Package 'integrationUser'

March 24, 2021

Title integrationUser

Version 1.36.0-1

API version v0.1

Description This is the API for layer 4 of the Roche pRed project. This swagger page describes the integrationUser APIs. These are typically used to find and retrieve study, sample and processed (signal) data and metadata for a given query. 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:

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

`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,..>

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

`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,..>

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

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.

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

`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.

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

`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.

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_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

`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.

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

`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.

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_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

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.

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

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_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

id	Unique identifier (accession) of the object.

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

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

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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 param-
                 eter 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

Retrieve expression levels streamingly

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_get_parents_by_study

Retrieve group metadata by querying study ID (accession)

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_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 end-
> points. 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 end-
> points.

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 param-
> eter 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

`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.

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_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. `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_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. `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_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.

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.