

On-Line Public Resources for Big Biological Data with data and tools combined

Cancer Focused Resources

OncoMine: <https://www.oncomine.org/resource/login.html>

GDOC Plus: <https://gdoc.georgetown.edu/gdoc/>

Cancer Cell Line Encyclopedia (CCLE): 1K cancer cell lines
<http://www.broadinstitute.org/ccle>

cBio Portal for Cancer genomics: <http://www.cbioportal.org/>

FireBrowse (TCGA collection): <http://firebrowse.org/>

Cancer Genomics Browser (UCSC): <https://genome-cancer.ucsc.edu>

Systems Biology Resources In Public Domain

WikiPathways: <http://www.wikipathways.org/index.php/WikiPathways>

PathVisio: a tool to edit and analyze pathways

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

NetPath: a manually curated resource of signal transduction pathways in humans

<http://www.netpath.org/index.html>

STRING: functional protein association networks <http://string-db.org/>

PANTHER – Gene Ontology and Pathways Classification System

<http://www.pantherdb.org/panther/prowler.jsp?>

ConsensusPathDB: integration of molecular interaction networks

<http://consensuspathdb.org/>

WikiPathways

<http://www.wikipathways.org/index.php/WikiPathways>

open, public platform dedicated to the curation of biological pathways by and for the scientific community

WikiPathways: capturing the full diversity of pathway knowledge

Martina Kutmon^{1,2,*}, Anders Riutta³, Nuno Nunes¹, Kristina Hanspers³, Egon L. Willighagen¹, Anwesha Bohler¹, Jonathan Mélius¹, Andra Waagmeester^{1,4}, Sravanthi R. Sinha⁵, Ryan Miller¹, Susan L. Coort¹, Elisa Cirillo¹, Bart Smeets¹, Chris T. Evelo^{1,2} and Alexander R. Pico^{3,*}

Author Affiliations

¹Department of Bioinformatics – BiGCaT, NUTRIM, Maastricht University, Maastricht, 6229 ER Maastricht, The Netherlands

²Maastricht Centre for Systems Biology (MaCSBio), Maastricht University, Maastricht, 6229 ER Maastricht, The Netherlands

³Gladstone Institutes, San Francisco, California, CA 94158, USA

⁴Micelio, Antwerp, 2180 Antwerp, Belgium

⁵Keshav Memorial Institute of Technology, Hyderabad, Telangana 500029, India

[« Previous](#) | [Next Article »](#)
[Table of Contents](#)

This Article

Nucl. Acids Res. (04 January 2016) 44 (D1): D488-D494.
doi: 10.1093/nar/gkv1024

First published online: October 19, 2015

This article appears in: [Database issue](#)

This article is Open Access

» Abstract **Free**

Full Text (HTML) **Free**

Full Text (PDF) **Free**

[SUPPLEMENTARY DATA](#)

All Versions of this Article:

[gkv1024v1](#)

[44/D1/D488](#) **most recent**

plos.org create account sign in


PLOS | COMPUTATIONAL BIOLOGY

Browse Publish About Search


OPEN ACCESS PEER-REVIEWED

RESEARCH ARTICLE

PathVisio 3: An Extendable Pathway Analysis Toolbox

Martina Kutmon , Martijn P. van Iersel, Anwesha Bohler, Thomas Kelder, Nuno Nunes, Alexander R. Pico, Chris T. Evelo 

Published: February 23, 2015 • DOI: 10.1371/journal.pcbi.1004085

Article	Authors	Metrics	Comments	Related Content
				

Abstract

Introduction

Design and Implementation

Abstract

PathVisio is a commonly used pathway editor, visualization and analysis software. Biological pathways have been used by biologists for many years to describe the detailed steps in

Loading metrics

Download PDF

Print Share

CrossMark

Subject Areas

[Data visualization](#)

WikiPathways



search

navigation

- Home
- Help

pathway

- Create
- Browse
- Wish List
- Download
- Web service API
- WikiPathways RDF

overview

- Recent Changes
- Most Viewed
- Most Edited
- New Pathways
- Statistics

community

- About us
- Contact us
- Report a bug
- How to cite
- Curation events
- CIRM portal
- Disease portal
- ExRNA portal
- Micronutrient portal
- NetPath portal
- Plants portal
- Reaction portal
- WormBase portal
- Development

toolbox

- What links here
- Related changes

[page](#) [discussion](#) [view source](#) [history](#)

Welcome to WikiPathways ^{BETA}

WikiPathways is an open, public platform dedicated to the curation of biological pathways by and for the scientific community. [More about WikiPathways...](#)

Finding Pathways

Search

Search

You can search by:

- Pathway name (*Apoptosis*)
- Gene or protein name (*p53*)
- Any page content (*cancer*)

Browse

Browse Pathways

Show pathway thumbnail | [Sort by](#) [Category](#) [Metabolic](#) [Protein](#)

- Apoptosis pathway
- Amino acid metabolism pathway
- Angiogenesis pathway
- Cholesterol metabolism pathway
- Citric acid cycle pathway
- DNA replication pathway
- Glycolysis pathway
- Hemoglobin synthesis pathway
- Insulin signaling pathway
- Lipid metabolism pathway
- Mitochondrial metabolism pathway
- Nitric oxide metabolism pathway
- Protein synthesis pathway
- Signal transduction pathway
- Tumor necrosis factor signaling pathway
- Vitamin metabolism pathway

Browse by species and category

Contributing New Pathways

Create



Create a new pathway page

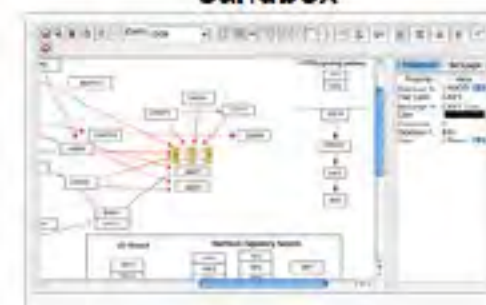
Suggest

Pathway title	Author	Date	Comments	View	Watch	Revert
Apoptosis pathway	John Doe	2007-10-10	Initial version of the pathway			
Cholesterol metabolism pathway	John Doe	2007-10-10	Initial version of the pathway			
DNA replication pathway	John Doe	2007-10-10	Initial version of the pathway			
Glycolysis pathway	John Doe	2007-10-10	Initial version of the pathway			

Add a pathway to the wish list

Sample Pathway Pages

Sandbox




Play with the editor tools

Check out the following pages:

- Show recent changes
- Show new pathways
- Show most edited pathways
- Show most viewed pathways
- Show pathway wish list
- Selected publications using WikiPathways

