Overview of NCIBI Suite of Tools

National Center for Integrative Biomedical Informatics
(NCIBI - www.ncibi.org)

Funding provided by NIH, NIDA Grant U54-DA021915

(NCBC Web Page: http://www.ncbcs.org)

NCIBI Tools

Navigation

- Home
- About
- Tools
- Biological Projects
- Working with NCIBI
- Education
- Outreach & Dissemination
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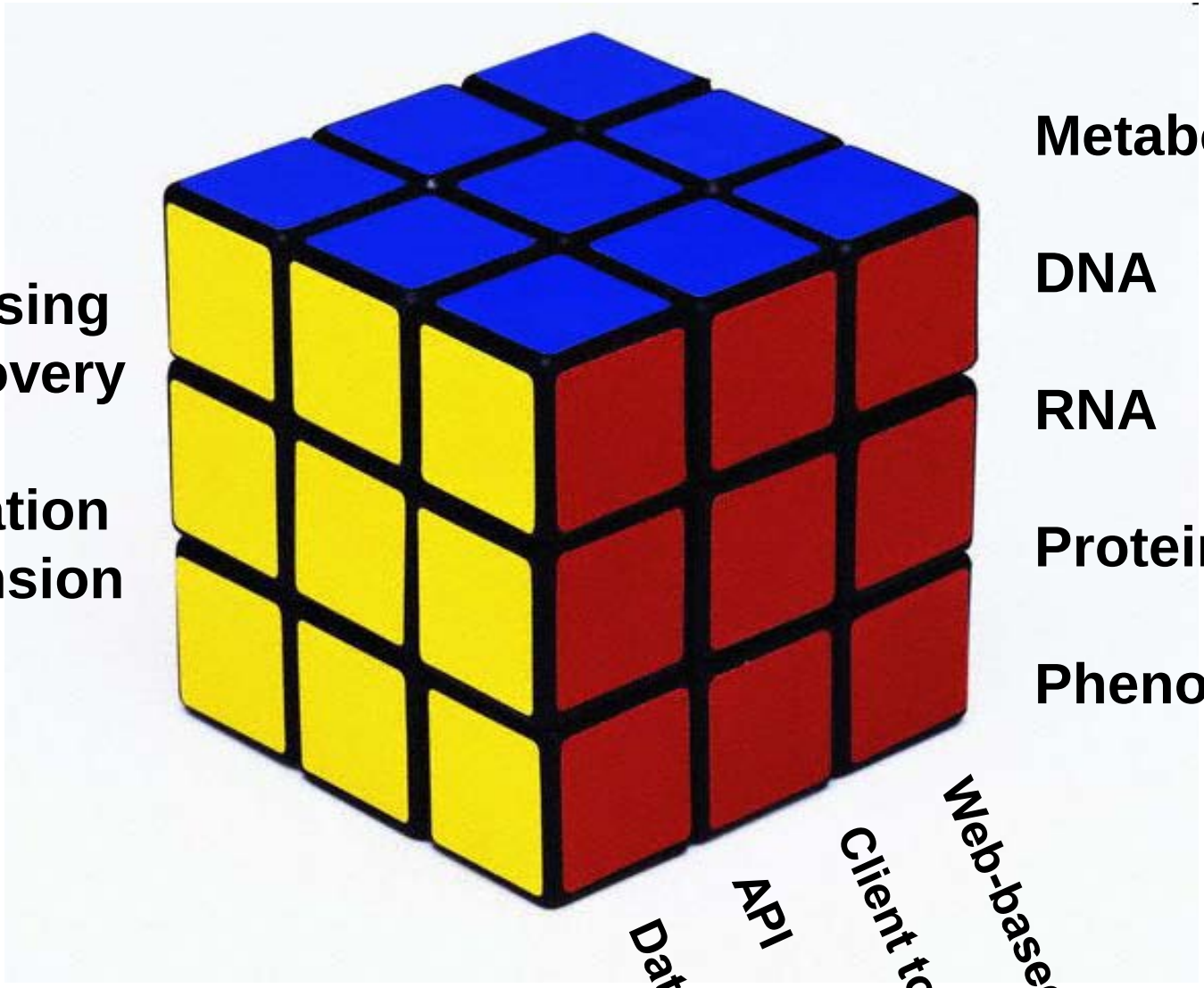
Try Our Tools: Getting started with NCIBI tools

Coming soon: Tools arranged by biological hierarchies.

Exploratory analysis | Conceptual literature searches | Databases | Other

To explore interactions

Use this tool	If you want to:
ConceptGen **ConceptGen** (tool) **ConceptGen** (tutorial) Related gene lists to enriched concepts and other genes enriched for the given concept.	Find concepts related to your list of genes Statistically validate enriched concepts Find genes enriched for the same concept as your genes
MetScape **MetScape Plug in for Cytoscape** (tool) **MetScapei Plug in for Cytoscape** (tutorial)	Query a compound or list of compounds Explore reactions and pathways. Add in your own data Link to details and matches to pathway databases

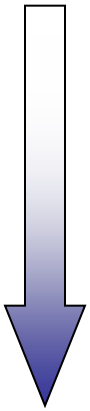

Browsing
Discovery
Validation
Expansion
Metabolite
DNA
RNA
Protein
Phenotypes
Databases
API
Client tools
Web-based

Integrating Tools and Data

- Integration occurs at several levels
  - User interface – making it easier for users to explore and gather information as they process data and form hypotheses
  - Data integration – identifying and developing methods to integrate different data types and sources.

Levels of Integration

User Interface:



- **Pencil and paper**
- **Copy, paste**
- **URL passing IDs, single authentication**
- **History of searches, persistence, memory**
- **Stored private datasets, workspace**

Core Databases:

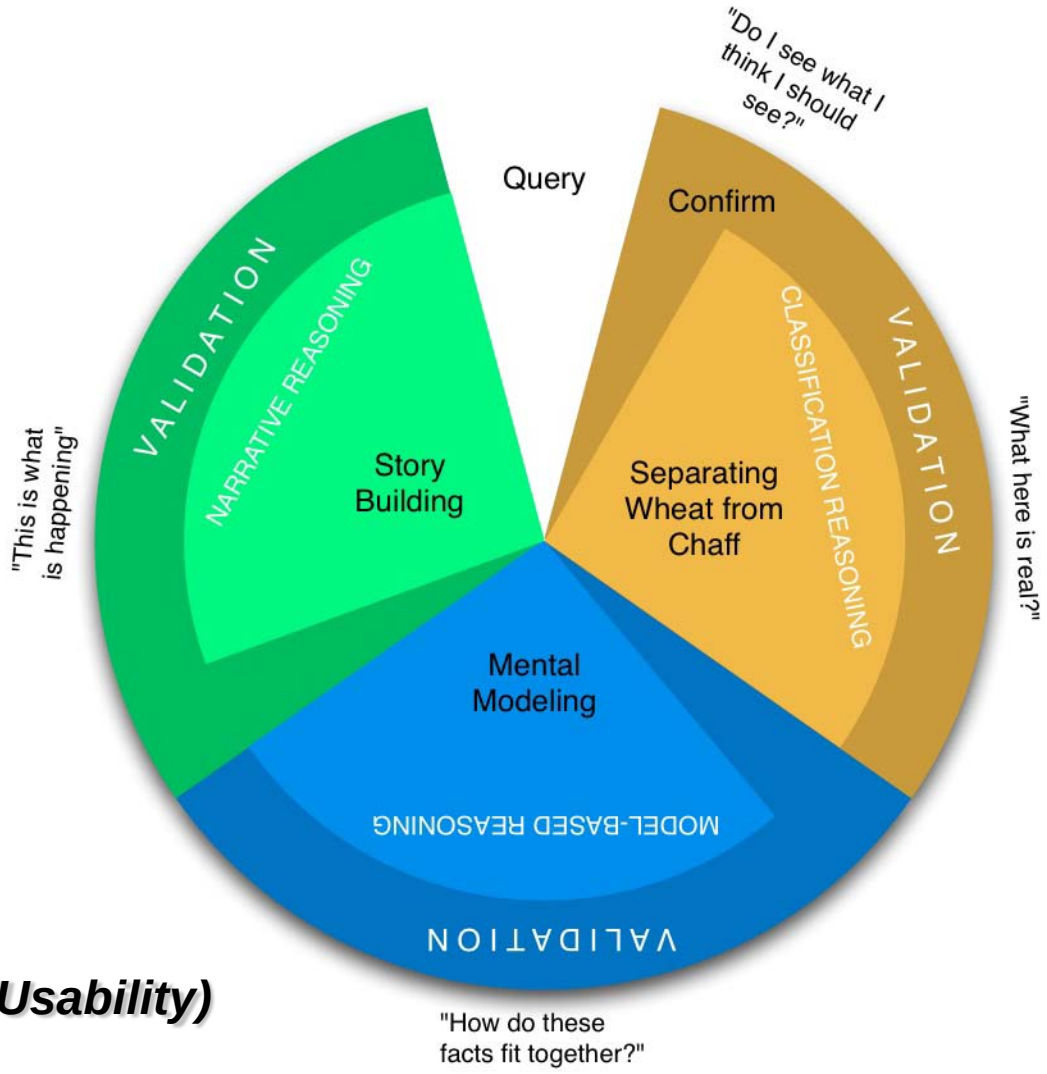
- Federated with common linkage of data
  - GeneID, ProteinID (Uniprot), PMID, *ConceptID, MoleculeID*

Poster #3: Alla Karnovsky (Metabolomics)

Understanding the User's Needs

- What do they expect?
- Where do they want to go?

- NCIBI is focused on usability and usefulness of tool development.



