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**

```{r}
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
{
    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/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**

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

**Arguments**

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

**Value**
A list of lists

**See Also**

- `findPathwaysByLiterature`

**Examples**

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

---

findPathwayNamesByOrcid

*Find Pathway Names By ORCID*

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

**Usage**

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

**Arguments**

- `query` The character ORCID to search for.

---
**findPathwayNamesByText**

*Find Pathway Names By Text*

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

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

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

**Value**
A list of pathway names

**See Also**
- findPathwaysByOrcid

**Examples**
```
{
  findPathwayNamesByOrcid('0000-0001-9773-4008')
}
```
```
{
  findPathwayNamesByText('cancer')
}
```
findPathwayNamesByXref

Find Pathway Names By Xref

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

Usage
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**

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

---

findPathwaysByOrcid Find Pathways By ORCID

**Description**

Retrieve pathways containing the query ORCID

**Usage**

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

**Arguments**

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

**Value**

- A dataframe of pathway attributes including the matching ORCIDs

**Examples**

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

**Description**  
Retrieve pathways matching the query text.

**Usage**  
`findPathwaysByText(query = NULL, field = NULL)`

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

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

**Value**  
A dataframe of pathway attributes including the matching attributes

**Examples**
```r  
{  
  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)`

**Examples**
```r  
{  
  findPathwaysByXref('identifier', 'systemCode')  
  findPathwaysByXref('identifier', 'systemCode', 'Xref')  
}
```
**findPathwayUrlsByLiterature**

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>identifier</td>
<td>(character) The official ID specified by a data source or system</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), 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

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

Usage
findPathwayUrlsByXref(identifier = NULL, systemCode = NULL)

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

Value
A list of lists

See Also
findPathwaysByXref

Examples
{
  findPathwayUrlsByXref('cancer')
}

{findPathwayUrlsByXref('ENSG00000100031','En')}
**getCounts**

*Get Counts for WikiPathways Stats*

**Description**

Retrieve information about various total counts at WikiPathways.

**Usage**

getCounts()

**Value**

A `data.frame` of counts

**Examples**

```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

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

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

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**
```r
getOntologyTermNames(pathway = NULL)
```

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

**Value**
A list of term names

**Examples**
```r
{
  getOntologyTermNames('WP554')
}
```

getOntologyTerms  
*Get Ontology Terms by Pathway*

**Description**
Retrieve information about ontology terms for a specific pathway.

**Usage**
```r
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')
}

ggetPathway  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')
}

ggetPathwayHistory  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

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

---

getPathwayIdsByCommunity

### Get Pathway IDs By Community

**Description**

Retrieve the list of pathway IDs per community

**Usage**

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

**Arguments**

- **community_tag**: Abbreviated name of community

**Value**

A list of pathway IDs

**Examples**

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

*DEPRECATED: Get Pathway WPIDs by Curation Tag*

**Description**

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

**Usage**

`getPathwayIdsByCurationTag(tag)`

**Arguments**

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

**Value**

A list of pathway WPIDs

---

**getPathwayIdsByOntologyTerm**

*Get Pathway WPIDs by Ontology Term*

**Description**

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

**Usage**

`getPathwayIdsByOntologyTerm(term = NULL)`

**Arguments**

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

**Value**

A list of pathway WPIDs

**Examples**

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

*Get Pathway WPIDs by Parent Ontology Term*

**Description**

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

**Usage**

```r
getPathwayIdsByParentOntologyTerm(term = NULL)
```

**Arguments**

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

**Value**

A list of pathway WPIDs

**Examples**

```r
getPathwayIdsByParentOntologyTerm('signaling pathway')
```

---

**getPathwayInfo**

*Get Pathway Info*

**Description**

Retrieve information for a specific pathway.

**Usage**

```r
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

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

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 list of pathway information, including WPID, url, name, species and revision
getPathwaysByParentOntologyTerm

Value
A data.frame of pathway information

Examples
{
  getPathwaysByParentOntologyTerm('signaling pathway')
}

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

gETCHWayURLsByCommunity(community_tag = NULL)

Arguments

community_tag  Abbreviated name of community

Value

A list of pathway URLs

Examples

{
  getPathwayUrlsByCommunity("AOP")
}

gETCHRecentChanges

Get Recent Changes

Description

Retrieve recently changed pathways at WikiPathways.

Usage

gETCHRecentChanges(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
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.
getXrefList

Description

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

Usage

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

Arguments

- **pathway**: WikiPathways identifier (WPID) for the pathway to download, e.g. WP554
- **systemCode**: (character) The BridgeDb code associated with the data source or system, e.g., En (Ensembl), L (NCBI gene), H (HGNC), S (UniProt), Wd (Wikidata), Ce (ChEBI), Ik (InChI). See column two of https://github.com/bridgedb/datasources/blob/main/datasources.tsv.
- **compact**: (Boolean) Whether to return compact identifiers, like ncbigene:1215. If FALSE (default), then just the identifier is returned, like 1215

Value

A list of Xrefs identifiers

Examples

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

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

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

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

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

listOrganisms

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

**Usage**
```r
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
{
  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
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-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**

```r
cleanPathwayGMT(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"))
```
**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.
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
```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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