For more information see the [Help](#) pages

WikiPathways

 **BETA**
WIKIPATHWAYS
Pathways for the People

special

Log in / create a

Browse pathways

Species: Collection: View:

search

navigation

- Home
- Help

pathway

- Create
- Browse
- Wish List
- Download
- Web service API
- WikiPathways RDF

overview

- Recent Changes
- Most Viewed
- Most Edited
- New Pathways
- Statistics

community

- About us
- Contact us
- Report a bug
- How to cite
- Curation events
- CIRM portal
- Disease portal
- ExRNA portal
- Micronutrient portal

ACE Inhibitor Pathway
★★

Acetylcholine Synthesis
★★

Alzheimers Disease
★★

AMPK Signaling
★★

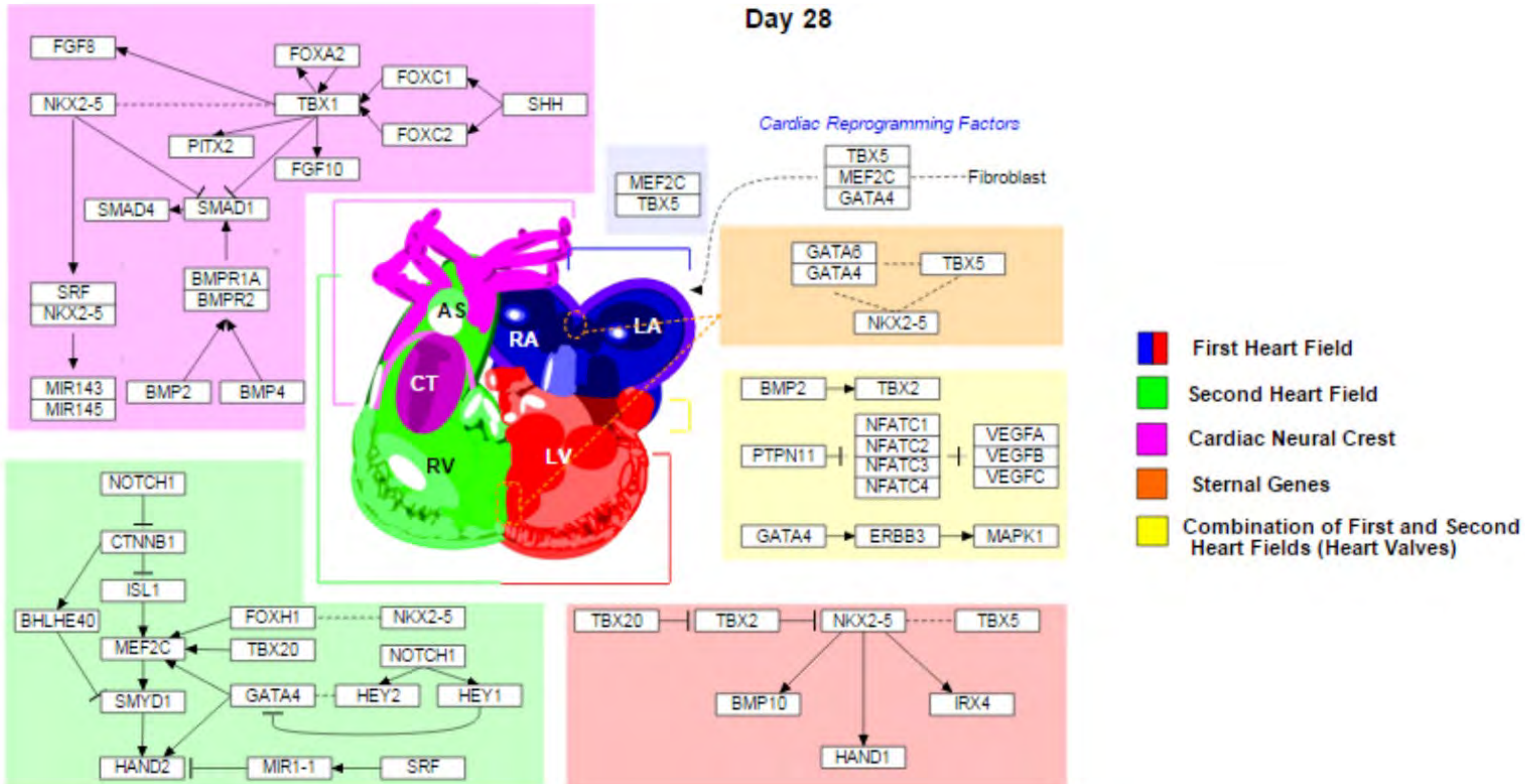
Amyotrophic lateral sclerosis (ALS)
★★

Angiogenesis
★★

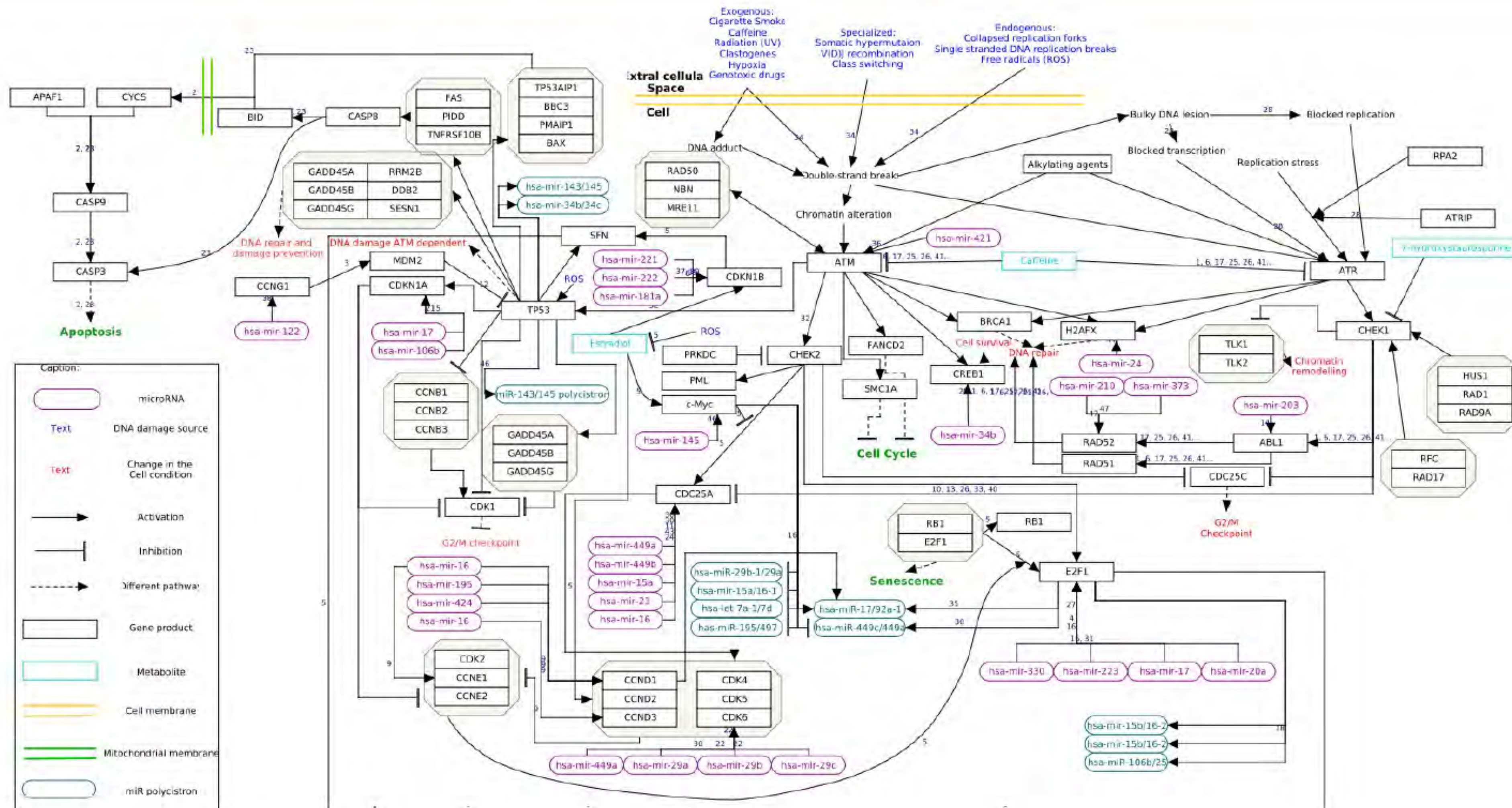
Apoptosis
★★★

Apoptosis Modulation and Signaling
★★★

Pathway Examples: Heart Development




Wiki Pathways Collection – Example 2: microRNA regulation of DNA damage



PathVisio: a tool to edit and analyze pathways

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



PathVisio

a tool to edit and analyze biological pathways

Home Getting Started ▾ Support/Help ▾ Downloads ▾ Plugins ▾ Cite Us About ▾ Tutorial 5

What is PathVisio?

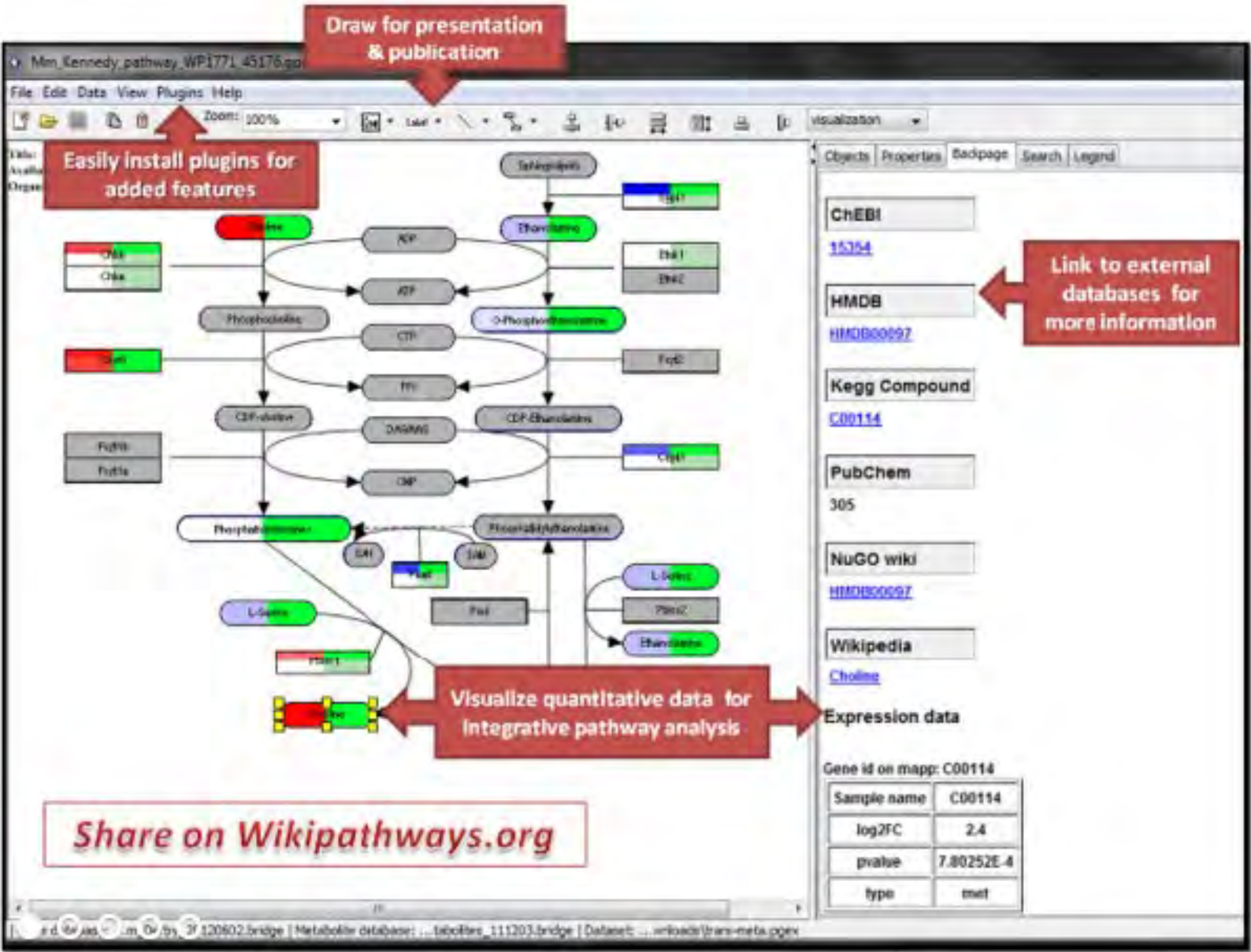
PathVisio is a free open-source biological pathway analysis software that allows you to draw, edit and analyze biological pathways. [Learn more.](#)

How to use PathVisio?

Learn how to download PathVisio and go through the tutorials to find out how to do pathway analysis and how to visualize and analyze your data. [Get started.](#)

