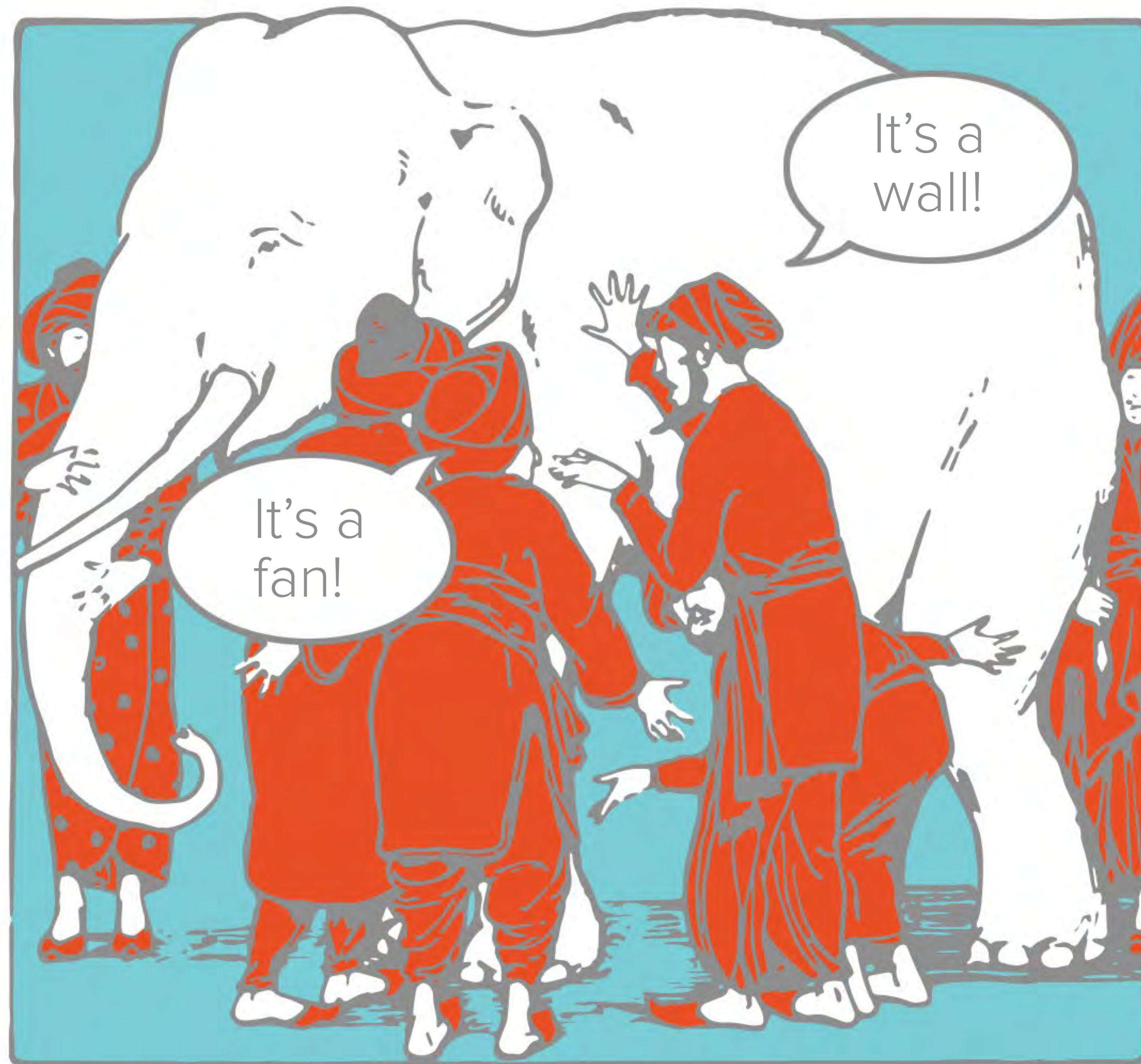


Introduction to Systems Biology

- Definitions and fundamental concepts
- Tools for Systems Biology analysis – overview
- Pathway Analysis: overview
- Gene Ontology Analysis: overview
- Public on-line resources – hands-on



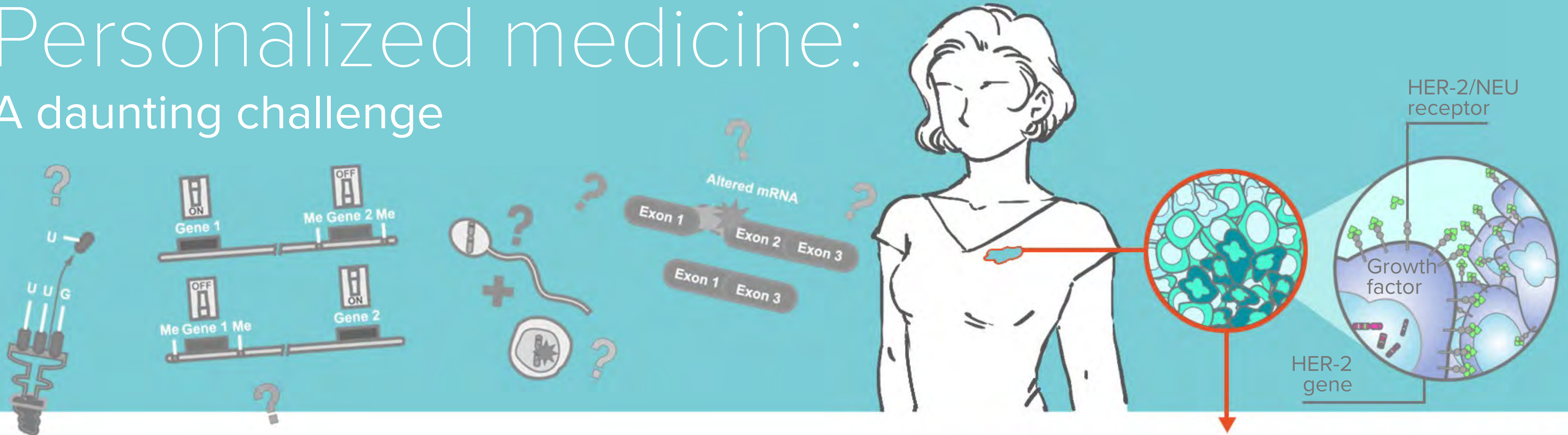
Blind men & the Elephant

It's a snake!

It's a wall!

It's a fan!

It's a rope!



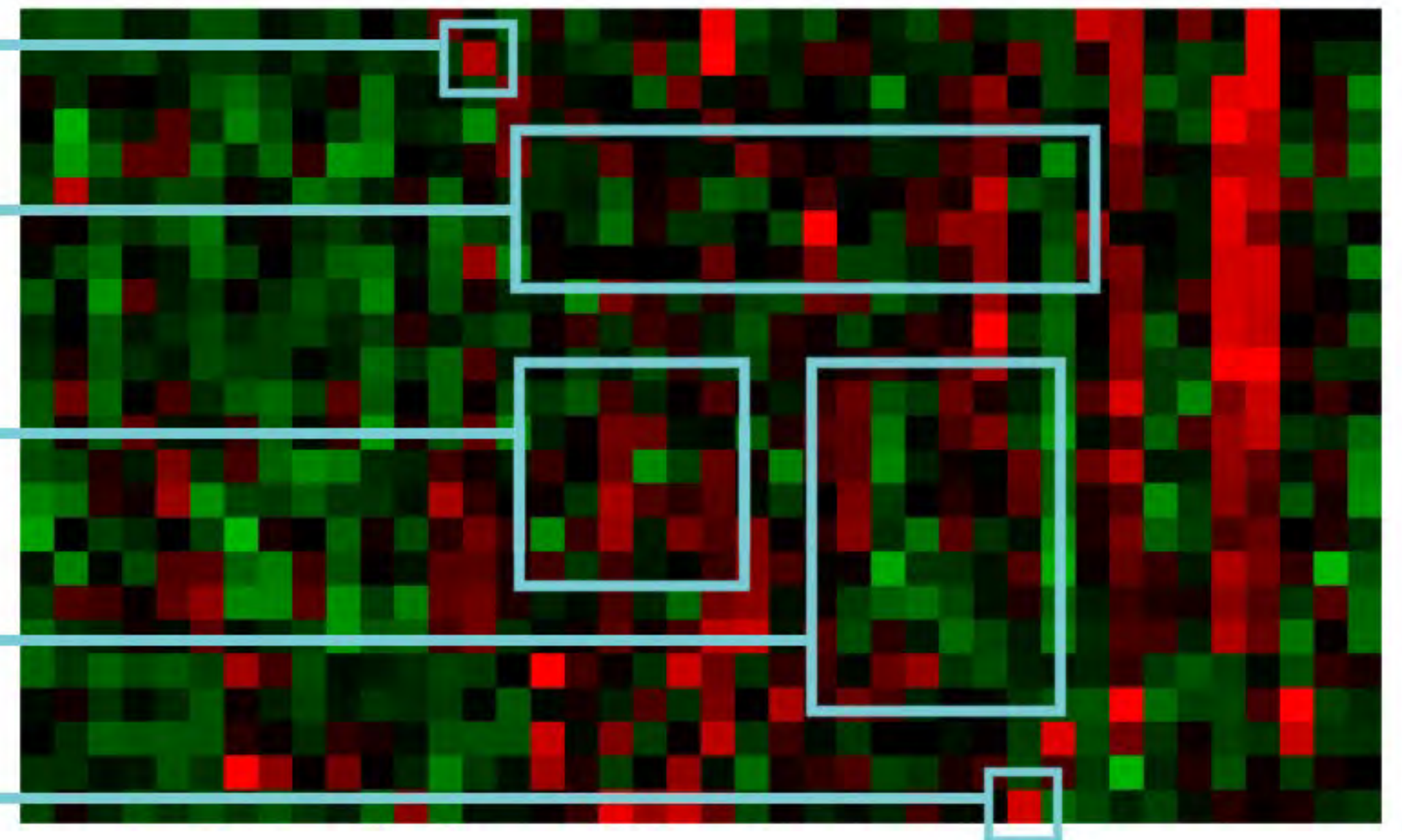
Growth receptor present

High risk of relapse

Not good candidate for conventional therapy

Mutated susceptibility genes

Vascular markers present



Systems Biology – Definitions

To understand complex biological systems requires the integration of experimental and computational research — in other words a systems biology approach. (Kitano, 2002)

Systems biology studies biological systems by systematically perturbing them (biologically, genetically, or chemically); monitoring the gene, protein, and informational pathway responses; integrating these data; and ultimately, formulating mathematical models that describe the structure of the system and its response to individual perturbations. (Ideker et al, 2001)

[...]the objective of systems biology [can be] defined as the understanding of network behavior, and in particular their dynamic aspects, which requires the utilization of mathematical modeling tightly linked to experiment. (Cassman, 2005)

Systems Biology – Definitions

By discovering how function arises in dynamic interactions, systems biology addresses the missing links between molecules and physiology. Top-down systems biology identifies molecular interaction networks on the basis of correlated molecular behavior observed in genome-wide “omics” studies. Bottom-up systems biology examines the mechanisms through which functional properties arise in the interactions of known components. (Bruggeman and Westerhoff, 2007)

Systems Biology – Definitions

Systems biology is the study of systems of biological components, which may be molecules, cells, organisms or entire species.

