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# Partial Integration of GO with the Ingenuity Ontology

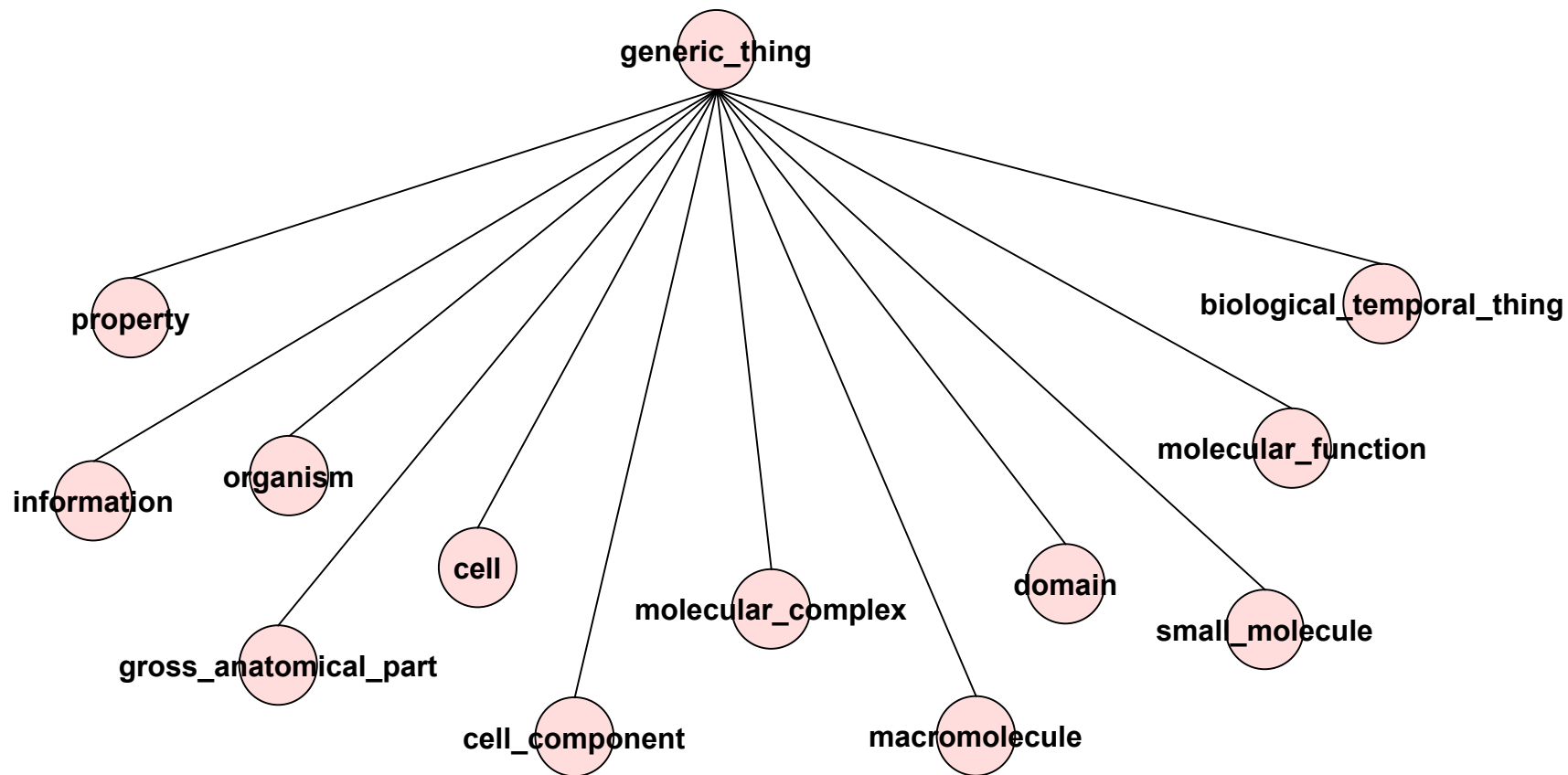
Molly James  
Ontology Modeling, Ingenuity System  
Mountain View, CA

