

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>)





Navigation

- Home
- About ▶
- Tools ▶
- Biological Projects ▶
- Working with NCIBI ▶
- Education ▶
- Outreach & Dissemination ▶
- NCIBI Publications
- Calendar
- NCBCs

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 ([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 Plug in for Cytoscape ([tool](#))

MetScapei Plug in for Cytoscape ([tutorial](#))

Query a compound or list of compounds

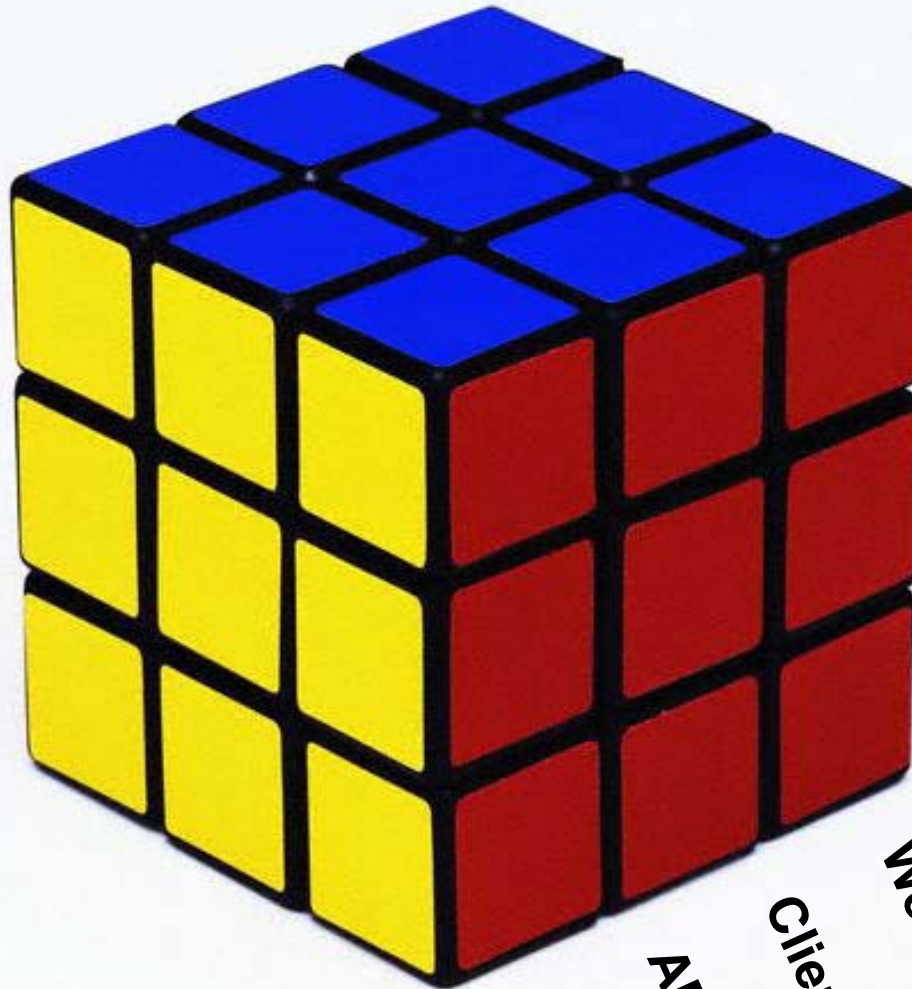
Explore reactions and pathways.

