Single-cell data submission through Annotare

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Submissions Project Lead
Functional Genomics Team

Additional information

EMBL-EBI

Functional Genomics Team – what we do

Data submission & archival

Repository for functional genomics data **ArrayExpress** and its submission tool, **Annotare**

Data integration & visualization

Knowledgebases: **Expression Atlas (EA)** and **Single cell Expression Atlas (SCEA)** – standardized re-analysis and integration of gene profiling data across species and conditions

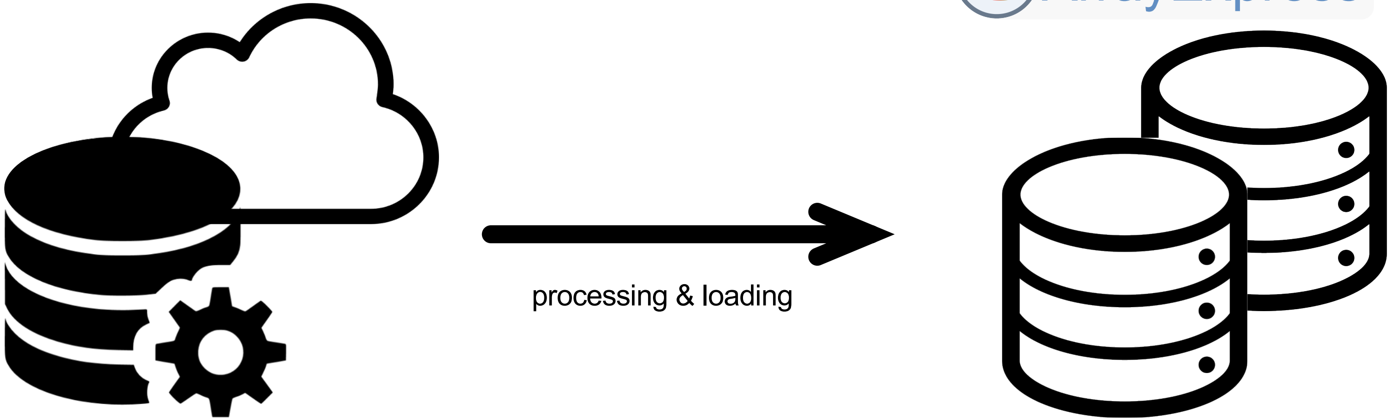
What is Annotare and ArrayExpress?

Annotare

BioStudies.

ArrayExpress

ENA
European Nucleotide Archive



processing & loading

submission assembly & temporary file holding storage

permanent and secure data archival

Annotare – submission tool for ArrayExpress

Promote reproducible research

Make data FAIR

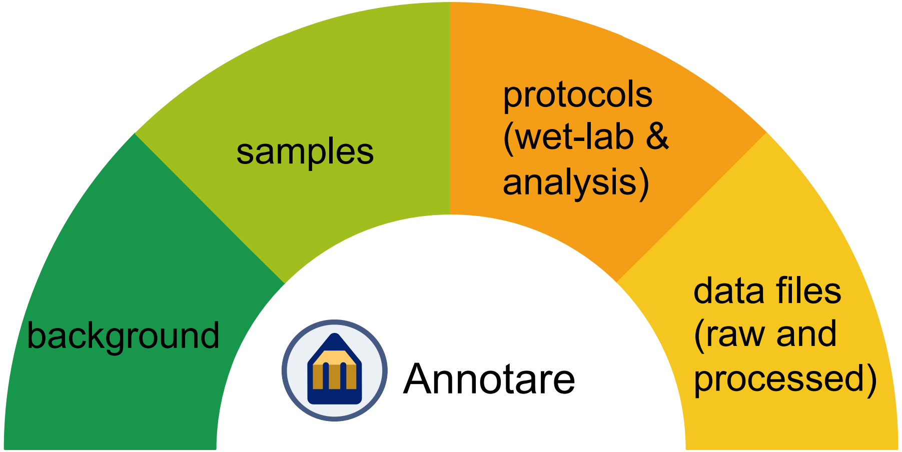
Findable
Accessible
Interoperable
Re-usable

Journal submission requirement

- Provides templates configured to each experiment and sample type
- Captures all data related to an experiment, including protocols
- Ensures high quality metadata by following MIAME/MINSEQE/MinSC data standards
- Defines unique links between samples and associated files
- Instant metadata validation feedback
- Quick automated accessioning

Annotare – submission tool for ArrayExpress

- for functional genomics data (microarray and sequencing)
- user-friendly web-form tool to collect all data and metadata about an experiment



background

samples

protocols (wet-lab & analysis)

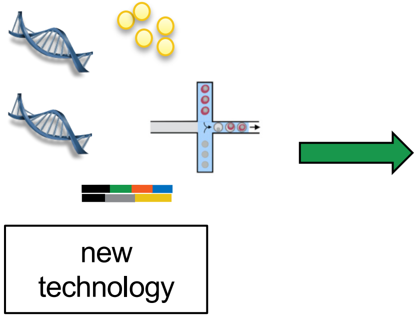
data files (raw and processed)

