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 Riutta[3], Nuno Nunes[1], Kristina Hanspers[3], Egon L. Willighagen[1], Anwesha Bohler[1], Jonathan Mélius[1], Andra Waagmeester[1,4], Sravanthi R. Sinha[5], Ryan Miller[1], Susan L. Coort[1], Elisa Cirillo[1], Bart Smeets[1], Chris T. Evelo[1,2] and Alexander R. Pico[3,*]

Author Affiliations

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

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

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

[4]Micelio, Antwerp, 2180 Antwerp, Belgium

[5]Keshav 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

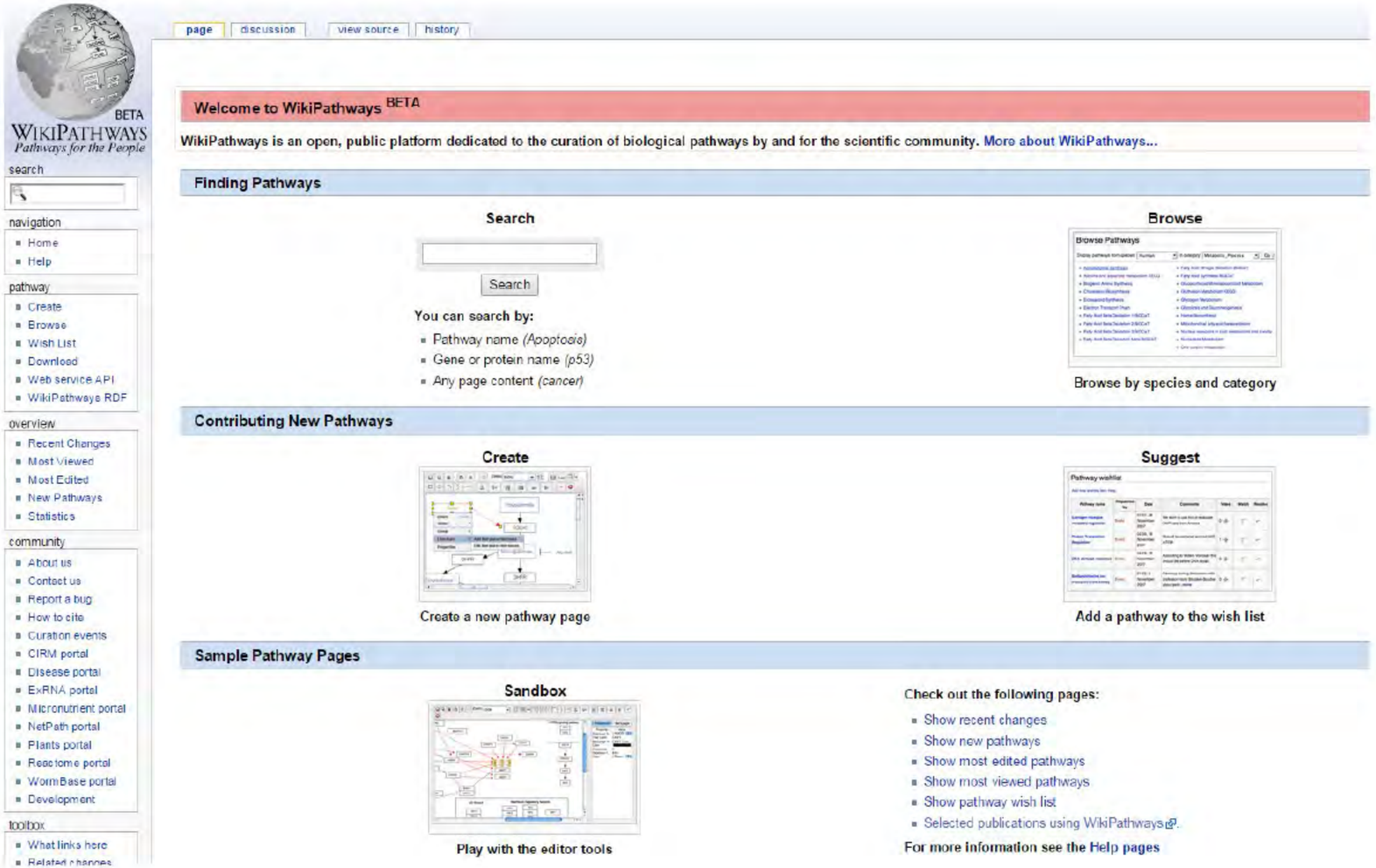
Print Share

CrossMark

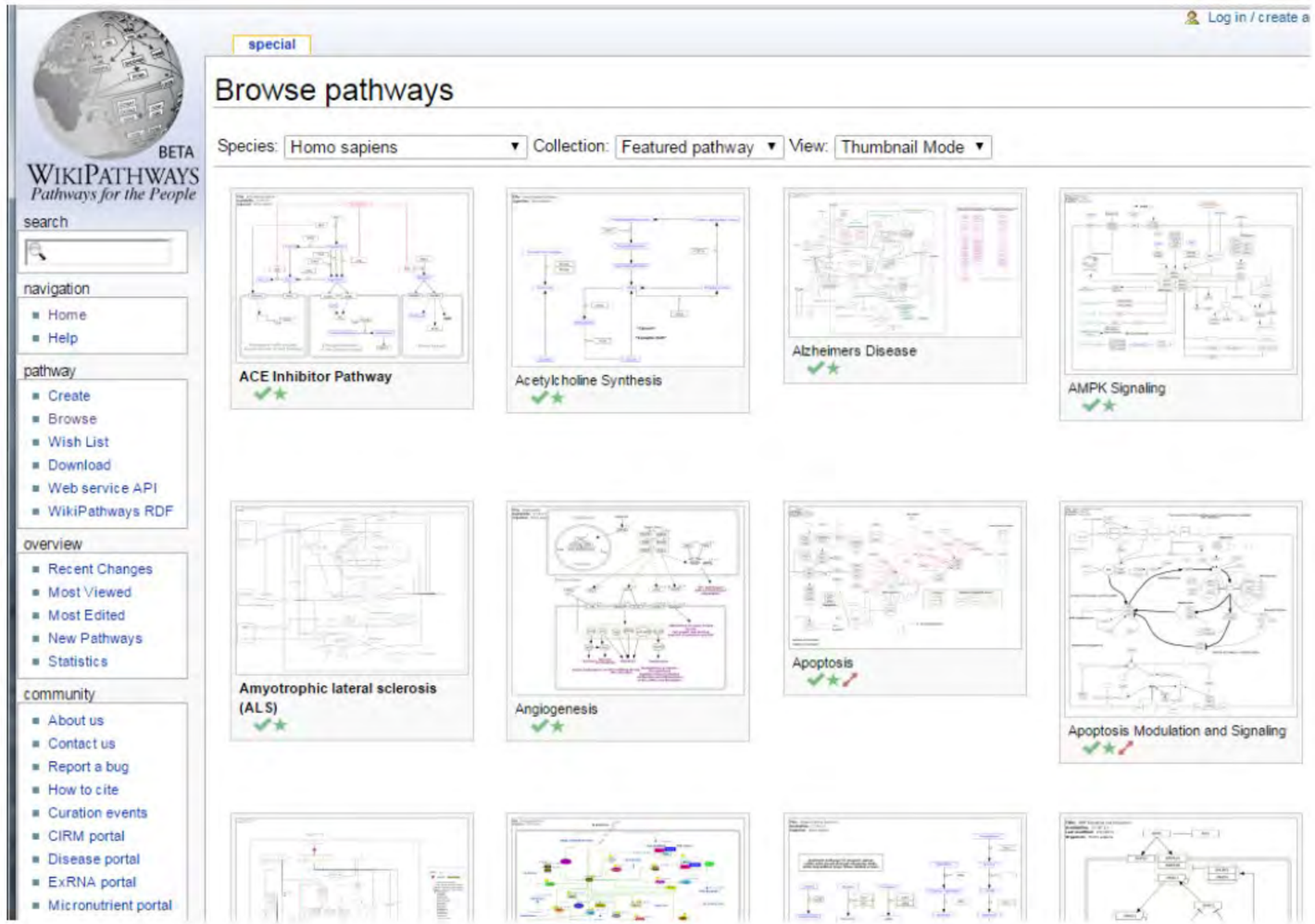
Subject Areas

Data visualization

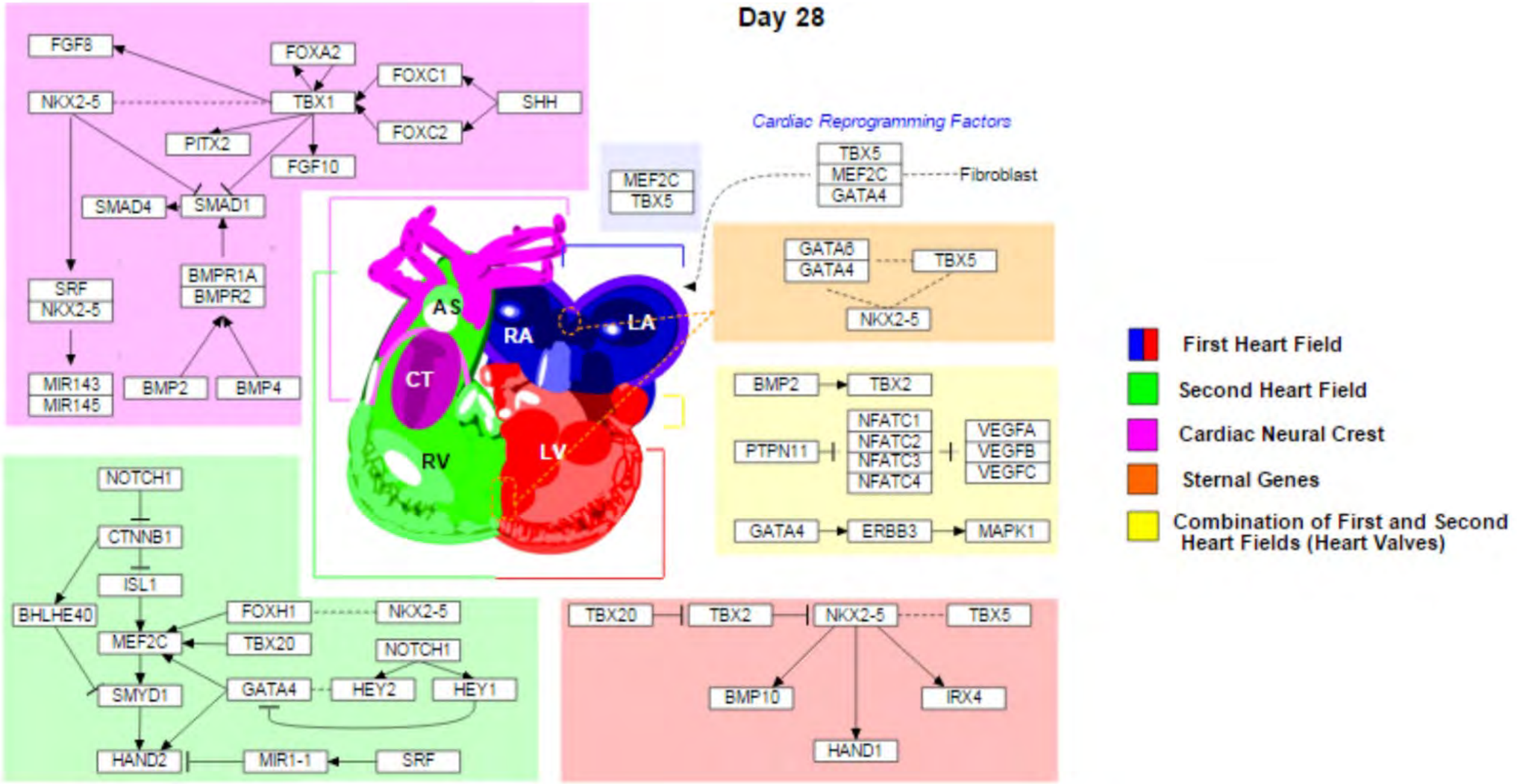
WikiPathways



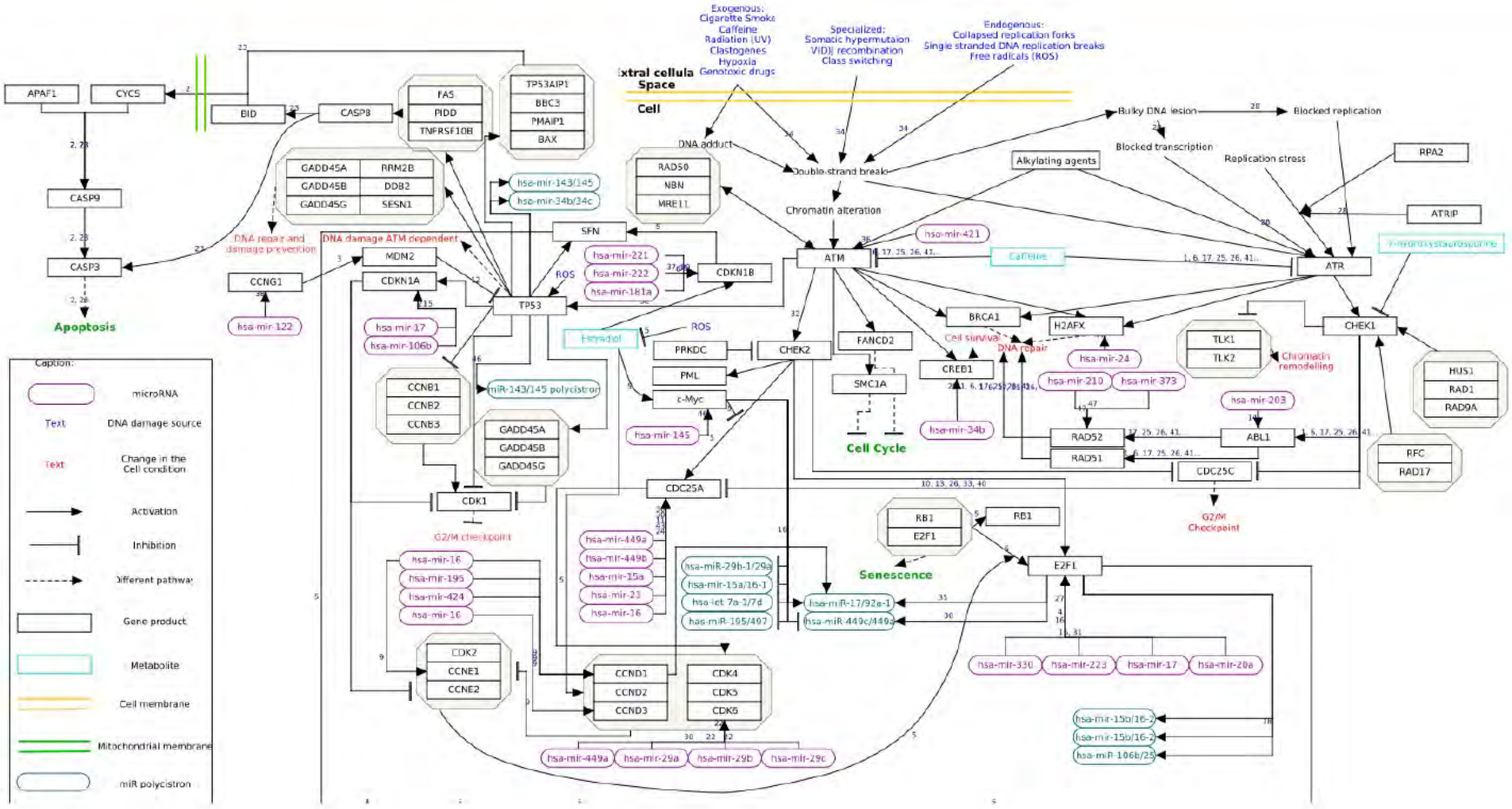
WikiPathways



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?

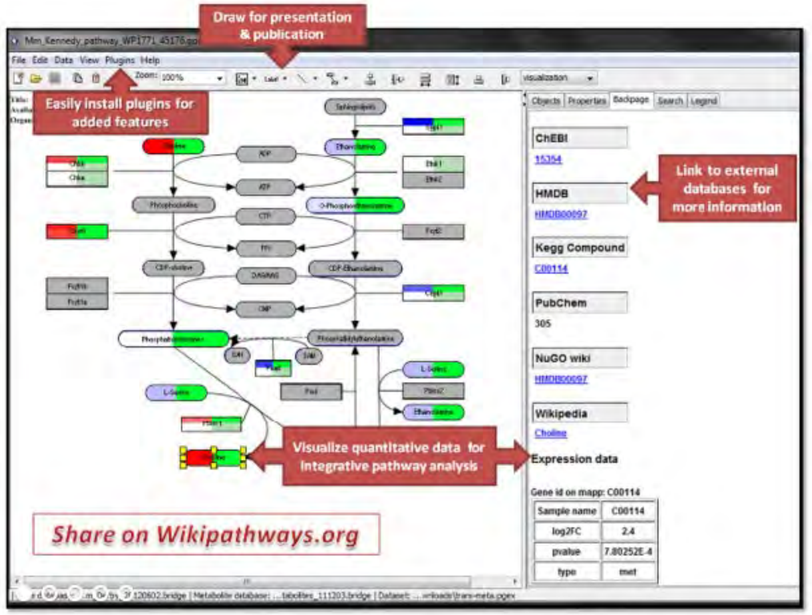
PathVisio is a free open-source biological pathway analysis software that allows you to draw, edit and analyze biological pathways. Learn more.

