Package 'rbioapi'

May 9, 2026

Type Package

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

Version 0.8.3

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 the technicalities of using web services API and creates a unified and easy-to-use interface to biological and medical web services. This is an ongoing project; New databases and services will be added periodically. Feel free to suggest any databases or services you often use.

License GPL-3

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

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

Imports httr, jsonlite, utils

Suggests DT, knitr, png, rmarkdown, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

Encoding UTF-8

RoxygenNote 7.3.2

NeedsCompilation no

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Repository CRAN

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Contents

`rba_connection_test` *Test if the Supported Services Are Responding*

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 provides a convenient one-step wrapper for performing enrichment analysis on a given gene list using Enrichr. It simplifies the process by internally calling the necessary functions in the correct order. See the details section for more information.

Usage

```
rba_enrichr(
  gene_list,
  description = NULL,
  gene_set_library = "all",
  regex_library_name = FALSE,
  organism = "human",
  background_genes = NULL,
```

```
  progress_bar = TRUE,
  ...
)
```

Arguments

gene_list	A character vector with Entrez gene symbols of test genes.
description	(optional) A description to be associated with your uploaded gene-set to Enrichr servers.
gene_set_library	One of the: 1. "all" to select all of the available Enrichr gene-set libraries. 2. A gene-set library name. You can retrieve the available options for a given species using rba_enrichr_libs. 3. If regex_library_name = TRUE, A partially-matching name a regex pattern that correspond to one or more of Enrichr library names.
regex_library_name	logical: (default = FALSE) if TRUE the supplied gene_set_library will be considered as a regex pattern. If FALSE, gene_set_library will be considered as an 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).
background_genes	A character vector of Entrez gene symbols of the background genes.
progress_bar	logical: (default = TRUE) if multiple Enrichr libraries are selected, should a progress bar be displayed?
...	rbioapi 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 for the given organism.
2. Call rba_enrichr_add_list to upload your gene-list and obtain a 'user list ID'.
3. (If necessary) Call rba_enrichr_add_background to upload your background gene-list and obtain a 'background list ID'.
4. Call rba_enrichr_enrich to perform enrichment analysis on 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"
"POST https://maayanlab.cloud/speedrichr/api/addList"
"POST https://maayanlab.cloud/speedrichr/api/addbackground"
"GET https://maayanlab.cloud/Enrichr/enrich"
"POST https://maayanlab.cloud/speedrichr/api/backgroundenrich"

References

- Chen, E.Y., Tan, C.M., Kou, Y. et al. Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. Bioinformatics 14, 128 (2013). https://doi.org/10.1186/1471-2105-14-128
- Maxim V. Kuleshov, Matthew R. Jones, Andrew D. Rouillard, Nicolas F. Fernandez, Qiaonan Duan, Zichen Wang, Simon Koplev, Sherry L. Jenkins, Kathleen M. Jagodnik, Alexander Lachmann, Michael G. McDermott, Caroline D. Monteiro, Gregory W. Gundersen, Avi Ma'ayan, Enrichr: a comprehensive gene set enrichment analysis web server 2016 update, Nucleic Acids Research, Volume 44, Issue W1, 8 July 2016, Pages W90–W97, https://doi.org/10.1093/nar/gkw377
- Xie, Z., Bailey, A., Kuleshov, M. V., Clarke, D. J. B., Evangelista, J. E., Jenkins, S. L., Lachmann, A., Wojciechowicz, M. L., Kropiwnicki, E., Jagodnik, K. M., Jeon, M., & Ma'ayan, A. (2021). Gene set knowledge discovery with Enrichr. Current Protocols, 1, e90. doi: 10.1002/cpz1.90
- Enrichr API Documentation
- Citations note on Enrichr website

See Also

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

Other "Enrichment/Over-representation": `rba_mieaa_enrich()`, `rba_panther_enrich()`, `rba_reactome_analysis()`, `rba_string_enrichment()`, `rba_string_enrichment_image()`

Examples

```
## Not run:
rba_enrichr(gene_list = c("TP53", "TNF", "EGFR"))

## End(Not run)

rba_enrichr(gene_list = c("TP53", "TNF", "EGFR"),
    gene_set_library = "GO_Molecular_Function_2025",
    regex_library_name = FALSE)


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

`rba_enrichr_add_background` *Upload Background Gene-List to Enrichr*

Description

In addition to the main gene list, you can also submit a background gene list to Enrichr. This gene list can be used later to compute the statistics of the enrichment analysis.

Usage

```
rba_enrichr_add_background(background_genes, ...)
```

Arguments

`background_genes`	A character vector of Entrez gene symbols of the background genes.
`...`	rbioapi option(s). See `rba_options`'s arguments manual for more information on available options.

Details

Please note that `rba_enrichr` provides a one-step and more convenient way to automatically handle this and other required function calls needed to perform gene set enrichment analysis with Enrichr.

Value

A list with the unique IDs for your uploaded background gene list.

Corresponding API Resources

"POST https://maayanlab.cloud/speedrichr/api/addbackground"

References

- Chen, E.Y., Tan, C.M., Kou, Y. et al. Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. Bioinformatics 14, 128 (2013). https://doi.org/10.1186/1471-2105-14-128
- Maxim V. Kuleshov, Matthew R. Jones, Andrew D. Rouillard, Nicolas F. Fernandez, Qiaonan Duan, Zichen Wang, Simon Koplev, Sherry L. Jenkins, Kathleen M. Jagodnik, Alexander Lachmann, Michael G. McDermott, Caroline D. Monteiro, Gregory W. Gundersen, Avi Ma'ayan, Enrichr: a comprehensive gene set enrichment analysis web server 2016 update, Nucleic Acids Research, Volume 44, Issue W1, 8 July 2016, Pages W90–W97, https://doi.org/10.1093/nar/gkw377
- Xie, Z., Bailey, A., Kuleshov, M. V., Clarke, D. J. B., Evangelista, J. E., Jenkins, S. L., Lachmann, A., Wojciechowicz, M. L., Kropiwnicki, E., Jagodnik, K. M., Jeon, M., & Ma'ayan, A. (2021). Gene set knowledge discovery with Enrichr. Current Protocols, 1, e90. doi: 10.1002/cpz1.90

- Enrichr API Documentation
- Citations note on Enrichr website

See Also

rba_enrichr

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

Examples

```
my_background_genes <- c(
"NSUN3", "POLRMT", "NLRX1", "SFXN5", "ZC3H12C", "SLC25A39", "ARSG",
"DEFB29", "PCMTD2", "ACAA1A", "LRRC1", "2810432D09RIK", "SEPHS2",
"SAC3D1", "TMLHE", "LOC623451", "TSR2", "PLEKHA7", "GYS2", "ARHGEF12",
"HIBCH", "LYRM2", "ZBTB44", "ENTPD5", "RAB11FIP2", "LIPT1",
"INTU", "ANXA13", "KLF12", "SAT2", "GAL3ST2", "VAMP8", "FKBPL",
"AQP11", "TRAP1", "PMPCB", "TM7SF3", "RBM39", "BRI3", "KDR", "ZFP748",
"NAP1L1", "DHRS1", "LRRC56", "WDR20A", "STXBP2", "KLF1", "UFC1",
"CCDC16", "9230114K14RIK", "RWDD3", "2610528K11RIK")

rba_enrichr_add_background(background_genes = my_background_genes)
```

---

rba_enrichr_add_list *Upload Your Gene-List to Enrichr*

Description

This function uploads your gene list to Enrichr and retrieves a unique 'user list ID' required for performing enrichment analysis.

Usage

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

Arguments

gene_list	A character vector with Entrez gene symbols of test genes.
description	(optional) A 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).
speedrichr	logical (default = FALSE) Set to TRUE if you will use this gene list with a background list; otherwise, set to FALSE. Only available for human libraries. Refer to the details section for more information.
...	rbioapi option(s). See rba_options's arguments manual for more information on available options.

Details

Enrichr uses separate APIs for analysis with or without a background gene list. Set 'speedrichr = TRUE' if this gene list will be used with a background gene list; otherwise, set it to FALSE. Gene lists submitted with 'speedrichr = TRUE' can only be analyzed with a background set, and those submitted with 'speedrichr = FALSE' can only be analyzed without one. Currently, background-based enrichment is supported only for human libraries.

Please note that rba_enrichr provides a one-step and more convenient way to automatically handle this and other required function calls needed to perform gene set enrichment analysis with Enrichr.

Value

A list with the unique IDs for your uploaded gene list. 'userListId' is the ID required for later steps.

Corresponding API Resources

"POST https://maayanlab.cloud/Enrichr/addList"
"POST https://maayanlab.cloud/speedrichr/api/addList"

References

- Chen, E.Y., Tan, C.M., Kou, Y. et al. Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. Bioinformatics 14, 128 (2013). https://doi.org/10.1186/1471-2105-14-128
- Maxim V. Kuleshov, Matthew R. Jones, Andrew D. Rouillard, Nicolas F. Fernandez, Qiaonan Duan, Zichen Wang, Simon Koplev, Sherry L. Jenkins, Kathleen M. Jagodnik, Alexander Lachmann, Michael G. McDermott, Caroline D. Monteiro, Gregory W. Gundersen, Avi Ma'ayan, Enrichr: a comprehensive gene set enrichment analysis web server 2016 update, Nucleic Acids Research, Volume 44, Issue W1, 8 July 2016, Pages W90–W97, https://doi.org/10.1093/nar/gkw377
- Xie, Z., Bailey, A., Kuleshov, M. V., Clarke, D. J. B., Evangelista, J. E., Jenkins, S. L., Lachmann, A., Wojciechowicz, M. L., Kropiwnicki, E., Jagodnik, K. M., Jeon, M., & Ma'ayan, A. (2021). Gene set knowledge discovery with Enrichr. Current Protocols, 1, e90. doi: 10.1002/cpz1.90

- Enrichr API Documentation
- Citations note on Enrichr website

See Also

rba_enrichr

Other "Enrichr": rba_enrichr(), rba_enrichr_add_background(), rba_enrichr_enrich(), rba_enrichr_gene_map(), rba_enrichr_libs(), rba_enrichr_view_list()

Examples

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


rba_enrichr_add_list(gene_list = c("RAG1", "RAG2", "DNTT", "LIG4", "ARTEMIS"),
     description = "TCR rearrangment",
     speedrichr = TRUE)
```

---

rba_enrichr_enrich *Get Enrichr Enrichment Results*

Description

This function retrieves enrichment analysis results for your supplied ‘user_list_id‘ against one or multiple Enrichr libraries.

Usage

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

Arguments

user_list_id	An ID returned after uploading a gene list using rba_enrichr_add_list, with the ‘speedrichr‘ set to TRUE or FALSE depending on whether you intend to analyze this gene list with or without a background gene list, respectively.

`gene_set_library`
: One of the:

1. "all" to select all of the available Enrichr gene-set libraries.
2. A gene-set library name. You can retrieve the available options for a given species using `rba_enrichr_libs`.
3. If regex_library_name = TRUE, A partially-matching name a regex pattern that correspond to one or more of Enrichr library names.

`regex_library_name`
: logical: (default = FALSE) if TRUE the supplied gene_set_library will be considered as a regex pattern. If FALSE, gene_set_library will be considered as an 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). If ‘background_id‘ is provided, the only available option is "human".

`background_id`
: An ID returned after uploading a background gene list using `rba_enrichr_add_background`

`progress_bar`
: logical: (default = TRUE) if multiple Enrichr libraries are selected, should a progress bar be displayed?

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

Details

If ‘background_id‘ is supplied, this function will interact with the speedrichr API. In this case, ‘user_list_id‘ must have been obtained from a `rba_enrichr_add_list` call with the ‘speedrichr‘ parameter set to ‘TRUE‘. Additionally, this feature is only available for "human" organism.

Please note that `rba_enrichr` provides a one-step and more convenient way to automatically handle this and other required function calls needed to perform gene set enrichment analysis with Enrichr.

