

Package ‘rbioapi’

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Type Package

Title User-Friendly R Interface to Biologic Web Services' API

Version 0.7.4

Description Currently fully supports Enrichr, JASPAR, miEAA, PANTHER, Reactome, STRING, and UniProt! The goal of rbioapi is to provide a user-friendly and consistent interface to biological databases and services: In a way that insulates the user from technicalities of using web services API and creates a unified and easy-to-use interface to biological and medical web services. This an ongoing project; New databases and services will be added periodically. Feel free to suggest any databases or services you often use.

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URL <https://rbioapi.moosa-r.com>, <https://github.com/moosa-r/rbioapi>

BugReports <https://github.com/moosa-r/rbioapi/issues>

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rba_connection_test	<i>Test if the Supported Services Are Responding</i>
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Description

Run this function to test the internet connectivity of your device and the current status of the supported Services.

Usage

```
rba_connection_test(print_output = TRUE, diagnostics = FALSE)
```

Arguments

print_output	(Logical) (default = TRUE) Send the tests' output to the console?
diagnostics	(Logical) (default = FALSE) Show diagnostics and detailed messages with internal information.

Details

This function attempts to send a simple query to the supported services. If the service successfully responded, you will be informed with a success message; If not, the content of the error will be reported to you.

Please run this function if you encounter any errors while using rbioapi. Also, if you need to contact support, kindly call this function with 'diagnostic = TRUE' and include the output messages in your support request.

Value

Connection test for the supported servers will be displayed in console and the results will be invisibly returned as a list.

See Also

Other "Helper functions": [rba_options\(\)](#), [rba_pages\(\)](#)

Examples

```
rba_connection_test()
```

rba_enrichr

A One-step Wrapper for Gene-list Enrichment Using Enrichr

Description

This function is an easy-to-use wrapper for the multiple function calls necessary to enrich a given gene-list using Enrichr. see details section for more information.

Usage

```
rba_enrichr(  
  gene_list,  
  description = NULL,  
  gene_set_library = "all",  
  regex_library_name = TRUE,  
  organism = "human",  
  progress_bar = FALSE,  
  ...  
)
```

Arguments

<code>gene_list</code>	A vector with Entrez gene symbols.
<code>description</code>	(optional) A name or description to be associated with your uploaded gene-set to Enrichr servers.
<code>gene_set_library</code>	One of the: <ol style="list-style-type: none">1. "all" to select all of the available Enrichr gene-set libraries.2. A gene-set library name existed in the results retrieved via rba_enrichr_libs3. If <code>regex_library_name = TRUE</code>, A partially-matching name a regex pattern that correspond to one or more of Enrichr library names.
<code>regex_library_name</code>	logical: if TRUE (default) the supplied <code>gene_set_library</code> will be regarded as a regex or partially matching name. if FALSE, <code>gene_set_library</code> will be considered exact match.

organism	(default = "human") Which model organism version of Enrichr to use? Available options are: "human", (H. sapiens & M. musculus), "fly" (D. melanogaster), "yeast" (S. cerevisiae), "worm" (C. elegans) and "fish" (D. rerio).
progress_bar	logical: In case of selecting multiple Enrichr libraries, should a progress bar be displayed?
...	rbiopi option(s). See rba_options 's arguments manual for more information on available options.

Details

This function will call other `rba_enrichr_***` functions with the following order:

1. (If necessary) Call `rba_enrichr_libs` to obtain a list of available libraries in Enrichr.
2. Call `rba_enrichr_add_list` to upload your gene-list and obtain a 'user list ID'.
3. Call `rba_enrichr_enrich` to enrich the gene-list against one or multiple Enrichr libraries

Value

A list containing data frames of the enrichment results of your supplied gene-list against the selected Enrichr libraries.

Corresponding API Resources

"GET <https://maayanlab.cloud/Enrichr/datasetStatistics>"
 "POST <https://maayanlab.cloud/Enrichr/addList>"
 "GET <https://maayanlab.cloud/Enrichr/enrich>"

References

- Chen EY, Tan CM, Kou Y, Duan Q, Wang Z, Meirelles GV, Clark NR, Ma'ayan A. Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. *BMC Bioinformatics*. 2013;128(14).
- Kuleshov MV, Jones MR, Rouillard AD, Fernandez NF, Duan Q, Wang Z, Koplev S, Jenkins SL, Jagodnik KM, Lachmann A, McDermott MG, Monteiro CD, Gundersen GW, Ma'ayan A. Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. *Nucleic Acids Research*. 2016; gkw377.
- [Enrichr API Documentation](#)

See Also

Other "Enrichr": `rba_enrichr_add_list()`, `rba_enrichr_enrich()`, `rba_enrichr_gene_map()`, `rba_enrichr_libs()`, `rba_enrichr_view_list()`

Examples

```
rba_enrichr(gene_list = c("TP53", "TNF", "EGFR"))
```

```
rba_enrichr(gene_list = c("TP53", "TNF", "EGFR"),  
  gene_set_library = "GO_Molecular_Function_2017",  
  regex_library_name = FALSE)
```

```
rba_enrichr(gene_list = c("TP53", "TNF", "EGFR"),  
  gene_set_library = "go",  
  regex_library_name = TRUE)
```

rba_enrichr_add_list *Upload Your Gene-List to Enrichr*

Description

Prior to perform enrichment, Enrichr requires you to upload your gene-list and retrieve a 'user list ID'.

Usage

```
rba_enrichr_add_list(gene_list, description = NULL, organism = "human", ...)
```

Arguments

gene_list	A vector with Entrez gene symbols.
description	(optional) A name or description to be associated with your uploaded gene-set to Enrichr servers.
organism	(default = "human") Which model organism version of Enrichr to use? Available options are: "human", (H. sapiens & M. musculus), "fly" (D. melanogaster), "yeast" (S. cerevisiae), "worm" (C. elegans) and "fish" (D. rerio).
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

Note that using [rba_enrichr](#) is a more convenient way to automatically perform this and other required function calls to enrich your input gene-set.

Value

A list with two unique IDs for your uploaded gene sets.

Corresponding API Resources

"POST <https://maayanlab.cloud/Enrichr/addList>"

References

- Chen EY, Tan CM, Kou Y, Duan Q, Wang Z, Meirelles GV, Clark NR, Ma'ayan A. Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. *BMC Bioinformatics*. 2013;128(14).
- Kuleshov MV, Jones MR, Rouillard AD, Fernandez NF, Duan Q, Wang Z, Koplev S, Jenkins SL, Jagodnik KM, Lachmann A, McDermott MG, Monteiro CD, Gundersen GW, Ma'ayan A. Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. *Nucleic Acids Research*. 2016; gkw377.
- [Enrichr API Documentation](#)

See Also

[rba_enrichr](#)

Other "Enrichr": [rba_enrichr_enrich\(\)](#), [rba_enrichr_gene_map\(\)](#), [rba_enrichr_libs\(\)](#), [rba_enrichr_view_list\(\)](#)
[rba_enrichr\(\)](#)

Examples

```
rba_enrichr_add_list(gene_list = c("TP53", "TNF", "EGFR"),  
                    description = "tumoral genes")
```

rba_enrichr_enrich *Get Enrichr Enrichment Results*

Description

This function which will retrieve the enrichment results of your supplied gene-list id against one or multiple Enrichr libraries.

Usage

```
rba_enrichr_enrich(  
  user_list_id,  
  gene_set_library = "all",  
  regex_library_name = TRUE,  
  organism = "human",  
  progress_bar = TRUE,  
  ...  
)
```


Arguments

user_list_id	An ID returned to you after uploading a gene list using rba_enrichr_add_list
gene_set_library	One of the: <ol style="list-style-type: none"> 1. "all" to select all of the available Enrichr gene-set libraries. 2. A gene-set library name existed in the results retrieved via rba_enrichr_libs 3. If <code>regex_library_name = TRUE</code>, A partially-matching name a regex pattern that correspond to one or more of Enrichr library names.
regex_library_name	logical: if TRUE (default) the supplied gene_set_library will be regarded as a regex or partially matching name. if FALSE, gene_set_library will be considered exact match.
organism	(default = "human") Which model organism version of Enrichr to use? Available options are: "human", (H. sapiens & M. musculus), "fly" (D. melanogaster), "yeast" (S. cerevisiae), "worm" (C. elegans) and "fish" (D. rerio).
progress_bar	logical: In case of selecting multiple Enrichr libraries, should a progress bar be displayed?
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

Note that using [rba_enrichr](#) is a more convenient way to automatically perform this and other required function calls to enrich your input gene-set.

Value

A list containing data frames of the enrichment results of your supplied gene-list against the selected Enrichr libraries.

Corresponding API Resources

"GET <https://maayanlab.cloud/Enrichr/enrich>"

References

- Chen EY, Tan CM, Kou Y, Duan Q, Wang Z, Meirelles GV, Clark NR, Ma'ayan A. Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. BMC Bioinformatics. 2013;128(14).
- Kuleshov MV, Jones MR, Rouillard AD, Fernandez NF, Duan Q, Wang Z, Koplev S, Jenkins SL, Jagodnik KM, Lachmann A, McDermott MG, Monteiro CD, Gunderson GW, Ma'ayan A. Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. Nucleic Acids Research. 2016; gkw377.
- [Enrichr API Documentation](#)

See Also[rba_enrichr](#)Other "Enrichr": [rba_enrichr_add_list\(\)](#), [rba_enrichr_gene_map\(\)](#), [rba_enrichr_libs\(\)](#), [rba_enrichr_view_list\(\)](#), [rba_enrichr\(\)](#)**Examples**

```
## Not run:
rba_enrichr_enrich(user_list_id = "11111")

## End(Not run)
## Not run:
rba_enrichr_enrich(user_list_id = "11111",
  gene_set_library = "GO_Molecular_Function_2017",
  regex_library_name = FALSE)

## End(Not run)
## Not run:
rba_enrichr_enrich(user_list_id = "11111",
  gene_set_library = "go",
  regex_library_name = TRUE)

## End(Not run)
```

rba_enrichr_gene_map *Find Enrichr Terms That Contain a Given Gene*

Description

This function will search the gene and retrieve a list of Enrichr Terms that contains that gene.

Usage

```
rba_enrichr_gene_map(gene, catagorize = FALSE, organism = "human", ...)
```

Arguments

gene	character: An Entrez gene symbol.
catagorize	logical: Should the category informations be included?
organism	(default = "human") Which model organism version of Enrichr to use? Available options are: "human", (H. sapiens & M. musculus), "fly" (D. melanogaster), "yeast" (S. cerevisiae), "worm" (C. elegans) and "fish" (D. rerio).
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

a list containing the search results of your supplied gene.

Corresponding API Resources

"GET <https://maayanlab.cloud/Enrichr/genemap>"

References

- Chen EY, Tan CM, Kou Y, Duan Q, Wang Z, Meirelles GV, Clark NR, Ma'ayan A. Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. *BMC Bioinformatics*. 2013;128(14).
- Kuleshov MV, Jones MR, Rouillard AD, Fernandez NF, Duan Q, Wang Z, Koplev S, Jenkins SL, Jagodnik KM, Lachmann A, McDermott MG, Monteiro CD, Gundersen GW, Ma'ayan A. Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. *Nucleic Acids Research*. 2016; gkw377.
- [Enrichr API Documentation](#)

See Also

Other "Enrichr": [rba_enrichr_add_list\(\)](#), [rba_enrichr_enrich\(\)](#), [rba_enrichr_libs\(\)](#), [rba_enrichr_view_list\(\)](#)
[rba_enrichr\(\)](#)

Examples

```
rba_enrichr_gene_map(gene = "p53")
```

```
rba_enrichr_gene_map(gene = "p53", catagorize = TRUE)
```

rba_enrichr_libs

Retrieve a List of available libraries from Enrichr

Description

This function will retrieve a list of available libraries in Enrichr with their statistics. And by default, will save those names as a global option ("rba_enrichr_libs") to be available for other Enrichr functions that internally require the names of Enrichr libraries.

Usage

```
rba_enrichr_libs(store_in_options = FALSE, organism = "human", ...)
```

Arguments

store_in_options	logical: (default = TRUE) Should a list of available Enrichr libraries be saved as a global option?
organism	(default = "human") Which model organism version of Enrichr to use? Available options are: "human", (H. sapiens & M. musculus), "fly" (D. melanogaster), "yeast" (S. cerevisiae), "worm" (C. elegans) and "fish" (D. rerio).
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

You should call this function once per R session with the argument 'store_in_options = TRUE' before using [rba_enrichr_enrich](#) or [rba_enrichr](#).

Nevertheless, rbioapi will do this for you in the background at the first time you call any function which requires this.

Note that using [rba_enrichr](#) is a more convenient way to automatically perform this and other required function calls to enrich your input gene-set.

Value

A data frame with the names of available library in Enrichr and their statistics.

Corresponding API Resources

"GET <https://maayanlab.cloud/Enrichr/datasetStatistics>"

References

- Chen EY, Tan CM, Kou Y, Duan Q, Wang Z, Meirelles GV, Clark NR, Ma'ayan A. Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. *BMC Bioinformatics*. 2013;128(14).
- Kuleshov MV, Jones MR, Rouillard AD, Fernandez NF, Duan Q, Wang Z, Koplev S, Jenkins SL, Jagodnik KM, Lachmann A, McDermott MG, Monteiro CD, Gundersen GW, Ma'ayan A. Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. *Nucleic Acids Research*. 2016; gkw377.
- [Enrichr API Documentation](#)

See Also

[rba_enrichr](#)

Other "Enrichr": [rba_enrichr_add_list\(\)](#), [rba_enrichr_enrich\(\)](#), [rba_enrichr_gene_map\(\)](#), [rba_enrichr_view_list\(\)](#), [rba_enrichr\(\)](#)

Examples

```
rba_enrichr_libs()
```

rba_enrichr_view_list *View an Uploaded Gene List*

Description

Retrieve a list of uploaded genes under a 'user list ID'.

Usage

```
rba_enrichr_view_list(user_list_id, organism = "human", ...)
```

Arguments

user_list_id	a user_list_id returned to you after uploading a gene list using rba_enrichr_add_list
organism	(default = "human") Which model organism version of Enrichr to use? Available options are: "human", (H. sapiens & M. musculus), "fly" (D. melanogaster), "yeast" (S. cerevisiae), "worm" (C. elegans) and "fish" (D. rerio).
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A list containing the genes and description available under the supplied user_list_id

Corresponding API Resources

"GET <https://maayanlab.cloud/Enrichr/view>"

References

- Chen EY, Tan CM, Kou Y, Duan Q, Wang Z, Meirelles GV, Clark NR, Ma'ayan A. Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. BMC Bioinformatics. 2013;128(14).
- Kuleshov MV, Jones MR, Rouillard AD, Fernandez NF, Duan Q, Wang Z, Koplev S, Jenkins SL, Jagodnik KM, Lachmann A, McDermott MG, Monteiro CD, Gundersen GW, Ma'ayan A. Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. Nucleic Acids Research. 2016; gkw377.
- [Enrichr API Documentation](#)

See Also

Other "Enrichr": [rba_enrichr_add_list\(\)](#), [rba_enrichr_enrich\(\)](#), [rba_enrichr_gene_map\(\)](#), [rba_enrichr_libs\(\)](#), [rba_enrichr\(\)](#)

Examples

```
## Not run:  
rba_enrichr_view_list(user_list_id = 11111)  
  
## End(Not run)
```

rba_jaspar_collections

List collections available in JASPAR

Description

JASPAR organizes matrix profiles into collections. Using this function, you can retrieve a list of available collections in a JASPAR release.

Usage

```
rba_jaspar_collections(release = 2020, ...)
```

Arguments

release	Numeric: (default = 2020) Which JASPAR database release to use? Available options are: 2014, 2016, 2018, and 2020.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A data frame with collections' names and URLs.

Corresponding API Resources

"GET "http://jaspar.genereg.net/api/v1/collections/"

References

- Fornes O, Castro-Mondragon JA, Khan A, et al. JASPAR 2020: update of the open-access database of transcription factor binding profiles. *Nucleic Acids Res.* 2019; doi: 10.1093/nar/gkz1001
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. *Bioinformatics*, 2017, doi: 10.1093/bioinformatics/btx804

- Khan, A. et al. JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework. *Nucleic Acids Res.* 2018; 46:D260–D266, doi: 10.1093/nar/gkx1126
- [JASPAR API Documentation](#)

See Also

Other "JASPAR": [rba_jaspar_collections_matrices\(\)](#), [rba_jaspar_matrix_search\(\)](#), [rba_jaspar_matrix_version\(\)](#), [rba_jaspar_matrix\(\)](#), [rba_jaspar_releases\(\)](#), [rba_jaspar_sites\(\)](#), [rba_jaspar_species_matrices\(\)](#), [rba_jaspar_species\(\)](#), [rba_jaspar_taxons_matrices\(\)](#), [rba_jaspar_taxons\(\)](#), [rba_jaspar_tffm_search\(\)](#), [rba_jaspar_tffm\(\)](#)

Examples

```
rba_jaspar_collections(release = 2020)
```

```
rba_jaspar_collections_matrices
```

List matrices available in a JASPAR collection

Description

Using this function you can list all matrix profiles that are available in a collection from a JASPAR release.

Usage

```
rba_jaspar_collections_matrices(  
  collection,  
  release = 2020,  
  only_last_version = FALSE,  
  search = NULL,  
  order = NULL,  
  page_size = 1000,  
  page = 1,  
  ...  
)
```

Arguments

collection	JASPAR Collection's name. See JASPAR Collections for information. The accepted values are: "CORE", "CNE", "PHYLOFACTS", "SPLICE", "POLII", "FAM", "PBM", "PBM_HOMEEO", "PBM_HLH", and "UNVALIDATED".
release	Numeric: (default = 2020) Which JASPAR database release to use? Available options are: 2014, 2016, 2018, and 2020.

<code>only_last_version</code>	Logical: (default = FALSE) If TRUE, only the latest version of a matrix profile will be returned.
<code>search</code>	Character: A search term.
<code>order</code>	Character: A character string or a vector of character strings of field names that will be used to order the results. Providing multiple field names is supported. You can also use prefix "-" before a field name to indicate reverse ordering.
<code>page_size</code>	Numeric: (default = 1000) This resource returns paginated results. What is the maximum numbers of results that you want to retrieve per a page? Accepted values are between 1 and 1000.
<code>page</code>	Numeric: Which page of the results to retrieve? The accepted values depend on the page size and number of results.
<code>...</code>	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

The results are paginated. You can control the page's size number with the function's arguments. Also, you can use [rba_pages](#) to automatically iterate over multiple pages.

Value

A list that contains a data frame with information of matrix profiles available in the collection.

Corresponding API Resources

"GET "http://jaspar.genereg.net/api/v1/collections/collection/"

References

- Fornes O, Castro-Mondragon JA, Khan A, et al. JASPAR 2020: update of the open-access database of transcription factor binding profiles. *Nucleic Acids Res.* 2019; doi: 10.1093/nar/gkz1001
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. *Bioinformatics*, 2017, doi: 10.1093/bioinformatics/btx804
- Khan, A. et al. JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework. *Nucleic Acids Res.* 2018; 46:D260–D266, doi: 10.1093/nar/gkx1126
- [JASPAR API Documentation](#)

See Also

Other "JASPAR": [rba_jaspar_collections\(\)](#), [rba_jaspar_matrix_search\(\)](#), [rba_jaspar_matrix_versions\(\)](#), [rba_jaspar_matrix\(\)](#), [rba_jaspar_releases\(\)](#), [rba_jaspar_sites\(\)](#), [rba_jaspar_species_matrices\(\)](#), [rba_jaspar_species\(\)](#), [rba_jaspar_taxons_matrices\(\)](#), [rba_jaspar_taxons\(\)](#), [rba_jaspar_tffm_search\(\)](#), [rba_jaspar_tffm\(\)](#)

Examples

```
rba_jaspar_collections_matrices(collection = "CORE",
  release = 2020,
  page_size = 100,
  page = 2)
```

rba_jaspar_matrix	<i>Get a Position Frequency Matrices (PFM) with annotations</i>
-------------------	---

Description

Using this function you can retrieve a Position Frequency Matrices (PFM) associated with a matrix profile Identifier along with its details and annotations. If a base ID (i.e. without version suffix) was supplied, the latest version will be returned.

Usage

```
rba_jaspar_matrix(matrix_id, file_format = NULL, save_to = NULL, ...)
```

Arguments

matrix_id	Character: A matrix profile Identifier. It has "base_id.version" naming schema.
file_format	Character: Instead of returning a R object, you can directly download the profile matrix in file with this format. Supported formats are: "yaml", "jaspar", "transfac", "meme" and "pfm"
save_to	NULL or Character: <ul style="list-style-type: none"> • NULL: (only if file_format was supplied) Save the file to an automatically-generated path. • Character string: A valid file or directory path to save the file to.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A list that contains the PFM along with its details and annotations. If file_format was supplied, an un-parsed character string with the file's content.

Corresponding API Resources

"GET "http://jaspar.genereg.net/api/v1/matrix/matrix_id/"

References

- Fornes O, Castro-Mondragon JA, Khan A, et al. JASPAR 2020: update of the open-access database of transcription factor binding profiles. *Nucleic Acids Res.* 2019; doi: 10.1093/nar/gkz1001
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. *Bioinformatics*, 2017, doi: 10.1093/bioinformatics/btx804
- Khan, A. et al. JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework. *Nucleic Acids Res.* 2018; 46:D260–D266, doi: 10.1093/nar/gkx1126
- [JASPAR API Documentation](#)

See Also

Other "JASPAR": [rba_jaspar_collections_matrices\(\)](#), [rba_jaspar_collections\(\)](#), [rba_jaspar_matrix_search\(\)](#), [rba_jaspar_matrix_versions\(\)](#), [rba_jaspar_releases\(\)](#), [rba_jaspar_sites\(\)](#), [rba_jaspar_species_matrices\(\)](#), [rba_jaspar_species\(\)](#), [rba_jaspar_taxons_matrices\(\)](#), [rba_jaspar_taxons\(\)](#), [rba_jaspar_tffm_search\(\)](#), [rba_jaspar_tffm\(\)](#)

Examples

```
rba_jaspar_matrix("MA0600.2")

## Not run:
rba_jaspar_matrix(matrix_id = "MA0600.2",
                  file_format = "meme",
                  save_to = "my_matrix.meme")

## End(Not run)
```

rba_jaspar_matrix_search

Search matrix profiles available in JASPAR

Description

You can use this function to list the JASPAR matrix profiles that match your search query, or run the function without any arguments to return a list of every matrix profile available in the latest release.

Usage

```
rba_jaspar_matrix_search(
  term = NULL,
  tf_name = NULL,
  tf_class = NULL,
  tf_family = NULL,
  tax_group = NULL,
```

```

    tax_id = NULL,
    data_type = NULL,
    collection = NULL,
    release = 2020,
    only_last_version = FALSE,
    order = NULL,
    page_size = 1000,
    page = 1,
    ...
)

```

Arguments

term	Character: A search term.
tf_name	Character: Transcription factor names (Case-sensitive).
tf_class	Character: Transcription factor class
tf_family	Character: Transcription factor family
tax_group	Character: Taxonomic group. Use rba_jaspar_taxons to get a list of supported Taxonomic groups.
tax_id	Numeric: NCBI taxonomic Identifier of species. Use rba_jaspar_species to get a list of supported Species.
data_type	Character: Type of the data (i.e The Methodology used for matrix construction). For example: "ChIP-seq", "PBM"
collection	Character: JASPAR matrix profile collection name. USE rba_jaspar_collections to get a list of collection names.
release	Numeric: (default = 2020) Which JASPAR database release to use? Available options are: 2014, 2016, 2018, and 2020.
only_last_version	Logical: (default = FALSE) If TRUE, only the latest version of a matrix profile will be returned.
order	Character: A character string or a vector of character strings of field names that will be used to order the results. Providing multiple field names is supported. You can also use prefix "-" before a field name to indicate reverse ordering.
page_size	Numeric: (default = 1000) This resource returns paginated results. What is the maximum numbers of results that you want to retrieve per a page? Accepted values are between 1 and 1000.
page	Numeric: Which page of the results to retrieve? The accepted values depend on the page size and number of results.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

Note that this is a search function. Thus, you are not required to fill every argument; You may use whatever combinations of arguments you see fit for your query.

The results are paginated. You can control the page's size number with the function's arguments. Also, you can use [rba_pages](#) to automatically iterate over multiple pages.

Value

A list that contains a data frame of matrix profiles' information.

Corresponding API Resources

"GET "http://jaspar.genereg.net/api/v1/api/v1/matrix/"

References

- Fornes O, Castro-Mondragon JA, Khan A, et al. JASPAR 2020: update of the open-access database of transcription factor binding profiles. *Nucleic Acids Res.* 2019; doi: 10.1093/nar/gkz1001
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. *Bioinformatics*, 2017, doi: 10.1093/bioinformatics/btx804
- Khan, A. et al. JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework. *Nucleic Acids Res.* 2018; 46:D260–D266, doi: 10.1093/nar/gkx1126
- [JASPAR API Documentation](#)

See Also

Other "JASPAR": [rba_jaspar_collections_matrices\(\)](#), [rba_jaspar_collections\(\)](#), [rba_jaspar_matrix_versions](#), [rba_jaspar_matrix\(\)](#), [rba_jaspar_releases\(\)](#), [rba_jaspar_sites\(\)](#), [rba_jaspar_species_matrices\(\)](#), [rba_jaspar_species\(\)](#), [rba_jaspar_taxons_matrices\(\)](#), [rba_jaspar_taxons\(\)](#), [rba_jaspar_tffm_search\(\)](#), [rba_jaspar_tffm\(\)](#)

Examples

```
rba_jaspar_matrix_search(term = "FOX")
rba_jaspar_matrix_search(tf_name = "FOXP3")
rba_jaspar_matrix_search(tf_name = "FOXP3", only_last_version = TRUE)
rba_jaspar_matrix_search(tf_class = "Zipper-Type")
rba_jaspar_matrix_search(tax_group = "insects")
rba_jaspar_matrix_search(page_size = 100)
```

`rba_jaspar_matrix_versions`*List matrix profile versions associated with a base ID*

Description

Since JASPAR release 2010, the matrix profiles are versioned; So, a matrix profile Identifier has "base_id.version" naming schema. Using this function you can retrieve a list of matrix profiles associated with a base (stable) ID.

Usage

```
rba_jaspar_matrix_versions(base_id, order = NULL, ...)
```

Arguments

<code>base_id</code>	Character: A base (stable) Identifier. A matrix profile identifier has "base_id.version" naming schema
<code>order</code>	Character: A character string or a vector of character strings of field names that will be used to order the results. Providing multiple field names is supported. You can also use prefix "-" before a field name to indicate reverse ordering.
<code>...</code>	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A data frame of matrix profiles' versions information.

Corresponding API Resources

```
"GET "http://jaspar.genereg.net/api/v1/matrix/base_id/versions/"
```

References

- Fornes O, Castro-Mondragon JA, Khan A, et al. JASPAR 2020: update of the open-access database of transcription factor binding profiles. *Nucleic Acids Res.* 2019; doi: 10.1093/nar/gkz1001
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. *Bioinformatics*, 2017, doi: 10.1093/bioinformatics/btx804
- Khan, A. et al. JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework. *Nucleic Acids Res.* 2018; 46:D260–D266, doi: 10.1093/nar/gkx1126
- [JASPAR API Documentation](#)

See Also

Other "JASPAR": [rba_jaspar_collections_matrices\(\)](#), [rba_jaspar_collections\(\)](#), [rba_jaspar_matrix_search\(\)](#), [rba_jaspar_matrix\(\)](#), [rba_jaspar_releases\(\)](#), [rba_jaspar_sites\(\)](#), [rba_jaspar_species_matrices\(\)](#), [rba_jaspar_species\(\)](#), [rba_jaspar_taxons_matrices\(\)](#), [rba_jaspar_taxons\(\)](#), [rba_jaspar_tffm_search\(\)](#), [rba_jaspar_tffm\(\)](#)

Examples

```
rba_jaspar_matrix_versions("MA0600")
```

rba_jaspar_releases *Get information about JASPAR database releases*

Description

If a release number was supplied, this function will return the details of that release. Otherwise, if the function was called without "release" argument, a list of all JASPAR database releases will be returned.

Usage

```
rba_jaspar_releases(release_number = NULL, ...)
```

Arguments

`release_number` Numeric: Which JASPAR database release number information's to retrieve? If left NULL (the default), a list of all JASPAR database releases will be returned. Available options are 1 to 8.

`...` rbioapi option(s). See [rba_options](#)'s arguments manual for more information on available options.

Value

A list that contains all JASPAR database releases' information or details of a particular release.