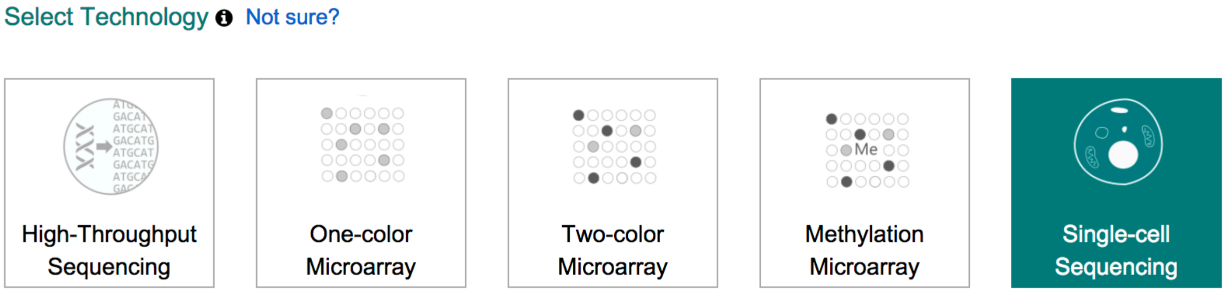
Annotare

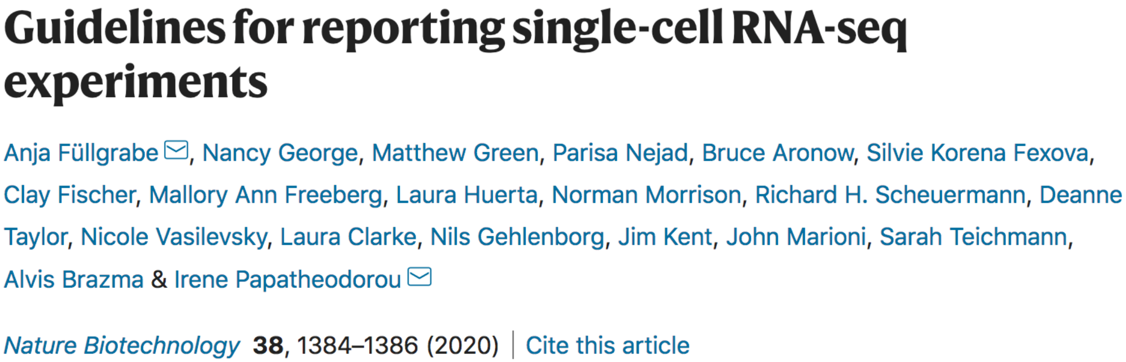
Annotare – submission tool for ArrayExpress

- for functional genomics data (microarray and sequencing)
- user-friendly web-form tool to collect all data and metadata about an experiment
- adopts standards and ontologies
- mix&match templates according to technology and sample type
- continue to develop templates in line with advancing technologies