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"
"POST https://maayanlab.cloud/speedrichr/api/backgroundenrich"

References

- Chen, E.Y., Tan, C.M., Kou, Y. et al. Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. Bioinformatics 14, 128 (2013). https://doi.org/10.1186/1471-2105-14-128
- Maxim V. Kuleshov, Matthew R. Jones, Andrew D. Rouillard, Nicolas F. Fernandez, Qiaonan Duan, Zichen Wang, Simon Koplev, Sherry L. Jenkins, Kathleen M. Jagodnik, Alexander Lachmann, Michael G. McDermott, Caroline D. Monteiro, Gregory W. Gundersen, Avi

Ma'ayan, Enrichr: a comprehensive gene set enrichment analysis web server 2016 update, Nucleic Acids Research, Volume 44, Issue W1, 8 July 2016, Pages W90–W97, https://doi.org/10.1093/nar/gkw377

- Xie, Z., Bailey, A., Kuleshov, M. V., Clarke, D. J. B., Evangelista, J. E., Jenkins, S. L., Lachmann, A., Wojciechowicz, M. L., Kropiwnicki, E., Jagodnik, K. M., Jeon, M., & Ma'ayan, A. (2021). Gene set knowledge discovery with Enrichr. Current Protocols, 1, e90. doi: 10.1002/cpz1.90
- Enrichr API Documentation
- Citations note on Enrichr website

See Also

rba_enrichr

Other "Enrichr": rba_enrichr(), rba_enrichr_add_background(), rba_enrichr_add_list(), rba_enrichr_gene_map(), rba_enrichr_libs(), rba_enrichr_view_list()

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, categorize = FALSE, organism = "human", ...)
```

Arguments

gene	character: An Entrez gene symbol.
categorize	logical: Should the category information 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 nested list containing the search results of your supplied gene.

Corresponding API Resources

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

References

- Chen, E.Y., Tan, C.M., Kou, Y. et al. Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. Bioinformatics 14, 128 (2013). https://doi.org/10.1186/1471-2105-14-128
- Maxim V. Kuleshov, Matthew R. Jones, Andrew D. Rouillard, Nicolas F. Fernandez, Qiaonan Duan, Zichen Wang, Simon Koplev, Sherry L. Jenkins, Kathleen M. Jagodnik, Alexander Lachmann, Michael G. McDermott, Caroline D. Monteiro, Gregory W. Gundersen, Avi Ma'ayan, Enrichr: a comprehensive gene set enrichment analysis web server 2016 update, Nucleic Acids Research, Volume 44, Issue W1, 8 July 2016, Pages W90–W97, https://doi.org/10.1093/nar/gkw377
- Xie, Z., Bailey, A., Kuleshov, M. V., Clarke, D. J. B., Evangelista, J. E., Jenkins, S. L., Lachmann, A., Wojciechowicz, M. L., Kropiwnicki, E., Jagodnik, K. M., Jeon, M., & Ma'ayan, A. (2021). Gene set knowledge discovery with Enrichr. Current Protocols, 1, e90. doi: 10.1002/cpz1.90
- Enrichr API Documentation
- Citations note on Enrichr website

See Also

Other "Enrichr": rba_enrichr(), rba_enrichr_add_background(), rba_enrichr_add_list(), rba_enrichr_enrich(), rba_enrichr_libs(), rba_enrichr_view_list()

Examples

```
rba_enrichr_gene_map(gene = "p53")


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

rba_enrichr_libs *Retrieve a List of available libraries from Enrichr*

Description

This function retrieves a list of libraries available in Enrichr along with their associated statistics. Each library represents a collection of gene sets that can be used for enrichment analysis.

Usage

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

Arguments

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).
store_in_options	logical: (default = TRUE) Should a list of available Enrichr libraries be saved as a global option?
...	rbioapi option(s). See rba_options's arguments manual for more information on available options.

Details

By default, this function will save the library names as a global option ("rba_enrichr_libs") for other Enrichr functions that internally require the names of Enrichr libraries. You should call this function once per R session with the argument 'store_in_options = TRUE' before using rba_enrichr_enrich or rba_enrichr. However, if you do not explicitly call it, rbioapi will automatically execute this function in the background the when it is needed.

Please note that rba_enrichr provides a one-step and more convenient way to automatically handle this and other required function calls needed to perform gene set enrichment analysis with Enrichr.

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, E.Y., Tan, C.M., Kou, Y. et al. Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. Bioinformatics 14, 128 (2013). https://doi.org/10.1186/1471-2105-14-128

- Maxim V. Kuleshov, Matthew R. Jones, Andrew D. Rouillard, Nicolas F. Fernandez, Qiaonan Duan, Zichen Wang, Simon Koplev, Sherry L. Jenkins, Kathleen M. Jagodnik, Alexander Lachmann, Michael G. McDermott, Caroline D. Monteiro, Gregory W. Gundersen, Avi Ma'ayan, Enrichr: a comprehensive gene set enrichment analysis web server 2016 update, Nucleic Acids Research, Volume 44, Issue W1, 8 July 2016, Pages W90–W97, https://doi.org/10.1093/nar/gkw377
- Xie, Z., Bailey, A., Kuleshov, M. V., Clarke, D. J. B., Evangelista, J. E., Jenkins, S. L., Lachmann, A., Wojciechowicz, M. L., Kropiwnicki, E., Jagodnik, K. M., Jeon, M., & Ma'ayan, A. (2021). Gene set knowledge discovery with Enrichr. Current Protocols, 1, e90. doi: 10.1002/cpz1.90
- Enrichr API Documentation
- Citations note on Enrichr website

See Also

rba_enrichr

Other "Enrichr": rba_enrichr(), rba_enrichr_add_background(), rba_enrichr_add_list(), rba_enrichr_enrich(), rba_enrichr_gene_map(), rba_enrichr_view_list()

Examples

```
rba_enrichr_libs()
```

---

rba_enrichr_view_list *View an Uploaded Gene List*

Description

Retrieve the list of uploaded genes with a given 'user list ID'.

Usage

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

Arguments

user_list_id	a user list ID returned 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).

speedrichr	logical (default = FALSE) Did you upload your gene list to speedrichr API? (i.e. did you intend to use this gene list along with a background gene list?)
...	rbioapi option(s). See rba_options's arguments manual for more information on available options.

Value

A list containing the genes and description associated to the supplied user_list_id.

Corresponding API Resources

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

References

- Chen, E.Y., Tan, C.M., Kou, Y. et al. Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. Bioinformatics 14, 128 (2013). https://doi.org/10.1186/1471-2105-14-128
- Maxim V. Kuleshov, Matthew R. Jones, Andrew D. Rouillard, Nicolas F. Fernandez, Qiaonan Duan, Zichen Wang, Simon Koplev, Sherry L. Jenkins, Kathleen M. Jagodnik, Alexander Lachmann, Michael G. McDermott, Caroline D. Monteiro, Gregory W. Gundersen, Avi Ma'ayan, Enrichr: a comprehensive gene set enrichment analysis web server 2016 update, Nucleic Acids Research, Volume 44, Issue W1, 8 July 2016, Pages W90–W97, https://doi.org/10.1093/nar/gkw377
- Xie, Z., Bailey, A., Kuleshov, M. V., Clarke, D. J. B., Evangelista, J. E., Jenkins, S. L., Lachmann, A., Wojciechowicz, M. L., Kropiwnicki, E., Jagodnik, K. M., Jeon, M., & Ma'ayan, A. (2021). Gene set knowledge discovery with Enrichr. Current Protocols, 1, e90. doi: 10.1002/cpz1.90
- Enrichr API Documentation
- Citations note on Enrichr website

See Also

Other "Enrichr": rba_enrichr(), rba_enrichr_add_background(), rba_enrichr_add_list(), rba_enrichr_enrich(), rba_enrichr_gene_map(), rba_enrichr_libs()

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 = 2024, ...)
```

Arguments

`release`	Numeric: (default = 2024) Which JASPAR database release to use? Available options are: 2024, 2022, 2020, 2018, 2016, and 2014.
`...`	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 https://jaspar.elixir.no/api/v1/collections/"

References

- Rauluseviciute I, Riudavets-Puig R, Blanc-Mathieu R, Castro-Mondragon JA, Ferenc K, Kumar V, Lemma RB, Lucas J, Chèneby J, Baranasic D, Khan A, Fornes O, Gundersen S, Johansen M, Hovig E, Lenhard B, Sandelin A, Wasserman WW, Parcy F, Mathelier A JASPAR 2024: 20th anniversary of the open-access database of transcription factor binding profiles Nucleic Acids Res. in_press; doi: 10.1093/nar/gkad1059
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. Bioinformatics, 2017, doi: 10.1093/bioinformatics/btx804
- JASPAR API Documentation
- Citations note on JASPAR website

See Also

Other "JASPAR": `rba_jaspar_collections_matrices()`, `rba_jaspar_matrix()`, `rba_jaspar_matrix_search()`, `rba_jaspar_matrix_versions()`, `rba_jaspar_releases()`, `rba_jaspar_sites()`, `rba_jaspar_species()`, `rba_jaspar_species_matrices()`, `rba_jaspar_taxons()`, `rba_jaspar_taxons_matrices()`, `rba_jaspar_tffm()`, `rba_jaspar_tffm_search()`

Examples

```
rba_jaspar_collections(release = 2024)
```

`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 = 2024,
  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_HOMEO", "PBM_HLH", and "UNVALIDATED".
`release`	Numeric: (default = 2024) Which JASPAR database release to use? Available options are: 2024, 2022, 2020, 2018, 2016, and 2014.
`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 alsoa 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 in the collection.

Corresponding API Resources

"GET https://jaspar.elixir.no/api/v1/collections/{collection}/"

References

- Rauluseviciute I, Riudavets-Puig R, Blanc-Mathieu R, Castro-Mondragon JA, Ferenc K, Kumar V, Lemma RB, Lucas J, Chèneby J, Baranasic D, Khan A, Fornes O, Gundersen S, Johansen M, Hovig E, Lenhard B, Sandelin A, Wasserman WW, Parcy F, Mathelier A JASPAR 2024: 20th anniversary of the open-access database of transcription factor binding profiles Nucleic Acids Res. in_press; doi: 10.1093/nar/gkad1059
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. Bioinformatics, 2017, doi: 10.1093/bioinformatics/btx804
- JASPAR API Documentation
- Citations note on JASPAR website

See Also

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

Examples

```
rba_jaspar_collections_matrices(collection = "CORE",
  release = 2024,
  page_size = 100,
  page = 2)
```

`rba_jaspar_matrix` *Get a Position Frequency Matrices (PFM) with annotations*

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: • 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 https://jaspar.elixir.no/api/v1/matrix/{matrix_id}/"

References

- Rauluseviciute I, Riudavets-Puig R, Blanc-Mathieu R, Castro-Mondragon JA, Ferenc K, Kumar V, Lemma RB, Lucas J, Chèneby J, Baranasic D, Khan A, Fornes O, Gundersen S, Johansen M, Hovig E, Lenhard B, Sandelin A, Wasserman WW, Parcy F, Mathelier A JASPAR 2024: 20th anniversary of the open-access database of transcription factor binding profiles Nucleic Acids Res. in_press; doi: 10.1093/nar/gkad1059
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. Bioinformatics, 2017, doi: 10.1093/bioinformatics/btx804
- JASPAR API Documentation
- Citations note on JASPAR website

See Also

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

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 = 2024,
  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 = 2024) Which JASPAR database release to use? Available options are: 2024, 2022, 2020, 2018, 2016, and 2014.
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 https://jaspar.elixir.no/api/v1/api/v1/matrix/"

References

- Rauluseviciute I, Riudavets-Puig R, Blanc-Mathieu R, Castro-Mondragon JA, Ferenc K, Kumar V, Lemma RB, Lucas J, Chèneby J, Baranasic D, Khan A, Fornes O, Gundersen S, Johansen M, Hovig E, Lenhard B, Sandelin A, Wasserman WW, Parcy F, Mathelier A JASPAR 2024: 20th anniversary of the open-access database of transcription factor binding profiles Nucleic Acids Res. in_press; doi: 10.1093/nar/gkad1059
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. Bioinformatics, 2017, doi: 10.1093/bioinformatics/btx804
- JASPAR API Documentation
- Citations note on JASPAR website

See Also

Other "JASPAR": `rba_jaspar_collections()`, `rba_jaspar_collections_matrices()`, `rba_jaspar_matrix()`, `rba_jaspar_matrix_versions()`, `rba_jaspar_releases()`, `rba_jaspar_sites()`, `rba_jaspar_species()`, `rba_jaspar_species_matrices()`, `rba_jaspar_taxons()`, `rba_jaspar_taxons_matrices()`, `rba_jaspar_tffm()`, `rba_jaspar_tffm_search()`

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

base_id	Character: A base (stable) Identifier. A matrix profile identifier has "base_id.version" naming schema
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 of matrix profiles' versions information.

Corresponding API Resources

"GET https://jaspar.elixir.no/api/v1/matrix/{base_id}/versions/"

References

- Rauluseviciute I, Riudavets-Puig R, Blanc-Mathieu R, Castro-Mondragon JA, Ferenc K, Kumar V, Lemma RB, Lucas J, Chèneby J, Baranasic D, Khan A, Fornes O, Gundersen S, Johansen M, Hovig E, Lenhard B, Sandelin A, Wasserman WW, Parcy F, Mathelier A JASPAR 2024: 20th anniversary of the open-access database of transcription factor binding profiles Nucleic Acids Res. in_press; doi: 10.1093/nar/gkad1059
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. Bioinformatics, 2017, doi: 10.1093/bioinformatics/btx804
- JASPAR API Documentation
- Citations note on JASPAR website

See Also

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

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 https://jaspar.elixir.no/api/v1/releases/"
"GET https://jaspar.elixir.no/api/v1/releases/{release_number}/"

References

- Rauluseviciute I, Riudavets-Puig R, Blanc-Mathieu R, Castro-Mondragon JA, Ferenc K, Kumar V, Lemma RB, Lucas J, Chèneby J, Baranasic D, Khan A, Fornes O, Gundersen S, Johansen M, Hovig E, Lenhard B, Sandelin A, Wasserman WW, Parcy F, Mathelier A JASPAR 2024: 20th anniversary of the open-access database of transcription factor binding profiles Nucleic Acids Res. in_press; doi: 10.1093/nar/gkad1059
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. Bioinformatics, 2017, doi: 10.1093/bioinformatics/btx804
- JASPAR API Documentation
- Citations note on JASPAR website

See Also

Other "JASPAR": `rba_jaspar_collections()`, `rba_jaspar_collections_matrices()`, `rba_jaspar_matrix()`, `rba_jaspar_matrix_search()`, `rba_jaspar_matrix_versions()`, `rba_jaspar_sites()`, `rba_jaspar_species()`, `rba_jaspar_species_matrices()`, `rba_jaspar_taxons()`, `rba_jaspar_taxons_matrices()`, `rba_jaspar_tffm()`, `rba_jaspar_tffm_search()`

Examples

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

`rba_jaspar_sites` *Get binding sites of a matrix profile*

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 https://jaspar.elixir.no/api/v1/sites/{matrix_id}/"

References

- Rauluseviciute I, Riudavets-Puig R, Blanc-Mathieu R, Castro-Mondragon JA, Ferenc K, Kumar V, Lemma RB, Lucas J, Chèneby J, Baranasic D, Khan A, Fornes O, Gundersen S, Johansen M, Hovig E, Lenhard B, Sandelin A, Wasserman WW, Parcy F, Mathelier A JASPAR 2024: 20th anniversary of the open-access database of transcription factor binding profiles Nucleic Acids Res. in_press; doi: 10.1093/nar/gkad1059
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. Bioinformatics, 2017, doi: 10.1093/bioinformatics/btx804
- JASPAR API Documentation
- Citations note on JASPAR website

See Also

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

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 = 2024, search = NULL, order = NULL, ...)
```

