Package ‘rWikiPathways’

March 23, 2024

Type Package
Title rWikiPathways - R client library for the WikiPathways API
Version 1.22.1
Date 2023-10-24
Imports httr, utils, XML, rjson, data.table, RCurl, dplyr, tidyr, readr, stringr, purrr, lubridate
Suggests testthat, BiocStyle, knitr, rmarkdown
Encoding UTF-8
Description Use this package to interface with the WikiPathways API. It provides programmatic access to WikiPathways content in multiple data and image formats, including official monthly release files and convenient GMT read/write functions.
License MIT + file LICENSE
URL https://github.com/wikipathways/rwikipathways
BugReports https://github.com/wikipathways/rwikipathways/issues
LazyLoad yes
biocViews Visualization, GraphAndNetwork, ThirdPartyClient, Network, Metabolomics
NeedsCompilation no
VignetteBuilder knitr
RoxygenNote 7.2.3

git_url https://git.bioconductor.org/packages/rWikiPathways

Author Egon Willighagen [aut, cre] (<https://orcid.org/0000-0001-7542-0286>), Alex Pico [aut] (<https://orcid.org/0000-0001-5706-2163>)
Maintainer Egon Willighagen <egon.willighagen@gmail.com>
R topics documented:

downloadPathwayArchive ........................................ 3
findPathwayIdsByLiterature ..................................... 4
findPathwayIdsByOrcid ............................................ 5
findPathwayIdsByText ............................................. 5
findPathwayIdsByXref ............................................. 6
findPathwayNamesByLiterature .................................... 7
findPathwayNamesByOrcid .......................................... 7
findPathwayNamesByText .......................................... 8
findPathwayNamesByXref .......................................... 8
findPathwaysByLiterature ......................................... 9
findPathwaysByOrcid ............................................. 10
findPathwaysByText ............................................. 11
findPathwaysByXref ............................................. 11
findPathwayUrlsByLiterature ..................................... 12
findPathwayUrlsByOrcid ......................................... 13
findPathwayUrlsByText ......................................... 13
findPathwayUrlsByXref ......................................... 14
getCounts .......................................................... 15
getCurationStatus ............................................... 15
getCurationTagNames .......................................... 16
getCurationTags ................................................. 16
getEveryCurationTag ........................................... 17
getOntologyTermIds ............................................ 17
getOntologyTermNames ......................................... 18
getOntologyTerms ............................................... 18
getPathway ....................................................... 19
getPathwayHistory ............................................... 19
getPathwayIdsByCommunity .................................... 20
getPathwayIdsByCurationTag .................................... 21
getPathwayIdsByOntologyTerm .................................. 21
getPathwayIdsByParentOntologyTerm ........................... 22
getPathwayInfo ................................................... 22
getPathwayNamesByCommunity ................................ 23
getPathwaysByCommunity ........................................ 23
getPathwaysByCurationTag ...................................... 24
getPathwaysByOntologyTerm .................................... 24
getPathwaysByParentOntologyTerm ............................. 25
getPathwayUrlsByCommunity .................................... 26
getRecentChanges ............................................... 26
getRecentChangesIds ............................................. 27
getRecentChangesNames ......................................... 27
getXrefList ....................................................... 28
listCommunities ................................................ 29
listOrganisms .................................................... 29
listPathwayIds ................................................... 30
listPathwayNames ................................................ 30
Description

Access the monthly archives of pathway content from WikiPathways.

Usage

downloadPathwayArchive(
  date = "current",
  organism = NULL,
  format = c("gpml", "gmt", "svg"),
  destpath = "./"
)

Arguments

date (optional) The timestamp for a monthly release (e.g., 20171010) or "current" (default) for latest release.
organism (optional) A particular species. See listOrganisms.
format (optional) Either gpml (default), gmt or svg.
destpath (optional) Destination path for file to be downloaded to. Default is current working directory.

Details

If you do not specify an organism, then an archive file will not be downloaded. Rather, the archive will be opened in a tab in your default browser.

