

# Package ‘metabolighteR’

April 5, 2021

**Type** Package

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

**Version** 0.1.2

**Date** 2021-03-29

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

**Depends** magrittr

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

**License** GPL (>= 3)

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

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

**RoxygenNote** 7.1.0

**Encoding** UTF-8

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

**VignetteBuilder** knitr

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2021-04-05 15:30:02 UTC

## R topics documented:

download_study_file	2
get_isa_investigation	2
get_private_studies	3
get_studies	4
get_study_contacts	4
get_study_desc	5

get_study_descriptors . . . . .	5
get_study_factors . . . . .	6
get_study_files . . . . .	6
get_study_meta . . . . .	7
get_study_org . . . . .	7
get_study_protocols . . . . .	8
get_study_pubs . . . . .	8
get_study_samples . . . . .	9
get_study_tech . . . . .	9
get_study_title . . . . .	10
get_webservice . . . . .	10
mtbls_key . . . . .	11

## Index 12

---

download\_study\_file *Download Study File Contents*

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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

---

get\_isa\_investigation *Get ISA Investigation File*

---

### 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      *Get Study Description*

---

**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      *Get Study Descriptors*

---

**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')
```

---

get\_study\_factors      *Get Study Factors*

---

**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      *Get Study Files*

---

**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)
```

---

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`     *Get Study Protocols*

---

**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`     *Get Study Publications*

---

**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*      *Get Study Samples*

---

**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*      *Get Study Technology*

---

**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      *Get Study Title*

---

**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      *Get Web-service details*

---

**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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mtbls_key	<i>Set API Token</i>
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**Description**

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

**Usage**

```
mtbls_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 `.Renvirom`  
  
mtbls_key()  
  
# If API Token is not set in `.Renvirom`  
  
mtbls_key('XXXX-0000-XXXX-0000')  
  
## End(Not run)
```

# Index

download\_study\_file, 2

get\_isa\_investigation, 2  
get\_private\_studies, 3  
get\_studies, 4  
get\_study\_contacts, 4  
get\_study\_desc, 5  
get\_study\_descriptors, 5  
get\_study\_factors, 6  
get\_study\_files, 6  
get\_study\_meta, 7  
get\_study\_org, 7  
get\_study\_protocols, 8  
get\_study\_pubs, 8  
get\_study\_samples, 9  
get\_study\_tech, 9  
get\_study\_title, 10  
get\_webservice, 10

mtbls\_key, 11