Talk in S24 by Barb Mirel (Usability)

How Users use our Tools

CONCEPT BROWSING

- Starting with a concept, disease term or other keyword
  - Refined literature search (MiSearch)
  - Gene-Disease interactions
    - GIN
    - Gene2Mesh
    - Metab2Mesh

DIRECTED EXPANSION / VALIDATION

- Starting with a list of genes
  - Sources
    - Expt data (GWAS, Expression Profile, Favorite Genes)
  - Expand set by looking for
    - Protein-protein interactions (MiMI, Cytoscape Plug-in)
    - Metabolites (MetScape <- reference poster)
    - Geneset enrichment by
      - ConceptGen
    - Pathway matching (SAGA / TALE)

Concept or Keyword

Browsing Discovery

Validation Expansion

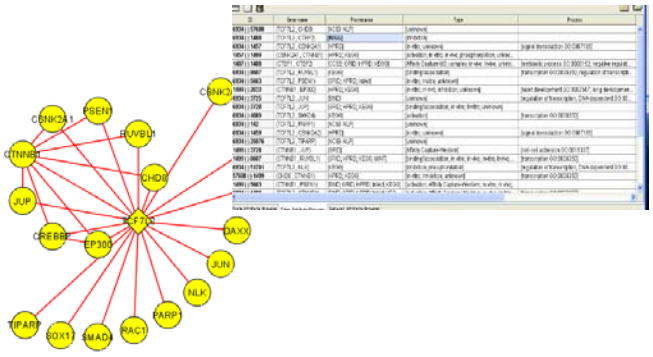
Gene Set

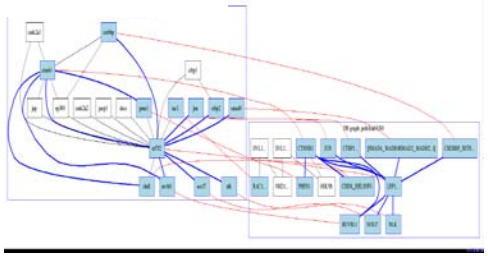
MiSearch

Gene2Mesh

GIN

BioSearch2D





MiMI Cytoscape

SAGA/TALE

ConceptGen

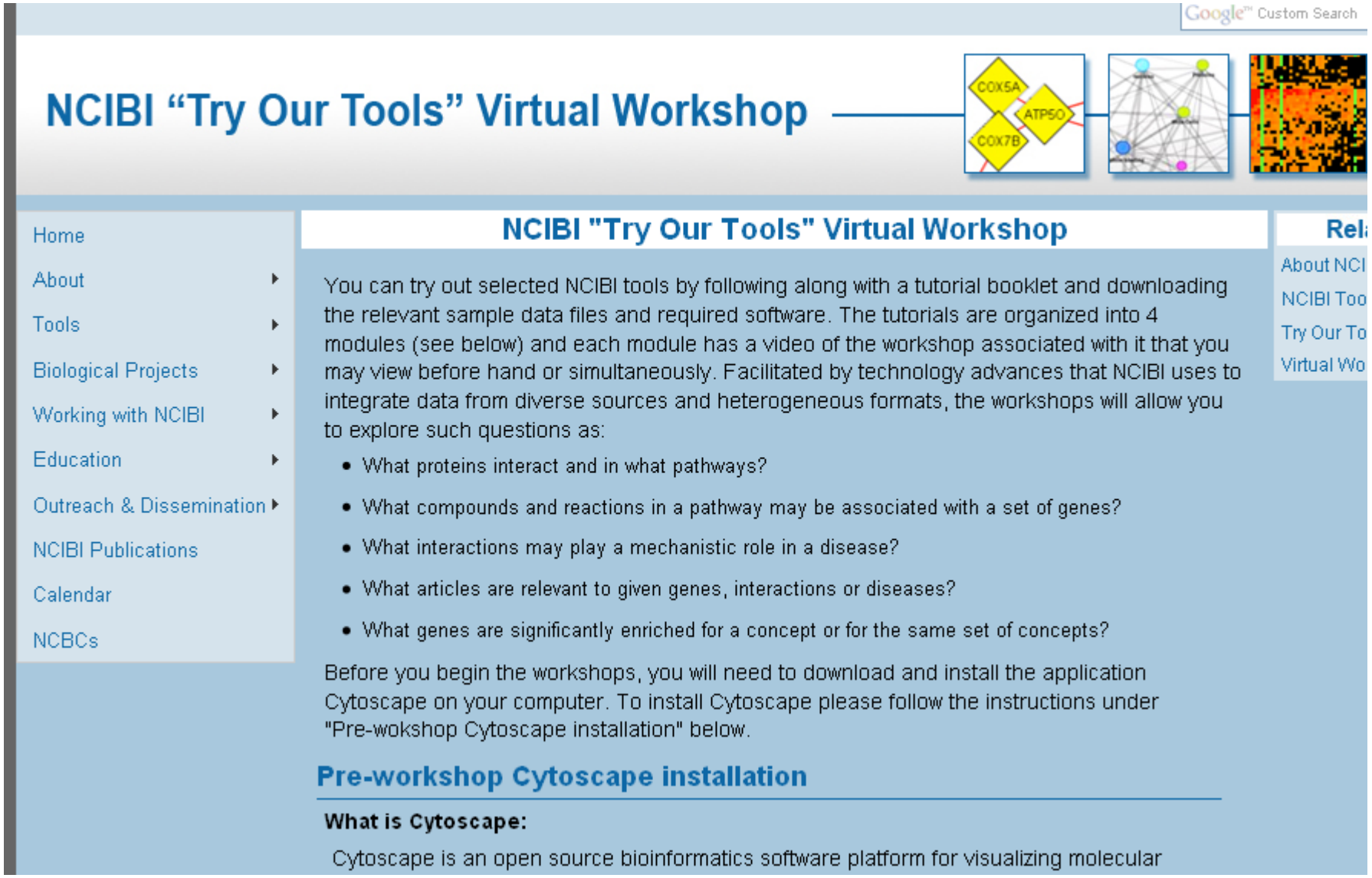
NLP Data

Private Data

MiMI Data

Today's Presentation

- Use a biological case-study to demonstrate the utility and integration of tools developed by NCIBI.
- Featured tools:
  - Gene2Mesh (Gene / Mesh Term matrix)
  - MiMI (Michigan Molecular Interactions)
    - MiMIWeb
    - MiMI Plugin for Cytoscape (API and visualization for the MiMI Data and linkage to other Cytoscape Plugin tools)
  - Metab2Mesh
  - MetScape (Cytoscape Plug-in)
  - SAGA / TALE (subgraph approximate matching tools for network similarity)
  - BioNLP (parsed and gene-tagged version of PubMed and PMCOA)
  - GIN (NLP literature summarization and centroiding)



http://portal.ncibi.org/gateway/virtual-workshop.html

Concept / Keyword Start

- Starting with a Keyword, Disease term. Explore and visualize the Gene space to generate hypotheses
  - Gene2Mesh (Gene/MeSH matrix)
  - MiMI (Protein-Protein interactions)
  - GIN

http://gene2mesh.ncibi.org

Gene2MeSH

NCIBI National Center for Integrative Biomedical Informatics

Automated Literature Based Genome Annotation Using MeSH

Get top genes for MeSH term:
example: *"prostatic neoplasms"*

Get top MeSH terms for gene:
example: *brca2*

TGFB1 Submit About

hint: use quotes to match a phrase

Human only | Substances only

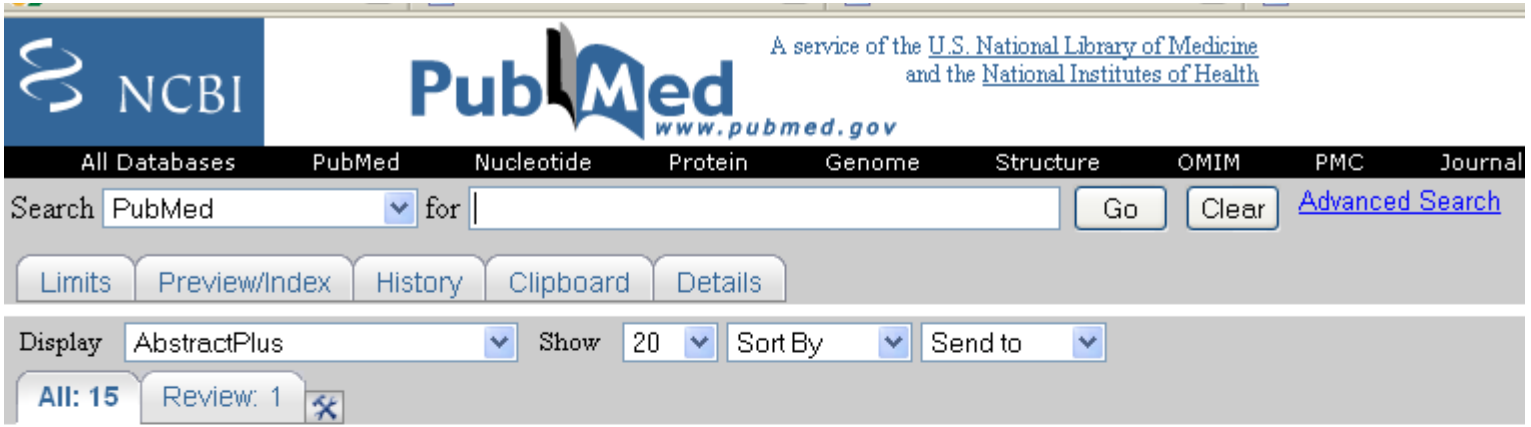
history : "Kidney Failure, Chronic" -> TGFB1

257 MeSH headings found matching gene symbol **"TGFB1"**

Show All Columns | download tab-delimited results

= lookup gene or MeSH heading; M = view interactions in MiMI

Gene Symbol	MeSH Heading	TaxID	Fisher's Exact	MeSH Qualifier	Gene Description	External Search
TGFB1 M	Transforming Growth Factor beta1	9606	0.0e-1	-	transforming growth factor, beta 1	658
TGFB1 M	Transforming Growth Factor beta	9606	0.0e-1	genetics	transforming growth factor, beta 1	789
Tgfb1 M	Transforming Growth Factor beta	10090	0.0e-1	metabolism	transforming growth factor, beta 1	585
Tgfb1 M	Transforming Growth Factor beta1	10090	0.0e-1	-	transforming growth factor, beta 1	236
Tgfb1 M	Transforming Growth Factor beta1	10116	1.5e-2611	-	transforming growth factor, beta 1	134
Tgfb1 M	Transforming Growth Factor beta	10116	4.6e-2111	metabolism	transforming growth factor, beta 1	134
TGFB1 M	Receptors, Transforming Growth Factor beta	9606	4.0e-1344	metabolism	transforming growth factor, beta 1	106
TGFB1 M	Smad3 Protein	9606	1.5e-1233	-	transforming growth factor, beta 1	91
Tgfb1 M	Receptors, Transforming Growth Factor beta	10090	1.2e-1122	metabolism	transforming growth factor, beta 1	81



Significance of the tissue kallikrein promoter and transforming growth factor-beta1 polymorphisms with renal progression in children with vesicoureteral reflux.

Lee-Chen GJ, Liu KP, Lai YC, Juang HS, Huang SY, Lin CY.

Department of Biological Science, National Taiwan Normal University, Taipei, Taiwan.

