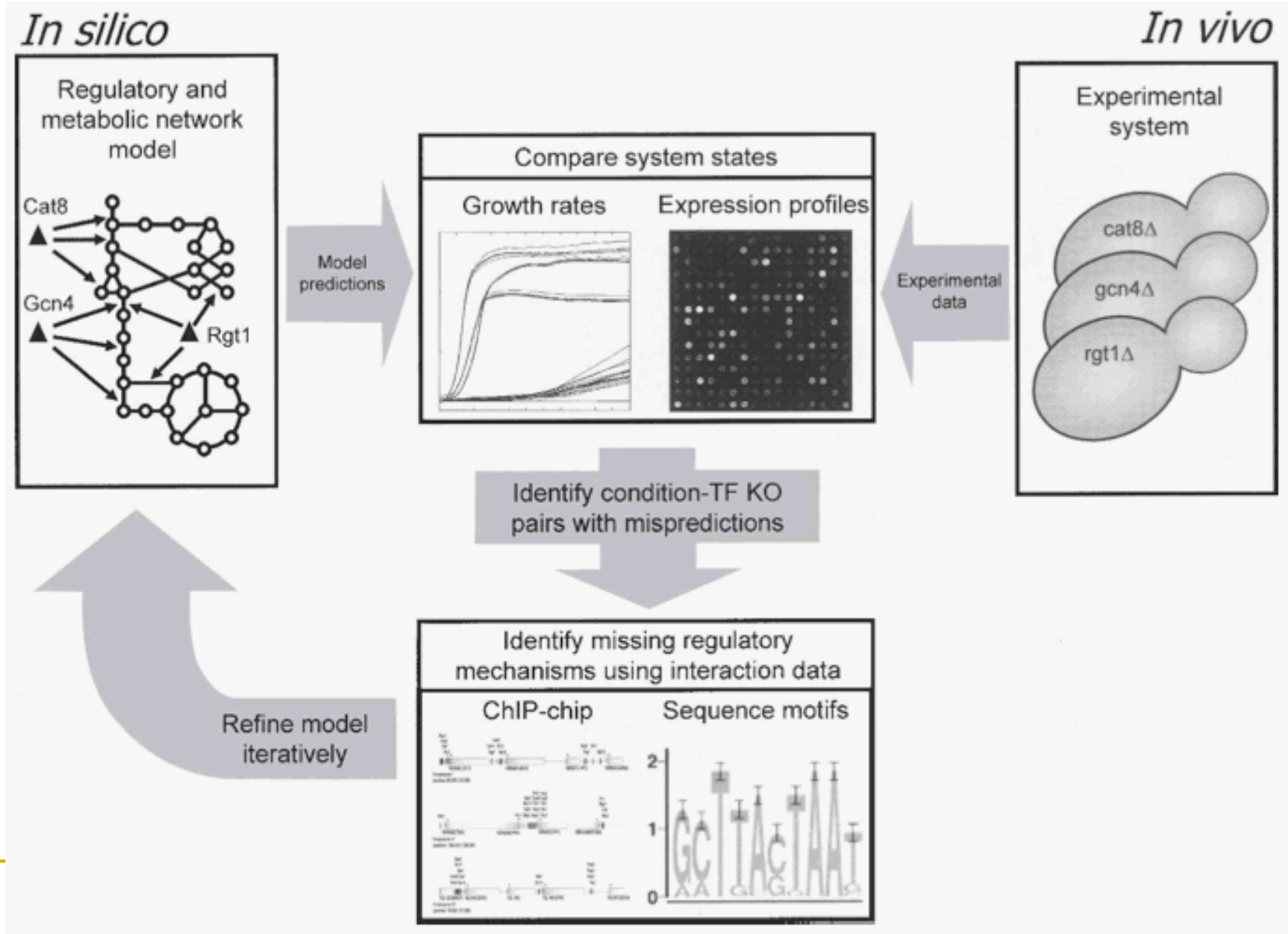
Protein RNA DNA Walls Membranes

- Linear
- Divergent
- Few connections

Macromolecule biosynthesis

[Integrated analysis of regulatory and metabolic networks reveals novel regulatory mechanisms in Saccharomyces cerevisiae]

MJ Herrgård, BS Lee, V Portnoy, BØ ... - Genome research, 2006 - genome.cshlp.org



2007

The human microbiome project
PJ Turnbaugh, RE Ley, M Hamady, CM Fraser-Liggett, … - Nature, 2007 - nature.com
... interpret mass-spectrometry data sets 38 . Given the limited knowledge of the biological transformations that human microbial communities support, **meta-metabolomics** is likely to be challenging. Tools and databases for metabolite **...**
引用元 269 - 関連記事 - 全 15 バージョン

[HTML] Structural and functional analysis of cellular networks with CellNetAnalyzer
S Klamt, J Saez-Rodriguez, ED Gilles - BMC Systems Biology, 2007 - biomedcentral.com
... CNA extends its predecessor FluxAnalyzer, originally developed for **metabolic network analysis** [7], by new methods for signalling and regulatory networks, ie for networks where signal flows are dominating (in contrast to mass flows in metabolic networks). **...**
引用元 86 - 関連記事 - キャッシュ - 全 9 バージョン

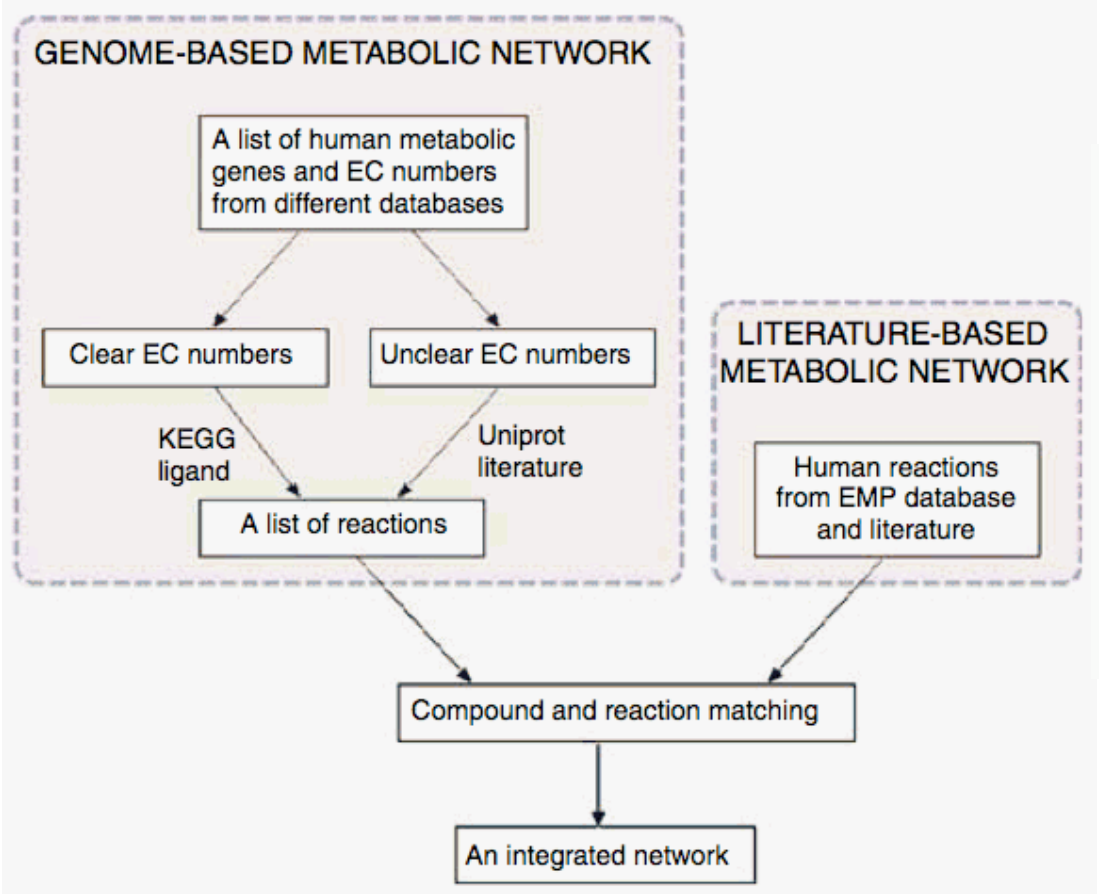
The Edinburgh human metabolic network reconstruction and its functional analysis
H Ma, A Sorokin, A Mazein, A Selkov, E … - Molecular systems …, 2007 - nature.com
... A main objective of human **metabolic network analysis** is to see how it is related with human disease. More than 10 000 human genes (half of the whole genome) have been reported to be related with one or more human diseases in the OMIM database (Hamosh et al, 2005). **...**
引用元 67 - 関連記事 - 全 13 バージョン

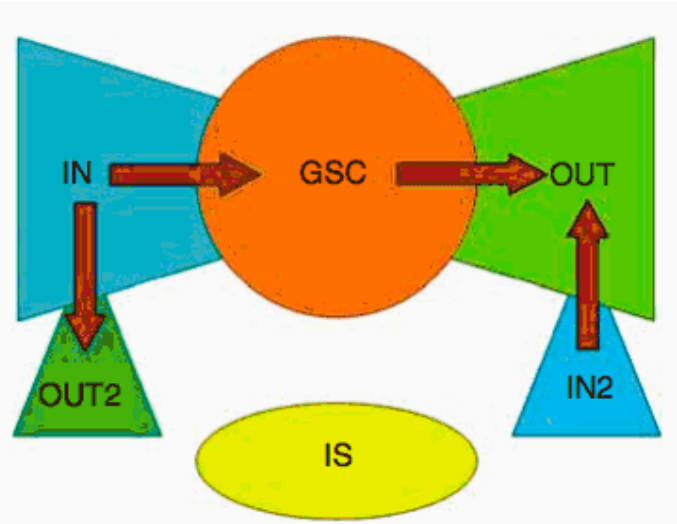
The Edinburgh human metabolic network reconstruction and its functional analysis

H Ma, A Sorokin, A Mazein, A Selkov, E ... - Molecular systems ..., 2007 - nature.com

... A main objective of human **metabolic network analysis** is to see how it is related with human disease. More than 10 000 human genes (half of the whole genome) have been reported to be related with one or more human diseases in the OMIM database (Hamosh et al, 2005). **...**

引用元 67 - 関連記事 - 全 13 バージョン



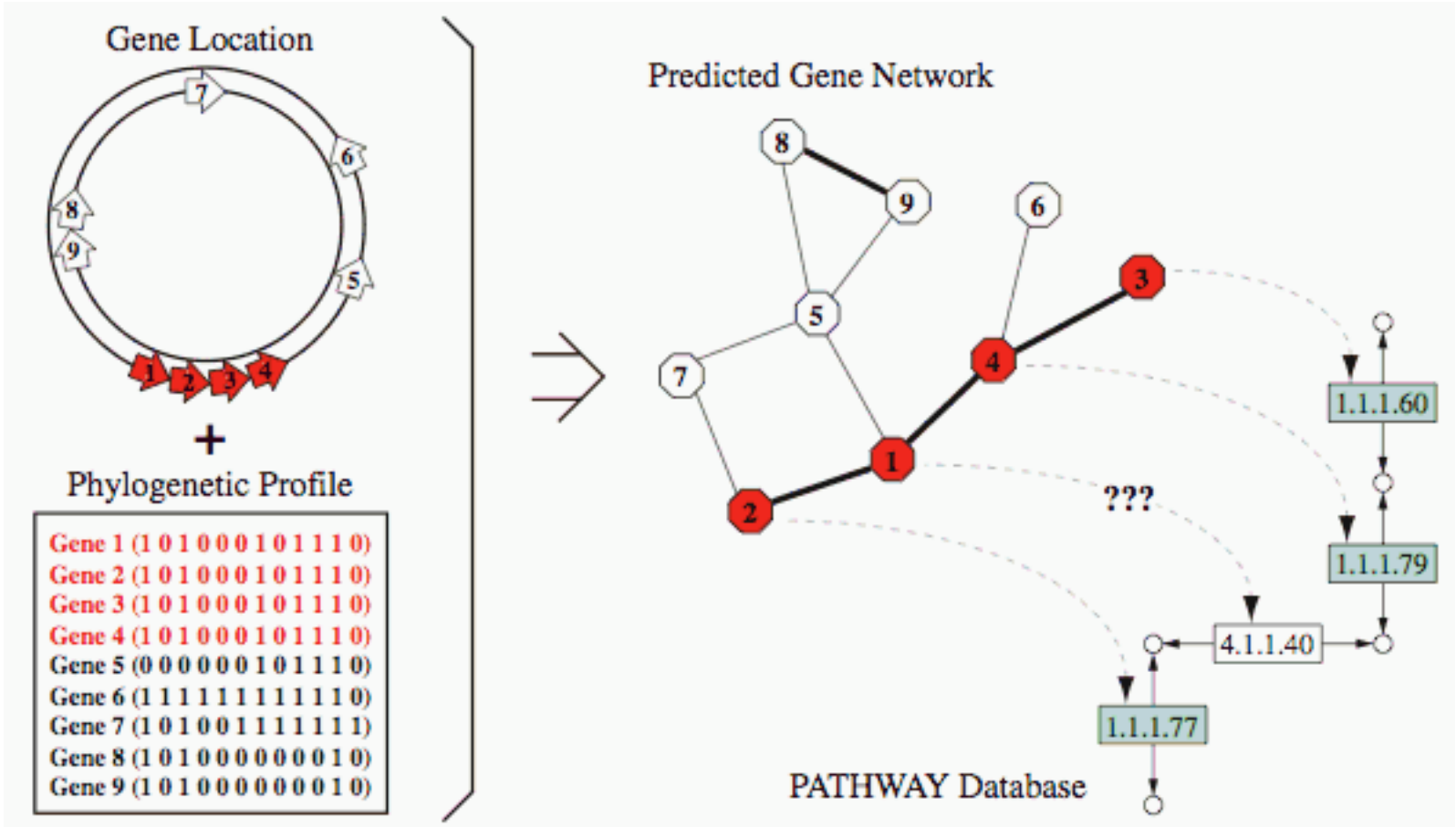


Prediction of missing enzyme genes in a bacterial metabolic network

Y Yamanishi, H Mihara, M Osaki, H ... - FEBS ..., 2007 - interscience.wiley.com

Prediction of missing enzyme genes in a bacterial ... Reconstruction of the lysine-degradation pathway of Pseudomonas aeruginosa ... Yoshihiro Yamanishi1, Hisaaki Mihara2, Motoharu Osaki2, Hisashi Muramatsu3, Nobuyoshi Esaki2, Tetsuya Sato1, Yoshiyuki Hizukuri1, ...

引用元 16 - 関連記事 - 全 5 バージョン



KAAS: an automatic genome annotation and pathway reconstruction server

Y Moriya, M Itoh, S Okuda, AC Yoshizawa, … - Nucleic Acids …, 2007 - Oxford Univ Press

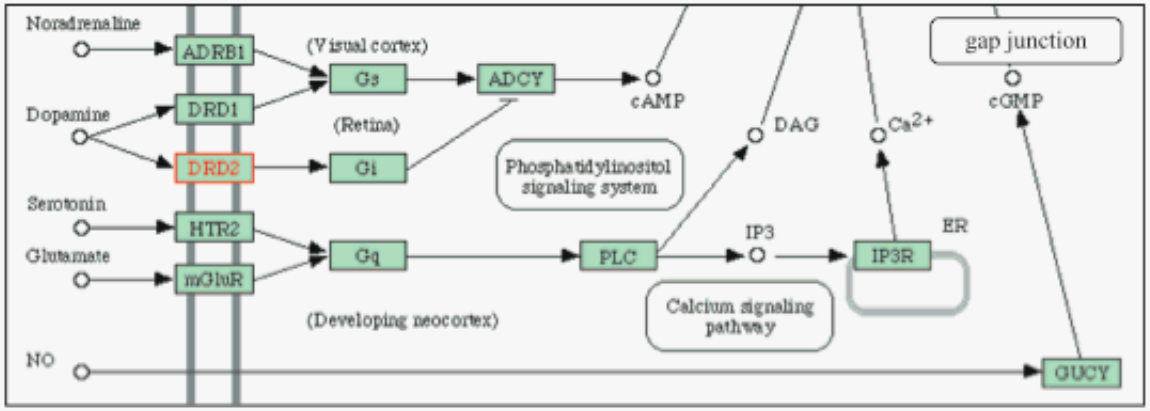
The number of complete and draft genomes is rapidly growing in recent years, and it has become increasingly important to automate the identification of functional properties and biological roles of genes in these genomes. In the KEGG database, genes in complete genomes are ...

