findGeneByCompartmentPaperCnt

*Get gene table of frequently found genes within compartments*

**Description**

Get gene table and paper count for genes mentioned *cnt* or more times in different compartment-paper pairs.

**Usage**

```r
findGeneByCompartmentPaperCnt(cnt = 1)
```

**Arguments**

- `cnt`: minimal number of times mentioned gene

**Value**

`data.frame` with 9 columns: 8 specified in `getGenesByID` and `Npmid` column for the paper count.

**See Also**

`getGenesByID`

Other Gene functions: `findGeneByPaperCnt()`, `findGeneByPapers()`, `findGenesByEntrez()`, `findGenesByName()`, `getAllGenes4Compartment()`, `getGenes4Compartment()`, `getGenesByID()`

**Examples**

```r
cntT <- findGeneByPaperCnt(47)
head(cntT)
```
findGeneByPaperCnt  Get gene table of frequently found genes

Description
Get gene table and paper count for genes mentioned cnt or more times in different papers.

Usage
findGeneByPaperCnt(cnt = 1)

Arguments
cnt  minimal number of papers that mentioned gene

Value
data.frame with 9 columns: 8 specified in getGenesByID and Npmid column for the paper count.

See Also
genesByID
Other Gene functions: findGeneByCompartmentPaperCnt(), findGeneByPapers(), findGenesByEntrez().
findGenesByName(), getAllGenes4Compartment(), getGenes4Compartment(), getGenesByID()

Examples
cntT <- findGeneByPaperCnt(47)
head(cntT)

findGeneByPapers  Get gene table of frequently found genes

Description
Get gene table and paper count for genes mentioned cnt or more times in different papers.

Usage
findGeneByPapers(pmids, cnt = 1)

Arguments
pmids  vector of PMIDs to search for genes
cnt  minimal number of papers that mentioned gene
findGenesByEntrez

Value
data.frame with 9 columns: 8 specified in getGenesByID and Npmid column for the paper count.

See Also
genesByID
Other Gene functions: findGeneByCompartmentPaperCnt(), findGeneByPaperCnt(), findGenesByEntrez(), findGenesByName(), getAllGenes4Compartment(), getGenes4Compartment(), getGenesByID()

Examples
res<- getAllGenes4Compartment(compartmentID = 1)
gnt<-getGeneInfoByIDs(res$GeneID)
pmids<-names(sort(table(gnt$PaperPMID)))[1:5]
cntT <- findGeneByPapers(pmids,cnt=3)
head(cntT)

findGenesByEntrez

Internal Gene representation for given list of gene Entrez IDs

Description
Get internal gene representation for set of gene Entrez IDs. Function lookups for provided values in Human Entrez ID, Mouse Entrez ID and Rat Entrez ID columns and return following features for all found genes: GeneID (internal database ID), MGI ID, Human Entrez ID, Mouse Entrez ID, Rat Entrez ID, Human gene name, Mouse gene name and Rat gene name.

Usage
findGenesByEntrez(entrez)

Arguments
entrez vector of Entrez IDs. Function accepts both integers and characters.

Details
Could be used as an intermediate step for building Protein-Protein interaction map from the list of Gene IDs returned in the first column. Also, this function provides a useful sanity check, e.g. how many Gene IDs correspond to the specific gene name or Entrez ID, which could be specie-specific.

Value
data.frame with columns specified above.
See Also

Other Lookup functions: `findGenesByEntrez()`
Other Gene functions: `findGeneByCompartmentPaperCnt()`, `findGeneByPaperCnt()`, `findGeneByPapers()`, `findGenesByName()`, `getAllGenes4Compartment()`, `getGenes4Compartment()`, `getGenesByID()`

Examples

```r
# get information for specific gene
t <- findGenesByEntrez(c(1742, 1741, 1739, 1740))
```

---

**Description**

Get internal gene representation for set of gene names. Function lookups for provided values in Human Name, Mouse Name and Rat Name columns and return following features for all found genes: GeneID (internal database ID), MGI ID, Human Entrez ID, Mouse Entrez ID, Rat Entrez ID, Human gene name, Mouse gene name and Rat gene name.