BACKGROUND: Tissue kallikrein regulates blood circulation. Low urinary kallikrein excretion was associated with hypertension and renal disease in blacks. The polymorphic KLK1 promoter includes -130 GN coupled with multiple single base substitutions. The -130 G12 allele in the KLK1 promoter was associated with lower transcriptional activity and hypertensive end-stage renal disease (ESRD) in blacks. Transforming growth factor-beta1 (TGF-beta1) regulates matrix production, and induces fibrosis in a variety of tissues. High circulating TGF-beta1 levels mediating renal fibrosis and loss of function in transgenic mice. The -509 T allele in the TGF-beta1 promoter showed marginally higher transcriptional activity, and was associated with increased TGF-beta1 production in humans. The aim of this study was to investigate whether the tissue KLK1 promoter and TGF-beta1 polymorphism are involved in primary vesicoureteric reflux (VUR) with renal progression in children. METHODS: Seventy-four primary VUR children were studied with regular annual follow-up for more than 18 years, all of them more than grade II (diagnosed by voiding

Gene2MeSH

- Gene2MeSH is an automated annotation tool that associates Medical Subject Heading (MeSH) terms with genes using the National Library of Medicine's PubMed literature database.

- The significance of association between genes and MeSH terms is evaluated using Fisher's exact test and displayed in an interface in order of significance score.

- Users may search by gene name or MeSH term and view or download results via the web interface. Gene2MeSH also provides relevant links to protein interactions in MiMI as well as reference links to Entrez, the MeSH browser, and PubMed.

- Website: http://gene2mesh.ncibi.org

- Programmatic Interface for direct query access (XML return):
  - http://gene2mesh.ncibi.org/about.html#programmatic

http://gene2mesh.ncibi.org

Gene2MeSH

Automated Literature Based Genome Annotation Using MeSH

(•) Get top genes for MeSH term:
example: *"prostatic neoplasms"*

( ) Get top MeSH terms for gene:
example: *brca2*

"Kidney Failure, Chronic" Submit About

hint: use quotes to match a phrase

☐ Human only | ☐ Substances only

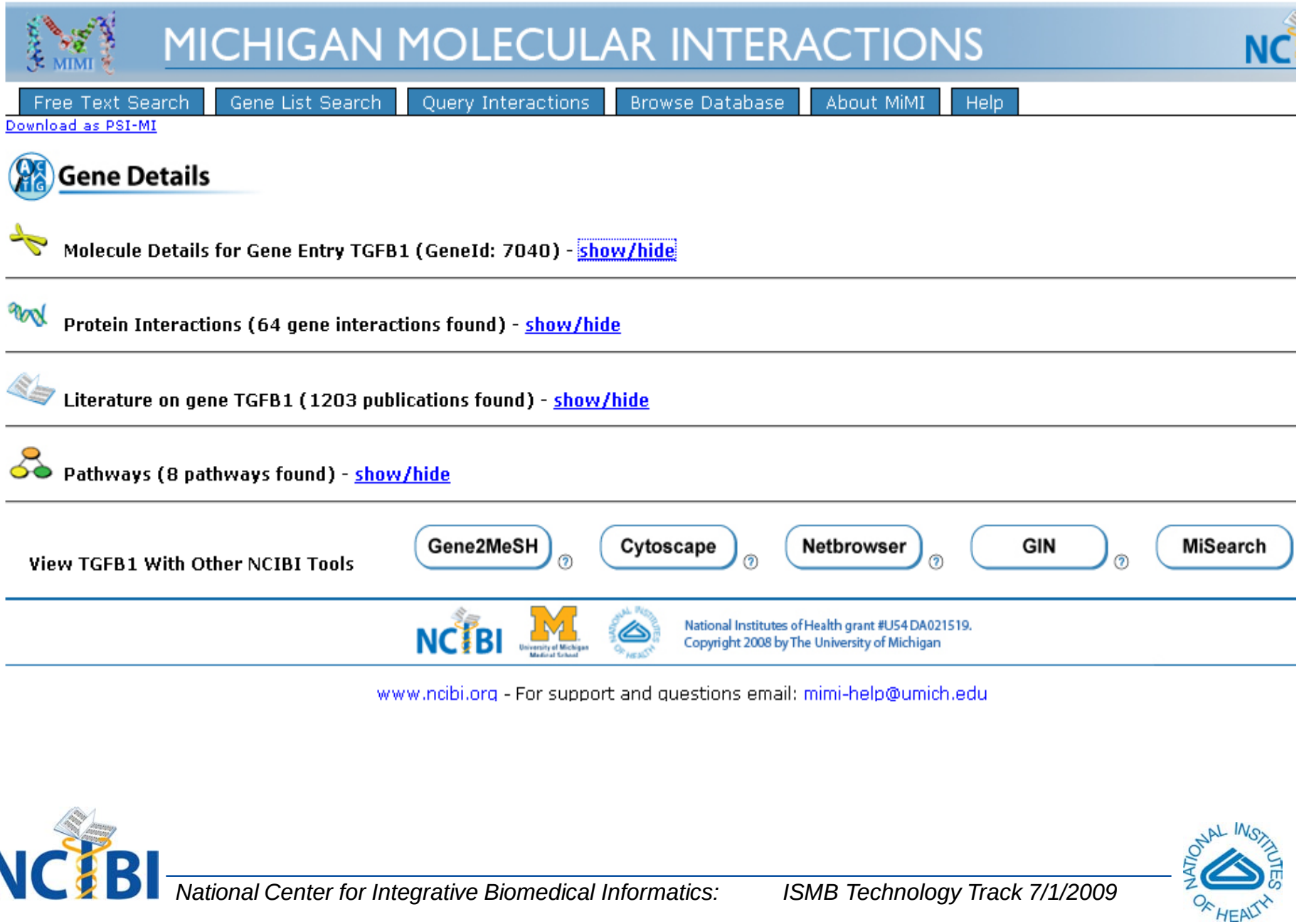
history : "Kidney Failure, Chronic"

21 genes found matching MeSH heading ""Kidney Failure, Chronic""

Show All Columns ☐ | download tab-delimited results

= lookup gene or MeSH heading; M = view interactions in MiMI

Gene Symbol	MeSH Heading	TaxID	Fisher's Exact	MeSH Qualifier	Gene Description	External Search
ACE M	Kidney Failure, Chronic	9606	1.5e-47	genetics	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	51
AGT M	Kidney Failure, Chronic	9606	4.9e-22	genetics	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	22
AGTR1 M	Kidney Failure, Chronic	9606	3.4e-18	genetics	angiotensin II receptor, type 1	18
MTHFR M	Kidney Failure, Chronic	9606	6.4e-17	genetics	5,10-methylenetetrahydrofolate reductase (NADPH)	26
NOS3 M	Kidney Failure, Chronic	9606	5.9e-15	genetics	nitric oxide synthase 3 (endothelial cell)	19
nph M	Kidney Failure, Chronic	10090	5.7e-12	pathology	nephrosis	4
AHSG M	Kidney Failure, Chronic	9606	2.9e-10	complications	alpha-2-HS-glycoprotein	7
IL6 M	Kidney Failure, Chronic	9606	1.8e-8	therapy	interleukin 6 (interferon, beta 2)	16


MICHIGAN MOLECULAR INTERACTIONS
Free Text Search
Gene List Search
Query Interactions
Browse Database
About MiMI
Help
Download as PSI-MI
Gene Details
Molecule Details for Gene Entry TGFB1 (GeneId: 7040) - show/hide
Protein Interactions (64 gene interactions found) - show/hide
Literature on gene TGFB1 (1203 publications found) - show/hide
Pathways (8 pathways found) - show/hide
View TGFB1 With Other NCIBI Tools
Gene2MeSH
Cytoscape
Netbrowser
GIN
MiSearch
National Institutes of Health grant #U54 DA021519.
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www.ncibi.org - For support and questions email: mimi-help@umich.edu

Gene Details

Molecule Details for Gene Entry TGFB1 (GeneId: 7040) - show/hide

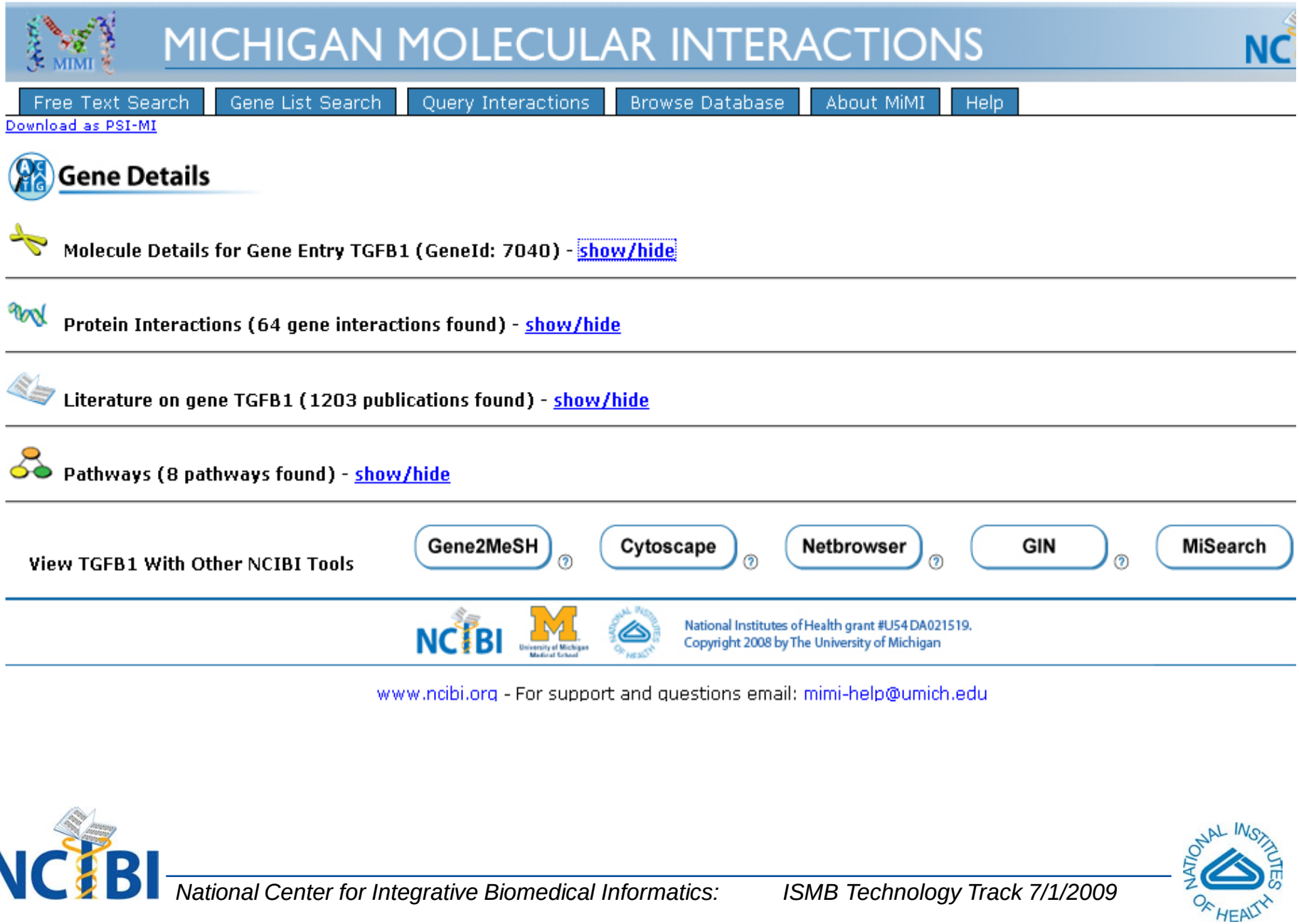
Protein Interactions (64 gene interactions found) - show/hide

Literature on gene TGFB1 (1203 publications found) - show/hide

Pathways (8 pathways found) - show/hide

8 pathways found, displaying all pathways.

