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)
Try Our Tools: Getting started with NCBI tools

Coming soon: Tools arranged by biological hierarchies.

To explore interactions

| Exploratory analysis | Conceptual literature searches | Databases | Other |

Use this tool

ConceptGen

ConceptGen (tool)
ConceptGen (tutorial)

Related gene lists to enriched concepts and other genes enriched for the given concept.

If you want to:

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)
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)
You can try out selected NCBI 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 NCBI 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

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: "prostate neoplasms"
  - TGFβ1

#### Get top MeSH terms for gene:
- Example: "beta2"
  - Human only | Substances only

**History:** "Kidney Failure, Chronic" → TGFβ1

257 MeSH headings found matching gene symbol "TGFβ1"

<table>
<thead>
<tr>
<th>Gene Symbol</th>
<th>MeSH Heading</th>
<th>TaxID</th>
<th>Fisher's Exact</th>
<th>MeSH Qualifier</th>
<th>Gene Description</th>
<th>External Search</th>
</tr>
</thead>
<tbody>
<tr>
<td>TGFβ1</td>
<td>Transforming Growth Factor beta</td>
<td>9606</td>
<td>0.0e-1</td>
<td>-</td>
<td>transforming growth factor, beta 1</td>
<td>658</td>
</tr>
<tr>
<td>TGFβ1</td>
<td>Transforming Growth Factor beta</td>
<td>9606</td>
<td>0.0e-1</td>
<td>genetics</td>
<td>transforming growth factor, beta 1</td>
<td>789</td>
</tr>
<tr>
<td>Tgf1</td>
<td>Transforming Growth Factor beta</td>
<td>10090</td>
<td>0.0e-1</td>
<td>metabolism</td>
<td>transforming growth factor, beta 1</td>
<td>585</td>
</tr>
<tr>
<td>Tgf1</td>
<td>Transforming Growth Factor beta</td>
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<td>0.0e-1</td>
<td>-</td>
<td>transforming growth factor, beta 1</td>
<td>238</td>
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<td>Tgf1</td>
<td>Transforming Growth Factor beta</td>
<td>10116</td>
<td>1.5e-2611</td>
<td>-</td>
<td>transforming growth factor, beta 1</td>
<td>134</td>
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<tr>
<td>Tgf1</td>
<td>Transforming Growth Factor beta</td>
<td>10116</td>
<td>4.6e-2111</td>
<td>metabolism</td>
<td>transforming growth factor, beta 1</td>
<td>134</td>
</tr>
<tr>
<td>TGFβ1</td>
<td>Receptors, Transforming Growth Factor beta</td>
<td>10116</td>
<td>4.0e-1344</td>
<td>metabolism</td>
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<td>TGFβ1</td>
<td>Smad3 Protein</td>
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<td>1.5e-1233</td>
<td>-</td>
<td>transforming growth factor, beta 1</td>
<td>94</td>
</tr>
<tr>
<td>Tgf1</td>
<td>Receptors, Transforming Growth Factor beta</td>
<td>10090</td>
<td>1.2e-1122</td>
<td>metabolism</td>
<td>transforming growth factor, beta 1</td>
<td>84</td>
</tr>
</tbody>
</table>
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: bpca2

- Human only
- Substances only

History: "Kidney Failure, Chronic"

