Systems Biology in Metabolomics

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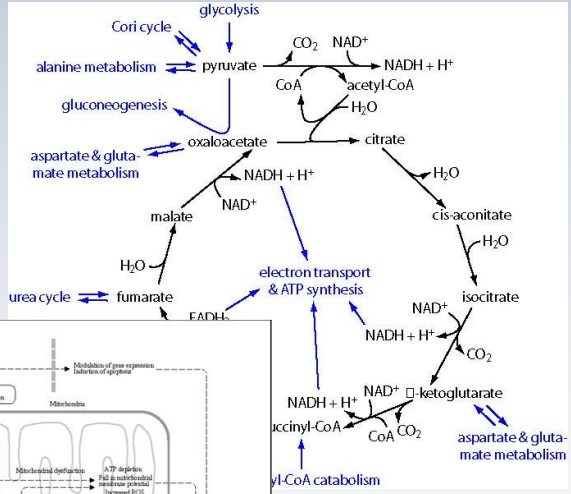
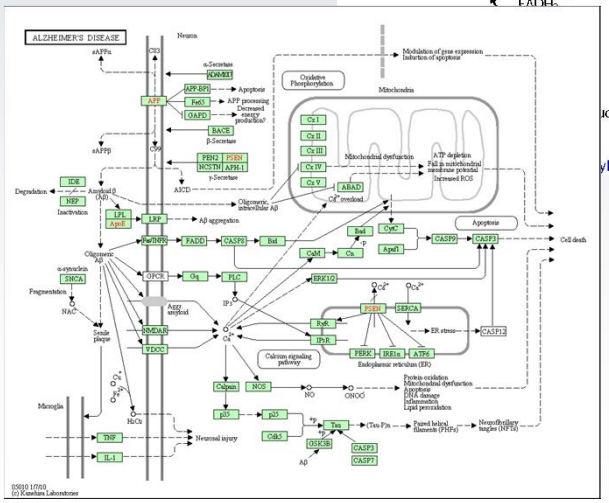




TrasMed Course 25.09.2014

Basic definitions:

- **Metabolites** - are the intermediates and products of metabolism. The term *metabolite* is usually restricted to small molecules. A **primary metabolite** is directly involved in normal growth, development, and reproduction, e.g. alcohol. A **secondary metabolite** is not directly involved in those processes, but usually has an important ecological function. Examples include antibiotics and pigments. Some antibiotics use primary metabolites as precursors, e.g. actinomycin, a product of primary metabolite tryptophan.

- **Metabolome** - The metabolome forms a large network of metabolic reactions, where outputs from one **enzymatic chain reaction** are inputs to other chemical reactions. The metabolome represents the collection of all metabolites in a biological cell, tissue, organ or organism, which are the end products of cellular processes.

- **Metabolomics** - "systematic study of the unique chemical fingerprints that specific cellular processes leave behind", the study of their small-molecule metabolite profiles.

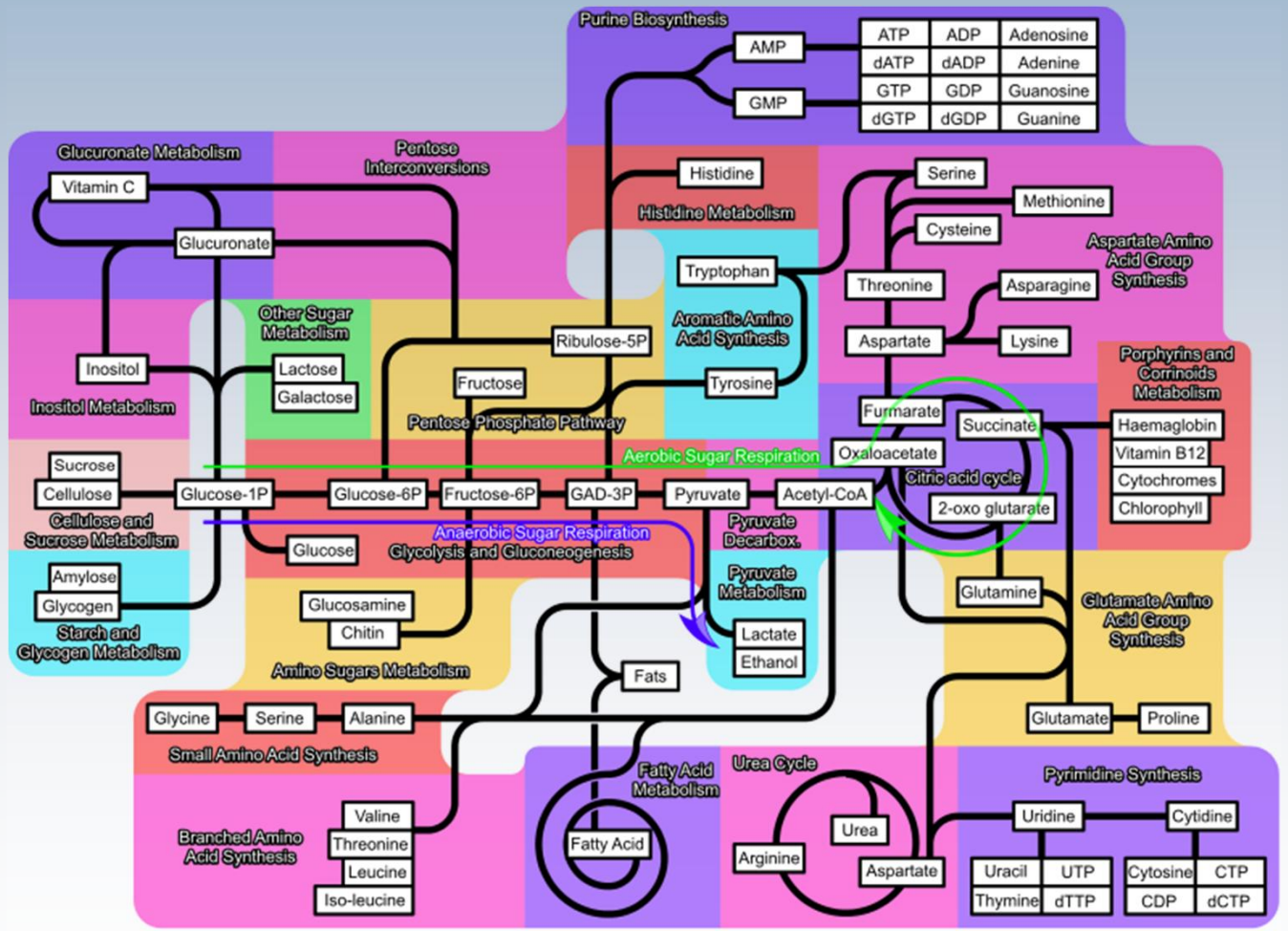
- **Metabolomic pathways** - are series of chemical reactions occurring within a cell. In each pathway, a principal chemical is modified by a series of chemical reactions. This collection of pathways is called the **metabolic network**. Pathways are important to the maintenance of **homeostasis** within an organism. **Catabolic** (**break-down**) and **anabolic** (**synthesis**) pathways often work interdependently to create new biomolecules as the final end-products.

Major metabolic pathways

A metabolic pathway involves the step-by-step modification of an initial molecule to form another product.

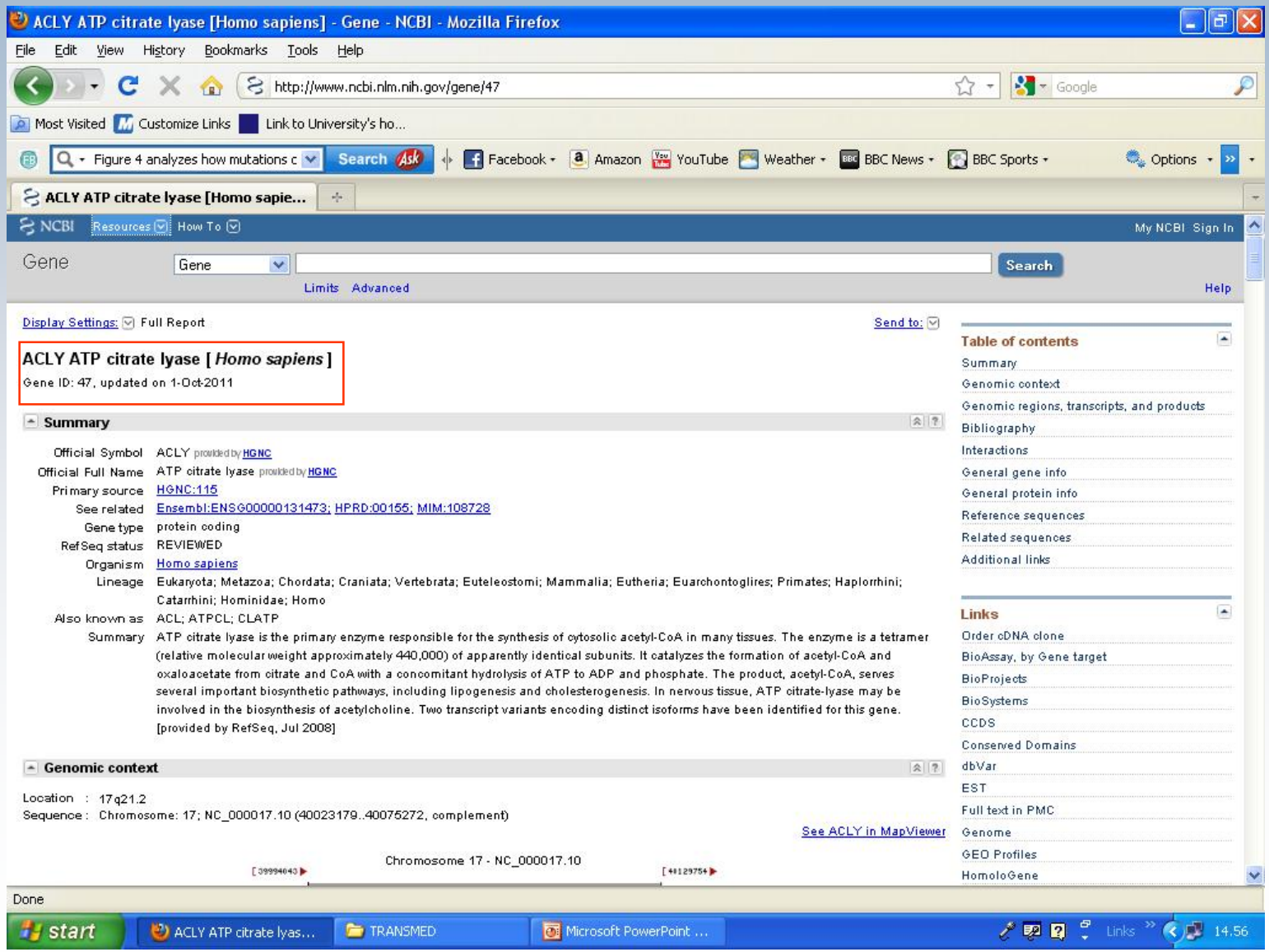
1) product is used immediately, as the end-product of a metabolic pathway
2) product initiates another metabolic pathway, called a flux generating step
3) product is stored by the cell.

A molecule called a substrate enters a metabolic pathway depending on the needs of the cell and the availability of the substrate. An increase in concentration of anabolic and catabolic intermediates and/or end-products may influence the metabolic rate for that particular pathway.



http://en.wikipedia.org/wiki/Metabolic_pathway

Entrez Gene: http://www.ncbi.nlm.nih.gov/gene/:



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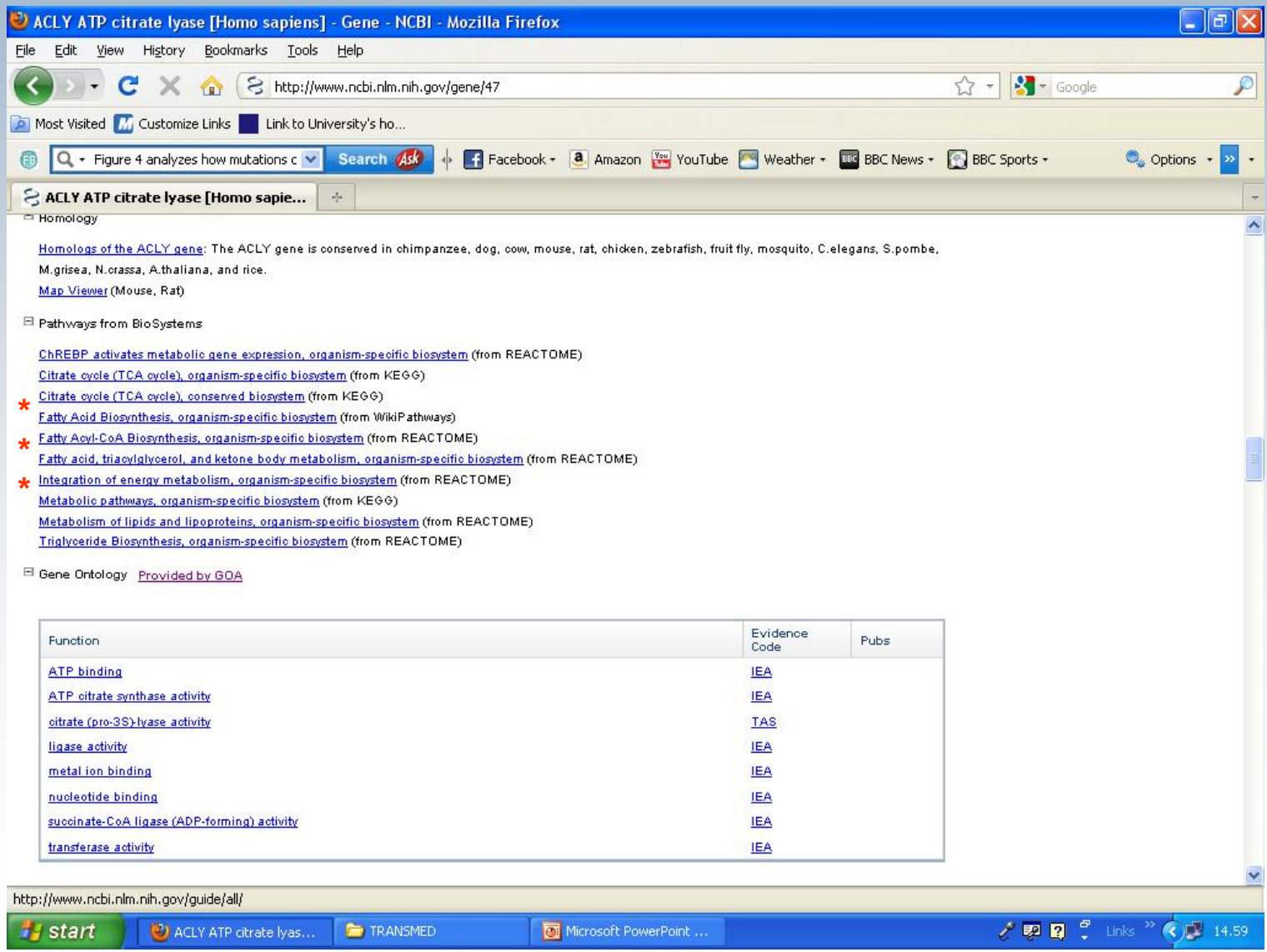
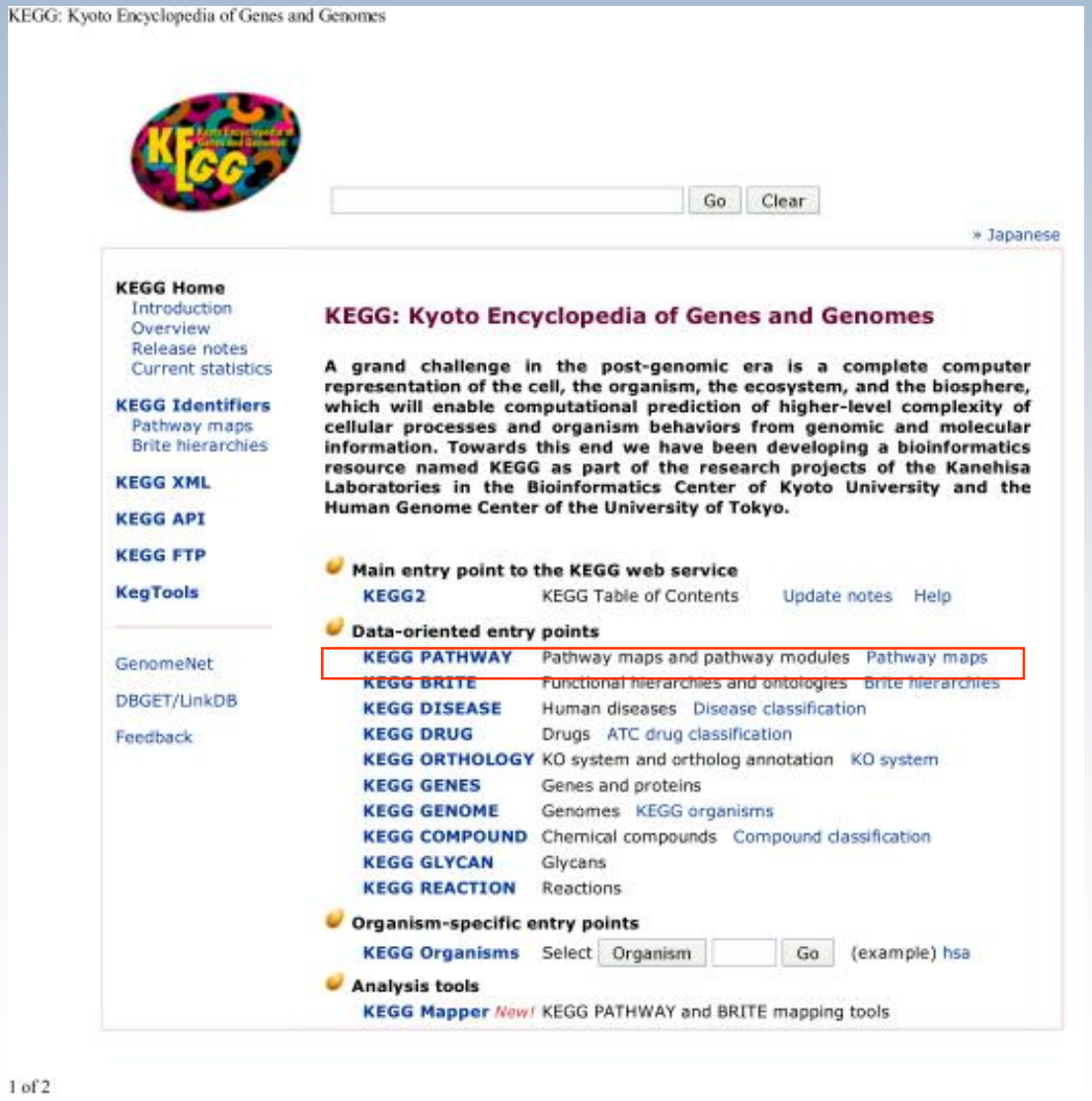


KEGG http://www.genome.jp/kegg/



KEGG: Kyoto Encyclopedia of Genes and Genomes

Go Clear

» Japanese

KEGG Home
Introduction
Overview
Release notes
Current statistics

KEGG Identifiers
Pathway maps
Brite hierarchies

KEGG XML

KEGG API

KEGG FTP

KegTools

GenomeNet

DBGET/LinkDB

Feedback

KEGG: Kyoto Encyclopedia of Genes and Genomes

A grand challenge in the post-genomic era is a complete computer representation of the cell, the organism, the ecosystem, and the biosphere, which will enable computational prediction of higher-level complexity of cellular processes and organism behaviors from genomic and molecular information. Towards this end we have been developing a bioinformatics resource named KEGG as part of the research projects of the Kanehisa Laboratories in the Bioinformatics Center of Kyoto University and the Human Genome Center of the University of Tokyo.