Pathway	Description	Genes Related to Path
KEGG:hsa04110 Image	Cell cycle	View Related
KEGG:hsa04350 Image	TGF-beta signaling pathway	View Related
KEGG:hsa05211 Image	Renal cell carcinoma	View Related
KEGG:hsa05220 Image	Chronic myeloid leukemia	View Related
KEGG:hsa05210 Image	Colorectal cancer	View Related
KEGG:hsa04010 Image	MAPK signaling pathway	View Related
KEGG:hsa05212 Image	Pancreatic cancer	View Related


MICHIGAN MOLECULAR INTERACTIONS
Free Text Search
Gene List Search
Query Interactions
Browse Database
About MiMI
Help
Download as PSI-MI
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Cytoscape
Netbrowser
GIN
MiSearch
National Institutes of Health grant #U54 DA021519.
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www.ncibi.org - For support and questions email: mimi-help@umich.edu

GIN: Gene Interaction Network

Information for TGFBR2

Interactions

SMAD2

- Two of four sites in SMAD2, three of four in Smad3 and all sites in TGFBR2 were effective in suppressing their targets down to 0Ã¢??10% (Figure 1A). (Article 1188087) (score = 2.26493)

TRADD

- Ninety-five genes were identified that distinguished the samples from all four autoimmune diseases from healthy controls, including those encoding the cell surface receptors TGFBR2, CSF3R, and BMPR2, which were overexpressed in the autoimmune patients, and several genes implicated in apoptosis (TRADD, TRAF2, CASP6, CASP8), which were underexpressed. (Article 333417) (score = 1.72039)

SMAD3

- Two of four sites in Smad2, three of four in SMAD3 and all sites in TGFBR2 were effective in suppressing their targets down to 0Ã¢??10% (Figure 1A). (Article 1188087) (score = 1.63958)

CSF1R

- CSF1R is a tyrosine kinase transmembrane receptor for the cytokine colony stimulating factor 1 (CSF1), and is involved in macrophage differentiation, function and production; and TGFBR2 is a Ser/Thr kinase transmembrane receptor for transforming growth factor-beta (TGFÃ?Â²), with a role in transcriptional regulation. (Article 1475747)

Global Network Statistic

Degree: 4

Clustering coefficient: 0.17 (1 out of 6)

MiMI

Information about TGFBR2 on MiMI

Cytoscape

Information about TGFBR2 on Cytoscap

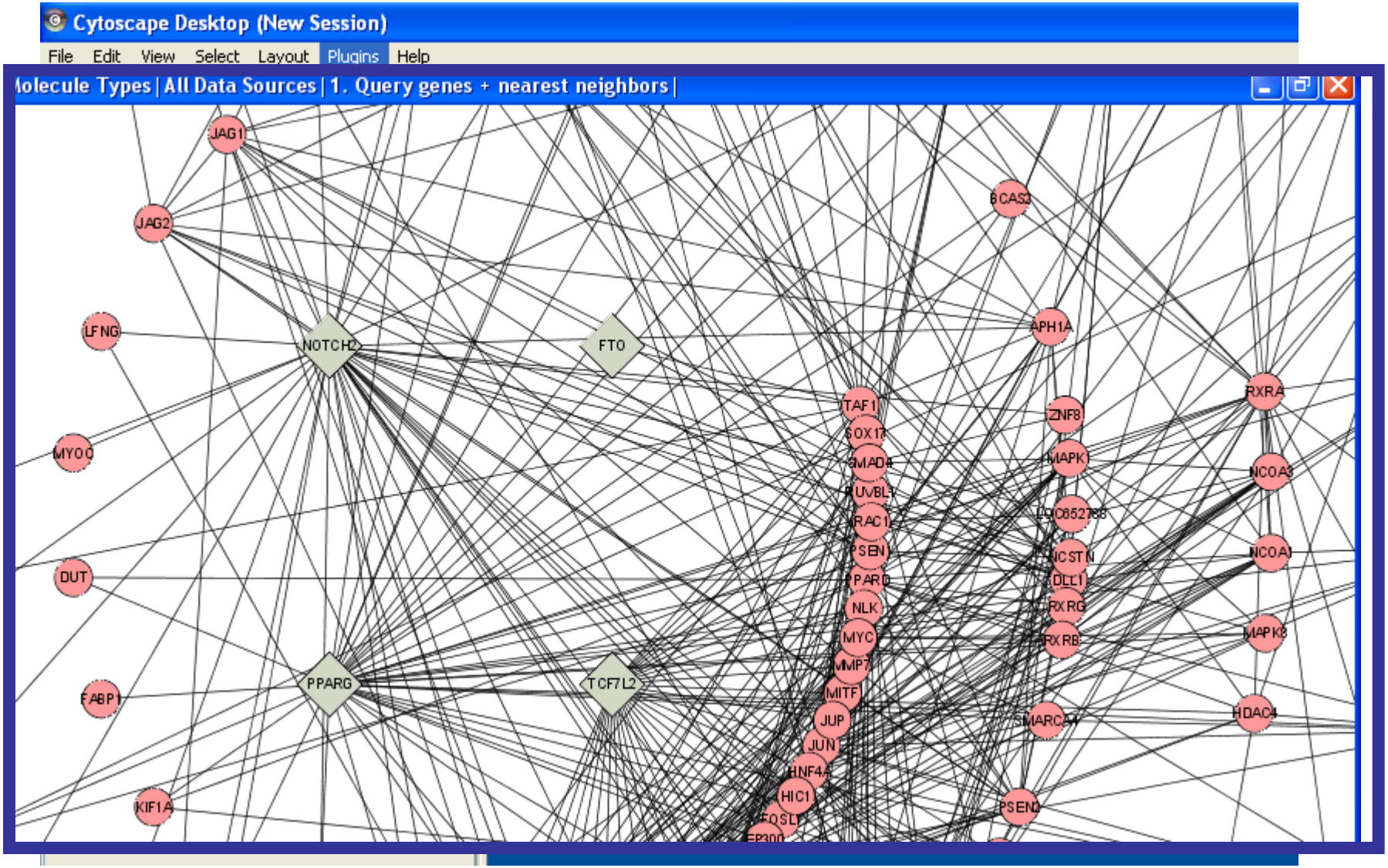
Second Neighbors

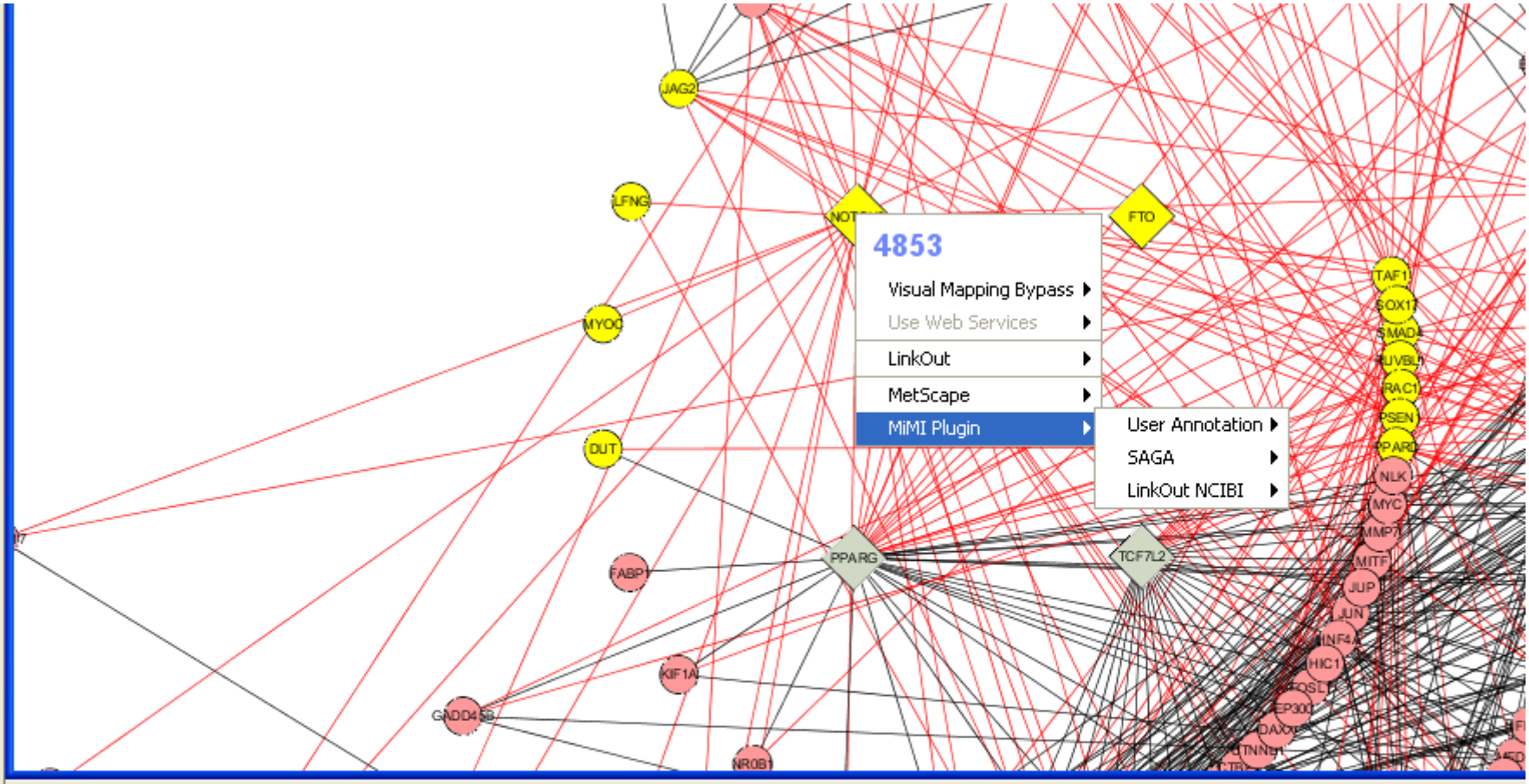
- MAPK8 through:
  - SMAD2
  - CSF1R
  - SMAD3
- TGFBR1 through:
  - SMAD2
  - SMAD3
- CD40 through:
  - SMAD3