**Usage**

```r
findGenesByName(name)
```

**Arguments**

- `name`: vector of gene names.

**Details**

Could be used as an intermediate step for building Protein-Protein interaction map from the list of Gene IDs returned in the first column. Also, this function provides a useful sanity check, e.g. how many Gene IDs correspond to the specific gene name or Entrez ID, which could be specie-specific.

**Value**

data.frame with columns specified above.

**See Also**

Other Lookup functions: `findGenesByEntrez()`
Other Gene functions: `findGeneByCompartmentPaperCnt()`, `findGeneByPaperCnt()`, `findGeneByPapers()`, `findGenesByEntrez()`, `getAllGenes4Compartment()`, `getGenes4Compartment()`, `getGenesByID()`

**Examples**

```r
# Find GeneIDs for names
t <- findGenesByName(c("Src", "Srcin1", "Fyn"))
```
getDescription

Get all genes annotated for specific brain region for specific specie. Function looks up Brain Region ID and Specie Tax ID columns and returns main information like internal Gene IDs, MGI ID, Human Entrez ID, Human Gene Name, Mouse Entrez ID, Mouse Gene Name, Localisation (presynaptic, postsynaptic, synaptosomal), PaperPMID and BrainRegion.

Usage

getAddress4BrainRegion(brainRegion, taxID)

Arguments

<table>
<thead>
<tr>
<th>brainRegion</th>
<th>ID for specific brain region</th>
</tr>
</thead>
<tbody>
<tr>
<td>taxID</td>
<td>specie ID</td>
</tr>
</tbody>
</table>

Value

data.frame with the following columns:

- GeneID
- Localisation
- MGI
- HumanEntrez
- MouseEntrez
- HumanName
- MouseName
- PMID
- Paper
- Year
- SpeciesTaxID
- BrainRegion

See Also

Other BrainRegion functions: `getBrainRegions()`, `getAllGenes4BrainRegion()`, `getPPIbyIDs4BrainRegion()`

Other BrainRegion Gene functions: `getAllGenes4BrainRegion()`

Examples

gns <- getAddress4BrainRegion(brainRegion = "Striatum", taxID = 10090)
head(gns)
getAllGenes4Compartment

Extract all genes found in compartment

Description

Get all genes annotated for specific compartment. Function returns main information like internal Gene IDs, MGI ID, Human Entrez ID, Human Gene Name, Mouse Entrez ID, Mouse Gene Name, Rat Entrez ID, Rat Gene Name.

Usage

ggetAllGenes4Compartment(compartmentID)

Arguments

compartmentID ID for specific compartment

Value

data.frame described in getGenesByID()

See Also

Other Gene functions: findGeneByCompartmentPaperCnt(), findGeneByPaperCnt(), findGeneByPapers(), findGenesByEntrez(), findGenesByName(), getGenes4Compartment(), getGenesByID()

Other Compartment functions: getCompartments(), getGenes4Compartment(), getPPIbyIDs4Compartment()

Examples

G <- getAllGenes4Compartment(compartmentID = 1) # 5560 rows

ggetBrainRegions

Get list of all Brain regions in the database

Description

Get full list of brain regions considered in the database. Returns table with regions and their respective IDs.

Usage

ggetBrainRegions()
getCompartments

Value
data.frame with following columns:

- ID: Brain region internal ID
- Name: name of the region
- Description: extended description of the region
- InterlexID
- ParentID: ID of the containing brain region

See Also
Other BrainRegion functions: getAllGenes4BrainRegion(), getGenes4BrainRegion(), getPPIbyIDs4BrainRegion()

Examples
t <- getBrainRegions()

c <- getCompartments()
getGeneDiseaseByEntres

*Disease information for Human Entrez IDs*

**Description**

Get Human disease information (HDO provided) for the set of Human Entrez IDs. Function lookups for diseases associated with Human Entrez IDs and returns list of available diseases.

