

PathwaysBrowser Web Application Documentation

Introduction

Cancer is the uncontrolled growth of abnormal cells in the body. For cancer to occur multiple signaling mechanisms must break down to allow the cell to avoid the many checks and balances in the body that prevent such uncontrolled growth from happening. An understanding of molecular interactions and biological processes that support or prevent this growth is a key element to finding the causes and cures for cancer. Scientists have grouped the molecular interactions and biological processes into signaling and regulatory pathways. This information includes data about the pathways, the genes that make up those pathways and interactions between the genes. The PathwaysBrowser Web Application was created to provide a mechanism by which users or software programs could easily access such information. It utilizes the PathwaysWeb Web Service to retrieve the requested information from an organized database.

The PathwaysBrowser Web Application

The PathwaysBrowser is a read-only resource-based web application that makes it possible to retrieve data regarding cancer-related biological pathways and related data using standard HTTP protocol GET requests. Resources may be objects (i.e. a single pathway) or collections of objects (i.e. a set of pathways that all contain certain genes). Resources accessible via the application include information about pathways, the genes within those pathways, interactions between genes, gene synonyms, references to multiple gene database ids for genes with an approved HUGO gene symbol, and references to PubMed ids for articles related to genes and interactions. The system contains multiple versions of data which are snapshots of the full collection of data from different sources at a given point in time. The API provides for data can be retrieved by version to help reproduce results or to easily retrieve the latest version of the data without knowing the beforehand what the latest version is.

Available Data

PathwaysBrowser includes data from the National Cancer Institute (NCI), the National Center for Biotechnology (NCBI), the HUGO Gene Nomenclature Committee (HGNC), and The Gene Ontology. The information is made available based on resources. As of 5/10/2014, resources include:

Resources	Record Count per latest data load (version)
Pathways and sub pathways	Total: 1600; NCI-Curated: 201; Reactome: 1399
Interactions	1,024,802
Interaction Types	79 specific, 11 generic
PubMed Documents Identifiers	28,734 for genes; 468,474 for interactions
Genes	Human: 38,674
Gene Name Synonyms	46,041
Gene Symbol Synonyms	87,524
Gene Ontology Taxa	2
Gene Ontology (GO) Terms	38,959
Gene Ontology (GO) Genes	Total: 44,047 Human: 18,991; Mouse: 25,416
GO Gene-Term Associations	Assigned By GO: 482,214; Calculated: 2,822,163 Human: 3,102,124; Mouse: 3,124,827 Common to Human and Mouse: 2,944,786

Resources

The PathwaysBrowser Application resources can be broken down into the following types:

Primary	Pathways and Interactions
Metadata	Additional Metadata regarding Genes and Interactions (sources, interaction types, etc.)
Supporting Data	Pubmed information for Genes and Interactions, Gene information, including gene name and symbol synonyms)
Gene Ontology	Gene Ontology Terms and relationships to genes.
Related Data	

Resource descriptions are divided into the groups listed above.

PathwaysBrowser Reference

(All calls support only HTTP GET unless specified otherwise)

Primary

Pathway(s)

Returns the following data:

- MDA Pathway Id
- Description
- Id from Source
- Source Id
- Number of Genes
- Genes (HGNC Symbols)
- Genes (Entrez Ids)
- Sub Pathway
- Parent Pathway Ids and Appropriate Links
- Link to Interactions
- Link[s] to related Pathway Diagram (NCI or Reactome)
- Version

Optional query parameters:

Query / Form parameter	Description of parameter	Default value
start	Starting record number (first record is 0)	0
count	Max number of records to return with each call.	20
sourceId	Id of pathway source (see sourceId in pathwaySources resource for acceptable values).	
allGenes	Comma separated list of HUGO gene symbols where all genes must be in pathway.	
anyGenes	Comma separated list of HUGO gene symbols where at least one must be in pathway.	
description	Text to search for in description field. (Case insensitive).	