引用元 71 - 関連記事 - 全 11 バージョン

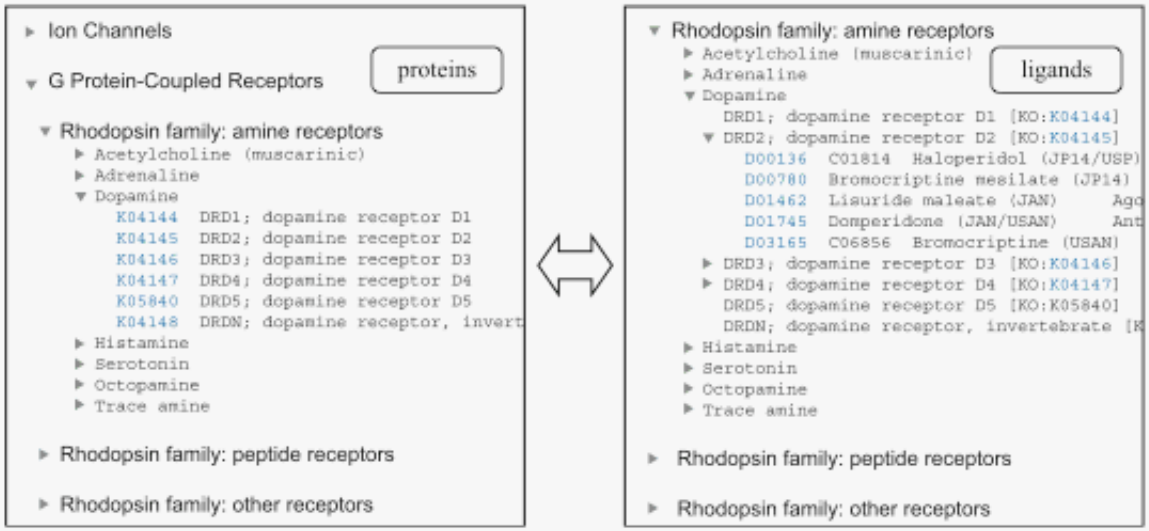
KO assignment

Gene	KO
1803	K01278
1806	K00207
1807	K01464
1808	K07528
1812	K04144
1813	K04145
1814	K04146
1815	K04147
1816	K05840
1819	K06944
1822	K05626
1823	K07600
1824	K07601
1825	K07602
1826	K06767
1828	K07596
1829	K07597
1830	K07598
1833	K08127
1839	K08523
1840	K06058

KEGG pathway mapping



KEGG BRITE mapping



2008

Molecular eco-systems biology: towards an understanding of community function
J Raes, P Bork - Nature Reviews Microbiology, 2008 - nature.com
... With the advent of various high-throughput techniques that aim to characterize complete microbial ecosystems (metagenomics, meta-transcriptomics and **meta-metabolomics**), we propose that the time is ripe to consider molecular systems biology at the ecosystem level (eco ...
引用元 44 - 関連記事 - 全 6 バージョン

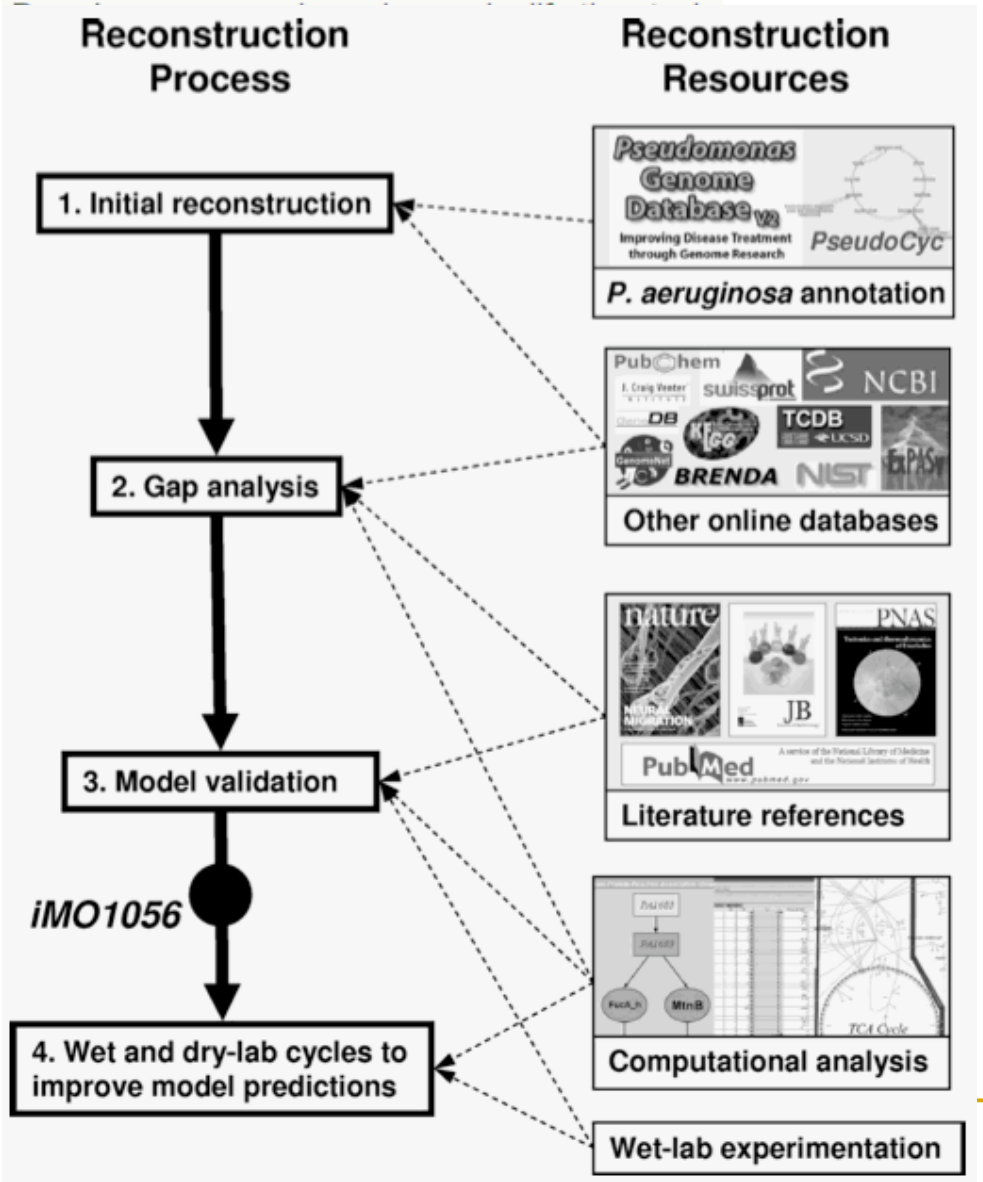
Genome-scale metabolic network analysis of the opportunistic pathogen Pseudomonas aeruginosa PAO1
MA Oberhardt, J Puchalka, KE Fryer, VAP ... - Journal of ..., 2008 - Am Soc Microbiol
Pseudomonas aeruginosa is a major life-threatening opportunistic pathogen that commonly infects immunocompromised patients. This bacterium owes its success as a pathogen largely to its metabolic versatility and flexibility. A thorough understanding of P. aeruginosa's ...
引用元 43 - 関連記事 - 全 8 バージョン

An invitation to the marriage of metagenomics and metabolomics
PJ Turnbaugh, JI Gordon - Cell, 2008 - Elsevier
... DNA, to identify specific functions such as antibiotic resistance (functional metagenomics), (3) profiling of RNAs and proteins produced by a microbiome (meta-transcriptomics and meta-proteomics), and (4) identification of a community's metabolic network (**meta-metabolomics**). ...
引用元 17 - 関連記事 - 全 9 バージョン

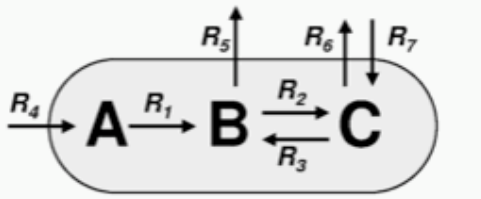
Host-bacterial coevolution and the search for new drug targets
J Zaneveld, PJ Turnbaugh, C Lozupone, RE ... - Current opinion in ..., 2008 - Elsevier
... of our human biology thus requires the understanding of our microbial communities and the genes that they harbor ('our' microbiome) (Figure 1). The notion that we have a 'meta-genome' composed of microbial and human components, and a '**meta-metabolome**' that reflects ...
引用元 12 - 関連記事 - 全 7 バージョン

Genome-scale metabolic network analysis of the opportunistic pathogen Pseudomonas aeruginosa PAO1

MA Oberhardt, J Puchalka, KE Fryer, VAP … - Journal of …, 2008 - Am Soc Microbiol



a.



(Reactions)

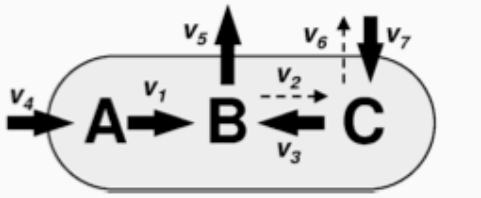
S = (compounds)

	R1	R2	R3	R4	R5	R6	R7
A	-1	0	0	1	0	0	0
B	1	-1	1	0	-1	0	0
C	0	1	-1	0	0	-1	1

b.

$$\max(v_5)$$

$$s.t. \begin{cases} lb_j \leq v_j \leq ub_j & \forall j \in \text{Reactions, R} \\ \sum_{j=1}^{C} S_{ij} v_j = 0 & \forall i \in \text{Compounds, C} \\ v_4 = \text{uptake} \end{cases}$$

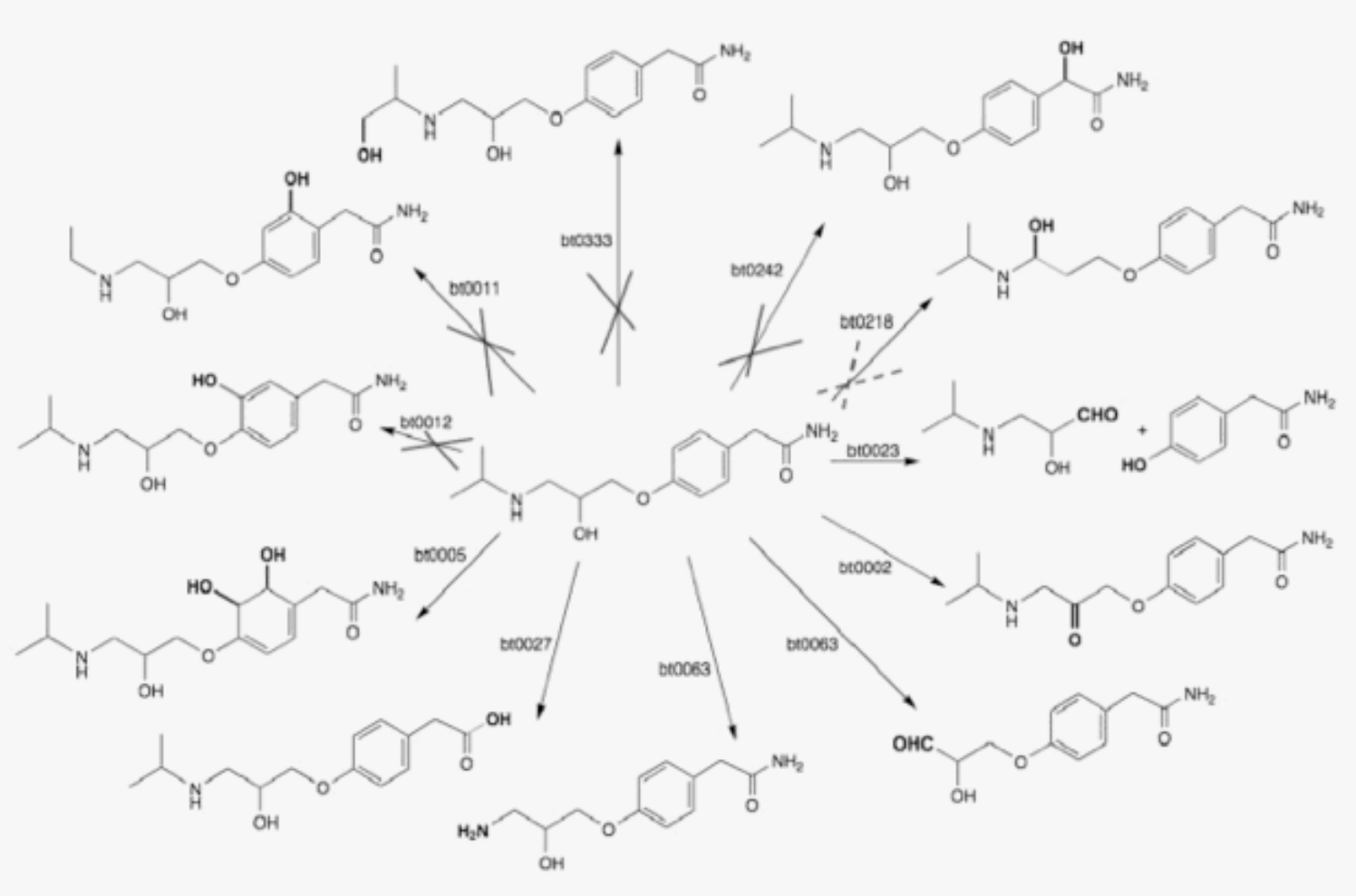


Data-driven extraction of relative reasoning rules to limit combinatorial explosion in biodegradation pathway prediction

K Fenner, J Gao, S Kramer, L Ellis, L Wackett - Bioinformatics, 2008 - Oxford Univ Press

Results: A total of 112 relative reasoning rules were identified and implemented. In one prediction step, ie as per one generation predicted, the use of relative reasoning decreases the predicted biotransformations by over 25% for 50 compounds used to generate the rules and by ...

引用元 8 - 関連記事 - 全 10 バージョン

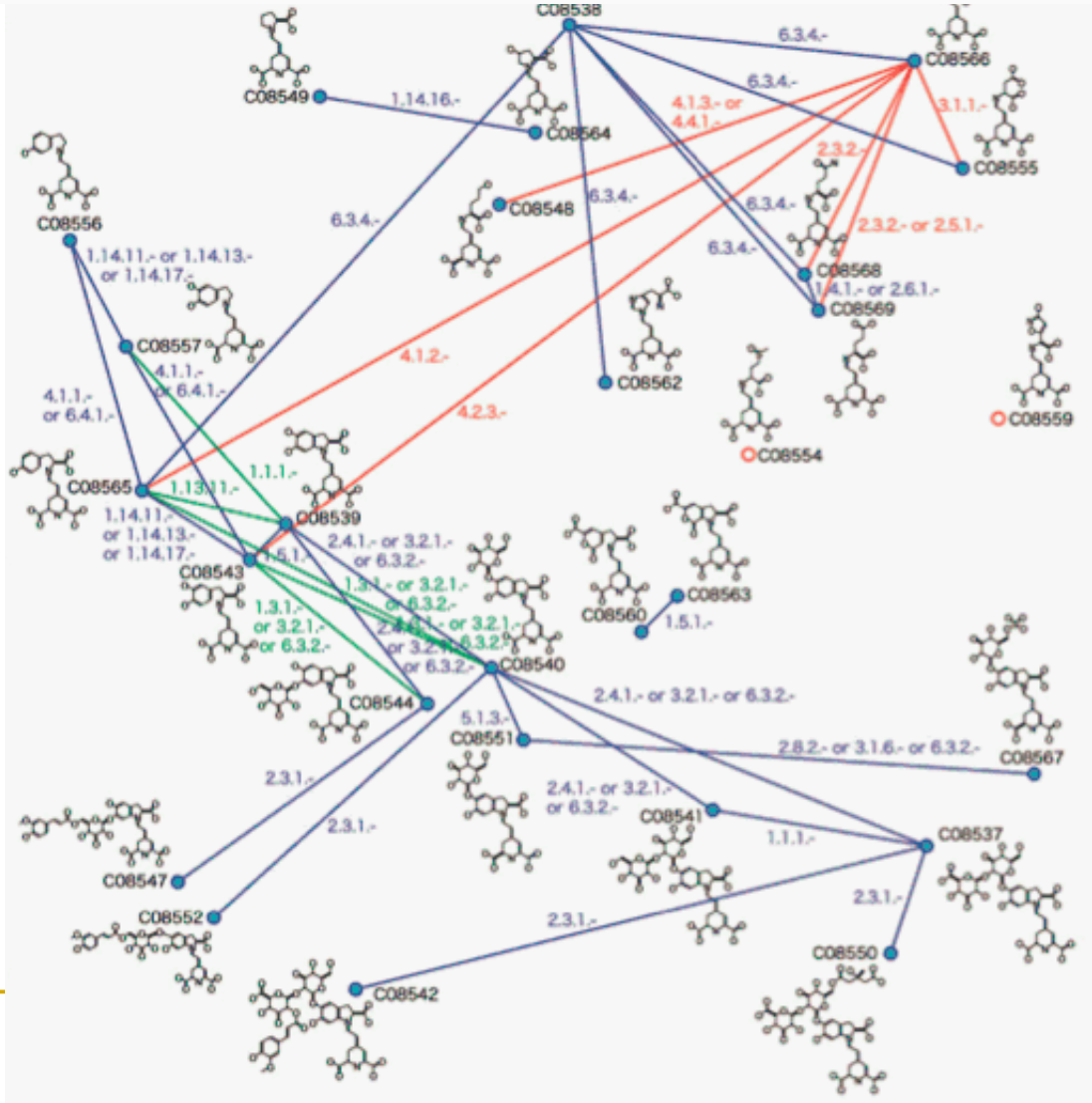


Eliciting possible reaction equations and metabolic pathways involving orphan metabolites

M Kotera, AG McDonald, S Boyce, KF … - Journal of Chemical …, 2008 - ACS Publications

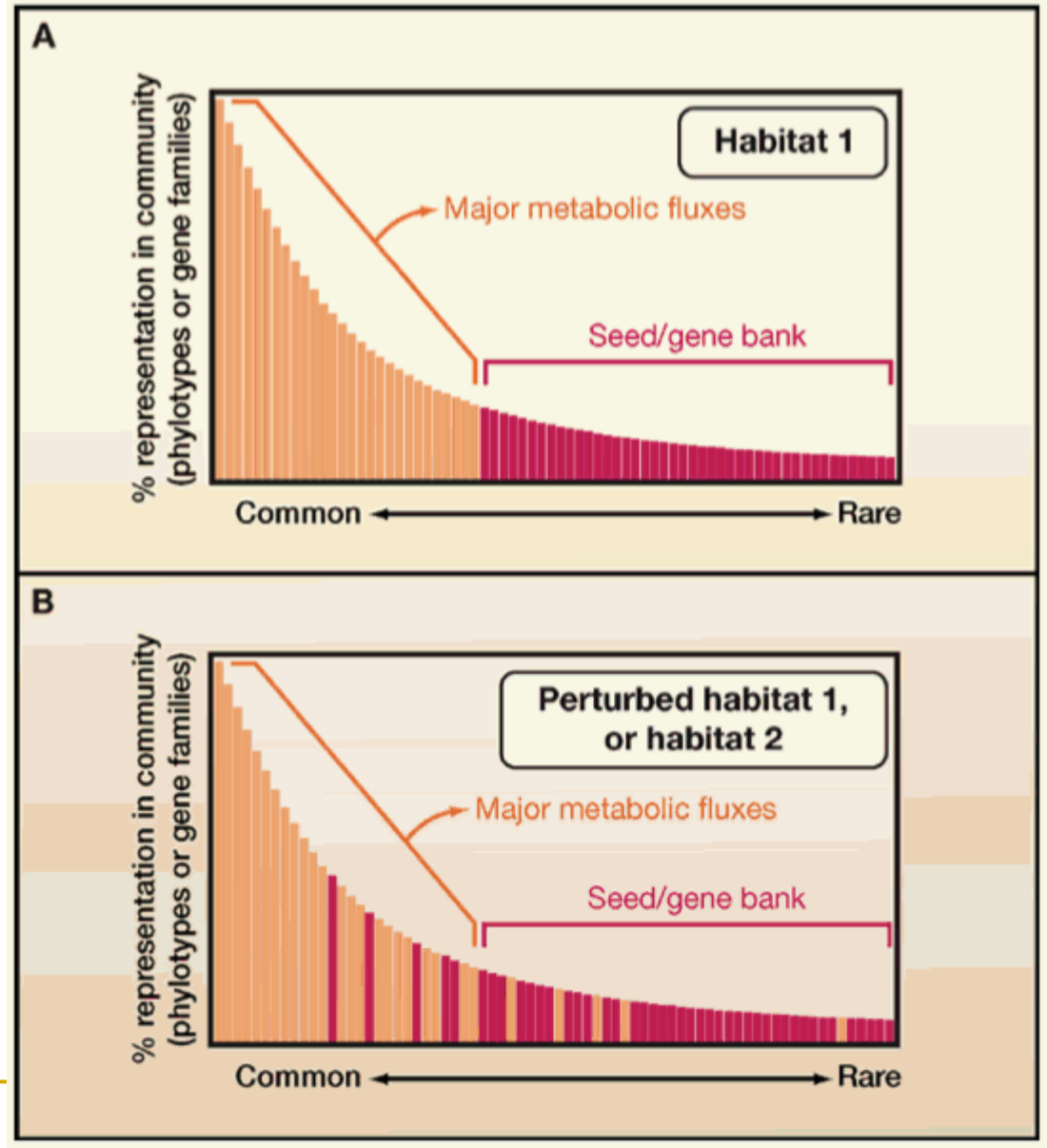
The development of metabolomics has resulted in the discovery of an increasing number of orphan metabolites, which are defined as compounds that are known to be present in living organisms but whose synthetic/degradation pathways are unknown. In this paper, we describe a ...

