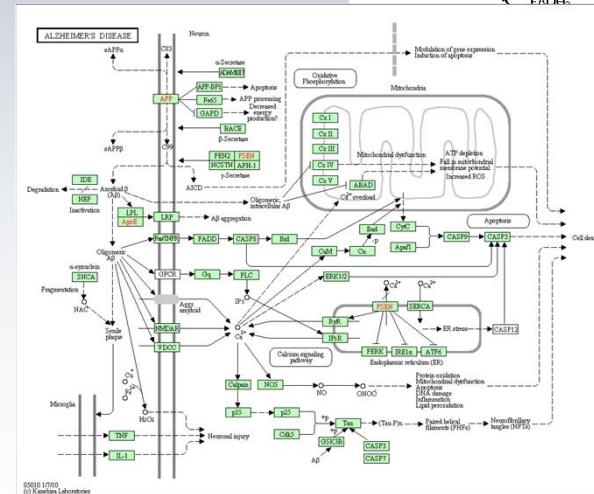
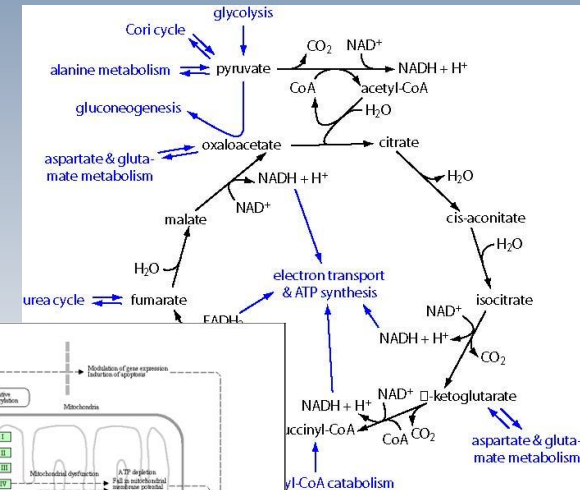


# Systems Biology in Metabolomics

Maciej Lalowski

Biomedicum Helsinki  
Helsinki University

TrasMed Course 12.10.2012



## Basic definitions:

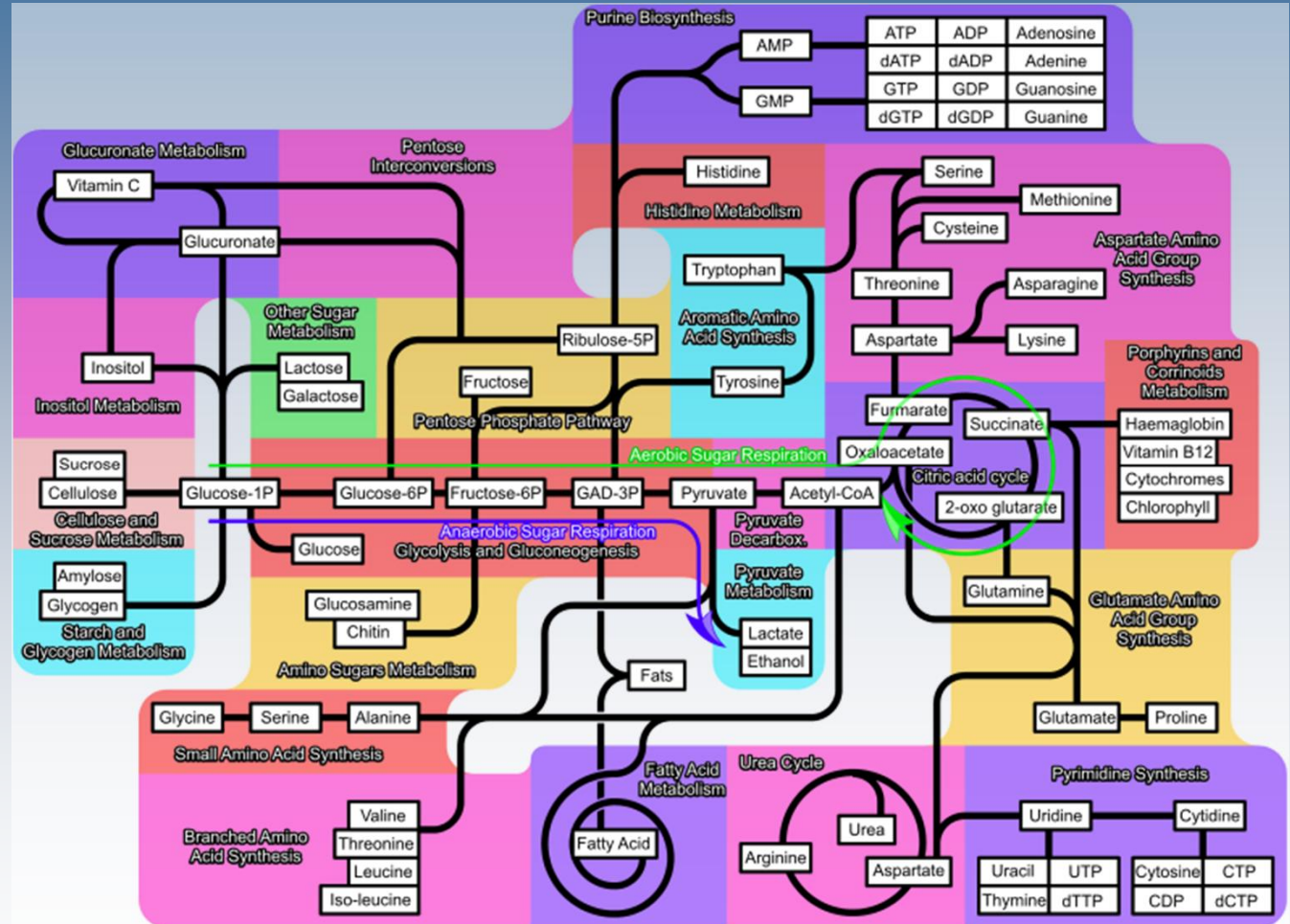
- **Metabolites** - are the intermediates and products of metabolism. The term *metabolite* is usually restricted to small molecules. A **primary metabolite** is directly involved in normal growth, development, and reproduction, e.g. alcohol. A **secondary metabolite** is not directly involved in those 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.



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

**ACLY ATP citrate lyase [Homo sapiens]**  
Gene ID: 47, updated on 1-Oct-2011

**Summary**

Official Symbol [ACLY](#) provided by [HGNC](#)  
 Official Full Name [ATP citrate lyase](#) provided by [HGNC](#)  
 Primary source [HGNC:115](#)  
 See related [Ensembl:ENS00000131473](#); [HPRD:00155](#); [MIM:108728](#)  
 Gene type protein coding  
 RefSeq status REVIEWED  
 Organism [Homo sapiens](#)  
 Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini; Catarrhini; Hominidae; Homo  
 Also known as [ACL](#); [ATPCL](#); [CLATP](#)  
 Summary ATP citrate lyase is the primary enzyme responsible for the synthesis of cytosolic acetyl-CoA in many tissues. The enzyme is a tetramer (relative molecular weight approximately 440,000) of apparently identical subunits. It catalyzes the formation of acetyl-CoA and oxaloacetate from citrate and CoA with a concomitant hydrolysis of ATP to ADP and phosphate. The product, acetyl-CoA, serves several important biosynthetic pathways, including lipogenesis and cholesterol synthesis. In nervous tissue, ATP citrate-lyase may be involved in the biosynthesis of acetylcholine. Two transcript variants encoding distinct isoforms have been identified for this gene. [provided by RefSeq, Jul 2008]

**Genomic context**

Location : 17q21.2  
 Sequence : Chromosome: 17; NC\_000017.10 (40023179..40075272, complement)

[See ACLY in MapViewer](#)

Chromosome 17 - NC\_000017.10

**Table of contents**

- Summary
- Genomic context
- Genomic regions, transcripts, and products
- Bibliography
- Interactions
- General gene info
- General protein info
- Reference sequences
- Related sequences
- Additional links

**Links**

- Order cDNA clone
- BioAssay, by Gene target
- BioProjects
- BioSystems
- CCDS
- Conserved Domains
- dbVar
- EST
- Full text in PMC
- Genome
- GEO Profiles
- HomoloGene



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

ACLY ATP citrate lyase [Homo sapiens] - Gene - NCBI - Mozilla Firefox

File Edit View History Bookmarks Tools Help

http://www.ncbi.nlm.nih.gov/gene/47

Most Visited Customize Links Link to University's ho...

Figure 4 analyzes how mutations c Search Ask Facebook Amazon YouTube Weather BBC BBC News BBC Sports Options

ACLY ATP citrate lyase [Homo sapie... +

Homology

[Homologs of the ACLY gene](#): The ACLY gene is conserved in chimpanzee, dog, cow, mouse, rat, chicken, zebrafish, fruit fly, mosquito, C.elegans, S.pombe, M.grisea, N.crassa, A.thaliana, and rice.  
[Map Viewer](#) (Mouse, Rat)

Pathways from BioSystems

- [ChREBP activates metabolic gene expression, organism-specific biosystem](#) (from REACTOME)
- \* [Citrate cycle \(TCA cycle\), organism-specific biosystem](#) (from KEGG)
- [Citrate cycle \(TCA cycle\), conserved biosystem](#) (from KEGG)
- \* [Fatty Acid Biosynthesis, organism-specific biosystem](#) (from WikiPathways)
- [Fatty Acyl-CoA Biosynthesis, organism-specific biosystem](#) (from REACTOME)
- \* [Fatty acid, triacylglycerol, and ketone body metabolism, organism-specific biosystem](#) (from REACTOME)
- [Integration of energy metabolism, organism-specific biosystem](#) (from REACTOME)
- [Metabolic pathways, organism-specific biosystem](#) (from KEGG)
- [Metabolism of lipids and lipoproteins, organism-specific biosystem](#) (from REACTOME)
- [Triglyceride Biosynthesis, organism-specific biosystem](#) (from REACTOME)

