



**Learning KEGG
via a web interface**

- KEGG PATHWAY part 1 -

**Wataru Honda
Bioinformatics Center
Kyoto University, JAPAN**



Genomic Information (GENES,KO)

Network Information

Chemical Information (LIGAND)

KEGG PATHWAY

Well-established knowledge on molecular interactions



Genomic Information (GENES, KO)

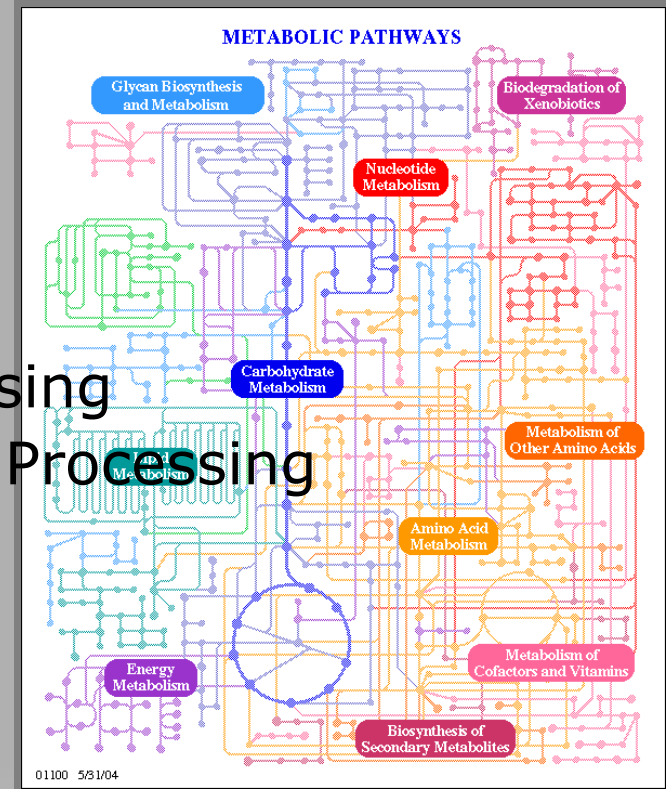
Network Information

Chemical Information (LIGAND)

KEGG PATHWAY

Well-established knowledge on molecular interactions

- Contents of DB
 - Metabolic pathways
 - Regulatory pathways
 - Genetic Information Processing
 - Environmental Information Processing
 - Cellular Processes
 - Human Diseases
 - Drug structure maps



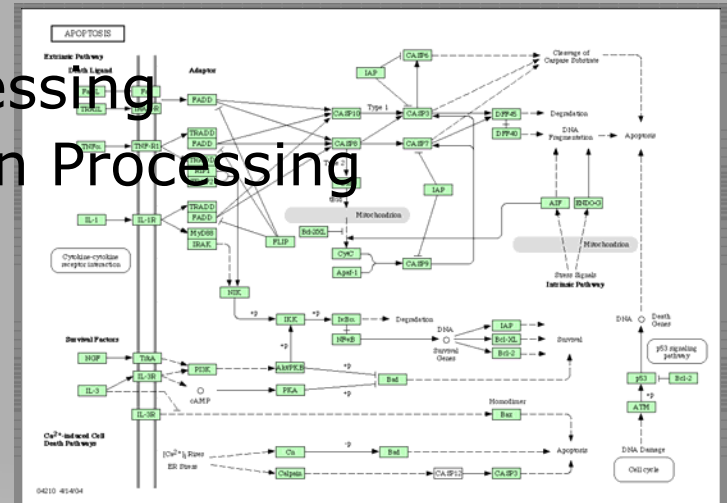
KEGG PATHWAY

- Contents of DB
 - Metabolic pathways

- Regulatory pathways

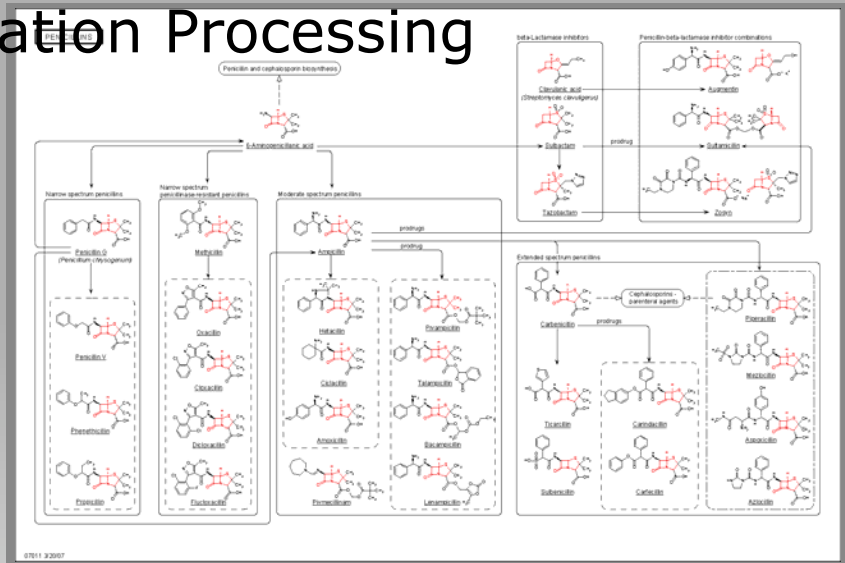
- Genetic Information Processing
- Environmental Information Processing
- Cellular Processes
- Human Diseases

- Drug structure maps



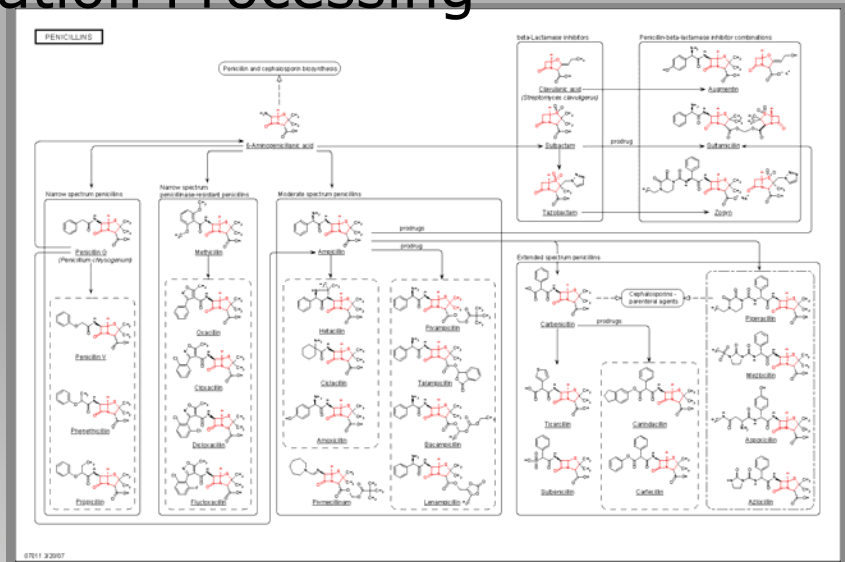
KEGG PATHWAY

- Contents of DB
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KEGG PATHWAY

- Contents of DB
 - Metabolic pathways
 - Regulatory pathways
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 - Human Diseases
 - Drug structure maps
→Next speaker



KEGG PATHWAY

- Contents of DB

- ➔ • Metabolic pathways

- ➔ • Regulatory pathways

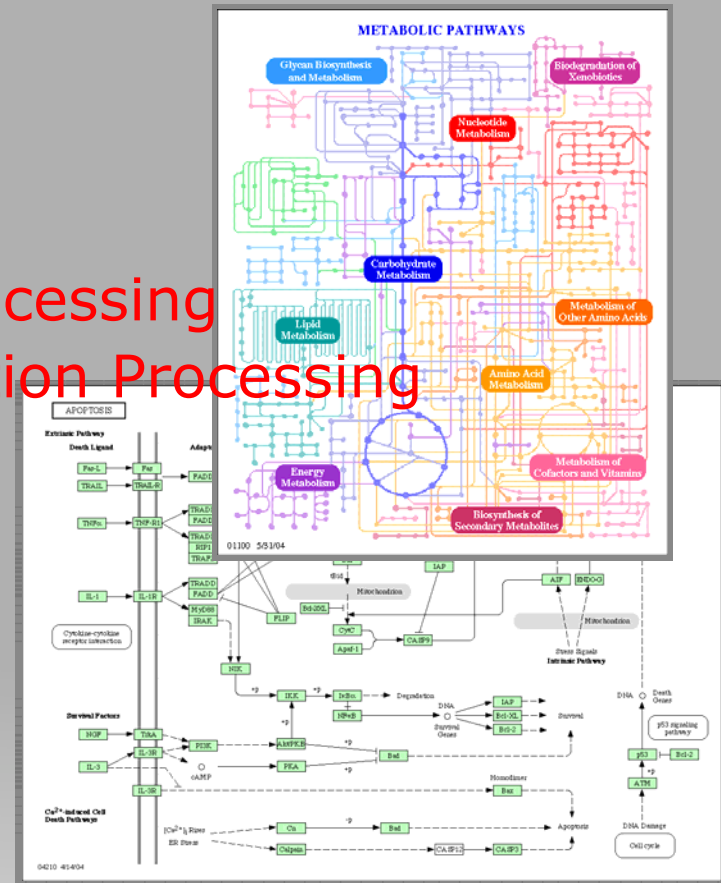
- Genetic Information Processing

- Environmental Information Processing

- Cellular Processes

- Human Diseases

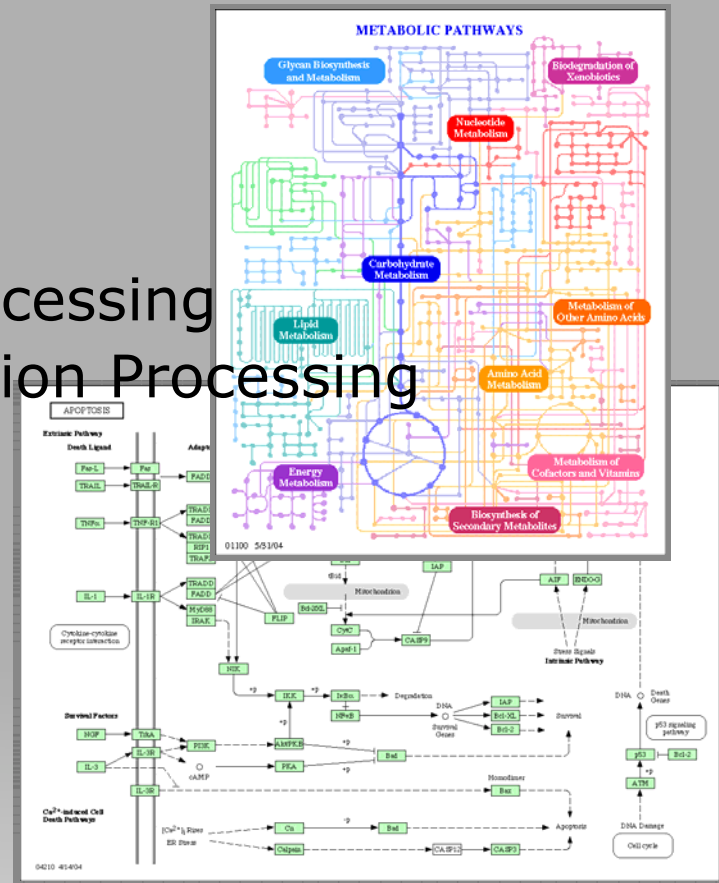
- Drug structure maps



KEGG PATHWAY

- Contents of DB
- ➔ • **Metabolic pathways**

- Regulatory pathways
 - Genetic Information Processing
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KEGG PATHWAY

http://www.genome.jp/kegg/pathway.html
or
you can find it by clicking ...

KEGG - Table of Contents

KEGG2 ATLAS PATHWAY BRITE GENES SSDB LIGAND DBGET

Search [KEGG] for [] Go Clear

Category	Entry Point	Release Info	Search & Compute	DBGET Search
Systems information	KEGG ATLAS	New maps Update status	KEGG metabolism map Search objects in pathways Color objects in pathways Map relations to hierarchies KEGG Orthology (KO)	PATHWAY BRITE MODULE DISEASE
	KEGG PATHWAY			
	KEGG BRITE			
Genomic information	KEGG GENES	New organisms Update status	SSDB search BLAST search FASTA search EGassembler for ESTs KAAS automatic annotation GENES network prediction	ORTHOLOGY GENES DGENES / EGENES GENOME VGENES / OGENES VGENOME
Chemical information	KEGG LIGAND	Update status	SIMCOMP compound search KCAH glycan search a-zyme reaction prediction PathComp computation	COMPOUND DRUG GLYCAN REACTION PAIR ENZYME

See Kanahisa et al. (2008) for the new features of KEGG.

KEGG2 DISEASE DRUG GLYCAN COMPOUND REACTION Organisms

KEGG for specific organisms

KEGG Organisms - the list of currently available organisms
Choose [Organism] [Go] [Clear] (examples) hsa mmu sce eco bsu svm

Customize the organism menu in pathway maps with selected organisms [Select]

Show currently selected organisms (All organisms in GENES)

KEGG for selected research areas

GenomeNet

KEGG KEGG2 PATHWAY BRITE DRUG DBGET

[English | Japanese]

Search [All databases] for [] Go Clear

GenomeNetlet
About GenomeNet
Announcements
Release notes
Access statistics
Acknowledgments

KEGG
Overview
DB release info

DBGET
Overview
DB release info
DB growth curve

Community DBs
Sequence analysis
Genome annotation
Chemical annotation
Feedback

GenomeNet Database Service

KEGG Kyoto Encyclopedia of Genes and Genomes
KEGG Top page

KEGG ATLAS - Global maps interface
KEGG PATHWAY - System information, pathways
KEGG BRITE - System information, ontologies

KEGG GENES - Genomic information
KEGG LIGAND - Chemical information
KEGG DISEASE - Disease information resource
KEGG DRUG - Drug information resource
KEGG GLYCAN - Glycan information resource

DBGET: Integrated Database Retrieval System
DBGET search
LinkDB search

Community Databases
CYORF - Cyanobacteria annotation database
BGIORF - Bacillus subtilis genome database
EXPRESSION - Gene expression profile database

GenomeNet Computation Service

Sequence Analysis
BLAST / FASTA - Sequence similarity search
MOTIF - Sequence motif search
CLUSTALW / MAFFT / PRIN - Multiple alignment

Genome Annotation
KAAS - KEGG automatic annotation server
EGassembler - EST consensus contigs
GENES - Gene network prediction

Chemical Annotation
SIMCOMP / SUBCOMP - Structure search
KCAH - Glycan structure search
a-zyme - Reaction prediction

KEGG Organisms
KEGG Update Notes (January 4, 2008)

New features of KEGG **NEW!**

1. KEGG Atlas global map
2. KEGG MODULE database
3. KEGG DISEASE database

Features of DBGET search

1. "All databases" search option
2. Combination of brite search and blnd search
3. Direct links to original sites
4. Direct program links by Java Web Start
5. Over 500 databases in LinkDB

Kyoto University Bioinformatics Center

Where is KEGG PATHWAY?



KEGG PATHWAY Database

Wiring diagrams of molecular interactions, reactions, and relations

[KEGG2](#) [ATLAS](#) [PATHWAY](#) [BRITE](#) [GENES](#) [SSDB](#) [LIGAND](#) [DBGET](#)

Pathway Maps

KEGG PATHWAY is a collection of manually drawn pathway maps representing our knowledge on the molecular interaction and reaction networks for:

1. Metabolism

[Carbohydrate](#) [Energy](#) [Lipid](#) [Nucleotide](#) [Amino acid](#) [Other amino acid](#)
[Glycan](#) [PK/NRP](#) [Cofactor/vitamin](#) [Secondary metabolite](#) [Xenobiotics](#)

2. Genetic Information Processing

3. Environmental Information Processing

4. Cellular Processes

5. Human Diseases

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

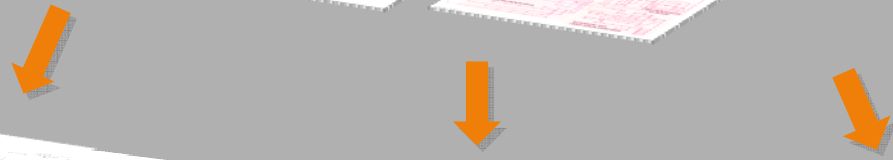
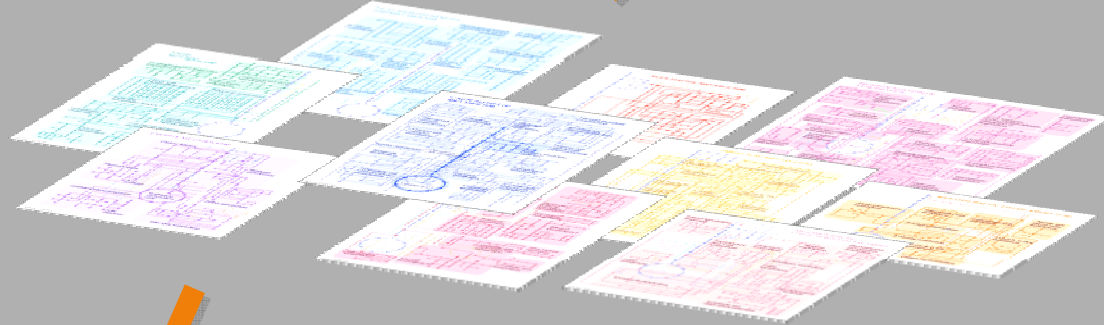
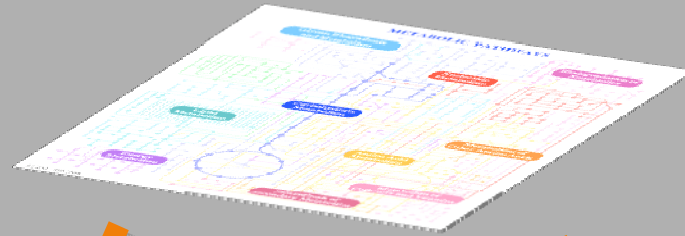
6. Drug Development

Pathway Modules

KEGG MODULE is a new collection of pathway modules, molecular complexes, and other functional

KEGG PATHWAY

Hierarchical structured



Metabolic Pathways

KEGG PATHWAY Database - Windows Internet Explorer

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

KEGG PATHWAY Database

1. Metabolism

1.1 Carbohydrate Metabolism

- Glycolysis / Gluconeogenesis
- Citrate cycle (TCA cycle)
- Pentose phosphate pathway
- Pentose and glucuronate interconversions
- Fructose and mannose metabolism
- Galactose metabolism
- Ascorbate and aldarate metabolism
- Starch and sucrose metabolism
- Aminosugars metabolism
- Nucleotide sugars metabolism
- Pyruvate metabolism
- Glyoxylate and dicarboxylate metabolism
- Propanoate metabolism
- Butanoate metabolism
- C5-Branched dibasic acid metabolism
- Inositol metabolism
- Inositol phosphate metabolism

1.2 Energy Metabolism

- Oxidative phosphorylation
- Photosynthesis
- Photosynthesis - antenna proteins
- Carbon fixation
- Reductive carboxylate cycle (CO2 fixation)
- Methane metabolism
- Nitrogen metabolism
- Sulfur metabolism

1.3 Lipid Metabolism

- Fatty acid biosynthesis
- Fatty acid elongation in mitochondria
- Fatty acid metabolism
- Synthesis and degradation of ketone bodies
- Biosynthesis of steroids
- Bile acid biosynthesis
- C21-Steroid hormone metabolism
- Androgen and estrogen metabolism
- Glycerolipid metabolism
- Glycerophospholipid metabolism
- Ether lipid metabolism
- Sphingolipid metabolism
- Arachidonic acid metabolism
- Linoleic acid metabolism
- alpha-Linolenic acid metabolism
- Polyunsaturated fatty acid biosynthesis

1.4 Nucleotide Metabolism

- Purine metabolism
- Pyrimidine metabolism

1.5 Amino Acid Metabolism

- Glutamate metabolism
- Alanine and aspartate metabolism
- Glycine, serine and threonine metabolism
- Methionine metabolism
- Cysteine metabolism

KEGG Orthology (KO)

KEGG pathway modules

Overview of biosynthetic pathways

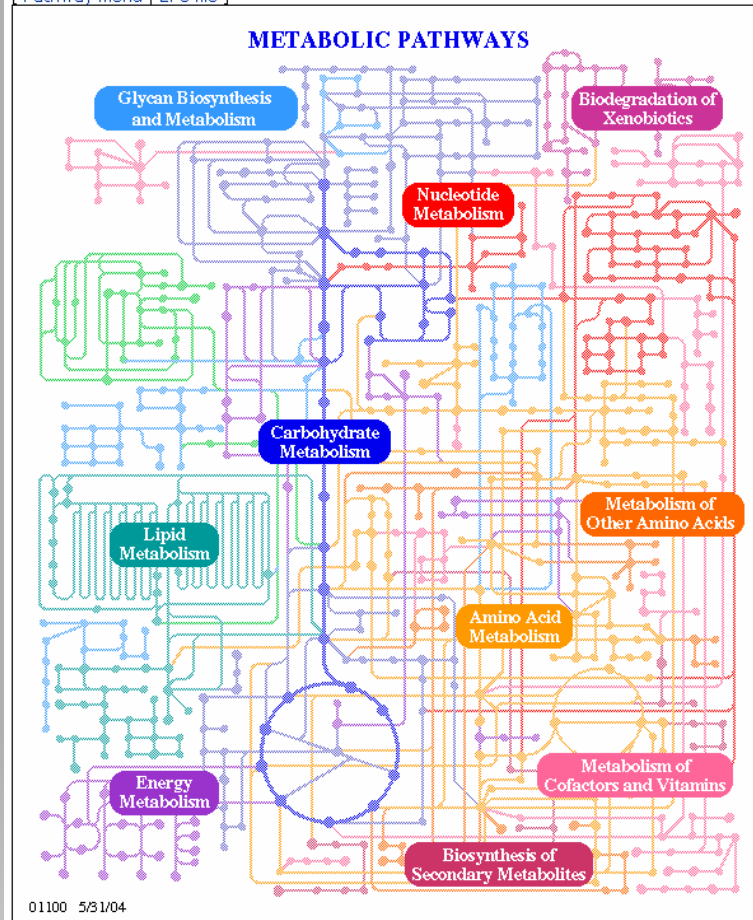
Enzymes (+diseases)

Compounds with biological roles

Photosynthesis proteins

Lipids

Metabolic Pathways



Metabolic Pathways

KEGG PATHWAY Database - Windows Internet Explorer

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

KEGG PATHWAY Database

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- Valine and leucine metabolism

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KEGG pathway modules

Overview of biosynthetic pathways

Enzymes (+diseases)

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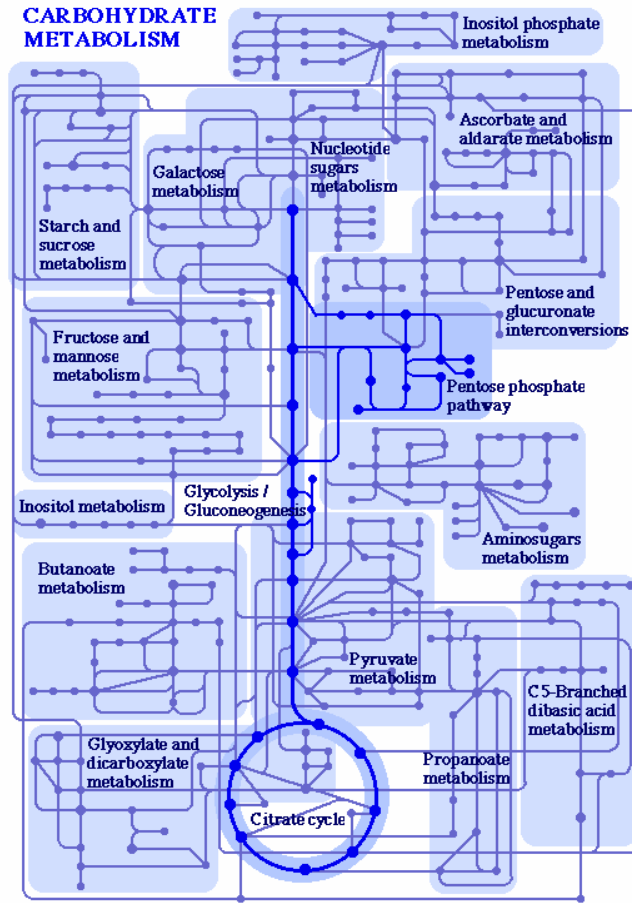
Lipids

インターネット 100%

KEGG PATHWAY

[Pathway menu]

CARBOHYDRATE METABOLISM



01110 8/10/04

Metabolic Pathways

KEGG PATHWAY Database - Windows Internet Explorer
http://www.genome.jp/kegg/pathway.html#metabolism

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1.5 Amino Acid Metabolism

- Glutamate metabolism
- Alanine and aspartate metabolism
- Glycine, serine and threonine metabolism
- Methionine metabolism
- Cysteine metabolism
- Alanine, leucine, isoleucine, and valine degradation

KEGG Orthology (KO)
KEGG pathway modules
Overview of biosynthetic pathways
Enzymes (+diseases)
Compounds with biological roles

Photosynthesis proteins

Lipids

Metabolic Pathways

KEGG PATHWAY Database - Windows Internet Explorer

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

KEGG PATHWAY Database

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Glycolysis / Gluconeogenesis KEGG Orthology (KO)

Citrate cycle (TCA cycle) KEGG pathway modules

Pentose phosphate pathway Overview of biosynthetic pathways

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Photosynthesis

Photosynthesis - antenna proteins Photosynthesis proteins

Carbon fixation

Reductive carboxylate cycle (CO2 fixation)

