Package ‘rWikiPathways’

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**downloadPathwayArchive**

Download Pathway Archive

**Description**

Access the monthly archives of pathway content from WikiPathways.

**Usage**

```r
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')
}
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.
findPathwayIdsByXref

**Value**

A list of WPIDs

**See Also**

findPathwaysByText

**Examples**

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

---

**findPathwayIdsByXref**  
*Find Pathway WPIDs By Xref*

**Description**

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

**Usage**

```r
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**

```r
{ findPathwayIdsByXref('ENSG0000010031','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.
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

**Examples**

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

```r
{
  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/datasources/blob/main/datasources.tsv.

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)
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

{  
  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

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

Description

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

Usage

findPathwaysByXref(identifier = NULL, systemCode = NULL)
Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>identifier</td>
<td>The official ID specified by a data source or system</td>
</tr>
<tr>
<td>systemCode</td>
<td>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 <a href="https://github.com/bridgedb/datasources/blob/main/datasources.tsv">https://github.com/bridgedb/datasources/blob/main/datasources.tsv</a>.</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>query</td>
<td>The character string to search for, e.g., a PMID, title keyword or author name.</td>
</tr>
</tbody>
</table>

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
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.
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
```r
{  
  findPathwayUrlsByXref('cancer')
}
```
```r
{  
  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**

ggetCurationStatus(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  
\textit{Get Ontology Term Names by Pathway}

\textbf{Description}  
Retrieve names of ontology terms for a specific pathway.

\textbf{Usage}  
getOntologyTermNames(pathway = NULL)

\textbf{Arguments}  
pathway \hspace{1cm} WikiPathways identifier (WPID) for the pathway to download, e.g. WP4

\textbf{Value}  
A list of term names

\textbf{Examples}  
{
  getOntologyTermNames('WP554')
}

getOntologyTerms  
\textit{Get Ontology Terms by Pathway}

\textbf{Description}  
Retrieve information about ontology terms for a specific pathway.

\textbf{Usage}  
getOntologyTerms(pathway = NULL)

\textbf{Arguments}  
pathway \hspace{1cm} WikiPathways identifier (WPID) for the pathway, e.g. WP554. If NULL, then ontology term information for all pathways is returned.

\textbf{Value}  
A \texttt{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**  
{  
    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
getPathwayIdsByCommunity(community_tag = NULL)

Arguments
community_tag  Abbreviated name of community

Value
A list of pathway IDs

Examples
{
  getPathwayIdsByCommunity("AOP")
}

Value
Opens the GitHub history for a pathway

Examples
#getPathwayHistory('WP554')
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**

```r
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**

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

**Arguments**

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

**Value**

A list of pathway WPIDs

**Examples**

```r
{
  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
getPathwaysByOntologyTerm

**Value**

A data.frame of pathway information

**Examples**

```r
{ 
  getPathsByCommunity("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**

```r
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**

```r
getPathwaysByOntologyTerm(term = NULL)
```

**Arguments**

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

**Value**

A data.frame of pathway information

**Examples**

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

**Description**

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

**Usage**

```r
getPathwaysByParentOntologyTerm(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

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

---

getRecentChangesIds  Get WPIDs of Recent Changes

Description

Retrieve WPIDs of recently changed pathways at WikiPathways.

Usage

generateRecentChangesIds(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

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

---

getRecentChangesNames  Get Pathway Names of Recent Changes

Description

Retrieve names of recently changed pathways at WikiPathways.

Usage

generateRecentChangesNames(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**

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

---

**getXrefList**

*Get Xref List*

**Description**

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

**Usage**

```r
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**  
`listCommunities()`

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

**Examples**

```r
{  
  listCommunities()
}
```

---

**listOrganisms**  
*List Organisms*

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

**Usage**  
`listOrganisms()`

**Value**  
A list of organisms

**Examples**

```r
{  
  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**
```r
{
  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') }
```

---

**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**
```r
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**
```r
{
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**
```r
readGMT(file)
```
readGMTnames

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

**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](https://github.com/YuLab-SMU/clusterProfiler/blob/master/R/GMT.R)

**See Also**
downloadPathwayArchive

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

---

**readGMTnames**

**Description**
See Also
readGMT

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

```r
wikopathwaysAPI(base.url = .baseUrl)
```

**Arguments**

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

**Value**

New tab in default browser

---

wikopathwaysGET  
*DEPRECATED: WikiPathways GET*

**Description**

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

**Usage**

```r
wikopathwaysGET(
  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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>df</td>
<td>Data frame with columns ordered as Identifiers, optional Description column and Genes. Identifiers must be first and Genes must be last.</td>
</tr>
<tr>
<td>outfile</td>
<td>Path to output GMT file</td>
</tr>
</tbody>
</table>

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

```R
#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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