Value

Filename of downloaded file or an opened tab in default browser
findPathwayIdsByLiterature

Find Pathway WPIDs By Literature

Description
Retrieve list of pathway WPIDs containing the query citation.

Usage
findPathwayIdsByLiterature(query = NULL)

Arguments
query The character string to search for, e.g., a PMID, title keyword or author name.

Value
A list of WPIDs

See Also
findPathwaysByLiterature

Examples
{
  findPathwayIdsByLiterature('19649250')
  findPathwayIdsByLiterature('smith')
  findPathwayIdsByLiterature('cancer')
}

See Also
readPathwayGMT

Examples
#downloadPathwayArchive() ## open in browser
#downloadPathwayArchive(format="gmt") ## open in browser
#downloadPathwayArchive(date="20230710", format="svg") ## open in browser
#downloadPathwayArchive(date="20230710", organism="Mus musculus", format="svg") ## download file
#downloadPathwayArchive(organism="Mus musculus") ## download file
**findPathwayIDsByOrcid**  
*Find Pathway WPIDs By ORCID*

**Description**
Retrieve list of pathway WPIDs containing the query ORCID

**Usage**
```r
findPathwayIDsByOrcid(query = NULL)
```

**Arguments**
- `query` The character ORCID to search for.

**Value**
A list of WPIDs

**See Also**
- `findPathwaysByOrcid`

**Examples**
```r
{  
  findPathwayIDsByOrcid('0000-0001-9773-408')
}
```

---

**findPathwayIdsByText**  
*Find Pathway WPIDs By Text*

**Description**
Retrieve list of pathway WPIDs containing the query text.

**Usage**
```r
findPathwayIdsByText(query = NULL, field = NULL)
```

**Arguments**
- `query` A character string to search for, e.g., "cancer"
- `field` Optional character string to restrict search to a single field, e.g., title, description, wpid, species, revision, authors, datanodes, annotations, or citedIn.
findPathwayIdsByXref

Description
Retrieve list of pathway WPIDs containing the query Xref by identifier and system code.

Usage
findPathwayIdsByXref(identifier = NULL, systemCode = NULL)

Arguments
- identifier (character) The official ID specified by a data source or system
- systemCode (character) The BridgeDb code associated with the data source or system, e.g., En (Ensembl), L (Entrez), Ch (HMDB), etc. See column two of https://github.com/bridgedb/datasources/blob/main/datasources.tsv.

Value
A list of WPIDs

See Also
findPathwaysByXref

Examples
{
  findPathwayIdsByXref('ENSG00000100031', 'En')
}

findPathwayIdsByXref  Find Pathway WPIDs By Xref

findPathwaysByXref
findPathwayNamesByLiterature

*Find Pathway Names By Literature*

**Description**
Retrieve list of pathway names containing the query citation.

**Usage**

```r
findPathwayNamesByLiterature(query = NULL)
```

**Arguments**

- **query**: The character string to search for, e.g., a PMID, title keyword or author name.

**Value**
A list of lists

**See Also**

- `findPathwaysByLiterature`

**Examples**

```r
{
  findPathwayNamesByLiterature('19649250')
  findPathwayNamesByLiterature('smith')
  findPathwayNamesByLiterature('cancer')
}
```

---

findPathwayNamesByOrcid

*Find Pathway Names By ORCID*

**Description**
Retrieve list of pathway names containing the query ORCID

**Usage**

```r
findPathwayNamesByOrcid(query = NULL)
```

**Arguments**

- **query**: The character ORCID to search for.

---
findPathwayNamesByText

Find Pathway Names By Text

Description
Retrieve list of pathway names containing the query text.

Usage
findPathwayNamesByText(query = NULL, field = NULL)

Arguments
query A character string to search for, e.g., "cancer"
field Optional character string to restrict search to a single field, e.g., title, description, wpid, species, revision, authors, datanodes, annotations, or citedIn.