Pathways

Returns all pathway names and ids and link in latest database version (HTTP GET and POST)

PathwaysBrowser/pathways/latest

Optional query/form parameters: start, count, sourceId, allGenes, anyGenes, description

Returns all pathway names and ids and links in specified database version (HTTP GET and POST)

PathwaysBrowser/pathways/version/{version_id}

Optional query/form parameters: start, count, sourceId, allGenes, anyGenes, description

Pathway

Returns all information for pathway of specified id in latest database version

PathwaysBrowser/pathway/latest/mdaPathwayId/{mdaPathwayId}

Returns all information for pathway of specified id in specified database version

First Order Interaction(s)

Returns the following data:

- Interaction Id
- Interaction details count
- Gene A
- Gene B
- Entrez Gene A
- Entrez Gene B
- Interaction Direction
- Type Id
- Specific Type
- Generic Type
- Is Descriptive
- Positive
- Predicate
- Source
- Source of source
- Text from Source
- Pubmed Count
- Version

Optional query parameters:

Query / Form parameter	Description of parameter	Comments	Default value
start	Starting record number (first record is 0)		0
count	Max number of records to return with each call.		100
genes	Comma separated list of gene symbols where if any gene in list is on left or right in interaction record is included.	Does not apply to URIs containing pathwayIds	
limitGenes	Comma separated list of gene symbols where both sides of interaction must be in this list for interaction to be included.	Does not apply to URIs containing pathwayIds	
interactionTypes	Comma separated list of interaction Type Ids that interaction must be labeled with to be included. (See interactionTypes resource for valid interaction type ids.)	Does not apply to URIs containing pathwayIds	

First Order Interactions

Returns first order interaction information in specified database version (HTTP GET and POST)

PathwaysBrowser/interactions/latest

Optional query/form parameters: start, count, genes, limitGenes, interactionTypes

Returns first order interaction information in specified database (HTTP GET and POST)

PathwaysBrowser/interactions/version/{version_id}

Optional query/form parameters: start, count, genes, limitGenes, interactionTypes

Returns first order interaction information for specified pathway ids in latest database version

PathwaysBrowser/interactions/latest/pathway/pathwayIds/{csv list of pathway Ids}

Optional query parameters: start, count

Returns first order interaction information for specified pathway ids in specified database version (HTTP GET and POST)

PathwaysBrowser/interactions/version/{version_id}/pathwayIds/{csv list of pathway Ids}

Optional query parameters: start, count

First Order Interaction

Returns first order interaction information for specified interaction id in latest database version

PathwaysBrowser/interaction/latest/interactionId/{interaction_id}

Returns first order interaction information for specified interaction id in specified database version

PathwaysBrowser/interaction/version/{version_id}/interactionId/{interaction_id}

Metadata

Interaction Direction(s)

Returns the following data:

Direction

Direction

Interaction Directions

Returns all information for all interaction directions (This resource is not versioned)

PathwaysBrowser/interactionDirections

Interaction Direction

Returns all information for interaction direction with specified interaction id

PathwaysBrowser/interactionDirection/{interactionDirectionId}

Pathway Source(s)

Returns the following data:

Source Id

Description

Version Id

Pathway Sources

Returns all information for pathway sources in latest database version

PathwaysBrowser/pathwaySources/latest

Returns all information for pathway sources in specified database version

PathwaysBrowser/pathwaySources/version/{versionId}

Pathway Source

Returns all information for pathway source with specified source id in latest database version

PathwaysBrowser/pathwaySource/latest/sourceId/{sourceId}

Returns all information for pathway source with specified source id in specified database version

PathwaysBrowser/pathwaySource/version/{versionId}/sourceId/{sourceId}

Data Version(s)

Returns the following data:

Version Data

Version Id

Data Archive Date

Description

General Resource Links

Pathways

Interactions

Genes

Pathway Sources

Gene Ontology Resource Links

- Genes
- Terms
- Genes To Terms
- Terms and All Gene Counts
- Terms and Associated Gene Counts
- Terms and Parent Terms

