

Package ‘integrationCurator’

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Title integrationCurator

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Description This is the API for layer 4 of the Roche pRed project. This swagger page describes the integrationCurator 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.

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R topics documented:

ExpressionIntegrationApi_create_expression_group_library_group_link	1
ExpressionIntegrationApi_create_expression_group_preparation_group_link	2
ExpressionIntegrationApi_create_expression_group_sample_group_link	3
ExpressionIntegrationApi_create_expression_library_link	3
ExpressionIntegrationApi_create_expression_preparation_link	4
ExpressionIntegrationApi_create_expression_sample_link	4
ExpressionIntegrationApi_delete_expression_group_library_group_link	5
ExpressionIntegrationApi_delete_expression_group_preparation_group_link	5
ExpressionIntegrationApi_delete_expression_group_sample_group_link	6
ExpressionIntegrationApi_delete_expression_library_link	6
ExpressionIntegrationApi_delete_expression_preparation_link	7
ExpressionIntegrationApi_delete_expression_sample_link	7
ExpressionIntegrationApi_get_expression_by_library	8
ExpressionIntegrationApi_get_expression_by_preparation	8

ExpressionIntegrationApi_get_expression_by_sample	9
ExpressionIntegrationApi_get_parents_by_study	10
ExpressionIntegrationApi_get_run_to_library_pairs	11
ExpressionIntegrationApi_get_run_to_preparation_pairs	11
ExpressionIntegrationApi_get_run_to_sample_pairs	12
FlowCytometryIntegrationApi_create_flow_cytometry_group_sample_group_link	12
FlowCytometryIntegrationApi_create_flow_cytometry_sample_link	13
FlowCytometryIntegrationApi_delete_flow_cytometry_group_sample_group_link	13
FlowCytometryIntegrationApi_delete_flow_cytometry_sample_link	14
FlowCytometryIntegrationApi_get_flow_cytometry_by_sample	14
FlowCytometryIntegrationApi_get_parents_by_study	15
FlowCytometryIntegrationApi_get_run_to_sample_pairs	16
LibraryIntegrationApi_create_library_group_sample_group_link	17
LibraryIntegrationApi_create_library_sample_link	17
LibraryIntegrationApi_delete_library_group_sample_group_link	18
LibraryIntegrationApi_delete_library_sample_link	18
LibraryIntegrationApi_get_libraries_by_samples	19
LibraryIntegrationApi_get_library_by_sample	20
LibraryIntegrationApi_get_library_links_to_samples	20
LibraryIntegrationApi_get_parents_by_study	21
LinkageApi_delete_link	21
LinkageApi_get_data_types	22
LinkageApi_get_data_types_links	22
LinkageApi_get_links_by_ids	22
LinkageApi_get_links_by_params	23
LinkageApi_save_links	23
OmicsQueriesApi_search_expression_data	24
OmicsQueriesApi_search_expression_groups	25
OmicsQueriesApi_search_flow_cytometry_data	26
OmicsQueriesApi_search_flow_cytometry_groups	28
OmicsQueriesApi_search_samples	29
OmicsQueriesApi_search_streamed_expression_data	31
OmicsQueriesApi_search_variant_data	32
OmicsQueriesApi_search_variant_groups	33
PreparationIntegrationApi_create_preparation_group_sample_group_link	34
PreparationIntegrationApi_create_preparation_sample_link	35
PreparationIntegrationApi_delete_preparation_group_sample_group_link	35
PreparationIntegrationApi_delete_preparation_sample_link	36
PreparationIntegrationApi_get_parents_by_study	36
PreparationIntegrationApi_get_preparations_by_samples	37
PreparationIntegrationApi_get_preparation_by_sample	38
PreparationIntegrationApi_get_preparation_links_to_samples	38
SampleIntegrationApi_create_sample_group_study_link	39
SampleIntegrationApi_create_sample_study_link	39
SampleIntegrationApi_delete_sample_group_study_link	40
SampleIntegrationApi_delete_sample_study_link	40
SampleIntegrationApi_get_samples_by_libraries	41
SampleIntegrationApi_get_samples_by_preparations	42

SampleIntegrationApi_get_samples_by_study	43
StudyIntegrationApi_get_studies_by_libraries	43
StudyIntegrationApi_get_studies_by_preparations	44
StudyIntegrationApi_get_studies_by_samples	45
StudyIntegrationApi_get_study_by_sample	46
ValidationSummaryApi_search_expression_data	47
VariantIntegrationApi_create_variant_group_sample_group_link	47
VariantIntegrationApi_create_variant_sample_link	48
VariantIntegrationApi_delete_variant_group_sample_group_link	48
VariantIntegrationApi_delete_variant_sample_link	49
VariantIntegrationApi_get_parents_by_study	49
VariantIntegrationApi_get_run_to_sample_pairs	50
VariantIntegrationApi_get_variant_by_sample	50

ExpressionIntegrationApi_create_expression_group_library_group_link
Create a link between a group of expression objects and a group of library objects

Description

Create a link between a group of expression objects and a group of library objects

Usage

```
ExpressionIntegrationApi_create_expression_group_library_group_link(
    source_id,
    target_id,
    ...
)
```

Arguments

source_id	The ID (accession) of the group of run-level objects (corresponding to a GCT file)
target_id	The ID (accession) of the library group object

ExpressionIntegrationApi_create_expression_group_preparation_group_link
Create a link between a group of expression objects and a group of preparation objects

Description

Create a link between a group of expression objects and a group of preparation objects

Usage

```
ExpressionIntegrationApi_create_expression_group_preparation_group_link(
    source_id,
    target_id,
    ...
)
```

Arguments

source_id	The ID (accession) of the group of run-level objects (corresponding to a GCT file)
target_id	The ID (accession) of the preparation group object

ExpressionIntegrationApi_create_expression_group_sample_group_link
Create a link between a group of expression objects and a group of sample objects

Description

Create a link between a group of expression objects and a group of sample objects

Usage

```
ExpressionIntegrationApi_create_expression_group_sample_group_link(
    source_id,
    target_id,
    ...
)
```

Arguments

source_id	The ID (accession) of the group of run-level objects (corresponding to a GCT file)
target_id	The ID (accession) of the sample group object

ExpressionIntegrationApi_create_expression_library_link
Create a link between an expression object and a library

Description

Create a link between an expression object and a library

Usage

```
ExpressionIntegrationApi_create_expression_library_link(  
    source_id,  
    target_id,  
    ...  
)
```

Arguments

source_id	The ID (accession) of the run-level object (corresponding to the column in a VCG/GCT file)
target_id	The ID (accession) of the library object

ExpressionIntegrationApi_create_expression_preparation_link
Create a link between an expression object and a preparation

Description

Create a link between an expression object and a preparation

Usage

```
ExpressionIntegrationApi_create_expression_preparation_link(  
    source_id,  
    target_id,  
    ...  
)
```

Arguments

source_id	The ID (accession) of the run-level object (corresponding to the column in a VCG/GCT file)
target_id	The ID (accession) of the preparation object

