# Package ‘rWikiPathways’

May 30, 2024

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downloadPathwayArchive

Description
Access the monthly archives of pathway content from WikiPathways.

Usage
```
downloadPathwayArchive(
  date = "current",
  organism = NULL,
  format = c("gpml", "gmt", "svg"),
  destpath = "./"
)
```

Arguments
- `date` (optional) The timestamp for a monthly release (e.g., 20171010) or "current" (default) for latest release.
- `organism` (optional) A particular species. See `listOrganisms`.
- `format` (optional) Either gpml (default), gmt or svg.
- `destpath` (optional) Destination path for file to be downloaded to. Default is current working directory.

Details
If you do not specify an organism, then an archive file will not be downloaded. Rather, the archive will be opened in a tab in your default browser.

Value
Filename of downloaded file or an opened tab in default browser
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

**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('ENSG000000031', '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

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('ENSG0000010031', '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  

**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  

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

**Usage**  
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** 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
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

```r
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')  
}
```
**getCounts**

*Get Counts for WikiPathways Stats*

**Description**
Retrieve information about various total counts at WikiPathways.

**Usage**
```r
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**
```r
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**

```python
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**

```python
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
{
  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

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

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**

```r
generatePathwayIdsByCurationTag(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
generatePathwayIdsByOntologyTerm(term = NULL)
```

**Arguments**

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

**Value**

A list of pathway WPIDs

**Examples**

```r
{
  generatePathwayIdsByOntologyTerm('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**

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

**Description**

Retrieve the list of pathway names per community

**Usage**

```r
generatePathwayNamesByCommunity(community_tag = NULL)
```

**Arguments**

- `community_tag`  Abbreviated name of community

**Value**

A list of pathway names

**Examples**

```r
{ 
  getPathwayNamesByCommunity("AQP")
}
```

**getPathwaysByCommunity**

*Get Pathways By Community*

**Description**

Retrieve pathways per community

**Usage**

```r
generatePathwaysByCommunity(community_tag = NULL)
```

**Arguments**

- `community_tag`  Abbreviated name of community
**getPathwaysByOntologyTerm**

**Value**

A data.frame of pathway information

**Examples**

```r
{  
  getPathwaysByCommunity("AOP")
}
```

---

**getPathsByCurationTag**

*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

Examples

```javascript
{
    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**

```javascript
{
    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

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/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**

*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 = "")
```
listPathways

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 \hspace{1cm} \textit{List Pathway URLs}

\textbf{Description}

Retrieve list of pathway URLs per species.

\textbf{Usage}

\begin{verbatim}
listPathwayUrls(organism = "")
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
\item \texttt{organism} \hspace{1cm} \texttt{(character, optional)} A particular species. See \texttt{listOrganisms}. Default is all species.
\end{itemize}

\textbf{Details}

Basically returns a subset of \texttt{listPathways} result.

\textbf{Value}

A list of URLs

\textbf{See Also}

\texttt{listPathways}

\textbf{Examples}

\begin{verbatim}
{  
  listPathwayUrls('Mus musculus')
}
\end{verbatim}

\textbf{readGMT \hspace{1cm} \textit{Read GMT File}}

\textbf{Description}

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

\textbf{Usage}

\begin{verbatim}
readGMT(file)
\end{verbatim}
**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**

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

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**

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

**Arguments**

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

**Value**

New tab in default browser

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**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**

```r
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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