Main entry point to the KEGG web service

KEGG2	KEGG Table of Contents	Update notes Help

Data-oriented entry points

KEGG PATHWAY	Pathway maps and pathway modules	Pathway maps
KEGG BRITE	Functional hierarchies and ontologies	Brite hierarchies
KEGG DISEASE	Human diseases	Disease classification
KEGG DRUG	Drugs	ATC drug classification
KEGG ORTHOLOGY	KO system and ortholog annotation	KO system
KEGG GENES	Genes and proteins	
KEGG GENOME	Genomes	KEGG organisms
KEGG COMPOUND	Chemical compounds	Compound classification
KEGG GLYCAN	Glycans	
KEGG REACTION	Reactions	

Organism-specific entry points

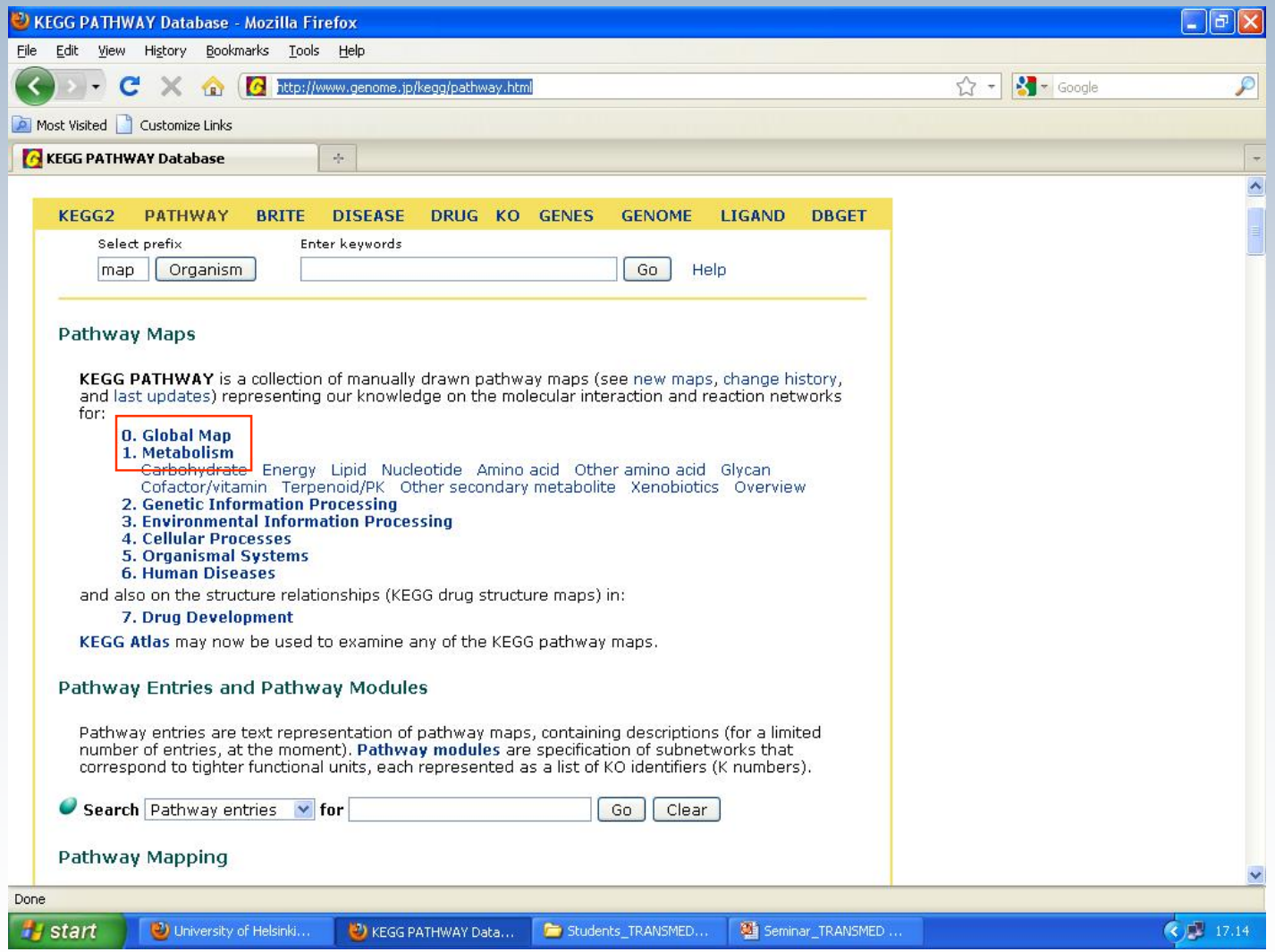
KEGG Organisms Select Organism Go (example) hsa

Analysis tools

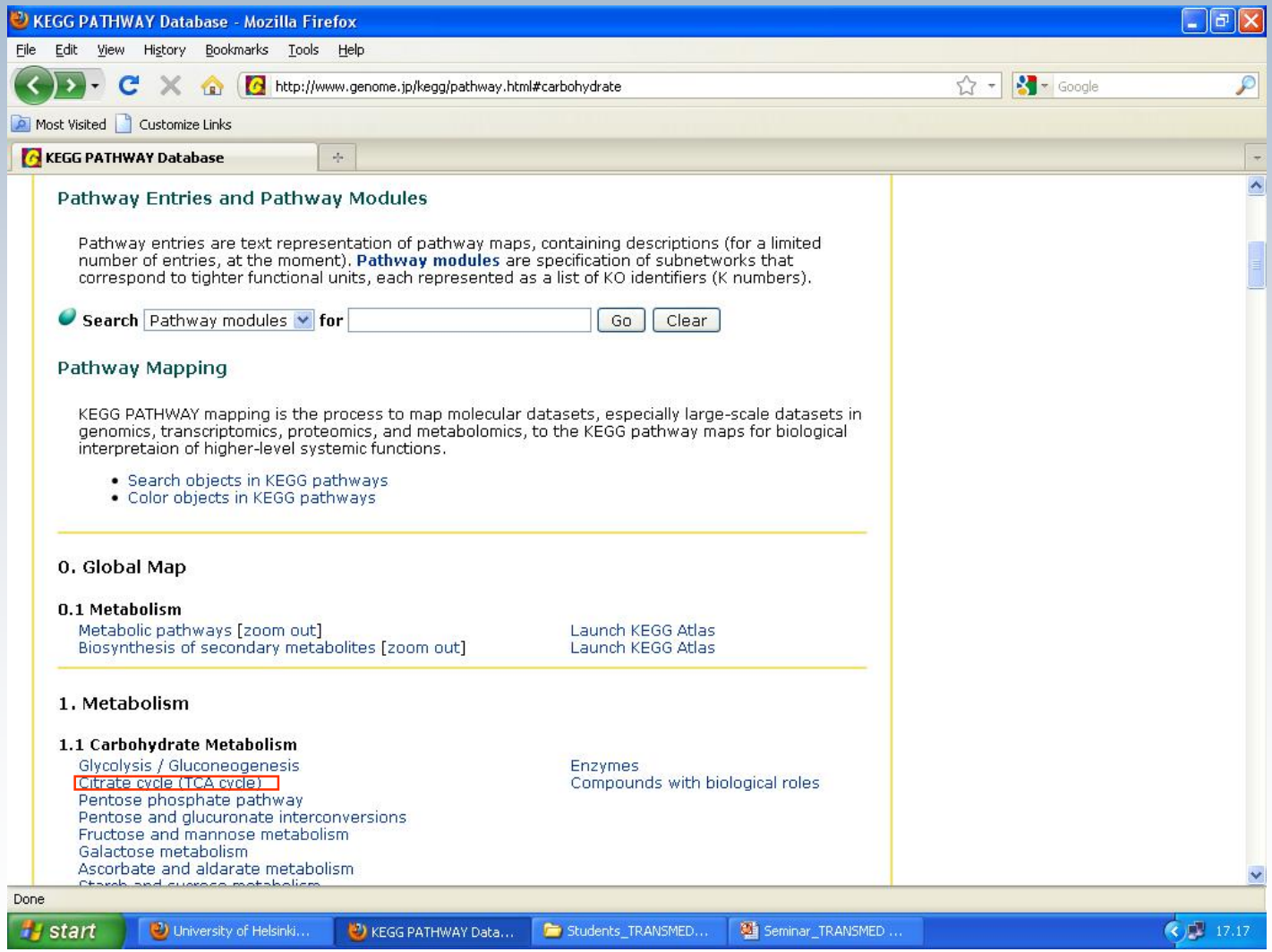
KEGG Mapper *New!* KEGG PATHWAY and BRITE mapping tools