Living systems are dynamic and complex, and their behavior may be hard to predict from the properties of individual parts.

To study them, we use quantitative measurements of the behavior of groups of interacting components, systematic measurement technologies such as genomics, bioinformatics and proteomics, and mathematical and computational models to describe and predict dynamical behavior.

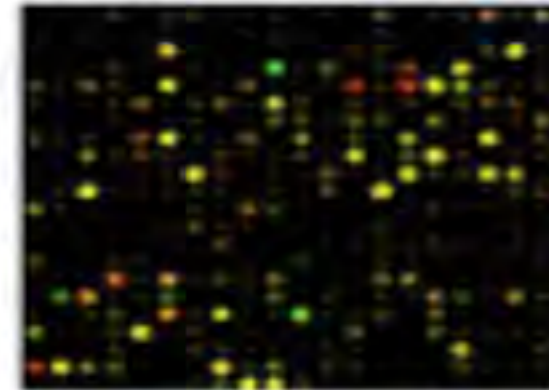
Systems problems are emerging as central to all areas of biology and medicine.

- Dep. Systems Biology, Harvard University

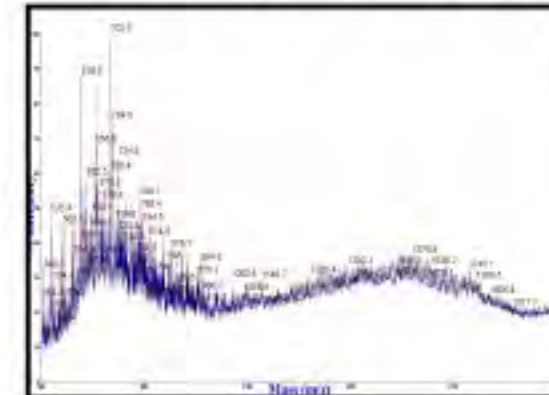
Systems Biology / Integrative Bioinformatics

DATA

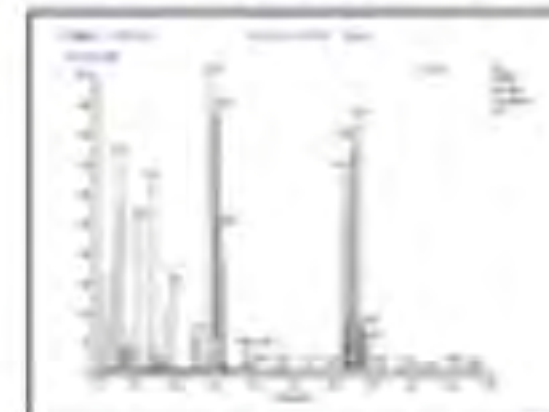
Gene Expression



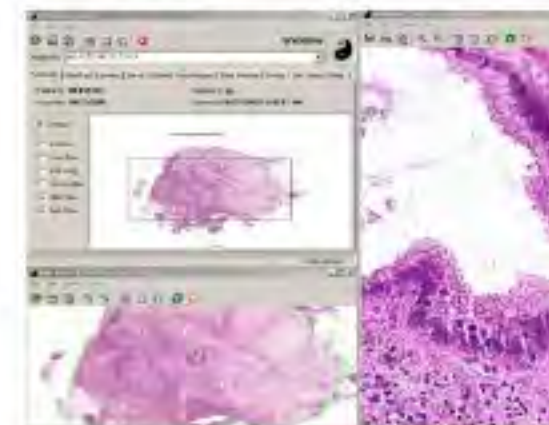
Proteome Profiling



Metabolomics

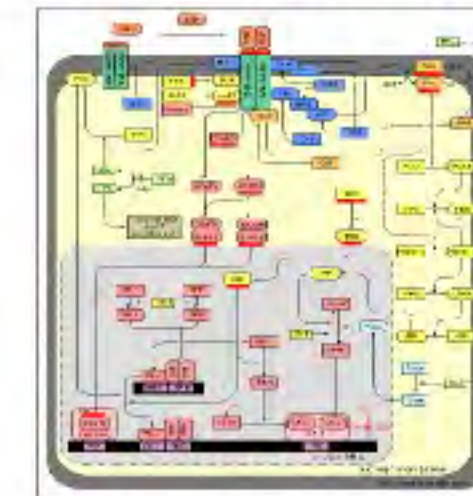


Histo-Morphometry



MODELS

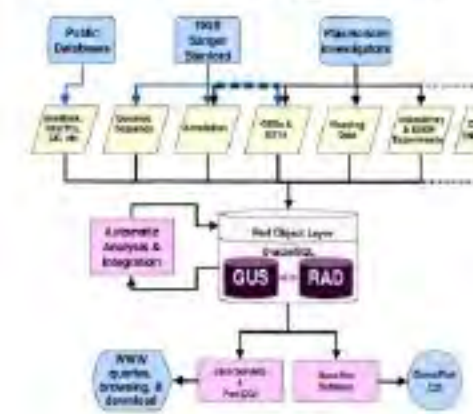
Pathway Linkage



Network Models



Knowledge Bases



DISCOVERY

Disease

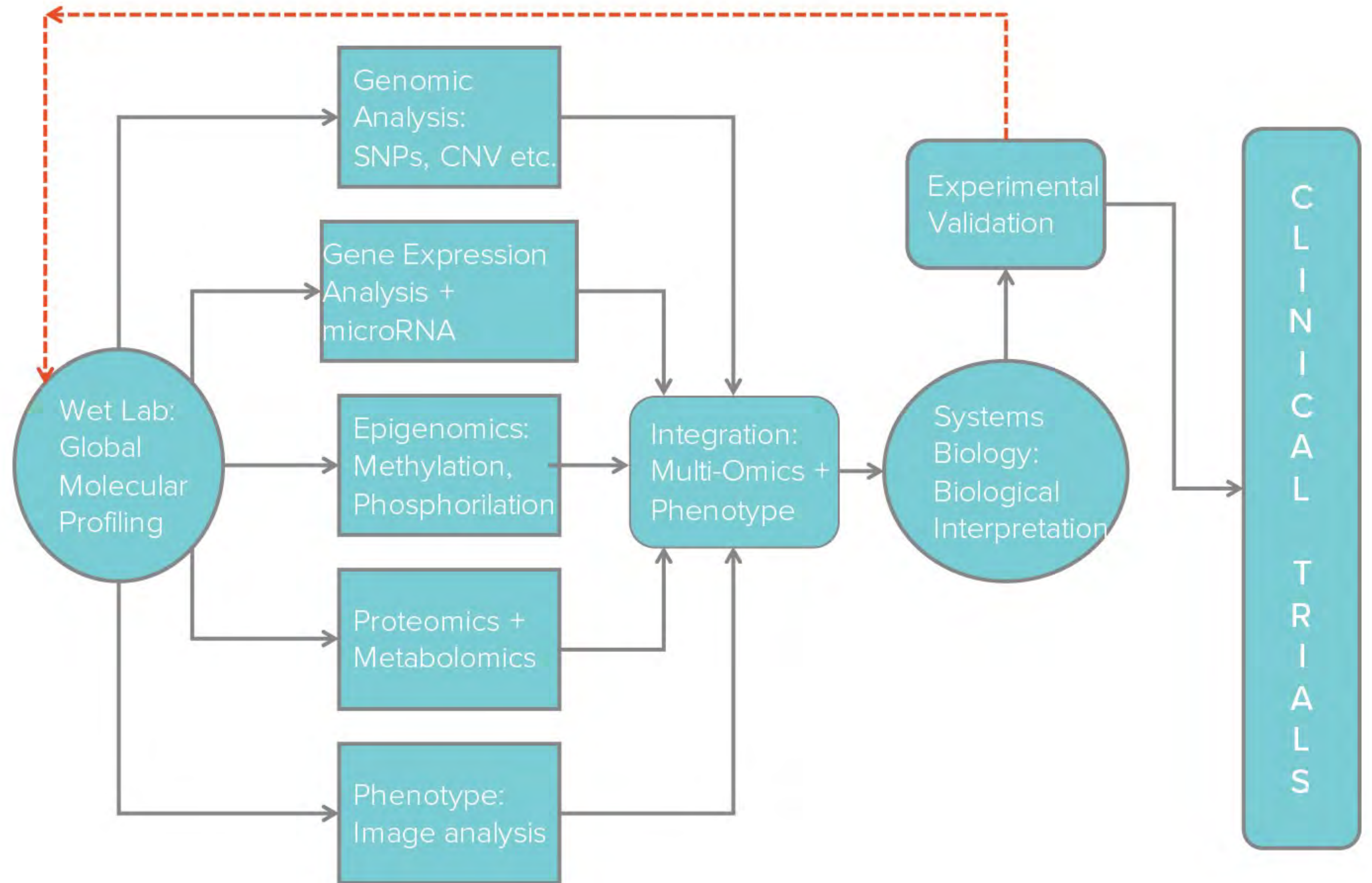


- Biomarkers
- Toxicology
- Diagnostics
- Disease Staging
- Drug Targets
- Drug Discovery
- Clinical Trials

Animal Models



How does it all fit together?



Systems Biology Methods/ Analysis tools

Pathway Analysis

Biological Pathways/ Signaling Pathways - overview

Bioinformatics Tools and Resources for Pathway Analysis

Pathway Studio (Ariadne/Elsevier)

GeneGo (Thomson Scientific/Reuters)

Ingenuity Pathway Analysis IPA (Ingenuity Systems)

Applications: micro-array and other omics- data analysis and text mining

Gene Ontology – GO Enrichment Analysis

Biological Interactions Networks

From Pathways and Networks to Biological Interpretation

Pathway Resources Central

Pathguide» the pathway resource list

Navigation

Protein-Protein Interactions

Metabolic Pathways

Signaling Pathways

Pathway Diagrams

Transcription Factors / Gene Regulatory Networks

Protein-Compound Interactions

Genetic Interaction Networks

Protein Sequence Focused

Other

Search

Organisms

All

Availability

All

Standards

All

Reset

Search

Analysis

Statistics

Database Interactions

Contact

Comments, Questions, Suggestions are Always Welcome!

Complete Listing of All Pathguide Resources

Pathguide contains information about **547** biological pathway related resources and molecular interaction related resources. Click on a link to go to the resource home page or 'Details' for a description page. Databases that are free and those supporting BioPAX, CellML, PSI-MI or SBML standards are respectively indicated.

If you know of a pathway resource that is not listed here, or have other questions or comments, please [send us an e-mail](#).