**Usage**

`getGeneDiseaseByEntres(entrez)`

**Arguments**

- `entrez` vector of Human Entrez gene IDs

**Value**

data.frame with following columns:

- HumanEntrez
- HumanName
- HDOID
- Description

**See Also**

Other Disease functions: `getGeneDiseaseByIDs()`, `getGeneDiseaseByName()`

**Examples**

```r
  t <- getGeneDiseaseByEntres(c(8573, 1742, 1739))  # (95 rows)
```

getGeneDiseaseByIDs

*Disease information for internal gene IDs.*

**Description**

Get Human disease information (HDO provided) for the set of internal gene IDs. Function lookups for diseases associated with internal GeneIDs and returns list of available diseases.

**Usage**

`getGeneDiseaseByIDs(ids)`
getGeneDiseaseByName

Arguments
ids vector of gene IDs.

Value
data.frame with following columns:
  • HumanEntrez
  • HumanName
  • HDOID
  • Description

See Also
Other Disease functions: getGeneDiseaseByEntres(), getGeneDiseaseByID()

Examples
t <- getGeneDiseaseByIDs(c(48, 585, 710))

t <- getGeneDiseaseByName(c("CASK", "DLG2", "DLG1")) # (115 rows)
getGeneInfoByEntrez

Gene information for given list of gene Entrez IDs

Description

Get gene information for set of gene Entrez IDs. Function lookup for name in Human Entrez ID and Mouse Entrez Id data and return following features for all found genes: GeneID (internal database ID), Localisation (presynaptic, postsynaptic, synaptosome), MGI (MGI ID), HumanEntrez (Human Entrez ID), MouseEntrez (Mouse Entrez ID), HumanName (Human gene name), MouseName (Mouse gene name), PaperPMID (PMID IDs for the publications where the genes were reported), Paper (papers where specific genes were reported in a format FIRSTAUTHOR_YEAR), Year, SpeciesTaxID (specie the original experiment was performed on), BrainRegion (Brain region where the specific genes were identified, according to the paper)

Usage

getGeneInfoByEntrez(entrez)

Arguments

entrez vector of Entrez IDs. Function accepts both integers and characters.

Value

data.frame with fields specified above.

See Also

Other GeneInfo functions: getGeneInfoByIDs(), getGeneInfoByName(), getGeneInfoByPapers()

Examples

# get information for specific gene
t <- getGeneInfoByEntrez(1742)
# get information for specific character string Entrez representation
t <- getGeneInfoByEntrez("1742")

# get information for the list of genes
t <- getGeneInfoByName(c(1741, 1742, 1739, 1740))
getGeneInfoByIDs

Description

Function lookup for internal GeneID values and return following features for all found genes: GeneID (internal database ID), Localisation (one of the following: presynaptic, postsynaptic, synapticosome), MGI (MGI ID), HumanEntrez (Human Entrez ID), MouseEntrez (Mouse Entrez ID), HumanName (Human gene name), MouseName (Mouse gene name), PaperPMID (PMID IDs for the publications where the genes were reported), Paper (papers where specific genes were reported in a format FIRSTAUTHOR_YEAR), Year, SpeciesTaxID (specie the original experiment was performed on), BrainRegion (Brain region where the specific genes were identified, according to the paper)

Usage

getGeneInfoByIDs(ids)

Arguments

ids vector of Gene IDs.

Details

This function then returns following features for all found genes:

- GeneID,
- Localisation,
- MGI,
- HumanEntrez,
- MouseEntrez,
- HumanName,
- MouseName,
- PaperPMID,
- Paper,
- Year,
- SpeciesTaxID,
- BrainRegion

Value

data.frame with column specified above.
getGeneInfoByName

See Also
Other GeneInfo functions: getGeneInfoByEntrez(), getGeneInfoByName(), getGeneInfoByPapers()

Examples

gdf <- getGeneInfoByIDs(c(46, 6, 15, 1))

Description
Function lookup for name in Human Gene name, Rat Gene name and Mouse Gene name data and return following features for all found genes: GeneID (internal database ID), Localisation (one of the following: presynaptic, postsynaptic, synaptosome), MGI (MGI ID), HumanEntrez (Human Entrez ID), MouseEntrez (Mouse Entrez ID), HumanName (Human gene name), MouseName (Mouse gene name), PaperPMID (PMID IDs for the publications where the genes were reported), Paper (papers where specific genes were reported in a format FIRSTAUTHOR_YEAR), Year, SpeciesTaxID (specie the original experiment was performed on), BrainRegion (Brain region where the specific genes were identified, according to the paper)