Data Versions

Returns list of all pathway database versions

PathwaysBrowser/versions

Data Version

Returns latest pathway database version

PathwaysBrowser/version/latest

Returns specified pathway database version

PathwaysBrowser/version/{version_id}

Returns active pathway database version at a specified date

PathwaysBrowser/version/date/{dateString}

(Date in format yyyy-MM-dd)

Interaction Type(s)

Returns the following data:

- Type Id
- Specific Type
- Generic Type
- Is Descriptive
- Version

Interaction Types

Returns all interaction types in latest database version

PathwaysBrowser/interactionTypes/latest

Optional query parameters: start, count

Returns all interaction types in specified database version

PathwaysBrowser/interactionTypes/version/{version_id}

Optional query parameters: start, count

Interaction Type

Returns information for specified interaction type in latest database version

PathwaysBrowser/interactionType/latest/typeId/{interaction_type_id}

Returns information for specified interaction type in specified database version

PathwaysBrowser/interactionType/version/{version_id}/typeId/{interaction_type_id}

Optional query parameters:

Query / Form parameter	Description of parameter	Comments	Default value
start	Starting record number (first record is 0)		0
count	Max number of records to return with each call.		100

Supporting Data

Gene Related Pubmed Documents

Returns the following data: Identifier

- Id
- Related PubMed IDs
- Version Id

Gene-related Pubmed Documents

Return list of PubMed ids for specified Hugo gene id in latest database version

PathwaysBrowser/pubmedList/latest/approvedHugoId/{hugo_gene_id}

Return list of PubMed ids for specified Hugo gene id in specified database version

PathwaysBrowser/pubmedList/version/{version_id}/approvedHugoId/{hugo_gene_id}

Interaction Related Pubmed Documents

Returns the following data:

- Interaction Id
- Interaction Detail Id
- Location (PubMed or PubMed Central)
- Related PubMed ID (link to PubMed documents)
- Version Id

Interaction-related Pubmed Documents

Return list of PubMed ids for specified interaction in latest database version

PathwaysBrowser/interactionDocumentationList/latest/interactionId/{interaction_id}

Return list of PubMed ids for specified interaction in specified database version

PathwaysBrowser/interactionDocumentationList/version/{version_id}/interactionId/{interaction_id}

Optional query parameters: start, count

HGNC Gene(s)

Returns the following data:

- Gene Symbol
- Gene Name
- Chromosome
- Ensembl Gene Id
- Ensembl Id
- Entrez Gene Id
- Entrez Gene Id (NCBI)
- HGNC ID
- Locus Group
- Locus Type
- OMIM Id
- Refseq
- UCSC Id
- UNIPROT Id
- Vega Id

Gene Family Tag
Name Synonyms
Symbol Synonyms
Pathways
Interactions
Pubmed Ids
Version Id

Optional query parameters:

Query parameter	Description of parameter	Default value
start	Starting record number (first record is 0)	0
count	Max number of records to return with each call.	100

HGNC Genes

Returns list of HUGO gene symbols for all genes in latest database version

PathwaysBrowser/genes/latest

Optional query parameters: start, count

Returns list of HUGO gene symbols for all genes in specified database version

PathwaysBrowser/genes/version/{version_id}

Optional query parameters: start, count

HGNC Gene

Return gene information for specified HUGO gene Id in latest database version

PathwaysBrowser/gene/latest/approvedHugold/{hugo_gene_id}

Return gene information for specified HUGO gene Id in specified database version

PathwaysBrowser/gene/version/{version_id}/approvedHugold/{hugo_gene_id}

HGNC Gene Name Synonym(s)

Returns the following data:

Gene Symbol

Names

Version Id

HGNC Gene Name Synonyms

Returns all various gene names for designated HUGO gene Id in latest database version

PathwaysBrowser/geneNameSynonyms/latest/approvedHugold/{hugo_gene_id}

Returns all various gene names for designated HUGO gene Id in latest database version

PathwaysBrowser/geneNameSynonyms/version/{version_id}/approvedHugold/{hugo_gene_id}