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.



News

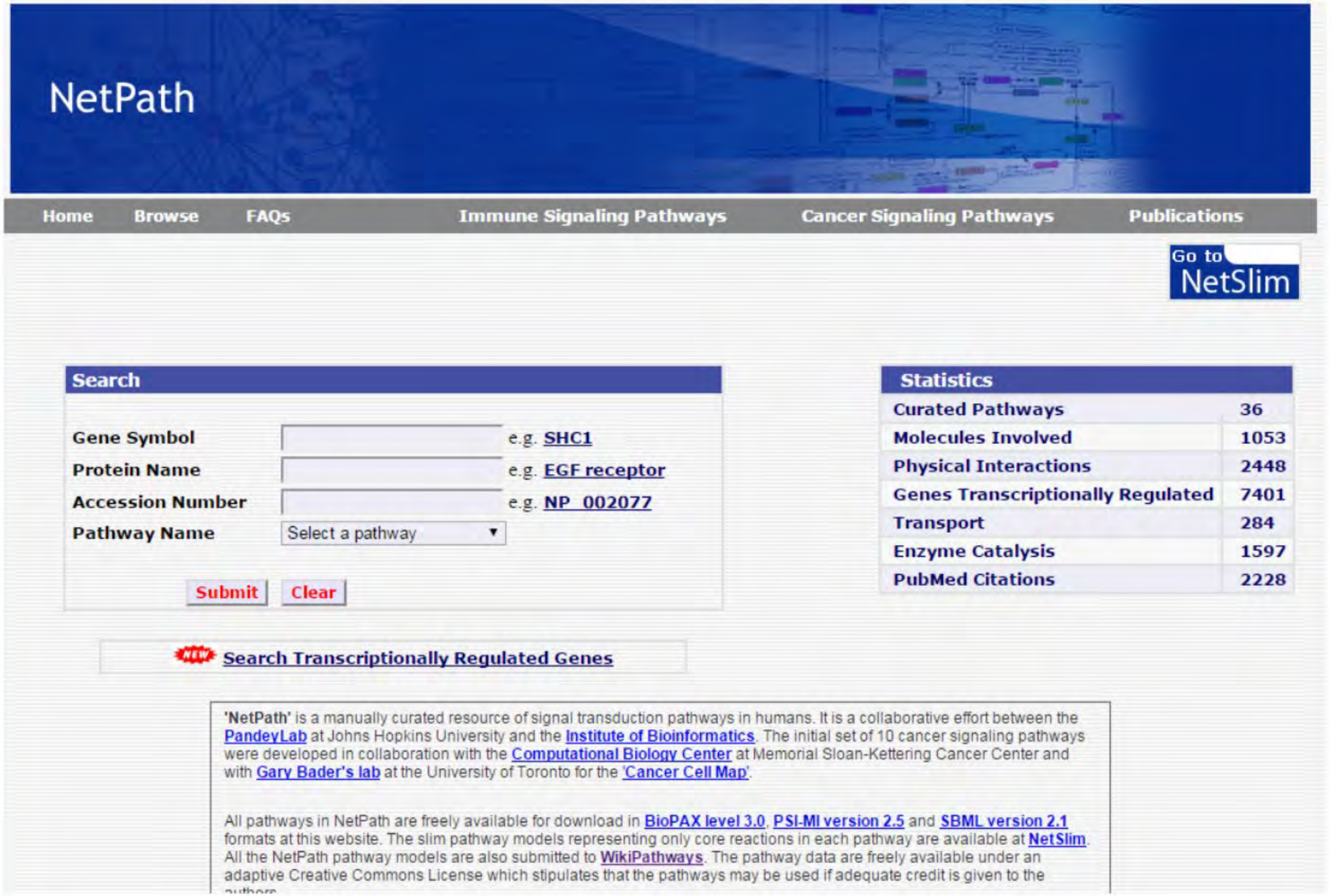
- **Check out the new WikiPathways paper!** "WikiPathways: capturing the full diversity of pathway knowledge." Nucl. Acids Res. first published online October 19, 2015. doi: 10.1093/nar/gkv1024
- **BioSB 2015 Application Showcase:** Martina Kutmon presented WikiPathways, PathVisio and the WikiPathways 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!**

