

# Package ‘ReactomeContentService4R’

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**Title** Interface for the Reactome Content Service

**Version** 1.2.0

**Description** Reactome is a free, open-source, open access, curated and peer-reviewed knowledgebase of bio-molecular pathways. This package is to interact with the Reactome Content Service API. Pre-built functions would allow users to retrieve data and images that consist of proteins, pathways, and other molecules related to a specific gene or entity in Reactome.

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**BugReports** <https://github.com/reactome/ReactomeContentService4R/issues>

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discover	<i>Search engines discovery schema</i>
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**Description**

Search engines discovery schema

**Usage**

```
discover(event.id)
```

**Arguments**

event.id      stable id or db id of an Event

**Value**

a list of the event schema

**Examples**

```
discover("R-HSA-73893")
```

---

exportEventFile	<i>File exporter</i>
-----------------	----------------------

---

## Description

Export Reactome pathway diagrams in SBGN or SBML format.

## Usage

```
exportEventFile(  
  id,  
  format = c("sbgn", "sbml"),  
  writeToFile = TRUE,  
  file = NULL  
)
```

## Arguments

id	a stable or db id of an Event (Pathway or Reaction)
format	either in "sbgn" (SBGN, Systems Biology Graphical Notation) or "sbml" (SBML, Systems Biology Markup Language)
writeToFile	If set to TRUE, the returned data would be written into a file. If file=NULL, the output file will be automatically saved into the working directory and named based on the id and format
file	full path of the output file

## Value

a character object with the content of SBGN/SBML for a given id, or a SBGN/SBML file saved into the specified path. If the output is empty character or list, please check on [ContentService](#) or contact HelpDesk <help@reactome.org>.

## See Also

Other exporter: [exportImage\(\)](#)

## Examples

```
exportEventFile("R-HSA-432047", "sbgn", writeToFile=FALSE)  
## Not run: exportEventFile("R-HSA-68616", "sbml", file="orc.assembly.sbml")
```

---

 exportImage

*Image exporter*


---

### Description

The diagram exporter allows researchers to include images of their favorite pathway diagrams into their publications, posters or presentations. For details see Reactome [diagram exporter](#) guide.

### Usage

```
exportImage(
  id = NULL,
  output = c("diagram", "fireworks", "reaction"),
  species = NULL,
  format = c("png", "jpg", "jpeg", "svg", "gif"),
  quality = 5,
  flg = NULL,
  flgInteractors = TRUE,
  sel = NULL,
  title = TRUE,
  margin = 15,
  ehld = TRUE,
  diagramProfile = "Modern",
  token = NULL,
  resource = "TOTAL",
  analysisProfile = "Standard",
  expColumn = NULL,
  fireworksCoverage = FALSE,
  file = NULL,
  ...
)
```

### Arguments

id	stable or db id of a ReactionLikeEvent for "reaction" output, or id of an Event for "diagram"
output	type of exported image including "diagram", "fireworks", "reaction"
species	name or db id or taxon id of a species. Used in "fireworks" output
format	output format including "png", "jpg", "jpeg", "svg", "gif"
quality	result image quality between 1-10, default is 5
flg	gene name, protein or chemical identifier or Reactome identifier used to flag elements in the diagram
flgInteractors	defines whether to take into account interactors for the flagging
sel	highlight element(s) selection in the diagram
title	whether the name of the pathway is shown below

margin	defines the image margin between 0-20, default is 15
ehld	whether textbook-like illustration are taken into account
diagramProfile	color profile, "modern" or "standard"
token	token from Reactome <a href="#">Analysis Service</a>
resource	the analysis resource for which the results will be overlaid on top of the given pathways overview
analysisProfile	analysis color profile including "Standard", "Strosobar", "Copper%20plus"
expColumn	the specific expression analysis results column to be overlaid. If it is not specified (null), the first one is selected. If it is not specified (null) and format is gif, then an animated gif is generated with all the columns.
fireworksCoverage	set TRUE to overlay analysis coverage values in a fireworks image
file	full path of the output file
...	additional parameters passed to <code>magick::image_write()</code>

**Value**

an image saved into the specified path or a magick image object. More magick processing see the [package](#).