Gene Ontology [Provided by GOA](#)


| Function  | Evidence Code | Pubs |
|---|---------------|------|
| <a href="#">ATP binding</a>                                 | IEA           |      |
| <a href="#">ATP citrate synthase activity</a>               | IEA           |      |
| <a href="#">citrate (pro-3S)-lyase activity</a>             | TAS           |      |
| <a href="#">ligase activity</a>                             | IEA           |      |
| <a href="#">metal ion binding</a>                           | IEA           |      |
| <a href="#">nucleotide binding</a>                          | IEA           |      |
| <a href="#">succinate-CoA ligase (ADP-forming) activity</a> | IEA           |      |
| <a href="#">transferase activity</a>                        | IEA           |      |

http://www.ncbi.nlm.nih.gov/guide/all/

start ACLY ATP citrate lyas... TRANSMED Microsoft PowerPoint ... Links 14.59

# KEGG <http://www.genome.jp/kegg/>

KEGG: Kyoto Encyclopedia of Genes and Genomes



» Japanese

**KEGG Home**  
[Introduction](#)  
[Overview](#)  
[Release notes](#)  
[Current statistics](#)

**KEGG Identifiers**  
[Pathway maps](#)  
[Brite hierarchies](#)

**KEGG XML**

**KEGG API**

**KEGG FTP**

**KegTools**

---

[GenomeNet](#)

[DBGET/UnkDB](#)

[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   (example) hsa
- **Analysis tools**  
[KEGG Mapper](#) *New!*    [KEGG PATHWAY and BRITE mapping tools](#)

# KEGG <http://www.genome.jp/kegg/>

KEGG PATHWAY Database - Mozilla Firefox

File Edit View History Bookmarks Tools Help

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

Most Visited Customize Links

KEGG PATHWAY Database

KEGG2 PATHWAY BRITE DISEASE DRUG KO GENES GENOME LIGAND DBGET

Select prefix: map Organism Enter keywords: Go Help

### Pathway Maps

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

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

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

- 7. Drug Development**

KEGG Atlas may now be used to examine any of the KEGG pathway maps.

### Pathway Entries and Pathway Modules

Pathway entries are text representation of pathway maps, containing descriptions (for a limited number of entries, at the moment). **Pathway modules** are specification of subnetworks that correspond to tighter functional units, each represented as a list of KO identifiers (K numbers).

Search Pathway entries for Go Clear

### Pathway Mapping

Done

start University of Helsinki... KEGG PATHWAY Data... Students\_TRANSMED... Seminar\_TRANSMED... 17.14

# KEGG <http://www.genome.jp/kegg/>

**KEGG PATHWAY Database - Mozilla Firefox**

File Edit View History Bookmarks Tools Help

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

Most Visited Customize Links

**KEGG PATHWAY Database**

## Pathway Entries and Pathway Modules

Pathway entries are text representation of pathway maps, containing descriptions (for a limited number of entries, at the moment). **Pathway modules** are specification of subnetworks that correspond to tighter functional units, each represented as a list of KO identifiers (K numbers).

Search  for

### Pathway Mapping

KEGG PATHWAY mapping is the process to map molecular datasets, especially large-scale datasets in genomics, transcriptomics, proteomics, and metabolomics, to the KEGG pathway maps for biological interpretation of higher-level systemic functions.

- Search objects in KEGG pathways
- Color objects in KEGG pathways

---

## 0. Global Map

### 0.1 Metabolism

Metabolic pathways [zoom out] [Launch KEGG Atlas](#)  
Biosynthesis of secondary metabolites [zoom out] [Launch KEGG Atlas](#)

---

## 1. Metabolism

### 1.1 Carbohydrate Metabolism

Glycolysis / Gluconeogenesis [Enzymes](#)  
**Citrate cycle (TCA cycle)** [Compounds with biological roles](#)  
Pentose phosphate pathway  
Pentose and glucuronate interconversions  
Fructose and mannose metabolism  
Galactose metabolism  
Ascorbate and aldarate metabolism  
Starch and sucrose metabolism

Done

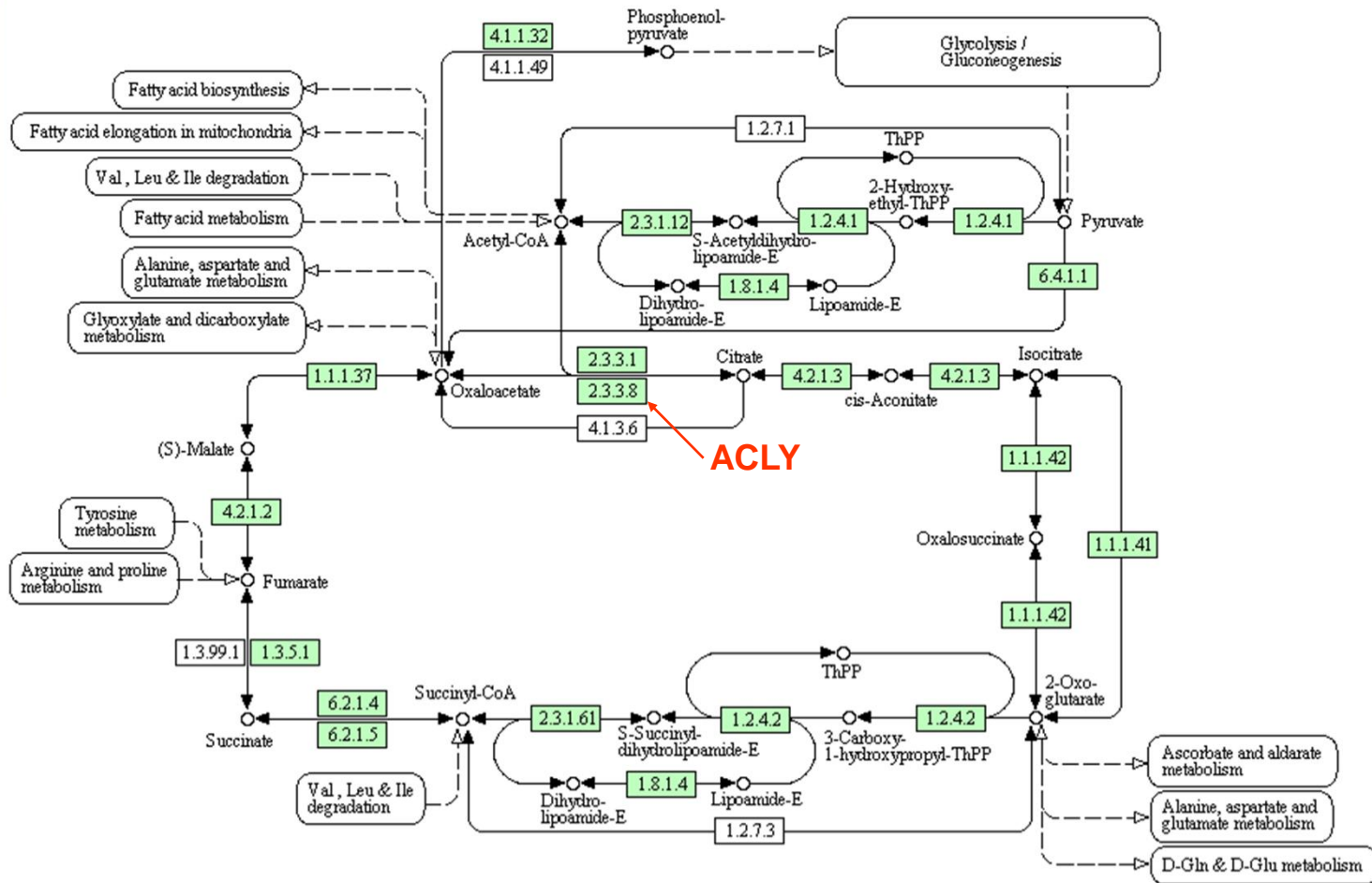
start University of Helsinki... KEGG PATHWAY Data... Students\_TRANSMED... Seminar\_TRANSMED ... 17.17



# KEGG <http://www.genome.jp/kegg/>

BSID: 82927 KEGG: hsa:00020

## CITRATE CYCLE (TCA CYCLE)



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

**Reactome - Mozilla Firefox**  
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 http://www.reactome.org/ReactomeGWT/entrypoint.html  
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**REACTOME**  
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**About Reactome**  
 REACTOME is an open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. These include NCBI Entrez Gene, Ensembl and UniProt databases, the UCSC and HapMap Genome Browsers, the KEGG Compound and ChEBI small molecule databases, PubMed, and Gene Ontology... [more]

**Reactome Milestone**  
 Reactome has achieved its milestone of curating reactions and pathways involving at least 5000 distinct human proteins... [more]

**Tutorial**  
 Reactome Introduction Us... [Video Player]

**Pathway of the Month: G2/M DNA damage checkpoint**  
 DNA Damage → kinase → Cyclin A/B Cdc 2 (Cdk 1) → pT14Y15

**Download**  
 The following links allow you to download Reactome data in various formats:  
 • BioPax  
 • SBML  
 • Textbook

Read it. yting.com

start Reactome - Mozilla Fir... Seminar\_TRANSMED... 17.00

## Reactome: pathways

Mozilla Firefox

File Edit View History Bookmarks Tools Help

http://www.reactome.org/entitylevelview/PathwayBrowser.html#DB=gk\_current&FOCUS\_SPECIES\_ID=48887&F...

