

# Package ‘flowCytometryCurator’

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**Title** flowCytometryCurator

**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 flowCytometryCurator 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

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FlowCytometrySPoTApi_add_atomic_flow_cytometry
<i>Create a single new object from a given data file with optional supplied metadata.</i>

---

**Description**

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

**Usage**

```
FlowCytometrySPoTApi_add_atomic_flow_cytometry(source, ...)
```

---

FlowCytometrySPoTApi_add_flow_cytometry
<i>Create multiple new objects from a multi-row data file with optional supplied metadata</i>

---

**Description**

Create multiple new objects from a multi-row data file with optional supplied metadata

**Usage**

```
FlowCytometrySPoTApi_add_flow_cytometry(source, ...)
```

**Arguments**

source

---

FlowCytometrySPoTApi_delete_atomic
<i>Delete the object</i>

---

**Description**

Delete the object

**Usage**

```
FlowCytometrySPoTApi_delete_atomic(id, ...)
```

**Arguments**

id                      Unique identifier (accession) of the object.

---

FlowCytometrySPoTApi\_delete\_group  
*Delete the object*

---

**Description**

Delete the object

**Usage**

FlowCytometrySPoTApi\_delete\_group(id, ...)

**Arguments**

id                      Unique identifier (accession) of the object.

---

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_get_group_curation_status`*Get curation status of a group by ID (accession)*

---

**Description**

Get curation status of a group by ID (accession)

**Usage**

```
FlowCytometrySPoTApi_get_group_curation_status(id, ...)
```

**Arguments**

`id` Unique identifier (accession) of the object.

---

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.

---

FlowCytometrySPoTApi\_update\_atomic\_metadata

*Update object metadata*

---

### Description

Update object metadata

### Usage

```
FlowCytometrySPoTApi_update_atomic_metadata(id, body, ...)
```

### Arguments

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

---

FlowCytometrySPoTApi_update_flow_cytometry
<i>Update object metadata</i>

---

**Description**

Update object metadata

**Usage**

FlowCytometrySPoTApi\_update\_flow\_cytometry(id, body, ...)

**Arguments**

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

---

FlowCytometrySPoTApi_update_group
<i>Set curation status of a group by ID (accession)</i>

---

**Description**

Set curation status of a group by ID (accession)

**Usage**

FlowCytometrySPoTApi\_update\_group(id, body, ...)

**Arguments**

- |    |  |
|----|--|
| id | Unique identifier (accession) of the object. |
|----|--|