

# Package ‘rWikiPathways’

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**Type** Package

**Title** rWikiPathways - R client library for the WikiPathways API

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**Suggests** testthat, BiocStyle, knitr, rmarkdown

**Description** Use this package to interface with the WikiPathways API. It provides programmatic access to WikiPathways content in multiple data and image formats, including official monthly release files and convenient GMT read/write functions.

**License** MIT + file LICENSE

**URL** <https://github.com/wikipathways/rwikipathways>

**BugReports** <https://github.com/wikipathways/rwikipathways/issues>

**LazyLoad** yes

**biocViews** Visualization, GraphAndNetwork, ThirdPartyClient, Network, Metabolomics

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---

`downloadPathwayArchive`*Download Pathway Archive*

---

## Description

Access the monthly archives of pathway content from WikiPathways.

## Usage

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

## Arguments

<code>date</code>	(optional) The timestamp for a monthly release (e.g., 20171010) or "current" (default) for latest release.
<code>organism</code>	(optional) A particular species. See <a href="#">listOrganisms</a> .
<code>format</code>	(optional) Either gpml (default), gmt or svg.
<code>destpath</code>	(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

## See Also

`readPathwayGMT`

## Examples

```
downloadPathwayArchive() ## open in browser  
downloadPathwayArchive(format="gmt") ## open in browser  
downloadPathwayArchive(date="20171010", format="svg") ## open in browser  
downloadPathwayArchive(date="20171010", organism="Mus musculus", format="svg") ## download file  
downloadPathwayArchive(organism="Mus musculus") ## download file
```

findPathwayIdsByLiterature

*Find Pathway WPIDs By Literature*

---

**Description**

Retrieve list of pathway WPIDs containing the query citation.

**Usage**

```
findPathwayIdsByLiterature(query)
```

**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')  
}
```

---

findPathwayIdsByText    *Find Pathway WPIDs By Text*

---

**Description**

Retrieve list of pathway WPIDs containing the query text.

**Usage**

```
findPathwayIdsByText(query)
```

**Arguments**

query                    A character string to search for, e.g., "cancer"

**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, systemCode)
```

**Arguments**

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

**Details**

Note: there will be multiple listings of the same pathway if the Xref is present mutiple times.

**Value**

A list of WPIDs

**See Also**

`findPathwaysByXref`

**Examples**

```
{  
  findPathwayIdsByXref('ENSG00000232810', 'En')  
}
```

findPathwayNamesByLiterature

*Find Pathway Names By Literature*

---

**Description**

Retrieve list of pathway names containing the query citation.

**Usage**

```
findPathwayNamesByLiterature(query)
```

**Arguments**

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

**Details**

Note: there will be multiple listings of the same pathway name if copies exist for multiple species.

**Value**

A list of lists

**See Also**

findPathwaysByLiterature

**Examples**

```
{
  findPathwayNamesByLiterature('19649250')
  findPathwayNamesByLiterature('smith')
  findPathwayNamesByLiterature('cancer')
}
```

---

findPathwayNamesByText

*Find Pathway Names By Text*

---

**Description**

Retrieve list of pathway names containing the query text.

**Usage**

```
findPathwayNamesByText(query)
```

**Arguments**

query            A character string to search for, e.g., "cancer"

**Details**

Note: there will be multiple listings of the same pathway name if copies exist for multiple species.

**Value**

A list of pathway names

**See Also**

findPathwaysByText

**Examples**

```
{
  findPathwayNamesByText('cancer')
}
```

---

findPathwayNamesByXref

*Find Pathway Names By Xref*

---

**Description**

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

**Usage**

```
findPathwayNamesByXref(identifier, systemCode)
```

**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/>

**Details**

Note: there will be multiple listings of the same pathway if the Xref is present mutiple times.

**Value**

A list of lists

**See Also**

findPathwaysByXref

**Examples**

```
{  
  findPathwayNamesByXref('ENSG00000232810', 'En')  
}
```

---

findPathwaysByLiterature

*Find Pathways By Literature*

---

**Description**

Retrieve pathways containing the query citation.