Add in your own data

Link to details and matches to pathway databases

**Browsing
Discovery**

**Validation
Expansion**



Metabolite

DNA

RNA

Protein

Phenotypes

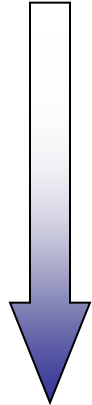
Databases
API
Client tools
Web-based

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

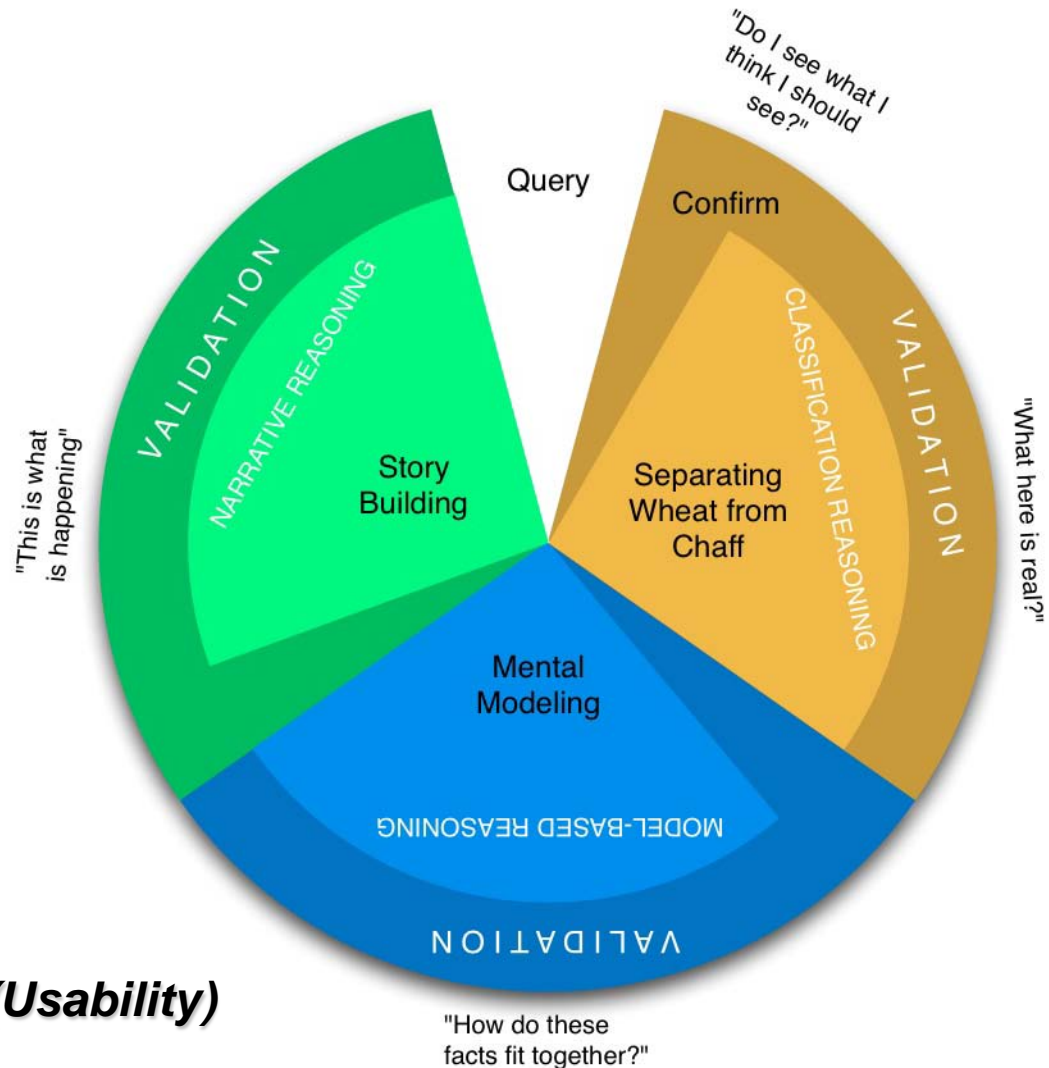
Core Databases:

- 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

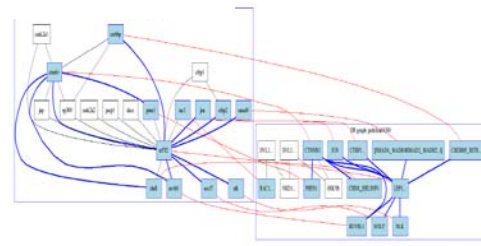
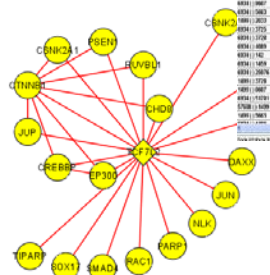
MiSearch