PathVisio Plugins

Plugins are extensions that provide advanced analysis methods, visualization options or additional import/export functionality. [Find out more.](#)



Draw for presentation & publication

Easily install plugins for added features

Link to external databases for more information

Visualize quantitative data for integrative pathway analysis

Share on Wikipathways.org

Gene id on map: C00114	
Sample name	C00114
log2FC	2.4
pvalue	7.80252E-4
type	met

News

- **Check out the new WikiPathways paper!** "WikiPathways: capturing the full diversity of pathway knowledge." Nucl. Acids Res. first published online October 19, 2015. doi: 10.1093/nar/gkv1024
- **BioSB 2015 Application Showcase:** Martina Kutmon presented WikiPathways, PathVisio and the WikiPathways App for Cytoscape and won the best application showcase prize. Congratulations!
- **New PathVisio 3 paper!!** "PathVisio 3: An Extendable Pathway Analysis Toolbox." PLoS Comput Biol. 2015 Feb 23;11(2):e1004085. doi: 10.1371/journal.pcbi.1004085
- **Developer website:** The previous website will stay available on developers.pathvisio.org and will be used as a developers website.
- **Plugin repository:** Find plugins in the [plugin repository](#) and install them through the [plugin manager](#)


Releases

- Oct 07 2015 PathVisio 3.2.1 has been released!
- Feb 28 2015 PathVisio 3.2.0 has been released!
- Jan 31 2014 PathVisio 3.1.3 has been released!
- Oct 29 2013 PathVisio 3.1.2 has been released!