Protein-Protein Interactions

Database Name (Order: alphabetically | [by web popularity](#))

	Full Record	Details
2P2Idb - The Protein-Protein Interaction Inhibition Database		Details
3D-Interologs - 3D-Interologs		Details
3DID - 3D interacting domains		Details
ADAN - Prediction of protein-protein interaction of modular domains		Details
AHD2.0 - Arabidopsis Hormone Database 2.0		Details
AlFuse - Functional Associations of Proteins in Complete Genomes		Details
aMAZE - Protein Function and Biochemical Pathways Project		Details
ANAP - Arabidopsis Network Analysis Pipeline		Details
AnimalTFDB - Animal Transcription Factor Database		Details
AntiJen - AntiJen a Kinetic, Thermodynamic and Cellular Database		Details
APID - Agile Protein Interaction DataAnalyzer		Details
AS-ALPS - Alternative Splicing - induced ALteration of Protein Structure		Details
ASD - Allosteric Database		Details
ASEdb - Alanine Scanning Energetics Database		Details
ASPD - Artificial Selected Proteins/Peptides Database		Details
ATDB - Animal Toxin Database		Details
AtPID - Arabidopsis thaliana Protein Interactome Database		Details
AtPIN - Arabidopsis thaliana Protein Interactome Network		Details
Bacteriome.org - Bacterial Protein Interaction Database for Escherichia Coli		Details

Home

BioPAX

Note that some enumerations, such as the resources under Availability, are exclusive while others, such as those under Tools, may count the same resource for every criteria it satisfies.

Unless otherwise noted, the values represent the number of resources that contain/satisfy the specified data/criteria.

The "Contents" section also includes values denoted as "Totals". This is a simple summation and does not account for any overlaps in data between the resources.

News

Major new update August 2013
We now have info ~550 resources!

Visual navigation 2010
Click the 'Databases' link on the left menu

General

Total Resources	547
Resources with Primary Data Sources	277
Resources with Secondary Data Sources	258

Availability

Free to all users	422
Not currently available	69
Free to academic users	34
License purchase required	22

Data Access Methods

Keyword searches	437
Browsing / Canned queries	351
Download in other format	344
Download in BioPAX format	39
Download in PSI format	36
Download in SBML format	26
SQL queries	8
Download in CellML format	2

Tools

Pathway diagram tools	84
-----------------------	----

Organisms

Homo sapiens	171
Mus musculus	101
Saccharomyces cerevisiae	75
Rattus norvegicus	67
Drosophila melanogaster	67
Arabidopsis thaliana	61
Caenorhabditis elegans	59
Escherichia coli	40
Oryza sativa	20
Schizosaccharomyces pombe	18
Bos taurus	17
Danio rerio	17
Helicobacter pylori	15
Plasmodium falciparum	14
Bacillus subtilis	12
Xenopus laevis	8
Zea mays	7
Human immunodeficiency virus	6
Hepatitis C virus	5
Chlamydomonas reinhardtii	4
Dictyostelium discoideum	4
Mycoplasma pneumoniae	2

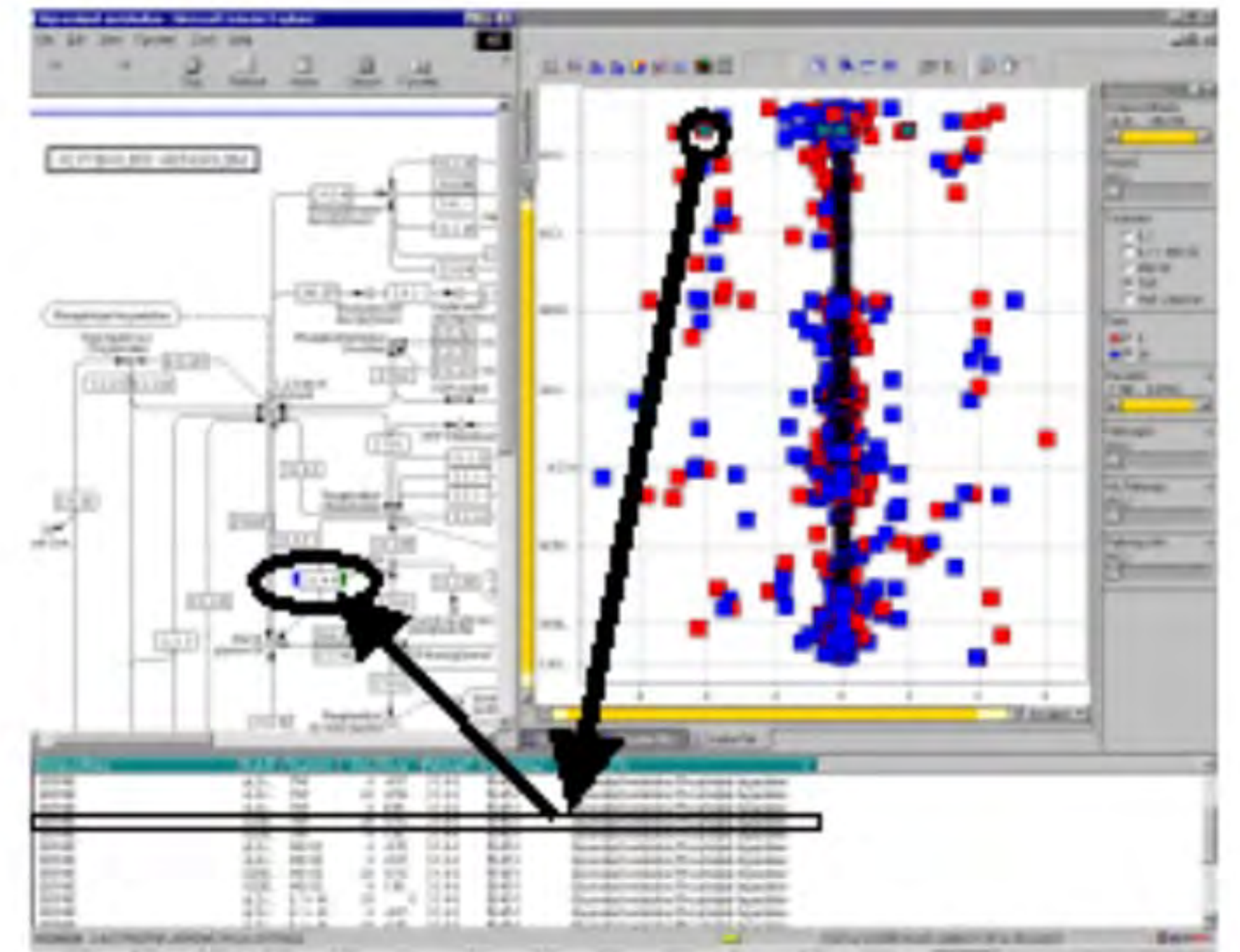
Contents

Resources containing small molecules	78
Total small molecules	33,680,655
Resources containing genes/proteins	277
Total genes/proteins	345,626,442
Resources containing interactions/reactions	261
Total interactions/reactions	1,311,363,048
Resources containing pathways	109
Total pathways	2,533,510
Resources containing experiments	88
Total experiments	2,547,553

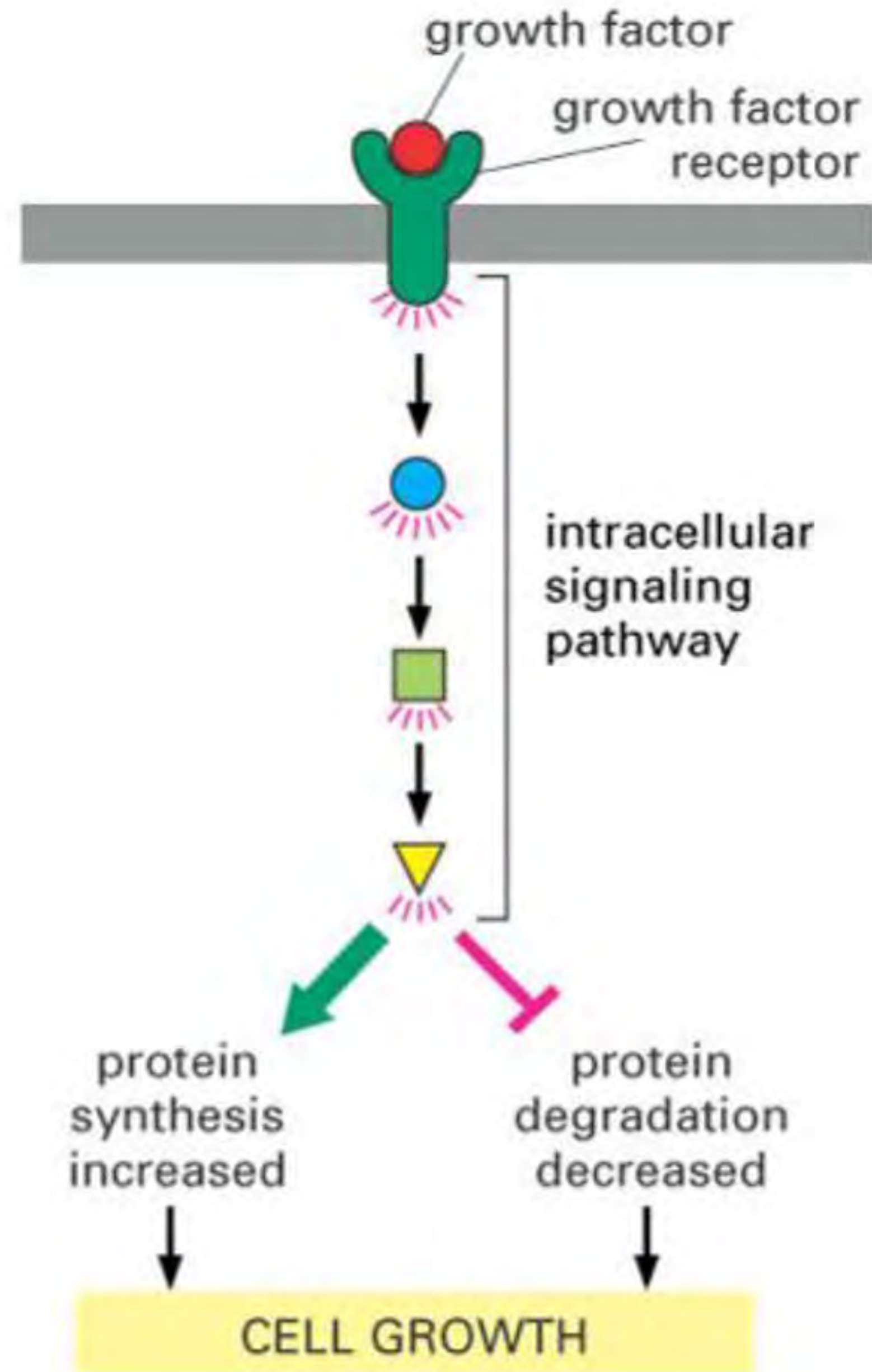
Pathguide: 547 resources <http://www.pathguide.org/>