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

- E = lookup gene or MeSH heading
- M = view interactions in MiMI

<table>
<thead>
<tr>
<th>Gene Symbol</th>
<th>MeSH Heading</th>
<th>TaxID</th>
<th>Fisher's Exact</th>
<th>MeSH Qualifier</th>
<th>Gene Description</th>
<th>External Search</th>
</tr>
</thead>
<tbody>
<tr>
<td>ACE</td>
<td>Kidney Failure, Chronic</td>
<td>9606</td>
<td>1.5e-47</td>
<td>genetics</td>
<td>angiotensin I converting enzyme (peptidyl-dipeptidase A) 1</td>
<td>51</td>
</tr>
<tr>
<td>AGT</td>
<td>Kidney Failure, Chronic</td>
<td>9606</td>
<td>4.9e-22</td>
<td>genetics</td>
<td>angiotensinogen (serpin peptidase inhibitor, clade A, member 8)</td>
<td>22</td>
</tr>
<tr>
<td>AGTRI</td>
<td>Kidney Failure, Chronic</td>
<td>9606</td>
<td>3.4e-18</td>
<td>genetics</td>
<td>angiotensin II receptor, type 1</td>
<td>18</td>
</tr>
<tr>
<td>MTHFR</td>
<td>Kidney Failure, Chronic</td>
<td>9606</td>
<td>6.4e-17</td>
<td>genetics</td>
<td>5,10-methylenetetrahydrofolate reductase (NADPH)</td>
<td>26</td>
</tr>
<tr>
<td>NOS3</td>
<td>Kidney Failure, Chronic</td>
<td>9606</td>
<td>5.9e-15</td>
<td>genetics</td>
<td>nitric oxide synthase 3 (endothelial cell)</td>
<td>19</td>
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<tr>
<td>nph</td>
<td>Kidney Failure, Chronic</td>
<td>10090</td>
<td>5.7e-12</td>
<td>pathology</td>
<td>nephrosis</td>
<td>4</td>
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<tr>
<td>AHSG</td>
<td>Kidney Failure, Chronic</td>
<td>9606</td>
<td>2.9e-10</td>
<td>complications</td>
<td>alpha-2-HS-glycoprotein</td>
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<tr>
<td>IL6</td>
<td>Kidney Failure, Chronic</td>
<td>9606</td>
<td>1.8e-9</td>
<td>therapy</td>
<td>interleukin 6 (interferon, beta)</td>
<td>18</td>
</tr>
</tbody>
</table>
### Literature on gene TGFβ1 (1203 publications found) - show/hide

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

<table>
<thead>
<tr>
<th>Pathway</th>
<th>Description</th>
<th>Genes Related to Pathway</th>
</tr>
</thead>
<tbody>
<tr>
<td>KEGG:hsa04110</td>
<td>Image</td>
<td>View Related</td>
</tr>
<tr>
<td></td>
<td>Cell cycle</td>
<td></td>
</tr>
<tr>
<td>KEGG:hsa04350</td>
<td>Image</td>
<td>View Related</td>
</tr>
<tr>
<td></td>
<td>TGF-beta signaling pathway</td>
<td></td>
</tr>
<tr>
<td>KEGG:hsa05211</td>
<td>Image</td>
<td>View Related</td>
</tr>
<tr>
<td></td>
<td>Renal cell carcinoma</td>
<td></td>
</tr>
<tr>
<td>KEGG:hsa05220</td>
<td>Image</td>
<td>View Related</td>
</tr>
<tr>
<td></td>
<td>Chronic myeloid leukemia</td>
<td></td>
</tr>
<tr>
<td>KEGG:hsa05210</td>
<td>Image</td>
<td>View Related</td>
</tr>
<tr>
<td></td>
<td>Colorectal cancer</td>
<td></td>
</tr>
<tr>
<td>KEGG:hsa04010</td>
<td>Image</td>
<td>View Related</td>
</tr>
<tr>
<td></td>
<td>MAPK signaling pathway</td>
<td></td>
</tr>
<tr>
<td>KEGG:hsa05212</td>
<td>Image</td>
<td>View Related</td>
</tr>
<tr>
<td></td>
<td>Pancreatic cancer</td>
<td></td>
</tr>
</tbody>
</table>
MICHIGAN MOLECULAR INTERACTIONS