Annotare – single cell sequencing template



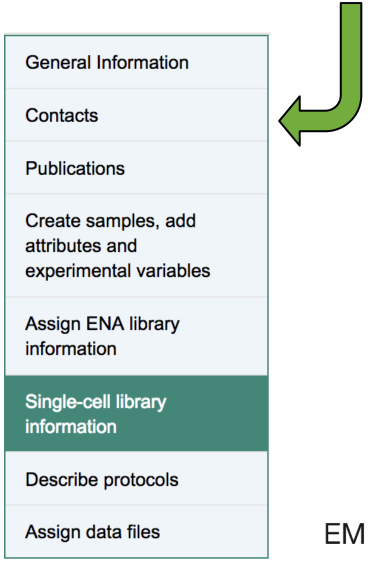




Guidelines for reporting single-cell RNA-seq experiments

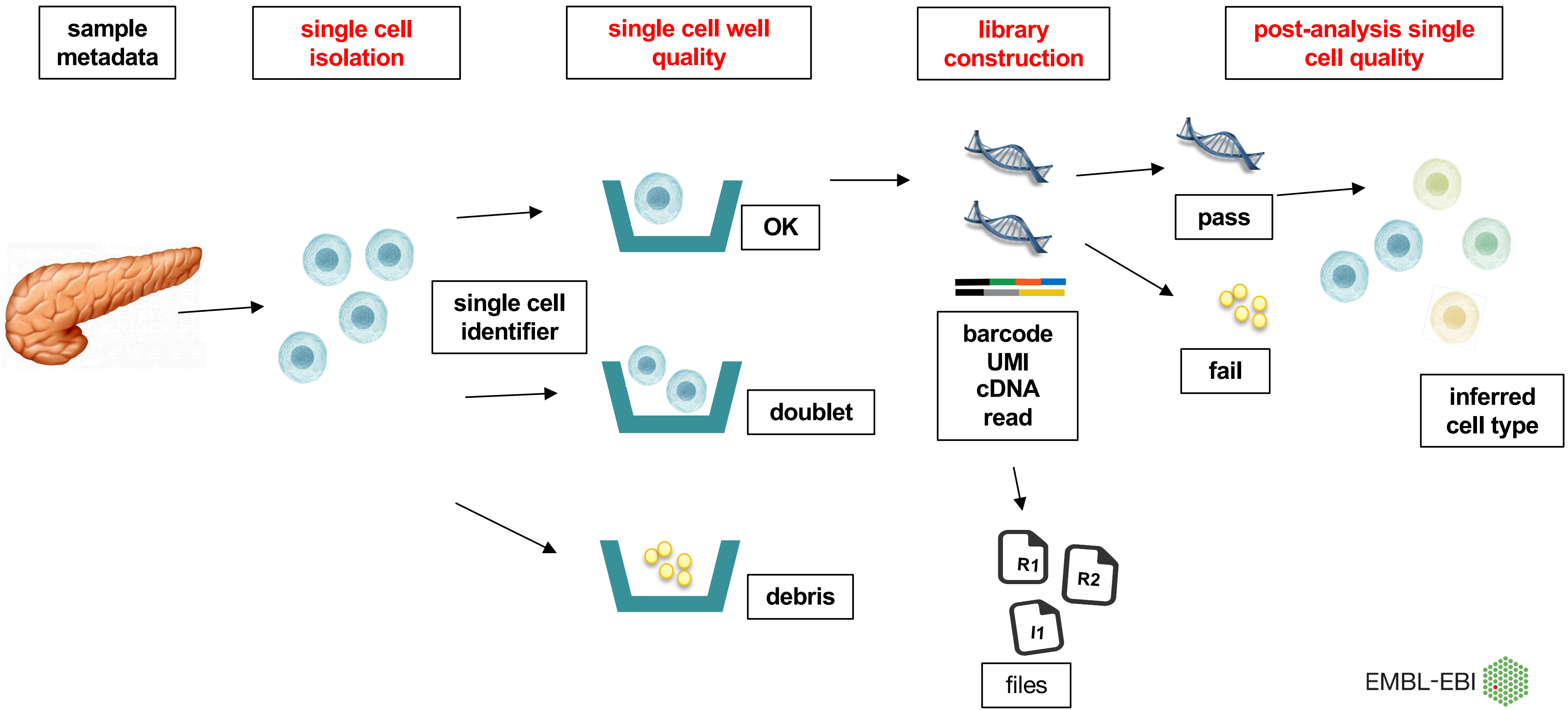
Anja Füllgrabe ✉, Nancy George, Matthew Green, Parisa Nejad, Bruce Aronow, Silvie Korena Fexova, Clay Fischer, Mallory Ann Freeberg, Laura Huerta, Norman Morrison, Richard H. Scheuermann, Deanne Taylor, Nicole Vasilevsky, Laura Clarke, Nils Gehlenborg, Jim Kent, John Marioni, Sarah Teichmann, Alvis Brazma & Irene Papatheodorou ✉

Nature Biotechnology **38**, 1384–1386 (2020) | Cite this article



joint proposal of ‘minSCe’ standard for scRNA-seq from SCEA, HCA, HuBMAP teams and others