Arguments

release	Numeric: (default = 2024) Which JASPAR database release to use? Available options are: 2024, 2022, 2020, 2018, 2016, and 2014.
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 https://jaspar.elixir.no/api/v1/species/"

References

- Rauluseviciute I, Riudavets-Puig R, Blanc-Mathieu R, Castro-Mondragon JA, Ferenc K, Kumar V, Lemma RB, Lucas J, Chèneby J, Baranasic D, Khan A, Fornes O, Gundersen S, Johansen M, Hovig E, Lenhard B, Sandelin A, Wasserman WW, Parcy F, Mathelier A JASPAR 2024: 20th anniversary of the open-access database of transcription factor binding profiles Nucleic Acids Res. in_press; doi: 10.1093/nar/gkad1059
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. Bioinformatics, 2017, doi: 10.1093/bioinformatics/btx804
- JASPAR API Documentation
- Citations note on JASPAR website

See Also

Other "JASPAR": `rba_jaspar_collections()`, `rba_jaspar_collections_matrices()`, `rba_jaspar_matrix()`, `rba_jaspar_matrix_search()`, `rba_jaspar_matrix_versions()`, `rba_jaspar_releases()`, `rba_jaspar_sites()`, `rba_jaspar_species_matrices()`, `rba_jaspar_taxons()`, `rba_jaspar_taxons_matrices()`, `rba_jaspar_tffm()`, `rba_jaspar_tffm_search()`

Examples

```
rba_jaspar_species(release = 2024)
```

`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 = 2024,
  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 = 2024) Which JASPAR database release to use? Available options are: 2024, 2022, 2020, 2018, 2016, and 2014.
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 https://jaspar.elixir.no/api/v1/species/{tax_id}/"

References

- Rauluseviciute I, Riudavets-Puig R, Blanc-Mathieu R, Castro-Mondragon JA, Ferenc K, Kumar V, Lemma RB, Lucas J, Chèneby J, Baranasic D, Khan A, Fornes O, Gundersen S, Johansen M, Hovig E, Lenhard B, Sandelin A, Wasserman WW, Parcy F, Mathelier A JASPAR 2024: 20th anniversary of the open-access database of transcription factor binding profiles Nucleic Acids Res. in_press; doi: 10.1093/nar/gkad1059
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. Bioinformatics, 2017, doi: 10.1093/bioinformatics/btx804
- JASPAR API Documentation
- Citations note on JASPAR website

See Also

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

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 = 2024, ...)
```

Arguments

release	Numeric: (default = 2024) Which JASPAR database release to use? Available options are: 2024, 2022, 2020, 2018, 2016, and 2014.
...	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 https://jaspar.elixir.no/api/v1/taxon/"

References

- Rauluseviciute I, Riudavets-Puig R, Blanc-Mathieu R, Castro-Mondragon JA, Ferenc K, Kumar V, Lemma RB, Lucas J, Chèneby J, Baranasic D, Khan A, Fornes O, Gundersen S, Johansen M, Hovig E, Lenhard B, Sandelin A, Wasserman WW, Parcy F, Mathelier A JASPAR 2024: 20th anniversary of the open-access database of transcription factor binding profiles Nucleic Acids Res. in_press; doi: 10.1093/nar/gkad1059

- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. Bioinformatics, 2017, doi: 10.1093/bioinformatics/btx804
- JASPAR API Documentation
- Citations note on JASPAR website

See Also

Other "JASPAR": `rba_jaspar_collections()`, `rba_jaspar_collections_matrices()`, `rba_jaspar_matrix()`, `rba_jaspar_matrix_search()`, `rba_jaspar_matrix_versions()`, `rba_jaspar_releases()`, `rba_jaspar_sites()`, `rba_jaspar_species()`, `rba_jaspar_species_matrices()`, `rba_jaspar_taxons_matrices()`, `rba_jaspar_tffm()`, `rba_jaspar_tffm_search()`

Examples

```
rba_jaspar_taxons(release = 2024)
```

---

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 = 2024,
  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 = 2024) Which JASPAR database release to use? Available options are: 2024, 2022, 2020, 2018, 2016, and 2014.

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 https://jaspar.elixir.no/api/v1/taxon/{tax_group}/"

References

- Rauluseviciute I, Riudavets-Puig R, Blanc-Mathieu R, Castro-Mondragon JA, Ferenc K, Kumar V, Lemma RB, Lucas J, Chèneby J, Baranasic D, Khan A, Fornes O, Gundersen S, Johansen M, Hovig E, Lenhard B, Sandelin A, Wasserman WW, Parcy F, Mathelier A JASPAR 2024: 20th anniversary of the open-access database of transcription factor binding profiles Nucleic Acids Res. in_press; doi: 10.1093/nar/gkad1059
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. Bioinformatics, 2017, doi: 10.1093/bioinformatics/btx804
- JASPAR API Documentation
- Citations note on JASPAR website

See Also

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

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 https://jaspar.elixir.no/api/v1/fttm/{tffm_id}/"

References

- Rauluseviciute I, Riudavets-Puig R, Blanc-Mathieu R, Castro-Mondragon JA, Ferenc K, Kumar V, Lemma RB, Lucas J, Chèneby J, Baranasic D, Khan A, Fornes O, Gundersen S, Johansen M, Hovig E, Lenhard B, Sandelin A, Wasserman WW, Parcy F, Mathelier A JASPAR 2024: 20th anniversary of the open-access database of transcription factor binding profiles Nucleic Acids Res. in_press; doi: 10.1093/nar/gkad1059
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. Bioinformatics, 2017, doi: 10.1093/bioinformatics/btx804
- JASPAR API Documentation
- Citations note on JASPAR website

See Also

Other "JASPAR": rba_jaspar_collections(), rba_jaspar_collections_matrices(), rba_jaspar_matrix(), rba_jaspar_matrix_search(), rba_jaspar_matrix_versions(), rba_jaspar_releases(), rba_jaspar_sites(), rba_jaspar_species(), rba_jaspar_species_matrices(), rba_jaspar_taxons(), rba_jaspar_taxons_matrices(), 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 = 2024,
  tax_group = NULL,
  search = NULL,
  order = NULL,
  page_size = 1000,
  page = 1,
  ...
)
```

Arguments

`term`	Character: A search term.
`release`	Numeric: (default = 2024) Which JASPAR database release to use? Available options are: 2024, 2022, 2020, 2018, 2016, and 2014.
`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 https://jaspar.elixir.no/api/v1/api/v1/tffm/"

References

- Rauluseviciute I, Riudavets-Puig R, Blanc-Mathieu R, Castro-Mondragon JA, Ferenc K, Kumar V, Lemma RB, Lucas J, Chèneby J, Baranasic D, Khan A, Fornes O, Gundersen S, Johansen M, Hovig E, Lenhard B, Sandelin A, Wasserman WW, Parcy F, Mathelier A JASPAR 2024: 20th anniversary of the open-access database of transcription factor binding profiles Nucleic Acids Res. in_press; doi: 10.1093/nar/gkad1059
- Khan, A. and Mathelier, A. JASPAR RESTful API: accessing JASPAR data from any programming language. Bioinformatics, 2017, doi: 10.1093/bioinformatics/btx804
- JASPAR API Documentation
- Citations note on JASPAR website

See Also

Other "JASPAR": rba_jaspar_collections(), rba_jaspar_collections_matrices(), rba_jaspar_matrix(), rba_jaspar_matrix_search(), rba_jaspar_matrix_versions(), rba_jaspar_releases(), rba_jaspar_sites(), rba_jaspar_species(), rba_jaspar_species_matrices(), rba_jaspar_taxons(), rba_jaspar_taxons_matrices(), 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` *Get Supported Enrichment Categories for a Species and miRNA Type*

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: 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
- Citations note on miEAA website

See Also

Other "miEAA": `rba_mieaa_convert_type()`, `rba_mieaa_convert_version()`, `rba_mieaa_enrich()`, `rba_mieaa_enrich_results()`, `rba_mieaa_enrich_status()`, `rba_mieaa_enrich_submit()`

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: A uniform system for microRNA annotation). 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
- Citations note on miEAA website

See Also

Other "miEAA": `rba_mieaa_cats()`, `rba_mieaa_convert_version()`, `rba_mieaa_enrich()`, `rba_mieaa_enrich_results()`, `rba_mieaa_enrich_status()`, `rba_mieaa_enrich_submit()`

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
- Citations note on miEAA website

See Also

Other "miEAA": rba_mieaa_cats(), rba_mieaa_convert_type(), rba_mieaa_enrich(), rba_mieaa_enrich_results(
rba_mieaa_enrich_status(), rba_mieaa_enrich_submit()

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 perform enrichment analysis on 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 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: 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

- 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
- Citations note on miEAA website

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()`

Other "Enrichment/Over-representation": `rba_enrichr()`, `rba_panther_enrich()`, `rba_reactome_analysis()`, `rba_string_enrichment()`, `rba_string_enrichment_image()`