ExpressionIntegrationApi_create_expression_sample_link
Create a link between an expression object and a sample

Description

Create a link between an expression object and a sample

Usage

```
ExpressionIntegrationApi_create_expression_sample_link(  
    source_id,  
    target_id,  
    ...  
)
```

Arguments

source_id	The ID (accession) of the run-level object (corresponding to the column in a VCG/GCT file)
target_id	The ID (accession) of the sample object

ExpressionIntegrationApi_delete_expression_group_library_group_link
Delete link between a group of expression objects and a group of library objects

Description

Delete link between a group of expression objects and a group of library objects

Usage

```
ExpressionIntegrationApi_delete_expression_group_library_group_link(  
    source_id,  
    target_id,  
    ...  
)
```

Arguments

source_id	The ID (accession) of the group of run-level objects (corresponding to a GCT file)
target_id	The ID (accession) of the library group object

ExpressionIntegrationApi_delete_expression_group_preparation_group_link
Delete link between a group of expression objects and a group of preparation objects

Description

Delete link between a group of expression objects and a group of preparation objects

Usage

```
ExpressionIntegrationApi_delete_expression_group_preparation_group_link(  
    source_id,  
    target_id,  
    ...  
)
```

Arguments

source_id	The ID (accession) of the group of run-level objects (corresponding to a GCT file)
target_id	The ID (accession) of the preparation group object

ExpressionIntegrationApi_delete_expression_group_sample_group_link
Delete link between a group of expression objects and a group of sample objects

Description

Delete link between a group of expression objects and a group of sample objects

Usage

```
ExpressionIntegrationApi_delete_expression_group_sample_group_link(  
    source_id,  
    target_id,  
    ...  
)
```

Arguments

source_id	The ID (accession) of the group of run-level objects (corresponding to a GCT file)
target_id	The ID (accession) of the sample group object

`ExpressionIntegrationApi_delete_expression_library_link`*Delete link between an expression object and a library*

Description

Delete link between an expression object and a library

Usage

```
ExpressionIntegrationApi_delete_expression_library_link(  
    source_id,  
    target_id,  
    ...  
)
```

Arguments

<code>source_id</code>	The ID (accession) of the run-level object (corresponding to the column in a VCG/GCT file)
<code>target_id</code>	The ID (accession) of the library object

`ExpressionIntegrationApi_delete_expression_preparation_link`*Delete link between an expression object and a preparation*

Description

Delete link between an expression object and a preparation

Usage

```
ExpressionIntegrationApi_delete_expression_preparation_link(  
    source_id,  
    target_id,  
    ...  
)
```

Arguments

<code>source_id</code>	The ID (accession) of the run-level object (corresponding to the column in a VCG/GCT file)
<code>target_id</code>	The ID (accession) of the preparation object

ExpressionIntegrationApi_delete_expression_sample_link
Delete link between an expression object and a sample

Description

Delete link between an expression object and a sample

Usage

```
ExpressionIntegrationApi_delete_expression_sample_link(  
    source_id,  
    target_id,  
    ...  
)
```

Arguments

source_id	The ID (accession) of the run-level object (corresponding to the column in a VCG/GCT file)
target_id	The ID (accession) of the sample object

ExpressionIntegrationApi_get_expression_by_library
Retrieve expression run-level data by querying related library ID (accession)

Description

Retrieve expression run-level data by querying related library ID (accession)

Usage

```
ExpressionIntegrationApi_get_expression_by_library(  
    id,  
    page_limit,  
    page_offset,  
    use_versions,  
    ...  
)
```

Arguments

<code>id</code>	Unique identifier (accession) of the object.
<code>page_limit</code>	Maximum number of results to return. This value must be between 0 and 2000 (inclusive).
<code>page_offset</code>	Show the page <code>pageOffset+1</code> 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.
<code>use_versions</code>	Specify which versions of omics data files are used in the query. By default the active version is used. See Versioning above. Syntax: <code>*</code> or <code>v<version number></code> or <code><CHAIN_ID>:v<version number></code> or <code><CHAIN_ID>:<accession1,accession2,...></code>

ExpressionIntegrationApi_get_expression_by_preparation

Retrieve expression run-level data by querying related preparation ID (accession)

Description

Retrieve expression run-level data by querying related preparation ID (accession)

Usage

```
ExpressionIntegrationApi_get_expression_by_preparation(
    id,
    page_limit,
    page_offset,
    use_versions,
    ...
)
```

Arguments

<code>id</code>	Unique identifier (accession) of the object.
<code>page_limit</code>	Maximum number of results to return. This value must be between 0 and 2000 (inclusive).
<code>page_offset</code>	Show the page <code>pageOffset+1</code> 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.
<code>use_versions</code>	Specify which versions of omics data files are used in the query. By default the active version is used. See Versioning above. Syntax: <code>*</code> or <code>v<version number></code> or <code><CHAIN_ID>:v<version number></code> or <code><CHAIN_ID>:<accession1,accession2,...></code>

ExpressionIntegrationApi_get_expression_by_sample

Retrieve expression run-level data by querying related sample ID (accession)

Description

Retrieve expression run-level data by querying related sample ID (accession)

Usage

```
ExpressionIntegrationApi_get_expression_by_sample(
    id,
    page_limit,
    page_offset,
    use_versions,
    returned_metadata_fields,
    ...
)
```

Arguments

<code>id</code>	Unique identifier (accession) of the object.
<code>page_limit</code>	Maximum number of results to return. This value must be between 0 and 2000 (inclusive).
<code>page_offset</code>	Show the page <code>pageOffset+1</code> 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.
<code>use_versions</code>	Specify which versions of omics data files are used in the query. By default the active version is used. See Versioning above. Syntax: <code>*</code> or <code>v<version number></code> or <code><CHAIN_ID>:v<version number></code> or <code><CHAIN_ID>:<accession1,accession2,...></code>
<code>returned_metadata_fields</code>	The parameter defines amount of metadata attributes to return: 1. <code>template</code> - 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. <code>all</code> - return all metadata attributes with values and null attributes, if they are present in the applied template. This is the default for Curator endpoints.

ExpressionIntegrationApi_get_parents_by_study

Retrieve group metadata by querying study ID (accession)

Description

Retrieve group metadata by querying study ID (accession)

Usage

```
ExpressionIntegrationApi_get_parents_by_study(
    id,
    use_versions,
    returned_metadata_fields,
    ...
)
```

Arguments

id	Unique identifier (accession) of the object.
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.

ExpressionIntegrationApi_get_run_to_library_pairs

Retrieve run-library pairs by group id. Pagination is based on unique runs, not unique pairs.

Description

Retrieve run-library pairs by group id. Pagination is based on unique runs, not unique pairs.

Usage

```
ExpressionIntegrationApi_get_run_to_library_pairs(  
    id,  
    page_limit,  
    page_offset,  
    ...  
)
```

Arguments

<code>id</code>	Unique identifier (accession) of the object.
<code>page_limit</code>	Maximum number of results to return. This value must be between 0 and 2000 (inclusive).
<code>page_offset</code>	Show the page <code>pageOffset+1</code> 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.