引用元 6 - 関連記事 - 全 2 バージョン



An invitation to the marriage of metagenomics and metabolomics

PJ Turnbaugh, JI Gordon - Cell, 2008 - Elsevier



2009

Mass spectrometry based metabolomics and enzymatic assays for functional genomics
R Baran, W Reindl, TR Northen - Current opinion in microbiology, 2009 - Elsevier
... We anticipate that these capabilities coupled with both the increased focus on microbial communities and integration with other '-omics' technologies provide tremendous opportunities for '**meta-metabolomic**' studies of microbial communities (Figure 3) [66] and will provide new ...
引用元 5 - 関連記事 - 全 4 バージョン

Intertwined interspecies relationships: approaches to untangle the microbial network
S Haruta, S Kato, K Yamamoto, Y ... - Environmental ..., 2009 - Wiley Online Library
... The quality of the results absolutely depends on the quantity and variety of data for learning. Biology has entered the omics age to comprehensively access the black box, ie metagenome, meta-transcriptome, meta-proteome, and **meta-metabolome**. ...
引用元 4 - 関連記事 - 全 5 バージョン

Symbionts, including pathogens, of the predatory mite Metaseiulus occidentalis: current and future analysis methods
MA Hoy, A Jeyaprakash - Diseases of Mites and Ticks, 2009 - Springer
Page 1. J. Bruin & LPS van der Geest (eds.), Diseases of Mites and Ticks. DOI: 10.1007/978-1-4020-9695-2_26 329 Symbionts, including pathogens, of the predatory mite Metaseiulus occidentalis: current and future analysis methods Marjorie A. Hoy · A. Jeyaprakash ...
引用元 3 - 関連記事 - 全 7 バージョン

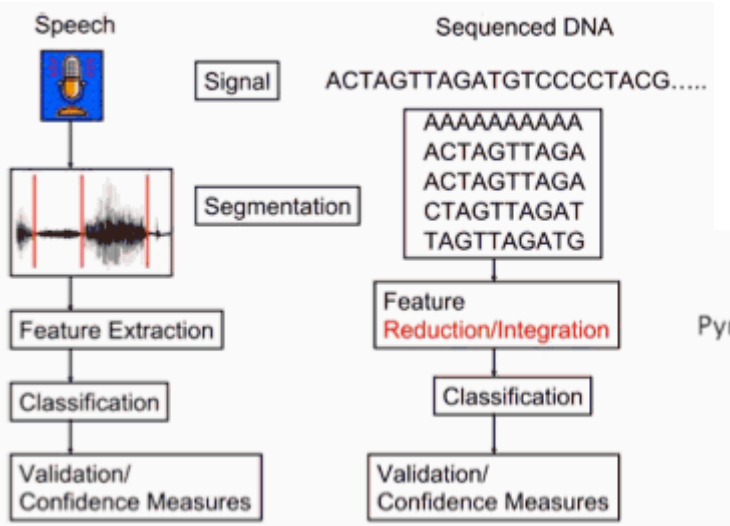
[HTML] **Signal Processing for Metagenomics**: Extracting Information from the Soup
GL Rosen, BA Sokhansanj, R Polikar, MA Bruns, J ... - 2009 - ncbi.nlm.nih.gov
Traditionally, studies in microbial genomics have focused on single-genomes from cultured species, thereby limiting their focus to the small percentage of species that can be cultured outside their natural environment. Fortunately, recent advances in high-throughput sequencing ...
引用元 1 - 関連記事 - 全 11 バージョン

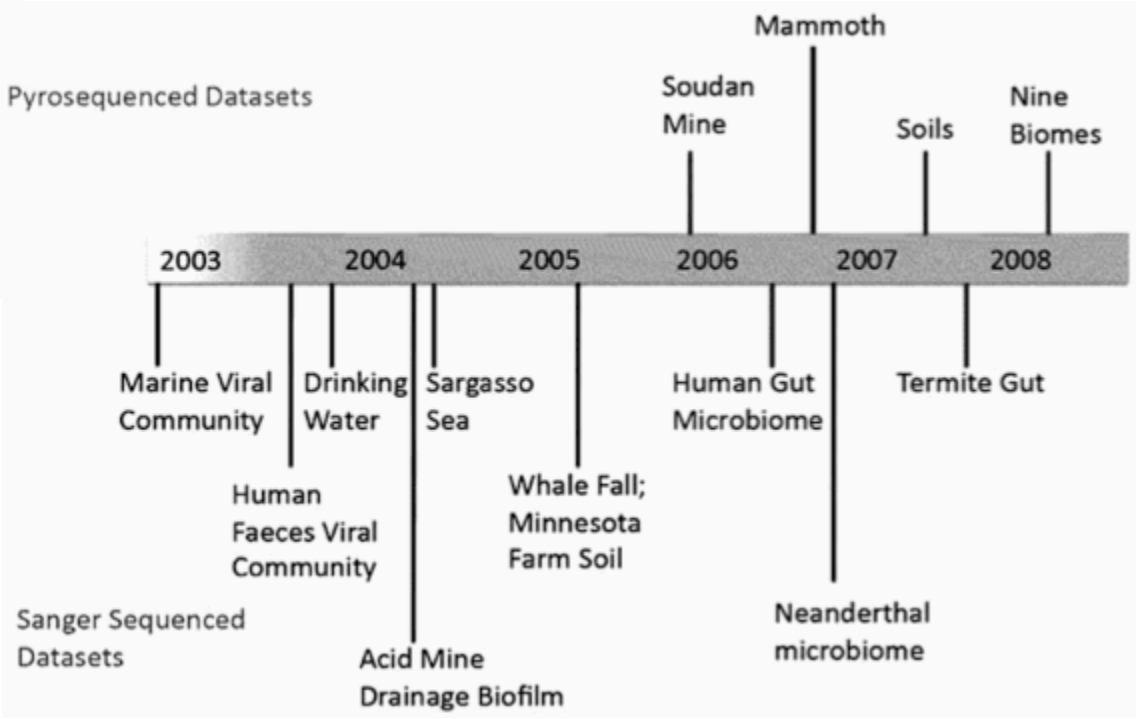
[HTML] **Signal Processing for Metagenomics**: Extracting Information from the Soup

GL Rosen, BA Sokhansanj, R Polikar, MA Bruns, J ... - 2009 - ncbi.nlm.nih.gov

Traditionally, studies in microbial genomics have focused on single-genomes from cultured species, thereby limiting their focus to the small percentage of species that can be cultured outside their natural environment. Fortunately, recent advances in high-throughput sequencing ...

引用元 1 - 関連記事 - 全 11 バージョン





2010

Acetylation of metabolic enzymes coordinates carbon source utilization and metabolic flux
Q Wang, Y Zhang, C Yang, H Xiong, Y Lin, J Yao, H Li, ... - Science, 2010 - sciencemag.org
... knockouts. J. Bacteriol. 185, 7053 (2003). [Abstract/Free Full Text]; 8. N. Zamboni, E. Fischer, U. Sauer, FiatFlux—a software for **metabolic flux analysis** from 13C-glucose experiments. BMC Bioinformatics 6, 209 (2005). [CrossRef ...
引用元 18 - 関連記事 - 全 10 バージョン

Metabolic networks: how to identify key components in the regulation of metabolism and growth
M Stitt, R Sulpice, J Keurentjes - Plant Physiology, 2010 - Am Soc Plant Biol
... They provide an overview of the available technology for analysis of metabolite levels (Kopka et al., 2004 Go ; Hall, 2006 Go ; Lisec et al., 2006 Go ; Last et al., 2007 Go), the use of **metabolic flux analysis** to analyze fluxes in complex metabolic systems (Fernie et al., 2005 Go ...
引用元 6 - 関連記事 - 全 5 バージョン

Tradeoff between enzyme and metabolite efficiency maintains metabolic homeostasis upon perturbations in enzyme capacity
SM Fendt, JM Buescher, F Rudroff, P Picotti, N ... - Molecular Systems ..., 2010 - **nature**.com
... **Metabolic control analysis** and its extensions, in particular regulation analysis, provide a coherent framework for sensitivity of the influence of enzyme activities and ... If you require assistance to access this image, or to obtain a text description, please contact npg@**nature**.com ...
引用元 3 - 関連記事 - 全 6 バージョン

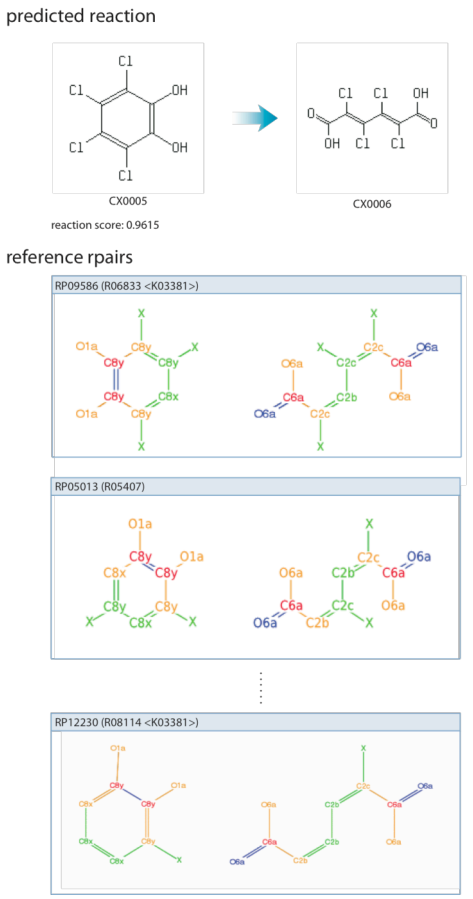
Metabolic flux distributions: genetic information, computational predictions, and experimental validation
LM Blank, L Kuepfer - Applied microbiology and biotechnology, 2010 - Springer
... Finally, the achievements are discussed in the context of future developments in Metabolic Engineering and Synthetic Biology. Keywords Flux balance analysis . **Metabolic network analysis** . 13C-**metabolic flux analysis** . Synthetic biology. Metabolic engineering . ...
引用元 2 - 関連記事 - 全 5 バージョン

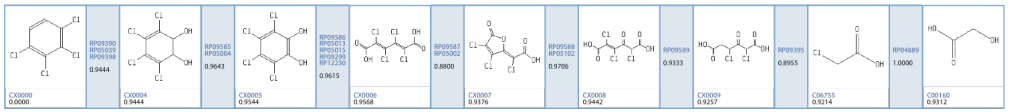
PathPred: an enzyme-catalyzed metabolic pathway prediction server

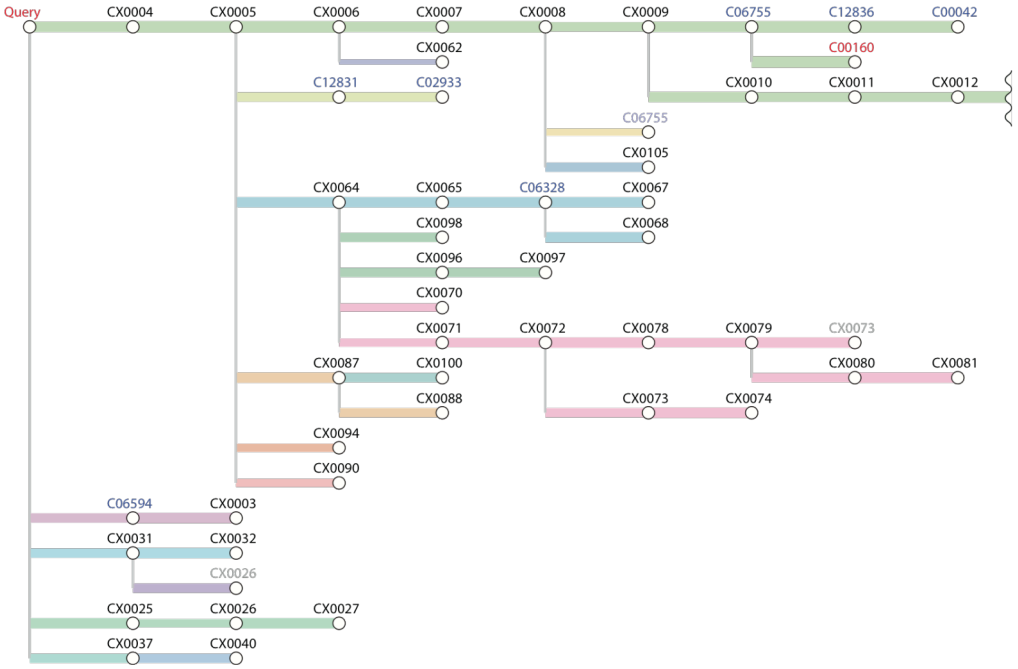
Y Moriya, D Shigemizu, M Hattori, T ... - Nucleic Acids ..., 2010 - Oxford Univ Press

The KEGG RPAIR database is a collection of biochemical structure transformation patterns, called RDM patterns, and chemical structure alignments of substrate-product pairs (reactant pairs) in all known enzyme-catalyzed reactions taken from the Enzyme Nomenclature and the ...