# Ingenuity Ontology

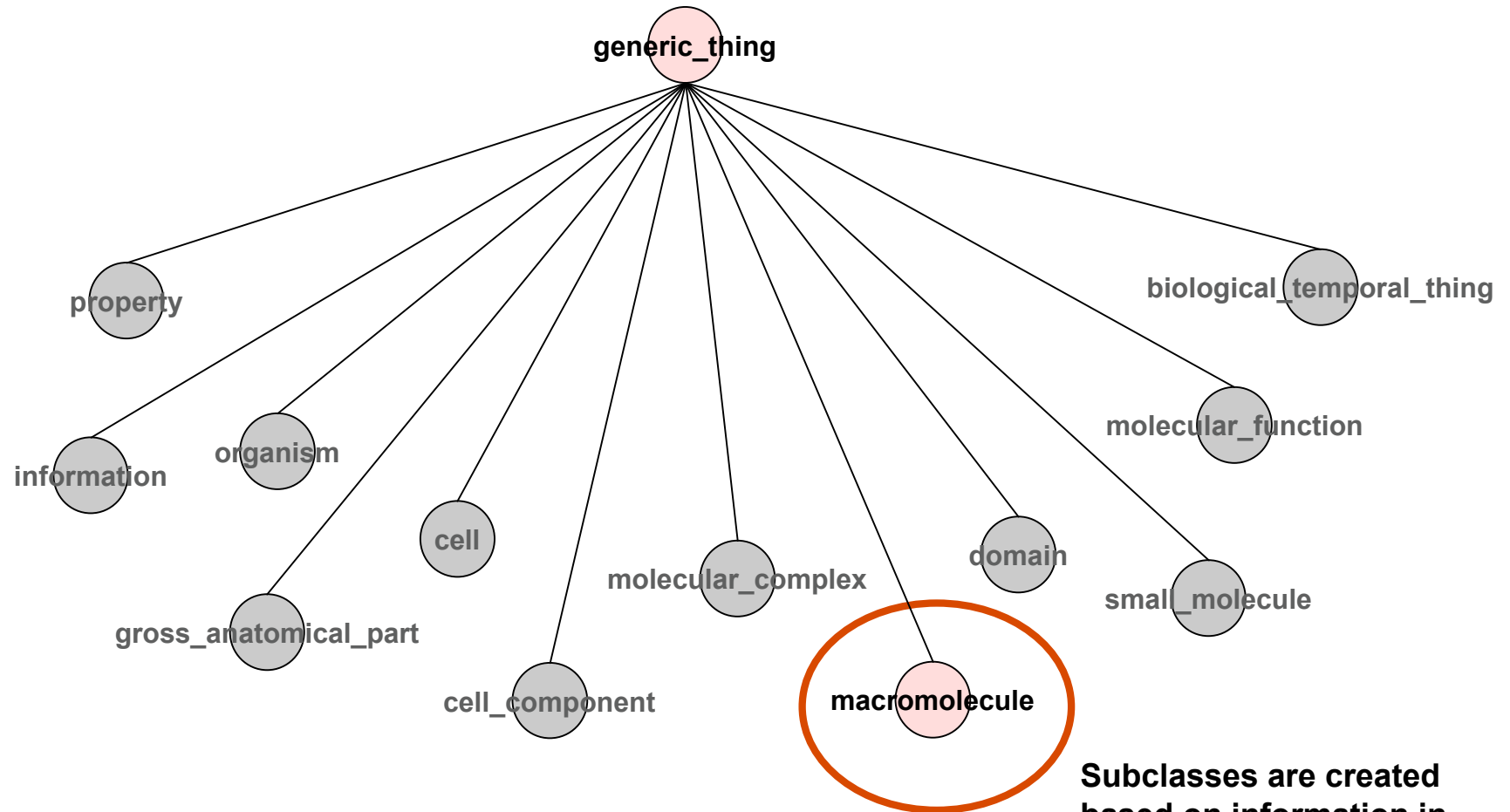
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- Private ontology
  - Stores information extracted from scientific literature
- Very large ontology
  - 575,000 classes
  - 10 million instances
  - 370 slots
- Uses frame-based knowledge representation system