ExpressionIntegrationApi_get_run_to_preparation_pairs

Retrieve run-preparation pairs by group id. Pagination is based on unique runs, not unique pairs.

Description

Retrieve run-preparation pairs by group id. Pagination is based on unique runs, not unique pairs.

Usage

```
ExpressionIntegrationApi_get_run_to_preparation_pairs(  
    id,  
    page_limit,  
    page_offset,  
    ...  
)
```

Arguments

<code>id</code>	Unique identifier (accession) of the object.
<code>page_limit</code>	Maximum number of results to return. This value must be between 0 and 2000 (inclusive).
<code>page_offset</code>	Show the page <code>pageOffset+1</code> 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.

ExpressionIntegrationApi_get_run_to_sample_pairs

Retrieve run-sample pairs by group id. Pagination is based on unique runs, not unique pairs.

Description

Retrieve run-sample pairs by group id. Pagination is based on unique runs, not unique pairs.

Usage

```
ExpressionIntegrationApi_get_run_to_sample_pairs(  
    id,  
    page_limit,  
    page_offset,  
    ...  
)
```

Arguments

id	Unique identifier (accession) of the object.
page_limit	Maximum number of results to return. This value must be between 0 and 2000 (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.

FlowCytometryIntegrationApi_create_flow_cytometry_group_sample_group_link

Create a link between a group of flow-cytometry objects and a group of sample objects

Description

Create a link between a group of flow-cytometry objects and a group of sample objects

Usage

```
FlowCytometryIntegrationApi_create_flow_cytometry_group_sample_group_link(  
    source_id,  
    target_id,  
    ...  
)
```

Arguments

source_id	The ID (accession) of the group of run-level objects (corresponding to the column in a FACS file)
target_id	The ID (accession) of the sample object

FlowCytometryIntegrationApi_create_flow_cytometry_sample_link

Create a link between a flow-cytometry object and a sample

Description

Create a link between a flow-cytometry object and a sample

Usage

```
FlowCytometryIntegrationApi_create_flow_cytometry_sample_link(  
  source_id,  
  target_id,  
  ...  
)
```

Arguments

source_id	The ID (accession) of the run-level data block
target_id	The ID (accession) of the sample object

FlowCytometryIntegrationApi_delete_flow_cytometry_group_sample_group_link

Delete link between a group of flow-cytometry objects and a group of sample objects

Description

Delete link between a group of flow-cytometry objects and a group of sample objects

Usage

```
FlowCytometryIntegrationApi_delete_flow_cytometry_group_sample_group_link(  
  source_id,  
  target_id,  
  ...  
)
```

Arguments

source_id	The ID (accession) of the group of run-level objects (corresponding to the column in a FACS file)
target_id	The ID (accession) of the sample object

FlowCytometryIntegrationApi_delete_flow_cytometry_sample_link
Delete link between a flow-cytometry object and a sample

Description

Delete link between a flow-cytometry object and a sample

Usage

```
FlowCytometryIntegrationApi_delete_flow_cytometry_sample_link(
  source_id,
  target_id,
  ...
)
```

Arguments

source_id	The ID (accession) of the run-level data block
target_id	The ID (accession) of the sample object

FlowCytometryIntegrationApi_get_flow_cytometry_by_sample
Retrieve flow cytometry run-level data by querying related sample ID (accession)

Description

Retrieve flow cytometry run-level data by querying related sample ID (accession)

Usage

```
FlowCytometryIntegrationApi_get_flow_cytometry_by_sample(
  id,
  page_limit,
  page_offset,
  use_versions,
  returned_metadata_fields,
  ...
)
```


Arguments

<code>id</code>	Unique identifier (accession) of the object.
<code>page_limit</code>	Maximum number of results to return. This value must be between 0 and 2000 (inclusive).
<code>page_offset</code>	Show the page <code>pageOffset+1</code> 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.
<code>use_versions</code>	Specify which versions of omics data files are used in the query. By default the active version is used. See Versioning above. Syntax: <code>*</code> or <code>v<version number></code> or <code><CHAIN_ID>:v<version number></code> or <code><CHAIN_ID>:<accession1,accession2,...></code>
<code>returned_metadata_fields</code>	The parameter defines amount of metadata attributes to return: 1. <code>template</code> - 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. <code>all</code> - return all metadata attributes with values and null attributes, if they are present in the applied template. This is the default for Curator endpoints.

FlowCytometryIntegrationApi_get_parents_by_study

Retrieve group metadata by querying study ID (accession)

Description

Retrieve group metadata by querying study ID (accession)

Usage

```
FlowCytometryIntegrationApi_get_parents_by_study(
    id,
    use_versions,
    returned_metadata_fields,
    ...
)
```

Arguments

<code>id</code>	Unique identifier (accession) of the object.
<code>use_versions</code>	Specify which versions of omics data files are used in the query. By default the active version is used. See Versioning above. Syntax: <code>*</code> or <code>v<version number></code> or <code><CHAIN_ID>:v<version number></code> or <code><CHAIN_ID>:<accession1,accession2,...></code>
<code>returned_metadata_fields</code>	The parameter defines amount of metadata attributes to return: 1. <code>template</code> - 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. <code>all</code> - return all metadata attributes with values and null attributes, if they are present in the applied template. This is the default for Curator endpoints.

FlowCytometryIntegrationApi_get_run_to_sample_pairs

Retrieve run-sample pairs by group id. Pagination is based on unique runs, not unique pairs.

Description

Retrieve run-sample pairs by group id. Pagination is based on unique runs, not unique pairs.

Usage

```
FlowCytometryIntegrationApi_get_run_to_sample_pairs(  
    id,  
    page_limit,  
    page_offset,  
    ...  
)
```

Arguments

id	Unique identifier (accession) of the object.
page_limit	Maximum number of results to return. This value must be between 0 and 2000 (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.