**See Also**

[magick](#) to further process the image object

Other exporter: [exportEventFile\(\)](#)

**Examples**

```
# fireworks
exportImage(species="9606", output="fireworks",
            format="jpg", quality=7)

## Not run:
# animated gifs of EHLs
# can use your own token from your Reactome Analysis
gif <- exportImage(id="R-HSA-69278", output="diagram", format="gif",
                  sel="R-HSA-69242", token="MjAyMDA2MTcyMDM5NDBfMzU2")
print(gif)

# reaction
exportImage(id="R-HSA-6787403", output="reaction", format="svg",
            flg="MT01", analysisProfile="Copper%20plus", file="R-HSA-6787403.svg")

## End(Not run)
```

---

`getEntities`*PhysicalEntity queries*

---

### Description

This method retrieves instances related to PhysicalEntity.

### Usage

```
getEntities(  
  id,  
  retrieval = c("subunits", "complexes", "componentOf", "otherForms"),  
  resource = "Reactome",  
  subunitsExcludeStructures = FALSE  
)
```

### Arguments

<code>id</code>	stable or db id of a Reactome PhysicalEntity, or id from resources other than Reactome
<code>retrieval</code>	entities to be retrieved, including "subunits", "complexes", "componentOf", "otherForms"
<code>resource</code>	resource other than Reactome, e.g. UniProt, Ensembl
<code>subunitsExcludeStructures</code>	whether contained Complexes and EntitySets are excluded when retrieving "subunits"

### Details

Details on options of retrieval arg:

- **subunits**: retrieves subunits that constitute any given Complex
- **complexes**: retrieves Complexes that contain the given id and resource
- **componentOf**: retrieves structures (Complexes and Sets) that include the given Entity as their component
- **otherForms**: retrieves Entities containing all other forms of the given PhysicalEntity

### Value

a dataframe containing requested information

### See Also

Other getContent: [getEventsHierarchy\(\)](#), [getOrthology\(\)](#), [getParticipants\(\)](#), [getPathways\(\)](#), [getPerson\(\)](#), [getSchemaClass\(\)](#), [getSpecies\(\)](#), [query\(\)](#)

### Examples

```
getEntities("R-HSA-5674003", retrieval="subunits")  
getEntities("P00533", retrieval="complexes", resource="UniProt")
```

---

getEventsHierarchy      *EventsHierarchy queries*

---

### Description

Events (Pathways and Reactions) in Reactome are organized in a hierarchical structure for every species. By following all hasEvent relationships, this method retrieves the full event hierarchy for any given **main species**.

### Usage

```
getEventsHierarchy(main.species)
```

### Arguments

main.species      name or taxon/db id or abbreviation of **main species** in Reactome

### Value

a nested dataframe containing full event hierarchy for a given main species

### See Also

[getSpecies](#) to get the main species list

Other getContent: [getEntities\(\)](#), [getOrthology\(\)](#), [getParticipants\(\)](#), [getPathways\(\)](#), [getPerson\(\)](#), [getSchemaClass\(\)](#), [getSpecies\(\)](#), [query\(\)](#)

### Examples

```
## Not run:  
getEventsHierarchy("chicken")  
getEventsHierarchy("XTR")  
  
## End(Not run)
```

---

getOrthology                      *Orthology related queries*

---

### Description

This function retrieves the orthology for any given Event or Entity in the specified species. More information on inferred events see <https://www.reactome.org/pages/documentation/electronically-inferred-events/>.

### Usage

```
getOrthology(id, species)
```

### Arguments

id	a stable or db id of an Event or Entity
species	name or taxon id or dbId or abbreviation of species

### Value

a list containing the orthology for given Event or Entity in the specified species

### See Also

Other getContent: [getEntities\(\)](#), [getEventsHierarchy\(\)](#), [getParticipants\(\)](#), [getPathways\(\)](#), [getPerson\(\)](#), [getSchemaClass\(\)](#), [getSpecies\(\)](#), [query\(\)](#)

### Examples

```
getOrthology("R-HSA-5674003", "pig")
```

---

getParticipants                      *Participants related queries*

---

### Description

Data in Reactome are organized in a hierarchical manner - Pathways contain Reactions, Reactions contain PhysicalEntities. This function is to get the participants of a given Event.