Usage

geneInfoByName(name)

Arguments
name vector of gene names

Details
This function then returns following features for all found genes:
- GeneID,
- Localisation,
- MGI,
- HumanEntrez,
- MouseEntrez,
- HumanName,
- MouseName,
- PaperPMID,
- Paper,
- Year,
- SpeciesTaxID,
- BrainRegion
Value

data.frame with fields specified above.

See Also

Other GeneInfo functions: `getGeneInfoByEntrez()`, `getGeneInfoByIDs()`, `getGeneInfoByPapers()`

Examples

```r
# get information for specific gene
t <- getGeneInfoByPapers("CASK")

# get information for the list of genes
t <- getGeneInfoByPapers(c("CASK", "DLG2"))
```

Description

Function lookup for specified PubMedIDs in the gene reference data and return following features for genes referenced by requested papers at least `cnt` times: GeneID (internal database ID), Localisation (one of the following: presynaptic, postsynaptic, synaptosome), MGI (MGI ID), HumanEntrez (Human Entrez ID), MouseEntrez (Mouse Entrez ID), HumanName (Human gene name), MouseName (Mouse gene name), PaperPMID (PMID IDs for the publications where the genes were reported if it is within `pmids` list), Paper (papers where specific genes were reported in a format FIRSTAUTHOR_YEAR), Year, SpeciesTaxID (specie the original experiment was performed on), BrainRegion (Brain region where the specific genes were identified, according to the paper)

Usage

```r
getGeneInfoByPapers(pmids, cnt = 1)
```

Arguments

- `pmids` vector of PMIDs to search for genes
- `cnt` minimal number of papers that mentioned gene

Details

This function then returns following features for all found genes:

- GeneID,
- Localisation,
- MGI,
- HumanEntrez,
getGenes4BrainRegion

Select genes from the list that found in brain region of particular specie

Description
Select genes from your list annotated for specific brain region. Should be used with findGenesByEntrez() or findGenesByName() functions to obtain list of internal IDs for your list of genes. Function lookups the Gene table for specified localisation and returns main gene information like internal Gene IDs, MGI ID, Human Entrez ID, Human Gene Name, Mouse Entrez ID, Mouse Gene Name, PaperPMID, Localisation and BrainRegion.

Usage
getGenes4BrainRegion(ids, brainRegion, taxID)

Arguments
<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ids</td>
<td>internal IDs for list of genes</td>
</tr>
<tr>
<td>brainRegion</td>
<td>ID for the brain region of interest</td>
</tr>
<tr>
<td>taxID</td>
<td>taxon ID specie tax ID</td>
</tr>
</tbody>
</table>

Value
data.frame with fields specified above.

See Also
Other GeneInfo functions: getGeneInfoByEntrez(), getGeneInfoByIDs(), getGeneInfoByName()

Examples
res<- getAllGenes4Compartment(compartmentID = 1)
gnt<-getGeneInfoByIDs(res$GeneID)
pmids<-names(sort(table(gnt$PaperPMID))[1:5])
cntT <- getGeneInfoByPapers(pmids,cnt=3)
head(cntT)
Value

data.frame with the following columns:

- GeneID
- Localisation
- MGI
- HumanEntrez
- MouseEntrez
- HumanName
- MouseName
- PMID
- Paper
- Year
- SpeciesTaxID
- BrainRegion

See Also

Other BrainRegion functions: `getAllGenes4BrainRegion()`, `getBrainRegions()`, `getPPIbyIDs4BrainRegion()`

Other BrainRegion Gene functions: `getAllGenes4BrainRegion()`

Examples

```r
Genes <- getGenes4BrainRegion(c(1, 15, 156, 1500, 3000, 7000),
                           brainRegion = "Striatum", taxID = 10090)
# 5 rows
```

```
getGenes4Compartment  Select genes from the list that found in compartment
```

Description

Select all genes from your list annotated for specific compartment. Should be used with `findGenesByEntrez()` or `findGenesByName()` functions to obtain list of internal IDs for your list of genes. Function lookups the Gene table for specified localisation and returns main gene information like internal Gene IDs, MGI ID, Human Entrez ID, Human Gene Name, Mouse Entrez ID, Mouse Gene Name, Rat Entrez ID, Rat Gene Name.