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Search Ask Facebook Amazon YouTube Weather BBC BBC News BBC Sports Options

http://www.rea...734&ID=75105& Reactome

Home & Search

Analyze, Annotate & Upload

Switch Species: Homo sapiens

Pathways Help

- Metabolism of carbohydrates
- Metabolism of lipids and lipoproteins
  - Lipid digestion, mobilization, and transport
  - Fatty acid, triacylglycerol, and ketone body met
  - Triglyceride Biosynthesis
    - Fatty Acyl-CoA Biosynthesis
      - Conversion of Dihydroxyacetone Phosp
      - Conversion of Glycerol to Glycerol-3-ph
      - glycerol 3-phosphate + acyl-CoA => 1-a
      - glycerol 3-phosphate + acyl-CoA => 1-a
      - 1-acyl-glycerol 3-phosphate + acyl-CoA
      - 1,2-diacyl-glycerol 3-phosphate + H2O =
      - 1,2-diacyl-glycerol + acyl-CoA => triacylg
      - 1,2-diacyl-glycerol + acyl-CoA => triacylg
    - Import of palmitoyl-CoA into the mitochon
    - Mitochondrial Fatty Acid Beta-Oxidation
    - Ketone body metabolism
      - Gly-3-P+FAD->DHAP+FADH2 (catalyzed by

Protein Small Molecule Complex Diagram key

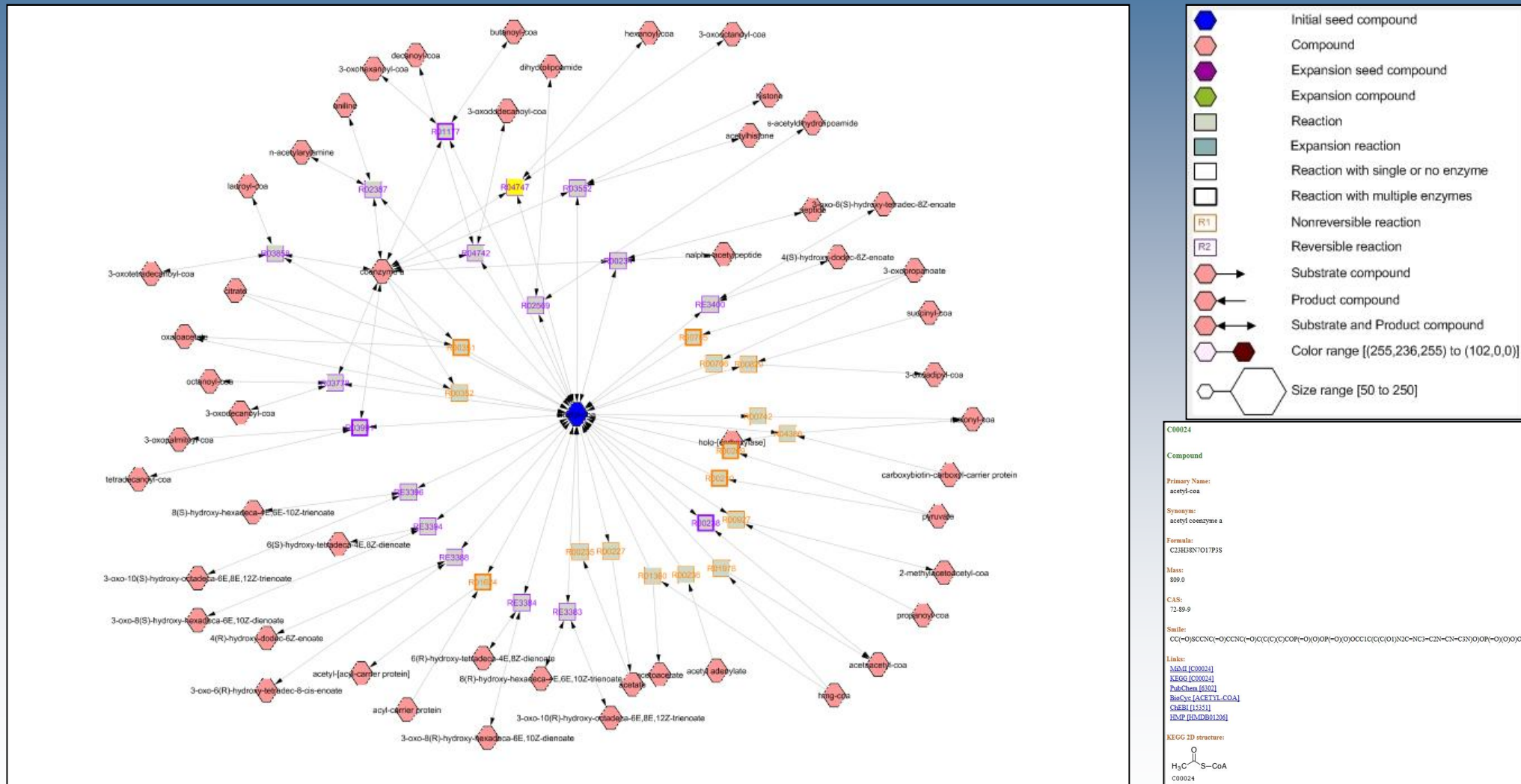
Done

start Mozilla Firefox Seminar\_TRANSMED\_... Links 16.56





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



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

MICHIGAN MOLECULAR INTERACTIONS

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### 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>

AmiGO: Gene Product Search Results - Mozilla Firefox

http://amigo.geneontology.org/cgi-bin/amigo/search.cgi?session\_id=8648amigo1317651794&search\_query=ACLY

the Gene Ontology AmiGO

Search Browse BLAST Homolog Annotations Tools & Resources Help

Search GO   GO terms  genes or proteins  exact match

## Gene Product Search Results

12 results for **ACLY** in genes or proteins fields **symbol, full name(s) and synonyms**

▼ Filter search results ?

| Filter Gene Products |             |                      | Filter Gene Products by Associations |               |
|----------------------|-------------|----------------------|--------------------------------------|---------------|
| Gene Product Type    | Data source | Species              | Ontology                             | Evidence Code |
| All                  | All         | All                  | All                                  | All           |
| complex              | ASAP        | Arabidopsis thaliana | biological process                   | IBA           |
| gene                 | AspGD       | Aspergillus fumig... | cellular component                   | IBD           |
| gene product         | CGD         | Aspergillus niger    | molecular function                   | IKR           |

Results are sorted by **relevance**. To change the sort order, click on the column headers.

Perform an action with this page's selected gene products...

| rel ↓                    | <u>Symbol</u> , <u>full name</u> | <u>Species</u>                                   |
|--------------------------|----------------------------------|--|
| <input type="checkbox"/> | <b>ACLY</b>                      | 24 associations protein from <i>Mus musculus</i> |

Done

start AmiGO: Gene Product... Seminar\_TRANSMED... 17.24



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

Gene  
Ontology:  
component

ACLY Homo sapiens P53396 - Mozilla Firefox

http://www.ebi.ac.uk/QuickGO/GProtein?ac=P53396

Search Ask | Facebook | Amazon | YouTube | Weather | BBC | BBC News | BBC Sports

University of Helsinki\_ Research Progra... | ACLY ATP citrate lyase [Homo sapiens] | ACLY Homo sapiens P53396

| UniProtKB        | ACLY | GO                         | Component   | C         | IEA | InterPro2GO               | InterPro:IPR016143         | 9606 | 20111001 | InterPro  |
|------------------|------|----------------------------|---|-----------|-----|---------------------------|----------------------------|------|----------|-----------|
| UniProtKB P53396 | ACLY | <a href="#">GO:0046912</a> | alkyl on transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer | F         | IEA | InterPro2GO               | InterPro:IPR016143         | 9606 | 20111001 | InterPro  |
| UniProtKB P53396 | ACLY | <a href="#">GO:0005634</a> | nucleus   | C         | IDA | PMID:18029348             |                            | 9606 | 20101115 | HPA       |
| UniProtKB P53396 | ACLY | <a href="#">GO:0005737</a> | cytoplasm   | C         | IEA | InterPro2GO               | InterPro:IPR014608         | 9606 | 20111001 | InterPro  |
| UniProtKB P53396 | ACLY | <a href="#">GO:0005737</a> | cytoplasm   | C         | IEA | Swiss-Prot<br>Keywords2GO | SP_KW:KW-0963              | 9606 | 20111001 | UniProtKB |
| UniProtKB P53396 | ACLY | <a href="#">GO:0005737</a> | cytoplasm   | C         | IEA | Subcellular Location2GO   | SP_SL:SL-0086              | 9606 | 20111001 | UniProtKB |
| UniProtKB P53396 | ACLY | <a href="#">GO:0005737</a> | cytoplasm   | C         | IDA | PMID:18029348             |                            | 9606 | 20101115 | HPA       |
| UniProtKB P53396 | ACLY | <a href="#">GO:0005739</a> | mitochondrion   | C         | IEA | Compara                   | Ensembl:ENSMUSP00000103012 | 9606 | 20111001 | ENSEMBL   |
| UniProtKB P53396 | ACLY | <a href="#">GO:0005829</a> | cytosol   | C         | TAS | Reactome:REACT_1141       |                            | 9606 | 20040609 | Reactome  |
| UniProtKB P53396 | ACLY | <a href="#">GO:0005829</a> | cytosol   | C         | TAS | Reactome:REACT_1577       |                            | 9606 | 20040609 | Reactome  |
| UniProtKB P53396 | ACLY | <a href="#">GO:0009346</a> | citrate lyase complex   | C         | TAS | PMID:1371749              |                            | 9606 | 20030904 | PINC      |
| UniProtKB P53396 | ACLY | NOT                        | <a href="#">GO:0005730</a>  | nucleolus | C   | IDA                       | PMID:18029348              | 9606 | 20101115 | HPA       |

Please send comments, suggestions or bug reports to [goa@ebi.ac.uk](mailto:goa@ebi.ac.uk). Click [here](#) for details of how to cite UniProtKB-GOA and QuickGO.

Javascript:  ON  OFF

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Done

start | ACLY Homo sapiens P... | Seminar\_TRANSMED... | 17.13



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

## Gene Ontology: process

ACLY Homo sapiens P53396 - Mozilla Firefox

http://www.ebi.ac.uk/QuickGO/GProtein?ac=P53396

Results: 1 to 48 of 48 Page size: 25 (Show All) Additional filters: None Bookmarkable link

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

Done

start | ACLY Homo sapiens P... | Seminar\_TRANSMED... | 17.17

# Gene Cards: <http://www.genecards.org/>

GeneCards V3 - Human Genes | Gene Database | Gene Search - Mozilla Firefox

File Edit View History Bookmarks Tools Help

http://www.genecards.org/

GeneCards V3 - Human Genes | Gen...