HGNC Gene Symbol Synonyms

Returns the following data:

Gene Symbol

Synonyms
Version Id

Returns all various gene symbols for specified HUGO gene Id in latest database version

PathwaysBrowser/geneSymbolSynonyms/latest/approvedHugold/{hugo_gene_id}

Returns all various gene symbols for specified HUGO gene Id in specified database version

PathwaysBrowser/geneSymbolSynonyms/version/{version_id}/approvedHugold/{hugo_gene_id}

Returns all various gene symbols for specified gene symbol synonym in latest database version

PathwaysBrowser/geneSymbolSynonyms/latest/synonym/{synonym}

Returns all various gene symbols for specified gene symbol synonym in specified database version

PathwaysBrowser/geneSymbolSynonyms/version/{version_id}/synonym/{synonym}

Returns approved gene symbols for list of specified gene symbol synonyms in latest database version

PathwaysBrowser/geneSymbolSynonyms/latest/genIds/{ csv list of synonyms }

Returns approved gene symbols for list of specified gene symbol synonyms in specified database version

PathwaysBrowser/geneSymbolSynonyms/version/{version_id}/genIds/{csv list of synonyms}

Gene Ontology (GO) Related

Gene Ontology Gene(s)

Returns the following data:

- Gene Symbol
- Gene Name
- Taxon
- HGNC Gene Link
- Version Id

Optional query parameters:

Query / Form parameter	Description of parameter	Default value
start	Starting record number (first record is 0)	0
count	Max number of records to return with each call.	1000
taxonId	NCBI Taxon (species) id of gene (see taxonId in goTaxa resource for acceptable values).	9606

Gene Ontology Gene Information

Return list of genes (according to GO) in the latest database version for the specified taxon (species) in specified database version. /PathwaysBrowser/goGene/version/{versionId}/geneSymbol/{geneSymbol}

Return list of genes (according to GO) in specified database version for the specified taxon (species) in latest database version. /PathwaysBrowser/goGene/latest/geneSymbol/{geneSymbol}

Gene Ontology Genes

Retrieve information on genes as defined in the Gene Ontology in specified database version.

/PathwaysBrowser/goGenes/version/{versionId}/

Optional query/form parameters: start, count, taxonId

Retrieve information on genes as defined in the Gene Ontology in latest database version.

/PathwaysBrowser/goGenes/latest/

Optional query/form parameters: start, count, taxonId

GO Gene To GO Term Association(s)

Retrieves list of genes imported from The Gene Ontology that are associated with Terms in the Gene Ontology. The list may contain gene symbols that do not match those imported from HGNC. (See goGenes resource for more information). The Gene Ontology associates genes and terms, but this list of GO Ids is not limited to those specific associations made by GO. All paths from a given term back to the root term of the three GO ontologies are determined. This resource returns all unique GO Ids for each gene associated by GO and all terms along the paths back to the root terms.

Returns the following data:

- Gene Symbol
- Gene Name
- Taxon
- HGNC Gene Link
- Related Go Ids
- Version Id

Optional query parameters:

Query / Form parameter	Description of parameter	Default value
start	Starting record number (first record is 0)	0
count	Max number of records to return with each call.	1000
taxonId	NCBI Taxon id of gene (see taxonId in goTaxa resource for values).	9606
genes	Comma separated list of gene symbols	

GO Gene To GO Term Associations

Retrieve information on a related Gene Ontology Terms for a specified list of genes in specified database version. (HTTP GET and POST)

/PathwaysBrowser/goGenesToTerms/version/{versionId}/

Optional query/form parameters: start, count, taxonId, genes.

Retrieve information on a related Gene Ontology Terms for a specified list of genes in latest database version. (HTTP GET and POST)

/PathwaysBrowser/goGenesToTerms/latest/

Optional query/form parameters: start, count, taxonId, genes.

Gene Ontology Term to Term Relationship Type(s)

Returns the following data:

- Relationship Id

Relationship Term
Version Id

Gene Ontology Term to Term Relationship Type

Returns the following data:

Retrieve information on a single GO Term used to associate other GO Terms to one another in specified database version.