STOP 1: Pathway Profiling / Compound Mapping

*A representation of
a peak (biochemical data)
being associated with
a compound in a database,
then with a compound in
a biological pathway map*



Biological Pathways/ Signaling Pathways



GenMAPP 2.1

GenMAPP

Gene Map Annotator and Pathway Profiler

Gladstone Institutes
University of California at San Francisco

Home

About Us

Contact Us

Help

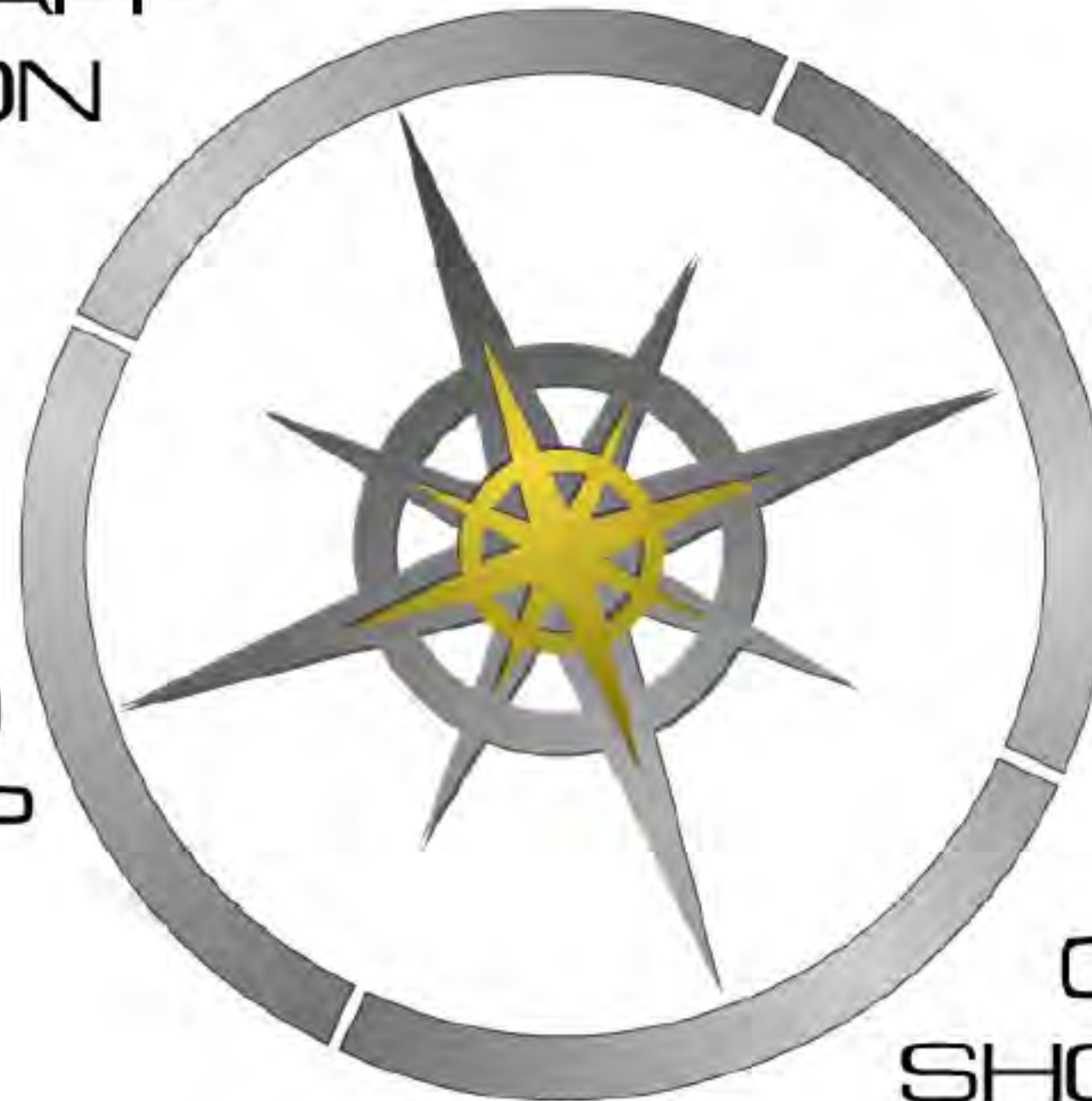
Downloads

Google Custom Search

Search

GenMAPP
INTRODUCTION

DOWNLOAD
GenMAPP



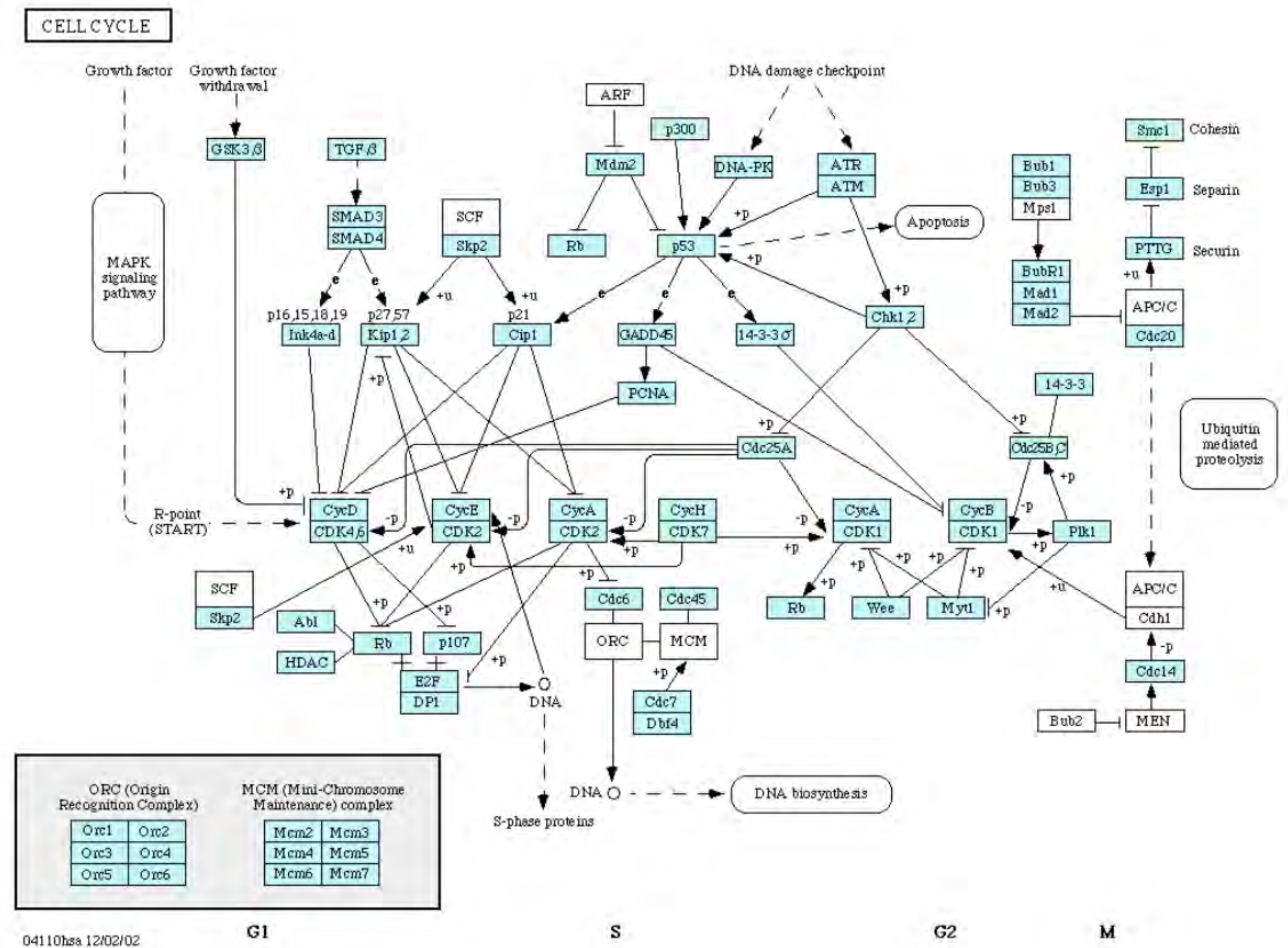
NEWS
ARCHIVE

GenMAPP
SHOWCASE

Pathways for Cellular Processes: Cell Cycle

KEGG Pathways Database
on-line :

<http://www.genome.ad.jp/kegg>



Signaling Pathways Examples

http://stke.sciencemag.org/content/sigtrans/suppl/2002/10/22/CMP_7966.DC1/wajant530.swf

http://stke.sciencemag.org/content/sigtrans/suppl/2002/10/22/CMP_7966.DC1/wajant530.swf



Science's **stke**

www.stke.org

Cell Death Mediated by Fas

H. Wajant, Fas Signaling Pathway. (Connections Map, as seen May 2002),
http://stke.sciencemag.org/cgi/cm/CMP_7966

Animation by : Cameron Slayden



Science's **stke**

www.stke.org

The Jak-STAT Pathway Stimulated by Interferon γ

D. Aaronson, C. M. Horvath, Interferon gamma Pathway. (Connections
Maps, as seen May 2002), http://stke.sciencemag.org/cgi/cm/CMP_9590

Animation by: Carin Cain



KEGG ▼

Search

Help

KEGG Home

[Release notes](#)
[Current statistics](#)
[Plea from KEGG](#)

KEGG Database

[KEGG overview](#)
[Searching KEGG](#)
[KEGG mapping](#)
[Color codes](#)

KEGG Objects

[Pathway maps](#)
[Brite hierarchies](#)

KEGG Software

[KegTools](#)
[KEGG API](#)
[KGML](#)

KEGG FTP

[Subscription](#)

GenomeNet

DBGET/LinkDB

Feedback

Kanehisa Labs

Current Statistics

KEGG Database as of 2015/1/23

Systems information

KEGG PATHWAY	Pathway maps, reference (total)	468 (346,709)
KEGG BRITE	Functional hierarchies, reference (total)	160 (120,942)
KEGG MODULE	KEGG modules, reference (total)	653 (279,875)

Genomic information

KEGG ORTHOLOGY	KEGG Orthology (KO) groups	18,384
KEGG GENOME	KEGG Organisms	3,565
KEGG GENES	Genes in high-quality genomes (303 eukaryotes, 3057 bacteria, 179 archaea)	15,768,634
KEGG SSDB	Best hit relations within GENES	82,423,307,159
	Bi-directional best hit relations within GENES	5,010,380,555
KEGG DGENES	Genes in draft genomes (26 eukaryotes)	654,883
KEGG MGENES	Genes in metagenomes (796 samples)	131,900,984