Value
A list of pathway names

See Also
findPathwaysByOrcid, findPathwaysByText

Examples
{
  findPathwayNamesByOrcid('0000-0001-9773-4008')
}

{
  findPathwayNamesByText('cancer')
}
**findPathwayNamesByXref**

*Find Pathway Names By Xref*

**Description**

Retrieve list of pathway names containing the query Xref by identifier and system code.

**Usage**

```r
defindPathwayNamesByXref(identifier = NULL, systemCode = NULL)
```

**Arguments**

- `identifier` (character) The official ID specified by a data source or system
- `systemCode` (character) The BridgeDb code associated with the data source or system, e.g., En (Ensembl), L (Entrez), Ch (HMDB), etc. See column two of https://github.com/bridgedb/datasources/blob/main/datasources.tsv.

**Value**

A list of lists

**See Also**

`findPathwaysByXref`

**Examples**

```r
findPathwayNamesByXref('ENSG00000100031', 'En')
```

---

**findPathwaysByLiterature**

*Find Pathways By Literature*

**Description**

Retrieve pathways containing the query citation.

**Usage**

```r
defindPathwaysByLiterature(query = NULL)
```

---
**findPathwaysByOrcid**

**Arguments**

query  
The character string to search for, e.g., a PMID, title keyword, journal abbreviation, year, or author name.

**Value**

A dataframe of pathway attributes including the matching citations

**Examples**

```r
{  
  findPathwaysByLiterature('15134803')
  findPathwaysByLiterature('Schwartz GL')
  findPathwaysByLiterature('Eur J Pharmacol')
  findPathwaysByLiterature('antihypertensive drug responses')
}
```

**findPathwaysByOrcid**  
*Find Pathways By ORCID*

**Description**

Retrieve pathways containing the query ORCID

**Usage**

```r
findPathwaysByOrcid(query = NULL)
```

**Arguments**

query  
The character ORCID to search for.

**Value**

A dataframe of pathway attributes including the matching ORCIDs

**Examples**

```r
{  
  findPathwaysByOrcid('0000-0001-9773-4008')
}
```
findPathwaysByText (Find Pathways By Text)

Description
Retrieve pathways matching the query text.

Usage
findPathwaysByText(query = NULL, field = NULL)

Arguments
- query: A character string to search for, e.g., "cancer". Case insensitive.
- field: Optional character string to restrict search to a single field, e.g., id, name, description, species, revision, authors, datanodes, annotations, or citedIn.

Details
Searches id, name, description, species, revision date, authors, datanode labels, ontology annotations, and citedIn (e.g., PMCIDs).

Value
A dataframe of pathway attributes including the matching attributes

Examples
{
  findPathwaysByText('cancer')
  findPathwaysByText('cancer','name')
}

findPathwaysByXref (Find Pathways By Xref)

Description
Retrieve pathways containing the query Xref by identifier and system code.

Usage
findPathwaysByXref(identifier = NULL, systemCode = NULL)
findPathwayUrlsByLiterature

**Arguments**

- **identifier** (character) The official ID specified by a data source or system
- **systemCode** (character) The BridgeDb code associated with the data source or system, e.g., En (Ensembl), L (NCBI gene), H (HGNC), U (UniProt), Wd (Wikidata), Ce (ChEBI), Ik (InChI). See column two of https://github.com/bridgedb/datasources/blob/main/datasources.tsv.

**Value**

A dataframe of pathway attributes including the matching identifiers

**Examples**

```r
findPathwaysByXref('ENSG00000100031', 'En')
```

findPathwayUrlsByLiterature

*Find Pathway URLs By Literature*

**Description**

Retrieve list of pathway URLs containing the query citation.

**Usage**

```r
findPathwayUrlsByLiterature(query = NULL)
```

**Arguments**

- **query** The character string to search for, e.g., a PMID, title keyword or author name.

