

Package ‘rWikiPathways’

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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.

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BugReports <https://github.com/wikipathways/rWikiPathways/issues>

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downloadPathwayArchive
Download Pathway Archive

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

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
```

`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')
}
```

`findPathwayIDsByOrcid` *Find Pathway WPIDs By ORCID*

Description

Retrieve list of pathway WPIDs containing the query ORCID

Usage

```
findPathwayIDsByOrcid(query = NULL)
```

Arguments

`query` The character ORCID to search for.

Value

A list of WPIDs

See Also

findPathwaysByOrcid

Examples

```
{
  findPathwayIdsByOrcid(' 0000-0001-9773-4008')
}
```

findPathwayIdsByText *Find Pathway WPIDs By Text*

Description

Retrieve list of pathway WPIDs containing the query text.

Usage

```
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.

Value

A list of WPIDs

See Also

findPathwaysByText

Examples

```
{
  findPathwayIdsByText('cancer')
}
```

`findPathwayIdsByXref` *Find Pathway WPIDs By Xref*

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>

Value

A list of WPIDs

See Also

`findPathwaysByXref`

Examples

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

`findPathwayNamesByLiterature`
 Find Pathway Names By Literature

Description

Retrieve list of pathway names containing the query citation.

Usage

```
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

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

findPathwayNamesByOrcid

Find Pathway Names By ORCID

Description

Retrieve list of pathway names containing the query ORCID

Usage

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

Arguments

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

Value

A list of lists

See Also

findPathwaysByOrcid

Examples

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

`findPathwayNamesByText`*Find Pathway Names By Text*

Description

Retrieve list of pathway names containing the query text.

Usage

```
findPathwayNamesByText(query = NULL, field = NULL)
```

Arguments

<code>query</code>	A character string to search for, e.g., "cancer"
<code>field</code>	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

`findPathwaysByText`

Examples

```
{  
  findPathwayNamesByText('cancer')  
}
```

`findPathwayNamesByXref`*Find Pathway Names By Xref*

Description

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

Usage

```
findPathwayNamesByXref(identifier = NULL, systemCode = NULL)
```

Arguments

<code>identifier</code>	(character) The official ID specified by a data source or system
<code>systemCode</code>	(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

Value

A list of lists

See Also

findPathwaysByXref

Examples

```
{  
  findPathwayNamesByXref('ENSG00000100031', 'En')  
}
```

findPathwaysByLiterature

Find Pathways By Literature

Description

Retrieve pathways containing the query citation.

Usage

```
findPathwaysByLiterature(query = NULL)
```

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

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

findPathwaysByOrcid	<i>Find Pathways By ORCID</i>
---------------------	-------------------------------

Description

Retrieve pathways containing the query ORCID

Usage

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

Arguments

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

Value

A dataframe of pathway attributes including the matching ORCIDs

Examples

```
{
  findPathwaysByOrcid(' 0000-0001-9773-4008')
}
```

findPathwaysByText	<i>Find Pathways By Text</i>
--------------------	------------------------------

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., PMCID).

Value

A dataframe of pathway attributes including the matching attributes

Examples

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

findPathwaysByXref	<i>Find Pathways By Xref</i>
--------------------	------------------------------

Description

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

Usage

```
findPathwaysByXref(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 (NCBI gene), H (HGNC), U (UniProt), Wd (Wikidata), Ce (ChEBI), Ik (InChI). See column two of https://github.com/bridgedb/datasources/blob/main/datasources

Value

A dataframe of pathway attributes including the matching identifiers

Examples

```
{
  findPathwaysByXref('ENSG00000100031', 'En')
}
```

findPathwayUrlsByLiterature	<i>Find Pathway URLs By Literature</i>
-----------------------------	--

Description

Retrieve list of pathway URLs containing the query citation.

Usage

```
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

```
{
  findPathwayUrlsByLiterature('19649250')
  findPathwayUrlsByLiterature('smith')
  findPathwayUrlsByLiterature('cancer')
}
```

findPathwayUrlsByOrcid

Find Pathway URLs By ORCID

Description

Retrieve list of pathway URLs containing the query ORCID

Usage

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

Arguments

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

Value

A list of lists

See Also

findPathwaysByOrcid

Examples

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

findPathwayUrlsByText *Find Pathway URLs By Text*

Description

Retrieve list of pathway URLs containing the query text.