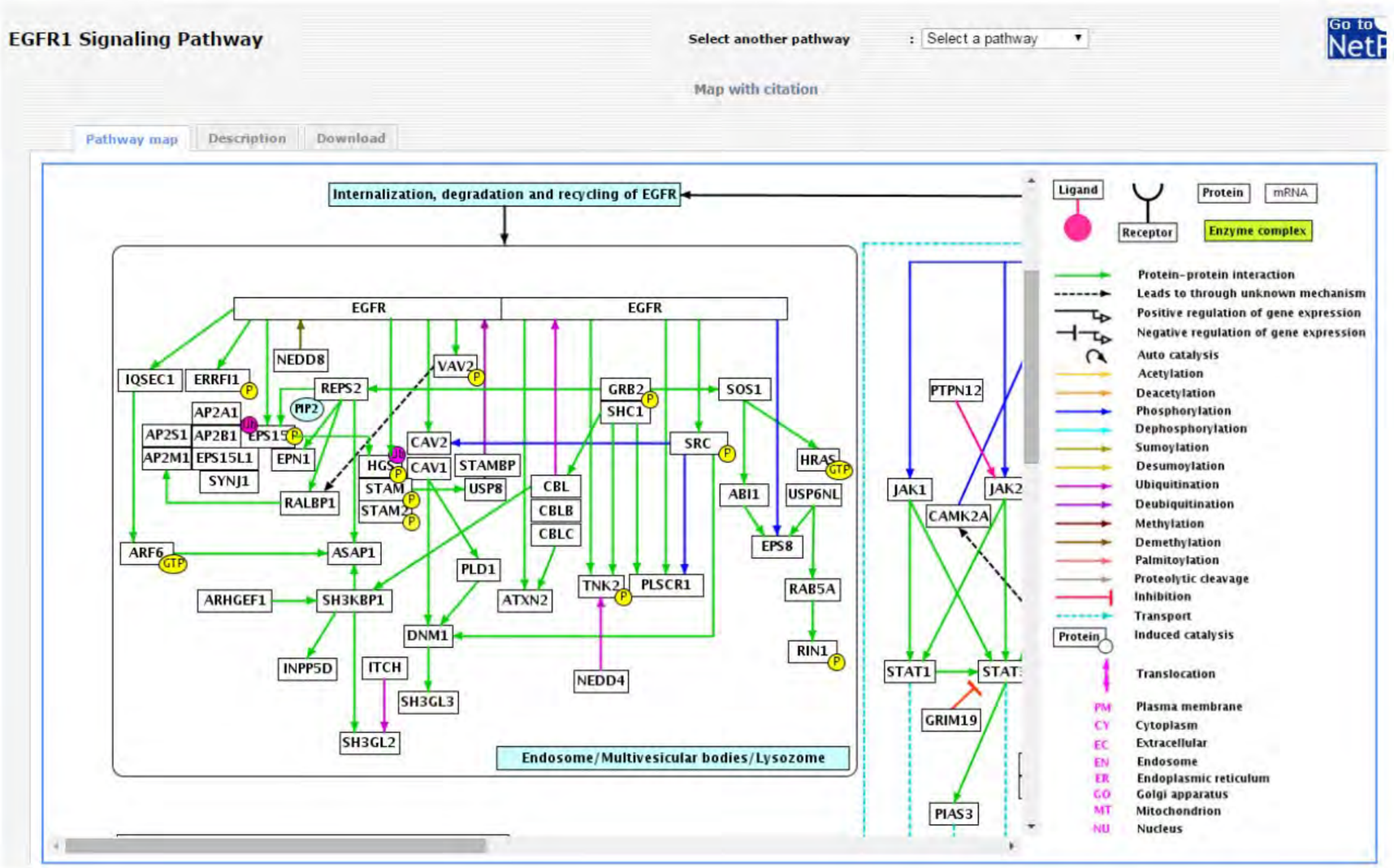
NetPath: a manually curated resource of signal transduction pathways in humans