LibraryIntegrationApi_create_library_group_sample_group_link

Create links between samples and libraries

Description

Create links between samples and libraries

Usage

```
LibraryIntegrationApi_create_library_group_sample_group_link(  
    source_id,  
    target_id,  
    ...  
)
```

Arguments

source_id	The ID (accession) of the library group object
target_id	The ID (accession) of the sample group object

`LibraryIntegrationApi_create_library_sample_link`*Create a link between a library and a sample*

Description

Create a link between a library and a sample

Usage

```
LibraryIntegrationApi_create_library_sample_link(source_id, target_id, ...)
```

Arguments

<code>source_id</code>	The ID (accession) of the library object
<code>target_id</code>	The ID (accession) of the sample object

`LibraryIntegrationApi_delete_library_group_sample_group_link`*Delete links between samples and libraries related to the specified group*

Description

Delete links between samples and libraries related to the specified group

Usage

```
LibraryIntegrationApi_delete_library_group_sample_group_link(  
  source_id,  
  target_id,  
  ...  
)
```

Arguments

<code>source_id</code>	The ID (accession) of the library group object
<code>target_id</code>	The ID (accession) of the sample group object

`LibraryIntegrationApi_delete_library_sample_link`*Delete a link between a library and a sample*

Description

Delete a link between a library and a sample

Usage

```
LibraryIntegrationApi_delete_library_sample_link(source_id, target_id, ...)
```

Arguments

<code>source_id</code>	The ID (accession) of the library object
<code>target_id</code>	The ID (accession) of the sample object

`LibraryIntegrationApi_get_libraries_by_samples`*Retrieve library metadata by querying related samples*

Description

Retrieve library metadata by querying related samples

Usage

```
LibraryIntegrationApi_get_libraries_by_samples(  
  filter,  
  query,  
  search_specific_terms,  
  page_limit,  
  page_offset,  
  returned_metadata_fields,  
  ...  
)
```

Arguments

<code>filter</code>	Filter by sample metadata (key-value metadata pair(s)). E.g. "Species or strain"="Homo sapiens"
<code>query</code>	Search for objects via a full-text query over all sample metadata fields. E.g. Clozapine

search_specific_terms	If the full-text query term is present in an RTS 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.
page_limit	Maximum number of results to return. This value must be between 0 and 2000 (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.
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.

LibraryIntegrationApi_get_library_by_sample

Retrieve library metadata by querying related sample ID (accession)

Description

Retrieve library metadata by querying related sample ID (accession)

Usage

```
LibraryIntegrationApi_get_library_by_sample(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.

`LibraryIntegrationApi_get_library_links_to_samples`

Retrieve library-samples pairs by group id. Pagination is based on unique libraries, not unique pairs.

Description

Retrieve library-samples pairs by group id. Pagination is based on unique libraries, not unique pairs.

Usage

```
LibraryIntegrationApi_get_library_links_to_samples(  
    id,  
    page_limit,  
    page_offset,  
    ...  
)
```

Arguments

<code>id</code>	Unique identifier (accession) of the object.
<code>page_limit</code>	Maximum number of results to return. This value must be between 0 and 2000 (inclusive).
<code>page_offset</code>	Show the page <code>pageOffset+1</code> 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.

`LibraryIntegrationApi_get_parents_by_study`

Retrieve group metadata by querying study ID (accession)

Description

Retrieve group metadata by querying study ID (accession)

Usage

```
LibraryIntegrationApi_get_parents_by_study(id, ...)
```

Arguments

<code>id</code>	Unique identifier (accession) of the object.
-----------------	--

`LinkageApi_delete_link`*Deletes existing links matching the specified criteria.*

Description

Deletes existing links matching the specified criteria.

Usage

```
LinkageApi_delete_link(first_id, second_id, first_type, second_type, ...)
```

Arguments

<code>first_id</code>	Object ID (accession) (e.g. accession of study)
<code>second_id</code>	Object ID (accession) (e.g. accession of study)
<code>first_type</code>	Type of the object (e.g. study)
<code>second_type</code>	Type of the object (e.g. study)

`LinkageApi_get_data_types`*Lists all available data types.*

Description

Lists all available data types.

Usage

```
LinkageApi_get_data_types(...)
```

`LinkageApi_get_data_types_links`

List all possible links between data types that match the specified criteria.

Description

List all possible links between data types that match the specified criteria.

Usage

```
LinkageApi_get_data_types_links(type, ...)
```

Arguments

type	Return only links with the specified data type.
------	---

`LinkageApi_get_links_by_ids`

Finds existing links by passing many IDs. Pagination goes through all links matched the criteria.

Description

Finds existing links by passing many IDs. Pagination goes through all links matched the criteria.

Usage

```
LinkageApi_get_links_by_ids(request, ...)
```

Arguments

request

`LinkageApi_get_links_by_params`*Finds existing links matching the specified criteria.*

Description

Finds existing links matching the specified criteria.

Usage

```
LinkageApi_get_links_by_params(  
    first_id,  
    first_type,  
    second_id,  
    second_type,  
    offset,  
    limit,  
    ...  
)
```

Arguments

<code>first_id</code>	Object ID (accession) (e.g. accession of study)
<code>first_type</code>	Type of the object (e.g. study)
<code>second_id</code>	Object ID (accession) (e.g. accession of study)
<code>second_type</code>	Type of the object (e.g. study)
<code>offset</code>	Param says to skip that many links before beginning to return links.
<code>limit</code>	Param says to limit the count of returned links.

`LinkageApi_save_links` *Creates new links between objects.*

Description

Creates new links between objects.

Usage

```
LinkageApi_save_links(links, ...)
```

Arguments

`links`

OmicsQueriesApi_search_expression_data

Retrieve expression data objects by searching across multiple data types

Description

Retrieve expression data objects by searching across multiple data types

Usage

```
OmicsQueriesApi_search_expression_data(
  study_filter,
  study_query,
  sample_filter,
  sample_query,
  search_specific_terms,
  vx_query,
  vx_filter,
  ex_query,
  ex_filter,
  fx_query,
  fx_filter,
  use_versions,
  cursor,
  page_limit,
  ...
)
```

Arguments

study_filter	Filter by study metadata (key-value metadata pair(s)). E.g. "Study Source"=ArrayExpress
study_query	Search for objects via a full-text query over all study metadata fields. E.g. "RNA-Seq of human dendritic cells"
sample_filter	Filter by sample metadata (key-value metadata pair(s)). E.g. "Species or strain"="Homo sapiens"
sample_query	Search for objects via a full-text query over all sample metadata fields. E.g. Clozapine
search_specific_terms	If the full-text query term is present in an RTS 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.

vx_query	Search for objects linked to variant data via data query (key-value pair(s)). E.g. VariationId=rs548419688 rs544419019 Intervals=12:23432-234324,30:234324-23432 Gene=ASPM,BRCA1 Reference=A T Alteration=C G Quality=(0.9:1.0) Type=SNP MNP INS DEL MI info_VT=DEL info_EUR_AF=(0.9:1.0) Start=12340 AllelesNumber=1 AlterationNumber=2
vx_filter	Filter by variant metadata (key-value metadata pair(s)). E.g. "Variant Source"=dbSNP
ex_query	Search for objects linked to expression data via data query (key-value pair(s)). E.g. Feature=ENSG00000230368,ENSG00000188976 MinValue=1.50
ex_filter	Filter by expression metadata (key-value metadata pair(s)). E.g. "Genome Version"=hg19-BROAD
fx_query	Search for objects linked to flow cytometry data via data query (key-value pair(s)). E.g. ReadoutType=Median Count CellPopulation="CD45+, live" MinValue=3.5
fx_filter	Filter by flow cytometry metadata (key-value metadata pair(s)). E.g. Organ=blood
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,...>
cursor	The page tag to resume results from (see paging above).
page_limit	How many results to retrieve per page. The default is 2000

OmicsQueriesApi_search_expression_groups

Retrieve group objects by searching across multiple data types

Description

Retrieve group objects by searching across multiple data types

Usage