Corresponding API Resources

"GET "http://jaspar.genereg.net/api/v1/releases/" "GET "http://jaspar.genereg.net/api/v1/releases/release_number/"

References

- Fornes O, Castro-Mondragon JA, Khan A, et al. JASPAR 2020: update of the open-access database of transcription factor binding profiles. *Nucleic Acids Res.* 2019; doi: 10.1093/nar/gkz1001
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. *Bioinformatics*, 2017, doi: 10.1093/bioinformatics/btx804
- Khan, A. et al. JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework. *Nucleic Acids Res.* 2018; 46:D260–D266, doi: 10.1093/nar/gkx1126
- [JASPAR API Documentation](#)

See Also

Other "JASPAR": [rba_jaspar_collections_matrices\(\)](#), [rba_jaspar_collections\(\)](#), [rba_jaspar_matrix_search\(\)](#), [rba_jaspar_matrix_versions\(\)](#), [rba_jaspar_matrix\(\)](#), [rba_jaspar_sites\(\)](#), [rba_jaspar_species_matrices\(\)](#), [rba_jaspar_species\(\)](#), [rba_jaspar_taxons_matrices\(\)](#), [rba_jaspar_taxons\(\)](#), [rba_jaspar_tffm_search\(\)](#), [rba_jaspar_tffm\(\)](#)

Examples

```
rba_jaspar_releases()
rba_jaspar_releases(7)
```

rba_jaspar_sites	<i>Get binding sites of a matrix profile</i>
------------------	--

Description

Use this function to retrieve a list of transcription factor binding sites associated with a matrix profile.

Usage

```
rba_jaspar_sites(matrix_id, ...)
```

Arguments

matrix_id	Character: A matrix profile Identifier. It has "base_id.version" naming schema.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A list that contains a data frame with binding sites information.

Corresponding API Resources

"GET "http://jaspar.genereg.net/api/v1/sites/matrix_id/"

References

- Fornes O, Castro-Mondragon JA, Khan A, et al. JASPAR 2020: update of the open-access database of transcription factor binding profiles. *Nucleic Acids Res.* 2019; doi: 10.1093/nar/gkz1001
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. *Bioinformatics*, 2017, doi: 10.1093/bioinformatics/btx804
- Khan, A. et al. JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework. *Nucleic Acids Res.* 2018; 46:D260–D266, doi: 10.1093/nar/gkx1126
- [JASPAR API Documentation](#)

See Also

Other "JASPAR": [rba_jaspar_collections_matrices\(\)](#), [rba_jaspar_collections\(\)](#), [rba_jaspar_matrix_search\(\)](#), [rba_jaspar_matrix_versions\(\)](#), [rba_jaspar_matrix\(\)](#), [rba_jaspar_releases\(\)](#), [rba_jaspar_species_matrices\(\)](#), [rba_jaspar_species\(\)](#), [rba_jaspar_taxons_matrices\(\)](#), [rba_jaspar_taxons\(\)](#), [rba_jaspar_tffm_search\(\)](#), [rba_jaspar_tffm\(\)](#)

Examples

```
rba_jaspar_sites("MA0600.1")
```

rba_jaspar_species *List available species in JASPAR*

Description

JASPAR organizes matrix profiles from multiple species in six taxonomic groups. Use this function to retrieve a list of available species in a JASPAR database release.

Usage

```
rba_jaspar_species(release = 2020, search = NULL, order = NULL, ...)
```

Arguments

release	Numeric: (default = 2020) Which JASPAR database release to use? Available options are: 2014, 2016, 2018, and 2020.
search	Character: A search term.

order	Character: A character string or a vector of character strings of field names that will be used to order the results. Providing multiple field names is supported. You can also use prefix "-" before a field name to indicate reverse ordering.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A data frame with information of available species.

Corresponding API Resources

"GET "http://jaspar.genereg.net/api/v1/species/"

References

- Fornes O, Castro-Mondragon JA, Khan A, et al. JASPAR 2020: update of the open-access database of transcription factor binding profiles. *Nucleic Acids Res.* 2019; doi: 10.1093/nar/gkz1001
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. *Bioinformatics*, 2017, doi: 10.1093/bioinformatics/btx804
- Khan, A. et al. JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework. *Nucleic Acids Res.* 2018; 46:D260–D266, doi: 10.1093/nar/gkx1126
- [JASPAR API Documentation](#)

See Also

Other "JASPAR": [rba_jaspar_collections_matrices\(\)](#), [rba_jaspar_collections\(\)](#), [rba_jaspar_matrix_search\(\)](#), [rba_jaspar_matrix_versions\(\)](#), [rba_jaspar_matrix\(\)](#), [rba_jaspar_releases\(\)](#), [rba_jaspar_sites\(\)](#), [rba_jaspar_species_matrices\(\)](#), [rba_jaspar_taxons_matrices\(\)](#), [rba_jaspar_taxons\(\)](#), [rba_jaspar_tffm_search\(\)](#), [rba_jaspar_tffm\(\)](#)

Examples

```
rba_jaspar_species(release = 2020)
```

 rba_jaspar_species_matrices

List matrices available in JASPAR of a species

Description

JASPAR curates matrix profiles from multiple species in six taxonomic groups. Using this function you can list all matrix profiles that are available in a JASPAR release from a species.

Usage

```
rba_jaspar_species_matrices(
  tax_id,
  release = 2020,
  only_last_version = FALSE,
  search = NULL,
  order = NULL,
  page_size = 1000,
  page = 1,
  ...
)
```

Arguments

tax_id	Numeric: NCBI taxonomic Identifier of species. Use rba_jaspar_species to get a list of supported Species.
release	Numeric: (default = 2020) Which JASPAR database release to use? Available options are: 2014, 2016, 2018, and 2020.
only_last_version	Logical: (default = FALSE) If TRUE, only the latest version of a matrix profile will be returned.
search	Character: A search term.
order	Character: A character string or a vector of character strings of field names that will be used to order the results. Providing multiple field names is supported. You can also use prefix "-" before a field name to indicate reverse ordering.
page_size	Numeric: (default = 1000) This resource returns paginated results. What is the maximum numbers of results that you want to retrieve per a page? Accepted values are between 1 and 1000.
page	Numeric: Which page of the results to retrieve? The accepted values depend on the page size and number of results.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

The results are paginated. You can control the page's size number with the function's arguments. Also, you can use [rba_pages](#) to automatically iterate over multiple pages.

Value

A list that contains a data frame with information of matrix profiles available for the species.

Corresponding API Resources

"GET "http://jaspar.genereg.net/api/v1/species/tax_id/"

References

- Fornes O, Castro-Mondragon JA, Khan A, et al. JASPAR 2020: update of the open-access database of transcription factor binding profiles. *Nucleic Acids Res.* 2019; doi: 10.1093/nar/gkz1001
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. *Bioinformatics*, 2017, doi: 10.1093/bioinformatics/btx804
- Khan, A. et al. JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework. *Nucleic Acids Res.* 2018; 46:D260–D266, doi: 10.1093/nar/gkx1126
- [JASPAR API Documentation](#)

See Also

Other "JASPAR": [rba_jaspar_collections_matrices\(\)](#), [rba_jaspar_collections\(\)](#), [rba_jaspar_matrix_search\(\)](#), [rba_jaspar_matrix_versions\(\)](#), [rba_jaspar_matrix\(\)](#), [rba_jaspar_releases\(\)](#), [rba_jaspar_sites\(\)](#), [rba_jaspar_species\(\)](#), [rba_jaspar_taxons_matrices\(\)](#), [rba_jaspar_taxons\(\)](#), [rba_jaspar_tffm_search\(\)](#), [rba_jaspar_tffm\(\)](#)

Examples

```
rba_jaspar_species_matrices(tax_id = 9606, page_size = 100)
```

rba_jaspar_taxons *List available taxonomic groups in JASPAR*

Description

JASPAR organizes matrix profiles from multiple species in six taxonomic groups. Use this function to retrieve a list of available taxonomic groups in a JASPAR database release.

Usage

```
rba_jaspar_taxons(release = 2020, ...)
```

Arguments

release	Numeric: (default = 2020) Which JASPAR database release to use? Available options are: 2014, 2016, 2018, and 2020.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A data frame with information of available species.

Corresponding API Resources

"GET "http://jaspar.genereg.net/api/v1/taxon/"

References

- Fornes O, Castro-Mondragon JA, Khan A, et al. JASPAR 2020: update of the open-access database of transcription factor binding profiles. *Nucleic Acids Res.* 2019; doi: 10.1093/nar/gkz1001
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. *Bioinformatics*, 2017, doi: 10.1093/bioinformatics/btx804
- Khan, A. et al. JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework. *Nucleic Acids Res.* 2018; 46:D260–D266, doi: 10.1093/nar/gkx1126
- [JASPAR API Documentation](#)

See Also

Other "JASPAR": [rba_jaspar_collections_matrices\(\)](#), [rba_jaspar_collections\(\)](#), [rba_jaspar_matrix_search\(\)](#), [rba_jaspar_matrix_versions\(\)](#), [rba_jaspar_matrix\(\)](#), [rba_jaspar_releases\(\)](#), [rba_jaspar_sites\(\)](#), [rba_jaspar_species_matrices\(\)](#), [rba_jaspar_species\(\)](#), [rba_jaspar_taxons_matrices\(\)](#), [rba_jaspar_tffm_search\(\)](#), [rba_jaspar_tffm\(\)](#)

Examples

```
rba_jaspar_taxons(release = 2020)
```

 rba_jaspar_taxons_matrices

List matrices available in JASPAR of a taxonomic group

Description

JASPAR organizes matrix profiles from multiple species in six taxonomic groups. Using this function you can list all matrix profiles that are available in a JASPAR release from a taxonomic group.

Usage

```
rba_jaspar_taxons_matrices(
  tax_group,
  release = 2020,
  only_last_version = FALSE,
  search = NULL,
  order = NULL,
  page_size = 1000,
  page = 1,
  ...
)
```

Arguments

tax_group	Character: Taxonomic group. Use rba_jaspar_taxons to get a list of supported Taxonomic groups.
release	Numeric: (default = 2020) Which JASPAR database release to use? Available options are: 2014, 2016, 2018, and 2020.
only_last_version	Logical: (default = FALSE) If TRUE, only the latest version of a matrix profile will be returned.
search	Character: A search term.
order	Character: A character string or a vector of character strings of field names that will be used to order the results. Providing multiple field names is supported. You can also use prefix "-" before a field name to indicate reverse ordering.
page_size	Numeric: (default = 1000) This resource returns paginated results. What is the maximum numbers of results that you want to retrieve per a page? Accepted values are between 1 and 1000.
page	Numeric: Which page of the results to retrieve? The accepted values depend on the page size and number of results.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

The results are paginated. You can control the page's size number with the function's arguments. Also, you can use [rba_pages](#) to automatically iterate over multiple pages.

Value

A list that contains a data frame with information of matrix profiles available for the taxonomic group.

Corresponding API Resources

"GET "http://jaspar.genereg.net/api/v1/taxon/tax_group/"

References

- Fornes O, Castro-Mondragon JA, Khan A, et al. JASPAR 2020: update of the open-access database of transcription factor binding profiles. *Nucleic Acids Res.* 2019; doi: 10.1093/nar/gkz1001
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. *Bioinformatics*, 2017, doi: 10.1093/bioinformatics/btx804
- Khan, A. et al. JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework. *Nucleic Acids Res.* 2018; 46:D260–D266, doi: 10.1093/nar/gkx1126
- [JASPAR API Documentation](#)

See Also

Other "JASPAR": [rba_jaspar_collections_matrices\(\)](#), [rba_jaspar_collections\(\)](#), [rba_jaspar_matrix_search\(\)](#), [rba_jaspar_matrix_versions\(\)](#), [rba_jaspar_matrix\(\)](#), [rba_jaspar_releases\(\)](#), [rba_jaspar_sites\(\)](#), [rba_jaspar_species_matrices\(\)](#), [rba_jaspar_species\(\)](#), [rba_jaspar_taxons\(\)](#), [rba_jaspar_tffm_search\(\)](#), [rba_jaspar_tffm\(\)](#)

Examples

```
rba_jaspar_taxons_matrices(tax_group = "plants", page_size = 100)
```

rba_jaspar_tffm

Get a TF flexible models (TFFMs) information

Description

Using this function you can retrieve details and annotations of Transcription Factor flexible models (TFFMs) associated with a TFFM ID. If a base ID (i.e. without version suffix) was supplied, the latest version will be returned.

Usage

```
rba_jaspar_tffm(tffm_id, ...)
```

Arguments

tffm_id	Character: A TF flexible model (TFFM) Identifier.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A list that contains the TFFM's information and annotations.

Corresponding API Resources

```
"GET "http://jaspar.genereg.net/api/v1/ftm/tffm_id/"
```

References

- Fornes O, Castro-Mondragon JA, Khan A, et al. JASPAR 2020: update of the open-access database of transcription factor binding profiles. *Nucleic Acids Res.* 2019; doi: 10.1093/nar/gkz1001
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. *Bioinformatics*, 2017, doi: 10.1093/bioinformatics/btx804
- Khan, A. et al. JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework. *Nucleic Acids Res.* 2018; 46:D260–D266, doi: 10.1093/nar/gkx1126
- [JASPAR API Documentation](#)

See Also

Other "JASPAR": [rba_jaspar_collections_matrices\(\)](#), [rba_jaspar_collections\(\)](#), [rba_jaspar_matrix_search\(\)](#), [rba_jaspar_matrix_versions\(\)](#), [rba_jaspar_matrix\(\)](#), [rba_jaspar_releases\(\)](#), [rba_jaspar_sites\(\)](#), [rba_jaspar_species_matrices\(\)](#), [rba_jaspar_species\(\)](#), [rba_jaspar_taxons_matrices\(\)](#), [rba_jaspar_taxons\(\)](#), [rba_jaspar_tffm_search\(\)](#)

Examples

```
rba_jaspar_tffm("TFFM0056.3")
```

 rba_jaspar_tffm_search

Search TF flexible models (TFFMs) available in JASPAR

Description

You can use this function to list the JASPAR TF flexible models (TFFMs) that match your search query, or run the function without any arguments to return a list of every matrix profile available in the latest release.

Usage

```
rba_jaspar_tffm_search(
  term = NULL,
  release = 2020,
  tax_group = NULL,
  search = NULL,
  order = NULL,
  page_size = 1000,
  page = 1,
  ...
)
```

Arguments

term	Character: A search term.
release	Numeric: (default = 2020) Which JASPAR database release to use? Available options are: 2014, 2016, 2018, and 2020.
tax_group	Character: Taxonomic group. Use rba_jaspar_taxons to get a list of supported Taxonomic groups.
search	Character: A search term.
order	Character: A character string or a vector of character strings of field names that will be used to order the results. Providing multiple field names is supported. You can also use prefix "-" before a field name to indicate reverse ordering.
page_size	Numeric: (default = 1000) This resource returns paginated results. What is the maximum numbers of results that you want to retrieve per a page? Accepted values are between 1 and 1000.
page	Numeric: Which page of the results to retrieve? The accepted values depend on the page size and number of results.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

Note that this is a search function. Thus, you are not required to fill every argument; You may use whatever combinations of arguments you see fit for your query.

The results are paginated. You can control the page's size number with the function's arguments. Also, you can use [rba_pages](#) to automatically iterate over multiple pages.

Value

A list that contains a data frame with information of query hits' TFFMs.

Corresponding API Resources

"GET "http://jaspar.genereg.net/api/v1/api/v1/tffm/"

References

- Fornes O, Castro-Mondragon JA, Khan A, et al. JASPAR 2020: update of the open-access database of transcription factor binding profiles. *Nucleic Acids Res.* 2019; doi: 10.1093/nar/gkz1001
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. *Bioinformatics*, 2017, doi: 10.1093/bioinformatics/btx804
- Khan, A. et al. JASPAR 2018: update of the open-access database of transcription factor binding profiles and its web framework. *Nucleic Acids Res.* 2018; 46:D260–D266, doi: 10.1093/nar/gkx1126
- [JASPAR API Documentation](#)

See Also

Other "JASPAR": [rba_jaspar_collections_matrices\(\)](#), [rba_jaspar_collections\(\)](#), [rba_jaspar_matrix_search\(\)](#), [rba_jaspar_matrix_versions\(\)](#), [rba_jaspar_matrix\(\)](#), [rba_jaspar_releases\(\)](#), [rba_jaspar_sites\(\)](#), [rba_jaspar_species_matrices\(\)](#), [rba_jaspar_species\(\)](#), [rba_jaspar_taxons_matrices\(\)](#), [rba_jaspar_taxons\(\)](#), [rba_jaspar_tffm\(\)](#)

Examples

```
rba_jaspar_tffm_search(term = "FOX")
rba_jaspar_tffm_search(tax_group = "insects")
rba_jaspar_tffm_search(page_size = 100)
```

rba_mieaa_cats	<i>Get Supported Enrichment Categories for a Species and miRNA Type</i>
----------------	---

Description

For each Combination of species and miRNA type, Only a pre-defined categories groups are supported. Use this function to retrieve a list of supported categories for a given combination of Species and miRNA type.

Usage

```
rba_mieaa_cats(mirna_type, species, ...)
```

Arguments

mirna_type	Type of your miRNA accession. either "mature" or "precursor".
species	Fully or partially matching Scientific name, abbreviation or NCBI taxon ID of one of the following species: <ol style="list-style-type: none"> 1. "Homo sapiens", "hsa" or 9606 2. "Mus musculus", "mmu" or 10090 3. "Rattus norvegicus", "rno" or 10116 4. "Arabidopsis thaliana", "ath" or 3702 5. "Bos taurus", "bta" or 9913 6. "Caenorhabditis elegans", "cel" or 6239 7. "Drosophila melanogaster", "dme" or 7227 8. "Danio rerio", "dre" or 7955 9. "Gallus gallus", "gga" or 9031 10. "Sus scrofa", "ssc" or 9823
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

a named character vector with the supported categories for your supplied input combination.

Corresponding API Resources

"GET "https://ccb-compute2.cs.uni-saarland.de/mieaa2/api/v1/enrichment_categories/species/mirna_type/"

References

- Fabian Kern, Tobias Fehlmann, Jeffrey Solomon, Louisa Schwed, Nadja Grammes, Christina Backes, Kendall Van Keuren-Jensen, David Wesley Craig, Eckart Meese, Andreas Keller, miEAA 2.0: integrating multi-species microRNA enrichment analysis and workflow management systems, *Nucleic Acids Research*, Volume 48, Issue W1, 02 July 2020, Pages W521–W528, <https://doi.org/10.1093/nar/gkaa309>
- [miEAA browsable API tutorial](#)

See Also

Other "miEAA": [rba_mieaa_convert_type\(\)](#), [rba_mieaa_convert_version\(\)](#), [rba_mieaa_enrich_results\(\)](#), [rba_mieaa_enrich_status\(\)](#), [rba_mieaa_enrich_submit\(\)](#), [rba_mieaa_enrich\(\)](#)

Examples

```
rba_mieaa_cats("mature", "Homo sapiens")
```

```
rba_mieaa_convert_type
```

Convert Between Mature and precursor miRNA Accession

Description

miRBase miRNA accession could refer to either mature or precursor miRNAs. (see: [miRNA naming conventions](#)). Use this function to mature miRNA accession to corresponding miRNA accessions or vice versa.

Usage

```
rba_mieaa_convert_type(
  mirna,
  input_type,
  only_unique = FALSE,
  simple_output = FALSE,
  ...
)
```

Arguments

mirna	A vector of miRNA accessions to be converted.
input_type	Type of your supplied miRNA accession. either "mature" or "precursor".
only_unique	(logical) miRBase precursor and mature miRNA accessions are not uniquely mapped. (i.e. you may get more than one results for a given accession). set this to TRUE to only retrieve the unique mappings. (default = FALSE)
simple_output	(logical) If FALSE (default), the result will be a two-columned data frame with your input and output accessions. Otherwise, if TRUE, only the output miRNA accessions will be returned.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

Depending on the arguments, a data frame or a character vectors containing the miRNA accessions in your output version.

Corresponding API Resources

"POST https://ccb-compute2.cs.uni-saarland.de/mieaa2/api/v1/mirna_precursor_converter/"

References

- Fabian Kern, Tobias Fehlmann, Jeffrey Solomon, Louisa Schwed, Nadja Grammes, Christina Backes, Kendall Van Keuren-Jensen, David Wesley Craig, Eckart Meese, Andreas Keller, miEAA 2.0: integrating multi-species microRNA enrichment analysis and workflow management systems, *Nucleic Acids Research*, Volume 48, Issue W1, 02 July 2020, Pages W521–W528, <https://doi.org/10.1093/nar/gkaa309>
- [miEAA browsable API tutorial](#)

See Also

Other "miEAA": [rba_mieaa_cats\(\)](#), [rba_mieaa_convert_version\(\)](#), [rba_mieaa_enrich_results\(\)](#), [rba_mieaa_enrich_status\(\)](#), [rba_mieaa_enrich_submit\(\)](#), [rba_mieaa_enrich\(\)](#)

Examples

```
Sys.sleep(1) # to prevent 429 error during R CMD check
rba_mieaa_convert_type(mirna = c("hsa-miR-20b-5p", "hsa-miR-144-5p"),
  input_type = "mature")
```

rba_mieaa_convert_version

Convert miRNA accession Between Different miRBase Versions

Description

miEAA works with miRBASE v22 accession. Using This function you can convert a set of mature or precursor miRNA accession between two given miRBase versions.

Usage

```
rba_mieaa_convert_version(
  mirna,
  mirna_type,
  input_version,
  output_version,
```

```

    simple_output = FALSE,
    ...
  )

```

Arguments

mirna	A vector of miRNA accessions to be converted.
mirna_type	Type of your supplied miRNA accession. either "mature" or "precursor".
input_version	(numeric) miRBase version of your supplied miRNA accessions.
output_version	(numeric) To what version should your miRNA accessions be converted?
simple_output	(logical) If FALSE (default), the result will be a two-columned data frame with your input and output accessions. Otherwise, if TRUE, only the output miRNA accessions will be returned.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

Depending on the arguments, a data frame or a character vectors containing the miRNA accessions in your output version.

Corresponding API Resources

"POST https://ccb-compute2.cs.uni-saarland.de/mieaa2/api/v1/mirbase_converter/"

References

- Fabian Kern, Tobias Fehlmann, Jeffrey Solomon, Louisa Schwed, Nadja Grammes, Christina Backes, Kendall Van Keuren-Jensen, David Wesley Craig, Eckart Meese, Andreas Keller, miEAA 2.0: integrating multi-species microRNA enrichment analysis and workflow management systems, *Nucleic Acids Research*, Volume 48, Issue W1, 02 July 2020, Pages W521–W528, <https://doi.org/10.1093/nar/gkaa309>
- [miEAA browsable API tutorial](#)

See Also

Other "miEAA": [rba_mieaa_cats\(\)](#), [rba_mieaa_convert_type\(\)](#), [rba_mieaa_enrich_results\(\)](#), [rba_mieaa_enrich_status\(\)](#), [rba_mieaa_enrich_submit\(\)](#), [rba_mieaa_enrich\(\)](#)

Examples

```

Sys.sleep(1) # to prevent 429 error during R CMD check
rba_mieaa_convert_version(mirna = c("hsa-miR-20b-5p", "hsa-miR-144-5p"),
  mirna_type = "mature", input_version = 22, output_version = 16)

```

rba_mieaa_enrich *A One-step Wrapper for miRNA Enrichment Using miEAA*

Description

This function is a wrapper for the multiple function calls necessary to enrich a given miRNA list using miEAA. see details section for more information.

Usage

```
rba_mieaa_enrich(
  test_set,
  mirna_type,
  test_type,
  species,
  categories = NULL,
  p_adj_method = "fdr",
  independent_p_adj = TRUE,
  sig_level = 0.05,
  min_hits = 2,
  ref_set = NULL,
  sort_by = "p_adjusted",
  sort_asc = TRUE,
  ...
)
```

Arguments

test_set	a character vector with your mature or precursor miRBase miRNA accessions. Note that <ol style="list-style-type: none"> 1. Only miRBase v22 miRNA accession are accepted. You can use rba_mieaa_convert_version to convert your accessions to miRBase v22. 2. Your list should be entirely consisted of either mature or precursor miRNA accession. A mixture of both is not accepted.
mirna_type	Type of your supplied miRNA accession. either "mature" or "precursor".
test_type	The analysis to perform. can be either "ORA" for 'Over Representation Analysis' or "GSEA" for miRNA (Gene) 'Set Enrichment Analysis'. Note that in GSEA, your list should be sorted beforehand based on some criterion.
species	Fully or partially matching Scientific name, abbreviation or NCBI taxon ID of one of the following species: <ol style="list-style-type: none"> 1. "Homo sapiens", "hsa" or 9606 2. "Mus musculus", "mmu" or 10090 3. "Rattus norvegicus", "rno" or 10116 4. "Arabidopsis thaliana", "ath" or 3702 5. "Bos taurus", "bta" or 9913

	<ol style="list-style-type: none"> 6. "Caenorhabditis elegans", "cel" or 6239 7. "Drosophila melanogaster", "dme" or 7227 8. "Danio rerio", "dre" or 7955 9. "Gallus gallus", "gga" or 9031 10. "Sus scrofa", "ssc" or 9823
categories	<p>one or multiple Category names to be used for miRNA set enrichment analysis. Note that</p> <ul style="list-style-type: none"> • Available categories varies based on your chosen specie and if your supplied miRNA type is mature or precursor. Use rba_mieaa_cats to retrieve a list of available category names for a given specie and miRNA type. • If you supply NULL, the analysis will be performed on all of the available categories.
p_adj_method	P-value adjustment method to be used. Should be one of: "none", "fdr" (default), "bonferroni", "BY", "hochberg", "holm" or "hommel"
independent_p_adj	(logical) The scope and level of p-value adjustment; if TRUE (default), the categories will be considered independent from each other and the p-value will be adjusted separately for each category. if FALSE, the p-value will be adjusted collectively over all categories.
sig_level	(numeric) The significance threshold of adjusted P-value. values equal to or greater than this threshold will be dropped from the results.
min_hits	(numeric) How many miRNA should a sub-category have from your supplied test-list to be included in the results? (default is 2)
ref_set	(Optional) Only applicable when test_type is "ORA". This character vector will be used as your reference (background or universe) set for p-value calculations.
sort_by	A column name to the result's table based on that. one of: "category", "subcategory", "enrichment", "p_value", "p_adjusted" (default), "q_value" or "observed"
sort_asc	(logical) If TRUE, the results will be sorted in ascending order. If FALSE, the results will be sorted in descending order.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

This function will call other `rba_mieaa_***` functions with the following order:

1. Call [rba_mieaa_enrich_submit](#) to Submit an enrichment analysis request to miEAA servers, using your supplied miRNA lists and other arguments.
2. Once your job was successfully submitted, it will call [rba_mieaa_enrich_status](#) every 5 seconds, to check the status of your running server-side job and whether your analysis job is finished and the results are available.
3. Call [rba_mieaa_enrich_results](#) to retrieve the results of your enrichment analysis.

See each function's manual for more details.

Value

A data frame with your enrichment analysis results.

Corresponding API Resources

"GET <https://ccb-compute2.cs.uni-saarland.de/mieaa2/api/>"

References

- Fabian Kern, Tobias Fehlmann, Jeffrey Solomon, Louisa Schwed, Nadja Grammes, Christina Backes, Kendall Van Keuren-Jensen, David Wesley Craig, Eckart Meese, Andreas Keller, miEAA 2.0: integrating multi-species microRNA enrichment analysis and workflow management systems, *Nucleic Acids Research*, Volume 48, Issue W1, 02 July 2020, Pages W521–W528, <https://doi.org/10.1093/nar/gkaa309>
- [miEAA browsable API tutorial](#)

See Also

Other "miEAA": [rba_mieaa_cats\(\)](#), [rba_mieaa_convert_type\(\)](#), [rba_mieaa_convert_version\(\)](#), [rba_mieaa_enrich_results\(\)](#), [rba_mieaa_enrich_status\(\)](#), [rba_mieaa_enrich_submit\(\)](#)

Examples

```
## Not run:
rba_mieaa_enrich(test_set = c("hsa-miR-20b-5p", "hsa-miR-144-5p"),
  mirna_type = "mature",
  test_type = "GSEA",
  species = 9606,
  categories = NULL)

## End(Not run)
```

rba_mieaa_enrich_results

Retrieve Results of a finished Enrichment Analysis from miEAA

Description

After your submitted enrichment analysis request has finished (check using [rba_mieaa_enrich_status](#)), you can retrieve the results using this function.

Usage

```
rba_mieaa_enrich_results(job_id, sort_by = "p_adjusted", sort_asc = TRUE, ...)
```


Arguments

job_id	The job-id (a character string) of a submitted enrichment analysis.
sort_by	A column name to the result's table based on that. one of: "category", "subcategory", "enrichment", "p_value", "p_adjusted" (default), "q_value" or "observed".
sort_asc	(logical) If TRUE, the results will be sorted in ascending order. If FALSE, the results will be sorted in descending order.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

Note that using [rba_mieaa_enrich](#) is a more convenient way to automatically perform this and other required function calls to enrich your input miRNA-set using miEAA.