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



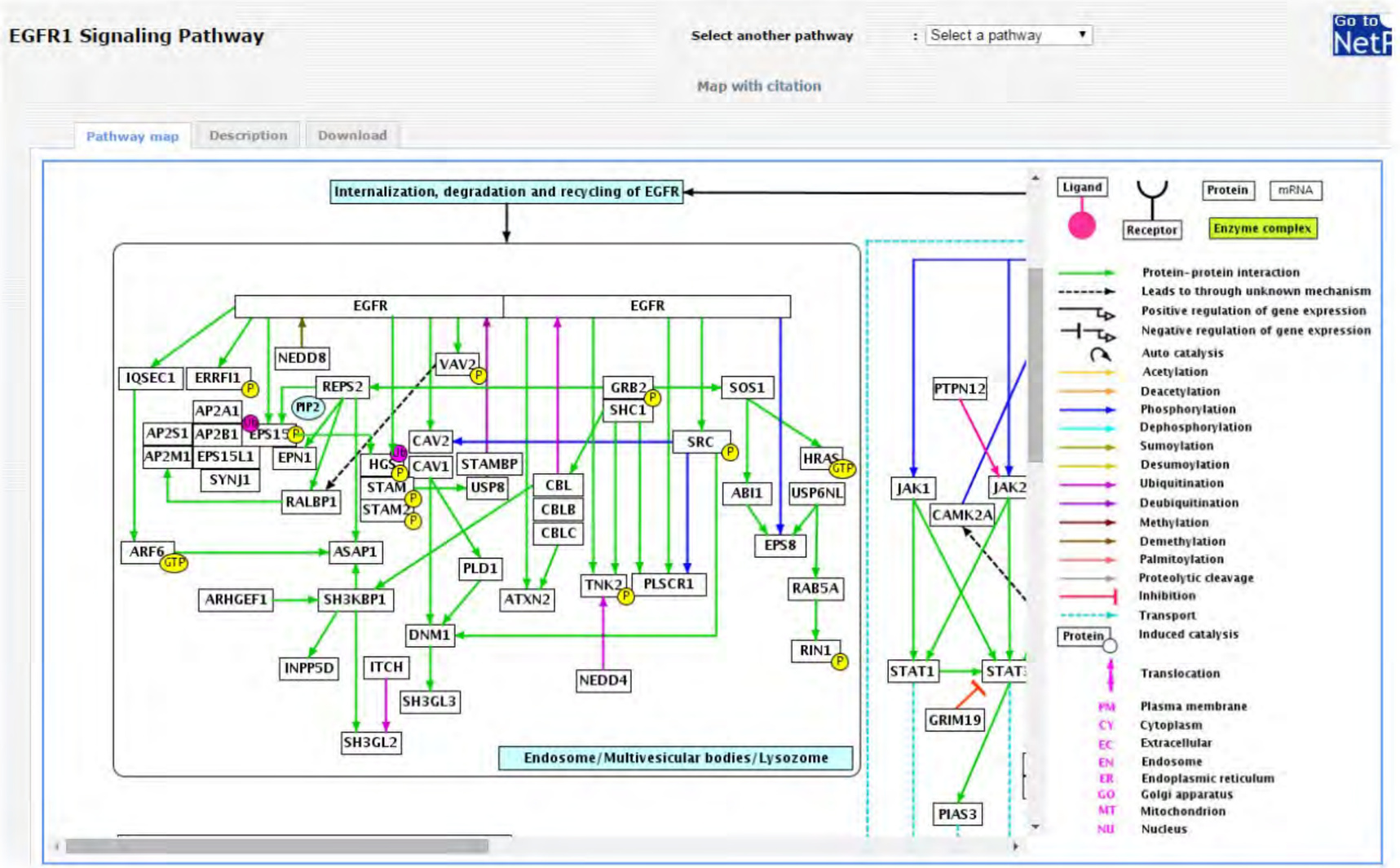
NetPath: a manually curated resource of signal transduction pathways in humans

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



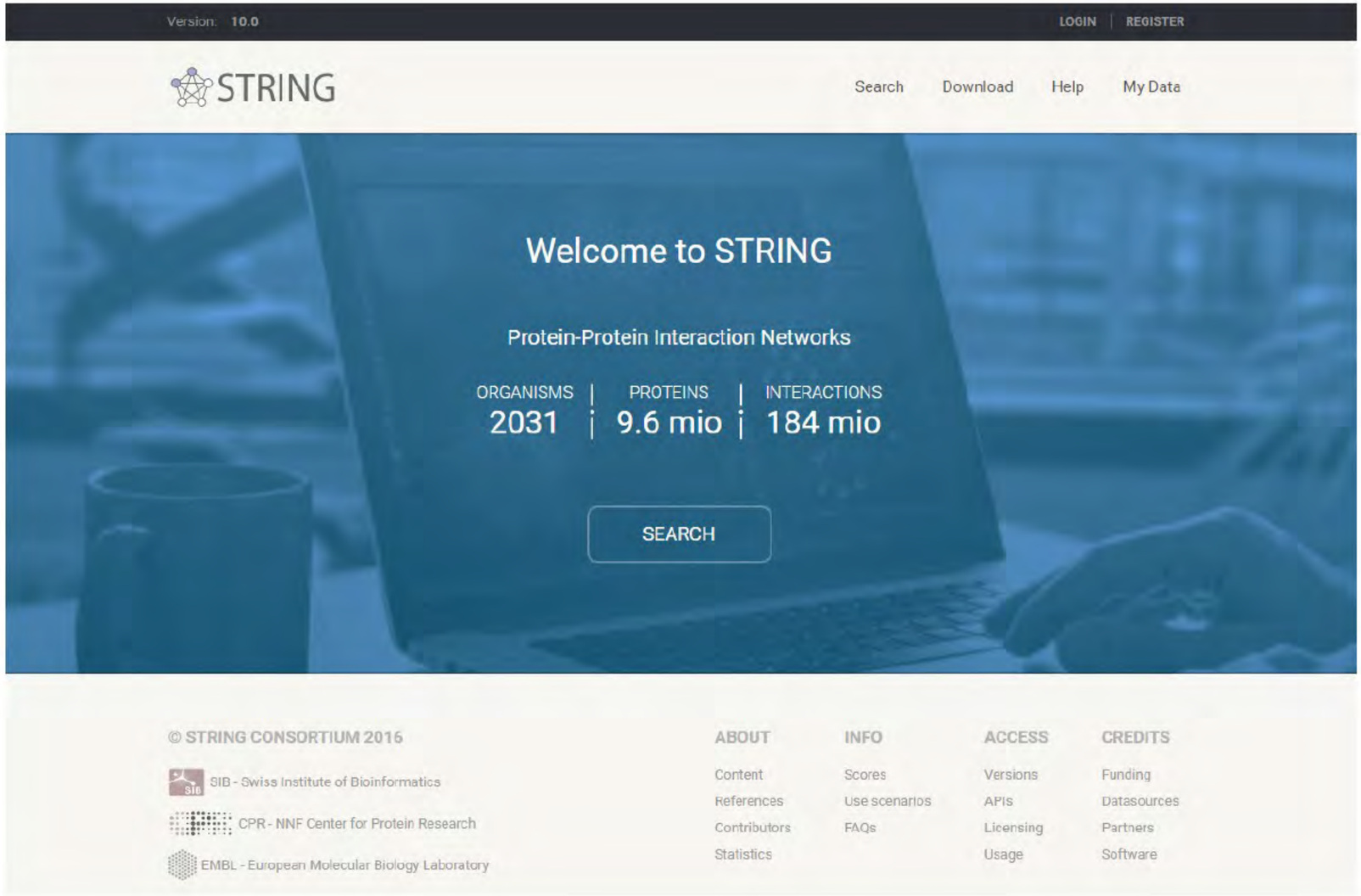
NetPath: a manually curated resource of signal transduction pathways in humans

