ODM Basic Training

Maria Borodaenko
Senior Solution Consultant

Genestack

Program

Welcome to ODM training

- Learning goals
- Brief overview of what ODM does and why
- Training
- Q&A Session

Learning Goals

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Learning Goals

- Get an impression how ODM can help me and my colleagues
- Get understanding of ODM capabilities
  - Know how to find relevant data
  - Learn how to import a study
  - Get knowledge about curation
  - Know how to share, export and delete a study

ODM Introduction

Genestack

Making Data FAIR and Action-Ready for Both Consumers & Curators

DATA CURATORS

Metadata Curation

Harmonise thousands of samples
Enforce minimum metadata model

RESEARCHERS

Integrated Data Catalog

Find data across sources
Explore study-sample-data links

DATA SCIENTISTS

Search Services

Slice-and-dice analysis-ready data
Write R Shiny apps rapidly

A Single Point of Truth for Your Data

Data Storage

E.g. S3

Public Data

E.g. TCGA, GEO

ELN/LIMS

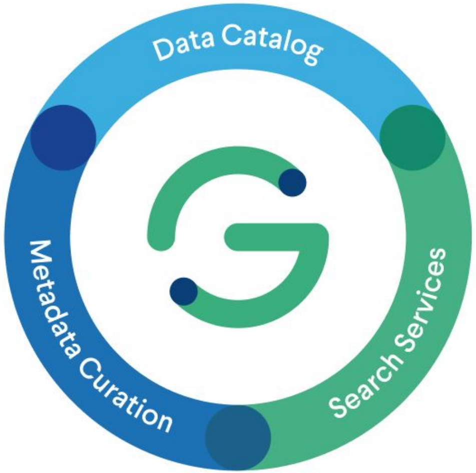
E.g. Benchling

Pipelines

E.g. DNANexus

Terminology Service

E.g. CenTree



Easier Collaboration

Reduced Experimental Redundancy

Increased Speed to Discovery

Data Viz

E.g. R Shiny, ArrayStudio, ...

Downstream Analytics

E.g. AI, Systems Biology, ...

Training

Genestack

Training Plan

- Getting started
- Exploring a Study in Metadata Editor
- Searching for available data in Study Browser
- Data loading
- Metadata templates
- Metadata curation
- Access to studies
- Study export
- Study deletion

Training Plan

- **Getting started**
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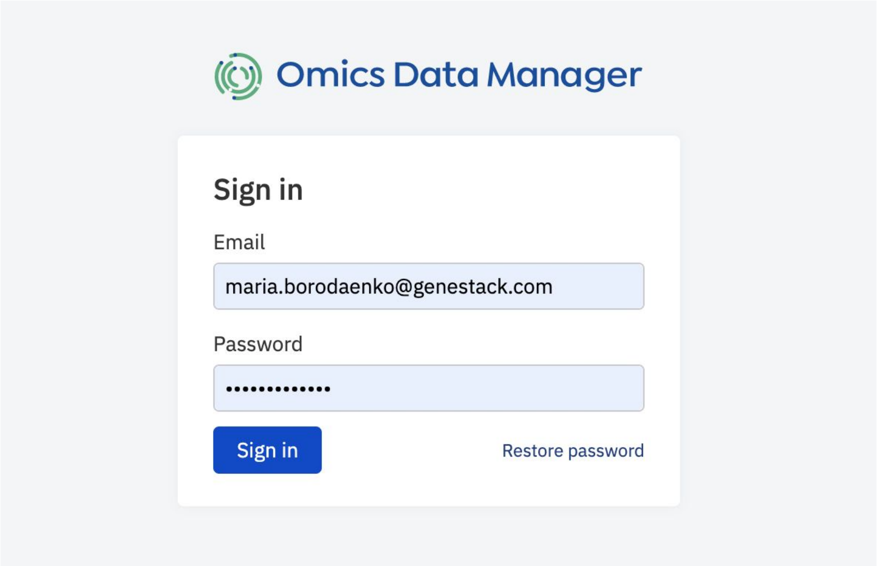
Login

The users are able to login into ODM via SSO

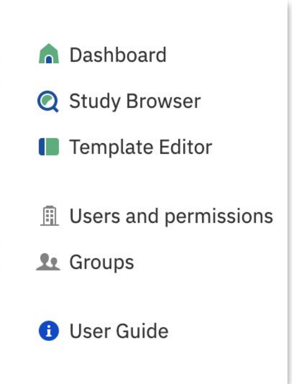


Email: maria.borodaenko@genestack.com

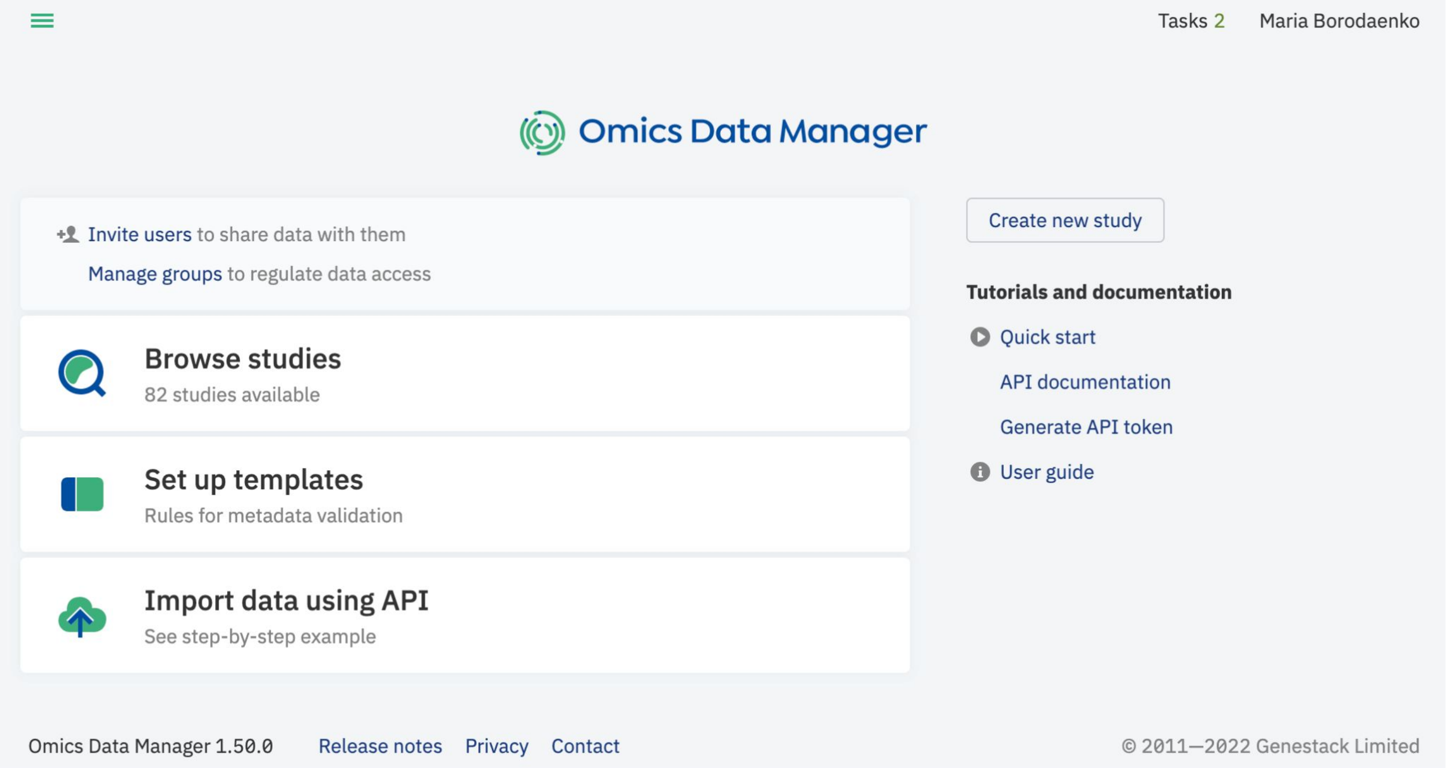
Password: •••••••••••••

Starting Page

Navigation



- Dashboard
- Study Browser
- Template Editor
- Users and permissions
- Groups
- User Guide



Tasks 2 Maria Borodaenko

Omics Data Manager

Invite users to share data with them

Manage groups to regulate data access

Browse studies

82 studies available

Set up templates

Rules for metadata validation

Import data using API

See step-by-step example

Create new study

Tutorials and documentation

- Quick start
- API documentation
- Generate API token
- User guide

Omics Data Manager 1.50.0 Release notes Privacy Contact

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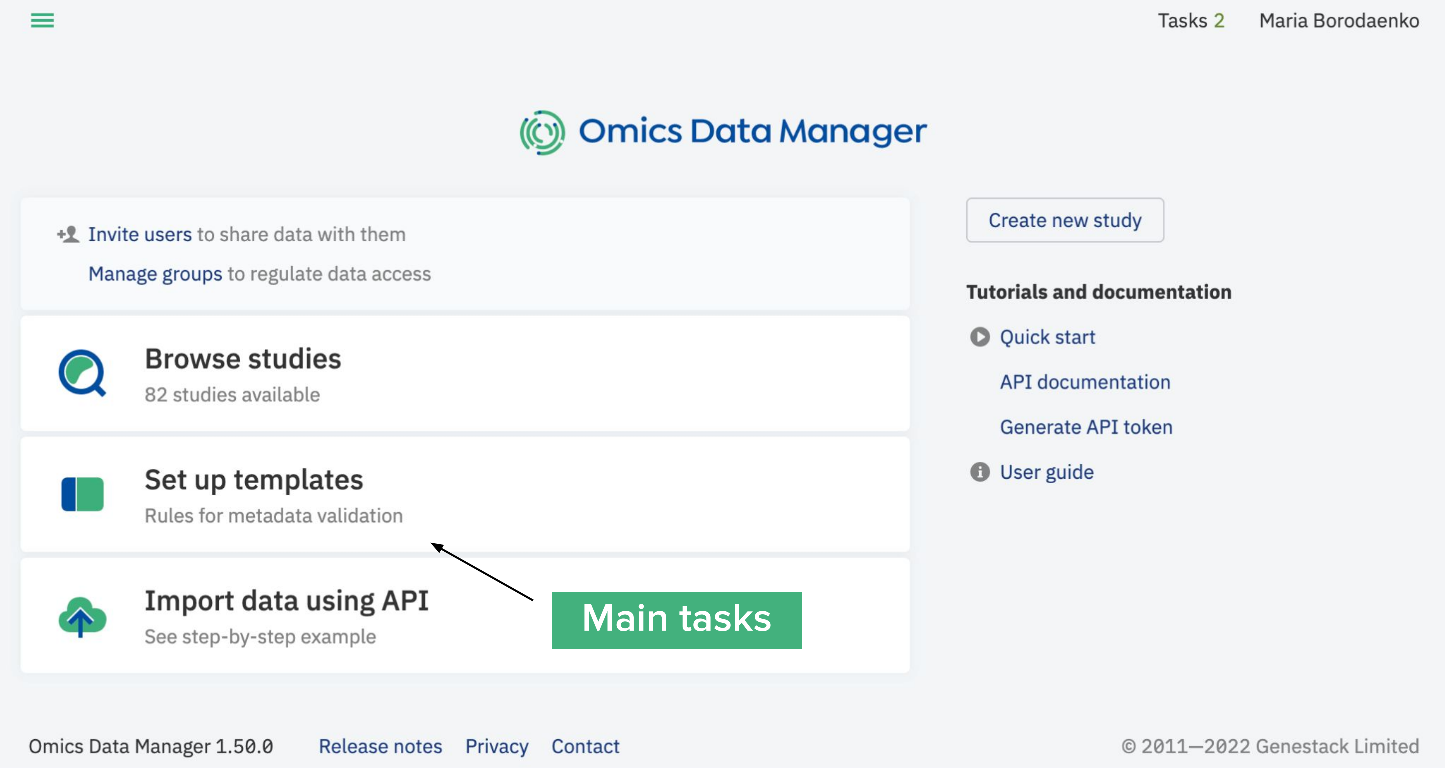
Starting Page



Tasks 2 Maria Borodaenko

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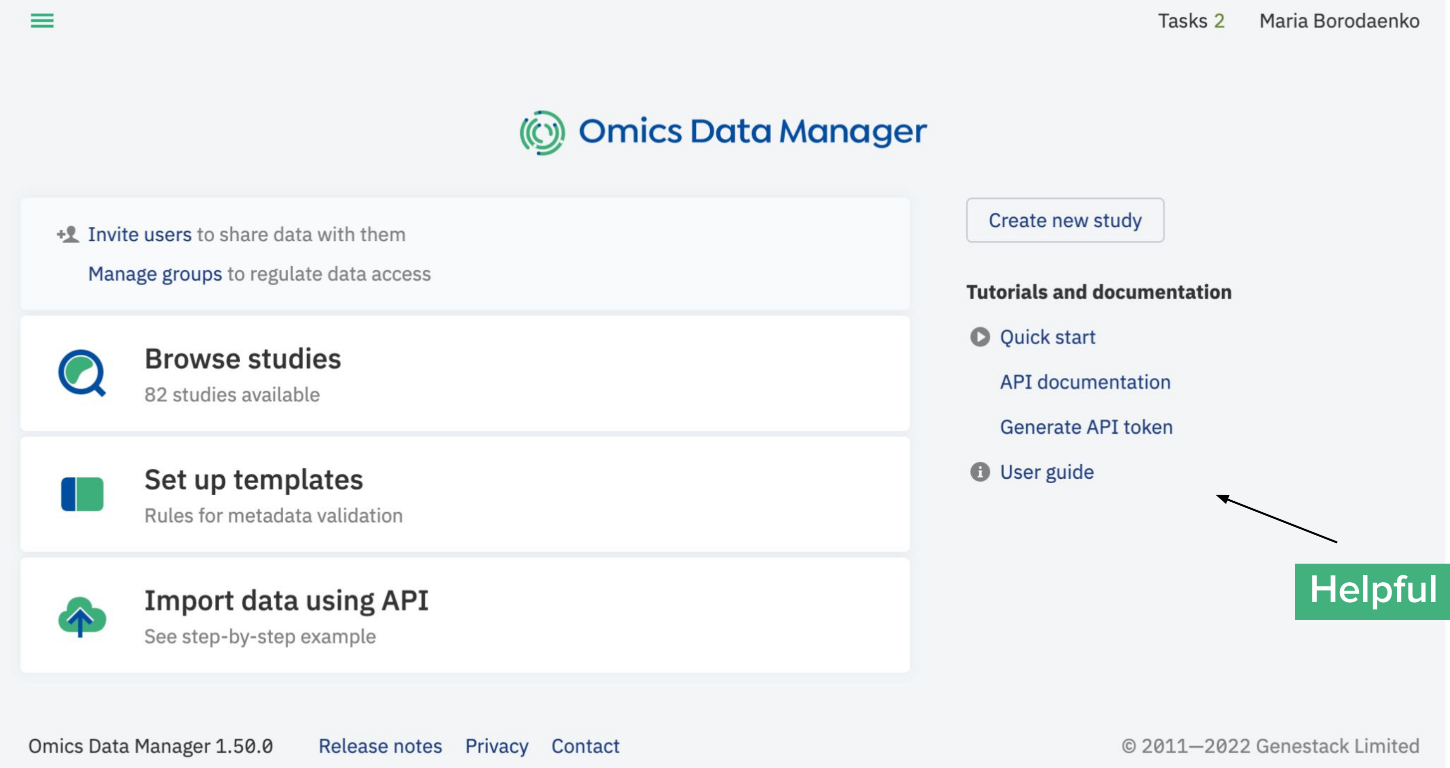
Main tasks