NetPath: a manually curated resource of signal transduction pathways in humans

<http://www.netpath.org/index.html>

NetPath



[Home](#) [Browse](#) [FAQs](#) [Immune Signaling Pathways](#) [Cancer Signaling Pathways](#) [Publications](#)

[Go to NetSlim](#)

Search

Gene Symbol	<input type="text"/>	e.g. SHC1
Protein Name	<input type="text"/>	e.g. EGF receptor
Accession Number	<input type="text"/>	e.g. NP_002077
Pathway Name	<input type="text" value="Select a pathway"/>	

[Submit](#) [Clear](#)

Statistics

Curated Pathways	36
Molecules Involved	1053
Physical Interactions	2448
Genes Transcriptionally Regulated	7401
Transport	284
Enzyme Catalysis	1597
PubMed Citations	2228

NEW [Search Transcriptionally Regulated Genes](#)

'NetPath' is a manually curated resource of signal transduction pathways in humans. It is a collaborative effort between the [PandeyLab](#) at Johns Hopkins University and the [Institute of Bioinformatics](#). The initial set of 10 cancer signaling pathways were developed in collaboration with the [Computational Biology Center](#) at Memorial Sloan-Kettering Cancer Center and with [Gary Bader's lab](#) at the University of Toronto for the ['Cancer Cell Map'](#).

All pathways in NetPath are freely available for download in [BioPAX level 3.0](#), [PSI-MI version 2.5](#) and [SBML version 2.1](#) formats at this website. The slim pathway models representing only core reactions in each pathway are available at [NetSlim](#). All the NetPath pathway models are also submitted to [WikiPathways](#). The pathway data are freely available under an adaptive Creative Commons License which stipulates that the pathways may be used if adequate credit is given to the authors.