Examples

```
## Not run:
rba_mieaa_enrich(test_set = c("hsa-miR-20b-5p", "hsa-miR-144-5p",
 "hsa-miR-17-5p", "hsa-miR-20a-5p"),
     mirna_type = "mature",
     test_type = "ORA",
     species = 9606,
     categories = "miRPathDB_GO_Biological_process_mature")

## 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 perform enrichment analysis on 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
- Citations note on miEAA website

See Also

Other "miEAA": rba_mieaa_cats(), rba_mieaa_convert_type(), rba_mieaa_convert_version(), rba_mieaa_enrich(), rba_mieaa_enrich_status(), rba_mieaa_enrich_submit()

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

`job_id`	The job-id (a character string) of a submitted enrichment analysis.
`...`	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 perform enrichment analysis on 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
- Citations note on miEAA website

See Also

Other "miEAA": `rba_mieaa_cats()`, `rba_mieaa_convert_type()`, `rba_mieaa_convert_version()`, `rba_mieaa_enrich()`, `rba_mieaa_enrich_results()`, `rba_mieaa_enrich_submit()`

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 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:

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

- 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 perform enrichment analysis on 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
- Citations note on miEAA website

See Also

Other "miEAA": `rba_mieaa_cats()`, `rba_mieaa_convert_type()`, `rba_mieaa_convert_version()`, `rba_mieaa_enrich()`, `rba_mieaa_enrich_results()`, `rba_mieaa_enrich_status()`

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 = 0) How many times should rbioapi retry in case of 5xx server responses, errors 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: • 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 = 90) 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: 1. : Wrap a quote() around it. meaning: quote(rba_example()) 2. : 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 or Enrichment Analysis*

Description

Use PANTHER services to perform over-representation enrichment analysis. You can either provide a character vector of gene IDs for over-representation analysis, or a data frame of gene IDs and expression analysis.
Please refer to the details section for more information on the statistical analysis.

Usage

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

Arguments

genes	Either a character vector or a data frame. Depending on this parameter, the analysis type is determined. **Character vector:** If a character vector is supplied, over-representation analysis will be performed using either Fisher's exact test (default), or binomial. **Data frame:** If a data.frame is supplied, statistical enrichment test is performed using Mann-Whitney U (Wilcoxon Rank-Sum) test. The data frame should have two columns: the first column is a character vector with gene identifiers and the second column is a numerical vector with expression values. In both cases, maximum of 10000 genes can be supplied. The gene identifiers can be any of: Ensemble gene ID, Ensembl protein ID, Ensembl transcript ID, Entrez gene ID, gene symbol, NCBI GI, HGNC ID, International protein index ID, NCBI UniGene ID, UniProt accession 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. Note that you should enter the "id" of the dataset, not its label (e.g. entering "biological_process" is incorrect, you should rather enter "GO:0008150").
test_type	statistical test type to calculate the p values. • If performing over-representation analysis (i.e. 'genes' parameter is a character vector), valid values are "FISHER" (default) or "BINOMIAL". • If performing statistical enrichment analysis (i.e. 'genes' parameter is a data.frame), the only valid value is "Mann-Whitney"
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, only valid if genes is a character vector) A character vector 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. The maximum length and supported IDs are the same as 'genes' argument.

`ref_organism` (Optional, only valid if genes is a character vector) 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.

Details

Over-representation Test: It assesses whether specific gene sets are represented in your input gene list differently from what is expected by chance. It uses Fisher's exact test or Binomial test to calculate p-values. Fisher's exact test determines the probability of observing the gene counts in a category based on a hypergeometric distribution; the binomial test compares the observed proportion of genes in a category to the expected proportion based on the reference list. A significant p-value indicates over-representation or under-representation of a gene set.

Statistical Enrichment Test: The statistical enrichment test uses the Mann-Whitney U (Wilcoxon Rank-Sum) test to assess if the expression values associated with genes in a specific category differ significantly from the overall distribution in the input list. This non-parametric test first ranks the numerical values and computes whether the expression values were randomly drawn from the overall distribution of values. A small p-value indicates that the numerical values for the genes in the category are significantly different from the background distribution, thus non-random patterns.

Please note that starting from rbioapi version 0.8.2, you can supply a gene expression data frame to perform statistical enrichment analysis. In earlier versions, only a character vector of gene IDs was possible, thus only over-representation analysis.

Value

A list with the parameters and results. If the analysis was successful, the results data frame are returned in the "results" element within the list. Otherwise, an error message will be returned under the "search$error" element in the returned list.

Corresponding API Resources

"POST https://www.pantherdb.org/services/oai/pantherdb/enrich/overrep"
"POST https://www.pantherdb.org/services/oai/pantherdb/enrich/statenrich"

References

- Huaiyu Mi, Dustin Ebert, Anushya Muruganujan, Caitlin Mills, Laurent-Philippe Albou, Tremayne Mushayamaha, Paul D Thomas, PANTHER version 16: a revised family classification, tree-based classification tool, enhancer regions and extensive API, Nucleic Acids Research, Volume 49, Issue D1, 8 January 2021, Pages D394–D403, https://doi.org/10.1093/nar/gkaa1106
- PANTHER Services Details
- Citations note on PANTHER website

See Also

Other "PANTHER": `rba_panther_family()`, `rba_panther_homolog()`, `rba_panther_info()`, `rba_panther_mapping()`, `rba_panther_ortholog()`, `rba_panther_tree_grafter()`

Other "Enrichment/Over-representation": rba_enrichr(), rba_mieaa_enrich(), rba_reactome_analysis(), rba_string_enrichment(), rba_string_enrichment_image()

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
  )



expression_df <- data.frame(
  genes = c("p53", "BRCA1", "cdk2", "Q99835", "CDC42",
    "CDK1", "KIF23", "PLK1", "RAC2", "RACGAP1"),
  expr = runif(10, 0, 100)
  )

rba_panther_enrich(
  genes = expression_df,
  organism = 9606,
  annot_dataset = "GO:0008150"
  )
```

---

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: • "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 https://www.pantherdb.org/services/oai/pantherdb/familyortholog"
"GET https://www.pantherdb.org/services/oai/pantherdb/familymsa"
"GET https://www.pantherdb.org/services/oai/pantherdb/treeinfo"

References

- Huaiyu Mi, Dustin Ebert, Anushya Muruganujan, Caitlin Mills, Laurent-Philippe Albou, Tremayne Mushayamaha, Paul D Thomas, PANTHER version 16: a revised family classification, tree-based classification tool, enhancer regions and extensive API, Nucleic Acids Research, Volume 49, Issue D1, 8 January 2021, Pages D394–D403, https://doi.org/10.1093/nar/gkaa1106
- PANTHER Services Details
- Citations note on PANTHER website

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 https://www.pantherdb.org/services/oai/pantherdb/ortholog/homologOther"

References

- Huaiyu Mi, Dustin Ebert, Anushya Muruganujan, Caitlin Mills, Laurent-Philippe Albou, Tremayne Mushayamaha, Paul D Thomas, PANTHER version 16: a revised family classification, tree-based classification tool, enhancer regions and extensive API, Nucleic Acids Research, Volume 49, Issue D1, 8 January 2021, Pages D394–D403, https://doi.org/10.1093/nar/gkaa1106
- PANTHER Services Details
- Citations note on PANTHER website

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: • "organisms": Retrieve supported organisms in PANTHER. • "datasets": Retrieve available annotation datasets. • "families" Retrieve available family IDs. • "species_tree" Retrieve the PANThER's species tree. • "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 and species tree, a list and otherwise a data frame with pertinent information.

Corresponding API Resources

"GET https://www.pantherdb.org/services/oai/pantherdb/supportedgenomes"
"GET https://www.pantherdb.org/services/oai/pantherdb/supportedannotdatasets"
"GET https://www.pantherdb.org/services/oai/pantherdb/supportedpantherfamilies"
"GET https://www.pantherdb.org/services/oai/pantherdb/supportedpantherpathways"
"GET https://www.pantherdb.org/services/oai/pantherdb/speciestree"

References

- Huaiyu Mi, Dustin Ebert, Anushya Muruganujan, Caitlin Mills, Laurent-Philippe Albou, Tremayne Mushayamaha, Paul D Thomas, PANTHER version 16: a revised family classification, tree-based classification tool, enhancer regions and extensive API, Nucleic Acids Research, Volume 49, Issue D1, 8 January 2021, Pages D394–D403, https://doi.org/10.1093/nar/gkaa1106
- PANTHER Services Details
- Citations note on PANTHER website

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 https://www.pantherdb.org/services/oai/pantherdb/geneinfo"

References

- Huaiyu Mi, Dustin Ebert, Anushya Muruganujan, Caitlin Mills, Laurent-Philippe Albou, Tremayne Mushayamaha, Paul D Thomas, PANTHER version 16: a revised family classification, tree-based classification tool, enhancer regions and extensive API, Nucleic Acids Research, Volume 49, Issue D1, 8 January 2021, Pages D394–D403, https://doi.org/10.1093/nar/gkaa1106
- PANTHER Services Details
- Citations note on PANTHER website

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 https://www.pantherdb.org/services/oai/pantherdb/ortholog/matchortho"
"POST https://www.pantherdb.org/services/oai/pantherdb/ortholog/homologpos"

References

- Huaiyu Mi, Dustin Ebert, Anushya Muruganujan, Caitlin Mills, Laurent-Philippe Albou, Tremayne Mushayamaha, Paul D Thomas, PANTHER version 16: a revised family classification, tree-based classification tool, enhancer regions and extensive API, Nucleic Acids Research, Volume 49, Issue D1, 8 January 2021, Pages D394–D403, https://doi.org/10.1093/nar/gkaa1106
- PANTHER Services Details
- Citations note on PANTHER website

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*

Description

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.

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.

Details

For more information, see: Haiming Tang, Robert D Finn, Paul D Thomas, TreeGrafter: phylogenetic tree-based annotation of proteins with Gene Ontology terms and other annotations, Bioinformatics, Volume 35, Issue 3, February 2019, Pages 518–520, doi:10.1093/bioinformatics/bty625

Value

A list containing PANTHER tree topology information.

Corresponding API Resources

"GET https://www.pantherdb.org/services/oai/pantherdb/graftsequence"

References

- Huaiyu Mi, Dustin Ebert, Anushya Muruganujan, Caitlin Mills, Laurent-Philippe Albou, Tremayne Mushayamaha, Paul D Thomas, PANTHER version 16: a revised family classification, tree-based classification tool, enhancer regions and extensive API, Nucleic Acids Research, Volume 49, Issue D1, 8 January 2021, Pages D394–D403, https://doi.org/10.1093/nar/gkaa1106
- PANTHER Services Details
- Citations note on PANTHER website

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 = TRUE,
  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: • "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 = TRUE) 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. Note that you cannot supply the species parameter when projection parameter is TRUE.
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, form 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

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028

- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Analysis Services API Documentation
- Citations note on Reactome website

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()

Other "Enrichment/Over-representation": rba_enrichr(), rba_mieaa_enrich(), rba_panther_enrich(), rba_string_enrichment(), rba_string_enrichment_image()

Examples

```
## Not run:
rba_reactome_analysis(input = c("p53", "BRCA1", "cdk2", "Q99835", "CDC42"))

## End(Not run)
## 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: • "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. • "results_gz" Same as "results", but the output will be compress (gzipped).
save_to	NULL or Character: • 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}/pathways/ {resource}/{filename}.csv"
GET https://reactome.org/AnalysisService/download/{token}/result.json"
GET https://reactome.org/AnalysisService/download/{token}/result.json.gz"

References

• Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng,

Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028

- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Analysis Services API Documentation
- Citations note on Reactome website

See Also

rba_reactome_analysis_pdf rba_reactome_analysis

Other "Reactome Analysis Service": rba_reactome_analysis(), rba_reactome_analysis_import(), rba_reactome_analysis_mapping(), rba_reactome_analysis_pdf(), rba_reactome_analysis_species(), rba_reactome_analysis_token()

Examples

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

## End(Not run)
## 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: • "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

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028
- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Analysis Services API Documentation
- Citations note on Reactome website

See Also

Other "Reactome Analysis Service": `rba_reactome_analysis()`, `rba_reactome_analysis_download()`, `rba_reactome_analysis_mapping()`, `rba_reactome_analysis_pdf()`, `rba_reactome_analysis_species()`, `rba_reactome_analysis_token()`

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 = TRUE,
  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: • "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 = TRUE) 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"
"GET https://reactome.org/AnalysisService/mapping/url"
"GET https://reactome.org/AnalysisService/mapping/url/projection"

References

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028
- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Analysis Services API Documentation
- Citations note on Reactome website

See Also

Other "Reactome Analysis Service": `rba_reactome_analysis()`, `rba_reactome_analysis_download()`, `rba_reactome_analysis_import()`, `rba_reactome_analysis_pdf()`, `rba_reactome_analysis_species()`, `rba_reactome_analysis_token()`

Examples

```
## Not run:
rba_reactome_analysis_mapping(c("Q8SQ34", "cd40"))

## End(Not run)
```

---

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

token	A token associated to your previous Reactome analysis.
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.
save_to	NULL or Character: • NULL: Save the file to an automatically-generated path. • Character string: A valid file path to save the file to.
number	Numeric: Maximum number of the reported pathways. Cannot not be greater than 50.
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".
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".
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

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028
- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Analysis Services API Documentation
- Citations note on Reactome website

See Also

rba_reactome_analysis_download rba_reactome_analysis

Other "Reactome Analysis Service": rba_reactome_analysis(), rba_reactome_analysis_download(), rba_reactome_analysis_import(), rba_reactome_analysis_mapping(), rba_reactome_analysis_species(), rba_reactome_analysis_token()

Examples

```
## Not run:
rba_reactome_analysis_pdf(token = "MjAyMDEwMTYwMTI3MTNfMjY1MjM%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

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028
- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Analysis Services API Documentation
- Citations note on Reactome website

See Also

`rba_reactome_orthology`

Other "Reactome Analysis Service": `rba_reactome_analysis()`, `rba_reactome_analysis_download()`, `rba_reactome_analysis_import()`, `rba_reactome_analysis_mapping()`, `rba_reactome_analysis_pdf()`, `rba_reactome_analysis_token()`

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.
`...`	rbioapi 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

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028
- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Analysis Services API Documentation
- Citations note on Reactome website

See Also

`rba_reactome_analysis`

Other "Reactome Analysis Service": `rba_reactome_analysis()`, `rba_reactome_analysis_download()`, `rba_reactome_analysis_import()`, `rba_reactome_analysis_mapping()`, `rba_reactome_analysis_pdf()`, `rba_reactome_analysis_species()`

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

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028

- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Content Services API Documentation
- Citations note on Reactome website

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.