Starting Page



Tasks 2 Maria Borodaenko

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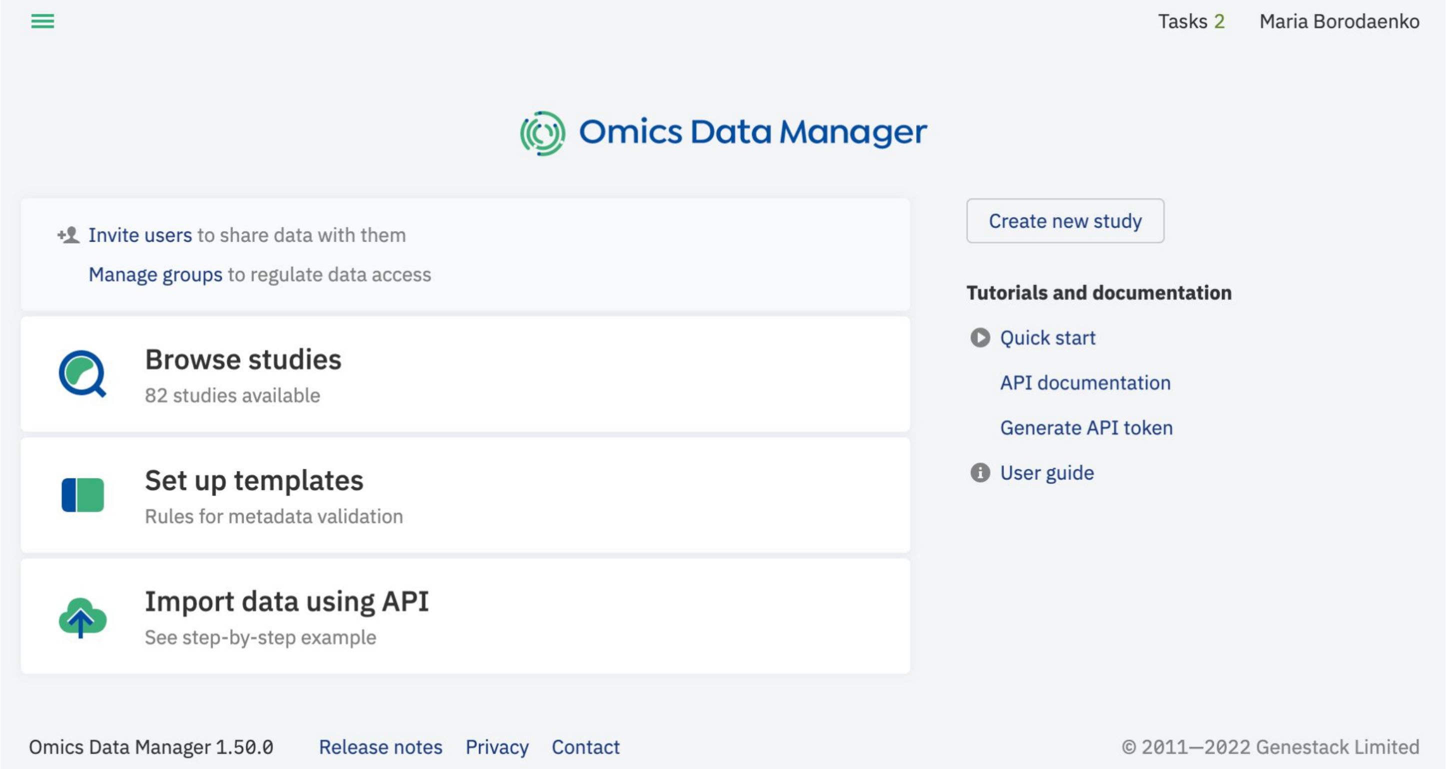
Helpful links

Starting Page



Your profile

Omics Data Manager

Invite users to share data with them

Manage groups to regulate data access

Browse studies

82 studies available

Set up templates

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Import data using API

See step-by-step example

Tutorials and documentation

- Quick start
- API documentation
- Generate API token
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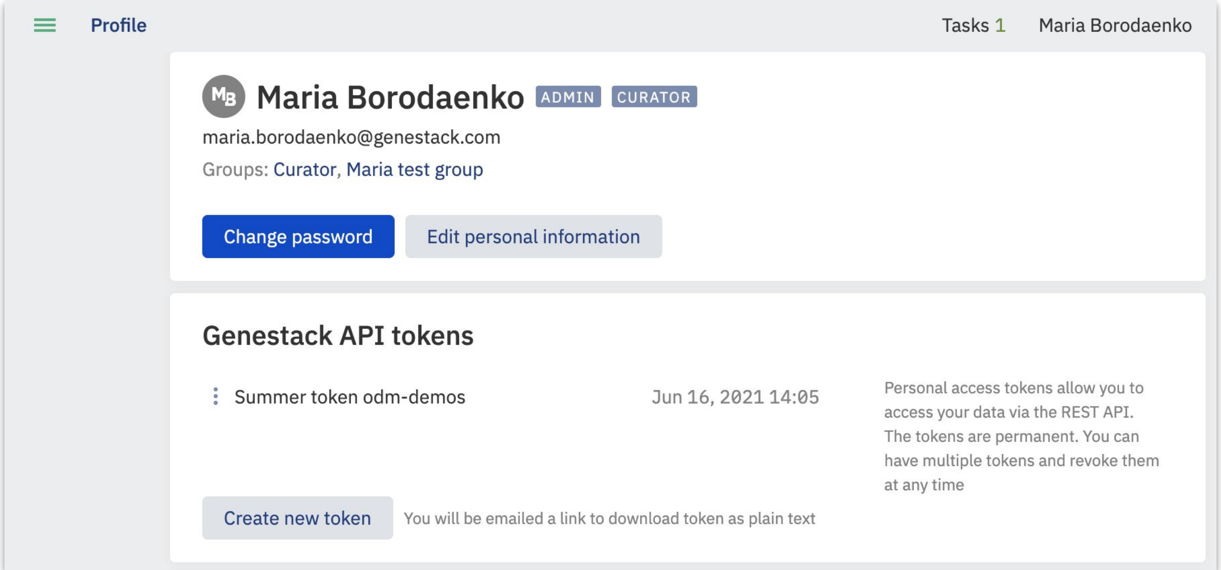
Omics Data Manager 1.50.0 Release notes Privacy Contact

Profile

Profile application shows your permission role, the list of available groups, allows you to edit personal information and to get a API access token.



Maria Borodaenko ADMIN CURATOR

maria.borodaenko@genestack.com

Groups: Curator, Maria test group

Genestack API tokens

Summer token odm-demos Jun 16, 2021 14:05

Personal access tokens allow you to access your data via the REST API. The tokens are permanent. You can have multiple tokens and revoke them at any time

You will be emailed a link to download token as plain text

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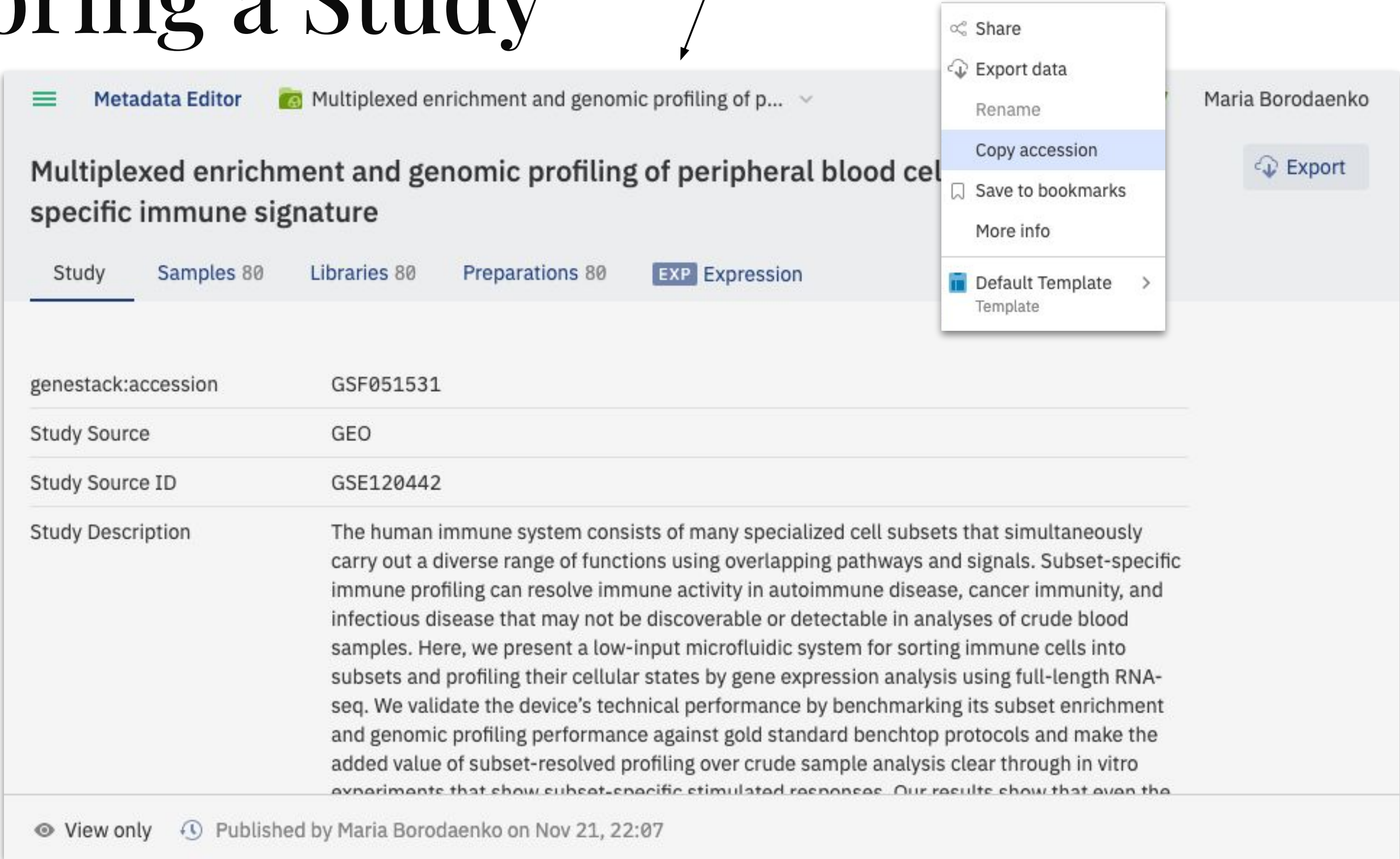
Exploring a Study

Study menu

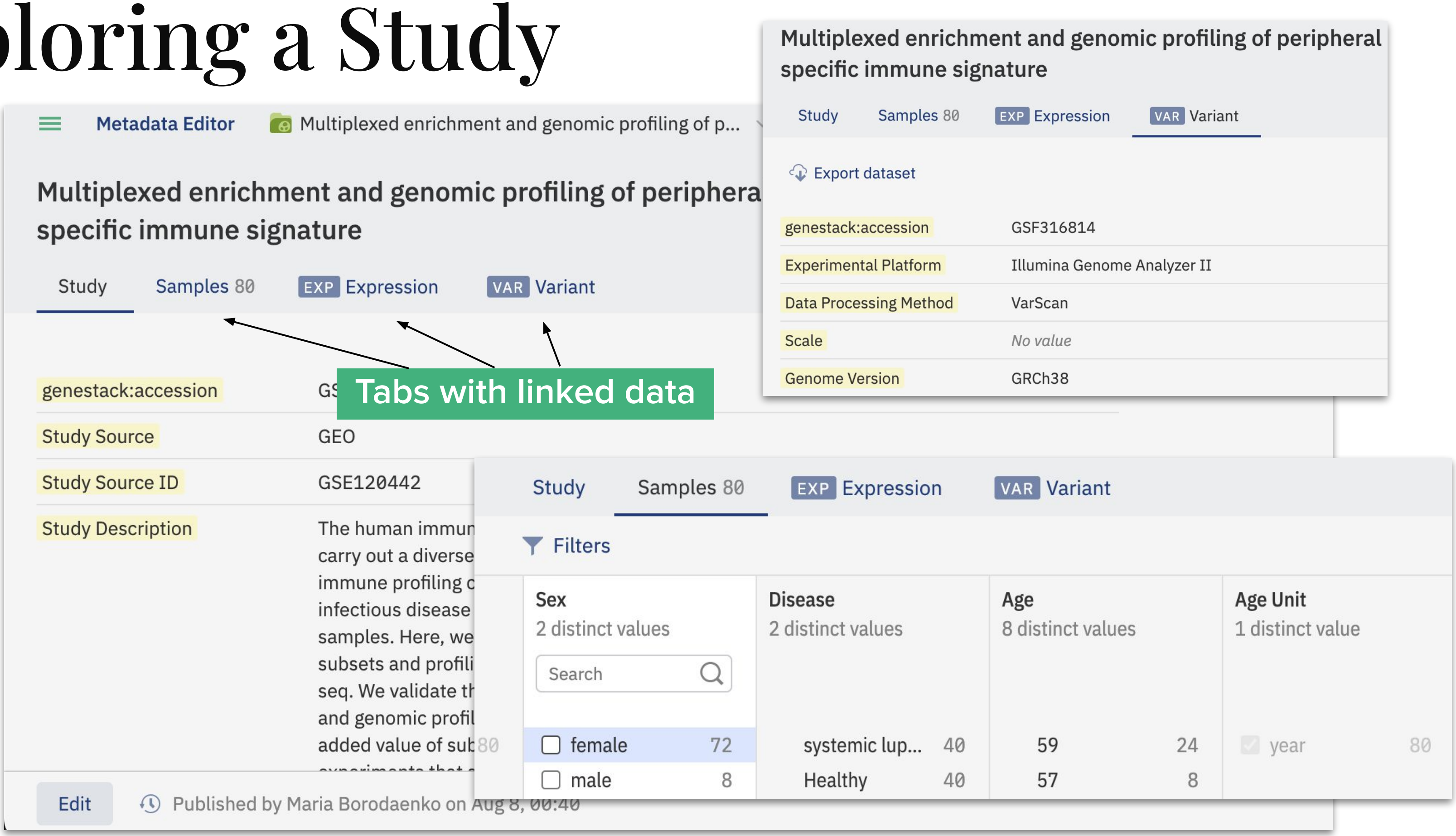


Multiplexed enrichment and genomic profiling of peripheral blood cel specific immune signature

genestack:accession	GSF051531
Study Source	GEO
Study Source ID	GSE120442
Study Description	The human immune system consists of many specialized cell subsets that simultaneously carry out a diverse range of functions using overlapping pathways and signals. Subset-specific immune profiling can resolve immune activity in autoimmune disease, cancer immunity, and infectious disease that may not be discoverable or detectable in analyses of crude blood samples. Here, we present a low-input microfluidic system for sorting immune cells into subsets and profiling their cellular states by gene expression analysis using full-length RNA-seq. We validate the device's technical performance by benchmarking its subset enrichment and genomic profiling performance against gold standard benchtop protocols and make the added value of subset-resolved profiling over crude sample analysis clear through in vitro

Published by Maria Borodaenko on Nov 21, 22:07

Exploring a Study



Multiplexed enrichment and genomic profiling of periphera
specific immune signature

Study | Samples 80 | EXP Expression | VAR Variant

Tabs with linked data

genestack:accession	GS
Study Source	GEO
Study Source ID	GSE120442
Study Description	The human immun carry out a diverse immune profiling c infectious disease samples. Here, we subsets and profili seq. We validate th and genomic profil added value of sub

Published by Maria Borodaenko on Aug 8, 00:40

Multiplexed enrichment and genomic profiling of peripheral specific immune signature

Study | Samples 80 | EXP Expression | VAR Variant

Export dataset

genestack:accession	GSF316814
Experimental Platform	Illumina Genome Analyzer II
Data Processing Method	VarScan
Scale	*No value*
Genome Version	GRCh38