関連記事 - 全 6 バージョン

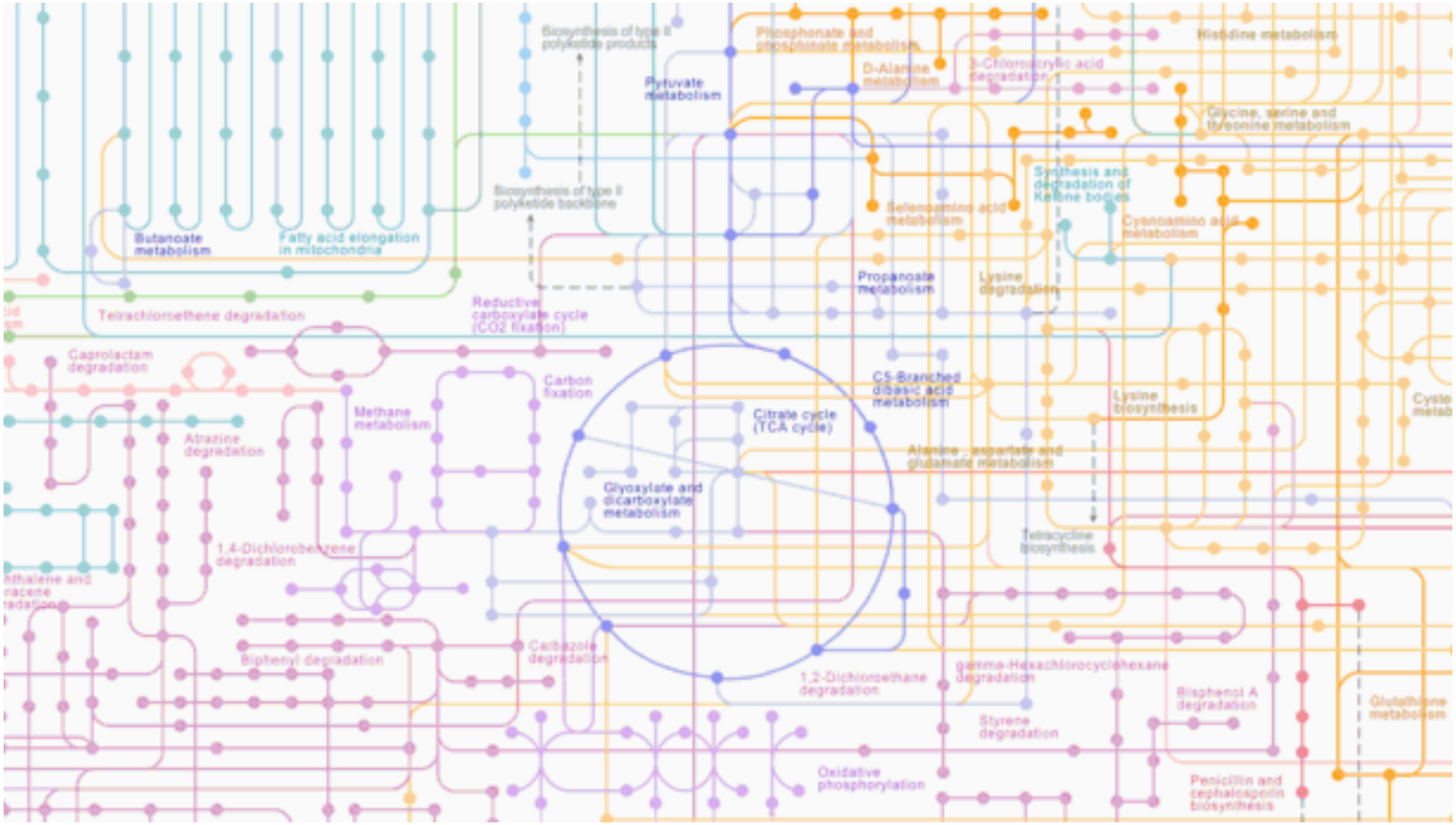






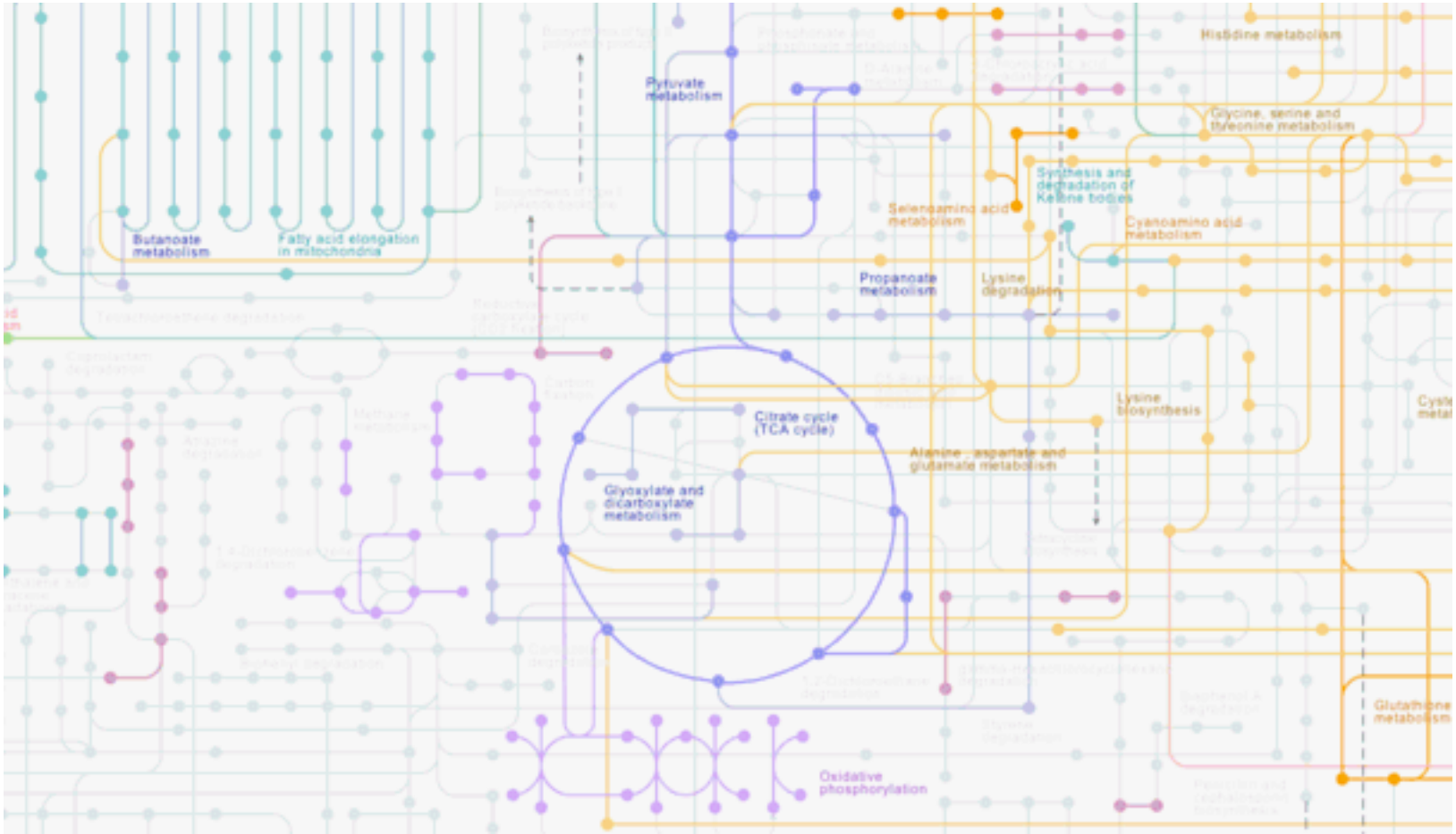
KEGG global map

http://www.genome.jp/kegg/pathway.html



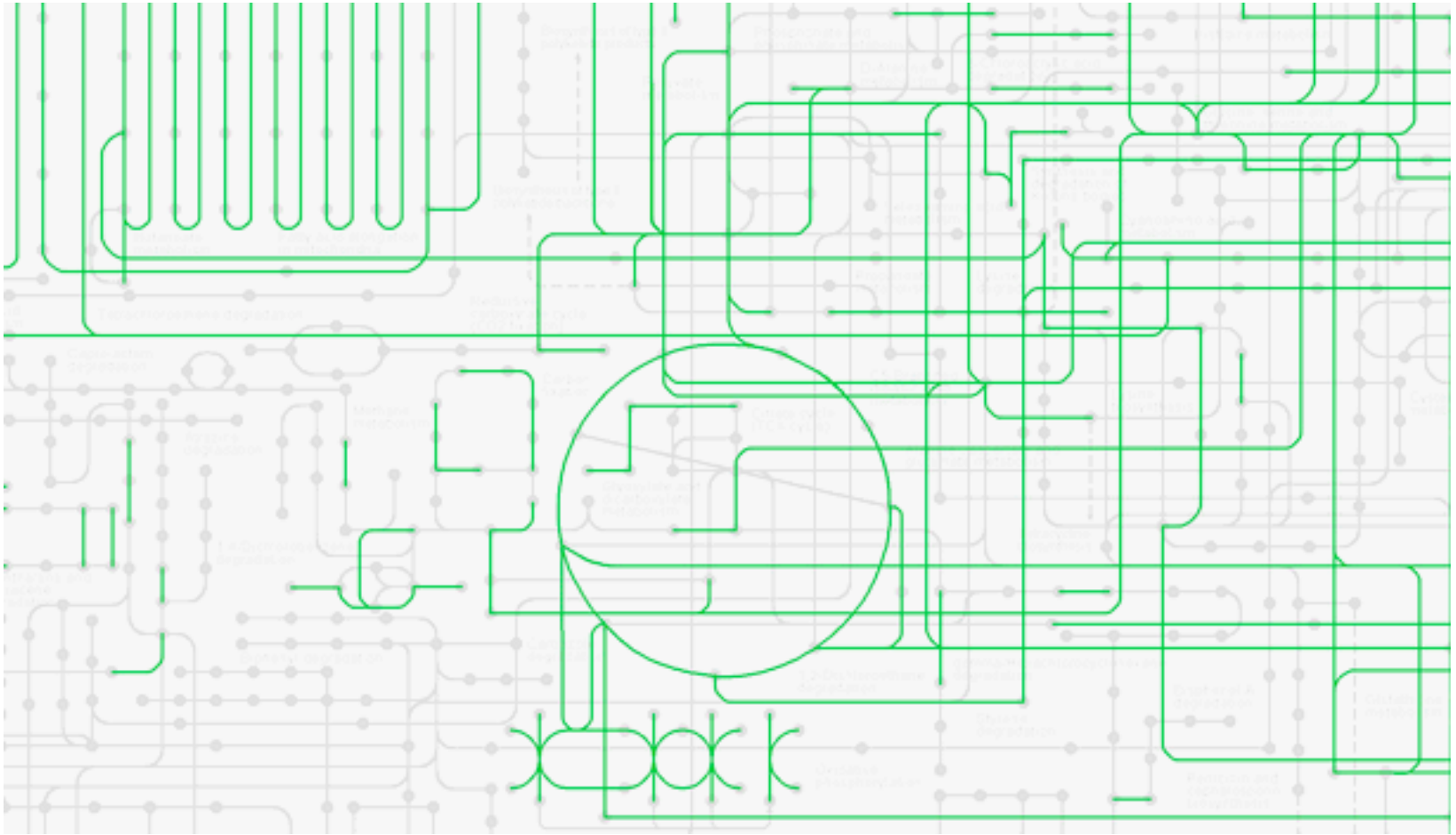
KEGG global map of human

http://www.genome.jp/kegg/pathway.html



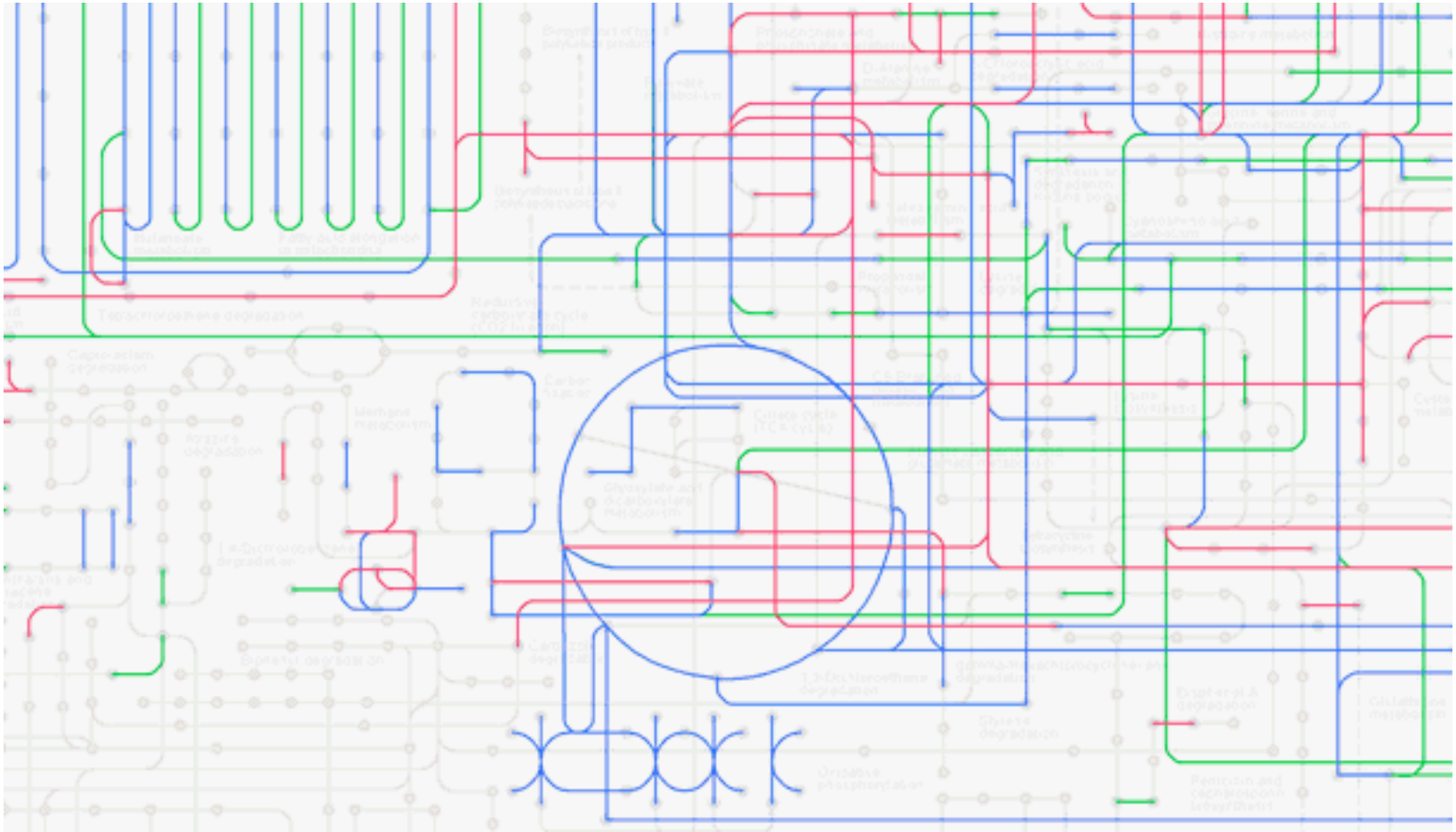
Human metabolome

http://www.genome.jp/kegg/pathway.html



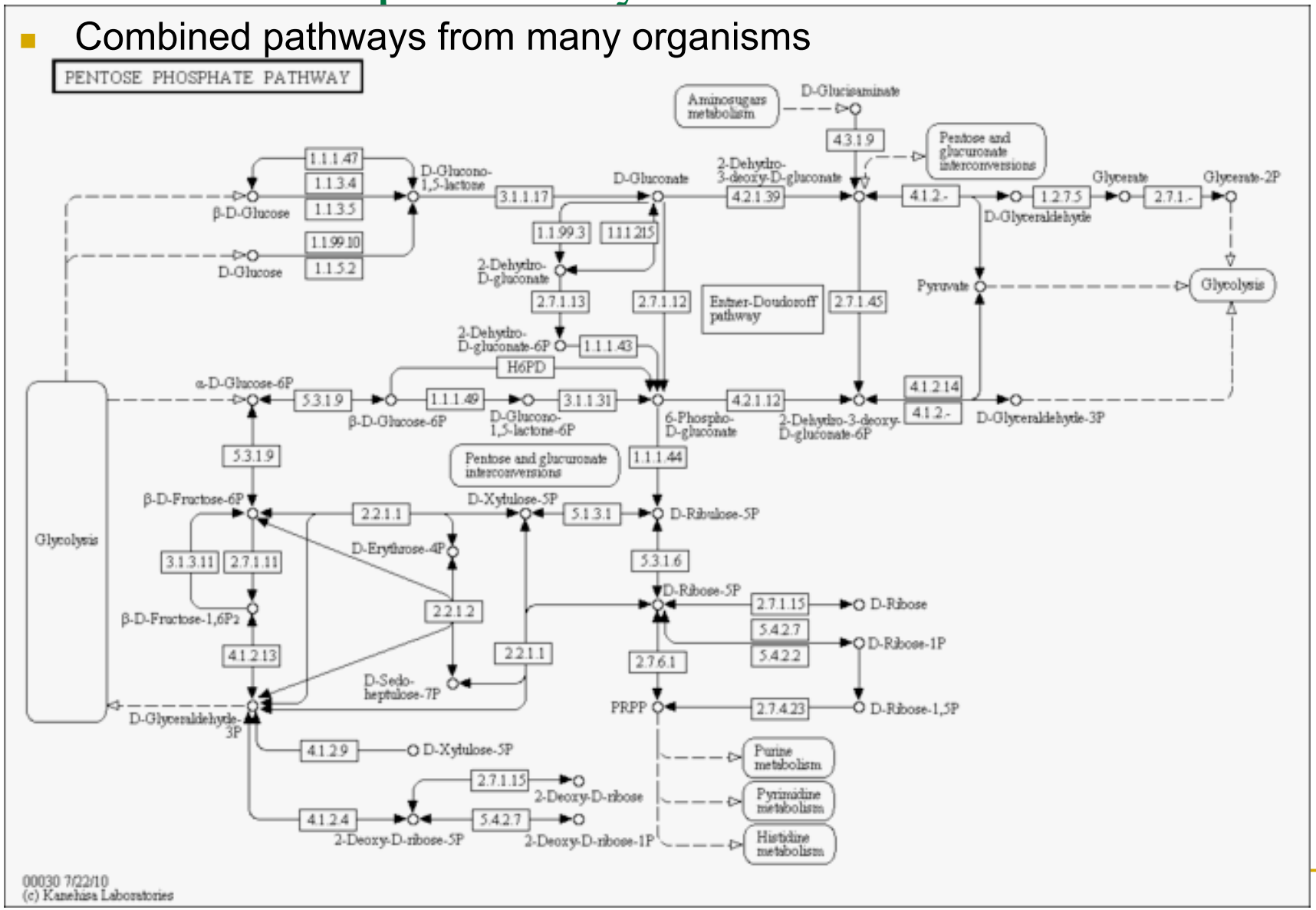
Human gut meta-metabolome

http://www.genome.jp/kegg/pathway.html



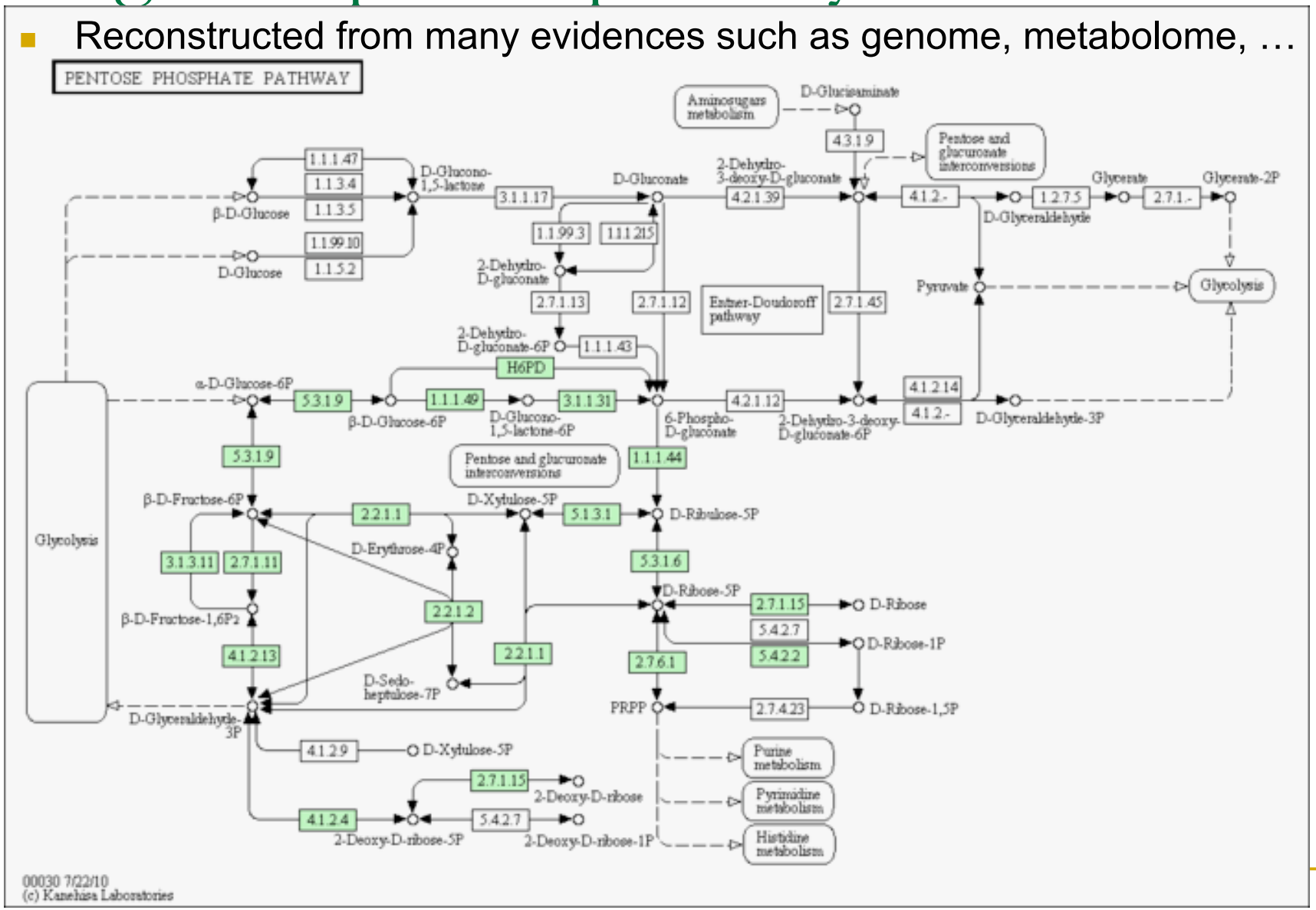
Reference pathways

- Combined pathways from many organisms



Organic-specific pathways

- Reconstructed from many evidences such as genome, metabolome, …

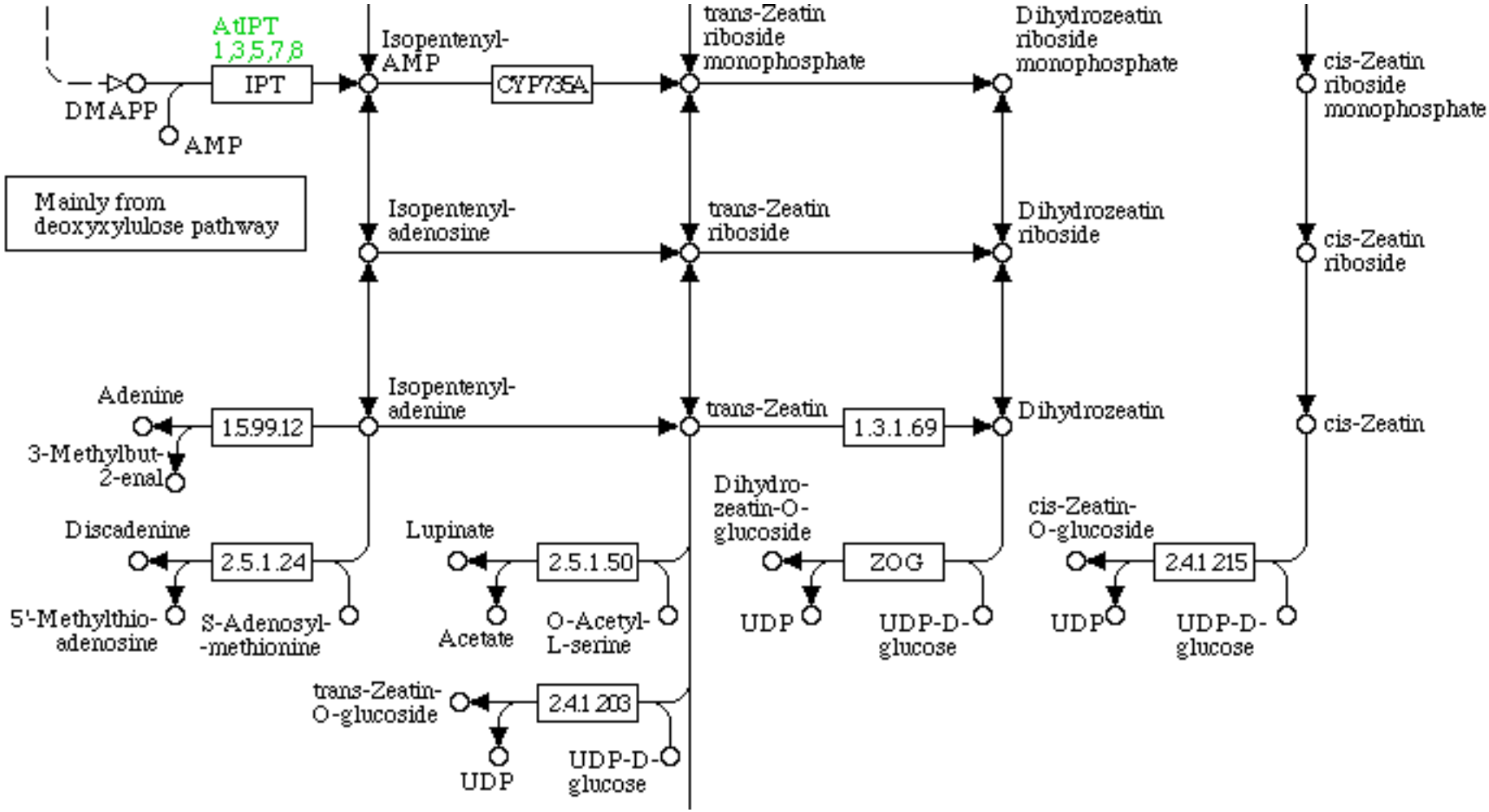


Reconstruction of metabolic networks

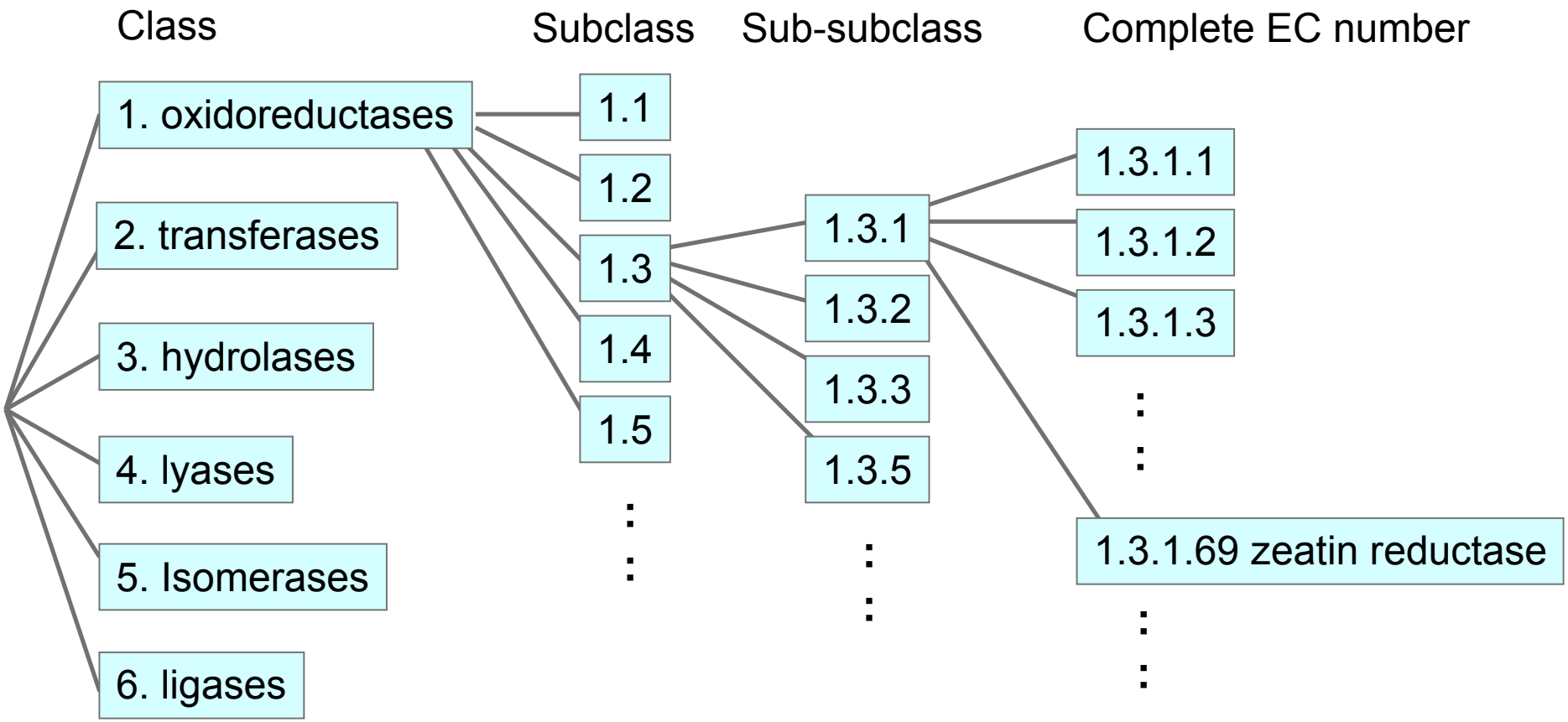
In the case a reference pathway…

- Exists,
  - Which gene is mapped onto where?
  - Are there any possible paths that are not found yet?
- Does not exist,
  - Which compound is converted into which compound?
  - Which gene is mapped onto that path?

EC numbers as the links beween genomic and metabolomic information



EC numbers as a classification of enzymes

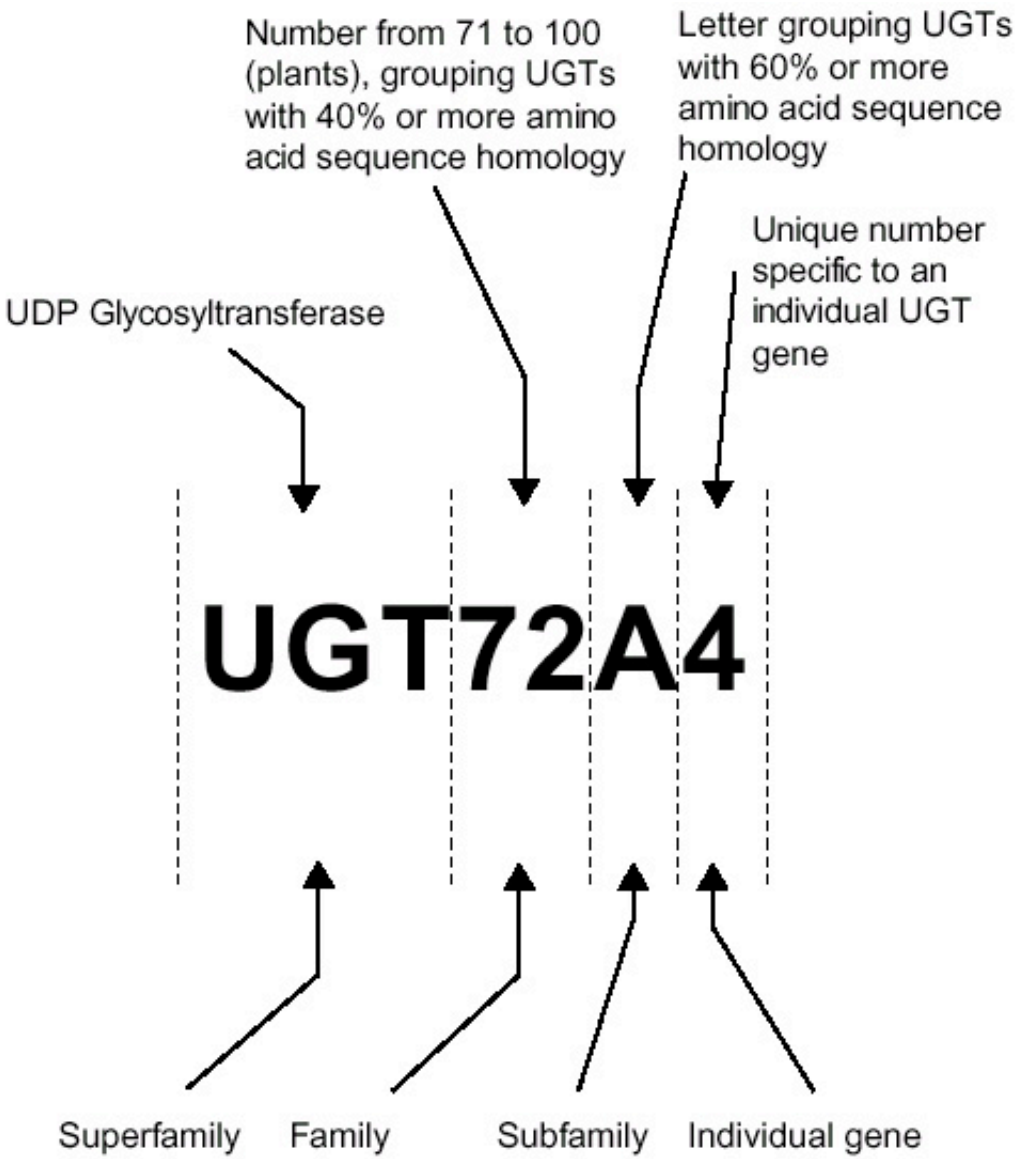


EC classification criteria

Class	Subclass	Sub-subclass	Remarks
1. Oxidoreductases	Functional groups of reductants	Oxidants	Which compounds are reductants, or oxidants?
2. Transferases	Transferred groups	Transferred groups in detail	From where to where?
3. Hydro-lases	Hydrolyzed bond	Hydrolyzed bond in detail	Nucleases and peptidases are classified in much more detail.
4. Lyases	Digested bond	Types of products	Some hydrolase-like reactions
5. Isomerases	Types of isomeration (RS, EZ, Redox, Transfer, Elimation)	Types of reacting bonds, or products	Any one-molecular reactions.
6. Ligases	Generated bond	Types of substrate	Multi-step reactions