Annotare – single cell sequencing template



sample metadata

single cell isolation

single cell well quality

library construction

post-analysis single cell quality

single cell identifier

OK

doublet

debris

barcode
UMI
cDNA
read

files

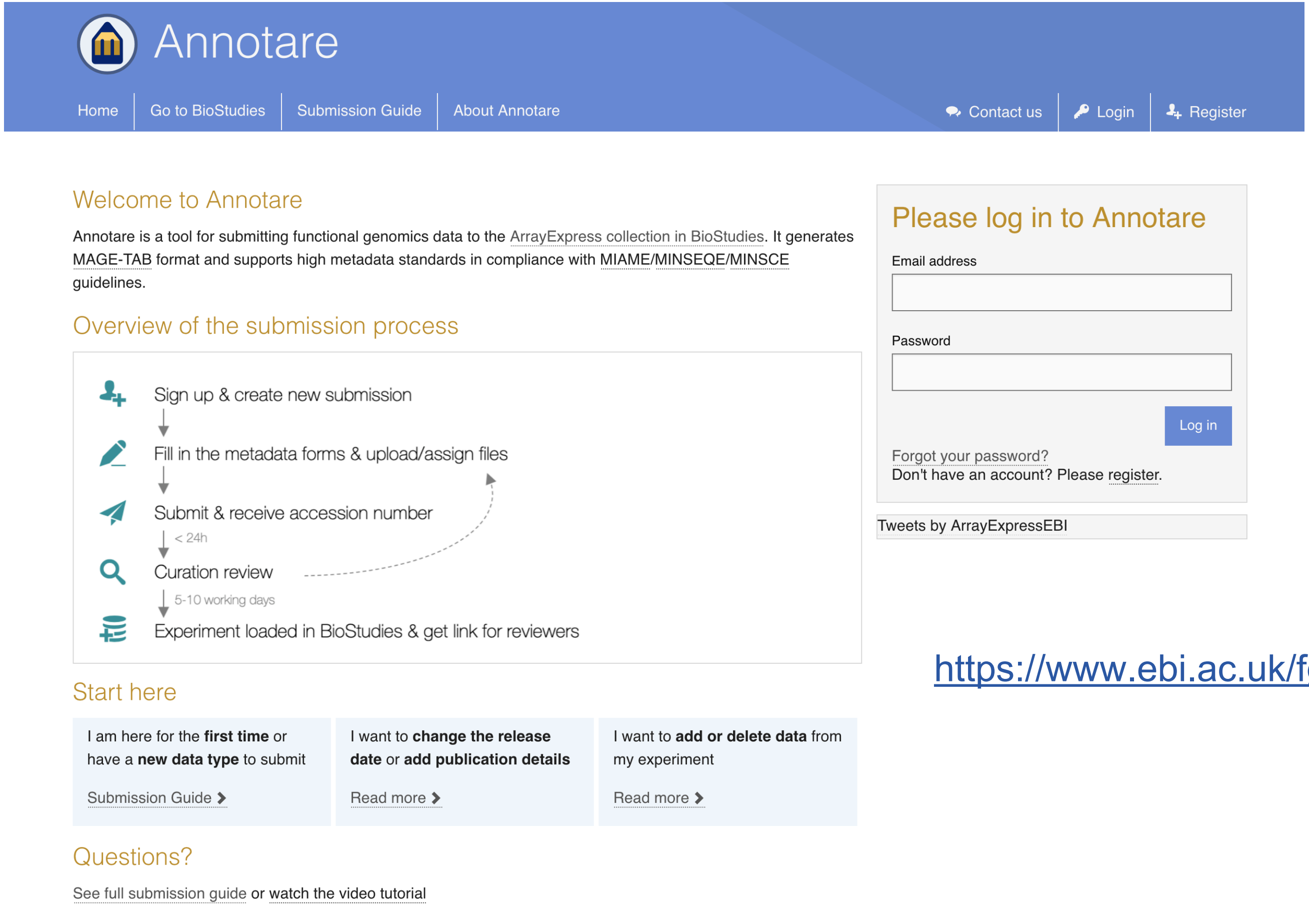
pass

fail

inferred cell type

EMBL-EBI

Using Annotare



Welcome to Annotare

Annotare is a tool for submitting functional genomics data to the ArrayExpress collection in BioStudies. It generates MAGE-TAB format and supports high metadata standards in compliance with MIAME/MINSEQE/MINSCE guidelines.

Overview of the submission process

Sign up & create new submission

Fill in the metadata forms & upload/assign files

Submit & receive accession number

< 24h

Curation review

5-10 working days

Experiment loaded in BioStudies & get link for reviewers

Start here

I am here for the **first time** or have a **new data type** to submit Submission Guide ›	I want to **change the release date** or **add publication details** Read more ›	I want to **add or delete data** from my experiment Read more ›

Questions?

See full submission guide or watch the video tutorial

Please log in to Annotare

Email address

Password

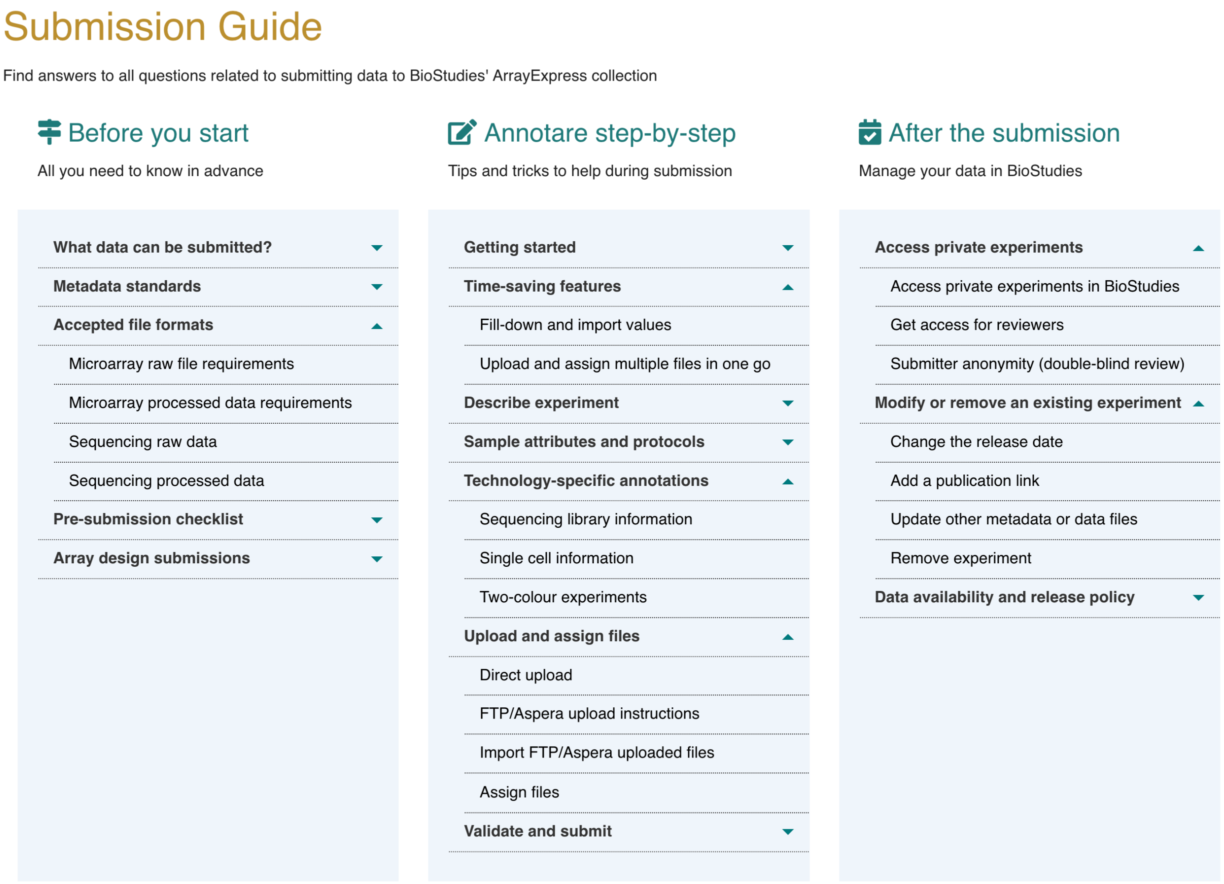
Forgot your password?
Don't have an account? Please register.