NetPath: a manually curated resource of signal transduction pathways in humans

<http://www.netpath.org/index.html>

EGFR1 Signaling Pathway

Select another pathway

: Select a pathway

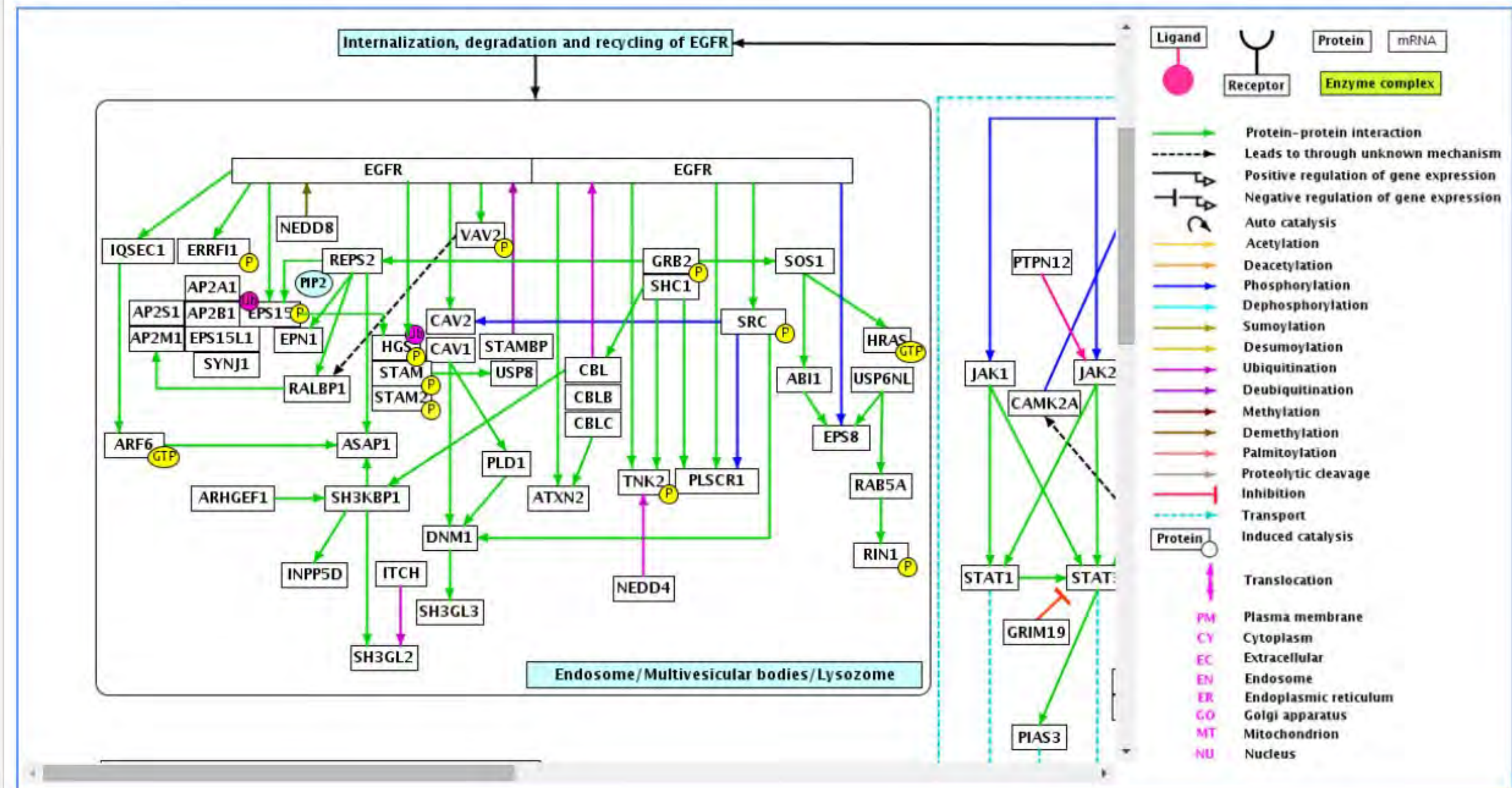
Go to
NetPath

Map with citation

Pathway map

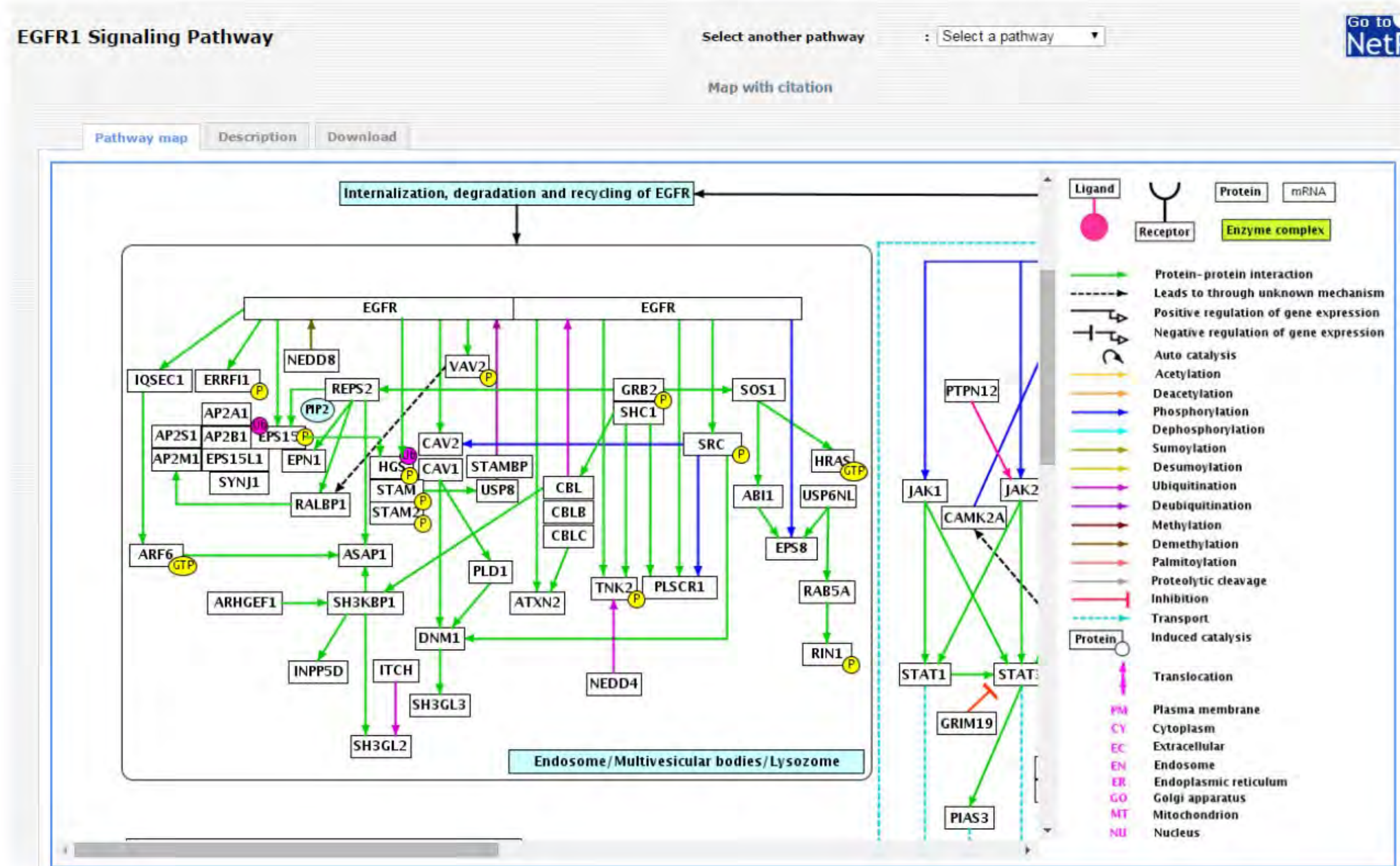
Description

Download



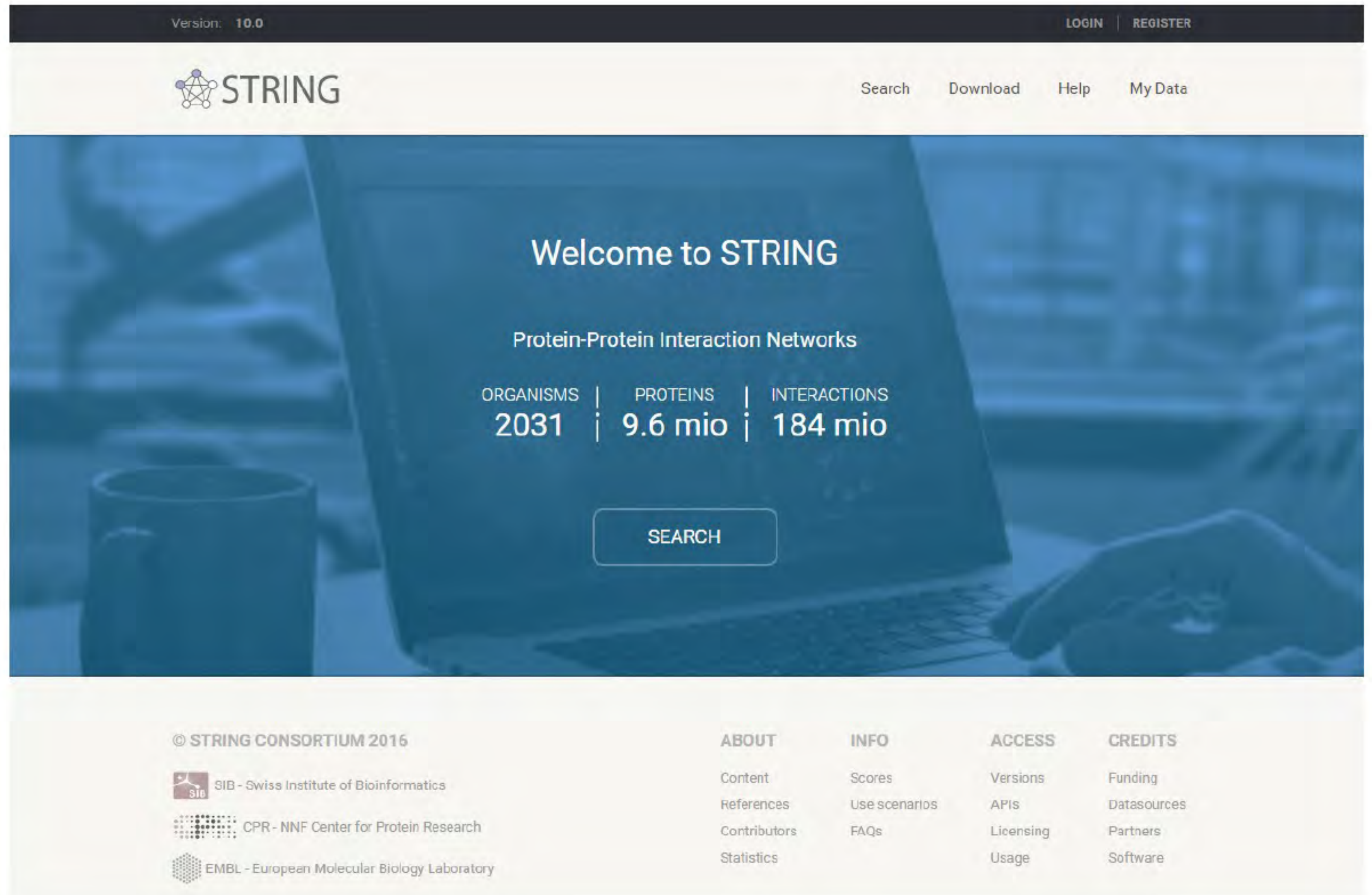
NetPath: a manually curated resource of signal transduction pathways in humans