Gene List Start

- Starting with a list of genes, Launch Cytoscape Plug-in for MiMI database and view protein protein interactions.
  - SAGA ← Approximate subgraph matching tool for pathway identification
  - BioNLP ← direct access to sentences in literature to support interactions
- Also other Cytoscape modules
  - Bingo, Dynamic Expression Module, MCode, others.

www.cytoscape.org **http://mimiplugin.ncibi.org/**





Data Panel

ID	Description	Gene Name	Pathway	
3955	LFNG O-fucosylpeptide 3-beta-N-acetylglucosamin...	LFNG	Notch signaling pathway [path:hsa04330]	compartment specifi
4653	myocilin, trabecular meshwork inducible glucocorti...	MYOC		anatomical structure
1854	deoxyuridine triphosphatase	DUT	Pyrimidine metabolism [path:hsa00240]	DNA replication [GO:
3714	jagged 2	JAG2	Notch signaling pathway [path:hsa04330]	auditory receptor cel
64321	SRY (sex determining region Y)-box 17	SOX17	Wnt signaling pathway [path:hsa04310]	angiogenesis [GO:0

Match No.	Match Graph Name (#Nodes, #Edges)	Graph Dist
Match #1	path:hsa04330 (17,16) [Notch signaling pathway]	29.00
Match #2	path:hsa04310 (59,70) [Wnt signaling pathway]	36.00

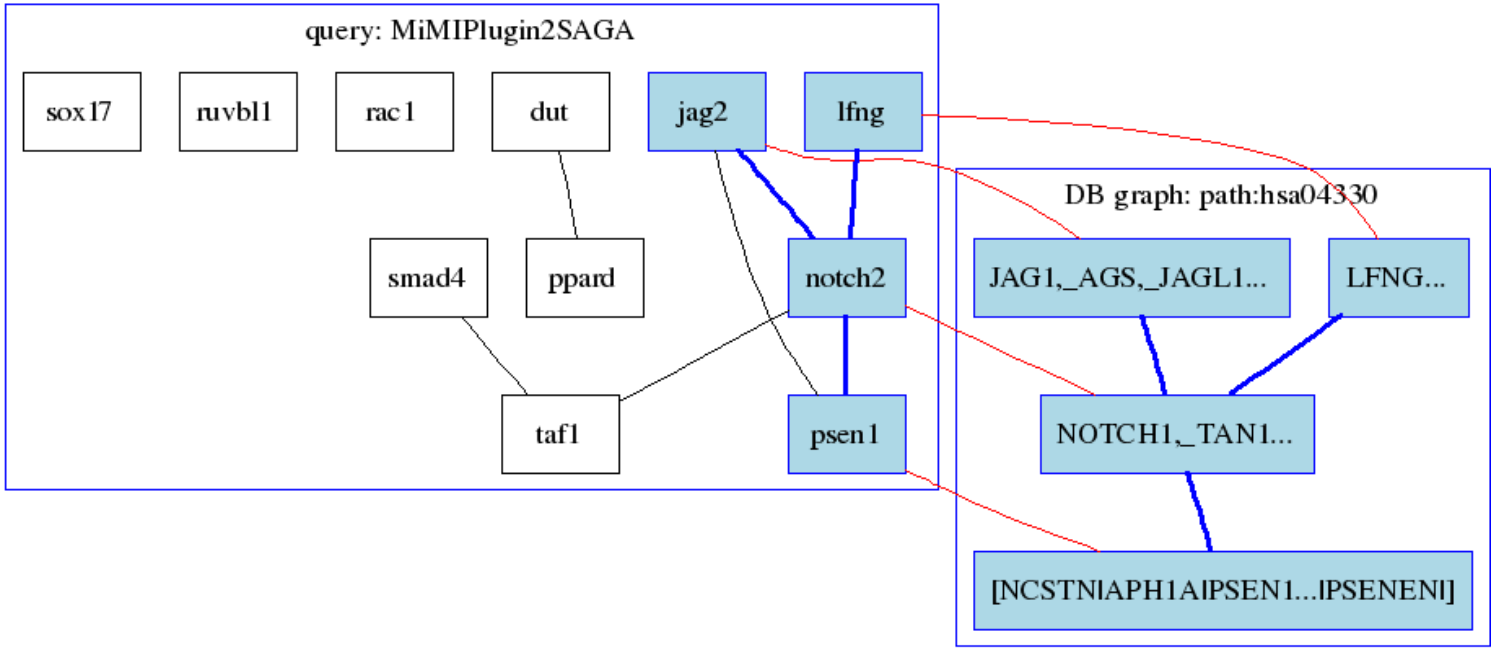
Details of the Matches:

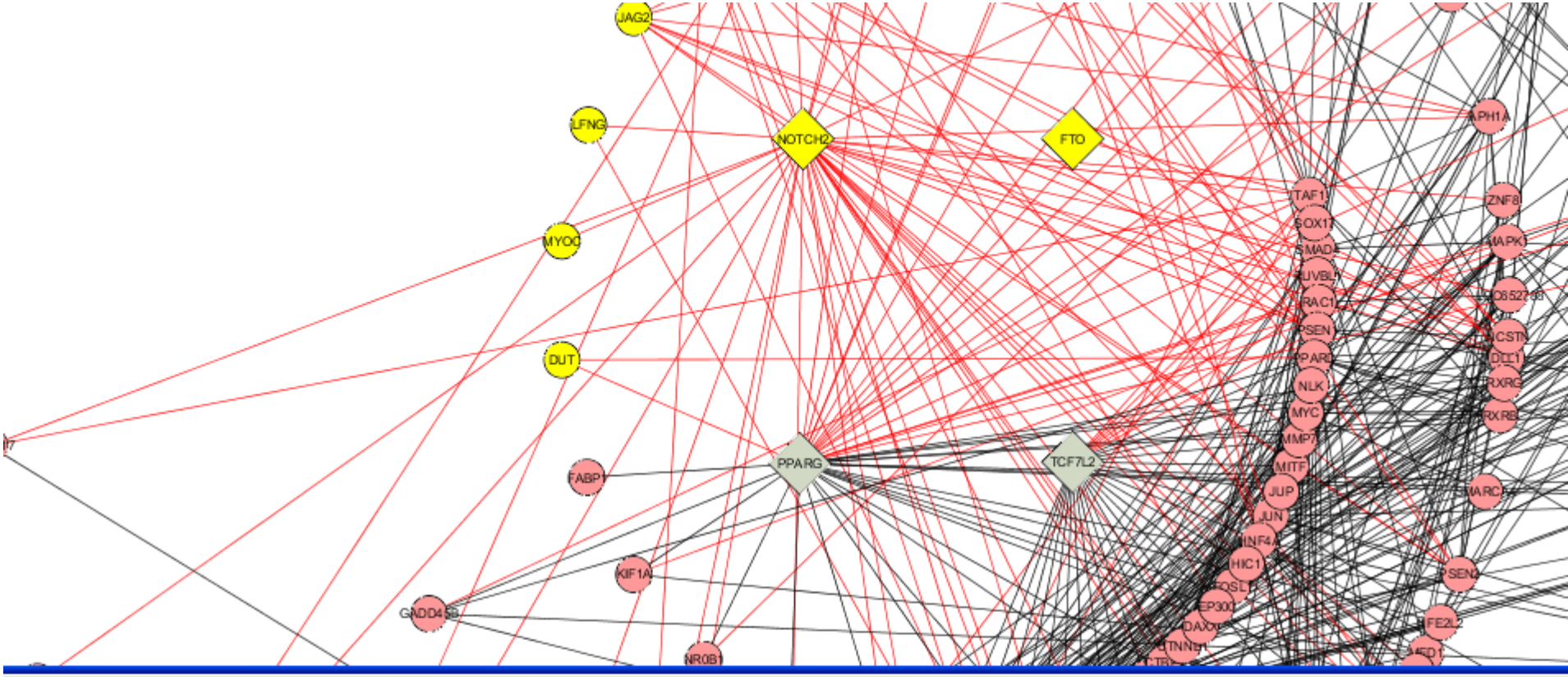
[Go Back to Matches Overview]

Match #1: path:hsa04330 (17 nodes, 16 edges) [Notch signaling pathway]

Graph Distance 29.00 (4 out of 11 nodes match)

[Link to KEGG Picture] (with the matching nodes highlighted)



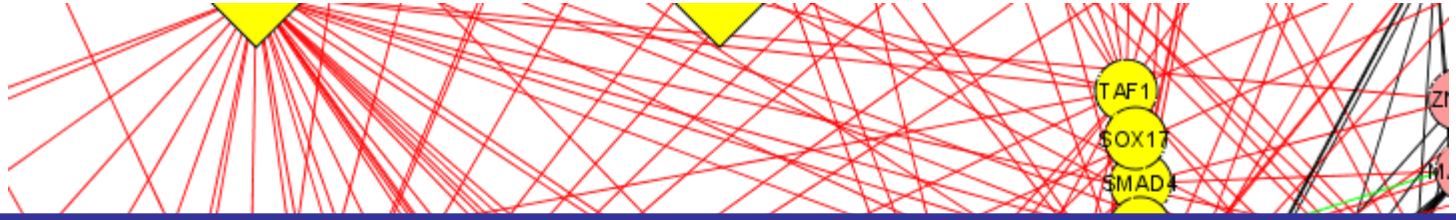


Data Panel

ID	Function	Gene name	Interactiontype	
4853 ( ) 4854	[calcium ion binding [GO:0005509]; protein binding ...	(NOTCH2 , NOTCH3)	[bidirectional]	[BIND]
6872 ( ) 8031	[protein binding [GO:0005515]]	(TAF1 , NCOA4)	[bidirectional]	[BIND]
4853 ( ) 23220	[protein binding [GO:0005515]]	(NOTCH2 , DTX4)	[PPrel]	[KEGG]
1840 ( ) 2033	[metal ion binding [GO:0046872]; transcription coac...	(DTX1 , EP300)	[bidirectional [reverse]; in vivo [reverse]; Invivo]	[GRID; HPRD
5468 ( ) 10987	[metal ion binding [GO:0046872]; protein binding [G...	(PPARG , COPS5)	[bidirectional]	[BIND]
5468 ( ) 6256	[metal ion binding [GO:0046872]; protein binding [G...	(PPARG , RXRA)	[Affinity Capture-MS; bidirectional; in vitro; Invitro [rev...	[CCSB; GRID
3714 ( ) 54567	[calcium ion binding [GO:0005509]; Notch binding [...	(JAG2 , DLL4)	[neighbouring_reaction [reverse]]	[reactome]
6934 ( ) 64321	[DNA binding [GO:0003677]]	(TCF7L2 , SOX17)	[PPrel [reverse]]	[KEGG]