/PathwaysBrowser/goRelationship/version/{versionId}/relationshipId/{relationshipId}

Retrieve information on a single GO Term used to associate other GO Terms to one another in latest database version.

/PathwaysBrowser/goRelationship/latest/relationshipId/{relationshipId}

Gene Ontology Term to Term Relationship Types

Retrieve information on GO Terms used to associate other GO Terms to one another in specified database version.

/PathwaysBrowser/goRelationships/versionId/{versionId}

Retrieve information on GO Terms used to associate other GO Terms to one another in latest database version.

/PathwaysBrowser/goRelationships/latest/

Gene Ontology Taxa (Species) Information

Returns the following data:

Taxon Id
Common Name
Genus
Species
Version Id

Gene Ontology Taxa (Species) Information

Retrieve information on the Taxons (species identifiers) imported from the Gene Ontology in specified database version.

/PathwaysBrowser/goTaxa/version/{versionId}/

Retrieve information on the Taxons (species identifiers) imported from the Gene Ontology in latest database version.

/PathwaysBrowser/goTaxa/latest/

Gene Ontology Individual Taxon (Species) Information

Retrieve information on a single Taxon Species imported from the Gene Ontology in specified database version.

/PathwaysBrowser/goTaxon/version/{versionId}/taxonId/{taxonId}

Retrieve information on a single Taxon Species imported from the Gene Ontology in latest database version.

/PathwaysBrowser/goTaxon/latest/taxonId/{taxonId}

Gene Ontology Term(s)

Returns the following data:

- GO Id
- Term
- Definition
- Term Type
- Version Id

Optional query parameters:

Query / Form parameter	Description of parameter	Default value
start	Starting record number (first record is 0)	0
count	Max number of records to return with each call.	20
termTypeId	Id of Term Type. Capitalized first letter of the text description of the particular Ontology within The Gene Ontology this term belongs. Choices are B,C, or M where B = Biological Process, C = Cellular Component, M = Molecular Function	

Gene Ontology Terms

Retrieve information on multiple Gene Ontology terms in specified database version.

/PathwaysBrowser/goTerms/version/{versionId}/

Optional query/form parameters: start, count, termTypeId

Retrieve information on multiple Gene Ontology terms in latest database version.

/PathwaysBrowser/goTerms/latest/

Optional query/form parameters: start, count, termTypeId

Gene Ontology Term

Retrieve information on a single Gene Ontology term in specified database version.

/PathwaysBrowser/goTerm/version/{versionId}/gold/{gold}

Retrieve information on a single Gene Ontology term in latest database version in specified database version.

/PathwaysBrowser/goTerm/latest/gold/{gold}

Gene Ontology Term and Related Genes

Returns the following data:

- GO Id
- Term
- Genes
- Definition
- TermType
- Version Id

Optional query parameters:

Query / Form parameter	Description of parameter	Default value
taxonId	NCBI Taxon Id as imported from The Gene Ontology.	9606

Gene Ontology Term and Related Genes

Retrieve information on Term imported from The Gene Ontology and the genes associated with that term in the specified database version.

/PathwaysWeb/goTermAndGenes/version/{versionId}/gold/{gold}

Retrieve information on Term imported from The Gene Ontology and the genes associated with that term in latest database version.

/PathwaysWeb/goTermAndGenes/latest /gold/{gold}

Gene Ontology Terms and Related and/or Associated Gene Counts

Returns the following data:

- GO Id
- Term
- Gene Counts (Associated and Selected where appropriate)
- Definition
- TermType
- Version Id

Optional query parameters:

Query / Form parameter	Description of parameter	Default value
start	Starting record number (first record is 0)	0
count	Max number of records to return with each call.	20
taxonId	NCBI Taxon Id as imported from The Gene Ontology.	9606
genes	Comma separated list of Gene Ontology gene symbols. Counts of the specified genes for each GO Term will be returned.	
golds	Comma separated list of Gene Ontology Ids for desired terms. Format: GO:1234567,GO:1234568	