<http://www.netpath.org/index.html>



STRING: functional protein association networks

<http://string-db.org/>



The screenshot shows the STRING database homepage. At the top, a dark header bar contains 'Version: 10.0' on the left and 'LOGIN | REGISTER' on the right. Below this is a light-colored navigation bar with the STRING logo (a network diagram) and the word 'STRING' on the left, and links for 'Search', 'Download', 'Help', and 'My Data' on the right. The main content area has a blue-tinted background image of a laptop and a mug. It features the text 'Welcome to STRING' and 'Protein-Protein Interaction Networks'. Below this, a table-like structure displays statistics: 'ORGANISMS 2031', 'PROTEINS 9.6 mio', and 'INTERACTIONS 184 mio'. A 'SEARCH' button is centered below the statistics. The footer is divided into four columns: '© STRING CONSORTIUM 2016' with logos for SIB, CPR, and EMBL; 'ABOUT' with links for Content, References, Contributors, and Statistics; 'INFO' with links for Scores, Use scenarios, and FAQs; and 'ACCESS' and 'CREDITS' with links for Versions, APIs, Licensing, Usage, Funding, Datasources, Partners, and Software.

Version: 10.0

LOGIN | REGISTER

STRING

Search Download Help My Data


Welcome to STRING


Protein-Protein Interaction Networks


ORGANISMS	PROTEINS	INTERACTIONS
2031	9.6 mio	184 mio

SEARCH

© STRING CONSORTIUM 2016

 SIB - Swiss Institute of Bioinformatics

 CPR - NNF Center for Protein Research

 EMBL - European Molecular Biology Laboratory

ABOUT

- Content
- References
- Contributors
- Statistics

INFO

- Scores
- Use scenarios
- FAQs

ACCESS

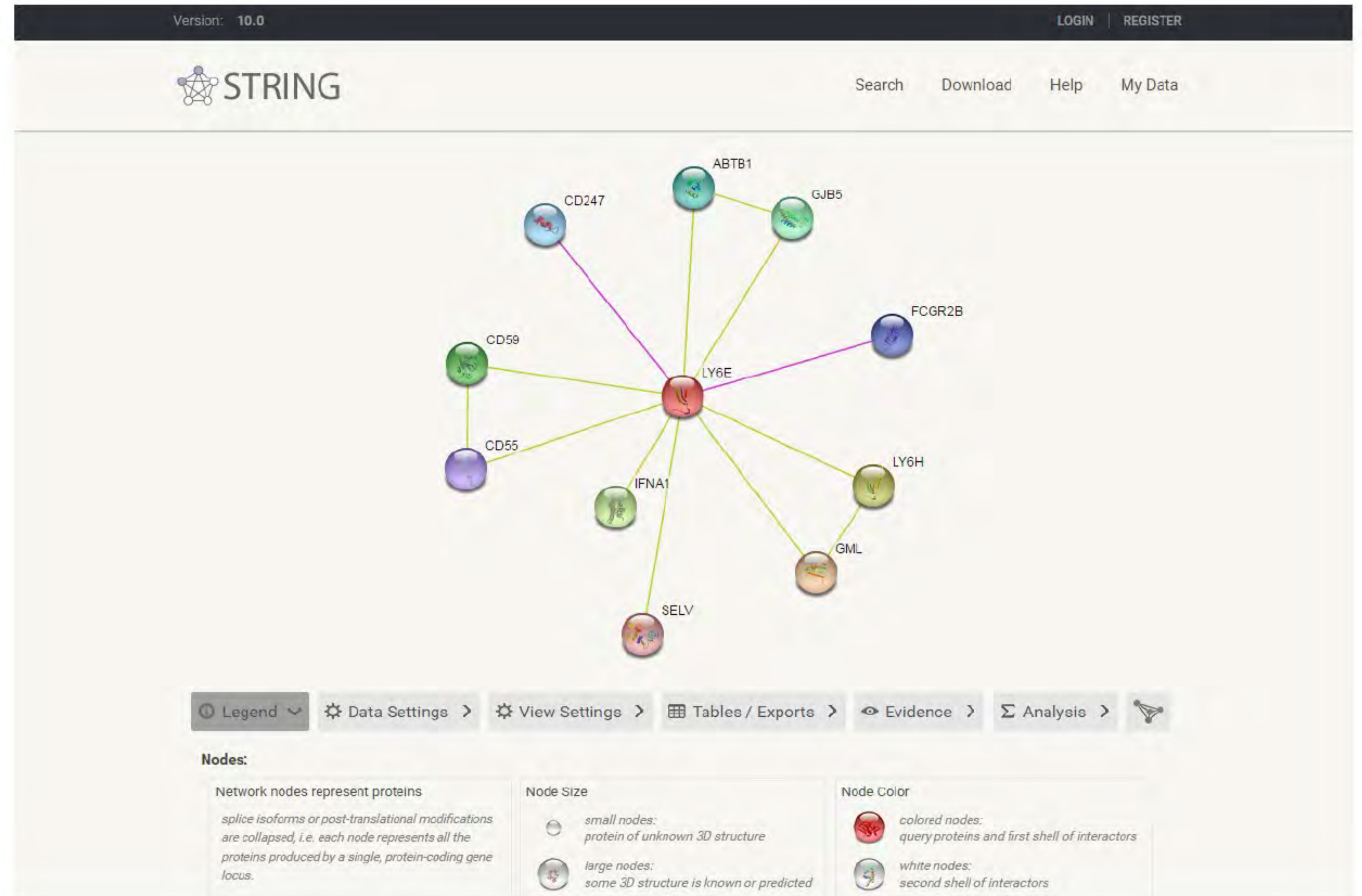
- Versions
- APIs
- Licensing
- Usage

CREDITS

- Funding
- Datasources
- Partners
- Software


STRING: functional protein association networks

<http://string-db.org/>




PANTHER – Gene Ontology and Pathways Classification System

<http://www.pantherdb.org/panther/prowler.jsp>



GENEONTOLOGY
Unifying Biology



PANTHER
Classification System

Home

About

PANTHER Data

PANTHER Tools

Workspace

Downloads

Help/Tutorial

Now includes comprehensive GO annotations directly imported from the GO database

Search

All

Go

Quick links

[Whole genome function views](#)

[Genome statistics](#)

[How to cite PANTHER](#)

[NEW! Recent publication describing PANTHER](#)

News


PANTHER gene analysis tools now support comprehensive GO annotations.