Gene2Mesh

GIN

BioSearch2D

ID	Gene	Protein	Type	Protein
MSM115898	PTGRL2	D-ERF	Interacts	
MSM115899	PTGRL2	IL1RN	Interacts	
MSM115900	PTGRL2	CHMP2C	Interacts	
MSM115901	PTGRL2	CHMP2B	Interacts	
MSM115902	PTGRL2	CHMP2A	Interacts	
MSM115903	PTGRL2	CHMP2D	Interacts	
MSM115904	PTGRL2	CHMP2E	Interacts	
MSM115905	PTGRL2	CHMP2F	Interacts	
MSM115906	PTGRL2	CHMP2G	Interacts	
MSM115907	PTGRL2	CHMP2H	Interacts	
MSM115908	PTGRL2	CHMP2I	Interacts	
MSM115909	PTGRL2	CHMP2J	Interacts	
MSM115910	PTGRL2	CHMP2K	Interacts	
MSM115911	PTGRL2	CHMP2L	Interacts	
MSM115912	PTGRL2	CHMP2M	Interacts	
MSM115913	PTGRL2	CHMP2N	Interacts	
MSM115914	PTGRL2	CHMP2O	Interacts	
MSM115915	PTGRL2	CHMP2P	Interacts	
MSM115916	PTGRL2	CHMP2Q	Interacts	
MSM115917	PTGRL2	CHMP2R	Interacts	
MSM115918	PTGRL2	CHMP2S	Interacts	
MSM115919	PTGRL2	CHMP2T	Interacts	
MSM115920	PTGRL2	CHMP2U	Interacts	
MSM115921	PTGRL2	CHMP2V	Interacts	
MSM115922	PTGRL2	CHMP2W	Interacts	
MSM115923	PTGRL2	CHMP2X	Interacts	
MSM115924	PTGRL2	CHMP2Y	Interacts	
MSM115925	PTGRL2	CHMP2Z	Interacts	
MSM115926	PTGRL2	CHMP3	Interacts	
MSM115927	PTGRL2	CHMP3B	Interacts	
MSM115928	PTGRL2	CHMP3C	Interacts	
MSM115929	PTGRL2	CHMP3D	Interacts	
MSM115930	PTGRL2	CHMP3E	Interacts	
MSM115931	PTGRL2	CHMP3F	Interacts	
MSM115932	PTGRL2	CHMP3G	Interacts	
MSM115933	PTGRL2	CHMP3H	Interacts	
MSM115934	PTGRL2	CHMP3I	Interacts	
MSM115935	PTGRL2	CHMP3J	Interacts	
MSM115936	PTGRL2	CHMP3K	Interacts	
MSM115937	PTGRL2	CHMP3L	Interacts	
MSM115938	PTGRL2	CHMP3M	Interacts	
MSM115939	PTGRL2	CHMP3N	Interacts	
MSM115940	PTGRL2	CHMP3O	Interacts	
MSM115941	PTGRL2	CHMP3P	Interacts	
MSM115942	PTGRL2	CHMP3Q	Interacts	
MSM115943	PTGRL2	CHMP3R	Interacts	
MSM115944	PTGRL2	CHMP3S	Interacts	
MSM115945	PTGRL2	CHMP3T	Interacts	
MSM115946	PTGRL2	CHMP3U	Interacts	
MSM115947	PTGRL2	CHMP3V	Interacts	
MSM115948	PTGRL2	CHMP3W	Interacts	
MSM115949	PTGRL2	CHMP3X	Interacts	
MSM115950	PTGRL2	CHMP3Y	Interacts	
MSM115951	PTGRL2	CHMP3Z	Interacts	
MSM115952	PTGRL2	CHMP4	Interacts	
MSM115953	PTGRL2	CHMP4B	Interacts	
MSM115954	PTGRL2	CHMP4C	Interacts	
MSM115955	PTGRL2	CHMP4D	Interacts	
MSM115956	PTGRL2	CHMP4E	Interacts	
MSM115957	PTGRL2	CHMP4F	Interacts	
MSM115958	PTGRL2	CHMP4G	Interacts	
MSM115959	PTGRL2	CHMP4H	Interacts	
MSM115960	PTGRL2	CHMP4I	Interacts	
MSM115961	PTGRL2	CHMP4J	Interacts	
MSM115962	PTGRL2	CHMP4K	Interacts	
MSM115963	PTGRL2	CHMP4L	Interacts	
MSM115964	PTGRL2	CHMP4M	Interacts	
MSM115965	PTGRL2	CHMP4N	Interacts	
MSM115966	PTGRL2	CHMP4O	Interacts	
MSM115967	PTGRL2	CHMP4P	Interacts	
MSM115968	PTGRL2	CHMP4Q	Interacts	
MSM115969	PTGRL2	CHMP4R	Interacts	
MSM115970	PTGRL2	CHMP4S	Interacts	
MSM115971	PTGRL2	CHMP4T	Interacts	
MSM115972	PTGRL2	CHMP4U	Interacts	
MSM115973	PTGRL2	CHMP4V	Interacts	
MSM115974	PTGRL2	CHMP4W	Interacts	
MSM115975	PTGRL2	CHMP4X	Interacts	
MSM115976	PTGRL2	CHMP4Y	Interacts	
MSM115977	PTGRL2	CHMP4Z	Interacts	
MSM115978	PTGRL2	CHMP5	Interacts	
MSM115979	PTGRL2	CHMP5B	Interacts	
MSM115980	PTGRL2	CHMP5C	Interacts	
MSM115981	PTGRL2	CHMP5D	Interacts	
MSM115982	PTGRL2	CHMP5E	Interacts	
MSM115983	PTGRL2	CHMP5F	Interacts	
MSM115984	PTGRL2	CHMP5G	Interacts	
MSM115985	PTGRL2	CHMP5H	Interacts	
MSM115986	PTGRL2	CHMP5I	Interacts	
MSM115987	PTGRL2	CHMP5J	Interacts	
MSM115988	PTGRL2	CHMP5K	Interacts	
MSM115989	PTGRL2	CHMP5L	Interacts	
MSM115990	PTGRL2	CHMP5M	Interacts	
MSM115991	PTGRL2	CHMP5N	Interacts	
MSM115992	PTGRL2	CHMP5O	Interacts	
MSM115993	PTGRL2	CHMP5P	Interacts	
MSM115994	PTGRL2	CHMP5Q	Interacts	
MSM115995	PTGRL2	CHMP5R	Interacts	
MSM115996	PTGRL2	CHMP5S	Interacts	
MSM115997	PTGRL2	CHMP5T	Interacts	
MSM115998	PTGRL2	CHMP5U	Interacts	
MSM115999	PTGRL2	CHMP5V	Interacts	
MSM116000	PTGRL2	CHMP5W	Interacts	
MSM116001	PTGRL2	CHMP5X	Interacts	
MSM116002	PTGRL2	CHMP5Y	Interacts	
MSM116003	PTGRL2	CHMP5Z	Interacts	



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)

NCIBI "Try Our Tools" Virtual Workshop



Home

About

Tools

Biological Projects

Working with NCIBI

Education

Outreach & Dissemination

NCIBI Publications

Calendar

NCBCs

NCIBI "Try Our Tools" Virtual Workshop

You can try out selected NCIBI tools by following along with a tutorial booklet and downloading the relevant sample data files and required software. The tutorials are organized into 4 modules (see below) and each module has a video of the workshop associated with it that you may view before hand or simultaneously. Facilitated by technology advances that NCIBI uses to integrate data from diverse sources and heterogeneous formats, the workshops will allow you to explore such questions as:

- What proteins interact and in what pathways?
- What compounds and reactions in a pathway may be associated with a set of genes?
- What interactions may play a mechanistic role in a disease?
- What articles are relevant to given genes, interactions or diseases?
- What genes are significantly enriched for a concept or for the same set of concepts?

Before you begin the workshops, you will need to download and install the application Cytoscape on your computer. To install Cytoscape please follow the instructions under "Pre-workshop Cytoscape installation" below.

Pre-workshop Cytoscape installation

What is Cytoscape:

Cytoscape is an open source bioinformatics software platform for visualizing molecular

Reli

About NCI

NCIBI Too

Try Our To

Virtual Wo

<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



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

Human only | Substances only

[About](#)

hint: use quotes to match a phrase

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; = view interactions in MiMI

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

[All Databases](#) [PubMed](#) [Nucleotide](#) [Protein](#) [Genome](#) [Structure](#) [OMIM](#) [PMC](#) [Journal](#)

Search PubMed for [Advanced Search](#)

Display AbstractPlus Show 20 Sort By Send to

Items 1 - 15 of 15

1: [Kidney Int.](#) 2004 Apr;65(4):1467-72.