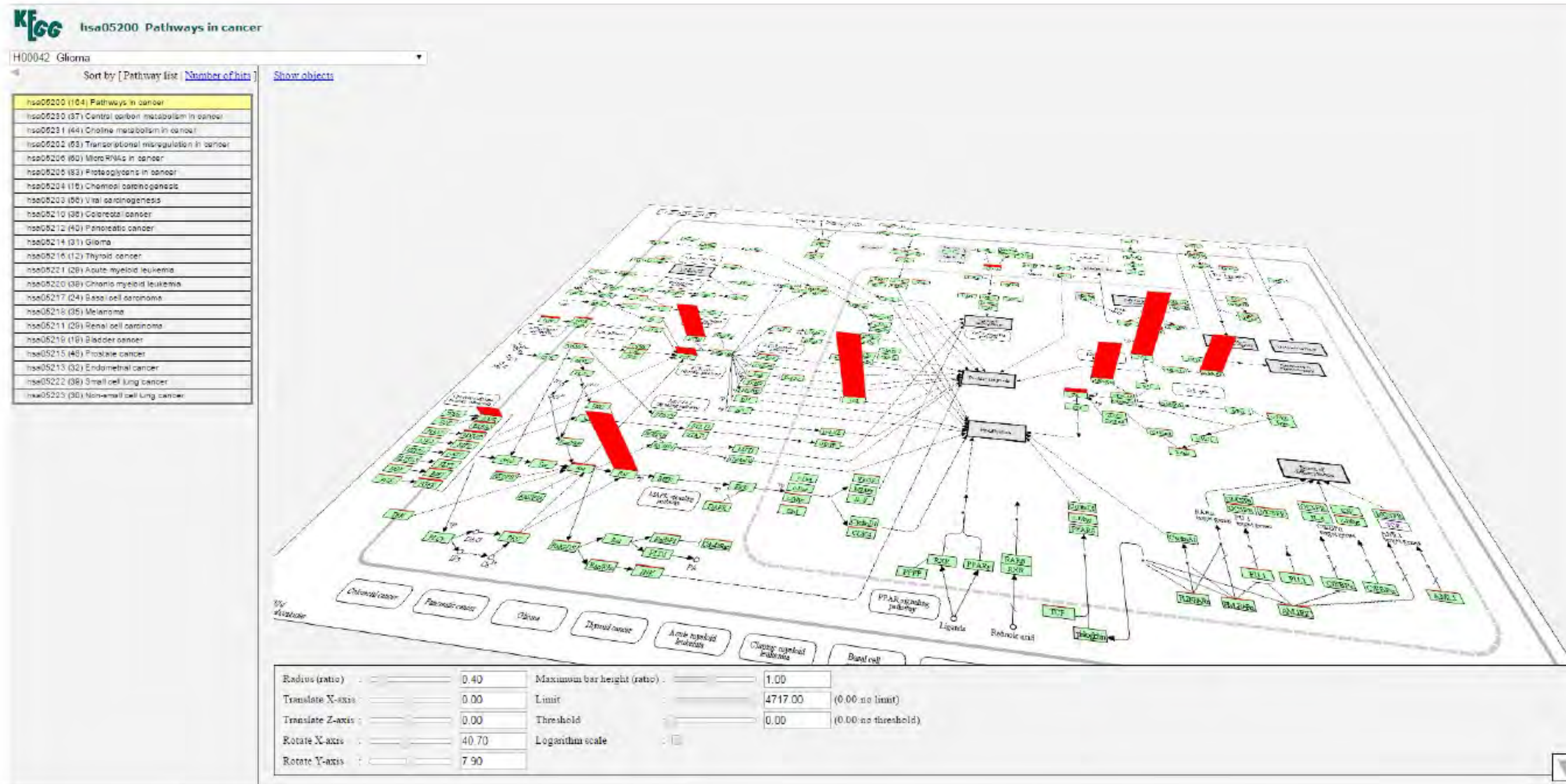
Chemical information

KEGG COMPOUND	Metabolites and other small molecules	17,361
KEGG GLYCAN	Glycans	10,987
KEGG REACTION	Biochemical reactions	9,790
KEGG RPAIR	Reactant pair chemical transformations	14,874
KEGG RCLASS	Reaction class	2,949
KEGG ENZYME	Enzyme nomenclature	6,415

Health information

KEGG DISEASE	Human diseases	1,402
KEGG DRUG	Drugs	10,142
KEGG DGROUP	Drug groups	1,741
KEGG ENVIRON	Crude drugs and health-related substances	850

KEGG Atlas: Cancer Pathways



Example: hsa05200
Pathways in cancer

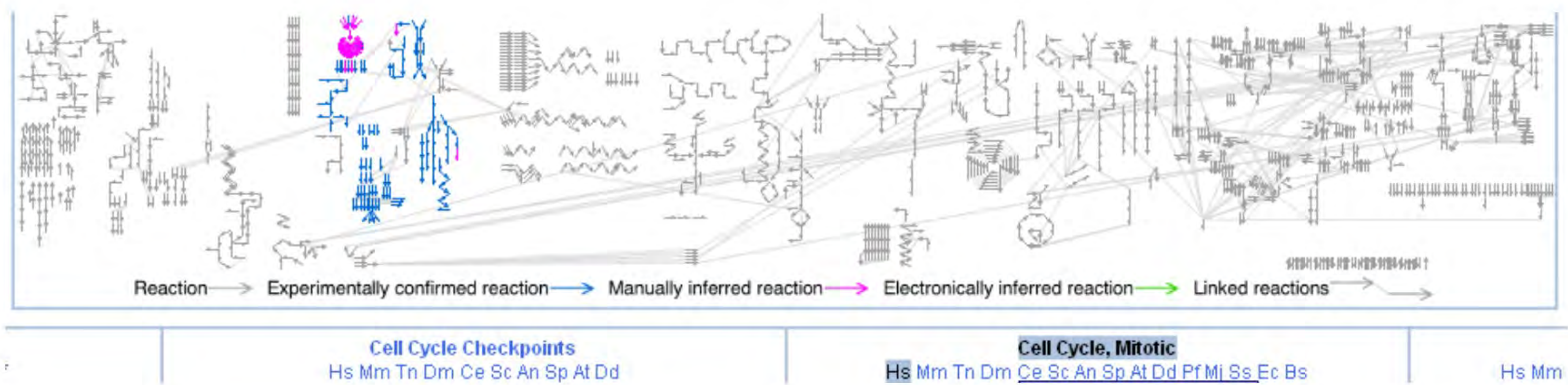
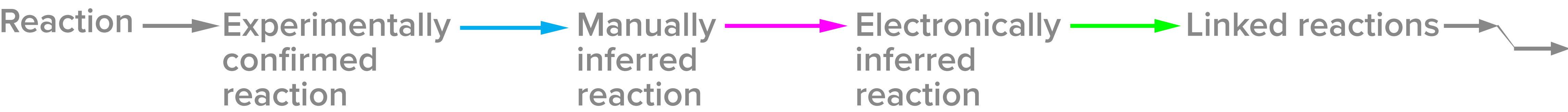
Reactome - a knowledgebase of biological processes

The Reactome project is a collaboration among Cold Spring Harbor Laboratory, The European Bioinformatics Institute, and The Gene Ontology Consortium to develop a curated resource of core pathways and reactions in human biology.

The information in this database is authored by biological researchers with expertise in their field, maintained by the Reactome editorial staff, and cross-referenced with PubMed, GO, and the sequence databases at NCBI, Ensembl and UniProt.

The image displays two screenshots of the Reactome project's online resources. The top screenshot is the main Reactome website, featuring a dark blue header with the 'REACTOME' logo and the tagline 'A CURATED PATHWAY DATABASE'. Below the header is a navigation bar with links: About, Content, Documentation, Tools, Community, Download, and Contact. A search bar on the right contains the text 'e.g. Q95631, NTN1, signalin'. The main content area has six large buttons: 'Browse Pathways', 'Analyze Data', 'Reactome FI Network', 'User Guide', 'Data Download', and 'Contact Us'. Below these buttons is an 'About Reactome' section stating that Reactome is a free, open-source, curated and peer-reviewed pathway database. At the bottom of this section are logos for OICR, NYU Langone Medical Center, CSH Cold Spring Harbor Laboratory, and EMBL-EBI. The bottom screenshot is the Reactome Wiki page, which has a similar header and navigation bar. The main content area of the Wiki page shows a 'Usersguide' link and a search bar.

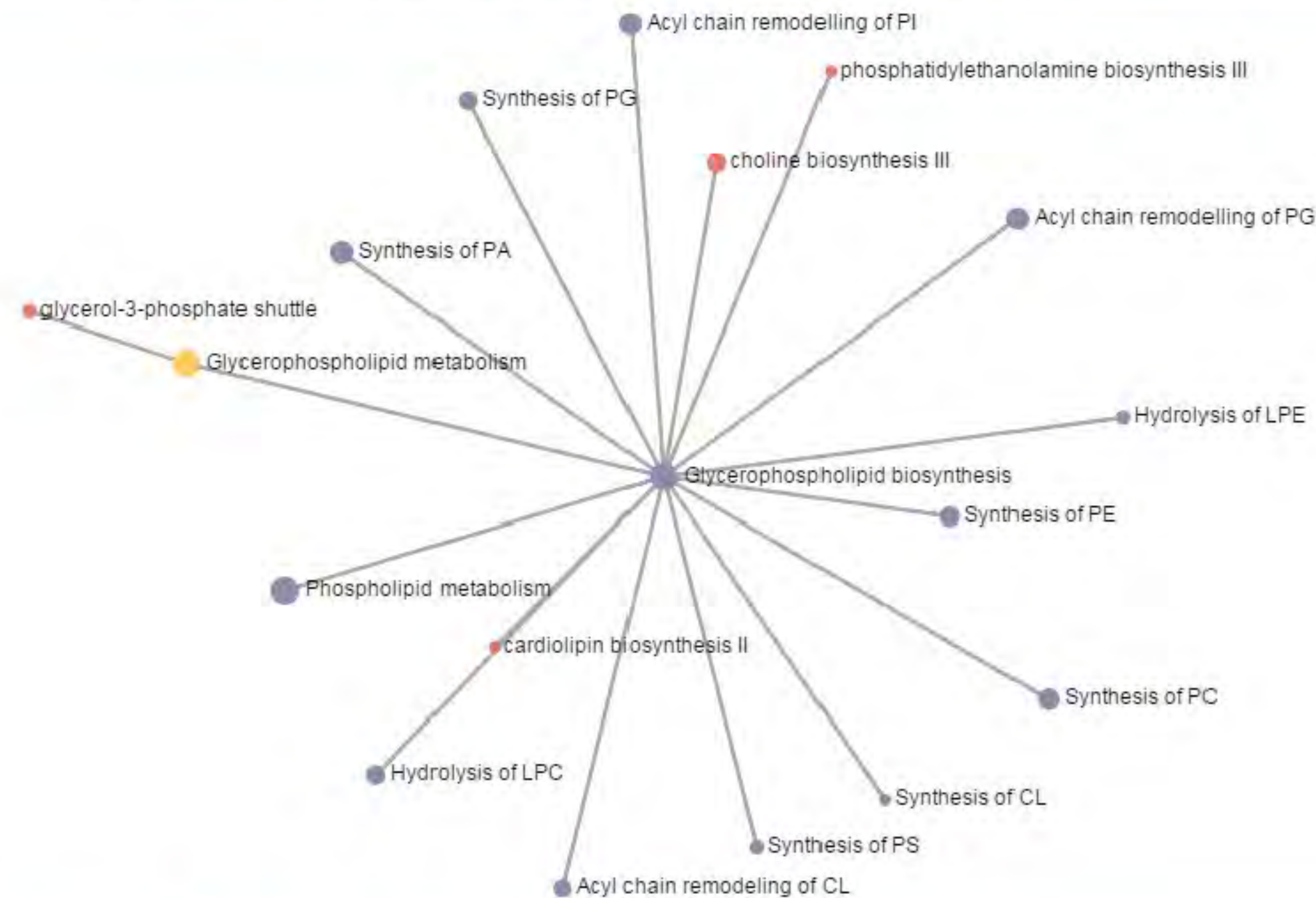
Reactome - a knowledgebase of biological processes





