

Package ‘flowCytometryUser’

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Title flowCytometryUser

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 flowCytometryUser API endpoints for ODM. These are typically used to find and retrieve flow cytometry data and metadata. Before carrying out any API calls you will need an API token. API tokens can be obtained under your profile within the Genestack software. Further instructions can be found [here](<https://odm-user-guide.readthedocs.io/en/latest/doc-odm-user-guide/getting-a-genestack-api-token.html>). 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:

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FlowCytometrySPoTApi_get_flow_cytometry

Retrieve a single sample flow cytometry by ID (accession)

Description

Retrieve a single sample flow cytometry by ID (accession)

Usage

```
FlowCytometrySPoTApi_get_flow_cytometry(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.

FlowCytometrySPoTApi_get_flow_cytometry_by_version

Retrieve a single sample flow cytometry by ID (accession)

Description

Retrieve a single sample flow cytometry by ID (accession)

Usage

```
FlowCytometrySPoTApi_get_flow_cytometry_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.

FlowCytometrySPoTApi_get_flow_cytometry_data

Retrieve multiple flow cytometry data and metadata objects

Description

Retrieve multiple flow cytometry data and metadata objects

Usage

```
FlowCytometrySPoTApi_get_flow_cytometry_data(
    filter,
    query,
    search_specific_terms,
    run_filter,
    readout_type,
    population,
    marker,
    min_value,
    use_versions,
    returned_metadata_fields,
    page_limit,
    cursor,
    ...
)
```

Arguments

filter	Filter by flow cytometry metadata (key-value metadata pair(s)). E.g. Organ=blood
query	Search for flow cytometry objects via a full text query over all flow cytometry metadata.
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.
run_filter	Genestack accession that corresponds to the fcy column used to link flow cytometry data from the same run to a sample
readout_type	Required value of "Readout type" column. E.g.: Count, Median
population	Value of "Cell Population" column. E.g.: "total cells", CD45+,live/CD45+, CD3+. Note that if this value contains special characters like / which is used as a URI path separator, such characters should be escaped manually before sending request. For example, / should be escaped as %2F.
marker	Marker value. E.g.: PD1, BV786
min_value	Minimum threshold (inclusive) for returned expression values.
use_versions	Specify which versions of omics data files are used in the query. By default the active version is used. See Versioning above. Syntax: * or v<version number> or <CHAIN_ID>:v<version number> or <CHAIN_ID>:<accession1,accession2,...>
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.
page_limit	Maximum number of results to return per page (see Paging above). This value must be between 0 and 2000 (inclusive). The default is 2000.
cursor	The page tag to resume results from (see paging above).

FlowCytometrySPoTApi_get_flow_cytometry_versions

Retrieve a list of object versions by ID

Description

Retrieve a list of object versions by ID

Usage

```
FlowCytometrySPoTApi_get_flow_cytometry_versions(id, ...)
```

Arguments

id Unique identifier (accession) of the object.

`FlowCytometrySPoTApi_get_group`*Retrieve a single group object by ID (accession)*

Description

Retrieve a single group object by ID (accession)

Usage

```
FlowCytometrySPoTApi_get_group(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.

`FlowCytometrySPoTApi_get_group_by_run`*Retrieve a single group object by run ID (accession)*

Description

Retrieve a single group object by run ID (accession)

Usage

```
FlowCytometrySPoTApi_get_group_by_run(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.

FlowCytometrySPoTApi_search_groups

Retrieve groups that match a query

Description

Retrieve groups that match a query

Usage

```
FlowCytometrySPoTApi_search_groups(
    filter,
    query,
    search_specific_terms,
    use_versions,
    returned_metadata_fields,
    page_offset,
    page_limit,
    ...
)
```

Arguments

filter	Filter by flow cytometry metadata (key-value metadata pair(s)). E.g. Organ=blood
query	Search for flow cytometry objects via a full text query over all flow cytometry metadata.
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.
use_versions	Specify which versions of omics data files are used in the query. By default the active version is used. See Versioning above. Syntax: * or v<version number> or <CHAIN_ID>:v<version number> or <CHAIN_ID>:<accession1,accession2,...>
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.
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.

page_limit	Maximum number of results to return per page (see Paging above). This value must be between 0 and 2000 (inclusive). The default is 2000.
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FlowCytometrySPoTApi_search_runs

Retrieve run objects related to the given group

Description

Retrieve run objects related to the given group

Usage

FlowCytometrySPoTApi_search_runs(id, page_offset, page_limit, ...)

Arguments

id	Unique identifier (accession) of the object.
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.
page_limit	Maximum number of results to return per page (see Paging above). This value must be between 0 and 2000 (inclusive). The default is 2000.