Version 3

GeneCards®

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WEIZMANN INSTITUTE OF SCIENCE

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GeneAnnot Mastering Gene Annotation

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Extract information for many genes at once: [GeneLaCart](#) [GeneDecks](#) [Hot genes](#) [Disease genes](#)

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Aliases Drugs Genome view Pathways Publications

Databases Expression Interactions Paralogs Summaries

Disorders External search IP/Patents Products Transcripts

Domains Function Orthologs Proteins Variants

View Random Gene

Category Protein-coding **SERPINA12**  
(GIFTS: 54)

News and Views

Version 3 features

New search engine:

- Speedy output
- Unlimited hits
- Field-specific input
- Better minicards
- Relational database

What's New

User comments

Xennex PR

Site Map

Version 3.06

19 June 2011

Revision 3.06.070

Previous V3 site

Done

start GeneCards V3 - Hum... TRANSMED Microsoft PowerPoint ... Links 9.58

# Gene Cards: aliases and descriptions

**Jump to Section...**

**Aliases & Descriptions for ACLY gene**

(According to <sup>1</sup>HGNC, <sup>2</sup>Entrez Gene, <sup>3</sup>UniProtKB/Swiss-Prot, <sup>4</sup>UniProtKB/TrEMBL, <sup>5</sup>OMIM, <sup>6</sup>GeneLoc, <sup>7</sup>Ensembl, <sup>8</sup>DME, and/or <sup>9</sup>miRBase)

[About This Section](#)

**Aliases & Descriptions**

|  |  |
|--|--|
| ATP citrate lyase <sup>1,2</sup>       | ATP-citrate (pro-S)-lyase <sup>2,3</sup> |
| ACL <sup>1,2,3</sup>                   | EC 2.3.3.8 <sup>3,8</sup>                |
| ATPCL <sup>1,2</sup>                   | OTTHUMP00000164773 <sup>2</sup>          |
| CLATP <sup>1,2</sup>                   | ATP citrate synthase <sup>2</sup>        |
| Citrate cleavage enzyme <sup>2,3</sup> | ATP-citrate synthase <sup>2</sup>        |

**External Ids:** HGNC: 115<sup>1</sup> Entrez Gene: 47<sup>2</sup> Ensembl: ENSG00000131473<sup>1</sup> UniProtKB: P53396<sup>3</sup>

[Export aliases for ACLY gene to outside databases](#)

Previous GC identifiers: GC17M039579 GC17M042174 GC17M039931 GC17M040396 GC17M037276 GC17M035785

---

**Jump to Section...**

**Summaries for ACLY gene**

(According to [Entrez Gene](#), [Toocris Bioscience](#), [Wikipedia's Gene Wiki](#), [UniProtKB/Swiss-Prot](#), and/or [UniProtKB/TrEMBL](#))

[About This Section](#)

**Entrez Gene summary for ACLY:**

ATP citrate lyase is the primary enzyme responsible for the synthesis of cytosolic acetyl-CoA in many tissues. The enzyme is a tetramer (relative molecular weight approximately 440,000) of apparently identical subunits. It catalyzes the formation of acetyl-CoA and oxaloacetate from citrate and CoA with a concomitant hydrolysis of ATP to ADP and phosphate. The product, acetyl-CoA, serves several important biosynthetic pathways, including lipogenesis and cholesterologenesis. In nervous tissue, ATP citrate-lyase may be involved in the biosynthesis of acetylcholine. Two transcript variants encoding distinct isoforms have been identified for this gene. (provided by RefSeq)

**UniProtKB/Swiss-Prot:** [ACLY\\_HUMAN, P53396](#)

**Function:** ATP citrate-lyase is the primary enzyme responsible for the synthesis of cytosolic acetyl-CoA in many tissues. Has a central role in de novo lipid synthesis. In nervous tissue it may be involved in the biosynthesis of acetylcholine

Done

start | ACLY Gene - GeneCa... | TRANSMED | Microsoft PowerPoint ... | Links | 10.01



# Gene Cards: compounds for ACLY

ACLY Gene - GeneCards | ACLY Protein | ACLY Antibody - Mozilla Firefox

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http://www.genecards.org/cgi-bin/carddisp.pl?gene=ACLY&search=ACLY

Most Visited Customize Links Link to University's ho...

Search Ask Facebook Amazon YouTube Weather BBC News BBC Sports Options

ACLY Gene - GeneCards | ACLY Prote...

Aldrich, Tocris Bioscience, HMDB, and/or Novoseek and Drugs according to DrugBank, Enzo Life Sciences PharmGKB, and/or TarThera  
[About This Section](#)

### 7 HMDB Compounds for ACLY NEW

| Compound               | Synonyms   | CAS #      | PubMed Ids |
|------------------------|--|------------|------------|
| ADP                    | adenosindiphosphorsaeure ( <a href="#">see all 8</a> )                   | 58-64-0    | --         |
| Acetyl-CoA             | S-Acetyl coenzyme A ( <a href="#">see all 13</a> )                       | 72-89-9    | --         |
| Adenosine triphosphate | 5'-(tetrahydrogen triphosphate) Adenosine ( <a href="#">see all 24</a> ) | 56-65-5    | --         |
| Citric acid            | 2-Hydroxy-1,2,3-propanetricarboxylate ( <a href="#">see all 20</a> )     | 77-92-9    | --         |
| Coenzyme A             | Acetoacetyl coenzyme A sodium salt ( <a href="#">see all 21</a> )        | 85-61-0    | --         |
| Oxalacetic acid        | 2-Ketosuccinate ( <a href="#">see all 20</a> )                           | 328-42-7   | --         |
| Phosphate              | NFB Orthophosphate ( <a href="#">see all 13</a> )                        | 14265-44-2 | --         |

[About this table](#)

**n|s**

### 10/28 Novoseek chemical compound relationships for ACLY gene ([see all 28](#))

| Compound                       | -log (P-Val) | Hits | PubMed IDs for Articles with Shared Sentences (# sentences)                          |
|--------------------------------|--------------|------|--|
| hydroxycitrate                 | 91           | 4    | 17476502 (1), 11319829 (1), 20372858 (1)   |
| (-)-hydroxycitrate             | 89.1         | 3    | 2176080 (1), 11101469 (1)  |
| acetyl-coa                     | 84           | 26   | 14681844 (2), 8207683 (1), 7911658 (1), 11171136 (1) ( <a href="#">see all 21</a> )  |
| citrate                        | 77.7         | 31   | 17928289 (2), 1765100 (2), 8207683 (1), 9820262 (1) ( <a href="#">see all 21</a> )   |
| oxaloacetate                   | 69.9         | 7    | 7669753 (2), 11171137 (1), 1675605 (1), 18922930 (1)                                 |
| phosphohistidine               | 69.2         | 2    | 1371749 (1)  |
| pyruvate                       | 62.2         | 14   | 8999918 (3), 17928289 (2), 11171136 (1), 7616129 (1) ( <a href="#">see all 10</a> )  |
| fatty acid                     | 62.1         | 26   | 10410463 (3), 8999918 (3), 15869874 (1), 17476502 (1) ( <a href="#">see all 15</a> ) |
| 6-phosphogluconate             | 60.9         | 2    | 14605988 (1), 8355562 (1)  |
| 3-hydroxy-3-methylglutaryl-coa | 57.8         | 7    | 8999918 (2), 18774944 (1), 19389950 (1)  |

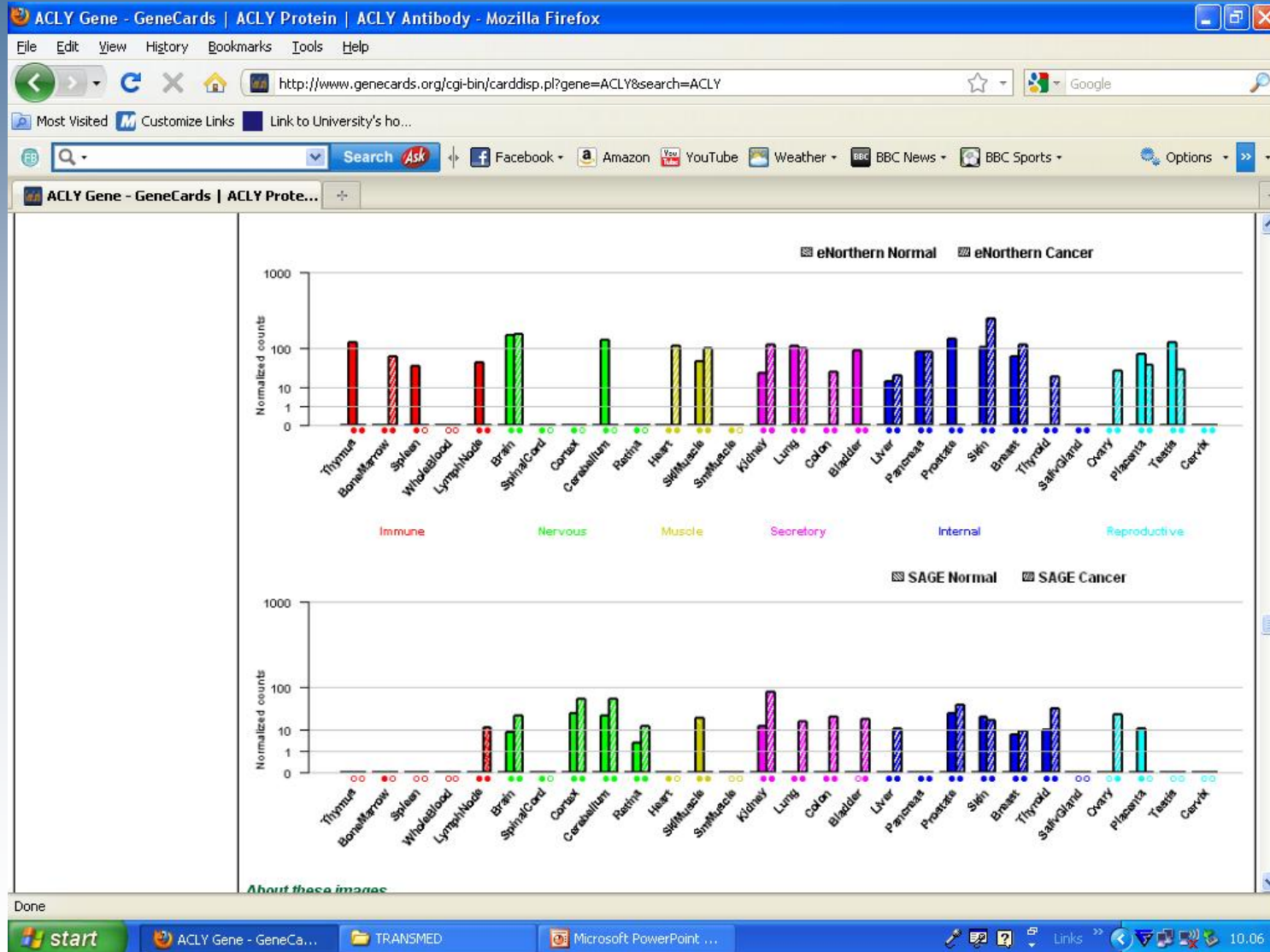
[About this table](#)