**Usage**

```
findPathwaysByLiterature(query)
```

**Arguments**

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

**Details**

The score is from a lucene index search engine, ranging from 0 to 1 with higher scores for better matches. The two literature columns are lists of pubmed ids and titles for the citations matching the query per pathway. The graphId column lists the id for any objects in the GPML pathway model that have been specifically annotated with the matching citations.

**Value**

A dataframe of pathway attributes in addition to query result score and literature details

**Examples**

```
{  
  findPathwaysByLiterature('19649250')  
  findPathwaysByLiterature('smith')  
  findPathwaysByLiterature('cancer')  
}
```



---

findPathwaysByText      *Find Pathways By Text*

---

**Description**

Retrieve pathways containing the query text.

**Usage**

```
findPathwaysByText(query)
```

**Arguments**

query                      A character string to search for, e.g., "cancer"

**Details**

The score is from a lucene index search engine, ranging from 0 to 1 with higher scores for better matches.

**Value**

A dataframe of pathway attributes in addition to query result score

**Examples**

```
{
  findPathwaysByText('cancer')
}
```

---

findPathwaysByXref      *Find Pathways By Xref*

---

**Description**

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

**Usage**

```
findPathwaysByXref(identifier, systemCode)
```

**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/>

**Details**

Note: there will be multiple listings of the same pathway if the Xref is present mutiple times.

The score is from a lucene index search engine, ranging from 0 to 1 with higher scores for better matches.

**Value**

A dataframe of pathway attributes in addition to query result score

**Examples**

```
{  
  findPathwaysByXref('ENSG00000232810', 'En')  
}
```

---

findPathwayUrlsByLiterature

*Find Pathway URLs By Literature*

---

**Description**

Retrieve list of pathway URLs containing the query citation.

**Usage**

```
findPathwayUrlsByLiterature(query)
```

**Arguments**

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

**Value**

A list of lists

**See Also**

findPathwaysByLiterature

**Examples**

```
{  
  findPathwayUrlsByLiterature('19649250')  
  findPathwayUrlsByLiterature('smith')  
  findPathwayUrlsByLiterature('cancer')  
}
```

---

findPathwayUrlsByText *Find Pathway URLs By Text*

---

**Description**

Retrieve list of pathway URLs containing the query text.

**Usage**

```
findPathwayUrlsByText(query)
```

**Arguments**

query                    A character string to search for, e.g., "cancer"

**Value**

A list of urls

**See Also**

findPathwaysByText

**Examples**

```
{
  findPathwayUrlsByText('cancer')
}
```

---

findPathwayUrlsByXref *Find Pathway URLs By Xref*

---

**Description**

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

**Usage**

```
findPathwayUrlsByXref(identifier, systemCode)
```

**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/>

**Details**

Note: there will be multiple listings of the same pathway if the Xref is present mutiple times.

**Value**

A list of lists

**See Also**

findPathwaysByXref

**Examples**

```
{
  findPathwayUrIsByXref('ENSG00000232810', 'En')
}
```

---

getCurationTagNames     *Get Curation Tag Names on a Pathway*

---

**Description**

Retrieve names of curation tags for a specific pathway.

**Usage**

```
getCurationTagNames(pathway)
```

**Arguments**

pathway             WikiPathways identifier (WPID) for the pathway to download, e.g. WP4

**Value**

A list of tag names

**Examples**

```
{
  getCurationTagNames('WP554')
}
```

---

getCurationTags	<i>Get Curation Tags on a Pathway</i>
-----------------	---------------------------------------

---

**Description**

Retrieve information about curation tags for a specific pathway.

**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

**Examples**

```
{
  getCurationTags('WP554')
}
```

---

getEveryCurationTag	<i>Get Every Instance of a Curation Tag</i>
---------------------	---

---

**Description**

Retrieve information about every instance of a given curation tag.

**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

**Examples**

```
{
  getEveryCurationTag('Curation:FeaturedPathway')
}
```

getOntologyTermIds     *Get Ontology Term IDs by Pathway*

---

**Description**

Retrieve identifiers of ontology terms for a specific pathway.

