

# Package ‘HuBMAPR’

April 3, 2026

**Title** Interface to 'HuBMAP'

**Version** 1.4.0

**Description** 'HuBMAP' provides an open, global bio-molecular atlas of the human body at the cellular level. The ``datasets()``, ``samples()``, ``donors()``, ``publications()``, and ``collections()`` functions retrieves the information for each of these entity types. ``*_details()`` are available for individual entries of each entity type. ``*_derived()`` are available for retrieving derived datasets or samples for individual entries of each entity type. Data files can be accessed using ``bulk_data_transfer()``.

**License** Artistic-2.0

**Depends** R (>= 4.4.0)

**Imports** htr2, dplyr, tidyr, tibble, rjsoncons, utils, stringr, whisker, purrr, rlang

**Collate** query.R datasets.R samples.R donors.R utilities.R publications.R publication\_information.R collections.R collection\_information.R provenance.R files.R organ.R template.R utils-globals.R

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.3

**Suggests** testthat (>= 3.0.0), knitr, ggplot2, rmarkdown, BiocStyle, pryr

**VignetteBuilder** knitr

**biocViews** Software, SingleCell, DataImport, ThirdPartyClient, Spatial, Infrastructure

**URL** <https://christinehou11.github.io/HuBMAPR/>,  
<https://github.com/christinehou11/HuBMAPR>

**BugReports** <https://github.com/christinehou11/HuBMAPR/issues>

**Config/testthat/edition** 3

**git\_url** <https://git.bioconductor.org/packages/HuBMAPR>

**git\_branch** RELEASE\_3\_22

**git\_last\_commit** e815208

**git\_last\_commit\_date** 2025-10-29

**Repository** Bioconductor 3.22

**Date/Publication** 2026-04-02

**Author** Christine Hou [aut, cre] (ORCID:

<<https://orcid.org/0009-0001-5350-0629>>),

Martin Morgan [aut] (ORCID: <<https://orcid.org/0000-0002-5874-8148>>),

Federico Marini [aut] (ORCID: <<https://orcid.org/0000-0003-3252-7758>>)

**Maintainer** Christine Hou <[chris2018hou@gmail.com](mailto:chris2018hou@gmail.com)>

## Contents

bulk_data_transfer . . . . .	2
collections . . . . .	3
collection_information . . . . .	4
datasets . . . . .	5
donors . . . . .	6
organ . . . . .	7
publications . . . . .	8
publication_information . . . . .	9
samples . . . . .	10
uuid_provenance . . . . .	11
<b>Index</b>	<b>12</b>

---

bulk_data_transfer	<i>HuBMAP File Querying</i>
--------------------	-----------------------------

---

## Description

bulk\_data\_transfer() takes a unique dataset or publication UUID to be used to query the HuBMAP API for information about available files.

## Usage

```
bulk_data_transfer(uuid)
```

## Arguments

uuid	character(1) corresponding to the HuBMAP Dataset UUID string. This is expected to be a 32-digit hex number. One unique Dataset UUID corresponds to one specific URL on Globus. Files corresponding to unique Dataset UUID are saved on Globus HuBMAP Public Collection webpage.
------	---

## Details

Additional details are provided on the HuBMAP consortium webpage, <https://software.docs.hubmapconsortium.org/apis>

## Value

bulk\_data\_transfer() display information about how to bulk download all files related to the dataset or publication.

## Examples

```
# Globus available
uuid_globus <- "2d3dbd5e5a3d9d5cfc7a46f06815a4eb"
uuid_sra_dbGaP <- "5ba6a5b81e95c93c26a33980f6e957d7"
uuid_not_available <- "0eb5e457b4855ce28531bc97147196b6"

# bulk_data_transfer(*_globus)
```

---

collections

*HuBMAP Collections*

---

## Description

`collections()` returns details about available collections, ordered by last modified dates  
`*_columns()` returns a tibble or named character vector describing the content of the tibble returned by `samples()`, `datasets()`, `donors()`, `collections()`, or `publications()`.

`collection_detail()` takes a unique `collection_id` and returns details about one specified collection as a tibble

`collection_contacts()` takes a unique `collection_id` and returns contacts information of one specified collection as a tibble

`collection_data()` takes a unique `collection_id` and returns related datasets of one specified collection as a tibble

`collection_contributors()` takes a unique `collection_id` and returns contributors information of one specified collection as a tibble

## Usage

```
collections()

collections_default_columns(as = c("tibble", "character"))

collection_detail(uuid)

collection_contacts(uuid)

collection_data(uuid)

collection_contributors(uuid)
```

## Arguments

`as` character(1) return format. One of "tibble" (default), or "character".

`uuid` character(1) corresponding to the HuBMAP Collection UUID string. This is expected to be a 32-digit hex number.