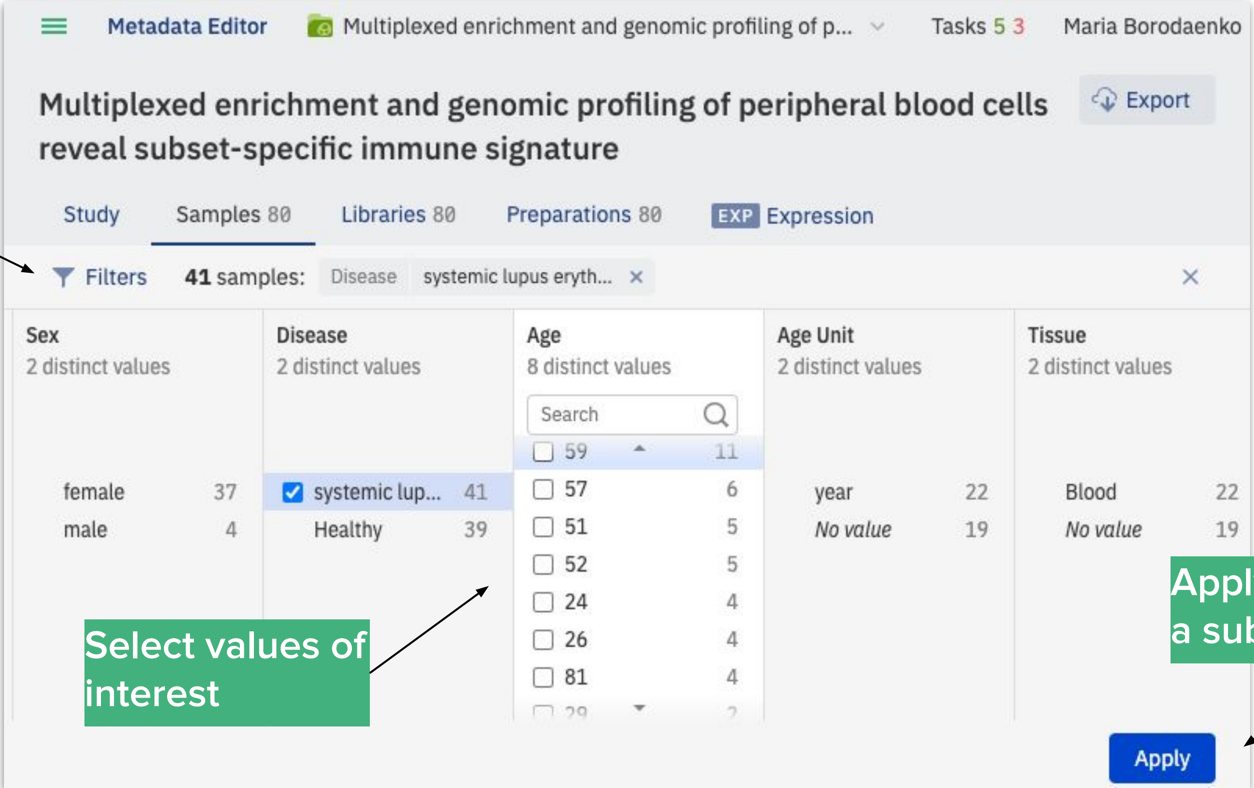
Study | Samples 80 | EXP Expression | VAR Variant

Filters

Sex	Disease	Age	Age Unit
2 distinct values	2 distinct values	8 distinct values	1 distinct value
Search			
☐ female 72	systemic lup... 40	59 24	☑ year 80
☐ male 8	Healthy 40	57 8	

Exploring Sample Filters

Open filters to analyse data



Multiplexed enrichment and genomic profiling of peripheral blood cells reveal subset-specific immune signature

41 samples: Disease systemic lupus eryth... ×

Sex		Disease		Age		Age Unit		Tissue	
2 distinct values		2 distinct values		8 distinct values		2 distinct values		2 distinct values	
				☐ 59	11				
female	37	☑ systemic lup...	41	☐ 57	6	year	22	Blood	22
male	4	Healthy	39	☐ 51	5	*No value*	19	*No value*	19
				☐ 52	5				
				☐ 24	4				
				☐ 26	4				
				☐ 81	4				

Select values of interest

Apply to explore a subset of samples

Study with Multiple Datasets

List of available datasets

Dataset in focus

Experiment's metadata

Multiplexed enrichment and genomic profiling of peripheral blood cells reveal subset-specific immune signature

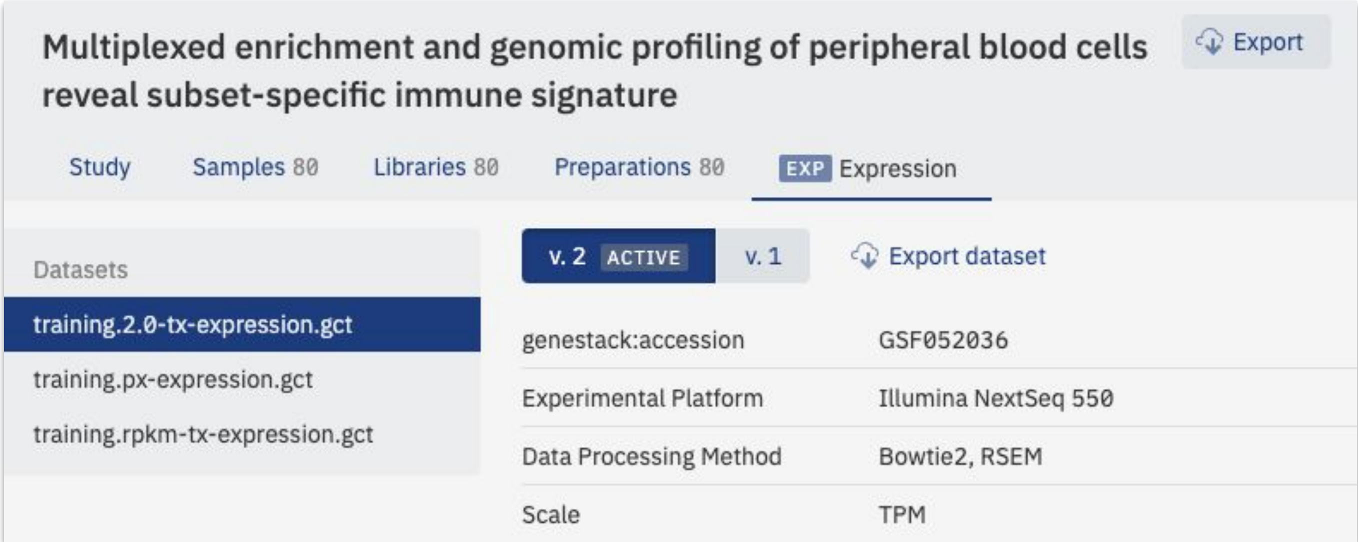
Datasets
- training.2.0-tx-expression.gct
- training.px-expression.gct
- training.rpkm-tx-expression.gct

genestack:accession	GSF051699
Experimental Platform	Illumina NextSeq 550
Data Processing Method	Bowtie2, RSEM
Scale	RPKM
Genome Version	GRCh37
Pipeline ID	*No value*
Data Files / Raw	*No value*

Published by Maria Borodaenko on Nov 21, 22:24

Multiple Versions of The Same Dataset

If few versions of dataset are available, they will be displayed. The latest version is active and focused by default, previous version available for exploring and exporting.

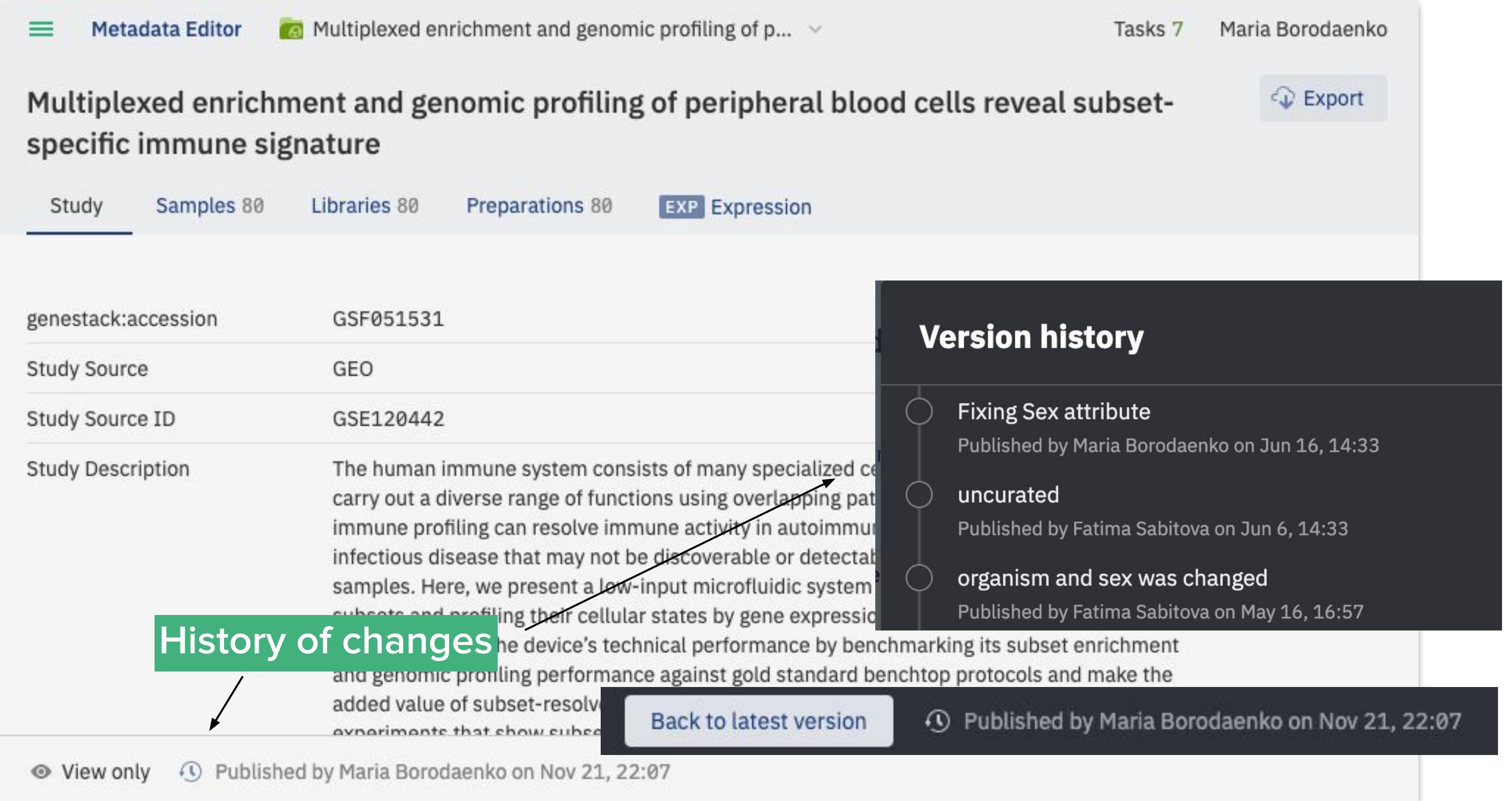


Multiplexed enrichment and genomic profiling of peripheral blood cells reveal subset-specific immune signature

training.2.0-tx-expression.gct
training.px-expression.gct
training.rpkm-tx-expression.gct

genestack:accession	GSF052036
Experimental Platform	Illumina NextSeq 550
Data Processing Method	Bowtie2, RSEM
Scale	TPM

Version History



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Published by Maria Borodaenko on Nov 21, 22:07

Version history

- Fixing Sex attribute
  Published by Maria Borodaenko on Jun 16, 14:33
- uncurated
  Published by Fatima Sabitova on Jun 6, 14:33
- organism and sex was changed
  Published by Fatima Sabitova on May 16, 16:57

Published by Maria Borodaenko on Nov 21, 22:07

Training Plan

- Getting started
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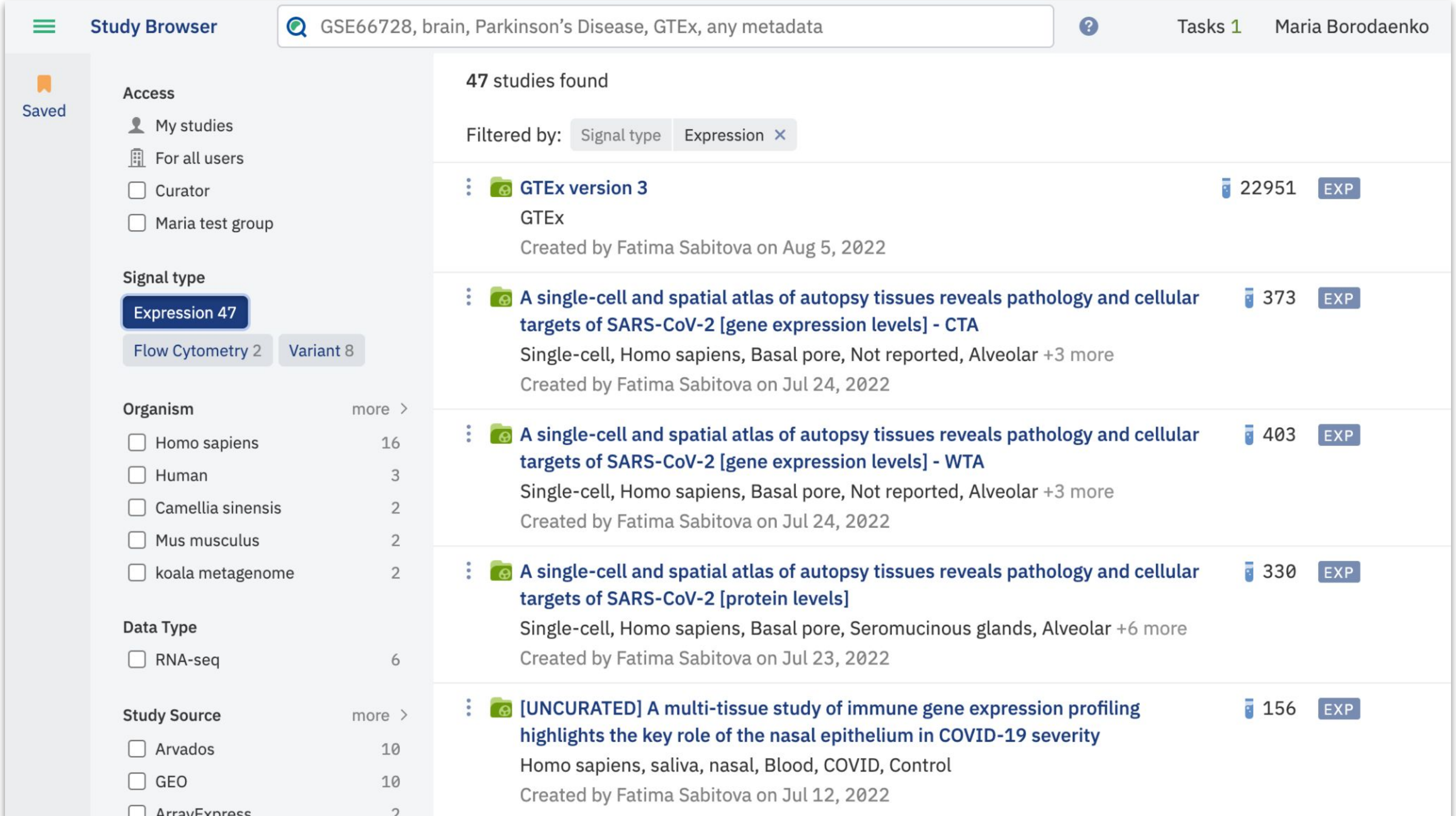
Searching for Available Data



Access
- My studies
- For all users
- ☐ Curator
- ☐ Maria test group

Signal type
- Expression 47
- Flow Cytometry 2
- Variant 8

Organism (more >)

☐ Homo sapiens	16
☐ Human	3
☐ Camellia sinensis	2
☐ Mus musculus	2
☐ koala metagenome	2

Data Type

☐ RNA-seq	6

Study Source (more >)

☐ Arvados	10
☐ GEO	10
☐ ArrayExpress	2

47 studies found

Filtered by: Signal type Expression ×

GTEx version 3 — 22951 EXP
GTEx
Created by Fatima Sabitova on Aug 5, 2022

A single-cell and spatial atlas of autopsy tissues reveals pathology and cellular targets of SARS-CoV-2 [gene expression levels] - CTA — 373 EXP
Single-cell, Homo sapiens, Basal pore, Not reported, Alveolar +3 more
Created by Fatima Sabitova on Jul 24, 2022