1 of 2

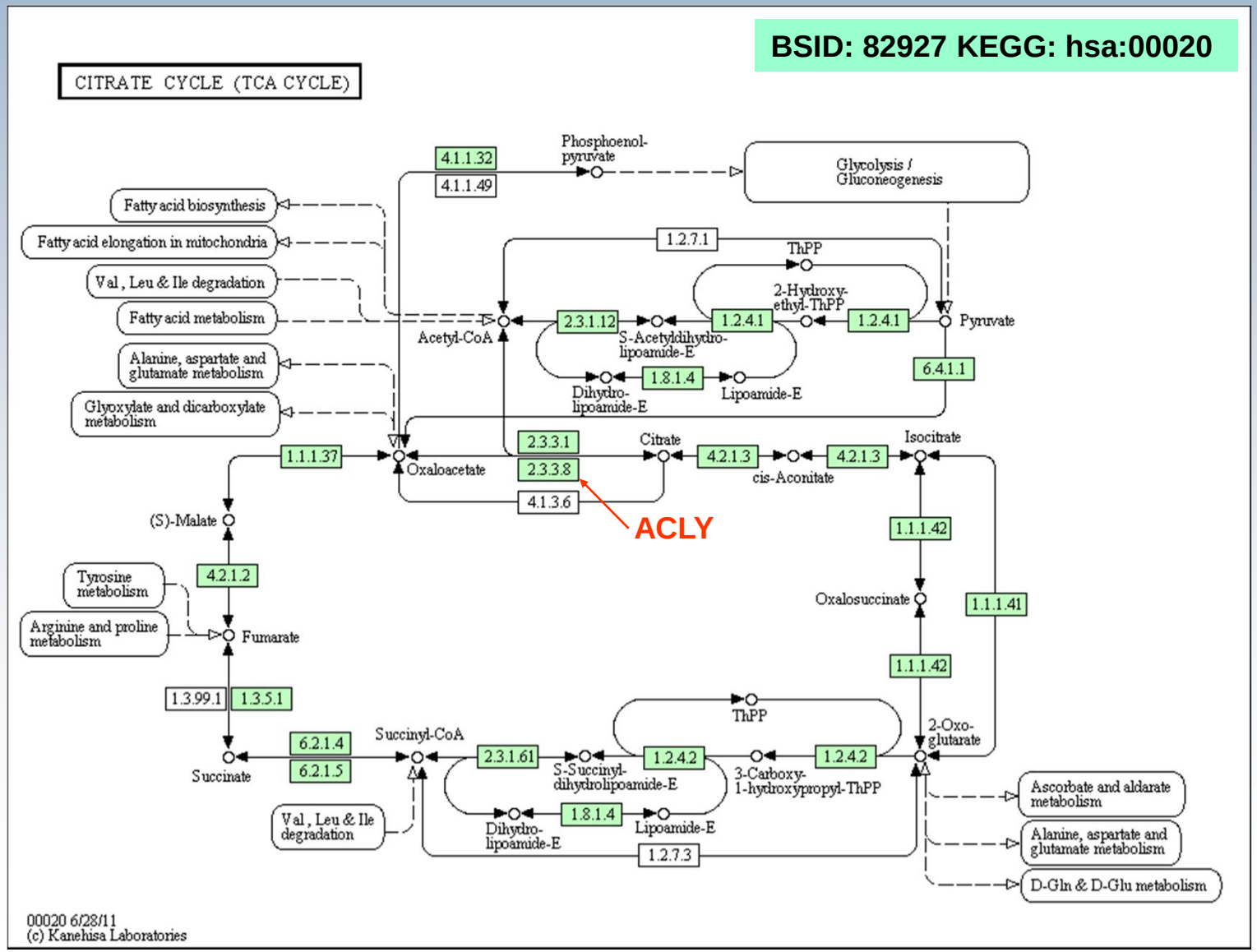
KEGG http://www.genome.jp/kegg/



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

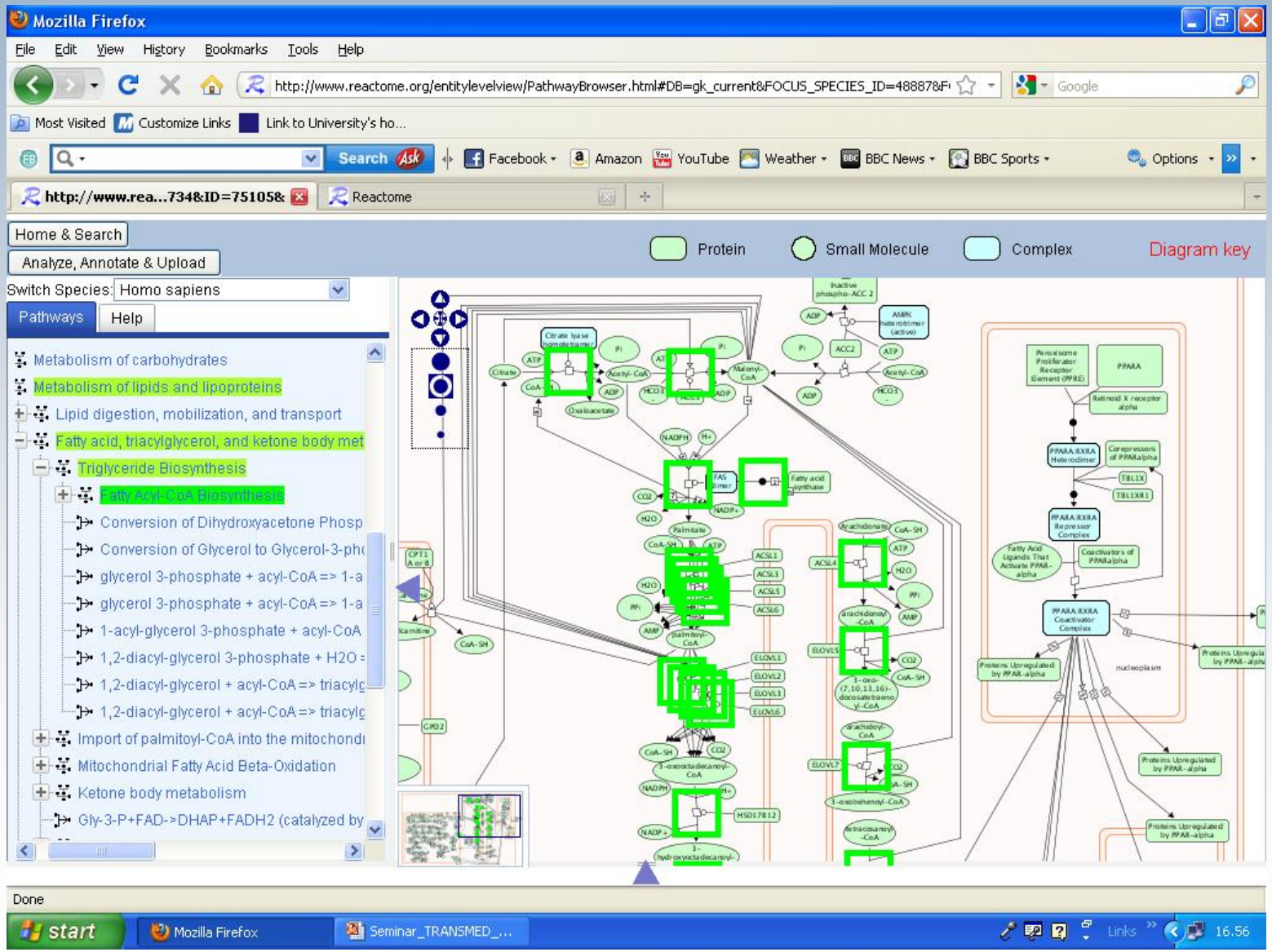


KEGG http://www.genome.jp/kegg/

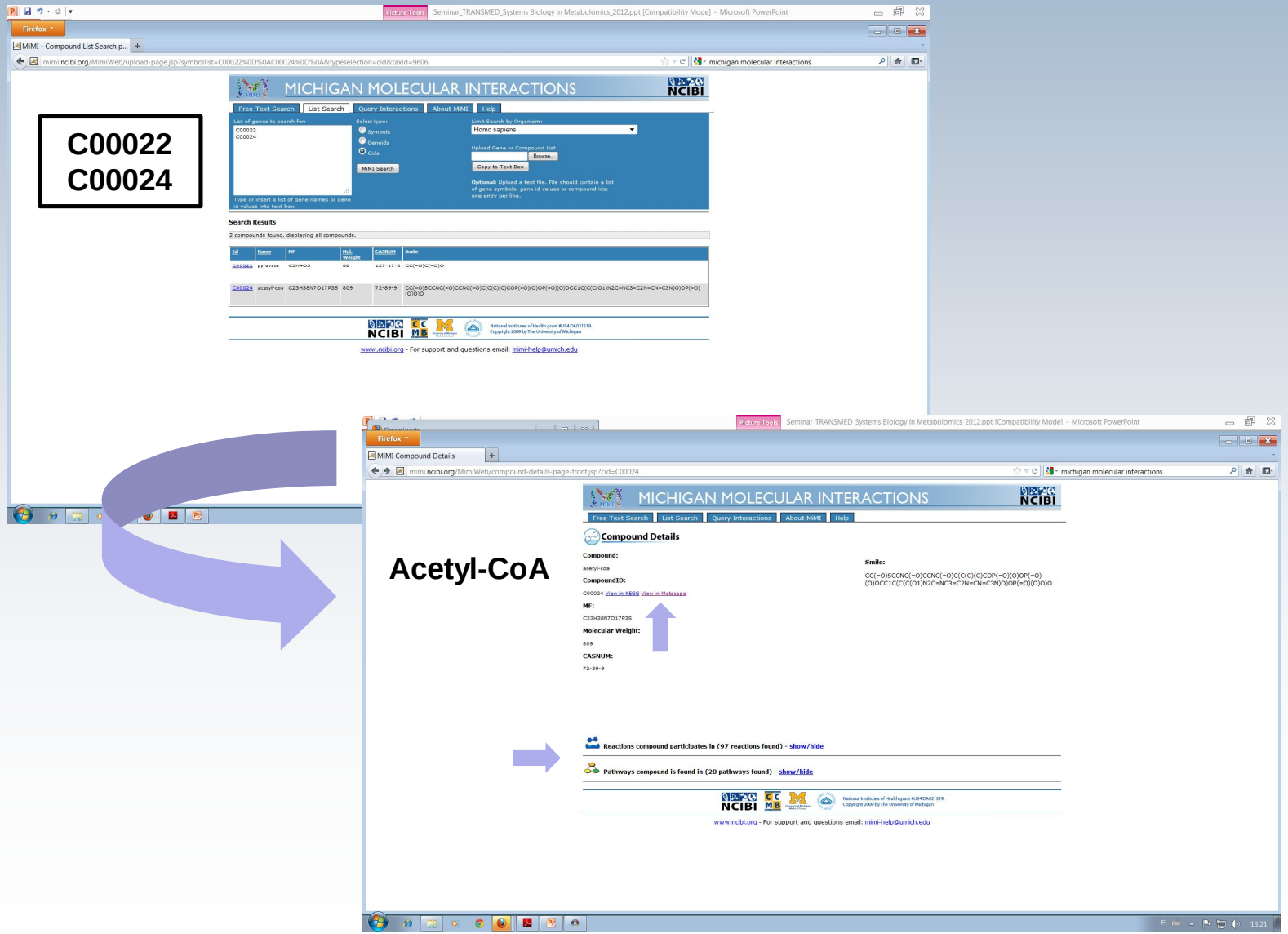


http://www.reactome.org/ReactomeGWT/entrypoint.html

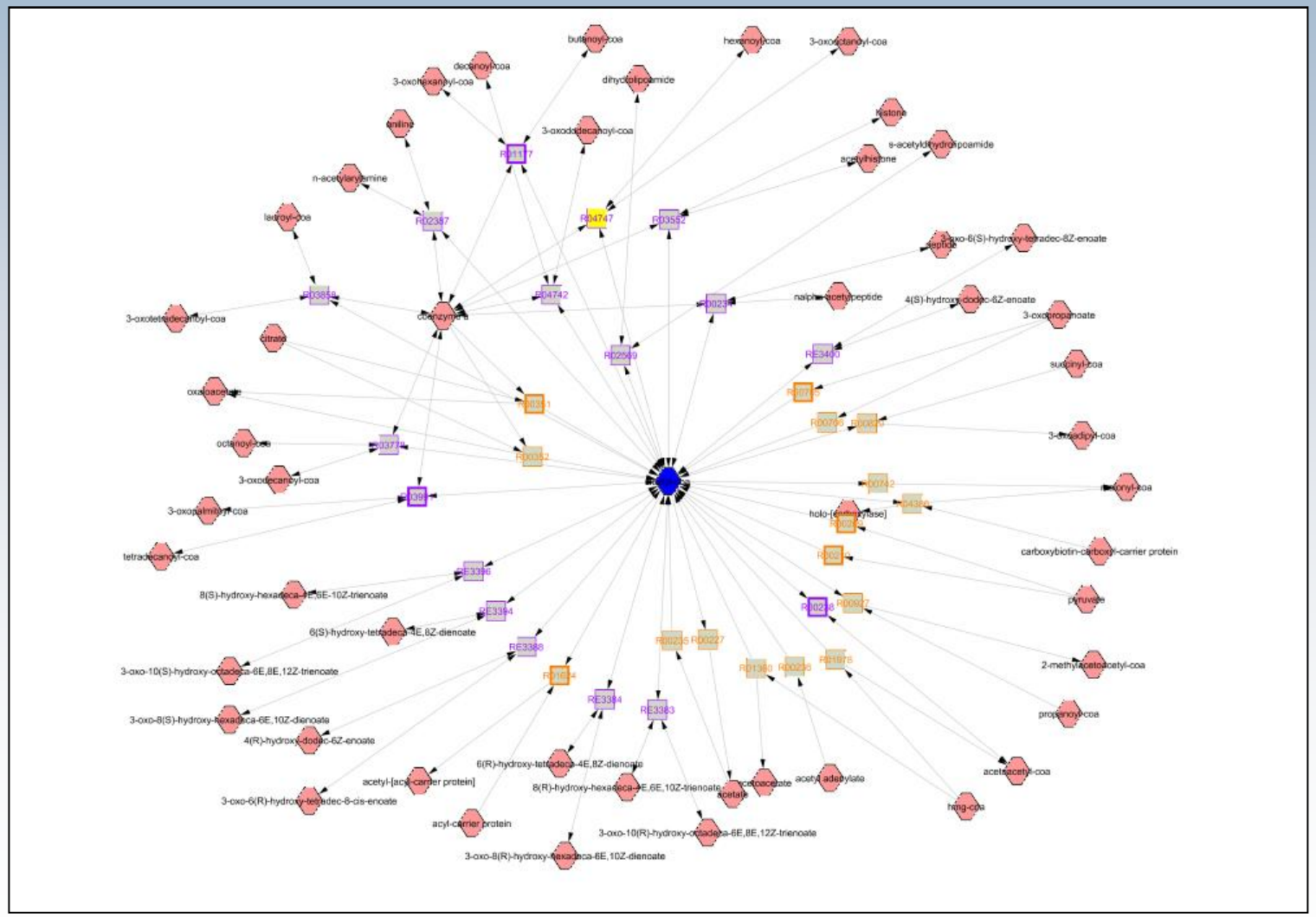
Reactome: pathways

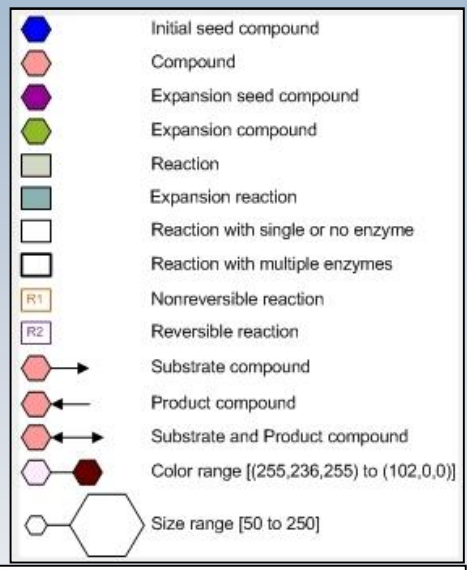


http://mimi.ncibi.org/MimiWeb/main-page.jsp



Acetyl-CoA (C00024) network (view in MetScape)





C00024

Compound

Primary Name:
acetyl-coa

Synonym:
acetyl coenzyme a

Formula:
C23H38N7O17P3S

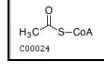
Mass:
809.0

CAS:
72-89-9

Smile:
CC(=O)SCCNC(=O)CCNC(=O)C(C(C)(C)COP(=O)(O)OP(=O)(O)OCC1C(C(C(O1)N2C=NC3=C2N=CN=C3N)O)OP(=O)(O)O)O

Links:
MiMI [C00024]
KEGG [C00024]
PubChem [6302]
BioCyc [ACETYL-COA]
ChEBI [13551]
HMP [HMDB01206]

KEGG 2D structure:



C00024

Lists of compound reactions

Reactions compound participates in (97 reactions found) - show/hide

97 reactions found, displaying page 1 of 5.
[First/Prev] 1, 2, 3, 4, 5 [Next/Last]

Id	Description	Reversible?	Equation
R00209	Pyruvate metabolism	false	pyruvate + coenzyme a + nad = acetyl-coa + carbon dioxide + nadh2
R00210	Glycolysis / Gluconeogenesis	false	pyruvate + coenzyme a + nadp = acetyl-coa + carbon dioxide + nadph2
R00227	Pyruvate metabolism	false	acetyl-coa + water = coenzyme a + acetate
R00234		true	acetyl-coa + peptide = coenzyme a + nalpha-acetylpeptide
R00235	Glycolysis / Gluconeogenesis	false	adenosine 5'-triphosphate + acetate + coenzyme a = adenosine 5'-monophosphate + pyrophosphate + acetyl-coa
R00236	Pyruvate metabolism	false	acetyl adenylate + coenzyme a = adenosine 5'-monophosphate + acetyl-coa
R00238	Fatty acid metabolism	true	2 acetyl-coa = coenzyme a + acetoacetyl-coa
R00259	Urea cycle and metabolism of amino groups	false	acetyl-coa + glutamic acid = coenzyme a + n-acetyl-l-glutamate
R00351	Citrate cycle (TCA cycle)	false	citrate + coenzyme a = acetyl-coa + water + oxaloacetate
R00352	Citrate cycle (TCA cycle)	false	adenosine 5'-triphosphate + citrate + coenzyme a = adenosine 5'-diphosphate + orthophosphate + acetyl-
R00371	Glycine, serine and threonine metabolism	false	acetyl-coa + glycine = coenzyme a + l-2-amino-3-oxobutanoate
R00705	Inositol metabolism	false	3-oxopropanoate + coenzyme a + nad = acetyl-coa + carbon dioxide + nadh2 + h+
R00706	Inositol metabolism	false	3-oxopropanoate + coenzyme a + nadp = acetyl-coa + carbon dioxide + nadph2 + h+
R00742	Tetracycline biosynthesis	false	adenosine 5'-triphosphate + acetyl-coa + hco3-icarbonate = adenosine 5'-diphosphate + orthophosphate
R00829	Benzoate degradation via hydroxylation	false	succinyl-coa + acetyl-coa = coenzyme a + 3-oxoadipyl-coa
R00927	Valine, leucine and isoleucine degradation	false	propanoyl-coa + acetyl-coa = coenzyme a + 2-methylacetoacetyl-coa

MICHIGAN MOLECULAR INTERACTIONS — NCIBI

Free Text Search | List Search | Query Interactions | ... | MiMI | Help

Reaction Details

Reaction Description:
Fatty acid metabolism

ReactionID:
R00238 View Reaction in KEGG

Reversible:
true

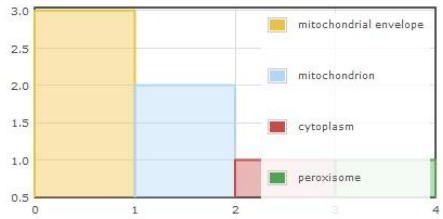
Reaction Text:
2 C00024=C00010+C00332

Equation:
2 Acetyl-CoA=CoA+Acetoacetyl-CoA

Enzymes for Reaction:
2.3.1.16 2.3.1.9

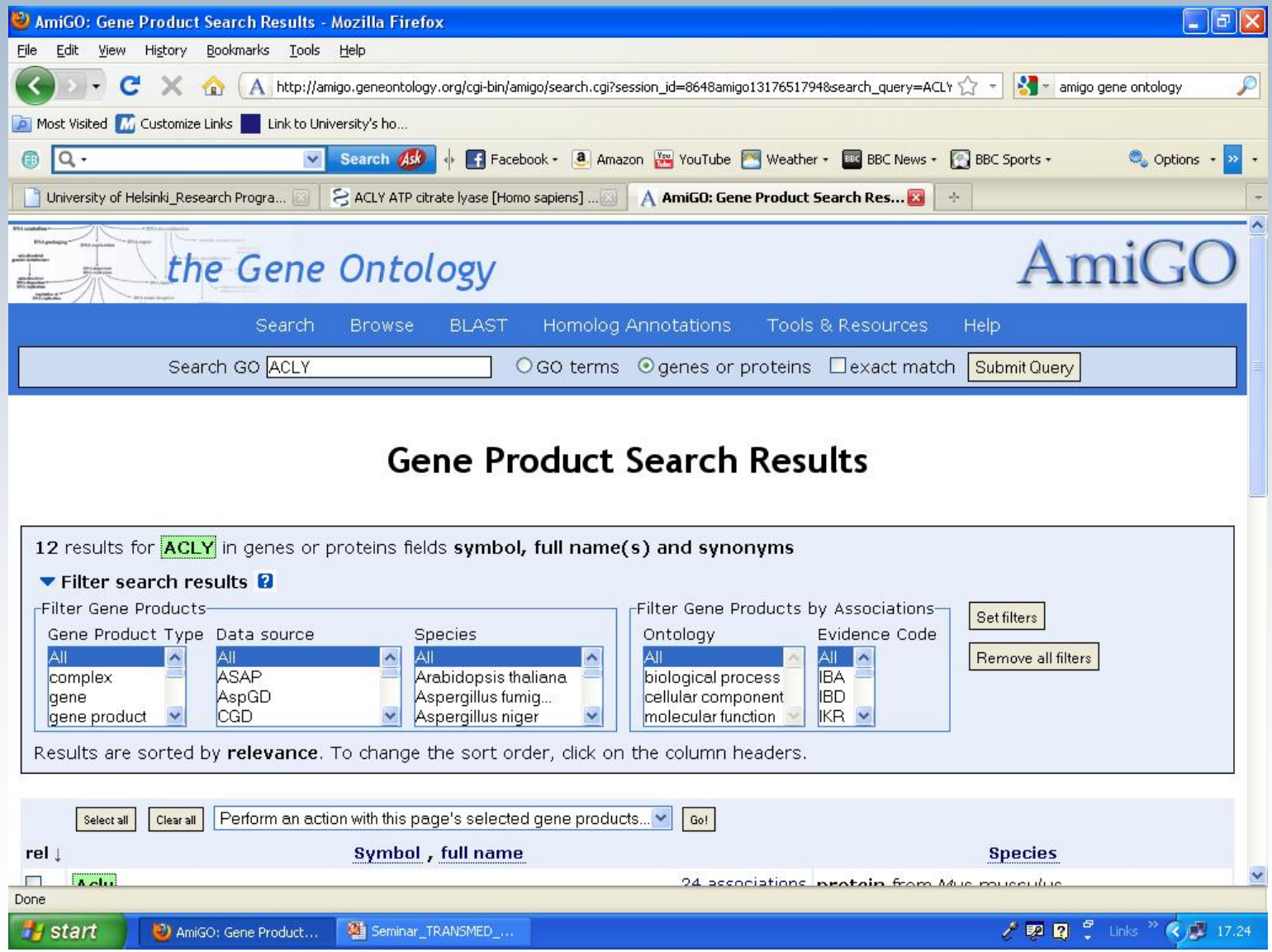
Genes for Reaction:
ACAA1 HADHB ACAA2 ACAT1 ACAT2

Subcellular Locations:



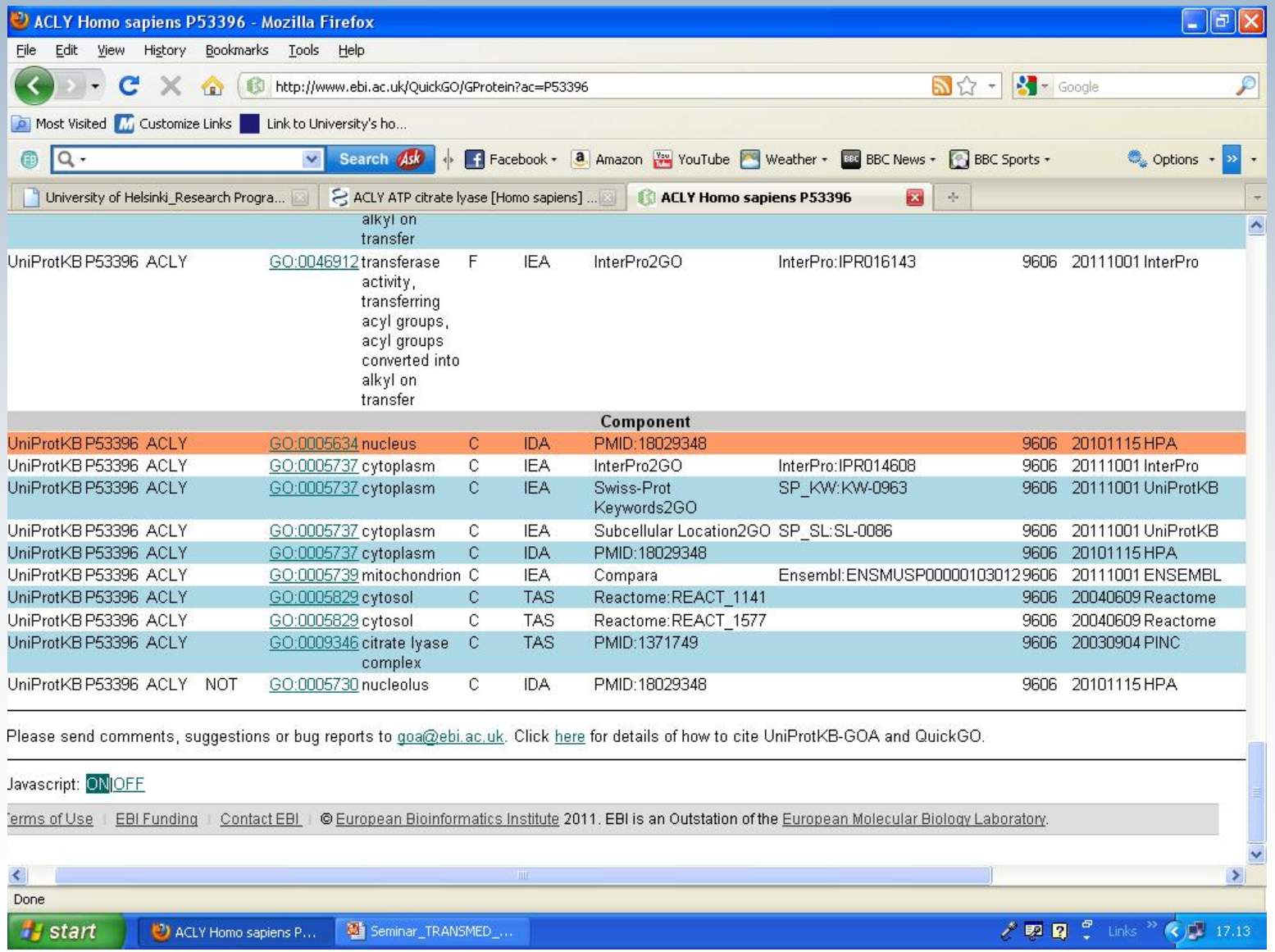
Compounds in reaction (3 compounds found) - show/hide