Usage

```r
getGenes4Compartment(ids, compartmentID)
```
getGenesByID

Arguments

ids  Gene IDs
compartmentID  compartment ID

Value

data.frame described in getGenesByID()

See Also

Other Gene functions: findGeneByCompartmentPaperCnt(), findGeneByPaperCnt(), findGeneByPapers(), findGenesByEntrez(), findGenesByName(), getAllGenes4Compartment(), getGenesByID()

Other Compartment functions: getAllGenes4Compartment(), getCompartments(), getPPIbyIDs4Compartment()

Examples

Genes <- getGenes4Compartment(c(1, 15, 156, 1500, 3000, 7000), compartmentID = 1)

getGenesByID  Get gene table from list of GeneIDs.

Description

Takes internal gene IDs as input and return the following features for all found genes:

GeneID  internal database ID
MGI  MGI ID
HumanEntrez  Human Entrez ID
MouseEntrez  Mouse Entrez ID
HumanName  Human gene name
MouseName  Mouse gene name
RatEntrez  Rat Entrez ID
RatName  Rat gene name

Usage

genesByID(ids)

Arguments

ids  vector of GeneID values.
getIGraphFromPPI

Value
data.frame with 8 columns specified above.

See Also
Other Gene functions: findGeneByCompartmentPaperCnt(), findGeneByPaperCnt(), findGeneByPapers(), findGenesByEntrez(), findGenesByName(), getAllGenes4Compartment(), getGenes4Compartment()

Examples
gdf <- getGenesByID(c(46, 6, 15, 1))

getIGraphFromPPI

Get Igraph representation of PPI

Description
Combine information from PPI data.frame obtained with functions like getPPIbyName or getPPIbyEntrez with information about genes obtained from getGenesByID to make interpretable undirected PPI graph in igraph format. In this format network could be further analysed and visualized by algorithms in igraph package.

Usage
getIGraphFromPPI(ppi)

Arguments
ppi
PPI data.frame with columns A and B, obtained from functions like getPPIbyName

Value
igraph object with specified PPI network.

See Also
getPPIbyName(), getPPIbyEntrez() and getPPIbyIDs() to get PPI data.frame, getTableFromPPI() to get interpretable table representation of the PPI data.frame.

Other PPI functions: getPPIbyEntrez(), getPPIbyIDs4BrainRegion(), getPPIbyIDs4Compartment(), getPPIbyIDs(), getPPIbyName(), getTableFromPPI()

Examples
library(igraph)
g <- getIGraphFromPPI(
  getPPIbyIDs(c(48, 129, 975, 4422, 5715, 5835), type = "lim")
)
plot(g, vertex.label = V(g)$RatName, vertex.size = 35)
getMutations4DiseaseByEntres

Get mutational information for Gene and Disease

Description
Function looks up the information for particular set of Entrez IDs and disease HDOID.

Usage
getMutations4DiseaseByEntres(entrez, hdoid)

Arguments
entrez        list of Entrez IDs for genes to select
hdoid         disease HDOID to get mutational association.

Value
data.frame as described in getMutations4DiseaseByIDs.

See Also
findGenesByEntrez

Other Mutation functions: getMutations4DiseaseByIDs(), getMutations4DiseaseByNames()

Examples
hdoid<- 'DOID:0060041'
entrez<-c("23859", "17754", "18673", "268566", "12293", "320840", "24012")
mdf<-getMutations4DiseaseByEntres(entrez, hdoid)
is.null(mdf)

generateMutations4DiseaseByIDs

Get mutational information for Gene and Disease

Description
Function looks up the information for particular set of GeneIDs and disease HDOID.