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



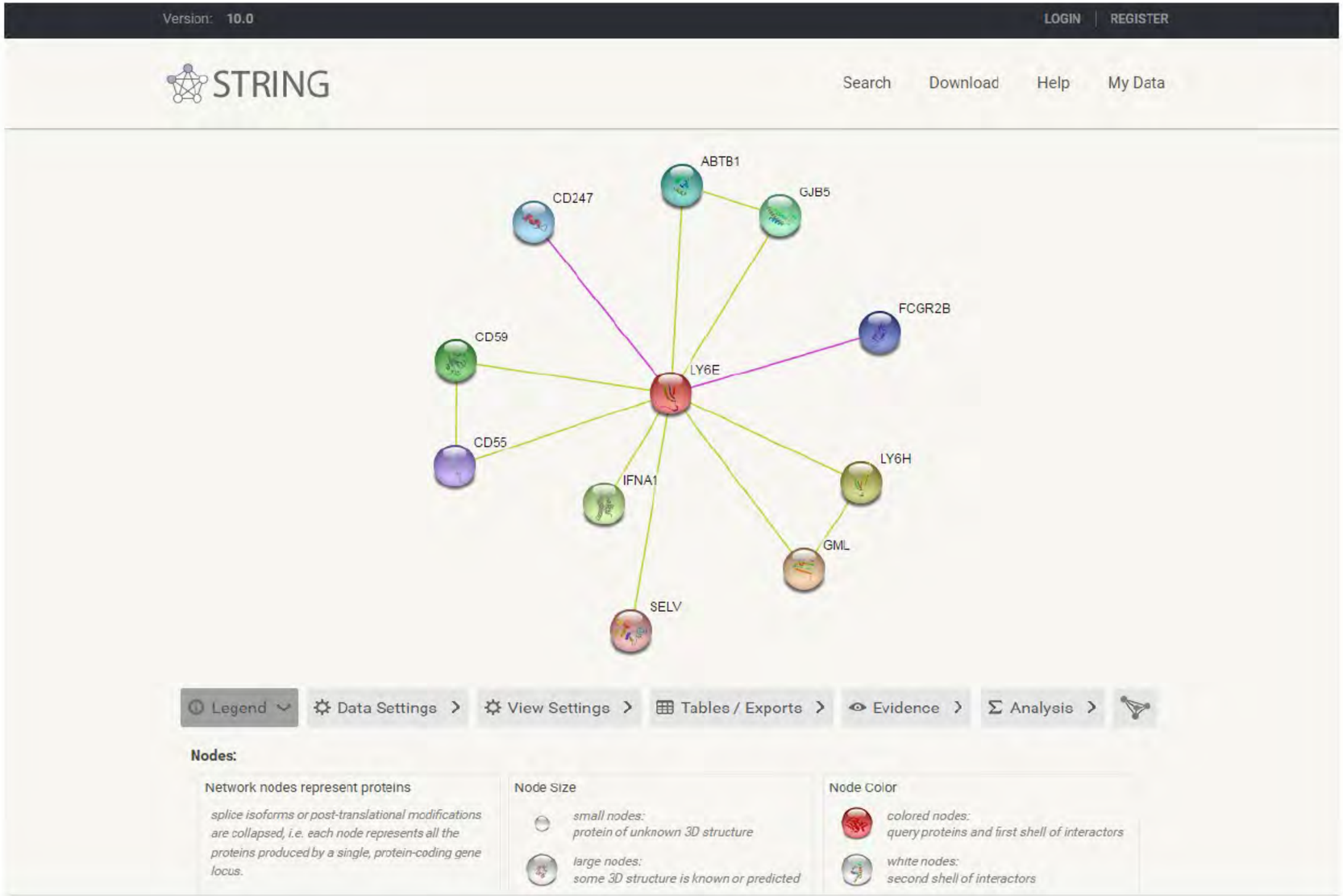
STRING: functional protein association networks

http://string-db.org/



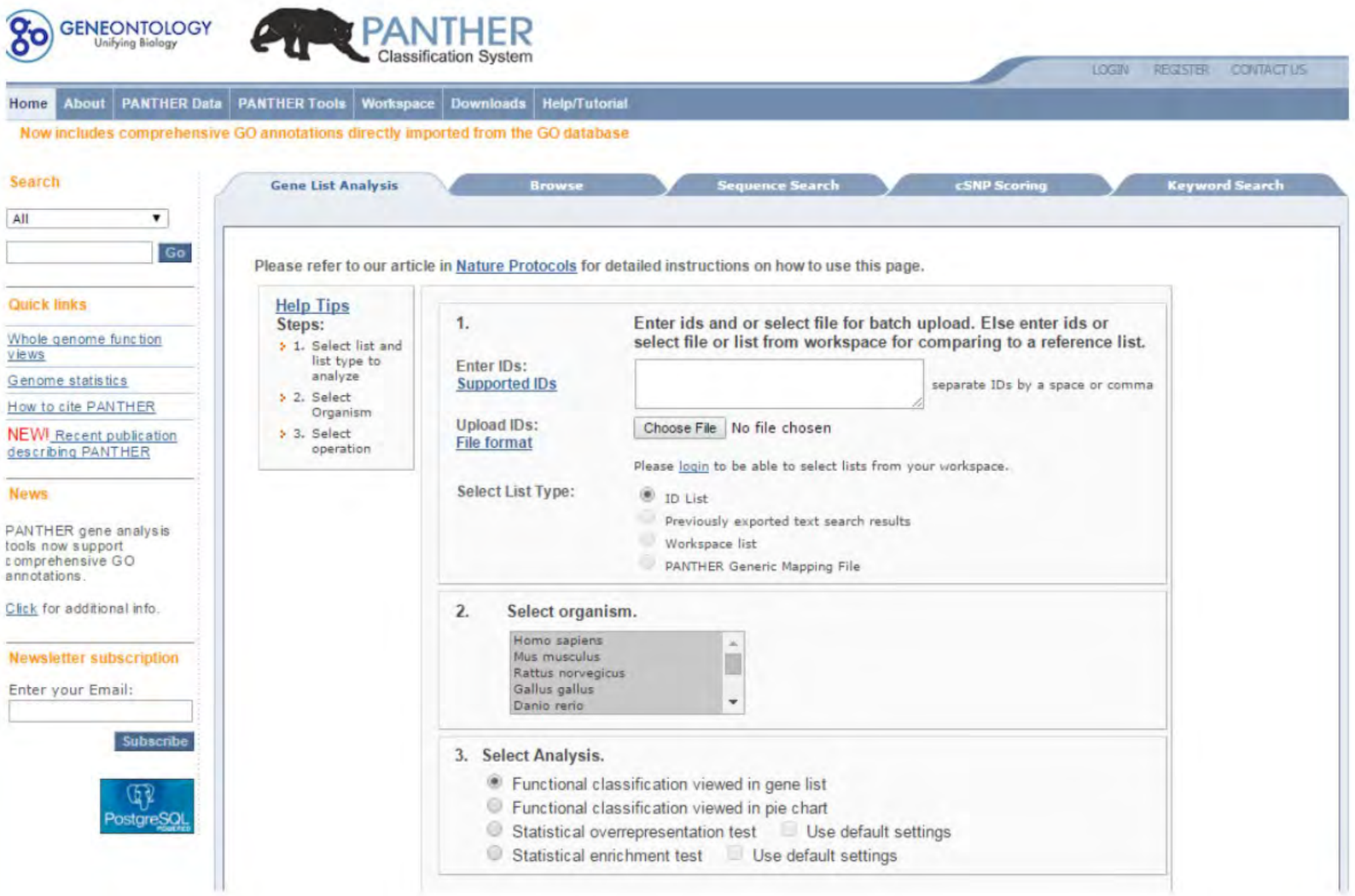
STRING: functional protein association networks