# High Level Classes

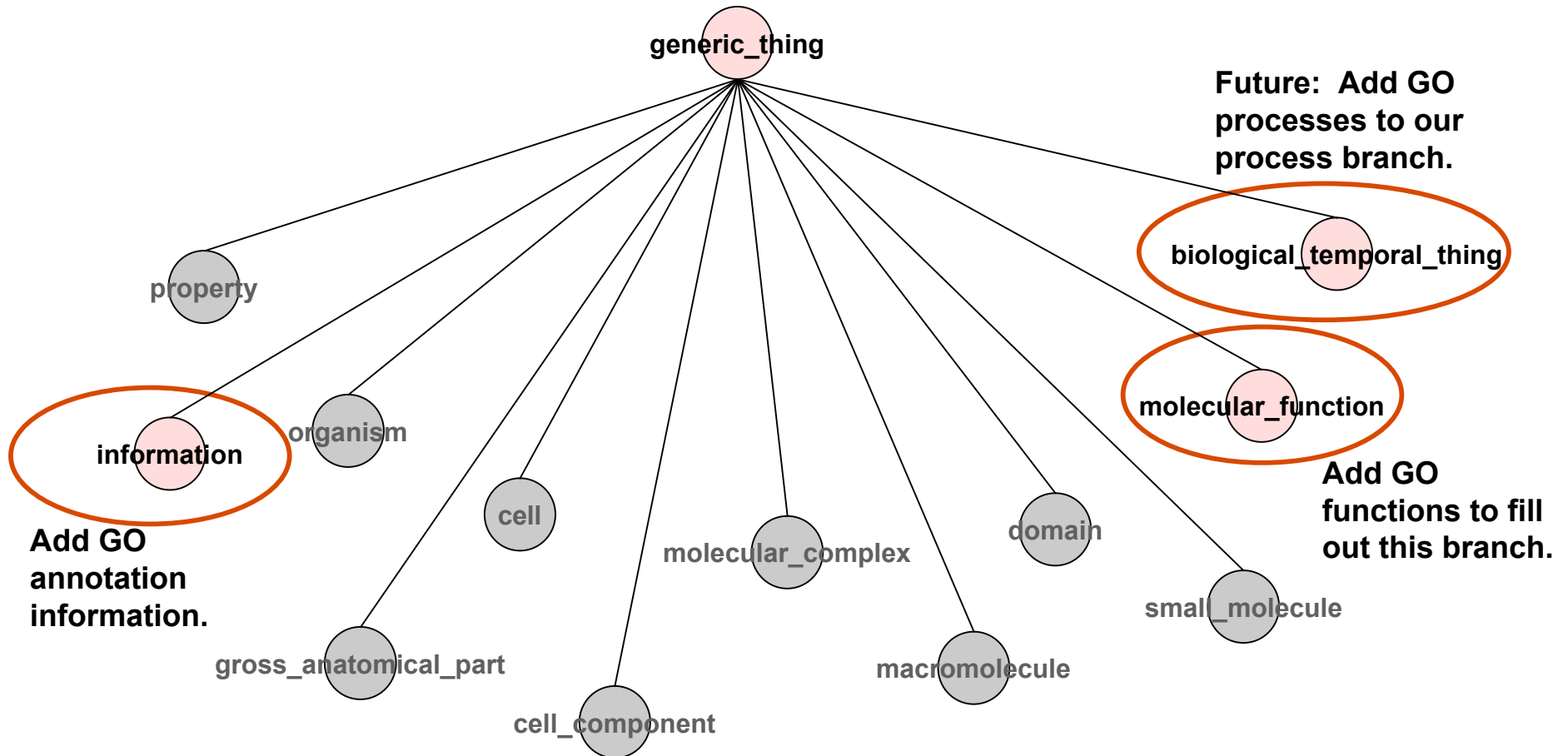


# Ontology Construction via Downloads



**Subclasses are created based on information in LocusLink.**

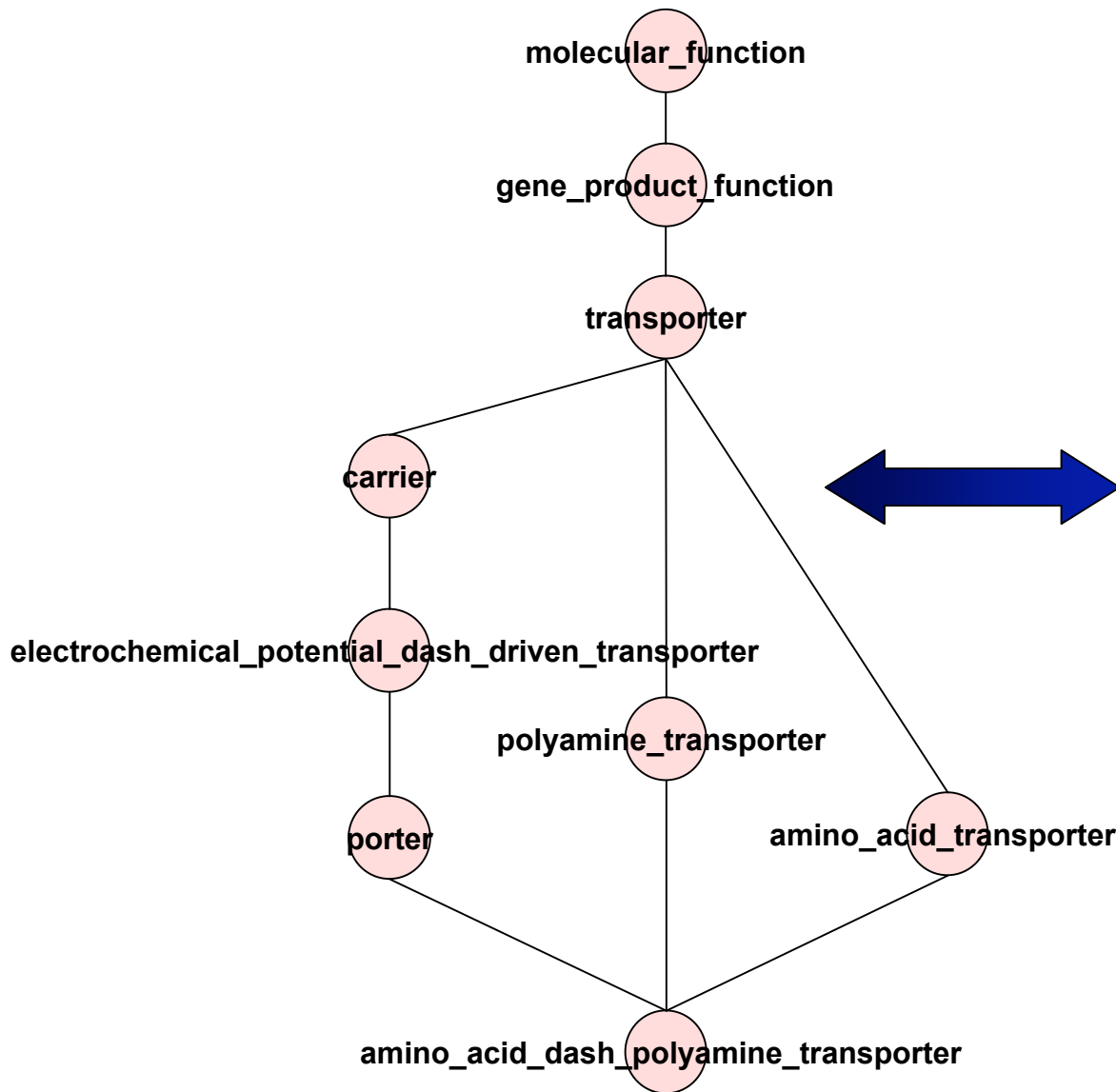
# Using GO to Supplement the Ontology



# Adding GO functions.

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- Took only "is-a" relationships from GO.