Sequence similarity-based enzyme classifications

- Cyt P450
  - EC 1.14
- Glycosyltransferases
  - EC 2.4



[PDF] **Higher plant glycosyltransferases**
J Ross, Y Li, EK Lim, DJ Bowles - Genome Biol, 2001 - biome
Uridine diphosphate (UDP) glycosyltransferases (UGTs) media
from activated nucleotide sugars to acceptor molecules (aglyc
of the acceptors such as their bioactivity, solubility and transp
引用元 110 - 関連記事 - HTMLバージョン - 全 11 バージョン

[PDF] **SCOPEC: a database of protein catalytic domains**
RA George, RV Spriggs, JM Thornton, B Al- ... - ..., 2004 - Oxford Univ Press
Page 1. BIOINFORMATICS Vol. 20 Suppl. 1 2004, pages i130–i136 DOI: 10.1093/bioinformatics/bth948 SCOPEC: a database of protein catalytic domains Richard A. George 1,2,* , Ruth V. Spriggs 1,2 , Janet M. Thornton 2 , Bissan Al-Lazikani 1 and Mark B. Swindells 1 ...
引用元 25 - 関連記事 - 全 8 バージョン

Thioesterase domain of polypeptide, polyketide and fatty acid synthases

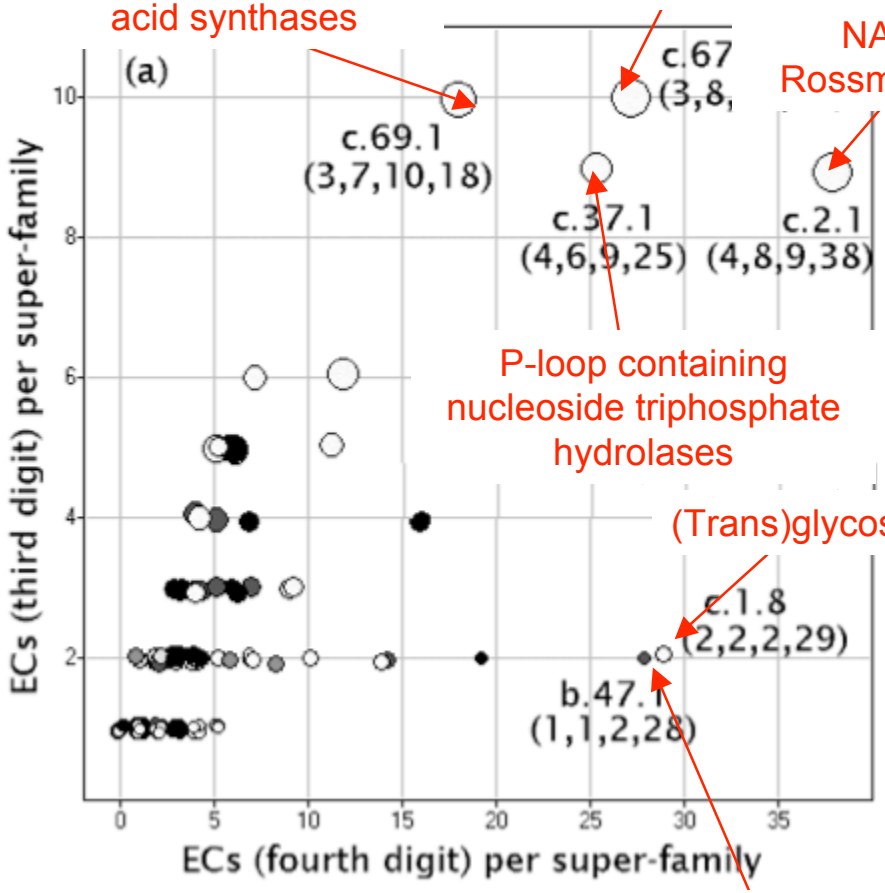
Aspartate aminotransferase-like domain

NAD(P)-binding Rossmann-fold domain

P-loop containing nucleoside triphosphate hydrolases

(Trans)glycosidases

Trypsin-like serine proteases



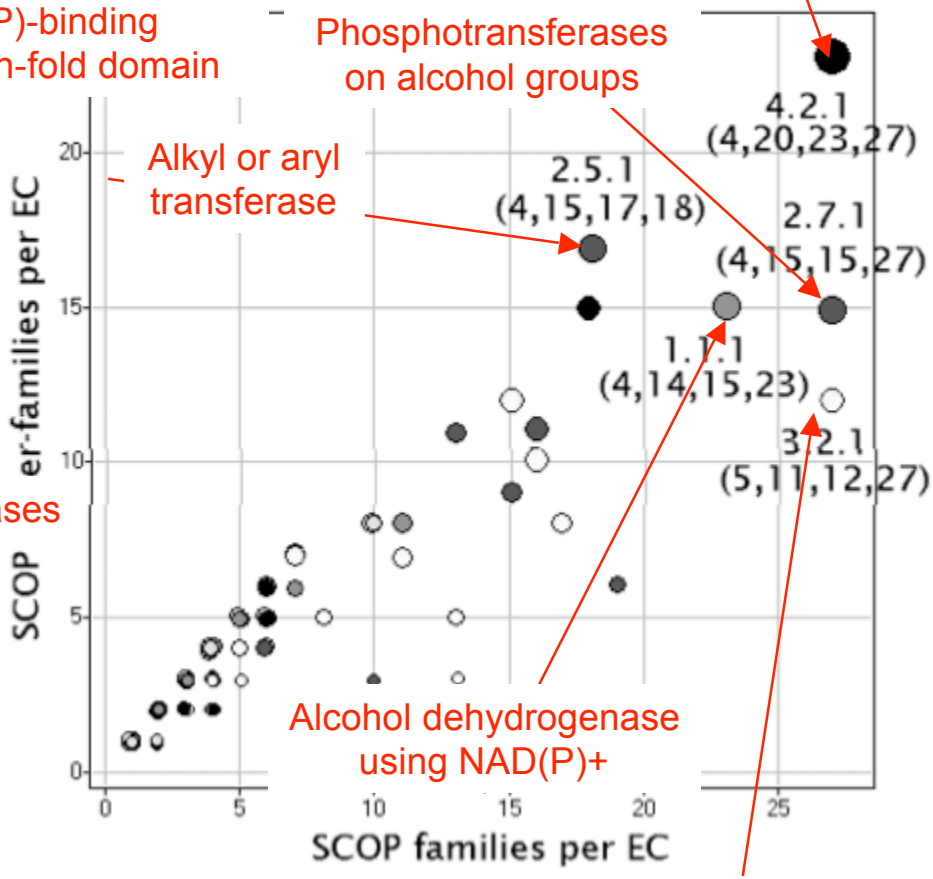
Hydro-lyase

Phosphotransferases on alcohol groups

Alkyl or aryl transferase

Alcohol dehydrogenase using NAD(P)+

O- or S-glycosidases

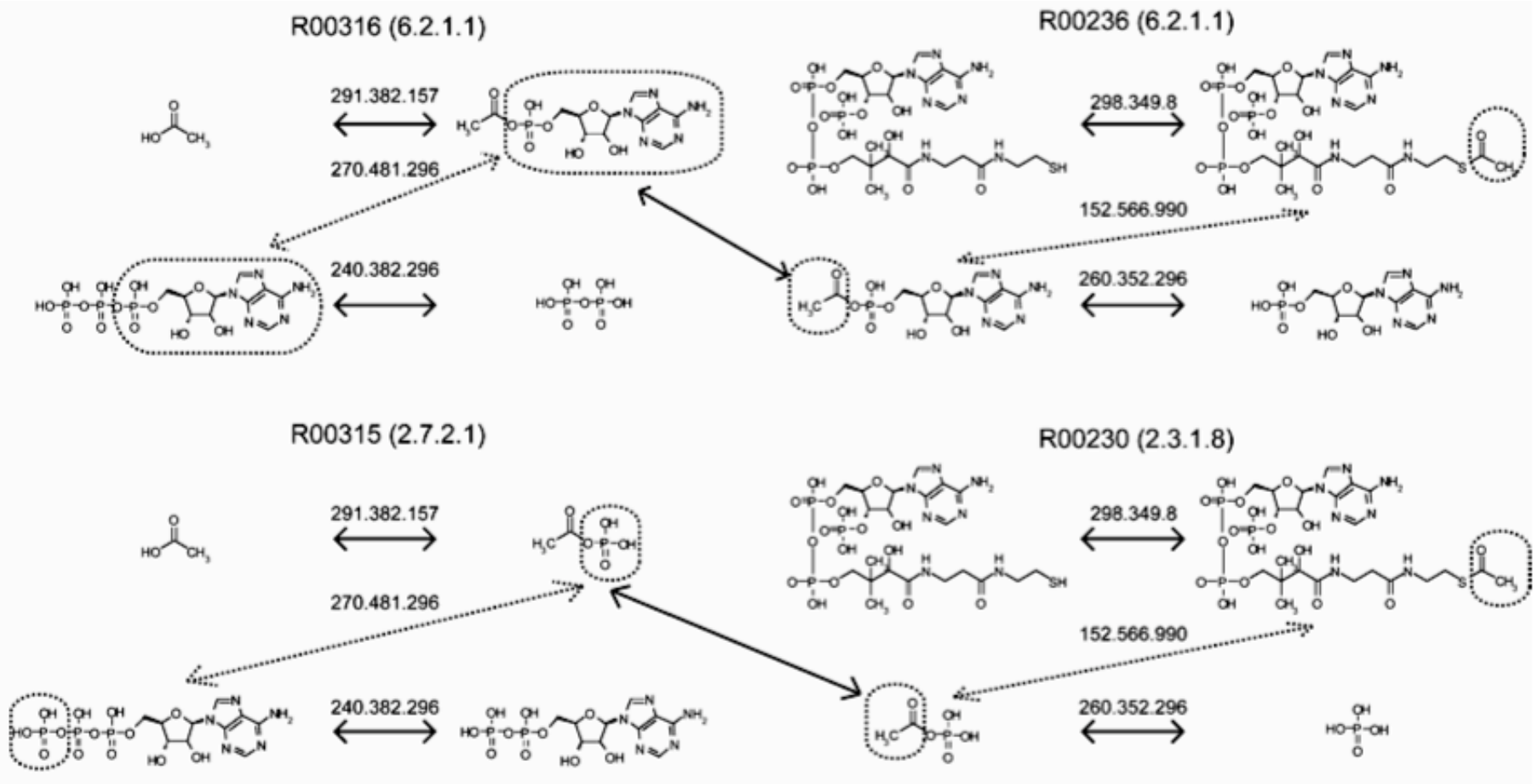


Computational assignment of the EC numbers for genomic-scale analysis of enzymatic reactions

M Kotera, Y Okuno, M Hattori, S Goto, M ... - J. Am. Chem. ..., 2004 - ACS Publications

The EC (Enzyme Commission) numbers represent a hierarchical classification of enzymatic reactions, but they are also commonly utilized as identifiers of enzymes or enzyme genes in the analysis of complete genomes. This duality of the EC numbers makes it possible to link ...