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>



Gene2MeSH



Automated Literature Based Genome Annotation Using MeSH

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

Get top MeSH terms for gene:
 example: *bcr2*

[About](#)

hint: use quotes to match a phrase

Human only | Substances only

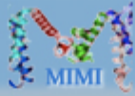
history : ["Kidney Failure, Chronic"](#)

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

Show All Columns | [download tab-delimited results](#)

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

Gene Symbol	MeSH Heading	TaxID	Fisher's Exact	MeSH Qualifier	Gene Description	External Search
ACE	Kidney Failure, Chronic	9606	1.5e-47	genetics	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	51
AGT	Kidney Failure, Chronic	9606	4.9e-22	genetics	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	22
AGTR1	Kidney Failure, Chronic	9606	3.4e-18	genetics	angiotensin II receptor, type 1	18
MTHFR	Kidney Failure, Chronic	9606	6.4e-17	genetics	5,10-methylenetetrahydrofolate reductase (NADPH)	26
NOS3	Kidney Failure, Chronic	9606	5.9e-15	genetics	nitric oxide synthase 3 (endothelial cell)	19
nph	Kidney Failure, Chronic	10090	5.7e-12	pathology	nephrosis	4
AHSG	Kidney Failure, Chronic	9606	2.9e-10	complications	alpha-2-HS-glycoprotein	7
IL6	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 #U54DA021519.
Copyright 2008 by The University of Michigan

www.ncibi.org - For support and questions email: mimi-help@umich.edu

[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](#)



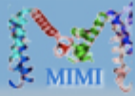
Literature on gene TGFB1 (1203 publications found) - [show/hide](#)



Pathways (8 pathways found) - [show/hide](#)

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](#)



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 #U54DA021519.
Copyright 2008 by The University of Michigan

www.ncibi.org - For support and questions email: mimi-help@umich.edu

GIN: Gene Interaction Network

[Search](#) [Article Search](#) [Disease-Specific Networks](#) [Seed Disease Genes](#) [Inferred Disease Genes](#) [About](#)

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 0-10% (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 0-10% (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 (TGF- β), with a role in transcriptional regulation. ([Article 1475747](#))

Global Network Statistics

Degree: 4

Clustering coefficient: 0.17 (1 out of 6)

MIMI

[Information about TGFBR2 on MIMI](#)

Cytoscape

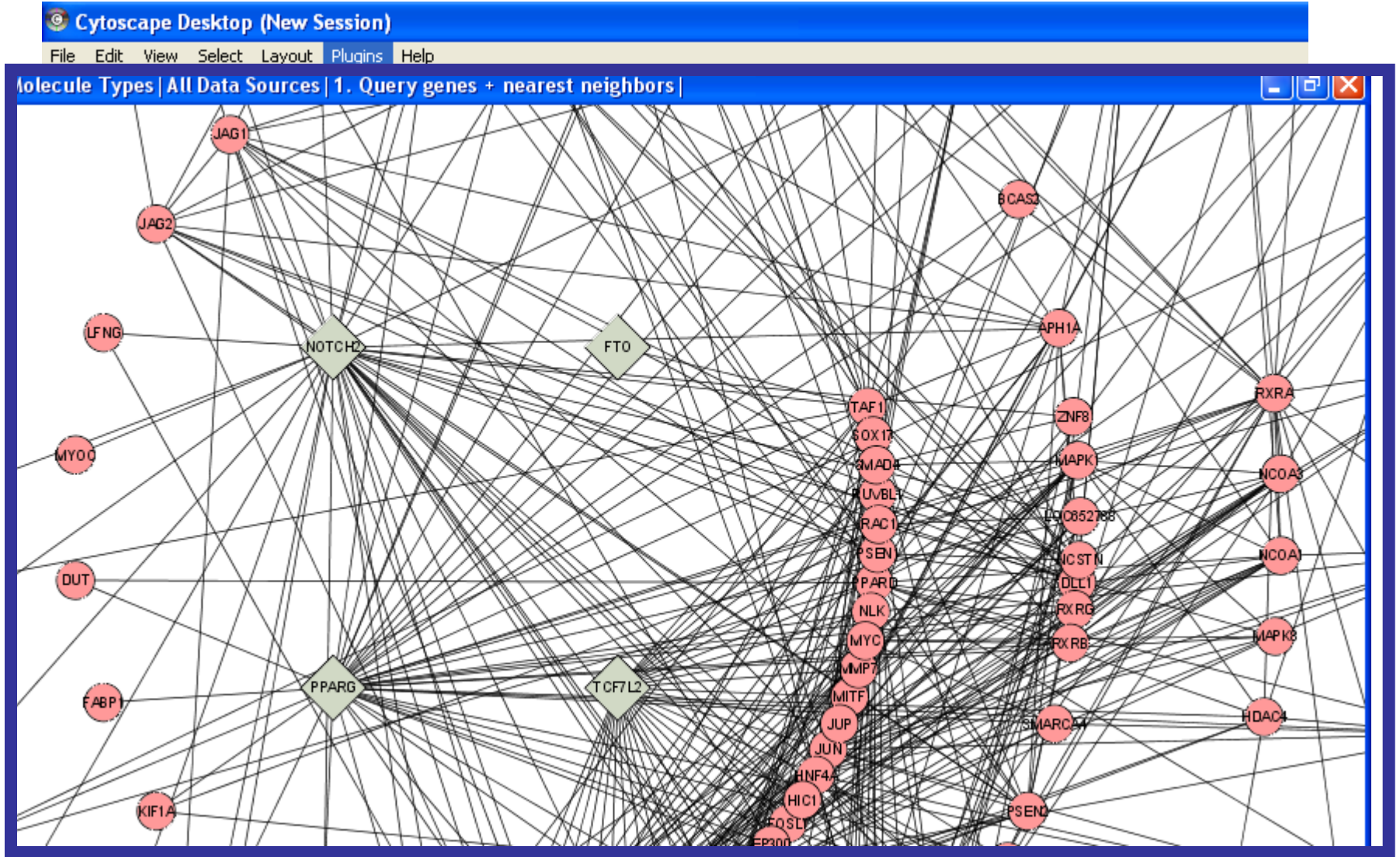
[Information about TGFBR2 on Cytoscape](#)