Value

A data frame with your enrichment analysis results.

Corresponding API Resources

"GET https://ccb-compute2.cs.uni-saarland.de/mieaa2/api/v1/results/job_id"

References

- Fabian Kern, Tobias Fehlmann, Jeffrey Solomon, Louisa Schwed, Nadja Grammes, Christina Backes, Kendall Van Keuren-Jensen, David Wesley Craig, Eckart Meese, Andreas Keller, miEAA 2.0: integrating multi-species microRNA enrichment analysis and workflow management systems, *Nucleic Acids Research*, Volume 48, Issue W1, 02 July 2020, Pages W521–W528, <https://doi.org/10.1093/nar/gkaa309>
- [miEAA browsable API tutorial](#)

See Also

Other "miEAA": [rba_mieaa_cats\(\)](#), [rba_mieaa_convert_type\(\)](#), [rba_mieaa_convert_version\(\)](#), [rba_mieaa_enrich_status\(\)](#), [rba_mieaa_enrich_submit\(\)](#), [rba_mieaa_enrich\(\)](#)

Examples

```
## Not run:  
rba_mieaa_enrich_results("f52d1aef-6d3d-4d51-9020-82e68fe99012")  
  
## End(Not run)
```

`rba_mieaa_enrich_status`*Check Status of a Submitted Enrichment Analysis in miEAA*

Description

After you have submitted your enrichment analysis (using [rba_mieaa_enrich_submit](#)) and retrieved a job-id, you can use this function to check the status of your job. Status value equal to 100 means that your requested analysis has finished and you may retrieve the results using [rba_mieaa_enrich_results](#).

Usage

```
rba_mieaa_enrich_status(job_id, ...)
```

Arguments

<code>job_id</code>	The job-id (a character string) of a submitted enrichment analysis.
<code>...</code>	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

Note that using [rba_mieaa_enrich](#) is a more convenient way to automatically perform this and other required function calls to enrich your input miRNA-set using miEAA.

Value

A list containing the status value for a analysis that corresponds to your supplied job-id.

Corresponding API Resources

"GET https://ccb-compute2.cs.uni-saarland.de/mieaa2/api/v1/job_status/job_id"

References

- Fabian Kern, Tobias Fehlmann, Jeffrey Solomon, Louisa Schwed, Nadja Grammes, Christina Backes, Kendall Van Keuren-Jensen, David Wesley Craig, Eckart Meese, Andreas Keller, miEAA 2.0: integrating multi-species microRNA enrichment analysis and workflow management systems, *Nucleic Acids Research*, Volume 48, Issue W1, 02 July 2020, Pages W521–W528, <https://doi.org/10.1093/nar/gkaa309>
- [miEAA browsable API tutorial](#)

See Also

Other "miEAA": [rba_mieaa_cats\(\)](#), [rba_mieaa_convert_type\(\)](#), [rba_mieaa_convert_version\(\)](#), [rba_mieaa_enrich_results\(\)](#), [rba_mieaa_enrich_submit\(\)](#), [rba_mieaa_enrich\(\)](#)

Examples

```
## Not run:
Sys.sleep(1) # to prevent 429 error during R CMD check
rba_mieaa_enrich_status("f52d1aef-6d3d-4d51-9020-82e68fe99012")

## End(Not run)
```

```
rba_mieaa_enrich_submit
```

Submit miEAA miRNA Enrichment Analysis Request

Description

Using This function you can submit a request in miEAA servers to perform Over-representation or GSEA Analysis for a given set of miRNA identifiers. see "arguments" section for more information.

Usage

```
rba_mieaa_enrich_submit(
  test_set,
  mirna_type,
  test_type,
  species = "hsa",
  categories = NULL,
  p_adj_method = "fdr",
  independent_p_adj = TRUE,
  sig_level = 0.05,
  min_hits = 2,
  ref_set = NULL,
  ...
)
```

Arguments

test_set	a character vector with your mature or precursor miRBase miRNA accessions. Note that <ol style="list-style-type: none"> 1. Only miRBase v22 miRNA accession are accepted. You can use rba_mieaa_convert_version to convert your accessions to miRBase v22. 2. Your list should be entirely consisted of either mature or precursor miRNA accession. A mixture of both is not accepted.
mirna_type	Type of your supplied miRNA accession. either "mature" or "precursor".
test_type	The analysis to perform. can be either "ORA" for 'Over Representation Analysis' or "GSEA" for miRNA (Gene) 'Set Enrichment Analysis'. Note that in GSEA, your list should be sorted beforehand based on some criterion.

species	Fully or partially matching Scientific name, abbreviation or NCBI taxon ID of one of the following species: <ol style="list-style-type: none"> 1. "Homo sapiens", "hsa" or 9606 2. "Mus musculus", "mmu" or 10090 3. "Rattus norvegicus", "rno" or 10116 4. "Arabidopsis thaliana", "ath" or 3702 5. "Bos taurus", "bta" or 9913 6. "Caenorhabditis elegans", "cel" or 6239 7. "Drosophila melanogaster", "dme" or 7227 8. "Danio rerio", "dre" or 7955 9. "Gallus gallus", "gga" or 9031 10. "Sus scrofa", "ssc" or 9823
categories	one or multiple Category names to be used for miRNA set enrichment analysis. Note that <ul style="list-style-type: none"> • Available categories varies based on your chosen specie and if your supplied miRNA type is mature or precursor. Use rba_mieaa_cats to retrieve a list of available category names for a given specie and miRNA type. • If you supply NULL, the analysis will be performed on all of the available categories.
p_adj_method	P-value adjustment method to be used. Should be one of: "none", "fdr" (default), "bonferroni", "BY", "hochberg", "holm" or "hommel"
independent_p_adj	(logical) The scope and level of p-value adjustment; if TRUE (default), the categories will be considered independent from each other and the p-value will be adjusted separately for each category. if FALSE, the p-value will be adjusted collectively over all categories.
sig_level	(numeric) The significance threshold of adjusted P-value. values equal to or greater than this threshold will be dropped from the results.
min_hits	(numeric) How many miRNA should a sub-category have from your supplied test-list to be included in the results? (default is 2)
ref_set	(Optional) Only applicable when test_type is "ORA". This character vector will be used as your reference (background or universe) set for p-value calculations.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

Note that using [rba_mieaa_enrich](#) is a more convenient way to automatically perform this and other required function calls to enrich your input miRNA-set using miEAA.

Value

A list that contains your submitted job's ID and a URL to manually check for your job status.

Corresponding API Resources

"POST https://ccb-compute2.cs.uni-saarland.de/mieaa2/api/v1/enrichment_analysis/species/type/test/"

References

- Fabian Kern, Tobias Fehlmann, Jeffrey Solomon, Louisa Schwed, Nadja Grammes, Christina Backes, Kendall Van Keuren-Jensen, David Wesley Craig, Eckart Meese, Andreas Keller, miEAA 2.0: integrating multi-species microRNA enrichment analysis and workflow management systems, *Nucleic Acids Research*, Volume 48, Issue W1, 02 July 2020, Pages W521–W528, <https://doi.org/10.1093/nar/gkaa309>
- [miEAA browsable API tutorial](#)

See Also

Other "miEAA": [rba_mieaa_cats\(\)](#), [rba_mieaa_convert_type\(\)](#), [rba_mieaa_convert_version\(\)](#), [rba_mieaa_enrich_results\(\)](#), [rba_mieaa_enrich_status\(\)](#), [rba_mieaa_enrich\(\)](#)

Examples

```
Sys.sleep(1) # to prevent 429 error during R CMD check
rba_mieaa_enrich_submit(test_set = c("hsa-miR-20b-5p", "hsa-miR-144-5p"),
  mirna_type = "mature",
  test_type = "GSEA",
  species = 9606,
  categories = NULL)
```

rba_options

Set rbioapi Global Options

Description

A safe way to change rbioapi's global options and behavior. see "arguments" section for available options.

Note that you are not limited to changing the options globally, you can include the option names and values in the `'...'` argument of any rbioapi function to alter the option(s) only in that function call; e.g. `example_function(x, diagnostics = TRUE, timeout = 300)`.

Alternatively, you can call this function with no arguments, i.e. `rba_options()`, to retrieve a data frame of available rbioapi options and their current values.

Usage

```
rba_options(
  diagnostics = NULL,
  dir_name = NULL,
  retry_max = NULL,
  retry_wait = NULL,
  progress = NULL,
  save_file = NULL,
  skip_error = NULL,
  timeout = NULL,
  verbose = NULL
)
```

Arguments

diagnostics	(Logical) (default = FALSE) Show diagnostics and detailed messages with internal information.
dir_name	(character) (default = "rbioapi") If the package needs to generate a file path to save the server's response, a directory with this name will be created in your working directory to save your files.
retry_max	(Numeric) (default = 1) How many times should rbioapi retry in case of 5xx server responses, errors un-related to the server or no internet connectivity?
retry_wait	(Numeric) (default = 10) Time in seconds to wait before next retry in case of internet connection or server problems.
progress	(Logical) (default = FALSE) Should a progress bar be displayed?
save_file	(Logical or character) (default = FALSE) Either: <ul style="list-style-type: none"> • TRUE: In this case, the raw server's response file will be automatically saved to a proper file path. use "dir_name" argument to change the file's parent directory. • FALSE: (default) Do not automatically save server's response file. • Character: (Only when changing the option via "..." in a functions call) A valid file path to save the server's response file to the function that you are calling.
skip_error	(Logical) (default = FALSE if R is in the interactive mode, TRUE otherwise) If TRUE, the code execution will not be stopped in case of errors (anything but HTTP status 200 from the server); Instead the error message will be returned as the function's output. However, if FALSE, in case of any error, the code execution will be halted and an error message will be issued.
timeout	(Numeric) (default = 30) The maximum time in seconds that you are willing to wait for a server response before giving up and stopping the function execution.
verbose	(Logical) (Default = TRUE) Generate short informative messages.

Details

Because this function validates your supplied changes, please *only change rbioapi options using this function* and avoid directly editing them.

Value

If called without any argument, a Data frame with available options and their information; If Called with an argument, will Return NULL but Alters that option globally.

See Also

Other "Helper functions": [rba_connection_test\(\)](#), [rba_pages\(\)](#)

Examples

```
rba_options()
## Not run:
rba_options(verbose = FALSE)

## End(Not run)
## Not run:
rba_options(save_file = TRUE)

## End(Not run)
## Not run:
rba_options(diagnostics = TRUE, progress = TRUE)

## End(Not run)
```

rba_pages

Get Multiple Pages of a Paginated Resource

Description

Some resources return paginated results, meaning that you have to make separate calls for each page. Using this function, you can iterate over up to 100 pages. Just supply your rbioapi function and change to page argument to "pages:start_page:end_page", for example "pages:1:5".

Usage

```
rba_pages(input_call, ...)
```

Arguments

input_call	A quoted call. supply a regular rbioapi function call, but with two differences: <ol style="list-style-type: none"> : Wrap a quote() around it. meaning: quote(rba_example()) : Set the argument that corresponds to the page number to "pages:start_page:end_page", for example "pages:1:5".
	See the "examples" section to learn more.
...	Experimental internal options.

Details

To prevent flooding the server, there will be a 1 second delay between calls, also the user cannot iterate on more than 100 pages. The function will also override `skip_error` option and will always set it to `TRUE`. This means that in case of server response error (e.g. requesting pages that do not exist) an error message be returned to you instead of halting function's execution.

Value

A named list where each element corresponds to a request's page.

See Also

Other "Helper functions": [rba_connection_test\(\)](#), [rba_options\(\)](#)

Examples

```
rba_pages(input_call = quote(rba_uniprot_taxonomy(ids = 189831,
  hierarchy = "siblings",
  page_size = 50,
  page_number = "pages:1:5")))
```

```
rba_pages(input_call = quote(rba_uniprot_taxonomy_name(name = "adenovirus",
  field = "scientific",
  search_type = "contain",
  page_size = 200,
  page_number = "pages:1:5",
  verbose = FALSE)))
```

```
rba_pages(input_call = quote(rba_panther_info(what = "families",
  families_page = "pages:9:11")))
```

rba_panther_enrich *PANTHER Over-Representation Enrichment Analysis*

Description

Using this function you can use PANTHER services to perform over-representation enrichment analysis. This statistical test will compare your input genes to a set of defined gene lists to determine if they are over/under-represented.

Usage

```
rba_panther_enrich(
  genes,
  organism,
  annot_dataset,
  test_type = "FISHER",
  correction = "FDR",
  cutoff = NULL,
  ref_genes = NULL,
  ref_organism = NULL,
  ...
)
```

Arguments

genes	Character vector of genes identifiers with maximum length of 10000. Can be any of: Ensemble gene ID, Ensemble protein ID, Ensemble transcript ID, Entrez gene ID, gene symbol, NCBI GI, HGNC ID, International protein index ID, NCBI UniGene ID, UniProt accession and/or UniProt ID.
organism	(numeric) NCBI taxon ID. run rba_panther_info with argument 'what = "organisms"' to get a list of PANTHER's supported organisms.
annot_dataset	A PANTHER dataset ID to test your input against it. run rba_panther_info with argument 'what = "datasets"' to get a list of PANTHER's supported datasets.
test_type	statistical test type to calculate the p values. either "FISHER" (default) or "BINOMIAL".
correction	p value correction method. either "FDR" (default), "BONFERRONI" or "NONE".
cutoff	(Numeric) (Optional) a threshold to filter the results. if correction is "FDR", the threshold will be applied to fdr column's values; if otherwise, the threshold will be applied to p value column.
ref_genes	(Optional) A set of genes that will be used as the test's background (reference/universe) gene set. If no value supplied, all of the genes in specified organism will be used. maximum length and supported IDs are the same as 'genes' argument.
ref_organism	(Optional) if 'ref_genes' is used, you can specify the organisms which correspond to your supplied IDs in 'ref_genes' argument. see 'organism' argument for supported values.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A list with the prov

Corresponding API Resources

"POST <http://www.pantherdb.org/services/oai/pantherdb/enrich/overrep>"

References

- Mi, H., Muruganujan, A., Ebert, D., Huang, X., & Thomas, P. D. (2019). PANTHER version 14: more genomes, a new PANTHER GO-slim and improvements in enrichment analysis tools. *Nucleic acids research*, 47(D1), D419-D426.
- Mi, H., Muruganujan, A., Huang, X., Ebert, D., Mills, C., Guo, X., & Thomas, P. D. (2019). Protocol Update for large-scale genome and gene function analysis with the PANTHER classification system (v. 14.0). *Nature protocols*, 14(3), 703-721.
- [PANTHER Services Details](#)

See Also

Other "PANTHER": [rba_panther_family\(\)](#), [rba_panther_homolog\(\)](#), [rba_panther_info\(\)](#), [rba_panther_mapping\(\)](#), [rba_panther_ortholog\(\)](#), [rba_panther_tree_grafter\(\)](#)

Examples

```
rba_panther_enrich(genes = c("p53", "BRCA1", "cdk2", "Q99835", "CDC42",
    "CDK1", "KIF23", "PLK1", "RAC2", "RACGAP1"),
    organism = 9606, annot_dataset = "GO:0008150",
    cutoff = 0.01)
```

rba_panther_family *Get PANTHER Families and Sub-Families*

Description

Using this function, you can retrieve Orthologs, MSA or Tree topology information of a given PANTHER family.

Usage

```
rba_panther_family(id, what, target_organisms = NULL, ...)
```

Arguments

id	Panther family id.
what	What to retrieve? One of: <ul style="list-style-type: none"> • "ortholog": Orthologs ('LDO' for least diverged and 'O' for more diverged). • "msa": Multiple Sequence Alignment Information, • "tree": Tree topology and nodes attributes.
target_organisms	(numeric) NCBI taxon ID(s) to filter the results. run rba_panther_info with argument 'what = "organisms"' to get a list of PANTHER's supported organisms.

... rbioapi option(s). See [rba_options](#)'s arguments manual for more information on available options.

Value

For trees a list and otherwise a data frame with the requested family's information.

Corresponding API Resources

"GET <http://www.pantherdb.org/services/oai/pantherdb/familyortholog>"

"GET <http://www.pantherdb.org/services/oai/pantherdb/familymsa>"

"GET <http://www.pantherdb.org/services/oai/pantherdb/treeinfo>"

References

- Mi, H., Muruganujan, A., Ebert, D., Huang, X., & Thomas, P. D. (2019). PANTHER version 14: more genomes, a new PANTHER GO-slim and improvements in enrichment analysis tools. *Nucleic acids research*, 47(D1), D419-D426.
- Mi, H., Muruganujan, A., Huang, X., Ebert, D., Mills, C., Guo, X., & Thomas, P. D. (2019). Protocol Update for large-scale genome and gene function analysis with the PANTHER classification system (v. 14.0). *Nature protocols*, 14(3), 703-721.
- [PANTHER Services Details](#)

See Also

Other "PANTHER": [rba_panther_enrich\(\)](#), [rba_panther_homolog\(\)](#), [rba_panther_info\(\)](#), [rba_panther_mapping\(\)](#), [rba_panther_ortholog\(\)](#), [rba_panther_tree_grafter\(\)](#)

Examples

```
rba_panther_family("PTHR10000", what = "ortholog")
```

rba_panther_homolog *Search PANTHER for Homologs of Gene(s)*

Description

Using this function you can search and retrieve homolog of given gene(s).

Usage

```
rba_panther_homolog(genes, organism, type = "P", target_organisms = NULL, ...)
```

Arguments

genes	Character vector of genes identifiers with maximum length of 10 or only one if seq_pos is supplied. Can be any of: Ensemble gene ID, Ensemble protein ID, Ensemble transcript ID, Entrez gene ID, gene symbol, NCBI GI, HGNC ID, International protein index ID, NCBI UniGene ID, UniProt accession and/or UniProt ID.
organism	(numeric) NCBI taxon ID of the organism of your supplied genes. run rba_panther_info with argument 'what = "organisms"' to get a list of PANTHER's supported organisms.
type	Homolog types to return. either "P" (default) for paralogs, "X" for horizontal gene transfer and "LDX" for diverged horizontal gene transfer.
target_organisms	(numeric) NCBI taxon ID(s) to filter the results. run rba_panther_info with argument 'what = "organisms"' to get a list of PANTHER's supported organisms. For Paralog, target organism and organism should be the same; Otherwise, the target organism should be different from the input organism.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A dataframe with homologs information.

Corresponding API Resources

"GET <http://www.pantherdb.org/services/oai/pantherdb/ortholog/homologOther>"

References

- Mi, H., Muruganujan, A., Ebert, D., Huang, X., & Thomas, P. D. (2019). PANTHER version 14: more genomes, a new PANTHER GO-slim and improvements in enrichment analysis tools. *Nucleic acids research*, 47(D1), D419-D426.
- Mi, H., Muruganujan, A., Huang, X., Ebert, D., Mills, C., Guo, X., & Thomas, P. D. (2019). Protocol Update for large-scale genome and gene function analysis with the PANTHER classification system (v. 14.0). *Nature protocols*, 14(3), 703-721.
- [PANTHER Services Details](#)

See Also

Other "PANTHER": [rba_panther_enrich\(\)](#), [rba_panther_family\(\)](#), [rba_panther_info\(\)](#), [rba_panther_mapping\(\)](#), [rba_panther_ortholog\(\)](#), [rba_panther_tree_grafter\(\)](#)

Examples

```
rba_panther_homolog("OR4F5", organism = 9606, type = "P")
```

rba_panther_info *Get PANTHER database Information*

Description

Using this function you can retrieve a list of available organisms, annotation datasets, families, and pathways which are supported in PANTHER.

Usage

```
rba_panther_info(what, organism_chr_loc = FALSE, families_page = 1, ...)
```

Arguments

what	what information to retrieve? should be one of: <ul style="list-style-type: none"> • "organisms": Retrieve supported organisms in PANTHER. • "datasets": Retrieve available annotation datasets. • "families" Retrieve available family IDs. • "pathways" Retrieve available pathway IDs.
organism_chr_loc	(Logical) (only when 'what = "organisms"') If TRUE, only organisms with chromosome location will be returned. If FALSE (default) every organisms will be returned.
families_page	(Numeric) (only when 'what = "families"') Family information is very long, so results are paginated. Use this argument to define the page to retrieve.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

For families, a list and otherwise a data frame with pertinent information.

Corresponding API Resources

```
"GET http://www.pantherdb.org/services/oai/pantherdb/supportedgenomes"
"GET http://www.pantherdb.org/services/oai/pantherdb/supportedannotdatasets"
"GET http://www.pantherdb.org/services/oai/pantherdb/supportedpantherfamilies"
"GET http://www.pantherdb.org/services/oai/pantherdb/supportedpantherpathways"
```

References

- Mi, H., Muruganujan, A., Ebert, D., Huang, X., & Thomas, P. D. (2019). PANTHER version 14: more genomes, a new PANTHER GO-slim and improvements in enrichment analysis tools. *Nucleic acids research*, 47(D1), D419-D426.

- Mi, H., Muruganujan, A., Huang, X., Ebert, D., Mills, C., Guo, X., & Thomas, P. D. (2019). Protocol Update for large-scale genome and gene function analysis with the PANTHER classification system (v. 14.0). *Nature protocols*, 14(3), 703-721.
- [PANTHER Services Details](#)

See Also

Other "PANTHER": [rba_panther_enrich\(\)](#), [rba_panther_family\(\)](#), [rba_panther_homolog\(\)](#), [rba_panther_mapping\(\)](#), [rba_panther_ortholog\(\)](#), [rba_panther_tree_grafter\(\)](#)

Examples

```
rba_panther_info(what = "organisms")
```

```
rba_panther_info(what = "families", families_page = 4)
```

rba_panther_mapping *Map A Gene-set to PANTHER Database*

Description

Using this function, you can search your genes in PANTHER database and retrieve attributes and annotations associated to your genes.

Usage

```
rba_panther_mapping(genes, organism, ...)
```

Arguments

genes	Character vector of genes identifiers with maximum length of 1000. Can be any of: Ensemble gene ID, Ensemble protein ID, Ensemble transcript ID, Entrez gene ID, gene symbol, NCBI GI, HGNC ID, International protein index ID, NCBI UniGene ID, UniProt accession and/or UniProt ID.
organism	(numeric) NCBI taxon ID. run rba_panther_info with argument 'what = "organisms"' to get a list of PANTHER's supported organisms.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A list containing your unmapped inputs and mapped genes with pertinent information.

Corresponding API Resources

"GET <http://www.pantherdb.org/services/oai/pantherdb/geneinfo>"

References

- Mi, H., Muruganujan, A., Ebert, D., Huang, X., & Thomas, P. D. (2019). PANTHER version 14: more genomes, a new PANTHER GO-slim and improvements in enrichment analysis tools. *Nucleic acids research*, 47(D1), D419-D426.
- Mi, H., Muruganujan, A., Huang, X., Ebert, D., Mills, C., Guo, X., & Thomas, P. D. (2019). Protocol Update for large-scale genome and gene function analysis with the PANTHER classification system (v. 14.0). *Nature protocols*, 14(3), 703-721.
- [PANTHER Services Details](#)

See Also

Other "PANTHER": [rba_panther_enrich\(\)](#), [rba_panther_family\(\)](#), [rba_panther_homolog\(\)](#), [rba_panther_info\(\)](#), [rba_panther_ortholog\(\)](#), [rba_panther_tree_grafter\(\)](#)

Examples

```
rba_panther_mapping(genes = c("Cd40", 7124, "ENSG00000203747", "P33681"),
  organism = 9606)
```

rba_panther_ortholog *Search PANTHER for Orthologs of Gene(s)*

Description

Using this function you can search and retrieve orthologs of given gene(s), and optionally return the corresponding position in the target organisms' protein sequences.

Usage

```
rba_panther_ortholog(  
  genes,  
  organism,  
  type = "all",  
  target_organisms = NULL,  
  seq_pos = NULL,  
  include_msa = NULL,  
  ...  
)
```

Arguments

genes	Character vector of genes identifiers with maximum length of 10 or only one if seq_pos is supplied. Can be any of: Ensemble gene ID, Ensemble protein ID, Ensemble transcript ID, Entrez gene ID, gene symbol, NCBI GI, HGNC ID, International protein index ID, NCBI UniGene ID, UniProt accession and/or UniProt ID.
organism	(numeric) NCBI taxon ID of the organism of your supplied genes. run rba_panther_info with argument 'what = "organisms"' to get a list of PANTHER's supported organisms.
type	Ortholog types to return. either "all" (default) or "LDO" to only return least diverged orthologs.
target_organisms	(numeric) NCBI taxon ID(s) to filter the results. run rba_panther_info with argument 'what = "organisms"' to get a list of PANTHER's supported organisms.
seq_pos	(Numeric) A position in the protein's sequence of the supplied gene. should be in the range of the protein's length.
include_msa	(Logical) Only if a sequence position is supplied, should MSA (Multiple Sequence Alignment) information be included in the results?
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A data frame with Orthologs information.

Corresponding API Resources

"POST <http://www.pantherdb.org/services/oai/pantherdb/ortholog/matchortho>"
 "POST <http://www.pantherdb.org/services/oai/pantherdb/ortholog/homologpos>"

References

- Mi, H., Muruganujan, A., Ebert, D., Huang, X., & Thomas, P. D. (2019). PANTHER version 14: more genomes, a new PANTHER GO-slim and improvements in enrichment analysis tools. *Nucleic acids research*, 47(D1), D419-D426.
- Mi, H., Muruganujan, A., Huang, X., Ebert, D., Mills, C., Guo, X., & Thomas, P. D. (2019). Protocol Update for large-scale genome and gene function analysis with the PANTHER classification system (v. 14.0). *Nature protocols*, 14(3), 703-721.
- [PANTHER Services Details](#)

See Also

Other "PANTHER": [rba_panther_enrich\(\)](#), [rba_panther_family\(\)](#), [rba_panther_homolog\(\)](#), [rba_panther_info\(\)](#), [rba_panther_mapping\(\)](#), [rba_panther_tree_grafter\(\)](#)

Examples

```
rba_panther_ortholog("CD40", organism = 9606, type = "LDO")
```

rba_panther_tree_grafter

PANTHER Tree Grafter Use this function to retrieve a PANTHER family's tree topology information with a node corresponding to your sequence grafted in the best location in that tree.

Description

For more information, see: [TreeGrafter: phylogenetic tree-based annotation of proteins with Gene Ontology terms and other annotations](#)

Usage

```
rba_panther_tree_grafter(protein_seq, target_organisms = NULL, ...)
```

Arguments

protein_seq	A character string with the protein's sequence. Maximum allowed sequence length is 50kb.
target_organisms	(numeric) NCBI taxon ID(s) to filter the results. run rba_panther_info with argument 'what = "organisms"' to get a list of PANTHER's supported organisms.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A list containing PANTHER tree topology information.

Corresponding API Resources

"GET <http://www.pantherdb.org/services/oai/pantherdb/graftsequence>"

References

- Mi, H., Muruganujan, A., Ebert, D., Huang, X., & Thomas, P. D. (2019). PANTHER version 14: more genomes, a new PANTHER GO-slim and improvements in enrichment analysis tools. *Nucleic acids research*, 47(D1), D419-D426.

- Mi, H., Muruganujan, A., Huang, X., Ebert, D., Mills, C., Guo, X., & Thomas, P. D. (2019). Protocol Update for large-scale genome and gene function analysis with the PANTHER classification system (v. 14.0). *Nature protocols*, 14(3), 703-721.
- [PANTHER Services Details](#)

See Also

Other "PANTHER": [rba_panther_enrich\(\)](#), [rba_panther_family\(\)](#), [rba_panther_homolog\(\)](#), [rba_panther_info\(\)](#), [rba_panther_mapping\(\)](#), [rba_panther_ortholog\(\)](#)

Examples

```
rba_panther_tree_grafter("MKVLWAALLVTFLAGCQAKVEQAVETE")
```

rba_reactome_analysis *Reactome Over-Representation or Expression Analysis*

Description

Using this function, you can perform Reactome Analysis In a convenient way. The Analysis Type will be chosen depending on your supplied input:

1. If you supply a vector or a single-columned table, "Over-Representation" analysis will be performed.
2. If you supply a multi-column table, with the first column being molecules identifiers and the rest being numeral expression values, "Expression" analysis will be performed.

See the details section for the accepted input types and format.