Done

start ACLY Gene - GeneCa... TRANSMED Microsoft PowerPoint ... 10.03



# Gene Cards: expression in tissues and disease



# OMIM: [www.ncbi.nlm.nih.gov/omim](http://www.ncbi.nlm.nih.gov/omim)

The screenshot shows a Mozilla Firefox browser window displaying the OMIM (Online Mendelian Inheritance in Man) website. The search results for 'ATP CITRATE LYASE; ACLY' are shown. A red box highlights the MIM ID \*108728 and the gene name. The page includes a search bar, navigation tabs (All Databases, PubMed, Nucleotide, Protein, Genome, Structure, PMC, OMIM), and a detailed description of the enzyme. The description states that ATP citrate lyase is the primary enzyme responsible for the synthesis of cytosolic acetyl-CoA in many tissues. It is a tetramer with a relative molecular weight of approximately 440,000. The enzyme catalyzes the formation of acetyl-CoA and oxaloacetate from citrate and CoA, with a concomitant hydrolysis of ATP to ADP and phosphate. The product, acetyl-CoA, serves several important biosynthetic pathways, including lipogenesis and cholesterol synthesis. In nervous tissue, ATP citrate-lyase may be involved in the biosynthesis of acetylcholine.

**MIM ID \*108728**  
**ATP CITRATE LYASE; ACLY**

*Alternative titles; symbols*  
CLATP  
ATPCL  
ACL

Gene map locus: [17q21.1](#)

**Description**  
ATP citrate lyase is the primary enzyme responsible for the synthesis of cytosolic acetyl-CoA in many tissues. The enzyme is a tetramer (relative molecular weight approximately 440,000) of apparently identical subunits. It catalyzes the formation of acetyl-CoA and oxaloacetate from citrate and CoA with a concomitant hydrolysis of ATP to ADP and phosphate. The product, acetyl-CoA, serves several important biosynthetic pathways, including lipogenesis and cholesterol synthesis. In nervous tissue, ATP citrate-lyase may be involved in the biosynthesis of acetylcholine.

**Cloning**  
Cloning of cDNAs has been reported for murine (Sul et al., 1984), rat (Elshourbagy et al., 1990), and human (Elshourbagy et al., 1992) ATP citrate lyase. Elshourbagy et al. (1992) found that the subunits of the enzyme have 1,105 amino acids and a calculated molecular mass of 121,419 Da. The human and rat ATPCL cDNAs showed 96.3% amino acid identity.

**Gene Function**

**Table of Contents**  
MIM \*108728  
Description  
Cloning  
Gene Function  
Mapping  
References  
Contributors  
Creation Date  
Edit History

**Links**  
Selected Gene Related Links  
G Entrez Gene  
N Nomenclature  
R RefSeq  
G GenBank  
P Protein  
U UniGene  
Other NCBI Links  
BioSystems  
GEO Profiles  
Gene  
Gene Genotype  
GeneView in dbSNP  
HomoloGene

# ChEBI: Chemical Entities of Biological Interest

[www.ebi.ac.uk/chebi/](http://www.ebi.ac.uk/chebi/)

Chemical Entities of Biological Interest (ChEBI) - Mozilla Firefox

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http://www.ebi.ac.uk/chebi/advancedSearchFT.do?searchString=ACLY&queryBean.stars=3&queryBean.star...

Most Visited Customize Links Link to University's ho...

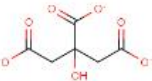
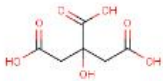
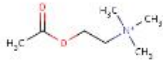
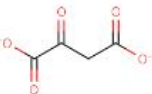
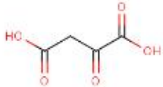
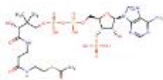
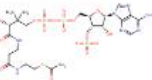
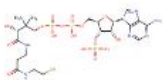
Search Ask Facebook Amazon YouTube Weather BBC News BBC Sports Options

Chemical Entities of Biological I... Mining metabolites: extracting the ye... Mining metabolites: extracting the ye... Mail :: Inbox

Preferences Contact ChEBI Printer Friendly View

**ACLY search** Download your search results: [Tab-delimited](#), [XML](#), [SDF](#)

46 entries found, displaying 1 to 15. << < 1 2 3 4 >>

|  |   |   |
|--|---|---|
| <a href="#">CHEBI:50744</a> citrate salt   |    |    |
|  | <a href="#">CHEBI:16947</a> citrate(3-)   | <a href="#">CHEBI:30769</a> citric acid   |
|    |    |    |
| <a href="#">CHEBI:15355</a> acetylcholine  | <a href="#">CHEBI:16452</a> oxaloacetate(2-)  | <a href="#">CHEBI:30744</a> oxaloacetic acid  |
|  |  |  |
| <a href="#">CHEBI:15351</a> acetyl-CoA   | <a href="#">CHEBI:57288</a> acetyl-CoA(4-)  | <a href="#">CHEBI:15346</a> coenzyme A  |

Done

start TRANSMED Microsoft PowerPoint ... Chemical Entities of Bi... Links 10.24

# HMDB: Human Metabolome Database

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## Human Metabolome Database Version 3.0



Search:

Search type: Metabolites

[\[Advanced\]](#)

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 ( $> 1 \mu\text{M}$ ) or relatively rare ( $< 1 \text{nM}$ ). 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

[www.hmdb.ca/](http://www.hmdb.ca/)




# 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<br><small>Locus</small> | Name                 | Type   | Metabolites   |
|--------------------------------------|-----------------------------------|----------------------|--------|---|
| P53396<br><a href="#">EnzymeCard</a> | ACLY<br>17q21.2                   | ATP-citrate synthase | Enzyme | <div style="border: 1px solid red; padding: 2px;"> <a href="#">Acetyl-CoA</a> </div> <a href="#">Oxalacetic acid</a><br><a href="#">Citric acid</a><br><a href="#">Coenzyme A</a><br><a href="#">Adenosine triphosphate</a><br>ADP<br>Phosphate |
| P53396<br><a href="#">EnzymeCard</a> | ACLY<br>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.

HMDB Version: 3.0 — [Contact us](#) | ©2005-2012 [Genome Alberta](#)

# HMDB: Human Metabolome Database

## Showing metabocard for Acetyl-CoA (HMDB01206)

Legend: metabolite field enzyme field

[Show XML](#) [Show Similar Structure](#)

### Record Information

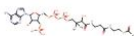
|                             |                           |
|-----------------------------|---------------------------|
| Version                     | 3.0                       |
| Creation Date               | 2005-11-16 08:48:42 -0700 |
| Update Date                 | 2009-05-05 14:58:35 -0600 |
| 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=ZSLZBFDCINBPY-ZSJKINUSA-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)