Gene Ontology Terms and All Gene Counts

Retrieve information on Terms imported from The Gene Ontology and the number of genes associated with those terms and the count of specified genes associated with that term in specified database version. (HTTP GET and POST)

/PathwaysBrowser/goTermsAndGeneCounts/version/{versionId}/

Optional query/form parameters: start, count, taxonId, genes, golds

Retrieve information on Terms imported from The Gene Ontology and the number of genes associated with those terms and the count of specified genes associated with that term in latest database version. (HTTP GET and POST)

/PathwaysBrowser/goTermsAndGeneCounts/latest/

Optional query/form parameters: start, count, taxonId, genes, golds

Retrieve information on Terms imported from The Gene Ontology and the total number of genes associated with those terms in specified database version. (HTTP GET and POST)

/PathwaysBrowser/goTermsAndAssociatedGeneCounts/version/{versionId}/

Optional query/form parameters: start, count, taxonId, golds

Retrieve information on Terms imported from The Gene Ontology and the total number of genes associated with those terms in latest database version. (HTTP GET and POST)

/PathwaysBrowser/goTermsAndAssociatedGeneCounts/latest/

Optional query/form parameters: start, count, taxonId, golds

Gene Ontology Terms and Parent Terms

Returns the following data:

GO Id

Parent Go Ids

Relationship Ids (Ids of Term to Term Relationship - One for each parent Term Id)

Version Id

Optional query parameters:

Query / Form parameter	Description of parameter	Default value
start	Starting record number (first record is 0)	0
count	Max number of records to return with each call.	20
golds	Comma separated list of Gene Ontology Ids for desired terms. Format: GO:1234567,GO:1234568	

Gene Ontology Terms and Parent Terms

Retrieve information on Terms imported from The Gene Ontology and their parent terms term in specified database version. (HTTP GET and POST)

/PathwaysBrowser/goTermsAndParents/version/{versionId}/

Optional query/form parameters: start, count, taxonId, golds

Retrieve information on Terms imported from The Gene Ontology and their parent terms term in latest database version. (HTTP GET and POST)

/PathwaysBrowser/goTermsAndParents/latest/

Optional query/form parameters: start, count, taxonId, golds

Sources of Data for API and Use of Data Sources:

HGNC Dataset

Use: Used in genes and gene resources and in providing correct HUGO gene names in pathways, pathway, interactions, and interaction resources.

Description: http://www.genenames.org/cgi-bin/hgnc_stats.pl

Data: http://www.genenames.org/cgi-bin/hgnc_downloads.cgi?title=HGNC+output+data&hgnc_dbtag=on&preset=all&status=Approved&status=Entry+Withdrawn&status_opt=2&level=pri&=on&where=&order_by=gd_app_sym_sorf&limit=&format=text&submit=submit&.cgifields=&.cgifields=level&.cgifields=chr&.cgifields=status&.cgifields=hgnc_dbtag

NCBI GeneRIFS (Gene Reference Into Function)

Use: Used in interactions and interaction resources.

Description: <http://www.ncbi.nlm.nih.gov/gene/about-generif>

Data: <ftp://ftp.ncbi.nlm.nih.gov/gene/GeneRIF/interactions.gz>

Pathway Commons: NCI Nature SIF (Simple Interaction Format)

Use: Used in interactions and interaction resources.

Description: http://www.pathwaycommons.org/pc/sif_interaction_rules.do

Data: http://www.pathwaycommons.org/pc-snapshot/current-release/sif/by_species/homo-sapiens-9606.sif.zip

Predictive Networks: CSV

Use: Used in interactions and interaction resources. Only data sources for functional interactions (2010) and pathways commons extractions (2010) were used. Interactions mined from Pubmed and Medline were determined to contain too much bad data to use.