Node Attribute Browser | Edge Attribute Browser | Network Attribute Browser

ZOOM Middle-click + drag to PAN



Cytoscape MiMI Plugin Query BioNLP

18 Sentences Related To [PPARG] And [RXRA] From BioNLP

SORT (SINGLE CLICK) Sentences by semantic similarity [May take several minutes for long lists] Computed by MEAD , a centroid-based extractive summarization system

PubmedID	Section	Symbol	Symbol	Sentence
8990192	ABSTRACT	PPARG	RXRA	The peroxisome proliferator-activated receptor gamma (PPAR gamma) and the retinoid X receptor alpha (RXR alpha) form a heterodimeric complex that functions as a central regulator of adipocyte differentiation.
9492033	ABSTRACT	PPARG	RXRA	No effect on the transient expression of leptin was noted upon treatment with a thiazolidinedione, BRL49653, or upon cotransfection with peroxisome proliferator-activated receptor-gamma/retinoid X receptor-alpha or sterol response element-binding protein-1.
10582693	ABSTRACT	PPARG	RXRA	Compared with normal human myometrium, leiomyomata had 3- to 5-fold higher levels of peroxisome proliferator-activated receptor gamma (PPARgamma), retinoid X receptor alpha proteins, and all-trans retinoic acid, but only during the follicular phase of the menstrual cycle.
10860864	ABSTRACT	PPARG	RXRA	In human coronary artery vascular smooth muscle (hcaVSM) cells, the mechanisms that mediate the antiproliferative effects of ligands for the peroxisome proliferator-activated receptor-gamma (PPAR gamma) and the retinoid X receptor-alpha (RXR alpha) are unclear.
10936484	ABSTRACT	PPARG	RXRA	We studied the effects of peroxisome proliferator-activated receptor (PPAR) gamma, alpha, and retinoid X receptor alpha (RXRalpha) ligands on MCP-1-directed migration and matrix metalloproteinase expression of a human acute monocytic leukemia cell line (THP-1).
				PIMT enhances the transcriptional activity of peroxisome proliferator-activated receptor gamma and

Additional Cytoscape Modules

- MetScape (beta release 0.8) mapping metabolites to proteins **(Poster # 3, Alla Karnovsky)**
  - **http://metabplugin.ncibi.org/index.html**
- Bingo (GO term overrepresentation/enrichment)
  - **Maere S, Heymans K, Kuiper M. Bioinformatics. 2005 Aug 15;21(16):3448-9**
- MCode (highly connected regions of a graph)
  - **Bader GD, Hogue CW. *BMC Bioinformatics*. 2003 Jan 13;4(1):2.**
- DynamicExpression (timecourse color / size)
  - **Iliana Avila-Campillo, Galitski Group, Institute for Systems Biology.**
- Many others ….

ConceptGen

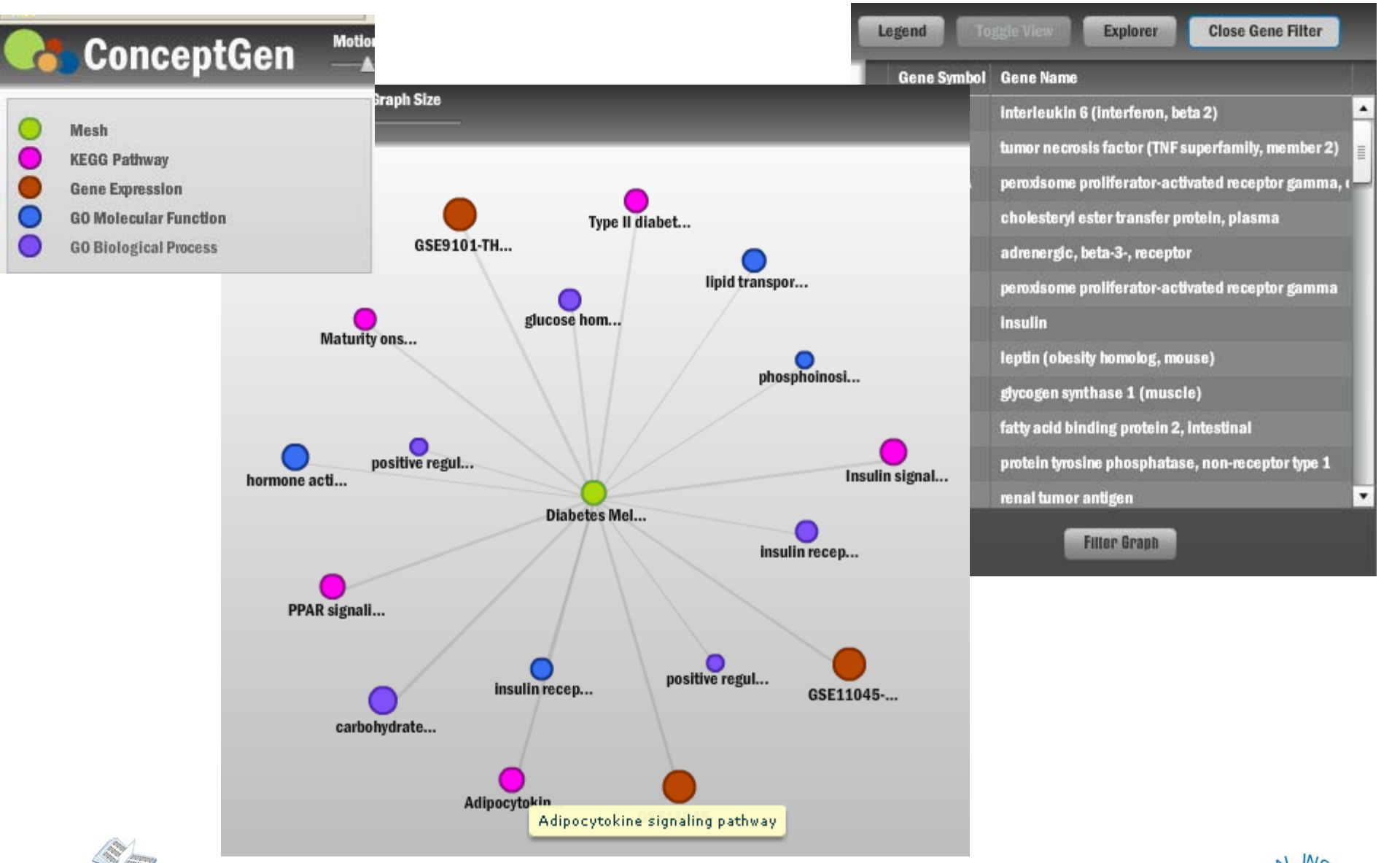
- ConceptGen is a web-based application that performs *gene set enrichment testing and concept mapping*, and offers private accounts and several visualization methods.
- The significance of association between uploaded gene sets and concepts, and *among* all pre-loaded concepts is assessed using a modified Fisher's Exact test.
- Concept mapping in a graph network allows users to explore *networks* of relationships among previously defined biological concepts.
- Several types of biological knowledge are represented in ConceptGen in addition to Gene Ontology (GO), including pathways (KEGG, Biocarta, and Panther), protein families, chromosomal locations, protein interactions, MeSH terms (concepts defined using Gene2MeSH), targets of transcription factors, drugs, and miRNAs, differential gene expression profiles, metabolic-centered gene sets, and human diseases.
- Gene expression profiles are analyzed using a custom-built pipeline that downloads raw Affymetrix .CEL files from Gene Expression Omnibus (GEO), assesses quality, normalizes data with RMA, and tests for differential expression with an empirical Bayesian method.