引用元 68 - 関連記事 - 全 7 バージョン



What is meant by being "similar"?

- Enzyme "proteins" are similar

	Sequence	3D
Globally	Full-length	Fold
Locally	Motif	Cavity

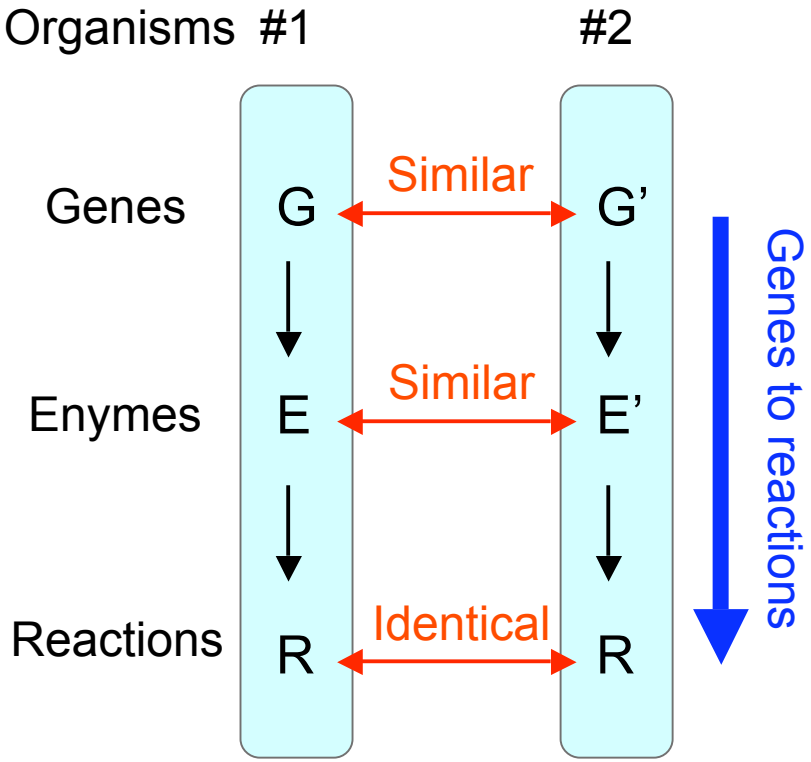
- Enzyme "reactions" are similar

	Reaction	Substrates
Globally	?	?
Locally	?	?

Genome annotation with chemical point of view

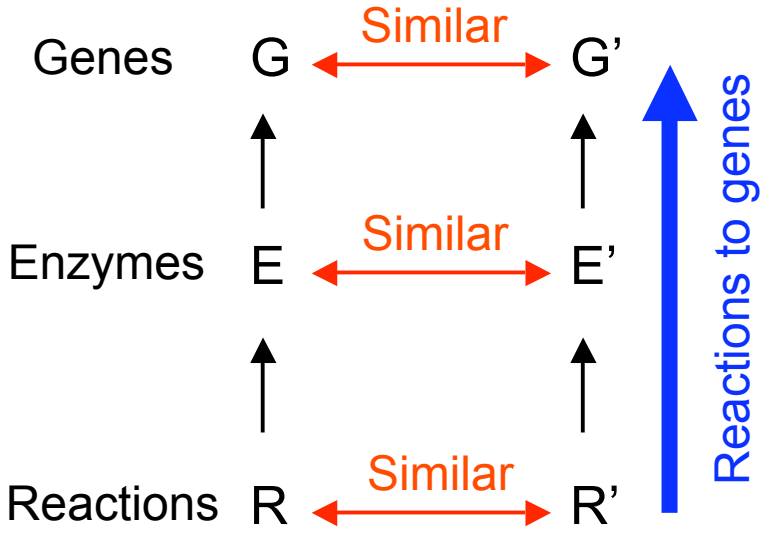
KEGG Orthology (KO)

Sequence similarity groups



Reaction Class (RC)

Reaction similarity groups



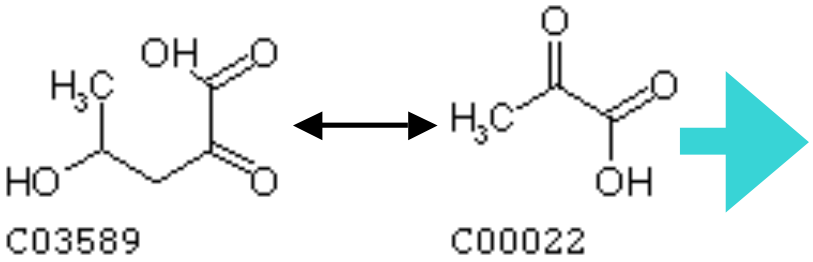
Development of a chemical structure comparison method for integrated analysis of chemical and genomic information in the metabolic pathways

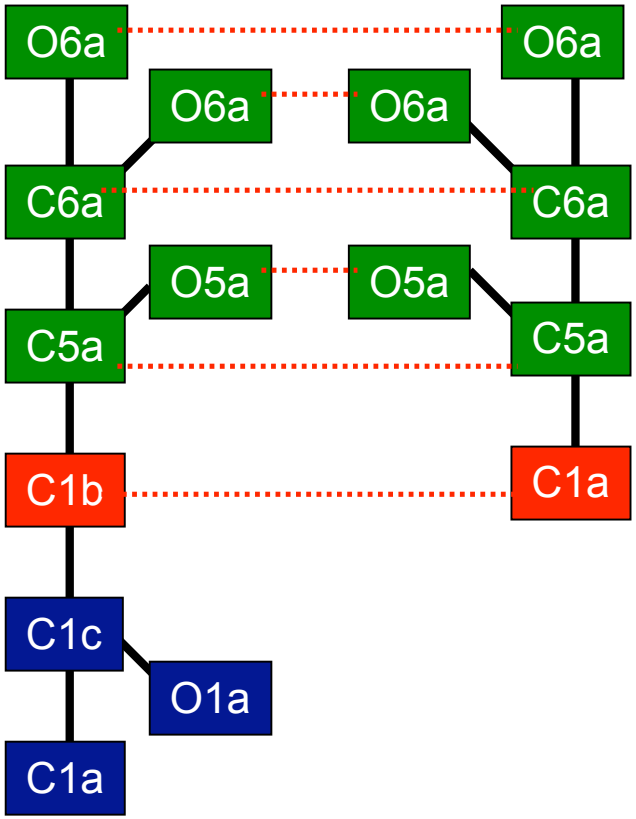
M Hattori, Y Okuno, S Goto, M Kanehisa - J. Am. Chem. Soc, 2003 - ACS Publications

Cellular functions result from intricate networks of molecular interactions, which involve not only proteins and nucleic acids but also small chemical compounds. Here we present an efficient algorithm for comparing two chemical structures of compounds, where the chemical ...

引用元 112 - 関連記事 - 全 4 バージョン

Atom alignment of the molecular graphs



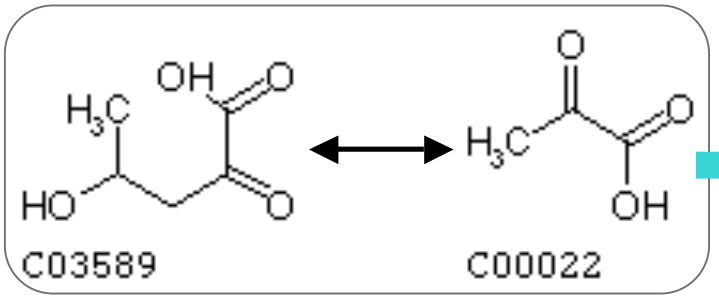


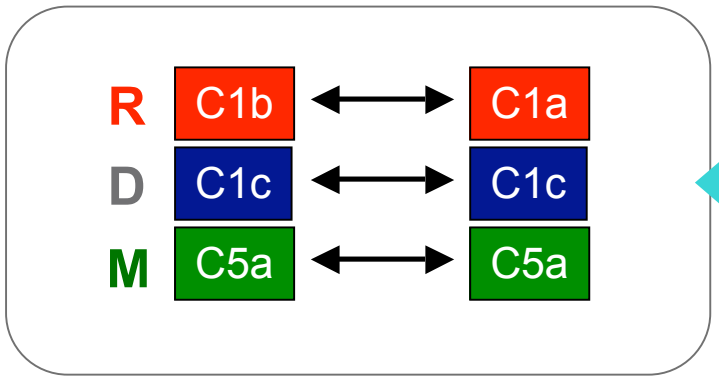
Computational assignment of the EC numbers for genomic-scale analysis of enzymatic reactions

M Kotera, Y Okuno, M Hattori, S Goto, M ... - J. Am. Chem. ..., 2004 - ACS Publications

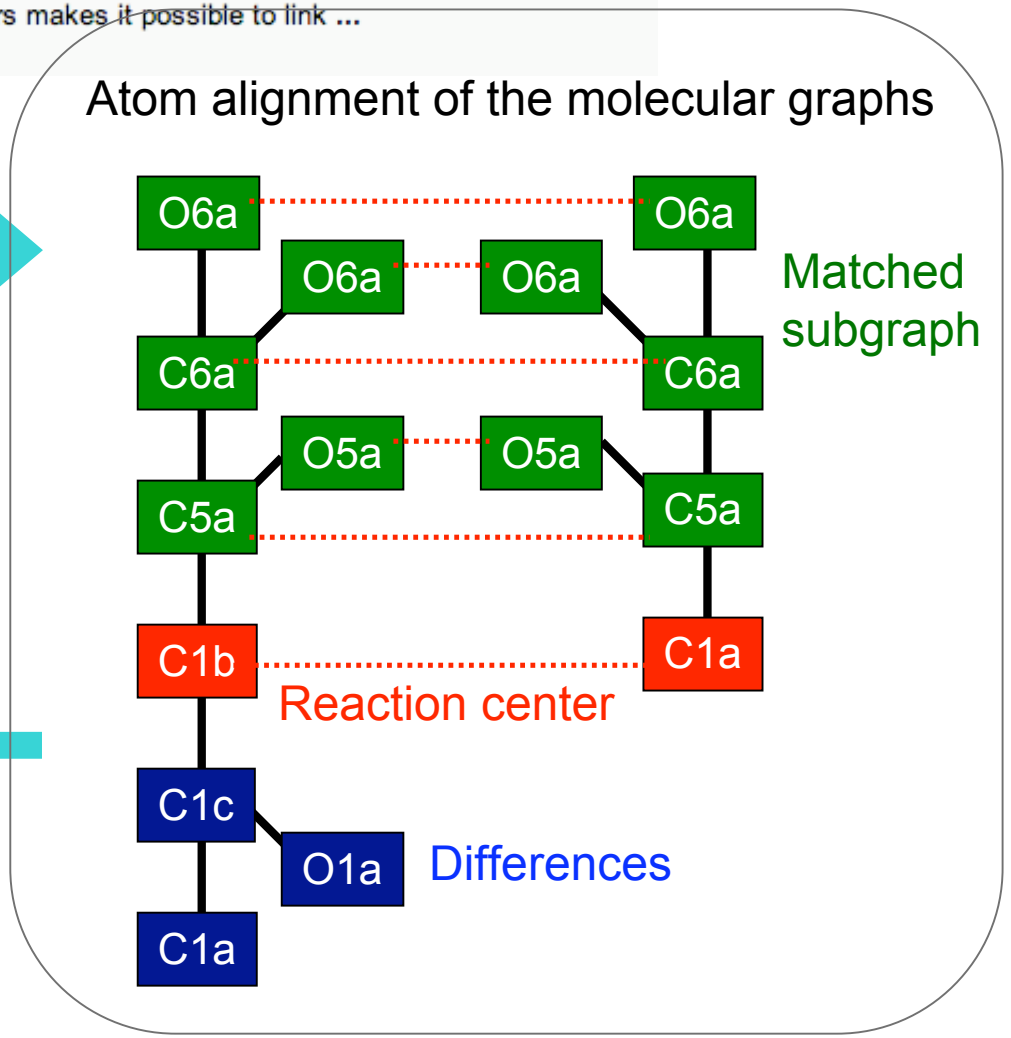
The EC (Enzyme Commission) numbers represent a hierarchical classification of enzymatic reactions, but they are also commonly utilized as identifiers of enzymes or enzyme genes in the analysis of complete genomes. This duality of the EC numbers makes it possible to link ...

引用元 68 - 関連記事 - 全 7 バージョン





RDM chemical transformation pattern

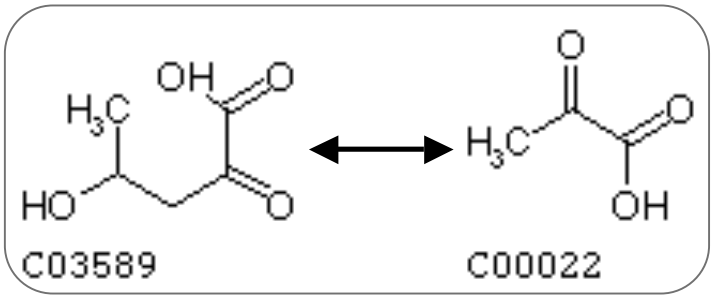


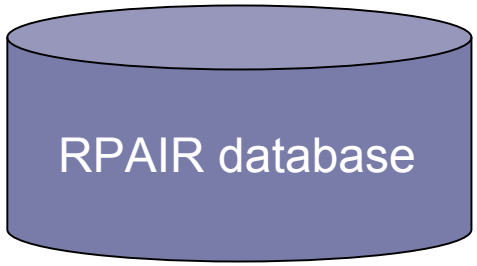
[HTML] **E-zyme: predicting potential EC numbers from the chemical transformation pattern of substrate-product pairs**

Y Yamanishi, M Hattori, M Kotera, S Goto, M ... - ..., 2009 - Oxford Univ Press

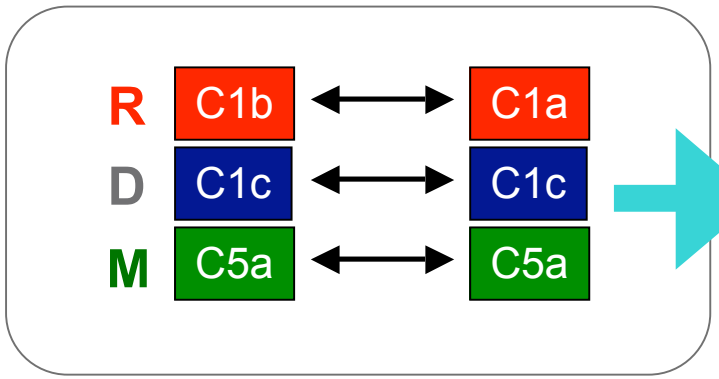
Results: In this article we propose a new method to predict the potential EC numbers to given reactant pairs (substrates and products) or uncharacterized reactions, and a web-server named E-zyme as an application. This technology is based on our original biochemical ...

引用元 10 - 関連記事 - 全 11 バージョン





Known correspondence between RDM patterns and enzyme classifications



RDM chemical transformation pattern

What kind of enzymes may catalyze this reaction?

!

KEGG PATHWAY

http://www.genome.jp/kegg/pathway.html

KEGG PATHWAY Database

Wiring diagrams of molecular interactions, reactions, and relations

KEGG2 PATHWAY BRITE DISEASE DRUG KO GENES GENOME LIGAND DBGET

Select prefix: map | Organism

Enter keywords: | Go | Help

Pathway Maps

KEGG PATHWAY is a collection of manually drawn pathway maps (see new maps, change history, and last updates) representing our knowledge on the molecular interaction and reaction networks for:

0. Global Map
1. Metabolism
Carbohydrate Energy Lipid Nucleotide Amino acid Other amino acid Glycan
Cofactor/vitamin Terpenoid/PK Other secondary metabolite Xenobiotics Overview
2. Genetic Information Processing
3. Environmental Information Processing
4. Cellular Processes
5. Organismal Systems
6. Human Diseases

and also on the structure relationships (KEGG drug structure maps) in:

7. Drug Development

KEGG MEDICUS

http://www.genome.jp/kegg/medicus.html

KEGG MEDICUS

Molecular network based information resource for diseases and drugs

KEGG2 | PATHWAY | BRITE | MEDICUS | DISEASE | DRUG | EDRUG | Atlas

KEGG MEDICUS

KEGG MEDICUS is a new interface under development for molecular network-based analysis of diseases, drugs, and environmental compounds. The following list of KEGG pathway maps presents a pathway-based view of known disease genes and drug targets. Disease genes in the Gene field of KEGG DISEASE (H number) entries and drug targets in the Target field of KEGG DRUG (D number) entries are summarized in each pathway map.