### Usage

```
getParticipants(  
  event.id,  
  retrieval = c("AllInstances", "PhysicalEntities", "ReferenceEntities",  
               "EventsInPathways")  
)
```



**Arguments**

event.id	a stable or db id of an Event (pathways and reactions)
retrieval	participants to be retrieved, including "AllInstances", "PhysicalEntities", "ReferenceEntities", "EventsInPathways"

**Details**

Details on options of retrieval arg:

- **AllInstances**: retrieves all participants (PhysicalEntities) from a given Event and their ReferenceEntities
- **PhysicalEntities**: retrieves all the PhysicalEntities that take part in a given Event
- **ReferenceEntities**: retrieves the ReferenceEntities for all PhysicalEntities in every constituent Pathway/Reaction
- **EventsInPathways**: recursively retrieves all the Events contained in any given Event

**Value**

a dataframe containing requested participants

**See Also**

Other getContent: [getEntities\(\)](#), [getEventsHierarchy\(\)](#), [getOrthology\(\)](#), [getPathways\(\)](#), [getPerson\(\)](#), [getSchemaClass\(\)](#), [getSpecies\(\)](#), [query\(\)](#)

**Examples**

```
getParticipants("R-HSA-6804741", "AllInstances")
getParticipants("R-HSA-69306", "EventsInPathways")
```

---

getPathways                      *Pathway related queries*

---

**Description**

To get the Events that contain the given PhysicalEntity or Event (i.e. subpathway).

**Usage**

```
getPathways(id, species = NULL, allForms = FALSE, top.level = FALSE)
```

**Arguments**

id	a stable or db id of a PhysicalEntity or Event present in the pathways
species	name or taxon id or dbId or abbreviation of species
allForms	if set to TRUE, all low level pathways that contain the given PhysicalEntity (not Event) in all forms returned
top.level	if set to TRUE, only top-level pathways returned

**Value**

a dataframe containing requested pathways

**See Also**

Other getContent: [getEntities\(\)](#), [getEventsHierarchy\(\)](#), [getOrthology\(\)](#), [getParticipants\(\)](#), [getPerson\(\)](#), [getSchemaClass\(\)](#), [getSpecies\(\)](#), [query\(\)](#)

**Examples**

```
getPathways("R-HSA-199420", "Homo sapiens")
```

---

getPerson

*Person queries*

---

**Description**

Retrieves a specific person's property by his/her name or OrcidId or dbId.

**Usage**

```
getPerson(name = NULL, id = NULL, attributes = NULL)
```

**Arguments**

name	Person's first or/and last name
id	Person's Orcid Id or DbId
attributes	Property for a person. Return all available attributes if it is not specified.

**Value**

a list of requested information

**See Also**

Other getContent: [getEntities\(\)](#), [getEventsHierarchy\(\)](#), [getOrthology\(\)](#), [getParticipants\(\)](#), [getPathways\(\)](#), [getSchemaClass\(\)](#), [getSpecies\(\)](#), [query\(\)](#)

**Examples**

```
getPerson(name="Robin Haw", attributes=c("displayName", "affiliation"))
```

---

getSchemaClass	<i>Schema class queries</i>
----------------	-----------------------------

---

### Description

Fetch instances by Class. All Classes see [Reactome data schema](#).

### Usage

```
getSchemaClass(  
  class,  
  species = NULL,  
  all = FALSE,  
  rows = 1000,  
  minimised = FALSE,  
  reference = FALSE  
)
```

### Arguments

class	schema class name
species	name or taxon id or dbId or abbreviation of species. Only Event and PhysicalEntity classes can specify species
all	to return ALL entries or not, default is FALSE
rows	the number of entries retrieved, default is 1000
minimised	to retrieve simplified entries (db id, stable id, displayName, type) or not, default is FALSE
reference	to retrieve simplified reference objects (db id, external identifier, external database name) or not, default is FALSE. Only for ReferenceEntity or ExternalOntology class

### Value

a sorted dataframe containing entries that belong to the specified schema class

### See Also

Other getContent: [getEntities\(\)](#), [getEventsHierarchy\(\)](#), [getOrthology\(\)](#), [getParticipants\(\)](#), [getPathways\(\)](#), [getPerson\(\)](#), [getSpecies\(\)](#), [query\(\)](#)

### Examples

```
## Not run:  
getSchemaClass(class="Drug", all=TRUE)  
  
## End(Not run)  
getSchemaClass(class="Regulation", rows=20, minimised=TRUE)  
getSchemaClass(class="Complex", species="pig", rows=10)
```

---

`getSpecies`*Species queries*

---

**Description**

This method retrieves the list of all or main species in Reactome knowledgebase.