Methane metabolism

Nitrogen metabolism

Sulfur metabolism

1.3 Lipid Metabolism

Fatty acid biosynthesis Lipids

Fatty acid elongation in mitochondria

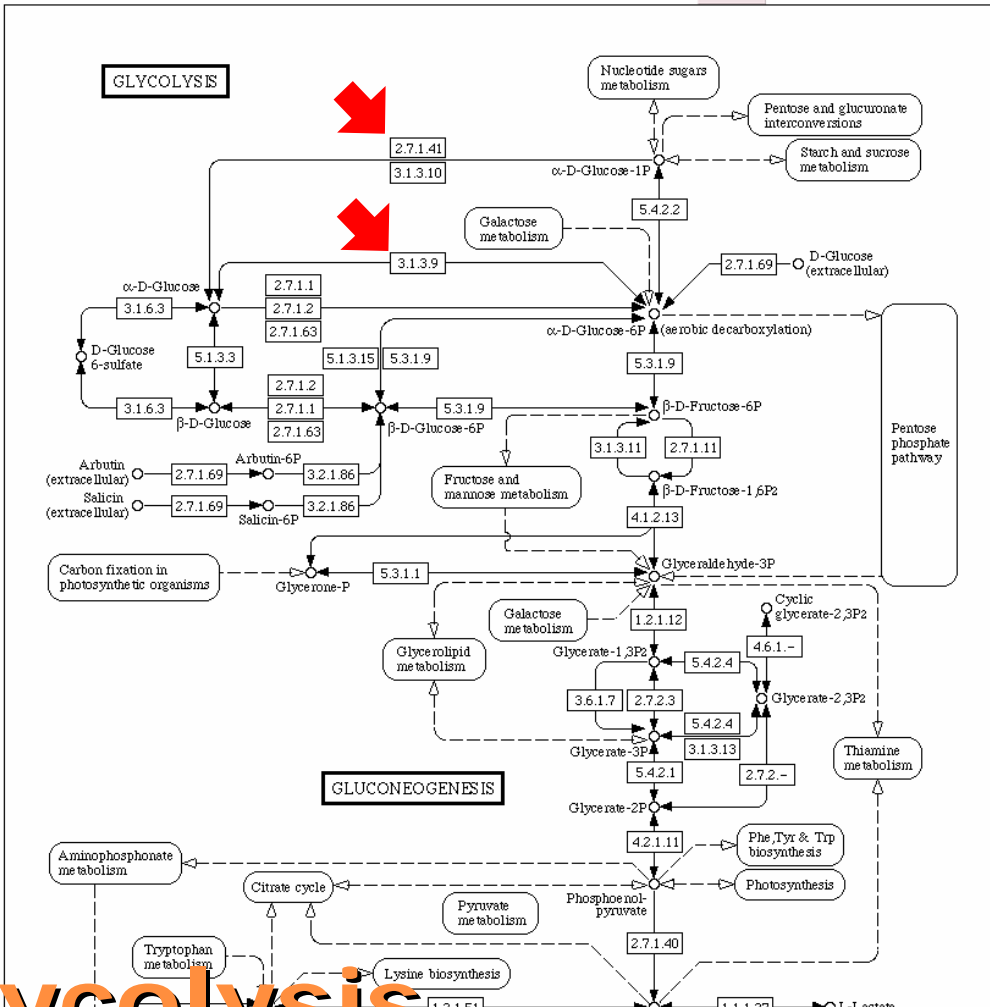
Fatty acid metabolism

Synthesis and degradation of ketone bodies

Biosynthesis of steroids

Bile acid biosynthesis

Metabolic Pathways



GLYCOLYSIS



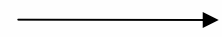
GLUCONEOGENESIS



Enzyme
or
reaction

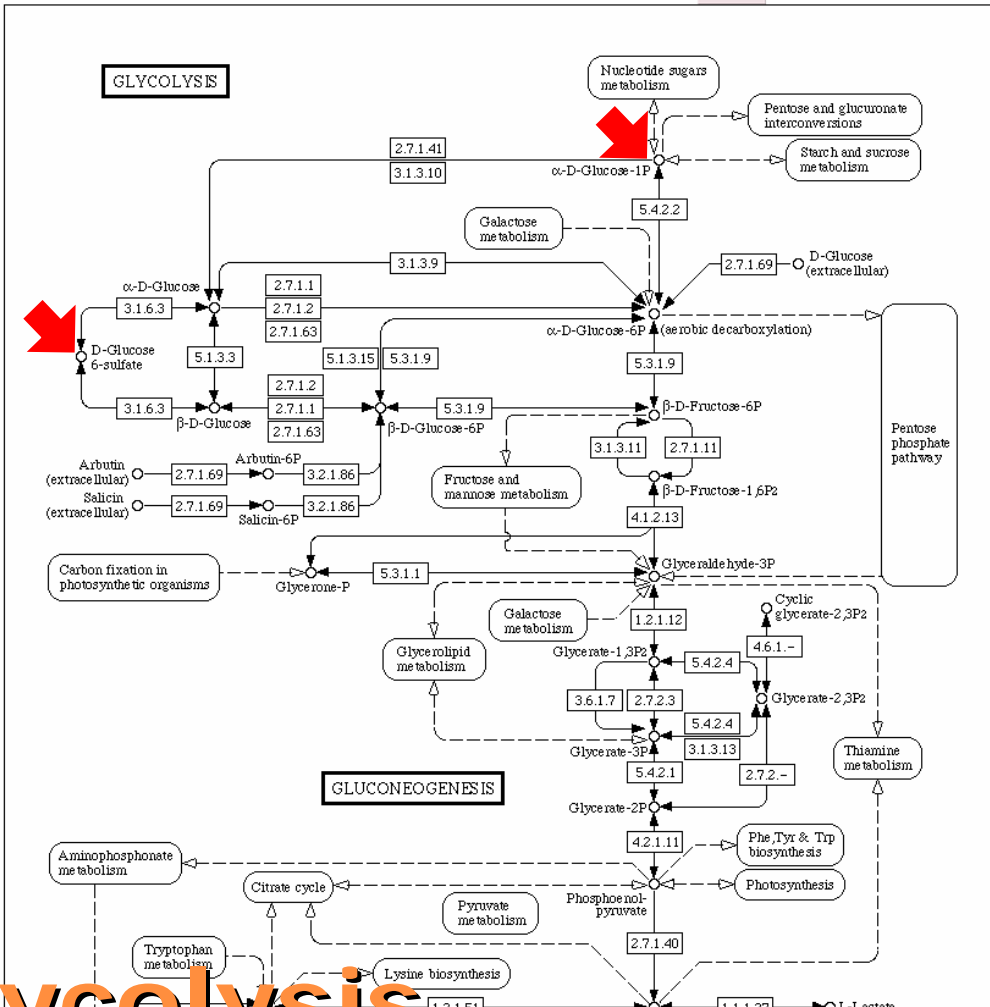



compound





Molecular
Interaction
or
relation

Glycolysis

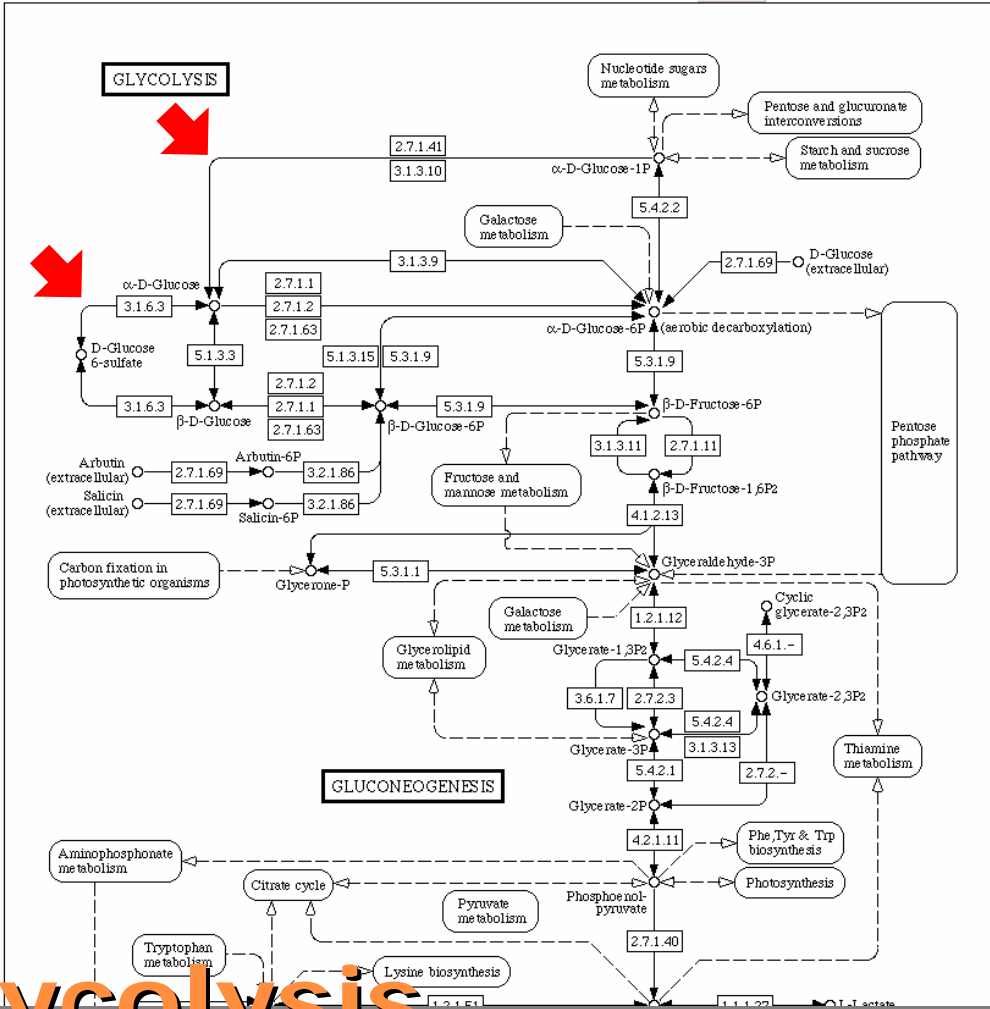




Enzyme
or
reaction



compound

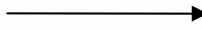

Molecular
Interaction
or
relation

Glycolysis

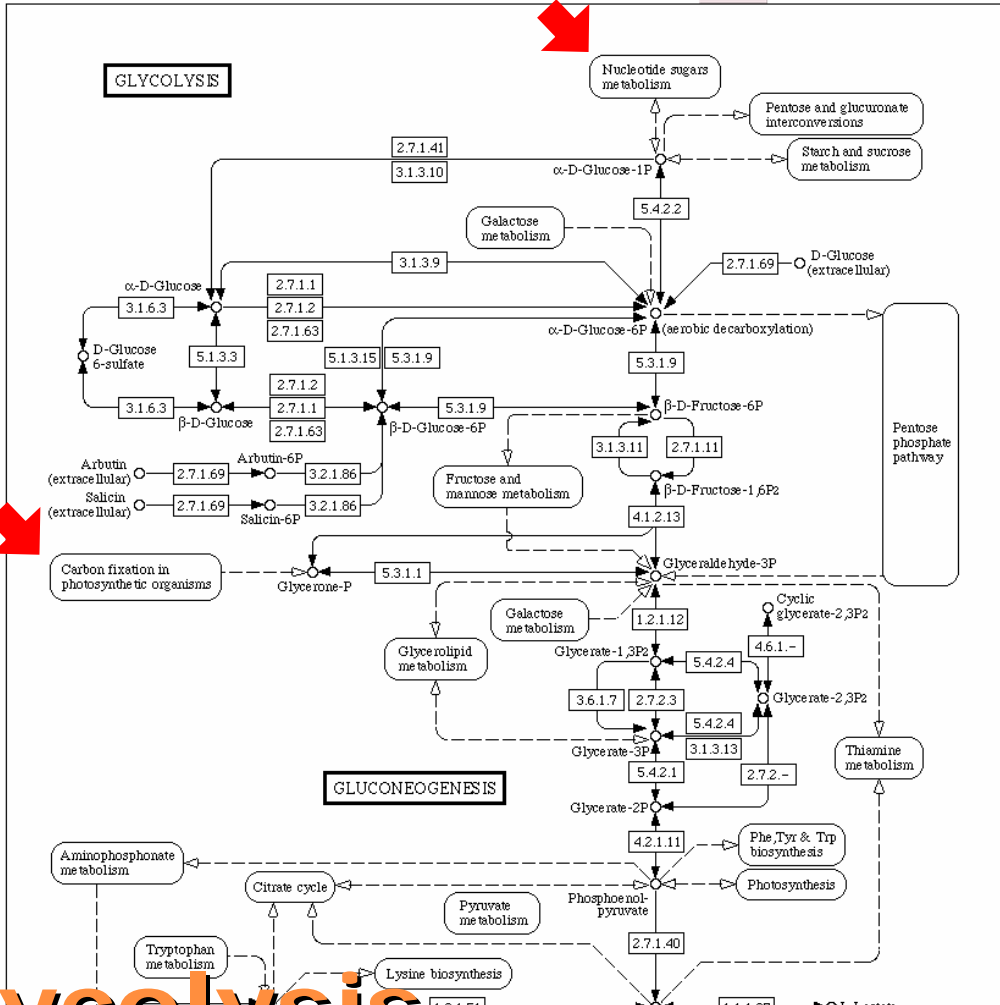



Enzyme
or
reaction


compound


Molecular
Interaction
or
relation

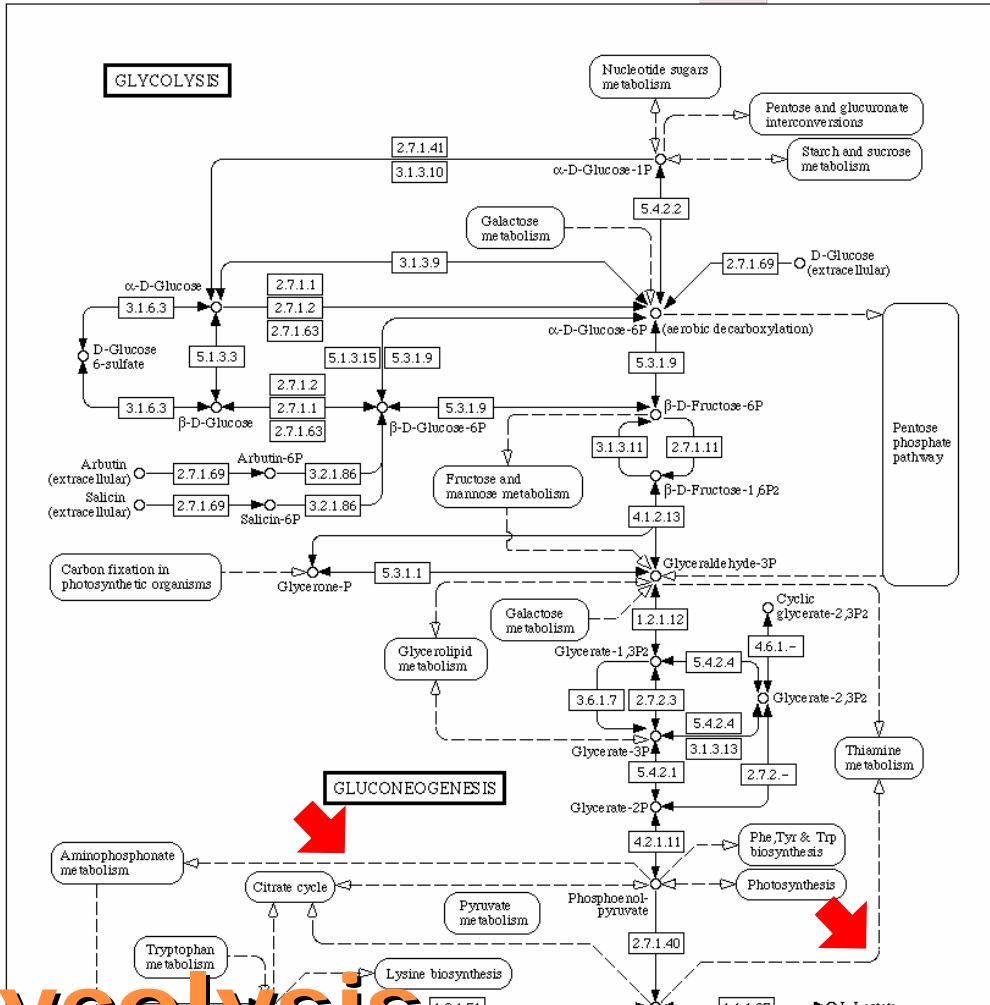
Glycolysis



Another map

Link to another map

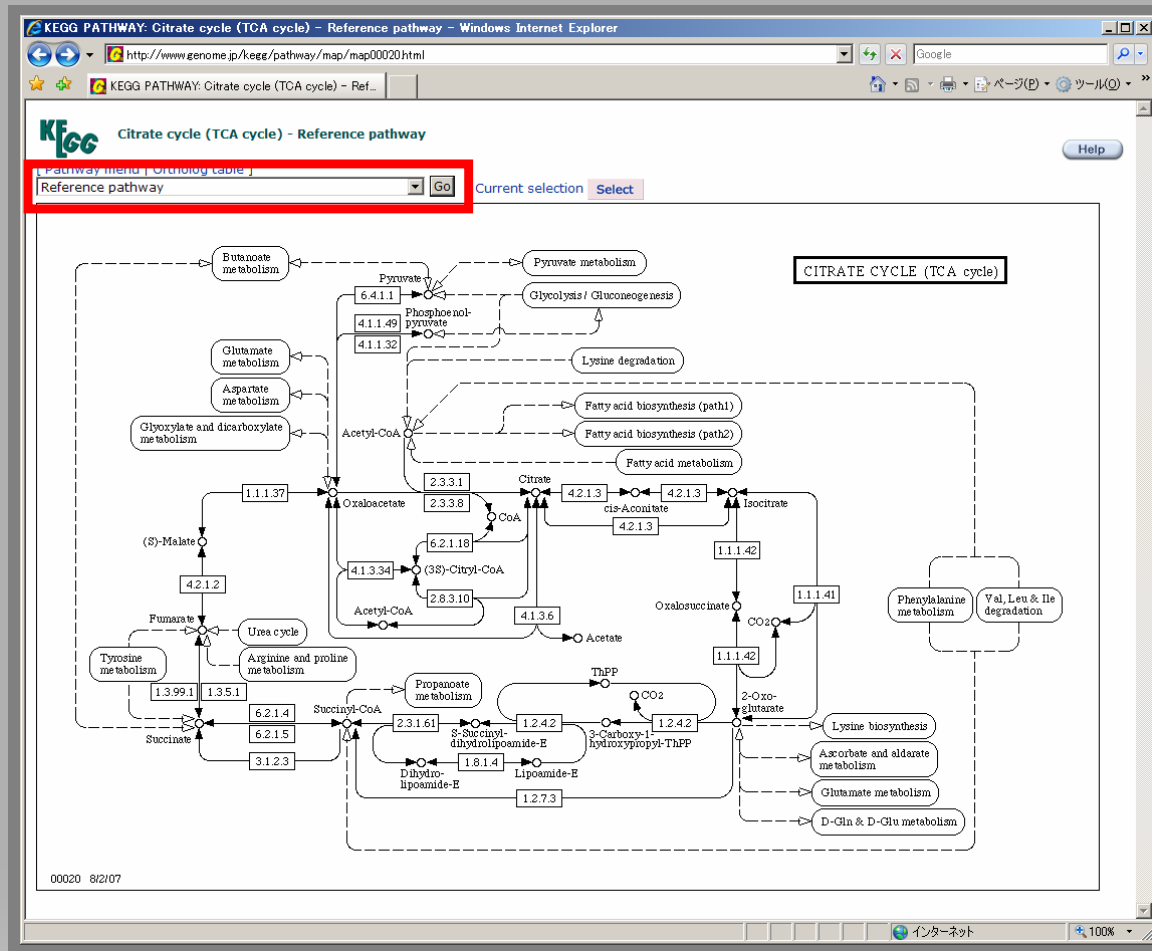
Glycolysis



Glycolysis

Another map

Link to another map



Metabolic – Reference

KEGG PATHWAY: Citrate cycle (TCA cycle) - Reference pathway - Windows Internet Explorer

http://www.genome.jp/kegg/pathway/map/map00020.html

KEGG PATHWAY: Citrate cycle (TCA cycle) - Ref...

KEGG PATHWAY: Citrate cycle (TCA cycle) - Reference pathway

COMPOUND: C00158

Entry: C00158 Compound

Name: Citrate; Citric acid; 2-Hydroxy-1,2,3-propanetricarboxylic acid; 2-Hydroxytricarballic acid

Formula: C₆H₈O₇

Mass: 192.027

Structure:

Remark: Same as: D00037

Reaction: R00351 R00352 R00362 R01322 R01323 R01324 R01325 R04357

Pathway: PATH: map00020 Citrate cycle (TCA cycle); PATH: map00251 Glutamate metabolism; PATH: map00252 Alanine and aspartate metabolism; PATH: map00630 Glyoxylate and dicarboxylate metabolism; PATH: map00720 Reductive carboxylate cycle (CO₂ fixation)

Enzyme: 2.3.3.1 2.3.3.3 2.3.3.8 2.8.3.10 3.4.13.20 (C) 4.1.3.6 4.2.1.3 4.2.1.4 6.2.1.18 6.3.2.27

Other DBs: CAS: 77-92-9; PubChem: 3458; ChEBI: 30769; PDB-CCD: CIT; 3DMET: B00046

LinkDB: All DBs

KCF data: Show

Enzyme: 4.2.1.3

Entry: EC 4.2.1.3 Enzyme

Name: aconitate hydratase; cis-aconitase; aconitase; AcnE; 2-methylaconitate hydratase; citrate(isocitrate) hydro-lyase

Class: Lyases; Carbon-oxygen lyases; Hydro-lyases (BRITE hierarchy)

Synname: citrate(isocitrate) hydro-lyase (cis-aconitate-forming)

Reaction(IUBMB): (1) citrate = isocitrate [RN:R01324]; (2) (1a) citrate = cis-aconitate + H₂O [RN:R01325]; (3) (1b) cis-aconitate + H₂O = isocitrate [RN:R01900]

Reaction(KEGG): R01324 R01325 R01900

Substrate: citrate [CPD:C00158]; cis-aconitate [CPD:C00417]; H₂O [CPD:C00001]

Product: isocitrate [CPD:C00311]; cis-aconitate [CPD:C00417]; H₂O [CPD:C00001]

Cofactor: Iron [CPD:C00023]; Sulfur [CPD:C00087]; Iron-sulfur [CPD:C00824]

Comment: Besides interconverting citrate and cis-aconitate, it also interconverts cis-aconitate with isocitrate and, hence, interconverts citrate and isocitrate. The equilibrium mixture is 91% citrate, 6% isocitrate and 3% aconitate. cis-Aconitate is used to designate the isomer (2Z)-prop-1-ene-1,2,3-tricarboxylate. An iron-sulfur protein, containing a [4Fe-4S] cluster to which the substrate binds.

Pathway: PATH: map00020 Citrate cycle (TCA cycle); PATH: map00630 Glyoxylate and dicarboxylate metabolism; PATH: map00720 Reductive carboxylate cycle (CO₂ fixation)

00020 8/2/07

インターネット 100%

Metabolic - Reference

KEGG PATHWAY: Citrate cycle (TCA cycle) - Reference pathway - Windows Internet Explorer

http://www.genome.jp/kegg/pathway/map/map00020.html

KEGG PATHWAY: Citrate cycle (TCA cycle) - Ref...

KEGG Citrate cycle (TCA cycle) - Reference pathway

Reference pathway (Reaction) selected

Reference pathway (KO)

All organisms in KEGG

-----< Sort below by alphabet >-----

- Homo sapiens (human)
- Pan troglodytes (chimpanzee)
- Macaca mulatta (rhesus monkey)
- Mus musculus (mouse)
- Rattus norvegicus (rat)
- Canis familiaris (dog)
- Bos taurus (cow)
- Sus scrofa (pig)
- Gallus gallus (chicken)
- Xenopus laevis (African clawed frog)
- Xenopus tropicalis (western clawed frog)
- Danio rerio (zebrafish)
- Strongylocentrotus purpuratus (purple sea urchin)
- Drosophila melanogaster (fruit fly)
- Caenorhabditis elegans (nematode)
- Arabidopsis thaliana (thale cress)
- Oryza sativa japonica (Japanese rice)
- Cyanidioschyzon merolae
- Ostreococcus lucimarinus
- Saccharomyces cerevisiae
- Ashbya gossypii (Eremothecium gossypii)
- Kluyveromyces fragilis
- Debaryomyces hansenii
- Pichia stipitis
- Candida albicans

Reaction: R01325

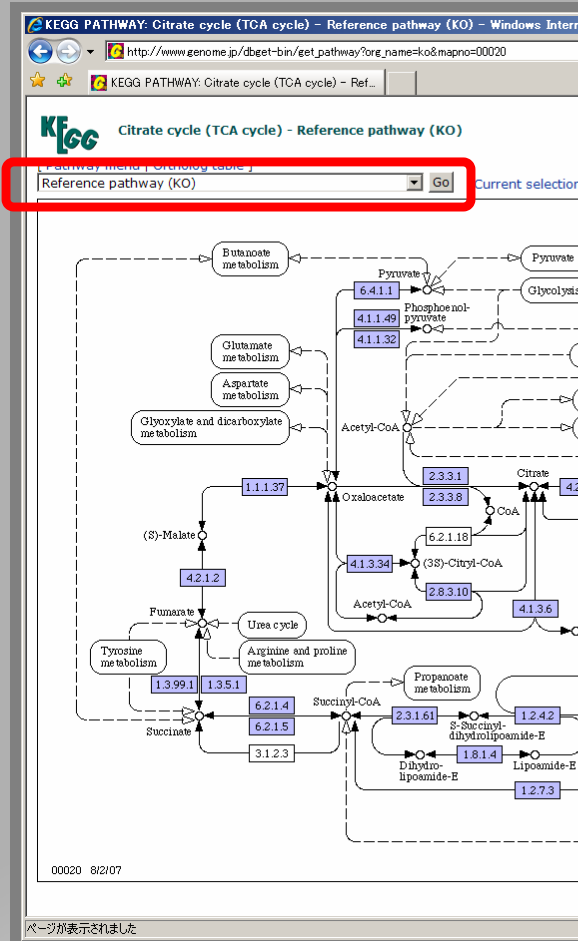
Reaction

Entry	R01325	Reaction
Name	citrate hydro-lyase	
Definition	Citrate <=> cis-Aconitate + H2O	
Equation	C00158 <=> C00417 + C00001	
RPair	RP: A01432 C00158_C00417 main RP: A06526 C00001_C00158 leave	
Pathway	PATH: rn00020 Citrate cycle (TCA cycle) PATH: rn00630 Glyoxylate and dicarboxylate metabolism PATH: rn00720 Reductive carboxylate cycle (CO2 fixation)	
Enzyme	4.2.1.3 4.2.1.4	
Orthology	KO: K01680 aconitate hydratase KO: K01681 aconitate hydratase 1 KO: K01682 aconitate hydratase 2	
LinkDB	All DBs	