Tweets by ArrayExpressEBI

https://www.ebi.ac.uk/fg/annotare/

EMBL-EBI

Using Annotare



Submission Guide

Find answers to all questions related to submitting data to BioStudies' ArrayExpress collection

Before you start

All you need to know in advance

- **What data can be submitted?**
- **Metadata standards**
- **Accepted file formats**
  - Microarray raw file requirements
  - Microarray processed data requirements
  - Sequencing raw data
  - Sequencing processed data
- **Pre-submission checklist**
- **Array design submissions**

Annotare step-by-step

Tips and tricks to help during submission

- **Getting started**
- **Time-saving features**
  - Fill-down and import values
  - Upload and assign multiple files in one go
- **Describe experiment**
- **Sample attributes and protocols**
- **Technology-specific annotations**
  - Sequencing library information
  - Single cell information
  - Two-colour experiments
- **Upload and assign files**
  - Direct upload
  - FTP/Aspera upload instructions
  - Import FTP/Aspera uploaded files
  - Assign files
- **Validate and submit**

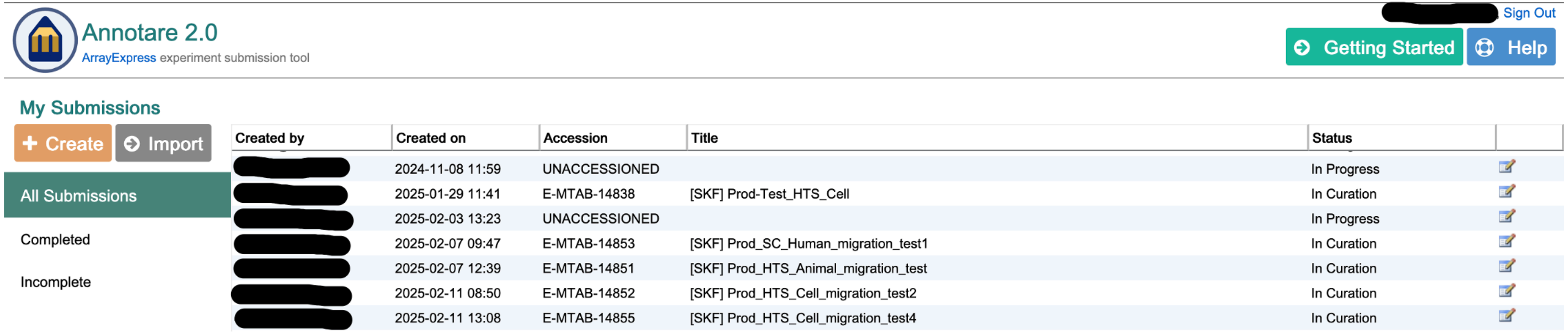
After the submission

Manage your data in BioStudies

- **Access private experiments**
  - Access private experiments in BioStudies
  - Get access for reviewers
  - Submitter anonymity (double-blind review)
- **Modify or remove an existing experiment**
  - Change the release date
  - Add a publication link
  - Update other metadata or data files
  - Remove experiment
- **Data availability and release policy**