```
OmicsQueriesApi_search_expression_groups(
    study_filter,
    study_query,
    sample_filter,
    sample_query,
    search_specific_terms,
    vx_query,
    vx_filter,
    ex_query,
    ex_filter,
    fx_query,
    fx_filter,
    use_versions,
    cursor,
    page_limit,
    ...
)
```

Arguments

study_filter	Filter by study metadata (key-value metadata pair(s)). E.g. "Study Source"=ArrayExpress
study_query	Search for objects via a full-text query over all study metadata fields. E.g. "RNA-Seq of human dendritic cells"
sample_filter	Filter by sample metadata (key-value metadata pair(s)). E.g. "Species or strain"="Homo sapiens"
sample_query	Search for objects via a full-text query over all sample metadata fields. E.g. Clozapine
search_specific_terms	If the full-text query term is present in an RTS 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.
vx_query	Search for objects linked to variant data via data query (key-value pair(s)). E.g. VariationId=rs548419688 rs544419019 Intervals=12:23432-234324,30:234324-23432 Gene=ASPM,BRCA1 Reference=A T Alteration=C G Quality=(0.9:1.0) Type=SNP MNP INS DEL MI info_VT=DEL info_EUR_AF=(0.9:1.0) Start=12340 AllelesNumber=1 AlterationNumber=2
vx_filter	Filter by variant metadata (key-value metadata pair(s)). E.g. "Variant Source"=dbSNP
ex_query	Search for objects linked to expression data via data query (key-value pair(s)). E.g. Feature=ENSG00000230368,ENSG00000188976 MinValue=1.50
ex_filter	Filter by expression metadata (key-value metadata pair(s)). E.g. "Genome Version"=hg19-BROAD
fx_query	Search for objects linked to flow cytometry data via data query (key-value pair(s)). E.g. ReadoutType=Median Count CellPopulation="CD45+, live" MinValue=3.5
fx_filter	Filter by flow cytometry metadata (key-value metadata pair(s)). E.g. Organ=blood
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,...>
cursor	The page tag to resume results from (see paging above).
page_limit	How many results to retrieve per page. The default is 2000

OmicsQueriesApi_search_flow_cytometry_data

Retrieve flow cytometry data objects by searching across multiple data types

Description

Retrieve flow cytometry data objects by searching across multiple data types

Usage

```
OmicsQueriesApi_search_flow_cytometry_data(
  study_filter,
  study_query,
  sample_filter,
  sample_query,
  search_specific_terms,
  vx_query,
  vx_filter,
  ex_query,
  ex_filter,
  fx_query,
  fx_filter,
  use_versions,
  page_offset,
  cursor,
  page_limit,
  ...
)
```

Arguments

study_filter	Filter by study metadata (key-value metadata pair(s)). E.g. "Study Source"=ArrayExpress
study_query	Search for objects via a full-text query over all study metadata fields. E.g. "RNA-Seq of human dendritic cells"
sample_filter	Filter by sample metadata (key-value metadata pair(s)). E.g. "Species or strain"="Homo sapiens"
sample_query	Search for objects via a full-text query over all sample metadata fields. E.g. Clozapine
search_specific_terms	If the full-text query term is present in an RTS 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.
vx_query	Search for objects linked to variant data via data query (key-value pair(s)). E.g. VariationId=rs548419688 rs544419019 Intervals=12:23432-234324,30:234324-23432 Gene=ASPM,BRCA1 Reference=A T Alteration=C G Quality=(0.9:1.0) Type=SNP MNP INS DEL MI info_VT=DEL info_EUR_AF=(0.9:1.0) Start=12340 AllelesNumber=1 AlterationNumber=2
vx_filter	Filter by variant metadata (key-value metadata pair(s)). E.g. "Variant Source"=dbSNP
ex_query	Search for objects linked to expression data via data query (key-value pair(s)). E.g. Feature=ENSG00000230368,ENSG00000188976 MinValue=1.50
ex_filter	Filter by expression metadata (key-value metadata pair(s)). E.g. "Genome Version"=hg19-BROAD
fx_query	Search for objects linked to flow cytometry data via data query (key-value pair(s)). E.g. ReadoutType=Median Count CellPopulation="CD45+, live" MinValue=3.5

fx_filter	Filter by flow cytometry metadata (key-value metadata pair(s)). E.g. Organ=blood
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,...>
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.
cursor	The page tag to resume results from (see paging above).
page_limit	How many results to retrieve per page. The default is 2000

OmicsQueriesApi_search_flow_cytometry_groups

Retrieve group objects by searching across multiple data types

Description

Retrieve group objects by searching across multiple data types

Usage

```
OmicsQueriesApi_search_flow_cytometry_groups(
    study_filter,
    study_query,
    sample_filter,
    sample_query,
    search_specific_terms,
    vx_query,
    vx_filter,
    ex_query,
    ex_filter,
    fx_query,
    fx_filter,
    use_versions,
    cursor,
    page_limit,
    ...
)
```

Arguments

study_filter	Filter by study metadata (key-value metadata pair(s)). E.g. "Study Source"=ArrayExpress
study_query	Search for objects via a full-text query over all study metadata fields. E.g. "RNA-Seq of human dendritic cells"
sample_filter	Filter by sample metadata (key-value metadata pair(s)). E.g. "Species or strain"="Homo sapiens"
sample_query	Search for objects via a full-text query over all sample metadata fields. E.g. Clozapine

search_specific_terms

If the full-text query term is present in an RTS 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.

vx_query

Search for objects linked to variant data via data query (key-value pair(s)). E.g. VariationId=rs548419688|rs544419019 Intervals=12:23432-234324,30:234324-23432 Gene=ASPM,BRCA1 Reference=A|T Alteration=C|G Quality=(0.9:1.0) Type=SNP|MNP|INS|DEL|MI info_VT=DEL info_EUR_AF=(0.9:1.0) Start=12340 AllelesNumber=1 AlterationNumber=2

vx_filter

Filter by variant metadata (key-value metadata pair(s)). E.g. "Variant Source"=dbSNP

ex_query

Search for objects linked to expression data via data query (key-value pair(s)). E.g. Feature=ENSG00000230368,ENSG00000188976 MinValue=1.50

ex_filter

Filter by expression metadata (key-value metadata pair(s)). E.g. "Genome Version"=hg19-BROAD

fx_query

Search for objects linked to flow cytometry data via data query (key-value pair(s)). E.g. ReadoutType=Median|Count CellPopulation="CD45+, live" MinValue=3.5

fx_filter

Filter by flow cytometry metadata (key-value metadata pair(s)). E.g. Organ=blood

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,...>

cursor

The page tag to resume results from (see paging above).

page_limit

How many results to retrieve per page. The default is 2000

OmicsQueriesApi_search_samples

Retrieve sample metadata objects by searching across multiple data types

Description

Retrieve sample metadata objects by searching across multiple data types

Usage