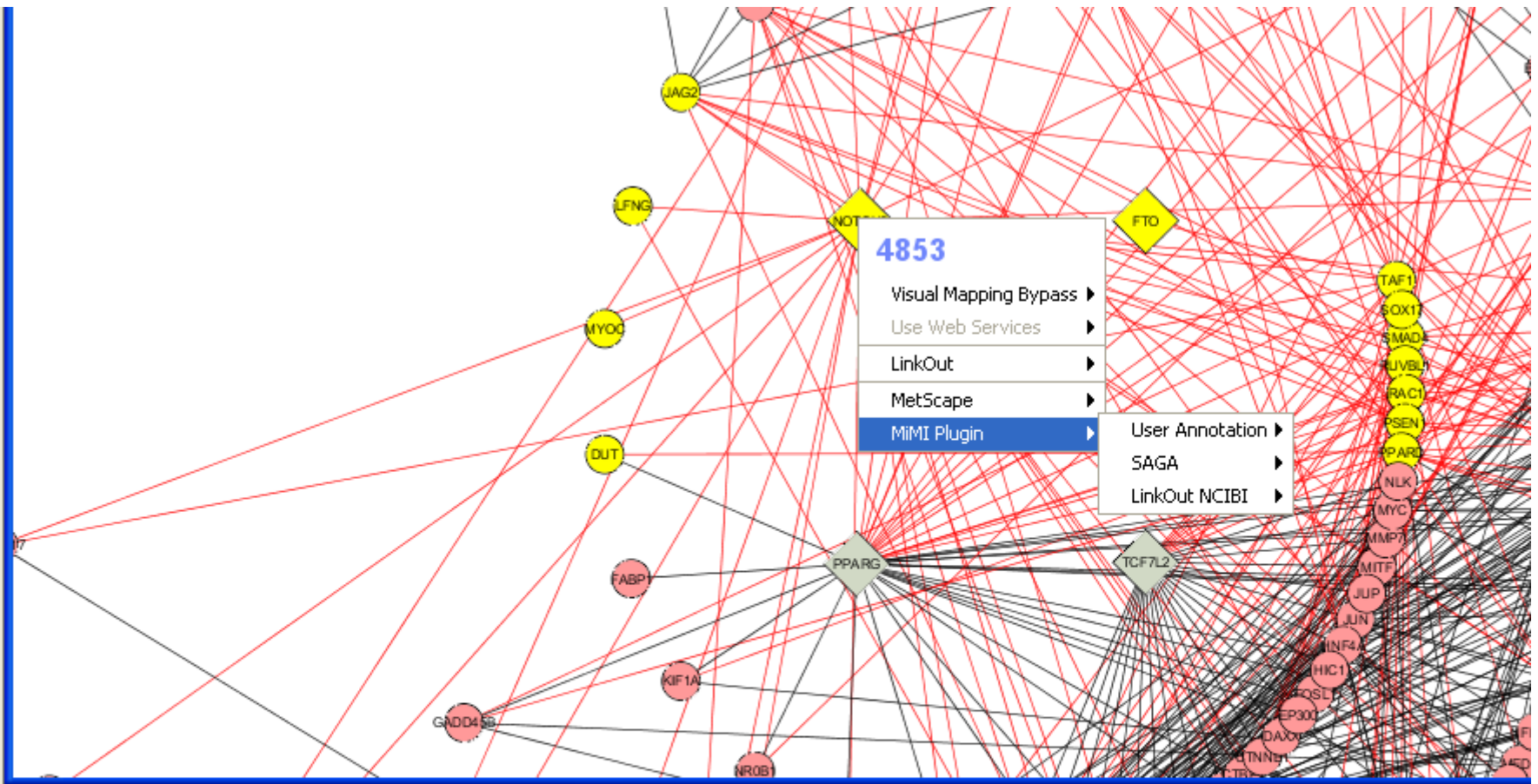
Second Neighbors

- [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.





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 Dis
Match #1	path:hsa04330 (17,16) [Notch signaling pathway]	29.00
Match #2	path:hsa04310 (59,70) [Wnt signaling pathway]	36.00