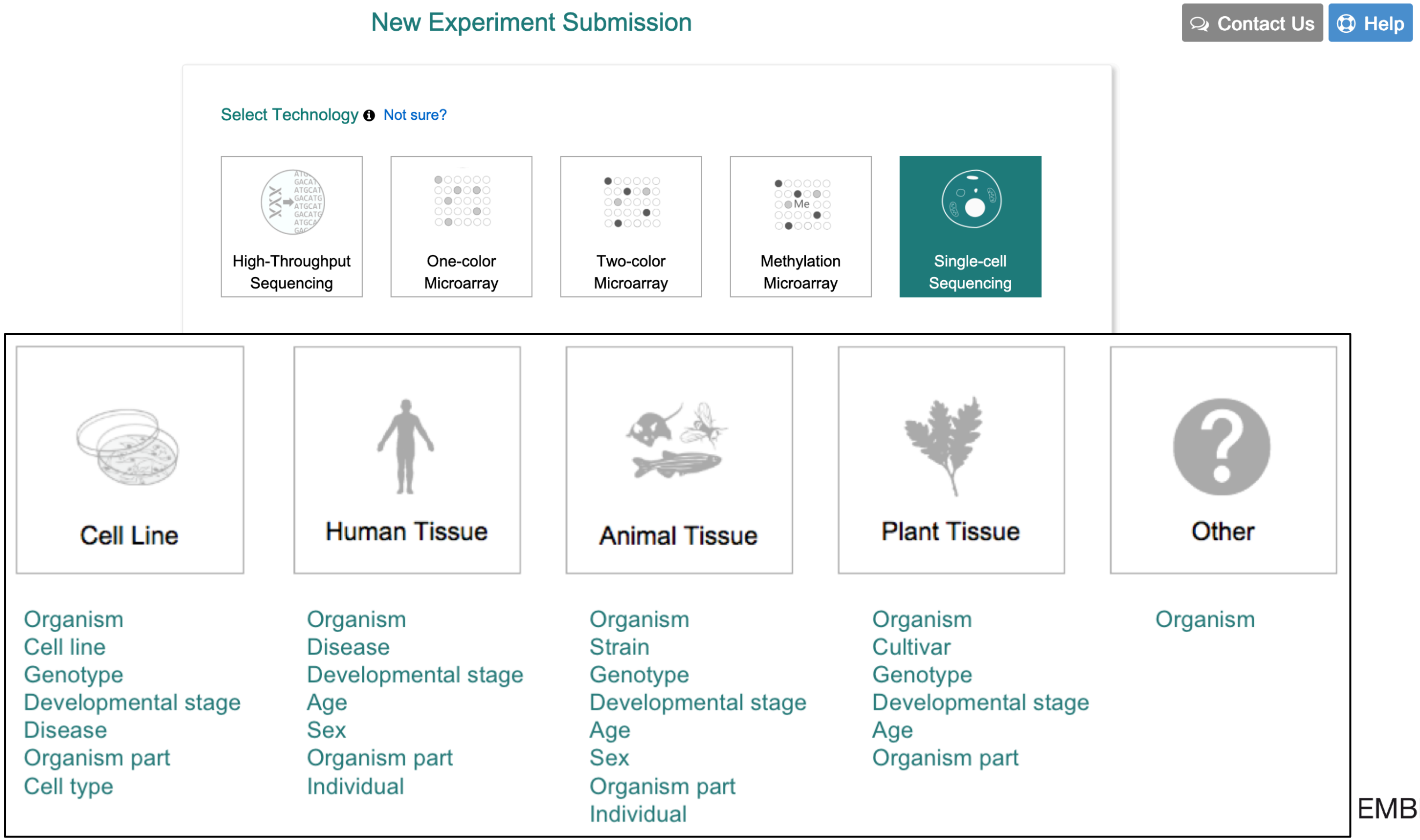
EMBL-EBI

Using Annotare



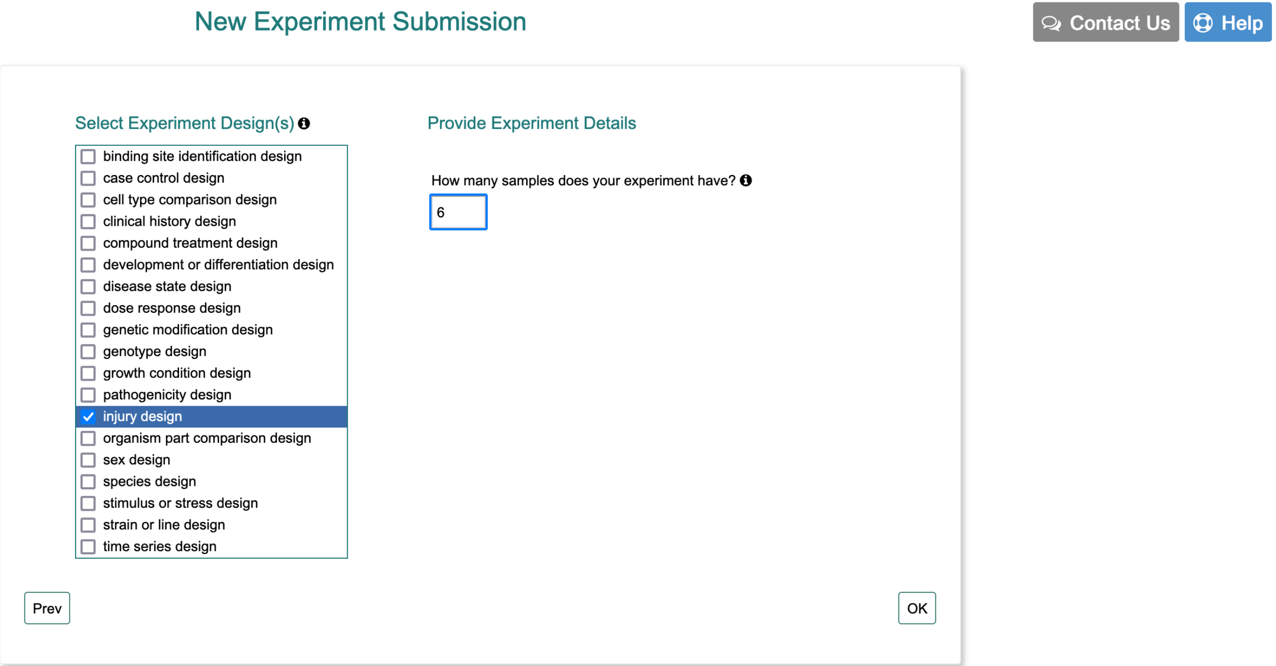
Created by	Created on	Accession	Title	Status	
[redacted]	2024-11-08 11:59	UNACCESSIONED		In Progress	✎
[redacted]	2025-01-29 11:41	E-MTAB-14838	[SKF] Prod-Test_HTS_Cell	In Curation	✎
[redacted]	2025-02-03 13:23	UNACCESSIONED		In Progress	✎
[redacted]	2025-02-07 09:47	E-MTAB-14853	[SKF] Prod_SC_Human_migration_test1	In Curation	✎
[redacted]	2025-02-07 12:39	E-MTAB-14851	[SKF] Prod_HTS_Animal_migration_test	In Curation	✎
[redacted]	2025-02-11 08:50	E-MTAB-14852	[SKF] Prod_HTS_Cell_migration_test2	In Curation	✎
[redacted]	2025-02-11 13:08	E-MTAB-14855	[SKF] Prod_HTS_Cell_migration_test4	In Curation	✎

