

# Package ‘metabolighteR’

February 9, 2022

**Type** Package

**Title** Interface to the 'Metabolights' RESTful API

**Version** 0.1.3

**Date** 2022-02-09

**Description** Access to the 'Metabolights' RESTful API <<https://www.ebi.ac.uk/metabolights/index>>. Retrieve elements of publically available 'Metabolights' studies.

**Depends** magrittr

**Imports** httr,  
dplyr,  
purrr,  
crayon

**License** GPL (>= 3)

**LazyData** true

**URL** <https://github.com/aberHRML/metabolighteR>

**BugReports** <https://github.com/aberHRML/metabolighteR/issues>

**RoxygenNote** 7.1.1

**Encoding** UTF-8

**Suggests** covr,  
testthat,  
tibble,  
knitr,  
rmarkdown,  
tidyr

**Roxygen** list(markdown = TRUE)

**VignetteBuilder** knitr

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download_study_file	<i>Download Study File Contents</i>
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**Description**

Download the contents of a specified file from a public study

**Usage**

download\_study\_file(study\_id, filename)

**Arguments**

- study\_id            a character string of a valid MTBLS study id
- filename           a character of the full filename and extension to download

**Value**

a tibble of file contents

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get\_isa\_investigation    *Get ISA Investigation File*

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**Description**

Retrieve the ISA Investigation for a specified Metabolights Study

**Usage**

```
get_isa_investigation(study_id)
```

**Arguments**

study\_id            A character string of a valid MTBLS study id

**Value**

the ISA-tab Investigation output

**Examples**

```
## Not run:  
ISA <- get_isa_investigation('MTBLS375')  
writeLines(isa_investigation_parse, con = paste0('outpath/ISA.txt'))  
  
## End(Not run)
```

---

get\_private\_studies    *Get Private Studies*

---

**Description**

Retrieve all private studies which belong to your user account

**Usage**

```
get_private_studies()
```

**Value**

a tibble of your private Study IDs

**Examples**

```
## Not run:  
get_private_studies()  
  
## End(Not run)
```

---

`get_studies`*Get Studies*

---

**Description**

Retrieve a list of all publically available Metabolights studies

**Usage**

```
get_studies()
```

**Value**

a tibble of Study IDs

**Examples**

```
get_studies()
```

---

`get_study_contacts`*Get Study Contacts*

---

**Description**

Retrieve the contact details for a specified public study '

**Usage**

```
get_study_contacts(study_id)
```

**Arguments**

`study_id` a character string of a valid MTBLS study id

**Value**

a tibble of study contacts

**Examples**

```
get_study_contacts('MTBLS375')
```

---

get_study_desc	<i>Get Study Description</i>
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**Description**

Retrieve the abstract based description of a public study

**Usage**

```
get_study_desc(study_id)
```

**Arguments**

study_id	A character string of a valid MTBLS study id
----------	--

**Value**

a character string of the study description

**Examples**

```
get_study_desc('MTBLS375')
```

---

get_study_descriptors	<i>Get Study Descriptors</i>
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**Description**

Retrieve the study descriptors and annotation values for a publically available study

**Usage**

```
get_study_descriptors(study_id)
```

**Arguments**

study_id	A character string of a valid MTBLS study id
----------	--

**Value**

a tibble of study descriptors

**Examples**

```
get_study_descriptors('MTBLS375')
```

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get_study_factors	<i>Get Study Factors</i>
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**Description**

Retrieve the study factors and annotation values for a publically available study

**Usage**

```
get_study_factors(study_id)
```

**Arguments**

study_id	A character string of a valid MTBLS study id
----------	--

**Value**

a tibble of study factors

**Examples**

```
get_study_factors('MTBLS375')
```

---

get_study_files	<i>Get Study Files</i>
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**Description**

Retrieve the names and type of all files that have been deposited with the public study. If raw\_data is TRUE then details of raw data files(ie, .mzML) are also returned.