Gene Details

Molecule Details for Gene Entry TGBF1 (GeneId: 7040) - show/hide

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

Literature on gene TGBF1 (1203 publications found) - show/hide

Pathways (8 pathways found) - show/hide

View TGBF1 With Other NCBI Tools

Gene2MeSH  Cytoscape  Netbrowser  GIN  MiSearch

www.ncbi.org - For support and questions email: mimi-help@umich.edu
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 0A%??10% (Figure 1A). (Article 1188057) (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 0A%??10% (Figure 1A). (Article 1188057) (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 (TGFβ) 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 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.
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)
<table>
<thead>
<tr>
<th>ID</th>
<th>Function</th>
<th>Gene name</th>
<th>Interactiontype</th>
</tr>
</thead>
<tbody>
<tr>
<td>4854</td>
<td>[calcium ion binding [GO:0005509]; protein binding ...</td>
<td>(NOTCH2 , NOTCH3)</td>
<td>[bidirectional]</td>
</tr>
<tr>
<td>6872</td>
<td>[protein binding [GO:0005515]]</td>
<td>(TAF1 , NCOA4)</td>
<td>[bidirectional]</td>
</tr>
<tr>
<td>4853</td>
<td>[protein binding [GO:0005515]]</td>
<td>(NOTCH2 , DTX4)</td>
<td>[PPrel]</td>
</tr>
<tr>
<td>1840</td>
<td>[metal ion binding [GO:0046872]; transcription coac...</td>
<td>(DTX1 , EP300)</td>
<td>[bidirectional [reverse]; in vivo [reverse]; Invivo]</td>
</tr>
<tr>
<td>5468</td>
<td>[metal ion binding [GO:0046872]; protein binding [G...</td>
<td>(PPARG , COPS5)</td>
<td>[bidirectional]</td>
</tr>
<tr>
<td>5468</td>
<td>[metal ion binding [GO:0046872]; protein binding [G...</td>
<td>(PPARG , RXRA)</td>
<td>[Affinity Capture-MS; bidirectional; in vitro; Invitro [rev...</td>
</tr>
<tr>
<td>3714</td>
<td>[calcium ion binding [GO:0005509]; Notch binding [...</td>
<td>(JAG2 , DLL4)</td>
<td>[neighbouring_reaction [reverse]]</td>
</tr>
<tr>
<td>6934</td>
<td>[DNA binding [GO:0003677]]</td>
<td>(TCF7L2 , SOX17)</td>
<td>[PPrel [reverse]]</td>
</tr>
</tbody>
</table>
### 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

<table>
<thead>
<tr>
<th>PubmedID</th>
<th>Section</th>
<th>Symbol</th>
<th>Symbol</th>
<th>Sentence</th>
</tr>
</thead>
<tbody>
<tr>
<td>8990192</td>
<td>ABSTRACT</td>
<td>PPARG</td>
<td>RXRA</td>
<td>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.</td>
</tr>
<tr>
<td>9492033</td>
<td>ABSTRACT</td>
<td>PPARG</td>
<td>RXRA</td>
<td>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.</td>
</tr>
<tr>
<td>10582693</td>
<td>ABSTRACT</td>
<td>PPARG</td>
<td>RXRA</td>
<td>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.</td>
</tr>
<tr>
<td>10860864</td>
<td>ABSTRACT</td>
<td>PPARG</td>
<td>RXRA</td>
<td>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.</td>
</tr>
<tr>
<td>10936484</td>
<td>ABSTRACT</td>
<td>PPARG</td>
<td>RXRA</td>
<td>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).</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>PIMT enhances the transcriptional activity of peroxisome proliferator-activated receptor gamma and</td>
</tr>
</tbody>
</table>
Additional Cytoscape Modules

• MetScape (beta release 0.8) mapping metabolites to proteins (Poster # 3, Alla Karnovsky)

• Bingo (GO term overrepresentation/enrichment)

• MCode (highly connected regions of a graph)

• DynamicExpression (timecourse color / size)
  – Iliana Avila-Campillo, Galitski Group, Institute for Systems Biology.