Usage
generateMutations4DiseaseByIDs(ids, hdoid)
getMutations4DiseaseByIDs

Arguments

- **ids**  
  internal GeneIDs to filter mutation data
- **hdoid**  
  disease HDOID to get mutational association.

Details

This function then returns following features for all found genes:

- GeneID,
- MGI,
- MouseEntrez,
- MouseName,
- HumanName,
- HumanEntrez,
- HDOID,
- Disease,
- Chromosome,
- Position,
- Variant,
- FunctionClass,
- cDNAvariant,
- ProteinVariant,
- DENOVO,
- SFARI,
- EpilepsyGene,
- ClinVar,
- PMID,
- Paper

Value

data.frame with fields specified above.

See Also

Other Mutation functions: `getMutations4DiseaseByEntres()`, `getMutations4DiseaseByName()`

Examples

```r
hdoid<- 'DOID:0060041'
ids<-c(6,32,127,181,240,267,558)
mdf<-getMutations4DiseaseByIDs(ids, hdoid)
is.null(mdf)
```
getMutations4DiseaseByName

*Get mutational information for Gene and Disease*

**Description**
Function lookups for provided values in Human Name, Mouse Name and Rat Name columns, extract known mutations, filter requested HDOID and return data.frame in the format described in `getMutations4DiseaseByIDs`.

**Usage**

```r
getMutations4DiseaseByName(name, hdoid)
```

**Arguments**

- `name`  
gene names to look for
- `hdoid`  
disease HDOID to get mutational association.

**Value**
data.frame as described in `getMutations4DiseaseByIDs`.

**See Also**

`findGenesByName`

Other Mutation functions: `getMutations4DiseaseByEntrez()`, `getMutations4DiseaseByIDs()`

**Examples**

```r
hdoid<- 'DOID:0060041'
name<-c("Dlg2", "Map1a", "Phb", "Gphn", "Cacna2d1", "Negr1", "Rgs7")
mdf<-getMutations4DiseaseByName(name, hdoid)
is.null(mdf)
```

getPPIbyEntrez

*Extract the PPIs for my list of genes defined by Entrez IDs*

**Description**
Get Protein-Protein interactions (PPIs) for the set of ID. Function lookups for PPIs for the list of Entrez IDs and returns either “induced” (all available interactions for these genes) or “limited” (only interactions between genes specified in the query) table of interacting genes A and B, where A and B are respective Internal IDs.
getPPIbyIDs

Usage

getPPIbyEntrez(entrez, type = c("induced", "limited"))

Arguments

entrez Entrez IDs

type type of the PPI network should be either induced (for all the PPIs for specific
genes, including external genes) or limited (for PPIs between the genes specified
in the query). Type could be shortened to recognizable minimum like 'ind'
or 'lim'.

Value
data.frame with interactors internal GeneID in columns A and B

See Also

getPPIbyName() and getPPIbyIDs() to get PPI data.frame, getIGraphFromPPI() to get igraph
representation of the PPI data.frame and getTableFromPPI() to get interpretable table representation
of the PPI data.frame.

Other PPI functions: getIGraphFromPPI(), getPPIbyIDs4BrainRegion(),
getPPIbyIDs4Compartment(),
getPPIbyIDs(),
getPPIbyName(),
getTableFromPPI()

Examples

t <- getPPIbyEntrez(c(1739, 1740, 1742, 1741), type = "ind")

getPPIbyIDs Extract the PPIs for my list of genes defined by GeneID

Description

Get Protein-Protein interactions (PPIs) for the set of internal GeneIDs. Function lookups for PPIs
for specific GeneID and returns either “induced” (all interaction for this GeneID) or “limited” (only
interactions between GeneIDs specified in the query) table of A and B interacting genes, where A
and B are respective GeneIDs.