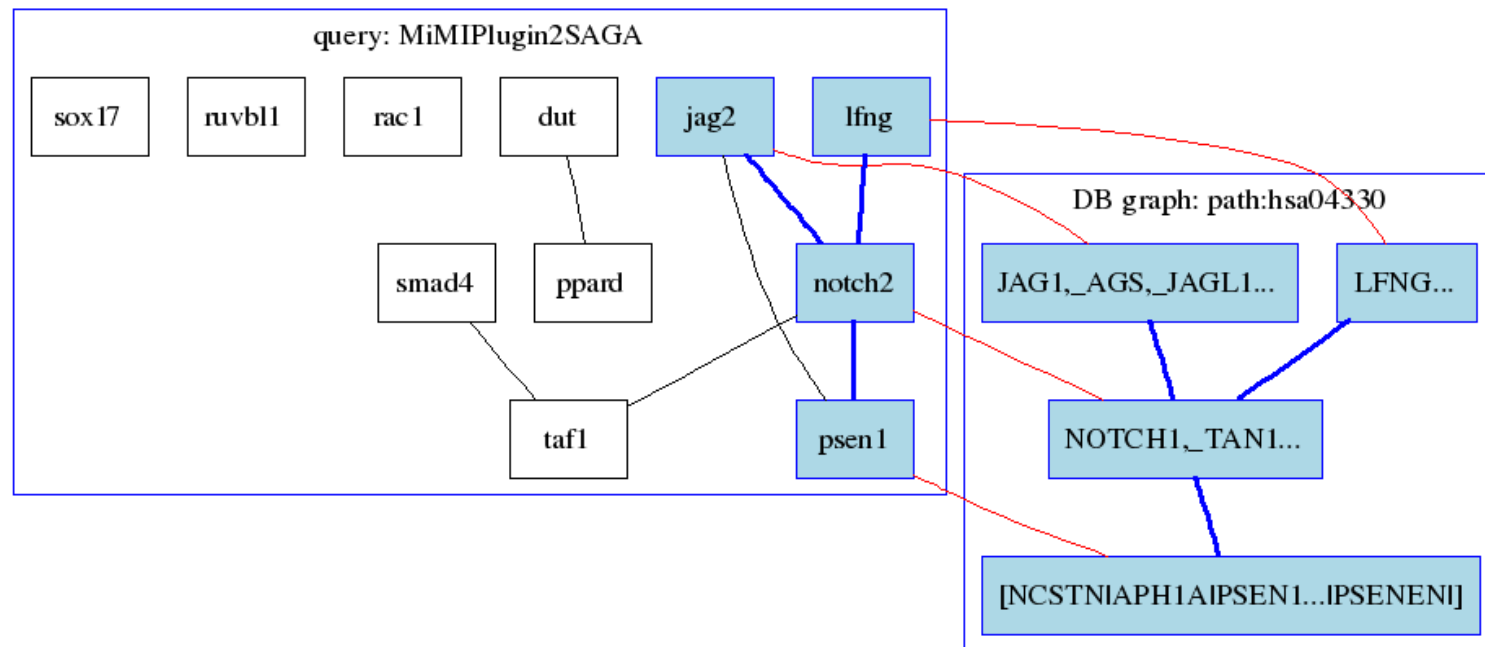
Details of the Matches:

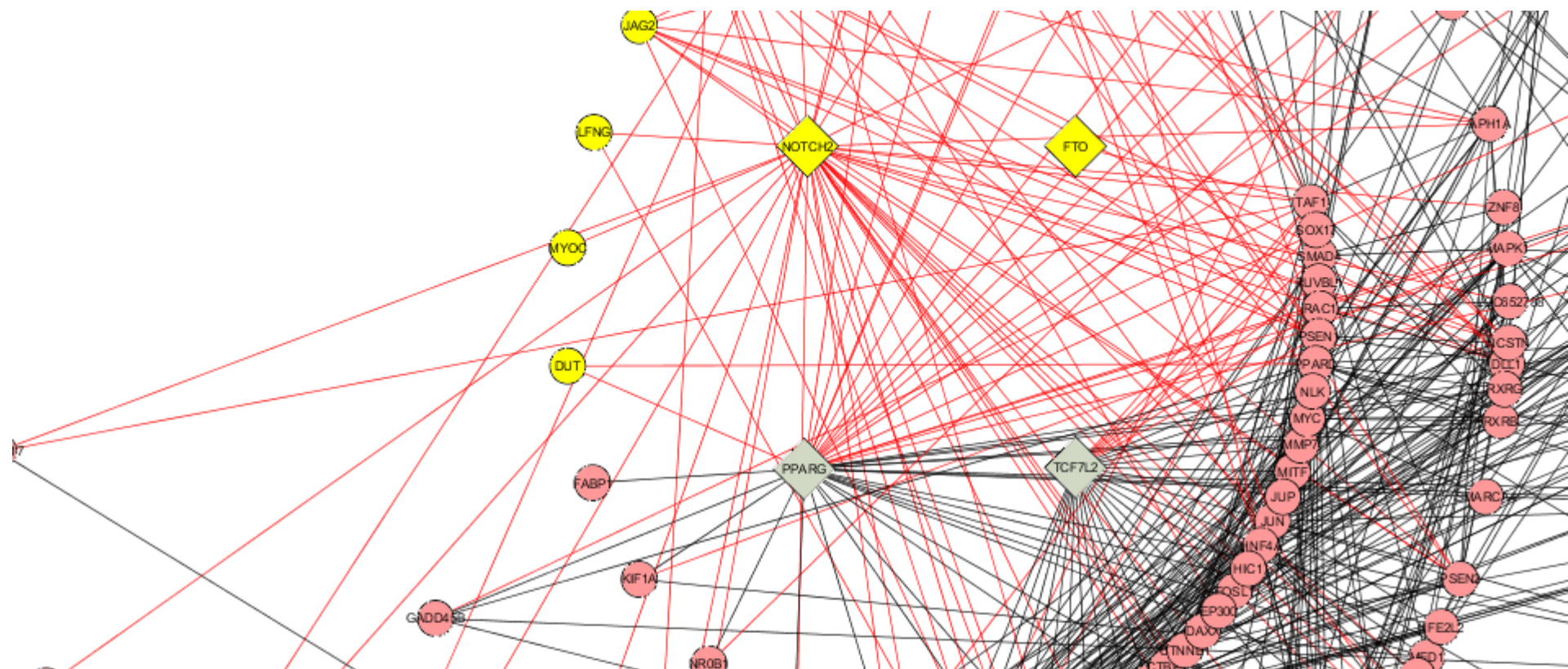
[\[Go Back to Matches Overview\]](#)