Disease genes and drug targets in KEGG pathways

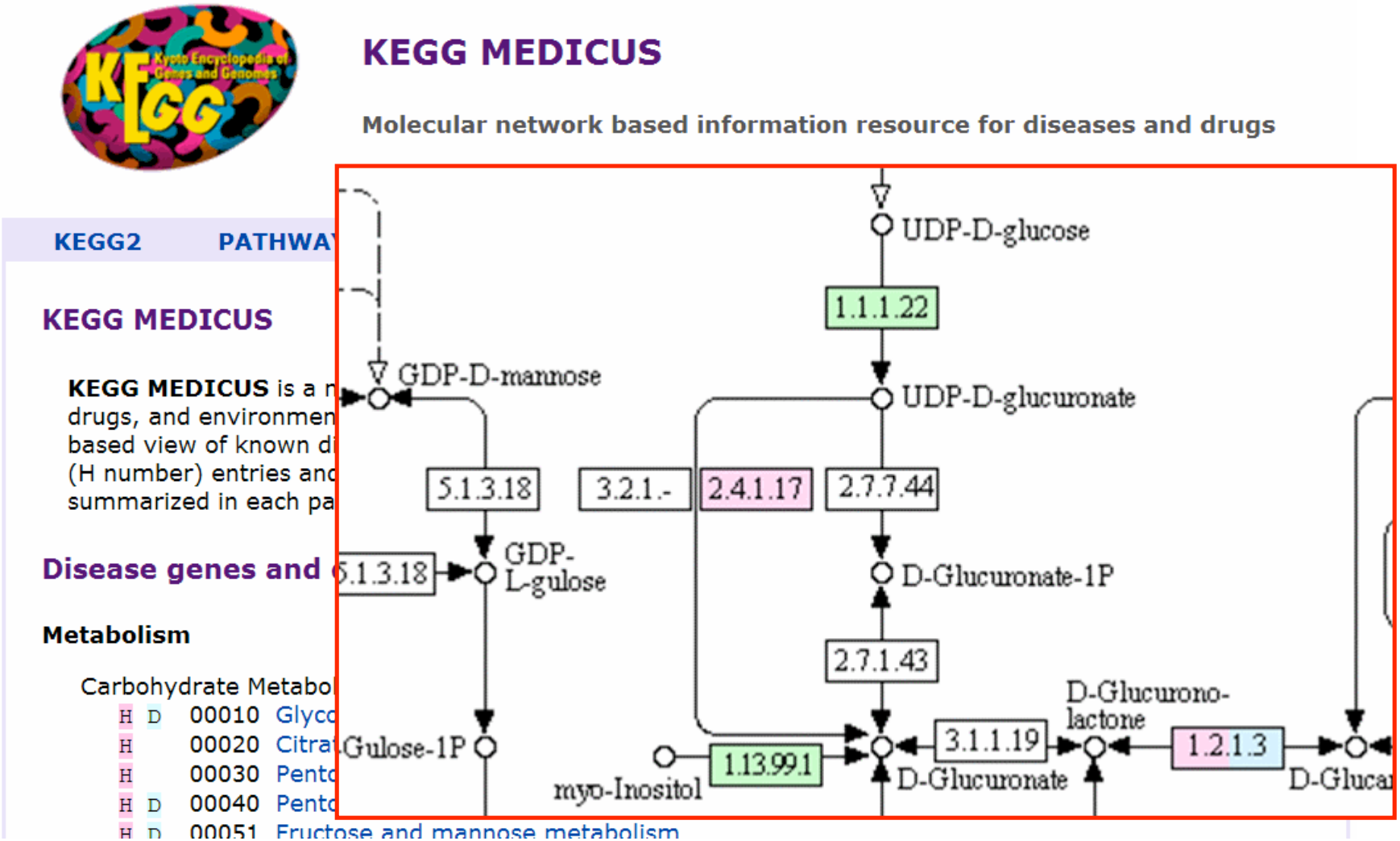
Metabolism

Carbohydrate Metabolism

H	D	00010	Glycolysis / Gluconeogenesis
H		00020	Citrate cycle (TCA cycle)
H		00030	Pentose phosphate pathway
H	D	00040	Pentose and glucuronate interconversions
H	D	00051	Fructose and mannose metabolism

KEGG MEDICUS

http://www.genome.jp/kegg/medicus.html



KEGG MEDICUS

http://www.genome.jp/kegg/medicus.html

KEGG2 PATH

KEGG MEDICUS

KEGG MEDICUS is
drugs, and environ
based view of know
(H number) entries
summarized in each

Disease genes ar

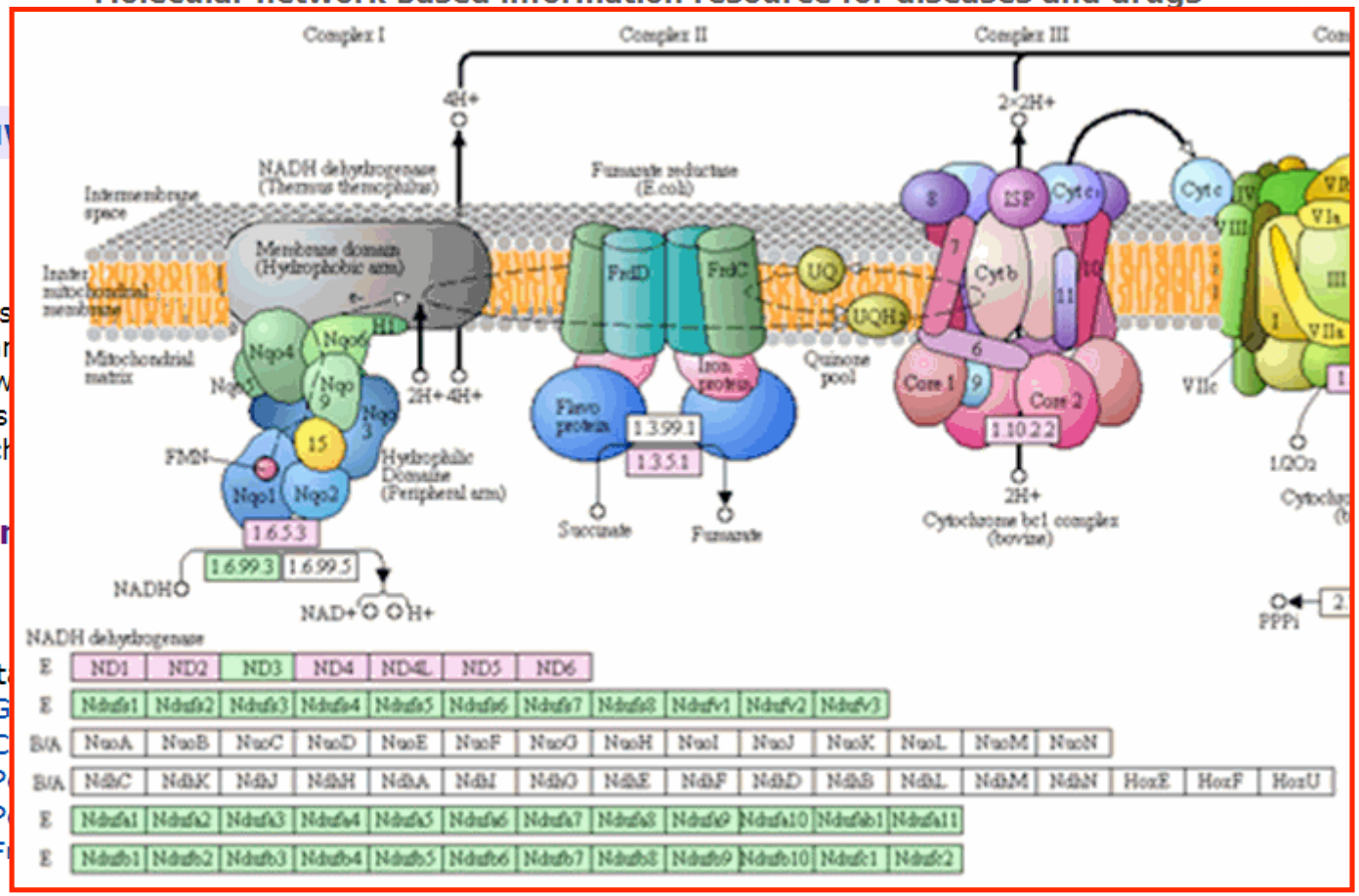
Metabolism

Carbohydrate Met

H	D	00010	G
H		00020	C
H		00030	P
H	D	00040	P
H	D	00051	F

KEGG MEDICUS

Molecular network based information resource for diseases and drugs



KEGG MEDICUS

http://www.genome.jp/kegg/medicus.html

KEGG MEDICUS

Molecular network based information resource for diseases and drugs

KEGG2 PA

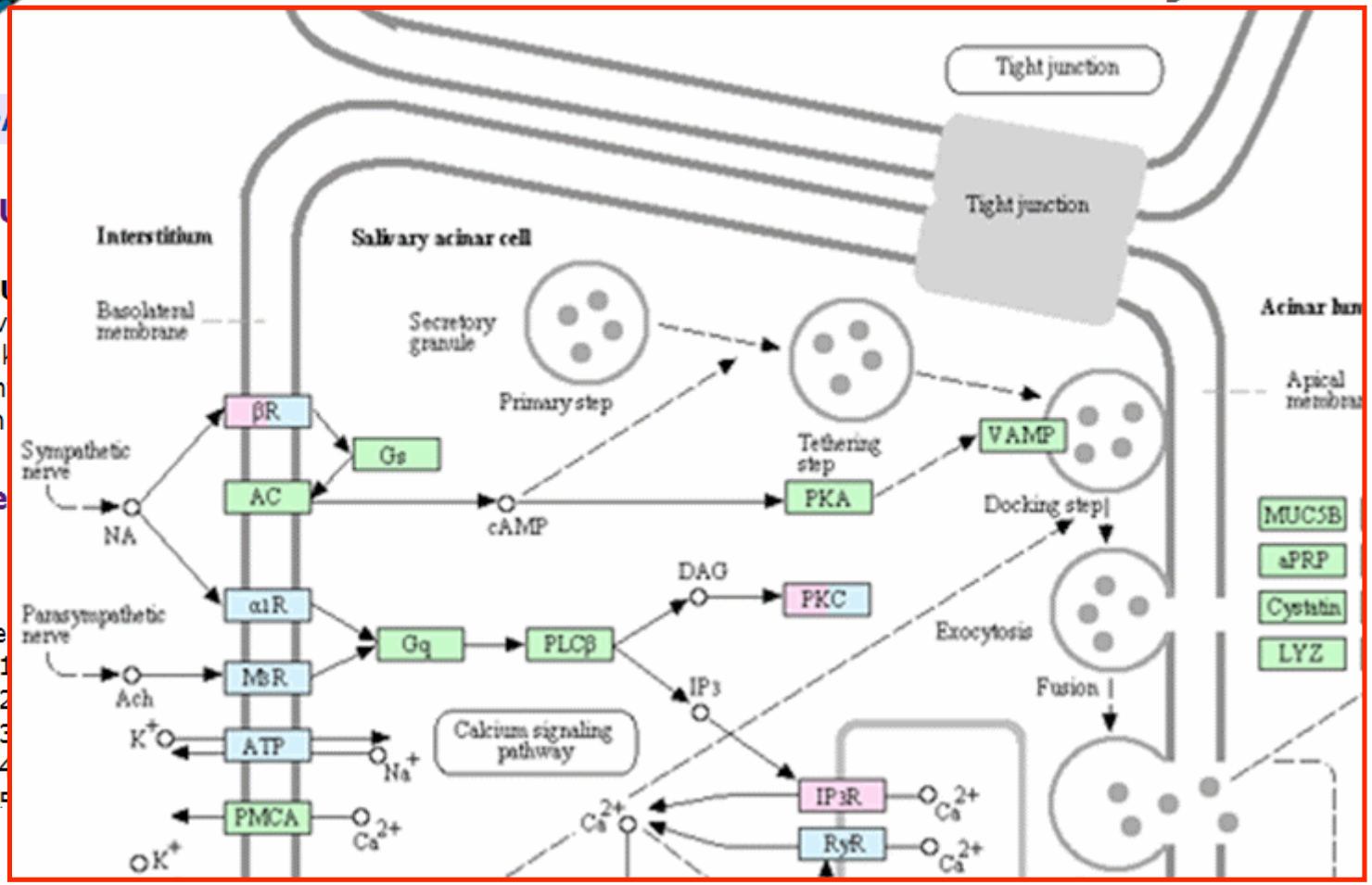
KEGG MEDICU

KEGG MEDICU
drugs, and env
based view of
(H number) en
summarized in

Disease gene

Metabolism

Carbohydrate
H D 0001
H 0002
H 0003
H D 0004
H D 0005



KEGG Mapper

http://www.genome.jp/kegg/mapper.html

KEGG Mapper: Overview

KEGG Mapper | Search Pathway | Color Pathway | Search Brite | Color Brite | Join Brite

KEGG Mapper

KEGG Mapper is a collection of KEGG mapping tools, both for KEGG pathway mapping and BRITE mapping (ontology enrichment). Two pathway mapping tools, "Search Pathway" and "Color Pathway", were made available from the beginning of the KEGG project. Although the naming of these tools is somewhat misleading since both involve searching and coloring procedures, similar naming was introduced to BRITE mapping as well. With the release of the third BRITE mapping tool, Join Brite, the collection of five tools shown below is now called KEGG Mapper.

Pathway mapping tools

- Search Pathway - basic pathway mapping tool where mapped objects are marked in red
- Color Pathway - modified pathway mapping tool where mapped objects are marked in any color

Brite mapping tools

- Search Brite - basic brite mapping tool where mapped objects are marked in red
- Color Brite - modified brite mapping tool where mapped objects are marked in any color
- Join Brite - enhanced brite mapping tool where, instead of coloring, given attributes of mapped objects are shown in an additional column or an additional level of hierarchy

KEGG Mapper

http://www.genome.jp/kegg/mapper.html

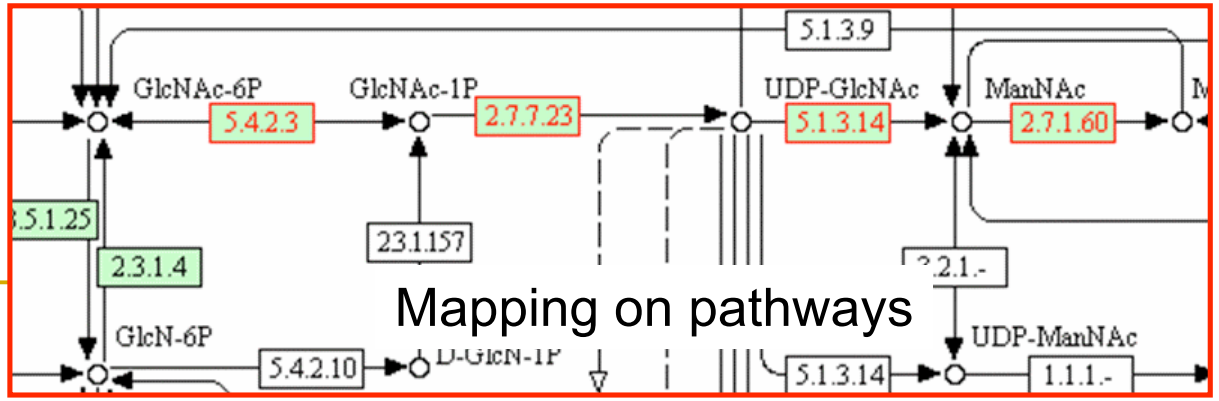
List of genes

11251
64579
27242
9331
51744
7436
8396
11001
8542
8611
26290
53340
7804
4585
55512
6361
6364
3579
914
5175
5553

KEGG Mapper

hsa04060 Cytokine-cytokine receptor interaction - Homo sapiens (human) (56)
hsa04510 Focal adhesion - Homo sapiens (human) (48)
hsa04062 Chemokine signaling pathway - Homo sapiens (human) (38)
tural killer cell mediated cytotoxicity - Homo sapiens (human) (34)
hsa05146 Amoebiasis - Homo sapiens (human) (34)
hsa04810 Regulation of actin cytoskeleton - Homo sapiens (human) (33)
hsa04142 Lysosome - Homo sapiens (human) (31)
hsa00564 Glycerophospholipid metabolism - Homo sapiens (human) (31)
hsa04512 ECM-receptor interaction - Homo sapiens (human) (30)
hsa04010 MAPK signaling pathway - Homo sapiens (human) (30)
hsa04310 Wnt signaling pathway - Homo sapiens (human) (28)
hsa00510 N-Glycan biosynthesis - Homo sapiens (human) (28)
hsa04070 Phosphatidylinositol signaling system
hsa04145 Phagosome - Homo sapiens (human) (27)
hsa04666 Fc gamma R-mediated phagocytosis - Homo sapiens (human) (26)
hsa00520 Amino sugar and nucleotide sugar metabolism - Homo sapiens (human) (25)
hsa04910 Insulin signaling pathway - Homo sapiens (human) (25)
hsa04664 Fc epsilon RI signaling pathway - Homo sapiens (human) (24)

List of pathways



Mapping on pathways

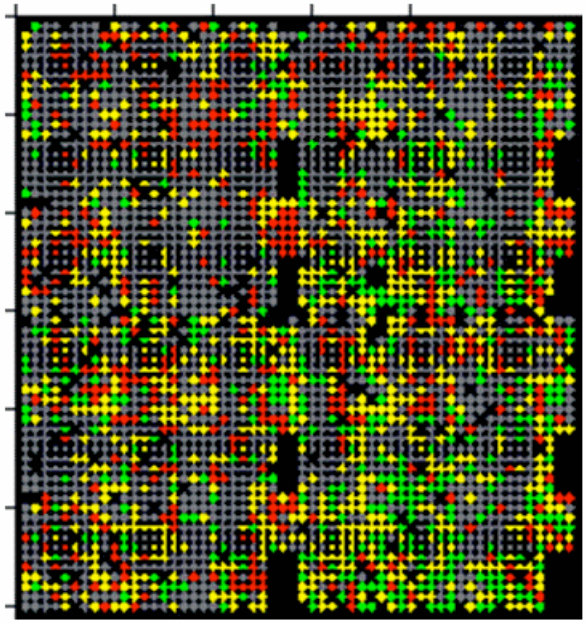
KEGG Expression

http://www.genome.jp/kegg/expression/

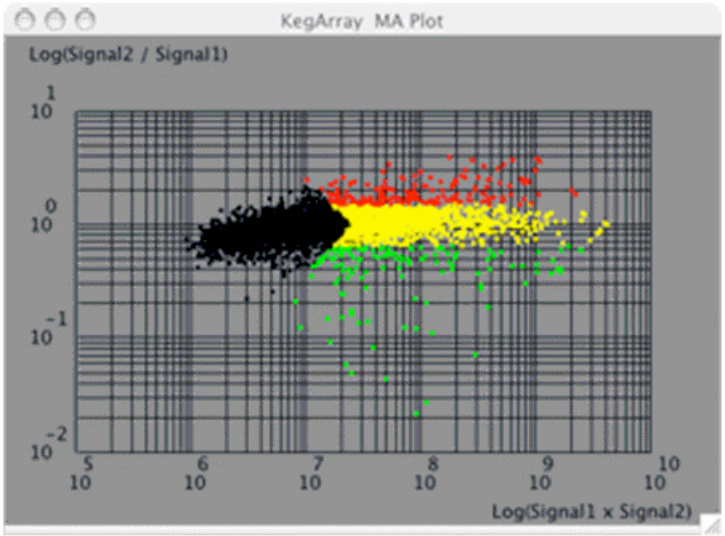
KEGG EXPRESSION Database

for mapping gene expression profiles to pathways and genomes

KEGG EXPRESSION Database



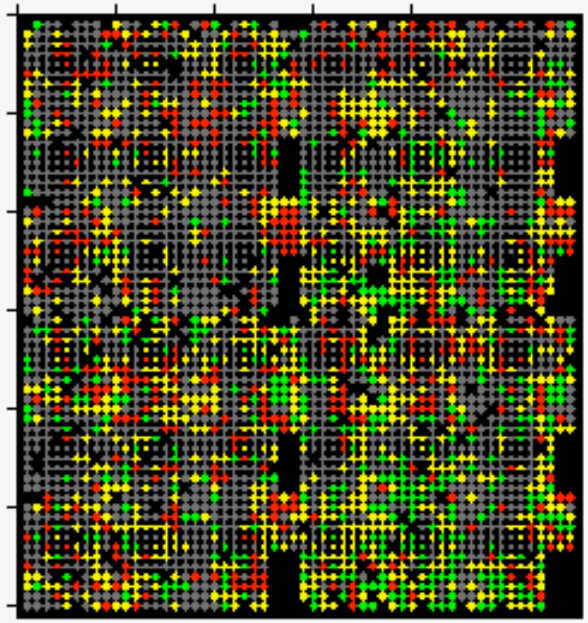
KegArray

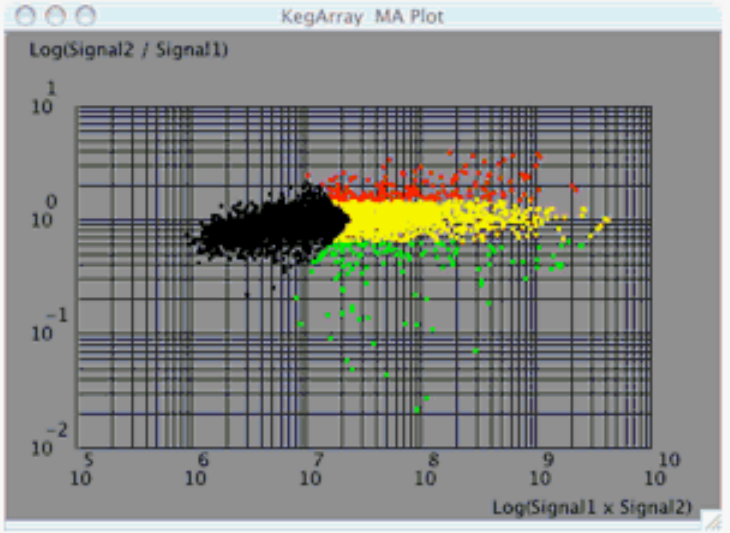


KegArray is a standalone Java application for integrated analysis of gene expression profiles

KEGG Expression

http://www.genome.jp/kegg/expression/





KEGG EXPRESSION is a repository of microarray gene expression profile data for Synechocystis PCC6803 (syn), Bacillus subtilis (bsu), Escherichia coli W3110 (ecj), Anabaena PCC7120 (ana), and other species contributed by the Japanese research community.