Usage

```
rba_reactome_analysis(  
  input,  
  input_format = NULL,  
  projection = FALSE,  
  interactors = FALSE,  
  species = NULL,  
  sort_by = "ENTITIES_PVALUE",  
  order = "ASC",  
  resource = "TOTAL",  
  p_value = 1,  
  include_disease = TRUE,  
  min = NULL,  
  max = NULL,  
  ...  
)
```

Arguments

input	A vector, data frame, matrix or a local file path or URL that points to your data. See "Details section" for more information of how to organize and supply your input.
input_format	(Optional) This function will automatically identify your supplied input's format. But in case of unexpected issues or if you want to be explicit, set this argument to one of: <ul style="list-style-type: none"> • "table": If you supplied a data frame or matrix as input. • "vector": If you supplied a simple vector (numeric or character) as input. • "file": If you supplied a local file path pointing to a correctly-formatted text file. • "url": If you supplied a URL pointing to a correctly-formatted text file.
projection	Logical (default = FALSE) Should non-human identifiers be projected to their human equivalents? (using Reactome orthology data)
interactors	Logical (default = FALSE) Should IntAct interaction data be used to increase the analysis background?
species	Numeric or Character: NCBI Taxonomy identifier (Human is 9606), species name (e.g. "Homo sapiens") or Reactome DbId (e.g Homo sapiens is 48887). See rba_reactome_species or Reactome Data Schema: Entries: Species .
sort_by	Sort the result based on what column? available choices are: "NAME", "TOTAL_ENTITIES", "TOTAL_INTERACTORS", "TOTAL_REACTIONS", "FOUND_ENTITIES", "FOUND_INTERACTORS", "FOUND_REACTIONS", "ENTITIES_RATIO", "ENTITIES_PVALUE", "ENTITIES_FDR" or "REACTIONS_RATIO"
order	Sort Order. Can be either "ASC" (default) or "DESC".
resource	Filter results based on the resource. Default is "TOTAL", available choices are: "TOTAL", "UNIPROT", "ENSEMBL", "CHEBI", "IUPHAR", "MIRBASE", "NCBI_PROTEIN", "EMBL", "COMPOUND", "ENTITIES_FDR" or "PUBCHEM_COMPOUND".
p_value	Set a P value threshold. Only results with P value equal to or less than your supplied threshold will be returned. (default = 1, Meaning no P value filtering)
include_disease	Logical (default = TRUE) Should the disease pathways be included in the results?
min	(numeric) Minimum number of entities that a pathways should have to be included in the results.
max	(numeric) Maximum number of entities that a pathways should have to be included in the results.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

You can supply your table or vector input in numerous formats:

1. A R object which can be data frame, matrix or a simple vector.
2. A path to a local text file in your device that contains the molecules data. (The file should be formatted correctly, see below.)
3. A URL pointing to a text file on the web that contains the molecules data. (The file should be formatted correctly, see below.)

If you supply a text file (as a local file path or URL), it should be in TSV (Tab-Separated Values) format; Column names should start with "#" character. Note that if you are providing the file for "Over-Representation" analysis (i.e. Single columned-data) this header line is optional and will be used as your 'Sample Name', otherwise it is required.

Also, from the "summary" element in the function's output, you can see how Reactome Interpreted your input and subsequently the type of analysis that has been performed.

There is no strict criteria about the type of your molecules Identifiers, Reactome will Map the IDs to it's internal database entities. Nevertheless, You can check if all your identifiers has been found in "identifiersNotFound" element in the function's output.

After Any Analysis, Reactome will associate a token to your analysis. It can be later used to in function that requires the token (e.g to retrieve the analysis results, download pdf).

Note that Reactome will store your token for only 7 days. You can download your full results with [rba_reactome_analysis_download](#), and re-import it anytime to reactome (using [rba_reactome_analysis_import](#)) to generate a new token.

Value

List containing the results and information of your analysis. Note that you can use the token returned in the "summary" sub-list of the results (i.e. `results$summary$token`) to retrieve your results later or in other Reactome analysis functions.

Corresponding API Resources

"POST <https://reactome.org/AnalysisService/identifiers/form>"

"POST <https://reactome.org/AnalysisService/identifiers/url>"

"POST <https://reactome.org/AnalysisService/identifiers/form/projection>"

"POST <https://reactome.org/AnalysisService/identifiers/url/projection>"

References

- Fabregat A, Sidiropoulos K, Viteri G, Forner O, Marin-Garcia P, Arnau V, D'Eustachio P, Stein L, Hermjakob H. Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*. 2017 Mar;18(1) 142. doi: 10.1186/s12859-017-1559-2. PubMed PMID: 28249561. PubMed Central PMCID: PMC5333408.
- [Reactome Analysis Services API Documentation](#)

See Also

Other "Reactome Analysis Service": [rba_reactome_analysis_download\(\)](#), [rba_reactome_analysis_import\(\)](#), [rba_reactome_analysis_mapping\(\)](#), [rba_reactome_analysis_pdf\(\)](#), [rba_reactome_analysis_species\(\)](#), [rba_reactome_analysis_token\(\)](#)

Examples

```
rba_reactome_analysis(input = c("p53", "BRCA1", "cdk2", "Q99835", "CDC42"))

## Not run:
rba_reactome_analysis(input = "c:/rbioapi/genes.txt")

## End(Not run)
## Not run:
rba_reactome_analysis(input = "https://qazwsx.com/genes.txt")

## End(Not run)
```

rba_reactome_analysis_download

Download Different Reactome Analysis Results

Description

Based on the "request" argument, you can download different analysis results data associated with a given token.

Usage

```
rba_reactome_analysis_download(  
  token,  
  request,  
  save_to = NULL,  
  resource = "TOTAL",  
  ...  
)
```

Arguments

token	A token associated to your previous Reactome analysis.
request	What to download? Should be one of: <ul style="list-style-type: none">"found_ids": Download a CSV file containing the found user-supplied identifiers in the analysis associated with your supplied token and resource."not_found_ids": Download a CSV file containing the user-supplied Identifiers which has not been found in the analysis associated with your supplied token."pathways": Download a CSV file containing Pathway analysis results of the analysis associated with your supplied token and resource."results": Download a JSON file containing the complete analysis results associated with your supplied token.

	<ul style="list-style-type: none"> • "results_gz" Same as "results", but the output will be compress (gzipped).
save_to	<p>NULL or Character:</p> <ul style="list-style-type: none"> • NULL: Save the file to an automatically-generated path. • Character string: A valid file path to save the file to.
resource	(Only when request is "found_ids" or "pathways") Filter results based on the resource. Default is "TOTAL", available choices are:"TOTAL", "UNIPROT", "ENSEMBL", "CHEBI", "IUPHAR", "MIRBASE", "NCBI_PROTEIN", "EMBL", "COMPOUND", "ENTITIES_FDR" or "PUBCHEM_COMPOUND".
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

Token is associated to each Reactome analysis results and kept by Reactome for at least 7 days. You can locate it in [rba_reactome_analysis](#)'s output, under a sub-list named "summary" (i.e. results\$summary\$token).

Use [rba_reactome_analysis_pdf](#) to save a full report in PDF format.

Value

NULL, a CSV,JSON or Gzipped JSON file will be saved to disk based on your input.

Corresponding API Resources

GET <https://reactome.org/AnalysisService/download/token/entities/found/resource/filename.csv>" GET <https://reactome.org/AnalysisService/download/token/entities/notfound/filename.csv>" GET <https://reactome.org/AnalysisService/download/token/result.json>" GET <https://reactome.org/AnalysisService/download/token/result.json.gz>"

References

- Fabregat A, Sidiropoulos K, Viteri G, Forner O, Marin-Garcia P, Arnau V, D'Eustachio P, Stein L, Hermjakob H. Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*. 2017 Mar;18(1) 142. doi: 10.1186/s12859-017-1559-2. PubMed PMID: 28249561. PubMed Central PMCID: PMC5333408.
- [Reactome Analysis Services API Documentation](#)

See Also

[rba_reactome_analysis_pdf](#) [rba_reactome_analysis](#)

Other "Reactome Analysis Service": [rba_reactome_analysis_import\(\)](#), [rba_reactome_analysis_mapping\(\)](#), [rba_reactome_analysis_pdf\(\)](#), [rba_reactome_analysis_species\(\)](#), [rba_reactome_analysis_token\(\)](#), [rba_reactome_analysis\(\)](#)

Examples

```
## Not run:
rba_reactome_analysis_download(token = "MjAyMDEwMTYwMTI3MTNfMjY1MjM",
  request = "found_ids", save_to = "found_ids.csv")

## End(Not run)
```

rba_reactome_analysis_import

Import Saved Analysis JSON to Reactome

Description

If you have a JSON file of analysis results (only obtained via [rba_reactome_analysis_download](#) with the result argument set to "results", or "results_gz"), you can import the results back to Reactome and retrieve a token.

This is useful when you want to use other Reactome services which require a token but you do not have a token or your token has been expired (i.e. more than 7 days passed from your analysis).

Usage

```
rba_reactome_analysis_import(input, input_format = NULL, ...)
```

Arguments

input	A local file path or URL that points to your -optionally gzipped- JSON file.
input_format	(Optional) This function will automatically identify your supplied input's format. But in case of unexpected issues or if you want to be explicit, set this argument to one of: <ul style="list-style-type: none">• "file": If you supplied a local file path pointing to the JSON file.• "url": If you supplied a URL pointing to the JSON file.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A list containing the new token and other information of your imported results.

Corresponding API Resources

```
"GET https://reactome.org/AnalysisService/import/"
"GET https://reactome.org/AnalysisService/import/form"
"GET https://reactome.org/AnalysisService/import/url"
```

References

- Fabregat A, Sidiropoulos K, Viteri G, Forner O, Marin-Garcia P, Arnau V, D'Eustachio P, Stein L, Hermjakob H. Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*. 2017 Mar;18(1) 142. doi: 10.1186/s12859-017-1559-2. PubMed PMID: 28249561. PubMed Central PMCID: PMC5333408.
- [Reactome Analysis Services API Documentation](#)

See Also

Other "Reactome Analysis Service": [rba_reactome_analysis_download\(\)](#), [rba_reactome_analysis_mapping\(\)](#), [rba_reactome_analysis_pdf\(\)](#), [rba_reactome_analysis_species\(\)](#), [rba_reactome_analysis_token\(\)](#), [rba_reactome_analysis\(\)](#)

Examples

```
## Not run:
rba_reactome_analysis_import("c:/rbioapi/res.json")

## End(Not run)
## Not run:
rba_reactome_analysis_import("https://qaz.com/res.json.gz")

## End(Not run)
```

rba_reactome_analysis_mapping
Maps Molecule Identifiers

Description

Use this function to map molecule identifiers of different species to Reactome Identifiers.

Usage

```
rba_reactome_analysis_mapping(  
  input,  
  input_format = NULL,  
  projection = FALSE,  
  interactors = FALSE,  
  ...  
)
```


Arguments

input	A vector, local file path or URL that points to your identifiers list.
input_format	(Optional) This function will automatically identify your supplied input's format. But in case of unexpected issues or if you want to be explicit, set this argument to one of: <ul style="list-style-type: none"> "vector": If you supplied a simple vector (numeric or character) as input. "file": If you supplied a local file path pointing to a correctly-formatted text file. "url": If you supplied a URL pointing to a correctly-formatted text file.
projection	Logical (default = FALSE) Should non-human identifiers be projected to their human equivalents? (using Reactome orthology data)
interactors	Logical (default = FALSE) Should IntAct interaction data be included?
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

List containing your identifiers and the IDS and resources they are mapped to.

Corresponding API Resources

"GET https://reactome.org/AnalysisService/mapping"
"GET https://reactome.org/AnalysisService/mapping/form"
"GET https://reactome.org/AnalysisService/mapping/form/projection"
"GET https://reactome.org/AnalysisService/mapping/url"
"GET https://reactome.org/AnalysisService/mapping/url/projection"

References

- Fabregat A, Sidiropoulos K, Viteri G, Forner O, Marin-Garcia P, Arnau V, D'Eustachio P, Stein L, Hermjakob H. Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*. 2017 Mar;18(1) 142. doi: 10.1186/s12859-017-1559-2. PubMed PMID: 28249561. PubMed Central PMCID: PMC5333408.
- [Reactome Analysis Services API Documentation](#)

See Also

Other "Reactome Analysis Service": [rba_reactome_analysis_download\(\)](#), [rba_reactome_analysis_import\(\)](#), [rba_reactome_analysis_pdf\(\)](#), [rba_reactome_analysis_species\(\)](#), [rba_reactome_analysis_token\(\)](#), [rba_reactome_analysis\(\)](#)

Examples

```
rba_reactome_analysis_mapping(c("Q8SQ34", "cd40"))
```

`rba_reactome_analysis_pdf`*Generate PDF file with Reactome Analysis Results*

Description

Use this function to save a detailed report of your previous analysis (That you have done with [rba_reactome_analysis](#)). You need to supply a 'token' associated to your previous analysis.

Usage

```
rba_reactome_analysis_pdf(  
  token,  
  species,  
  save_to = NULL,  
  number = 25,  
  resource = "TOTAL",  
  diagram_profile = "Modern",  
  analysis_profile = "Standard",  
  fireworks_profile = "Barium Lithium",  
  ...  
)
```

Arguments

<code>token</code>	A token associated to your previous Reactome analysis.
<code>species</code>	Numeric or Character: NCBI Taxonomy identifier (Human Taxonomy ID is 9606.) or species name (e.g. "Homo sapiens"). See rba_reactome_species or Reactome Data Schema: Entries: Species .
<code>save_to</code>	NULL or Character: <ul style="list-style-type: none">• NULL: Save the file to an automatically-generated path.• Character string: A valid file path to save the file to.
<code>number</code>	Numeric: Maximum number of the reported pathways. Cannot not be greater than 50.
<code>resource</code>	Filter results based on the resource. Default is "TOTAL", available choices are: "TOTAL", "UNIPROT", "ENSEMBL", "CHEBI", "IUPHAR", "MIRBASE", "NCBI_PROTEIN", "EMBL", "COMPOUND", "ENTITIES_FDR" or "PUB-CHEM_COMPOUND".
<code>diagram_profile</code>	Color profile of diagrams, should be either "Modern" (default) or "Standard".
<code>analysis_profile</code>	Color profile of analysis, should be one of: "Standard" (default), "Strosobar" or "Copper Plus".

fireworks_profile
Color profile of overview diagram, should be one of: "Copper", "Copper Plus", "Barium Lithium" or "calcium salts".

...
rbioapi option(s). See [rba_options](#)'s arguments manual for more information on available options.

Details

Token is associated to each Reactome analysis results and kept by Reactome for at least 7 days. You can locate it in [rba_reactome_analysis](#)'s output, under a sub-list named "summary" (i.e. results\$summary\$token).

Note that Reactome will store your token for only 7 days. You can download your full results with [rba_reactome_analysis_download](#), and re-import it anytime to reactome (using [rba_reactome_analysis_import](#)) to generate a new token. Use [rba_reactome_analysis_download](#) to save your results in other formats.

Value

NULL, a PDF file will be saved to disk.

Corresponding API Resources

"GET <https://reactome.org/AnalysisService/report/token/species/> filename.pdf"

References

- Fabregat A, Sidiropoulos K, Viteri G, Forner O, Marin-Garcia P, Arnau V, D'Eustachio P, Stein L, Hermjakob H. Reactome pathway analysis: a high-performance in-memory approach. BMC bioinformatics. 2017 Mar;18(1) 142. doi: 10.1186/s12859-017-1559-2. PubMed PMID: 28249561. PubMed Central PMCID: PMC5333408.
- [Reactome Analysis Services API Documentation](#)

See Also

[rba_reactome_analysis_download](#) [rba_reactome_analysis](#)

Other "Reactome Analysis Service": [rba_reactome_analysis_download\(\)](#), [rba_reactome_analysis_import\(\)](#), [rba_reactome_analysis_mapping\(\)](#), [rba_reactome_analysis_species\(\)](#), [rba_reactome_analysis_token\(\)](#), [rba_reactome_analysis\(\)](#)

Examples

```
## Not run:  
rba_reactome_analysis_pdf(token = "MjAyMDEwMTYwMTI3MTNmMjY1MjM%3D",  
  species = 9606, save_to = "my_analysis.pdf")  
  
## End(Not run)
```

 rba_reactome_analysis_species

Compare Human Pathways with with Other Species

Description

Use This function to Compare human's manually-curated pathways and computationally inferred pathways (orthologous) in other species.

Usage

```
rba_reactome_analysis_species(
  species_dbid,
  sort_by = "ENTITIES_PVALUE",
  order = "ASC",
  resource = "TOTAL",
  p_value = 1,
  min = NULL,
  max = NULL,
  ...
)
```

Arguments

species_dbid	Numeric: Reactome DbId (e.g Mus musculus is 48892) of the species you want to compare with Homo sapiens. See rba_reactome_species or Reactome Data Schema: Entries: Species .
sort_by	Sort the result based on what column? available choices are: "NAME", "TOTAL_ENTITIES", "TOTAL_INTERACTORS", "TOTAL_REACTIONS", "FOUND_ENTITIES", "FOUND_INTERACTORS", "FOUND_REACTIONS", "ENTITIES_RATIO", "ENTITIES_PVALUE", "ENTITIES_FDR" or "REACTIONS_RATIO"
order	Sort Order. Can be either "ASC" (default) or "DESC".
resource	Filter results based on the resource. Default is "TOTAL", available choices are: "TOTAL", "UNIPROT", "ENSEMBL", "CHEBI", "IUPHAR", "MIRBASE", "NCBI_PROTEIN", "EMBL", "COMPOUND", "ENTITIES_FDR" or "PUBCHEM_COMPOUND".
p_value	Set a P value threshold. Only results with P value equal to or less than your supplied threshold will be returned. (default = 1, Meaning no P value filtering)
min	(numeric) Minimum number of entities that a pathways should have to be included in the results.
max	(numeric) Maximum number of entities that a pathways should have to be included in the results.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

Reactome incorporate manually curated human reactions and PANTHER's protein homology data to Computationally infer events in other eukaryotic species.

In version 73 (11 June 2020), using an orthology-based approach, Homo sapiens events was projected to 18,654 orthologous pathways (with 81,835 orthologous proteins) in 15 non-human species. See [Reactome Computationally Inferred Events](#) for more information.

Value

List with the results of the comparison.

Corresponding API Resources

"GET <https://reactome.org/AnalysisService/species/homoSapiens/species>"

References

- Fabregat A, Sidiropoulos K, Viteri G, Forner O, Marin-Garcia P, Arnau V, D'Eustachio P, Stein L, Hermjakob H. Reactome pathway analysis: a high-performance in-memory approach. BMC bioinformatics. 2017 Mar;18(1) 142. doi: 10.1186/s12859-017-1559-2. PubMed PMID: 28249561. PubMed Central PMCID: PMC5333408.
- [Reactome Analysis Services API Documentation](#)

See Also

[rba_reactome_orthology](#)

Other "Reactome Analysis Service": [rba_reactome_analysis_download\(\)](#), [rba_reactome_analysis_import\(\)](#), [rba_reactome_analysis_mapping\(\)](#), [rba_reactome_analysis_pdf\(\)](#), [rba_reactome_analysis_token\(\)](#), [rba_reactome_analysis\(\)](#)

Examples

```
rba_reactome_analysis_species(species_dbid = 48892)
```

rba_reactome_analysis_token

Return the Results Associated with a Token

Description

Use a token generated After a Reactome analysis (via [rba_reactome_analysis](#)) to Retrieve the analysis results. The output format is identical to the returned object of [rba_reactome_analysis](#).

Usage

```
rba_reactome_analysis_token(
  token,
  species,
  sort_by = "ENTITIES_PVALUE",
  order = "ASC",
  resource = "TOTAL",
  p_value = NULL,
  include_disease = TRUE,
  min = NULL,
  max = NULL,
  ...
)
```

Arguments

token	A token associated to your previous Reactome analysis.
species	Numeric or Character: NCBI Taxonomy identifier (Human is 9606), species name (e.g. "Homo sapiens") or Reactome DbId (e.g Homo sapiens is 48887). See rba_reactome_species or Reactome Data Schema: Entries: Species .
sort_by	Sort the result based on what column? available choices are: "NAME", "TOTAL_ENTITIES", "TOTAL_INTERACTORS", "TOTAL_REACTIONS", "FOUND_ENTITIES", "FOUND_INTERACTORS", "FOUND_REACTIONS", "ENTITIES_RATIO", "ENTITIES_PVALUE", "ENTITIES_FDR" or "REACTIONS_RATIO"
order	Sort Order. Can be either "ASC" (default) or "DESC".
resource	Filter results based on the resource. Default is "TOTAL", available choices are: "TOTAL", "UNIPROT", "ENSEMBL", "CHEBI", "IUPHAR", "MIRBASE", "NCBI_PROTEIN", "EMBL", "COMPOUND", "ENTITIES_FDR" or "PUBCHEM_COMPOUND".
p_value	Set a P value threshold. Only results with P value equal to or less than your supplied threshold will be returned. (default = 1, Meaning no P value filtering)
include_disease	Logical (default = TRUE) Should the disease pathways be included in the results?
min	(numeric) Minimum number of entities that a pathways should have to be included in the results.
max	(numeric) Maximum number of entities that a pathways should have to be included in the results.
...	rbaapi option(s). See rba_options 's arguments manual for more information on available options.

Details

After Any Analysis, Reactome will associate a token to your analysis. It can be later used to in function that requires the token (e.g to retrieve the analysis results, download pdf).

Note that Reactome will store your token for only 7 days. You can download your full results with

[rba_reactome_analysis_download](#), and re-import it anytime to reactome (using [rba_reactome_analysis_import](#)) to generate a new token.

Value

List containing the results and information of your analysis.

Corresponding API Resources

"GET <https://reactome.org/AnalysisService/token/token>"

References

- Fabregat A, Sidiropoulos K, Viteri G, Forner O, Marin-Garcia P, Arnau V, D'Eustachio P, Stein L, Hermjakob H. Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*. 2017 Mar;18(1) 142. doi: 10.1186/s12859-017-1559-2. PubMed PMID: 28249561. PubMed Central PMCID: PMC5333408.
- [Reactome Analysis Services API Documentation](#)

See Also

[rba_reactome_analysis](#)

Other "Reactome Analysis Service": [rba_reactome_analysis_download\(\)](#), [rba_reactome_analysis_import\(\)](#), [rba_reactome_analysis_mapping\(\)](#), [rba_reactome_analysis_pdf\(\)](#), [rba_reactome_analysis_species\(\)](#), [rba_reactome_analysis\(\)](#)

Examples

```
## Not run:
rba_reactome_analysis_token(token = "MjAyMDEwMTYwMTI3MTNFMjY1MjM",
  species = 9606)

## End(Not run)
```

rba_reactome_complex_list

Get Complexes That Include a Molecule

Description

This function will retrieve a list of complexes that include your supplied molecule as a component.

Usage

```
rba_reactome_complex_list(id, resource, ...)
```

Arguments

id	Molecule's external Identifier
resource	What is the resource of your supplied ID? see: Reactome External Identifiers
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

Data frame where each row is a complex containing your supplied molecule and columns are pertinent information.

Corresponding API Resources

"GET https://reactome.org/ContentService/data/complexes/resource/ identifier"

References

- Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorsler S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. *Nucleic Acids Res.* 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031. PubMed PMID: 31691815.
- [Reactome Content Services API Documentation](#)

See Also

Other "Reactome Content Service - Physical Entity Queries": [rba_reactome_complex_subunits\(\)](#), [rba_reactome_entity_other_forms\(\)](#), [rba_reactome_participant_of\(\)](#)

Examples

```
rba_reactome_complex_list(id = "3845", resource = "NCBI Gene")
```

```
rba_reactome_complex_list(id = "P00533", resource = "UniProt")
```

rba_reactome_complex_subunits

Get a Complex's Subunits

Description

This function will return a list of subunits which are participants of your supplied complex.

rba_reactome_diseases *Reactome Diseases*

Description

This function Retrieve a list of all diseases or disease DOIDs annotated in Reactome.

Usage

```
rba_reactome_diseases(doid = FALSE, ...)
```

Arguments

doid	(logical) Return disease DOIDs instead of diseases? (default = FALSE)
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

Data frame containing all the disease annotation available at Reactome. If doid was set to TRUE, DOID info will be returned instead.

Corresponding API Resources

"GET https://reactome.org/ContentService/GET data/diseases" "GET https://reactome.org/ContentService/GET data/diseases/doid"

References

- Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorsler S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. *Nucleic Acids Res.* 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031. PubMed PMID: 31691815.
- [Reactome Content Services API Documentation](#)

Examples

```
rba_reactome_diseases()
```

```
rba_reactome_diseases(doid = TRUE)
```

`rba_reactome_entity_other_forms`*Get Other forms of a Reactome Entity*

Description

This function retrieve a list containing all other forms of your supplied Physical Entity ID.

Usage

```
rba_reactome_entity_other_forms(entity_id, ...)
```

Arguments

<code>entity_id</code>	Reactome's entity ID.
<code>...</code>	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

According to Reactome API documentation, "These other forms are Physical Entities that share the same Reference Entity identifier, e.g. PTEN H93R R-HSA-2318524 and PTEN C124R R-HSA-2317439 are two forms of PTEN."

Value

Data frame where each row is other forms of your supplied Entity ID and columns are pertinent information.

Corresponding API Resources

"GET <https://reactome.org/ContentService/data/entity/id/otherForms>"

References

- Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorsler S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. *Nucleic Acids Res.* 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031. PubMed PMID: 31691815.
- [Reactome Content Services API Documentation](#)

See Also

Other "Reactome Content Service - Physical Entity Queries": [rba_reactome_complex_list\(\)](#), [rba_reactome_complex_subunits\(\)](#), [rba_reactome_participant_of\(\)](#)

Examples

```
rba_reactome_entity_other_forms("R-HSA-199420")
```

```
rba_reactome_event_ancestors
```

Get Reactome Events Ancestors

Description

Along with Reactome's events hierarchy, This function will retrieve all the events beginning from your supplied event up to the "Top level Pathway". see "Details section" for more information.

Usage

```
rba_reactome_event_ancestors(event_id, ...)
```

Arguments

event_id	Reactome event's identifier.
...	rbaapi option(s). See rba_options 's arguments manual for more information on available options.

Details

By Reactome's definition, Events are the building blocks of biological processes and could be of two main classes: "Pathway" or "Reaction-like events". The events are organized in a hierarchical structure; and each event could be child or parent to another event; The hierarchy will always begin with a "Top level pathway" event. Also note that a given event could be part of more than one hierarchies.

Value

List which every element is a Data frame listing your supplied event along with it's ancestor events. Because any given event can be part of more than one pathway hierarchy, the list may contain multiple data frames.

Corresponding API Resources

"GET <https://reactome.org/ContentService/data/event/id/ancestors>"

References

- Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorsler S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. *Nucleic Acids Res.* 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031. PubMed PMID: 31691815.
- [Reactome Content Services API Documentation](#)

See Also

Other "Reactome Content Service - Queries Related to Events": [rba_reactome_event_hierarchy\(\)](#)

Examples

```
rba_reactome_event_ancestors("R-HSA-5673001")
```

```
rba_reactome_event_hierarchy
```

Get Full Event Hierarchy of a Species

Description

This function will retrieve the full Events hierarchy of your supplied species. Directly under each species, each child element is a "top Level Pathway". You can traverse the events tree down by following the "children" element.

Usage

```
rba_reactome_event_hierarchy(species, ...)
```

Arguments

species	Numeric or Character: NCBI Taxonomy identifier (Human Taxonomy ID is 9606.) or species name (e.g. "Homo sapiens"). See rba_reactome_species or Reactome Data Schema: Entries: Species .
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

By Reactome's definition, Events are the building blocks of biological processes and could be of two main classes: "Pathway" or "Reaction-like events". The events are organized in a hierarchical structure; and each event could be child or parent to another event; The hierarchy will always begin with a "Top level pathway" event. Also note that a given event could be part of more than one hierarchies.

Value

List which is a representation of the species's events hierarchy described in the "Details section".