**Details**

Additional details are provided on the HuBMAP consortium webpage, <https://software.docs.hubmapconsortium.org/apis>

Additional details are provided on the HuBMAP consortium webpage, <https://software.docs.hubmapconsortium.org/apis>

Additional details are provided on the HuBMAP consortium webpage, <https://software.docs.hubmapconsortium.org/apis>

Additional details are provided on the HuBMAP consortium webpage, <https://software.docs.hubmapconsortium.org/apis>

**Value**

\*\_columns() returns a named list name containing the column name used in the tibble returned by samples(), datasets(), donors(), collections(), or publications(). When as = "tibble", the return value is a tibble with paths as elements and abbreviations as names.

**Examples**

```
collections()
collections_default_columns()

uuid <- "a320abcf56241be2e5e453401efeaaf3"
collection_detail(uuid)
uuid <- "381f65e58d5e2c1d16a9cef2cc203aab"
collection_contacts(uuid)
uuid <- "381f65e58d5e2c1d16a9cef2cc203aab"
collection_data(uuid)
uuid <- "590b0485a196956284b8f3344276bc50"
collection_contributors(uuid)
```

---

collection\_information

*Collection Information Summaries from Collection UUID*

---

**Description**

collection\_information() queries the HuBMAP collection for title, description, DOI, URL, creation date, and last modified time date.

print.collection\_information() organizes the returned tibble from collection\_information() in a more legible format.

**Usage**

```
collection_information(uuid)

## S3 method for class 'collection_information'
print(x, ...)
```

**Arguments**

uuid	character(1) corresponding to the HuBMAP Collection UUID string. This is expected to be a 32-digit hex number.
x	an object of class collection_information, the result of a call to collection_information().
...	additional arguments, required to conform with the print generic but not used.

**Value**

`collection_information()` returns a tibble, and columns containing information about the collection. The tibble is of class `collection_information` and is printed in character.

`print.collection_information()` is invoked automatically when the result of `collection_information()` is displayed for its side effect of displaying the object.

**Examples**

```
uuid <- "90399057f6ff0ff18d4c46a378f0b069"
collection_information(uuid)
```

---

 datasets

*HuBMAP Datasets*


---

**Description**

`datasets` returns the details available datasets, ordered by last modified dates

`*_columns()` returns a tibble or named character vector describing the content of the tibble returned by `samples()`, `datasets()`, `donors()`, `collections()`, or `publications()`.

`dataset_detail()` takes a unique `dataset_id` and returns details about one specified dataset as a tibble

`dataset_derived()` takes a unique `sample_id` and returns the derived (support) dataset details. Support datasets normally belong to Image Pyramid, with image files available to download via Globus Collection. See details to download in `files_globus_url()`.

`dataset_metadata()` takes a unique `dataset_id` and returns the metadata of the dataset.

`dataset_contributors()` takes a unique `dataset_id` and returns the contributors of the dataset. For questions for this dataset, reach out to the individuals listed as contacts, either via the email address listed in the table or contact information provided on their ORCID profile page.

**Usage**

```
datasets()
```

```
datasets_default_columns(as = c("tibble", "character"))
```

```
dataset_detail(uuid)
```

```
dataset_derived(uuid)
```

```
dataset_metadata(uuid)
```

```
dataset_contributors(uuid)
```

**Arguments**

`as` character(1) return format. One of "tibble" (default), or "character".

`uuid` character(1) corresponding to the HuBMAP Donor UUID string. This is expected to be a 32-digit hex number.

**Details**

Additional details are provided on the HuBMAP consortium webpage, <https://software.docs.hubmapconsortium.org/apis>

Additional details are provided on the HuBMAP consortium webpage, <https://software.docs.hubmapconsortium.org/apis>

Additional details are provided on the HuBMAP consortium webpage, <https://software.docs.hubmapconsortium.org/apis>

Additional details are provided on the HuBMAP consortium webpage, <https://software.docs.hubmapconsortium.org/apis>

**Value**

\*\_columns() returns a named list name containing the column name used in the tibble returned by samples(), datasets(), donors(), collections(), or publications(). When as = "tibble", the return value is a tibble with paths as elements and abbreviations as names.

**Examples**

```
datasets()
datasets_default_columns()

uuid <- "7754aa5ebde628b5e92705e33e74a4ef"
dataset_detail(uuid)
# no derived dataset
uuid <- "3acdb3ed962b2087fbe325514b098101"
dataset_derived(uuid)

# with derived dataset
uuid <- "2c77b1cdf33dbed3dbfb74e4b578300e"
dataset_derived(uuid)
uuid <- "564167adbbb2fdd64c24e7ea409c23f1"
dataset_metadata(uuid)

uuid <- "564167adbbb2fdd64c24e7ea409c23f1"
dataset_contributors(uuid)
```

---

donors

*HuBMAP Donors*

---

**Description**

donors() returns details about available samples, ordered by last modified dates

\*\_columns() returns a tibble or named character vector describing the content of the tibble returned by samples(), datasets(), donors(), collections(), or publications().

donor\_detail() takes a unique donor\_id and returns details about one specified sample as a tibble

donor\_derived() takes a unique donor\_id and returns the derived dataset or/and sample details.

donor\_metadata() takes a unique donor\_id and returns the metadata of the donor.