```
OmicsQueriesApi_search_samples(
  study_filter,
  study_query,
  sample_filter,
  sample_query,
  search_specific_terms,
  vx_query,
  vx_filter,
```

```

    ex_query,
    ex_filter,
    fx_query,
    fx_filter,
    use_versions,
    cursor,
    page_limit,
    ...
)

```

Arguments

study_filter	Filter by study metadata (key-value metadata pair(s)). E.g. "Study Source"=ArrayExpress
study_query	Search for objects via a full-text query over all study metadata fields. E.g. "RNA-Seq of human dendritic cells"
sample_filter	Filter by sample metadata (key-value metadata pair(s)). E.g. "Species or strain"="Homo sapiens"
sample_query	Search for objects via a full-text query over all sample metadata fields. E.g. Clozapine
search_specific_terms	If the full-text query term is present in an RTS 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.
vx_query	Search for objects linked to variant data via data query (key-value pair(s)). E.g. VariationId=rs548419688 rs544419019 Intervals=12:23432-234324,30:234324-23432 Gene=ASPM,BRCA1 Reference=A T Alteration=C G Quality=(0.9:1.0) Type=SNP MNP INS DEL MI info_VT=DEL info_EUR_AF=(0.9:1.0) Start=12340 AllelesNumber=1 AlterationNumber=2
vx_filter	Filter by variant metadata (key-value metadata pair(s)). E.g. "Variant Source"=dbSNP
ex_query	Search for objects linked to expression data via data query (key-value pair(s)). E.g. Feature=ENSG00000230368,ENSG00000188976 MinValue=1.50
ex_filter	Filter by expression metadata (key-value metadata pair(s)). E.g. "Genome Version"=hg19-BROAD
fx_query	Search for objects linked to flow cytometry data via data query (key-value pair(s)). E.g. ReadoutType=Median Count CellPopulation="CD45+, live" MinValue=3.5
fx_filter	Filter by flow cytometry metadata (key-value metadata pair(s)). E.g. Organ=blood
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,...>
cursor	The page tag to resume results from (see paging above).
page_limit	How many results to retrieve per page. The default is 2000

OmicsQueriesApi_search_streamed_expression_data
<i>Retrieve expression levels streamingly</i>

Description

Retrieve expression levels streamingly

Usage

```
OmicsQueriesApi_search_streamed_expression_data(  
  group_accession,  
  sample_filter,  
  sample_query,  
  search_specific_terms,  
  feature_list,  
  ...  
)
```

Arguments

group_accession	Accession of the group which contains the reference to the expression matrix
sample_filter	Filter by sample metadata (key-value metadata pair(s)). E.g. "Species or strain"="Homo sapiens"
sample_query	Search for objects via a full-text query over all sample metadata fields. E.g. Clozapine
search_specific_terms	If the full-text query term is present in an RTS 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.
feature_list	Filter results by specific feature (eg. Gene identifier). The feature parameter value must match the name of the identifier in the GCT file (under the NAME column). Example: ENSG00000077044

OmicsQueriesApi_search_variant_data

Retrieve variant data objects by searching across multiple data types

Description

Retrieve variant data objects by searching across multiple data types

Usage

```
OmicsQueriesApi_search_variant_data(
  study_filter,
  study_query,
  sample_filter,
  sample_query,
  search_specific_terms,
  vx_query,
  vx_filter,
  ex_query,
  ex_filter,
  fx_query,
  fx_filter,
  use_versions,
  page_offset,
  cursor,
  page_limit,
  ...
)
```

Arguments

study_filter	Filter by study metadata (key-value metadata pair(s)). E.g. "Study Source"=ArrayExpress
study_query	Search for objects via a full-text query over all study metadata fields. E.g. "RNA-Seq of human dendritic cells"
sample_filter	Filter by sample metadata (key-value metadata pair(s)). E.g. "Species or strain"="Homo sapiens"
sample_query	Search for objects via a full-text query over all sample metadata fields. E.g. Clozapine
search_specific_terms	If the full-text query term is present in an RTS 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.

vx_query	Search for objects linked to variant data via data query (key-value pair(s)). E.g. VariationId=rs548419688 rs544419019 Intervals=12:23432-234324,30:234324-23432 Gene=ASPM,BRCA1 Reference=A T Alteration=C G Quality=(0.9:1.0) Type=SNP MNP INS DEL MI info_VT=DEL info_EUR_AF=(0.9:1.0) Start=12340 AllelesNumber=1 AlterationNumber=2
vx_filter	Filter by variant metadata (key-value metadata pair(s)). E.g. "Variant Source"=dbSNP
ex_query	Search for objects linked to expression data via data query (key-value pair(s)). E.g. Feature=ENSG00000230368,ENSG00000188976 MinValue=1.50
ex_filter	Filter by expression metadata (key-value metadata pair(s)). E.g. "Genome Version"=hg19-BROAD
fx_query	Search for objects linked to flow cytometry data via data query (key-value pair(s)). E.g. ReadoutType=Median Count CellPopulation="CD45+, live" MinValue=3.5
fx_filter	Filter by flow cytometry metadata (key-value metadata pair(s)). E.g. Organ=blood
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,...>
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.
cursor	The page tag to resume results from (see paging above).
page_limit	How many results to retrieve per page. The default is 2000

OmicsQueriesApi_search_variant_groups

Retrieve group objects by searching across multiple data types

Description

Retrieve group objects by searching across multiple data types

Usage

```
OmicsQueriesApi_search_variant_groups(
    study_filter,
    study_query,
    sample_filter,
    sample_query,
    search_specific_terms,
    vx_query,
    vx_filter,
    ex_query,
    ex_filter,
    fx_query,
    fx_filter,
    use_versions,
    cursor,
    page_limit,
    ...
)
```

Arguments

study_filter	Filter by study metadata (key-value metadata pair(s)). E.g. "Study Source"=ArrayExpress
study_query	Search for objects via a full-text query over all study metadata fields. E.g. "RNA-Seq of human dendritic cells"
sample_filter	Filter by sample metadata (key-value metadata pair(s)). E.g. "Species or strain"="Homo sapiens"
sample_query	Search for objects via a full-text query over all sample metadata fields. E.g. Clozapine
search_specific_terms	If the full-text query term is present in an RTS 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.
vx_query	Search for objects linked to variant data via data query (key-value pair(s)). E.g. VariationId=rs548419688 rs544419019 Intervals=12:23432-234324,30:234324-23432 Gene=ASPM,BRCA1 Reference=A T Alteration=C G Quality=(0.9:1.0) Type=SNP MNP INS DEL MI info_VT=DEL info_EUR_AF=(0.9:1.0) Start=12340 AllelesNumber=1 AlterationNumber=2
vx_filter	Filter by variant metadata (key-value metadata pair(s)). E.g. "Variant Source"=dbSNP
ex_query	Search for objects linked to expression data via data query (key-value pair(s)). E.g. Feature=ENSG00000230368,ENSG00000188976 MinValue=1.50
ex_filter	Filter by expression metadata (key-value metadata pair(s)). E.g. "Genome Version"=hg19-BROAD
fx_query	Search for objects linked to flow cytometry data via data query (key-value pair(s)). E.g. ReadoutType=Median Count CellPopulation="CD45+, live" MinValue=3.5
fx_filter	Filter by flow cytometry metadata (key-value metadata pair(s)). E.g. Organ=blood
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,...>
cursor	The page tag to resume results from (see paging above).
page_limit	How many results to retrieve per page. The default is 2000

PreparationIntegrationApi_create_preparation_group_sample_group_link
Create links between samples and preparations

Description

Create links between samples and preparations

Usage