Glycerophospholipid biosynthesis SuperPath

Pathway network for *Glycerophospholipid biosynthesis* SuperPath



18 Pathways in the *Glycerophospholipid biosynthesis* SuperPath

http://pathcards.genecards.org/card/glycerophospholipid_biosynthesis

STOP 2: Beyond Pathways: FUNCTIONAL CLASSIFICATION using Gene Ontologies (GO)



The screenshot shows the Gene Ontology Home page. At the top left is a logo with a hierarchical tree structure and the text "the Gene Ontology". Below this is a sidebar menu with links: "Open menus", "Home", "Downloads" (with sub-links: "Ontologies", "Annotations", "Database", "Mappings to GO", "Teaching Resources", "Monthly Reports"), "GO Tools", "Documentation", "About GO", "GO Editor Guides", "Contact GO", and "Site Map". The main content area is titled "Gene Ontology Home" and contains a paragraph: "The Gene Ontology project provides a controlled vocabulary to describe gene and gene product attributes in any organism. [Read more...](#)". Below this is a "Popular Links" section with a heading "Search the Gene Ontology Database". It features a search input field, a "GO!" button, and radio buttons for "gene or protein name" (selected) and "GO term or ID". A note states: "This search uses the browser [AmiGO](#). [Browse](#) the Gene Ontology using AmiGO." At the bottom is a "GO website" section with a bulleted list of links: "GO downloads: including [ontology files](#), [annotations](#) and the [GO database](#)", "Tools for using GO", "Request new terms or ontology changes via the [SourceForge](#) tracker system; [help with new term submission](#) is available.", "Documentation on all aspects of the GO project and [the FAQ](#)", and "Gene Ontology mailing lists and [contact details](#)".

<http://www.geneontology.org/>

The Gene Ontologies

A Common Language for Annotation of Genes from Yeast, Flies and Mice

...and Plants and Worms

...and Humans

...and anything else!

Gene Ontology Objectives

GO represents concepts used to classify specific parts of our biological knowledge

- Biological Process
- Molecular Function
- Cellular Component

GO develops a common language applicable to any organism

GO terms can be used to annotate gene products from any species, allowing comparison of information across species

GO

Three (Orthogonal) Ontologies

Molecular Function

elemental activity or task
e.g. DNA binding, catalysis of a reaction

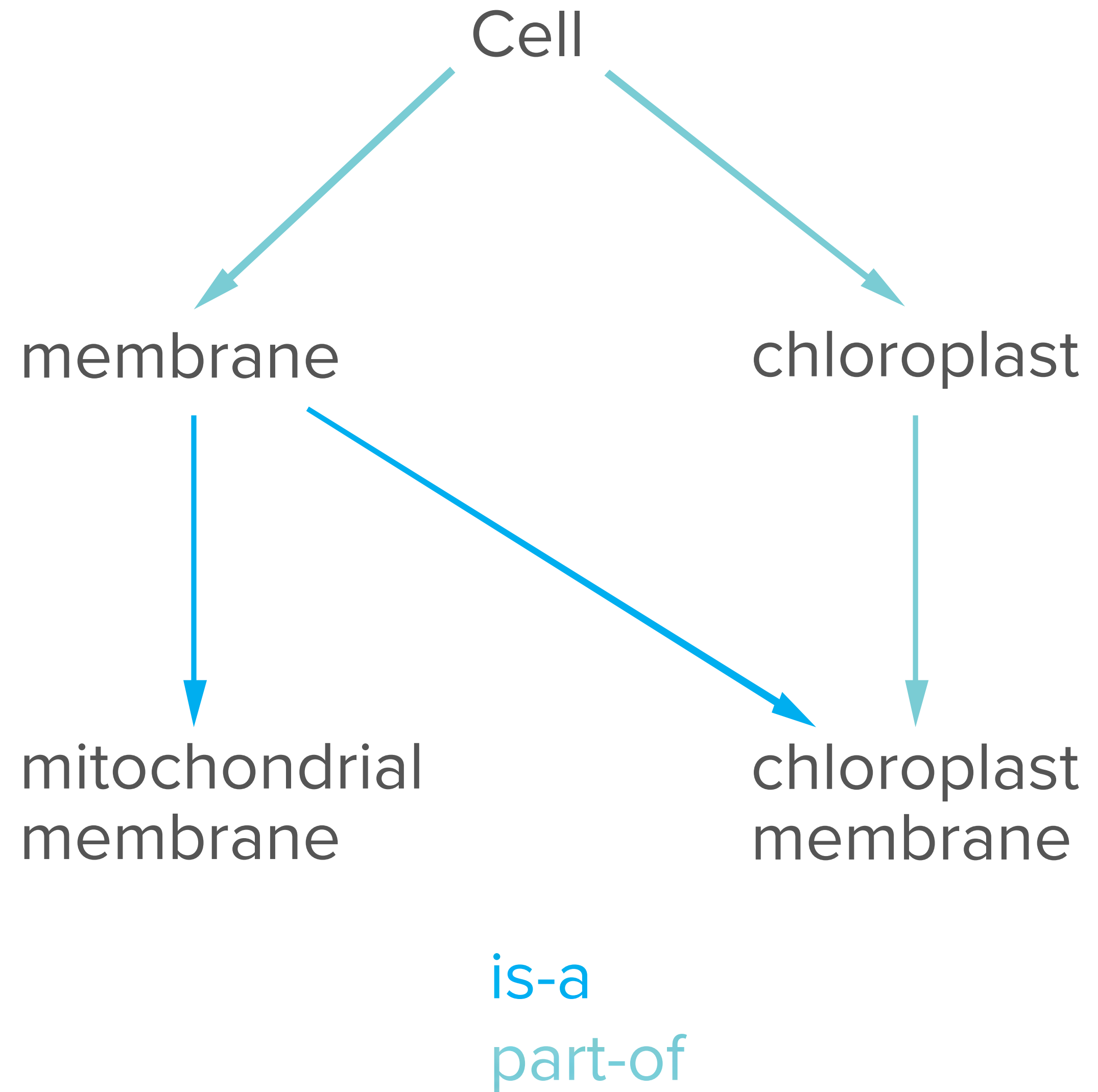
Biological Process

broad objective or goal
e.g. mitosis, signal transduction, metabolism

Cellular Component

location or complex
e.g. nucleus, ribosome

Directed Acyclic Graph



Example: Gene Product = Hammer

Function (what)

Drive nail (into wood)

Drive stake (into soil)

Smash roach

Clown's juggling object



Process (why)

Carpentry

Gardening

Pest Control

Entertainment

What can scientists do with GO?

Access gene product functional information

Provide a link between biological knowledge, gene expression profiles and proteomics data

Find how much of a proteome is involved in a process/ function/ component in the cell

using a GO-Slim

(a slimmed down version of GO to summarize biological attributes of a proteome)

Map GO terms and incorporate manual GOA annotation into own databases

to enhance your dataset

or to validate automated ways of deriving information about gene function (text-mining)

Access to the Gene Ontology

Downloads

formats available:

OBO GO

XML OWL

MySQL

(<http://www.geneontology.org/GO.downloads>)

Web-based tools

AmiGO

(<http://www.godatabase.org>)

QuickGO

(<http://www.ebi.ac.uk/ego>)

GO-based Tools

*Functional profiling of microarray
and proteomics data*

Tools for gene expression/microarray analysis

BiNGO

CLENCH

DAVID

EASE

eGOn v2.0

ermineJ

FatiGO

FuncAssociate

FuncExpression

GARBAN

GeneMerge

GFINDER: Genome Function

GOArray

GOdist

GOODIES

GoMiner and MatchMiner

GOstat

GoSurfer

GO Term Finder

GOTM (Gene Ontology Tree Machine)

Combining Pathways and GO ontology enrichment analysis

DAVID National Institute of Allergy and Infectious Disease
Integrated solutions for the annotation and analysis of genome-scale datasets (DAVID 2.1)

[Home](#) | [Functional Annotation Tool](#) | [Gene ID Conversion Tool](#) | [Pathogen Genome Browser](#) | [Find Related Genes](#) | [Functional](#)
[Licensing Information](#) | [Acknowledgement](#) | [Accessibility](#) | [Publications](#) | [Collaborators](#) | [Linking to DAVID](#) | [Contact](#)

UPLOAD GENE LIST

DAVID Database for Annotation, Visualization and Integrated Discovery

[HOME](#) | [Annotation Tool](#) | [GOCharts](#) | [KEGGCharts](#) | [DomainCharts](#)

DAVID Tools

- [DAVID 2.1 Beta](#)
- [DAVID 2.0](#)
- [Annotation Tool](#)
- [GOCharts](#)
- [KEGGCharts](#)

Convert your Genes to Themes with EASE...

EASE: the Expression Analysis Systematic Explorer

EASE is a customizable, standalone software application that facilitates the biological interpretation of gene lists, generates gene annotation tables, and provides statistical methods for discovering enriched biological themes within gene lists.