[Click](#) for additional info.

Newsletter subscription

Enter your Email:

Subscribe



Gene List Analysis

Browse

Sequence Search

cSNP Scoring

Keyword Search

Please refer to our article in [Nature Protocols](#) for detailed instructions on how to use this page.

Help Tips

Steps:

1. Select list and list type to analyze

2. Select Organism

3. Select operation

1.

Enter ids and or select file for batch upload. Else enter ids or select file or list from workspace for comparing to a reference list.

Enter IDs:
[Supported IDs](#)

Upload IDs:
[File format](#)

Choose File No file chosen

Please [login](#) to be able to select lists from your workspace.

Select List Type:

☒ ID List

☐ Previously exported text search results

☐ Workspace list

☐ PANTHER Generic Mapping File

2.

Select organism.

Homo sapiens

Mus musculus

Rattus norvegicus

Gallus gallus

Danio rerio

3. Select Analysis.

☒ Functional classification viewed in gene list


☐ Functional classification viewed in pie chart

☐ Statistical overrepresentation test ☐ Use default settings


☐ Statistical enrichment test ☐ Use default settings

PANTHER – Gene Ontology and Pathways Classification System

<http://www.pantherdb.org/panther/prowler.jsp>



GENE ONTOLOGY
Unifying Biology



PANTHER
Classification System

LOGINREGISTERCONTACT US

HomeAboutPANTHER DataPANTHER ToolsWorkspaceDownloadsHelp/Tutorial

Now includes comprehensive GO annotations directly imported from the GO database

Search

AllGo

Quick links

[Whole genome function views](#)

[Genome statistics](#)

[How to cite PANTHER](#)

[NEW! Recent publication describing PANTHER](#)

News

PANTHER gene analysis tools now support comprehensive GO annotations.

[Click for additional info.](#)

Newsletter subscription

Enter your Email:

Subscribe

Gene List AnalysisBrowseSequence SearchcSNP ScoringKeyword Search

Prowler ⓘ

Browse the PANTHER system using the Prowler, and retrieve results for different data associated with the ontology and pathway terms, such as individual genes or families and subfamilies of proteins. [About the PANTHER Ontologies](#)

Biological ProcessMolecular FunctionCellular ComponentProtein ClassPathwaySpecies

Type a search term for live filtering

☐

apoptotic process

☒

induction of apoptosis

☐

negative regulation of apoptotic process

☐

biological adhesion

☐

biological regulation

☐

cell killing

☐

cellular component organization or biogenesis

☐

cellular process

☐

developmental process

☐

growth

☐

immune system process

☐

localization

3044 - Genes

276 - Families

52 - Pathways

All results must belong to the following Biological Process, or its subcategories:

I. induction of apoptosis

CPDB

http://consensuspathdb.org/

ConsensusPathDB – human: integrates interaction networks in Homo sapiens

includes: binary and complex protein-protein,genetic, metabolic, signaling, gene regulatory and drug-target interactions, as well as biochemical pathways




human yeast mouse
Release 31 (01. Sept. 2015)

ConsensusPathDB-human integrates interaction networks in *Homo sapiens* including **binary and complex protein-protein, genetic, metabolic, signaling, gene regulatory** and **drug-target** interactions, as well as biochemical pathways. Data originate from currently **32** public resources for interactions (listed below) and interactions that we have curated from the literature. The interaction data are integrated in a complementary manner (avoiding redundancies), resulting in a seamless interaction network containing different types of interactions.

Kamburov, A. *et al.* (2013) The ConsensusPathDB interaction database: 2013 update. *Nucleic Acids Res.*
Kamburov, A. *et al.* (2011) ConsensusPathDB: toward a more complete picture of cell biology. *Nucleic Acids Res.*
Kamburov, A. *et al.* (2009) ConsensusPathDB—a database for integrating human interaction networks. *Nucleic Acids Res.*
Pentchev, K. *et al.* (2010) Evidence mining and novelty assessment of protein-protein interactions with the ConsensusPathDB plugin for Cytoscape. *Bioinformatics*
A poster about ConsensusPathDB is available [here](#).

Current statistics:

unique physical entities:	158,523
unique interactions:	468,570
gene regulations:	17,086
protein interactions:	261,085
genetic interactions:	443
biochemical reactions:	21,070
drug-target interactions:	158,874
pathways:	4,593

Integrated databases:

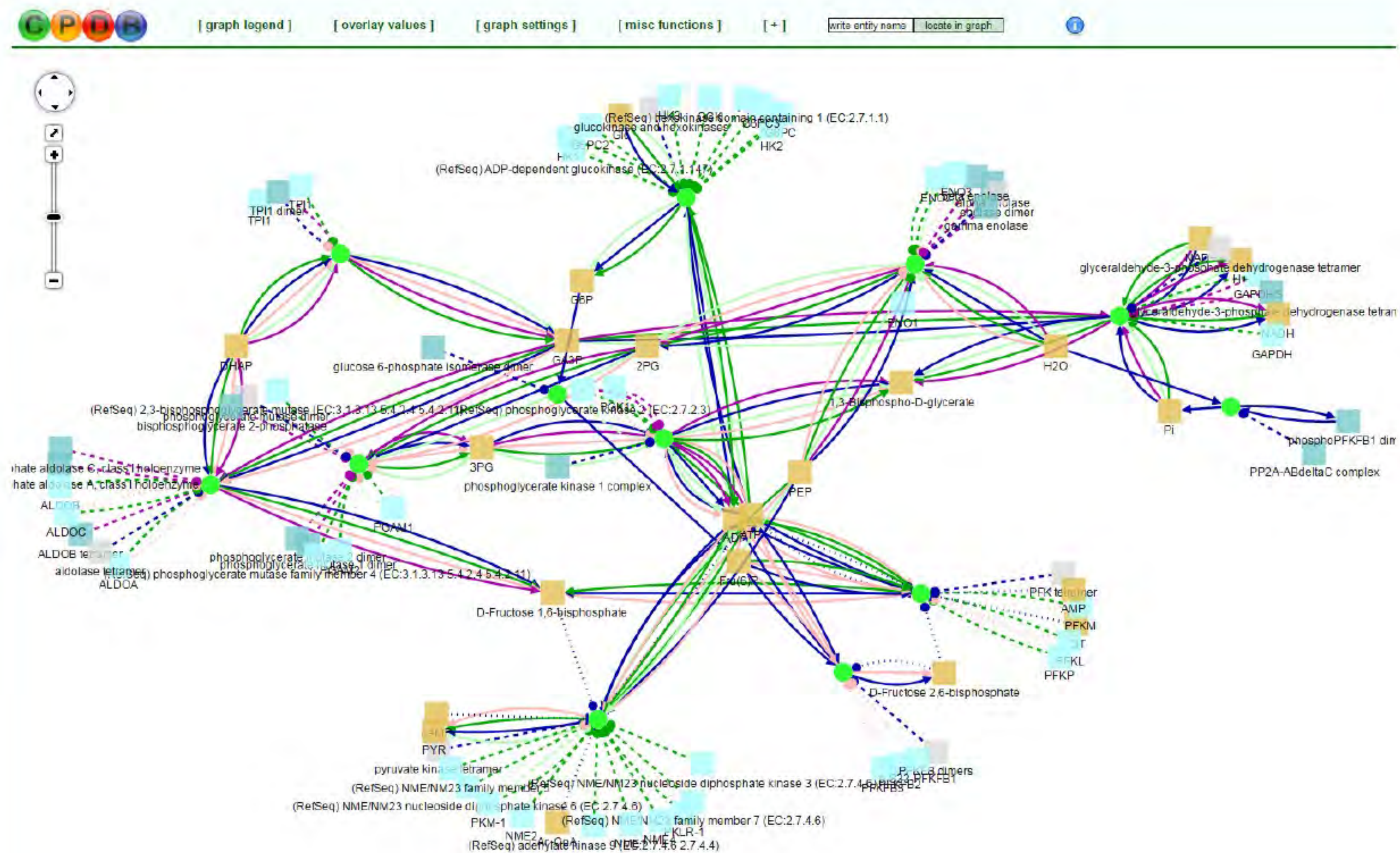
	name	protein interactions	signaling reactions	metabolic reactions	gene regulations	genetic interactions	drug-target interactions	biochemical pathways
	BIND	✓	✗	✗	✓	✗	✗	✗
	BioCarta	✗	✓	✗	✓	✗	✗	✓
	Biogrid	✓	✗	✗	✗	✓	✗	✗
	CORUM	✓	✗	✗	✗	✗	✗	✗
	ChEMBL	✗	✗	✗	✗	✗	✓	✗
	DIP	✓	✗	✗	✗	✗	✗	✗
	DrugBank	✓	✗	✗	✗	✗	✓	✗
	EHMN	✗	✗	✓	✗	✗	✗	✓
	HPRD	✓	✗	✗	✗	✗	✗	✗
	HumanCyc	✗	✗	✓	✗	✗	✗	✓
	INOH	✗	✓	✓	✗	✗	✗	✓
	InnateDB	✓	✓	✗	✓	✗	✗	✗
	IntAct	✓	✗	✗	✗	✗	✗	✗