```
PreparationIntegrationApi_create_preparation_group_sample_group_link(  
    source_id,  
    target_id,  
    ...  
)
```

Arguments

source_id	The ID (accession) of the preparation group object
target_id	The ID (accession) of the sample group object

PreparationIntegrationApi_create_preparation_sample_link
<i>Create a link between a preparation and a sample</i>

Description

Create a link between a preparation and a sample

Usage

```
PreparationIntegrationApi_create_preparation_sample_link(  
    source_id,  
    target_id,  
    ...  
)
```

Arguments

source_id	The ID (accession) of the preparation object
target_id	The ID (accession) of the sample object

PreparationIntegrationApi_delete_preparation_group_sample_group_link
<i>Delete links between samples and preparations related to the specified group</i>

Description

Delete links between samples and preparations related to the specified group

Usage

```
PreparationIntegrationApi_delete_preparation_group_sample_group_link(  
    source_id,  
    target_id,  
    ...  
)
```

Arguments

- source_id The ID (accession) of the preparation group object
- target_id The ID (accession) of the sample group object

PreparationIntegrationApi_delete_preparation_sample_link
<i>Delete a link between a preparation and a sample</i>

Description

Delete a link between a preparation and a sample

Usage

```
PreparationIntegrationApi_delete_preparation_sample_link(  
    source_id,  
    target_id,  
    ...  
)
```

Arguments

- source_id The ID (accession) of the preparation object
- target_id The ID (accession) of the sample object

PreparationIntegrationApi_get_parents_by_study
<i>Retrieve group metadata by querying study ID (accession)</i>

Description

Retrieve group metadata by querying study ID (accession)

Usage

```
PreparationIntegrationApi_get_parents_by_study(id, ...)
```

Arguments

id Unique identifier (accession) of the object.

PreparationIntegrationApi_get_preparations_by_samples

Retrieve preparation metadata by querying related samples

Description

Retrieve preparation metadata by querying related samples

Usage

```
PreparationIntegrationApi_get_preparations_by_samples(
    filter,
    query,
    search_specific_terms,
    page_limit,
    page_offset,
    returned_metadata_fields,
    ...
)
```

Arguments

filter	Filter by sample metadata (key-value metadata pair(s)). E.g. "Species or strain"="Homo sapiens"
query	Search for objects via a full-text query over all sample metadata fields. E.g. Clozapine
search_specific_terms	If the full-text query term is present in an RTS 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.
page_limit	Maximum number of results to return. This value must be between 0 and 2000 (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.
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.

```
PreparationIntegrationApi_get_preparation_by_sample
```

Retrieve preparation metadata by querying related sample ID (accession)

Description

Retrieve preparation metadata by querying related sample ID (accession)

Usage

```
PreparationIntegrationApi_get_preparation_by_sample(
    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.

```
PreparationIntegrationApi_get_preparation_links_to_samples
```

Retrieve run-sample pairs by group id. Pagination is based on unique preparations, not unique pairs.

Description

Retrieve run-sample pairs by group id. Pagination is based on unique preparations, not unique pairs.

Usage

```
PreparationIntegrationApi_get_preparation_links_to_samples(
    id,
    page_limit,
    page_offset,
    ...
)
```


Arguments

id	Unique identifier (accession) of the object.
page_limit	Maximum number of results to return. This value must be between 0 and 2000 (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.

SampleIntegrationApi_create_sample_group_study_link

Create a link between a group of sample objects and a study

Description

Create a link between a group of sample objects and a study

Usage

SampleIntegrationApi_create_sample_group_study_link(source_id, target_id, ...)

Arguments

source_id	The ID (accession) of the sample group object
target_id	The ID (accession) of the study object

SampleIntegrationApi_create_sample_study_link

Create a link between a sample and a study

Description

Create a link between a sample and a study

Usage

SampleIntegrationApi_create_sample_study_link(source_id, target_id, ...)

Arguments

source_id	The ID (accession) of the sample object
target_id	The ID (accession) of the study object

`SampleIntegrationApi_delete_sample_group_study_link`*Delete link between a group of sample objects and a study*

Description

Delete link between a group of sample objects and a study

Usage

```
SampleIntegrationApi_delete_sample_group_study_link(source_id, target_id, ...)
```

Arguments

<code>source_id</code>	The ID (accession) of the sample group object
<code>target_id</code>	The ID (accession) of the study object

`SampleIntegrationApi_delete_sample_study_link`*Delete link between a sample and a study*

Description

Delete link between a sample and a study

Usage

```
SampleIntegrationApi_delete_sample_study_link(source_id, target_id, ...)
```

Arguments

<code>source_id</code>	The ID (accession) of the sample object
<code>target_id</code>	The ID (accession) of the study object

SampleIntegrationApi_get_samples_by_libraries

Retrieve sample metadata by querying related libraries

Description

Retrieve sample metadata by querying related libraries

Usage

```
SampleIntegrationApi_get_samples_by_libraries(
    filter,
    query,
    search_specific_terms,
    page_limit,
    page_offset,
    returned_metadata_fields,
    ...
)
```

Arguments

filter	Filter by library metadata (key-value metadata pair(s)). E.g. "Species or strain"="Homo sapiens"
query	Search for objects via a full-text query over all library metadata fields. E.g. "RNA-Seq of human dendritic cells"
search_specific_terms	If the full-text query term is present in an RTS 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.
page_limit	Maximum number of results to return. This value must be between 0 and 2000 (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.
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.

SampleIntegrationApi_get_samples_by_preparations

Retrieve sample metadata by querying related preparations

Description

Retrieve sample metadata by querying related preparations

Usage

```
SampleIntegrationApi_get_samples_by_preparations(
    filter,
    query,
    search_specific_terms,
    page_limit,
    page_offset,
    returned_metadata_fields,
    ...
)
```

Arguments

filter	Filter by preparation metadata (key-value metadata pair(s)). E.g. "Species or strain"="Homo sapiens"
query	Search for study metadata objects via a full-text query over all preparation metadata fields. E.g. "RNA-Seq of human dendritic cells"
search_specific_terms	If the full-text query term is present in an RTS 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.
page_limit	Maximum number of results to return. This value must be between 0 and 2000 (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.
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.