**Value**

A list of lists

**See Also**

findPathwaysByLiterature

**Examples**

```r
findPathwayUrlsByLiterature('19649250')
findPathwayUrlsByLiterature('smith')
findPathwayUrlsByLiterature('cancer')
```
### findPathwayUrlsByOrcid

*Find Pathway URLs By ORCID*

**Description**
Retrieve list of pathway URLs containing the query ORCID

**Usage**

```r
findPathwayUrlsByOrcid(query = NULL)
```

**Arguments**
- `query` (character) The character ORCID to search for.

**Value**
A list of lists

**See Also**
- findPathwaysByOrcid

**Examples**

```r
{  
findPathwayUrlsByOrcid('0000-0001-9773-4008')
}
```

---

### findPathwayUrlsByText

*Find Pathway URLs By Text*

**Description**
Retrieve list of pathway URLs containing the query text.

**Usage**

```r
findPathwayUrlsByText(query = NULL, field = NULL)
```

**Arguments**
- `query` (character) A character string to search for, e.g., "cancer"
- `field` (character) Optional character string to restrict search to a single field, e.g., title, description, wpid, species, revision, authors, datanodes, annotations, or citedIn.
findPathwayUrlsByXref

Find Pathway URLs By Xref

Description
Retrieve list of pathway URLs containing the query Xref by identifier and system code.

Usage
findPathwayUrlsByXref(identifier = NULL, systemCode = NULL)

Arguments
identifier (character) The official ID specified by a data source or system
systemCode (character) The BridgeDb code associated with the data source or system, e.g., En (Ensembl), L (Entrez), Ch (HMDB), etc. See column two of https://github.com/bridgedb/datasources/blob/main/datasources.tsv.

Value
A list of lists

See Also
findPathwaysByXref

Examples
{
  findPathwayUrlsByXref('cancer')
}
{
  findPathwayUrlsByXref('ENSG00000100031', 'En')
}
getCounts

Get Counts for WikiPathways Stats

Description
Retrieve information about various total counts at WikiPathways.

Usage
getCounts()

Value
A data.frame of counts

Examples
{
  getCounts()
}

cgetCurationStatus

Get Curation Status of a Pathway

Description
Retrieve information about curation status for a specific pathway.

Usage
gCurationStatus(pathway)

Arguments
pathway WikiPathways identifier (WPID) for the pathway, e.g. WP554

Value
A data.frame of status details

Examples
{
  getCurationStatus('WP554')
}
**getCurationTagNames**  
DEPRECATED: Get Curation Tag Names on a Pathway

**Description**

This function is provided for compatibility with older web services only and will be defunct at the next release.

**Usage**

getCurationTagNames(pathway)

**Arguments**

- **pathway**  
  WikiPathways identifier (WPID) for the pathway to download, e.g. WP4

**Value**

A list of tag names

---

**getCurationTags**  
DEPRECATED: Get Curation Tags on a Pathway

**Description**

This function is provided for compatibility with older web services only and will be defunct at the next release.

**Usage**

getCurationTags(pathway)

**Arguments**

- **pathway**  
  WikiPathways identifier (WPID) for the pathway to download, e.g. WP4

**Value**

A list of tag name, display name, revision, text, timestamp and user
**getEveryCurationTag**  
*DEPRECATED: Get Every Instance of a Curation Tag*

**Description**
This function is provided for compatibility with older web services only and will be defunct at the next release.

**Usage**

```r
getEveryCurationTag(tag)
```

**Arguments**

- `tag` *(character)* Official name of curation tag, e.g., "Curation:FeaturedPathway"

**Value**

A list of tag name, display name, revision, text, timestamp and user

---

**getOntologyTermIds**  
*Get Ontology Term IDs by Pathway*

**Description**

Retrieve identifiers of ontology terms for a specific pathway.

**Usage**

```r
getOntologyTermIds(pathway = NULL)
```

**Arguments**

- `pathway` WikiPathways identifier (WPID) for the pathway to download, e.g. WP4

**Value**

A list of term identifiers

**Examples**

```r
{
  getOntologyTermIds('WP554')
}
```
getOntologyTermNames  Get Ontology Term Names by Pathway

Description
Retrieve names of ontology terms for a specific pathway.