• Many others ....
• 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
NetBrowser

Gene Annotation

- **Gene ID:** 19637
- **Gene Type:** protein-coding
- **Organism:** Homo sapiens
- **Chromosome:** 1
- **Map Location:** 1q42.1
- **Locus Tag:**
  - **Alias:** LEFTY1, LEFTB, LEFTY8
  - **Kegg Pathway:** hsa:19637
  - **Gene Complex:** KEGG:pathc5a04350:29

<table>
<thead>
<tr>
<th>GO Term</th>
<th>Category</th>
</tr>
</thead>
<tbody>
<tr>
<td>extracellular region</td>
<td>Component</td>
</tr>
<tr>
<td>extracellular space</td>
<td>Component</td>
</tr>
<tr>
<td>cytokine activity</td>
<td>Function</td>
</tr>
<tr>
<td>growth factor activity</td>
<td>Function</td>
</tr>
</tbody>
</table>

**Path Name**

- **pathc5a04350**

**Description**

- TGF-beta signaling pathway

Diagram showing gene interactions with LEFTY1 and TGFBR3 as central nodes.
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
List of genes to search for:

C00213

Select type:
- Symbols
- Gene IDs
- CIDs

Limit search by organism:
- Homo sapiens

Optional: Upload a text file. File should contain a list of gene symbols, gene ID values or compound IDs; one entry per line.

www.ncbi.org - For support and questions email: mimi-help@umich.edu
### Metab2MeSH

**Get top substances for MeSH term:**
- example: aspirin

**Get top MeSH terms for substance:**
- example: phosloest

History: glucose - insulin - TZD - glitazone - "diabetic mice" - "diabetic model" - "diabetes model" - "diabetes" - diabetes - Thiazolidinediones

Showing top 1000 MeSH headings found matching substance **"Thiazolidinediones"**

<table>
<thead>
<tr>
<th>Substance Name</th>
<th>Registry #</th>
<th>MeSH Heading</th>
<th>MeSH Qualifier</th>
<th>PubMed Articles</th>
<th>Fisher's Exact</th>
<th>Ratio</th>
</tr>
</thead>
<tbody>
<tr>
<td>Thiazolidinediones</td>
<td>-</td>
<td>Thiazolidinediones</td>
<td>therapeutic use</td>
<td>4968</td>
<td>-4.2e+4</td>
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<td>Thiazolidinediones</td>
<td>-</td>
<td>Hypoglycemic Agents</td>
<td>therapeutic use</td>
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<td>-1.5e+4</td>
<td>235</td>
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<td>-</td>
<td>Thiazoles</td>
<td>pharmacology</td>
<td>2016</td>
<td>-9.4e+3</td>
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<td>-</td>
<td>Chromams</td>
<td>pharmacology</td>
<td>1353</td>
<td>-8.3e+3</td>
<td>807.4</td>
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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
examples: gab2 or prostate cancer AND androgen receptor
Submit

The query returned 4504 citations from NCBI Entrez.

Key Authors
Increased plasma urotensin-II levels are associated with diabetic retinopathy and carotid atherosclerosis in Type 2 diabetes. Suguro T, Watanabe T, Kodate S, Xu G, Hirano T, Adachi M, Miyazaki A
1 18388983 Clin Sci (Lond) 115(11):327-34 1969

Defining human diabetic nephropathy on the molecular level: Martini S, Eichinger F, Nair V, Kretzler M

New insights into the mechanisms of fibrosis and sclerosis Brosius FC
8 16726161 Rev Endocr Metab Disord 9(4):245-54 1969

AVPR2 variants and mutations in nephrogenic diabetes insipidus Spanakis E, Milord E, Gragnoli C
9 16726699 J Cell Physiol 217(3):605-17 1969

Mass spectrometric quantification of amino acid oxidation in Vivokeyanan-Giri A, Wang JH, Byun J, Pennathur S

"A novel mutation of SLC34A12 gene causing primary renal..."
Gene2Mesh API

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

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http://gene2mesh.ncibi.org/about
NLP Pubmed Programmatic Interface

- http://nlp.ncibi.org/about.html
- Example:

```xml
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