A single-cell and spatial atlas of autopsy tissues reveals pathology and cellular targets of SARS-CoV-2 [gene expression levels] - WTA — 403 EXP
Single-cell, Homo sapiens, Basal pore, Not reported, Alveolar +3 more
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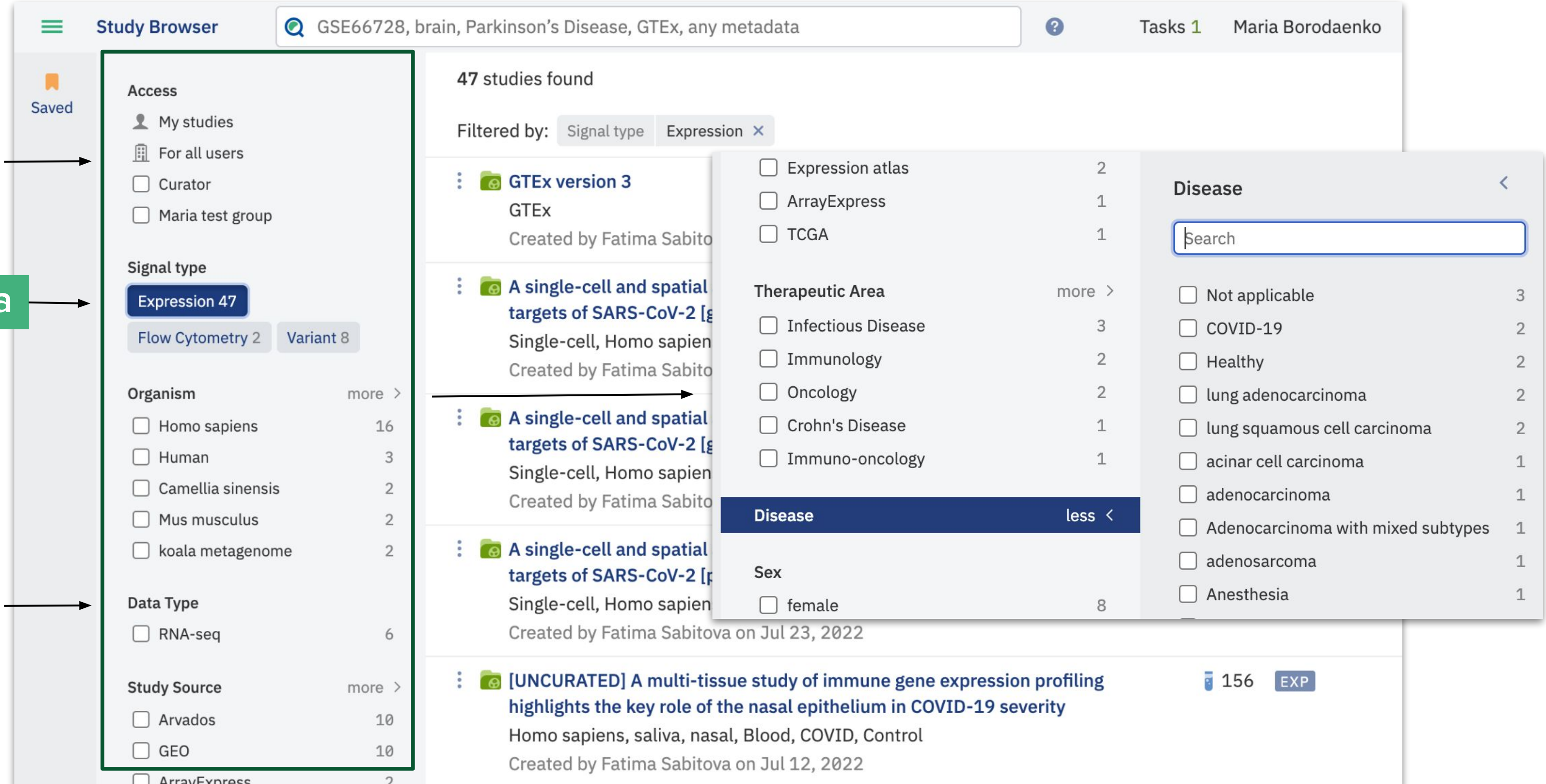
A single-cell and spatial atlas of autopsy tissues reveals pathology and cellular targets of SARS-CoV-2 [protein levels] — 330 EXP
Single-cell, Homo sapiens, Basal pore, Seromucinous glands, Alveolar +6 more
Created by Fatima Sabitova on Jul 23, 2022

[UNCURATED] A multi-tissue study of immune gene expression profiling highlights the key role of the nasal epithelium in COVID-19 severity — 156 EXP
Homo sapiens, saliva, nasal, Blood, COVID, Control
Created by Fatima Sabitova on Jul 12, 2022

Faceted Search



Access

Linked data

Metadata

Study Browser

GSE66728, brain, Parkinson's Disease, GTEx, any metadata

Tasks 1 Maria Borodaenko

Saved

Access
- My studies
- For all users
- ☐ Curator
- ☐ Maria test group

Signal type

Expression 47 | Flow Cytometry 2 | Variant 8

Organism more

☐ Homo sapiens	16
☐ Human	3
☐ Camellia sinensis	2
☐ Mus musculus	2
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Data Type

☐ RNA-seq	6

Study Source more

☐ Arvados	10
☐ GEO	10
☐ ArrayExpress	2

47 studies found

Filtered by: Signal type Expression ×

GTEx version 3
GTEx
Created by Fatima Sabito

A single-cell and spatial
targets of SARS-CoV-2 [g
Single-cell, Homo sapien
Created by Fatima Sabito

A single-cell and spatial
targets of SARS-CoV-2 [g
Single-cell, Homo sapien
Created by Fatima Sabito

A single-cell and spatial
targets of SARS-CoV-2 [p
Single-cell, Homo sapien
Created by Fatima Sabitova on Jul 23, 2022

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Homo sapiens, saliva, nasal, Blood, COVID, Control
Created by Fatima Sabitova on Jul 12, 2022

☐ Expression atlas	2
☐ ArrayExpress	1
☐ TCGA	1

Therapeutic Area more

☐ Infectious Disease	3
☐ Immunology	2
☐ Oncology	2
☐ Crohn's Disease	1
☐ Immuno-oncology	1

Disease less

Sex

☐ female	8

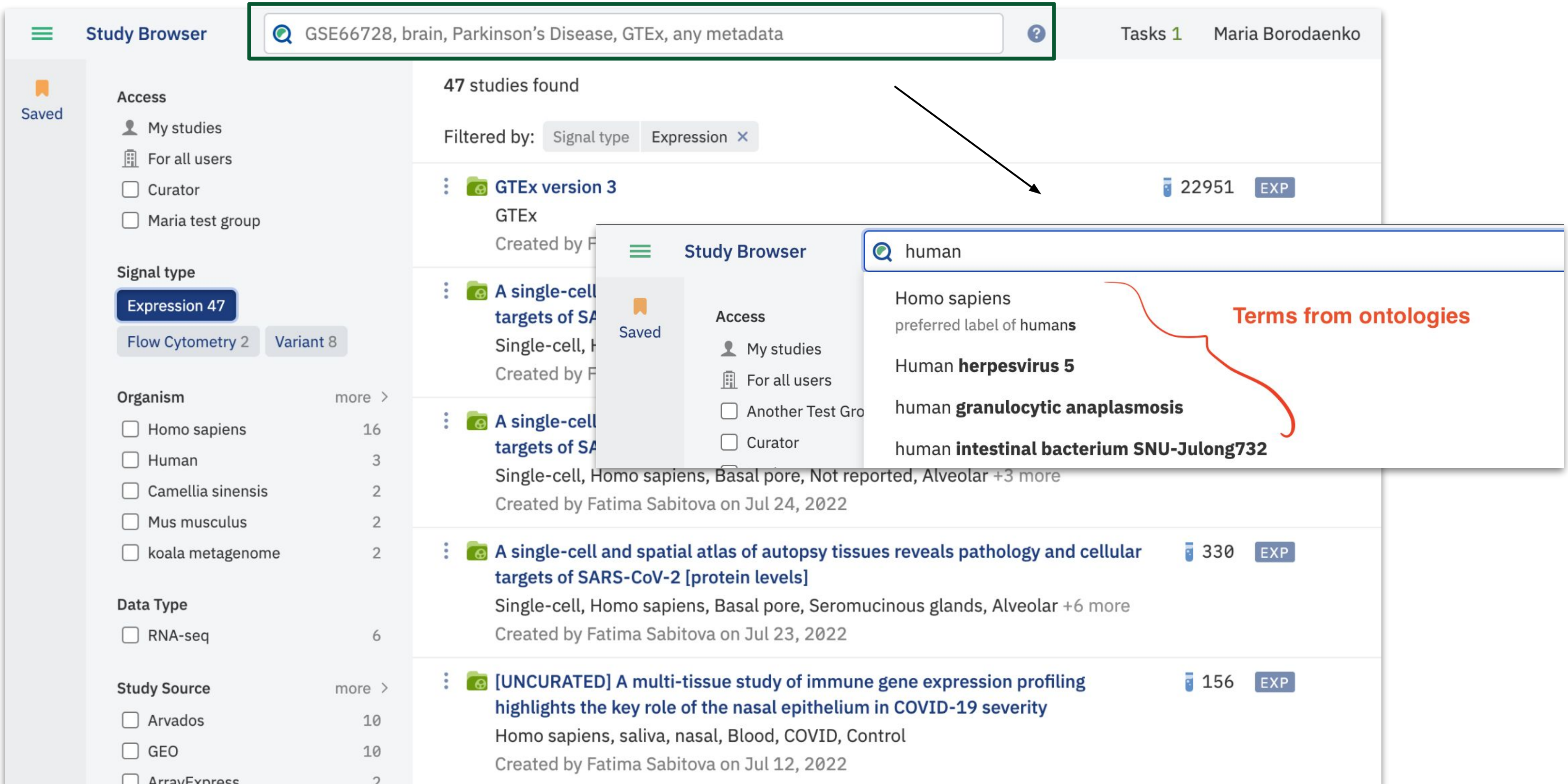
Disease

Search

☐ Not applicable	3
☐ COVID-19	2
☐ Healthy	2
☐ lung adenocarcinoma	2
☐ lung squamous cell carcinoma	2
☐ acinar cell carcinoma	1
☐ adenocarcinoma	1
☐ Adenocarcinoma with mixed subtypes	1
☐ adenosarcoma	1
☐ Anesthesia	1

Genestack

Full-Text Search



Access
- My studies
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Signal type
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Organism (more)

☐ Homo sapiens	16
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☐ Mus musculus	2
☐ koala metagenome	2

Data Type

☐ RNA-seq	6

Study Source (more)

☐ Arvados	10
☐ GEO	10
☐ ArrayExpress	2

47 studies found

Filtered by: Signal type Expression ✕

GTEx version 3 — 22951 EXP
GTEx
Created by F

A single-cell … targets of SA
Single-cell, H
Created by F

A single-cell … targets of SA
Single-cell, Homo sapiens, Basal pore, Not reported, Alveolar +3 more
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Homo sapiens, saliva, nasal, Blood, COVID, Control
Created by Fatima Sabitova on Jul 12, 2022

Homo sapiens
preferred label of **humans**

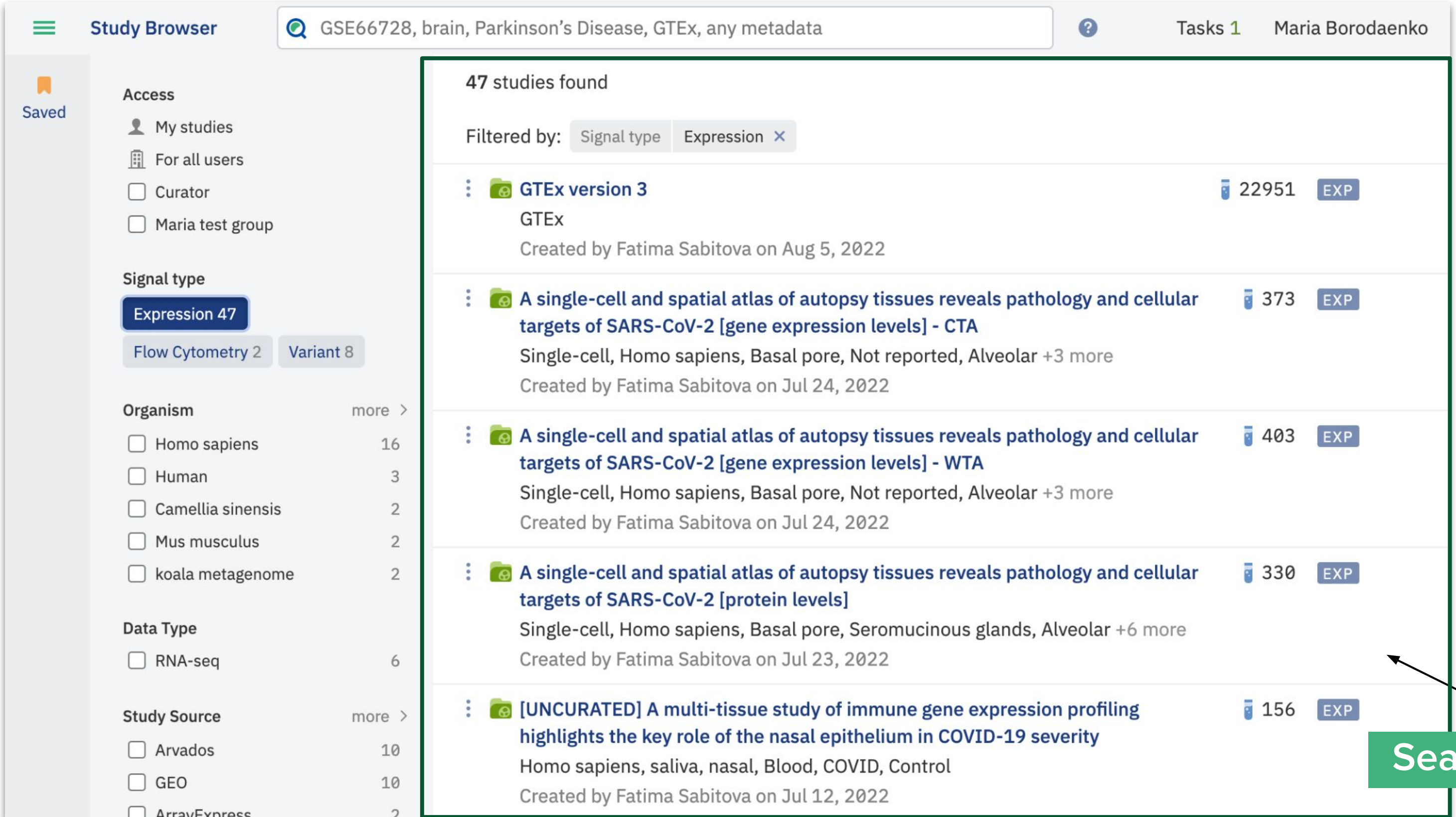
Human **herpesvirus 5**

human **granulocytic anaplasmosis**

human **intestinal bacterium SNU-Julong732**

Terms from ontologies

Search Results



47 studies found

Filtered by: Signal type: Expression ×

GTEx version 3 — 22951 — EXP
GTEx
Created by Fatima Sabitova on Aug 5, 2022

A single-cell and spatial atlas of autopsy tissues reveals pathology and cellular targets of SARS-CoV-2 [gene expression levels] - CTA — 373 — EXP
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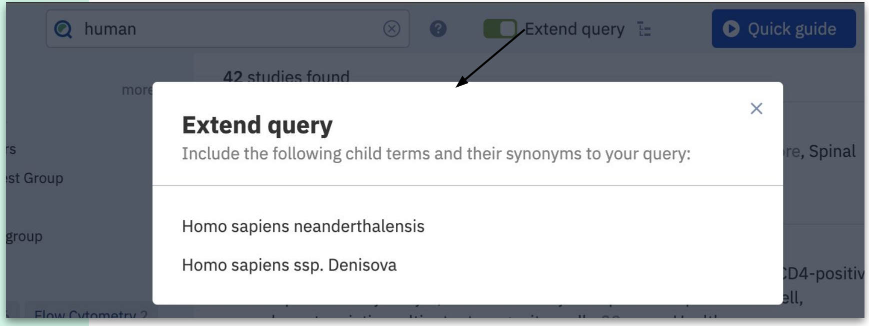
Homo sapiens, saliva, nasal, Blood, COVID, Control
Created by Fatima Sabitova on Jul 12, 2022

Search results

Advanced Search Capabilities

The query can be extended based to include child terms from the ontology



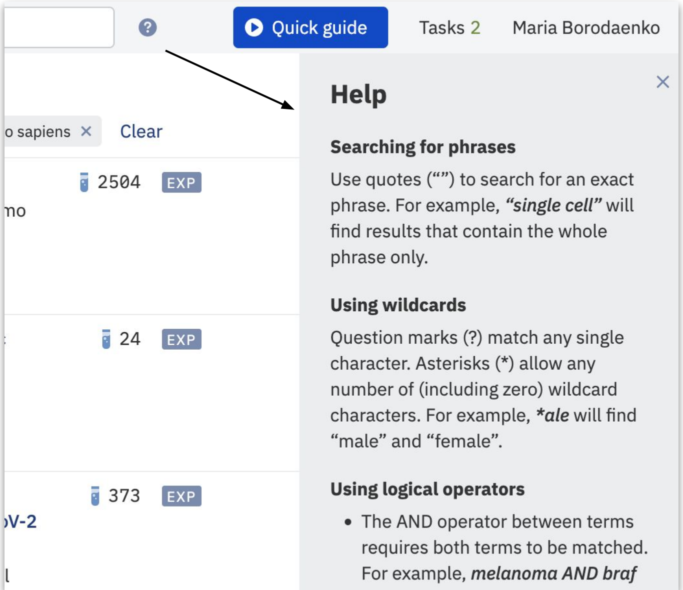
Extend query

Include the following child terms and their synonyms to your query:

Homo sapiens neanderthalensis

Homo sapiens ssp. Denisova

Help button for using logical operators, wildcards and more



Help

Searching for phrases

Use quotes (“”) to search for an exact phrase. For example, ***“single cell”*** will find results that contain the whole phrase only.