**Usage**

```
getOntologyTermIds(pathway)
```

**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)
```

**Arguments**

pathway             WikiPathways identifier (WPID) for the pathway to download, e.g. WP4

**Value**

A list of term names

**Examples**

```
{
  getOntologyTermNames('WP554')
}
```

---

getOntologyTerms	<i>Get Ontology Terms by Pathway</i>
------------------	--------------------------------------

---

**Description**

Retrieve information about ontology terms for a specific pathway.

**Usage**

```
getOntologyTerms(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

**Examples**

```
{  
  getOntologyTerms('WP554')  
}
```

---

getPathway	<i>Get Pathway</i>
------------	--------------------

---

**Description**

Retrieve a specific pathway in the GPML format

**Usage**

```
getPathway(pathway, revision = 0)
```

**Arguments**

pathway            WikiPathways identifier (WPID) for the pathway to download, e.g. WP4  
revision            (integer, optional) Number to indicate a specific revision to download

**Value**

GPML

**Examples**

```
{
  getPathway('WP554')
}
```

---

getPathwayHistory      *Get Pathway History*

---

**Description**

Retrieve the revision history of a pathway.

**Usage**

```
getPathwayHistory(pathway, timestamp)
```

**Arguments**

pathway	WikiPathways identifier (WPID) for the pathway to download, e.g. WP4
timestamp	(integer) Limit by time, only history items after the given time, e.g., 20180201 for revisions since Feb 1st, 2018. Any length of timestamp is accepted, upto 14 digits, e.g., 2018, 201802, 20180201063011, etc.

**Value**

A list of revisions, including user and comment

**Examples**

```
{
  getPathwayHistory('WP554', 20180201)
}
```

---

getPathwayIdsByCurationTag  
*Get Pathway WPIDs by Curation Tag*

---

**Description**

Retrieve pathway WPIDs for every pathway with a given curation tag.

**Usage**

```
getPathwayIdsByCurationTag(tag)
```



**Arguments**

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

**Value**

A list of pathway WPIDs

**Examples**

```
{
  getPathwayIdsByCurationTag('Curation:FeaturedPathway')
}
```

---

*getPathwayIdsByOntologyTerm*  
*Get Pathway WPIDs by Ontology Term*

---

**Description**

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

**Usage**

```
getPathwayIdsByOntologyTerm(term)
```

**Arguments**

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

**Value**

A list of pathway WPIDs

**Examples**

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

---

getPathwayIdsByParentOntologyTerm  
*Get Pathway WPIDs by Parent Ontology Term*

---

**Description**

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

**Usage**

```
getPathwayIdsByParentOntologyTerm(term)
```

**Arguments**

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

**Value**

A list of pathway WPIDs

**Examples**

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

---

getPathwayInfo *Get Pathway Info*

---

**Description**

Retrieve information for a specific pathway

**Usage**

```
getPathwayInfo(pathway)
```

**Arguments**

pathway WikiPathways identifier (WPID) for the pathway to download, e.g. WP4

**Value**

A dataframe of pathway WPID, URL, name, species and latest revision

**Examples**

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

---

`getPathwaysByCurationTag`*Get Pathways by Curation Tag*

---

**Description**

Retrieve pathway information for every pathway with a given curation tag.

**Usage**

```
getPathwaysByCurationTag(tag)
```

**Arguments**

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

**Value**

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

**Examples**

```
{
  getPathwaysByCurationTag('Curation:FeaturedPathway')
}
```

---

`getPathwaysByOntologyTerm`*Get Pathways by Ontology Term*

---

**Description**

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

**Usage**

```
getPathwaysByOntologyTerm(term)
```

**Arguments**

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

**Value**

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

**Examples**

```
{  
  getPathwaysByOntologyTerm('PW:0000045')  
}
```

---

getPathwaysByParentOntologyTerm

*Get Pathways by Parent Ontology Term*

---

**Description**

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

**Usage**

```
getPathwaysByParentOntologyTerm(term)
```

**Arguments**

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

**Value**

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

**Examples**

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

---

getRecentChanges	<i>Get Recent Changes</i>
------------------	---------------------------

---

**Description**

Retrieve recent changes to pathways at WikiPathways.

**Usage**

```
getRecentChanges(timestamp)
```

**Arguments**

timestamp	(14 digits, YYYYMMDDhhmmss) Limit by time, only history items after the given time, e.g., 20180201000000 for changes since Feb 1st, 2018.
-----------	---

**Value**

A list of changes, including pathway WPID, name, url, species and revision

**Examples**

```
{  
  getRecentChanges('20180201000000')  
}
```

---

getRecentChangesIds	<i>Get WPIDs of Recent Changes</i>
---------------------	------------------------------------

---

**Description**

Retrieve WPIDs of recently changed pathways at WikiPathways.