Corresponding API Resources

"GET <https://reactome.org/ContentService/data/eventsHierarchy/species>"

References

- Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorsler S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. *Nucleic Acids Res.* 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031. PubMed PMID: 31691815.
- [Reactome Content Services API Documentation](#)

See Also

Other "Reactome Content Service - Queries Related to Events": [rba_reactome_event_ancestors\(\)](#)

Examples

```
rba_reactome_event_hierarchy("Homo sapiens")
```

```
rba_reactome_event_hierarchy(9606)
```

```
rba_reactome_exporter_diagram
```

Get a Reactome Event Diagram

Description

This function could be called in two scenarios:

1. With `create_document = FALSE`: To retrieve an image of that event's Diagram.
2. With `create_document = TRUE`: To retrieve a PDF document with the event's diagram image and additional information.

see "Details section" for more information

Usage

```

rba_reactome_exporter_diagram(
  event_id,
  save_to = NULL,
  create_document = FALSE,
  resource = "TOTAL",
  diagram_profile = "Modern",
  analysis_profile = "Standard",
  token = NULL,
  exp_column = NULL,
  document_level = 1,
  output_format = "png",
  image_quality = 5,
  flag_element = NULL,
  flg_interactors = TRUE,
  sel = NULL,
  title = TRUE,
  margin = 15,
  ehld = FALSE,
  ...
)

```

Arguments

event_id	Reactome event's identifier.
save_to	NULL or Character: <ul style="list-style-type: none"> • NULL: Save the file to an automatically-generated path. • Character string: A valid file path to save the file to.
create_document	logical: Create PDF document instead of image? (default = FALSE)
resource	The analysis resource for which the results will be overlaid on top of the given pathways overview,
diagram_profile	Color profile of diagrams, should be either "Modern" (default) or "Standard".
analysis_profile	Color profile of analysis, should be one of: "Standard" (default), "Strosobar" or "Copper Plus"
token	The analysis Token for which the results will be overlaid on top of the given pathways overview. see: rba_reactome_analysis .
exp_column	numeric: (only if token is supplied) Specify the expression column for the overlay.
document_level	numeric: (Only if "create_document" is TRUE) if 0 (default) the event's children will not be included in the PDF document. Set this to 1 to include event's children.
output_format	(Only if "create_document" is FALSE) Image format of the saved diagram. Can be one of: png (default), jpeg, svg or gif.

image_quality	Numeric: (Only if "create_document" is FALSE), a number ranging from 1 to 10. 1 is the lowest quality and 10 is the highest (default = 5).
flag_element	(Only if "create_document" is FALSE) gene name, protein ID, chemical ID or Reactome ID of a diagram's element to be flagged.
flg_interactors	Logical: (Only if "create_document" is FALSE) Should the interactor be considered when flagging a diagram element? (default = TRUE)
sel	(Only if "create_document" is FALSE) CSV line for highlighting element(s) selection in the diagram.
title	Logical: (Only if "create_document" is FALSE) Should the pathway name be displayed below the image? (default = TRUE)
margin	Numeric: (Only if "create_document" is FALSE) A number ranging from 0 to 20 to set as the image's margin. (default = 15)
ehld	logical: (Only if "create_document" is FALSE) Should "Enhanced High Level Diagram" be considered?
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

If the function is called with `create_document = FALSE`:

The result will be an image with the format supplied in "output_format" argument. If the supplied event ID refers to a pathway, the image's content will be the that pathways diagram. If the supplied event ID refers to a sub-pathway or reaction event, the parent pathway's diagram will be exported, with that reaction or sub-pathway's events highlighted.

Note that to export an image of reaction-like event separately, you should use [rba_reactome_exporter_reaction](#).

If the function is called with `create_document = TRUE`:

A PDF document will contain an image of the event's diagram and the following information of that events: Summation, Literature references, Edit history type, location, compartments and diseases. note that if you call the function with "document level = 1", information of your supplied event's children will also be included.

Value

NULL, Based to the inputs, an image or PDF file will be saved to disk.

Corresponding API Resources

"GET <https://reactome.org/ContentService/exporter/diagram/identifier.ext>" "GET <https://reactome.org/ContentService/exporter/diagram/identifier.pdf>"

References

- Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorser S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. *Nucleic Acids Res.* 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031. PubMed PMID: 31691815.

- [Reactome Content Services API Documentation](#)

See Also

[rba_reactome_exporter_reaction](#) [rba_reactome_analysis](#)

Other "Reactome Content Service - Format Exporter": [rba_reactome_exporter_event\(\)](#), [rba_reactome_exporter_overview\(\)](#), [rba_reactome_exporter_reaction\(\)](#)

Examples

```
## Not run:
rba_reactome_exporter_diagram(event_id = "R-HSA-177929",
  create_document = FALSE)

## End(Not run)
## Not run:
rba_reactome_exporter_diagram(event_id = "R-HSA-6787403",
  create_document = FALSE)

## End(Not run)
## Not run:
rba_reactome_exporter_diagram(event_id = "R-HSA-177929",
  create_document = TRUE)

## End(Not run)
## Not run:
rba_reactome_exporter_diagram(event_id = "R-HSA-177929",
  output_format = "svg",
  save_to = "reactome_event_diagram.svg")

## End(Not run)
```

rba_reactome_exporter_event

Exports A Reactome Event to SBGN or SBML

Description

This function will export a supplied Reactome Event (Pathway or Reaction) to a SBGN (Systems Biology Graphical Notation) or SBML (Systems Biology Markup Language)

Usage

```
rba_reactome_exporter_event(event_id, output_format, save_to = NULL, ...)
```

Arguments

event_id	Reactome event's database IDs (DbId) or Stable IDs (StId).
output_format	Either "sbgn" or "sbml".
save_to	NULL or Character: <ul style="list-style-type: none"> • NULL: Save the file to an automatically-generated path. • Character string: A valid file path to save the file to.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

NULL, According to the inputs, a SBGN or SBML file will be saved to disk.

Corresponding API Resources

"GET https://reactome.org/ContentService//exporter/event/ identifier.sbgn" "GET https://reactome.org/ContentService//expo identifier.sbml"

References

- Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorsler S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. *Nucleic Acids Res.* 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031. PubMed PMID: 31691815.
- [Reactome Content Services API Documentation](#)

See Also

Other "Reactome Content Service - Format Exporter": [rba_reactome_exporter_diagram\(\)](#), [rba_reactome_exporter_ov](#), [rba_reactome_exporter_reaction\(\)](#)

Examples

```
## Not run:
rba_reactome_exporter_event(event_id = "R-HSA-177929",
  output_format = "sbgn",
  save_to = "R-HSA-177929.sbgn")

## End(Not run)
## Not run:
rba_reactome_exporter_event(event_id = "R-HSA-177929",
  output_format = "sbgn")

## End(Not run)
```

`rba_reactome_exporter_overview`*Get a Reactome Pathway Overview*

Description

This function will Save a Pathway Overview of the supplied specie as an image file.

Usage

```
rba_reactome_exporter_overview(  
  species,  
  output_format = "png",  
  save_to = NULL,  
  image_quality = 5,  
  flag_element = NULL,  
  flg_interactors = TRUE,  
  sel = NULL,  
  title = TRUE,  
  margin = 15,  
  diagram_profile = "Copper",  
  token = NULL,  
  resource = "TOTAL",  
  exp_column = NULL,  
  coverage = FALSE,  
  ...  
)
```

Arguments

<code>species</code>	Numeric or Character: NCBI Taxonomy identifier (Human Taxonomy ID is 9606.) or species name (e.g. "Homo sapiens"). See rba_reactome_species or Reactome Data Schema: Entries: Species .
<code>output_format</code>	Images format, Can be one of: png (default), jpeg, svg or gif.
<code>save_to</code>	NULL or Character: <ul style="list-style-type: none">• NULL: Save the file to an automatically-generated path.• Character string: A valid file path to save the file to.
<code>image_quality</code>	Numeric: A number ranging from 1 to 10. 1 is the lowest quality and 10 is the highest (default = 5).
<code>flag_element</code>	Gene name, protein ID, chemical ID or Reactome ID of a diagram's element to be flagged.
<code>flg_interactors</code>	Logical: Should the interactor be considered when flagging a diagram element? (default = TRUE)
<code>sel</code>	CSV line for highlighting element(s) selection in the diagram.

title	Logical: Should the pathway name be displayed below the image? (default = TRUE)
margin	Numeric: A number ranging from 0 to 20 to set as the image's margin. (default = 15)
diagram_profile	Color profile of diagrams, should be one of "Copper" (default), "Copper Plus", "Barium Lithium" or "calcium salts".
token	The analysis Token for which the results will be overlaid on top of the given pathways overview. see: rba_reactome_analysis .
resource	The analysis resource for which the results will be overlaid on top of the given pathways overview.
exp_column	numeric: (only if token is supplied) Specify the expression column for the overlay.
coverage	Logical: Should the analysis coverage values be overlaid? (default = FALSE)
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

NULL, Based to the inputs, an image file will be saved to disk.

Corresponding API Resources

"GET <https://reactome.org/ContentService/exporter/fireworks/species.ext>"

References

- Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorser S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. *Nucleic Acids Res.* 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031. PubMed PMID: 31691815.
- [Reactome Content Services API Documentation](#)

See Also

[rba_reactome_analysis](#)

Other "Reactome Content Service - Format Exporter": [rba_reactome_exporter_diagram\(\)](#), [rba_reactome_exporter_ev](#), [rba_reactome_exporter_reaction\(\)](#)

Examples

```
## Not run:
rba_reactome_exporter_overview(species = 9606,
  output_format = "svg",
  save_to = "human_pathways.svg")
```

```
## End(Not run)
## Not run:
rba_reactome_exporter_overview(species = 9606,
  token = 123456789)

## End(Not run)
```

```
rba_reactome_exporter_reaction
  Get a Reactome Reaction Event
```

Description

This function will Save a Reactome event of class "ReactionLikeEvent" as an image file.

Usage

```
rba_reactome_exporter_reaction(
  event_id,
  save_to = NULL,
  output_format = "png",
  resource = "TOTAL",
  diagram_profile = "Modern",
  analysis_profile = "Standard",
  token = NULL,
  exp_column = NULL,
  image_quality = 5,
  flag_element = NULL,
  flg_interactors = TRUE,
  sel = NULL,
  title = TRUE,
  margin = 15,
  ...
)
```

Arguments

event_id	Reactome Reaction-like event 's identifier.
save_to	NULL or Character: <ul style="list-style-type: none">• NULL: Save the file to an automatically-generated path.• Character string: A valid file path to save the file to.
output_format	Images format, Can be one of: png (default), jpeg, svg or gif.
resource	The analysis resource for which the results will be overlaid on top of the given pathways overview.

diagram_profile	Color profile of diagrams, should be one of "Copper" (default), "Copper Plus", "Barium Lithium" or "calcium salts".
analysis_profile	Color profile of analysis, should be one of: "Standard" (default), "Strosobar" or "Copper Plus".
token	The analysis Token for which the results will be overlaid on top of the given pathways overview. see: rba_reactome_analysis .
exp_column	numeric: (only if token is supplied) Specify the expression column for the overlay.
image_quality	Numeric: A number ranging from 1 to 10. 1 is the lowest quality and 10 is the highest (default = 5).
flag_element	Gene name, protein ID, chemical ID or Reactome ID of a diagram's element to be flagged.
flg_interactors	Logical: Should the interactor be considered when flagging a diagram element? (default = TRUE)
sel	CSV line for highlighting element(s) selection in the diagram.
title	Logical: Should the pathway name be displayed below the image? (default = TRUE)
margin	Numeric: A number ranging from 0 to 20 to set as the image's margin. (default = 15)
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

Note that this function will save Reaction-like event separately and out of it's parent pathway context. To overlay a Reaction on it's parent pathway, use [rba_reactome_exporter_diagram](#).

Value

NULL, Based to the inputs, an image file will be saved to disk.

Corresponding API Resources

"GET [https://reactome.org/ContentService//exporter/reaction/ identifier.ext](https://reactome.org/ContentService//exporter/reaction/identifier.ext)"

References

- Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorser S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. *Nucleic Acids Res.* 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031. PubMed PMID: 31691815.
- [Reactome Content Services API Documentation](#)

See Also

[rba_reactome_exporter_diagram](#) [rba_reactome_analysis](#)

Other "Reactome Content Service - Format Exporter": [rba_reactome_exporter_diagram\(\)](#), [rba_reactome_exporter_ev](#)
[rba_reactome_exporter_overview\(\)](#)

Examples

```
## Not run:
rba_reactome_exporter_diagram(event_id = "R-HSA-6787403",
  create_document = FALSE)

## End(Not run)
## Not run:
rba_reactome_exporter_diagram(event_id = "R-HSA-6787403",
  output_format = "svg",
  save_to = "reactome_reacion_image.svg")

## End(Not run)
```

rba_reactome_interactors_psicquic

The interface From Reactome to PSICQUIC

Description

You can call this function in two scenarios: 1- To retrieve information of all available PSICQUIC resources, call the function without providing any argument; i.e `rba_reactome_interactors_psicquic()`. 2-To retrieve a list of interactors of specific protein(s), fill out the function's arguments.

Usage

```
rba_reactome_interactors_psicquic(
  proteins = NULL,
  resource = NULL,
  details = TRUE,
  ...
)
```

Arguments

<code>proteins</code>	Proteins to retrieve PSICQUIC interactors.
<code>resource</code>	The PSICQUIC resource for your supplied proteins. Call <code>rba_reactome_interactors_psicquic()</code> without argument to get the available options.
<code>details</code>	Logical: If TRUE (default) a detailed list of interactors will be returned. If FALSE, only a summary of available interactors will be returned.
<code>...</code>	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

Depending your input, a list containing the detailed or summary of PSICQUIC interactions or a data frame of all registered PSICQUIC resources.

Corresponding API Resources

"POST https://reactome.org/ContentService/interactors/psicquic/molecules/resource/details" "POST https://reactome.org/ContentService/interactors/psicquic/molecules/resource/summary" "GET https://reactome.org/ContentService/interactors/psicquic/molecules/resource/details"

References

- Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorser S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. *Nucleic Acids Res.* 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031. PubMed PMID: 31691815.
- [Reactome Content Services API Documentation](#)

See Also

Other "Reactome Content Service - Molecule Interactors": [rba_reactome_interactors_static\(\)](#)

Examples

```
rba_reactome_interactors_psicquic()
```

```
rba_reactome_interactors_psicquic(proteins = c("TP53", "MYC"),  
  resource = "BioGrid",  
  details = FALSE)
```

```
rba_reactome_interactors_psicquic(proteins = c("TP53", "MYC"),  
  resource = "BioGrid",  
  details = TRUE)
```

rba_reactome_interactors_static

Get Static(IntAct) Interaction Information of a Protein

Description

Reactome maintain a locally host a version of IntAct(Static) interactions database. Using this function, you can retrieve IntAct information of a protein(s) in two scenarios:

1. If endpoint = "details" or "summary": Retrieve a detailed/summary information of your supplied protein accession(s) from IntAct database.
2. If endpoint = "pathway", Retrieve a list of Reactome pathways which include your supplied protein accession. Pathways with the class "TopLevelPathway" will be excluded.

Usage

```
rba_reactome_interactors_static(
  proteins,
  endpoint = "details",
  only_diagrammed = FALSE,
  species = NULL,
  ...
)
```

Arguments

proteins	Uniprot proteins accession(s). If endpoint = "pathway", only a single protein accession can be supplied.
endpoint	Can be one of: <ol style="list-style-type: none"> 1. "details": To return a detailed information of your supplied protein(s) accession. 2. "summary": To return a summary of your supplied protein(s) accession 3. "pathway": To return a list of pathways containing the interacting molecules (excluding TopLevelPathway class).
only_diagrammed	Logical: (only when "endpoint = "pathway") If TRUE, pathways without diagram will be excluded. (default = FALSE)
species	Only when "endpoint = "pathway", The scientific name of the species to search for the pathways. See rba_reactome_species or Reactome Data Schema: Entries: Species .
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

List which it's content varies based on the supplied "endpoint" argument.

Corresponding API Resources

"POST <https://reactome.org/ContentService/interactors/static/ molecules/details>"
 "POST <https://reactome.org/ContentService/interactors/static/ molecules/summary>"
 "GET <https://reactome.org/ContentService/interactors/static/ molecules/pathways>"

References

- Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorser S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. *Nucleic Acids Res.* 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031. PubMed PMID: 31691815.
- [Reactome Content Services API Documentation](#)

See Also

Other "Reactome Content Service - Molecule Interactors": [rba_reactome_interactors_psicquic\(\)](#)

Examples

```
rba_reactome_interactors_static(proteins = "Q9BXM7-1",  
                               endpoint = "pathways", species = "Homo sapiens")
```

```
rba_reactome_interactors_static(proteins = c("Q9BXM7-1", "Q13501"),  
                               endpoint = "details")
```

```
rba_reactome_interactors_static(proteins = c("Q9BXM7-1", "Q13501"),  
                               endpoint = "summary")
```

rba_reactome_mapping *Map External ID to Reactome Pathways/Reactions*

Description

By providing an external identifier from a given resource, you can retrieve a list of pathways/reactions that include your supplied ID.

Usage

```
rba_reactome_mapping(id, resource, map_to, species = "Homo sapiens", ...)
```

Arguments

id	Molecule's external Identifier
resource	What is the resource of your supplied ID? see: Reactome External Identifiers
map_to	Either "pathways" or "reactions".

species	Numeric or Character: NCBI Taxonomy identifier (Human is 9606), species name (e.g. "Homo sapiens") or Reactome DbId (e.g Homo sapiens is 48887). See rba_reactome_species or Reactome Data Schema: Entries: Species .
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

Data frame where each row is a pathway/reaction and columns are pertinent information.

Corresponding API Resources

"GET [https://reactome.org/ContentService/data/mapping/resource/ identifier/pathways](https://reactome.org/ContentService/data/mapping/resource/identifier/pathways)"
"GET [https://reactome.org/ContentService/data/mapping/resource/ identifier/reactions](https://reactome.org/ContentService/data/mapping/resource/identifier/reactions)"

References

- Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorser S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. *Nucleic Acids Res.* 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031. PubMed PMID: 31691815.
- [Reactome Content Services API Documentation](#)

Examples

```
rba_reactome_mapping(id = "PTEN", resource = "UniProt",  
  map_to = "reactions", species = 9606)
```

rba_reactome_orthology

Get Orthologous (Computationally Inferred) Events

Description

Reactome incorporate manually curated human reactions and PANTHER's protein homology data to Computationally infer events in other eukaryotic species.

Usage

```
rba_reactome_orthology(event_ids, species_dbid, ...)
```

Arguments

event_ids	Human Reactome event ID(s) to retrieve their orthologous events.
species_dbid	Reactome database ID (DbId) of the target species. (e.g Mus musculus is 48892). See rba_reactome_species or Reactome Data Schema: Entries: Species .
...	rbiapi option(s). See rba_options 's arguments manual for more information on available options.

Details

In version 73 (11 June 2020), using an orthology-based approach, Homo sapiens events was projected to 18,654 orthologous pathways (with 81,835 orthologous proteins) in 15 non-human species. See [Reactome Computationally Inferred Events](#) for more information.

Value

List containing found Orthologous event(s) in your supplied species and their pertinent information.

Corresponding API Resources

"POST <https://reactome.org/ContentService/data/orthologies/ids/species/speciesId>"

References

- Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorser S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. *Nucleic Acids Res.* 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031. PubMed PMID: 31691815.
- [Reactome Content Services API Documentation](#)

See Also

[rba_reactome_analysis_species](#)

Examples

```
rba_reactome_orthology(event_ids = c("R-HSA-6799198", " R-HSA-72764"),  
  species_dbid = 49633)
```

`rba_reactome_participants`*Get Participants of a Reactome Event*

Description

Participating molecules in a Reactome comprises set of 'Physical Entity' and 'Reference Entities' class objects. Use this function to retrieve all, only 'Physical Entity' or only 'Reference Entities' participants of given event.

Usage

```
rba_reactome_participants(  
  event_id,  
  only_physical_entities = FALSE,  
  only_reference_entities = FALSE,  
  ...  
)
```

Arguments

<code>event_id</code>	Reactome event's database ID (DbId) or Stable ID (StId).
<code>only_physical_entities</code>	Logical: If TRUE, only participating 'Physical Entities' will be returned.
<code>only_reference_entities</code>	Logical: If TRUE, only participating 'Reference Entities' will be returned.
<code>...</code>	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

A 'Physical Entity' Instance could include an individual molecule, a multi-molecular complex or a set of molecule forming a group based on some characteristics. a single molecule can have different 'Physical Entity' instances based on it's associated attributes. For example, IgK Ig kappa chain, has two 'Physical Entity' instances; one, with ID "[R-HSA-197041](#)" refers to the secreted antibody protein to the extra-cellular region; And the second one is with ID "[R-HSA-2038819](#)" and refers to the plasma-membrane-integrated form of the antibody protein.

To make it possible to link multiple 'Physical Entity' instances of a molecule, Reactome uses a data class named "'Reference Entities'" which correspond to the invariant attribute of a molecule. for example, both of the above-mentioned 'Physical Entities' see a 'Reference Entities' named "[UniProt:P01834 IGKC](#)".

See [Reactome Data Model](#) for more information about the data model and Physical Entities.

Value

List with the participant of your supplied Event ID. A Data frame if only physical or 'Reference Entities' was requested.

Corresponding API Resources

```
"GET https://reactome.org/ContentService/data/participants/id"  
"GET https://reactome.org/ContentService/data/participants/id/ participatingPhysicalEntities"  
"GET https://reactome.org/ContentService/data/participants/id/ referenceEntities"
```

References

- Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorsler S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. *Nucleic Acids Res.* 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031. PubMed PMID: 31691815.
- [Reactome Content Services API Documentation](#)

See Also

[rba_reactome_participant_of](#)

Examples

```
rba_reactome_participants("R-HSA-5682012")
```

```
rba_reactome_participants("R-HSA-5682012", only_physical_entities = TRUE)
```

```
rba_reactome_participants("R-HSA-5682012", only_reference_entities = TRUE)
```

rba_reactome_participant_of

Get Larger Reactome Structures Which Include an Entity

Description

This function will retrieve a list of complexes and sets that Your supplied entity ID participates in (e.g. as a complex component, reaction output).

Usage

```
rba_reactome_participant_of(entity_id, ...)
```

Arguments

entity_id	Reactome's entity ID.
...	rbaapi option(s). See rba_options 's arguments manual for more information on available options.

Value

List of Reactome database Entities which Your supplied ID is a participant in them.

Corresponding API Resources

"GET <https://reactome.org/ContentService/data/entity/id/componentOf>"

References

- Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorsler S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. *Nucleic Acids Res.* 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031. PubMed PMID: 31691815.
- [Reactome Content Services API Documentation](#)

See Also

[rba_reactome_participants](#)

Other "Reactome Content Service - Physical Entity Queries": [rba_reactome_complex_list\(\)](#), [rba_reactome_complex_subunits\(\)](#), [rba_reactome_entity_other_forms\(\)](#)

Examples

```
rba_reactome_participant_of(entity_id = "R-HSA-199420")
```

rba_reactome_pathways_events

Get Events Contained in an Upstream Events

Description

A Reactome Event could be comprised of other events (meaning, a pathway that include other pathways itself). Use this function to recursively return all the events which reside downstream of your supplied event ID (or an attribute of that events).

Usage

```
rba_reactome_pathways_events(event_id, attribute_name = NULL, ...)
```

Arguments

event_id	Reactome event's database ID (DbId) or Stable ID (StId).
attribute_name	An attribute of the events to be returned instead of the whole events. see Reactome Data Schema: Event for available options.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

By Reactome's definition, Events are the building blocks of biological processes and could be of two main classes: "Pathway" or "Reaction-like events". The events are organized in a hierarchical structure; and each event could be child or parent to another event; The hierarchy will always begin with a "Top level pathway" event. Also note that a given event could be part of more than one hierarchies.

Value

Data frame where each row is a contained event and columns are event's attributes. If an "attribute_name" argument was supplied, a character vector will be returned.

Corresponding API Resources

"GET <https://reactome.org/ContentService/data/pathway/id/> containedEvents"

"GET <https://reactome.org/ContentService/data/pathway/id/> containedEvents/attributeName"

References

- Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorser S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. *Nucleic Acids Res.* 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031. PubMed PMID: 31691815.
- [Reactome Content Services API Documentation](#)

See Also

Other "Reactome Content Service - Pathway Related Queries": [rba_reactome_pathways_low\(\)](#), [rba_reactome_pathways_top\(\)](#)

Examples

```
rba_reactome_pathways_events(event_id = "R-HSA-5673001")
```

```
rba_reactome_pathways_events(event_id = "R-HSA-5673001",
  attribute_name = "displayName")
```

 rba_reactome_pathways_low

Get lower level pathways Containing a 'Physical Entity' or Event

Description

Use this function to search the event hierarchy and retrieve a list of all lower level pathways (non TopLevelPathway class) that contain a given 'Physical Entity' or Event. See "Arguments section" on how to modify your search.

Usage

```
rba_reactome_pathways_low(
  entity_id,
  with_diagram = FALSE,
  all_forms = FALSE,
  species = NULL,
  ...
)
```

Arguments

entity_id	The entity that should exist in the pathways.
with_diagram	Logical: only include pathways with diagram?
all_forms	Logical: should other variants of your supplied entity_id be considered? (e.g. same molecule but in different compartment, secretory form etc.) see rba_reactome_participants's "Details section" to learn more about how Reactome classifies molecules.
species	(optional) Numeric or Character: confine your search to a specific species by providing it's NCBI Taxonomy identifier (Human Taxonomy ID is 9606) or species name (e.g. "Homo sapiens"). See rba_reactome_species or Reactome Data Schema: Entries: Species .
...	rbioapi option(s). See rba_options's arguments manual for more information on available options.

Value

Data frame where each row is a pathway that contains your supplied entity and columns are pertinent information.

Corresponding API Resources

"GET <https://reactome.org/ContentService/data/pathways/low/entity/id>"

"GET <https://reactome.org/ContentService/data/pathways/low/diagram/entity/id>"

"GET <https://reactome.org/ContentService/data/pathways/low/diagram/entity/id/allForms>"

References

- Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorser S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. *Nucleic Acids Res.* 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031. PubMed PMID: 31691815.
- [Reactome Content Services API Documentation](#)

See Also

Other "Reactome Content Service - Pathway Related Queries": [rba_reactome_pathways_events\(\)](#), [rba_reactome_pathways_top\(\)](#)

Examples

```
rba_reactome_pathways_low(entity_id = "R-HSA-199420")
```

```
rba_reactome_pathways_low(entity_id = "R-HSA-199420", with_diagram = TRUE)
```

```
rba_reactome_pathways_low(entity_id = "R-HSA-199420", with_diagram = TRUE,  
  all_forms = TRUE)
```

```
rba_reactome_pathways_top
```

Get Top Level Pathways in a Species

Description

This function will Return a list of all pathways with the class "TopLevelPathway" which are annotated in your supplied species.

Usage

```
rba_reactome_pathways_top(species, ...)
```

Arguments

species	Numeric or Character: NCBI Taxonomy identifier (Human Taxonomy ID is 9606.) or species name (e.g. "Homo sapiens"). See rba_reactome_species or Reactome Data Schema: Entries: Species .
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

Reactome's Events hierarchy for any specie will begin with pathways with class "TopLevelPathway" (e.g. "Immune System", "Metabolism of proteins"). further down in the event's hierarchy tree, each TopLevelPathway has other events itself (e.g. "Adaptive immune system", "Innate immune system"). Based on the chosen pathway, the hierarchy tree would typically goes further down.

Value

Data frame where each row is a Top Level Pathway and columns are pertinent information.

Corresponding API Resources

"GET <https://reactome.org/ContentService/data/pathways/top/species>"

References

- Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorsler S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. *Nucleic Acids Res.* 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031. PubMed PMID: 31691815.
- [Reactome Content Services API Documentation](#)

See Also

Other "Reactome Content Service - Pathway Related Queries": [rba_reactome_pathways_events\(\)](#), [rba_reactome_pathways_low\(\)](#)

Examples

```
rba_reactome_pathways_top(species = 9606)
```

```
rba_reactome_pathways_top(species = "Saccharomyces cerevisiae")
```

rba_reactome_people_id

A person by his identifiers

Description

A person by his identifiers

Usage

```
rba_reactome_people_id(
  person_id,
  authored_pathways = FALSE,
  publications = FALSE,
  attribute_name = NULL,
  ...
)
```

Arguments

person_id	Reactome database ID (DbId) or ORCHID ID
authored_pathways	Logical: Only return Pathway list authored by the person? (default = FALSE)
publications	Logical: Only return publications list authored by the person? (Default = FALSE)
attribute_name	(optional) A Reactome person attribute to return only. see Reactome Data Schema: person for available options.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

List containing the requested informations of your supplied person.

Corresponding API Resources

"GET <https://reactome.org/ContentService>"

References

- Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorsler S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. *Nucleic Acids Res.* 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031. PubMed PMID: 31691815.
- [Reactome Content Services API Documentation](#)

See Also

Other "Reactome Content Service - Person Queries": [rba_reactome_people_name\(\)](#)

Examples

```
rba_reactome_people_id("391309")
```

```
rba_reactome_people_id(person_id = "391309", authored_pathways = TRUE)
```

rba_reactome_people_name

Get Persons Information by Name

Description

Using this function you can query people by partially matching or exact name and retrieve a list of matching people in Reactome.

Usage

```
rba_reactome_people_name(person_name, exact_match = FALSE, ...)
```

Arguments

person_name	first and last name of the person
exact_match	Logical: should the supplied name be considered as an exact match? (default = FALSE)
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

List where each element is a search hit contains the person's information.