Using wildcards

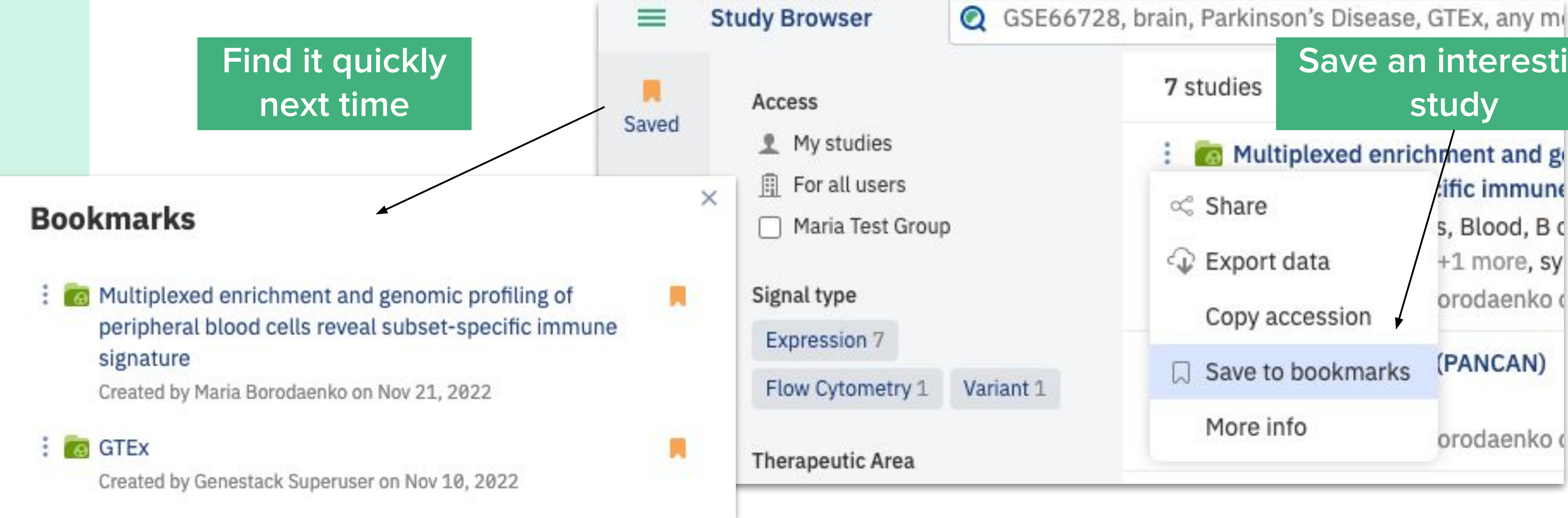
Question marks (?) match any single character. Asterisks (*) allow any number of (including zero) wildcard characters. For example, ***ale** will find “male” and “female”.

Using logical operators

- The AND operator between terms requires both terms to be matched. For example, ***melanoma AND braf***

Bookmarks

In case you have some studies which you regularly work with, it could be easier and faster to find them among bookmarks.



Find it quickly next time

Save an interesting study

Bookmarks

Multiplexed enrichment and genomic profiling of peripheral blood cells reveal subset-specific immune signature
Created by Maria Borodaenko on Nov 21, 2022

GTEx
Created by Genestack Superuser on Nov 10, 2022

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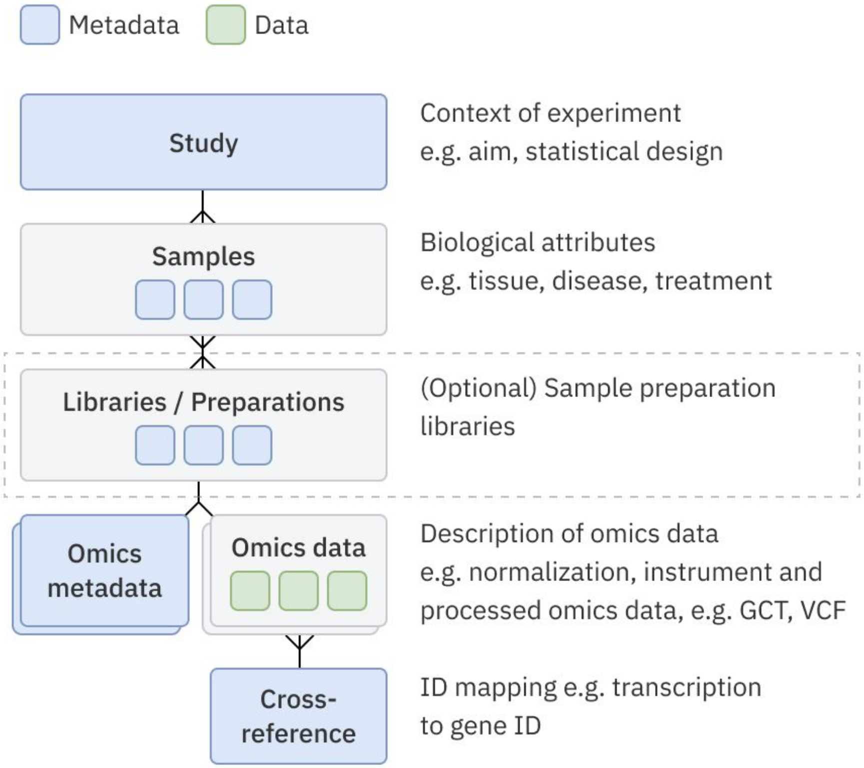
Data Model and Supported formats



🟦 Metadata 🟩 Data

Study – Context of experiment e.g. aim, statistical design

Samples – Biological attributes e.g. tissue, disease, treatment

Libraries / Preparations – (Optional) Sample preparation libraries

Omics metadata, **Omics data** – Description of omics data e.g. normalization, instrument and processed omics data, e.g. GCT, VCF

Cross-reference – ID mapping e.g. transcription to gene ID

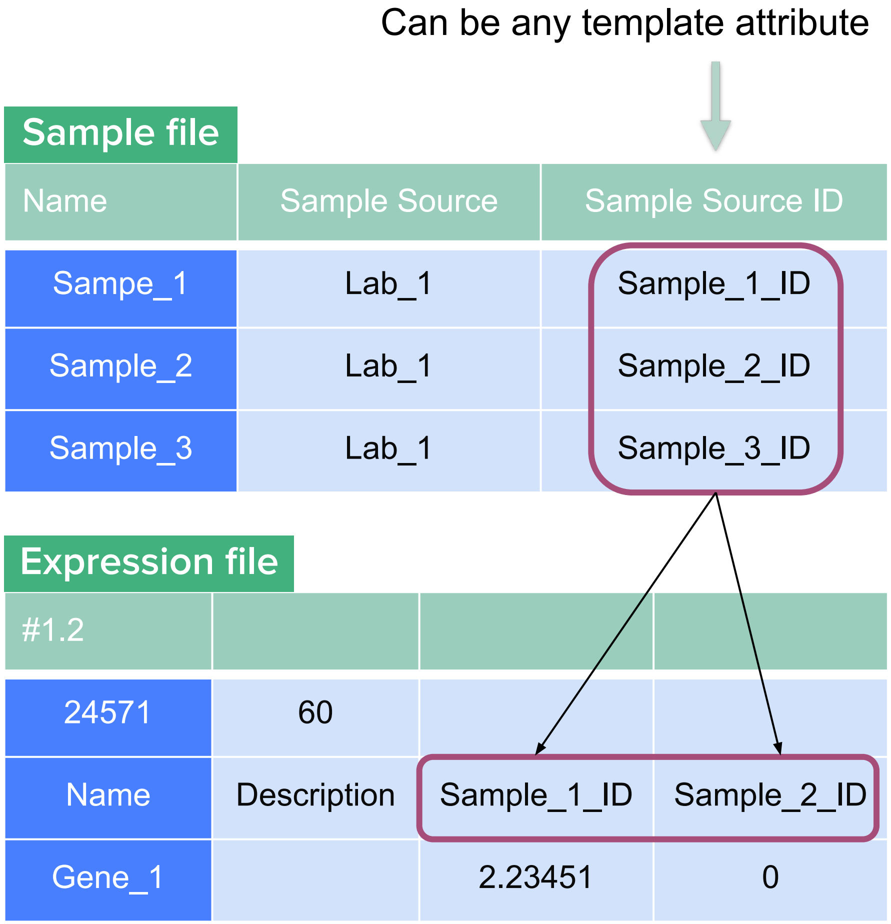
Import	GUI	Python Script
Study	Manual	TSV
Samples	Manual or TSV import	TSV
Libraries / Preparations (optional)	✗	TSV
Omics metadata	✗	TSV
Omics data	✗	GCT, VCF, FACS

Linking Attributes

Headers in the expression file should correspond to sample metadata so the system recognise what column relates to what sample.

During import user can specify which attribute from the template should be used for linking during import.

If nothing is specified the “Sample Source ID” attribute is used.



Can be any template attribute

Sample file

Name	Sample Source	Sample Source ID
Sampe_1	Lab_1	Sample_1_ID
Sample_2	Lab_1	Sample_2_ID
Sample_3	Lab_1	Sample_3_ID

Expression file

#1.2			
24571	60		
Name	Description	Sample_1_ID	Sample_2_ID
Gene_1		2.23451	0

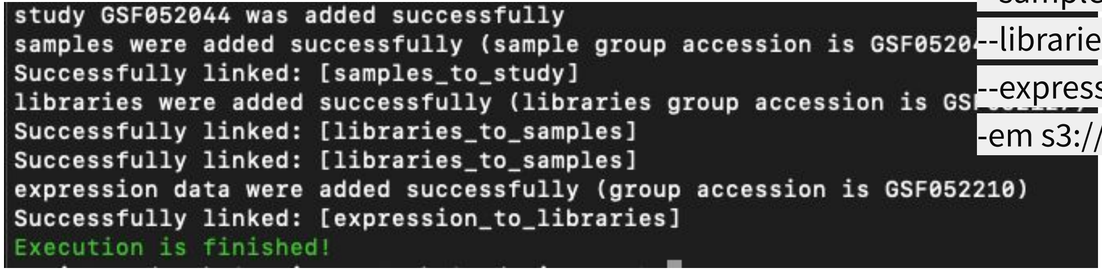
Data Loading via Script

During study import a study itself and associated data objects are created sequentially and linked to each other based on the data model.

This is done by the import data script which calls REST APIs. The user should be a curator and should provide an access token, links to the files and the server address. More details about the parameters can be found in the script’s help.

Example command

```
python3 import_ODM_data.py \
--token YOUR_TOKEN \
--server YOUR_SERVER \
--study s3://data_source/study.tsv \
--samples s3://data_source/samples.tsv \
--libraries s3://data_source/libraries.tsv \
--expression s3://data_source/expression.gct \
-em s3://data_source/expression.gct.tsv
```



```
study GSF052044 was added successfully
samples were added successfully (sample group accession is GSF0520
Successfully linked: [samples_to_study]
libraries were added successfully (libraries group accession is GS
Successfully linked: [libraries_to_samples]
Successfully linked: [libraries_to_samples]
expression data were added successfully (group accession is GSF052210)
Successfully linked: [expression_to_libraries]
Execution is finished!
```

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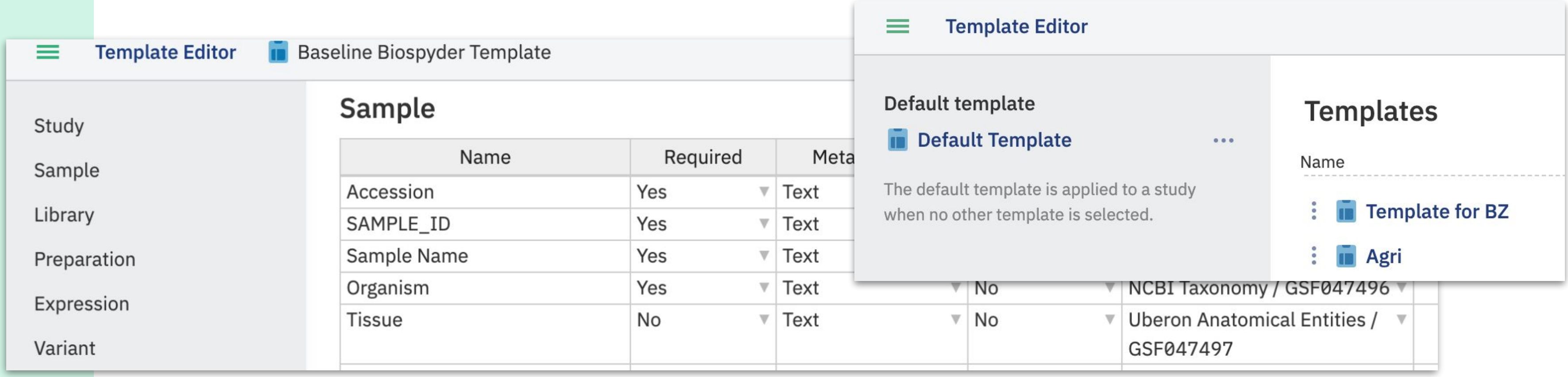
- **Metadata templates**
- Metadata curation
- Access to studies
- Study export
- Study deletion

Metadata Templates

For effective metadata curation the Templates are used. Template are set by users with “Manage templates” permission in Template Editor.

They describe the attributes and select ontologies for metadata validation. There could be more than 1 template on the instance to have set of attributes specific to a study type. The default template can be set.



Sample

Name	Required	Meta		
Accession	Yes	Text		
SAMPLE_ID	Yes	Text		
Sample Name	Yes	Text		
Organism	Yes	Text	No	NCBI Taxonomy / GSF047496
Tissue	No	Text	No	Uberon Anatomical Entities / GSF047497

Default template

Default Template

The default template is applied to a study when no other template is selected.