**Usage**

```
donors()
```

```
donors_default_columns(as = c("tibble", "character"))
```

```
donor_detail(uuid)
```

```
donor_derived(uuid, entity_type = c("Dataset", "Sample"))
```

```
donor_metadata(uuid)
```

### Arguments

<code>as</code>	character(1) return format. One of "tibble" (default), or "character".
<code>uuid</code>	character(1) corresponding to the HuBMAP Donor UUID string. This is expected to be a 32-digit hex number.
<code>entity_type</code>	character(1) selected derived entity type. One of "Sample" or "Dataset" (default).

### Details

Additional details are provided on the HuBMAP consortium webpage, <https://software.docs.hubmapconsortium.org/apis>

Additional details are provided on the HuBMAP consortium webpage, <https://software.docs.hubmapconsortium.org/apis>

Additional details are provided on the HuBMAP consortium webpage, <https://software.docs.hubmapconsortium.org/apis>

Additional details are provided on the HuBMAP consortium webpage, <https://software.docs.hubmapconsortium.org/apis>

### Value

\*\_columns() returns a named list name containing the column name used in the tibble returned by samples(), datasets(), donors(), collections(), or publications(). When as = "tibble", the return value is a tibble with paths as elements and abbreviations as names.

### Examples

```
donors()
donors_default_columns()

uuid <- "1dcde05aea3509b2cf89a41ceb3d700f"
donor_detail(uuid)
uuid <- "1dcde05aea3509b2cf89a41ceb3d700f"
donor_derived(uuid, "Sample")

uuid <- "d37df2cad4e80dc368763caefccf7140"
donor_metadata(uuid)
```

---

organ

*HuBMAP Organs*

---

### Description

organ retrieves available organ categories and abbreviations

### Usage

```
organ()
```

**Value**

organ returns the tibble with all available organs' abbreviations and corresponding full name.

**Examples**

```
organs <- organ()
organs |>
  dplyr::select("name") |>
  dplyr::distinct()
```

---

publications	<i>HuBMAP Samples</i>
--------------	-----------------------

---

**Description**

publications() returns details about available samples, ordered by last modified dates. publication\_status == TRUE: peer reviewed publication; publication\_status == FALSE: pre-print publication.

\*\_columns() returns a tibble or named character vector describing the content of the tibble returned by samples(), datasets(), donors(), collections(), or publications().

publication\_data() takes a unique publication\_id and returns details about one specified publication.

publication\_authors() takes a unique publication\_id and returns authors information of one specified collection as a tibble

**Usage**

```
publications()

publications_default_columns(as = c("tibble", "character"))

publication_data(uuid, entity_type = c("Dataset", "Sample", "Donor"))

publication_authors(uuid)
```

**Arguments**

as	character(1) return format. One of "tibble" (default), or "character".
uuid	character(1) corresponding to the HuBMAP Publication UUID string. This is expected to be a 32-digit hex number.
entity_type	character(1) selected derived entity type. One of "Sample", "Donor" or "Dataset" (default).

**Details**

Additional details are provided on the HuBMAP consortium webpage, <https://software.docs.hubmapconsortium.org/apis>

Additional details are provided on the HuBMAP consortium webpage, <https://software.docs.hubmapconsortium.org/apis>

Additional details are provided on the HuBMAP consortium webpage, <https://software.docs.hubmapconsortium.org/apis>

**Value**

\*\_columns() returns a named list name containing the column name used in the tibble returned by samples(), datasets(), donors(), collections(), or publications(). When as = "tibble", the return value is a tibble with paths as elements and abbreviations as names.

**Examples**

```
publications()
publications_default_columns()

uuid <- "3c7273660cdf9ab91a7901533b2cd9a5"
publication_data(uuid)

uuid <- "3c7273660cdf9ab91a7901533b2cd9a5"
publication_authors(uuid)
```

---

publication\_information

*Publication Information Summaries from Publication UUID*

---

**Description**

publication\_information() queries the HuBMAP publication for title, abstract, manuscript, corresponding authors, dataset types, and organ.

publication\_information() organizes the returned tibble from publication\_information() in a more legible format.

**Usage**

```
publication_information(uuid)

## S3 method for class 'publication_information'
print(x, ...)
```

**Arguments**

uuid	character(1) corresponding to the HuBMAP Publication UUID string. This is expected to be a 32-digit hex number.
x	an object of class publication_information, the result of a call to publication_information().
...	additional arguments, required to conform with the print generic but not used.