DAVID

Database for Annotation,
Visualisation and
Integrated Discovery

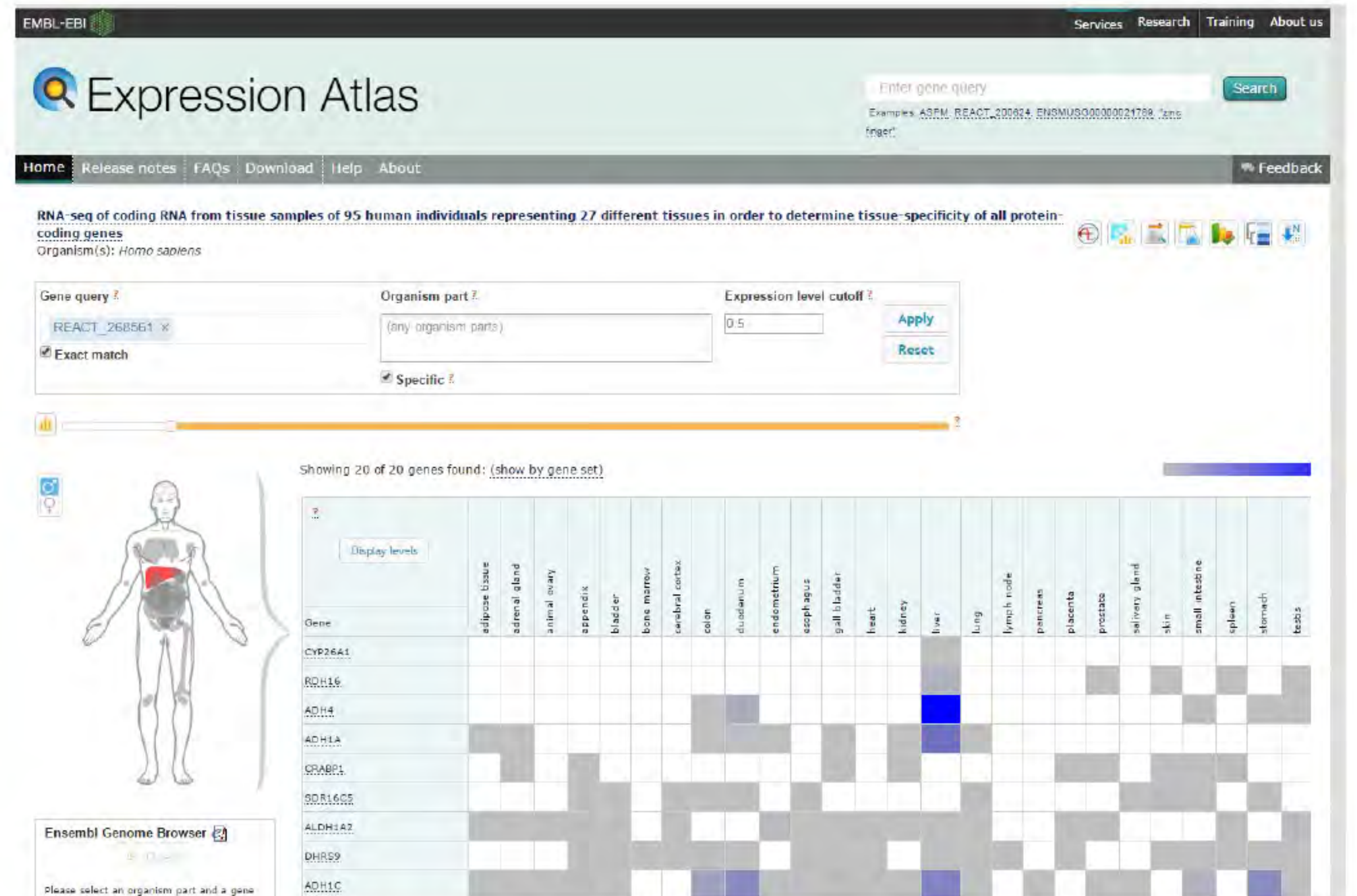
NEXT STOP: Next Generation of Systems Biology Tools

Bringing Tools and Data together

Open Access Web-based applications

Data Resources on-line: Expression Atlas (EBI)

http://www.ebi.ac.uk/gxa/experiments/E-MTAB-1733?gene-Query=REACT_268561&serializedFilterFactors



Pathway and Network analysis on-line: Public Domain

<http://www.pathwaycommons.org/about/>

<http://www.ndexbio.org/>

<http://amp.pharm.mssm.edu/Enrichr/>

CellMiner: <http://discover.nci.nih.gov/-cellminer/>

The screenshot shows the Pathway Commons website. At the top is a dark blue navigation bar with the 'Pathway Commons' logo and links for 'Download', 'F.A.Q.', 'Publications', and 'Contact'. Below this is a light green banner with a date 'March 4, 2015' and a message about a new version of Pathway Commons 2 (v7) that serves 31,698 pathways, 1,151,476 interactions, and 18 data sources. The main content area has a large 'Pathway Commons' title and a subtitle 'Search and visualize public biological pathway information. Single point of access.' Below this is a search bar containing 'BRCA1, BRCA2, MDM2' and a green 'Start exploring »' button. A paragraph describes Pathway Commons as a network biology resource. At the bottom, there is a section titled 'For biologists' with a link to search, visualize, and download pathways as part of an integrated network analysis. Below this are three small thumbnail images showing pathway visualizations.

Pathway Commons

Download F.A.Q. Publications Contact

March 4, 2015 - We have released [a new version of Pathway Commons 2 \(v7\)](#), which serves **31,698 pathways** and **1,151,476 interactions** from **18 data sources**.

Pathway Commons


Search and visualize public biological pathway information. Single point of access.

BRCA1, BRCA2, MDM2 **Start exploring »**

Pathway Commons is a network biology resource and acts as a convenient point of access to biological pathway information collected from public pathway databases, which you can search, visualize and download. All data is freely available, under the license terms of each contributing database.

For biologists

Search, visualize and download Pathway Commons pathways as part of an integrated network analysis ([more](#))



Systems Biology and Big Data: connecting tools to data (hands-on)

GEO2Enrichr

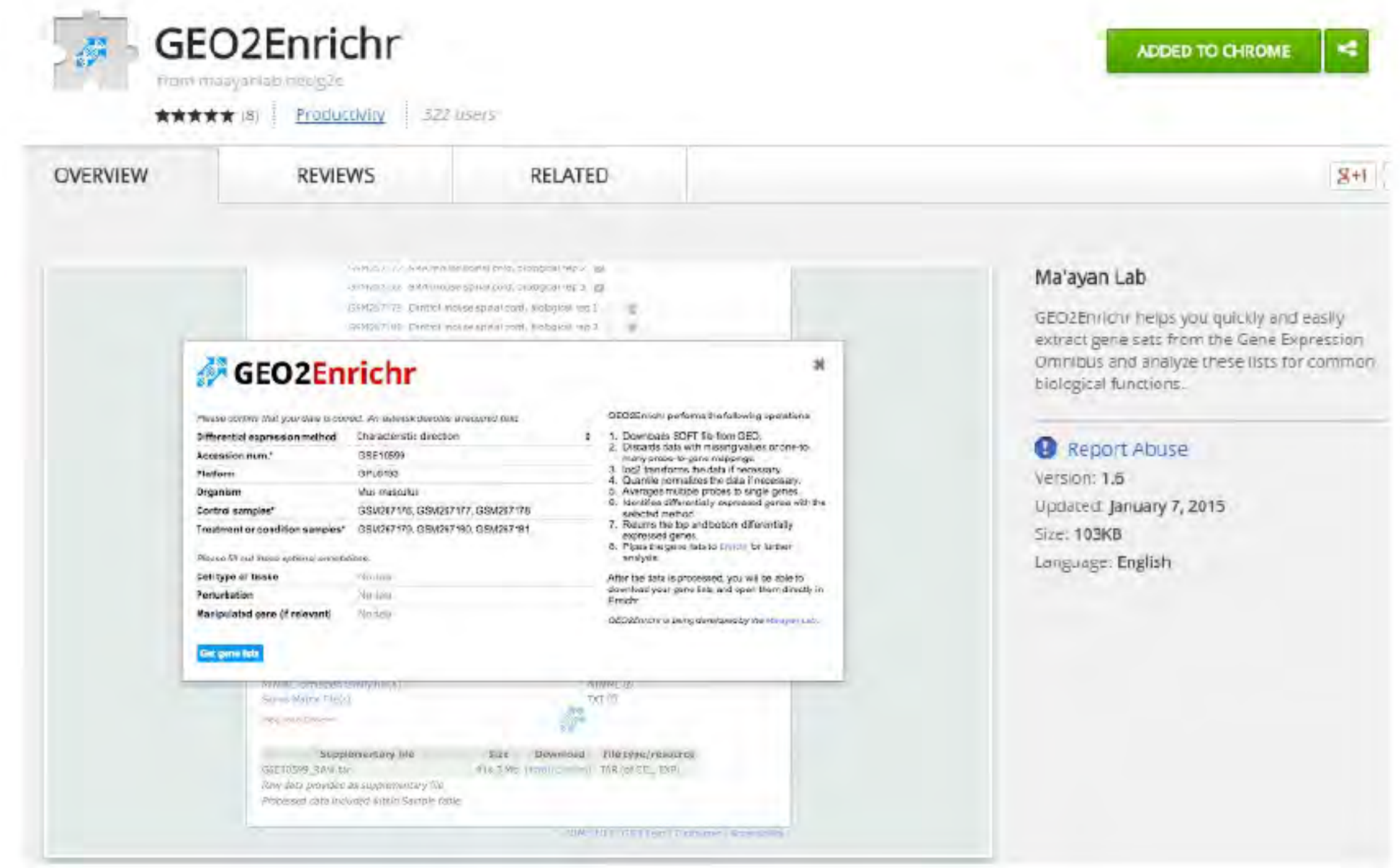
Google Chrome Extension to extract gene sets from GEO and analyze using Systems Biology Tools on-line

Data Public Repositories

Gene Omnibus - GEO
Express Array
Short Reads Archive - SRA

Systems Biology Tools

Pathway Analysis
Gene Ontology
Network Analysis



Enrichr



[Login](#) | [Register](#)

102799 lists analyzed!

[Analyze](#) [What's New?](#) [Dataset Statistics](#) [Find A Gene](#) [About](#) [Help](#)

Input data

Choose an input file to upload. Either in BED format or a list of genes. For a list of genes: separate each gene symbol with a new line. For a quantitative set, add a comma and the level of membership of that gene between 0 and 1 after each gene symbol. Try an example [BED file](#).

No file chosen

Or paste in a list of gene symbols optionally followed by a comma and levels of membership between 0 and 1 with each gene separated by a new line. Try a [regular example](#) or an [example of a quantitative set](#).

```
Mrpl9
LOC100046168
Zfp11
Asf1a
Plscr2
Mettl7a
Rab1
Lrrc19
LOC100047214
Phf7
```

0 gene(s) entered

Enter a brief description for the list in case you want to share it. (Optional)

Sample gene list

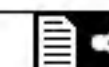
Please acknowledge Enrichr in your publications by citing the following reference:
Chen EY, Tan CM, Kou Y, Duan Q, Meirelles GV, Clark NR, Ma'ayan A. Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. *BMC Bioinformatics*. 2013;128(14).