Usage

```
rba_reactome_complex_subunits(complex_id, exclude_structures = FALSE, ...)
```

Arguments

`complex_id`	Reactome stable Identifier of the complex.
`exclude_structures`	(logical) Should the contained complexes and entity sets be excluded from the results? (default = FALSE)
`...`	rbioapi option(s). See `rba_options`'s arguments manual for more information on available options.

Details

Subunits will be returned recursively; Which means that if a subunit was itself a complex, subunit of that complex will be also returned in the results.

Value

Data frame which each row is a subunit of your supplied complex and the columns are pertinent information of that subunit.

Corresponding API Resources

"GET https://reactome.org/ContentService/data/complex/{id}/subunits"

References

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028
- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Content Services API Documentation
- Citations note on Reactome website

See Also

Other "Reactome Content Service - Physical Entity Queries": `rba_reactome_complex_list()`, `rba_reactome_entity_other_forms()`, `rba_reactome_participant_of()`

Examples

```
rba_reactome_complex_subunits(complex_id = "R-HSA-5674003",
    exclude_structures = FALSE)
```

---

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

References

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028
- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Content Services API Documentation
- Citations note on Reactome website

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

`entity_id`	Reactome's entity ID.
`...`	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

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028
- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Content Services API Documentation
- Citations note on Reactome website

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.
`...`	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 that 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

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028
- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Content Services API Documentation
- Citations note on Reactome website

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 that 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

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028
- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Content Services API Documentation
- Citations note on Reactome website

See Also

Other "Reactome Content Service - Queries Related to Events": `rba_reactome_event_ancestors()`

Examples

```
## Not run:
#very large response!
rba_reactome_event_hierarchy("Homo sapiens")

## End(Not run)
## Not run:
#very large response!
rba_reactome_event_hierarchy(9606)

## End(Not run)
```

`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: • 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/document/event/ {identifier}.pdf"

References

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028
- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Content Services API Documentation
- Citations note on Reactome website

See Also

rba_reactome_exporter_reaction rba_reactome_analysis

Other "Reactome Content Service - Format Exporter": rba_reactome_exporter_event(), rba_reactome_exporter_over
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: • 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/exporter/event/ {identifier}.sbml"

References

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028

- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Content Services API Documentation
- Citations note on Reactome website

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

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.
output_format	Images format, Can be one of: png (default), jpeg, svg or gif.
save_to	NULL or Character: • NULL: Save the file to an automatically-generated path. • Character string: A valid file path to save the file to.
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)
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

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028
- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Content Services API Documentation
- Citations note on Reactome website

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: • 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}"

References

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028
- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Content Services API Documentation
- Citations note on Reactome website

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

`proteins`	Proteins to retrieve PSICQUIC interactors.
`resource`	The PSICQUIC resource for your supplied proteins. Call rba_reactome_interactors_psicquic() without argument to get the available options.
`details`	Logical: If TRUE (default) a detailed list of interactors will be returned. If FALSE, only a summary of available interactors will be returned.
`...`	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/resources"

References

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028
- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Content Services API Documentation
- Citations note on Reactome website

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: 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

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028
- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Content Services API Documentation
- Citations note on Reactome website

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"
"GET https://reactome.org/ContentService/data/mapping/{resource}/ {identifier}/reactions"

References

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028
- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Content Services API Documentation
- Citations note on Reactome website

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.
`...`	rbioapi 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

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028

- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Content Services API Documentation
- Citations note on Reactome website

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

event_id	Reactome event's database ID (DbId) or Stable ID (StId).
only_physical_entities	Logical: If TRUe, only participating 'Physical Entities' will be returned.
only_reference_entities	Logical: If TRUe, only participating 'Reference Entities' will be returned.
...	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

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028
- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Content Services API Documentation
- Citations note on Reactome website

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.
`...`	rbioapi 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

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028
- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.

- Reactome Content Services API Documentation
- Citations note on Reactome website

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 that 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

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028
- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Content Services API Documentation
- Citations note on Reactome website

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

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning

Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028

- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Content Services API Documentation
- Citations note on Reactome website

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 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

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028
- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Content Services API Documentation
- Citations note on Reactome website

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? (Defalt = 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

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028

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- Reactome Content Services API Documentation
- Citations note on Reactome website

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

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028
- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Content Services API Documentation
- Citations note on Reactome website

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}"
"GET https://reactome.org/ContentService/data/query/enhanced/{id}"
"GET https://reactome.org/ContentService/data/query/{id}/{attributeName}"

References

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028
- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Content Services API Documentation
- Citations note on Reactome website

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.
`...`	rbioapi 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

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028
- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Content Services API Documentation
- Citations note on Reactome website

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

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser, Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028
- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Content Services API Documentation
- Citations note on Reactome website

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.
`...`	rbioapi 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

- Marc Gillespie, Bijay Jassal, Ralf Stephan, Marija Milacic, Karen Rothfels, Andrea Senff-Ribeiro, Johannes Griss, Cristoffer Sevilla, Lisa Matthews, Chuqiao Gong, Chuan Deng, Thawfeek Varusai, Eliot Ragueneau, Yusra Haider, Bruce May, Veronica Shamovsky, Joel Weiser, Timothy Brunson, Nasim Sanati, Liam Beckman, Xiang Shao, Antonio Fabregat, Konstantinos Sidiropoulos, Julieth Murillo, Guilherme Viteri, Justin Cook, Solomon Shorser,

Gary Bader, Emek Demir, Chris Sander, Robin Haw, Guanming Wu, Lincoln Stein, Henning Hermjakob, Peter D'Eustachio, The reactome pathway knowledgebase 2022, Nucleic Acids Research, 2021;, kab1028, https://doi.org/10.1093/nar/gkab1028

- Griss J, Viteri G, Sidiropoulos K, Nguyen V, Fabregat A, Hermjakob H. ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Mol Cell Proteomics. 2020 Sep 9. doi: 10.1074/mcp. PubMed PMID: 32907876.
- Reactome Content Services API Documentation
- Citations note on Reactome website

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 o 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, among with information for each term.

Usage

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

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.
split_df	(logical, default = TRUE), If TRUE, instead of one data frame, results from different categories will be split into multiple data frames based on their 'category'.
...	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_paramete

References

- Damian Szklarczyk, Rebecca Kirsch, Mikaela Koutrouli, Katerina Nastou, Farrokh Mehryary, Radja Hachilif, Annika L Gable, Tao Fang, Nadezhda T Doncheva, Sampo Pyysalo, Peer Bork, Lars J Jensen, Christian von Mering, The STRING database in 2023: protein–protein association networks and functional enrichment analyses for any sequenced genome of interest, Nucleic Acids Research, Volume 51, Issue D1, 6 January 2023, Pages D638–D646, https://doi.org/10.1093/nar/gkac1000
- STRING API Documentation
- Citations note on STRING website

See Also

rba_string_map_ids, rba_string_enrichment, rba_string_enrichment_image

Other "STRING": rba_string_enrichment(), rba_string_enrichment_image(), 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_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 o 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, among with pertinent information for each term. Use `rba_string_enrichment_image` to retrieve the analysis results as a plot.

Usage

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

Arguments

`ids`	Your protein ID(s). It is strongly recommended to supply STRING IDs. See `rba_string_map_ids` for more information. Note that if only one id is supplied, STRING expands the network by 10 proteins.
`species`	Numeric: NCBI Taxonomy identifier; Human Taxonomy ID is 9606. (Recommended, but optional if your input is less than 100 IDs.)
`background`	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.)
`split_df`	(logical, default = TRUE), If TRUE, instead of one data frame, results from different categories will be split into multiple data frames based on their 'category'.
`...`	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_annotations`.

Value

A list of data frames 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}"

References

- Damian Szklarczyk, Rebecca Kirsch, Mikaela Koutrouli, Katerina Nastou, Farrokh Mehryary, Radja Hachilif, Annika L Gable, Tao Fang, Nadezhda T Doncheva, Sampo Pyysalo, Peer Bork, Lars J Jensen, Christian von Mering, The STRING database in 2023: protein–protein association networks and functional enrichment analyses for any sequenced genome of interest, Nucleic Acids Research, Volume 51, Issue D1, 6 January 2023, Pages D638–D646, https://doi.org/10.1093/nar/gkac1000
- STRING API Documentation
- Citations note on STRING website

See Also

`rba_string_map_ids`, `rba_string_annotations`, `rba_string_enrichment_image`

Other "STRING": `rba_string_annotations()`, `rba_string_enrichment_image()`, `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()`

Other "Enrichment/Over-representation": `rba_enrichr()`, `rba_mieaa_enrich()`, `rba_panther_enrich()`, `rba_reactome_analysis()`, `rba_string_enrichment_image()`

Examples

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

rba_string_enrichment_image *Get STRING Enrichment Plot*

Description

In addition to performing enrichment analysis, STRING allows you to also visualize the analysis results. Use rba_string_enrichment to retrieve the analysis results as a data frame.

Usage

```
rba_string_enrichment_image(
  ids,
  species,
  category = "Process",
  image_format = "image",
  save_image = TRUE,
  group_by_similarity = NULL,
  color_palette = "mint_blue",
  number_of_term_shown = 10,
  x_axis = "signal",
  ...
)
```

Arguments

ids	Your protein ID(s). It is strongly recommended to supply STRING IDs. See rba_string_map_ids for more information. Note that if only one id is supplied, STRING expands the network by 10 proteins.
species	Numeric: NCBI Taxonomy identifier; Human Taxonomy ID is 9606.
category	The terms set to use to perform enrichment analysis. valid values are (See details for more info): "Process" (default), "Function", "Component", "Keyword", "KEGG", "RCTM", "HPO", "MPO", "DPO", "WPO", "ZPO", "FYPO", "Pfam", "SMART", "InterPro", "PMID", "NetworkNeighborAL", "COMPARTMENTS", "TISSUES", "DISEASES", or "WikiPathways"
image_format	one of: • "image": PNG image with normal resolution. • "highres_image": High-resolution PNG image. • "svg": Scalable Vector Graphics image.
save_image	Logical or Character: • 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.

`group_by_similarity`
: Jackard index treshold to visually group the related terms. Valid values are between 0.1 to 1 with increment of 0.1. Default value is NULL (i.e. no grouping).

`color_palette`
: Color pallet to code FDR values. Valid values are: "mint_blue" (default), "lime_emerald", "green_blue", "peach_purple", "straw_navy", or "yellow_pink"

`number_of_term_shown`
: (default: 10) Maximum number of results to include in the plot.

`x_axis`
: The variable to show on the x axis and rank the results based on it. Valid values are: "signal" (default), "strength", "FDR", or "gene_count"

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

Details

Available values for category are as follow. Default value is "Process".

- Process: Biological Process (Gene Ontology)
- Function: Molecular Function (Gene Ontology)
- Component: Cellular Component (Gene Ontology)
- Keyword: Annotated Keywords (UniProt)
- KEGG: KEGG Pathways
- RCTM: Reactome Pathways
- HPO: Human Phenotype (Monarch)
- MPO: The Mammalian Phenotype Ontology (Monarch)
- DPO: Drosophila Phenotype (Monarch)
- WPO: C. elegans Phenotype Ontology (Monarch)
- ZPO: Zebrafish Phenotype Ontology (Monarch)
- FYPO: Fission Yeast Phenotype Ontology (Monarch)
- Pfam: Protein Domains (Pfam)
- SMART: Protein Domains (SMART)
- InterPro: Protein Domains and Features (InterPro)
- PMID: Reference Publications (PubMed)
- NetworkNeighborAL: Local Network Cluster (STRING)
- COMPARTMENTS: Subcellular Localization (COMPARTMENTS)
- TISSUES: Tissue Expression (TISSUES)
- DISEASES: Disease-gene Associations (DISEASES)
- WikiPathways: WikiPathways

Value

A plot summarizing the enrichment results, which can be PNG or SVG depending on the inputs.