Using Annotare



Cell Line	Human Tissue	Animal Tissue	Plant Tissue	Other
Organism	Organism	Organism	Organism	Organism
Cell line	Disease	Strain	Cultivar	
Genotype	Developmental stage	Genotype	Genotype	
Developmental stage	Age	Developmental stage	Developmental stage	
Disease	Sex	Age	Age	
Organism part	Organism part	Sex	Organism part	
Cell type	Individual	Organism part		
		Individual		

Using Annotare



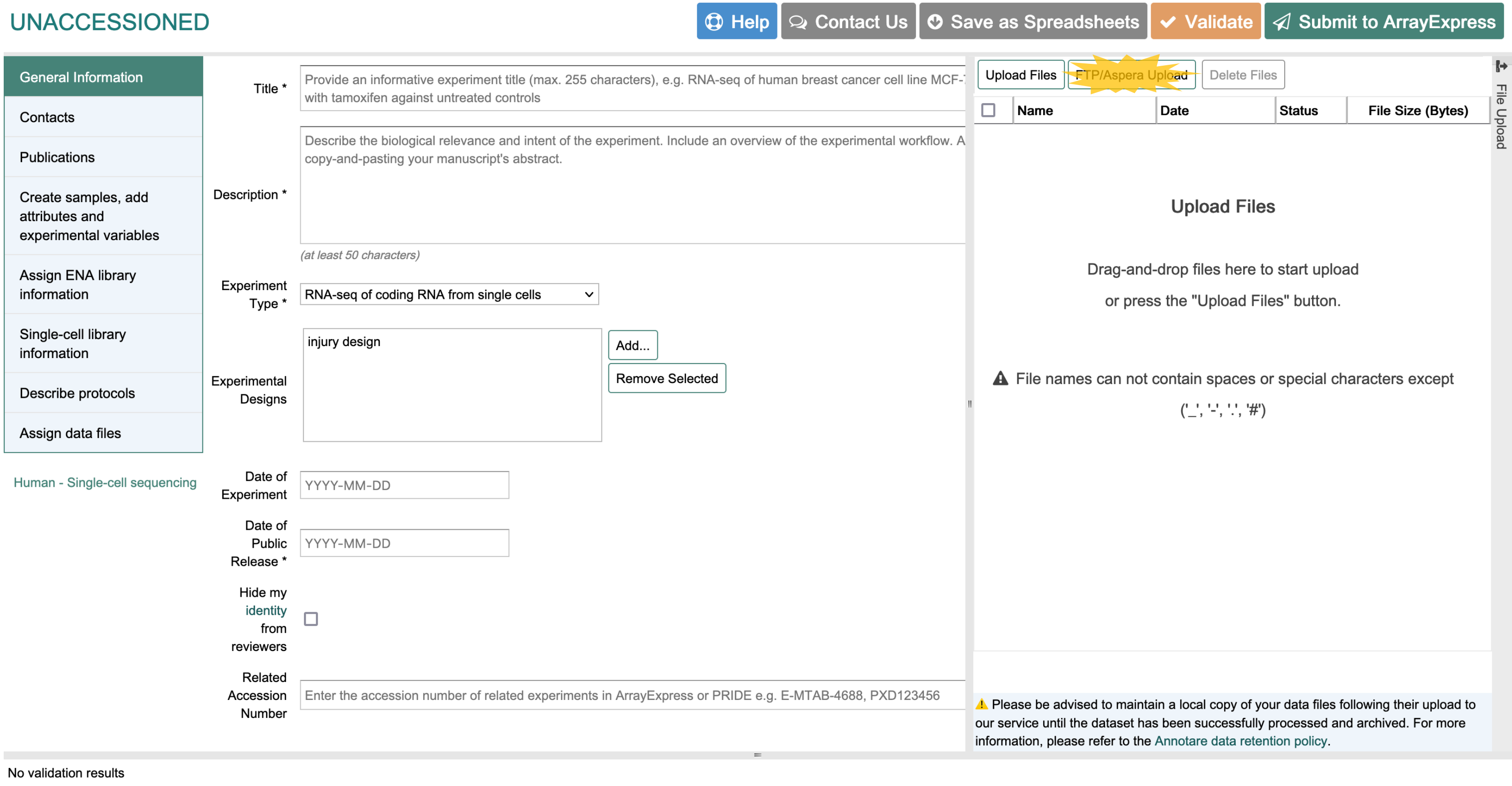
Select Experiment Design(s)

- ☐ binding site identification design
- ☐ case control design
- ☐ cell type comparison design
- ☐ clinical history design
- ☐ compound treatment design
- ☐ development or differentiation design
- ☐ disease state design
- ☐ dose response design
- ☐ genetic modification design
- ☐ genotype design
- ☐ growth condition design
- ☐ pathogenicity design
- ☑ injury design
- ☐ organism part comparison design
- ☐ sex design
- ☐ species design
- ☐ stimulus or stress design
- ☐ strain or line design
- ☐ time series design

Provide Experiment Details

How many samples does your experiment have? 6

Using Annotare



Title * Provide an informative experiment title (max. 255 characters), e.g. RNA-seq of human breast cancer cell line MCF- with tamoxifen against untreated controls

Description * Describe the biological relevance and intent of the experiment. Include an overview of the experimental workflow. A copy-and-pasting your manuscript's abstract.

