

# 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.

**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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---

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 <a href="#">listOrganisms</a> .
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

**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

**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

**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**

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/BridgeDb>

**Details**

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

**Value**

A list of WPIDs

**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

**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 lists

**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/BridgeDB>

**Details**

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

**Value**

A list of lists

**Examples**

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

---

findPathwaysByLiterature      *Find Pathways By Literature*

---

**Description**

Retrieve a list of 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.

**Value**

A list of lists

**Examples**

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

---

findPathwaysByText      *Find Pathways By Text*

---

**Description**

Retrieve a list of pathways containing the query text.

**Usage**

```
findPathwaysByText(query)
```

**Arguments**

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

**Value**

A list of lists

**Examples**

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

---

findPathwaysByXref      *Find Pathways By Xref*

---

**Description**

Retrieve a list of 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 <a href="https://github.com/bridgedb/BridgeDb">https://github.com/bridgedb/BridgeDb</a>

**Details**

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

**Value**

A list of lists

**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

**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 lists

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

### Details

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

### Value

A list of lists

### Examples

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

---

getColoredPathway *Get Colored Pathway*

---

### Description

Retrieve a pathway image file with specified nodes colored by specified colors

### Usage

```
getColoredPathway(pathway, revision = 0, graphId = NULL,
  color = NULL, fileType = c("svg", "png", "pdf"))
```

### Arguments

pathway	WikiPathways identifier (WPID) for the pathway to download, e.g. WP4
revision	(integer, optional) Number to indicate a specific revision to download
graphId	A character string or vector indicating the nodes to color
color	(optional) String or vector indicating the highlighting color, e.g., #FF8855. Default is red. You can provide a single color for multiple nodes; otherwise color list and graphId must be the same length.
fileType	(optional) Image file format, e.g., svg (default), png or pdf.

**Value**

Image file

**Examples**

```
{
  svg = getColoredPathway(pathway="WP554", graphId="ef1f3")
  svg = getColoredPathway(pathway="WP554", graphId=c("ef1f3","e68e0"))
  svg = getColoredPathway(pathway="WP554", graphId=c("ef1f3","e68e0"),
                           color="00FF00")
  svg = getColoredPathway(pathway="WP554", graphId=c("ef1f3","e68e0"),
                           color=c("FF0000", "0000FF"))
  # writelines(svg, "pathway.svg")
}
```

---

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      *Get Curation Tags on a Pathway*

---

**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, timestampe and user

**Examples**

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

---

getEveryCurationTag      *Get Every Instance of a Curation Tag*

---

**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, timestampe 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, timestampe 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	<i>Get Pathway Info</i>
----------------	-------------------------

---

**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 list of pathway WPID, URL, name, species and latest revision

**Examples**

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

---

getPathwaysByCurationTag	<i>Get Pathways by Curation Tag</i>
--------------------------	-------------------------------------

---

**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      *Get Recent Changes*

---

**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      *Get WPIDs of Recent Changes*

---

**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 <https://github.com/bridgedb/BridgeDb>

### 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

**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

**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 list of lists

**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

**Examples**

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

---

wikipathwaysAPI	<i>Open Swagger docs for WikiPathways API</i>
-----------------	---

---

**Description**

Opens swagger docs in default browser for available API calls.

**Usage**

```
wikipathwaysAPI(base.url = .baseUr1)
```

**Arguments**

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

**Value**

New tab in default browser

**Examples**

```
{
  wikipathwaysAPI()
}
```

---

wikipathwaysGET

*WikiPathways GET*

---

**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')
}
```



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