Corresponding API Resources

"GET https://reactome.org/ContentService/data/people/name/name"

"GET https://reactome.org/ContentService/data/people/name/name/exact"

References

- Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorsler S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. *Nucleic Acids Res.* 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031. PubMed PMID: 31691815.
- [Reactome Content Services API Documentation](#)

See Also

Other "Reactome Content Service - Person Queries": [rba_reactome_people_id\(\)](#)

Examples

```
rba_reactome_people_name("Jupe")
```

```
rba_reactome_people_name("Steve Jupe", exact_match = TRUE)
```

rba_reactome_query *Query and Retrieve any Reactome knowledge-base Object*

Description

Using this Comprehensive function, You can Retrieve any object from **Reactome knowledge-base**

Usage

```
rba_reactome_query(
  ids,
  enhanced = FALSE,
  map = FALSE,
  attribute_name = NULL,
  ...
)
```

Arguments

ids	A single or Multiple database IDs (DbId), Stable IDs (StId) or a mixture of both.
enhanced	Logical: (Default = FALSE) If 'TRUE' more information on the supplied entry will be returned. (You can set this argument to 'TRUE' Only when you supply a single ID).
map	(Default = FALSE) Should the supplied IDs be mapped? This argument will only be considered when you supply multiple IDs. (e.g. when you supply previous version of stable identifiers.)
attribute_name	(Optional) Only Return an Attribute of the supplied Database Object. (You can use this argument Only when you supply a single ID)
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

List containing your query outputs.

Corresponding API Resources

```
"POST https://reactome.org/ContentService/data/query/ids"  
"POST https://reactome.org/ContentService/data/query/ids/map"  
"GET https://reactome.org/ContentService/data/query/id"  
s"GET https://reactome.org/ContentService//data/query/enhanced/id"  
"GET https://reactome.org/ContentService/data/query/id/attributeName"
```

References

- Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorsler S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. *Nucleic Acids Res.* 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031. PubMed PMID: 31691815.
- [Reactome Content Services API Documentation](#)

Examples

```
rba_reactome_query(ids = c("8953958", "11982506", "R-ALL-9649879"))
```

```
rba_reactome_query(ids = "R-HSA-9656256", enhanced = TRUE)
```

```
rba_reactome_query(ids = "8863054", attribute_name = "displayName")
```

```
rba_reactome_species Get Reactome Species
```

Description

Use this function to retrieve a table of Available species in Reactome.

Usage

```
rba_reactome_species(only_main = FALSE, ...)
```

Arguments

only_main	Logical: If set to TRUE, will only return species which have either manually-curated or computationally inferred pathways.
...	rbiapi option(s). See rba_options 's arguments manual for more information on available options.

Value

Data frame where each row is a species and columns are pertinent information.

Corresponding API Resources

"GET https://reactome.org/ContentService/data/species/all"

"GET https://reactome.org/ContentService/data/species/main"

References

- Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorsler S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. *Nucleic Acids Res.* 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031. PubMed PMID: 31691815.
- [Reactome Content Services API Documentation](#)

Examples

```
rba_reactome_species()
```

```
rba_reactome_species(only_main = TRUE)
```

rba_reactome_version *The version number of current database*

Description

Returns the current version of Reactome database.

Usage

```
rba_reactome_version(...)
```

Arguments

... `rbioapi` option(s). See [rba_options](#)'s arguments manual for more information on available options.

Value

Character string containing the version of Reactome database.

Corresponding API Resources

"GET <https://reactome.org/ContentService/data/database/version>"

References

- Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorser S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. *Nucleic Acids Res.* 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031. PubMed PMID: 31691815.
- [Reactome Content Services API Documentation](#)

Examples

```
rba_reactome_version()
```

rba_reactome_xref *Map Cross References IDs to Reactome ReferenceEntity*

Description

Use this function To retrieve a list of Reactome ReferenceEntity associated to your supplied Cross Reference (i.e. External) ID.

Usage

```
rba_reactome_xref(xref_id, ...)
```

Arguments

xref_id	molecule's cross-reference (external) identifier.
...	rbaapi option(s). See rba_options 's arguments manual for more information on available options.

Details

Reactome cross-references external database's identifiers to it's database Entries named ReferenceEntity, which resembles the invariant aspect of a molecule. Thus there is a one-to-many relationship between Reactome's ReferenceEntity object and the molecule's ID in external databases, which in Reactome's terms is called Cross Reference.

See [rba_reactome_participants](#)'s "Details section" to learn more about how Reactome classifies molecules.

Value

List containing the ReferenceEntity corresponding to your supplied cross-reference (external) ID.

Corresponding API Resources

"GET https://reactome.org/ContentService/references/mapping/identifier"

References

- Jassal B, Matthews L, Viteri G, Gong C, Lorente P, Fabregat A, Sidiropoulos K, Cook J, Gillespie M, Haw R, Loney F, May B, Milacic M, Rothfels K, Sevilla C, Shamovsky V, Shorsler S, Varusai T, Weiser J, Wu G, Stein L, Hermjakob H, D'Eustachio P. The reactome pathway knowledgebase. *Nucleic Acids Res.* 2020 Jan 8;48(D1):D498-D503. doi: 10.1093/nar/gkz1031. PubMed PMID: 31691815.
- [Reactome Content Services API Documentation](#)

Examples

```
rba_reactome_xref("CD40")
```

```
rba_reactome_xref("ENSP00000361350")
```

rba_string_annotations

Retrieving Functional Annotation

Description

STRING cross-reference the proteins with several databases (see "Details" section). By providing your input set of proteins (and optionally background or universe protein set), you can use this function to retrieve full set of terms (annotations) pertinent to your input proteins in each database, along with information for each term.

Usage

```
rba_string_annotations(ids, species = NULL, allow_pubmed = FALSE, ...)
```

Arguments

ids	Your protein ID(s). It is strongly recommended to supply STRING IDs. See rba_string_map_ids for more information.
species	Numeric: NCBI Taxonomy identifier; Human Taxonomy ID is 9606. (Recommended, but optional if your input is less than 100 IDs.)

- allow_pubmed logical: (default = FALSE) PubMed usually assigns a large number of reference publications to each protein. In order to reduce the output size, PubMed's results will be excluded from the results, unless stated otherwise (By setting this argument to TRUE).
- ... rbioapi option(s). See [rba_options](#)'s arguments manual for more information on available options.

Details

STRING currently maps to and retrieve enrichment results based on Gene Ontology (GO), KEGG pathways, UniProt Keywords, PubMed publications, Pfam domains, InterPro domains, and SMART domains.

Note that this function will return a full list of the terms containing your supplied proteins. To perform enrichment and only retrieve a enriched subset of the terms, use [rba_string_enrichment](#).

Value

A data frame which every row is an assigned terms and the columns are the terms category, description, number of genes, and other pertinent information.

Corresponding API Resources

"POST [https://string-db.org/api/\[output_format\]/functional_annotation? identifiers=\[your_identifiers\]&\[optional_parameters\]](https://string-db.org/api/[output_format]/functional_annotation? identifiers=[your_identifiers]&[optional_parameters])

References

- Szklarczyk D, Gable AL, Lyon D, Junge A, Wyder S, Huerta-Cepas J, Simonovic M, Doncheva NT, Morris JH, Bork P, Jensen LJ, Mering CV. STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. *Nucleic Acids Res.* 2019 Jan 8;47(D1):D607-D613. doi: 10.1093/nar/gky1131. PMID: 30476243; PMCID: PMC6323986.
- [STRING API Documentation](#)

See Also

[rba_string_map_ids](#), [rba_string_enrichment](#)

Other "STRING": [rba_string_enrichment_ppi\(\)](#), [rba_string_enrichment\(\)](#), [rba_string_homology_inter\(\)](#), [rba_string_homology_intra\(\)](#), [rba_string_interaction_partners\(\)](#), [rba_string_interactions_network\(\)](#), [rba_string_map_ids\(\)](#), [rba_string_network_image\(\)](#), [rba_string_version\(\)](#)

Examples

```
rba_string_annotations(ids = "TP53", species = 9606)
```

rba_string_enrichment *Getting Functional Enrichment*

Description

STRING cross-reference the proteins with several databases (see "Details" section). By providing your input set of proteins (and optionally background or universe protein set), you can use this function to perform enrichment test and retrieve a list of enriched terms in each database, along with pertinent information for each term.

Usage

```
rba_string_enrichment(  
  ids,  
  species = NULL,  
  background = NULL,  
  split_df = FALSE,  
  ...  
)
```

Arguments

<code>ids</code>	Your protein ID(s). It is strongly recommended to supply STRING IDs. See rba_string_map_ids for more information.
<code>species</code>	Numeric: NCBI Taxonomy identifier; Human Taxonomy ID is 9606. (Recommended, but optional if your input is less than 100 IDs.)
<code>background</code>	character vector: A set of STRING protein IDs to be used as the statistical background (or universe) when computing P-value for the terms. Only STRING IDs are acceptable. (See rba_string_map_ids to map your IDs.)
<code>split_df</code>	(logical, default = FALSE), If TRUE, instead of one data frame, results from different categories will be split into multiple data frames based on their 'category'.
<code>...</code>	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

STRING currently maps to and retrieve enrichment results based on Gene Ontology (GO), KEGG pathways, UniProt Keywords, PubMed publications, Pfam domains, InterPro domains, and SMART domains.

Note that this function will only return the enriched terms pertinent to your proteins that have a p-value lesser than 0.1. To retrieve a full list of the terms -unfiltered by enrichment p-values-, use [rba_string_annotatations](#).

Value

A data frame which every row is an enriched terms with p-value smaller than 0.1 and the columns are the terms category, description, number of genes, p-value, fdr and other pertinent information.

Corresponding API Resources

"POST [https://string-db.org/api/\[output_format\]/enrichment?identifiers= \[your_identifiers\]&\[optional_parameters\]](https://string-db.org/api/[output_format]/enrichment?identifiers=[your_identifiers]&[optional_parameters])"

References

- Szklarczyk D, Gable AL, Lyon D, Junge A, Wyder S, Huerta-Cepas J, Simonovic M, Doncheva NT, Morris JH, Bork P, Jensen LJ, Mering CV. STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. *Nucleic Acids Res.* 2019 Jan 8;47(D1):D607-D613. doi: 10.1093/nar/gky1131. PMID: 30476243; PMCID: PMC6323986.
- [STRING API Documentation](#)

See Also

[rba_string_map_ids](#), [rba_string_annotations](#)

Other "STRING": [rba_string_annotations\(\)](#), [rba_string_enrichment_ppi\(\)](#), [rba_string_homology_inter\(\)](#), [rba_string_homology_intra\(\)](#), [rba_string_interaction_partners\(\)](#), [rba_string_interactions_network\(\)](#), [rba_string_map_ids\(\)](#), [rba_string_network_image\(\)](#), [rba_string_version\(\)](#)

Examples

```
rba_string_enrichment(ids = c("TP53", "TNF", "EGFR"), species = 9606)
```

rba_string_enrichment_ppi

Get Protein-Protein Interaction Enrichment

Description

Even when there is no annotation for your input proteins, STRING can Compare your Given proteins interactions pattern with the background proteome-wide interaction distribution to determine if your given set of proteins are functionally related.

Usage

```
rba_string_enrichment_ppi(ids, species = NULL, required_score = NULL, ...)
```

Arguments

ids	Your protein ID(s). It is strongly recommended to supply STRING IDs. See rba_string_map_ids for more information.
species	Numeric: NCBI Taxonomy identifier; Human Taxonomy ID is 9606. (Recommended, but optional if your input is less than 100 IDs.)
required_score	Numeric: A minimum of interaction score for an interaction to be included in the image. if not supplied, the threshold will be applied by STRING Based in the network. (low Confidence = 150, Medium Confidence = 400, High Confidence = 700, Highest confidence = 900)
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A list with protein-protein interaction enrichment results.

Corresponding API Resources

"POST [https://string-db.org/api/\[output_format\]/ppi_enrichment?identifiers=\[your_identifiers\]&\[optional_parameters\]](https://string-db.org/api/[output_format]/ppi_enrichment?identifiers=[your_identifiers]&[optional_parameters])"

References

- Szklarczyk D, Gable AL, Lyon D, Junge A, Wyder S, Huerta-Cepas J, Simonovic M, Doncheva NT, Morris JH, Bork P, Jensen LJ, Mering CV. STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. *Nucleic Acids Res.* 2019 Jan 8;47(D1):D607-D613. doi: 10.1093/nar/gky1131. PMID: 30476243; PMCID: PMC6323986.
- [STRING API Documentation](#)

See Also

[rba_string_map_ids](#)

Other "STRING": [rba_string_annotations\(\)](#), [rba_string_enrichment\(\)](#), [rba_string_homology_inter\(\)](#), [rba_string_homology_intra\(\)](#), [rba_string_interaction_partners\(\)](#), [rba_string_interactions_network\(\)](#), [rba_string_map_ids\(\)](#), [rba_string_network_image\(\)](#), [rba_string_version\(\)](#)

Examples

```
rba_string_enrichment_ppi(ids = c("p53", "BRCA1", "cdk2", "Q99835",
  "CDC42", "CDK1", "KIF23", "PLK1", "RAC2", "RACGAP1"),
  species = 9606)
```

`rba_string_homology_inter`*Get Similarity Scores Hits of Proteins in Different Species*

Description

Using this function, you can retrieve highest Smith-Waterman bit scores among your input proteins and proteins in every other STRING species (e.g. the closest homologous protein of your input protein in other species). Bit Scores serve as similarity scores between protein sequence; And, according to STRING documentations, as a proxy for protein homology.

Usage

```
rba_string_homology_inter(ids, species = NULL, species_b = NULL, ...)
```

Arguments

<code>ids</code>	Your protein ID(s). It is strongly recommended to supply STRING IDs. See rba_string_map_ids for more information.
<code>species</code>	Numeric: NCBI Taxonomy identifier of your input proteins; Human Taxonomy ID is 9606. (Recommended, but optional if your input is less than 100 IDs.)
<code>species_b</code>	(optional) Numeric: one or more NCBI Taxonomy identifiers of species to limit the closets homologous proteins search.
<code>...</code>	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

Note that this function will return the highest similarity score hits of your given protein(s) and their closets homologous proteins in other species. to retrieve similarity scores of different proteins within the same species see [rba_string_homology_intra](#).

Similarity matrix is imported -by STRING- from: [Similarity Matrix of Proteins \(SIMAP\)](#)

Value

A data frame with Your input proteins and it's closest homologous proteins among all other (or a defined) STRING species.

Corresponding API Resources

"POST [https://string-db.org/api/\[output-format\]/homology_best? identifiers=\[your_identifiers\]](https://string-db.org/api/[output-format]/homology_best? identifiers=[your_identifiers])"

References

- Szklarczyk D, Gable AL, Lyon D, Junge A, Wyder S, Huerta-Cepas J, Simonovic M, Doncheva NT, Morris JH, Bork P, Jensen LJ, Mering CV. STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. *Nucleic Acids Res.* 2019 Jan 8;47(D1):D607-D613. doi: 10.1093/nar/gky1131. PMID: 30476243; PMCID: PMC6323986.
- [STRING API Documentation](#)

See Also

[rba_string_map_ids](#), [rba_string_homology_intra](#)

Other "STRING": [rba_string_annotations\(\)](#), [rba_string_enrichment_ppi\(\)](#), [rba_string_enrichment\(\)](#), [rba_string_homology_intra\(\)](#), [rba_string_interaction_partners\(\)](#), [rba_string_interactions_network\(\)](#), [rba_string_map_ids\(\)](#), [rba_string_network_image\(\)](#), [rba_string_version\(\)](#)

Examples

```
rba_string_homology_inter(ids = "p53",  
  species = 9606,  
  species_b = c(6087, 7070))
```

```
rba_string_homology_inter(ids = "ENSP00000269305", species = 9606)
```

rba_string_homology_intra

Get Similarity Scores Hits of Proteins in a Species

Description

Using this function, you can retrieve the Smith-Waterman bit scores among proteins of the same species. Bit Scores serve as similarity scores between protein sequence; And, according to STRING documentations, as a proxy for protein homology.

Usage

```
rba_string_homology_intra(ids, species = NULL, ...)
```

Arguments

ids	Your protein ID(s). It is strongly recommended to supply STRING IDs. See rba_string_map_ids for more information.
species	Numeric: NCBI Taxonomy identifier; Human Taxonomy ID is 9606. (Recommended, but optional if your input is less than 100 IDs.)

... rbioapi option(s). See [rba_options](#)'s arguments manual for more information on available options.

Details

Note that this function will retrieve similarity scores of different proteins "within the same species". To Get a similarity scores of a given protein and it's closets homologous proteins in other species, see [rba_string_homology_inter](#).

Similarity matrix is imported -by STRING- from: [Similarity Matrix of Proteins \(SIMAP\)](#)

Value

A data frame with bit scores between your supplied proteins and their self-hit. To Reduce the transferred data, STRING returns only one half of the similarity matrix; This will not pose a problem because similarity matrix is symmetrical.

Corresponding API Resources

"POST [https://string-db.org/api/\[output-format\]/homology?identifiers= \[your_identifiers\]](https://string-db.org/api/[output-format]/homology?identifiers=[your_identifiers])"

References

- Szklarczyk D, Gable AL, Lyon D, Junge A, Wyder S, Huerta-Cepas J, Simonovic M, Doncheva NT, Morris JH, Bork P, Jensen LJ, Mering CV. STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. *Nucleic Acids Res.* 2019 Jan 8;47(D1):D607-D613. doi: 10.1093/nar/gky1131. PMID: 30476243; PMCID: PMC6323986.
- [STRING API Documentation](#)

See Also

[rba_string_map_ids](#), [rba_string_homology_inter](#)

Other "STRING": [rba_string_annotations\(\)](#), [rba_string_enrichment_ppi\(\)](#), [rba_string_enrichment\(\)](#), [rba_string_homology_inter\(\)](#), [rba_string_interaction_partners\(\)](#), [rba_string_interactions_network\(\)](#), [rba_string_map_ids\(\)](#), [rba_string_network_image\(\)](#), [rba_string_version\(\)](#)

Examples

```
rba_string_homology_intra(ids = c("CDK1", "CDK2"), species = 9606)
```

```
rba_string_interactions_network
    Get STRING Network Interactions
```

Description

This function will retrieve Sting interaction pairs among your input protein ids, with the combined score and separate score for each STRING score channels. You can further expand your network to a defined size by providing "add_node" parameter.

Usage

```
rba_string_interactions_network(
    ids,
    species = NULL,
    required_score = NULL,
    add_nodes = NULL,
    network_type = "functional",
    ...
)
```

Arguments

ids	Your protein IDs. It is strongly recommended to supply STRING IDs. See rba_string_map_ids for more information.
species	Numeric: NCBI Taxonomy identifier; Human Taxonomy ID is 9606. (Recommended, but optional if your input is less than 100 IDs.)
required_score	Numeric: A minimum of interaction score for an interaction to be included in the image. if not supplied, the threshold will be applied by STRING Based in the network. (low Confidence = 150, Medium Confidence = 400, High Confidence = 700, Highest confidence = 900)
add_nodes	Numeric: Number of neighboring proteins to be added to the network. If none supplied by the user, this argument value will depend on the number of supplied "ids" argument: <ol style="list-style-type: none"> 1. Single id: add_node will be set to 10 to retrieve the interaction neighborhood of you input protein. 2. Multiple ids: add_node will be set to 0, thus the output will be the interactions between your input proteins.
network_type	should be one of: <ul style="list-style-type: none"> • "functional": (default) The edge's indicate both physical and functional associations. • "physical": The edges indicate that two proteins have a physical interaction or are parts of a complex.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

Note that this function will return interactions between your set of supplied proteins, or at most, expand the interaction network by the given parameters. TO retrieve a list of all possible interacting proteins with your given input, see [rba_string_interaction_partners](#).

Value

A data frame which each row is a network interaction and the columns contains interactor information and interaction scores:

- stringId_A: STRING identifier (protein A)
- stringId_B: STRING identifier (protein B)
- preferredName_A: common protein name (protein A)
- preferredName_B: common protein name (protein B)
- ncbiTaxonId: NCBI taxon identifier
- score: combined score
- nscore: gene neighborhood score
- fscore: gene fusion score
- pscore: phylogenetic profile score
- ascore: co-expression score
- escore: experimental score
- dscore: database score
- tscore: textmining score

Corresponding API Resources

"POST [https://string-db.org/api/\[output-format\]/network?identifiers=\[your_identifiers\]&\[optional_parameters\]](https://string-db.org/api/[output-format]/network?identifiers=[your_identifiers]&[optional_parameters])"

References

- Szklarczyk D, Gable AL, Lyon D, Junge A, Wyder S, Huerta-Cepas J, Simonovic M, Doncheva NT, Morris JH, Bork P, Jensen LJ, Mering CV. STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. *Nucleic Acids Res.* 2019 Jan 8;47(D1):D607-D613. doi: 10.1093/nar/gky1131. PMID: 30476243; PMCID: PMC6323986.
- [STRING API Documentation](#)

See Also

[rba_string_map_ids](#), [rba_string_interaction_partners](#)

Other "STRING": [rba_string_annotations\(\)](#), [rba_string_enrichment_ppi\(\)](#), [rba_string_enrichment\(\)](#), [rba_string_homology_inter\(\)](#), [rba_string_homology_intra\(\)](#), [rba_string_interaction_partners\(\)](#), [rba_string_map_ids\(\)](#), [rba_string_network_image\(\)](#), [rba_string_version\(\)](#)

Examples

```
rba_string_interactions_network(ids = c("9606.ENSP00000269305",
    "9606.ENSP00000398698",
    "9606.ENSP00000275493"),
    network_type = "functional")
```

```
rba_string_interactions_network(ids = c("9606.ENSP00000269305",
    "9606.ENSP00000398698",
    "9606.ENSP00000275493"),
    species = 9606,
    add_nodes = 10)
```

rba_string_interaction_partners

Get All STRING Interaction Partners

Description

This function will retrieve all the STRING interactions which include your proteins as one party of the interaction. (e.g. interaction between your proteins and every other STRING proteins.)

Given the size of STRING database, this function could return a very long results. See "Arguments" section for information on how to filter the interactions.

Usage

```
rba_string_interaction_partners(
  ids,
  species = NULL,
  required_score = NULL,
  network_type = "functional",
  limit = NULL,
  ...
)
```

Arguments

ids	Your protein ID(s). It is strongly recommended to supply STRING IDs. See rba_string_map_ids for more information.
species	Numeric: NCBI Taxonomy identifier; Human Taxonomy ID is 9606. (Recommended, but optional if your input is less than 100 IDs.)
required_score	Numeric: A minimum of interaction score for an interaction to be included in the image. if not supplied, the threshold will be applied by STRING Based in the network. (low Confidence = 150, Medium Confidence = 400, High Confidence = 700, Highest confidence = 900)

network_type	should be one of: <ul style="list-style-type: none"> • "functional": (default) The edge's indicate both physical and functional associations.
limit	Limit the number returned interaction partners per each of your input proteins. (e.g. Number of the most confident interaction partner to return per each input protein.)
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

Note that this function will retrieve the interactions between your input proteins and every other STRING proteins. To retrieve the interaction among your input protein-set, see [rba_string_interactions_network](#).

Value

A data frame which each row is a network interaction and the columns contains interactor information and interaction scores.

Corresponding API Resources

"POST [https://string-db.org/api/\[output-format\]/interaction_partners?identifiers=\[your_identifiers\]&\[optional_parameters\]](https://string-db.org/api/[output-format]/interaction_partners?identifiers=[your_identifiers]&[optional_parameters])"

References

- Szklarczyk D, Gable AL, Lyon D, Junge A, Wyder S, Huerta-Cepas J, Simonovic M, Doncheva NT, Morris JH, Bork P, Jensen LJ, Mering CV. STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. *Nucleic Acids Res.* 2019 Jan 8;47(D1):D607-D613. doi: 10.1093/nar/gky1131. PMID: 30476243; PMCID: PMC6323986.
- [STRING API Documentation](#)

See Also

[rba_string_map_ids](#), [rba_string_interactions_network](#)

Other "STRING": [rba_string_annotations\(\)](#), [rba_string_enrichment_ppi\(\)](#), [rba_string_enrichment\(\)](#), [rba_string_homology_inter\(\)](#), [rba_string_homology_intra\(\)](#), [rba_string_interactions_network\(\)](#), [rba_string_map_ids\(\)](#), [rba_string_network_image\(\)](#), [rba_string_version\(\)](#)

Examples

```
rba_string_interaction_partners(ids = c("9606.ENSP00000269305",
  "9606.ENSP00000398698",
  "9606.ENSP00000275493"),
  network_type = "functional")
```

```
rba_string_interaction_partners(ids = "9606.ENSP00000269305",
```

```
species = 9606,
required_score = 700)
```

rba_string_map_ids *Map a Set of Identifiers to STRING Identifiers*

Description

This function Calls STRING's API to Convert a set of identifiers to STRING Identifiers. Although You can call STRING services with a variety of common identifiers, It is recommended by STRING's documentations that you first map Your Protein/genes IDs to STRING IDs and then proceed with other STRING's functions.

Usage

```
rba_string_map_ids(ids, species = NULL, echo_query = FALSE, limit = NULL, ...)
```

Arguments

ids	Your Common gene/protein Identifier(s) to be mapped.
species	Numeric: NCBI Taxonomy identifier; Human Taxonomy ID is 9606. (Recommended, but optional if your input is less than 100 IDs.)
echo_query	(default = FALSE) Include your input IDs as a column of the results.
limit	(Numeric, Optional) A limit on the number of matches per input ID.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A data frame with the mapped STRING IDs and other pertinent information.

Corresponding API Resources

"POST [https://string-db.org/api/\[output-format\]/get_string_ids?identifiers=\[your_identifiers\]&\[optional_parameters\]](https://string-db.org/api/[output-format]/get_string_ids?identifiers=[your_identifiers]&[optional_parameters])"

References

- Szklarczyk D, Gable AL, Lyon D, Junge A, Wyder S, Huerta-Cepas J, Simonovic M, Doncheva NT, Morris JH, Bork P, Jensen LJ, Mering CV. STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. *Nucleic Acids Res.* 2019 Jan 8;47(D1):D607-D613. doi: 10.1093/nar/gky1131. PMID: 30476243; PMCID: PMC6323986.
- [STRING API Documentation](#)

See Also

Other "STRING": [rba_string_annotations\(\)](#), [rba_string_enrichment_ppi\(\)](#), [rba_string_enrichment\(\)](#), [rba_string_homology_inter\(\)](#), [rba_string_homology_intra\(\)](#), [rba_string_interaction_partners\(\)](#), [rba_string_interactions_network\(\)](#), [rba_string_network_image\(\)](#), [rba_string_version\(\)](#)

Examples

```
rba_string_map_ids(ids = c("TP53", "TNF", "EGFR"), species = 9606)
```

```
rba_string_network_image
```

Get STRING Network Image

Description

Depending on that you supplied a single protein ID or more than one protein ID, this function will produce a static image of the interaction networks among your input proteins or/and with other proteins. See the "Arguments" section to learn more about how you can modify the network image.

Usage

```
rba_string_network_image(  
  ids,  
  image_format = "image",  
  save_image = TRUE,  
  species = NULL,  
  add_color_nodes = NULL,  
  add_white_nodes = NULL,  
  required_score = NULL,  
  network_flavor = "confidence",  
  network_type = "functional",  
  hide_node_labels = FALSE,  
  hide_disconnected_nodes = FALSE,  
  hide_structure_pics = FALSE,  
  ...  
)
```

Arguments

ids	Your protein ID(s). It is strongly recommended to supply STRING IDs. See rba_string_map_ids for more information.
image_format	one of: <ul style="list-style-type: none">"image": PNG image with normal resolution.

	<ul style="list-style-type: none"> • "highres_image": High-resolution PNG image. • "svg": Scalable Vector Graphics image.
save_image	<p>Logical or Character:</p> <ul style="list-style-type: none"> • TRUE: Save the image to an automatically-generated path. • FALSE: Do not save the image, just return it as an R object. • Character string: A valid file path to save the image to.
species	Numeric: NCBI Taxonomy identifier; Human Taxonomy ID is 9606. (Recommended, but optional if your input is less than 100 IDs.)
add_color_nodes	Numeric: The number of colored nodes (queried proteins and first shell of interactors) to be added.
add_white_nodes	Numeric: The number of white nodes (second shell of interactors) to be added after colored nodes.
required_score	Numeric: A minimum of interaction score for an interaction to be included in the image. if not supplied, the threshold will be applied by STRING Based in the network. (low Confidence = 150, Medium Confidence = 400, High Confidence = 700, Highest confidence = 900)
network_flavor	<p>The style of network edges, should be one of:</p> <ul style="list-style-type: none"> • "confidence": (default) Line's thickness is an indicator of the interaction's confidence score. • "evidence": Line's color is based on the type of evidences that support the interaction. • "action": Line's Shape is an indicator of the interaction's predicted mode of actions.
network_type	<p>should be one of:</p> <ul style="list-style-type: none"> • "functional": (default) The edge's indicate both physical and functional associations. • "physical": The edges indicate that two proteins have a physical interaction or are parts of a complex.
hide_node_labels	Logical: (Default = FALSE) Hide proteins names from the image?
hide_disconnected_nodes	Logical: (Default = FALSE) Hide proteins that are not connected to any other proteins from the image?
hide_structure_pics	Logical: (Default = FALSE) Hide protein's structure picture from inside the bubbles?
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A network images which can be PNG or SVG depending on the inputs.