- Excluded functions not applicable to human, mouse, or rat.
- Excluded functions not part of our function model.
  - E.g. anticoagulant is a drug in our ontology.
- Converted GO names into our naming format.
- Fix duplicates that were imported.



**%transporter ; GO:0005215**

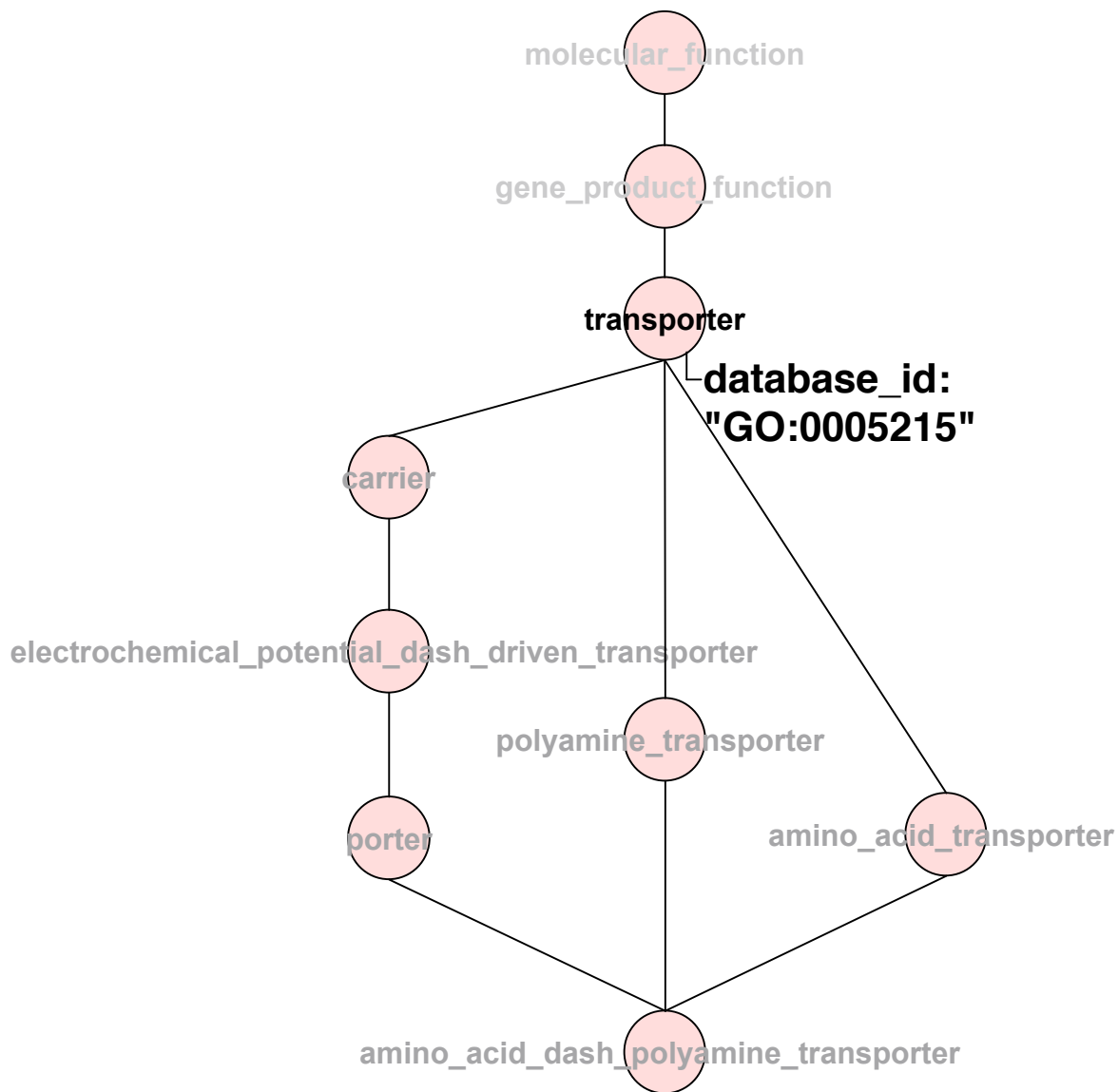
**%carrier ; GO:0005386 ;  
synonym:carrier type transporter**