CPDB

<http://consensuspathdb.org/>

ConsensusPathDB – human: integrates interaction networks in Homo sapiens

includes: binary and complex protein-protein, genetic, metabolic, signaling, gene regulatory and drug-target interactions, as well as biochemical pathways

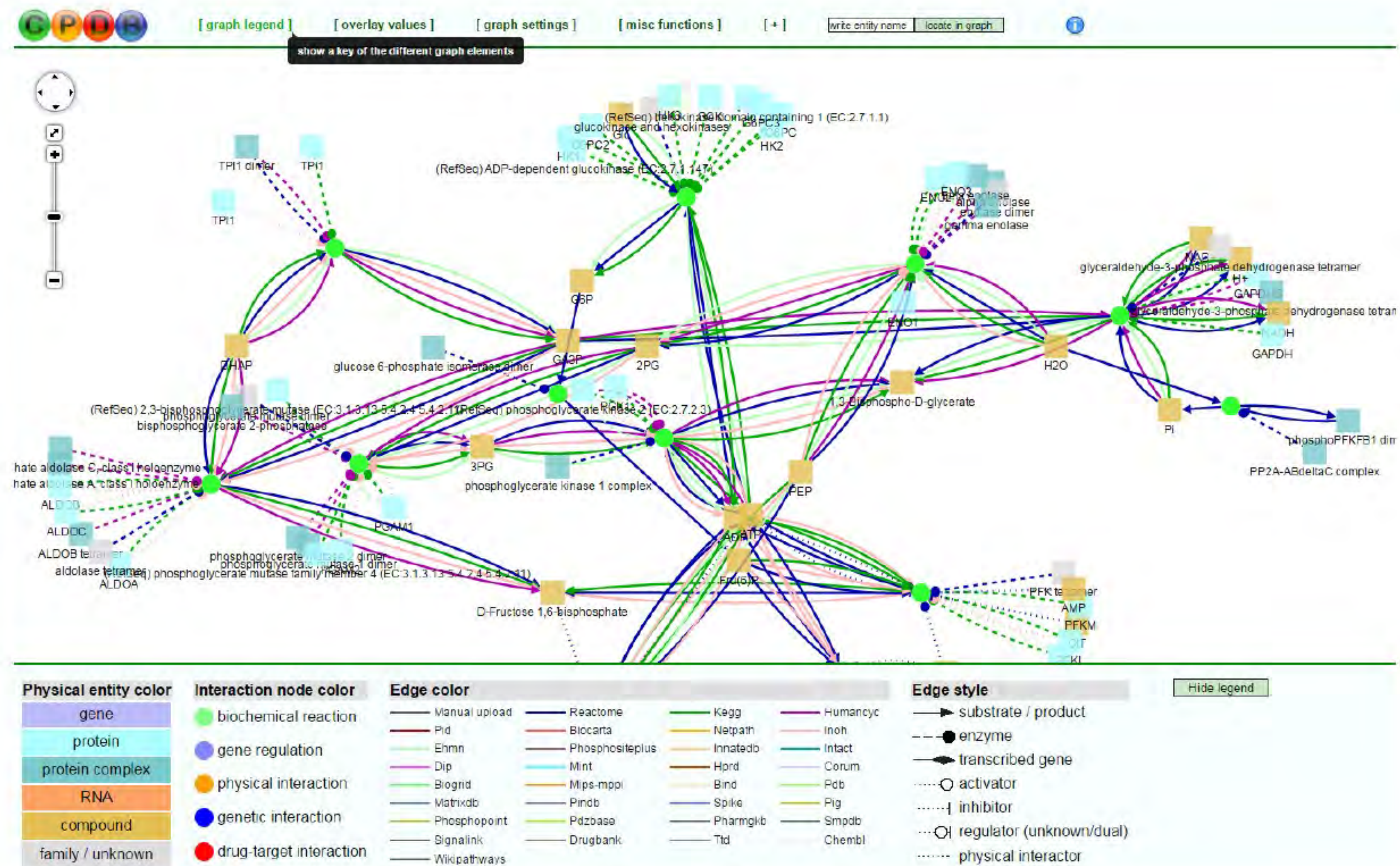


CPDB

<http://consensuspathdb.org/>

ConsensusPathDB – human: integrates interaction networks in Homo sapiens

includes: binary and complex protein-protein, genetic, metabolic, signaling, gene regulatory and drug-target interactions, as well as biochemical pathways



Pathway Analysis— next section: a short demo/hands-on

Major types of Pathway Analysis

Mapping genes of interest to known Pathways
Pathway Enrichment Analysis

Focusing on Analysis of Gene Lists