[Login](#) | [Register](#)

[Transcription](#) [Pathways](#) [Ontologies](#) [Disease/Drugs](#) [Cell Types](#) [Misc](#) [Legacy](#)

[Description](#) Sample gene list (375 genes)



ChEA

TRANSFAC and JASPAR PWMs

Genome Browser PWMs

Epigenomics Roadmap HM ChIP-seq

TargetScan microRNA


ENCODE TF ChIP-seq 2015

TF-LOF Expression from GEO

ENCODE Histone Modifications 2015

Transcription Factor PPIs

Enrichr



Login | Register

Transcription **Pathways** Ontologies Disease/Drugs Cell Types Misc Legacy

Description

Sample gene list (375 genes)

KEGG 2015

WikiPathways 2015

Reactome 2015

BioCarta 2015

PPI Hub Proteins

KEA

NURSA Human Endogenous Complexome

CORUM

Panther

Bar Graph **Table** 

Hover each row to see the overlapping genes.

10 entries per page

Search:

Index	Name	P-value	Z-score	Combined Score
1	Beta1 adrenergic receptor signaling pathway*	0.02936	-1.80	1.29
2	Purine metabolism*	0.01387	-1.50	1.07
3	Metabotropic glutamate receptor group II pathway*	0.07184	-1.37	0.88
4	Thyrotropin-releasing hormone receptor signaling pathway*	0.1257	-1.12	0.72
5	Muscarinic acetylcholine receptor 2 and 4 signaling pathway*	0.1114	-1.09	0.70
6	Heme biosynthesis*	0.02116	-0.89	0.64
7	Insulin/IGF pathway-mitogen activated protein kinase kinase/MAP kinase cascade*	0.07184	-0.91	0.58
8	Beta2 adrenergic receptor signaling pathway*	0.1352	1.61	0.00
9	Coenzyme A biosynthesis*	0.1352	3.69	0.00
10	Beta3 adrenergic receptor signaling pathway*	0.1601	2.51	0.00

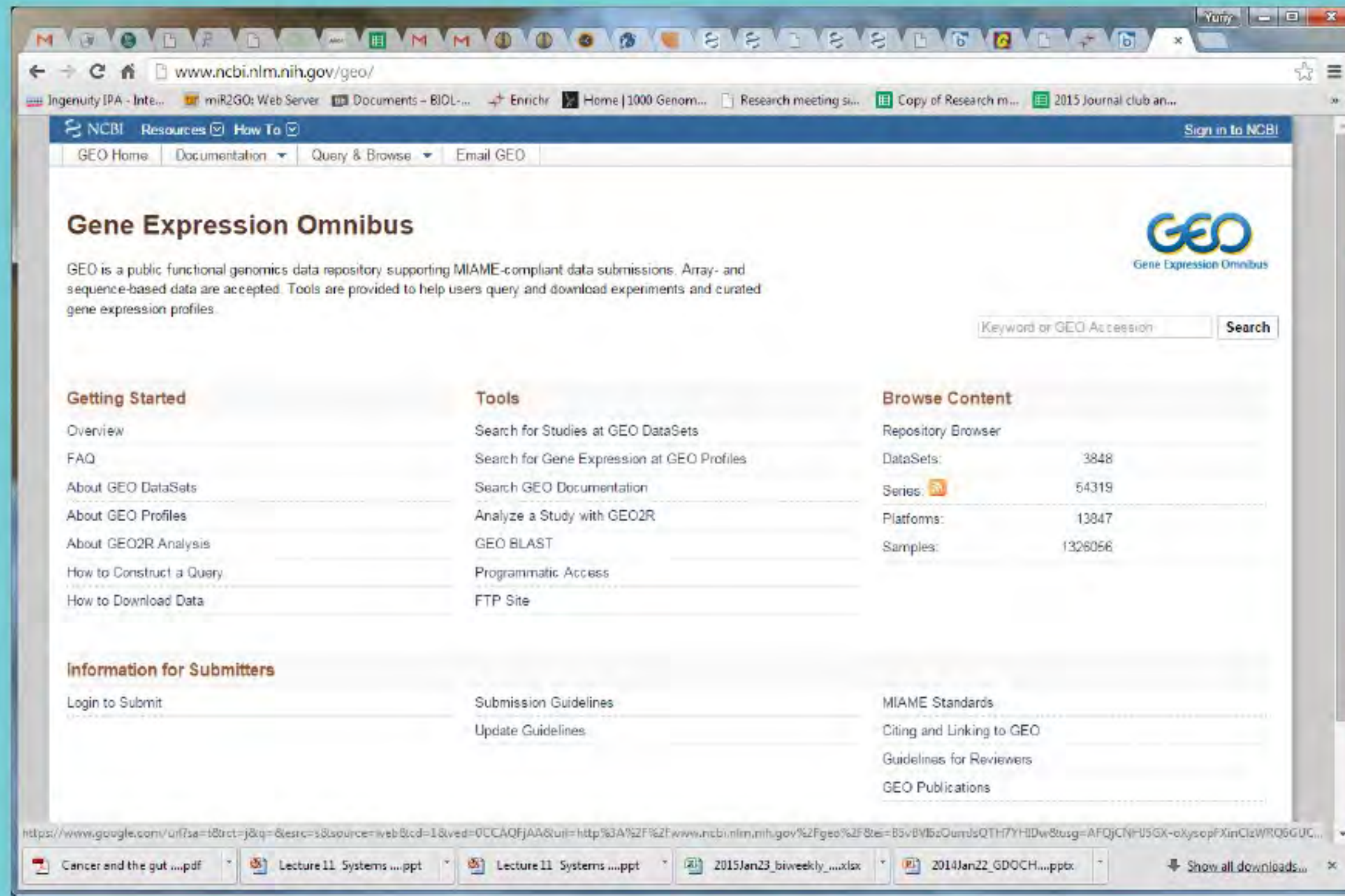
Showing 1 to 10 of 50 entries | [Export entries to table](#)

Terms marked with an * have an overlap of less than 5

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Scope: Self Format: HTML Amount: Quick GEO accession: GSE46141 GO

Series GSE46141

Query DataSets for GSE46141

Status	Public on Dec 02, 2013
Title	Expression data from fine-needle aspiration biopsies of breast cancer metastases from different anatomical sites
Organism	Homo sapiens
Experiment type	Expression profiling by array
Summary	Breast cancer molecular subtypes preferentially metastasize to specific organs and the anatomical location of the metastasis is associated with the length of survival post-recurrence. We used microarrays to provide a detailed characterization of breast cancer site-specific metastases with particular focus on identifying genes predictive of breast cancer liver metastatic propensity
Overall design	We performed global gene expression profiling on fine-needle aspirates of metastatic lesions from different anatomical sites obtained from breast cancer patients treated within the Swedish randomized trial (TEX) of first-line chemotherapy for locally advanced or metastatic breast cancer. Samples were collected before commencement of treatment.
Contributor(s)	Hedenfalk I , Hatschek T
Citation(s)	Kimbung S, Kovács A, Bendahl PO, Malmström P et al. Claudin-2 is an independent negative prognostic factor in breast cancer and specifically predicts early liver recurrences. <i>Mol Oncol</i> 2014 Feb;8(1):119-28. PMID: 24287398
Submission date	Apr 17, 2013
Last update date	Jul 09, 2014
Contact name	Siker Kimbung
Organization name	Lund University
Department	Department of Oncology and Pathology, Clinical Sciences, Lund
Lab	Lund University Cancer Center/Medicon Village/ Building 404:C2
Street address	Scheelevägen 2
City	Lund
ZIP/Postal code	SE-22381
Country	Sweden
Platforms (1)	GPL10379 Rosetta/Merck Human RSTA Custom Affymetrix 2.0 microarray [HuRSTA-2a520709]
Samples (91)	
More...	
	<div>Ctrl Expt</div> <div>GSM1124867 KI_TEX_2791_112 liver <input type="checkbox"/> <input type="checkbox"/></div> <div>GSM1124868 KI_TEX_2987_146 liver <input type="checkbox"/> <input type="checkbox"/></div> <div>GSM1124869 KI_TEX_1594_94 breast <input type="checkbox"/> <input type="checkbox"/></div>

<http://www.ncbi.nlm.nih.gov/geo/>

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE46141>

Platforms (1) [GPL10379](#) Rosetta/Merck Human RSTA Custom Affymetrix 2.0 microarray [HuRSTA-2a520709]

Samples (91) [More...](#)

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GSM1124867	KI_TEX_2791_112 liver	<input type="checkbox"/>	<input type="checkbox"/>
GSM1124868	KI_TEX_2987_146 liver	<input type="checkbox"/>	<input type="checkbox"/>
GSM1124869	KI_TEX_1594_94 breast	<input type="checkbox"/>	<input type="checkbox"/>

Relations

BioProject [PRJNA197346](#)

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Series Matrix File(s)

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TXT [?](#)

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Supplementary file	Size	Download	File type/resource
GSE46141_Probeset_Annotation_20100204.txt.gz	9.3 Mb	(ftp) (http)	TXT
GSE46141_RAW.tar	469.9 Mb	(http) (custom)	TAR (of CEL)

Raw data provided as supplementary file

Processed data included within Sample table

Contributor(s) [Hedenfalk I, Hatschek T](#)
Citation(s) Kimbung S, Kovács A, Bendahl PO, Malmström P et al. Claudin-2 is an independent negative prognostic factor in breast cancer and specifically predicts early liver recurrences. *Mol Oncol* 2014 Feb;8(1):119-28. PMID: [24287398](#)

Submission date Apr 17, 2013
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Contact name Siker Kimbung
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Country Sweden

Platforms (1) [GPL10379](#) Rosetta/Merck Human RSTA Custom Affymetrix 2.0 microarray [HuRSTA-2a520709]

Samples (91) [Less...](#)

		Ctrl	Expmt
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GSM1124868	KI_TEX_2987_146 liver	<input type="checkbox"/>	<input checked="" type="checkbox"/>
GSM1124869	KI_TEX_1594_94 breast	<input checked="" type="checkbox"/>	<input type="checkbox"/>

GSM1124870	KI_TEX_1583_8 breast	<input checked="" type="checkbox"/>	<input type="checkbox"/>
GSM1124871	KI_TEX_1524_35 lymph node	<input type="checkbox"/>	<input type="checkbox"/>
GSM1124872	KI_TEX_1467_82 skin local-regional	<input type="checkbox"/>	<input type="checkbox"/>
GSM1124873	KI_TEX_2904_71 skin local-regional	<input type="checkbox"/>	<input type="checkbox"/>
GSM1124874	KI_TEX_2850_62 lymph node	<input type="checkbox"/>	<input type="checkbox"/>
GSM1124875	KI_TEX_2917_74 lymph node	<input type="checkbox"/>	<input type="checkbox"/>
GSM1124876	KI_TEX_2777_105 skin local-regional	<input type="checkbox"/>	<input type="checkbox"/>
GSM1124877	KI_TEX_1451_81 skin local-regional	<input type="checkbox"/>	<input type="checkbox"/>
GSM1124878	KI_TEX_1560_10 liver	<input type="checkbox"/>	<input checked="" type="checkbox"/>
GSM1124879	KI_TEX_2782_60 skin	<input type="checkbox"/>	<input type="checkbox"/>

Questions?