`SampleIntegrationApi_get_samples_by_study`*Retrieve sample metadata by querying related study ID (accession)*

Description

Retrieve sample metadata by querying related study ID (accession)

Usage

```
SampleIntegrationApi_get_samples_by_study(  
    id,  
    page_limit,  
    page_offset,  
    returned_metadata_fields,  
    ...  
)
```

Arguments

<code>id</code>	Unique identifier (accession) of the object.
<code>page_limit</code>	Maximum number of results to return. This value must be between 0 and 2000 (inclusive).
<code>page_offset</code>	Show the page <code>pageOffset+1</code> 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.
<code>returned_metadata_fields</code>	The parameter defines amount of metadata attributes to return: 1. <code>template</code> - 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. <code>all</code> - return all metadata attributes with values and null attributes, if they are present in the applied template. This is the default for Curator endpoints.

`StudyIntegrationApi_get_studies_by_libraries`*Retrieve study metadata objects by querying related libraries*

Description

Retrieve study metadata objects by querying related libraries

Usage

```
StudyIntegrationApi_get_studies_by_libraries(
    filter,
    query,
    search_specific_terms,
    page_limit,
    page_offset,
    returned_metadata_fields,
    ...
)
```

Arguments

filter	Filter by library metadata (key-value metadata pair(s)). E.g. "Species or strain"="Homo sapiens"
query	Search for objects via a full-text query over all library metadata fields. E.g. "RNA-Seq of human dendritic cells"
search_specific_terms	If the full-text query term is present in an RTS 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.
page_limit	Maximum number of results to return. This value must be between 0 and 2000 (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.
returned_metadata_fields	The parameter defines amount of metadata attributes to return: 1. <code>template</code> - 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. <code>all</code> - return all metadata attributes with values and null attributes, if they are present in the applied template. This is the default for Curator endpoints.

StudyIntegrationApi_get_studies_by_preparations

Retrieve study metadata objects by querying related preparations

Description

Retrieve study metadata objects by querying related preparations

Usage

```
StudyIntegrationApi_get_studies_by_preparations(
    filter,
    query,
    search_specific_terms,
    page_limit,
    page_offset,
    returned_metadata_fields,
    ...
)
```

Arguments

filter	Filter by preparation metadata (key-value metadata pair(s)). E.g. "Species or strain"="Homo sapiens"
query	Search for study metadata objects via a full-text query over all preparation metadata fields. E.g. "RNA-Seq of human dendritic cells"
search_specific_terms	If the full-text query term is present in an RTS 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.
page_limit	Maximum number of results to return. This value must be between 0 and 2000 (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.
returned_metadata_fields	The parameter defines amount of metadata attributes to return: 1. <code>template</code> - 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. <code>all</code> - return all metadata attributes with values and null attributes, if they are present in the applied template. This is the default for Curator endpoints.

StudyIntegrationApi_get_studies_by_samples

Retrieve study metadata objects by querying related samples

Description

Retrieve study metadata objects by querying related samples

Usage

```
StudyIntegrationApi_get_studies_by_samples(
    filter,
    query,
    search_specific_terms,
    page_limit,
    page_offset,
    returned_metadata_fields,
    ...
)
```

Arguments

filter	Filter by sample metadata (key-value metadata pair(s)). E.g. "Species or strain"="Homo sapiens"
query	Search for study metadata objects via a full-text query over all sample metadata fields. E.g. "RNA-Seq of human dendritic cells"
search_specific_terms	If the full-text query term is present in an RTS 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.
page_limit	Maximum number of results to return. This value must be between 0 and 2000 (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.
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.

StudyIntegrationApi_get_study_by_sample

Retrieve study metadata by querying sample ID (accession)

Description

Retrieve study metadata by querying sample ID (accession)

Usage

```
StudyIntegrationApi_get_study_by_sample(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.

ValidationSummaryApi_search_expression_data

Retrieve validation summary by querying study ID (accession)

Description

Retrieve validation summary by querying study ID (accession)

Usage

```
ValidationSummaryApi_search_expression_data(id, ...)
```

Arguments

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

VariantIntegrationApi_create_variant_group_sample_group_link

Create a link between a group of variant objects and a group of sample objects

Description

Create a link between a group of variant objects and a group of sample objects

Usage

```
VariantIntegrationApi_create_variant_group_sample_group_link(
    source_id,
    target_id,
    ...
)
```

Arguments

source_id	The ID (accession) of the group of run-level objects (corresponding to the column in a VCF file)
target_id	The ID (accession) of the sample group object

VariantIntegrationApi_create_variant_sample_link
<i>Create a link between a variant object and a sample</i>

Description

Create a link between a variant object and a sample

Usage

VariantIntegrationApi_create_variant_sample_link(source_id, target_id, ...)

Arguments

source_id	The ID (accession) of the run-level object (corresponding to the column in a VCG/GCT file)
target_id	The ID (accession) of the sample object

VariantIntegrationApi_delete_variant_group_sample_group_link
<i>Delete link between a group of variant objects and a group of sample objects</i>

Description

Delete link between a group of variant objects and a group of sample objects

Usage

```
VariantIntegrationApi_delete_variant_group_sample_group_link(  
  source_id,  
  target_id,  
  ...  
)
```

Arguments

source_id	The ID (accession) of the group of run-level objects (corresponding to the column in a VCF file)
target_id	The ID (accession) of the sample group object

VariantIntegrationApi_delete_variant_sample_link

Delete link between a variant object and a sample

Description

Delete link between a variant object and a sample

Usage

```
VariantIntegrationApi_delete_variant_sample_link(source_id, target_id, ...)
```

Arguments

source_id	The ID (accession) of the run-level object (corresponding to the column in a VCG/GCT file)
target_id	The ID (accession) of the sample object

VariantIntegrationApi_get_parents_by_study

Retrieve group metadata by querying study ID (accession)

Description

Retrieve group metadata by querying study ID (accession)

Usage

```
VariantIntegrationApi_get_parents_by_study(
    id,
    use_versions,
    returned_metadata_fields,
    ...
)
```

Arguments

id	Unique identifier (accession) of the object.
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.

VariantIntegrationApi_get_run_to_sample_pairs

Retrieve run-sample pairs by group id. Pagination is based on unique runs, not unique pairs.

Description

Retrieve run-sample pairs by group id. Pagination is based on unique runs, not unique pairs.

Usage

```
VariantIntegrationApi_get_run_to_sample_pairs(id, page_limit, page_offset, ...)
```

Arguments

id	Unique identifier (accession) of the object.
page_limit	Maximum number of results to return. This value must be between 0 and 2000 (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.

VariantIntegrationApi_get_variant_by_sample

Retrieve variant run-level data by querying related sample ID (accession)

Description

Retrieve variant run-level data by querying related sample ID (accession)

Usage

```
VariantIntegrationApi_get_variant_by_sample(
    id,
    page_limit,
    page_offset,
    use_versions,
    returned_metadata_fields,
    ...
)
```

Arguments

id	Unique identifier (accession) of the object.
page_limit	Maximum number of results to return. This value must be between 0 and 2000 (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.
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.