http://conceptgen.ncibi.org

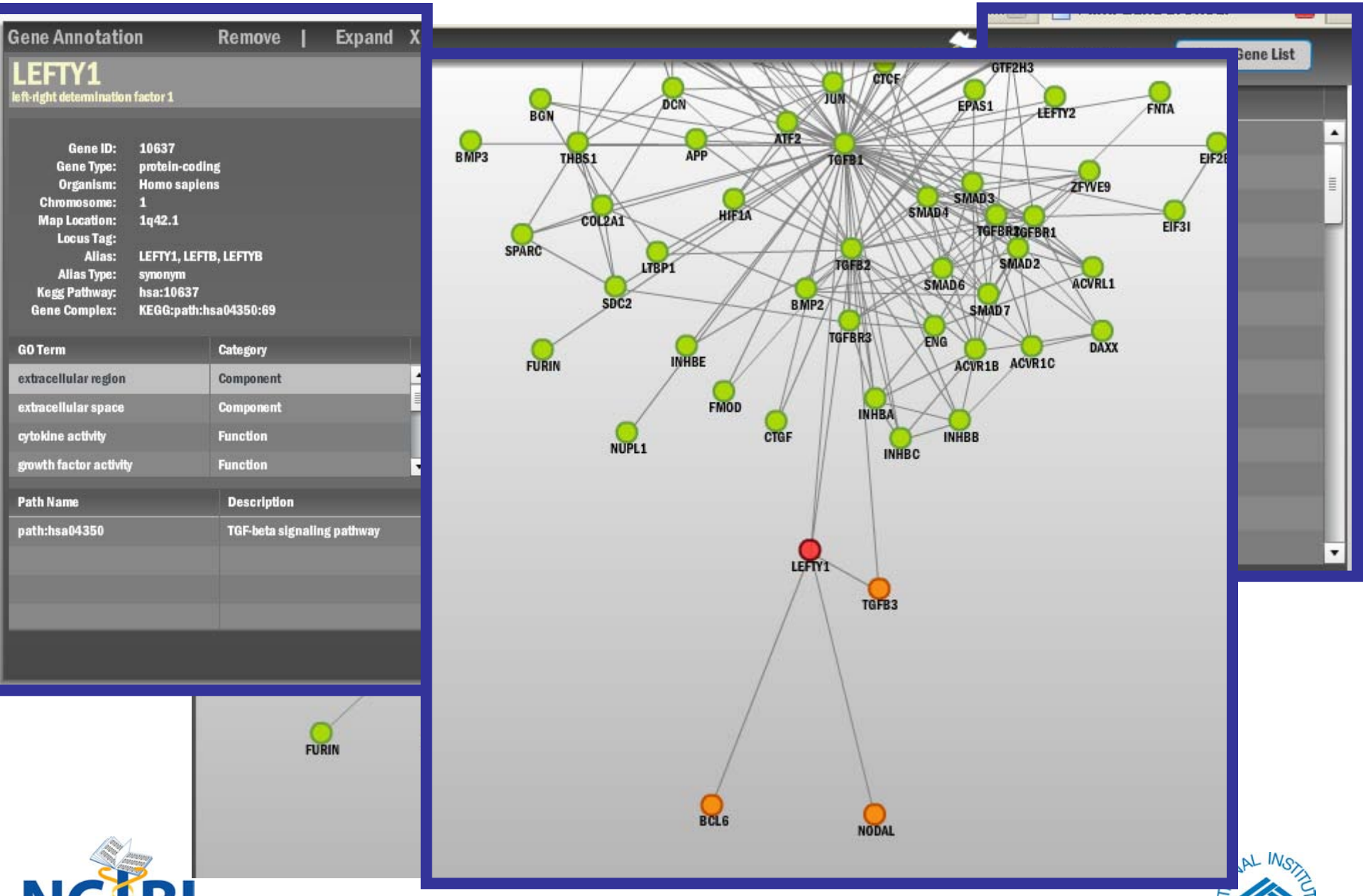
ConceptGen

Select enriched concepts by concept type

Conceptgen.ncibi.org

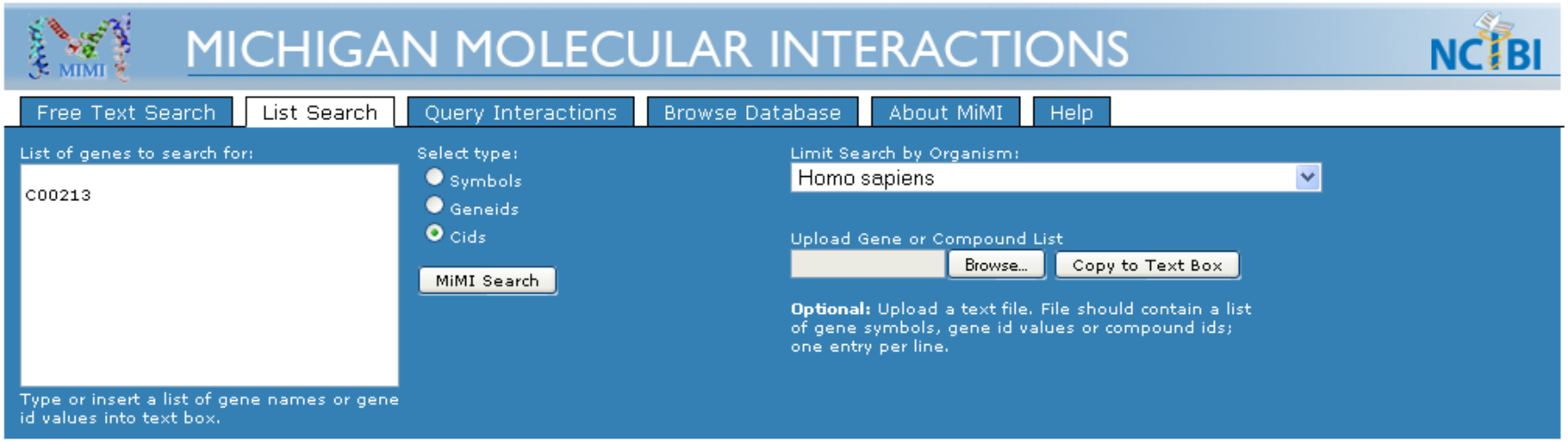


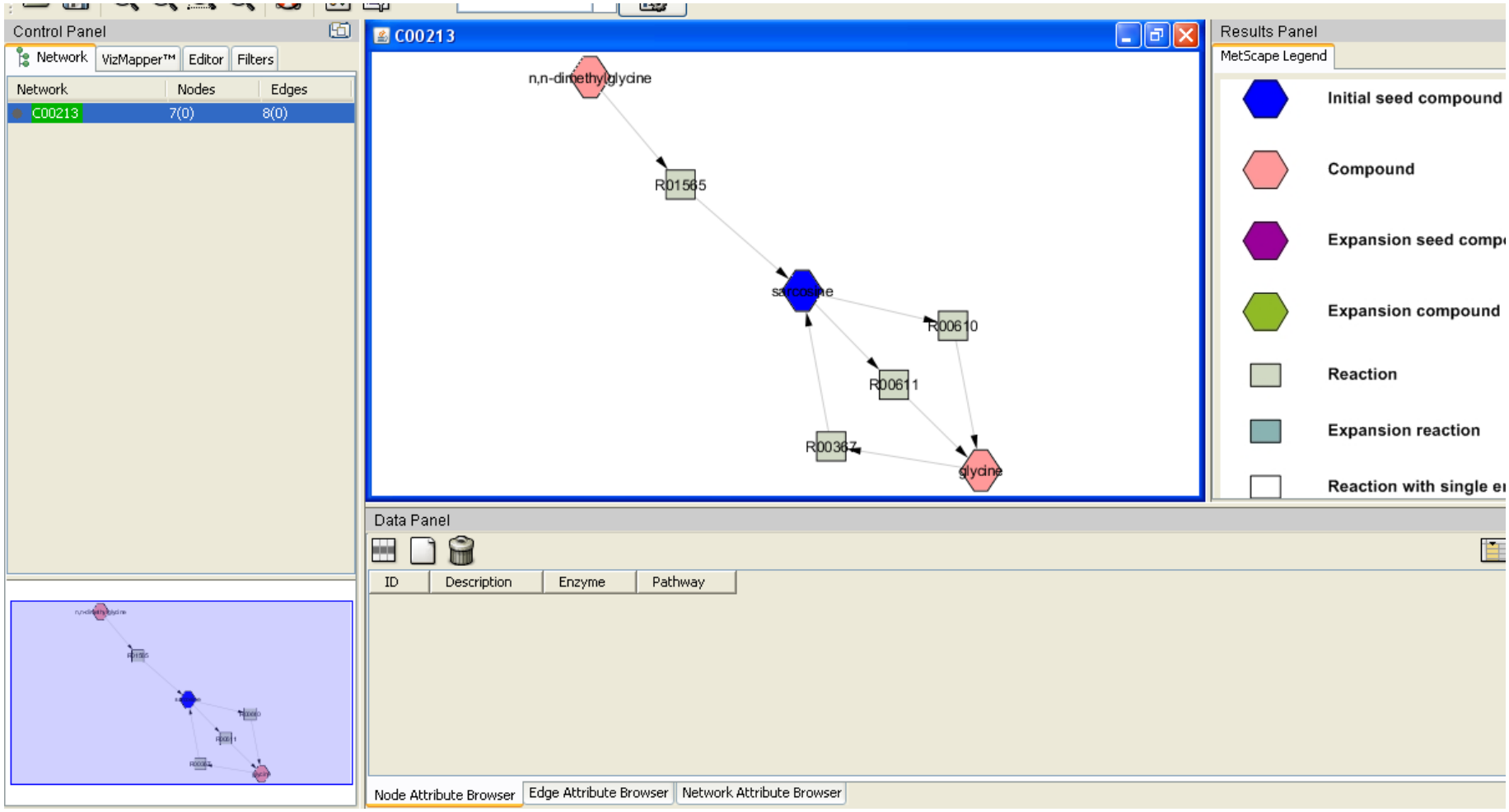
NetBrowser

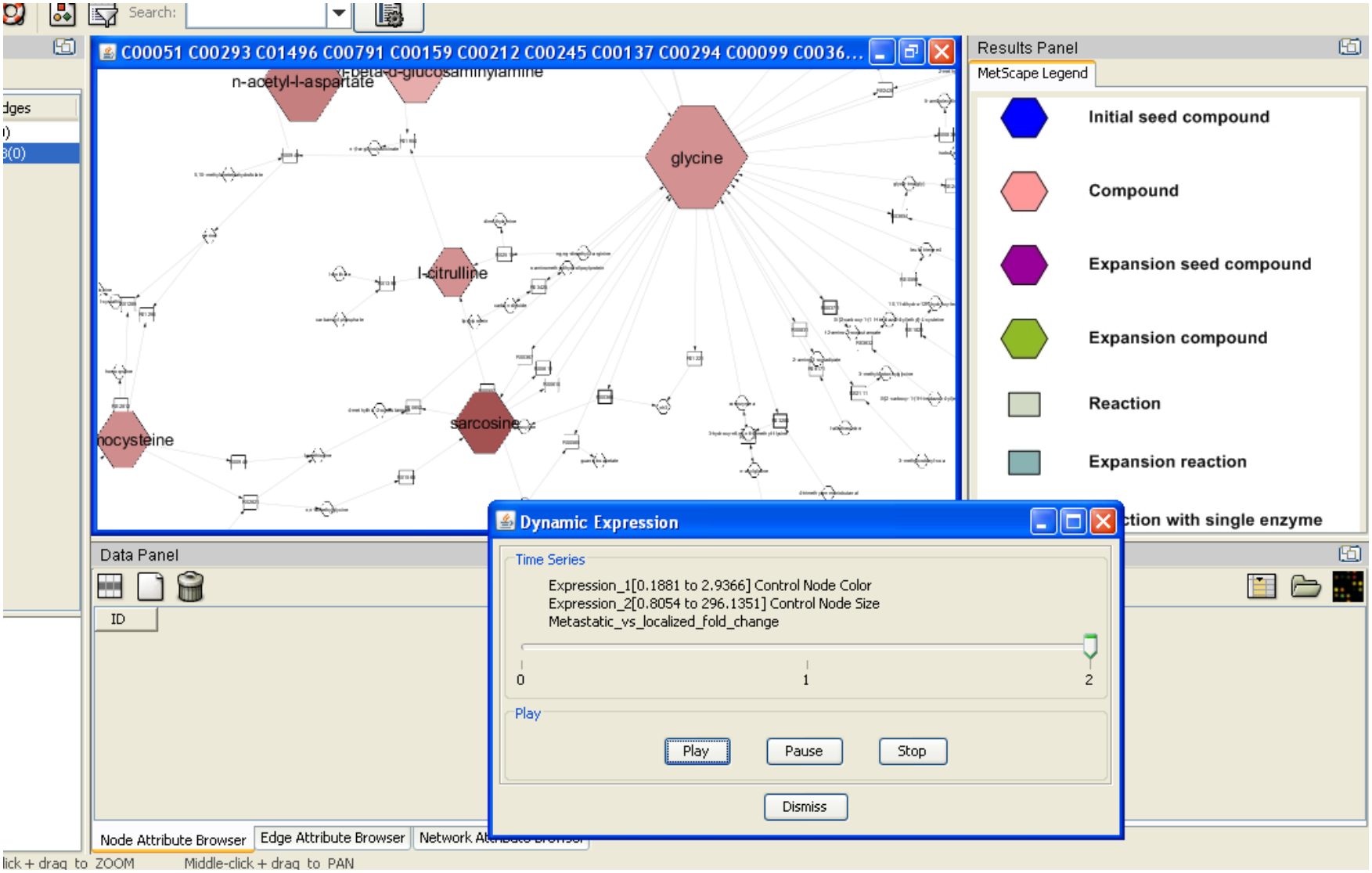

Gene Annotation
Remove | Expand X
LEFTY1
left-right determination factor 1
Gene ID: 10637
Gene Type: protein-coding
Organism: Homo sapiens
Chromosome: 1
Map Location: 1q42.1
Locus Tag:
Alias: LEFTY1, LEFTB, LEFTYB
Alias Type: synonym
Kegg Pathway: hsa:10637
Gene Complex: KEGG:path:hsa04350:69
GO Term
Category
extracellular region
Component
extracellular space
Component
cytokine activity
Function
growth factor activity
Function
Path Name
Description
path:hsa04350
TGF-beta signaling pathway
Gene List
GTF2H3
CTCF
JUN
DCN
BGN
EPAS1
LEFTY2
FNTA
BMP3
THBS1
APP
ATF2
TGFB1
EIF2B
ZFYVE9
SMAD3
SMAD4
HIF1A
COL2A1
TGFBR2
TGFBR1
EIF3I
SPARC
LTBP1
TGFB2
SMAD2
ACVRL1
SMAD6
SDC2
BMP2
SMAD7
TGFBR3
ENG
DAXX
FURIN
INHBE
ACVR1B
ACVR1C
FMOD
INHBA
CTGF
INHBB
NUPL1
INHBC
LEFTY1
TGFB3
BCL6
NODAL
FURIN

Metscape through MiMI

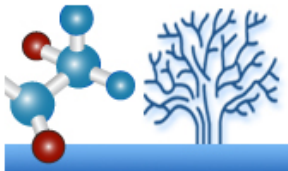
- Currently using Beta site: http://mimi.ncibi.org/MimiWebBeta/upload-page.jsp
- Use molecule ID to search for now – upgrade coming. Sarcosine=C00213


MICHIGAN MOLECULAR INTERACTIONS
NCIBI
Free Text Search
List Search
Query Interactions
Browse Database
About MiMI
Help
List of genes to search for:
C00213
Type or insert a list of gene names or gene id values into text box.
Select type:
Symbols
Geneids
Cids
MiMI Search
Limit Search by Organism:
Homo sapiens
Upload Gene or Compound List
Browse...
Copy to Text Box
Optional: Upload a text file. File should contain a list of gene symbols, gene id values or compound ids; one entry per line.
National Institutes of Health grant #U54 DA021519.
Copyright 2008 by The University of Michigan
www.ncibi.org - For support and questions email: mimi-help@umich.edu


Control Panel
Network
VizMapper™
Editor
Filters
Network
Nodes
Edges
C00213
7(0)
8(0)
C00213
n,n-dimethylglycine
R01565
sarcosine
R00610
R00611
R00367
glycine
Results Panel
MetScape Legend
Initial seed compound
Compound
Expansion seed compo
Expansion compound
Reaction
Expansion reaction
Reaction with single e
Data Panel
ID
Description
Enzyme
Pathway
Node Attribute Browser
Edge Attribute Browser
Network Attribute Browser


Search:
C00051 C00293 C01496 C00791 C00159 C00212 C00245 C00137 C00294 C00099 C0036...
n-acetyl-l-aspartate
glycine
l-citrulline
sarcosine
Results Panel
MetScape Legend
Initial seed compound
Compound
Expansion seed compound
Expansion compound
Reaction
Expansion reaction
Dynamic Expression
Time Series
Expression_1[0.1881 to 2.9366] Control Node Color
Expression_2[0.8054 to 296.1351] Control Node Size
Metastatic_vs_localized_fold_change
0
1
2
Play
Play
Pause
Stop
Dismiss
Data Panel
ID
Node Attribute Browser
Edge Attribute Browser
Middle-click + drag to PAN

Metab2mesh.ncibi.org



Metab2MeSH

Get top substances for MeSH term:
example: *macrophages*

Get top MeSH terms for substance:
example: *phorbol ester*

Thiazolidinediones Submit About

history : glucose -> rosiglitazone -> tzd -> glitazone -> "diabetic mice" -> "diabetic model" -> "diabetes model" -> "diabetes" -> diabetes -> Thiazolidinediones

Showing top 1000 MeSH headings found matching substance **"Thiazolidinediones"** [download tab-delimited results]

Substance Name	Registry #	MeSH Heading	MeSH Qualifier	PubMed Articles	Fisher's Exact	Ratio
Thiazolidinediones	-	Thiazolidinediones	therapeutic use	4968	-4.2e+4	1778.4
Thiazolidinediones	-	Hypoglycemic Agents	therapeutic use	3125	-1.5e+4	235
Thiazolidinediones	-	Thiazoles	pharmacology	2016	-9.4e+3	213.1
Thiazolidinediones	-	Chromans	pharmacology	1353	-8.3e+3	807.4
Thiazolidinediones	-	Diabetes Mellitus, Type 2	drug therapy	1674	-5.6e+3	62.9
Thiazolidinediones	-	PPAR gamma	agonists	851	-4.9e+3	615.7