Description: <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3245161/> and <https://compbio.dfci.harvard.edu/predictivenetworks/>

Data:

<https://compbio.dfci.harvard.edu/predictivenetworks/network/download/3?format=csv&extension=csv>

<https://compbio.dfci.harvard.edu/predictivenetworks/network/download/4?format=csv&extension=csv>

NCBI Gene To PubMed

Use: Used in genes and gene resources.

Description: <http://www.ncbi.nlm.nih.gov/entrez/query/static/entrezlinks.html#gene>

Data: <ftp://ftp.ncbi.nlm.nih.gov/gene/DATA/gene2pubmed.gz>

Pathways and Genes

Use: Used in pathways, pathway, and interactions resources.

Description: List of NCI-Nature Curated and Reactome pathways and genes in those pathways imported from caBio Web service.

<https://wiki.nci.nih.gov/display/caBIO/caBIO+Wiki+Home+Page>

Data: Read via client software from caBio web service using caBio Java API.

NCI pathways and sub pathways (Scraped from web page)

Use: Used in pathway resources.

Description: Used to determine if pathway from caBio API is a sub pathway and parent if it is.

Data: http://pid.nci.nih.gov/browse_pathways.shtml

Reactome

Use: Used in pathway resources.

Description: Pathways and related genes for curated Reactome pathways and visualizations.

Data: http://pid.nci.nih.gov/browse_pathways.shtml

The Gene Ontology

Use: Used in gene ontology related goGenes, goGene, goTaxa, goTaxon, goTerms, goTerm, goRelationships, goRelationship, goGenesToTerms, and goTermsAndGeneCounts resources.

Description: Latest SQL dump of assocdb-data form of data is downloaded from archive.geneontology.org/latest-lite. SQL is filtered to retrieve only the tables we want and the SQL is parsed, filtered, and reformatted.

Interaction Search Terms

Use: Used in interactions and interaction resources to create translate interaction descriptions to interaction types.

Description: Manually created list from review of interactions descriptions from multiple sources used to search interaction details and determine type of interaction.

Interaction Types

Use: Used in interactions, interaction, interactionTypes, and interactionType resources.

Description: Manually created list used to categorize types of interactions (somewhat detailed types and generic types). Created from review of descriptions of interactions in interaction source files and online documentation.

Appendix: Interaction Types

Interaction Types were constructed to group the various descriptions provided by different sources of interaction information into a smaller subset of different interaction types. Some of the interaction descriptions provided by different sources were very descriptive whereas others were not. There was no standard. The descriptions given by the various sources were searched for certain key terms that were then used to compile a list of fairly specific interaction types and more generic interaction types to group those. Some descriptions provided by the sources hinted how the interaction was discovered and not what type of interaction it was. Those that actually described the interaction in such a manner that the true type of interaction could be identified were assigned a Y value in the IS_DESCRIPTIVE field where as others were assigned a value of N. The interaction ids are assigned and an attempt is made to keep them consistent between data versions.