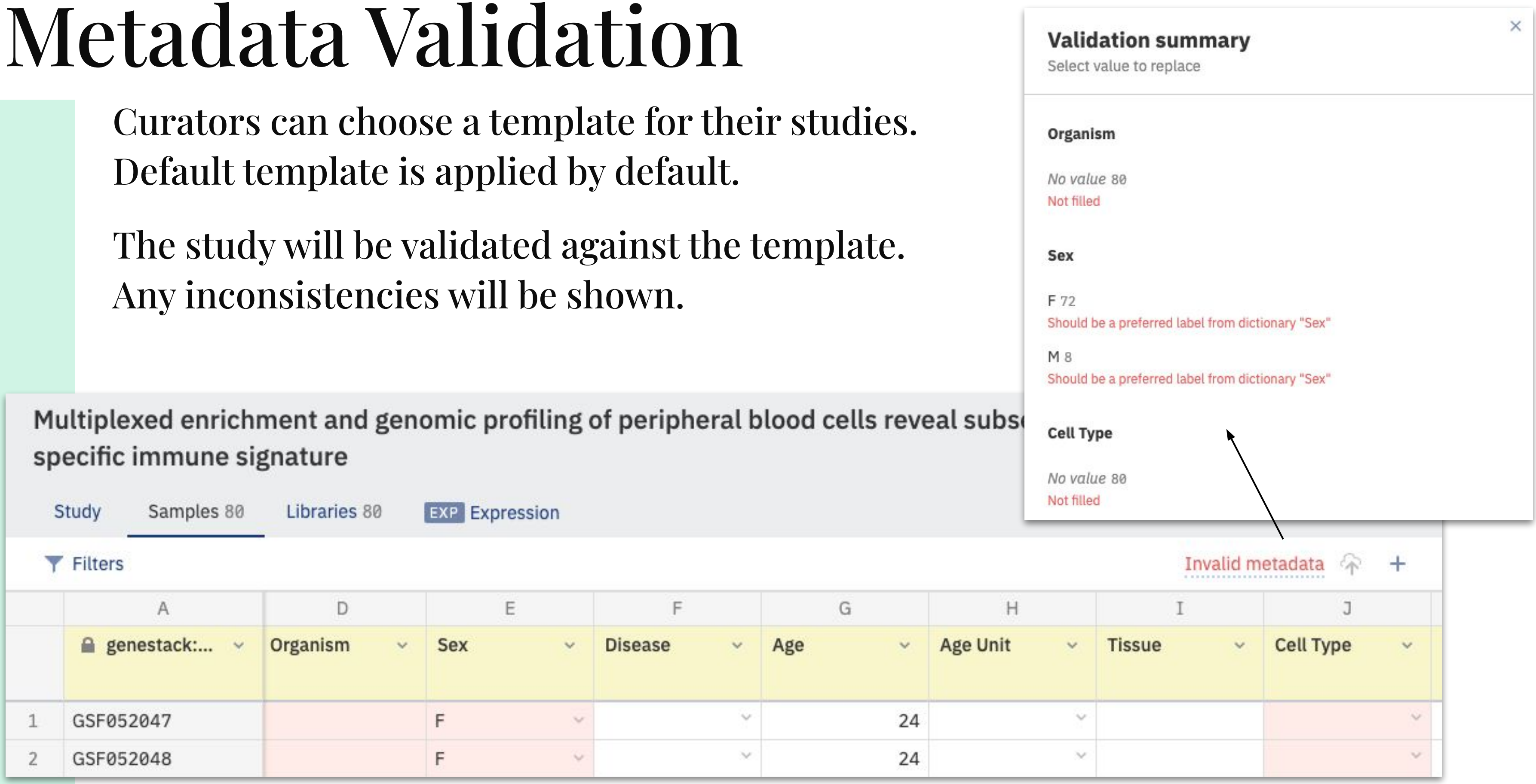
Templates

Name
Template for BZ
Agri

Metadata Validation

Curators can choose a template for their studies.
Default template is applied by default.

The study will be validated against the template.
Any inconsistencies will be shown.



Validation summary
Select value to replace

Organism

No value 80
Not filled

Sex

F 72
Should be a preferred label from dictionary "Sex"

M 8
Should be a preferred label from dictionary "Sex"

Cell Type

No value 80
Not filled

Multiplexed enrichment and genomic profiling of peripheral blood cells reveal subs
specific immune signature

	A	D	E	F	G	H	I	J
	genestack:...	Organism	Sex	Disease	Age	Age Unit	Tissue	Cell Type
1	GSF052047		F		24			
2	GSF052048		F		24			

Required Templates Attributes

There are a few attributes required by the system. These attributes should be presented in any template to allow ODM work properly. The following attributes should not be removed from the attribute or altered in spelling.

ATTRIBUTE	ENTITY	COMMENT
“Accession”	All entities	Mandatory for the template. Without these attributes the users will get errors upon opening a study in the GUI
“Study Title”	Study	
“Sample Source ID” (or alternative linking attribute)	Samples	Linking attribute should present in the template for proper linkage

Training Plan

- Getting started
- Exploring a Study in Metadata Editor
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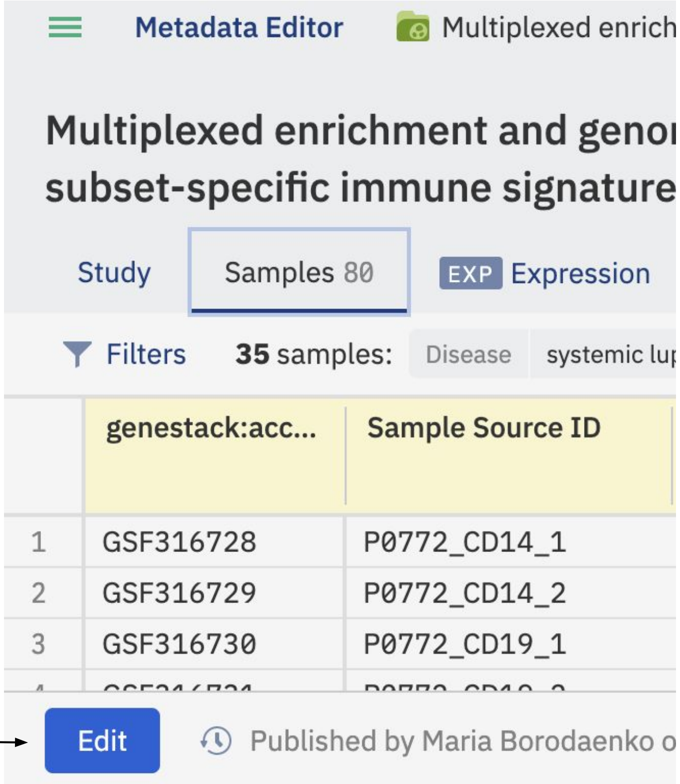
Metadata Curation

For curating metadata one should be a member of the Curator group.

The studies is opened in a view mode, to check validation and to apply changes the curator should switch to the Edit mode.

Changes made in the Edit mode are available for other curators but they are not seen by the researcher.



Multiplexed enrichment and genor
subset-specific immune signature

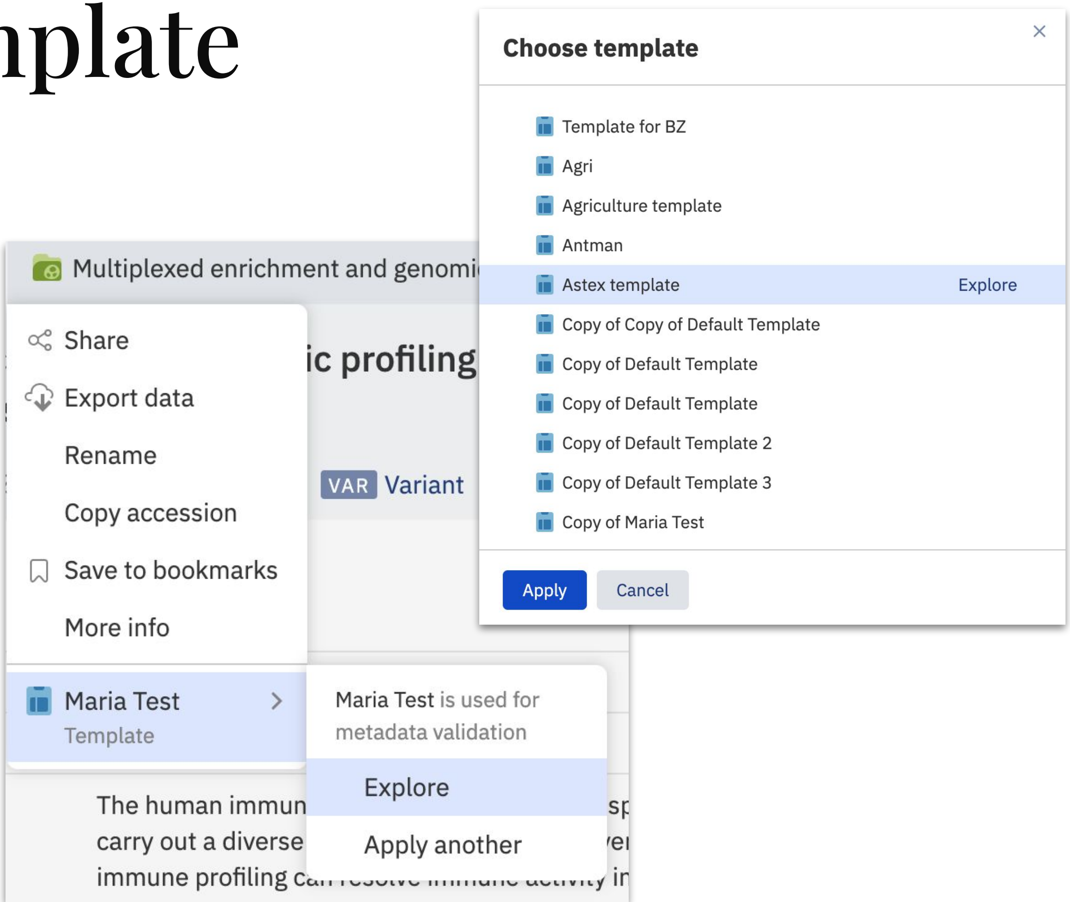
	genestack:acc...	Sample Source ID
1	GSF316728	P0772_CD14_1
2	GSF316729	P0772_CD14_2
3	GSF316730	P0772_CD19_1

Start curation →

Changing a Template

Prior to curating a study it is better to verify that the proper template is used.

The applied template is available in the study menu. It can be explored and changed if needed.

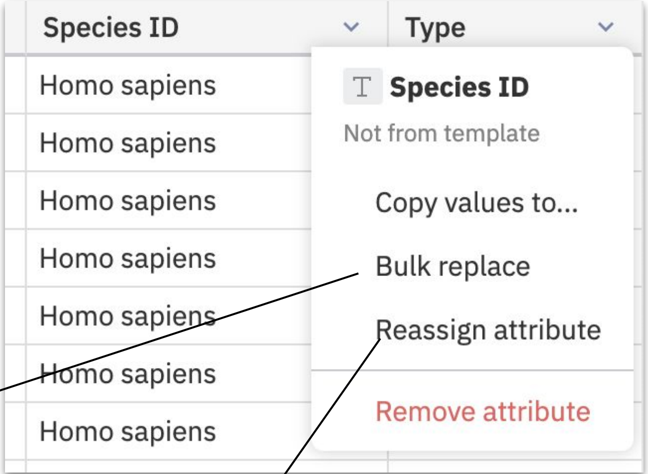


Maria Test is used for metadata validation

The human immun
carry out a diverse
immune profiling ca

Metadata Curation

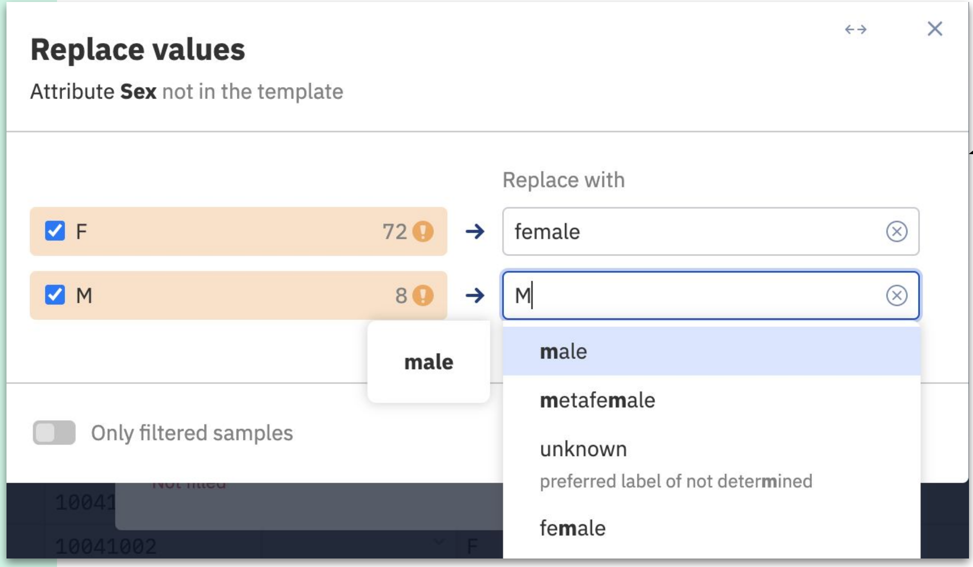
Curators can bulk replace values and reassign attributes to make metadata valid.



Species ID	Type
Homo sapiens	
Homo sapiens	
Homo sapiens	
Homo sapiens	
Homo sapiens	
Homo sapiens	
Homo sapiens	

Species ID

Not from template



Replace values

Attribute **Sex** not in the template

		Replace with
☑ F	72	female
☑ M	8	M

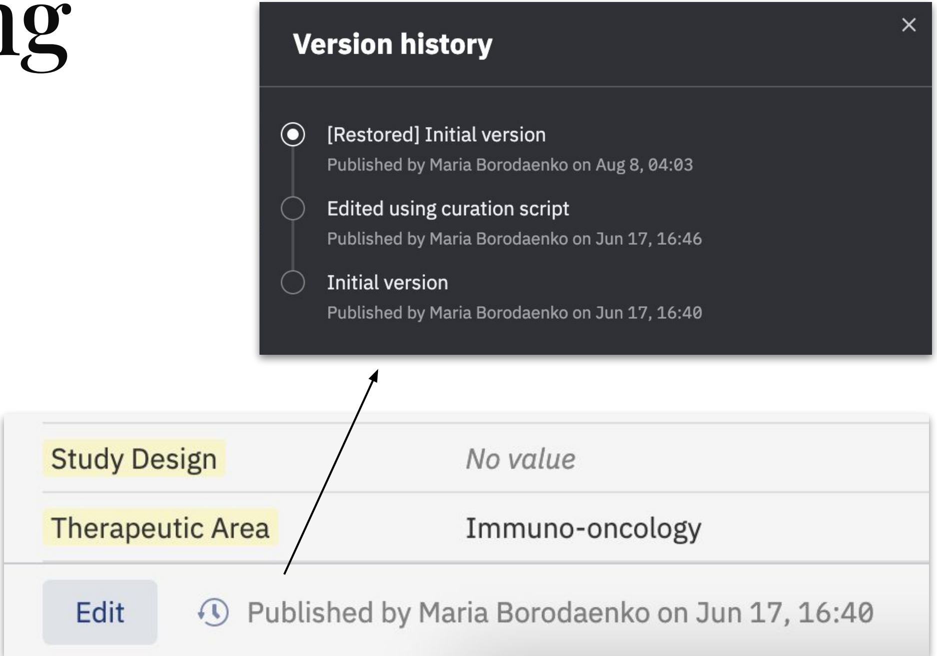
Reassign attribute

Species ID to

Organism

Metadata Versioning

- Once the changes are made study should be published.
- The history of published versions is available for each study.
- Any of previous version can be viewed and restored.