**Value**

publication\_information() returns a tibble, and columns containing information about the publication. The tibble is of class publication\_information and is printed in character.

print.publication\_information() is invoked automatically when the result of publication\_information() is displayed for it's side effect of displaying the object.

**Examples**

```
uuid <- "e8338966c69e759157d6c6ad24847989"
publication_information(uuid)
```

---

 samples

*HuBMAP Samples*


---

## Description

`samples()` returns details about available samples, ordered by last modified dates. There are multiple tissue sample types displayed in `sample_category` column which are block, organ, suspension, and section.

`*_columns()` returns a tibble or named character vector describing the content of the tibble returned by `samples()`, `datasets()`, `donors()`, `collections()`, or `publications()`.

`sample_detail()` takes a unique `sample_id` and returns details about one specified sample as a tibble

`sample_derived()` takes a unique `sample_id` and returns the derived dataset or/and sample details.

`sample_metadata()` takes a unique `donor_id` and returns the metadata of the sample.

## Usage

```
samples()
```

```
samples_default_columns(as = c("tibble", "character"))
```

```
sample_detail(uuid)
```

```
sample_derived(uuid, entity_type = c("Dataset", "Sample"))
```

```
sample_metadata(uuid)
```

## Arguments

`as` character(1) return format. One of "tibble" (default), or "character".

`uuid` character(1) corresponding to the HuBMAP Donor UUID string. This is expected to be a 32-digit hex number.

`entity_type` character(1) selected derived entity type. One of "Sample" or "Dataset" (default).

## Details

Additional details are provided on the HuBMAP consortium webpage, <https://software.docs.hubmapconsortium.org/apis>

Additional details are provided on the HuBMAP consortium webpage, <https://software.docs.hubmapconsortium.org/apis>

Additional details are provided on the HuBMAP consortium webpage, <https://software.docs.hubmapconsortium.org/apis>

Additional details are provided on the HuBMAP consortium webpage, <https://software.docs.hubmapconsortium.org/apis>

## Value

`*_columns()` returns a named list name containing the column name used in the tibble returned by `samples()`, `datasets()`, `donors()`, `collections()`, or `publications()`. When `as = "tibble"`, the return value is a tibble with paths as elements and abbreviations as names.

**Examples**

```
samples()
samples_default_columns()

uuid <- "d3525d35f6d5ee3dc3186613b0ab1762"
sample_detail(uuid)
uuid <- "3e7dc14313262af577f686dcb09f5119"
sample_derived(uuid, "Sample")
uuid <- "8d7ce3aab7013e416263d23b0c048900"
sample_metadata(uuid)
```

---

uuid_provenance	<i>HuBMAP Provenance</i>
-----------------	--------------------------

---

**Description**

HuBMAP Provenance

**Usage**

```
uuid_provenance(uuid)
```

**Arguments**

uuid	character(1) corresponding to the HuBMAP Dataset or Sample UUID string. This is expected to be a 32-digit hex number.
------	---

**Details**

Additional details are provided on the HuBMAP consortium webpage, <https://software.docs.hubmapconsortium.org/apis>

**Value**

uuid\_provenance() takes a Dataset or Sample UUID, and returns the provenance details as a list of characters, from the most recent ancestor to the furthest ancestor. The entity type of ancestors include Dataset, Sample, and Donor. Note that there is no ancestor for Donor entity such that the returned result will be an empty list.

**Examples**

```
uuid <- "acf816bed56dd6ba55da82960d937ec4"
uuid_provenance(uuid)
```

# Index

bulk\_data\_transfer, 2

collection\_contacts (collections), 3  
collection\_contributors (collections), 3  
collection\_data (collections), 3  
collection\_detail (collections), 3  
collection\_information, 4  
collections, 3  
collections\_default\_columns  
    (collections), 3

dataset\_contributors (datasets), 5  
dataset\_derived (datasets), 5  
dataset\_detail (datasets), 5  
dataset\_metadata (datasets), 5  
datasets, 5  
datasets\_default\_columns (datasets), 5  
donor\_derived (donors), 6  
donor\_detail (donors), 6  
donor\_metadata (donors), 6  
donors, 6  
donors\_default\_columns (donors), 6

organ, 7

print.collection\_information  
    (collection\_information), 4  
print.publication\_information  
    (publication\_information), 9  
publication\_authors (publications), 8  
publication\_data (publications), 8  
publication\_information, 9  
publications, 8  
publications\_default\_columns  
    (publications), 8

sample\_derived (samples), 10  
sample\_detail (samples), 10  
sample\_metadata (samples), 10  
samples, 10  
samples\_default\_columns (samples), 10

uuid\_provenance, 11