Package 'studyCurator'

March 24, 2021

Title studyCurator

Version 1.36.0-1

API version v0.1

Description

This is the API for layer 3 of the Roche pRed project. This swagger page describes the studyCurator APIs. Before carrying out any API calls you will need an API token. API tokens can be obtained under your profile within the Genestack software. To try out calls in this swagger page: 1. Click the 'Authorize' button below to enter your API token 2. Scroll to the 'Parameters' section for the method you wish to try out and click the 'Try it out' button 3. Enter parameter values that you wish to try 4. Scroll to the bottom of the Parameters section and click the 'Execute' bar that appears The server response will be in the section that follows.

Depends R (>= 3.3.2)

License Proprietary

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

R topics documented:

StudySPoTApi_add_atomic_study

Create a single new object from a given data file with optional supplied metadata.

Description

Create a single new object from a given data file with optional supplied metadata.

Usage

```
StudySPoTApi_add_atomic_study(source, ...)
```

StudySPoTApi_add_study

Add new study object

Description

Add new study object

Usage

```
StudySPoTApi_add_study(source, ...)
```

Arguments

source

StudySPoTApi_delete_study

Delete a given study object. This will not delete related objects or links to related objects.

Description

Delete a given study object. This will not delete related objects or links to related objects.

Usage

```
StudySPoTApi_delete_study(id, ...)
```

Arguments

id   Unique identifier (accession) of the object.

```
StudySPoTApi_get_study
```
Retrieve a single study object by ID (accession)

Description

Retrieve a single study object by ID (accession)

Usage

```
StudySPoTApi_get_study(id, returned_metadata_fields, ...)
```

Arguments

id   Unique identifier (accession) of the object.

returned_metadata_fields

The parameter defines amount of metadata attributes to return: 1. `template` - return metadata attributes according to applied template, if object doesn't have applied template default template will be used. This is the default for User endpoints. 2. `all` - return all metadata attributes with values and null attributes, if they are present in the applied template. This is the default for Curator endpoints.

```
StudySPoTApi_get_study_by_version
```
Retrieve a single study object by ID (accession)

Description

Retrieve a single study object by ID (accession)

Usage

```
StudySPoTApi_get_study_by_version(id, version, returned_metadata_fields, ...)
```

Arguments

id   Unique identifier (accession) of the object.

version   Unique version of the object.

returned_metadata_fields

The parameter defines amount of metadata attributes to return: 1. `template` - return metadata attributes according to applied template, if object doesn't have applied template default template will be used. This is the default for User endpoints. 2. `all` - return all metadata attributes with values and null attributes, if they are present in the applied template. This is the default for Curator endpoints.

StudySPoTApi_get_study_versions

Retrieve a list of object versions by ID

Description

Retrieve a list of object versions by ID

Usage

```
StudySPoTApi_get_study_versions(id, ...)
```

Arguments

id   Unique identifier (accession) of the object.

StudySPoTApi_search_studies

List or search for study metadata objects

Description

List or search for study metadata objects

Usage

```
StudySPoTApi_search_studies(
  filter,
  query,
  search_specific_terms,
  returned_metadata_fields,
  sort,
  page_limit,
  page_offset,
  ...
)
```

Arguments

filter   Filter by study metadata (key-value metadata pair(s)). E.g. "Study Source"=ArrayExpress

query   Search for study objects via a full-text query over all study metadata fields. E.g.
                "RNA-Seq of human dendritic cells"

search_specific_terms

> If the full-text query term is present in an ODM dictionary, enabling this parameter will modify the query to include child terms of the full-text query. For example, the search query "Body fluid" can be expanded to include the term "Blood" (a child term of "Body fluid") so files containing either "Body fluid" or "Blood" in their metadata will be returned in the search results. The parent-child relationship is defined by the key "broaders" in the dictionary. If the full query term is not present in a dictionary then this parameter has no effect.

returned_metadata_fields

> The parameter defines amount of metadata attributes to return: 1. `template` - return metadata attributes according to applied template, if object doesn't have applied template default template will be used. This is the default for User endpoints. 2. `all` - return all metadata attributes with values and null attributes, if they are present in the applied template. This is the default for Curator endpoints.

sort

> Attribute to sort by, with optional ascending/descending marker, of the form `"[+|-]<key_name>"`. No marker or `"+"` indicates ascending sort, and `"-"` indicates descending sort. *Default:* sort by ID in ascending order.

page_limit

> Maximum number of results to return. This value must be between 0 and 100 (inclusive).

page_offset

> Show the page pageOffset+1 results from the start of the results. E.g. 100 will show a page of results starting from the 101st result. The default value is 0.

StudySPoTApi_update_atomic_metadata
Update object metadata

Description

Update object metadata

Usage

```
StudySPoTApi_update_atomic_metadata(id, body, ...)
```

Arguments

id

> Unique identifier (accession) of the object.

body

> Metadata in the form of `{key: value, key2: value2, ...}`

StudySPoTApi_update_study
Update a study object

Description

Update a study object

Usage

```
StudySPoTApi_update_study(id, body, ...)
```

Arguments

id	Unique identifier (accession) of the object.
body	Metadata in the form of {key: value, key2: value2, ...}