

# Package ‘rWikiPathways’

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**Type** Package

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

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readr, stringr, purrr, lubridate

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

**Encoding** UTF-8

**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>

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Metabolomics

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## Contents

downloadPathwayArchive . . . . .	3
findPathwayIdsByLiterature . . . . .	4
findPathwayIdsByOrcid . . . . .	4
findPathwayIdsByText . . . . .	5
findPathwayIdsByXref . . . . .	6
findPathwayNamesByLiterature . . . . .	6
findPathwayNamesByOrcid . . . . .	7
findPathwayNamesByText . . . . .	8
findPathwayNamesByXref . . . . .	8
findPathwaysByLiterature . . . . .	9
findPathwaysByOrcid . . . . .	10
findPathwaysByText . . . . .	10
findPathwaysByXref . . . . .	11
findPathwayUrlsByLiterature . . . . .	11
findPathwayUrlsByOrcid . . . . .	12
findPathwayUrlsByText . . . . .	13
findPathwayUrlsByXref . . . . .	13
getCounts . . . . .	14
getCurationStatus . . . . .	14
getCurationTagNames . . . . .	15
getCurationTags . . . . .	15
getEveryCurationTag . . . . .	16
getOntologyTermIds . . . . .	16
getOntologyTermNames . . . . .	17
getOntologyTerms . . . . .	17
getPathway . . . . .	18
getPathwayHistory . . . . .	18
getPathwayIdsByCommunity . . . . .	19
getPathwayIdsByCurationTag . . . . .	19
getPathwayIdsByOntologyTerm . . . . .	20
getPathwayIdsByParentOntologyTerm . . . . .	20
getPathwayInfo . . . . .	21
getPathwayNamesByCommunity . . . . .	21
getPathwaysByCommunity . . . . .	22
getPathwaysByCurationTag . . . . .	22
getPathwaysByOntologyTerm . . . . .	23
getPathwaysByParentOntologyTerm . . . . .	23
getPathwayUrlsByCommunity . . . . .	24
getRecentChanges . . . . .	24
getRecentChangesIds . . . . .	25
getRecentChangesNames . . . . .	25
getXrefList . . . . .	26
listCommunities . . . . .	26
listOrganisms . . . . .	27
listPathwayIds . . . . .	27
listPathwayNames . . . . .	28
listPathways . . . . .	29
listPathwayUrls . . . . .	29
readGMT . . . . .	30
readGMTnames . . . . .	31

*downloadPathwayArchive* 3

readPathwayGMT . . . . .	31
wikipathwaysAPI . . . . .	32
wikipathwaysGET . . . . .	33
writeGMT . . . . .	33

**Index** 35

---

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**

- 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

**See Also**

readPathwayGMT

**Examples**

```
#downloadPathwayArchive() ## open in browser  
#downloadPathwayArchive(format="gmt") ## open in browser  
#downloadPathwayArchive(date="20230710", format="svg") ## open in browser  
#downloadPathwayArchive(date="20230710", 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 = 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.

**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 <a href="https://github.com/bridgedb/datasour">https://github.com/bridgedb/datasour</a>

### 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.

**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

```
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 <a href="https://github.com/bridgedb/datasour">https://github.com/bridgedb/datasour</a>



**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)
```

**Arguments**

<code>query</code>	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 *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., PMCID).

**Value**

A dataframe of pathway attributes including the matching attributes

**Examples**

```
{
  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)
```

**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 <a href="https://github.com/bridgedb/datasources/blob/main/datasources">https://github.com/bridgedb/datasources/blob/main/datasources</a>

**Value**

A dataframe of pathway attributes including the matching identifiers

**Examples**

```
{
  findPathwaysByXref('ENSG00000100031', 'En')
}
```

---

findPathwayUrlsByLiterature  
*Find Pathway URLs By Literature*

---

**Description**

Retrieve list of pathway URLs containing the query citation.

**Usage**

```
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**

```
{
  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.

**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 = 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 <a href="https://github.com/bridgedb/datasour">https://github.com/bridgedb/datasour</a>

**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**

```
{
  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**

```
{
  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, timestampe 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, timestampe 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	<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 retrieve, e.g. WP554
revision	<ignored> Only the latest version is available.

**Value**

GPML as string

**Examples**

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

---

getPathwayHistory	<i>Get Pathway History</i>
-------------------	----------------------------

---

**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**