Version history

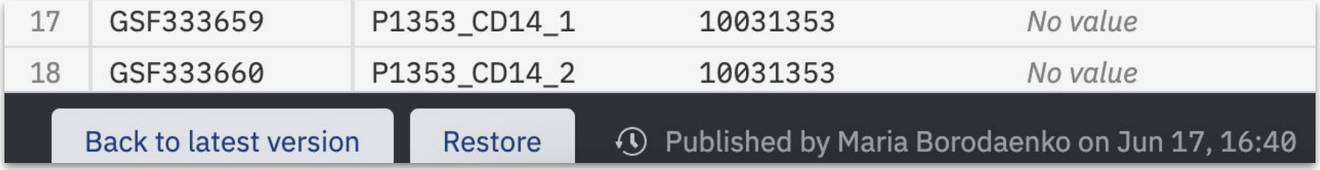
● [Restored] Initial version
Published by Maria Borodaenko on Aug 8, 04:03

○ Edited using curation script
Published by Maria Borodaenko on Jun 17, 16:46

○ Initial version
Published by Maria Borodaenko on Jun 17, 16:40

Study Design	*No value*
Therapeutic Area	Immuno-oncology

Published by Maria Borodaenko on Jun 17, 16:40



17	GSF333659	P1353_CD14_1	10031353	*No value*
18	GSF333660	P1353_CD14_2	10031353	*No value*

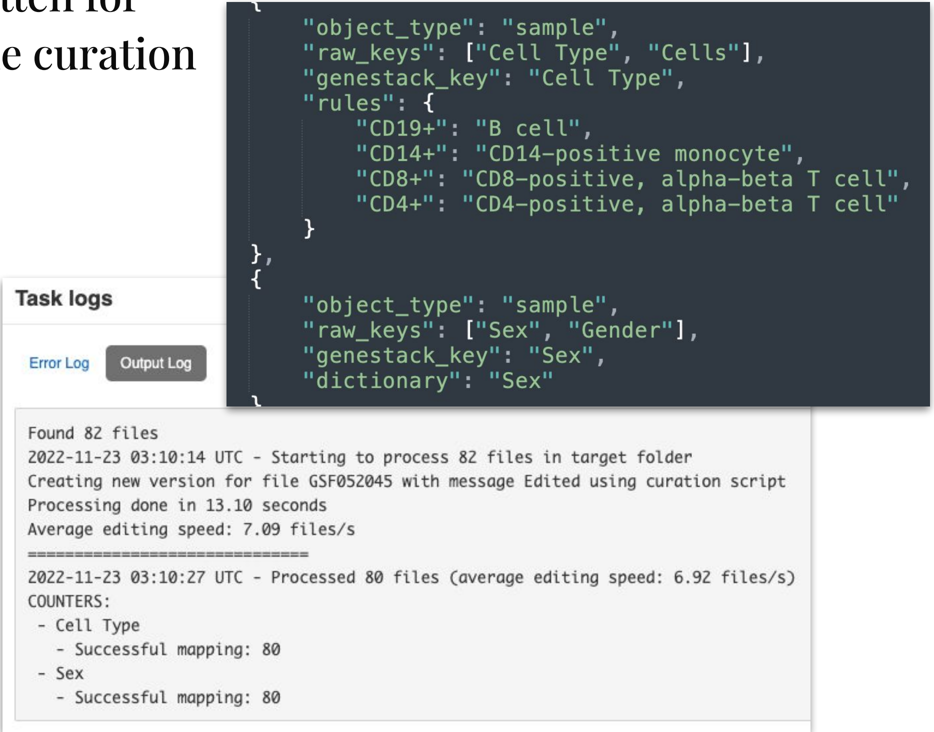
Published by Maria Borodaenko on Jun 17, 16:40

Curation Script

Curation script is a python script written for automating frequent operations in the curation process.

The main purpose of the script is to facilitate the curation process, reduce manual operations and reduce errors in metadata curation.

The script could be run on a particular study(ies). Changes done by the script are regulated by JSON file with predefined rules.



```
        "object_type": "sample",
        "raw_keys": ["Cell Type", "Cells"],
        "genestack_key": "Cell Type",
        "rules": {
            "CD19+": "B cell",
            "CD14+": "CD14-positive monocyte",
            "CD8+": "CD8-positive, alpha-beta T cell",
            "CD4+": "CD4-positive, alpha-beta T cell"
        }
    },
    {
        "object_type": "sample",
        "raw_keys": ["Sex", "Gender"],
        "genestack_key": "Sex",
        "dictionary": "Sex"
```

```
Found 82 files
2022-11-23 03:10:14 UTC - Starting to process 82 files in target folder
Creating new version for file GSF052045 with message Edited using curation script
Processing done in 13.10 seconds
Average editing speed: 7.09 files/s
==============================
2022-11-23 03:10:27 UTC - Processed 80 files (average editing speed: 6.92 files/s)
COUNTERS:
 - Cell Type
   - Successful mapping: 80
 - Sex
   - Successful mapping: 80
```

Training Plan

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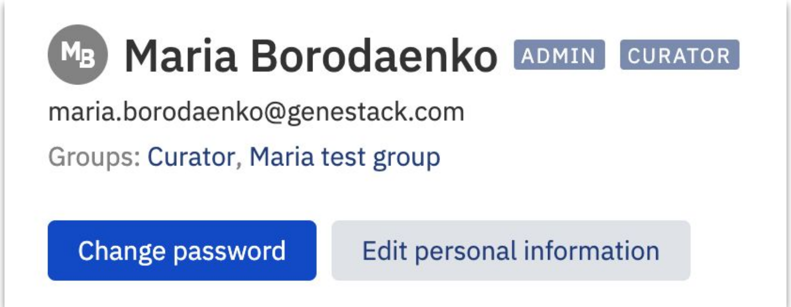
- Metadata curation
- **Access to studies**

- Study export
- Study deletion

Access to Studies

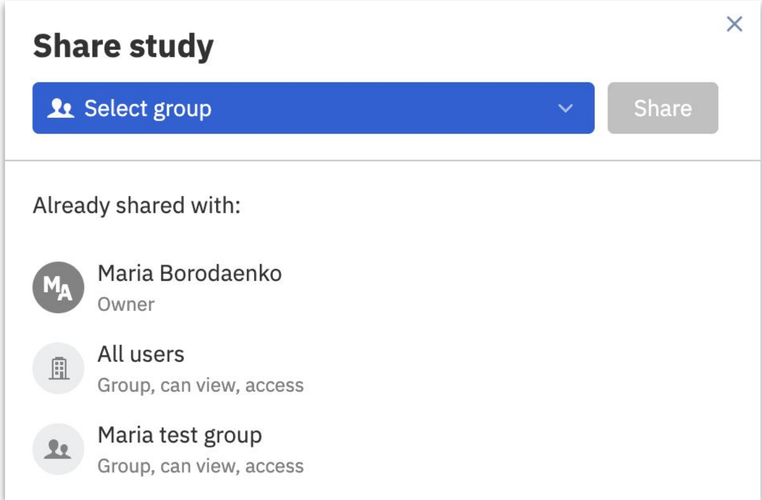
- The list of groups available in your profile.
- Curator group is a special group granting edit permissions.
- You can share your study with any group you are a member of.
- You can view with which groups a study is shared.



Maria Borodaenko

maria.borodaenko@genestack.com

Groups: Curator, Maria test group



Share study

Already shared with:

Maria Borodaenko
Owner

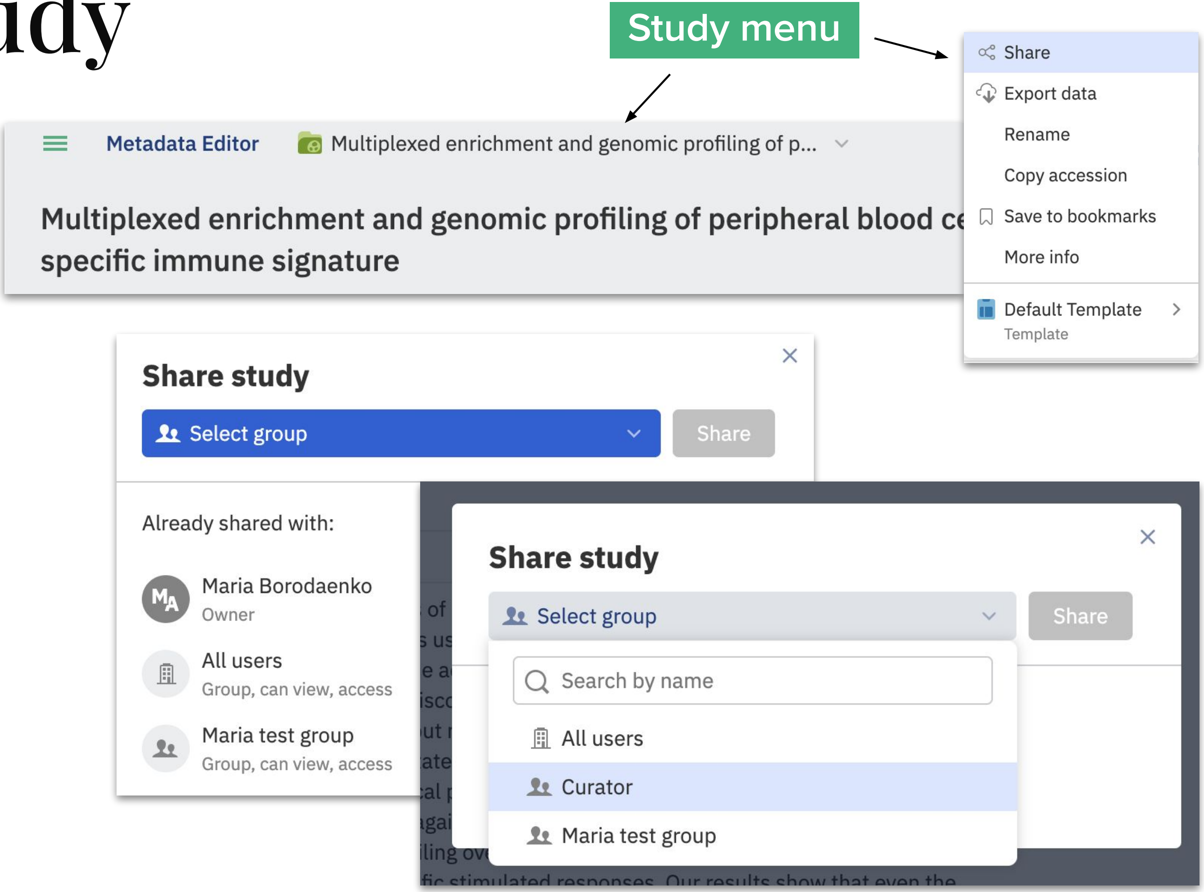
All users
Group, can view, access

Maria test group
Group, can view, access

Sharing a Study

To share a study user should be the owner of a study - the one who created it in ODM.

Share option is available in the Study menu.



Training Plan

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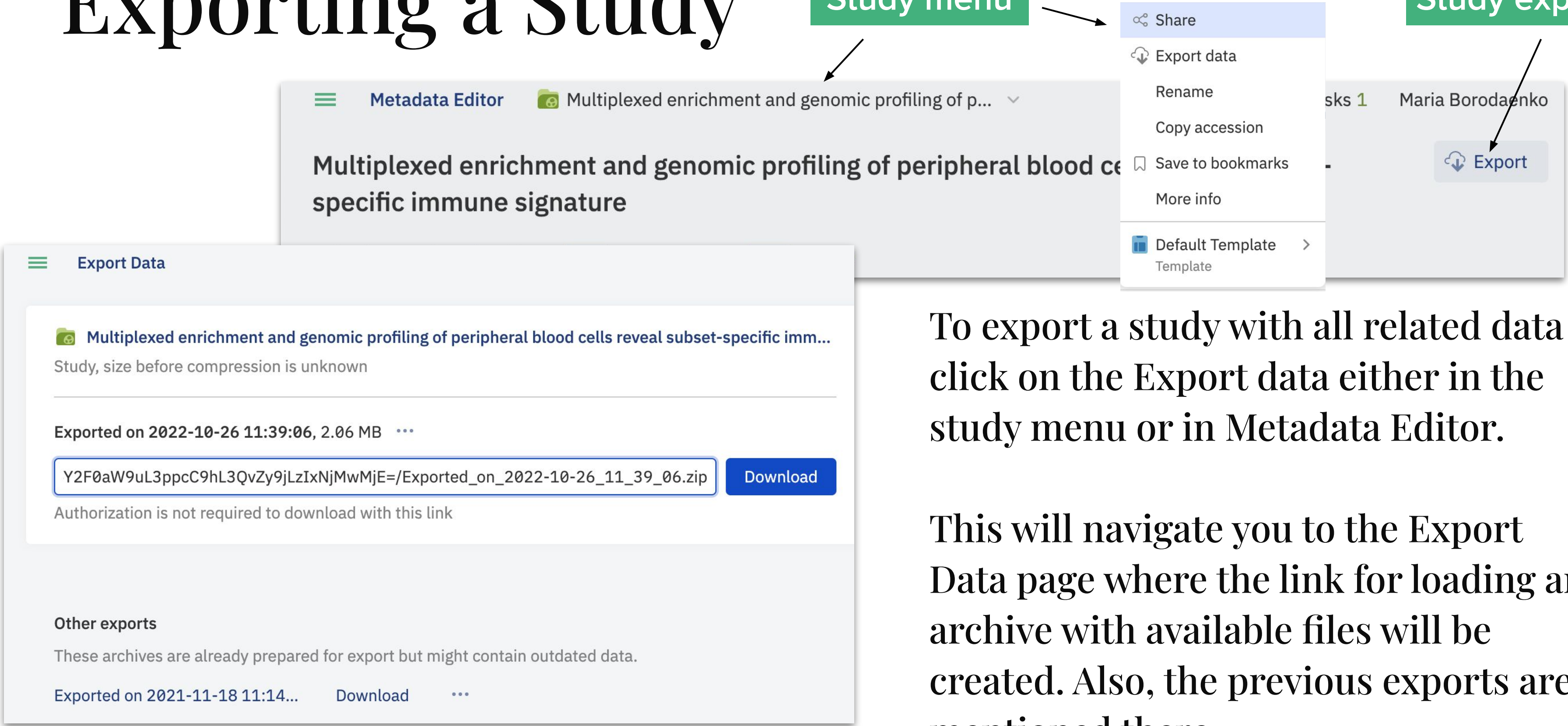
Exporting a Study

Study menu

Study export



Multiplexed enrichment and genomic profiling of peripheral blood ce... specific immune signature

Multiplexed enrichment and genomic profiling of peripheral blood cells reveal subset-specific imm...

Study, size before compression is unknown

Exported on 2022-10-26 11:39:06, 2.06 MB ···

Y2F0aW9uL3ppcC9hL3QvZy9jLzIxNjMwMjE=/Exported_on_2022-10-26_11_39_06.zip

Authorization is not required to download with this link

These archives are already prepared for export but might contain outdated data.

Exported on 2021-11-18 11:14... Download ···

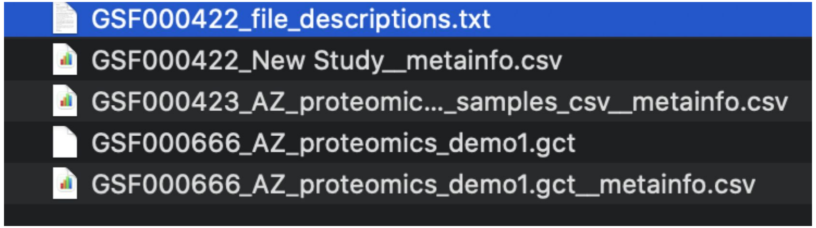
To export a study with all related data click on the Export data either in the study menu or in Metadata Editor.

This will navigate you to the Export Data page where the link for loading an archive with available files will be created. Also, the previous exports are mentioned there.

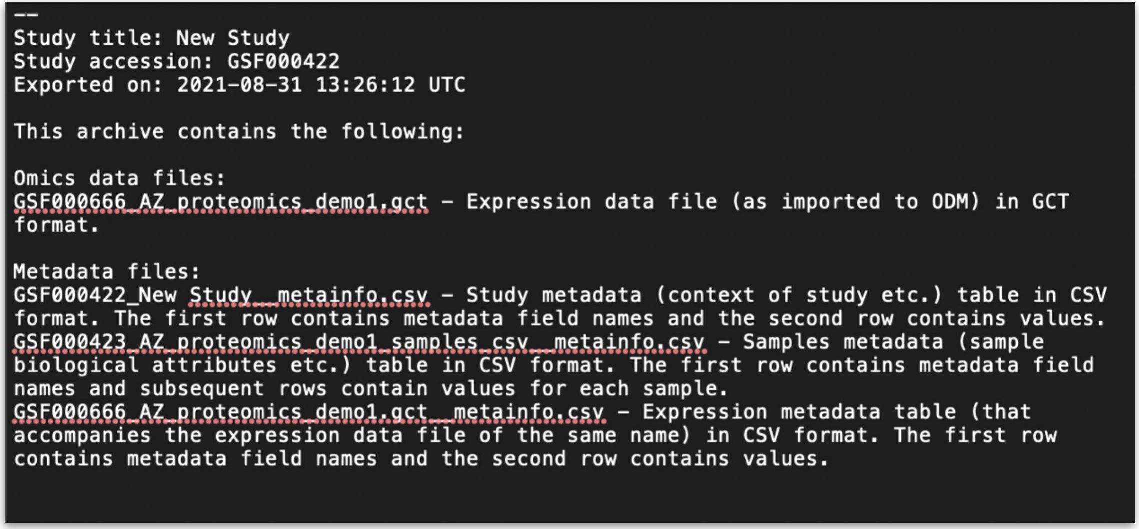
Exporting a Study

The archive contains all available files and a ReadMe file with the description.