INTERACTION_TYPE_ID	INTERACTION_TYPE	INTERACTION_GENERIC_TYPE	IS_DESCRIPTIVE
1	BINDS	BIND	Y
2	BINDS_TO	BIND	Y
3	FORM_BOND	BIND	Y
4	CATALYZES_PALMITOYLATION	CATALYSIS	Y
5	METABOLIC_CATALYSIS	CATALYSIS	Y
6	CLEAVES	CLEAVAGE_OF_BOND	Y
7	DEMETHYLIMINATES	CLEAVAGE_OF_BOND	Y
8	DEPHOSPHORYLATES	CLEAVAGE_OF_BOND	Y
9	DESUMOYLATES	CLEAVAGE_OF_BOND	Y
10	DEUBIQUITINATION	CLEAVAGE_OF_BOND	Y
11	STATE_CHANGE	CONVERSION	Y
12	ACETYLATION	COVALENT_MODIFICATION	Y
13	MYRISTOYLATION	COVALENT_MODIFICATION	Y
14	PHOSPHORYLATION	COVALENT_MODIFICATION	Y
15	POLY(ADP_RIBOSYL)ATES	COVALENT_MODIFICATION	Y
16	S_NITROSYLATED	COVALENT_MODIFICATION	Y
17	SUMOYLATION	COVALENT_MODIFICATION	Y
18	UBIQUITINATION	COVALENT_MODIFICATION	Y
19	DIMERIZES	DIMERIZATION	Y
20	FORM_DIAMER	DIMERIZATION	Y
21	FORM_HOMOMERIC_COMPLEX	DIMERIZATION	Y
22	FORM_HOMOOLOGOMER	DIMERIZATION	Y
23	HETERODIMERIZATION	DIMERIZATION	Y
24	HOMODIMERIZATION	DIMERIZATION	Y
25	OLIGOMERIZATION	DIMERIZATION	Y
26	ACTIVATES	ENHANCES	Y
27	ENHANCES	ENHANCES	Y
28	PHENOTYPIC_ENHANCEMENT	ENHANCES	Y
29	PROMOTES_UBIQUITINATION	ENHANCES	Y
30	FORM_COMPLEX	FORM_COMPLEX	Y
31	INHIBITS	INHIBITS	Y
32	PHENOTYPIC_SUPPRESSION	INHIBITS	Y
33	PREVENTS_ACTIVATION	INHIBITS	Y
34	REPRESSES	INHIBITS	Y
35	ACTS_ON	REACTION_TYPE_UNKNOWN	Y
36	ASSOCIATES_WITH	REACTION_TYPE_UNKNOWN	Y
37	INTERACTION	REACTION_TYPE_UNKNOWN	Y
38	INTERACTS_WITH	REACTION_TYPE_UNKNOWN	Y
39	IS_A	REACTION_TYPE_UNKNOWN	Y
40	IS_COVALENTLY_ATTACHED	REACTION_TYPE_UNKNOWN	Y

41	NEIGHBOURING_REACTION	REACTION_TYPE_UNKNOWN	Y
42	UBIQUITIN_LIGASE_ACTIVITY	COVALENT_MODIFICATION	Y
43	REACTION	REACTION_TYPE_UNKNOWN	Y
44	REACTS_WITH	REACTION_TYPE_UNKNOWN	Y
45	NON_INTERACTION	OTHER	N
46	AFFINITY_CAPTURE	OTHER	N
47	BIDIRECTIONAL	OTHER	N
48	BIOCHEMICAL_ACTIVITY	OTHER	N
49	CO_CONTROL	OTHER	N
50	CO_CRYSTAL_STRUCTURE	OTHER	N
51	CO_FRACTIONATION	OTHER	N
52	CO_LOCALIZATION	OTHER	N
53	CO_PURIFICATION	OTHER	N
54	ECREL	OTHER	N
55	FAR_WESTERN	OTHER	N
56	FRET	OTHER	N
57	G_EREL	OTHER	N
58	IN_SAME_COMPONENT	OTHER	N
59	IN_VITRO	OTHER	N
60	IN_VIVO	OTHER	N
61	INDIRECT_COMPLEX	OTHER	N
62	PCA	OTHER	N
63	PROTEIN_PEPTIDE	OTHER	N
64	PROTEIN_RNA	OTHER	N
65	RECONSTITUTED_COMPLEX	OTHER	N
66	SYNTHETIC_RESCUE	OTHER	N
67	TARGETS_CHIP	OTHER	N
68	TARGETS_CORE	OTHER	N
69	TWO_HYBRID	OTHER	N
70	SEQUENTIAL_CATALYSIS	OTHER	N
71	IS_CLEAVED	CLEAVAGE_OF_BOND	Y
72	UBC9 WITH	OTHER	N
73	NO_DESCRIPTION_PROVIDED	OTHER	N
74	HOMOMULTIMERIZES	BIND	Y
75	FUNCTIONAL_INTERACTION	OTHER	N
76	DOSAGE_RESCUE	OTHER	N
77	DOSAGE_LETHALITY	OTHER	N
78	PROXIMITY_LABEL_MS	OTHER	N
79	SYNTHETIC_GROWTH_DEFECT	OTHER	N