Usage
getOntologyTermNames(pathway = NULL)

Arguments
pathway  WikiPathways identifier (WPID) for the pathway to download, e.g. WP4

Value
A list of term names

Examples
{
  getOntologyTermNames('WP554')
}

getOntologyTerms  Get Ontology Terms by Pathway

Description
Retrieve information about ontology terms for a specific pathway.

Usage
getOntologyTerms(pathway = NULL)

Arguments
pathway  WikiPathways identifier (WPID) for the pathway, e.g. WP554. If NULL, then ontology term information for all pathways is returned.

Value
A data.frame pathway id and term information
**getPathway**  

**Get Pathway**

**Description**

Retrieve a specific pathway in the GPML format

**Usage**

`getPathway(pathway, revision = 0)`

**Arguments**

- **pathway**: WikiPathways identifier (WPID) for the pathway to retrieve, e.g. WP554
- **revision**: <ignored> Only the latest version is available.

**Value**

GPML as string

**Examples**

```r
{  
  getOntologyTerms('WP554')  
}
```

**getPathwayHistory**  

**Get Pathway History**

**Description**

View the revision history of a pathway.

**Usage**

`getPathwayHistory(pathway = NULL, timestamp = NULL)`

**Arguments**

- **pathway**: WikiPathways identifier (WPID) for the pathway, e.g. WP554
- **timestamp**: <ignored>
**getPathwayIdsByCommunity**

*Get Pathway IDs By Community*

**Description**

Retrieve the list of pathway IDs per community

**Usage**

```r
getPathwayIdsByCommunity(community_tag = NULL)
```

**Arguments**

- `community_tag` Abbreviated name of community

**Value**

A list of pathway IDs

**Examples**

```r
{  
  getPathwayIdsByCommunity("AOP")
}
```
**getPathwayIdsByCurationTag**

**DEPRECATED: Get Pathway WPIDs by Curation Tag**

**Description**
This function is provided for compatibility with older web services only and will be defunct at the next release.

**Usage**

```
getPathwayIdsByCurationTag(tag)
```

**Arguments**

- **tag**
  - (character) Official name of curation tag, e.g., "Curation:FeaturedPathway"

**Value**
A list of pathway WPIDs

---

**getPathwayIdsByOntologyTerm**

**Get Pathway WPIDs by Ontology Term**

**Description**
Retrieve pathway WPIDs for every pathway with a given ontology term.

**Usage**

```
getPathwayIdsByOntologyTerm(term = NULL)
```

**Arguments**

- **term**
  - (character) Official ID of ontology term, e.g., "PW:0000045"

**Value**
A list of pathway WPIDs

**Examples**

````
{
    getPathwayIdsByOntologyTerm('PW:0000045')
}
```
getPathwayIdsByParentOntologyTerm

*Get Pathway WPIDs by Parent Ontology Term*

**Description**
Retrieves pathway WPIDs for every pathway with a child term of a given ontology term.

**Usage**
```
getPathwayIdsByParentOntologyTerm(term = NULL)
```

**Arguments**
- `term` (character) Official name of ontology term, e.g., "signaling pathway".

**Value**
A list of pathway WPIDs.

**Examples**
```
{  
  getPathwayIdsByParentOntologyTerm('signaling pathway') 
}
```

getPathwayInfo

*Get Pathway Info*

**Description**
Retrieve information for a specific pathway.

**Usage**
```
getPathwayInfo(pathway = NULL)
```

**Arguments**
- `pathway` WikiPathways identifier (WPID) for the pathway to download, e.g. WP554. If NULL, then all pathways are returned.