**Usage**

```
getSpecies(main = FALSE)
```

**Arguments**

`main` determine whether return main species, which are those have either manually curated or computationally inferred pathways

**Value**

a dataframe of species information

**See Also**

Other `getContent`: [getEntities\(\)](#), [getEventsHierarchy\(\)](#), [getOrthology\(\)](#), [getParticipants\(\)](#), [getPathways\(\)](#), [getPerson\(\)](#), [getSchemaClass\(\)](#), [query\(\)](#)

**Examples**

```
# get a list of main species
getSpecies(main=TRUE)
```

---

`listSearchItems`*List filter items*

---

**Description**

To list the available filtering options for `searchQuery()`, and their counts.

**Usage**

```
listSearchItems(
  items = c("all", "species", "types", "compartments", "keywords"),
  facet = FALSE
)
```

**Arguments**

items	categories of query, including "species", "types", "compartments", "keywords", or "all"
facet	return faceting information or not

**Value**

available search items

**See Also**

[searchQuery](#) to search in Reactome

**Examples**

```
listSearchItems()
```

---

nonReactomeId	<i>Non-Reactome id mappings</i>
---------------	---------------------------------

---

**Description**

Mappings between non-Reactome identifiers and Reactome objects.

**Usage**

```
map2RefEntities(external.id)
```

```
map2Events(external.id, resource, species, mapTo = c("pathways", "reactions"))
```

```
event2Ids(event.id)
```

**Arguments**

external.id	an id from external dabatases, e.g. ChEBI, UniProt
resource	database name other than Reactome (e.g. UniProt, GeneCards)
species	name or taxon id or dbId or abbreviation of species
mapTo	retrieve Pathways or Reactions where an identifier can be mapped to
event.id	a stable or db id of an Event (Pathways and Reactions)

**Details**

Descriptions of functions:

- [map2RefEntities](#) maps a non-Reactome id to ReferenceEntities that store the given external id
- [map2Events](#) fetches Events related to a given non-Reactome id
- [event2Ids](#) gets all non-Reactome ids associated with a given Event

**Value**

a list of ReferenceEntity information  
a dataframe of Events associated with the given id  
non-Reactome ids associated with a given Event

**Examples**

```
## Not run:  
map2RefEntities("15377") #ChEBI id  
  
## End(Not run)  
map2Events("Q7Z569", resource="GeneCards", species="human", mapTo="reactions")  
event2Ids("R-HSA-69541")
```

---

query

*Common data retrieval*

---

**Description**

This function retrieves a Reactome Database object that has all its properties and direct relationships (relationships of depth 1) filled, while it also includes any second level relationships regarding regulations and catalysts.

**Usage**

```
query(id)
```

**Arguments**

id                    a stable or db id of **any** Reactome entry

**Value**

a list containing comprehensive information (all attributes) for a given id

**See Also**

[searchQuery](#) to search in Reactome

Other getContent: [getEntities\(\)](#), [getEventsHierarchy\(\)](#), [getOrthology\(\)](#), [getParticipants\(\)](#), [getPathways\(\)](#), [getPerson\(\)](#), [getSchemaClass\(\)](#), [getSpecies\(\)](#)

**Examples**

```
query("R-HSA-60140")
```

---

searchQuery	<i>Search query</i>
-------------	---------------------

---

### Description

Search for Reactome objects by name or identifiers.

### Usage

```
searchQuery(  
  query,  
  species = NULL,  
  types = NULL,  
  compartments = NULL,  
  keywords = NULL,  
  cluster = TRUE,  
  range = NULL  
)
```

### Arguments

query	name or dbId or stId of a search term from any class
species	name or taxon id or dbId or abbreviation of species
types	type filter, such as "Protein", "Complex", "Reaction", etc
compartments	compartment filter, such as "cytosol", "plasma membrane", "nucleoplasm", etc
keywords	keyword filter, such as "binds", "phosphorylates", "transports", etc
cluster	cluster returned data or not
range	start row and the number of rows to include, e.g. range = c(0, 2)

### Value

a list of information about the search term

### See Also

[listSearchItems](#) for available filters

### Examples

```
searchQuery(query="Biological oxidation", species="Mus musculus", types=c("Pathway", "Reaction"))
```

---

`spellCheck`*Spell-check suggestions for a given query*

---

**Description**

Spell-check suggestions for a given query

**Usage**

```
spellCheck(query)
```

**Arguments**

`query`            a search term

**Value**

spell-check suggestions for a given search term

**Examples**

```
spellCheck("intelukin")
```



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