**%electrochemical potential-  
driven transporter ; GO:0015290**

**%porter ; GO:0015291  
synonym:active transporter**

**%amino acid-polyamine  
transporter ; GO:0005279 ; %  
amino acid transporter ;  
GO:0015171 % polyamine  
transporter ; GO:0015203**





**%transporter ; GO:0005215**

%carrier ; GO:0005386 ;  
synonym:carrier type transporter

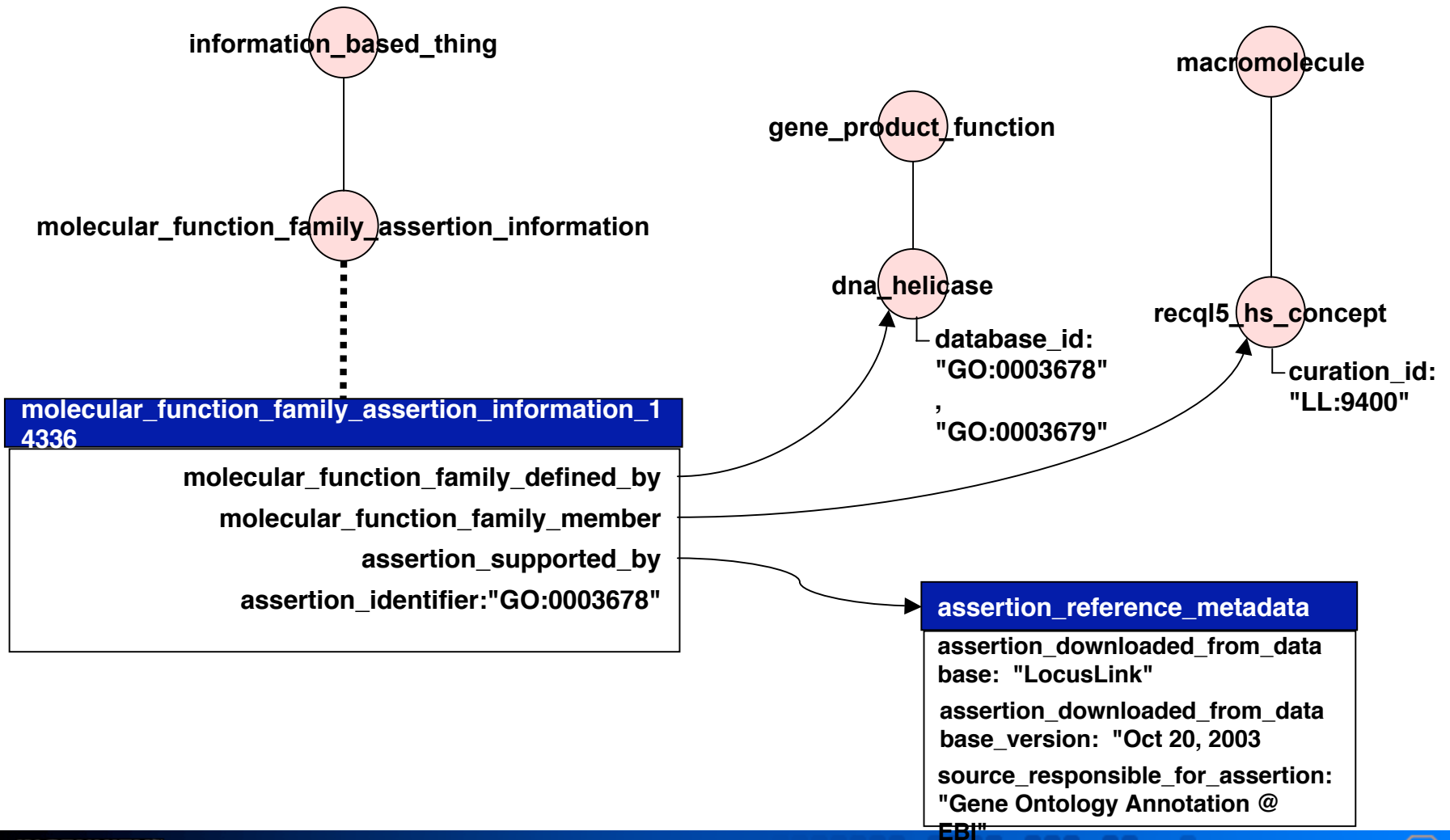
%electrochemical potential-  
driven transporter ; GO:0015290