00020 8/2/07

インターネット 100%

Metabolic – Reaction



KEGG ORTHOLOGY: K00024 K00025 K00026 - Windows Internet Explorer

http://www.genome.jp/dbget-bin/www_beet?ko+K00024+

KEGG ORTHOLOGY: K00024 K00025 K00026

KEGG ORTHOLOGY: K00024

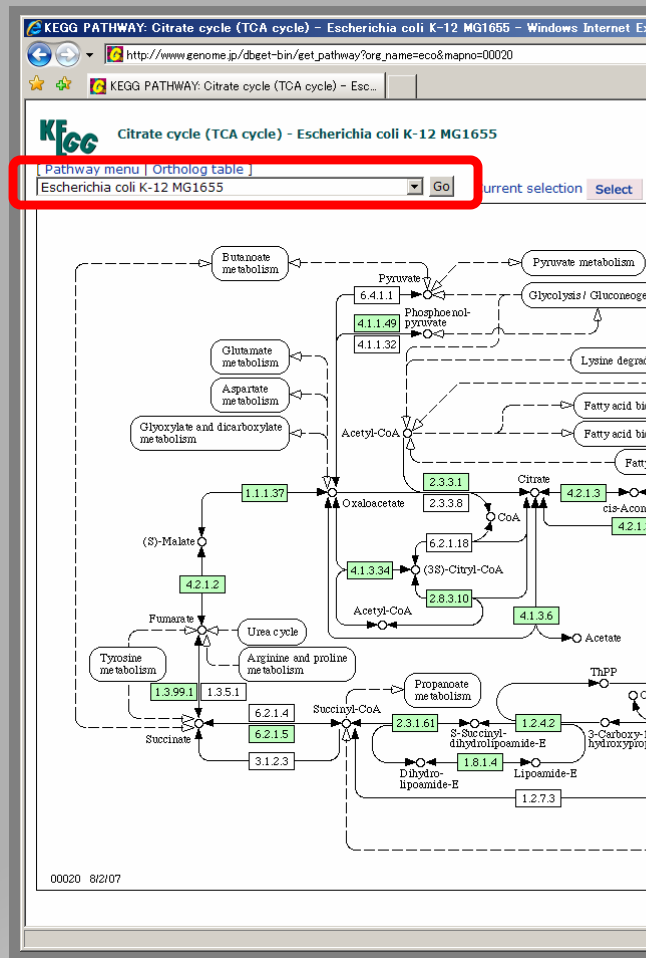
Help

Entry	K00024	KO
Name	E1.1.1.37	
Definition	malate dehydrogenase	
Class	Metabolism; Carbohydrate Metabolism; Citrate cycle (TCA cycle) [PATH:ko00020]	
	Metabolism; Carbohydrate Metabolism; Pyruvate metabolism [PATH:ko00620]	
	Metabolism; Carbohydrate Metabolism; Glyoxylate and dicarboxylate metabolism [PATH:ko00630]	
	Metabolism; Energy Metabolism; Carbon fixation [PATH:ko00710]	
	Metabolism; Energy Metabolism; Reductive carboxylate cycle (CO2 fixation) [PATH:ko00720]	
	BRITE hierarchy	
Other DBs	RN: R00342	
	EC: 1.1.1.37	
	GO: 0030060	
Genes	DRE: 399662 (mdh1a)	
	SCE: YDL078C (MDH3) YOL126C (MDH2)	
	DHA: DEHA0F09911g	
	PIC: PICST_78343 (MDH2)	
	PFA: PFF0895w	
	TBR: Tb10.70.5120	
	TCR: 507883.100	
	LMA: LmjF34.0130	
	ECW: EcE24377A_3719 (mdh)	
	ECX: EcHS_A3425	
	YPG: YpAngola_A3971 (mdh)	
	YPI: YpsIP31758_3616 (mdh)	
	SPE: Spro_3596	
	HIP: CGSH1E_05985	
	HIQ: CGSH1G_09775	
	APL: APL_1296 (mdh)	
	ASU: Asuc_0893	
VCO: VC0395_A2850 (mdh)		
VFI: VF1252		
PMY: Pmen_3486		
FRW: PsycFRwf_1261		
SBM: Shew185_2999		
SBN: Sball195_3142		
SSE: Seed_3124		
SPL: Spea_1313		

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インターネット 100%

Metabolic - KO



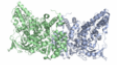

KEGG E.coli: b0118 b1276 - Windows Internet Explorer

http://www.genome.jp/dbget-bin/www_get?eco+b0118+b1276

KEGG E.coli: b0118 b1276

KEGG Escherichia coli K-12 MG1655: b0118

Help

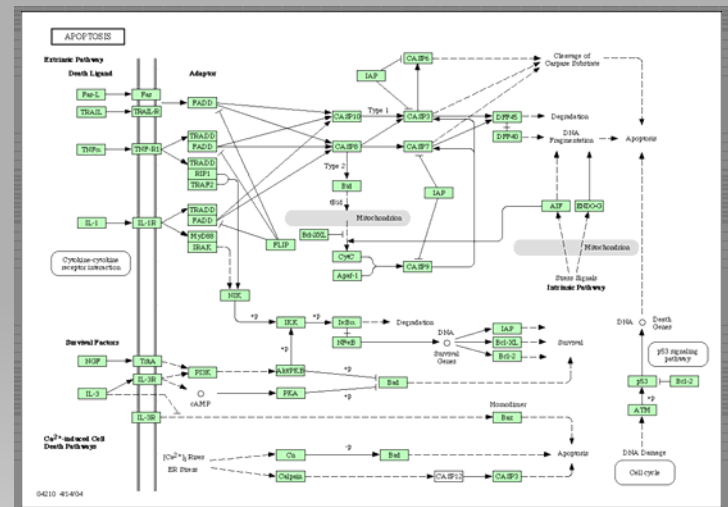
Entry	b0118	CDS	E.coli
Gene name	acnB, yacJ, yacI		
Definition	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase [EC:4.2.1.3]		
Orthology	KO: K01682 aconitate hydratase 2		
Pathway	PATH: eco00020 Citrate cycle (TCA cycle) PATH: eco00630 Glyoxylate and dicarboxylate metabolism PATH: eco00720 Reductive carboxylate cycle (CO2 fixation)		
Class	BRITE hierarchy		
SSDB	Ortholog Paralog Gene cluster		
Motif	Pfam: Aconitase_2_N Aconitase PROSITE: ACONITASE_1 ACONITASE_2 Motif		
Other DBs	Wisconsin: b0118 Colibri: acnB RegulonDB: B0118 NCBI-GI: 16128111 NCBI-GeneID: 944864 UniProt: P36683		
LinkDB	All DBs		
Structure	PDB: 1L5J Thumbnails  Jmol 		
Position	131615..134212 Genome map		
AA seq	865 aa AA seq DB search		
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Metabolic – Organism specific

- Contents of DB
 - Metabolic pathways



- **Regulatory pathways**
 - Genetic Information Processing
 - Environmental Information Processing
 - Cellular Processes
 - Human Diseases
- Drug structure maps



Regulatory Pathways

2. Genetic Information Processing

2.1 Transcription

RNA biosynthesis (illustration)
RNA polymerase
Basal transcription factors

Transcription factors

2.2 Translation

Protein biosynthesis (illustration)
Ribosome
Aminoacyl-tRNA biosynthesis

Translation factors
Ribosome

2.3 Folding, Sorting and Degradation

Protein export
Type II secretion system
Type III secretion system
Type IV secretion system
SNARE interactions in vesicular transport
Regulation of autophagy
Ubiquitin mediated proteolysis
Proteasome

SNAREs

2.4 Replication and Repair

DNA replication
Base excision repair *New!*
Nucleotide excision repair *New!*
Mismatch repair *New!*

DNA replication proteins

3. Environmental Information Processing

3.1 Membrane Transport

ABC transporters
Phosphotransferase system (PTS)

Transporters (+diseases)

3.2 Signal Transduction

Two-component system
MAPK signaling pathway
ErbB signaling pathway
Wnt signaling pathway
Notch signaling pathway
Hedgehog signaling pathway
TGF-beta signaling pathway
VEGF signaling pathway
Jak-STAT signaling pathway
Calcium signaling pathway
Phosphatidylinositol signaling system
mTOR signaling pathway

Two-component system

3.3 Signaling Molecules and Interaction

Neuroactive ligand-receptor interaction
Cytokine-cytokine receptor interaction
ECM-receptor interaction
Cell adhesion molecules (CAMs)

Receptors and channels (+diseases)
Cytokines
Cell adhesion molecules (CAMs)
CAM ligands
CD molecules
GTP-binding proteins

Regulatory Pathways

Cellular Processes

4.1 Cell Motility

2. Genetic Information Processing

2.1 Transcription

RNA biosynthesis (illustration)

Transcription factors

Basal transcription factors

2.2 Translation

Protein biosynthesis (illustration)

Translation factors

Ribosome

Ribosome

Aminoacyl-tRNA biosynthesis

2.3 Folding, Sorting and Degradation

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2.4 Replication and Repair

DNA replication

DNA replication proteins

Base excision repair *New!*

Nucleotide excision repair *New!*

Mismatch repair *New!*

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3.1 Membrane Transport

ABC transporters

Transporters (+diseases)

Phosphotransferase system (PTS)

3.2 Signal Transduction

Two-component system

Two-component system

MAPK signaling pathway

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Cell adhesion molecules (CAMs)

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CD molecules

GTP-binding proteins

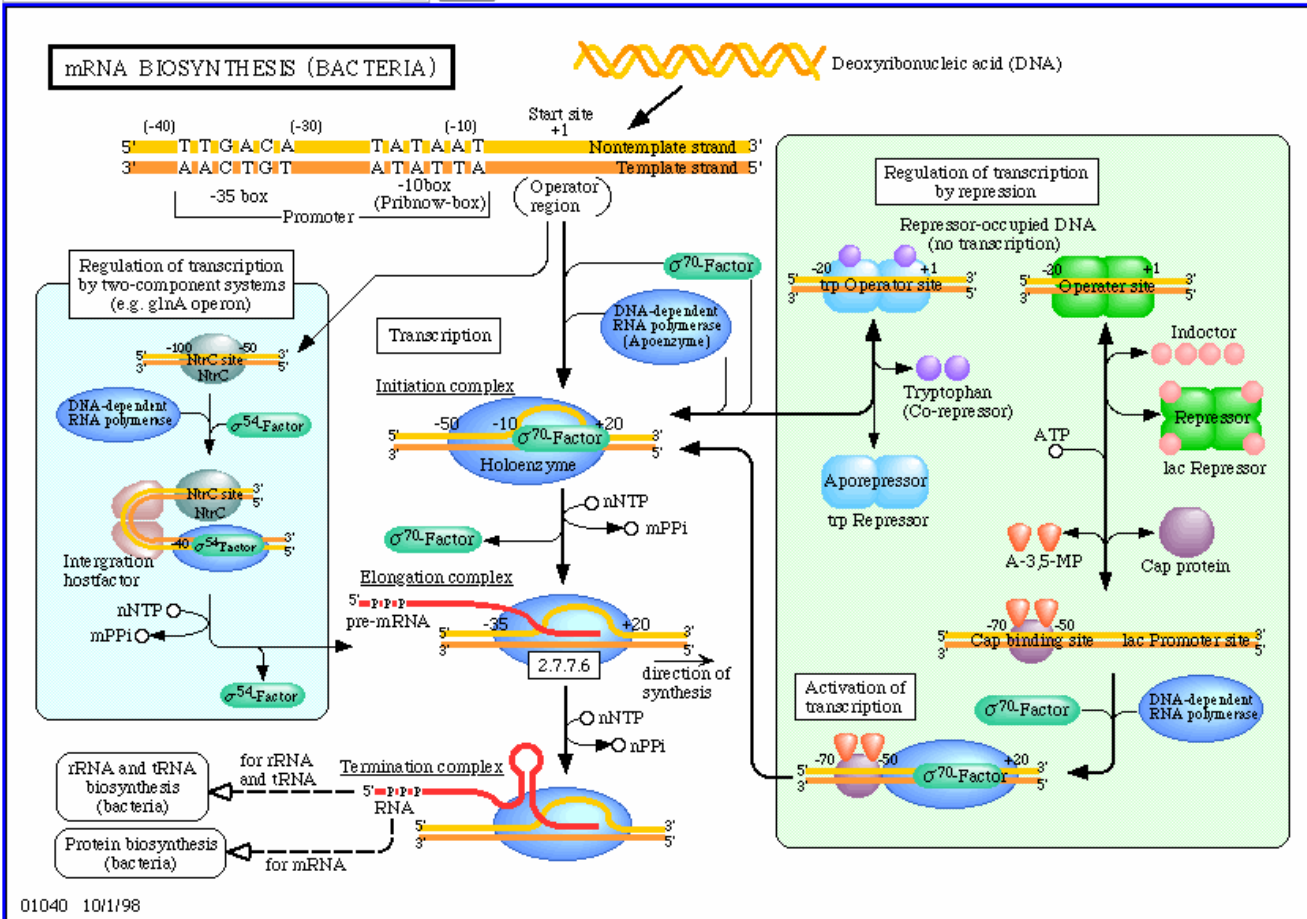
Regulatory Pathways

Cellular Processes

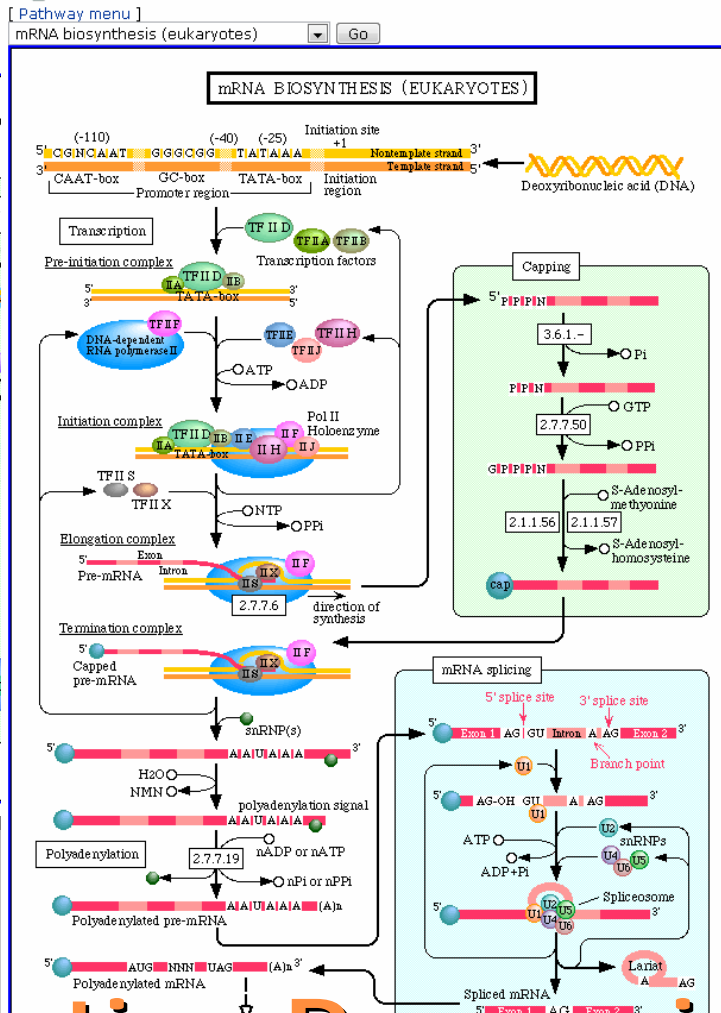
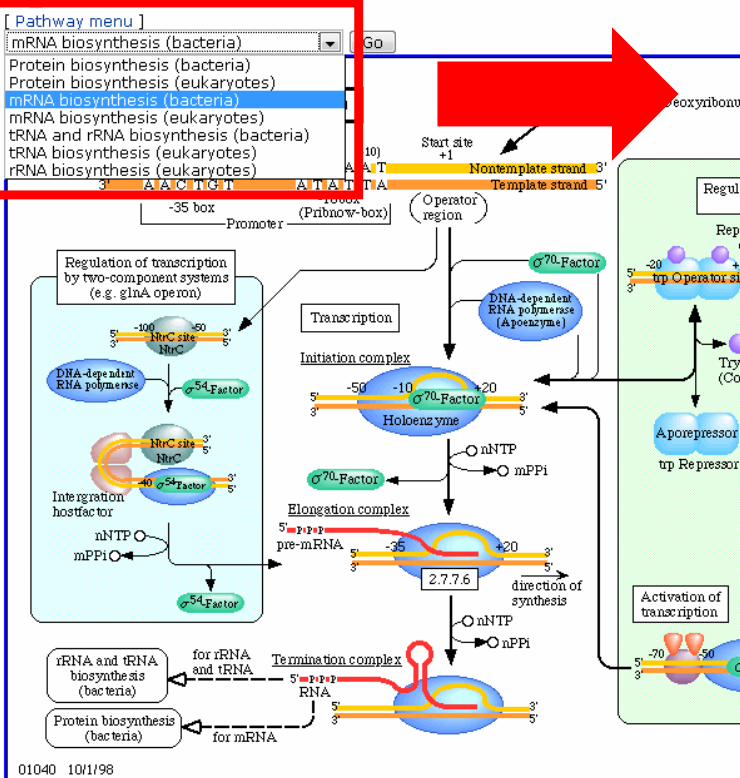
4.1 Cell Motility

[Pathway menu]

mRNA biosynthesis (bacteria)



Genetic Information Processing



Genetic Information Processing

2. Genetic Information Processing

2.1 Transcription

RNA biosynthesis (illustration)
RNA polymerase
Basal transcription factors

Transcription factors

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Cytokines
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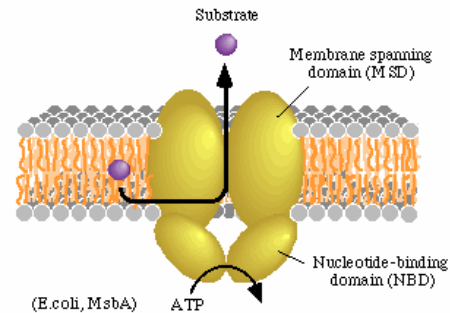
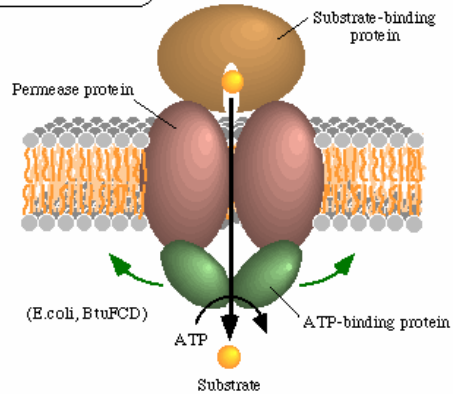
Regulatory Pathways