Usage

```
findPathwayUrlsByText(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 urls

See Also

findPathwaysByText

Examples

```
{
  findPathwayUrlsByText('cancer')
}
```

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

Value

A list of lists

See Also

findPathwaysByXref

Examples

```
{  
  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()  
}
```

getCurationStatus

Get Curation Status of a Pathway

Description

Retrieve information about curation status for a specific pathway.

Usage

getCurationStatus(pathway)

Arguments

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

Value

A data.frame of status details

Examples

```
{
  getCurationStatus('WP554')
}
```

getCurationTagNames	<i>DEPRECATED: Get Curation Tag Names on a Pathway</i>
---------------------	--

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	<i>DEPRECATED: Get Curation Tags on a Pathway</i>
-----------------	---

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, timestampe and user

getEveryCurationTag	<i>DEPRECATED: Get Every Instance of a Curation Tag</i>
---------------------	---

Description

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

Usage

```
getEveryCurationTag(tag)
```

Arguments

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

Value

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

getOntologyTermIds	<i>Get Ontology Term IDs by Pathway</i>
--------------------	---

Description

Retrieve identifiers of ontology terms for a specific pathway.

Usage

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

Arguments

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

Value

A list of term identifiers

Examples

```
{
  getOntologyTermIds('WP554')
}
```

getOntologyTermNames	<i>Get Ontology Term Names by Pathway</i>
----------------------	---

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	<i>Get Ontology Terms by Pathway</i>
------------------	--------------------------------------

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

Examples

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

 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

```
{
  getPathway('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>

Value

Opens the GitHub history for a pathway

Examples

```
#getPathwayHistory('WP554')
```

`getPathwayIdsByCommunity`*Get Pathway IDs By Community*

Description

Retrieve the list of pathway IDs per community

Usage

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

Arguments

`community_tag` Abbreviated name of community

Value

A list of pathway IDs

Examples

```
{
  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

Retrieve pathway WPIDs for every pathway with a child term of 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	<i>Get Pathway Info</i>
----------------	-------------------------

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

Examples

```
{
  getPathwayInfo('WP554')
}
```

getPathwayNamesByCommunity	<i>Get Pathway Names By Community</i>
----------------------------	---------------------------------------

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")
}
```

`getPathwaysByCommunity`*Get Pathways By Community*

Description

Retrieve pathways per community

Usage

```
getPathwaysByCommunity(community_tag = NULL)
```

Arguments

`community_tag` Abbreviated name of community

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"

Value

A `data.frame` of pathway information

Examples

```
{
  getPathwaysByOntologyTerm('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

```
getPathwaysByParentOntologyTerm(term = NULL)
```

Arguments

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

Value

A `data.frame` of pathway information

Examples

```
{
  getPathwaysByParentOntologyTerm('signaling pathway')
}
```

```
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")
}
```

```
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

Examples

```
{
  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

```
{  
  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.
-----------	---

Value

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

Examples

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

getXrefList	<i>Get Xref List</i>
-------------	----------------------

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
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

```
{
  xrefs = getXrefList("WP2338", "L")
}
```

listCommunities	<i>List Communities</i>
-----------------	-------------------------

Description

Retrieve the list of communities hosted by WikiPathways

Usage

```
listCommunities()
```

Value

A data.frame of community information

Examples

```
{
  listCommunities()
}
```

listOrganisms	<i>List Organisms</i>
---------------	-----------------------

Description

Retrieve the list of organisms supported by WikiPathways

Usage

```
listOrganisms()
```

Value

A list of organisms

Examples

```
{  
  listOrganisms()  
}
```

listPathwayIds	<i>List Pathway WPIDs</i>
----------------	---------------------------

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	<i>List Pathway Names</i>
------------------	---------------------------

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	<i>List Pathways</i>
--------------	----------------------

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	<i>List Pathway URLs</i>
-----------------	--------------------------

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	<i>Read GMT File</i>
---------	----------------------

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")
```

readGMTnames	<i>Read GMT File for Names</i>
--------------	--------------------------------

Description

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

Usage

```
readGMTnames(file)
```

Arguments

file	Path to GMT file
------	------------------

Details

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

Value

Data frame of term-name associations

See Also

readGMT

Examples

```
#readGMTnames(system.file("extdata", "my_gmt_file.gmt", package="rWikiPathways"))
#readGMTnames("path_to_your_gmt_file.gmt")
```

readPathwayGMT	<i>Read Pathway GMT File</i>
----------------	------------------------------

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.

Value

query result content

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")
```

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