**Value**
A dataframe of pathway WPID, URL, name, species, revision, authors, description, and citedIn.
getPathwayNamesByCommunity

Description
Retrieve the list of pathway names per community

Usage
getPathwayNamesByCommunity(community_tag = NULL)

Arguments
community_tag  Abbreviated name of community

Value
A list of pathway names

Examples
{
  getPathwayNamesByCommunity("AOP")
}

gPathwaysByCommunity

Description
Retrieve pathways per community

Usage
getPathwaysByCommunity(community_tag = NULL)

Arguments
community_tag  Abbreviated name of community
**getPathwaysByOntologyTerm**

**Value**
A data.frame of pathway information

**Examples**
```
{
    getPathwaysByCommunity("AOP")
}
```

**getPathwaysByCurationTag**

*DEPRECATED: Get Pathways by Curation Tag*

**Description**
This function is provided for compatibility with older web services only and will be defunct at the next release.

**Usage**
```
getPathwaysByCurationTag(tag)
```

**Arguments**
- `tag` (character) Official name of curation tag, e.g., "Curation:FeaturedPathway"

**Value**
A list of pathway information, including WPID, url, name, species and revision

**getPathwaysByOntologyTerm**

*Get Pathways by Ontology Term*

**Description**
Retrieve pathway information for every pathway with a given ontology term.

**Usage**
```
getPathwaysByOntologyTerm(term = NULL)
```

**Arguments**
- `term` (character) Official ID of ontology term, e.g., "PW:0000045"
**getDescriptionByParentOntologyTerm**

Value

A *data.frame* of pathway information

Examples

```r
{| 
    getPathwaysByParentOntologyTerm('PW:0000045') 
|}
```

---

**getPathwaysByParentOntologyTerm**

*Get Pathways by Parent Ontology Term*

Description

Retrieve pathway information for every pathway with a child term of given ontology term.

Usage

```r
gAtPathwaysByParentOntologyTerm(term = NULL)
```

Arguments

- `term` *(character)* Official name of ontology term, e.g., "signaling pathway"

Value

A *data.frame* of pathway information

Examples

```r
{| 
    getPathwaysByParentOntologyTerm('signaling pathway') 
|}
```
getRecentChanges

Get Recent Changes

Description
Retrieve recently changed pathways at WikiPathways.

Usage
getRecentChanges(timestamp = NULL)

Arguments
timestamp (8 digits, YYYYMMDD) Limit by time, only pathways changed after the given date, e.g., 20180201 for changes since Feb 1st, 2018.

Value
A data.frame of recently changed pathways, including id, name, url, species and revision

getPathwayUrlsByCommunity

Get Pathway URLs By Community

Description
Retrieve the list of pathway URLs per community

Usage
getPathwayUrlsByCommunity(community_tag = NULL)

Arguments
community_tag Abbreviated name of community

Value
A list of pathway URLs

Examples
{
  getPathwayUrlsByCommunity("AOP")
}
getRecentChangesIds  

**Examples**

```python
{
    getRecentChanges('20180201')
}
```

---

**getRecentChangesIds**  
Get WPIDs of Recent Changes  

**Description**  
Retrieve WPIDs of recently changed pathways at WikiPathways.

**Usage**  
getRecentChangesIds(timestamp)

**Arguments**  

- **timestamp**  
  (8 digits, YYYYMMDD) Limit by time, only pathways changed after the given date, e.g., 20180201 for changes since Feb 1st, 2018.

**Value**  
A list of WPIDs

**Examples**

```python
{
    getRecentChangesIds('20180201')
}
```

---

**getRecentChangesNames**  
Get Pathway Names of Recent Changes  

**Description**  
Retrieve names of recently changed pathways at WikiPathways.

**Usage**  
getRecentChangesNames(timestamp)

**Arguments**  

- **timestamp**  
  (8 digits, YYYYMMDD) Limit by time, only pathways changed after the given date, e.g., 20180201 for changes since Feb 1st, 2018.
getValue

A list of pathway names. Note: pathway deletions will be listed as blank names.