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

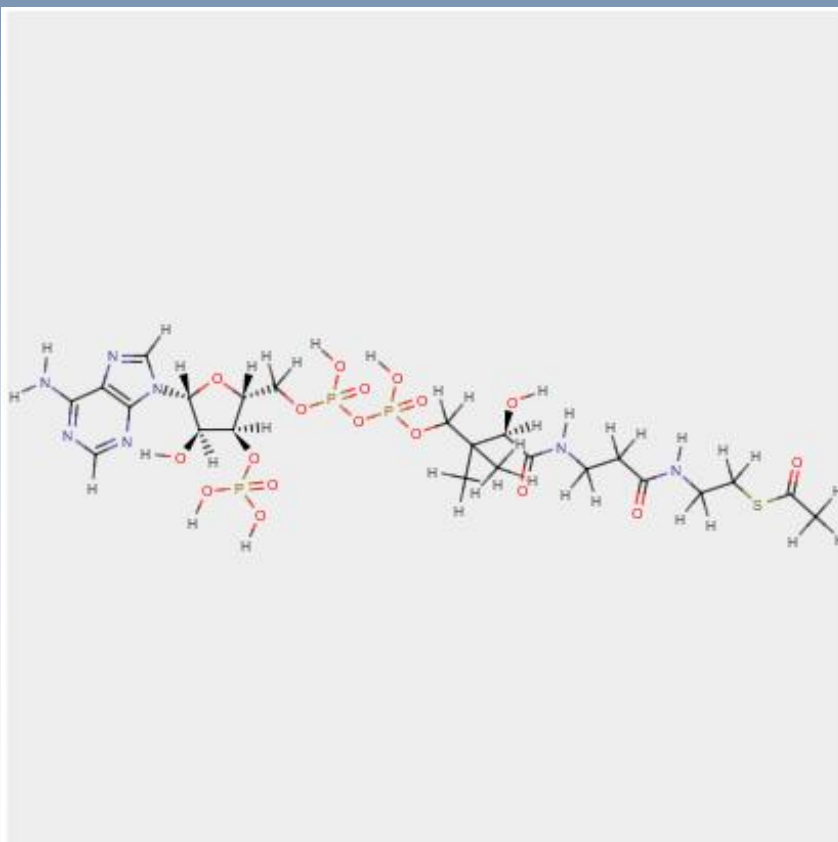
Status Detected and not quantified

Origin Endogenous  
Food

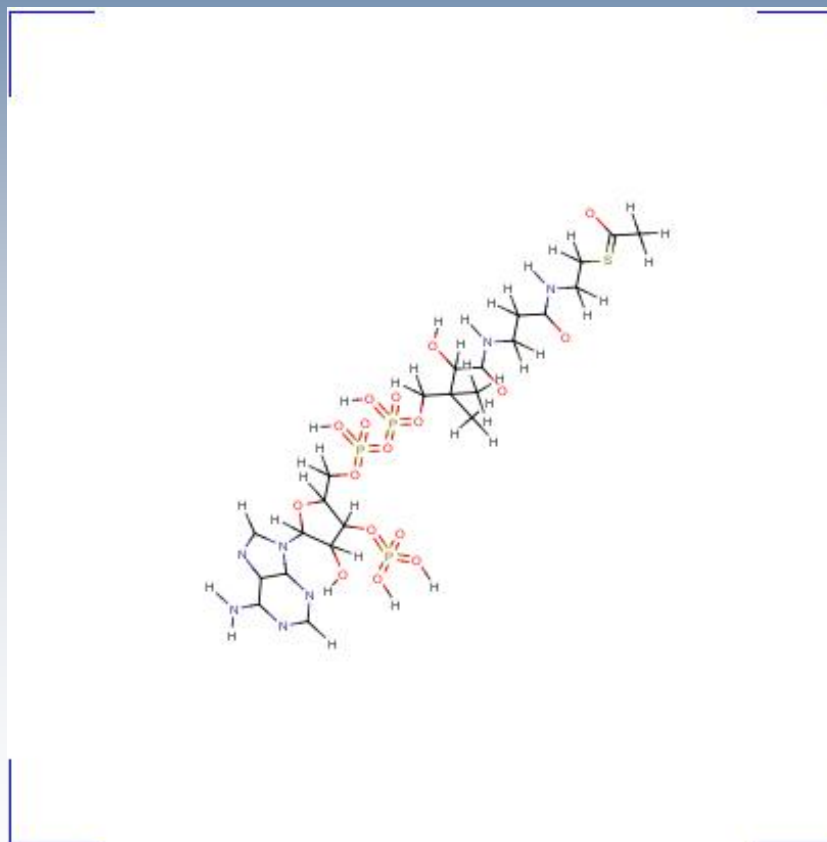
Cell signaling  
Component of Alanine and acetate metabolism

# HMDB: Human Metabolome Database

2D-structure of Acetyl CoA



3D-structure of Acetyl CoA



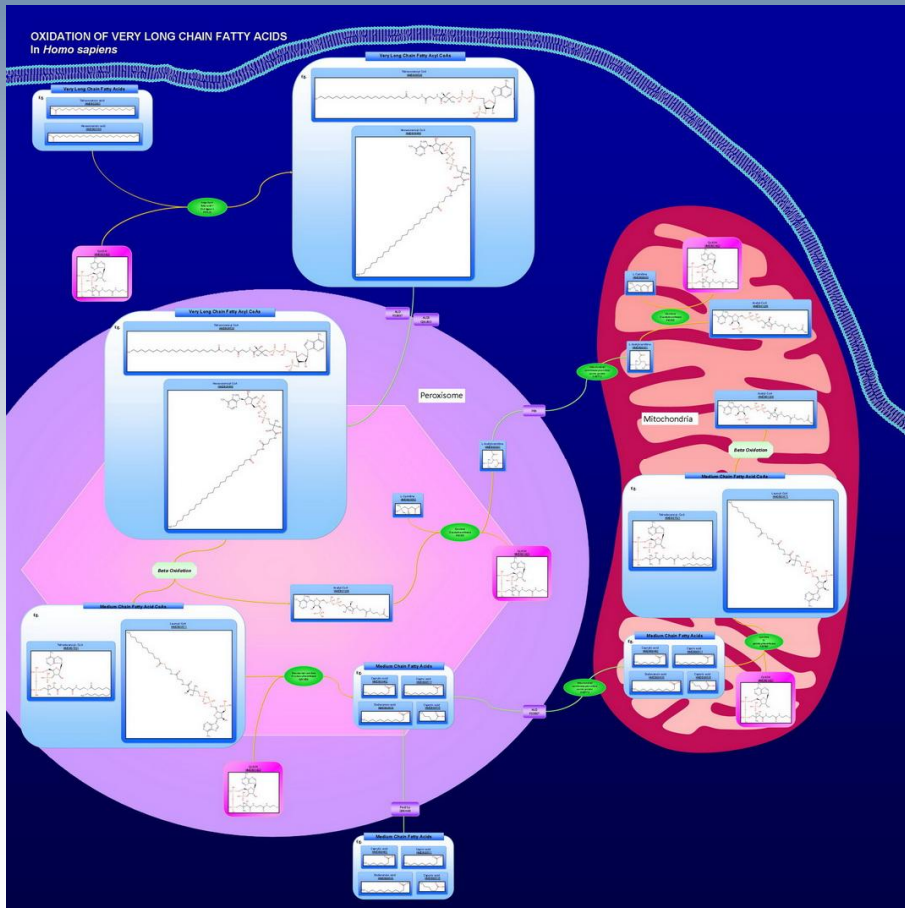
# HMDB: Human Metabolome Database

|  |  |                          |                          |
|--|--|--------------------------|--------------------------|
|  | nucleus  |                          |                          |
|  | peroxisome   |                          |                          |
| Biofluid Locations                       | Not Available  |                          |                          |
| Tissue Location                          | Adipose Tissue   |                          |                          |
|  | Brain  |                          |                          |
|  | Muscle   |                          |                          |
|  | Platelet   |                          |                          |
|  | Prostate   |                          |                          |
|  | Skeletal Muscle  |                          |                          |
|  | Spleen   |                          |                          |
| Pathways                                 | <b>Name</b>  | <b>SMPDB Link</b>        | <b>KEGG Link</b>         |
|  | Amino Sugar Metabolism   | <a href="#">SMP00045</a> | <a href="#">map00520</a> |
|  | Beta Oxidation of Very Long Chain Fatty Acids                      | <a href="#">SMP00052</a> | <a href="#">map01040</a> |
|  | Beta-Alanine Metabolism  | <a href="#">SMP00007</a> | <a href="#">map00410</a> |
|  | Butyrate Metabolism  | <a href="#">SMP00073</a> | <a href="#">map00650</a> |
|  | Citric Acid Cycle  | <a href="#">SMP00057</a> | <a href="#">map00020</a> |
|  | Ethanol Degradation  | <a href="#">SMP00449</a> | Not Available            |
|  | Fatty Acid Biosynthesis  | <a href="#">SMP00456</a> | Not Available            |
|  | Fatty acid Metabolism  | <a href="#">SMP00051</a> | <a href="#">map00071</a> |
|  | Glycine and Serine Metabolism                                      | <a href="#">SMP00004</a> | <a href="#">map00260</a> |
|  | Ketone Body Metabolism   | <a href="#">SMP00071</a> | <a href="#">map00072</a> |
|  | Lysine Degradation   | <a href="#">SMP00037</a> | <a href="#">map00310</a> |
|  | Mitochondrial Beta-Oxidation of Long Chain Saturated Fatty Acids   | <a href="#">SMP00482</a> | Not Available            |
|  | Mitochondrial Beta-Oxidation of Medium Chain Saturated Fatty Acids | <a href="#">SMP00481</a> | Not Available            |
|  | Mitochondrial Beta-Oxidation of Short Chain Saturated Fatty Acids  | <a href="#">SMP00480</a> | Not Available            |
|  | Oxidation of Branched Chain Fatty Acids                            | <a href="#">SMP00030</a> | Not Available            |
|  | Phytanic Acid Peroxisomal Oxidation                                | <a href="#">SMP00450</a> | Not Available            |
|  | Propanoate Metabolism  | <a href="#">SMP00016</a> | <a href="#">map00640</a> |
|  | Pyruvate Metabolism  | <a href="#">SMP00060</a> | <a href="#">map00620</a> |
|  | Steroid Biosynthesis   | <a href="#">SMP00023</a> | <a href="#">map00100</a> |
|  | Transfer of Acetyl Groups into Mitochondria                        | <a href="#">SMP00466</a> | Not Available            |
|  | Valine, Leucine and Isoleucine Degradation                         | <a href="#">SMP00032</a> | <a href="#">map00280</a> |
|  | <b>Normal Concentrations</b>                                       |                          |                          |
|  | Not Available  |                          |                          |
| <b>Abnormal Concentrations</b>           |  |                          |                          |
|  | Not Available  |                          |                          |
| <b>Associated Disorders and Diseases</b> |  |                          |                          |
|  | ..   |                          |                          |