Cellular Processes

4.1 Cell Motility

ABC TRANSPORTERS

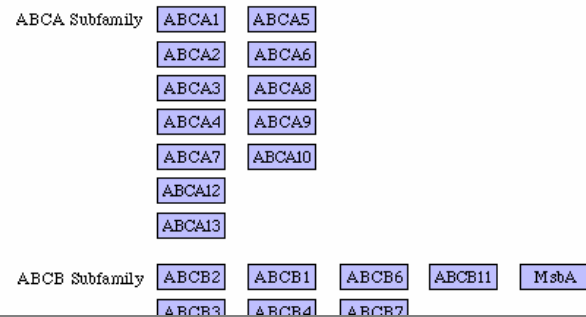
See also
organism-specific diagram



Prokaryotic-type ABC transporters

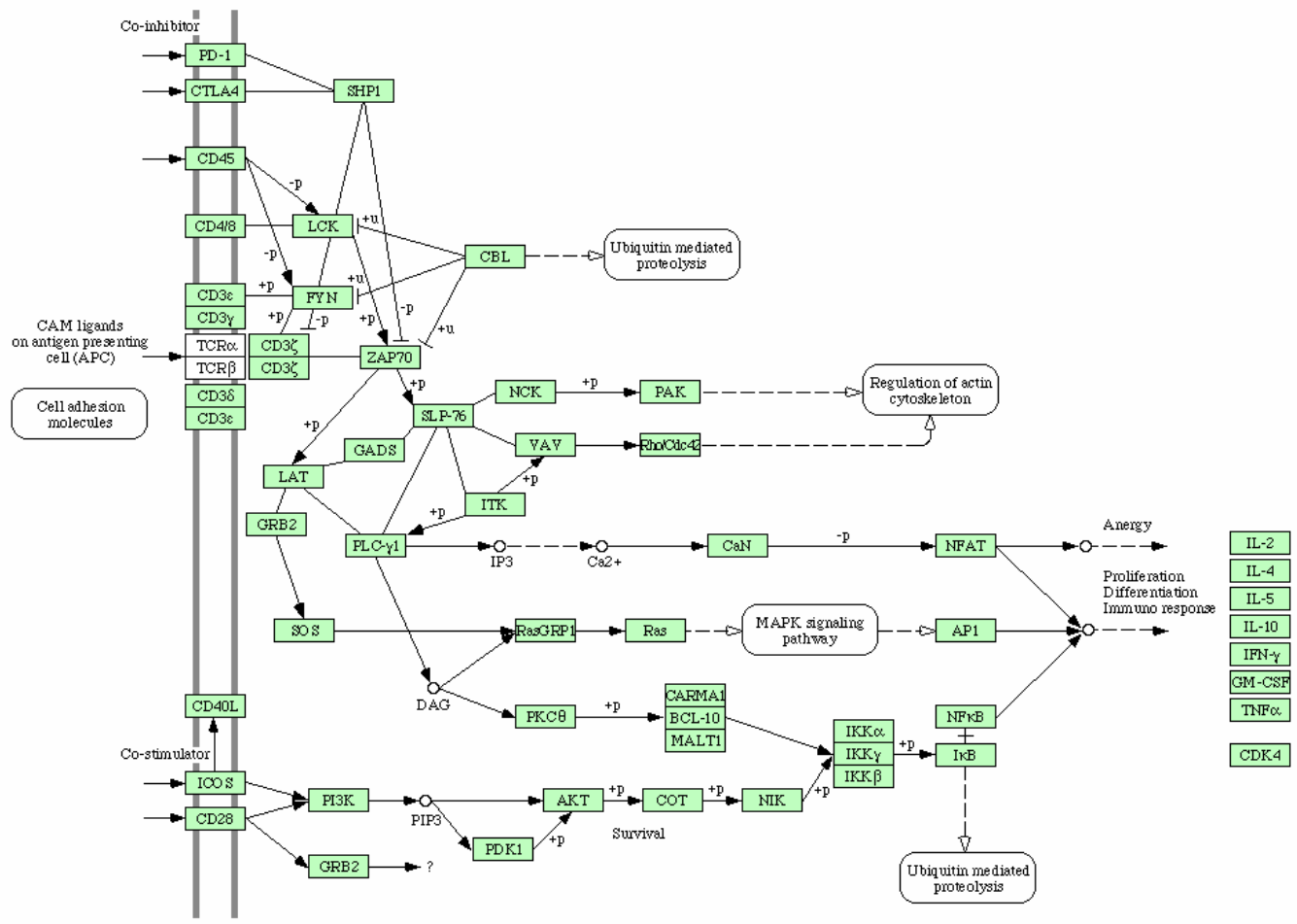


Eukaryotic-type ABC transporters



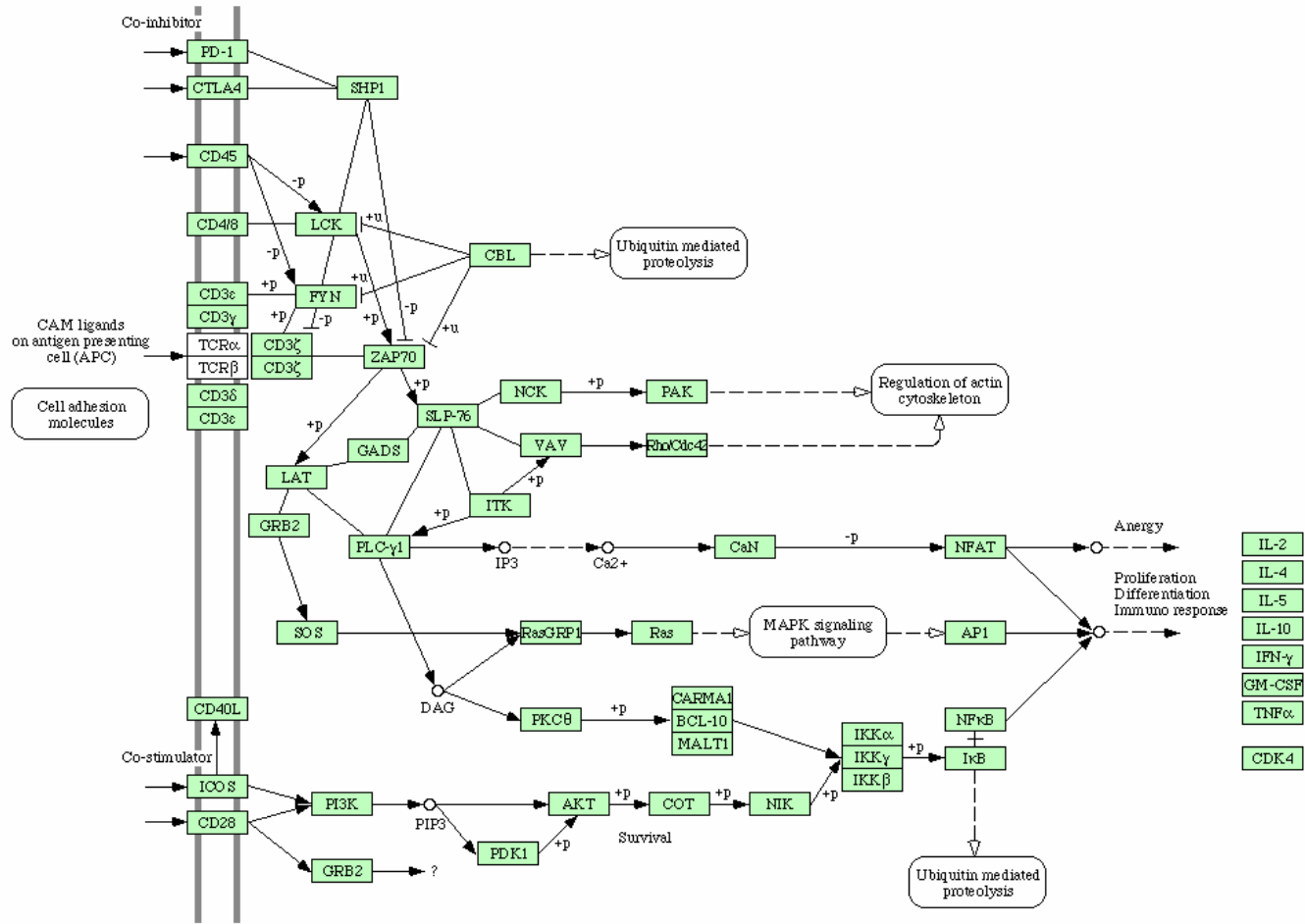
Environmental Information Processing

T CELL RECEPTOR SIGNALING PATHWAY



Cellular Processes

T CELL RECEPTOR SIGNALING PATHWAY



Cellular Processes

COLORECTAL CANCER

Chromosome Unstable (CIN) pathway
Microsatellite Unstable (MSI) pathway

Normal epithelium

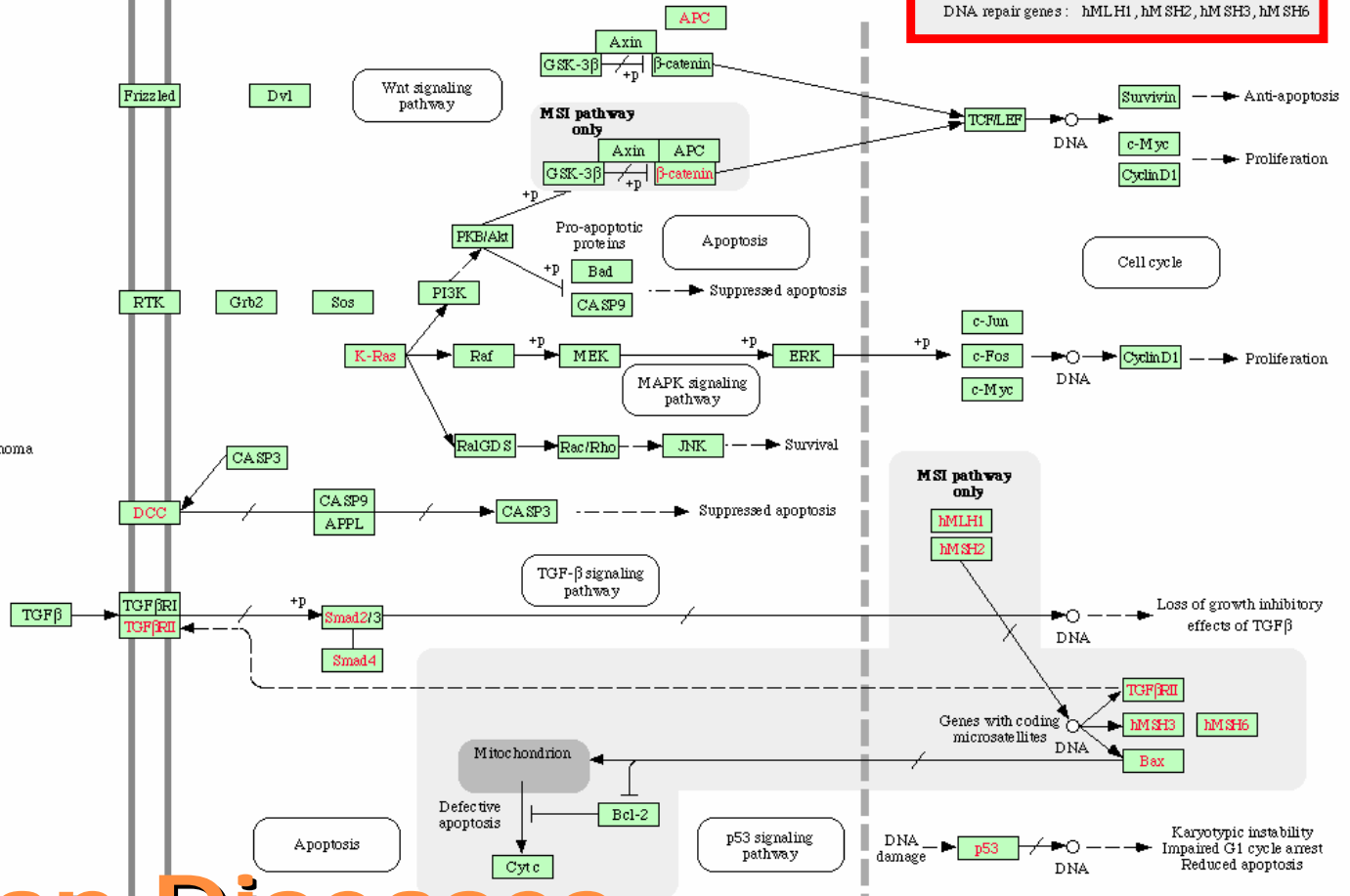
Dysplastic ACF

Early adenoma

Intermediate adenoma

Late adenoma

Colorectal epithelial cell



Human Diseases

COLORECTAL CANCER

Chromosome Unstable (CIN) pathway
Microsatellite Unstable (MSI) pathway

Normal epithelium

Dysplastic ACF

Early adenoma

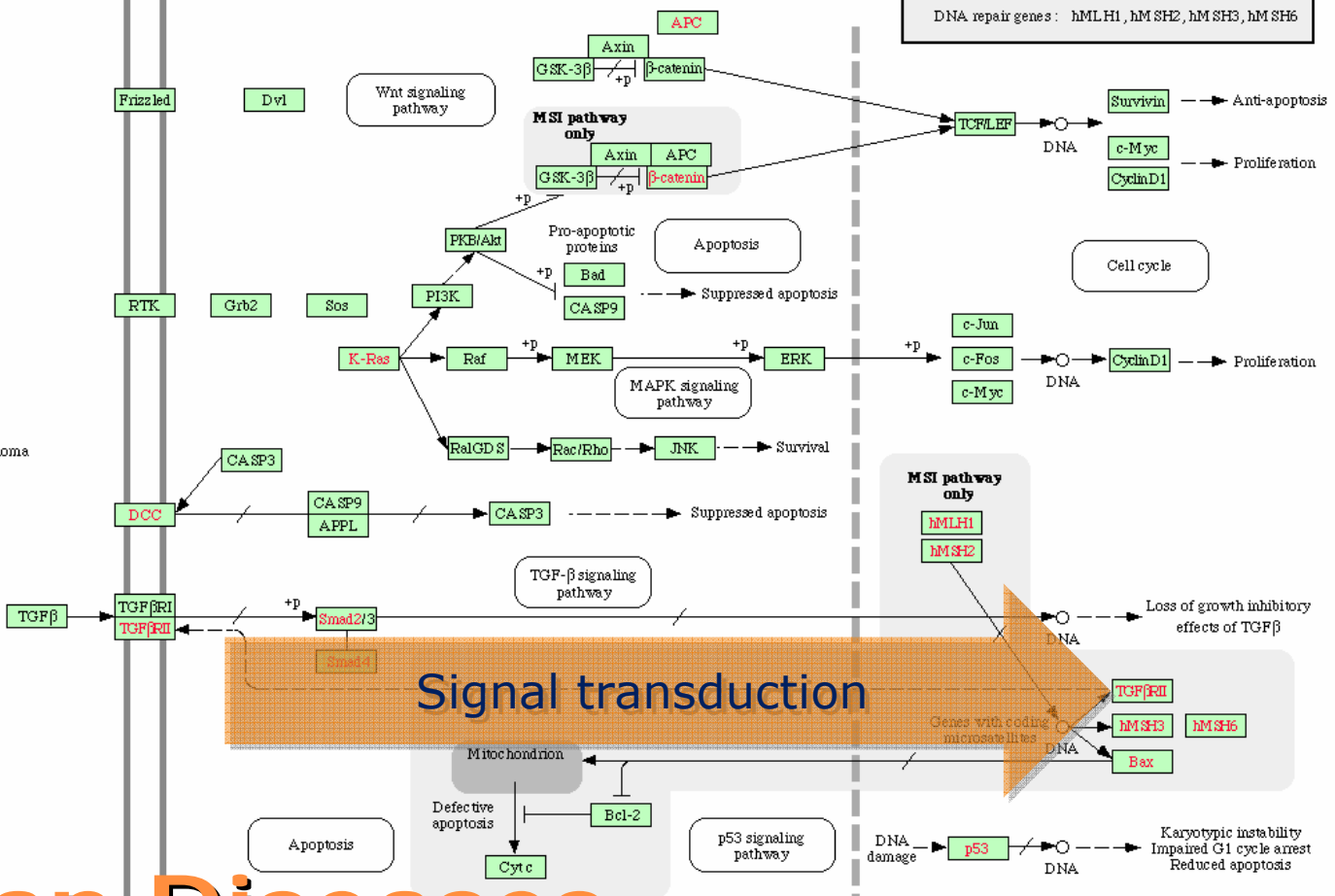
Intermediate adenoma

Late adenoma

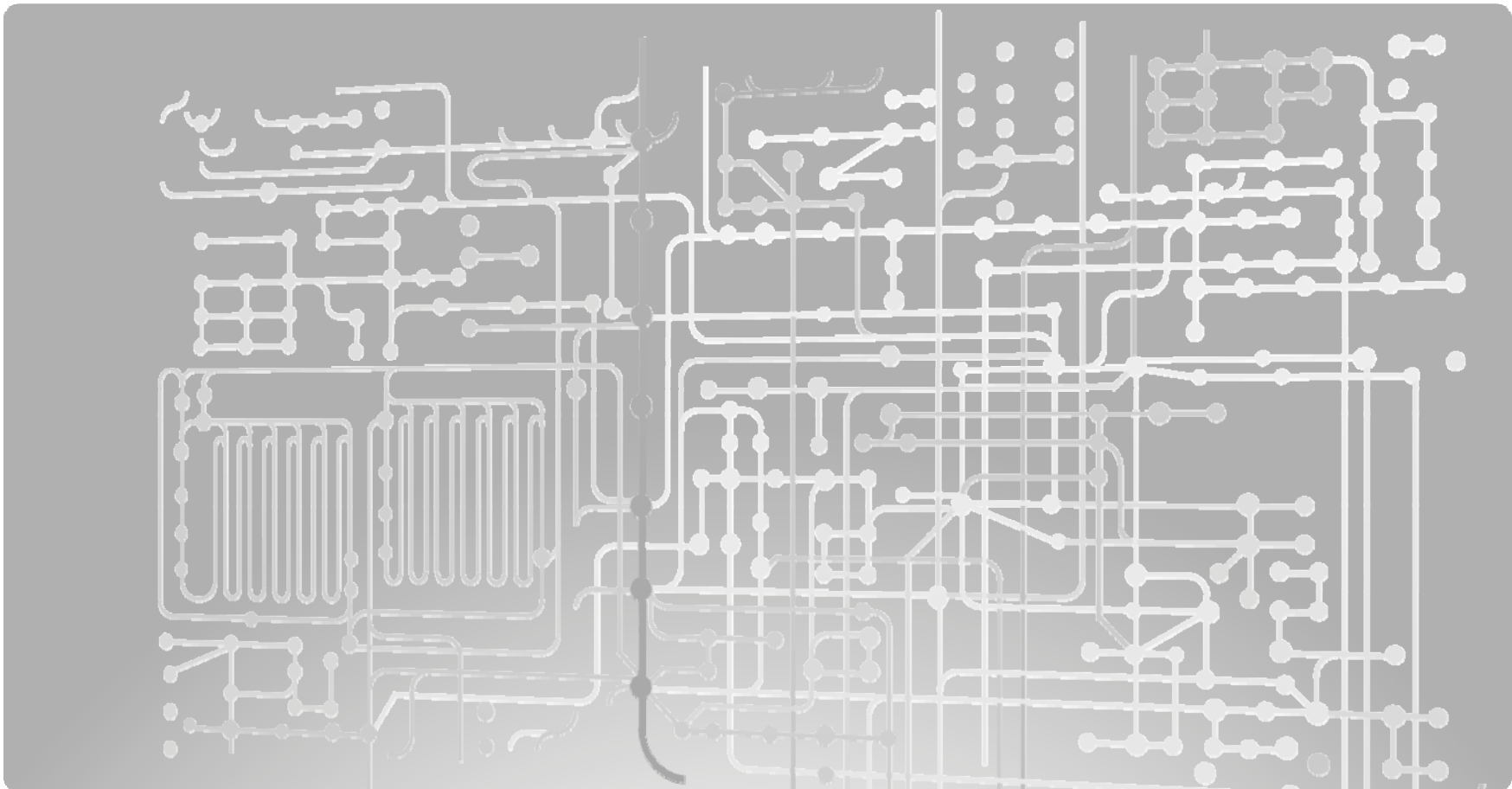
Cancer progression

Colorectal epithelial cell

- Genetic alterations**
- Oncogenes : β -catenin, K-Ras
 - Tumor suppressors : APC, DCC, TGF β RII, Smad2, Smad4, Bax, p53
 - DNA repair genes : hMLH1, hMSH2, hMSH3, hMSH6

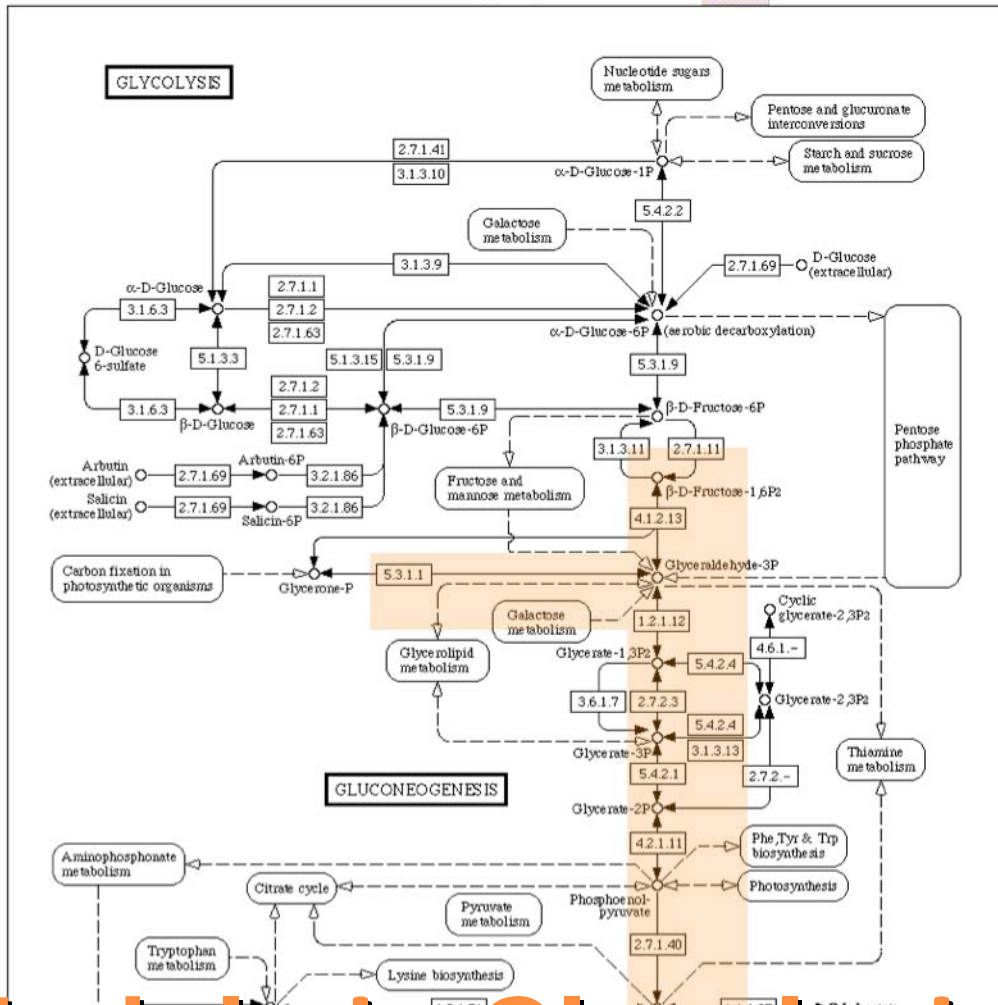


Human Diseases

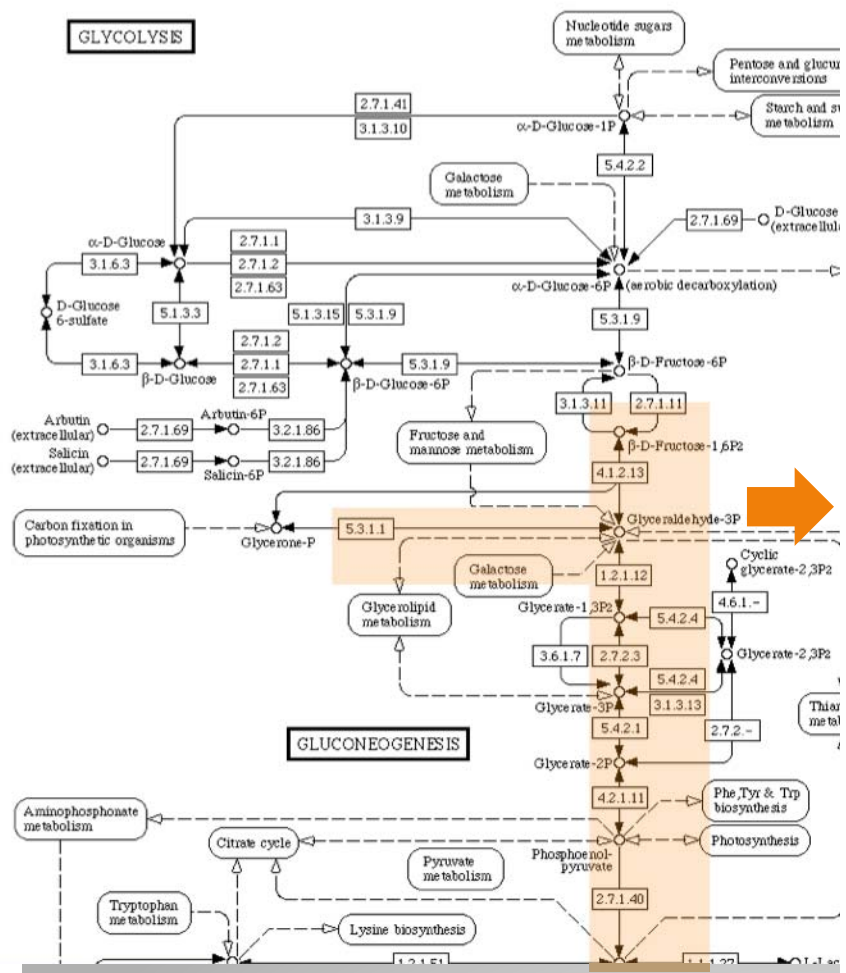


KEGG Modules

Small functional units in pathways



Module in Glycolysis



Entry	M10001	Pathway	Module
Name	Glycolysis		
Definition	K00850 (K01624 K01623 K01622) K01803 K00134 K00927 K01834 K01689 K00873 ((K00163 K00161+K00162)+K00627+K00382)		
Pathway	ko00010 Glycolysis / Gluconeogenesis		
Orthology	<p>K00850 6-phosphofructokinase [EC:2.7.1.11] [RN:R04779]</p> <p>K01624,K01623,K01622 fructose-bisphosphate aldolase [EC:4.1.2.13] [RN:R01070]</p> <p>K01803 triosephosphate isomerase [EC:5.3.1.1] [RN:R01015]</p> <p>K00134 glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12] [RN:R01061 R01063]</p> <p>K00927 phosphoglycerate kinase [EC:2.7.2.3] [RN:R01512]</p> <p>K01834 phosphoglycerate mutase [EC:5.4.2.1] [RN:R01518]</p> <p>K01689 enolase [EC:4.2.1.11] [RN:R00658]</p> <p>K00873 pyruvate kinase [EC:2.7.1.40] [RN:R02320]</p> <p>(K00163,K00161+K00162)+K00627+K00382 pyruvate dehydrogenase complex [EC:1.2.1.51] [RN:R00209 R00210]</p>		
Reaction	<p>R04779 C05345 -> C05378</p> <p>R01070 C05378 -> C00111 + C00118</p> <p>R01015 C00111 -> C00118</p> <p>R01061,R01063 C00118 -> C00236</p> <p>R01512 C00236 -> C00197</p> <p>R01518 C00197 -> C00631</p> <p>R00658 C00631 -> C00074</p> <p>R02320 C00074 -> C00022</p> <p>R00209,R00210 C00022 -> C00024</p>		
Compound	<p>C05345 beta-D-Fructose 6-phosphate</p> <p>C05378 beta-D-Fructose 1,6-bisphosphate</p> <p>C00111 Glycerone phosphate</p> <p>C00118 (2R)-2-Hydroxy-3-(phosphonoxy)-propanal</p> <p>C00236 3-Phospho-D-glyceroyl phosphate</p> <p>C00197 3-Phospho-D-glycerate</p> <p>C00631 2-Phospho-D-glycerate</p> <p>C00074 Phosphoenolpyruvate</p> <p>C00022 Pyruvate</p> <p>C00024 Acetyl-CoA</p>		
LinkDB	All DBs		

Module in Glycolysis

▼ **Metabolism**

▼ **Central metabolism**

- M10001 Glycolysis [PATH:ko00010]
- M10002 Glycolysis, core module [PATH:ko00010]
- M10003 Gluconeogenesis [PATH:ko00010]
- M10004 Pentose phosphate pathway [PATH:ko00030]
- M10005 Pentose phosphate pathway and PRPP biosynthesis [PATH:ko00030]
- M10006 Pentose phosphate pathway, oxidative phase [PATH:ko00030]
- M10007 Pentose phosphate pathway, non-oxidative phase [PATH:ko00030]
- M10008 Entner-Doudoroff pathway [PATH:ko00030]
- M10009 Citrate cycle [PATH:ko00020]
- M10010 Citrate cycle, module 1 [PATH:ko00020]
- M10011 Citrate cycle, module 2 [PATH:ko00020]
- M10012 Glyoxylate cycle [PATH:ko00630]
- M10013 Glyoxylate biosynthesis, glycolate => glyoxylate [PATH:ko00630]
- M10014 Glyoxylate biosynthesis, glycine => glyoxylate [PATH:ko00260]
- M10015 Malonate semialdehyde pathway [PATH:ko00640]
- M10016 Glucuronate pathway (uronate pathway) [PATH:ko00040]

▼ **Amino acid metabolism**

- M10017 Glutamate biosynthesis, oxoglutarate => glutamate (glutamate [PATH:ko00251])
- M10018 Glutamine biosynthesis, glutamate => glutamine [PATH:ko00251]
- M10019 Glutamate biosynthesis, oxoglutarate => glutamate (glutamate [PATH:ko00251])
- M10020 Proline biosynthesis, glutamate => proline [PATH:ko00220]
- M10021 Aspartate biosynthesis, oxaloacetate => aspartate [PATH:ko00252]
- M10022 Asparagine biosynthesis, aspartate => asparagine [PATH:ko00252]
- M10023 Lysine biosynthesis, aspartate => lysine [PATH:ko00300]
- M10024 Methionine biosynthesis, aspartate => homoserine => methionine [PATH:ko00260]
- M10025 Threonine biosynthesis, aspartate => homoserine => threonine [PATH:ko00260]
- M10026 Alanine biosynthesis, pyruvate => alanine [PATH:ko00252]
- M10027 Valine biosynthesis, pyruvate => valine [PATH:ko00290]
- M10028 Leucine biosynthesis, pyruvate => leucine [PATH:ko00290]
- M10029 Isoleucine biosynthesis, pyruvate => isoleucine [PATH:ko00290]
- M10030 Serine biosynthesis, glycerate-3P => serine [PATH:ko00260]
- M10031 Glycine biosynthesis, serine => glycine [PATH:ko00260]
- M10032 Cysteine biosynthesis, serine => cysteine [PATH:ko00272]
- M10033 Chorismate biosynthesis, phosphoenolpyruvate + erythrose-4P => [PATH:ko00400]
- M10034 Tryptophan biosynthesis, chorismate => tryptophan [PATH:ko00400]
- M10035 Phenylalanine biosynthesis, chorismate => phenylalanine [PATH:ko00400]
- M10036 Tyrosine biosynthesis, chorismate => tyrosine [PATH:ko00400]
- M10037 Histidine biosynthesis, PRPP => histidine [PATH:ko00340]
- M10038 Glutamine degradation, glutamine => glutamate + NH3 [PATH:ko00251]
- M10039 Selenocysteinyl-tRNA biosynthesis [PATH:ko00450]
- M10040 GABA (gamma-Aminobutyrate) shunt [PATH:ko00251]
- M10041 Ornithine biosynthesis, glutamate => ornithine [PATH:ko00220]
- M10042 Urea cycle [PATH:ko00220]
- M10043 Arginine degradation, arginine => citrulline [PATH:ko00330]
- M10044 Aspartate degradation, aspartate => fumarate [PATH:ko00252]

KEGG Modules

▼ **Metabolism**

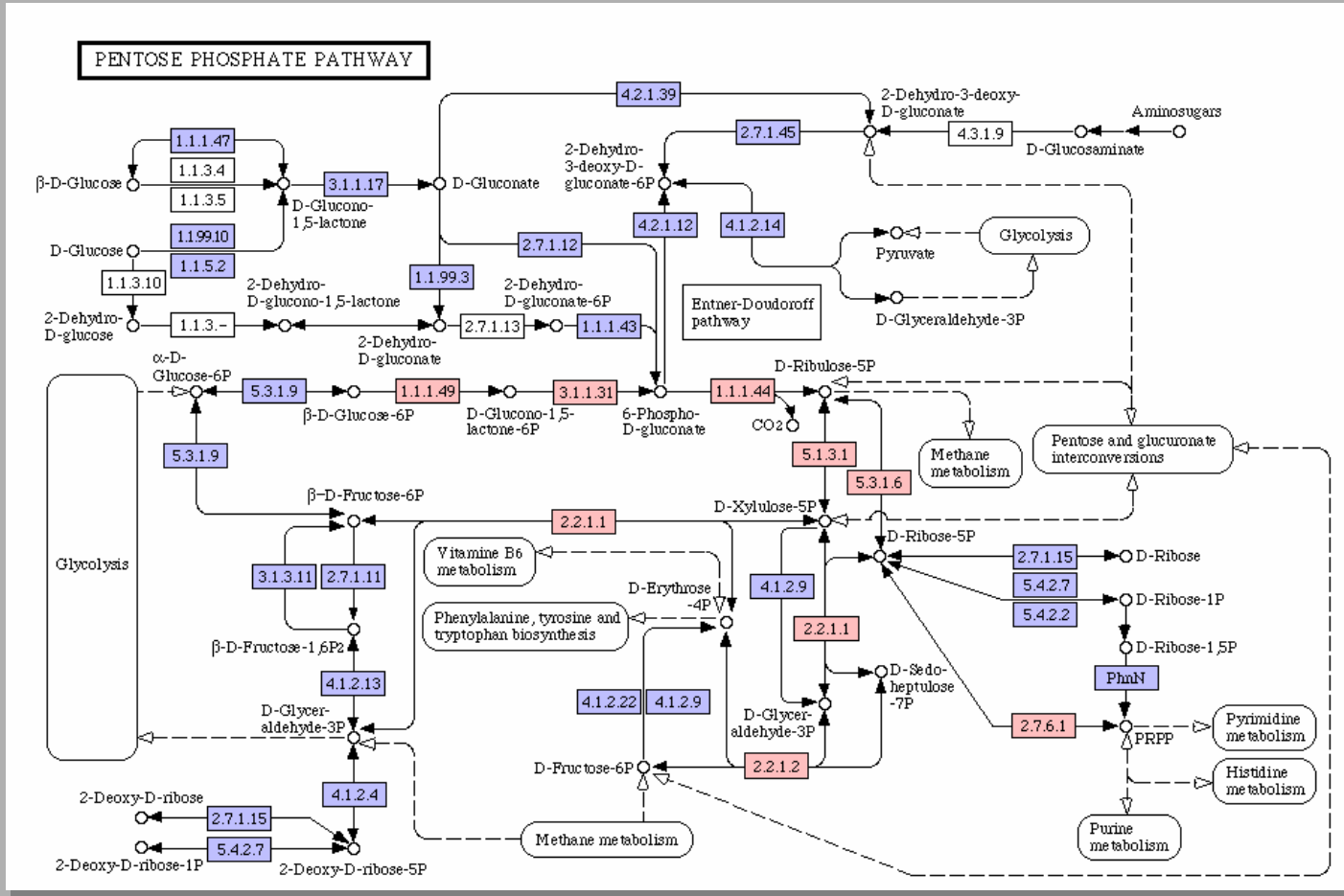
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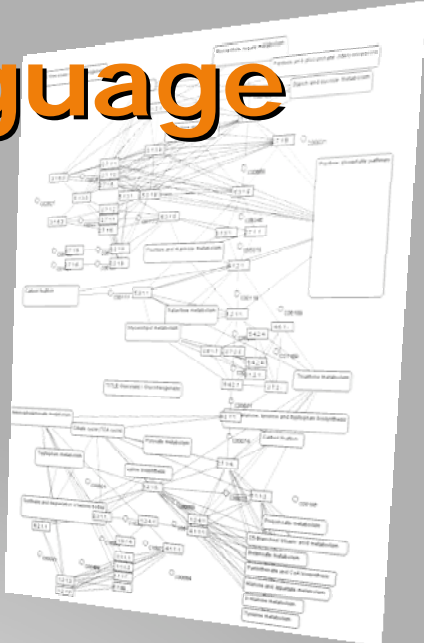
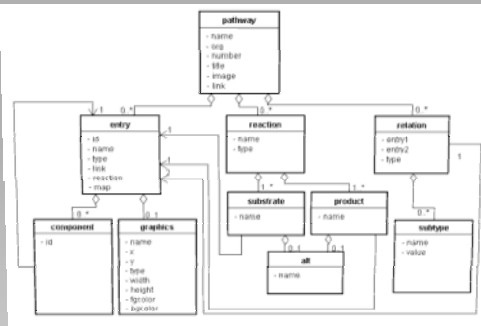
KEGG Modules



KEGG Modules

KEGG Markup Language

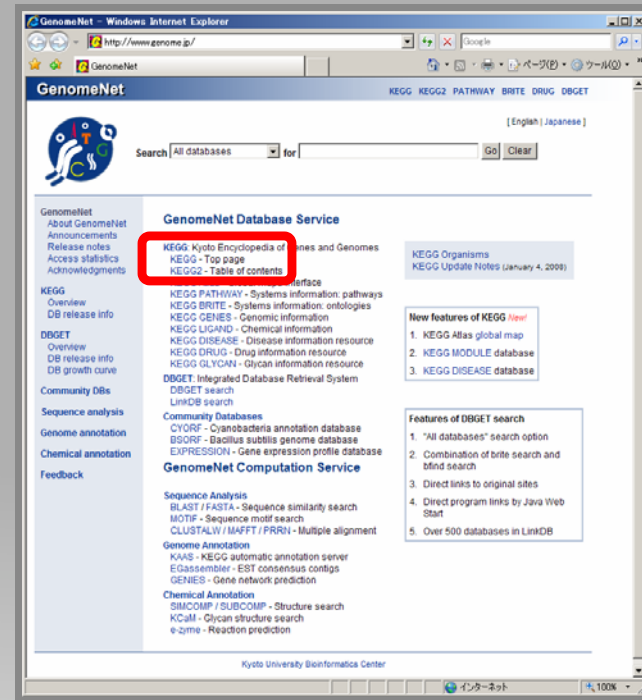
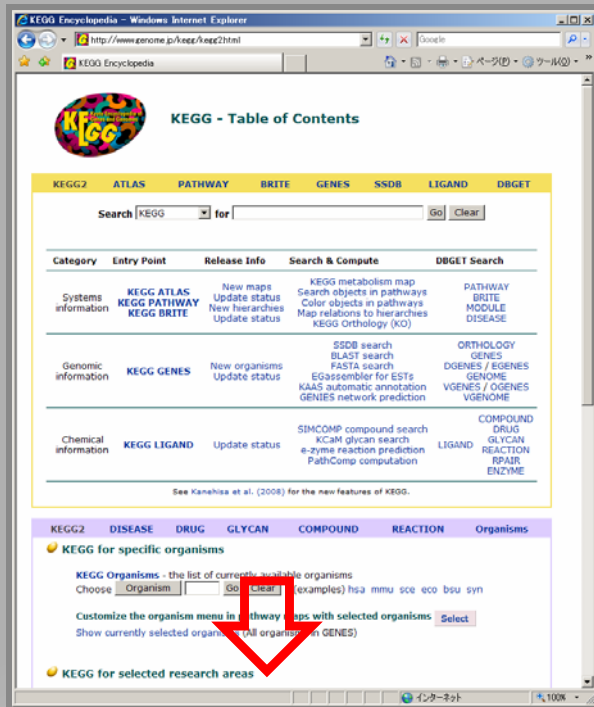
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KGML


Another expression of KEGG PATHWAY

http://www.genome.jp/kegg/xml/
or
you can find it by clicking ...