Corresponding API Resources

"POST [https://string-db.org/api/\[output-format\]/network?identifiers=\[your_identifiers\]&\[optional_parameters\]](https://string-db.org/api/[output-format]/network?identifiers=[your_identifiers]&[optional_parameters])"

References

- Szklarczyk D, Gable AL, Lyon D, Junge A, Wyder S, Huerta-Cepas J, Simonovic M, Doncheva NT, Morris JH, Bork P, Jensen LJ, Mering CV. STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. *Nucleic Acids Res.* 2019 Jan 8;47(D1):D607-D613. doi: 10.1093/nar/gky1131. PMID: 30476243; PMCID: PMC6323986.
- [STRING API Documentation](#)

See Also

[rba_string_map_ids](#)

Other "STRING": [rba_string_annotations\(\)](#), [rba_string_enrichment_ppi\(\)](#), [rba_string_enrichment\(\)](#), [rba_string_homology_inter\(\)](#), [rba_string_homology_intra\(\)](#), [rba_string_interaction_partners\(\)](#), [rba_string_interactions_network\(\)](#), [rba_string_map_ids\(\)](#), [rba_string_version\(\)](#)

Examples

```
## Not run:
rba_string_network_image(ids = c("9606.ENSP00000269305",
  "9606.ENSP00000398698",
  "9606.ENSP00000275493"),
  network_type = "functional",
  save_image = FALSE)

## End(Not run)
## Not run:
rba_string_network_image(ids = c("TP53", "TNF", "EGFR"),
  species = 9606,
  save_image = TRUE)

## End(Not run)
## Not run:
rba_string_network_image(ids = "9606.ENSP00000269305",
  image_format = "highres_image",
  save_image = file.path(getwd(), "TP53_network.png"))

## End(Not run)
```

rba_string_version *Get Current STRING Version*

Description

Get STRING version and stable Address that this package currently uses.

Usage

```
rba_string_version(...)
```

Arguments

... rbioapi option(s). See [rba_options](#)'s arguments manual for more information on available options.

Details

Note that STRING releases new version at approximately 2 years cycle. Nevertheless, to insure reproducibility, STRING dedicates a stable address for each release. Thus you can always reproduce research and results obtained via a certain STRING version. If the version that rbioapi returns is outdated, Kindly contact me.

Value

A list with STRING version and stable address.

Corresponding API Resources

"GET [https://string-db.org/api/\[output_format\]/version](https://string-db.org/api/[output_format]/version)"

References

- Szklarczyk D, Gable AL, Lyon D, Junge A, Wyder S, Huerta-Cepas J, Simonovic M, Doncheva NT, Morris JH, Bork P, Jensen LJ, Mering CV. STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. *Nucleic Acids Res.* 2019 Jan 8;47(D1):D607-D613. doi: 10.1093/nar/gky1131. PMID: 30476243; PMCID: PMC6323986.
- [STRING API Documentation](#)

See Also

Other "STRING": [rba_string_annotations\(\)](#), [rba_string_enrichment_ppi\(\)](#), [rba_string_enrichment\(\)](#), [rba_string_homology_inter\(\)](#), [rba_string_homology_intra\(\)](#), [rba_string_interaction_partners\(\)](#), [rba_string_interactions_network\(\)](#), [rba_string_map_ids\(\)](#), [rba_string_network_image\(\)](#)

Examples

```
rba_string_version()
```

rba_uniprot_antigens *Get Antigens by UniProt Accession*

Description

UniProt maps Antigenic features from different sources to the proteins' sequences. Using this function, you can retrieve all the Antigenic features that has been map to a given UniProt protein's sequence.

Usage

```
rba_uniprot_antigens(accession, ...)
```

Arguments

accession	UniProtKB primary or secondary accession(s).
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A list containing the Antigenic features of your supplied UniProt protein's sequence.

Corresponding API Resources

"GET <https://www.ebi.ac.uk/prot eins/api/antigen/accession>"

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, Nucleic Acids Research, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - Antigen": [rba_uniprot_antigens_search\(\)](#)

Examples

```
rba_uniprot_antigens("P04626")
```

 rba_uniprot_antigens_search

Search Antigens in UniProt

Description

UniProt maps Antigenic (Antibody-binding) features from different sources to the proteins' sequences. Using this function, you can search for Antigenic sequences that has been map to UniProt proteins. You may also refine your search with modifiers such as score etc. See "Arguments section" for more information.

Usage

```
rba_uniprot_antigens_search(
  accession = NULL,
  antigen_sequence = NULL,
  antigen_id = NULL,
  ensembl_id = NULL,
  match_score = NULL,
  ...
)
```

Arguments

accession	UniProtKB primary or secondary accession(s). You can supply up to 100 accession numbers.
antigen_sequence	Protein sequence in the antigenic site.
antigen_id	Human Protein Atlas (HPA) antigen ID. You can supply up to 20 IDs.
ensembl_id	Ensembl Stable Transcript ID. You can supply up to 20 IDs.
match_score	(Numeric) Minimum alignment score for the antigen sequence and the target protein sequence.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

Note that this is a search function. Thus, you are not required to fill every argument; You may use whatever combinations of arguments you see fit for your query.

Value

A list Where each element correspond to a UniProt protein (search hit) and Antigenic features are organized under the "features" sub-list.

Corresponding API Resources

"GET <https://www.ebi.ac.uk/proteins/api/antigen>"

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - Antigen": [rba_uniprot_antigens\(\)](#)

Examples

```
rba_uniprot_antigens_search(antigen_id = "HPA001060")
```

rba_uniprot_coordinates

Get Genomic Coordinates of a Protein

Description

Using this function you can retrieve genomic Coordinates of a Protein by either providing the protein's UniProt accession or it's ID in a cross-reference database (Ensembl, CCDC, HGNC or RefSeq). You should supply either 'accession' alone or 'db_type' and 'db_id' together.

Usage

```
rba_uniprot_coordinates(accession = NULL, db_type = NULL, db_id = NULL, ...)
```

Arguments

accession	UniProtKB primary or secondary accession.
db_type	cross-reference database name, Should be one of: "Ensembl", "CCDC", "HGNC" or "RefSeq".
db_id	Protein's ID in the cross-reference database
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

For more information about how UniProt imports and calculates genomic coordinates data, see: McGarvey, P. B., Nightingale, A., Luo, J., Huang, H., Martin, M. J., Wu, C., & UniProt Consortium (2019). UniProt genomic mapping for deciphering functional effects of missense variants. *Human mutation*, 40(6), 694–705. <https://doi.org/10.1002/humu.23738>

Value

A list with genome coordinates of your supplied protein.

Corresponding API Resources

"GET <https://ebi.ac.uk/proteins/api/coordinates/accession>"

"GET <https://ebi.ac.uk/proteins/api/coordinates/dbtype:dbid>"

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - Coordinates": [rba_uniprot_coordinates_location\(\)](#), [rba_uniprot_coordinates_search\(\)](#), [rba_uniprot_coordinates_sequence\(\)](#)

Examples

```
rba_uniprot_coordinates(accession = "P25942")
```

```
rba_uniprot_coordinates(db_type = "HGNC", db_id = "CD40")
```

rba_uniprot_coordinates_location

Search UniProt entries by taxonomy and genomic coordinates

Description

For more information about how UniProt imports and calculates genomic coordinates data, see: McGarvey, P. B., Nightingale, A., Luo, J., Huang, H., Martin, M. J., Wu, C., & UniProt Consortium (2019). UniProt genomic mapping for deciphering functional effects of missense variants. *Human mutation*, 40(6), 694–705. <https://doi.org/10.1002/humu.23738>

Usage

```
rba_uniprot_coordinates_location(  
    taxid,  
    locations,  
    in_range = TRUE,  
    feature = FALSE,  
    ...  
)
```

Arguments

taxid	NIH-NCBI Taxon ID .
locations	genomic location formatted as: chromosome:start-end. (e.g. "Y:17100001-19600000"). If you omit chromosome, it will be interpreted as any chromosome (e.g. "1-10000").
in_range	Only return proteins that are in range.
feature	(logical) Get features?
...	rbaapi option(s). See rba_options 's arguments manual for more information on available options.

Value

a list containing UniProt proteins which match the supplied genomic location and taxonomy ID.

Corresponding API Resources

```
"GET https://ebi.ac.uk/proteins/api/coordinates/taxonomy/locations/feature"  
"GET https://ebi.ac.uk/proteins/api/coordinates/taxonomy/locations"
```

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - Coordinates": [rba_uniprot_coordinates_search\(\)](#), [rba_uniprot_coordinates_sequence\(\)](#), [rba_uniprot_coordinates\(\)](#)

Examples

```
rba_uniprot_coordinates_location(taxid = 9606,  
    locations = "Y:17100001-19600000", in_range = TRUE)
```

```
rba_uniprot_coordinates_location(taxid = 9606,
  locations = "20:39000001", in_range = FALSE)
```

```
rba_uniprot_coordinates_search
```

Search Genomic Coordinates of UniProt entries

Description

Use this function to search genomic coordinates of UniProt entries. You may also refine your search with modifiers such as chromosome, taxon id etc. See "Arguments section" for more information.

Usage

```
rba_uniprot_coordinates_search(
  accession = NULL,
  chromosome = NULL,
  ensembl_id = NULL,
  gene = NULL,
  protein = NULL,
  taxid = NULL,
  location = NULL,
  ...
)
```

Arguments

accession	UniProtKB primary or secondary accession(s) . You can supply up to 100 accession numbers.
chromosome	chromosome name, such as "X", "Y", 1, 20, etc. You can supply up to 20 values.
ensembl_id	Ensembl Stable gene ID, transcript ID or translation ID. You can supply up to 20 IDs.
gene	UniProt gene name(s) . You can supply up to 20 gene names.
protein	UniProt protein name
taxid	NIH-NCBI Taxon ID . You can supply up to 20 taxon IDs.
location	Genome location range such as "58205437-58219305"
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

Note that this is a search function. Thus, you are not required to fill every argument; You may use whatever combinations of arguments you see fit for your query.

For more information about how UniProt imports and calculates genomic coordinates data, see: McGarvey, P. B., Nightingale, A., Luo, J., Huang, H., Martin, M. J., Wu, C., & UniProt Consortium (2019). UniProt genomic mapping for deciphering functional effects of missense variants. *Human mutation*, 40(6), 694–705. <https://doi.org/10.1002/humu.23738>

Value

List where each element corresponds to one UniProt entity returned by your search query. The element itself is a sub-list containing that protein's coordinates information.

Corresponding API Resources

"GET <https://ebi.ac.uk/proteins/api/coordinates>"

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - Coordinates": [rba_uniprot_coordinates_location\(\)](#), [rba_uniprot_coordinates_sequence\(\)](#), [rba_uniprot_coordinates\(\)](#)

Examples

```
rba_uniprot_coordinates_search(taxid = 9606, chromosome = "y")
```

rba_uniprot_coordinates_sequence

Get Genome coordinate by Protein Sequence position

Description

Using this function you can retrieve genome coordinates of a given UniProt protein by providing protein position or position range. You can either supply 'p_position' alone or supply 'p_start' and 'p_end' together.

Usage

```
rba_uniprot_coordinates_sequence(  
    accession,  
    p_position = NULL,  
    p_start = NULL,  
    p_end = NULL,  
    ...  
)
```

Arguments

accession	UniProtKB primary or secondary accession.
p_position	(numeric) Protein sequence position
p_start	(numeric) Protein sequence position start
p_end	(numeric) Protein sequence position end
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

For more information about how UniProt imports and calculates genomic coordinates data, see: McGarvey, P. B., Nightingale, A., Luo, J., Huang, H., Martin, M. J., Wu, C., & UniProt Consortium (2019). UniProt genomic mapping for deciphering functional effects of missense variants. *Human mutation*, 40(6), 694–705. <https://doi.org/10.1002/humu.23738>

Value

Genome coordinates of your supplied proteins.

Corresponding API Resources

"GET <https://ebi.ac.uk/proteins/api/coordinates/location/accession:pPosition>"
"GET <https://ebi.ac.uk/proteins/api/coordinates/location/accession:pStart-pEnd>"

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - Coordinates": [rba_uniprot_coordinates_location\(\)](#), [rba_uniprot_coordinates_search\(\)](#), [rba_uniprot_coordinates\(\)](#)

Examples

```
rba_uniprot_coordinates_sequence(accession = "P25942", p_position = 1)
```

```
rba_uniprot_coordinates_sequence(accession = "P25942",
    p_start = 1, p_end = 277)
```

rba_uniprot_features *Get UniProt protein sequence features by accession*

Description

Use this function to retrieve **sequence annotations (features)** of a protein by its UniProt accession.

Usage

```
rba_uniprot_features(accession, types = NULL, categories = NULL, ...)
```

Arguments

accession	UniProtKB primary or secondary accession.
types	Sequence annotation (Features) types. accepted values are: "INIT_MET", "SIGNAL", "PROPEP", "TRANSIT", "CHAIN", "PEPTIDE", "TOPO_DOM", "TRANSMEM", "DOMAIN", "REPEAT", "CA_BIND", "ZN_FING", "DNA_BIND", "NP_BIND", "REGION", "COILED", "MOTIF", "COMPBIAS", "ACT_SITE", "METAL", "BINDING", "SITE", "NON_STD", "MOD_RES", "LIPID", "CARBOHYD", "DISULFID", "CROSSLNK", "VAR_SEQ", "VARIANT", "MUTAGEN", "UNSURE", "CONFLICT", "NON_CONS", "NON_TER", "HELIX", "TURN", "STRAND" and/or "INTRAMEM". You can supply up to 20 types.
categories	Sequence annotation (Features) categories (subsection). accepted values are: "MOLECULE_PROCESSING", "TOPOLOGY", "SEQUENCE_INFORMATION", "STRUCTURAL", "DOMAINS_AND_SITES", "PTM", "VARIANTS" and/or "MUTAGENESIS". You can supply up to 8 categories.
...	rbiapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A list in which you can find all of your given protein's sequence annotations in a sub-list named "features".

Corresponding API Resources

"GET <https://www.ebi.ac.uk/protins/api/features/accession>"

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - Features": [rba_uniprot_features_search\(\)](#)

Examples

```
rba_uniprot_features("Q99616")
```

```
rba_uniprot_features(accession = "Q99616", types = "DISULFID")
```

rba_uniprot_features_search

UniProt maintains [Rhrefhttps://www.uniprot.org/help/sequence_annotation](https://www.uniprot.org/help/sequence_annotation) sequence annotations (features) that describe regions in the protein sequence. Using this function, you can search and retrieve UniProt proteins' sequence annotations (features). you may also refine your search query with variety of modifiers.

Description

Note that this is a search function. Thus, you are not required to fill every argument; You may use whatever combinations of arguments you see fit for your query.

UniProt Entries are grouped in two sections:

1. Reviewed(Swiss-Prot): Manually annotated records with information extracted from literature and curator-evaluated computational analysis.
2. Unreviewed (TrEMBL): Computationally analyzed records that await full manual annotation.

Usage

```
rba_uniprot_features_search(  
  accession = NULL,  
  gene = NULL,  
  exact_gene = NULL,  
  protein = NULL,  
  reviewed = NULL,
```

```

    organism = NULL,
    taxid = NULL,
    categories = NULL,
    types = NULL,
    ...
)

```

Arguments

accession	UniProtKB primary or secondary accession(s) . You can supply up to 100 accession numbers.
gene	UniProt gene name(s) . You can supply up to 20 gene names. e.g. if you supply "CD40", "CD40 ligand" will also be included.
exact_gene	UniProt exact gene name(s) . You can supply up to 20 exact gene names. e.g. if you supply "CD40", "CD40 ligand" will not be included in the results.
protein	UniProt protein name
reviewed	Logical: If TRUE, only return "UniProtKB/Swiss-Prot" (reviewed) entries; If FALSE, only return TrEMBL (un-reviewed) entries.
organism	Organism name .
taxid	NIH-NCBI Taxon ID . You can supply up to 20 taxon IDs.
categories	Sequence annotation (Features) categories (subsection). accepted values are: "MOLECULE_PROCESSING", "TOPOLOGY", "SEQUENCE_INFORMATION", "STRUCTURAL", "DOMAINS_AND_SITES", "PTM", "VARIANTS" and/or "MUTAGENESIS". You can supply up to 8 categories.
types	Sequence annotation (Features) types . accepted values are: "INIT_MET", "SIGNAL", "PROPEP", "TRANSIT", "CHAIN", "PEPTIDE", "TOPO_DOM", "TRANSMEM", "DOMAIN", "REPEAT", "CA_BIND", "ZN_FING", "DNA_BIND", "NP_BIND", "REGION", "COILED", "MOTIF", "COMPBIAS", "ACT_SITE", "METAL", "BINDING", "SITE", "NON_STD", "MOD_RES", "LIPID", "CARBOHYD", "DISULFID", "CROSSLNK", "VAR_SEQ", "VARIANT", "MUTAGEN", "UNSURE", "CONFLICT", "NON_CONS", "NON_TER", "HELIX", "TURN", "STRAND" and/or "INTRAMEM". You can supply up to 20 types.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

List where each element corresponds to one UniProt entity returned by your search query. The element itself is a sub-list containing all information that UniProt has about that entity.

Corresponding API Resources

"GET <https://www.ebi.ac.uk/proteins/api/features>"

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - Features": [rba_uniprot_features\(\)](#)

Examples

```
rba_uniprot_features_search(accession = "Q99616")
```

```
rba_uniprot_features_search(gene = "cd40")
```

```
rba_uniprot_features_search(gene = "cd40 ligand")
```

```
rba_uniprot_features_search(gene = "cd40", reviewed = TRUE)
```

```
rba_uniprot_features_search(accession = "Q99616",  
  categories = c("MOLECULE_PROCESSING", "TOPOLOGY"))
```

```
rba_uniprot_features_search(accession = "Q99616", types = "DISULFID")
```

```
rba_uniprot_genecentric
```

Get Gene-Centric proteins by UniProt Accession

Description

Using this function you can retrieve gene-centrics data. For more information, see [What are proteomes?](#) and [Automatic gene-centric isoform mapping for eukaryotic reference proteome entries..](#)

Usage

```
rba_uniprot_genecentric(accession, ...)
```

Arguments

accession **UniProtKB primary or secondary accession.**
... rbioapi option(s). See [rba_options](#)'s arguments manual for more information on available options.

Value

A list containing information of Gene-Centric proteins.

Corresponding API Resources

"GET <https://ebi.ac.uk/proteins/api/genecentric/accession>"

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - Proteomes": [rba_uniprot_genecentric_search\(\)](#), [rba_uniprot_proteomes_search\(\)](#), [rba_uniprot_proteomes\(\)](#)

Examples

```
rba_uniprot_genecentric("P29965")
```

rba_uniprot_genecentric_search
Search Gene-Centric Proteins

Description

Using this function you can search UniProt for available gene-centrics from proteomes. For more information, see [What are proteomes?](#) and [Automatic gene-centric isoform mapping for eukaryotic reference proteome entries](#). You may also refine your search with modifiers upid, accession and gene. See "Arguments section" for more information.

Usage

```
rba_uniprot_genecentric_search(upid = NULL, accession = NULL, gene = NULL, ...)
```

Arguments

upid	UniProt Proteome identifier (UPID) . You can supply up to 100 UPIDs.
accession	UniProtKB primary or secondary accession(s) . You can supply up to 100 accession numbers.
gene	unique gene identifier(s) found in MOD, Ensembl , Ensembl Genomes, OLN , ORF or UniProt Gene Name .
...	rbaapi option(s). See rba_options 's arguments manual for more information on available options.

Details

Note that this is a search function. Thus, you are not required to fill every argument; You may use whatever combinations of arguments you see fit for your query.

Value

a list containing gene-centric proteins search hits.

Corresponding API Resources

"GET <https://ebi.ac.uk/proteins/api/genecentric>"

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - Proteomes": [rba_uniprot_genecentric\(\)](#), [rba_uniprot_proteomes_search\(\)](#), [rba_uniprot_proteomes\(\)](#)

Examples

```
rba_uniprot_genecentric_search(accession = "P59594")
```

```
rba_uniprot_genecentric_search(gene = "Spike")
```

```
rba_uniprot_genecentric_search(upid = "UP000000354")
```

rba_uniprot_proteins *Get UniProt entry by accession*

Description

Use this function to retrieve a UniProt Entry by its UniProt accession. You can also use "isoform" or "interaction" arguments to retrieve isoforms or interactor proteins of that entry. Note that in one function call you can only set none or only one of "isoform" or "interaction" as TRUE, not both of them.

Usage

```
rba_uniprot_proteins(accession, interaction = FALSE, isoforms = FALSE, ...)
```

Arguments

accession	UniProtKB primary or secondary accession.
interaction	Logical: (default = FALSE) Only retrieve interaction information of your supplied UniProt entity?
isoforms	Logical: (default = FALSE) Only retrieve isoforms of your supplied UniProt entity?
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A list that contains UniProt protein informations with your supplied accession.

Corresponding API Resources

```
"GET https://ebi.ac.uk/proteins/api/proteins/accession"  
"GET https://ebi.ac.uk/proteins/api/proteins/interaction/accession"  
"GET https://ebi.ac.uk/proteins/api/proteins/accession/isoforms"
```

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - Proteins": [rba_uniprot_proteins_crossref\(\)](#), [rba_uniprot_proteins_search\(\)](#)

Examples

```
rba_uniprot_proteins(accession = "P01730")

rba_uniprot_proteins(accession = "P01730", interaction = TRUE)

rba_uniprot_proteins(accession = "Q29983", isoforms = TRUE)
```

```
rba_uniprot_proteins_crossref
```

Get UniProt Entry by UniProt Cross-Reference Database and ID

Description

UniProt Cross-Reference links protein Entities with cross-reference (external) databases. Using this function, you can retrieve a UniProt entity using external database name and protein ID in that database.

Usage

```
rba_uniprot_proteins_crossref(
  db_id,
  db_name,
  reviewed = NULL,
  isoform = NULL,
  ...
)
```

Arguments

db_id	The protein ID in the cross-reference (external) database.
db_name	cross-reference (external database) name.
reviewed	Logical: (Optional) If TRUE, only returns "UniProtKB/Swiss-Prot" (reviewed) entries; If FALSE, only returns TrEMBL (un-reviewed) entries.
isoform	Numeric: (Optional) you have two options: <ul style="list-style-type: none"> • 0: Exclude isoforms. • 1: Return isoforms only. see: Alternative products
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

List which each element is a UniProt entity that correspond to your supplied cross-reference database name and ID.

Corresponding API Resources

"GET <https://www.ebi.ac.uk/protproteins/api/protproteins/dbtype:dbid>"

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - Proteins": [rba_uniprot_proteins_search\(\)](#), [rba_uniprot_proteins\(\)](#)

Examples

```
rba_uniprot_proteins_crossref("cd40", "hgnc")
```

```
rba_uniprot_proteins_crossref("cd40", "hgnc", reviewed = TRUE)
```

```
rba_uniprot_proteins_crossref("mica", "hgnc", isoform = 0)
```

```
rba_uniprot_proteins_search
```

Search UniProt entries

Description

Using this function, you can search and retrieve UniProt Knowledge-base (UniProtKB) protein entries using variety of options. You may also refine your search with modifiers such as sequence length, review status etc. See "Arguments" section" for more information.

Usage

```

rba_uniprot_proteins_search(
  accession = NULL,
  reviewed = NULL,
  isoform = NULL,
  go_term = NULL,
  keyword = NULL,
  ec = NULL,
  gene = NULL,
  exact_gene = NULL,
  protein = NULL,
  organism = NULL,
  taxid = NULL,
  pubmed = NULL,
  seq_length = NULL,
  md5 = NULL,
  ...
)

```

Arguments

accession	UniProtKB primary or secondary accession(s) . You can supply up to 100 accession numbers.
reviewed	Logical: If TRUE, only return "UniProtKB/Swiss-Prot" (reviewed) entries; If FALSE, only return TrEMBL (un-reviewed) entries.
isoform	Numeric: you have three options: <ul style="list-style-type: none"> • 0: Exclude isoforms. • 1: Return isoforms only. • 2: Return both. see: Alternative products
go_term	Limit the search to entries associated with your supplied GO (Gene Ontology) term. You can supply Either GO ID or a character string -partially or fully-matching the term. e.g. "GO:0001776" or "leukocyte homeostasis". if You supply "leukocyte", any term containing that word will be included, e.g "leukocyte chemotaxis", "leukocyte activation".
keyword	Limit the search to entries that contain your supplied keyword. see: UniProt Keywords
ec	EC (Enzyme Commission) number(s) . You can supply up to 20 EC numbers.
gene	UniProt gene name(s) . You can supply up to 20 gene names. e.g. if you supply "CD40", "CD40 ligand" will also be included.
exact_gene	UniProt exact gene name(s) . You can supply up to 20 exact gene names. e.g. if you supply "CD40", "CD40 ligand" will not be included in the results.
protein	UniProt protein name
organism	Organism name .

taxid	NIH-NCBI Taxon ID . You can supply up to 20 taxon IDs.
pubmed	Entries which cite to the article with your supplied PubMed ID.
seq_length	An exact sequence length (e.g. 150) or a range of sequence lengths (e.g. "130-158").
md5	Sequence md5 value.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

Note that this is a search function. Thus, you are not required to fill every argument; You may use whatever combinations of arguments you see fit for your query.s

UniProt Entries are grouped in two sections:

1. Reviewed(Swiss-Prot): Manually annotated records with information extracted from literature and curator-evaluated computational analysis.
2. Unreviewed (TrEMBL): Computationally analyzed records that await full manual annotation.

Value

A List where each element corresponds to one UniProt entity returned by your search query. The element itself is a sub-list containing all information that UniProt has about that entity.

Corresponding API Resources

"GET <https://www.ebi.ac.uk/prot eins/api/prot eins>"

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - Proteins": [rba_uniprot_proteins_crossref\(\)](#), [rba_uniprot_proteins\(\)](#)

Examples

```
rba_uniprot_proteins_search(accession = "Q99616")
```

```
rba_uniprot_proteins_search(gene = "cd40")
```

```
rba_uniprot_proteins_search(gene = "cd40 ligand")
```

```
rba_uniprot_proteins_search(gene = "cd40", reviewed = TRUE)
```

```
rba_uniprot_proteins_search(gene = "cd40", reviewed = TRUE, isoform = 1)
```

```
rba_uniprot_proteins_search(keyword = "Inhibition of host chemokines by virus")
```

```
rba_uniprot_proteins_search(keyword = "chemokines")
```

rba_uniprot_proteomes *Get proteome by proteome/proteins UPID*

Description

UniProt collects and annotates proteomes (Protein sets expressed in an organism). Using this function you can search UniProt for available proteomes. see [What are proteomes?](#) for more information.

Usage

```
rba_uniprot_proteomes(upid, get_proteins = FALSE, reviewed = NULL, ...)
```

Arguments

upid	UniProt Proteome identifier (UPID) . You can supply up to 100 UPIDs.
get_proteins	logical: set FALSE (default) to only return information of the proteome with supplied UPID, set TRUE to also return the proteins of the supplied proteome UPID.
reviewed	Logical: Only considered when get_proteins is TRUE. If TRUE, only return "UniProtKB/Swiss-Prot" (reviewed) proteins; If FALSE, only return TrEMBL (un-reviewed) entries. leave it as NULL if you do not want to filter proteins based on their review status.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

a list containing information of the proteome with your supplied UPID that can contain the proteomes protein entries based on the value of get_proteins argument.

Corresponding API Resources

"GET <https://ebi.ac.uk/proteins/api/proteomes/proteins/upid>"

"GET <https://ebi.ac.uk/proteins/api/proteomes/upid>"

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>

- [Proteins API Documentation](#)

See Also

Other "UniProt - Proteomes": [rba_uniprot_genecentric_search\(\)](#), [rba_uniprot_genecentric\(\)](#), [rba_uniprot_proteomes_search\(\)](#)

Examples

```
rba_uniprot_proteomes(upid = "UP000000354")
```

```
rba_uniprot_proteomes(upid = "UP000000354", get_proteins = TRUE)
```

rba_uniprot_proteomes_search

Search Proteomes in UniProt

Description

UniProt collects and annotates proteomes (Protein sets expressed in an organism). Using this function you can search UniProt for available proteomes. see [What are proteomes?](#) for more information. You may also refine your search with modifiers such as keyword, taxon id etc. See "Arguments section" for more information.