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]



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

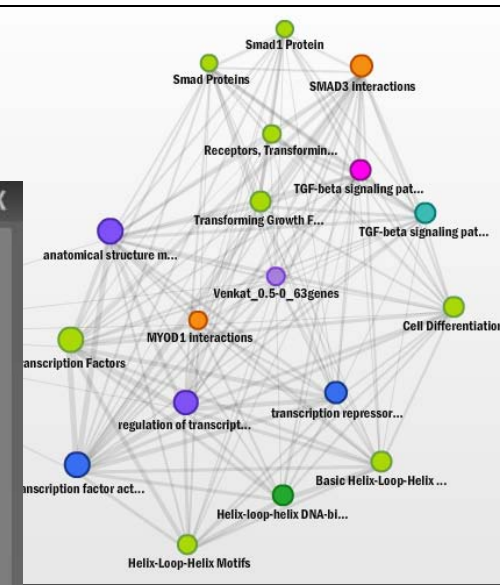
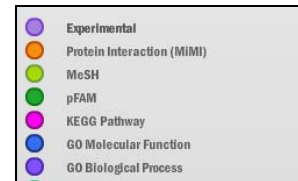
The logo for ConceptGen features four overlapping circles: a large green one on the left, a smaller orange one in the middle, a smaller red one on top, and a blue one on the right. To the right of these circles is the text "ConceptGen" in a bold, blue, sans-serif font.

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



Concept Explorer

TGFb_02hr

Queried Concept Name: TGFb_02hr Enriched Concept: JUN Interactions
 Concept Type: Experimental Concept Type: Protein Interactio...
 Gene List Size: 245 Gene List Size: 362
 Export Data: Export Data: ⚙️
 Overlap: 21

Gene Symbol	Gene Name
BCL6	B-cell CLL/lymphoma 6 (zinc finger protein 51)
SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), me
JUN	jun oncogene
JUNB	jun B proto-oncogene

Select None Select All

Enriched Concepts Filter Concepts

Draw complete Interactions Selected 0 of 106 Concepts | 🖨️ ✕

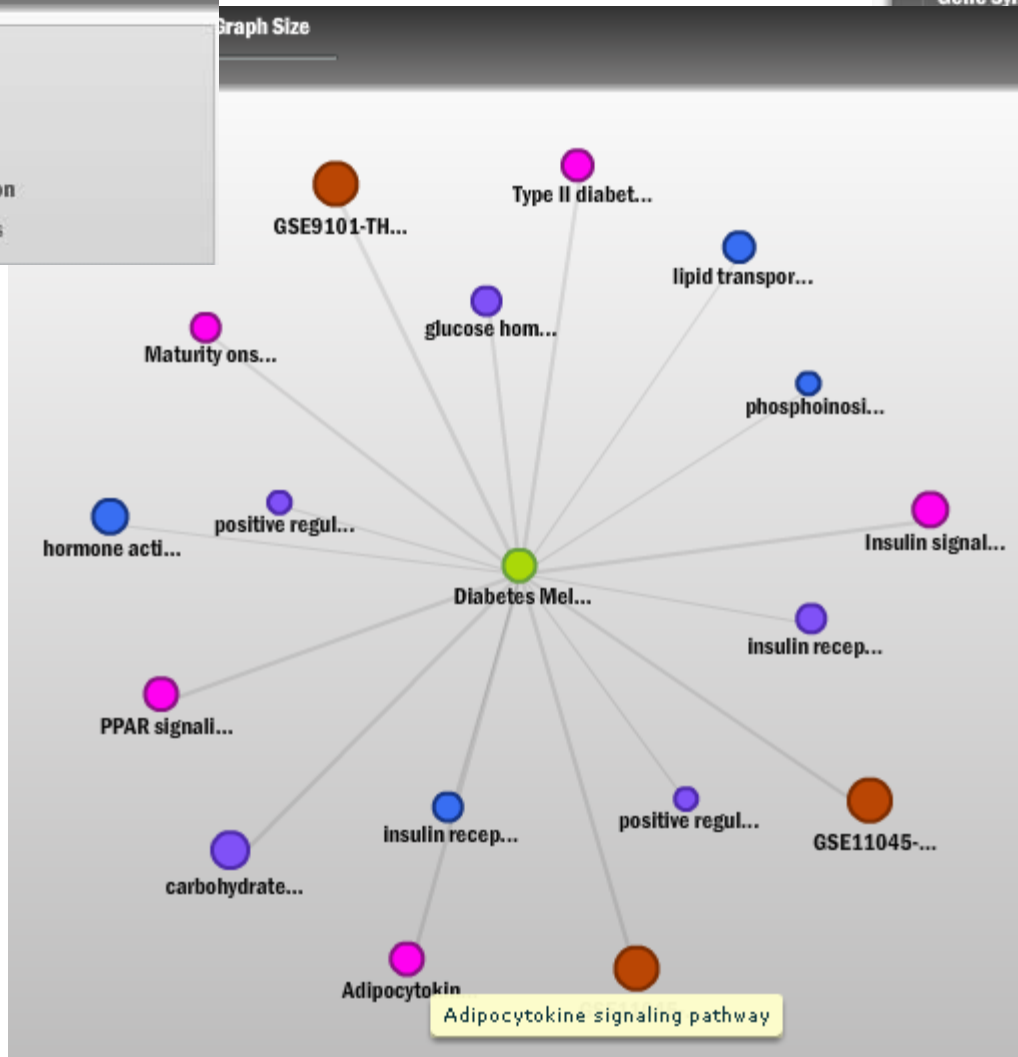
Concept Name	Concept Type Name	Category	Gene List Size	Overlap	P-value	Q-value
Transcription Factors	MeSH	Literature derived	716	42	8.58842E-17	1.729708E-13
transcription factor activity	GO Molecular Funct	Functional Annotati	928	44	5.705869E-13	3.765873E-10
sequence-specific DNA binding	GO Molecular Funct	Functional Annotati	508	32	9.308375E-13	3.071764E-10
Trans-Activators	MeSH	Literature derived	303	24	2.84646E-12	3.821847E-9
transcription from RNA polymerase II promoter	GO Biological Proce	Functional Annotati	625	34	1.466151E-11	1.529196E-8
Transforming Growth Factor beta	MeSH	Literature derived	91	14	5.950798E-11	5.992453E-8
Smad Proteins	MeSH	Literature derived	32	10	8.236528E-11	6.635347E-8
regulation of transcription from RNA polymerase II promot	GO Biological Proce	Functional Annotati	430	26	8.951237E-10	4.66807E-7
JUN Interactions	Protein Interaction	Interactions	362	21	1.990604E-8	1.403376E-4