Where is KGML?

KEGG (KEGG Markup Language)



KEGG Home
Introduction
Overview
Release notes

KEGG Databases
Current statistics

KEGG Identifiers

KEGG Software

KGML
The KEGG objects update facilities, chemical types, circles, contrast, how to use KO (KEG reason), actual

KEGG API

KEGG FTP

Feedback
GenomeNet

KGML (KEGG Markup Language) XML re

Docum

Data

Pathw

Previs

ページが表示されました

http://www.genome.jp/kegg-bin/xml/xmlview?~v+0.6.1+map+00010 - Windows Internet Explorer

http://www.genome.jp/kegg-bin/xml/xmlview?~v+0.6.1+map+00010

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  image="http://www.genome.jp/kegg/pathway/map/map00010.gif"
  link="http://www.genome.jp/dbget-bin/show_pathway?map00010">
  <entry id="1" name="ec:1.2.1.3" type="enzyme" reaction="xn:R00710"
    link="http://www.genome.jp/dbget-bin/www_bget?enzyme+1.2.1.3">
    <graphics name="1.2.1.3" fgcolor="#000000" bgcolor="#FFFFFF"
      type="rectangle" x="170" y="1018" width="45" height="17"/>
  </entry>
  <entry id="2" name="ec:6.2.1.1" type="enzyme" reaction="xn:R00235"
    link="http://www.genome.jp/dbget-bin/www_bget?enzyme+6.2.1.1">
    <graphics name="6.2.1.1" fgcolor="#000000" bgcolor="#FFFFFF"
      type="rectangle" x="102" y="916" width="46" height="17"/>
  </entry>
  <entry id="3" name="ec:1.2.1.5" type="enzyme" reaction="xn:R00711"
    link="http://www.genome.jp/dbget-bin/www_bget?enzyme+1.2.1.5">
    <graphics name="1.2.1.5" fgcolor="#000000" bgcolor="#FFFFFF"
      type="rectangle" x="170" y="1039" width="45" height="17"/>
  </entry>
  <entry id="4" name="cpd:C00033" type="compound"
    link="http://www.genome.jp/dbget-bin/www_bget?compound+C00033">
    <graphics name="C00033" fgcolor="#000000" bgcolor="#FFFFFF"
      type="circle" x="102" y="971" width="8" height="8"/>
  </entry>
  <entry id="5" name="path:map00650" type="map"
    link="http://www.genome.jp/kegg/pathway/map/map00650.html">
    <graphics name="Butanoate metabolism" fgcolor="#000000" bgcolor="#FFFFFF"
      type="roundrectangle" x="645" y="926" width="128" height="25"/>
  </entry>
  <entry id="6" name="path:map00660" type="map"
    link="http://www.genome.jp/kegg/pathway/map/map00660.html">
    <graphics name="C5-Branched dibasic acid metabolism" fgcolor="#000000" bgcolor="#FFFFFF"
      type="roundrectangle" x="683" y="898" width="205" height="25"/>
  </entry>
  <entry id="7" name="path:map00640" type="map"
    link="http://www.genome.jp/kegg/pathway/map/map00640.html">
    <graphics name="Propanoate metabolism" fgcolor="#000000" bgcolor="#FFFFFF"
      type="roundrectangle" x="677" y="866" width="131" height="25"/>
  </entry>
  <entry id="8" name="path:map00710" type="map"
    link="http://www.genome.jp/kegg/pathway/map/map00710.html">
    <graphics name="Carbon fixation" fgcolor="#000000" bgcolor="#FFFFFF"
      type="roundrectangle" x="643" y="720" width="90" height="25"/>
  </entry>
  <entry id="9" name="path:map00030" type="map">
```

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インターネット 100%

Google

ects, especially the KEGG
rawing of KEGG pathways
s and chemical networks.

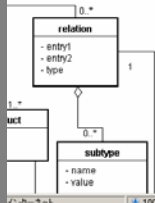
tracting molecules

on reference pathways.

relations in the KEGG
G GENES database.

s as its nodes and the
indicate the connection
chemical compounds),
ling of entry and relation
in network and the
as a network of proteins
pathways is:

orks and



インターネット 100%

KGML

KGML Document - Windows Internet Explorer

http://www.genome.jp/kegg/docs/xml/

KEGG Markup Language

The KEGG Markup Language (KGML) is an exchange format of the KEGG graph objects, especially the KEGG pathway maps that are manually drawn and updated. KGML enables automatic drawing of KEGG pathways and provides facilities for computational analysis and modeling of protein networks and chemical networks.

- <URL: <http://www.genome.jp/kegg/xml/>>

Background

The KEGG pathway maps are graphical image maps representing networks of interacting molecules responsible for specific cellular functions. There are two types of KEGG pathways:

- reference pathways which are manually drawn and
- organism-specific pathways which are computationally generated based on reference pathways.

The KGML files contain computerized information about graphical objects and their relations in the KEGG pathways as well as information about orthologous gene assignments in the KEGG GENES database.

In KGML the **pathway** element specifies one graph object with the **entry** elements as its nodes and the **reaction** and **relation** elements as its edges. The **reaction** and **relation** elements indicate the connection patterns of rectangles (gene products) and the connection patterns of circles (chemical compounds), respectively, in the KEGG pathways. The two types of graph objects, those consisting of entry and relation elements and those consisting of entry and reaction elements, are called the protein network and the chemical network, respectively. Since the metabolic pathway can be viewed both as a network of proteins (enzymes) and as a network of chemical compounds, another distinction of KEGG pathways is:

- metabolic pathways viewed as both protein networks and chemical networks and
- regulatory pathways viewed as protein networks only.

Overview

The following figure shows an overview of KGML.

```

classDiagram
    class pathway {
        - name
        - org
        - number
        - title
        - image
        - link
    }
    class entry {
        - id
        - name
        - type
        - link
        - reaction
        - map
    }
    class reaction {
        - name
        - type
    }
    class relation {
        - entry1
        - entry2
        - type
    }
    class component {
        - id
    }
    class graphics {
        - name
        - x
        - y
    }
    class substrate {
        - name
    }
    class product {
        - name
    }
    class subtype {
        - name
        - value
    }