http://string-db.org/



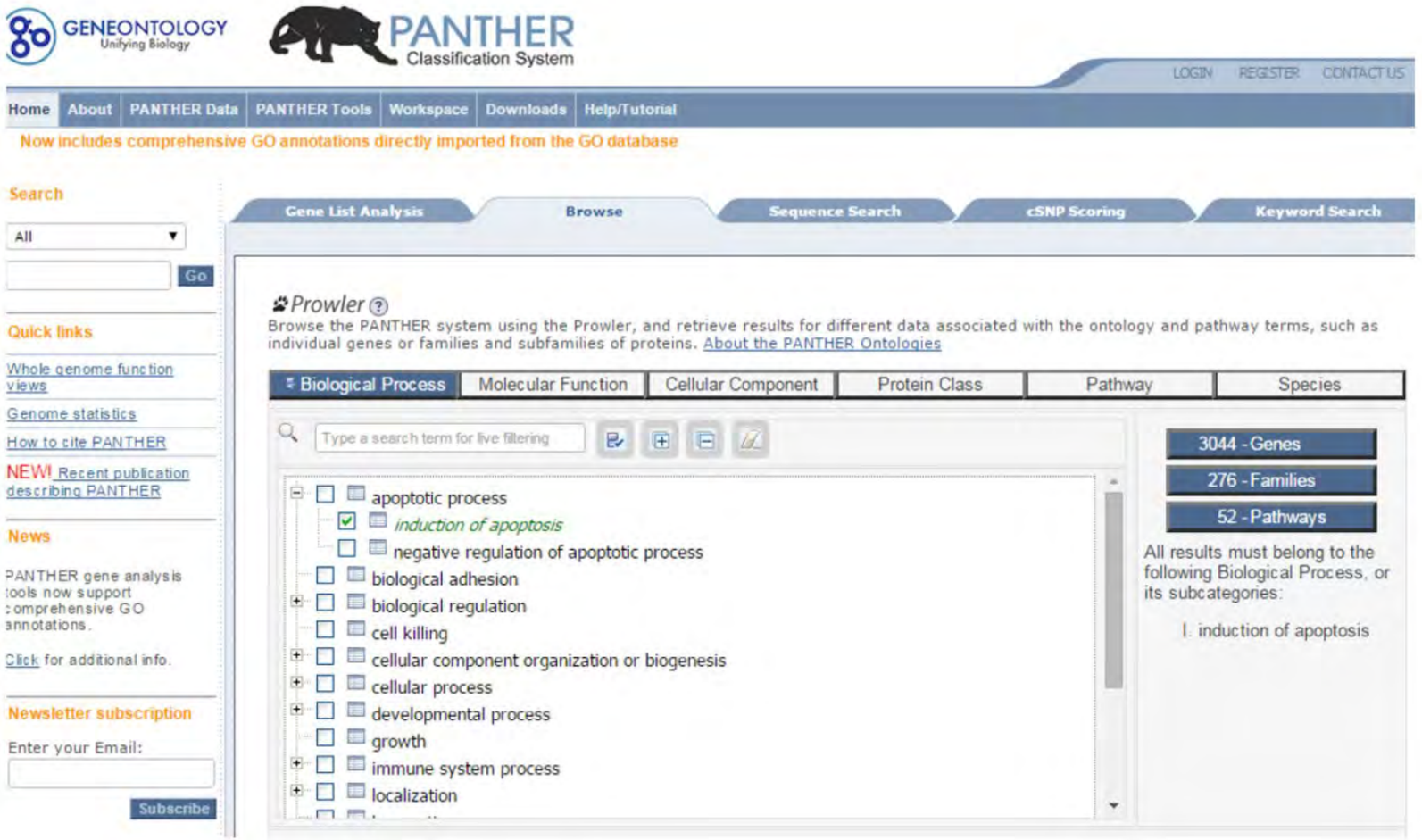
PANTHER – Gene Ontology and Pathways Classification System

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



PANTHER – Gene Ontology and Pathways Classification System

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



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

Max Planck Institute for Molecular Genetics

home
content information
search
- interactions of molecules/pathways
- shortest interaction paths

gene set analysis
metabolite set analysis
download / data access
documentation
news
contact

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:	**458,570**
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:

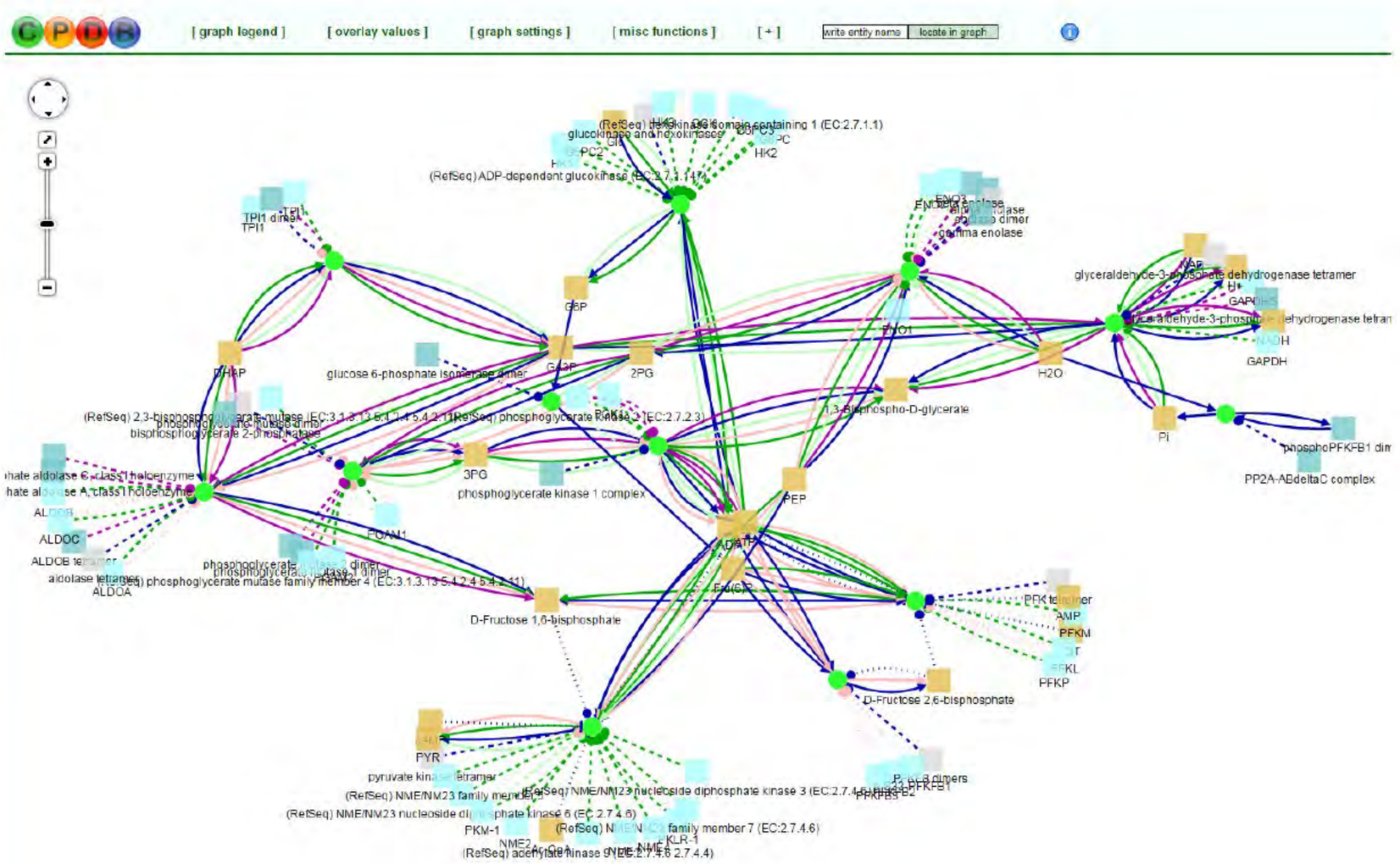
name	protein interactions	signaling reactions	metabolic reactions	gene regulations	genetic interactions	drug-target interactions	biochemical pathways
BIND	✔	✖	✖	✔	✖	✖	✖
BioCarta	✖	✔	✖	✔	✖	✖	✔
Biogrid	✔	✖	✖	✖	✔	✖	✖
CORUM	✔	✖	✖	✖	✖	✖	✖
Chembl	✖	✖	✖	✖	✖	✔	✖
DIP	✔	✖	✖	✖	✖	✖	✖
DrugBank	✔	✖	✖	✖	✖	✔	✖
EHMN	✖	✖	✔	✖	✖	✖	✔
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

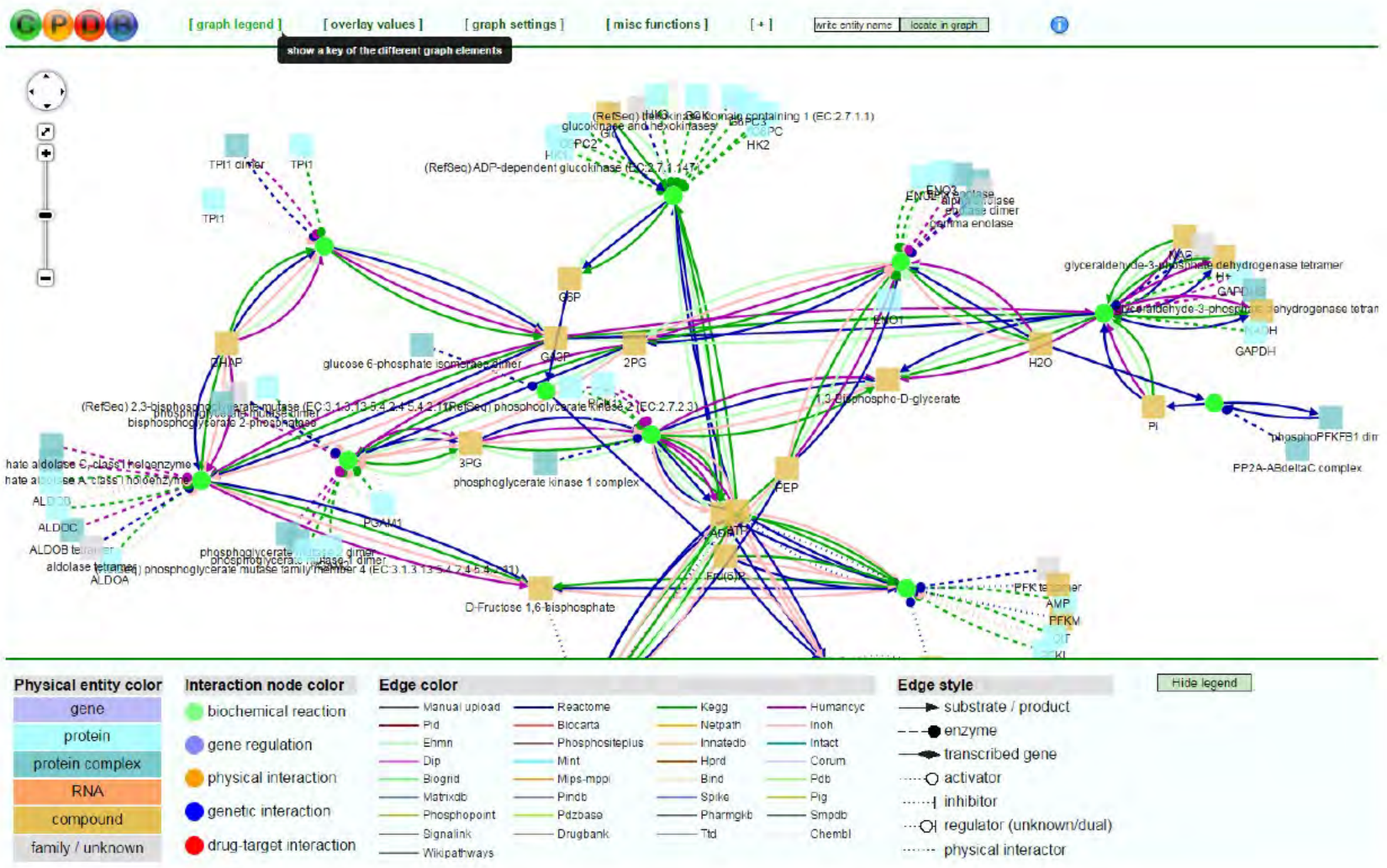


CPDB

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