Examples

```r
{  
  getRecentChangesNames('20180201')
}
```

---

**getXrefList**  
*Get Xref List*

**Description**

Retrieve the Xref identifiers for a specific pathway in a particular system code

**Usage**

```
getXrefList(pathway = NULL, systemCode = NULL, compact = FALSE)
```

**Arguments**

- **pathway**  
  WikiPathways identifier (WPID) for the pathway to download, e.g. WP554

- **systemCode**  
  (character) The BridgeDb code associated with the data source or system, e.g., En (Ensembl), L (NCBI gene), H (HGNC), S (UniProt), Wd (Wikidata), Ce (ChEBI), Ik (InChI). See column two of https://github.com/bridgedb/datasources/blob/main/datasources.tsv.

- **compact**  
  (Boolean) Whether to return compact identifiers, like ncbigene:1215. If FALSE (default), then just the identifier is returned, like 1215

**Value**

A list of Xrefs identifiers

**Examples**

```r
{  
  xrefs = getXrefList("WP2338", "L")
}
```
listCommunities | List Communities

**Description**
Retrieve the list of communities hosted by WikiPathways

**Usage**
```r
listCommunities()
```

**Value**
A `data.frame` of community information

**Examples**
```r
{
  listCommunities()
}
```

---

listOrganisms | List Organisms

**Description**
Retrieve the list of organisms supported by WikiPathways

**Usage**
```r
listOrganisms()
```

**Value**
A `list` of organisms

**Examples**
```r
{
  listOrganisms()
}
```
listPathwayIds

Description
Retrieve list of pathway WPIDs per species.

Usage
listPathwayIds(organism ="")

Arguments
organism (character, optional) A particular species. See listOrganisms. Default is all species.

Details
Basically returns a subset of listPathways result

Value
A list of WPIDs

See Also
listPathways

Examples
{
    listPathwayIds('Mus musculus')
}

listPathwayNames

Description
Retrieve list of pathway names per species.

Usage
listPathwayNames(organism ="")
Arguments

organism (character, optional) A particular species. See listOrganisms. Default is all species.

Details

Basically returns a subset of listPathways result

Value

A list of names

See Also

listPathways

Examples

{
  listPathwayNames('Mus musculus')
}

listPathways

List Pathways

Description

Retrieve list of pathways per species, including WPID, name, species, URL and latest revision number.

Usage

listPathways(organism = '')

Arguments

organism (character, optional) A particular species. See listOrganisms. Default is all species.

Value

A dataframe of pathway information

Examples

{
  listPathways('Mus musculus')
}
listPathwayUrls  List Pathway URLs

Description
Retrieve list of pathway URLs per species.

Usage
listPathwayUrls(organism = "")

Arguments
organism (character, optional) A particular species. See listOrganisms. Default is all species.

Details
Basically returns a subset of listPathways result

Value
A list of URLs

See Also
listPathways

Examples
{
  listPathwayUrls('Mus musculus')
}

readGMT  Read GMT File

Description
Reads any generic GMT file to produce a data frame of term-gene associations useful in enrichment analyses and other applications.

Usage
readGMT(file)
Arguments

file Path to GMT file

Details

The returned data frame includes only terms and genes. If you want another data frame with terms and names, then see readGMTnames.

Value

Data frame of term-gene associations

See Also

readGMTnames

Examples

#readGMT(system.file("extdata","my_gmt_file.gmt", package="rWikiPathways"))
#readGMT("path_to_your_gmt_file.gmt")
readPathwayGMT

Read Pathway GMT File

Description

Reads a WikiPathways GMT file to produce a data frame of pathway-gene associations useful in enrichment analyses and other applications.

Usage

readPathwayGMT(file)

Arguments

file  Path to GMT file

Details

The returned data frame includes pathway name, version, identifier, and organism. The gene content is provided as NCBI Entrez Gene identifiers. The input file can be retrieved by using downloadPathwayArchive(organism="Homo sapiens", format="gmt").

Value

Data frame of pathway-gene associations

References

Adapted from the generic GMT reader provided by clusterProfiler, https://github.com/YuLab-SMU/clusterProfiler/blob/master/R/GMT.R

See Also

downloadPathwayArchive

Examples

#readPathwayGMT(system.file("extdata", "wikipathways-20201010-gmt-Homo_sapiens.gmt", package="rWikiPathways"))
**wikipathwaysAPI**

DEPRECATED: Open Swagger docs for WikiPathways API

**Description**

This function is provided for compatibility with older web services only and will be defunct at the next release.