    pathway "1" *-- "0..*" entry
    pathway "1" *-- "0..*" reaction
    pathway "1" *-- "0..*" relation
    entry "0..*" *-- "1" component
    entry "0..*" *-- "0..1" graphics
    reaction "1..*" *-- "1..*" substrate
    reaction "1..*" *-- "1..*" product
    relation "1" *-- "0..*" subtype
  
```

KGML (KEGG Markup Language) - Windows Internet Explorer

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

KGML (KEGG Markup Language)

Search KEGG

KEGG Home
Introduction
Overview
Release notes

KEGG Databases
Current statistics

KEGG Identifiers

KEGG Software

KGML

KEGG API

KEGG FTP

Feedback
GenomeNet

KGML (KEGG Markup Language)

XML representation of KEGG pathway maps

The KEGG Markup Language (KGML) enables automatic drawing of KEGG pathways and provides facilities for computational analysis and modeling of protein networks and chemical networks. The KGML files for KEGG pathways consist of two types of graph objects, those consisting of entry and relation elements and those consisting of entry and reaction elements, are called the protein network and the chemical network, respectively. Since the metabolic pathway can be viewed both as a network of proteins (enzymes) and as a network of chemical compounds, another distinction of KEGG pathways is:

Documents

- KEGG Markup Language manual
- KGML v0.6.1 DTD [dtd]
- KGML v0.6.1 Readme [txt]

Data

- KEGG reference metabolic pathways
- KEGG reference metabolic pathways
- KEGG reference regulatory pathways
- KEGG organism-specific pathways

Pathway viewer using KGML

- Original viewer [map00770]
- VisANT viewer

Previous Versions

- KGML v0.6
- KGML v0.5
- KGML v0.4
- KGML v0.3
- KGML v0.2
- KGML v0.1

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KGML

Google

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KGML Data - Windows Internet Explorer

http://www.genome.jp/kegg/xml/map/ender.html

KGML Data

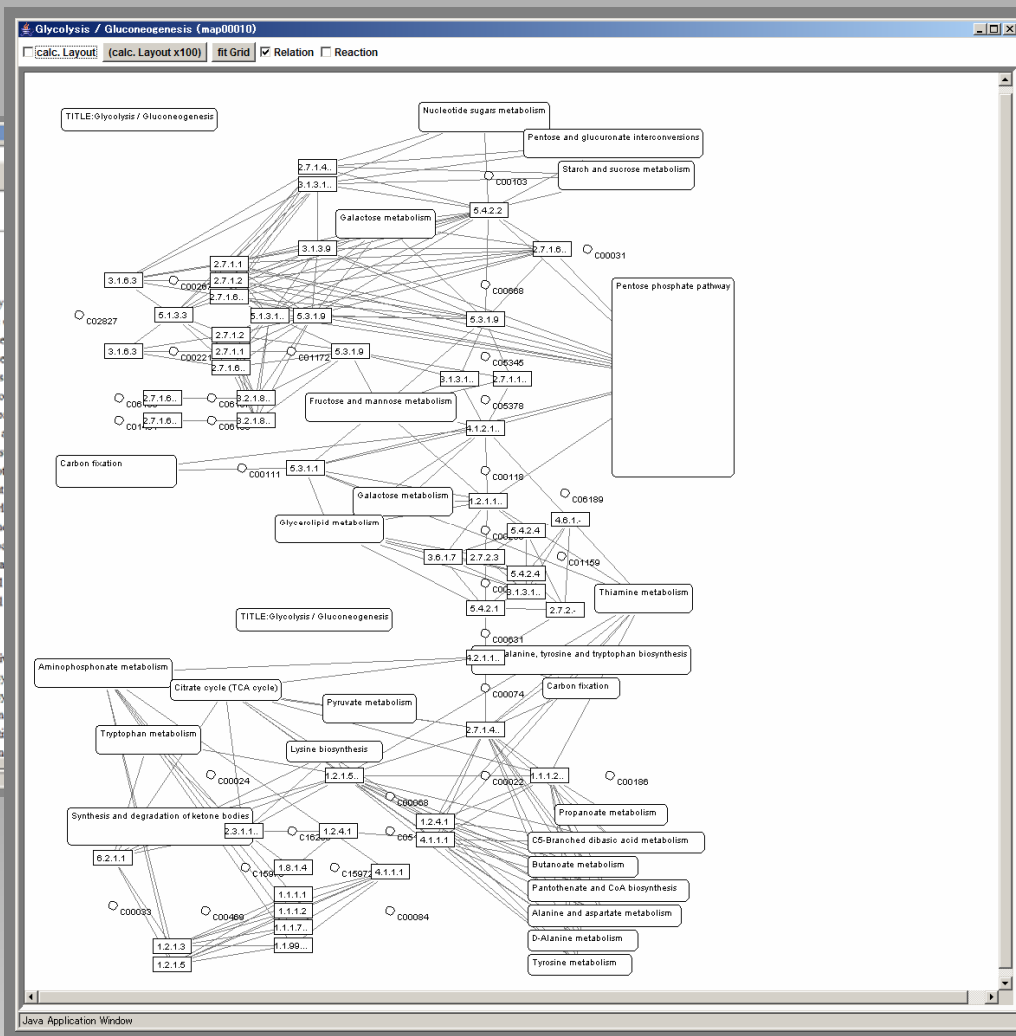
KEGG metabolic pathways

Carbohydrate Metabolism

map00010	[xml text KGMLViewer (Applet, Java Web Start)]	Aug 22, 2007	Glycoly
map00020	[xml text KGMLViewer (Applet, Java Web Start)]	Aug 22, 2007	Citrate
map00030	[xml text KGMLViewer (Applet, Java Web Start)]	Nov 20, 2007	Pentose
map00040	[xml text KGMLViewer (Applet, Java Web Start)]	Jan 18, 2007	Pentose
map00051	[xml text KGMLViewer (Applet, Java Web Start)]	Feb 06, 2007	Fructos
map00052	[xml text KGMLViewer (Applet, Java Web Start)]	Jun 09, 2006	Galacto
map00053	[xml text KGMLViewer (Applet, Java Web Start)]	Dec 12, 2007	Ascorb
map00500	[xml text KGMLViewer (Applet, Java Web Start)]	Sep 01, 2007	Starch
map00530	[xml text KGMLViewer (Applet, Java Web Start)]	Aug 20, 2007	Amino
map00520	[xml text KGMLViewer (Applet, Java Web Start)]	Sep 01, 2007	Nucleo
map00620	[xml text KGMLViewer (Applet, Java Web Start)]	Oct 13, 2007	Pyruvat
map00630	[xml text KGMLViewer (Applet, Java Web Start)]	Jun 21, 2006	Glyoxy
map00640	[xml text KGMLViewer (Applet, Java Web Start)]	Aug 10, 2007	Propano
map00650	[xml text KGMLViewer (Applet, Java Web Start)]	Aug 08, 2007	Butano
map00660	[xml text KGMLViewer (Applet, Java Web Start)]	Oct 13, 2007	C5-Bran
map00031	[xml text KGMLViewer (Applet, Java Web Start)]	Nov 20, 2007	Inositol
map00562	[xml text KGMLViewer (Applet, Java Web Start)]	Jun 09, 2006	Inositol

Energy Metabolism

map00190	[xml text KGMLViewer (Applet, Java Web Start)]	Oct 03, 2006	Oxidati
map00195	[xml text KGMLViewer (Applet, Java Web Start)]	Sep 26, 2006	Photosy
map00196	[xml text KGMLViewer (Applet, Java Web Start)]	Nov 20, 2007	Photosy
map00710	[xml text KGMLViewer (Applet, Java Web Start)]	Feb 20, 2007	Carbon
map00720	[xml text KGMLViewer (Applet, Java Web Start)]	Jun 27, 2006	Reduct
map00680	[xml text KGMLViewer (Applet, Java Web Start)]	Jun 15, 2007	Methan



KGML Viewer by KEGG

VisANT with KGML (KEGG Markup Language) - Opera

ファイル(F) 編集(E) 表示(V) ブックマーク(B) ウィジェット(G) ツール(T) ヘルプ(H)

新しいタブ VisANT with KGML (KE) x

http://visant.keg.jp/index.html

VisANT

KEGG Pathway Visualization by VisANT

KGML

Example

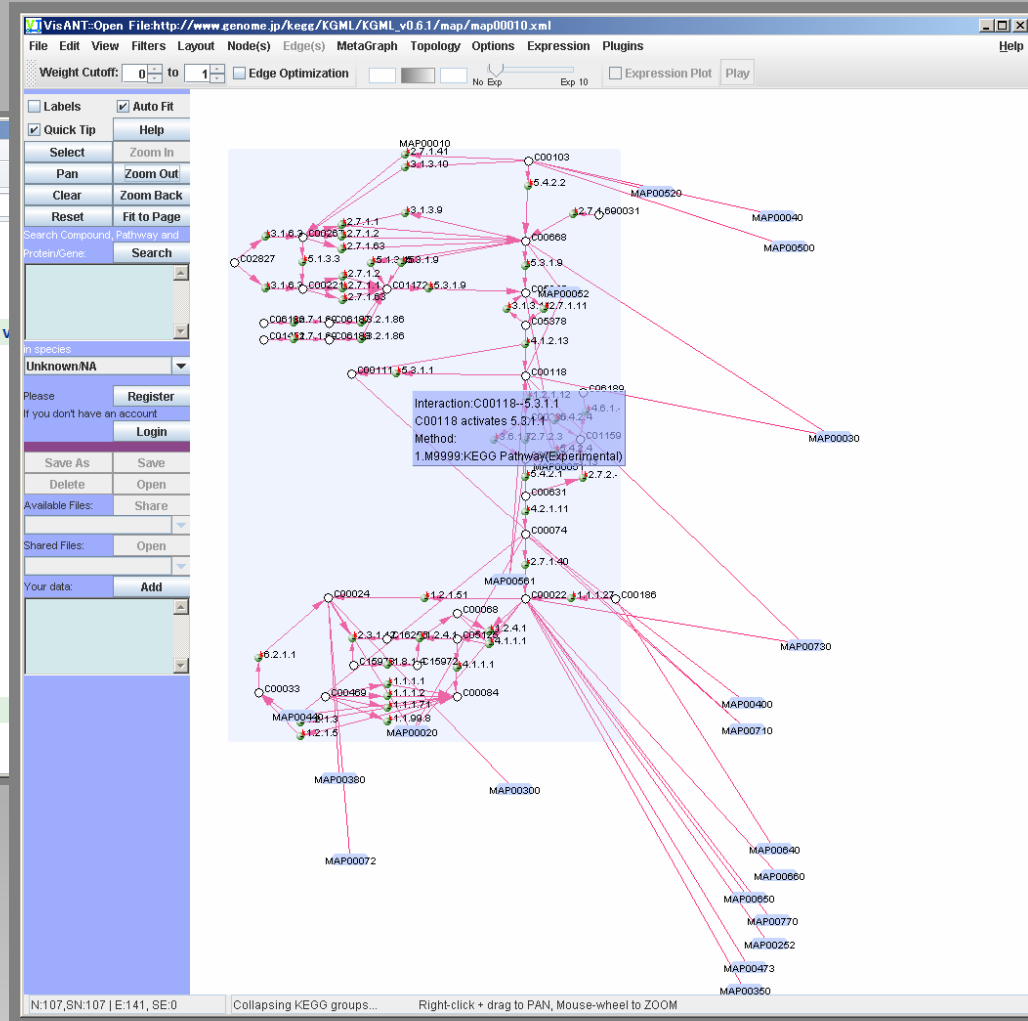
eco00010

KGML Data

- KEGG reference metabolic pathways linked to EC
- KEGG reference metabolic pathways linked to KO
- KEGG reference regulatory pathways linked to KO
- KEGG organism-specific pathways

Enter KEGG organism code (ex. hsa): Go

KEGG HGC



KGML Viewer by VisANT

(<http://visant.bu.edu/>)



A graphical interface of integrated global map

KEGG Atlas

New feature to explorer the KEGG

http://www.genome.jp/kegg/atlas.html
or
you can find it by clicking ...

KEGG - Table of Contents

KEGG2 ATLAS PATHWAY BRITE GENES SSDB LIGAND DBGET

Search [KEGG] for [] Go Clear

Category	Entry Point	Release Info	Search & Compute	DBGET Search
Systems information	KEGG ATLAS	New maps Update status Hierarchies Update status	KEGG metabolism map Search objects in pathways Color objects in pathways Map relations to hierarchies KEGG Orthology (KO)	PATHWAY BRITE MODULE DISEASE
	KEGG PATHWAY			
Genomic information	KEGG GENES	New organisms Update status	SSDB search BLAST search FASTA search EGassembler for ESTs KAAS automatic annotation GENES network prediction	ORTHOLOGY GENES DGENES / EGENES GENOME VGENES / OGENES VGENOME
Chemical information	KEGG LIGAND	Update status	SIMCOMP compound search KICAM glycan search a-zyme reaction prediction PathComp computation	COMPOUND DRUG GLYCAN REACTION PAIR ENZYME

See Kanahisa et al. (2008) for the new features of KEGG.

KEGG2 DISEASE DRUG GLYCAN COMPOUND REACTION Organisms

KEGG for specific organisms

KEGG Organisms - the list of currently available organisms
Choose [Organism] [Go] [Clear] (examples) hsa mmu sce eco bsu svm

Customize the organism menu in pathway maps with selected organisms [Select]

Show currently selected organisms (All organisms in GENES)

KEGG for selected research areas

GenomeNet

KEGG KEGG2 PATHWAY BRITE DRUG DBGET

[English | Japanese]

Search [All databases] for [] Go Clear

GenomeNet Database Service

KEGG Multi-Organismal Genes and Genomes

KEGG - Top page
KEGG2 - Table of contents
KEGG Atlas - Global maps
KEGG Pathway - Pathway information

KEGG
Overview
DB release info

DBGET
Overview
DB release info
DB growth curve

Community DBs

Sequence analysis

Genome annotation

Chemical annotation

Feedback

GenomeNet Database Service

KEGG BRITE - Systems information, ontologies
KEGG GENES - Genomic information
KEGG LIGAND - Chemical information
KEGG DISEASE - Disease information resource
KEGG DRUG - Drug information resource
KEGG GLYCAN - Glycan information resource

DBGET: Integrated Database Retrieval System

DBGET search
LinkDB search

Community Databases

CYORF - Cyanobacteria annotation database
BIOGRF - Bacillus subtilis genome database
EXPRESSION - Gene expression profile database

GenomeNet Computation Service

Sequence Analysis

BLAST / FASTA - Sequence similarity search
MOTIF - Sequence motif search
CLUSTALW / MAFFT / PRN - Multiple alignment

Genome Annotation

KAAS - KEGG automatic annotation server
EGassembler - EST consensus contigs
GENES - Gene network prediction

Chemical Annotation

SIMCOMP / SUBCOMP - Structure search
KICAM - Glycan structure search
a-zyme - Reaction prediction

1. KEGG Atlas global map
2. KEGG MODULE database
3. KEGG DISEASE database

Features of DBGET search

1. "All databases" search option
2. Combination of brite search and blnd search
3. Direct links to original sites
4. Direct program links by Java Web Start
5. Over 500 databases in LinkDB

Kyoto University Bioinformatics Center

Where is KEGG Atlas?



KEGG Atlas

Global maps for exploring KEGG virtual cells and organisms

KEGG2 ATLAS PATHWAY BRITE GENES SSDB LIGAND DBGET

KEGG Atlas

KEGG Atlas is a new graphical interface to the KEGG suite of databases, especially to the systems information in the PATHWAY and BRITE databases. It currently consists of a global metabolism map with an organism-specific view and a cancer map with the traditional KEGG map viewer.

[Metabolism map](#)
[Cancer map](#) *New!*

Other global maps are being developed or planned including:

- Cell map
- Body map
- Brain map

The new **KEGG metabolism map** is created as an SVG file by manually combining about 120 existing metabolic pathway maps. Each node (circle) is a chemical compound identified by the C number. Each line (curved or straight) connecting two nodes is manually defined as a segment lacking branches in the existing maps, named NetElement, and identified by the N number. Each NetElement corresponds to one to several KO's (such as [this](#)) in the reference pathway view, or one to several genes (such as [this](#)) in an organism-specific view.

KEGG Atlas Mapping

The new KEGG metabolism map allows the user to view and compare the entire metabolism, such as by mapping genomic, transcriptomic, metagenomic, or metabolomic data. The following interface allows mapping of genes/compounds as colored segments/nodes in the KEGG metabolism map.

Select

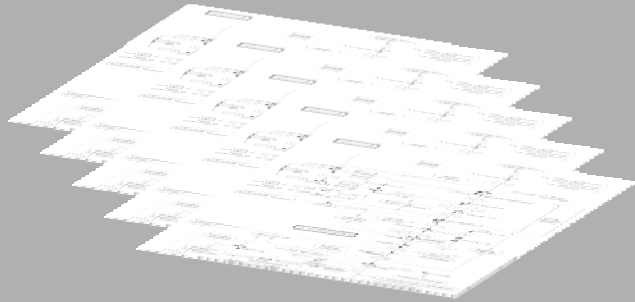
Reference pathway
 Organism

Enter objects one per line, optionally followed by color:

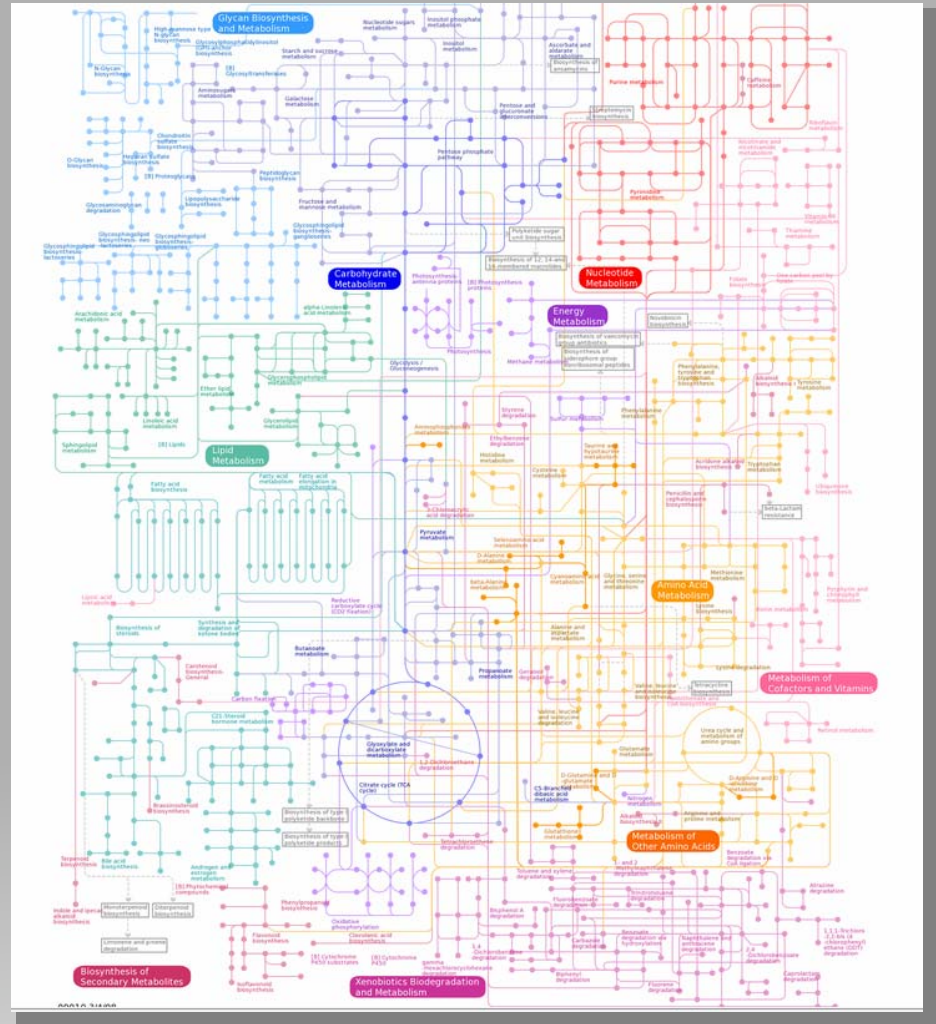
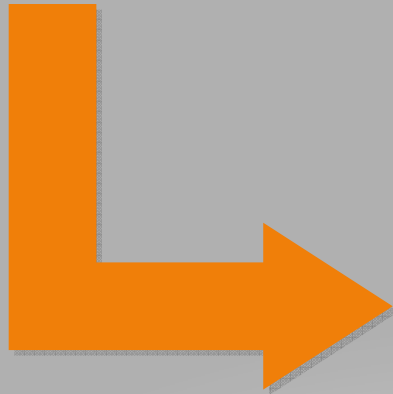
(Example)
Reference pathway:
K01689 #ff99cc
K00873 black
C00024 yellow
C00189

H. sapiens (hsa):
ENO1 red
PKLR #3300FF

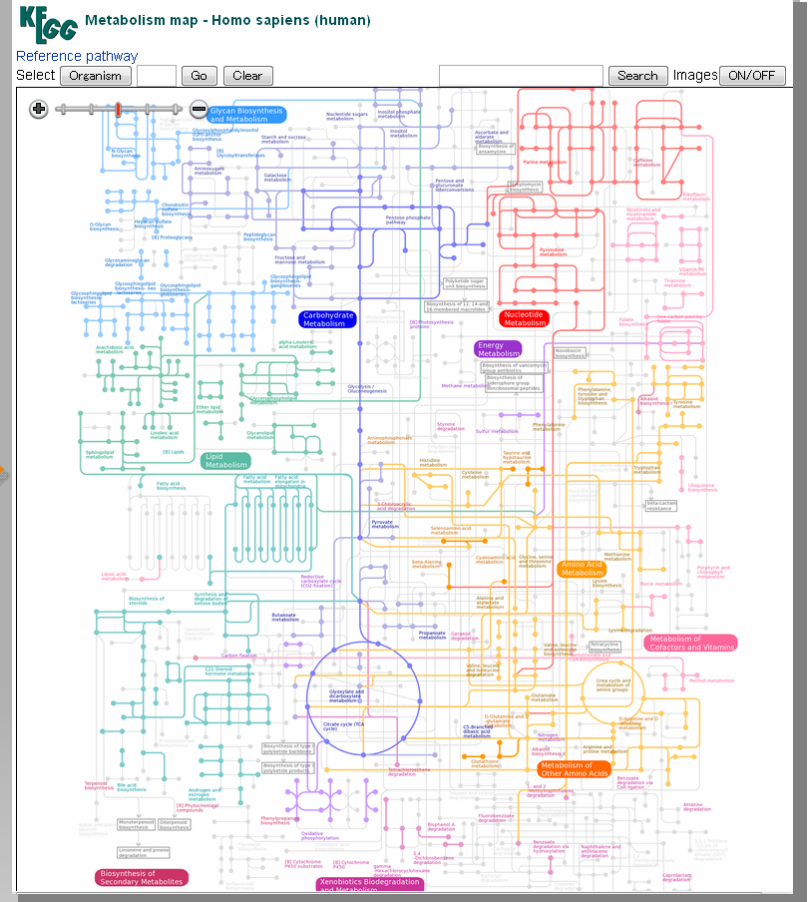
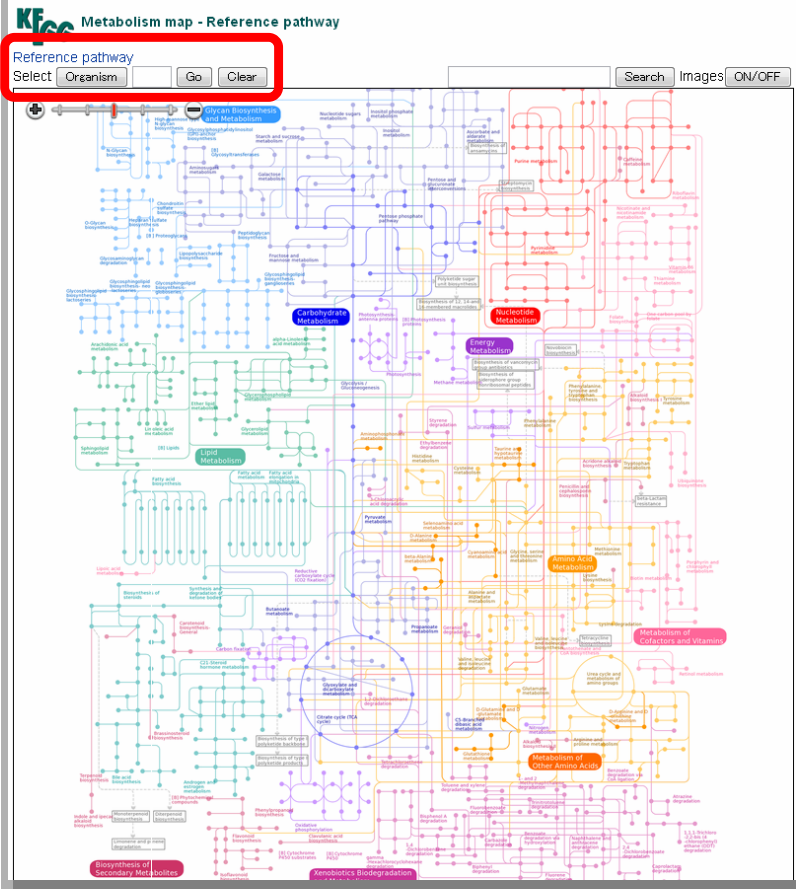
KEGG Atlas



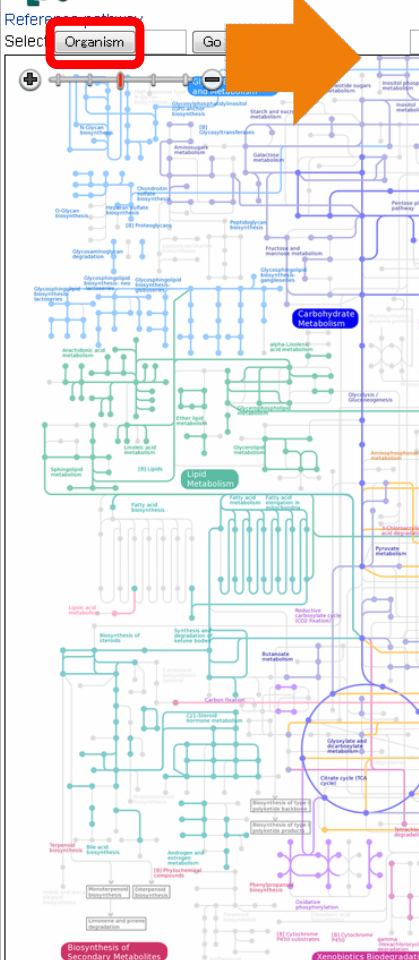
About 120 metabolic pathways



KEGG Atlas metabolism map



KEGG Atlas – Organism specific



Organism:



Organism:

- Encephalitozoon cuniculi [ecu]
- Entamoeba histolytica [ehi]
- Escherichia coli K-12 MG1655 [eco]
- Escherichia coli K-12 W3110 [ecj]
- Escherichia coli K-12 DH10B [ecd]
- Escherichia coli O157 EDL933 (EHEC) [ece]

KEGG Atlas – Organism specific

KEGG Atlas - Windows Internet Explorer

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

KEGG Atlas

Body map
Cancer map

The new **KEGG metabolism map** is created as an SVG file b metabolic pathway maps. Each node (circle) is a chemical o Each line (curved or straight) connecting two nodes is man branches in the existing maps, named NetElement, and ide NetElement corresponds to one to several KO's (such as th to several genes (such as [this](#)) in an organism-specific view

KEGG Atlas Mapping

The new KEGG metabolism map allows the user to view and by mapping genomic, transcriptomic, metagenomic, or meta allows mapping of genes/compounds as colored segments,

Enter objects one per line, optionally followed by color:

Alternatively, enter the file name containing the data:

Partial match of NetElements not allowed

Default color:

Last updated: January 1, 2008

[Feedback](#) [KEGG](#) [GenomeNet](#)

ページが表示されました

KEGG Atlas - Metabolism map - Windows Internet Explorer

http://www.genome.jp/kegg/atlas/mark.rb

KEGG Atlas - Metabolism map

KEGG Metabolism map - Reference pathway

Reference pathway

Select organisms

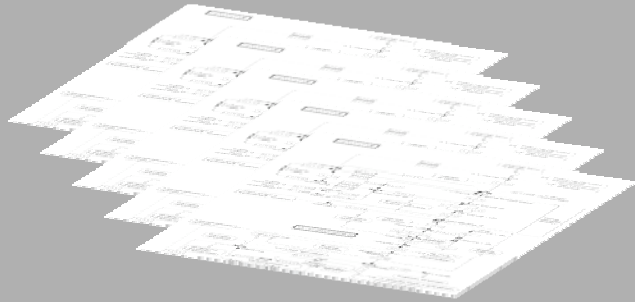
+

← →

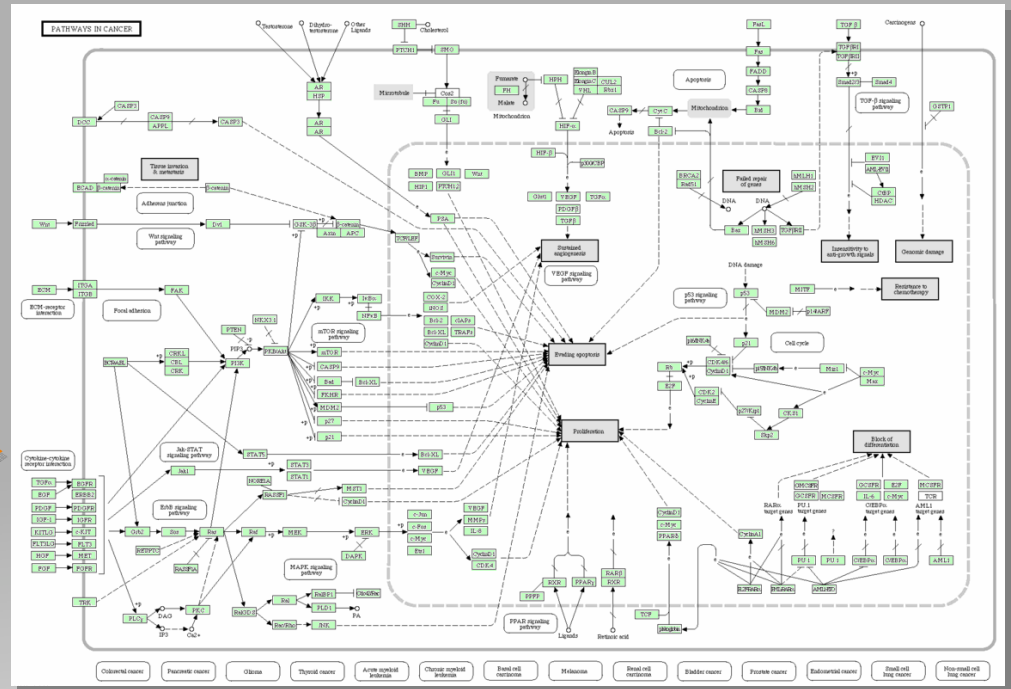
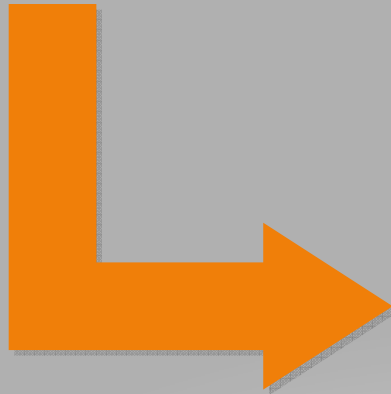
ページが表示されました

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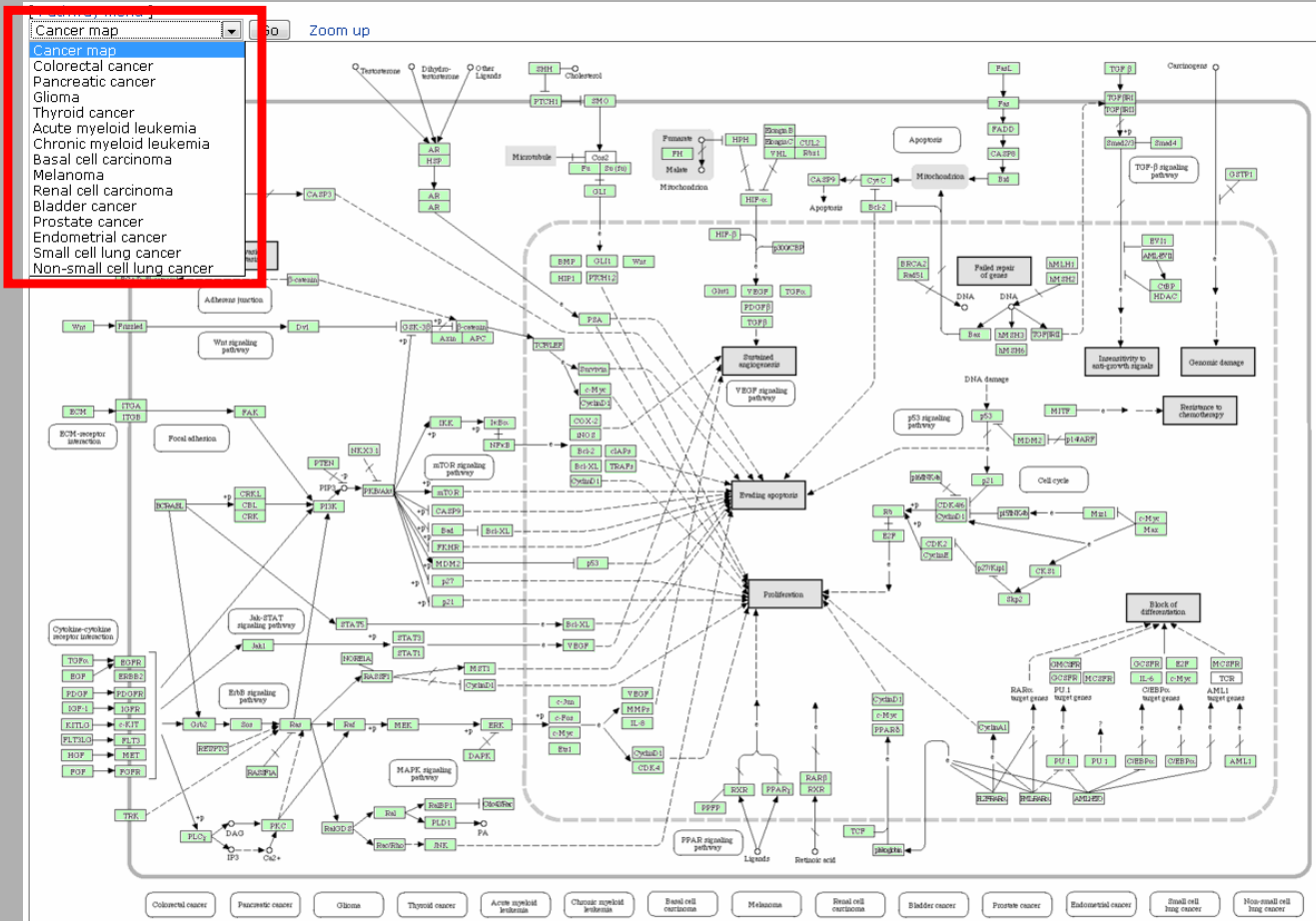
KEGG Atlas Mapping



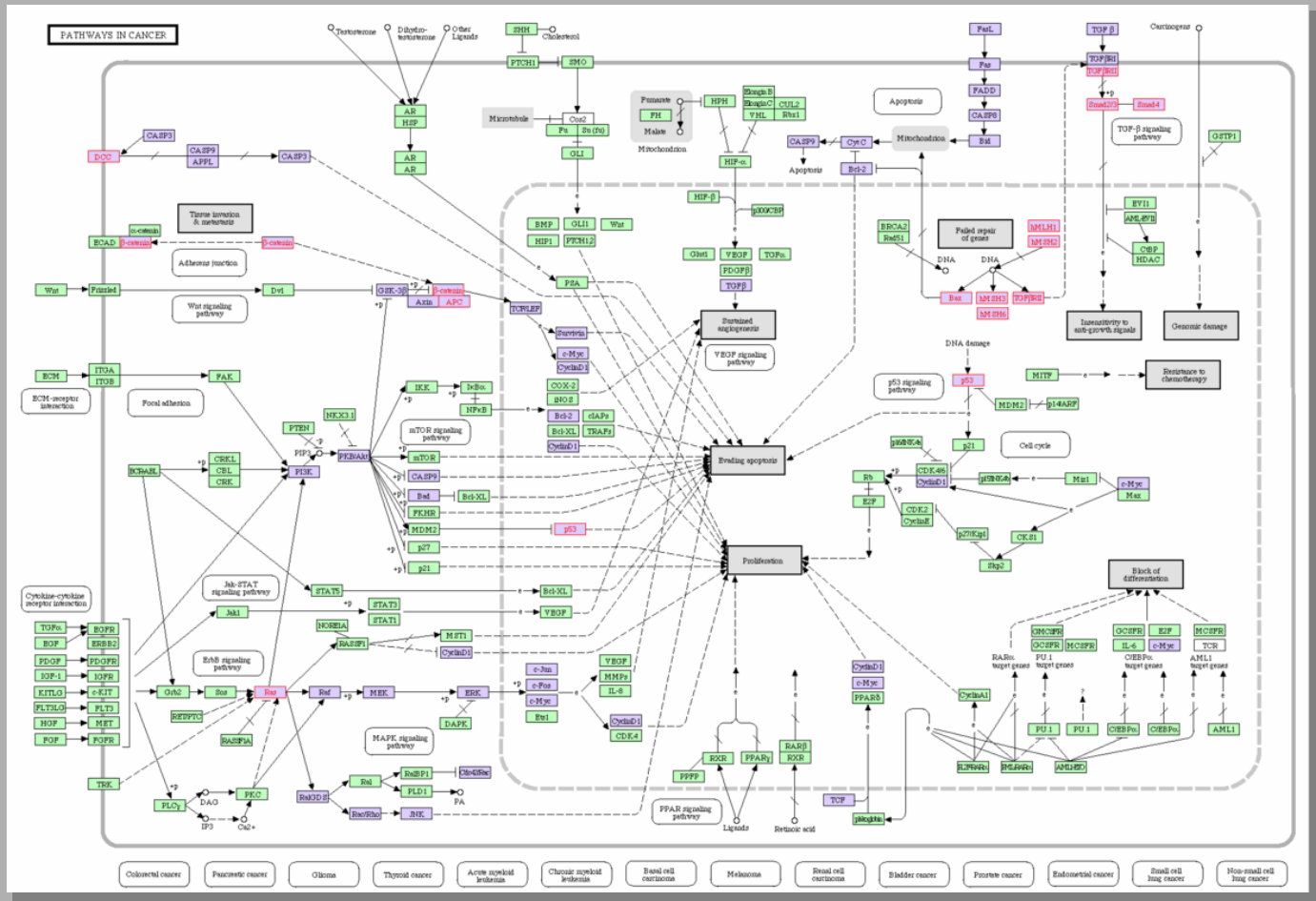
14 cancer pathways



KEGG Atlas Cancer map



KEGG Atlas Cancer map



KEGG Atlas Cancer map

- The original SVG file will be provided at the KEGG FTP site soon.
- Other types of maps, like Cell Map etc., will be added into the KEGG Atlas in the future.

KEGG Atlas – Future



**A collection of simple
entries for diseases**

KEGG DISEASES

Toward an understanding of molecular mechanisms of diseases



KEGG DISEASE

Genetic and genomic information resource for human diseases

KEGG2	DISEASE	DRUG	GLYCAN	COMPOUND	REACTION	Organisms
-------	---------	------	--------	----------	----------	-----------

KEGG DISEASE Database

Entry	H00004	Disease
Name	Chronic myeloid leukemia	
Category	Cancer	
Pathway	hsa05222 Chronic myeloid leukemia	
Gene	BCR-ABL (translocation) [BSA1611 25] JTK1 (overexpression) [BSA1222] ABL1 (translocation) [BSA1611] p16/INK4 (mutation) [BSA1029] p53 (mutation) [BSA1157] B2 (mutation) [BSA1923]	
Carcinogen	1,3-Butadiene [CPD014430] Rubber Industry	
Marker	BCR-ABL (translocation) [BSA1611 25] WT1 [BSA1740]	
Drug	Imatinib mesylate (Gleevec) [DRD01441] hydroxyurea [DRD0141] interferon-alpha [DRD00745 D02745 D03305 D04552 D04553]	
Comment	[C0-Dr: 91753], Tumor type: Chronic myelogenous leukemia	
Reference	[PMD:1571931] (tumor type, gene)	
Authors	Sun R.	
Title	Mechanism of BCR-ABL in the pathogenesis of chronic myelogenous leukemia.	
Journal	Nat Rev Cancer 5:172-83 (2005)	
Reference	[PMD:1040185] (gene)	
Authors	Faderl S, et al.	
Title	The biology of chronic myeloid leukemia.	
Journal	N Engl J Med 341:104-12 (1999)	

(Example) H00004