Usage

getPPIbyIDs(ids, type = c("induced", "limited"))

Arguments

ids Gene IDs

type type of the PPI network should be either induced (for all the PPIs for specific
genes, including external genes) or limited (for PPIs between the genes specified
in the query). Type could be shortened to recognizable minimum like 'ind'
or 'lim'.
getPPIbyIDs4BrainRegion

Prepare induced or limited network for brain region

Description
Prepare PPI network for genes from your list annotated for specific brain region. Should be used with `findGenesByEntrez()` or `findGenesByName()` functions to obtain list of internal IDs for your list of genes. Could be used with `getAllGenes4BrainRegion` functions to obtain all genes belonging to respective brain region. Function lookups the PPI table for gene IDs from the list and returns "limited" or "induced" interactors GeneIDs for the specified region.

Usage
```
getPPIbyIDs4BrainRegion(
  ids, 
  brainRegion, 
  taxID, 
  type = c("induced", "limited")
)
```

Arguments
- `ids` gene IDs
- `brainRegion` region ID
- `taxID` taxon ID
- `type` type of the PPI network should be either induced (for all the PPIs for specific genes, including external genes) or limited (for PPIs between the genes specified in the query). Type could be shortened to recognizable minimum like 'ind' or 'lim'.

Examples
```
t <- getPPIbyIDs(c(48, 585, 710), type = "limited") # (16 rows)
t <- getPPIbyIDs(c(48, 585, 710), type = "induced") # 306 rows
```
getPPIbyIDs4Compartment

Value

data.frame with interactors internal GeneID in columns A and B

See Also

Other PPI functions: getIGraphFromPPI(), getPPIbyEntrez(), getPPIbyIDs4Compartment(),
ge PTRbyIDs(), getPPIbyName(), getTableFromPPI()
Other BrainRegion functions: getAllGenes4BrainRegion().getBrainRegions().getGenes4BrainRegion()

Examples

# getting all genes for mouse Striatum
gns <- getAllGenes4BrainRegion(brainRegion = "Striatum", taxID = 10090)
head(gns)

# getting full PPI network for postsynaptic compartment
ppi <- getPPIbyIDs4BrainRegion(
  gns$GeneID,
  brainRegion = "Striatum",
  taxID = 10090,
  type = "limited"
)
head(ppi)

getPPIbyIDs4Compartment

Prepare induced or limited network for compartment

Description

Prepare PPI network for genes from your list annotated for specific compartment. Should be used with
findGenesByEntrez or findGenesByName functions to obtain list of internal IDs for your list
of genes. Could be used with getAllGenes4Compartment functions to obtain all genes belonging
to respective compartment. Function lookups the PPI table for gene IDs from the list and returns
“limited” or “induced” interactors GeneIDs from the same compartment.

Usage

getPPIbyIDs4Compartment(ids, compartmentID, type = c("induced", "limited"))

Arguments

ids internal gene IDs
compartmentID ID for specific compartment
type type of the PPI network should be either ‘induced’ (for all the PPIs for specific
genes, including external genes) or ‘limited’ (for PPIs between the genes specified
in the query). Type could be shortened to recognizable minimum like ‘ind’
or ‘lim’.
getPPIbyName

Value

data.frame with interactors internal GeneID in columns A and B

See Also

Other PPI functions: `getIGraphFromPPI()`, `getPPIbyEntrez()`, `getPPIbyIDs4BrainRegion()`, `getPPIbyIDs()`, `getPPIbyName()`, `getTableFromPPI()`

Other Compartment functions: `getAllGenes4Compartment()`, `getCompartments()`, `getGenes4Compartment()`

Examples

```r
ppi <- getPPIbyIDs4Compartment(c(1, 15, 156, 1500, 3000, 7000),
                                 compartmentID = 1, type = "induced"
                               )  # 201 rows
```

getPPIbyName

Extract the PPIs for my list of genes defined by Gene name

Description

Get Protein-Protein interactions (PPIs) for the set of gene names. Function lookups for PPIs for the list of GeneIDs and returns either “induced” (all interaction for this GeneID) or “limited” (only interactions between GeneIDs specified in the query) table of interacting genes A and B, where A and B are respective gene names.

Usage

```r
getPPIbyName(name, type = c("induced", "limited"))
```

Arguments

- **name**: Gene names
- **type**: type of the PPI network should be either induced (for all the PPIs for specific genes, including external genes) or limited (for PPIs between the genes specified in the query). Type could be shortened to recognizable minimum like 'ind' or 'lim'.