[accession]_file_descriptions.txt contains the accessions of the exported files, their names and the descriptions of the files.



GSF000422_file_descriptions.txt
GSF000422_New Study__metainfo.csv
GSF000423_AZ_proteomic..._samples_csv__metainfo.csv
GSF000666_AZ_proteomics_demo1.gct
GSF000666_AZ_proteomics_demo1.gct__metainfo.csv

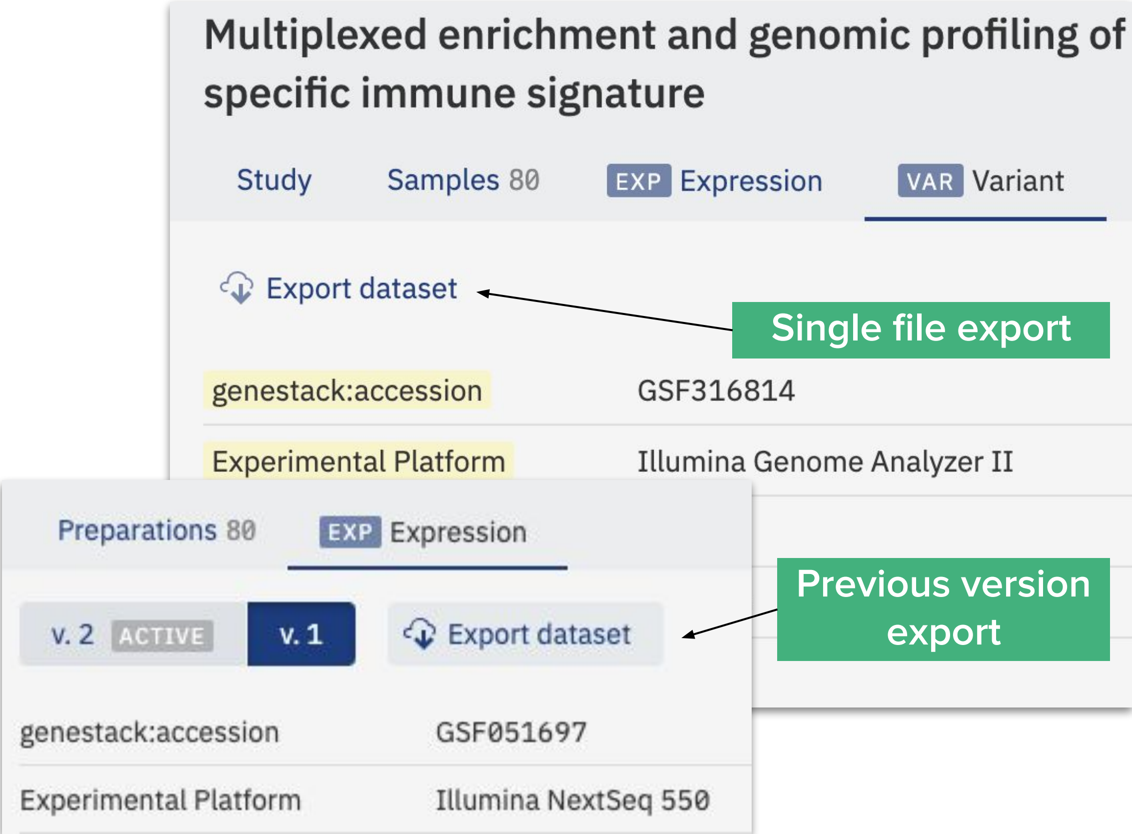


```
--
Study title: New Study
Study accession: GSF000422
Exported on: 2021-08-31 13:26:12 UTC

This archive contains the following:

Omics data files:
GSF000666_AZ_proteomics_demo1.gct - Expression data file (as imported to ODM) in GCT
format.

Metadata files:
GSF000422_New Study__metainfo.csv - Study metadata (context of study etc.) table in CSV
format. The first row contains metadata field names and the second row contains values.
GSF000423_AZ_proteomics_demo1_samples_csv__metainfo.csv - Samples metadata (sample
biological attributes etc.) table in CSV format. The first row contains metadata field
names and subsequent rows contain values for each sample.
GSF000666_AZ_proteomics_demo1.gct__metainfo.csv - Expression metadata table (that
accompanies the expression data file of the same name) in CSV format. The first row
contains metadata field names and the second row contains values.
```

Exporting a Dataset

It is possible to export just one dataset of interest. For doing it navigate to a tab with analysis of interest and click on “Export dataset” button.

The data file with the corresponding metadata file and the description will be compress into archive.



Multiplexed enrichment and genomic profiling of specific immune signature

genestack:accession	GSF316814
Experimental Platform	Illumina Genome Analyzer II

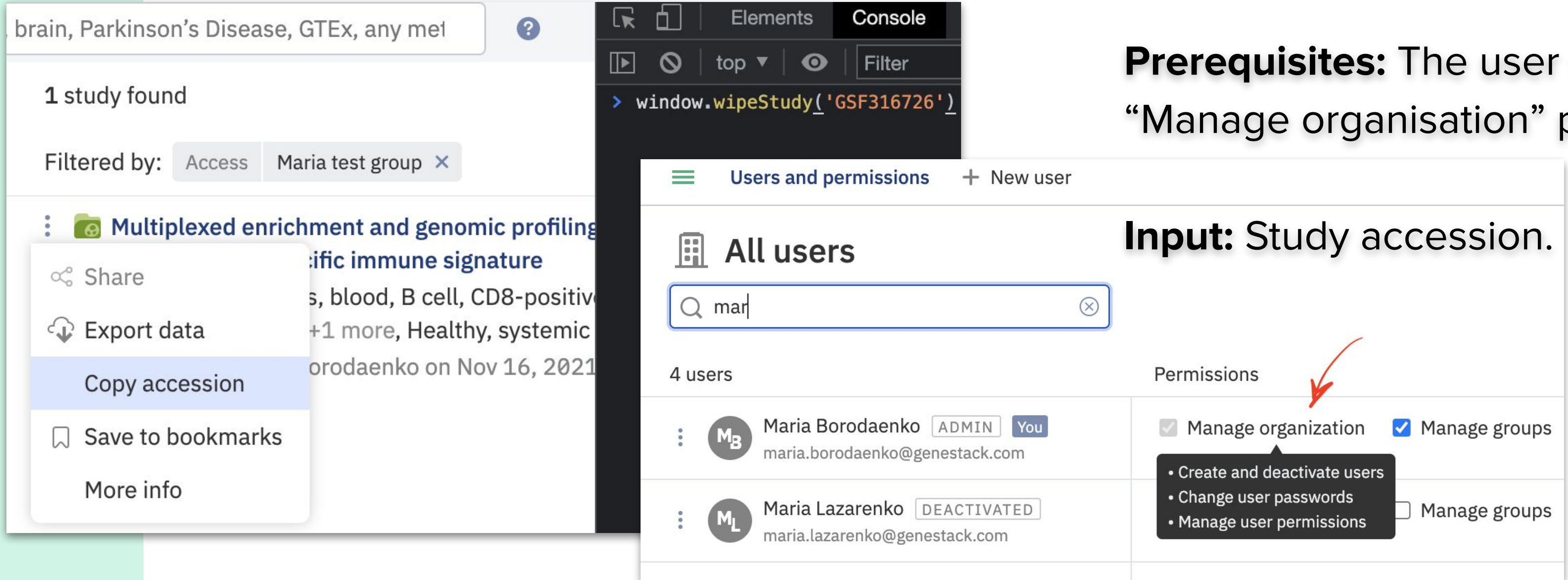
genestack:accession	GSF051697
Experimental Platform	Illumina NextSeq 550

Study Deletions

To delete a study “wipeStudy” method can be called either from the Browser console or via the python script. The method finds all entities linked to the study and delete them one by one.

Prerequisites: The user should have “Manage organisation” permission.

Input: Study accession.



```
> window.wipeStudy('GSF316726')
```

Study Design within ODM

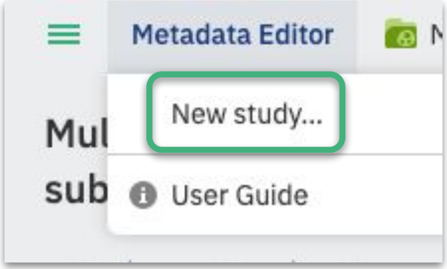
Genestack

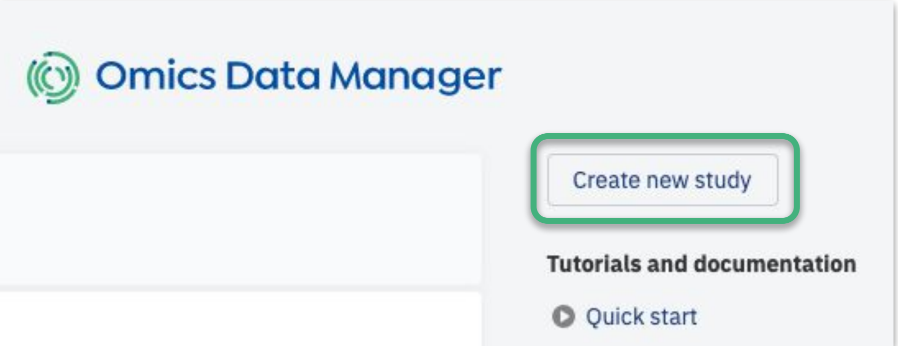
Study Design

A new study can be created directly in ODM without the need of filling in Excel spreadsheets or tsv files. The benefits are:

- Always synced and up-to-date attributes
- Suggestions from the ontologies while filling metadata
- Immediate validation based on the template

New study can be created from Dashboard or from Metadata Editor menu.

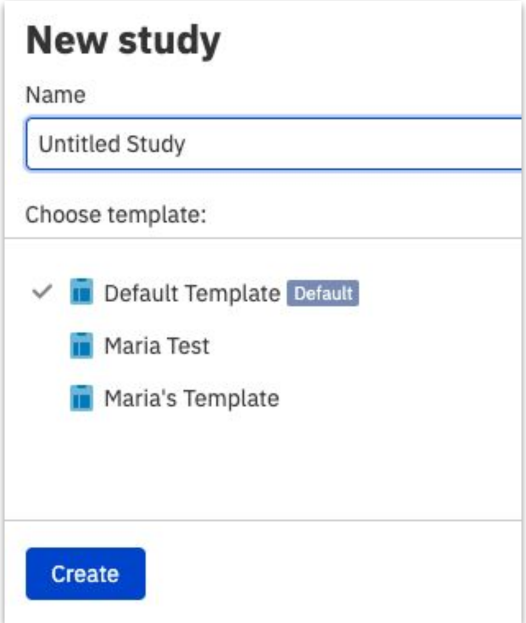




Study Design

After clicking on New study, the user will be prompted to enter a name and choose a template.

A new study with the chosen name and blank attributes from the template will be created.

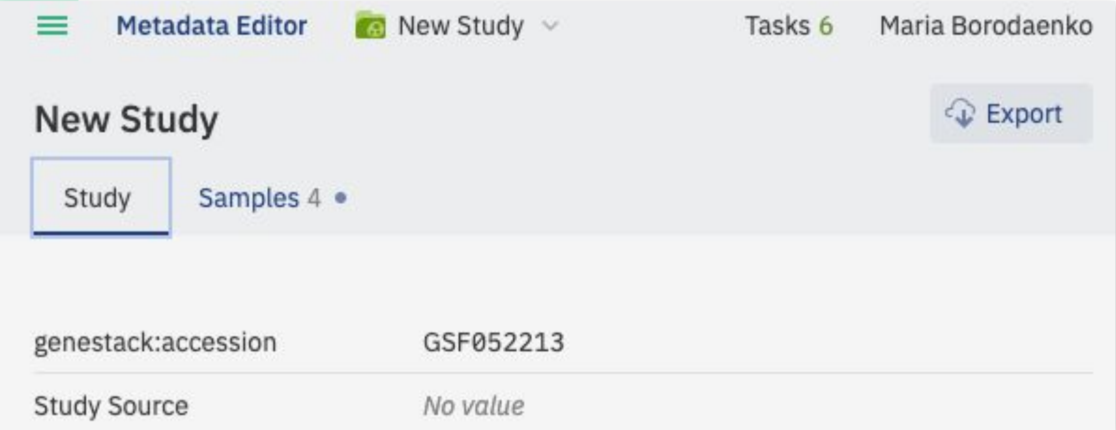


New study

Name: Untitled Study

Choose template:

- ✓ Default Template Default
- Maria Test
- Maria's Template



New Study

genestack:accession	GSF052213
Study Source	*No value*

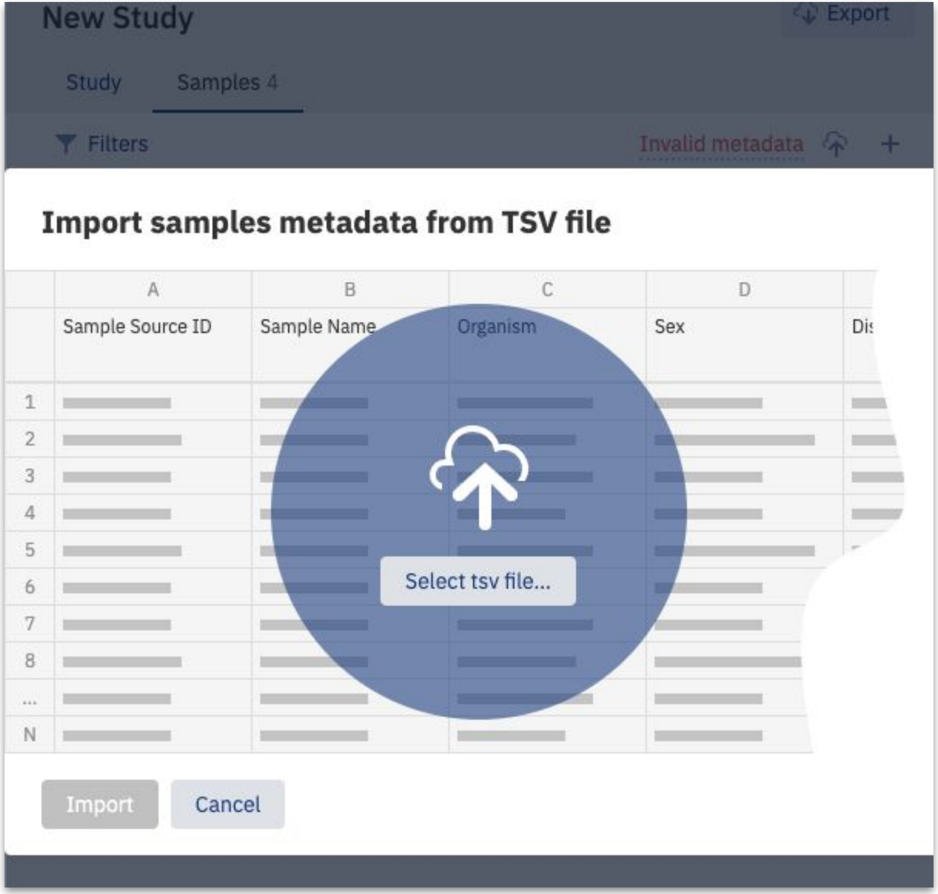
Adding Samples

A few blank samples will be created with the new study.

New samples can be created by “+” button or imported from .tsv file.

25

Maximum 100 samples at a time



Congratulations

You are now
a trained ODM user!

Q&A

Genestack

Thank You!

Maria Borodaenko
Senior Solution Consultant
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www.genestack.com

Genestack

Unlocking the Power of Life-Sciences Data