**Usage**

`wikipathwaysAPI(base.url = .baseUrl)`

**Arguments**

- `base.url` (optional) Ignore unless you need to specify a custom domain.

**Value**

New tab in default browser

---

**wikipathwaysGET**

DEPRECATED: WikiPathways GET

**Description**

This function is provided for compatibility with older web services only and will be defunct at the next release.

**Usage**

`wikipathwaysGET(`

    operation,
    parameters = NULL,
    format = c("json", "xml", "html", "jpg", "pdf", "dump"),
    base.url = .baseUrl
)

**Arguments**

- `operation` A character string to be converted to the query namespace
- `parameters` A named list of values to be converted to query parameters
- `format` (character) The format of the return, e.g., json (default), xml, html, jpg, pdf, dump
- `base.url` (optional) Ignore unless you need to specify a custom domain.
writeGMT

Write GMT File

Description

Writes a GMT (Gene Matrix Transposed) file from a data frame.

Usage

writeGMT(df, outfile)

Arguments

df  Data frame with columns ordered as Identifiers, optional Description column and Genes. Identifiers must be first and Genes must be last.
outfile  Path to output GMT file

Details

The input data frame must include at least two columns: Identifiers (first column) and Genes (last column). The Identifiers will be duplicated to fill the Description column in the output GMT file if none is provided. If more than three columns are provided, then the first n columns will be concatenated with number of columns.

Value

None

References

Adapted from the GMT writer in MAGeCKFlute, https://github.com/WubingZhang/MAGeCKFlute/blob/master/R/readGMT.R

See Also

readPathwayGMT

Examples

#my.df <- data.frame(id=c("WP1000","WP1000","WP1000","WP1001","WP1001"),
#                    description=c("cancer","cancer","cancer","diabetes","diabetes"),
#                    gene=c("574413","2167","4690","5781","11184"))
#writeGMT(my.df, "my_gmt_file.gmt")
Index

downloadPathwayArchive, 3
findPathwayIdsByLiterature, 4
findPathwayIdsByOrcid, 5
findPathwayIdsByText, 5
findPathwayIdsByXref, 6
findPathwayNamesByLiterature, 7
findPathwayNamesByOrcid, 7
findPathwayNamesByText, 8
findPathwayNamesByXref, 9
findPathwaysByLiterature, 9
findPathwaysByOrcid, 10
findPathwaysByText, 11
findPathwaysByXref, 11
findPathwayUrlsByLiterature, 12
findPathwayUrlsByOrcid, 13
findPathwayUrlsByText, 13
findPathwayUrlsByXref, 14
getCounts, 15
getCurationStatus, 15
getCurationTagNames, 16
getCurationTags, 16
getEveryCurationTag, 17
getOntologyTermIds, 17
getOntologyTermNames, 18
getOntologyTerms, 18
getPathway, 19
getPathwayHistory, 19
getPathwayIdsByCommunity, 20
getPathwayIdsByCurationTag, 21
getPathwayIdsByOntologyTerm, 21
getPathwayIdsByParentOntologyTerm, 22
getPathwayInfo, 22
getPathwayNamesByCommunity, 23
getPathwaysByCommunity, 23
getPathwaysByCurationTag, 24
getPathwaysByOntologyTerm, 24
getPathwaysByParentOntologyTerm, 25
getPathwayUrlsByCommunity, 26
getRecentChanges, 26
getRecentChangesIds, 27
getRecentChangesNames, 27
getXrefList, 28
listCommunities, 29
listOrganisms, 3, 29, 30–32
listPathwayIds, 30
listPathwayNames, 30
listPathways, 30, 31, 32
listPathwayUrls, 32
readGMT, 32
readGMTnames, 33
readPathwayGMT, 34
wikipathwaysAPI, 35
wikipathwaysGET, 35
writeGMT, 36