KEGG DISEASE is a collection of simple entries for diseases. Each entry is identified by the H number, and contains a list of diseases genes and other lists of molecules such as environmental factors, markers, drugs, etc. These lists are intended for integrating various KEGG databases including PATHWAY, GENES, DRUG, and COMPOUND in order to understand molecular mechanisms of diseases.

- DBGET search

Disease Classification

The KEGG BRITE database contains two disease classifications based on genomic and genetic perspectives.

- Pathogens and infectious diseases
- Human diseases

Last updated: March 18, 2008

Disease Pathway

The KEGG PATHWAY database contains pathway maps for certain types of diseases in its "Human diseases" category. Diseases genes are marked red in these pathway maps.

Cancers

- Colorectal cancer
- Pancreatic cancer
- Glioma
- Thyroid cancer
- Acute myeloid leukemia
- Chronic myeloid leukemia
- Basal cell carcinoma
- Melanoma
- Renal cell carcinoma
- Bladder cancer
- Prostate cancer
- Endometrial cancer
- Small cell lung cancer
- Non-small cell lung cancer

Neurodegenerative Disorders

- Alzheimer's disease
- Parkinson's disease
- Amyotrophic lateral sclerosis (ALS)
- Huntington's disease
- Dentatorubropallidolusian atrophy (DRPLA)
- Prion disease

Metabolic Disorders

- Type I diabetes mellitus
- Type II diabetes mellitus
- Maturity onset diabetes of the young

Infectious Diseases

- Cholera
- Epithelial cell signaling in H.pylori infection
- Pathogenic Escherichia coli infection

Feedback
KEGG
GenomeNet
Kanehisa Laboratories

KEGG DISEASES



KEGG DISEASE

Genetic and genomic information resource for human diseases

KEGG2	DISEASE	DRUG	GLYCAN	COMPOUND	REACTION	Organisms
-------	---------	------	--------	----------	----------	-----------

KEGG DISEASE Database

Disease Pathway

Entry	H00004	Disease
Name	Chronic myeloid leukemia	
Category	Cancer	
Pathway	hsa01228 Chronic myeloid leukemia	
Gene	BCR-ABL (translocation) [BSA:611 25] BCL1 (overexpression) [BSA:2122] ABL1 (translocation) [BSA:181] p16/INK4 (mutation) [BSA:1029] P53 (mutation) [BSA:1573] Rb (mutation) [BSA:5925]	
Carcinogen	1,3-butadiene [CDD:018438] Rubber industry	
Marker	BCR-ABL (translocation) [BSA:611 25] WT1 [BSA:1832]	
Drug	imatinib mesylate (Gleevec) [DRD01441] hydroxyurea [DRD00161] interferon-alpha [DRD00745 D02745 D03305 D04552 D04553]	
Comment	[CDD: 00757], Tumor type: Chronic myelogenous leukaemia	
Reference	PMID:15719151 (gene)	
Authors	Sun R	
Title	Mechanism of BCR-ABL in the pathogenesis of chronic myelogenous leukaemia.	
Journal	Nat Rev Cancer 5:172-83 (2005)	
Reference	PMID:10421855 (gene)	
Authors	Faderl S, et al.	
Title	The biology of chronic myeloid leukemia.	
Journal	N Engl J Med 341:164-72 (1999)	

(Example) H00004

KEGG DISEASE is a collection of simple entries for diseases. Each entry is identified by the H number, and contains a list of diseases genes and other lists of molecules such as environmental factors, markers, drugs, etc. These lists are intended for integrating various KEGG databases including PATHWAY, GENES, DRUG, and COMPOUND in order to understand molecular mechanisms of diseases.

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Last updated: March 18, 2008

Feedback KEGG GenomeNet Kanehisa Laboratories

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KEGG DISEASES



KEGG DISEASE

Genetic and genomic information resource for human diseases

KEGG2 DISEASE DRUG GLYCAN COMPOUND REACTION Organisms

KEGG DISEASE Database

Entry	H00004	Disease
Name	Chronic myeloid leukemia	
Category	Cancer	
Pathway	hsa05222: Chronic myeloid leukemia	
Gene	BCR-ABL (translocation) [BSA1611 25] JTK1 (overexpression) [BSA1222] ABL1 (translocation) [BSA1861] p16/INK4 (mutation) [BSA1029] p53 (mutation) [BSA1157] B2 (mutation) [BSA1923]	
Carotenoid	1,3-Butadiene [CP001443] Rubber Industry	
Marker	BCR-ABL (translocation) [BSA1611 25] WT1 [BSA1780]	
Drug	Imatinib mesylate (Gleevec) [DRD01441] hydroxyurea [DR02041] interferon-alpha [DR000745 002745 003305 004552 004553]	
Comment	[C0-Dr: 91757], Tumor type: Chronic myelogenous leukemia	
Reference	[PWID:1571931] (tumor type, gene)	
Authors	Pan R.	
Title	Mechanism of BCR-ABL in the pathogenesis of chronic myelogenous leukemia.	
Journal	Nat Rev Cancer 5:172-83 (2005)	
Reference	[PWID:1040185] (gene)	
Authors	Faderl S, et al.	
Title	The biology of chronic myeloid leukemia.	
Journal	N Engl J Med 341:104-12 (1999)	

(Example) H00004

KEGG DISEASE is a collection of simple entries for diseases. Each entry is identified by the H number, and contains a list of diseases genes and other lists of molecules such as environmental factors, markers, drugs, etc. These lists are intended for integrating various KEGG databases including PATHWAY, GENES, DRUG, and COMPOUND in order to understand molecular mechanisms of diseases.

- DBGET search

Disease Classification

The KEGG BRITE database contains two disease classifications based on genomic and genetic perspectives.

- Pathogens and infectious diseases
- Human diseases



Infectious Diseases
Cholera

Epithelial cell signaling in H.pylori infection
Pathogenic Escherichia coli infection

Last updated: March 18, 2008

Feedback

KEGG

GenomeNet

Kanehisa Laboratories

Disease Pathway

The KEGG PATHWAY database contains pathway maps for certain types of diseases in its "Human diseases" category. Diseases genes are marked red in these pathway maps.

Cancers

Colorectal cancer
Pancreatic cancer
Glioma
Thyroid cancer
Acute myeloid leukemia
Chronic myeloid leukemia
Basal cell carcinoma
Melanoma
Renal cell carcinoma
Bladder cancer
Prostate cancer
Endometrial cancer
Small cell lung cancer
Non-small cell lung cancer

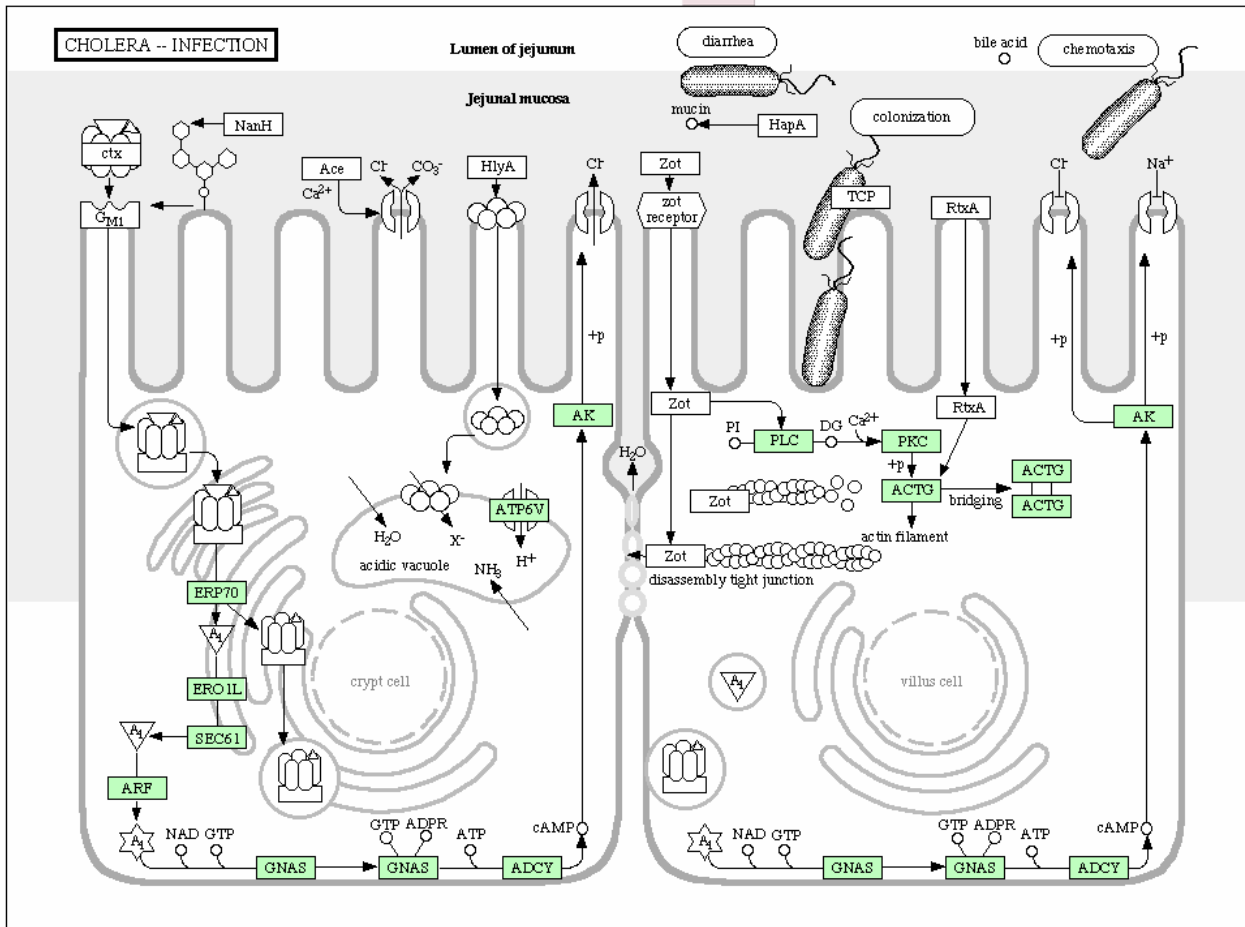
Neurodegenerative Disorders

Alzheimer's disease
Parkinson's disease
Amyotrophic lateral sclerosis (ALS)
Huntington's disease
Dentatorubropallidolusian atrophy (DRPLA)
Prion disease

Metabolic Disorders

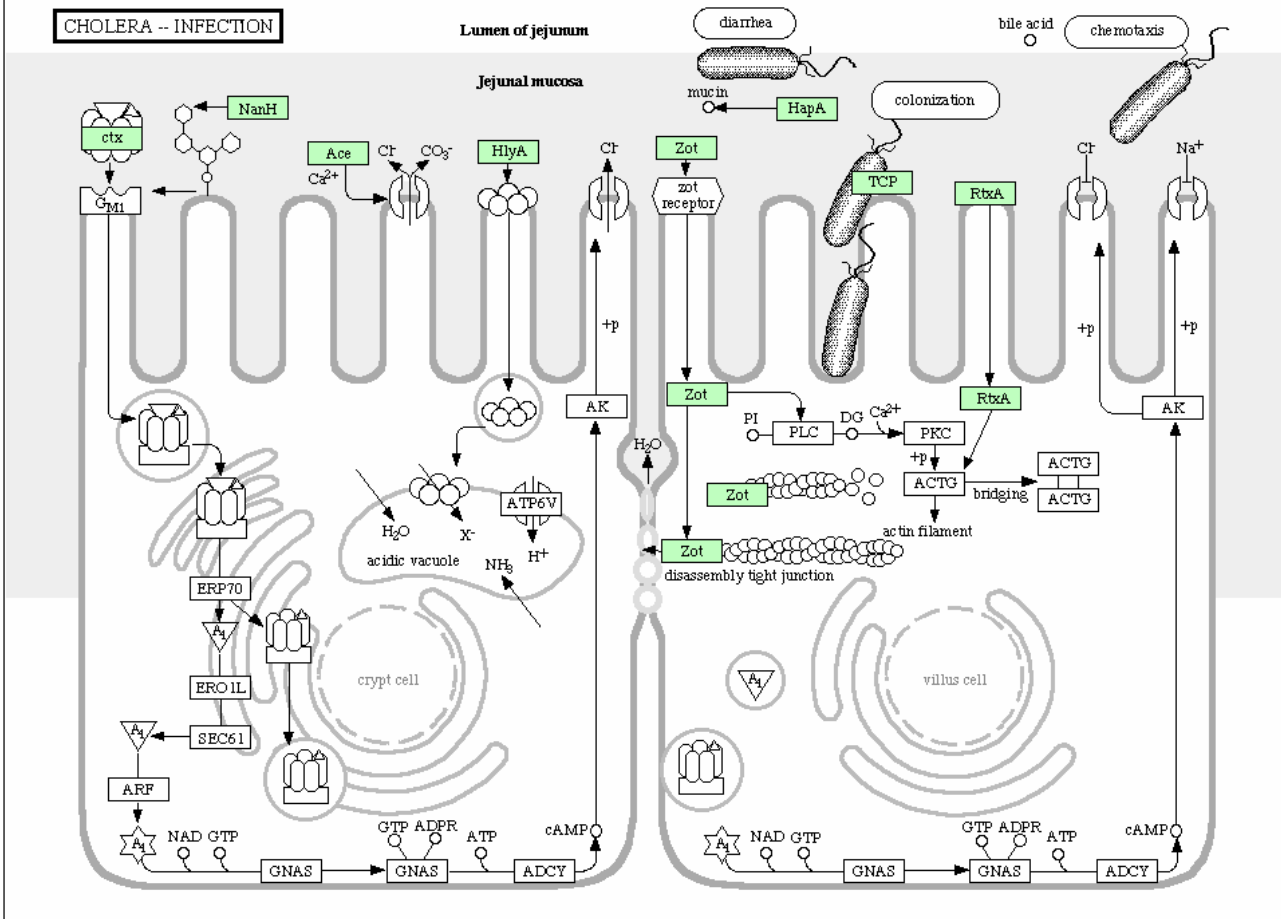
Type I diabetes mellitus
Type II diabetes mellitus
Maturity onset diabetes of the young

KEGG DISEASES



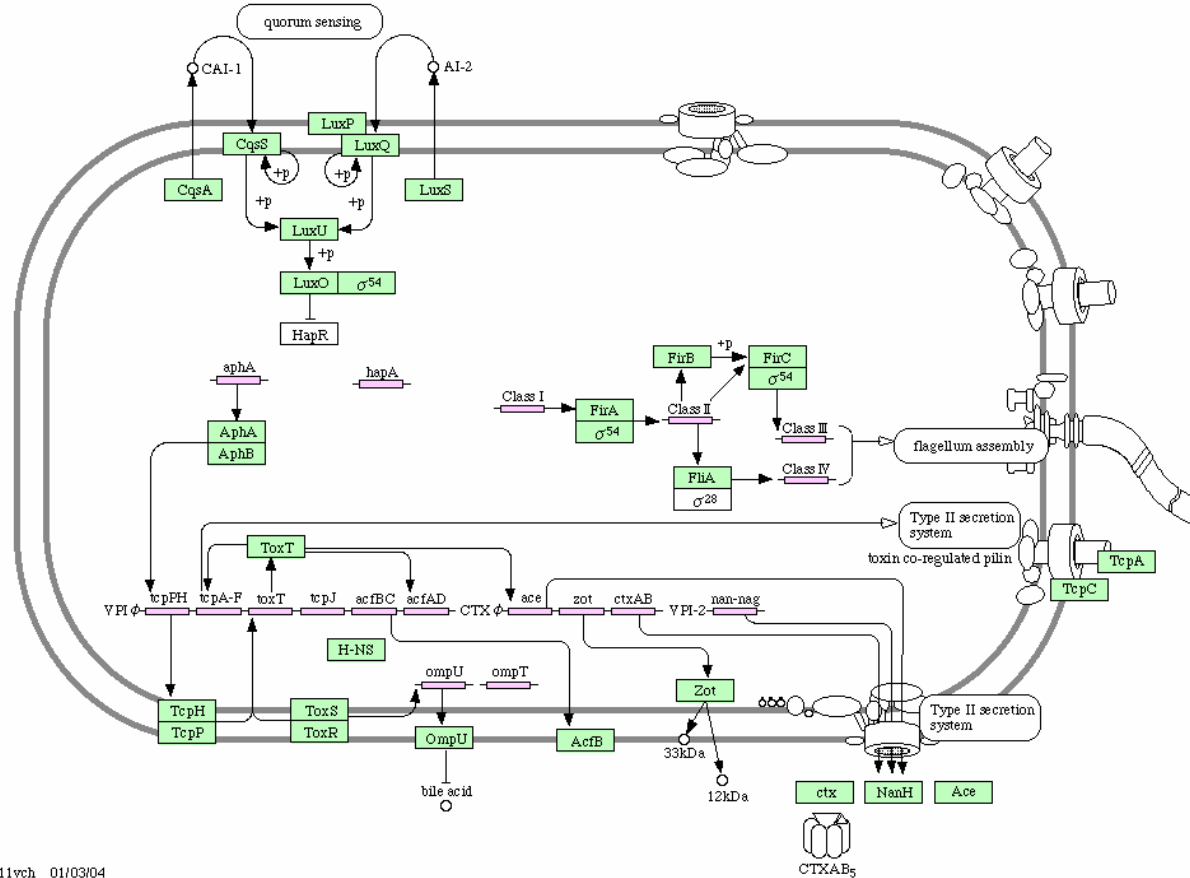
KEGG DISEASES

CHOLERA -- INFECTION



KEGG DISEASES

CHOLERA - COLONIZATION



05111vch 01/03/04



KEGG DISEASE

Genetic and genomic information resource for human diseases

KEGG2	DISEASE	DRUG	GLYCAN	COMPOUND	REACTION	Organisms
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KEGG DISEASE Database

Entry	H00004	Disease
Name	Chronic myeloid leukemia	
Category	Cancer	
Pathway	hsa05222 Chronic myeloid leukemia	
Gene	BCR-ABL (translocation) [BSA1611 25] JTK1 (overexpression) [BSA1222] ABL1 (translocation) [BSA1611] p16/INK4 (mutation) [BSA1029] p53 (mutation) [BSA1157] B2 (mutation) [BSA2747]	
Carcinogen	1,3-Butadiene [DB001443] Rubber Industry	
Marker	BCR-ABL (translocation) [BSA1611 25] WT1 [BSA1740]	
Drug	Imatinib mesylate (Gleevec) [DB001441] hydroxyurea [DB00141] interferon-alpha [DB000745 002745 003305 004552 004553]	
Comment	[CSD: 91757], Tumor type: Chronic myelogenous leukemia	
Reference	[PMID:1571931] (tumor type, gene)	
Authors	Sun R.	
Title	Mechanism of BCR-ABL in the pathogenesis of chronic myelogenous leukemia.	
Journal	Nat Rev Cancer 5:172-83 (2005)	
Reference	[PMID:1040185] (gene)	
Authors	Faderl S, et al.	
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(Example) H00004

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- DBGET search

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The KEGG BRITE database contains two disease classifications based on genomic and genetic perspectives.

- Pathogens and infectious diseases

Last updated: March 18, 2008

Feedback KEGG GenomeNet Kanehisa Laboratories

Disease Pathway

The KEGG PATHWAY database contains pathway maps for certain types of diseases in its "Human diseases" category. Diseases genes are marked red in these pathway maps.

Cancers

- Colorectal cancer
- Pancreatic cancer
- Glioma
- Thyroid cancer
- Acute myeloid leukemia
- Chronic myeloid leukemia
- Basal cell carcinoma
- Melanoma
- Renal cell carcinoma
- Bladder cancer
- Prostate cancer
- Endometrial cancer
- Small cell lung cancer
- Non-small cell lung cancer

Neurodegenerative Disorders

- Alzheimer's disease
- Parkinson's disease
- Amyotrophic lateral sclerosis (ALS)
- Huntington's disease
- Dentatorubropallidolusian atrophy (DRPLA)
- Prion disease

Metabolic Disorders

- Type I diabetes mellitus
- Type II diabetes mellitus
- Maturity onset diabetes of the young

Infectious Diseases

- Cholera
- Epithelial cell signaling in H.pylori infection
- Pathogenic Escherichia coli infection

KEGG DISEASES



Pathogens and Infectious Diseases



- ▶ **Human pathogens**
- ▶ **Animal pathogens**
- ▶ **Plant pathogens**

Search

[[DISEASE](#) | [BRITE](#) | [KEGG2](#) | [KEGG](#)]

Last updated: March 25, 2008

» [Japanese version](#)

KEGG DISEASES



▼ ▼ ▼ ▼

 Search

▼ **Human pathogens**

- ▶ Gamma proteobacteria
- ▶ Beta proteobacteria
- ▶ Delta/epsilon proteobacteria
- ▶ Alpha proteobacteria
- ▶ Gram-positive bacteria
- ▶ Actinobacteria
- ▶ Fusobacteria
- ▶ Chlamydia
- ▶ Spirochetes
- ▶ Bacteroides
- ▶ Protozoa
- ▶ Mycoses
- ▶ dsDNA viruses
- ▶ Retroviruses
- ▶ ssRNA viruses
- ▶ ssDNA viruses



▼ **Animal pathogens**

- ▶ Gamma proteobacteria
- ▶ Beta proteobacteria
- ▶ Delta/epsilon proteobacteria
- ▶ Alpha proteobacteria
- ▶ Gram-positive bacteria
- ▶ Actinobacteria
- ▶ Fusobacteria

KEGG DISEASES



▼ ▼ ▼ ▼


Search

▼ Human pathogens

- ▼ Gamma proteobacteria
 - ▼ Escherichia coli O157:H7 [GN:ece ecs] [PATH:hsa05130] A04.3
 - Enterohaemorrhagic Escherichia coli (EHEC)
 - ▼ Escherichia coli (UPEC) [GN:eci ecp ecc]
 - Cystitis N30
 - Urinary tract infections N39
 - ▼ Salmonella typhi [GN:sty stt]
 - Typhoid fever A01.0
 - ▼ Salmonella enterica [GN:spt spq]
 - Paratyphoid fever A01.1, A01.2
 - ▼ Salmonella typhimurium [GN:stm]
 - Salmonellosis A02
 - ▼ Salmonella enterica [GN:ses sec]
 - Salmonellosis A02
 - ▼ Yersinia pestis [GN:ype ypk ypm ypa ypn ypg ypp] / Xenopsylla cheopis (rat flea)
 - Plague A20
 - ▼ Yersinia pseudotuberculosis [GN:yps ypi]
 - Extraintestinal yersiniosis A28.2
 - Gastroenteritis
 - ▼ Yersinia enterocolitica [GN:yen]
 - Enteritis due to Yersinia enterocolitica A04.6
 - ▼ Shigella flexneri [GN:sfl sfx sfv]
 - Shigellosis A03
 - ▼ Shigella sonnei [GN:ssn]
 - Shigellosis A03
 - ▼ Shigella boydii [GN:sbo]
 - Shigellosis A03
 - ▼ Shigella dysenteriae [GN:sdv]
 - Shigellosis A03
 - ▼ Enterobacter sakazakii [GN:esa]
 - Septicemia A41
 - Meningitis G00
 - Necrotizing enterocolitis
 - ▼ Klebsiella pneumoniae [GN:kpn]
 - Pneumonia due to Klebsiella pneumoniae J15.0
 - Urinary tract infections N39
 - ▼ Citrobacter koseri [GN:cko]
 - Meningoencephalitis
 - Bacteremia
 - Multiple brain abscesses
 - ▼ Serratia proteamaculans [GN:spe]
 - Bacterial pneumonia J15
 - ▼ Haemophilus influenzae [GN:hin hit hip hiq]
 - Septicaemia due to Haemophilus influenzae A41.3
 - Haemophilus influenzae infections A49.2
 - Haemophilus meningitis G00.0
 - Pneumonia due to Haemophilus influenzae J14
 - Acute bronchitis due to Haemophilus influenzae J20.1

KEGG DISEASES



- ▼ ▼ ▼ ▼
- ▼ Human pathogens
- ▼ Gamma proteobacteria
 - ▼ Escherichia coli O157:H7 [GN:[ece ecs](#)] PATH:  PATH: [ecolx](#) A41.3
 - Enterohaemorrhagic [Escherichia coli](#) (EHEC)
 - ▼ Escherichia coli (UPEC) [GN:[eci ecp ecc](#)]
 - Cystitis N30
 - Urinary tract infections N39
 - ▼ Salmonella typhi [GN:[sty stt](#)]
 - Typhoid fever A01.0
 - ▼ Salmonella enterica [GN:[spt spq](#)]
 - Paratyphoid fever A01.1, A01.2
 - ▼ Salmonella typhimurium [GN:[stm](#)]
 - Salmonellosis A02
 - ▼ Salmonella enterica [GN:[ses sec](#)]
 - Salmonellosis A02
 - ▼ Yersinia pestis [GN:[ype ypk ypm ypa ypn ypg ypp](#)] / Xenopsylla cheopis
 - Plague A20
 - ▼ Yersinia pseudotuberculosis [GN:[yps ypi](#)]
 - Extraintestinal yersiniosis A28.2
 - Gastroenteritis
 - ▼ Yersinia enterocolitica [GN:[yen](#)]
 - Enteritis due to Yersinia enterocolitica A04.6
 - ▼ Shigella flexneri [GN:[sfl sfx sfv](#)]
 - Shigellosis A03
 - ▼ Shigella sonnei [GN:[ssn](#)]
 - Shigellosis A03
 - ▼ Shigella boydii [GN:[sbo](#)]
 - Shigellosis A03
 - ▼ Shigella dysenteriae [GN:[sdy](#)]
 - Shigellosis A03
 - ▼ Enterobacter sakazakii [GN:[esa](#)]
 - Septicemia A41
 - Meningitis G00
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 - ▼ Klebsiella pneumoniae [GN:[kpn](#)]
 - Pneumonia due to Klebsiella pneumoniae J15.0
 - Urinary tract infections N39
 - ▼ Citrobacter koseri [GN:[cko](#)]
 - Meningoencephalitis
 - Bacteremia
 - Multiple brain abscesses
 - ▼ Serratia proteamaculans [GN:[spe](#)]
 - Bacterial pneumonia J15
 - ▼ Haemophilus influenzae [GN:[hin hit hip hiq](#)]
 - Septicaemia due to Haemophilus influenzae A41.3
 - Haemophilus influenzae infections A49.2
 - Haemophilus meningitis G00.0
 - Pneumonia due to Haemophilus influenzae J14
 - Acute bronchitis due to Haemophilus influenzae J20.1

	Genome info	Pathway maps	Gene catalogs	Genome map	Organism list
Organism	ece				
Name	E.coli_O157, ECOLX, 155864				