AmiGO: http://geneontology.org



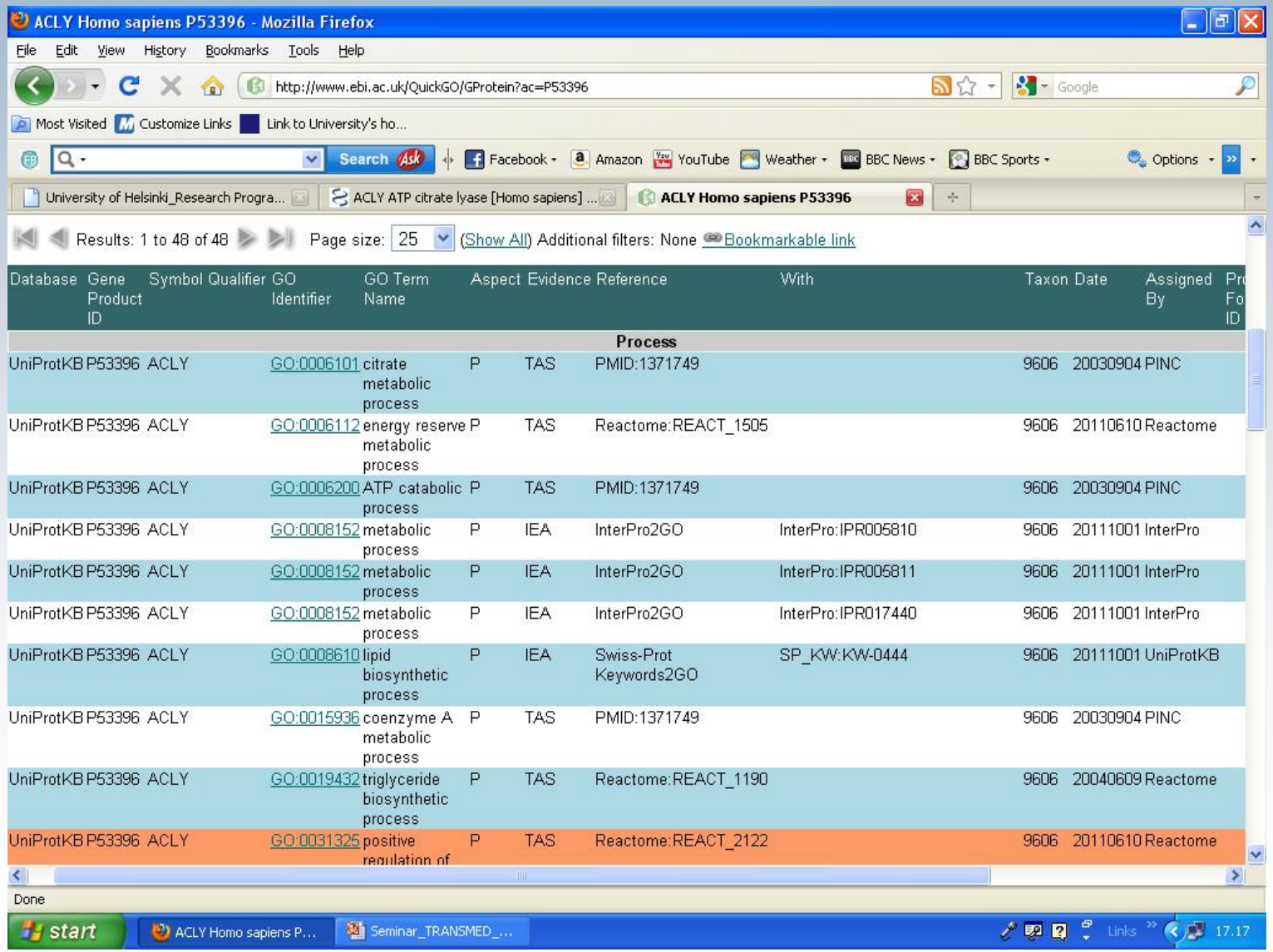
Gene Ontology annotation: http://www.ebi.ac.uk/GOA/

Gene Ontology: component



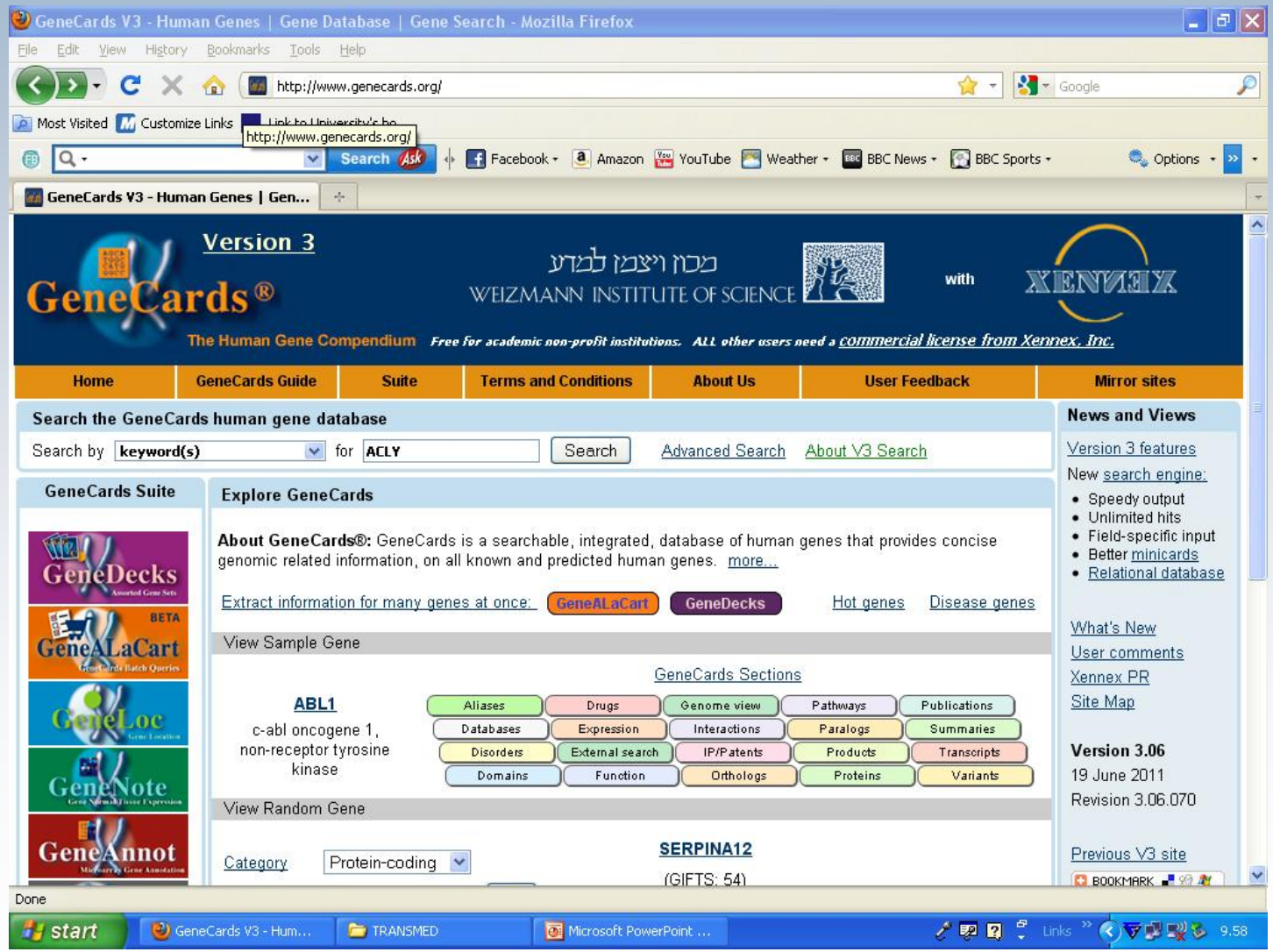
Gene Ontology annotation: http://www.ebi.ac.uk/GOA/

Gene Ontology: process



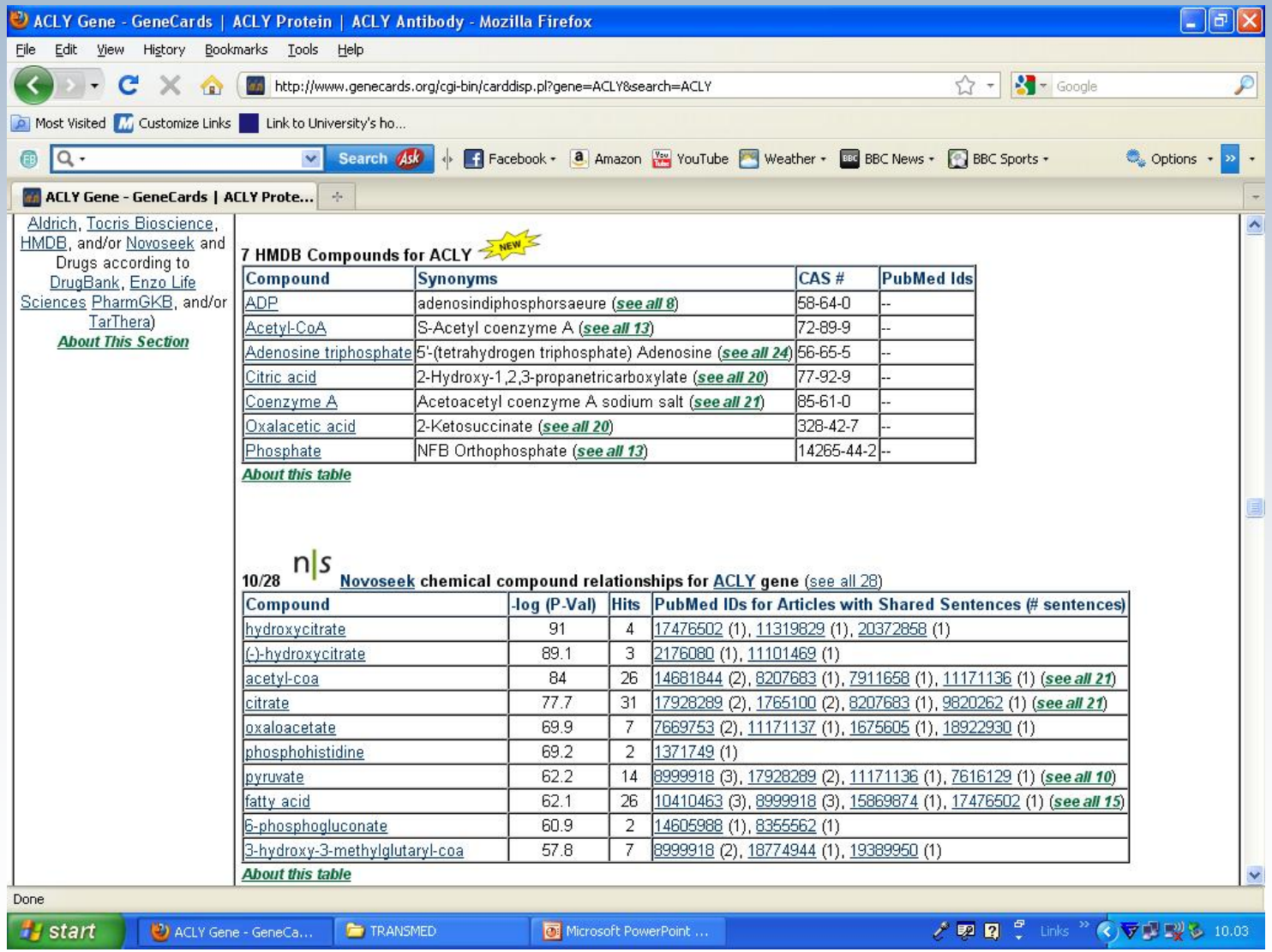
Database	Gene Product ID	Symbol	Qualifier	GO Identifier	GO Term Name	Aspect	Evidence	Reference	With	Taxon	Date	Assigned By	Pr Fo ID
					Process								
UniProtKB	P53396	ACLY		GO:0006101	citrate metabolic process	P	TAS	PMID:1371749		9606	20030904	PINC	
UniProtKB	P53396	ACLY		GO:0006112	energy reserve metabolic process	P	TAS	Reactome:REACT_1505		9606	20110610	Reactome	
UniProtKB	P53396	ACLY		GO:0006200	ATP catabolic process	P	TAS	PMID:1371749		9606	20030904	PINC	
UniProtKB	P53396	ACLY		GO:0008152	metabolic process	P	IEA	InterPro2GO	InterPro:IPR005810	9606	20111001	InterPro	
UniProtKB	P53396	ACLY		GO:0008152	metabolic process	P	IEA	InterPro2GO	InterPro:IPR005811	9606	20111001	InterPro	
UniProtKB	P53396	ACLY		GO:0008152	metabolic process	P	IEA	InterPro2GO	InterPro:IPR017440	9606	20111001	InterPro	
UniProtKB	P53396	ACLY		GO:0008610	lipid biosynthetic process	P	IEA	Swiss-Prot Keywords2GO	SP_KW:KW-0444	9606	20111001	UniProtKB	
UniProtKB	P53396	ACLY		GO:0015936	coenzyme A metabolic process	P	TAS	PMID:1371749		9606	20030904	PINC	
UniProtKB	P53396	ACLY		GO:0019432	triglyceride biosynthetic process	P	TAS	Reactome:REACT_1190		9606	20040609	Reactome	
UniProtKB	P53396	ACLY		GO:0031325	positive regulation of	P	TAS	Reactome:REACT_2122		9606	20110610	Reactome	

Gene Cards: http://www.genecards.org/



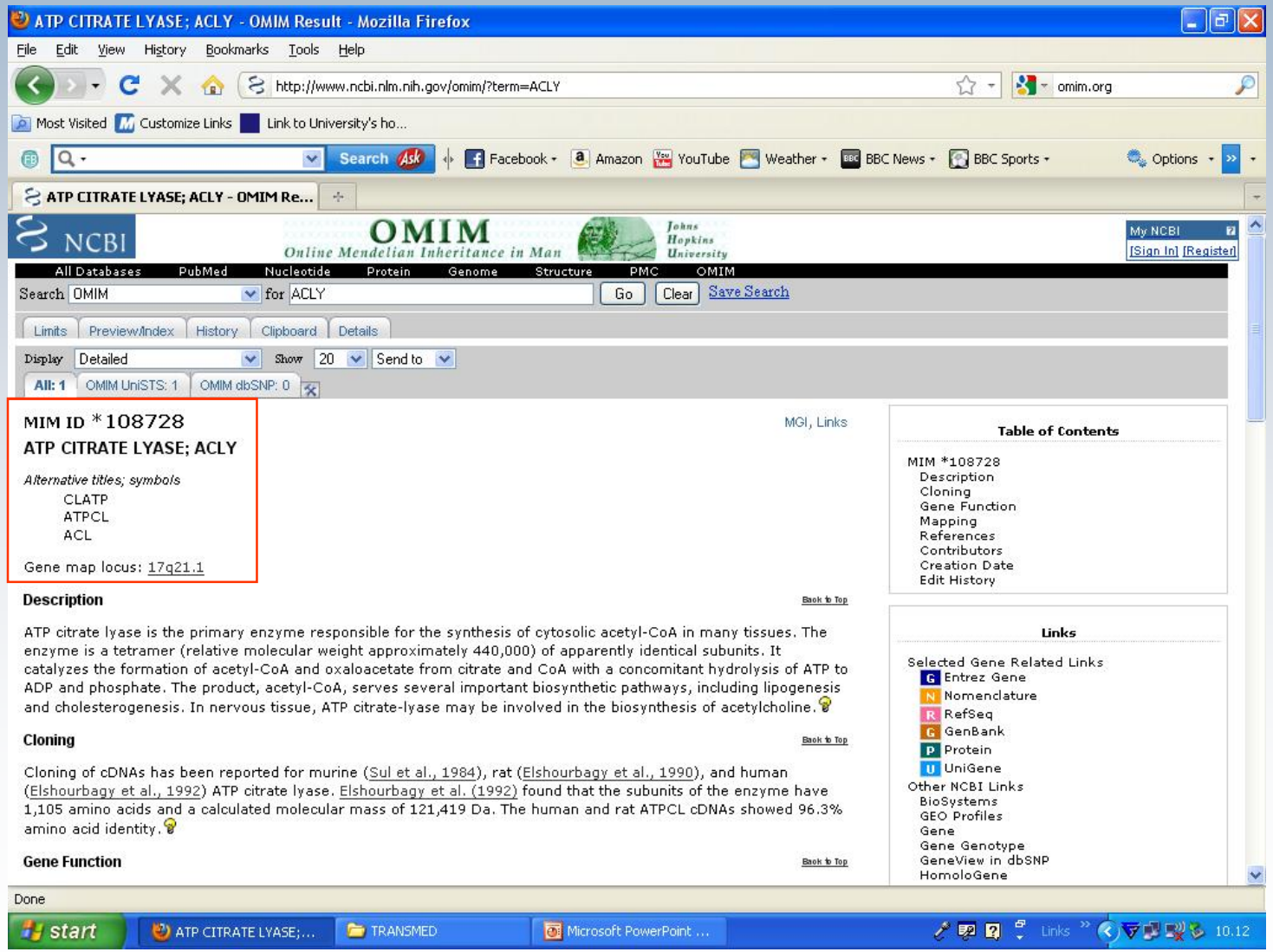
Gene Cards: aliases and descriptions

Gene Cards: compounds for ACLY



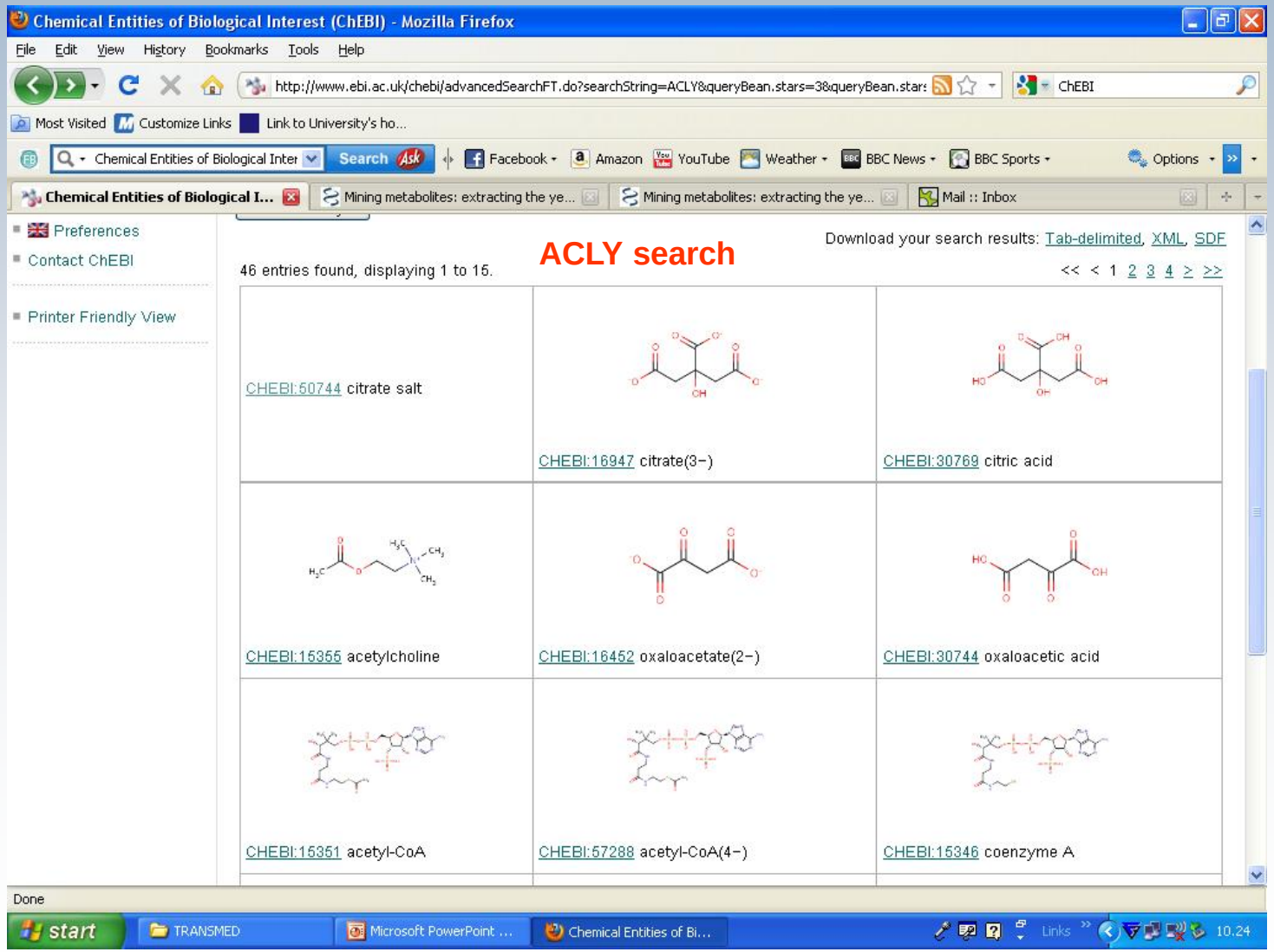
Gene Cards: expression in tissues and disease