```
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**

```
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	<i>Get Pathway Info</i>
----------------	-------------------------

---

**Description**

Retrieve information for a specific pathway

**Usage**

```
getPathwayInfo(pathway = NULL)
```

**Arguments**

pathway	WikiPathways identifier (WPID) for the pathway to download, e.g. WP554. If NULL, then all pathways are returned.
---------	--

**Value**

A dataframe of pathway WPID, URL, name, species, revision, authors, description, and citedIn

**Examples**

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

---

getPathwayNamesByCommunity	<i>Get Pathway Names By Community</i>
----------------------------	---------------------------------------

---

**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**

```
{
  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**

```
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**

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

**Arguments**

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

**Value**

A data.frame of pathway information

**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 = 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**

```
getPathwayUrlsByCommunity(community_tag = NULL)
```

**Arguments**

community\_tag    Abbreviated name of community

**Value**

A list of pathway URLs

**Examples**

```
{  
  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

**Examples**

```
{  
  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**

```
{
  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.

**Value**

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

**Examples**

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

---

getXrefList	<i>Get Xref List</i>
-------------	----------------------

---

**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 <a href="https://github.com/bridgedb/datasources/blob/main/datasources">https://github.com/bridgedb/datasources/blob/main/datasources</a>
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	<i>List Communities</i>
-----------------	-------------------------

---

**Description**

Retrieve the list of communities hosted by WikiPathways

**Usage**

```
listCommunities()
```

**Value**

A data.frame of community information

**Examples**

```
{
  listCommunities()
}
```

---

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')  
}
```

---

<code>listPathwayNames</code>	<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"))
#readGMT("path_to_your_gmt_file.gmt")
```

---

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"))  
#readGMTnames("path_to_your_gmt_file.gmt")
```

---

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

*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

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

## Arguments

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

## Value

New tab in default browser



---

 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

```
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")
```

# Index

[downloadPathwayArchive](#), 3

[findPathwayIdsByLiterature](#), 4

[findPathwayIDsByOrcid](#), 4

[findPathwayIdsByText](#), 5

[findPathwayIdsByXref](#), 6

[findPathwayNamesByLiterature](#), 6

[findPathwayNamesByOrcid](#), 7

[findPathwayNamesByText](#), 8

[findPathwayNamesByXref](#), 8

[findPathwaysByLiterature](#), 9

[findPathwaysByOrcid](#), 10

[findPathwaysByText](#), 10

[findPathwaysByXref](#), 11

[findPathwayUrlsByLiterature](#), 11

[findPathwayUrlsByOrcid](#), 12

[findPathwayUrlsByText](#), 13

[findPathwayUrlsByXref](#), 13

  

[getCounts](#), 14

[getCurationStatus](#), 14

[getCurationTagNames](#), 15

[getCurationTags](#), 15

[getEveryCurationTag](#), 16

[getOntologyTermIds](#), 16

[getOntologyTermNames](#), 17

[getOntologyTerms](#), 17

[getPathway](#), 18

[getPathwayHistory](#), 18

[getPathwayIdsByCommunity](#), 19

[getPathwayIdsByCurationTag](#), 19

[getPathwayIdsByOntologyTerm](#), 20

[getPathwayIdsByParentOntologyTerm](#), 20

[getPathwayInfo](#), 21

[getPathwayNamesByCommunity](#), 21

[getPathwaysByCommunity](#), 22

[getPathwaysByCurationTag](#), 22

[getPathwaysByOntologyTerm](#), 23

[getPathwaysByParentOntologyTerm](#), 23

[getPathwayUrlsByCommunity](#), 24

[getRecentChanges](#), 24

[getRecentChangesIds](#), 25

[getRecentChangesNames](#), 25

[getXrefList](#), 26

  

[listCommunities](#), 26

[listOrganisms](#), 3, 27, 27, 28, 29

[listPathwayIds](#), 27

[listPathwayNames](#), 28

[listPathways](#), 27–29, 29

[listPathwayUrls](#), 29

  

[readGMT](#), 30

[readGMTnames](#), 31

[readPathwayGMT](#), 31

  

[wikipathwaysAPI](#), 32

[wikipathwaysGET](#), 33

[writeGMT](#), 33