Draw Network Graph Draw Heatmap Back to Search

Select enriched concepts by concept type

ConceptGen Motion

- Mesh
- KEGG Pathway
- Gene Expression
- GO Molecular Function
- GO Biological Process



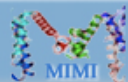
Legend Toggle View Explorer Close Gene Filter

Gene Symbol	Gene Name
	Interleukin 6 (Interferon, beta 2)
	tumor necrosis factor (TNF superfamily, member 2)
	peroxisome proliferator-activated receptor gamma, c
	cholesterol ester transfer protein, plasma
	adrenergic, beta-3-, receptor
	peroxisome proliferator-activated receptor gamma
	Insulin
	leptin (obesity homolog, mouse)
	glycogen synthase 1 (muscle)
	fatty acid binding protein 2, intestinal
	protein tyrosine phosphatase, non-receptor type 1
	renal tumor antigen

Filter Graph

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



Free Text Search

List Search

Query Interactions

Browse Database

About MiMI

Help

List of genes to search for:

C00213

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.

Type or insert a list of gene names or gene id values into text box.



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)

Results Panel

MetScape Legend

- Initial seed compound
- Compound
- Expansion seed compound
- Expansion compound
- Reaction
- Expansion reaction
- Reaction with single enzyme

Data Panel

ID	Description	Enzyme	Pathway

Node Attribute Browser Edge Attribute Browser Network Attribute Browser

```

graph TD
    A[n,n-dimethylglycine] -- R01565 --> B[sarcosine]
    B -- R00610 --> C[glycine]
    B -- R00611 --> D[ ]
    D -- R00367 --> E[ ]
    E -- R00611 --> C
  
```

Search:

C00051 C00293 C01496 C00791 C00159 C00212 C00245 C00137 C00294 C00099 C0036...

Results Panel
MetScape Legend

- Initial seed compound
- Compound
- Expansion seed compound
- Expansion compound
- Reaction
- Expansion reaction

Data Panel

ID

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

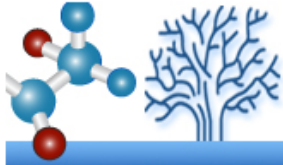
Play

Play Pause Stop

Dismiss

Node Attribute Browser | Edge Attribute Browser | Network Attribute Browser

Click + drag to ZOOM Middle-click + drag to PAN



Metab2MeSH



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

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

[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 (use the unique profile ID provided for this session or enter a username)

Query [MiSearch Help](#)

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

The query returned 4504 citations from NCBI Entrez.

Key Increased plasma urotensin-II levels are associated with diabetic retinopathy and carotid atherosclerosis in Type 2 diabetes.

Authors Suguro T, Watanabe T, Kodate S, Xu G, Hirano T, Adachi M, Miyazaki A

+ KA,Jacobson 1 [18338983](#) **Clin Sci (Lond)** 115(11):327-34 1969

+ GM,Clore

- + RT,
- + MD
- + GP
- 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 level
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 sclerosis
Brosius FC
8 [18726161](#) **Rev Endocr Metab Disord** 9(4):245-54

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

Mass spectrometric quantification of amino acid oxidations in urine
Vivekanadan-Giri A, Wang JH, Byun J, Pennathur S
10 [18752069](#) **Rev Endocr Metab Disord** 9(4):275-87

Angiotensin-aldosterone system on diabetic nephropathy risk.
Suguro T, Ugarph-Morawski A, Brismar K, Eriksson JW, Dahlquist G
22(6):377-83 1969

Angiotensin-converting enzyme inhibitors as markers of diabetic nephropathy in Type 2 diabetes mellitus.
Hilow H
22(6):384-8 1969

Angiotensin-converting enzyme inhibition and protein kinase-9 in the diabetic nephropathy of Kkay mice.
Hui L, Xiao-Man Z, Yi-Ming M
22(6):408-12 1969

Angiotensin-converting enzyme inhibition in diabetic nephropathy-role of mRNA translation.
Suguro T, Lee MJ, Ghosh Choudhury G, Feliers D
9(4):255-56 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>
    </ResultSet>
  </Response>
</NCIBI>
```

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