Value

data.frame with interactors internal GeneID in columns A and B

See Also

`getPPIbyEntrez()` and `getPPIbyIDs()` to get PPI data.frame, `getIGraphFromPPI()` to get igraph representation of the PPI data.frame and `getTableFromPPI()` to get interpretable table representation of the PPI data.frame.

Other PPI functions: `getIGraphFromPPI()`, `getPPIbyEntrez()`, `getPPIbyIDs4BrainRegion()`, `getPPIbyIDs4Compartment()`, `getPPIbyIDs()`, `getTableFromPPI()`
Examples

t <- getPPIbyName(c("CASK", "DLG4", "GRIN2A", "GRIN2B", "GRIN1"),
    type = "lim"
)

Description

Get synaptome papers overview

Usage

getPapers()

Value

data.frame with following columns:

• PaperPMID
• SpeciesTaxID
• Year
• Name
• Localisation
• BrainRegion
• Method
• Ngenes

Examples

p <- getPapers()
head(p)
getTableFromPPI

Get table representation of the PPI.

Description

Combine information from PPI data.frame obtained with functions like `getPPIbyName` or `getPPIbyEntrez` with information about genes obtained from `getGenesByID` to make interpretable table representation.

Usage

`getTableFromPPI(ppi)`

Arguments

- `ppi` PPI data.frame with columns A and B, obtained from functions like `getPPIbyName`

Value

Table with the following columns added for both interactors (A and B):

- GeneID internal database ID
- MGI MGI ID
- HumanEntrez Human Entrez ID
- MouseEntrez Mouse Entrez ID
- HumanName Human gene name
- MouseName Mouse gene name
- RatEntrez Rat Entrez ID
- RatName Rat gene name

See Also

`getPPIbyName()`, `getPPIbyEntrez()` and `getPPIbyIDs()` to get PPI data.frame, `getIGraphFromPPI()` to get igraph representation of the PPI data.frame.

Other PPI functions: `getIGraphFromPPI()`, `getPPIbyEntrez()`, `getPPIbyIDs4BrainRegion()`, `getPPIbyIDs4Compartments()`, `getPPIbyIDs()`, `getPPIbyName()`

Examples

```r
tbl <- getTableFromPPI(getPPIbyIDs(c(48, 585, 710), type = "limited"))
```
graphFromSynaptomeByEntrez

Utility function to create network from synaptome.db data

Description

Utility function to create network from synaptome.db data

Usage

graphFromSynaptomeByEntrez(entrez, LCC = TRUE, simplify = TRUE)

Arguments

entrez vector of EntrezIDs for network vertices
LCC if TRUE only largest connected component is returned
simplify if TRUE loops and multiple edges will be removed

Value

network defined by the gene table

Examples

library(synaptome.db)
cid<-match('Presynaptic', getCompartments()$Name)
geneTable<-getAllGenes4Compartment(cid)
gg<-graphFromSynaptomeByEntrez(geneTable$HumanEntrez)

graphFromSynaptomeGeneTable

Utility function to create network from synaptome.db data

Description

Utility function to create network from synaptome.db data

Usage

graphFromSynaptomeGeneTable(geneTable, LCC = FALSE, simplify = FALSE)

Arguments

geneTable data.frame described in getGenesByID
LCC if TRUE only largest connected component is returned
simplify if TRUE loops and multiple edges will be removed
**Value**

network defined by the gene table

**Examples**

```r
library(synaptome.db)
cid<-match('Presynaptic', getCompartments()$Name)
geneTable<-getAllGenes4Compartment(cid)
gg<-graphFromSynaptomeGeneTable(geneTable)
```

**Description**

The package obtains a local copy of the Synaptic proteome database from AnnotationHub package `synaptome.data` and provides a set of utility R functions to query and analyse its content.

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**References**

\insertRefSorokina:2021hlsynaptome.db

**See Also**

Useful links:

- Report bugs at https://github.com/lptolik/synaptome.db/issues/
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