Corresponding API Resources

"POST https://string-db.org/api/{output_format}/enrichmentfigure"

References

- Damian Szklarczyk, Rebecca Kirsch, Mikaela Koutrouli, Katerina Nastou, Farrokh Mehryary, Radja Hachilif, Annika L Gable, Tao Fang, Nadezhda T Doncheva, Sampo Pyysalo, Peer Bork, Lars J Jensen, Christian von Mering, The STRING database in 2023: protein–protein association networks and functional enrichment analyses for any sequenced genome of interest, Nucleic Acids Research, Volume 51, Issue D1, 6 January 2023, Pages D638–D646, https://doi.org/10.1093/nar/gkac1000
- STRING API Documentation
- Citations note on STRING website

See Also

rba_string_map_ids, rba_string_enrichment, rba_string_annotations

Other "STRING": rba_string_annotations(), rba_string_enrichment(), 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()

Other "Enrichment/Over-representation": rba_enrichr(), rba_mieaa_enrich(), rba_panther_enrich(), rba_reactome_analysis(), rba_string_enrichment()

Examples

```
## Not run:
  rba_string_enrichment_image(
  ids = c("TP53", "TNF", "EGFR"),
  species = 9606,
  category = "KEGG"
  )

## End(Not run)
## Not run:
  rba_string_enrichment_image(
  ids = c("TP53", "TNF", "EGFR"),
  species = 9606,
  x_axis = "strength",
  number_of_term_shown = 20
  )

## End(Not run)
## Not run:
  rba_string_enrichment_image(
  ids = c("TP53", "TNF", "EGFR"),
  species = 9606,
  color_palette = "straw_navy"
  )
```

```
## End(Not run)
```

`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,
  background = 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)
`background`	character vector: A set of STRING protein IDs to be used as the background proteome. Only STRING IDs are acceptable. (See `rba_string_map_ids` to map your IDs.)
`...`	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}"

References

- Damian Szklarczyk, Rebecca Kirsch, Mikaela Koutrouli, Katerina Nastou, Farrokh Mehryary, Radja Hachilif, Annika L Gable, Tao Fang, Nadezhda T Doncheva, Sampo Pyysalo, Peer Bork, Lars J Jensen, Christian von Mering, The STRING database in 2023: protein–protein association networks and functional enrichment analyses for any sequenced genome of interest, Nucleic Acids Research, Volume 51, Issue D1, 6 January 2023, Pages D638–D646, https://doi.org/10.1093/nar/gkac1000
- STRING API Documentation
- Citations note on STRING website

See Also

rba_string_map_ids

Other "STRING": rba_string_annotations(), rba_string_enrichment(), rba_string_enrichment_image(), 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

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 of your input proteins; Human Taxonomy ID is 9606. (Recommended, but optional if your input is less than 100 IDs.)
species_b	(optional) Numeric: one or more NCBI Taxonomy identifiers of species to limit the closets homologous proteins search.
...	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}"

References

- Damian Szklarczyk, Rebecca Kirsch, Mikaela Koutrouli, Katerina Nastou, Farrokh Mehryary, Radja Hachilif, Annika L Gable, Tao Fang, Nadezhda T Doncheva, Sampo Pyysalo, Peer Bork, Lars J Jensen, Christian von Mering, The STRING database in 2023: protein–protein association networks and functional enrichment analyses for any sequenced genome of interest, Nucleic Acids Research, Volume 51, Issue D1, 6 January 2023, Pages D638–D646, https://doi.org/10.1093/nar/gkac1000
- STRING API Documentation
- Citations note on STRING website

See Also

rba_string_map_ids, rba_string_homology_intra

Other "STRING": rba_string_annotations(), rba_string_enrichment(), rba_string_enrichment_image(), rba_string_enrichment_ppi(), 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 = 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}"

References

- Damian Szklarczyk, Rebecca Kirsch, Mikaela Koutrouli, Katerina Nastou, Farrokh Mehryary, Radja Hachilif, Annika L Gable, Tao Fang, Nadezhda T Doncheva, Sampo Pyysalo, Peer Bork, Lars J Jensen, Christian von Mering, The STRING database in 2023: protein–protein association networks and functional enrichment analyses for any sequenced genome of interest, Nucleic Acids Research, Volume 51, Issue D1, 6 January 2023, Pages D638–D646, https://doi.org/10.1093/nar/gkac1000
- STRING API Documentation
- Citations note on STRING website

See Also

rba_string_map_ids, rba_string_homology_inter

Other "STRING": rba_string_annotations(), rba_string_enrichment(), rba_string_enrichment_image(), rba_string_enrichment_ppi(), 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",
```

```
  use_query_labels = FALSE,
  ...
)
```

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: 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: • "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.
use_query_labels	Logical: (Default = FALSE) Use the names supplied with the 'ids' argument as the nodes labels instead of STRING's default ones.
...	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}"

References

- Damian Szklarczyk, Rebecca Kirsch, Mikaela Koutrouli, Katerina Nastou, Farrokh Mehryary, Radja Hachilif, Annika L Gable, Tao Fang, Nadezhda T Doncheva, Sampo Pyysalo, Peer Bork, Lars J Jensen, Christian von Mering, The STRING database in 2023: protein–protein association networks and functional enrichment analyses for any sequenced genome of interest, Nucleic Acids Research, Volume 51, Issue D1, 6 January 2023, Pages D638–D646, https://doi.org/10.1093/nar/gkac1000
- STRING API Documentation
- Citations note on STRING website

See Also

rba_string_map_ids, rba_string_interaction_partners

Other "STRING": rba_string_annotations(), rba_string_enrichment(), rba_string_enrichment_image(), rba_string_enrichment_ppi(), 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: • "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

References

- Damian Szklarczyk, Rebecca Kirsch, Mikaela Koutrouli, Katerina Nastou, Farrokh Mehryary, Radja Hachilif, Annika L Gable, Tao Fang, Nadezhda T Doncheva, Sampo Pyysalo, Peer Bork, Lars J Jensen, Christian von Mering, The STRING database in 2023: protein–protein association networks and functional enrichment analyses for any sequenced genome of interest, Nucleic Acids Research, Volume 51, Issue D1, 6 January 2023, Pages D638–D646, https://doi.org/10.1093/nar/gkac1000
- STRING API Documentation
- Citations note on STRING website

See Also

rba_string_map_ids, rba_string_interactions_network

Other "STRING": rba_string_annotations(), rba_string_enrichment(), rba_string_enrichment_image(), rba_string_enrichment_ppi(), 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. The output are sorted to have the best matches first.
`...`	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}"

References

- Damian Szklarczyk, Rebecca Kirsch, Mikaela Koutrouli, Katerina Nastou, Farrokh Mehryary, Radja Hachilif, Annika L Gable, Tao Fang, Nadezhda T Doncheva, Sampo Pyysalo, Peer Bork, Lars J Jensen, Christian von Mering, The STRING database in 2023: protein–protein association networks and functional enrichment analyses for any sequenced genome of interest, Nucleic Acids Research, Volume 51, Issue D1, 6 January 2023, Pages D638–D646, https://doi.org/10.1093/nar/gkac1000
- STRING API Documentation
- Citations note on STRING website

See Also

Other "STRING": rba_string_annotations(), rba_string_enrichment(), rba_string_enrichment_image(), rba_string_enrichment_ppi(), 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 = "evidence",
  network_type = "functional",
  hide_node_labels = FALSE,
  use_query_labels = FALSE,
  hide_disconnected_nodes = FALSE,
  hide_structure_pics = FALSE,
  flat_nodes = FALSE,
  node_labels_center = FALSE,
  node_labels_font_size = 12,
  ...
)
```

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: • "image": PNG image with normal resolution. • "highres_image": High-resolution PNG image. • "svg": Scalable Vector Graphics image.
save_image	Logical or Character: • 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 (Between 0 to 1000): 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	The style of network edges, should be one of: • "evidence": (default) Line's color is based on the type of evidences that support the interaction. • "confidence": Line's thickness is an indicator of the interaction's confidence score. • "action": Line's Shape is an indicator of the interaction's predicted mode of actions.
network_type	should be one of: • "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
use_query_labels	Logical: (Default = FALSE) Use the names supplied with the 'ids' argument as the nodes labels instead of STRING's default ones.
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

`flat_nodes`
: Logical: (Default = FALSE) Make the nodes design flat instead of the default 3D design

`node_labels_center`
: Logical: (Default = FALSE) Position the protein names labels center aligned on the nodes

`node_labels_font_size`
: Numeric (Between 5 to 50, Default = 12) Font size of the protein nodes labels

`...`
: 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}"

References

- Damian Szklarczyk, Rebecca Kirsch, Mikaela Koutrouli, Katerina Nastou, Farrokh Mehryary, Radja Hachilif, Annika L Gable, Tao Fang, Nadezhda T Doncheva, Sampo Pyysalo, Peer Bork, Lars J Jensen, Christian von Mering, The STRING database in 2023: protein–protein association networks and functional enrichment analyses for any sequenced genome of interest, Nucleic Acids Research, Volume 51, Issue D1, 6 January 2023, Pages D638–D646, https://doi.org/10.1093/nar/gkac1000
- STRING API Documentation
- Citations note on STRING website

See Also

`rba_string_map_ids`

Other "STRING": `rba_string_annotations()`, `rba_string_enrichment()`, `rba_string_enrichment_image()`, `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_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"

References

- Damian Szklarczyk, Rebecca Kirsch, Mikaela Koutrouli, Katerina Nastou, Farrokh Mehryary, Radja Hachilif, Annika L Gable, Tao Fang, Nadezhda T Doncheva, Sampo Pyysalo, Peer Bork, Lars J Jensen, Christian von Mering, The STRING database in 2023: protein–protein association networks and functional enrichment analyses for any sequenced genome of interest, Nucleic Acids Research, Volume 51, Issue D1, 6 January 2023, Pages D638–D646, https://doi.org/10.1093/nar/gkac1000
- STRING API Documentation
- Citations note on STRING website

See Also

Other "STRING": `rba_string_annotations()`, `rba_string_enrichment()`, `rba_string_enrichment_image()`, `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()`

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/proteins/api/antigen/{accession}"

References

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

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

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

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

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Coordinates": `rba_uniprot_coordinates_location()`, `rba_uniprot_coordinates_location_genome`
`rba_uniprot_coordinates_location_protein()`, `rba_uniprot_coordinates_search()`

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?
`...`	rbioapi 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

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Coordinates": `rba_uniprot_coordinates()`, `rba_uniprot_coordinates_location_genome()`, `rba_uniprot_coordinates_location_protein()`, `rba_uniprot_coordinates_search()`

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_location_genome

Get Genome coordinate by Gene Sequence position

Description

Using this function you can retrieve genome coordinates of a given UniProt protein by providing Genome location position or range. You can either supply 'g_position' alone or supply 'g_start' and 'g_end' together.

Usage

```
rba_uniprot_coordinates_location_genome(
  taxid,
  chromosome,
  g_position = NULL,
  g_start = NULL,
  g_end = NULL,
  ...
)
```

Arguments

taxid	NIH-NCBI Taxon ID. You can supply up to 20 taxon IDs.
chromosome	(Character or Numeric): Chromosome name, e.g. 1, 20, X.
g_position	(numeric) Genome location position
g_start	(numeric) Genome location position start
g_end	(numeric) Genome location 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/glocation /{accession}:{pPosition}"
"GET https://ebi.ac.uk/proteins/api/coordinates/glocation /{accession}:{pStart}-{pEnd}"

References

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Coordinates": rba_uniprot_coordinates(), rba_uniprot_coordinates_location(), rba_uniprot_coordinates_location_protein(), rba_uniprot_coordinates_search()

Examples

```
rba_uniprot_coordinates_location_genome(
taxid = 9606, chromosome = 11, g_position = 36573305)
```

---

rba_uniprot_coordinates_location_protein

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_location_protein(
  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

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Coordinates": `rba_uniprot_coordinates()`, `rba_uniprot_coordinates_location()`, `rba_uniprot_coordinates_location_genome()`, `rba_uniprot_coordinates_search()`

Examples

```
rba_uniprot_coordinates_location_protein(accession = "P25942", p_position = 1)


rba_uniprot_coordinates_location_protein(accession = "P25942",
    p_start = 1, p_end = 277)
```

---

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

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Coordinates": `rba_uniprot_coordinates()`, `rba_uniprot_coordinates_location()`, `rba_uniprot_coordinates_location_genome()`, `rba_uniprot_coordinates_location_protein()`

Examples

```
rba_uniprot_coordinates_search(taxid = 9606, chromosome = "y")
```

`rba_uniprot_epitope` *Retrieve Epitopes by Accession*

Description

Use this function to retrieve epitope annotations linked to a UniProt entry.