OMIM: www.ncbi.nlm.nih.gov/omim



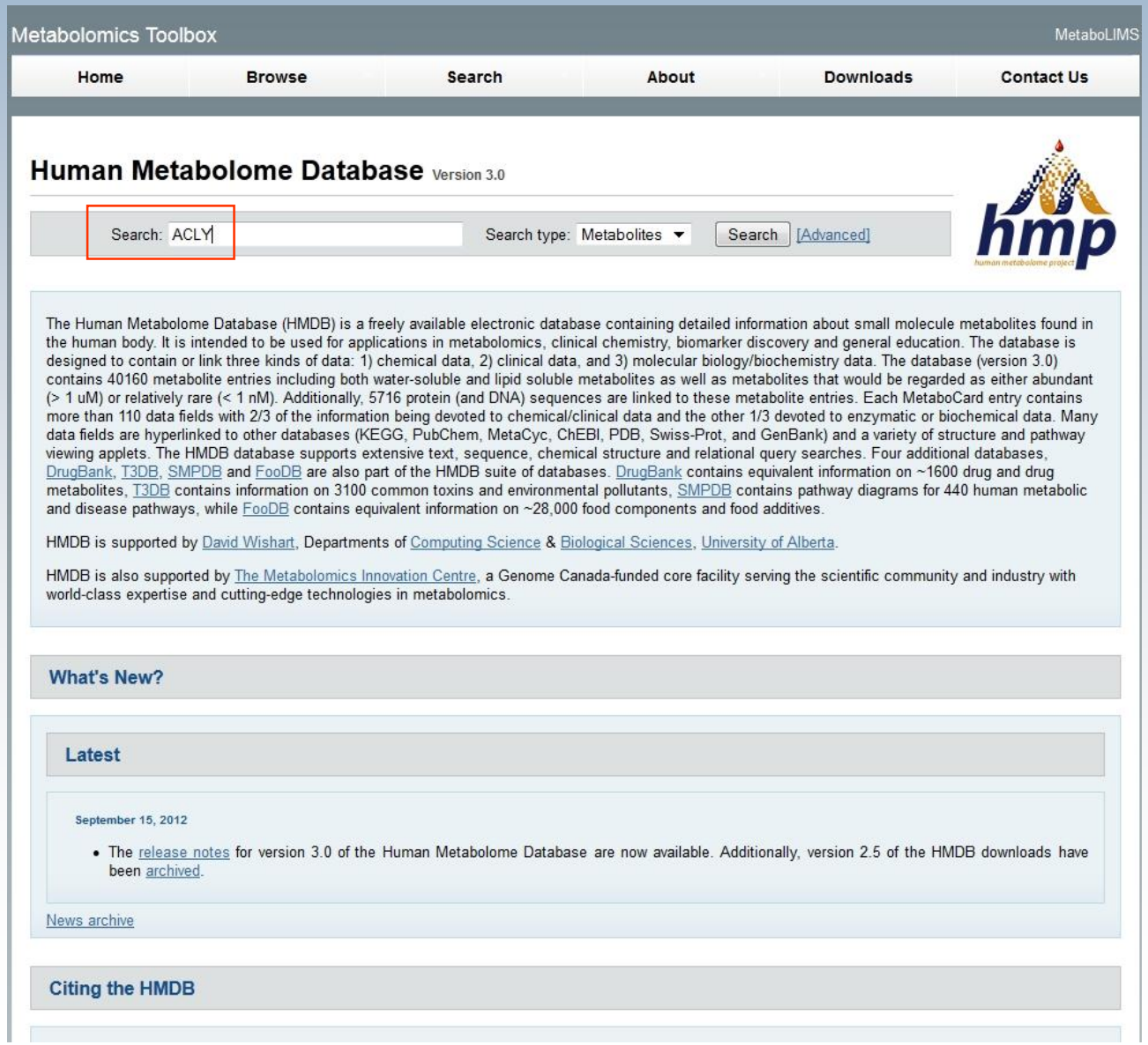
ChEBI: Chemical Entities of Biological Interest

www.ebi.ac.uk/chebi/



HMDB: Human Metabolome Database

www.hmdb.ca/



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Human Metabolome Database Version 3.0

Search: ACLY Search type: Metabolites Search [Advanced]

The Human Metabolome Database (HMDB) is a freely available electronic database containing detailed information about small molecule metabolites found in the human body. It is intended to be used for applications in metabolomics, clinical chemistry, biomarker discovery and general education. The database is designed to contain or link three kinds of data: 1) chemical data, 2) clinical data, and 3) molecular biology/biochemistry data. The database (version 3.0) contains 40160 metabolite entries including both water-soluble and lipid soluble metabolites as well as metabolites that would be regarded as either abundant (> 1 uM) or relatively rare (< 1 nM). Additionally, 5716 protein (and DNA) sequences are linked to these metabolite entries. Each MetaboCard entry contains more than 110 data fields with 2/3 of the information being devoted to chemical/clinical data and the other 1/3 devoted to enzymatic or biochemical data. Many data fields are hyperlinked to other databases (KEGG, PubChem, MetaCyc, ChEBI, PDB, Swiss-Prot, and GenBank) and a variety of structure and pathway viewing applets. The HMDB database supports extensive text, sequence, chemical structure and relational query searches. Four additional databases, DrugBank, T3DB, SMPDB and FooDB are also part of the HMDB suite of databases. DrugBank contains equivalent information on ~1600 drug and drug metabolites, T3DB contains information on 3100 common toxins and environmental pollutants, SMPDB contains pathway diagrams for 440 human metabolic and disease pathways, while FooDB contains equivalent information on ~28,000 food components and food additives.

HMDB is supported by David Wishart, Departments of Computing Science & Biological Sciences, University of Alberta.

HMDB is also supported by The Metabolomics Innovation Centre, a Genome Canada-funded core facility serving the scientific community and industry with world-class expertise and cutting-edge technologies in metabolomics.

What's New?

Latest

September 15, 2012

- The release notes for version 3.0 of the Human Metabolome Database are now available. Additionally, version 2.5 of the HMDB downloads have been archived.

News archive

Citing the HMDB

HMDB: Human Metabolome Database

Metabolomics Toolbox MetaboLIMS

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Human Metabolome Database Version 3.0

Search: ACLY Search type: Proteins Search [Advanced]

Search Results

Proteins search for "ACLY" returned 2 results

Filter metabolites by status: Detected and quantified | Detected and not quantified | Expected and not quantified | Apply | Clear Filter

Uniprot ID	Gene Name / Locus	Name	Type	Metabolites
P53396 EnzymeCard	ACLY / 17q21.2	ATP-citrate synthase	Enzyme	Acetyl-CoA, Oxalacetic acid, Citric acid, Coenzyme A, Adenosine triphosphate, ADP, Phosphate
P53396 EnzymeCard	ACLY / 17q21.2	ATP-citrate synthase	Enzyme	

This project is supported by Genome Alberta & Genome Canada, a not-for-profit organization that is leading Canada's national genomics strategy with $600 million in funding from the federal government.

GenomeCanada GenomeAlberta

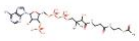
HMDB: Human Metabolome Database

Showing metabocard for Acetyl-CoA (HMDB01206)

Legend: metabolite field | enzyme field

Show XML | Show Similar Structure

Record Information	
Version	3.0
Creation Date	2005-11-16 08:48:42 -0700
Update Date	2009-05-05 14:58:35 -0600
Accession Number	HMDB01206
Secondary Accession Numbers	None

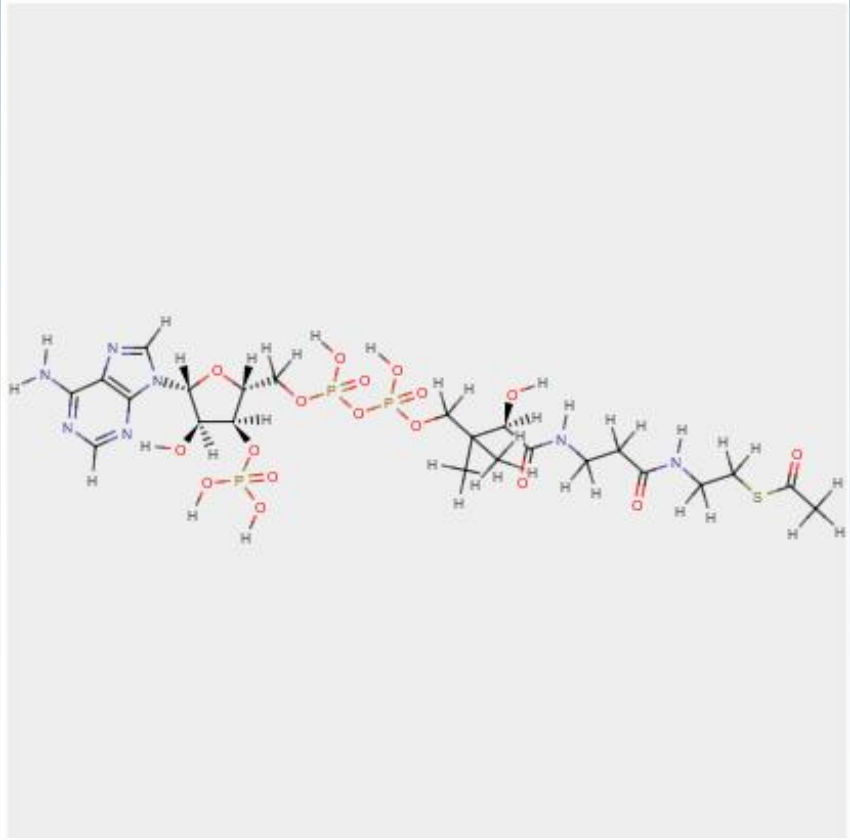
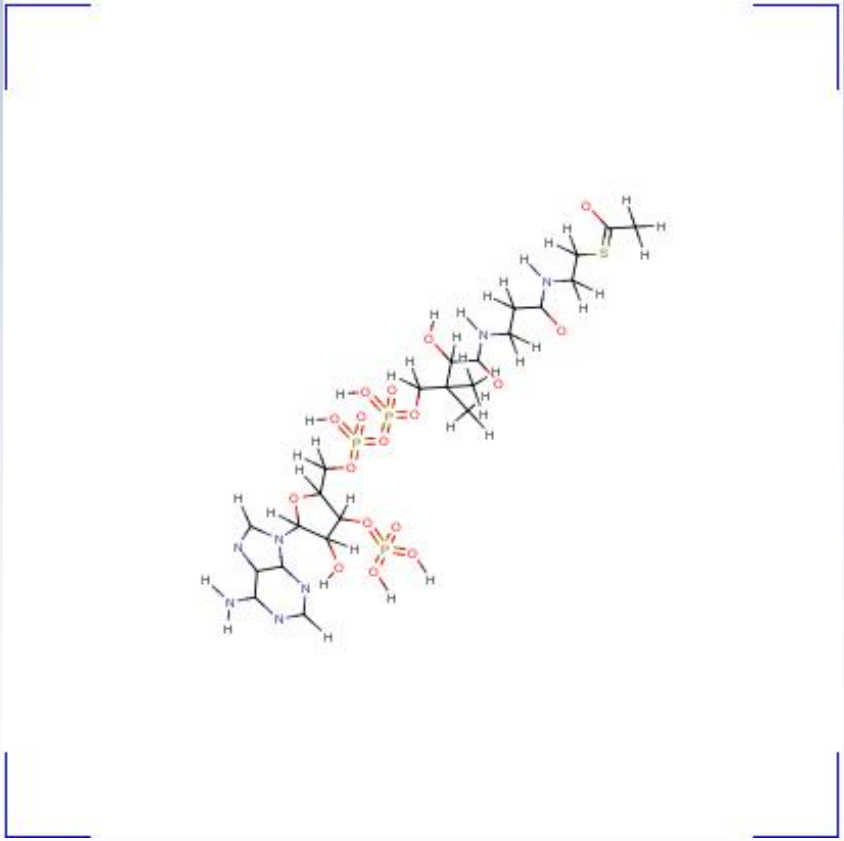
Metabolite Identification	
Common Name	**Acetyl-CoA**
Description	The main function of coenzyme A is to carry acyl groups (such as the acetyl group) or thioesters. Acetyl-CoA is an important molecule itself. It is the precursor to HMG CoA, which is a vital component in cholesterol and ketone synthesis. (wikipedia) acetyl CoA participates in the biosynthesis of fatty acids and sterols, in the oxidation of fatty acids and in the metabolism of many amino acids. It also acts as a biological acetylating agent.
Structure	 Download: MOL | SDF | SMILES | InChI Display: 2D Structure | 3D Structure
Synonyms	1. S-Acetyl coenzyme A 2. S-acetate CoA 3. S-acetate Coenzyme A 4. ac-CoA 5. ac-Coenzyme A 6. ac-S-CoA 7. ac-S-Coenzyme A 8. acetyl coenzyme-A 9. acetyl-CoA 10. acetyl-Coenzyme A 11. acetyl-S-CoA 12. acetyl-S-Coenzyme A 13. acetylcoenzyme-A
Chemical Formula	$C_{23}H_{38}N_7O_{17}P_3S$

InChI Key	InChIKey=ZSLZBFCDCINBPY-ZSJPKINUSA-N

Chemical Taxonomy	
Kingdom	Organic Compounds
Super Class	Lipids
Class	Fatty Acid Esters
Sub Class	Acyl CoAs
Other Descriptors	Aromatic Heteropolycyclic Compounds acyl-CoA(ChEBI)
Substituents	1 Phosphoribosyl Imidazole Aminopyrimidine Carboxamide Group Carboxylic Thioester Coenzyme A Glycosyl Compound Imidazole Imidazopyrimidine Monosaccharide Phosphate N Glycosyl Compound Organic Hypophosphite Organic Phosphite Organic Pyrophosphate Oxolane Pentose Monosaccharide Phosphoric Acid Ester Purine Purine Ribonucleoside 3',5' Bisphosphate Pyrimidine Saccharide Secondary Alcohol Secondary Carboxylic Acid Amide Thiocarboxylic Acid Ester
Direct Parent	Acyl CoAs

Ontology	
Status	Detected and not quantified
Origin	Endogenous Food
	Cell signaling Component of Alanine and aspartate metabolism

HMDB: Human Metabolome Database

2D-structure of Acetyl CoA	3D-structure of Acetyl CoA
	

HMDB: Human Metabolome Database

	nucleus
	peroxisome
Biofluid Locations	Not Available
Tissue Location	Adipose Tissue
	Brain
	Muscle
	Platelet
	Prostate
	Skeletal Muscle
	Spleen

Pathways

Name	SMPDB Link	KEGG Link
Amino Sugar Metabolism	SMP00045	map00520
Beta Oxidation of Very Long Chain Fatty Acids	SMP00052	map01040
Beta-Alanine Metabolism	SMP00007	map00410
Butyrate Metabolism	SMP00073	map00650
Citric Acid Cycle	SMP00057	map00020
Ethanol Degradation	SMP00449	Not Available
Fatty Acid Biosynthesis	SMP00456	Not Available
Fatty acid Metabolism	SMP00051	map00071
Glycine and Serine Metabolism	SMP00004	map00260
Ketone Body Metabolism	SMP00071	map00072
Lysine Degradation	SMP00037	map00310
Mitochondrial Beta-Oxidation of Long Chain Saturated Fatty Acids	SMP00482	Not Available
Mitochondrial Beta-Oxidation of Medium Chain Saturated Fatty Acids	SMP00481	Not Available
Mitochondrial Beta-Oxidation of Short Chain Saturated Fatty Acids	SMP00480	Not Available
Oxidation of Branched Chain Fatty Acids	SMP00030	Not Available
Phytanic Acid Peroxisomal Oxidation	SMP00450	Not Available
Propanoate Metabolism	SMP00016	map00640
Pyruvate Metabolism	SMP00060	map00620
Steroid Biosynthesis	SMP00023	map00100
Transfer of Acetyl Groups into Mitochondria	SMP00466	Not Available
Valine, Leucine and Isoleucine Degradation	SMP00032	map00280