%porter ; GO:0015291  
synonym:active transporter

%amino acid-polyamine  
transporter ; GO:0005279 ; %  
amino acid transporter ;  
GO:0015171 % polyamine  
transporter ; GO:0015203



# Adding Functional Annotation Information



# Use of Functions in Ingenuity Pathway Analysis

**Ingenuity  
PATHWAYS ANALYSIS** User: Not signed in

### Sign In

Welcome. Please sign in.

E-mail address:   Remember my e-mail address.

Password:

**>> Sign in**

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Done Internet

Network 1



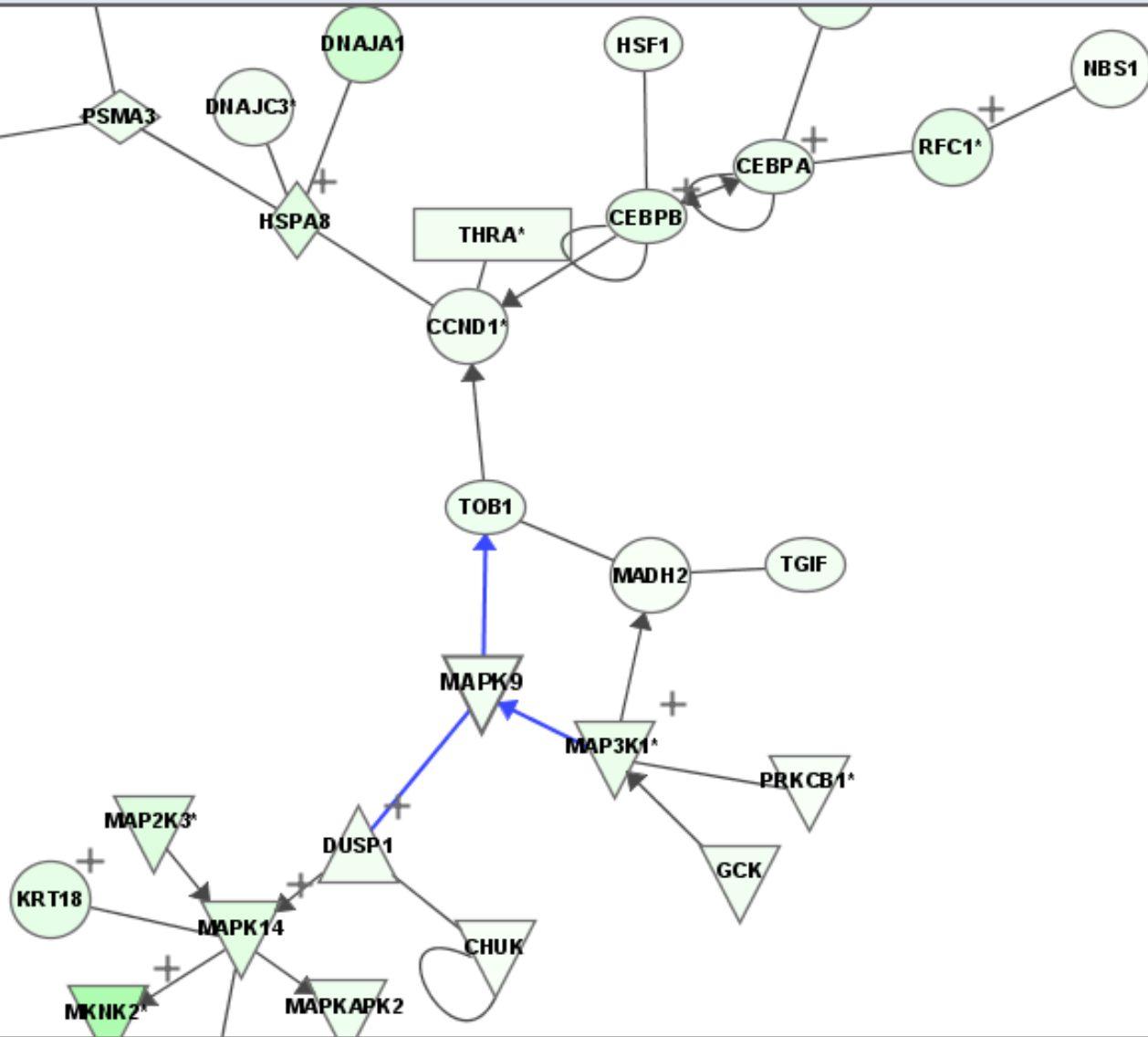
Shapes indicate function

Kinase

Nuclear Receptor

Transcription Factor

Enzyme



Network 1



**Node Name:** [RXRA \(Neighborhood Explorer\)](#)

**Source Id**

NM\_002957

**Synonyms**

NR2B1, Nr2b1, Retinoid X receptor alpha, Rxr alpha 1, Rxr alpha

**Protein Family, Domain**

AF-1 domain, AF-2 transcription activation domain, C4 type zinc finger domain, DNA binding domain, E domain, Hedgehog N-terminal signaling domain, hormone binding domain, ligand-binding domain, ligand-dependent nuclear receptor, receptor, retinoic acid receptor, steroid binding protein, steroid hormone receptor, transcription activation domain, transcription co-activator

**Subcellular Location**

chromatin, cytoplasm, nuclear fraction, nucleus

**LL Description**

retinoid X receptor, alpha