Usage

```
rba_uniprot_epitope(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 UniProt epitope features details for the given accession.

Corresponding API Resources

"GET https://www.ebi.ac.uk/proteins/api/epitope/{accession}"

See Also

Other "UniProt - Epitopes": `rba_uniprot_epitope_search()`, `rba_uniprot_rna_edit()`

Examples

```
rba_uniprot_epitope(accession = "P36222")
```

`rba_uniprot_epitope_search` *Search UniProt Epitopes*

Description

Use this function to search epitope data associated to UniProt entities, using various criteria such as UniProt accession, epitope sequence, IEDB ID, and match score.

Usage

```
rba_uniprot_epitope_search(
  accession = NULL,
  epitope_sequence = NULL,
  iedb_id = NULL,
  match_score = NULL,
  ...
)
```

Arguments

`accession`	UniProtKB primary or secondary accession(s). You can supply up to 100 accession numbers.
`epitope_sequence`	(Character) Epitope's proteins sequence
`iedb_id`	(Numeric) EIDB epitope Identifier(s). You can supply up to 20 accession numbers.
`match_score`	Integer: 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.

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/proteins/api/epitope"

See Also

Other "UniProt - Epitopes": `rba_uniprot_epitope()`, `rba_uniprot_rna_edit()`

Examples

```
rba_uniprot_epitope_search(accession = c("Q84ZX5", "P36222"))


rba_uniprot_epitope_search(epitope_sequence = "DKKCIEWEKAQHGA")


rba_uniprot_epitope_search(iedb_id = 20354)
```

---

rba_uniprot_features *Get UniProt protein sequence features by accession*

Description

Use this function to retrieve sequence annotations (features) of a protein by it's UniProt accession.

Usage

```
rba_uniprot_features(
  accession,
  types = NULL,
  categories = NULL,
  location = 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.
location	(character) Filter the features by the amino acid position in the sequence(s). Provide the range as a character string with the format "begin-end", e.g. "35-70"
...	rbioapi 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/proteins/api/features/{accession}"

References

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

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` *Search UniProt protein sequence features*

Description

UniProt maintains 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.

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.

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.
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

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

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

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

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Proteomes": `rba_uniprot_genecentric_search()`, `rba_uniprot_proteomes()`, `rba_uniprot_proteomes_search()`

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.
`...`	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 containing gene-centric proteins search hits.

Corresponding API Resources

"GET https://ebi.ac.uk/proteins/api/genecentric"

References

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Proteomes": `rba_uniprot_genecentric()`, `rba_uniprot_proteomes()`, `rba_uniprot_proteomes_sear`

Examples

```
rba_uniprot_genecentric_search(accession = "P59594")


rba_uniprot_genecentric_search(gene = "Spike")


rba_uniprot_genecentric_search(upid = "UP000000354")
```

`rba_uniprot_mutagenesis`

Get Mutagenesis by UniProt Accession

Description

UniProt describes the effects of mutations in proteins' amino acid sequence on the biological properties of the protein, cell or the organism. Using this function, you can get the Mutagenesis description that has been mapped to a given UniProt protein.

Usage

```
rba_uniprot_mutagenesis(accession, location = NULL, ...)
```

Arguments

accession	UniProtKB primary or secondary accession(s).
location	A valid amino acid range (e.g. 10-25) within the sequence range of the given proein.
...	rbioapi option(s). See rba_options's arguments manual for more information on available options.

Value

A list containing the mutagenesis description of your supplied UniProt protein's sequence.

Corresponding API Resources

"GET https://www.ebi.ac.uk/proteins/api/mutagenesis/{accession}"

References

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Mutagenesis": rba_uniprot_mutagenesis_search()

Examples

```
rba_uniprot_mutagenesis(accession = "P0DTC2", location = "300-400")
```

`rba_uniprot_mutagenesis_search` *Search Mutagenesis in UniProt*

Description

UniProt describes the effects of mutations in proteins' amino acid sequence on the biological properties of the protein, cell or the organism. Using this function, you can search for mutagenesis description in UniProt proteins. You may also refine your search. See "Arguments section" for more information.

Usage

```
rba_uniprot_mutagenesis_search(
  accession = NULL,
  taxid = NULL,
  db_id = NULL,
  ...
)
```

Arguments

`accession`	UniProtKB primary or secondary accession(s). You can supply up to 100 accession numbers.
`taxid`	NIH-NCBI Taxon ID. You can supply up to 20 taxon IDs.
`db_id`	The ID in a Cross-reference (external) database. You can supply up to 20 values.
`...`	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 mutagenesis description are organized under the "features" sub-list.

Corresponding API Resources

"GET https://www.ebi.ac.uk/proteins/api/mutagenesis"

References

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Mutagenesis": `rba_uniprot_mutagenesis()`

Examples

```
#search all mutations in COVID19 proteins
rba_uniprot_mutagenesis_search(taxid = 2697049)
```

---

rba_uniprot_proteins *Get UniProt entry by accession*

Description

Use this function to retrieve a UniProt Entry by it's 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

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

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: • 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/proteins/api/proteins/{dbtype}:{dbid}"

References

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Proteins": rba_uniprot_proteins(), rba_uniprot_proteins_search()

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: • 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/proteins/api/proteins"

References

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Proteins": `rba_uniprot_proteins()`, `rba_uniprot_proteins_crossref()`

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

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Proteomes": rba_uniprot_genecentric(), rba_uniprot_genecentric_search(), 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.
`...`	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 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

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Proteomes": `rba_uniprot_genecentric()`, `rba_uniprot_genecentric_search()`, `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 (Deprecated)*

Description

This function is Deprecated. Please use `rba_uniprot_proteomics_non_ptm` instead.
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/proteins/api/proteomics/{accession}"

References

- The UniProt Consortium, UniProt: the universal protein knowledgebase in 2021, Nucleic Acids Research, Volume 49, Issue D1, 8 January 2021, Pages D480–D489, https://doi.org/10.1093/nar/gkaa1100
- 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
- Citations note on UniProt website

See Also

Other "Deprecated functions": `rba_uniprot_proteomics_search()`, `rba_uniprot_ptm()`, `rba_uniprot_ptm_search()`

Examples

```
## Not run:
#Deprecated
rba_uniprot_proteomics(accession = "P25942")

## End(Not run)
```

`rba_uniprot_proteomics_hpp`

Get HPP Proteomics data in UniProt

Description

UniProt maps post-translational modification proteomics data from different sources to the proteins' sequences. Using this function, you can retrieve all the HPP (Human Proteome Project) proteomics features that has been map to a given UniProt protein's sequence.

Usage

```
rba_uniprot_proteomics_hpp(accession, ...)
```

Arguments

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

Details

UniProt categorizes proteomics data sources into three main data categories: PTM (Post-Translational Modification), non-PTM, and HPP (Human Proteome Project); each with corresponding API endpoints, and thus, rbioapi functions.

Value

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

Corresponding API Resources

"GET https://www.ebi.ac.uk/proteins/api/proteomics/nonPtm/{accession}"

References

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Proteomics": `rba_uniprot_proteomics_hpp_search()`, `rba_uniprot_proteomics_non_ptm()`, `rba_uniprot_proteomics_non_ptm_search()`, `rba_uniprot_proteomics_ptm()`, `rba_uniprot_proteomics_ptm_sea`
`rba_uniprot_proteomics_species()`

Examples

```
rba_uniprot_proteomics_hpp(accession = "P04234")
```

`rba_uniprot_proteomics_hpp_search`

Search HPP Proteomics data in UniProt

Description

Using this function, you can search for HPP (Human Proteome Project) proteomics features 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_hpp_search(
  accession = NULL,
  taxid = NULL,
  data_source = NULL,
  upid = NULL,
  peptide = NULL,
  unique = NULL,
  ...
)
```

Arguments

accession	UniProtKB primary or secondary accession(s). You can supply up to 100 accession numbers.
taxid	NIH-NCBI Taxon ID. You can supply up to 20 taxon IDs.
data_source	Proteomics data source. In addition to manual curation, UniProt also import PTM annotations from the following databases: • "HPP" Please use 'rba_uniprot_proteomics_species()' for more information on the available data sources for a given species.
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.

UniProt categorizes proteomics data sources into three main data categories: PTM (Post-Translational Modification), non-PTM, and HPP (Human Proteome Project); each with corresponding API endpoints, and thus, rbioapi functions.

Value

A list Where each element correspond to a UniProt protein and proteomics data are organized under the "features" sub-list.

Corresponding API Resources

"GET https://www.ebi.ac.uk/proteins/api/proteomics/ptm"

References

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Proteomics": rba_uniprot_proteomics_hpp(), rba_uniprot_proteomics_non_ptm(), rba_uniprot_proteomics_non_ptm_search(), rba_uniprot_proteomics_ptm(), rba_uniprot_proteomics_ptm_sea
rba_uniprot_proteomics_species()

Examples

```
rba_uniprot_proteomics_hpp_search(peptide = "NDQVYQPLRDRDDAQYSHLGGNWAR")
```

`rba_uniprot_proteomics_non_ptm`

Get Proteomics data in UniProt

Description

UniProt maps proteomics data from different sources to the proteins' sequences. Using this function, you can retrieve all the non-post-translational modification proteomics features that has been map to a given UniProt protein's sequence.

Usage

```
rba_uniprot_proteomics_non_ptm(accession, ...)
```

Arguments

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

Details

UniProt categorizes proteomics data sources into three main data categories: PTM (Post-Translational Modification), non-PTM, and HPP (Human Proteome Project); each with corresponding API endpoints, and thus, rbioapi functions.

Value

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

Corresponding API Resources

"GET https://www.ebi.ac.uk/proteins/api/proteomics/nonPtm/{accession}"

References

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Proteomics": `rba_uniprot_proteomics_hpp()`, `rba_uniprot_proteomics_hpp_search()`, `rba_uniprot_proteomics_non_ptm_search()`, `rba_uniprot_proteomics_ptm()`, `rba_uniprot_proteomics_ptm_sea`
`rba_uniprot_proteomics_species()`

Examples

```
rba_uniprot_proteomics_non_ptm(accession = "P04234")
```

`rba_uniprot_proteomics_non_ptm_search`

Search Proteomics data in UniProt

Description

Using this function, you can search for non-Post-Translational Modification proteomics features 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_non_ptm_search(
  accession = NULL,
  taxid = NULL,
  data_source = NULL,
  upid = NULL,
  peptide = NULL,
  unique = NULL,
  ...
)
```

Arguments

accession	UniProtKB primary or secondary accession(s). You can supply up to 100 accession numbers.
taxid	NIH-NCBI Taxon ID. You can supply up to 20 taxon IDs.
data_source	Proteomics data source. In addition to manual curation, UniProt also import PTM annotations from the following databases: • "MaxQB" • "PeptideAtlas" • "EPD" • "ProteomicsDB" Please use 'rba_uniprot_proteomics_species()' for more information on the available data sources for a given species.
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.

UniProt categorizes proteomics data sources into three main data categories: PTM (Post-Translational Modification), non-PTM, and HPP (Human Proteome Project); each with corresponding API endpoints, and thus, rbioapi functions.

Value

A list Where each element correspond to a UniProt protein and proteomics data are organized under the "features" sub-list.

Corresponding API Resources

"GET https://www.ebi.ac.uk/proteins/api/proteomics/nonPtm"

References

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Proteomics": rba_uniprot_proteomics_hpp(), rba_uniprot_proteomics_hpp_search(), rba_uniprot_proteomics_non_ptm(), rba_uniprot_proteomics_ptm(), rba_uniprot_proteomics_ptm_search(), rba_uniprot_proteomics_species()

Examples

```
rba_uniprot_proteomics_non_ptm_search(peptide = "NDQVYQPLRDRDDAQYSHLGGNWAR")
```

---

rba_uniprot_proteomics_ptm

Get Post-Translational Modification of UniProt Protein

Description

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

Usage

```
rba_uniprot_proteomics_ptm(accession, confidence_score = NULL, ...)
```

Arguments

accession	UniProtKB primary or secondary accession.
confidence_score	(Character) Valid values: "Bronze", "Silver", or "gold". UniProt classifies modified residues into three categories based on its false localization rate (FLR) across multiple dataset. See Large scale modified residue for more information.
...	rbioapi option(s). See rba_options's arguments manual for more information on available options.