Thiazolidinediones	-	Receptors, Cytoplasmic and Nuclear	metabolism	847	-3.2e+3	109
Thiazolidinediones	-	Insulin Resistance	physiology	906	-3.1e+3	76.9
Thiazolidinediones	-	Metformin	therapeutic use	491	-2.3e+3	262.8
Thiazolidinediones	-	Transcription Factors	metabolism	880	-1.7e+3	16.7
Thiazolidinediones	-	Insulin	blood	946	-1.7e+3	13.3
Thiazolidinediones	-	Blood Glucose	metabolism	806	-1.5e+3	14.8

Adaptive PubMed Search Tool

Profile 216.70.181.113:090315:095248 (use the unique profile ID provided for this session or enter a username)

Query Diabetes AND Nephropathy AND Kidney Failure, Chronic Submit MiSearch Help

examples: *gab2* or *prostate cancer AND androgen receptor*

The query returned 4504 citations from NCBI Entrez.

Key Authors
+ KA,Jacobson
+ GM,Clore

Increased plasma urotensin-II levels are associated with diabetic retinopathy and carotid atherosclerosis in Type 2 di
Suguro T, Watanabe T, Kodate S, Xu G, Hirano T, Adachi M, Miyazaki A
1 ☐ 18338983 **Clin Sci (Lond)** 115(11):327-34 **1969**

MeSH Terms
show/hide
+ Diabetic Nephropathies
+ Kidney Failure, Chronic
+ Diabetes Mellitus, Type 2
+ Kidney Diseases
+ Albuminuria
+ Cardiovascular Diseases
+ Diabetes Mellitus, Type 1
+ Hypertension
+ Diabetes

Defining human diabetic nephropathy on the molecular le
Martini S, Eichinger F, Nair V, Kretzler M
7 ☐ 18704688 **Rev Endocr Metab Disord** 9(4):267-74

New insights into the mechanisms of fibrosis and scleros
Brosius FC
8 ☐ 18726161 **Rev Endocr Metab Disord** 9(4):245-54

AVPR2 variants and mutations in nephrogenic diabetes i
Spanakis E, Milord E, Gragnoli C
9 ☐ 18726898 **J Cell Physiol** 217(3):605-17 **1969**

Mass spectrometric quantification of amino acid oxidatio
Vivekanadan-Giri A, Wang JH, Byun J, Pennathur S
10 ☐ 18752069 **Rev Endocr Metab Disord** 9(4):275-87

iotensin-aldosterone system on diabetic nephropathy risk.
g S, Ugarph-Morawski A, Brismar K, Eriksson JW, Dahlquist G
22(6):377-83 **1969**

markers of diabetic nephropathy in Type 2 diabetes mellitus.
Hilow H
22(6):384-8 **1969**

einase-9 in the diabetic nephropathy of Kkay mice.
Hui L, Xiao-Man Z, Yi-Ming M
22(6):408-12 **1969**

abetic nephropathy-role of mRNA translation.
an K, Lee MJ, Ghosh Choudhury G, Feliers D
9(4):255-66 **1969**

Gene2Mesh API

This XML file does not appear to have any style information associated with it. The document tree is shown below.


```
- <NCIBI>
  - <Gene2MeSH>
    - <Request type="fetch">
      - <ParameterSet>
          <GeneID type="entrez">1436</GeneID>
          <TaxonomyID>ALL</TaxonomyID>
          <Limit>1000</Limit>
        </ParameterSet>
      </Request>
    - <Response>
      - <ResultSet sort="P-Value" order="ascending">
        - <Result>
            <GeneID type="entrez">1436</GeneID>
            <GeneSymbol>CSF1R</GeneSymbol>
            <MeSHDescriptor>Receptor, Macrophage Colony-Stimulating Factor</MeSHDescriptor>
            <TaxonomyID>9606</TaxonomyID>
            <Fover>1354.3</Fover>
            <Chi-Square>63558</Chi-Square>
            <P-Value test="FisherExact">7.8e-1422</P-Value>
            <MeSHQualifier>metabolism</MeSHQualifier>
          - <GeneDescription>
              colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog
            </GeneDescription>
```


http://gene2mesh.ncibi.org/about

NLP Pubmed Programmatic Interface

- http://nlp.ncibi.org/about.html
- Example:
  - http://nlp.ncibi.org/fetch.php?pmid=17523140&tagger=nametagger&type=gene


```
- <NCIBI>
  - <BioNLP>
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          <Tagger>nametagger</Tagger>
          <Type>gene</Type>
          <Limit>1000</Limit>
        </ParameterSet>
      </Request>
    - <Response>
      - <ResultSet>
        - <Result>
          - <Article pmid="17523140">
            - <Section type="abstract">
              - <Paragraph>
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