**Top Findings**

**regulates:** SORBS1, CYP3A1, CYP7A1, FABP1, CYP4A1, APOA1, APOC3, CYP2B10, RXRG, FABP4, LPL, DLK1, RARA, ACOX1, ACADM

**regulated by:** IGFBP3, MAPK8, MAPK2K4, RARG, RARA, NCOA6, MYOD1, V-ERB A, POU1F1, PPARGC1, IFNG, STAT1, CSF2, IL3, NR0B2

**binds:** NCOA4, PPAR GAMMA, Malic Enzyme, THRA, NR1H3, ACC ALPHA, PPARG, APOA2, NCOR1, PCK1, POU1F1, NR1H2, NR0B2, NR1I2, CYP3A4

**role in cell:** size, apoptosis, density, organization, proliferation, developmental process

**disease:** cardiovascular disease, skeletomuscular disorder, tumorigenesis, immunological disease

**Descriptions**

**LocusLink Summary:** Retinoid X receptors (RXRs) and retinoic acid receptors (RARs), are nuclear receptors that mediate the biological effects of retinoids by their involvement in retinoic acid-mediated gene activation. These receptors exert their action by binding, as homodimers or heterodimers, to specific sequences in the promoters of target genes and regulating their transcription. The protein encoded by this gene is a member of the steroid and thyroid hormone receptor superfamily of transcriptional regulators.

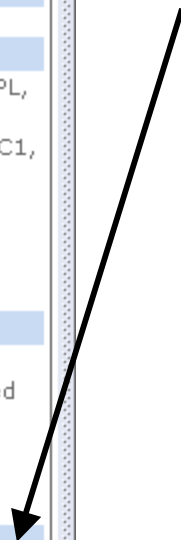
**GO Annotations**

**Molecular Function:** DNA binding; retinoic acid receptor activity; transcription co-activator activity; retinoid-X receptor activity

**Biological Process:** vitamin metabolism; signal transduction

**Cellular Component:** nucleus

GO Annotations are imported and displayed on NodeView pages.



# Processes are used to annotate groups of genes

**Functional Analysis: Network 1**

Click the plus icon to expand details.

**Network genes:** BRCA1↑, CCNA2↑, CDKN1A↓, ERBB2↓, ERBB3↓, FOS↑, HES1↓, ID2↓, IGFBP5↑, JAK1↑, MADH3↓, MYB↑, MYBL2↑, MYC↑, NCOA2↓, RARA↑, RBL2↓, RFC4↑, RXRA↓, TGFBR2↓

