Package ‘rWikiPathways’

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**downloadPathwayArchive**

#### 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**

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

**Arguments**

- `query` The character ORCID to search for.

**Value**

A list of WPIDs

**See Also**

`findPathwaysByOrcid`

**Examples**

```r
findPathwayIDsByOrcid('0000-0001-9773-4008')
```

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

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/blob/main/datasources.tsv.

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.
findPathwayNamesByText

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**

```r
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**

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

findPathwaysByLiterature

*Find Pathways By Literature*

**Description**

Retrieve pathways containing the query citation.

**Usage**

```r
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**

```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**

```r
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**

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

findPathwaysByXref  
*Find Pathways By Xref*

**Description**

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

**Usage**

```r
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** (character) 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` 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` 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

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('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**

```r
{
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**

```r
{
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

ggetCurationTags  

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**

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**

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

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>
getPathwayIdsByCommunity

Get Pathway IDs By Community

Value

Opens the GitHub history for a pathway

Examples

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

getPathwayIdsByCommunity

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**

```r
gapathwayIdsByCurationTag(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
gapathwayIdsByOntologyTerm(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
getPathwayNamesByCommunity

*Get Pathway Names By Community*

**Examples**

{  
    getPathwayInfo('WP554')  
}

**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

```r
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**

```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')
}
```

---

**getPathwaysByParentOntologyTerm**

*Get Pathways by Parent Ontology Term*

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

*Get WPIDs of Recent Changes*

### Description

Retrieve WPIDs of recently changed pathways at WikiPathways.

### Usage

```python
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

```python
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

```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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>pathway</td>
<td>WikiPathways identifier (WPID) for the pathway to download, e.g. WP554</td>
</tr>
<tr>
<td>systemCode</td>
<td>(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 <a href="https://github.com/bridgedb/datasources/blob/main/datasources.tsv">https://github.com/bridgedb/datasources/blob/main/datasources.tsv</a>.</td>
</tr>
<tr>
<td>compact</td>
<td>(Boolean) Whether to return compact identifiers, like ncbigene:1215. If FALSE (default), then just the identifier is returned, like 1215</td>
</tr>
</tbody>
</table>

Value

A list of Xrefs identifiers

Examples

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

**Description**

Retrieve the list of communities hosted by WikiPathways

**Usage**

listCommunities()

**Value**

A data.frame of community information

**Examples**

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

listOrganisms  

**Description**

Retrieve the list of organisms supported by WikiPathways

**Usage**

listOrganisms()

**Value**

A list of organisms

**Examples**

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

/listPathwayIds

**Description**

Retrieve list of pathway WPIDs per species.

**Usage**

```r
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  

/listPathwayNames

**Description**

Retrieve list of pathway names per species.

**Usage**

```r
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')
}
```
### 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)
```
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 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-name associations
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](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"))
```
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
deprecated_function <- wikipathwaysAPI(base.url = .baseUrl)
```

**Arguments**

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

---

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
deprecated_function <- 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

```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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