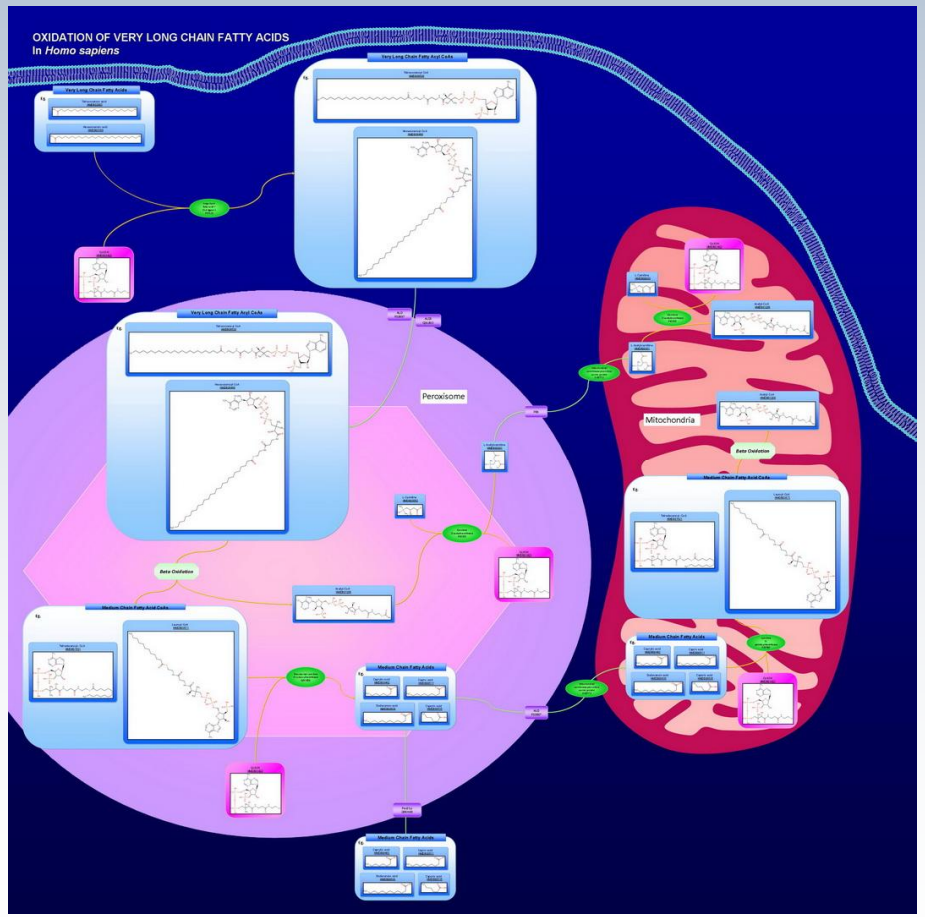
Normal Concentrations
Not Available

Abnormal Concentrations
Not Available

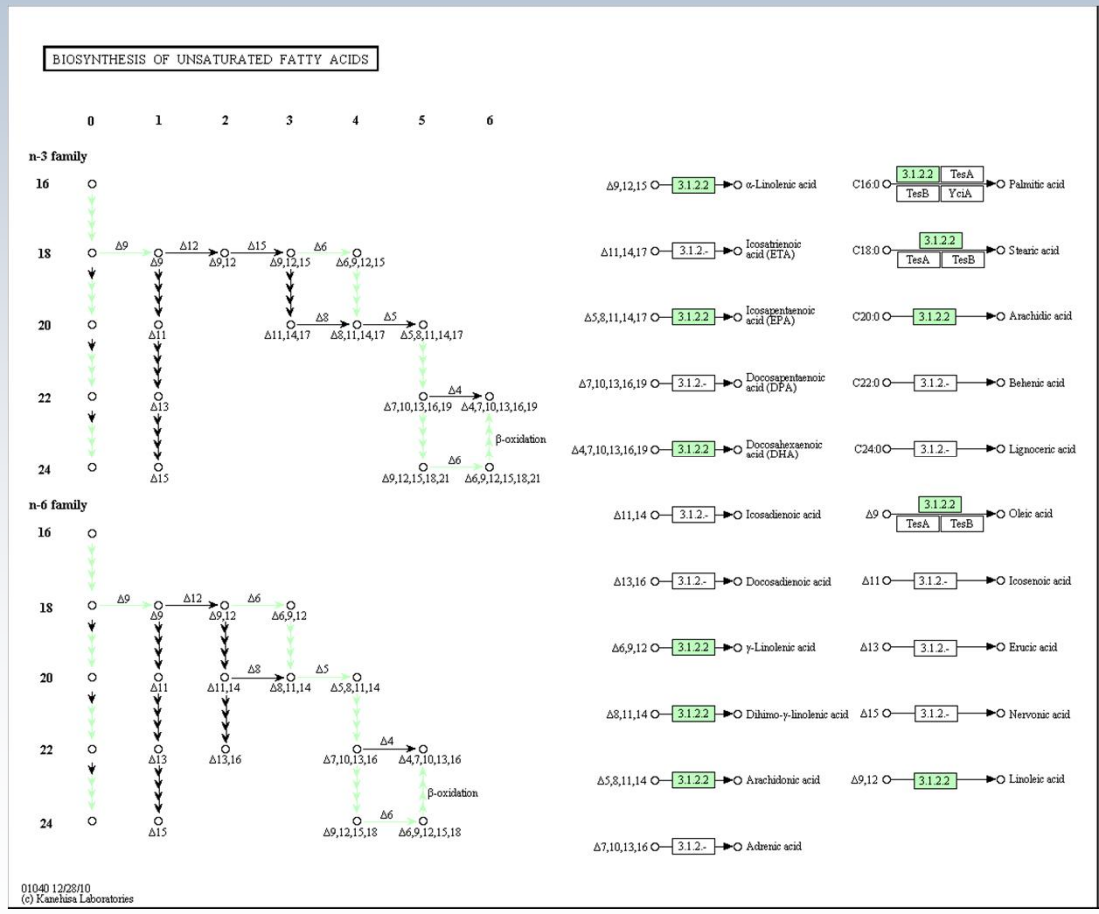
Associated Disorders and Diseases

HMDB: Human Metabolome Database

Beta Oxidation of Very Long Chain Fatty Acids SMP0052; http://pathman.smpdb.ca/



Biosynthesis of unsaturated fatty acids - Homo sapiens (human) KEGG 010140



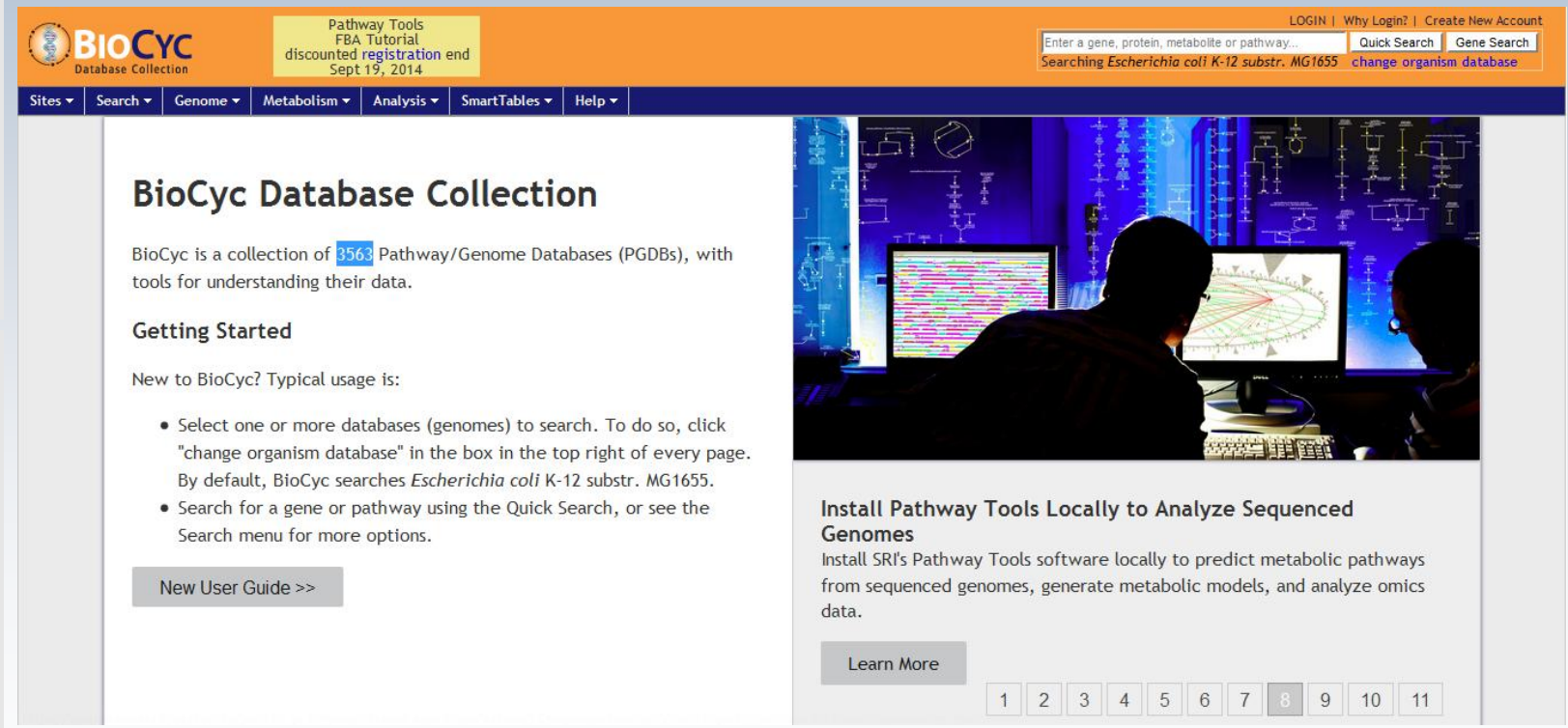
BioCyc Database collection

www.biocyc.org

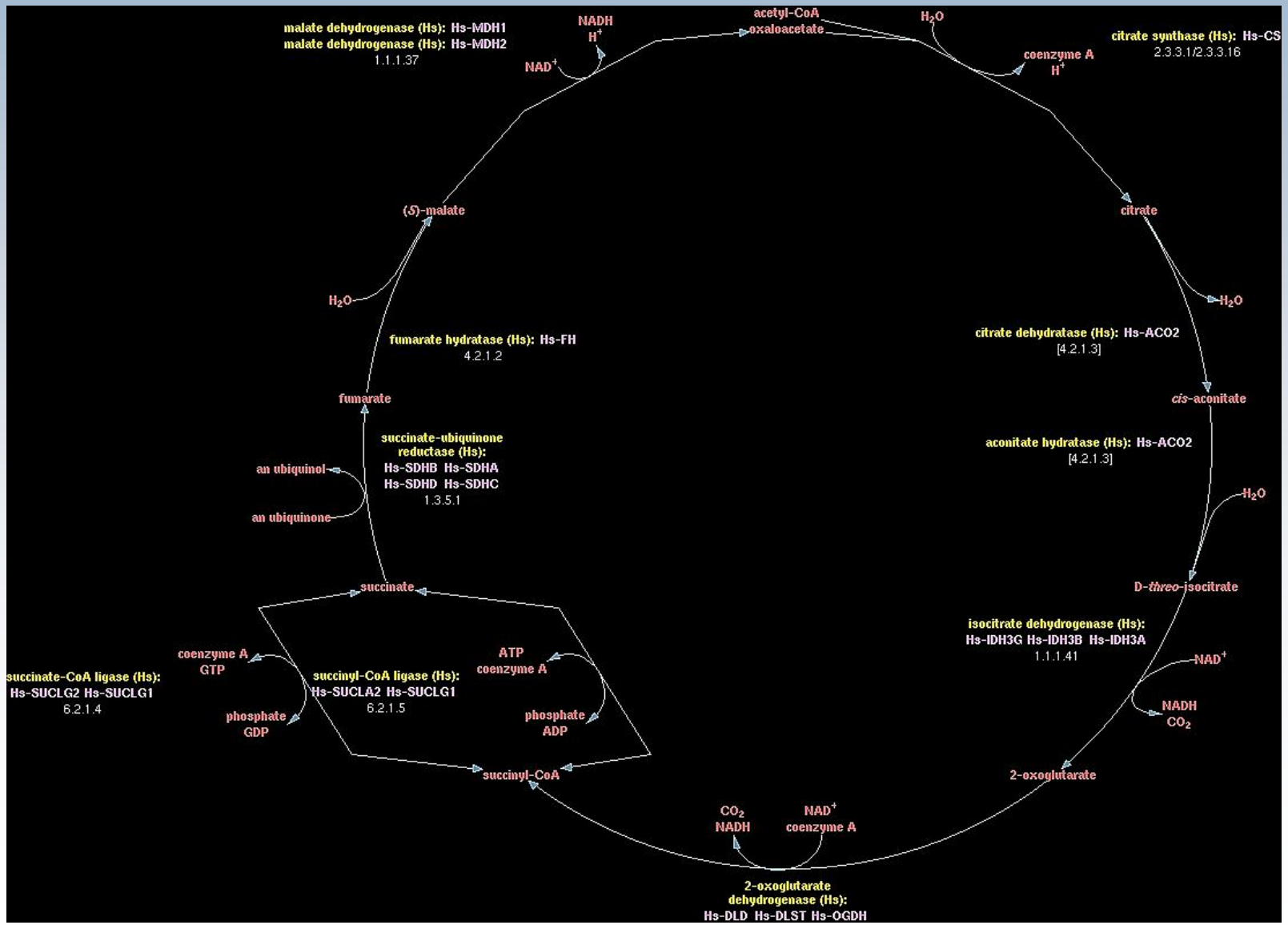
Collection of 3563 Pathway/Genome databases. Each database describes the genome and pathways of a single organism.

Tier 1: literature-based curation
Tier 2 and Tier 3: computational

HumanCyc:
250 pathways
MetaCyc:
2202 pathways from 2063 organisms

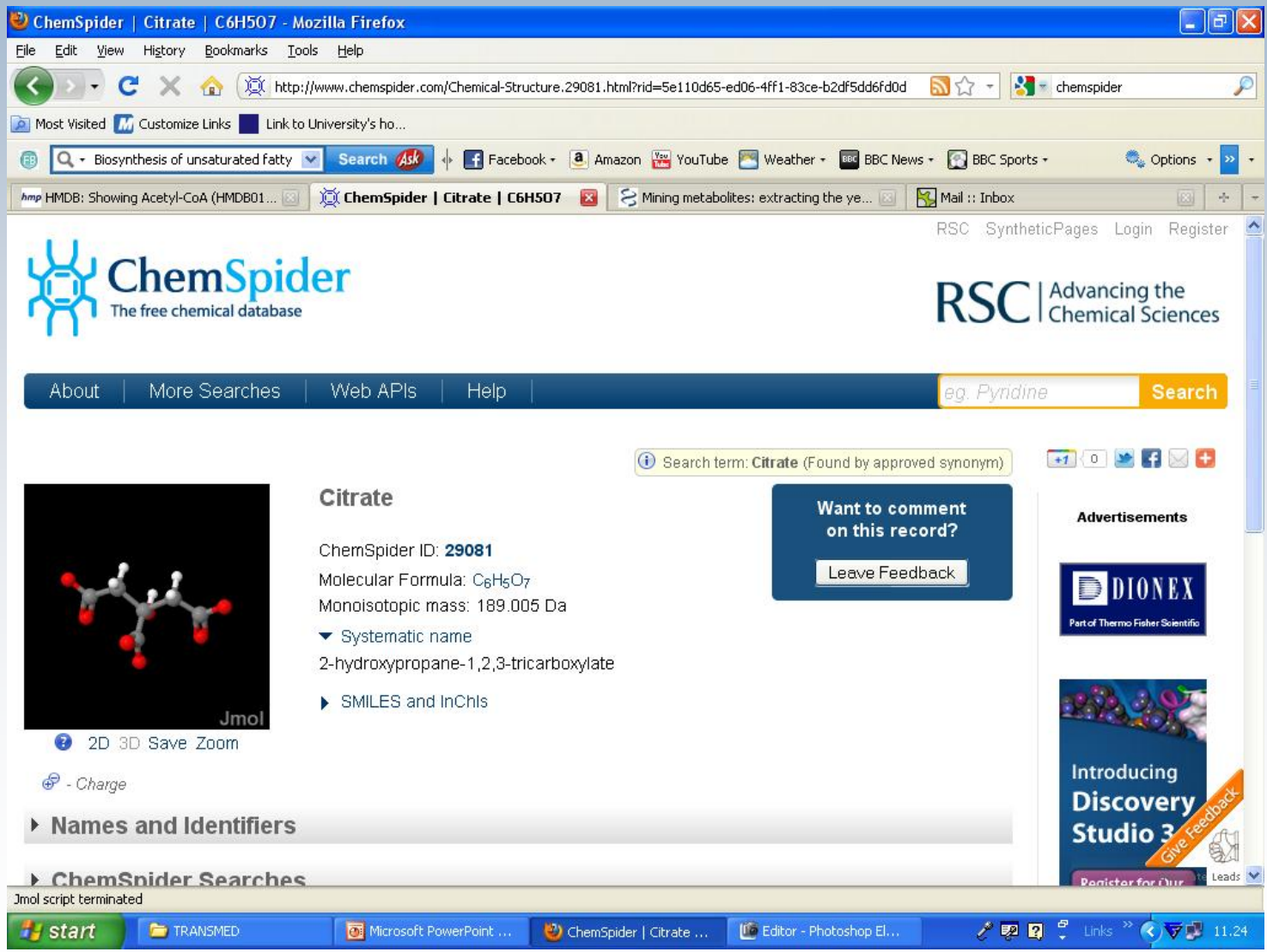


BioCyc Database collection: example TCA (human)



ChemSpider: the free chemical database

http://www.chemspider.com/



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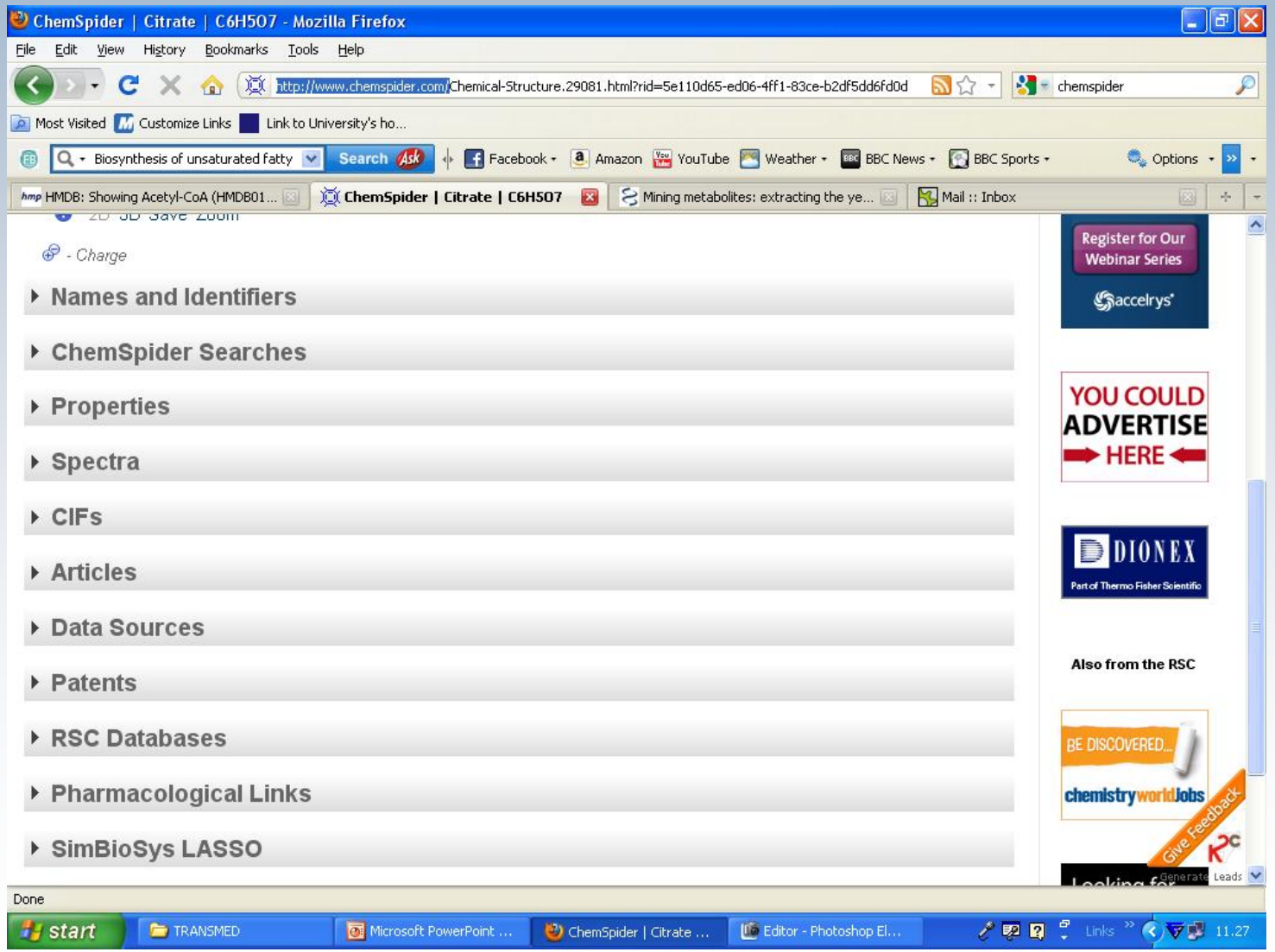
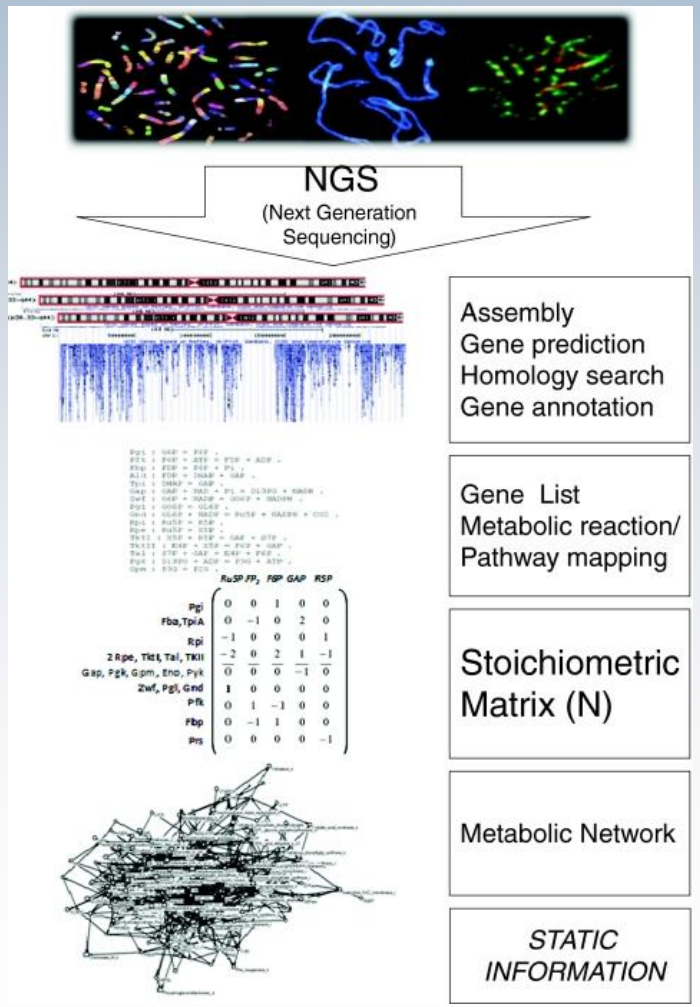
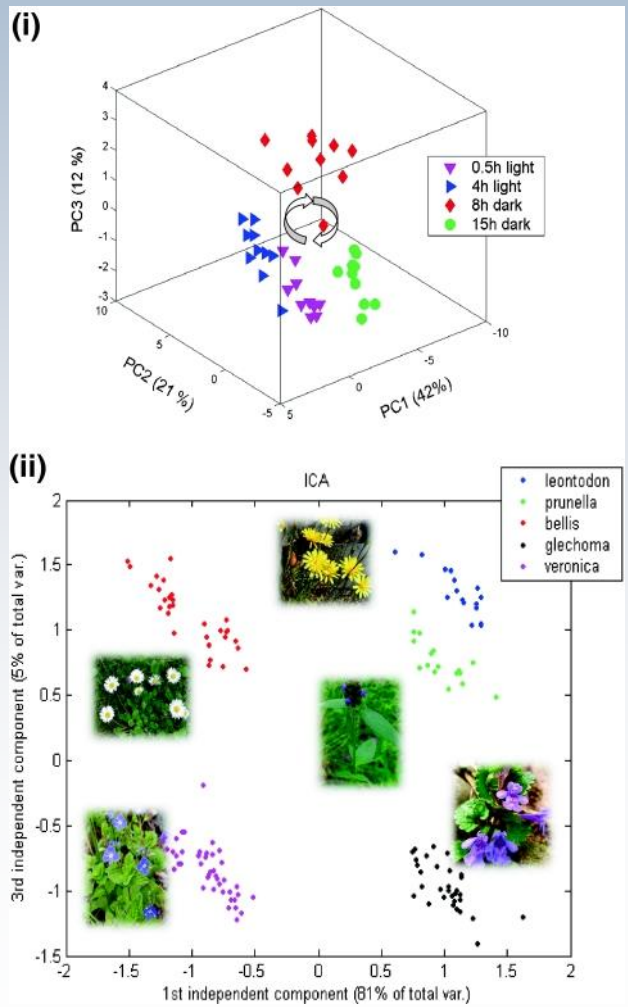