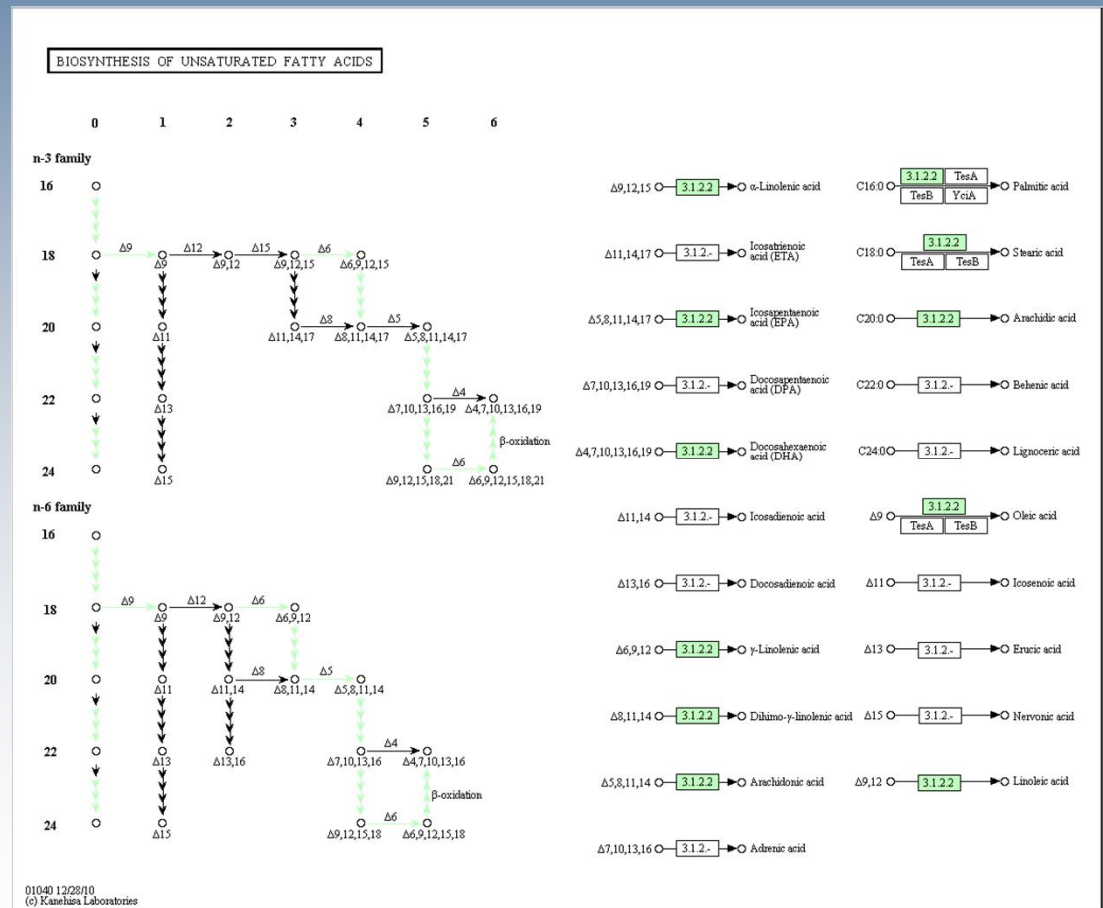


# HMDB: Human Metabolome Database

## 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 1962  
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:  
1877 pathways  
from 2263  
organisms

**ABOUT BIOCYC**

BioCyc is a collection of 1962 Pathway/Genome Databases (PGDBs). Each PGDB in the BioCyc collection describes the genome and metabolic pathways of a single organism. The BioCyc Web site contains many tools for navigating, visualizing, and analyzing these databases, and for analyzing omics data, including the following:

- Genome browser
- Display of individual metabolic pathways, and of full metabolic maps
- Visual analysis of user-supplied omics datasets by painting onto metabolic maps, regulatory maps, and genome maps
- Enrichment analysis of omics datasets
- Store groups of genes and pathways in your account; share, analyze, transform those groups
- Comparative analysis tools

**New to BioCyc? Typical usage:**

- Select a database [genome] to search by clicking "change organism database" at top right
- Enter a gene name or pathway name in the box at top right and click Quick Search

Windows users: We strongly suggest you use Firefox instead of Internet Explorer to interact with this web site [more]. To learn more about BioCyc, read the [Introduction to BioCyc](#) or watch our [Instructional videos](#).

**BIOCYC SOFTWARE: PATHWAY TOOLS**

The downloadable version of BioCyc that includes the [Pathway Tools](#) software provides more speed and power than the BioCyc Web site [more], and allows you to create your own PGDBs and build metabolic flux models. Multiple database configurations are available with Pathway Tools including multiple *E. coli* and *Shigella* genomes, multiple *Bacillus* genomes, multiple *Mycobacterium* genomes, and multiple mammalian genomes.

**BIOCYC PATHWAY/GENOME DATABASES**

The BioCyc databases are divided into three tiers, based on their quality. Tier 1 databases have received person-decades of literature-based curation, and are the most accurate. Tier 2 and Tier 3 databases contain computationally predicted metabolic pathways, predictions as to which genes code for missing enzymes in metabolic pathways, and predicted operons. PGDBs for many other organisms are available outside the BioCyc collection, created by other users of Pathway Tools [more].

**BioCyc Tier 1: Intensively Curated Databases**

| DATABASE | SCOPE   | HIGHLIGHTS   | ORGANIZATION                      |
|----------|---|--|-----------------------------------|
| EscoCyc  | <i>Escherichia coli</i> K-12 MG1625 Model Organism Database | <ul style="list-style-type: none"> <li>• Literature curation of complete genome</li> <li>• Information from 23,382 publications</li> <li>• Transcriptional regulatory network</li> <li>• Flux-balance metabolic model</li> </ul> | <a href="#">SRI International</a> |
| MetaCyc  | Multispecies  | <ul style="list-style-type: none"> <li>• 1,877 metabolic pathways</li> </ul>   | <a href="#">SRI International</a> |

# ChemSpider: the free chemical database

<http://www.chemspider.com/>

ChemSpider | Citrate | C6H5O7 - Mozilla Firefox

File Edit View History Bookmarks Tools Help

http://www.chemspider.com/Chemical-Structure.29081.html?rid=5e110d65-ed06-4ff1-83ce-b2df5dd6fd0d

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HMDB: Showing Acetyl-CoA (HMDB01... ChemSpider | Citrate | C6H5O7 Mining metabolites: extracting the ye... Mail: Inbox

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**ChemSpider**  
The free chemical database

RSC | Advancing the Chemical Sciences

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Search term: Citrate (Found by approved synonym)

**Citrate**

ChemSpider ID: **29081**

Molecular Formula: C<sub>6</sub>H<sub>5</sub>O<sub>7</sub>

Monoisotopic mass: 189.005 Da

▼ Systematic name  
2-hydroxypropane-1,2,3-tricarboxylate

▶ SMILES and InChIs

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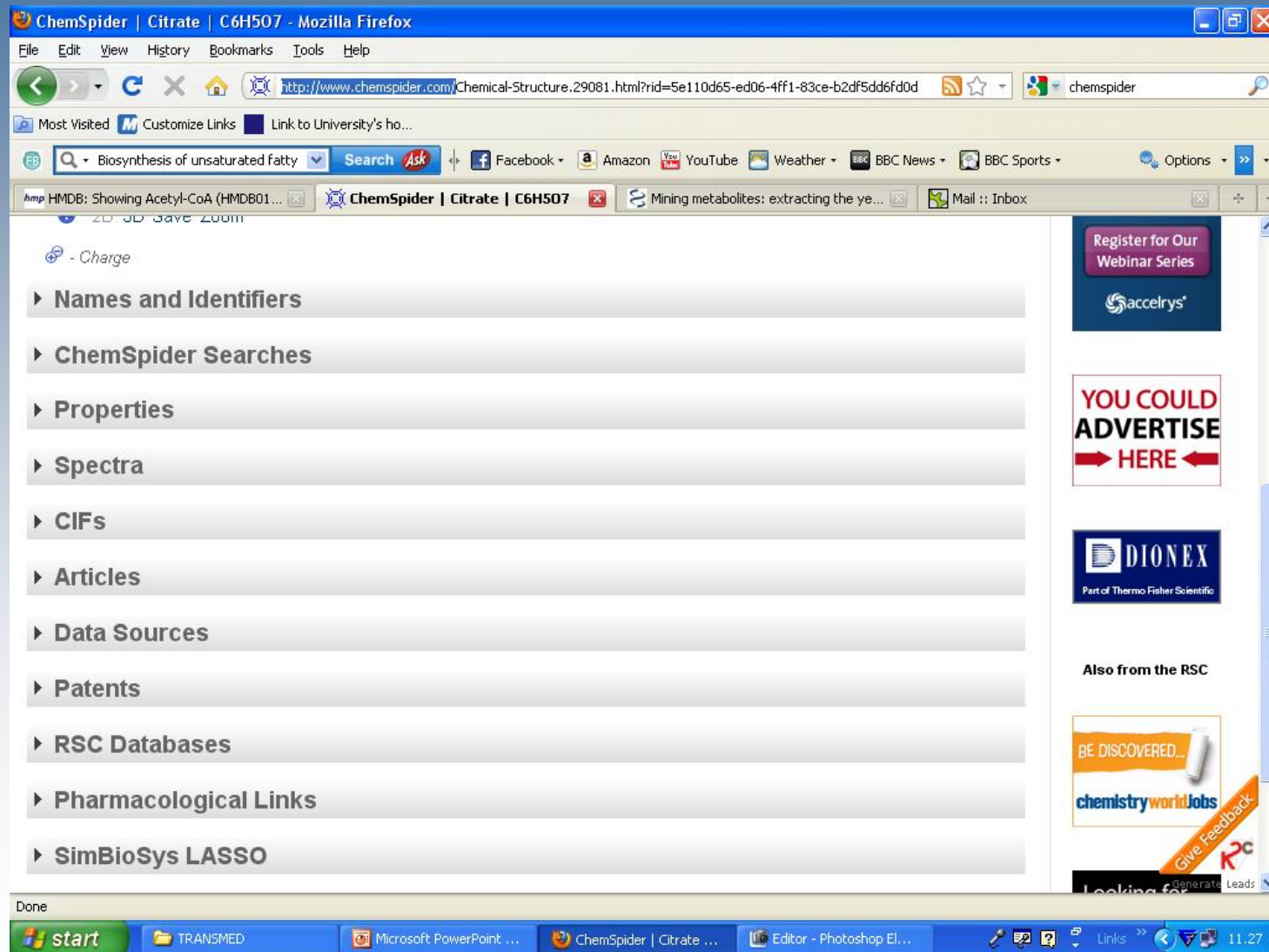
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## ChemSpider: the free chemical database