**Usage**

```
get_study_files(study_id, raw_data = FALSE)
```

**Arguments**

study_id	A character string of a valid MTBLS study id
raw_data	logical; if TRUE then raw data file info is also returned. (Default is FALSE)

**Value**

a tibble of file info

**Examples**

```
get_study_files('MTBLS375', raw_data = FALSE)
```

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get_study_meta	<i>Get Study Meta</i>
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**Description**

Retrieve the meta data for a publically available study

**Usage**

```
get_study_meta(study_id)
```

**Arguments**

study_id	A character string of a valid MTBLS study id
----------	--

**Value**

a tibble of study meta data

**Examples**

```
get_study_meta('MTBLS375')
```

---

get_study_org	<i>Get Study Organisms</i>
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**Description**

Retrieve the organisms used within a study

**Usage**

```
get_study_org(study_id)
```

**Arguments**

study_id	A character string of a valid MTBLS study id
----------	--

**Value**

a tibble of study organism data

**Examples**

```
## Not run:  
get_study_org('MTBLS375')  
  
## End(Not run)
```

---

get_study_protocols	<i>Get Study Protocols</i>
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---

**Description**

Retrieve the protocol information that has been deposited for a public study

**Usage**

```
get_study_protocols(study_id)
```

**Arguments**

study_id	A character string of a valid MTBLS study id
----------	--

**Value**

a tibble of study protocols

**Examples**

```
get_study_protocols('MTBLS375')
```

---

get_study_pubs	<i>Get Study Publications</i>
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---

**Description**

Retrieve details on any publications that have been associated with the study

**Usage**

```
get_study_pubs(study_id)
```

**Arguments**

study_id	A character string of a valid MTBLS study id
----------	--

**Value**

a tibble of study publications

**Examples**

```
get_study_pubs('MTBLS375')
```



---

get_study_samples	<i>Get Study Samples</i>
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**Description**

Get a list of all sample names mapped to files within the study

**Usage**

```
get_study_samples(study_id)
```

**Arguments**

study_id	A character string of a valid MTBLS study id
----------	--

**Value**

a tibble of filename sample name and reliability score. 1.0 indicates a perfect match

**Examples**

```
## Not run:  
get_study_samples('MTBLS375')  
  
## End(Not run)
```

---

get_study_tech	<i>Get Study Technology</i>
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**Description**

Retrieve a tibble of all Study IDs and the analytical technology used in the study

**Usage**

```
get_study_tech()
```

**Value**

a tibble of study id and technology

**Examples**

```
get_study_tech()
```

---

get_study_title	<i>Get Study Title</i>
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**Description**

Retrieve the full title of the study

**Usage**

```
get_study_title(study_id)
```

**Arguments**

study_id	A character string of a valid MTBLS study id
----------	--

**Value**

a character string of the study title

**Examples**

```
get_study_title('MTBLS375')
```

---

get_webservice	<i>Get Web-service details</i>
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**Description**

Retrieve details about the Metabolights RESTful WebService

**Usage**

```
get_webservice()
```

**Value**

a list of the MTBLS webservice information

**Examples**

```
get_webservice()
```

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mtbbs\_key

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*Set API Token***Description**

Set your Metabolights API Token as global option. If MTBLS\_API\_KEY is set in .Renviron then this variable will be passed directly to the MTBLS\_API\_KEY option. If no MTBLS\_API\_KEY is set in .Renviron, then the API Token must be passed as an input in the set\_api\_token function

**Usage**

```
mtbbs_key(API_KEY = NULL)
```

**Arguments**

API\_KEY            a character string of your Metabolights API Token (Default is NULL)

**Examples**

```
## Not run:

# If API Token is set in `.Renviron`

mtbbs_key()

# If API Token is not set in `.Renviron`

mtbbs_key('XXXX-0000-XXXX-0000')

## End(Not run)
```

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