- List of experimental data available
- DBGET search
- Download data by FTP

- CYORF: cyanobacteria database
- BSORF: Bacillus subtilis database

KegArray is a standalone Java application for integrated analysis of gene expression profiles together with KEGG pathways and KEGG genomes. KegArray runs on Mac and Windows and is made freely available to both academic and non-academic users.

Click here.

- KEGG API - for software developers
- LinkDB - for finding genes that are mapped to KEGG pathways
- Color genes in the KEGG pathway map

EXPRESSION Database

[Brite menu]

▼ ▼ ▼

▼ **Synechocystis sp. PCC6803**

- ▶ Suzuki et al. (2001), Synechocystis PCC6803 cold shock response [PMID:11298290] ==> Cluster analysis
- ▶ Hihara et al. (2001), Synechocystis PCC6803 acclimation from low to high light intensity [PMID:11283337] ==> Cluster analysi
- ▶ Yoshimura et al. (2001), Synechocystis PCC6803 cAMP receptor protein sycrp1 (sll1371) mutant [PMID:12085767]
- ▶ Hihara et al. (2003), Synechocystis PCC6803 redox-responsive genes [PMID:12591891]
- ▶ Kobayashi et
- ▶ and regulate distinct
- ▶ Kucho et al.
- ▶ Shoumskaya et al. (2005), Synechocystis PCC6803 identical Hik-Rre systems [PMID:15805106]
- ▶ Panichkin et al. (2006), Synechocystis PCC6803 serine/threonine protein kinase SpkA [PMID:16916897]
- ▶ Dmitry et al. (2006), Cold-inducible genes in Synechocystis sp. PCC 6803
- ▶ Kanesaki et al. (2007), Sensors and signal transducers of environmental stress in cyanobacteria [PMID:17181779]
- ▶ Prakash et al. (2007), DNA supercoiling regulates the stress-inducible expression of genes in Synechocystis sp. PCC 6803
- ▶ Panichkin et al. (2008), Ser/Thr protein linases are involved in cold-signal transduction in a cyanobacterium
- ▶ Prakash et al. (2009), RNA helicase, CrhR, enhances the low temperature-inducible expression of heat shock genes groESL and

▼ **Bacillus subtilis** ==> Cluster analysis

- ▶ Yoshida et al. (2001), Bacillus subtilis glucose repression [PMID:11160890]
- ▶ Ogura et al. (2001), Bacillus subtilis DegU, ComA and PhoP regulons [PMID:11557812]

Click one of these triangles.

EXPRESSION Database

[Brite menu]

▼ ▼ ▼

▼ **Synechocystis sp. PCC6803**

▼ Suzuki et al. (2001), Synechocystis PCC6803 cold shock response [PMID:11298290] ==> Cluster analysis

exn0000001 wild type transferred from 34C to 22C (normalized data only). Download data
ex0000012 wild type transferred from 34C to 22C [WT 34C/22C-1]
ex0000013 wild type t
ex0000014 wild type t
ex0000015
ex0000002 wild type t
ex0000003 wild type t

exn0000002 hik33 disru
ex0000008 hik33 disru
ex0000009 hik33 disru
ex0000010 hik33 disruptant transferred from 34C to 22C [Hik33 34C/22C-3]
ex0000011 hik33 disruptant transferred from 34C to 22C [Hik33 34C/22C-4]
ex0000004 hik33 disruptant transferred from 34C to 22C [Hik33 34C/22C-5]
ex0000005 hik33 disruptant transferred from 34C to 22C [Hik33 34C/22C-6]

exn0000003 hik33 disruptant vs. wild type at 34C (normalized data only). Download data
ex0000016 hik33 disruptant vs. wild type at 34C [WT/Hik33-1]
ex0000017 hik33 disruptant vs. wild type at 34C [WT/Hik33-2]
ex0000018 hik33 disruptant vs. wild type at 34C [WT/Hik33-3]
ex0000019 hik33 disruptant vs. wild type at 34C [WT/Hik33-4]
ex0000006 hik33 disruptant vs. wild type at 34C [WT/Hik33-5]
ex0000007 hik33 disruptant vs. wild type at 34C [WT/Hik33-6]

▶ Hihara et al. (2001), Synechocystis PCC6803 acclimation from low to high light intensity [PMID:11283337] ==> Cluster analysi

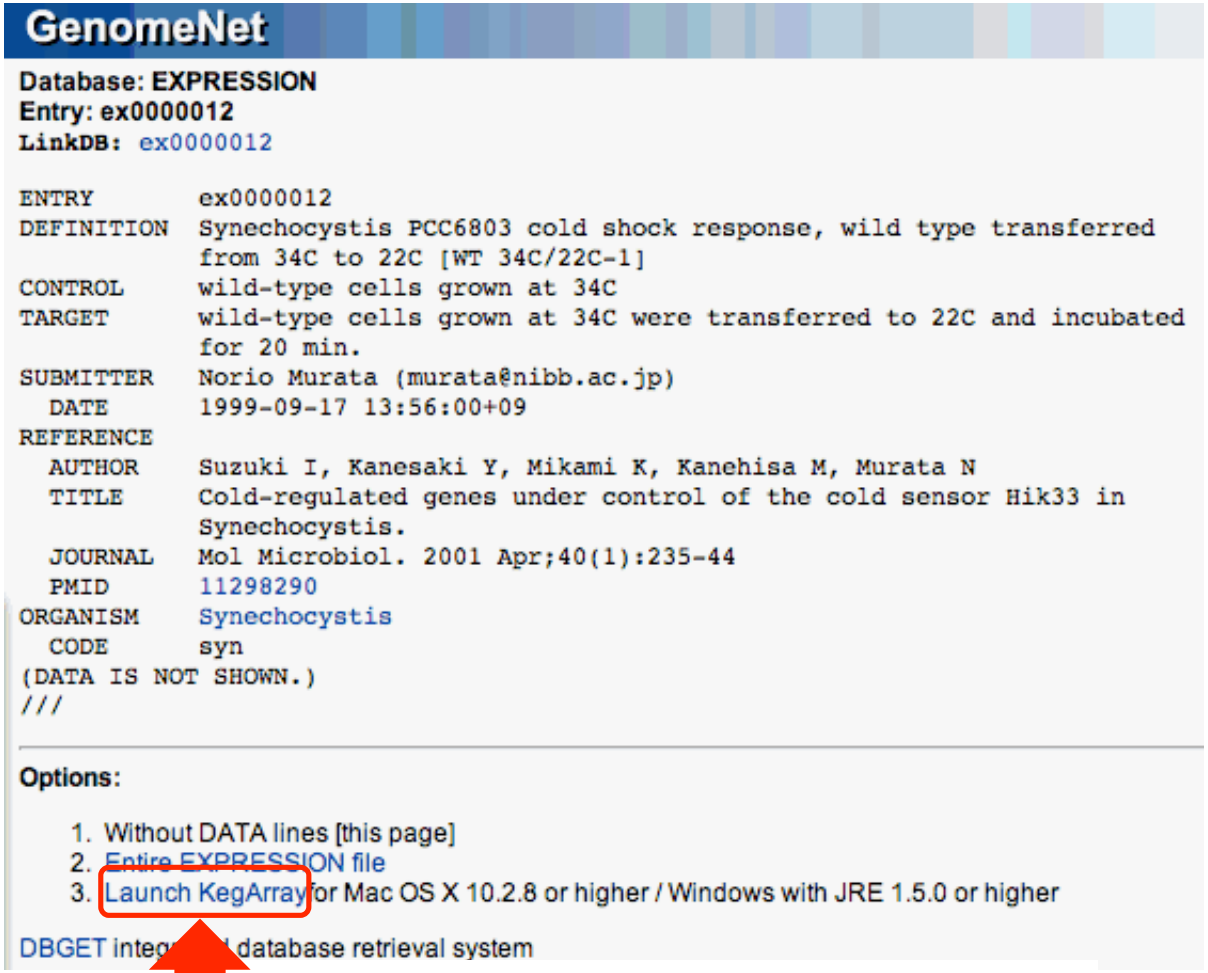
▶ Yoshimura et al. (2001), Synechocystis PCC6803 cAMP receptor protein sycrp1 (sll1371) mutant [PMID:12085767]

▶ Hihara et al. (2003), Synechocystis PCC6803 redox-responsive genes [PMID:12591891]

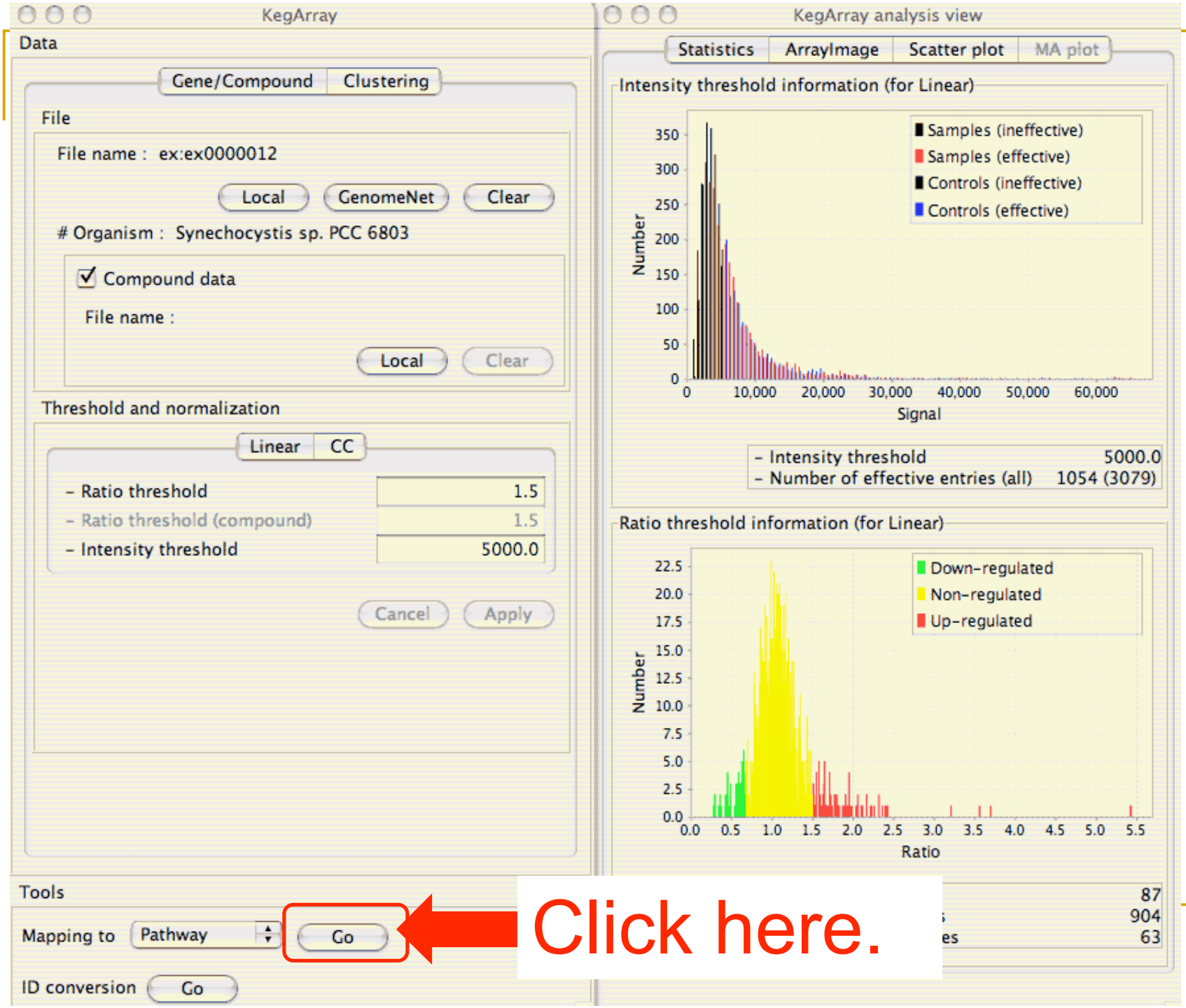
Select one of these experiments.

KEGG Expression

http://www.genome.jp/kegg/expression/



Launch KegArray

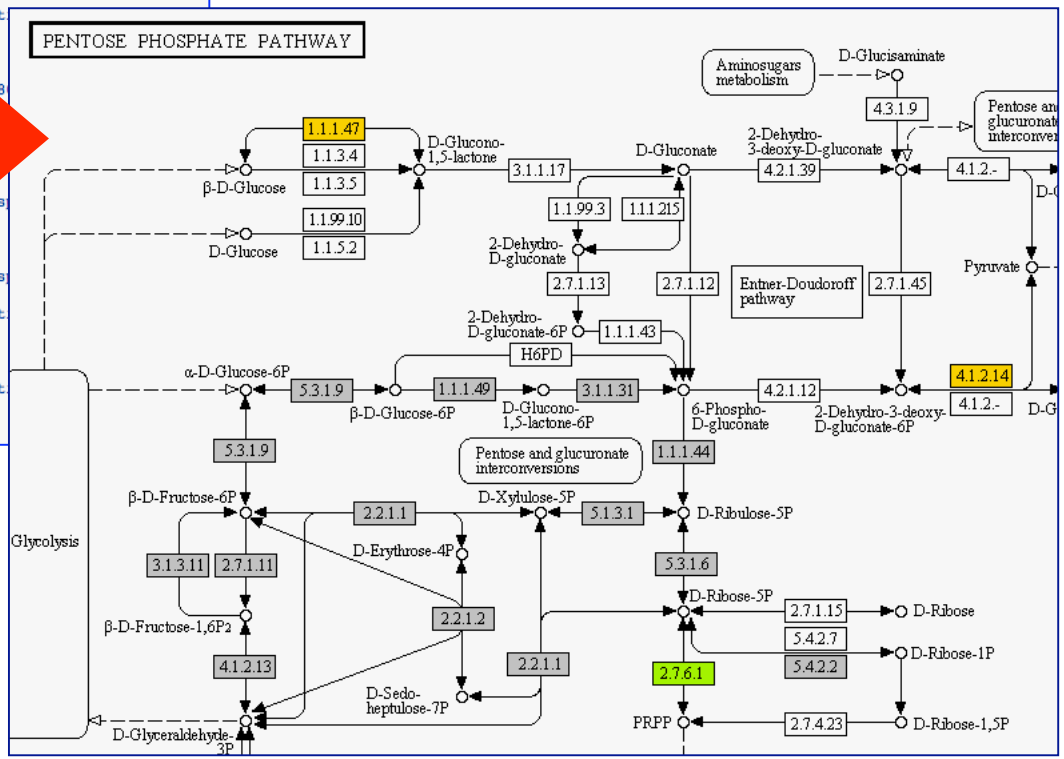

KegArray
Data
Gene/Compound
Clustering
File
File name : ex:ex0000012
Local
GenomeNet
Clear
Organism : Synechocystis sp. PCC 6803
Compound data
File name :
Local
Clear
Threshold and normalization
Linear
CC
- Ratio threshold 1.5
- Ratio threshold (compound) 1.5
- Intensity threshold 5000.0
Cancel
Apply
Tools
Mapping to
Pathway
Go
ID conversion
Go
KegArray analysis view
Statistics
ArrayImage
Scatter plot
MA plot
Intensity threshold information (for Linear)
Samples (ineffective)
Samples (effective)
Controls (ineffective)
Controls (effective)
Number
Signal
- Intensity threshold 5000.0
- Number of effective entries (all) 1054 (3079)
Ratio threshold information (for Linear)
Down-regulated
Non-regulated
Up-regulated
Number
Ratio
87
904
63
Click here.

Pathway Search Result

Sort by the pathway list

Show all objects

- syn01100 Metabolic pathways - Synechocystis sp. PCC6803 (48)
- syn00195 Photosynthesis - Synechocystis sp. PCC6803 (12)
- syn01110 Biosynthesis of secondary metabolites - Synechocystis sp. PCC6803 (12)
- syn03010 Ribosome - Synechocystis sp. PCC6803 (10)
- syn00196 Photosynthesis - antenna proteins - Synechocystis sp. PCC6803 (8)
- syn02010 ABC transporters - Synechocystis sp. PCC6803 (8)
- syn00190 Oxidative phosphorylation - Synechocystis sp. PCC6803 (4)
- syn03018 RNA degradation - Synechocystis sp. PCC6803 (4)
- syn00030 Pentose phosphate pathway - Synechocystis sp. PCC6803 (3)
- syn00520 Amino sugar and nucleotide sugar metab… Synechocyst…
- syn00230 Purine metabolism - Synechocystis sp. … (3)
- syn00330 Arginine and proline metabolism - Syne… is sp. PC…
- syn00010 Glycolysis / Gluconeogenesis - Synechocy…
- syn02020 Two-component system - Synechocystis sp. PCC6803 …
- syn00630 Glyoxylate and dicarboxylate metabolism - Synechocystis s…
- syn00061 Fatty acid biosynthesis - Synechocystis sp. PCC6803 (2)
- syn01040 Biosynthesis of unsaturated fatty acids - Synechocystis s…
- syn00710 Carbon fixation in photosynthetic organisms - Synechocyst…
- syn00680 Methane metabolism - Synechocystis sp. PCC6803 (2)
- syn00250 Alanine, aspartate and glutamate metabolism - Synechocyst…
- syn00480 Glutathione metabolism - Synechocystis sp. PCC6803 (1)



レポート課題

- KEGG Expression データベースから好きな実験を選び、KegArray を用いて Pathway 上へマッピングし、その結果を考察せよ。
- 提出先：kyomu@bic.kyoto-u.ac.jp
- 締切：2010年11月15日（月）