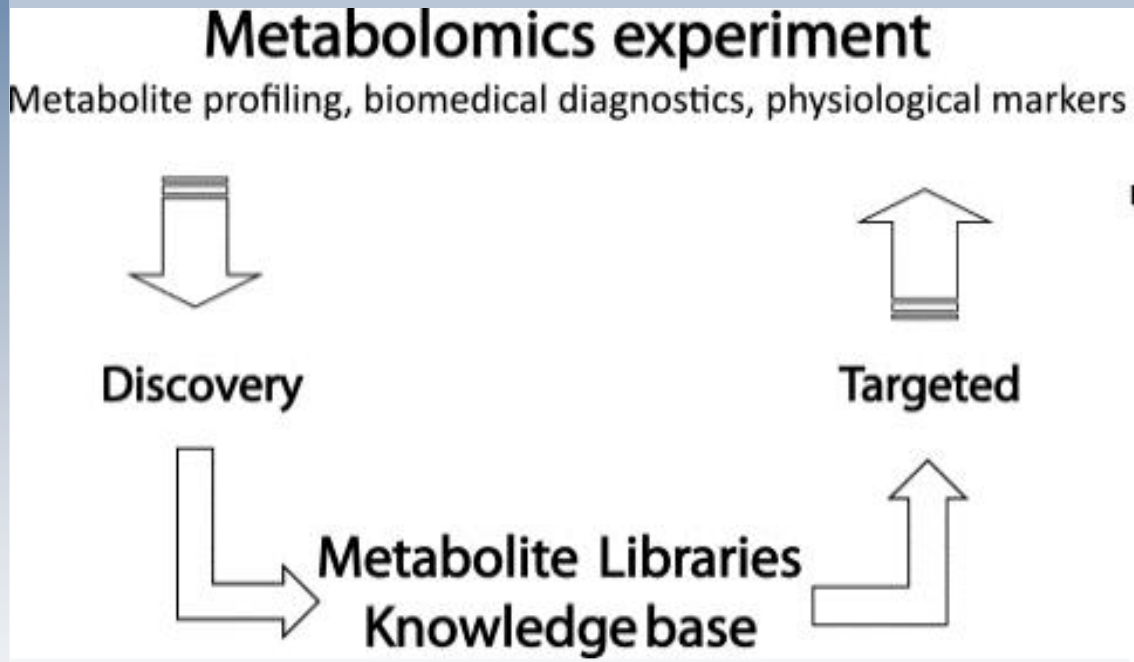
Unpredictability of metabolism--the key role of metabolomics science in combination with next-generation genome sequencing

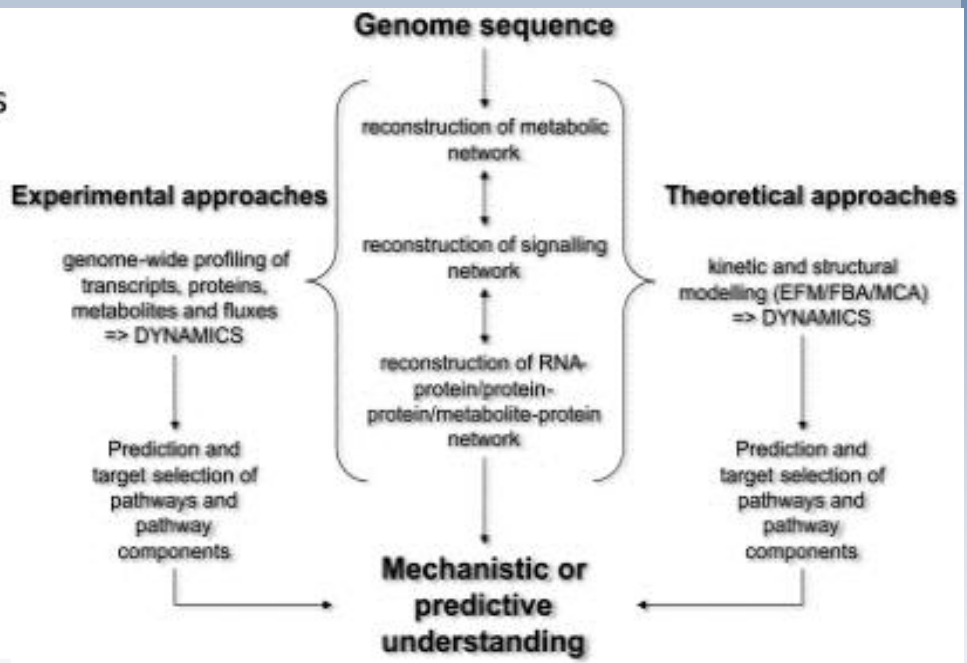




Weckwerth W. Anal Biochem Chem. 2011 Jun;400(7):1967-78.

Unpredictability of metabolism--the key role of metabolomics science in combination with next-generation genome sequencing



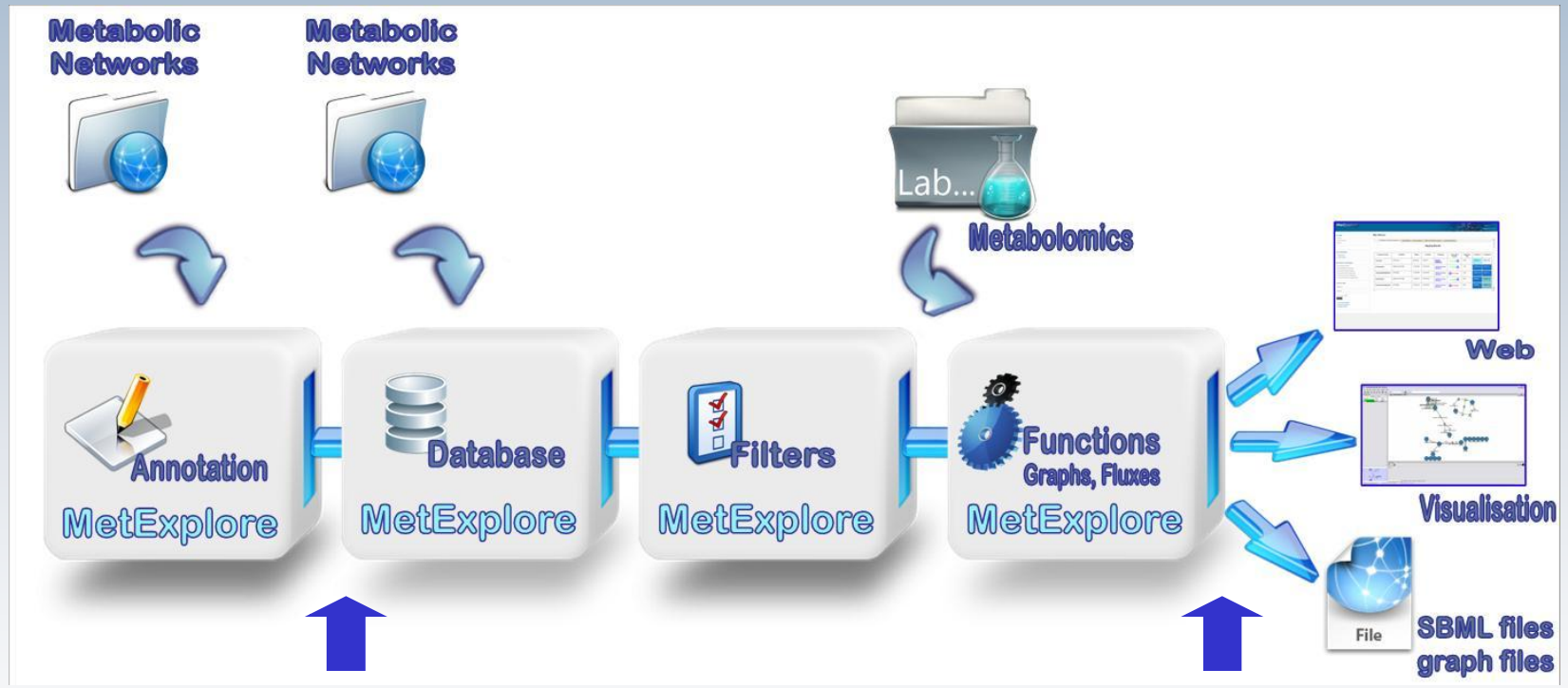


Overall strategy combining full-scan mass spectrometry analyses of metabolites and targeted analysis. Physiological markers are identified in HTP-manner with MRM MS technology.

Integrative approach combining genome sequencing, dynamic modeling and *omics* analysis. EFM-elementary flux models, FBA- flux balance analysis MCA-metabolic control analysis.

Weckwerth W. Anal Biochem Chem. 2011 Jun;400(7):1967-78.

MetExplore: a web server to link metabolomic experiments and genome-scale metabolic networks



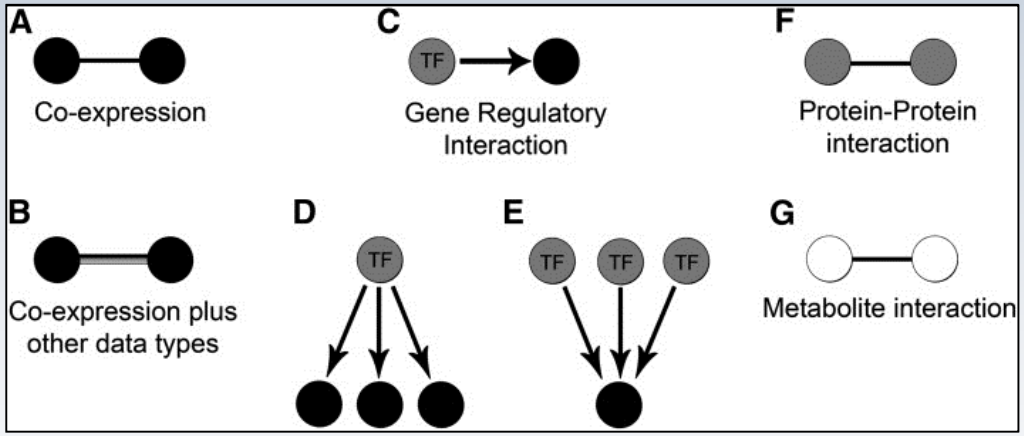
Metabolic networks from ~200 organisms

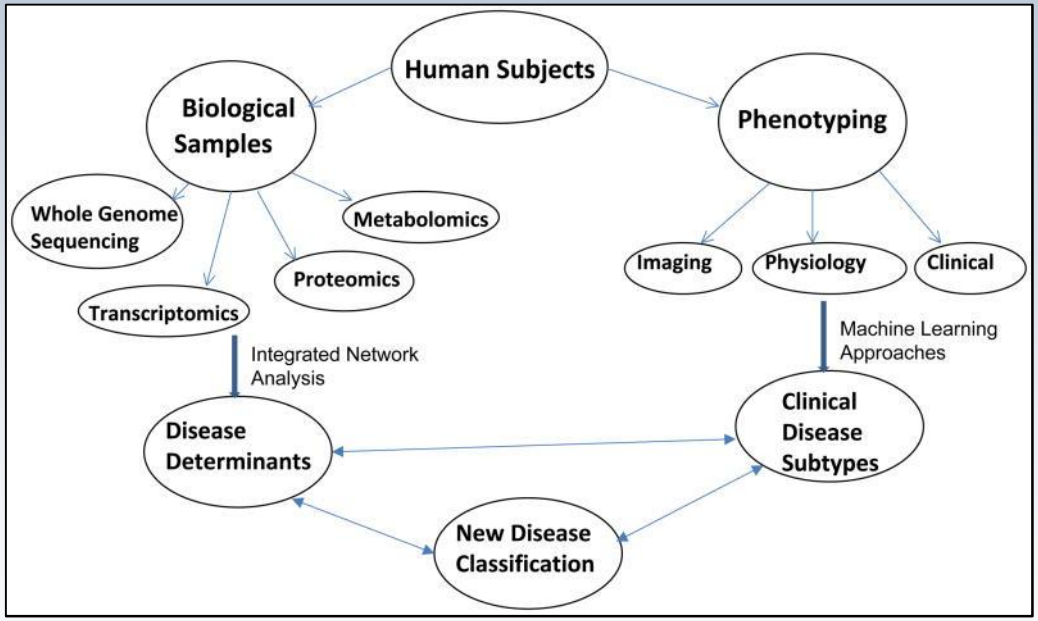
http://metexplore.toulouse.inra.fr

- Maps lists of metabolites to genome-inferred metabolic networks
- Provides computational functions that allow investigation of features, e.g. potential drug targets

Cotrett L. et al., Nucleic Acid Res. 2010 Jul;38 (Web Server issue):W132-7.

Network medicine approaches to the genetics of complex diseases

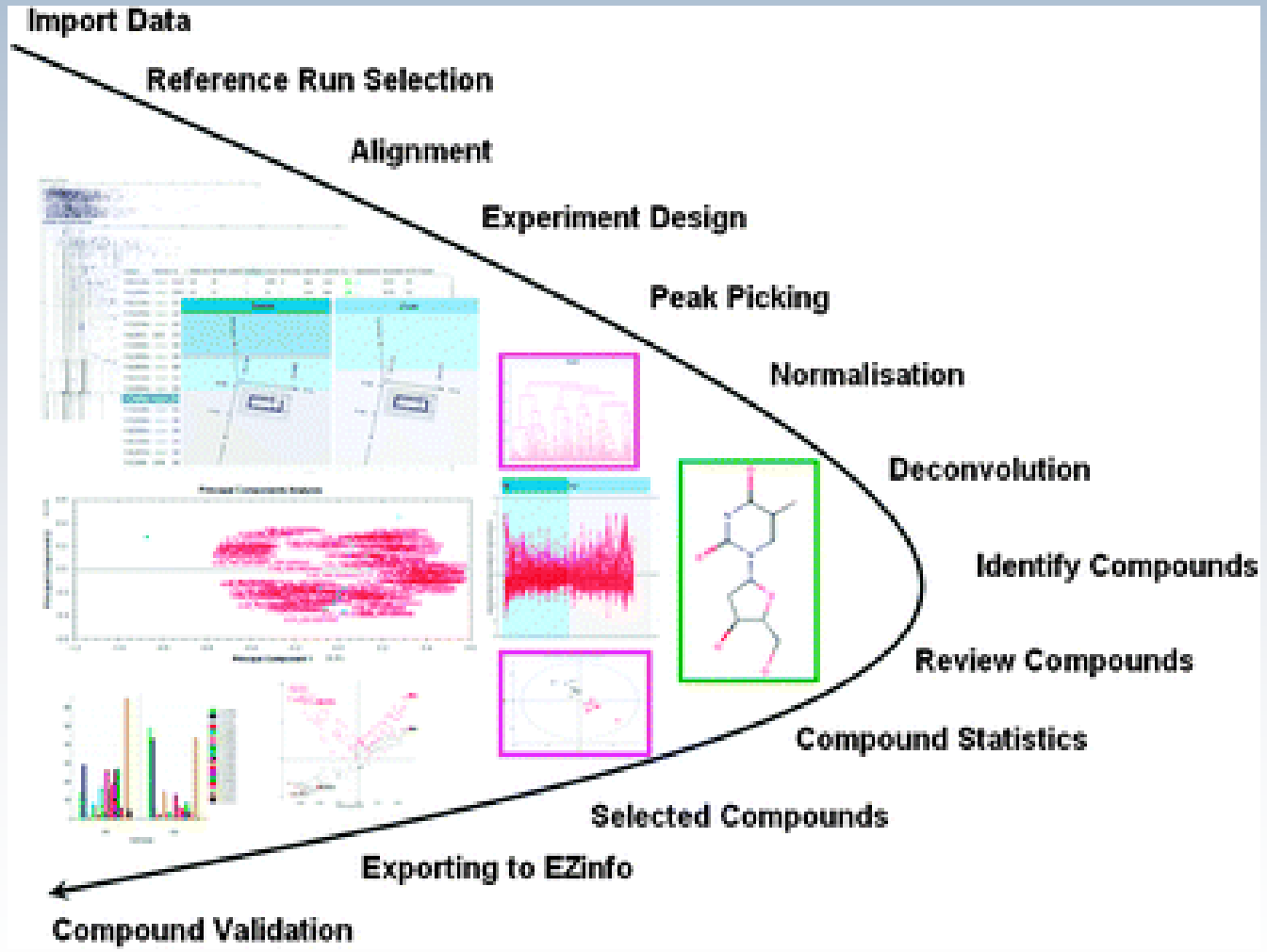




Silverman E. et al., Discovery Medicine 2012, 14(75):143-152.

http://www.youtube.com/watch?v=6EbWdWa2rF0

Rapidly improved determination of metabolites from biological data sets using the high-efficient TransOmics software tool



Detailed analysis workflow of TransOmics informatics for metabolomics (Waters/Nonlinear)

Zhang A. et al., Mol Biosyst 2014, 10: 2061-65.

