

Package: thermos (via r-universe)

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Title Interface with IonReporter from R

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Description thermos allows you to use the IonReporter API with R

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Repository <https://kaiaragaki.r-universe.dev>

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Contents

analysis	2
download	3
download_bam	3
getvcf	4
get_associated_bamfiles	5
key_setup	6
Index	7

`analysis`*Get analysis details*

Description

Get analysis details

Usage

```
analysis(  
  type = c("sample", "analysis"),  
  name = NULL,  
  id = NULL,  
  start_date = NULL,  
  end_date = NULL,  
  duration = NULL,  
  exclude = NULL,  
  view = NULL,  
  tidy = TRUE  
)
```

Arguments

<code>type</code>	character. Either "sample" (the default) or "analysis"
<code>name</code>	character. See details.
<code>id</code>	character. Optional. ID of analysis.
<code>start_date, end_date</code>	character. Optional. YYYY-MM-DD format.
<code>duration</code>	Optional. Parameter to filter the results by days/months. Valid value starts with "-" follow by a numeric value and ending with "d" or "m"
<code>exclude</code>	Optional. Can be "reports", "unfilteredvariants", "filteredvariants", or NULL. If NULL (default), downloads all.
<code>view</code>	Optional. Can be "summary", which will include a list of all analyses without links to the analyses (which can be faster to call)
<code>tidy</code>	boolean. Ignored if <code>view</code> is NULL. Should the results be presented as a tidy tibble?

Value

A JSON-like list or, if `view = "summary"` and `tidy = TRUE`, a tibble.

download	<i>Download an IonReporter file</i>
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Description

Download an IonReporter file

Usage

```
download(file_path, type = NULL, dest = NULL)
```

Arguments

file_path	Path where the file is stored on the server. See details.
type	Format of file. By default, file will be downloaded enclosed in a .zip
dest	Location where the file should be saved. If NULL, will be downloaded to temp-file.

Value

Path to downloaded files

download_bam	<i>Download a BAM file</i>
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Description

In a typical workflow, this will be used with `get_associated_bamfiles` to obtain the `file_path` argument

Usage

```
download_bam(file_path, type = NULL)
```

Arguments

file_path	character. Typically the output of <code>get_associated_bamfiles</code> .
type	character. Honestly no idea what this does. If NULL (default), downloads a zip. Other options are "" and "pdf"

getvcf	<i>Get a link to a VCF file</i>
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Description

If you want to download a VCF to a file, `download_vcf` is a better option.

Usage

```
getvcf(
  type = c("sample", "analysis"),
  name,
  id = NULL,
  start_date = NULL,
  end_date = NULL,
  duration = NULL,
  exclude = NULL
)

get_vcf(...)

download_vcf(dest = NULL, ...)
```

Arguments

<code>type</code>	character. Either "sample" (the default) or "analysis"
<code>name</code>	character. See details.
<code>id</code>	character. Optional. ID of analysis.
<code>start_date, end_date</code>	character. Optional. YYYY-MM-DD format.
<code>duration</code>	Optional. Parameter to filter the results by days/months. Valid value starts with "-" follow by a numeric value and ending with "d" or "m"
<code>exclude</code>	Optional. Can be "unfilteredvariants", "filteredvariants", or NULL. If NULL (default), downloads both.
<code>...</code>	Additional arguments passed to <code>getvcf</code> .
<code>dest</code>	Where the file should be saved. Should generally be a .zip. If null, will be saved as a tempfile with a .zip extension

Details

`download_vcf` provides a slightly more ergonomic way to directly download files, rather than just get links to them.

Sample names are the names in the 'Sample' field in under the 'Samples' tab on IonReporter. They are also under the 'samples' column in the output of `get_analysis_details`, *not* the 'name' column.

Analysis names can also be used to select a vcf to download/get links to download. They exist in the 'name' column in the output of get_analysis_details

Although the original API documentation seems to imply that the name argument isn't needed if type == "analysis", it appears that it is still needed.

All other arguments - except exclude - are further filters of the hits where type and name match.

I wish I could give a better explanation of "duration" but honestly the API documentation was sparse and gave no examples

Value

- download_vcf: The path to the downloaded file
- getvcf: A JSON-like list containing the link to download the file, the name, and the id of the analysis that the sample was in

get_associated_bamfiles

Get BAM files associated with samples or analyses

Description

Get BAM files associated with samples or analyses

Usage

```
get_associated_bamfiles(name, type = c("analysis", "sample"))
```

Arguments

name	character vector of either sample or analysis names
type	character, either "sample" or "analysis"

Details

You can get a list of analysis names using the list_analyses function. It's unclear if there's a way to get a list of sample names from the API.

`key_setup`*Helper to set up IonReporter envvar*

Description

Helper to set up IonReporter envvar

Usage

```
key_setup()
```

Value

boolean. Has key been set? Will return FALSE after setup since session hasn't been restarted

Index

analysis, [2](#)

download, [3](#)

download_bam, [3](#)

download_vcf (getvcf), [4](#)

get_associated_bamfiles, [5](#)

get_vcf (getvcf), [4](#)

getvcf, [4](#)

key_setup, [6](#)