Details

see also: PTM / Processing section in UniProtKB

UniProt categorizes proteomics data sources into three main data categories: PTM (Post-Translational Modification), non-PTM, and HPP (Human Proteome Project); each with corresponding API endpoints, and thus, rbioapi functions.

Value

A list containing the post-translational modification features of your supplied UniProt protein's sequence.

Corresponding API Resources

"GET https://www.ebi.ac.uk/proteins/api/proteomics/ptm/{accession}"

References

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Proteomics": `rba_uniprot_proteomics_hpp()`, `rba_uniprot_proteomics_hpp_search()`, `rba_uniprot_proteomics_non_ptm()`, `rba_uniprot_proteomics_non_ptm_search()`, `rba_uniprot_proteomics_ptm`, `rba_uniprot_proteomics_species()`

Examples

```
rba_uniprot_proteomics_ptm(accession = "P04234")
```

---

rba_uniprot_proteomics_ptm_search

Search Post-Translational Modification Proteomics in UniProt

Description

Using this function, you can search for Post-Translational Modification proteomics features 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_ptm_search(
  accession = NULL,
  ptm = NULL,
  taxid = NULL,
  data_source = NULL,
  upid = NULL,
  peptide = NULL,
  unique = NULL,
  confidence_score = NULL,
  ...
)
```

Arguments

accession	UniProtKB primary or secondary accession(s). You can supply up to 100 accession numbers.
ptm	Post-translational modification name. Valid values are: "Acetylation ", "ADP-ribosylation ", "Amidation ", "Autocatalytic cleavage ", "Bromination ", "Citrullination ", "Cleavage on pair of basic residues ", "Covalent protein-DNA linkage ", "Covalent protein-RNA linkage ", "CTQ ", "D-amino acid ", "Disulfide bond ", "Formylation ", "Gamma-carboxyglutamic acid ", "Glutathionylation ", "Glycoprotein ", "Lipoprotein ", "Hydroxylation ", "Hypusine ", "Iodination ", "Isopeptide bond ", "LTQ ", "Methylation ", "Nitration ", "Organic radical ", "Oxidation ", "Peptidoglycan-anchor ", "Phosphopantetheine ", "Phosphoprotein ", "Pyrrolidone carboxylic acid ", "Quinone ", "S-nitrosylation ", "Sulfation ", "Thioester bond ", "Thioether bond ", "TPQ ", "TTQ ", "Ubl conjugation ", or "Zymogen".
taxid	NIH-NCBI Taxon ID. You can supply up to 20 taxon IDs.
data_source	Proteomics data source. In addition to manual curation, UniProt also import PTM annotations from the following databases: • "PRIDE" • "PTMeXchange" Please use ‘rba_uniprot_proteomics_species()‘ for more information on the available data sources for a given species.
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.
confidence_score	(Character) Valid values: "Bronze", "Silver", or "gold". UniProt classifies modified residues into three categories based on its false localization rate (FLR) across multiple dataset. See Large scale modified residue for more information.

... 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: PTM / Processing section in UniProtKB

UniProt categorizes proteomics data sources into three main data categories: PTM (Post-Translational Modification), non-PTM, and HPP (Human Proteome Project); each with corresponding API endpoints, and thus, rbioapi functions.

Value

A list Where each element correspond to a UniProt protein and post-translational modification are organized under the "features" sub-list.

Corresponding API Resources

"GET https://www.ebi.ac.uk/proteins/api//proteomics/ptm"

References

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Proteomics": rba_uniprot_proteomics_hpp(), rba_uniprot_proteomics_hpp_search(), rba_uniprot_proteomics_non_ptm(), rba_uniprot_proteomics_non_ptm_search(), rba_uniprot_proteomics_ptm
rba_uniprot_proteomics_species()

Examples

```
rba_uniprot_proteomics_ptm_search(peptide = "NDQVYQPLRDRDDAQYSHLGGNWAR")
```

`rba_uniprot_proteomics_search` *Search Proteomics Peptides in UniProt (Deprecated)*

Description

This function is Deprecated. Please use `rba_uniprot_proteomics_non_ptm_search` instead. 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: • "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/proteins/api/proteomics"

References

- The UniProt Consortium, UniProt: the universal protein knowledgebase in 2021, Nucleic Acids Research, Volume 49, Issue D1, 8 January 2021, Pages D480–D489, https://doi.org/10.1093/nar/gkaa1100
- 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
- Citations note on UniProt website

See Also

Other "Deprecated functions": `rba_uniprot_proteomics()`, `rba_uniprot_ptm()`, `rba_uniprot_ptm_search()`

Examples

```
## Not run:
#Deprecated
rba_uniprot_proteomics_search(peptide = "MEDYTKIEK")

## End(Not run)
## Not run:
#Deprecated
rba_uniprot_proteomics_search(peptide = "MEDYTKIEK")

## End(Not run)
## Not run:
#Deprecated
### 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_proteomics_species` *Get UniProt Proteomics Metadata*

Description

Retrieve information on the available Species proteomics data sources in UniProt.

Usage

```
rba_uniprot_proteomics_species(...)
```

Arguments

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

Details

UniProt categorizes proteomics data sources into three main data categories: PTM (Post-Translational Modification), non-PTM, and HPP (Human Proteome Project); each with corresponding API endpoints, and thus, rbioapi functions.

Value

A data frame with the available species as rows, and the columns indicating the proteomics data sources, separated by three main data categories: PTM (Post-Translational Modification), non-PTM, and HPP (Human Proteome Project)

Corresponding API Resources

"GET https://www.ebi.ac.uk/proteins/api/proteomics/species"

References

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Proteomics": rba_uniprot_proteomics_hpp(), rba_uniprot_proteomics_hpp_search(), rba_uniprot_proteomics_non_ptm(), rba_uniprot_proteomics_non_ptm_search(), rba_uniprot_proteomics_ptm(), rba_uniprot_proteomics_ptm_search()

Examples

```
rba_uniprot_proteomics_species()
```

---

rba_uniprot_ptm *Get Post-Translational Modification of UniProt Protein (Deprecated)*

Description

This function is Deprecated. Please use rba_uniprot_proteomics_ptm instead.
UniProt maps post-translational modification features from different sources to the proteins' sequences. Using this function, you can retrieve all the post-translational modification features that has been map to a given UniProt protein's sequence.

Usage

```
rba_uniprot_ptm(accession, ...)
```

Arguments

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

Details

see also: PTM / Processing section in UniProtKB

Value

A list containing the post-translational modification features of your supplied UniProt protein's sequence.

Corresponding API Resources

"GET https://www.ebi.ac.uk/proteins/api/proteomics-ptm/{accession}"

References

- The UniProt Consortium, UniProt: the universal protein knowledgebase in 2021, Nucleic Acids Research, Volume 49, Issue D1, 8 January 2021, Pages D480–D489, https://doi.org/10.1093/nar/gkaa1100
- 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
- Citations note on UniProt website

See Also

Other "Deprecated functions": `rba_uniprot_proteomics()`, `rba_uniprot_proteomics_search()`, `rba_uniprot_ptm_search()`

Examples

```
## Not run:
#Deprecated
rba_uniprot_ptm(accession = "P04234")

## End(Not run)
```

---

rba_uniprot_ptm_search

Search Post-Translational Modification in UniProt (Deprecated)

Description

This function is Deprecated. Please use `rba_uniprot_proteomics_ptm_search` instead.
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_ptm_search(
  accession = NULL,
  ptm = 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.
ptm	Post-translational modification name
data_source	Proteomics data source. You can choose up to two of: • "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: PTM / Processing section in UniProtKB

Value

A list Where each element correspond to a UniProt protein and post-translational modification are organized under the "features" sub-list.

Corresponding API Resources

"GET https://www.ebi.ac.uk/proteins/api/proteomics-ptm"

References

- The UniProt Consortium, UniProt: the universal protein knowledgebase in 2021, Nucleic Acids Research, Volume 49, Issue D1, 8 January 2021, Pages D480–D489, https://doi.org/10.1093/nar/gkaa1100
- 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
- Citations note on UniProt website

See Also

Other "Deprecated functions": rba_uniprot_proteomics(), rba_uniprot_proteomics_search(), rba_uniprot_ptm()

Examples

```
## Not run:
#Deprecated
rba_uniprot_ptm_search(peptide = "NDQVYQPLRDRDDAQYSHLGGNWAR")

## End(Not run)
```

---

rba_uniprot_rna_edit *Retrieve Epitope by Accession*

Description

Use this function to retrieve RNA-editing events (conversion, insertion, deletion of nucleotides) annotations linked to a UniProt entry.

Usage

```
rba_uniprot_rna_edit(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 UniProt RNA-editing features details for the given accession.

Corresponding API Resources

"GET https://www.ebi.ac.uk/proteins/api/rna-edit/{accession}"

See Also

Other "UniProt - Epitopes": rba_uniprot_epitope(), rba_uniprot_epitope_search()

Examples

```
rba_uniprot_rna_edit(accession = "Q16851")
```

`rba_uniprot_rna_edit_search` *Search RNA Editing in UniProt*

Description

UniProt Curates RNA-editing events (conversion, insertion, deletion of nucleotides). Use this function to search RNA editing records in UniProt using various criteria such as accession, taxon ID, or variant location.

Usage

```
rba_uniprot_rna_edit_search(
  accession = NULL,
  taxid = NULL,
  variantlocation = NULL,
  ...
)
```

Arguments

`accession`	UniProtKB primary or secondary accession(s). You can supply up to 100 accession numbers.
`taxid`	(Numeric) NIH-NCBI Taxon ID. You can supply up to 20 taxon IDs.
`variantlocation`	Character: RNA editing variant location(s). 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 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/rna-editing"

Examples

```
rba_uniprot_rna_edit_search(accession = c("Q16851", "Q16849"))
```

`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

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

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

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Taxonomy": rba_uniprot_taxonomy(), rba_uniprot_taxonomy_lineage(), rba_uniprot_taxonomy_name(), rba_uniprot_taxonomy_path(), rba_uniprot_taxonomy_relationship()

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
...	rbioapi 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}"

References

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Taxonomy": rba_uniprot_taxonomy(), rba_uniprot_taxonomy_lca(), rba_uniprot_taxonomy_name(
rba_uniprot_taxonomy_path(), rba_uniprot_taxonomy_relationship()

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 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

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Taxonomy": `rba_uniprot_taxonomy()`, `rba_uniprot_taxonomy_lca()`, `rba_uniprot_taxonomy_linea`
`rba_uniprot_taxonomy_path()`, `rba_uniprot_taxonomy_relationship()`

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

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Taxonomy": `rba_uniprot_taxonomy()`, `rba_uniprot_taxonomy_lca()`, `rba_uniprot_taxonomy_linea`
`rba_uniprot_taxonomy_name()`, `rba_uniprot_taxonomy_relationship()`

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

`from`	NCBI taxonomic identifier of your initial node.
`to`	NCBI taxonomic identifier of your final node.
`...`	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

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - Taxonomy": `rba_uniprot_taxonomy()`, `rba_uniprot_taxonomy_lca()`, `rba_uniprot_taxonomy_linea`
`rba_uniprot_taxonomy_name()`, `rba_uniprot_taxonomy_path()`

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: • 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/proteome/{upid}"
"GET https://ebi.ac.uk/proteins/api/uniparc/upi/{upi}"

References

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

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

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - UniParc": rba_uniprot_uniparc(), rba_uniprot_uniparc_search(), rba_uniprot_uniparc_sequenc

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: • 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.
...	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 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

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - UniParc": rba_uniprot_uniparc(), rba_uniprot_uniparc_bestguess(), rba_uniprot_uniparc_sequ

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: • 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

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

See Also

Other "UniProt - UniParc": `rba_uniprot_uniparc()`, `rba_uniprot_uniparc_bestguess()`, `rba_uniprot_uniparc_sea`

Examples

```
rba_uniprot_uniparc_sequence("GMRSCPRGCSQRGRCENGRCVCNPGYTGEDC")
```

---

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: • 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/proteins/api/variation/dbsnp/{dbid}"
"GET https://www.ebi.ac.uk/proteins/api/variation/hgvs/{hgvs}"
"GET https://www.ebi.ac.uk/proteins/api/variation/{accession}"

References

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

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 = "O43593", 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: • "dbSNP": NIH-NCBI dbSNP database. • "cosmic curate": COSMIC (the Catalogue of Somatic Mutations in Cancer)

- "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:

- 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.

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

- The UniProt Consortium , UniProt: the Universal Protein Knowledgebase in 2025, Nucleic Acids Research, 2024;, gkae1010, https://doi.org/10.1093/nar/gkae1010
- 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
- Citations note on UniProt website

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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