**Usage**

```
getRecentChangesIds(timestamp)
```

**Arguments**

timestamp	(14 digits, YYYYMMDDhhmmss) Limit by time, only history items after the given time, e.g., 20180201000000 for changes since Feb 1st, 2018.
-----------	---

**Value**

A list of WPIDs

**Examples**

```
{
  getRecentChangesIds('20180201000000')
}
```

---

getRecentChangesNames *Get Pathway Names of Recent Changes*

---

**Description**

Retrieve names of recently changed pathways at WikiPathways.

**Usage**

```
getRecentChangesNames(timestamp)
```

**Arguments**

timestamp	(14 digits, YYYYMMDDhhmmss) Limit by time, only history items after the given time, e.g., 20180201000000 for changes since Feb 1st, 2018.
-----------	---

**Value**

A list of pathway names. Note: pathway deletions will be listed as blank names.

**Examples**

```
{
  getRecentChangesNames('20180201000000')
}
```

---

getXrefList *Get Xref List*

---

**Description**

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

**Usage**

```
getXrefList(pathway, systemCode)
```

**Arguments**

pathway	WikiPathways identifier (WPID) for the pathway to download, e.g. WP4
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 <a href="https://github.com/bridgedb/datasources/">https://github.com/bridgedb/datasources/</a>

**Value**

A list of Xrefs identifiers

**Examples**

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

---

listOrganisms	<i>List Organisms</i>
---------------	-----------------------

---

**Description**

Retrieve the list of organisms supported by WikiPathways

**Usage**

```
listOrganisms()
```

**Value**

A list of organisms

**Examples**

```
{
  listOrganisms()
}
```

---

listPathwayIds	<i>List Pathway WPIDs</i>
----------------	---------------------------

---

**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	<i>List Pathway Names</i>
------------------	---------------------------

---

**Description**

Retrieve list of pathway names per species.

**Usage**

```
listPathwayNames(organism = "")
```

**Arguments**

organism (character, optional) A particular species. See [listOrganisms](#). Default is all species.

**Details**

Basically returns a subset of [listPathways](#) result

**Value**

A list of names

**See Also**

[listPathways](#)

**Examples**

```
{  
  listPathwayNames('Mus musculus')  
}
```



---

listPathways	<i>List Pathways</i>
--------------	----------------------

---

**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	<i>List Pathway URLs</i>
-----------------	--------------------------

---

**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"))
```

---

readGMTnames	<i>Read GMT File for Names</i>
--------------	--------------------------------

---

**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

**See Also**

readGMT

**Examples**

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

---

readPathwayGMT	<i>Read Pathway GMT File</i>
----------------	------------------------------

---

**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

*Open Swagger docs for WikiPathways API*

---

**Description**

Opens swagger docs in default browser for available API calls.

**Usage**

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

**Arguments**

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

**Value**

New tab in default browser

**Examples**

```
{
  wikipathwaysAPI()
}
```

---

wikipathwaysGET	<i>WikiPathways GET</i>
-----------------	-------------------------

---

**Description**

Constructs the query, makes GET call and processes the result

**Usage**

```
wikipathwaysGET(
  operation,
  parameters = NULL,
  format = c("json", "xml", "html", "jpg", "pdf", "dump"),
  base.url = .baseUrl
)
```

**Arguments**

- operation      A character string to be converted to the query namespace
- parameters    A named list of values to be converted to query parameters
- format        (character) The format of the return, e.g., json (default), xml, html, jpg, pdf, dump
- base.url      (optional) Ignore unless you need to specify a custom domain.

**Value**

query result content

**Examples**

```
{
  wikipathwaysGET('listOrganisms')
}
```

---

`writeGMT`*Write GMT File*

---

**Description**

Writes a GMT (Gene Matrix Transposed) file from a data frame.

**Usage**

```
writeGMT(df, outfile)
```

**Arguments**

<code>df</code>	Data frame with columns ordered as Identifiers, optional Description column and Genes. Identifiers must be first and Genes must be last.
<code>outfile</code>	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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