Usage

```
rba_uniprot_proteomes_search(  
  name = NULL,  
  upid = NULL,  
  taxid = NULL,  
  keyword = NULL,  
  xref = NULL,  
  genome_acc = NULL,
```

```

    is_ref_proteome = NULL,
    is_redundant = NULL,
    ...
)

```

Arguments

name	a keyword in proteome's name
upid	UniProt Proteome identifier (UPID) . You can supply up to 100 UPIDs.
taxid	NIH-NCBI Taxon ID . You can supply up to 20 taxon IDs.
keyword	Limit the search to entries that contain your supplied keyword. see: UniProt Keywords
xref	Proteome cross-references such as Genome assembly ID or Biosample ID. You can supply up to 20 cross-reference IDs.
genome_acc	Genome accession associated with the proteome's components.
is_ref_proteome	(logical) If TRUE, only return reference proteomes; If FALSE, only returns non-reference proteomes; If NULL (default), the results will not be filtered by this criteria see ' What are reference proteomes? ' for more information.
is_redundant	(logical) If TRUE, only return redundant proteomes; If FALSE, only returns non-redundant proteomes; If NULL (default), the results will not be filtered by redundancy. see ' Reducing proteome redundancy ' for more information.
...	rbaapi option(s). See rba_options 's arguments manual for more information on available options.

Details

Note that this is a search function. Thus, you are not required to fill every argument; You may use whatever combinations of arguments you see fit for your query.

Value

A list where each element is a list that corresponds to a single proteome (search hit) and contains informations pertinent to that proteome.

Corresponding API Resources

"GET <https://ebi.ac.uk/proteins/api/proteomes>"

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- **Proteins API Documentation**

See Also

Other "UniProt - Proteomes": [rba_uniprot_genecentric_search\(\)](#), [rba_uniprot_genecentric\(\)](#), [rba_uniprot_proteomes\(\)](#)

Examples

```
rba_uniprot_proteomes_search(name = "SARS-CoV")
```

```
rba_uniprot_proteomes_search(name = "SARS-CoV", is_ref_proteome = TRUE)
```

```
rba_uniprot_proteomes_search(name = "SARS-CoV", is_ref_proteome = TRUE)
```

```
rba_uniprot_proteomes_search(genome_acc = "AY274119")
```

rba_uniprot_proteomics

Get Proteomics Peptides Mapped to UniProt Protein

Description

UniProt maps proteomics peptides from different sources to the proteins' sequences. Using this function, you can retrieve all the proteomics peptides features that has been map to a given UniProt protein's sequence.

Usage

```
rba_uniprot_proteomics(accession, ...)
```

Arguments

accession	UniProtKB primary or secondary accession.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A list containing the proteomics peptides features of your supplied UniProt protein's sequence.

Corresponding API Resources

"GET <https://www.ebi.ac.uk/protproteomics/accession>"

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - Proteomics": [rba_uniprot_proteomics_search\(\)](#)

Examples

```
rba_uniprot_proteomics(accession = "P25942")
```

rba_uniprot_proteomics_search

Search Proteomics Peptides in UniProt

Description

UniProt maps proteomics peptides from different sources to the proteins' sequences. Using this function, you can search for proteomics peptides that has been map to UniProt proteins. You may also refine your search with modifiers such as `data_source`, `peptide` etc. See "Arguments section" for more information.

Usage

```
rba_uniprot_proteomics_search(  
  accession = NULL,  
  data_source = NULL,  
  taxid = NULL,  
  upid = NULL,  
  peptide = NULL,  
  unique = NULL,  
  ...  
)
```

Arguments

accession	UniProtKB primary or secondary accession(s) . You can supply up to 100 accession numbers.
data_source	Proteomics data source. You can choose up to two of:

	<ul style="list-style-type: none"> • "MaxQB" • "PeptideAtlas" • "EPD" • "ProteomicsDB"
taxid	NIH-NCBI Taxon ID . You can supply up to 20 taxon IDs.
upid	UniProt Proteome identifier (UPID) . You can supply up to 100 UPIDs.
peptide	Peptide sequence(s). You can supply up to 20 sequences.
unique	Logical: Should the results be filtered based on the Peptide's uniqueness (the fact that a peptide maps to only 1 protein). If TRUE, Only unique peptides will be returned, if FALSE only un-unique peptides will be returned; If NULL (default) the results will not be filtered based on this.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Details

Note that this is a search function. Thus, you are not required to fill every argument; You may use whatever combinations of arguments you see fit for your query.

see also: [Mass spectrometry-based proteomics data in UniProtKB](#)

Value

A list Where each element correspond to a UniProt protein and proteomics peptides are organized under the "features" sub-list.

Corresponding API Resources

"GET <https://www.ebi.ac.uk/protins/api/proteomics>"

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - Proteomics": [rba_uniprot_proteomics\(\)](#)

Examples

```
rba_uniprot_proteomics_search(peptide = "MEDYTKIEK")
```

```
rba_uniprot_proteomics_search(peptide = "MEDYTKIEK")
```

```

## Not run:
### this will generate a very large response!
  rba_uniprot_proteomics_search(taxid = 9606,
    data_source = "PeptideAtlas",
    progress = TRUE, timeout = 999999, unique = TRUE)

## End(Not run)

```

rba_uniprot_taxonomy *Get UniProt Taxonomy Nodes*

Description

Using this function, you can retrieve taxonomic nodes information by providing their **NCBI taxonomic identifiers**. also, you can explicitly retrieve other nodes in relation to your supplied node's hierarchy in **UniProt Taxonomy database**.

Usage

```

rba_uniprot_taxonomy(
  ids,
  hierarchy = NULL,
  node_only = TRUE,
  page_size = 200,
  page_number = 1,
  ...
)

```

Arguments

ids	(numeric) a single or a numeric vector of NCBI taxonomic identifier(s)
hierarchy	Retrieve taxonomic nodes that have specific hierarchical relation to your supplied taxonomic node. should be one of: "children", "parent" or "siblings".
node_only	Retrieve only the node(s) information and exclude URL links to parents, siblings and children nodes.
page_size	(numeric) Only when hierarchy is supplied. hierarchy information may be very long, thus UniProt API will paginate the results, you may use this argument to control the pagination. maximum value is 200.
page_number	(numeric) Only when hierarchy is supplied. hierarchy information may be very long, thus UniProt API will paginate the results, you may use this argument to control the pagination.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

a list containing your supplied nodes or their related nodes taxonomic information.

Corresponding API Resources

```
"GET https://ebi.ac.uk/proteins/api/ids/ids"  
"GET https://ebi.ac.uk/proteins/api/ids/id/id/node"  
"GET https://ebi.ac.uk/proteins/api/id/id/node"  
"GET https://ebi.ac.uk/proteins/api/id/id/children"  
"GET https://ebi.ac.uk/proteins/api/id/id/children/node"  
"GET https://ebi.ac.uk/proteins/api/id/id/parent"  
"GET https://ebi.ac.uk/proteins/api/id/id/parent/node"  
"GET https://ebi.ac.uk/proteins/api/id/id/siblings"  
"GET https://ebi.ac.uk/proteins/api/id/id/siblings/node"
```

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - Taxonomy": [rba_uniprot_taxonomy_lca\(\)](#), [rba_uniprot_taxonomy_lineage\(\)](#), [rba_uniprot_taxonomy_name\(\)](#), [rba_uniprot_taxonomy_path\(\)](#), [rba_uniprot_taxonomy_relationship\(\)](#)

Examples

```
rba_uniprot_taxonomy(ids = c(9606, 10090))
```

```
rba_uniprot_taxonomy(ids = 9989, hierarchy = "children")
```

rba_uniprot_taxonomy_lca

Get Lowest Common Ancestor (LCA) of Two Taxonomy Nodes

Description

Use this function to retrieve lowest common ancestor (LCA) of two taxonomy nodes in [UniProt Taxonomy database](#)

Usage

```
rba_uniprot_taxonomy_lca(ids, ...)
```

Arguments

ids	(numeric) Numeric vector of NCBI taxonomic identifiers , with minimum length of two.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A list with UniProt taxonomy information of your supplied taxonomy elements.

Corresponding API Resources

"GET <https://ebi.ac.uk/proteins/api/ancestor/ids>"

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - Taxonomy": [rba_uniprot_taxonomy_lineage\(\)](#), [rba_uniprot_taxonomy_name\(\)](#), [rba_uniprot_taxonomy_path\(\)](#), [rba_uniprot_taxonomy_relationship\(\)](#), [rba_uniprot_taxonomy\(\)](#)

Examples

```
rba_uniprot_taxonomy_lca(c(9606,10090,9823,7712))
```

```
rba_uniprot_taxonomy_lineage  
Get Taxonomic Lineage
```

Description

Use this function to retrieve the taxonomic lineage of your supplied taxonomy node.

Usage

```
rba_uniprot_taxonomy_lineage(id, ...)
```

Arguments

id	(numeric) a NCBI taxonomic identifier
...	rbaapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A list with a data frame containing All the nodes that preceded your supplied node in the taxonomic tree. with your node as the first row and the root node in the last row.

Corresponding API Resources

```
"GET https://ebi.ac.uk/proteins/api/lineage/id"  
"GET https://ebi.ac.uk/proteins/api/lineage/id"
```

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - Taxonomy": [rba_uniprot_taxonomy_lca\(\)](#), [rba_uniprot_taxonomy_name\(\)](#), [rba_uniprot_taxonomy_path\(\)](#), [rba_uniprot_taxonomy_relationship\(\)](#), [rba_uniprot_taxonomy\(\)](#)

Examples

```
rba_uniprot_taxonomy_lineage(id = 9989)
```

 rba_uniprot_taxonomy_name

Search UniProt Taxonomic Names

Description

Using this function, you can search and retrieve taxonomic nodes using their names from [UniProt Taxonomy database](#).

Usage

```
rba_uniprot_taxonomy_name(
  name,
  field = "scientific",
  search_type = "equal_to",
  node_only = TRUE,
  page_size = 200,
  page_number = 1,
  ...
)
```

Arguments

name	a name to be used as search query.
field	Specify the field that your supplied name should be searched. It should be one of: "scientific" (default), "common" or "mnemonic".
search_type	The logical relationship between your supplied search query and the taxonomic name field. It should be one of "equal_to" (default), "start_with", "end_with" or "contain".
node_only	(logical) Retrieve only the node(s) information and exclude URL links to parents, siblings and children nodes. default = TRUE
page_size	(numeric) Your search results may be very long, thus UniProt API will paginate the results, you may use this argument to control the pagination. maximum value is 200.
page_number	(numeric) Your search results may be very long, thus UniProt API will paginate the results, you may use this argument to control the pagination. maximum value is 200.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

a list containing taxonomic nodes that match your supplied inputs.

Corresponding API Resources

```
"GET https://ebi.ac.uk/proteins/api/name/name"  
"GET https://ebi.ac.uk/proteins/api/name/name/node"
```

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - Taxonomy": [rba_uniprot_taxonomy_lca\(\)](#), [rba_uniprot_taxonomy_lineage\(\)](#), [rba_uniprot_taxonomy_path\(\)](#), [rba_uniprot_taxonomy_relationship\(\)](#), [rba_uniprot_taxonomy\(\)](#)

Examples

```
rba_uniprot_taxonomy_name(name = "homo", field = "scientific",  
  search_type = "start_with")
```

```
rba_uniprot_taxonomy_name(name = "adenovirus", field = "scientific",  
  search_type = "contain", page_size = 200, page_number = 2)
```

rba_uniprot_taxonomy_path

Traverse UniProt Taxonomic Tree Path

Description

Using this function you can retrieve nodes that are located in the top or the bottom of your supplied node in [UniProt Taxonomy database tree](#)

Usage

```
rba_uniprot_taxonomy_path(id, direction, depth = 5, ...)
```

Arguments

id	(numeric) a NCBI taxonomic identifier
direction	direction of the taxonomic path, either "TOP" or "BOTTOM".
depth	(numeric) How many levels should be traversed on the taxonomic tree? (from 1 to 5, default = 5)
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

a nested list containing the node which are in the path specified by your supplied argument in the UniProt taxonomic tree.

Corresponding API Resources

"GET <https://ebi.ac.uk/proteins/api/path>"

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - Taxonomy": [rba_uniprot_taxonomy_lca\(\)](#), [rba_uniprot_taxonomy_lineage\(\)](#), [rba_uniprot_taxonomy_name\(\)](#), [rba_uniprot_taxonomy_relationship\(\)](#), [rba_uniprot_taxonomy\(\)](#)

Examples

```
rba_uniprot_taxonomy_path(id = 9606, direction = "TOP", depth = 3)
```

```
rba_uniprot_taxonomy_path(id = 207598, direction = "BOTTOM", depth = 3)
```

`rba_uniprot_taxonomy_relationship`*Get Shortest Path Between Two Taxonomy Nodes*

Description

Use this function to retrieve the shortest path between two nodes in the taxonomy tree of **UniProt Taxonomy database**.

Usage

```
rba_uniprot_taxonomy_relationship(from, to, ...)
```

Arguments

<code>from</code>	NCBI taxonomic identifier of your initial node.
<code>to</code>	NCBI taxonomic identifier of your final node.
<code>...</code>	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

a nested list containing the node which are in the shortest path between your supplied nodes.

Corresponding API Resources

"GET <https://ebi.ac.uk/proteins/api/relationship>"

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - Taxonomy": [rba_uniprot_taxonomy_lca\(\)](#), [rba_uniprot_taxonomy_lineage\(\)](#), [rba_uniprot_taxonomy_name\(\)](#), [rba_uniprot_taxonomy_path\(\)](#), [rba_uniprot_taxonomy\(\)](#)

Examples

```
rba_uniprot_taxonomy_relationship(from = 9606, to = 10090)
```

 rba_uniprot_uniparc *Get UniParc entry*

Description

Use this function to retrieve UniParc entries. You can use either -and only one of- UniProt accession, Cross-reference database id, UniParc ID or UniProt Proteome UPID. You can also filter the returned content of the returned UniParc entry. see "Argument" section for more details.

Usage

```
rba_uniprot_uniparc(
  upi = NULL,
  accession = NULL,
  db_id = NULL,
  upid = NULL,
  rf_dd_type = NULL,
  rf_db_id = NULL,
  rf_active = NULL,
  rf_tax_id = NULL,
  ...
)
```

Arguments

upi	unique UniParc Identifier.
accession	UniProtKB primary or secondary accession.
db_id	Protein ID in the cross-reference (external) database.
upid	UniProt Proteome identifier (UPID). You can supply up to 100 UPIDs.
rf_dd_type	Filter the content of the UniParc entry by cross-reference names. You can supply multiple values.
rf_db_id	Filter the content of the UniParc entry by protein identifiers in any cross-reference database. You can supply multiple values.
rf_active	(logical) Filter the content of UniParc entry based on active status on source database: <ul style="list-style-type: none"> • NULL: (default) don't filter contents based on active status. • TRUE: only return contents which are still active. • FALSE: Only return contents which are not active.
rf_tax_id	(Numeric) Filter the content of the UniParc entry by NIH-NCBI Taxon ID . You can supply multiple values.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A list which correspond to a UniParc entry.

Corresponding API Resources

"GET https://ebi.ac.uk/proteins/api/uniparc/accession/accession "

"GET https://ebi.ac.uk/proteins/api/uniparc/dbreference/dbid"

"GET https://ebi.ac.uk/proteins/api/uniparc/peptide/upid"

"GET https://ebi.ac.uk/proteins/api/uniparc/upi/upi"

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - UniParc": [rba_uniprot_uniparc_bestguess\(\)](#), [rba_uniprot_uniparc_search\(\)](#), [rba_uniprot_uniparc_sequence\(\)](#)

Examples

```
rba_uniprot_uniparc(upi = "UPI00000000C9")
```

```
rba_uniprot_uniparc(upi = "UPI00000000C9")
```

```
rba_uniprot_uniparc(upi = "UPI00000000C9", rf_active = FALSE)
```

rba_uniprot_uniparc_bestguess

Get UniParc Longest Sequence for Entries

Description

This function returns the UniParc Entry with a cross-reference to the longest active UniProtKB sequence (preferably from Swiss-Prot and if not then TrEMBL). If it finds more than one longest active UniProtKB sequence it returns 400 (Bad Request) error response with the list of cross references found.

Usage

```
rba_uniprot_uniparc_bestguess(  
  upi = NULL,  
  accession = NULL,  
  db_id = NULL,  
  gene = NULL,  
  taxid = NULL,  
  ...  
)
```

Arguments

upi	unique UniParc Identifier.
accession	UniProtKB primary or secondary accession(s) . You can supply up to 100 accession numbers.
db_id	Protein ID in the cross-reference (external) database. You can supply up to 100 IDs.
gene	UniProt gene name(s) . You can supply up to 20 gene names.
taxid	NIH-NCBI Taxon ID . You can supply up to 20 taxon IDs.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A list where each element correspond to a UniParc entry.

Corresponding API Resources

"GET <https://ebi.ac.uk/proteins/api/uniparc/bestguess>"

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - UniParc": [rba_uniprot_uniparc_search\(\)](#), [rba_uniprot_uniparc_sequence\(\)](#), [rba_uniprot_uniparc\(\)](#)

Examples

```
rba_uniprot_uniparc_bestguess("UPI00000000C9")
```

```
rba_uniprot_uniparc_search  
                                  Search UniParc Entries
```

Description

Use this function to search **UniProt Archive (UniParc)** entries. You may also refine your search with modifiers such as sequence length, taxon id etc. See "Arguments section" for more information.

Usage

```
rba_uniprot_uniparc_search(  
  upi = NULL,  
  accession = NULL,  
  db_type = NULL,  
  db_id = NULL,  
  gene = NULL,  
  protein = NULL,  
  taxid = NULL,  
  organism = NULL,  
  sequence_checksum = NULL,  
  ipr = NULL,  
  signature_db = NULL,  
  signature_id = NULL,  
  upid = NULL,  
  seq_length = NULL,  
  rf_dd_type = NULL,  
  rf_db_id = NULL,  
  rf_active = NULL,  
  rf_tax_id = NULL,  
  ...  
)
```

Arguments

upi	unique UniParc Identifier(s). You can supply up to 100 IDs.
accession	UniProtKB primary or secondary accession (s). You can supply up to 100 accession numbers.
db_type	cross-reference (external database) name.

db_id	Protein ID in the cross-reference (external) database. You can supply up to 100 IDs.
gene	UniProt gene name(s) . You can supply up to 20 gene names.
protein	UniProt protein name .
taxid	NIH-NCBI Taxon ID . You can supply up to 20 taxon IDs.
organism	Organism name .
sequence_checksum	Sequence CRC64 checksum.
ipr	InterPro identifier(s) . You can supply up to 20 IDs.
signature_db	InterPro's signature database . You can supply up to 13 of the following values: "CATH", "CDD", "HAMAP", "MobiDB Lite", "Panther", "Pfam", "PIRSF", "PRINTS", "Prosite", "SFLD", "SMART", "SUPERFAMILY" and/or "TIGRFams"
signature_id	Signature ID in the InterPro's signature database . You can supply up to 20 IDs.
upid	UniProt Proteome identifier (UPID) . You can supply up to 100 UPIDs.
seq_length	An exact sequence length (e.g. 150) or a range of sequence lengths (e.g. "130-158").
rf_dd_type	Filter the content of the each UniParc entry by cross-reference names. You can supply multiple values.
rf_db_id	Filter the content of the each UniParc entry by protein identifiers in any cross-reference database. You can supply multiple values.
rf_active	(logical) Filter the content of each UniParc entry based on active status on source database: <ul style="list-style-type: none"> • NULL: (default) don't filter contents based on active status. • TRUE: only return contents which are still active. • FALSE: Only return contents which are not active.
rf_tax_id	(Numeric) Filter the content of each UniParc entry by NIH-NCBI Taxon ID . You can supply multiple values.
...	rbaapi option(s). See rba_options 's arguments manual for more information on available options.

Details

Note that this is a search function. Thus, you are not required to fill every argument; You may use whatever combinations of arguments you see fit for your query.

Value

A List where each element corresponds to one UniParc entry returned by your search query. The element itself is a sub-list containing sequence information and reference entries.

Corresponding API Resources

"GET <https://ebi.ac.uk/proteins/api/uniparc>"

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - UniParc": [rba_uniprot_uniparc_bestguess\(\)](#), [rba_uniprot_uniparc_sequence\(\)](#), [rba_uniprot_uniparc\(\)](#)

Examples

```
rba_uniprot_uniparc_search(upi = "UPI00000000C9")
```

```
rba_uniprot_uniparc_search(accession = "P30914")
```

```
rba_uniprot_uniparc_search(accession = "P30914", rf_active = TRUE)
```

```
rba_uniprot_uniparc_search(taxid = "694009", protein = "Nucleoprotein")
```

```
rba_uniprot_uniparc_sequence
```

Get UniParc Entries by Sequence

Description

Retrieve UniParc Entry by providing an exact sequence. Note that partial matches will not be accepted. You can also filter the returned content of the returned UniParc entry. see "Argument" section for more details.

Usage

```
rba_uniprot_uniparc_sequence(  
  sequence,  
  rf_dd_type = NULL,  
  rf_db_id = NULL,  
  rf_active = NULL,  
  rf_tax_id = NULL,  
  ...  
)
```

Arguments

sequence	Exact UniParc protein sequence. Partial matches will not be accepted.
rf_dd_type	Filter the content of the UniParc entry by cross-reference names. You can supply multiple values.
rf_db_id	Filter the content of the UniParc entry by protein identifiers in any cross-reference database. You can supply multiple values.
rf_active	(logical) Filter the content of UniParc entry based on active status on source database: <ul style="list-style-type: none"> • NULL: (default) don't filter contents based on active status. • TRUE: only return contents which are still active. • FALSE: Only return contents which are not active.
rf_tax_id	(Numeric) Filter the content of the UniParc entry by NIH-NCBI Taxon ID . You can supply multiple values.
...	rbioapi option(s). See rba_options 's arguments manual for more information on available options.

Value

A list which correspond to a UniParc entry.

Corresponding API Resources

"POST <https://ebi.ac.uk/proteins/api/uniparc/sequence>"

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - UniParc": [rba_uniprot_uniparc_bestguess\(\)](#), [rba_uniprot_uniparc_search\(\)](#), [rba_uniprot_uniparc\(\)](#)

Examples

```
rba_uniprot_uniparc_sequence("GMRSCPRGCSQRRCENGRCVCNPGYTGEDC")
```

rba_uniprot_variation *Get natural variants in UniProt by NIH-NCBI SNP database identifier*

Description

Retrieve natural variant annotations of a sequence using UniProt protein accession, dbSNP or HGVS expression.

Usage

```
rba_uniprot_variation(
  id,
  id_type,
  source_type = NULL,
  consequence_type = NULL,
  wild_type = NULL,
  alternative_sequence = NULL,
  location = NULL,
  save_peff = FALSE,
  ...
)
```

Arguments

id	An ID which can be either a UniProt primary or secondary accession , NIH-NCBI dbSNP ID or HGVS expression . NIH-NCBI dbSNP id or HGVS Expression .
id_type	The type of supplied ID argument, one of: "uniprot" , "dbSNP" or "hgvs"
source_type	Variation's source type. You can choose up to two of: "UniProt" , "large scale study" and/or "mixed" .
consequence_type	Variation's consequence type. You can choose up to two of: "missense" , "stop gained" or "stop lost" .
wild_type	Wild type amino acid. Accepted values are IUPAC single-letter amino acid (e.g. D for Aspartic acid) and "*" for stop codon. You can supply up to 20 values.
alternative_sequence	Alternative amino acid. Accepted values are IUPAC single-letter amino acid (e.g. D for Aspartic acid) and "*" for stop codon and "-" for deletion. You can supply up to 20 values.
location	A valid amino acid range (e.g. 10-25) within the sequence range where the variation occurs. You can supply up to 20 values.
save_peff	Logical or Character: <ul style="list-style-type: none"> FALSE: (default) Do not save PEFF file, just return as a list object. TRUE: Save as PEFF file to an automatically-generated path.

- Character string: A valid file path to save the PEFf file.
- ... rbioapi option(s). See [rba_options](#)'s arguments manual for more information on available options.

Value

A list where each element is a list that corresponds to a UniProt protein entry.

Corresponding API Resources

"GET <https://www.ebi.ac.uk/protins/api/variation/dbsnp/dbid>"

"GET <https://www.ebi.ac.uk/protins/api/variation/hgvs/hgvs>"

"GET <https://www.ebi.ac.uk/protins/api/variation/accession>"

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - Variation": [rba_uniprot_variation_search\(\)](#)

Examples

```
rba_uniprot_variation(id = "rs121434451", id_type = "dbsnp")
```

```
rba_uniprot_variation(id = "NC_000008.11:g.22119227C>T", id_type = "hgvs")
```

```
rba_uniprot_variation(id = "043593", id_type = "uniprot")
```

rba_uniprot_variation_search

Search UniProt Natural Variants

Description

Using this function, you can search and retrieve **Natural variant(s)** that has been annotated in the protein's sequences. You may also refine your search with modifiers such as source type, disease etc. See "Arguments section" for more information.

Usage

```

rba_uniprot_variation_search(
  accession = NULL,
  source_type = NULL,
  consequence_type = NULL,
  wild_type = NULL,
  alternative_sequence = NULL,
  location = NULL,
  disease = NULL,
  omim = NULL,
  evidence = NULL,
  taxid = NULL,
  db_type = NULL,
  db_id = NULL,
  save_peff = FALSE,
  ...
)

```

Arguments

accession	UniProtKB primary or secondary accession(s) . You can supply up to 100 accession numbers.
source_type	Variation's source type. You can choose up to two of: "UniProt", "large scale study" and/or "mixed".
consequence_type	Variation's consequence type. You can choose up to two of: "missense", "stop gained" or "stop lost".
wild_type	Wild type amino acid. Accepted values are IUPAC single-letter amino acid (e.g. D for Aspartic acid) and "*" for stop codon. You can supply up to 20 values.
alternative_sequence	Alternative amino acid. Accepted values are IUPAC single-letter amino acid (e.g. D for Aspartic acid) and "*" for stop codon and "-" for deletion. You can supply up to 20 values.
location	A valid amino acid range (e.g. 10-25) within the sequence range where the variation occurs. You can supply up to 20 values.
disease	Human disease that are associated with a sequence variation. Accepted values are disease name (e.g. Alzheimer disease 18), partial disease name (Alzheimer) and/or disease acronym (e.g. AD). You can supply up to 20 values.
omim	OMIM ID that is associated with a variation. You can supply up to 20 values.
evidence	Pubmed ID of the variation's citation . You can supply up to 20 values.
taxid	NIH-NCBI Taxon ID . You can supply up to 20 taxon IDs.
db_type	cross-reference database of the variation. You can supply up to two of the following: <ul style="list-style-type: none"> "dbSNP": NIH-NCBI dbSNP database. "cosmic curate": COSMIC (the Catalogue of Somatic Mutations in Cancer)

	<ul style="list-style-type: none"> • "ClinVar": NIH-NCBI ClinVar
db_id	The variation ID in a Cross-reference (external) database. You can supply up to 20 values.
save_peff	Logical or Character: <ul style="list-style-type: none"> • FALSE: (default) Do not save PEFF file, just return as a list object. • TRUE: Save as PEFF file to an automatically-generated path. • Character string: A valid file path to save the PEFF file.
...	rbaapi option(s). See rba_options 's arguments manual for more information on available options.

Details

Note that this is a search function. Thus, you are not required to fill every argument; You may use whatever combinations of arguments you see fit for your query.

Value

List where each element corresponds to one UniProt entity returned by your search query. The element itself is a sub-list containing all information that UniProt has about that Variation.

Corresponding API Resources

"GET <https://www.ebi.ac.uk/proteins/api/variation>"

References

- Andrew Nightingale, Ricardo Antunes, Emanuele Alpi, Borisas Bursteinas, Leonardo Gonzales, Wudong Liu, Jie Luo, Guoying Qi, Edd Turner, Maria Martin, The Proteins API: accessing key integrated protein and genome information, *Nucleic Acids Research*, Volume 45, Issue W1, 3 July 2017, Pages W539–W544, <https://doi.org/10.1093/nar/gkx237>
- [Proteins API Documentation](#)

See Also

Other "UniProt - Variation": [rba_uniprot_variation\(\)](#)

Examples

```
rba_uniprot_variation_search(accession = "P05067")
```

```
rba_uniprot_variation_search(disease = "alzheimer disease, 18")
```

```
rba_uniprot_variation_search(disease = "alzheimer",
  wild_type = "A", alternative_sequence = "T")
```

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