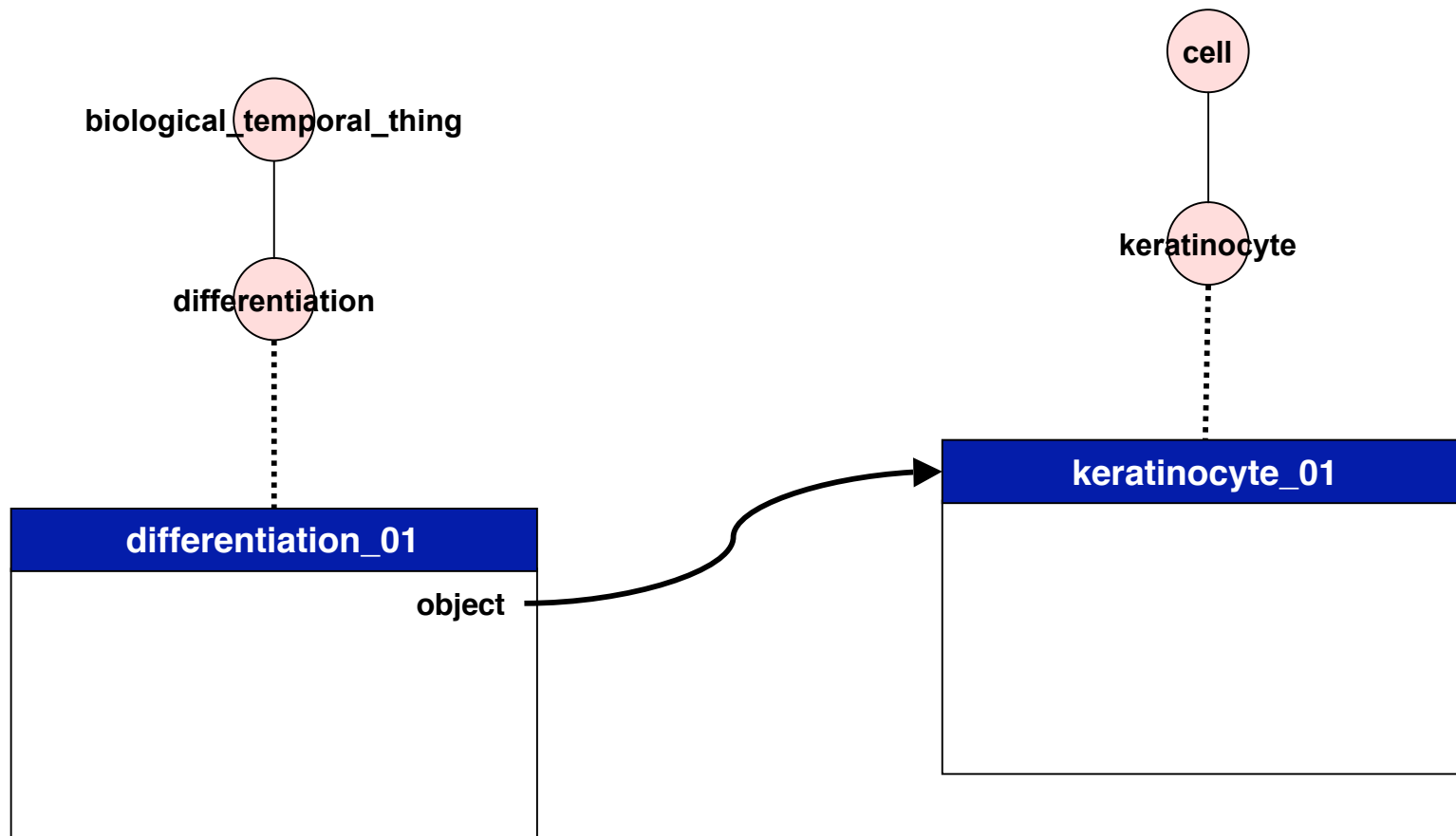
General Function (expand all)	p-value Range	Number of Associated Genes
<input type="checkbox"/> differentiation	1.60E-10 to 8.16E-3	15

Specific Function	Genes from Network	# Genes	p-value
differentiation of cells	BRCA1↑, CDKN1A↓, ERBB3↓, FOS↑, HES1↓, ID2↓, IGFBP5↑, MADH3↓, MYB↑, MYBL2↑, MYC↑, NCOA2↓, RARA↑, RBL2↓, RXRA↓	15	1.60E-10
differentiation of tumor cell lines	CDKN1A↓, FOS↑, HES1↓, MYB↑, MYC↑, RARA↑, RBL2↓	7	2.75E-6
differentiation of connective tissue cells	FOS↑, MADH3↓, MYB↑, MYC↑, RARA↑, RBL2↓	6	7.81E-6
differentiation of bone cell lines	CDKN1A↓, MYB↑, MYC↑, RBL2↓	4	2.06E-5
differentiation of myeloid cells	MYB↑, MYBL2↑, MYC↑, RARA↑	4	5.23E-5
differentiation of cancer cells	CDKN1A↓, MYC↑, RARA↑	3	5.43E-5
differentiation of leukocyte cell lines	MYB↑, MYBL2↑, MYC↑, RARA↑, RBL2↓	5	5.94E-5
differentiation of endocrine cell lines	CDKN1A↓, FOS↑, HES1↓, RBL2↓	4	6.98E-5
differentiation of keratinocytes	CDKN1A↓, MYC↑, RXRA↓	3	8.56E-5
differentiation of epithelial cells	CDKN1A↓, ID2↓, MYC↑, RXRA↓	4	1.04E-4
differentiation of blood cells	ID2↓, MYB↑, MYBL2↑, MYC↑, RARA↑, RXRA↓	6	1.55E-4
differentiation of neuroglia	ERBB3↓, HES1↓, ID2↓	3	3.52E-4
differentiation of muscle cell lines	IGFBP5↑, MADH3↓, RBL2↓	3	4.50E-4

Internet

# Aligning GO Processes with Ingenuity Processes

%keratinocyte differentiation; GO:0030216



# www.ingenuity.com

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Ingenuity Pathways Analysis  
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