The detailed information for identification of metabolites by TransOmics software online

A

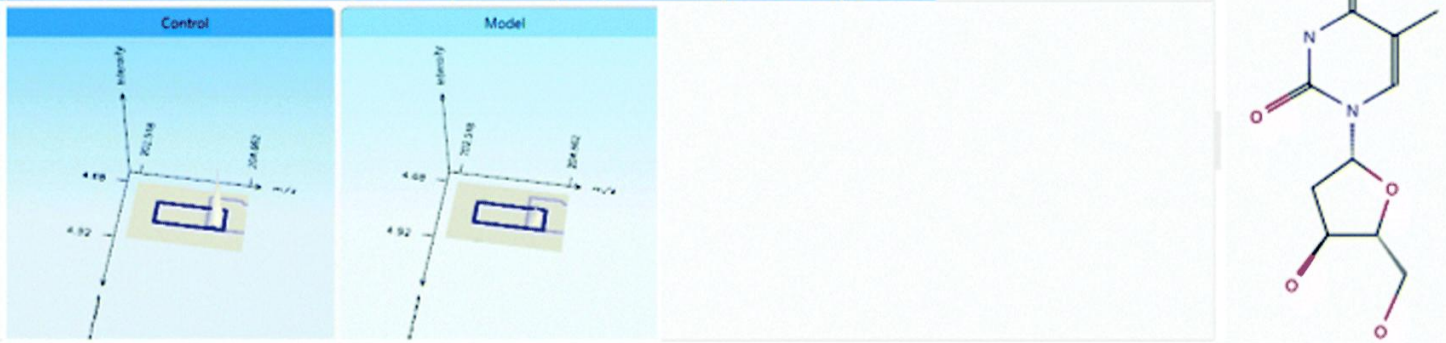
Compound	Neutral mass	m/z	z	Retention time	Peak Width	Accepted ID	Identifications	Anova (p)	Max fold change	Highest mean	Lowest mean	Tag	Isotope distribution	Max Abundance	Min CV%	Description
4.86_191.1145m/z	<unknown>	191.1145	1	4.86	0.08		1	0.00296	2.6	Model	Control			647.2017	45.74	
4.91_220.0010m/z	<unknown>	220.0010	1	4.91	0.10		1	0.41	1	Control	Model			966.7981	51.82	
5.09_215.1187m/z	<unknown>	215.1187	1	5.09	0.07		1	0.677	1.07	Control	Model			294.0438	28.65	
4.79_231.0754m/z	<unknown>	231.0754	1	4.79	0.08		1	0.193	6.31	Model	Control			403.8447	31.41	
4.79_203.0794m/z	<unknown>	203.0794	1	4.79	0.08		1	0.675	9.94	Model	Control			241.9278	48.81	
4.84_254.0571n	254.0571	277.0469	1	4.84	0.10		1	0.39	1.16	Control	Model			2378.6927	23.17	
5.18_268.0694m/z	<unknown>	268.0694	1	5.18	0.15		1	6.3E-05	3.18	Control	Model			2662.4642	36.48	
5.81_238.0083m/z	<unknown>	238.0083	1	5.81	0.04		1	0.352	1.24	Model	Control			238.0212	50.46	
5.84_288.0626m/z	<unknown>	288.0626	1	5.84	0.06		1	0.348	1.24	Control	Model			678.9418	44.36	
5.94_313.1112m/z	<unknown>	313.1112	1	5.94	0.09		1	0.148	1.96	Model	Control			993.7521	36.32	
5.26_300.0834m/z	<unknown>	300.0834	1	5.26	0.08		1	0.274	1.66	Control	Model			640.7929	39.32	
5.77_243.0989m/z	<unknown>	243.0989	1	5.77	0.15		1	0.0293	3.42	Model	Control			2342.7042	58.72	
5.78_291.1306m/z	<unknown>	291.1306	1	5.78	0.06		1	0.000858	1.44	Control	Model			565.3010	16.54	
4.78_220.0106m/z	<unknown>	220.0106	1	4.78	0.13		1	4.46E-05	6.42	Control	Model			2608.7112	59.02	
3.88_258.0839m/z	<unknown>	258.0839	1	3.88	0.04		1	0.0252	1.92	Model	Control			219.1541	30.12	
3.90_121.0323m/z	<unknown>	121.0323	1	3.90	0.12		1	0.218	1.2	Model	Control			967.6142	23.88	
3.98_128.0715m/z	<unknown>	128.0715	1	3.98	0.05		1	0.016	2.66	Model	Control			82.4211	75.98	
3.67_163.0664n	163.0664	164.0742	1	3.67	0.21		1	0.0399	1.53	Model	Control			3439.5021	27.60	

B

Compound 5.77_243.0989m/z:

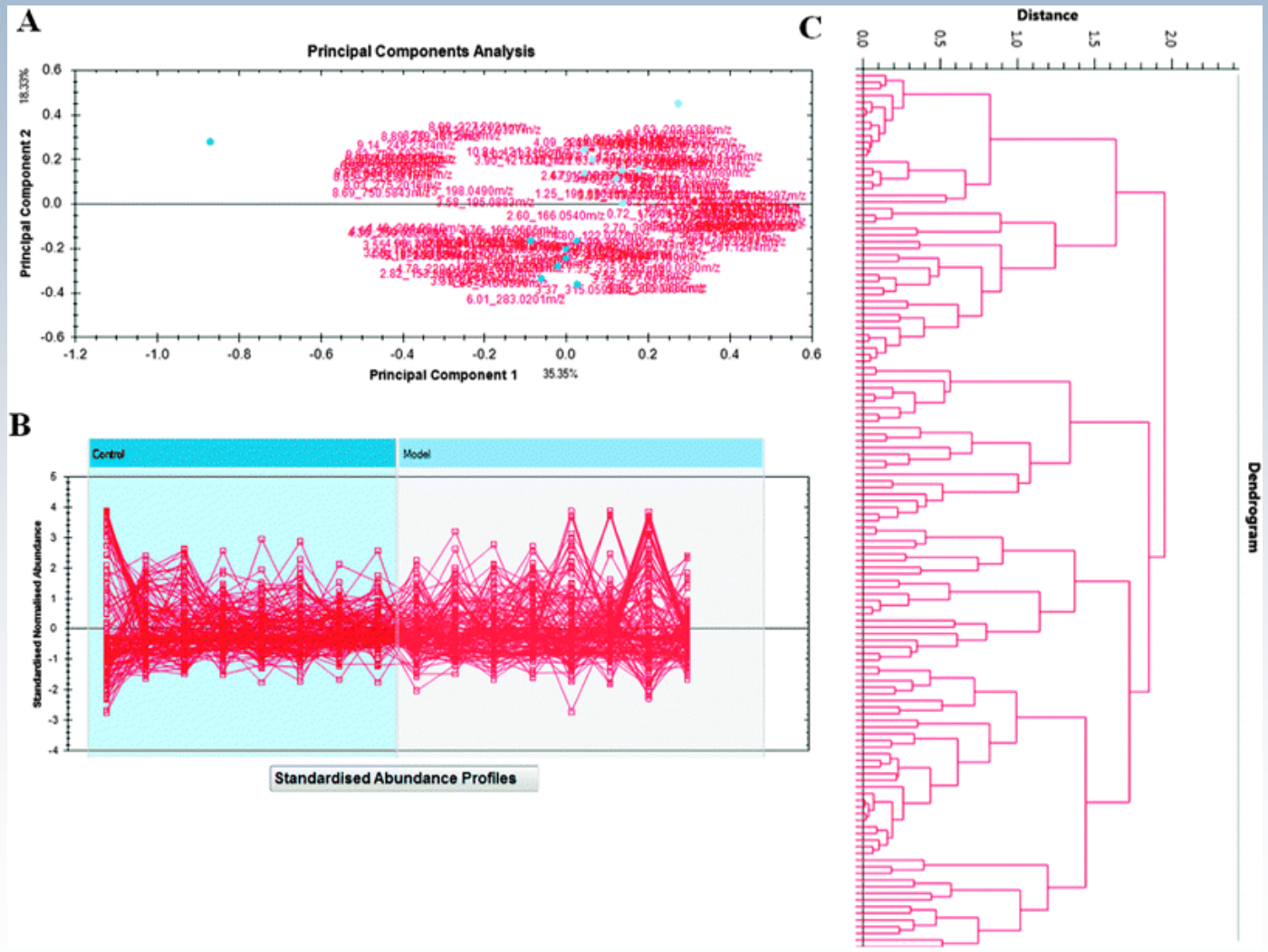
Compound abundance | Possible identifications (1) | 3D Montage

Compound ID	Description	Adducts	Formula	Retention time	Score	Mass error (ppm)	Isotope similarity	Link
HMDB00273	Thymidine	M+H	$C_{10}H_{14}N_2O_5$		63.9	3.24	95.41	nonlinear



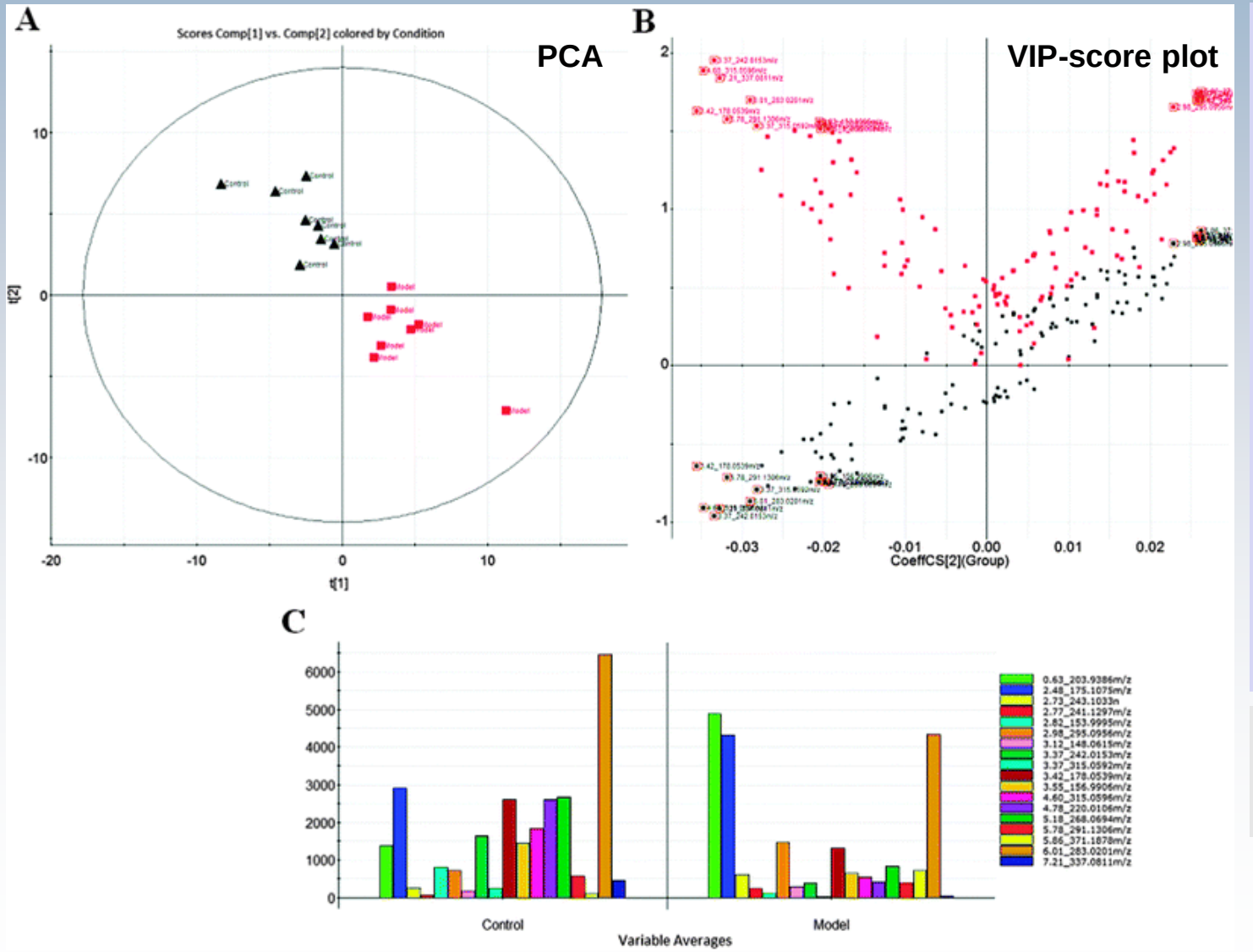
Zhang A. et al., Mol Biosyst 2014, 10: 2061-65.

Compound statistics (TransOmics software)



Zhang A. et al., Mol Biosyst 2014, 10: 2061-65.

Compound statistics (EZinfo)



***Ezinfo* software for compound statistics (PCA) and Orthogonal Projections to Latent Square Discriminant Analysis (OPLS-DA), correlation analysis and compound validation**

Orthogonal partial least square discriminant analysis finds a linear regression model by projecting the predicted variables and the observable variables to a new space OPLS-DA (2002) works best with discrete variables in classification and biomarker studies

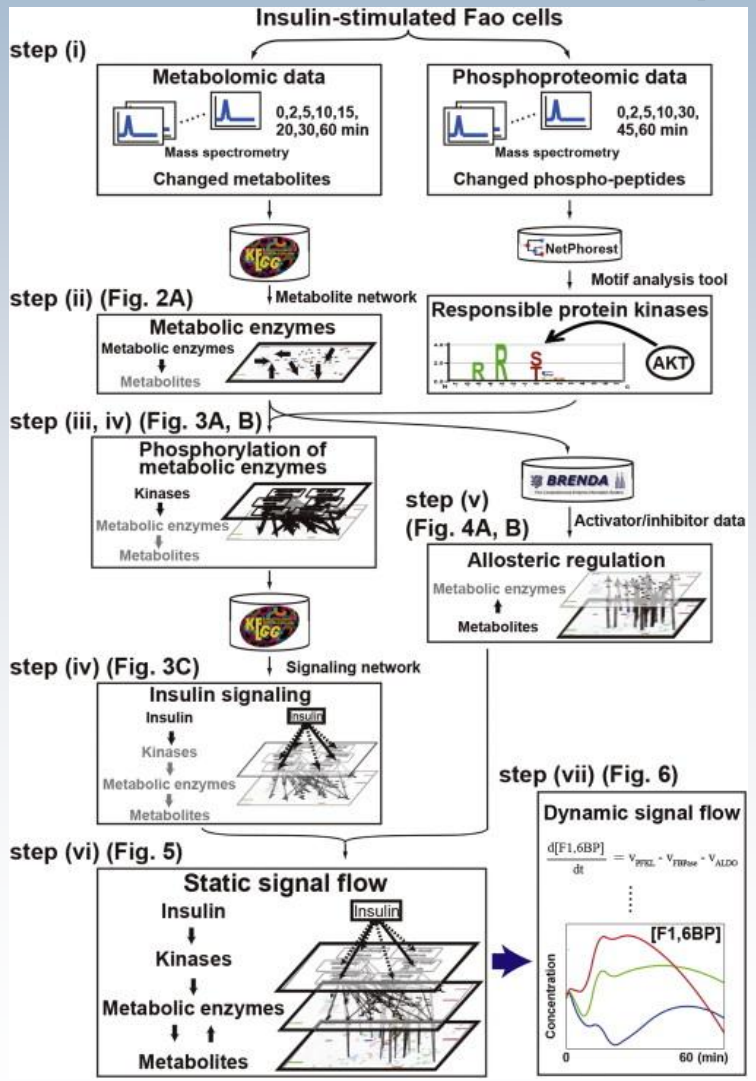
Assigned:
17 features in 14 KEGG pathways

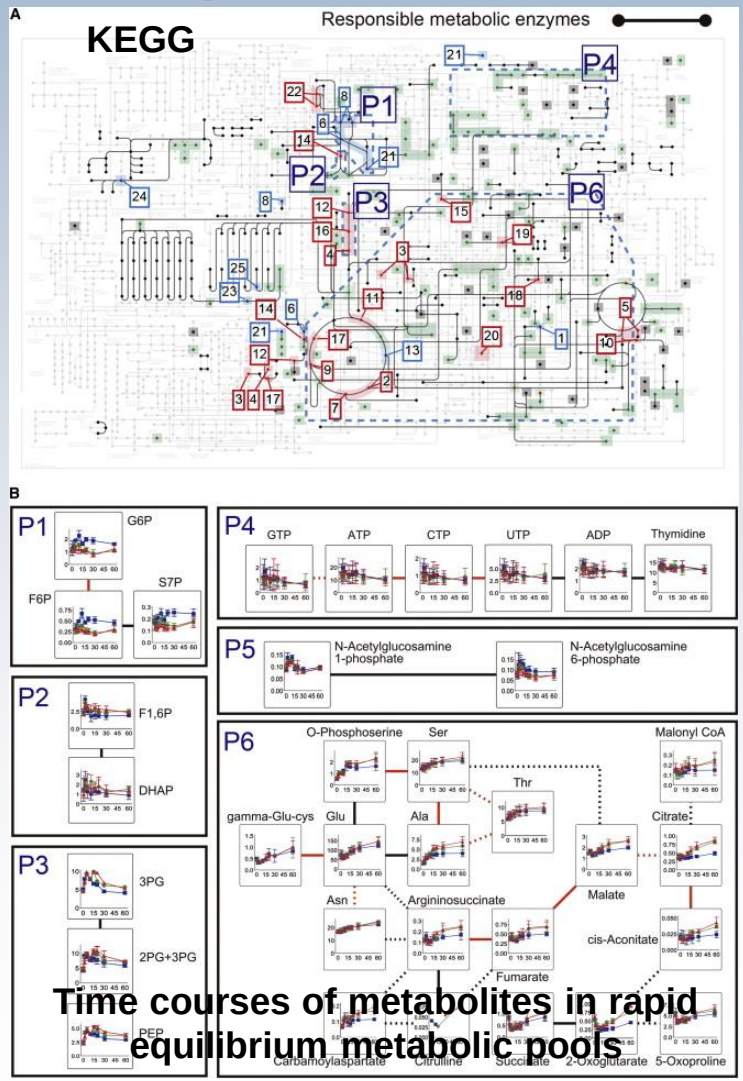
Zhang A. et al., Mol Biosyst 2014, 10: 2061-65.

Procedures of Reconstruction of Signal Flow in the Trans-Omic Network of Acute Insulin Action (< 60 minutes)

FAO cells

Simultaneous measurement of 304 metabolites, 7,277 P-sites on 3,458 proteins 19,778 RNA probes





Time courses of metabolites in rapid equilibrium metabolic pools

Yugi K. et al., Cell Reports 2014, 8(4): 1171-83.