Full name	Escherichia coli O157 EDL933 (EHEC)				
Definition	Escherichia coli O157:H7 EDL933 (EHEC)				
Annotation	manual				
Taxonomy	TAX: 155864				
Lineage	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia				
Data source	RefSeq				
Original DB	Wisconsin , TIGR				
Disease	Hemorrhagic colitis				
Chromosome	Circular				
Sequence	RS: NC_002655				
Length	5528445				
Plasmid	pO157; Circular				
Sequence	RS: NC_007414				
Length	92077				
Statistics	Number of nucleotides: 5620522 Number of protein genes: 5423 Number of RNA genes: 129				
Reference	PMID: 11206551				
Authors	Perna NT, et al.				
Title	Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.				
Journal	Nature 409:529-33 (2001)				
	KEGG2	PATHWAY	BRITE	GENES	LIGAND DBGET

KEGG DISEASES



KEGG DISEASE

Genetic and genomic information resource for human diseases

KEGG2	DISEASE	DRUG	GLYCAN	COMPOUND	REACTION	Organisms
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KEGG DISEASE Database

Entry	H00004	Disease
Name	Chronic myeloid leukemia	
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Carcinogen	1,3-Butadiene [CPD014430] Rubber Industry	
Marker	BCR-ABL (translocation) [BSA1611 25] WT1 [BSA1740]	
Drug	Imatinib mesylate (Gleevec) [DRD01441] hydroxyurea [DRD0141] interferon-alpha [DRD00745 D02745 D03305 D04552 D04553]	
Comment	[CSD: 91757], Tumor type: Chronic myelogenous leukemia	
Reference	[PWID:1571931] (tumor type, gene)	
Authors	Pan R.	
Title	Mechanism of BCR-ABL in the pathogenesis of chronic myelogenous leukemia.	
Journal	Nat Rev Cancer 5:172-83 (2005)	
Reference	[PWID:1040185] (gene)	
Authors	Faderl S, et al.	
Title	The biology of chronic myeloid leukemia.	
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(Example) H00004

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Feedback KEGG GenomeNet Kanehisa Laboratories

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- Thyroid cancer
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- Melanoma
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- Bladder cancer
- Prostate cancer
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- Alzheimer's disease
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- Prion disease

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- Type II diabetes mellitus
- Maturity onset diabetes of the young

Infectious Diseases

- Cholera
- Epithelial cell signaling in H.pylori infection
- Pathogenic Escherichia coli infection

KEGG DISEASES

- **Cancers**

- **Cancers of the Nervous System**
- **Cancers of the Digestive System**
- **Cancers of Haematopoietic and Lymphoid Tissues**
- **Cancers of the Breast and Female Genital Organs**
- **Cancers of Soft Tissues and Bone**
- **Skin Cancers**
- **Cancers of the Urinary System and Male Genital Organs**
- **Cancers of Endocrine Organs**
- **Head and Neck Cancers**
- **Cancers of the Lung and Pleura**

- **Nervous System Diseases**

- **Neurodegenerative Diseases**

- **Metabolic Disorders**

- **Disorders of Carbohydrate Metabolism**
- **Disorders of Lipid Metabolism**
- **Disorders of Glycan Metabolism**
- **Disorders of Amino Acid Metabolism**

KEGG DISEASES Classification



▼ Cancers

▼ Cancers of the Nervous System

- [H00042](#) Glioma [PATH:[hsa05214](#)]
- [H00043](#) Neuroblastoma
- Schwannoma
- Meningioma

▼ Cancers of the Digestive System

- [H00017](#) Esophageal cancer
- [H00018](#) Gastric cancer
- [H00034](#) Carcinoid
- [H00020](#) Colorectal cancer [PATH:[hsa05210](#)]
- [H00044](#) Cancer of the anal canal
- [H00048](#) Hepatocellular carcinoma
- [H00047](#) Gallbladder cancer
- [H00046](#) Cholangiocarcinoma
- [H00019](#) Pancreatic cancer [PATH:[hsa05212](#)]

▼ Cancers of Haematopoietic and Lymphoid Tissues

- [H00003](#) Acute myeloid leukemia (AML) [PATH:[hsa05221](#)]
- [H00001](#) Acute lymphoblastic leukemia (ALL) (Precursor B lymphoblastic leukemia)
- [H00002](#) Acute lymphoblastic leukemia (ALL) (Precursor T lymphoblastic leukemia)
- [H00004](#) Chronic myeloid leukemia (CML) [PATH:[hsa05220](#)]
- [H00005](#) Chronic lymphocytic leukemia (CLL)
- [H00007](#) Hodgkin lymphoma
- [H00006](#) Hairy-cell leukemia
- [H00008](#) Burkitt lymphoma
- [H00009](#) Adult T-cell leukemia
- [H00010](#) Multiple myeloma
- [H00011](#) Lymphoplasmacytic lymphoma
- [H00012](#) Polycythemia vera

▼ Cancers of the Breast and Female Genital Organs

- [H00031](#) Breast cancer
- [H00027](#) Ovarian cancer
- [H00028](#) Choriocarcinoma
- [H00026](#) Endometrial cancer [PATH:[hsa05213](#)]

KEGG DISEASES



▼ **Cancers**

▼ **Cancers of the Nervous System**

- H00042 Glioma [PATH:hsa05214]
- H00043 Neuroblastoma
- Schwannoma
- Meningioma

▼ **Cancers of the Digestive System**

- H00017 Esophageal cancer
- H00018 Gastric cancer
- H00034 Carcinoid
- H00020 Colorectal cancer [PATH:hsa05210]
- H00044 Cancer of the anal canal
- H00048 Hepatocellular carcinoma
- H00047 Gallbladder cancer
- H00046 Cholangiocarcinoma
- H00019 Pancreatic cancer [PATH:hsa05212]

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- H00003 Acute myeloid leukemia (AML) [PATH:hsa05221]
- H00001 Acute lymphoblastic leukemia (ALL) (Precursor B lymphoblastic leukemia)
- H00002 Acute lymphoblastic leukemia (ALL) (Precursor T lymphoblastic leukemia)
- H00004 Chronic myeloid leukemia (CML) [PATH:hsa05220]
- H00005 Chronic lymphocytic leukemia (CLL)
- H00007 Hodgkin lymphoma
- H00006 Hairy-cell leukemia
- H00008 Burkitt lymphoma
- H00009 Adult T-cell leukemia
- H00010 Multiple myeloma
- H00011 Lymphoplasmacytic lymphoma
- H00012 Polycythemia vera

▼ **Cancers of the Breast and Female Genital Organs**

- H00031 Breast cancer
- H00027 Ovarian cancer
- H00028 Choriocarcinoma
- H00026 Endometrial cancer [PATH:hsa05213]

KEGG DISEASES



Search

▼ **Cancers**

▼ **Cancers of the Nervous System**

- H00042 Glioma [PATH:[hsa05214](#)]
- H00043 Neuroblastoma
- Schwannoma
- Meningioma

▼ **Cancers of the Digestive System**

- H00017 Esophageal cancer
- H00018 Gastric cancer
- H00034 Carcinoid
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- H00048 Hepatocellular carcinoma
- H00047 Gallbladder cancer
- H00046 Cholangiocarcinoma
- H00019 Pancreatic cancer [PATH:[hsa05212](#)]

▼ **Cancers of Haematopoietic and Lymphoid Tissues**

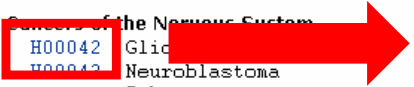
- H00003 Acute myeloid leukemia (AML) [PATH:[hsa05221](#)]
- H00001 Acute lymphoblastic leukemia (ALL) (Precursor B lymphoblastic leukemia)
- H00002 Acute lymphoblastic leukemia (ALL) (Precursor T lymphoblastic leukemia)
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- H00005 Chronic lymphocytic leukemia (CLL)
- H00007 Hodgkin lymphoma
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- H00009 Adult T-cell leukemia
- H00010 Multiple myeloma
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- H00012 Polycythemia vera

▼ **Cancers of the Breast and Female Genital Organs**

- H00031 Breast cancer
- H00027 Ovarian cancer
- H00028 Choriocarcinoma
- H00026 Endometrial cancer [PATH:[hsa05213](#)]

KEGG DISEASES

- ▼ ▼ ▼
- ▼ Cancers
 - ▼ Cancers of the Nervous System
 - H00042** Glioma
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 - ▼ Cancers of Haematopoietic and Lymphoid T
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 - H00001 Acute lymphoblastic leuke
 - H00002 Acute lymphoblastic leuke
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 - H00009 Adult T-cell leukemia
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 - H00012 Polycythemia vera
 - ▼ Cancers of the Breast and Female Genital C
 - H00031 Breast cancer
 - H00027 Ovarian cancer
 - H00028 Choriocarcinoma
 - H00026 Endometrial cancer [PATH:h



Entry	H00042	Disease
Name	Glioma	
Category	Cancer	
Pathway	hsa05214 Glioma	
Gene	EGFR (amplification, overexpression) [HSA:1956] MDM2 (amplification, overexpression) [HSA:4193] PTEN (mutation) [HSA:5728] p16/INK4A (deletion) [HSA:1029] PDGF-A (overexpression) [HSA:5154] PDGF-B (overexpression) [HSA:5155] PDGFR-alpha (overexpression, amplification) [HSA:5156] PDGFR-beta (overexpression, amplification) [HSA:5159] CDK4 (amplification) [HSA:1019] p53 (mutation) [HSA:7157] RB1 (loss) [HSA:5925]	
Carcinogen	X- and gamma-radiation	
Marker	p53 (mutation) [HSA:7157] PTEN (mutation) [HSA:5728] EGFR (amplification) [HSA:1956]	
Drug	Carmustine [DR:D00254] Lomustine [DR:D00363] Procarbazine [DR:D00478] Vincristine [DR:D02197] Temozolomide [DR:D06067]	
Comment	ICD-O: 9401/3, Tumor type: Anaplastic astrocytoma ICD-O: 9440/3, Tumor type: Glioblastoma	
Reference	PMID:15639402 (gene, tumor type) Soni D, et al. Genetics of glioblastoma multiforme: mitogenic signaling and cell cycle pathways converge. J Clin Neurosci 12:1-5 (2005)	
Reference	PMID:11253051 (gene) Holland EC. Gliomagenesis: genetic alterations and mouse models. Nat Rev Genet 2:120-9 (2001)	
Reference	PMID:12154354 (gene) Zhu Y, Parada LF.	

KEGG DISEASES

Summary

- KEGG Pathway
 - Metabolic pathways
 - Regulatory pathways
 - Human diseases etc
- KEGG Module
- KGML
- KEGG Atlas
 - Metabolism map
 - Cancer map
- KEGG DISEASE
 - Disease map
 - Pathogens
 - Disease entries

Afternoon...

- KEGG Pathway
 - Metabolic pathways
 - Regulatory pathways
 - Human diseases
- KEGG Module
- KGML
- KEGG Atlas
 - Metabolism map
 - Cancer map
- KEGG DISEASE
 - Disease map
 - Pathogens
 - Disease entries

Tack så mycket!

<http://web.kuicr.kyoto-u.ac.jp/~honda/temp/sweden/>

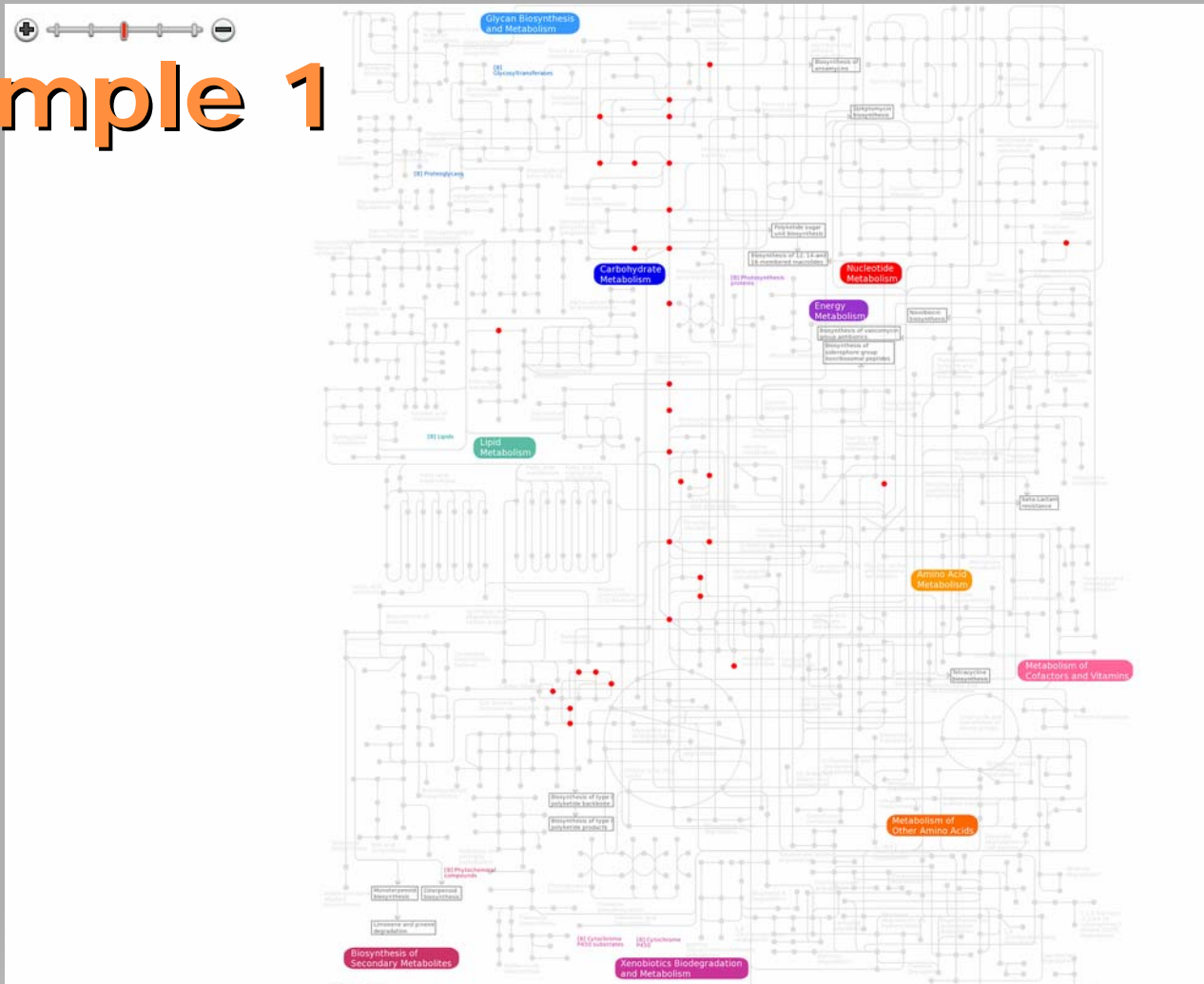
Filename : sweden_afternoon.rtf

- Example1 Compounds in Carbohydrate metabolism
- Example2 Oxidative phosphorylation
- Nucleotides from BRITE
- Vitamins from BRITE

Contact : honda@kuicr.kyoto-u.ac.jp

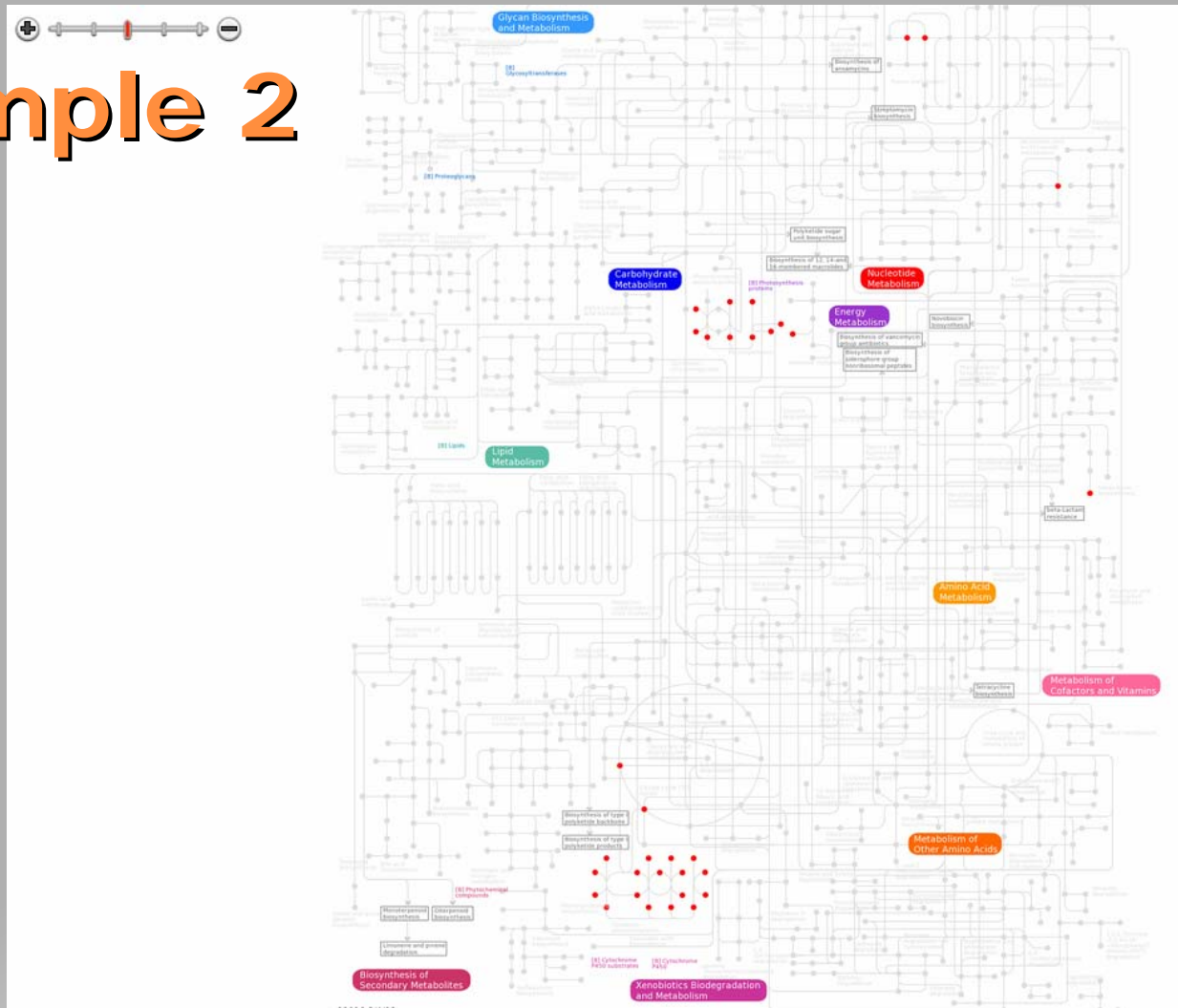
A file for example

Example 1



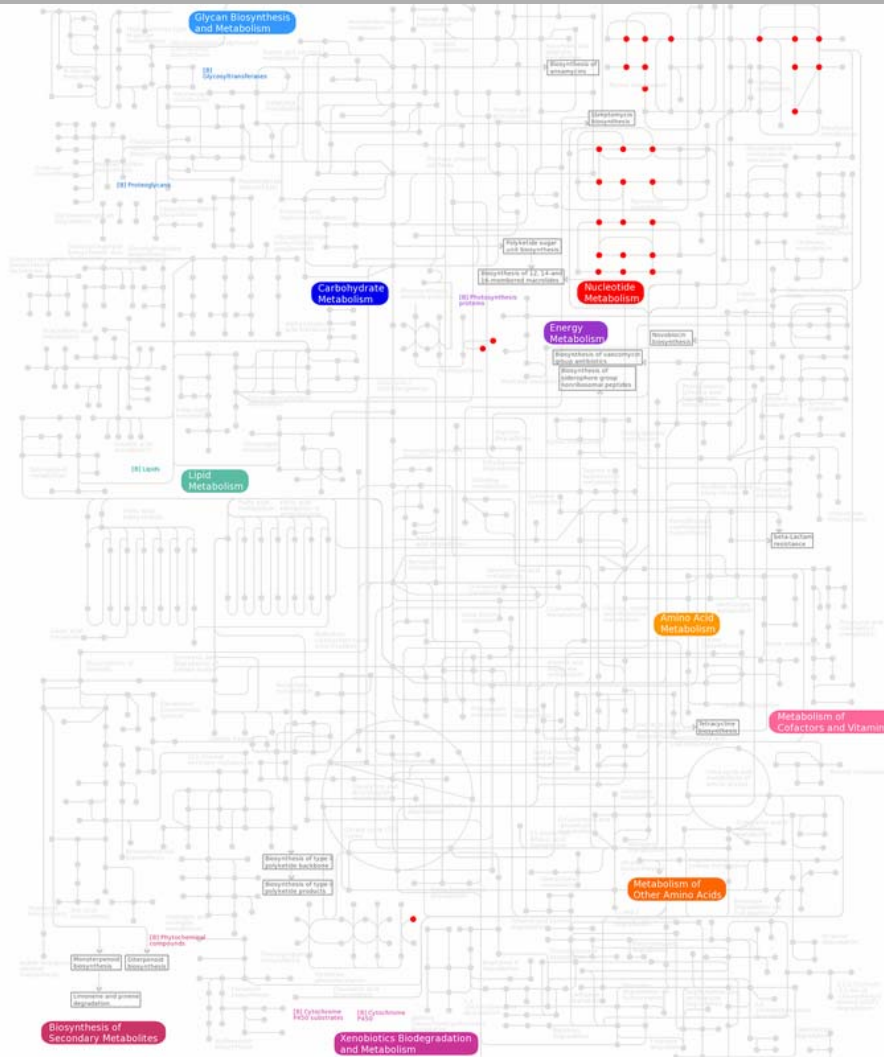
Search and compute

Example 2



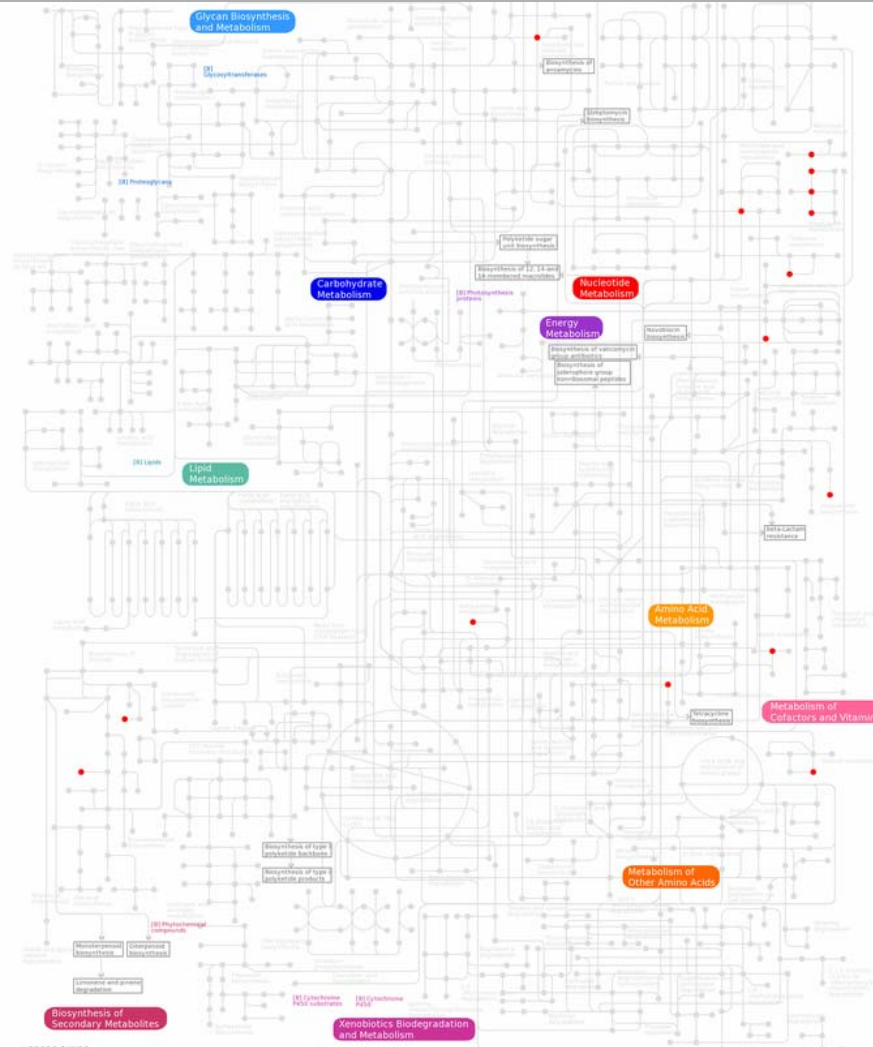
Search and compute

Distribution Of nucleotides

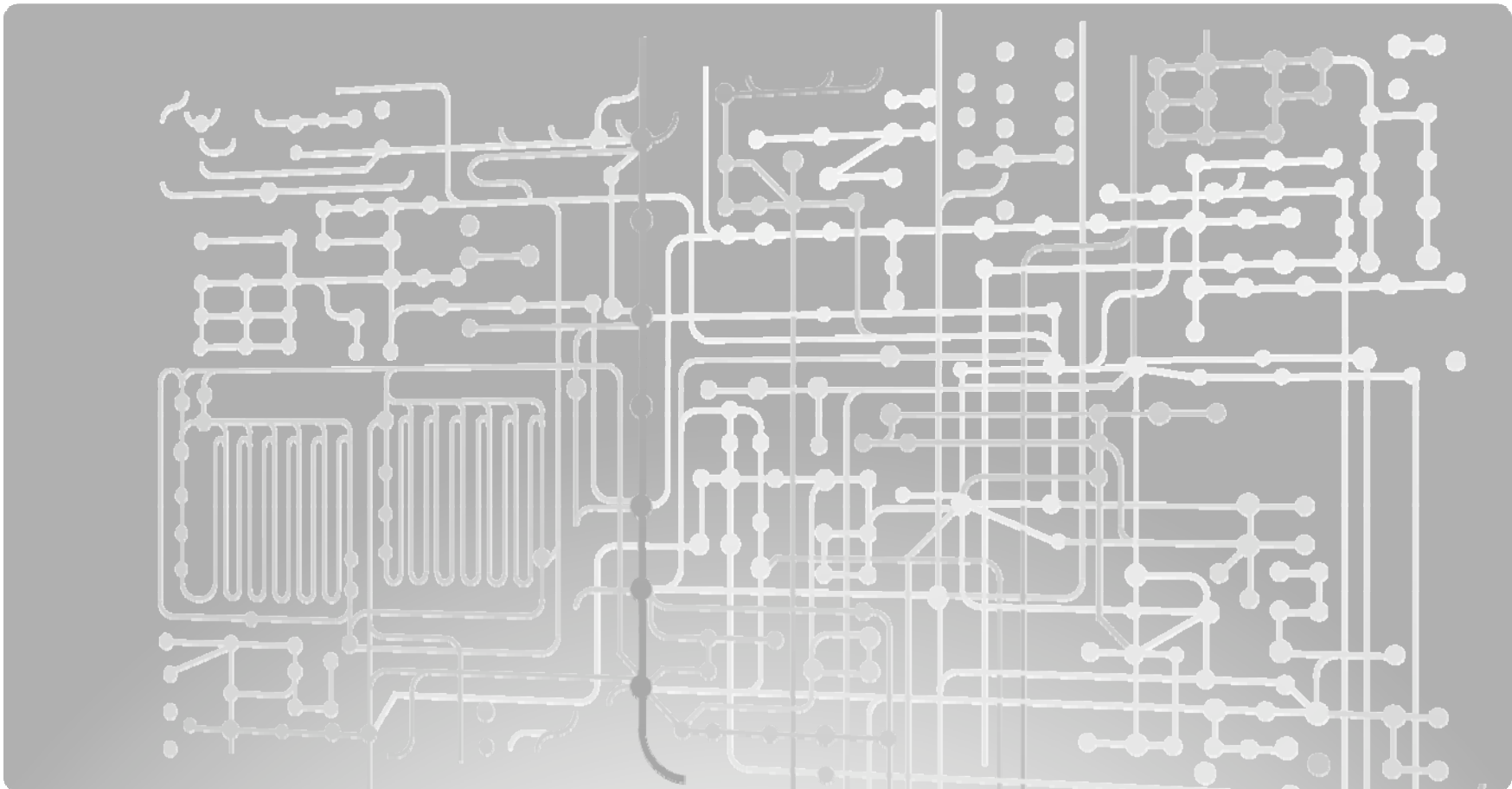


Search and compute

Distribution Of Vitamins



Search and compute



KEGG Web links

Creating web links to KEGG

Retrieve entries

http://www.genome.jp/dbget-bin/www_bget?....

- `www_bget?dbname1:identifier1+dbname2:identifier2+...`
- `www_bget?dbname+identifier1+identifier2+...`

dbname = Organism name or database name in full name or in abbreviation
identifier = Entry name (accession number) or gene name

The second form is applicable to multiple entries in a single database.
The pair "dbname:identifier" is called **keggid**.

(PATHWAY database) http://www.genome.jp/dbget-bin/www_bget?path:hsa05010

(GENES database) http://www.genome.jp/dbget-bin/www_bget?hsa:351

http://www.genome.jp/dbget-bin/www_bget?H.sapiens+APP+PSEN1

(LIGAND database) http://www.genome.jp/dbget-bin/www_bget?cpd:C00002

http://www.g.jp/dbget-bin/www_bget?rn:R05972

(Other databases) http://www.genome.jp/dbget-bin/www_bget?sp:P05067

http://www.genome.jp/dbget-bin/www_bget?swissprot+A4_HUMAN

Retrieve sequence entries in FASTA format

http://www.genome.jp/dbget-bin/www_bget?...

www_bget?-f+dbname1:identifier1+dbname2:identifier2+...
www_bget?-f+dbname+identifier1+identifier2+...

When the entry contains multiple sequences, specify as follows:

- f+-n+1 first sequence in FASTA format
- f+-n+2 second sequence in FASTA format
- f+-n+a amino acid sequence in FASTA format (GENES database only)
- f+-n+n nucleotide sequence in FASTA format (GENES database only)

http://www.genome.jp/dbget-bin/www_bget?-f+hsa:351

http://www.genome.jp/dbget-bin/www_bget?-f+-n+a+hsa:351

http://www.genome.jp/dbget-bin/www_bget?-f+-n+2+hsa:351

The list of options may be viewed by the **-h** option:

http://www.genome.jp/dbget-bin/www_bget?-h

Mark pathway objects in red

http://www.genome.jp/dbget-bin/show_pathway...

show_pathway?mapid+identifier1+identifier2+...

mapid = pathway map identifier, such as map00010 and hsa00010

identifier = gene identifier, compound identifier, ec number, etc.

(Examples)

http://www.genome.jp/dbget-bin/show_pathway?map00400+1.14.16.1+C00079+C00166

http://www.genome.jp/dbget-bin/show_pathway?hsa00400+5053+C00079+C00166

Mark pathway objects in any color

http://www.genome.jp/kegg-bin/mark_pathway_www?...

[mark_pathway_www?@mapid/keggid1/keggid2/...](http://www.genome.jp/kegg-bin/mark_pathway_www?@mapid/keggid1/keggid2/...)

[mark_pathway_www?@mapid/default%3ddcolor/keggid1%09bgcolor,fgcolor/...](http://www.genome.jp/kegg-bin/mark_pathway_www?@mapid/default%3ddcolor/keggid1%09bgcolor,fgcolor/...)

mapid = pathway map identifier, such as map00010 and hsa00010

keggid = dbname:identifier, where dbname: can be omitted

dcolor = default background color, "%3d" represents "=" in ASCII code

bgcolor = background color, "%09" represents TAB in ASCII code

fgcolor = foreground color

(Examples)

http://www.genome.jp/kegg-bin/mark_pathway_www?@map00400/ec:1.14.16.1/cpd:C00079/cpd:C00166

http://www.genome.jp/kegg-bin/mark_pathway_www?@map00400/default%3dpink/1.14.16.1%09,blue/C00079%09,red/cpd:C00166%09%23005050



