Package ‘rWikiPathways’

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Type Package

Title rWikiPathways - R client library for the WikiPathways API

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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.

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URL `https://github.com/wikipathways/rWikiPathways`

BugReports `https://github.com/wikipathways/rWikiPathways/issues`

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Contents

`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 workding 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/datasourc

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

`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

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

`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/datasourc

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` *Find Pathways By ORCID*

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` *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)
```

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/datasourc

Value

A `dataframe` of pathway attributes including the matching identifiers

Examples

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

`findPathwayUrlsByLiterature` *Find Pathway URLs By Literature*

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/datasourc

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` *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, timestampe 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

```
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` *Get Ontology Term IDs by Pathway*

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` *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

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` *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

Examples

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

`getPathwayNamesByCommunity` *Get Pathway Names By Community*

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` *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/datasourc
`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` *List Communities*

Description

Retrieve the list of communities hosted by WikiPathways

Usage

```
listCommunities()
```

Value

A `data.frame` of community information

Examples

```
{
listCommunities()
}
```

`listOrganisms` *List Organisms*

Description

Retrieve the list of organisms supported by WikiPathways

Usage

```
listOrganisms()
```

Value

A `list` of organisms

Examples

```
{
listOrganisms()
}
```

`listPathwayIds` *List Pathway WPIDs*

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` *List Pathway Names*

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")
```

`readGMTnames` *Read GMT File for Names*

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-namee associations

See Also

readGMT

Examples

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

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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