<http://www.chemspider.com/>



ChemSpider | Citrate | C<sub>6</sub>H<sub>5</sub>O<sub>7</sub> - Mozilla Firefox

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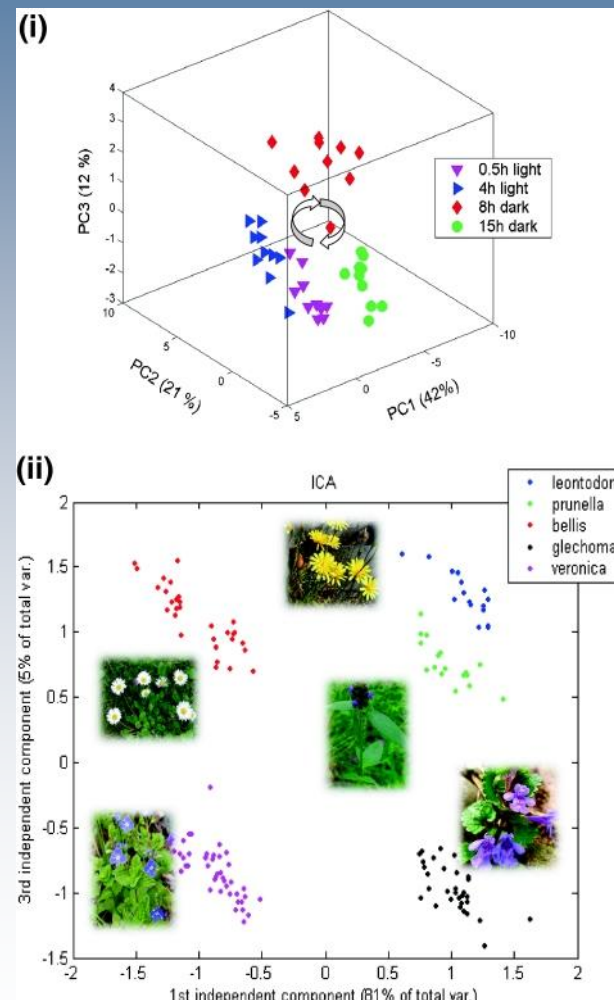
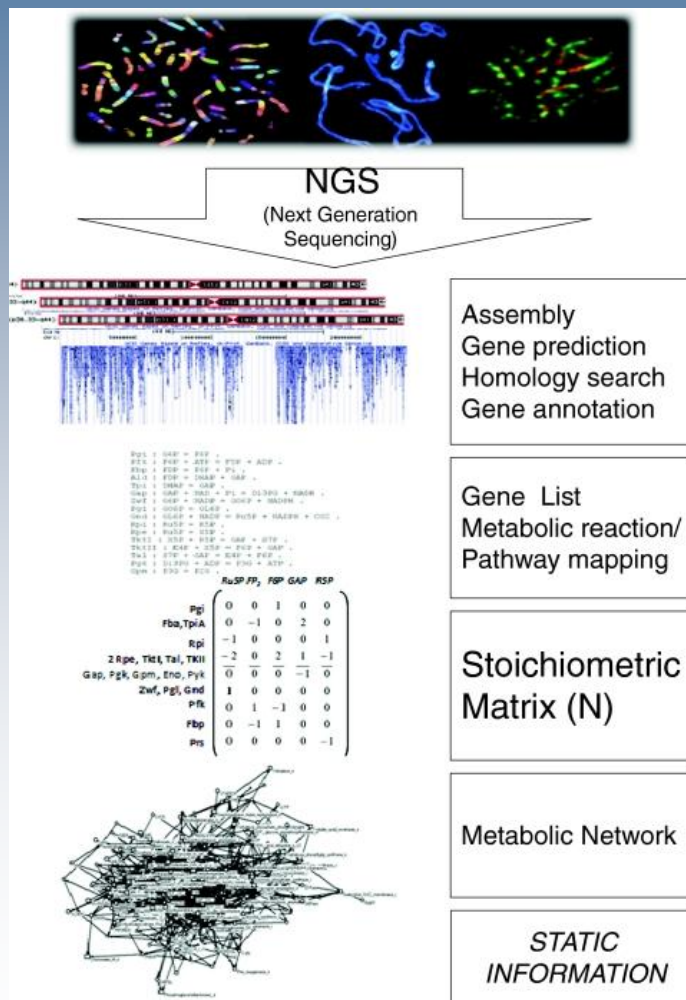
Give Feedback

Looking for Leads

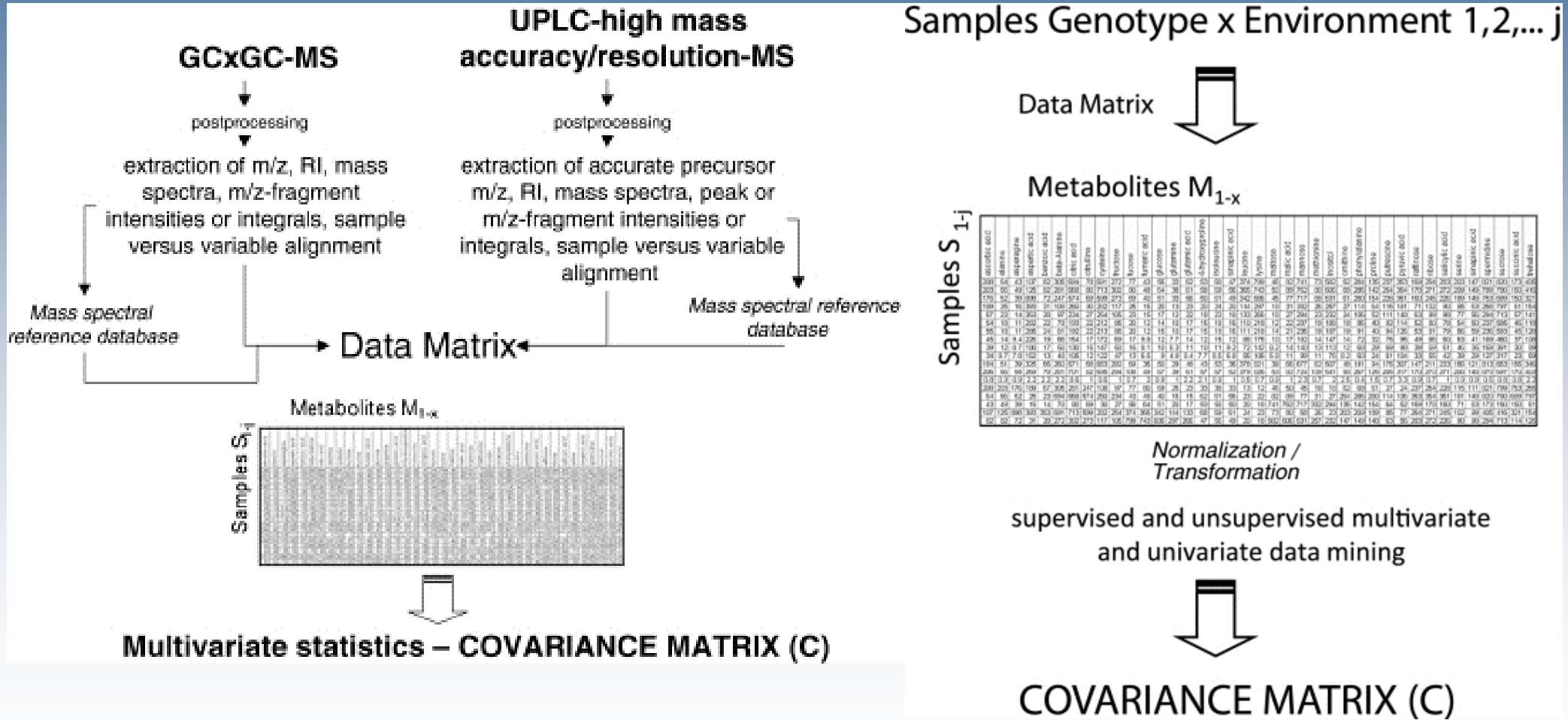
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# Unpredictability of metabolism--the key role of metabolomics science in combination with next-generation genome sequencing



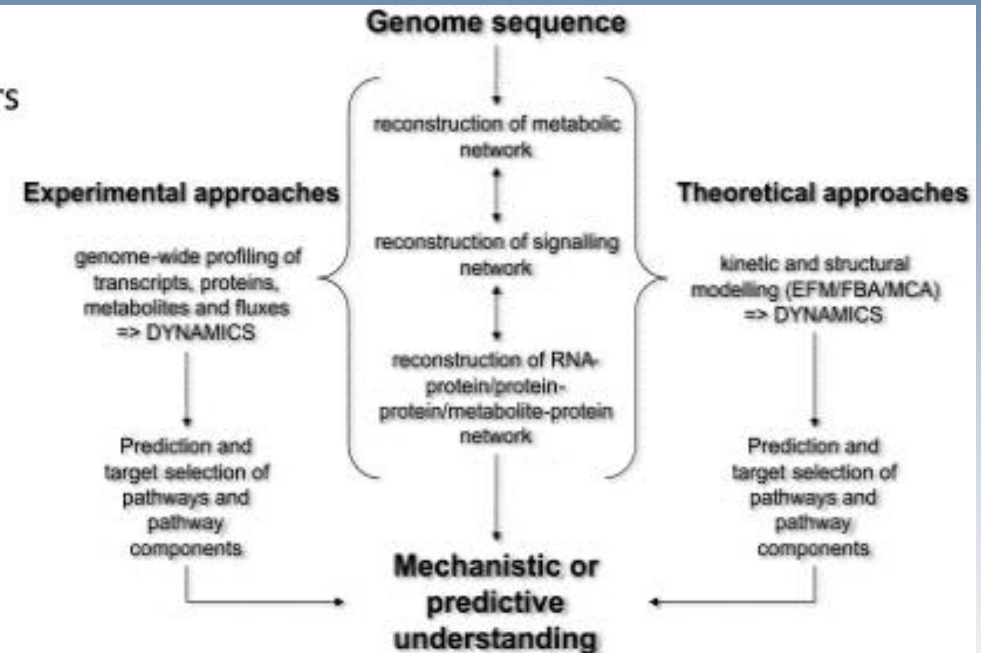
# Unpredictability of metabolism--the key role of metabolomics science in combination with next-generation genome sequencing



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

## Metabolomics experiment

Metabolite profiling, biomedical diagnostics, physiological markers



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.

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



Metabolic networks from 50 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



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