(at least 50 characters)

Experiment Type * RNA-seq of coding RNA from single cells

Experimental Designs: injury design

Date of Experiment: YYYY-MM-DD

Date of Public Release *: YYYY-MM-DD

Hide my identity from reviewers ☐

Related Accession Number: Enter the accession number of related experiments in ArrayExpress or PRIDE e.g. E-MTAB-4688, PXD123456

Upload Files

Drag-and-drop files here to start upload

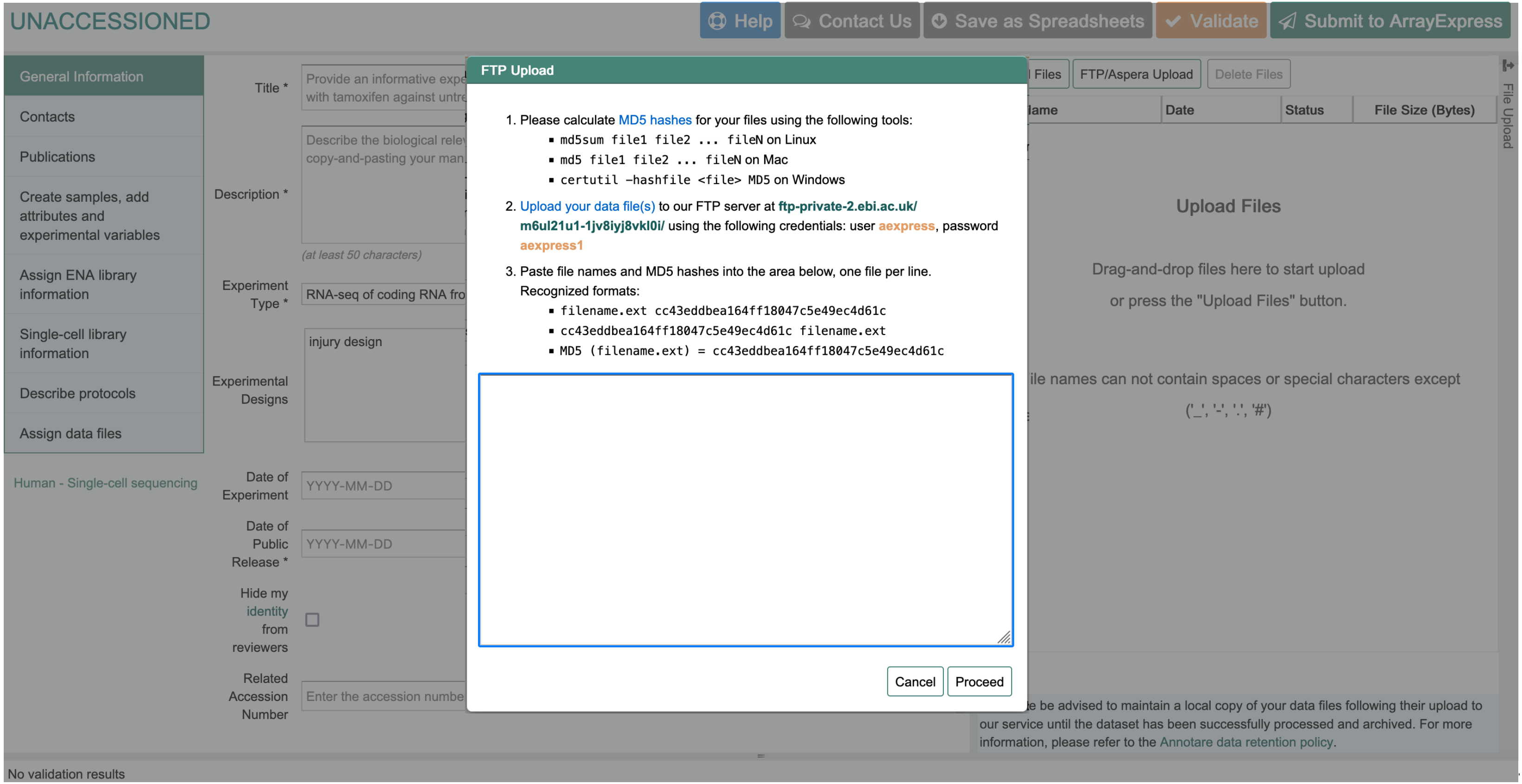
or press the "Upload Files" button.

⚠ File names can not contain spaces or special characters except ('_', '-', '.', '#')

⚠ Please be advised to maintain a local copy of your data files following their upload to our service until the dataset has been successfully processed and archived. For more information, please refer to the Annotare data retention policy.

No validation results

Using Annotare – file upload



Provide an informative expe with tamoxifen against untre

Describe the biological rele copy-and-pasting your man

(at least 50 characters)

RNA-seq of coding RNA fro

injury design

YYYY-MM-DD

YYYY-MM-DD

☐

Enter the accession numbe

FTP Upload

1. Please calculate MD5 hashes for your files using the following tools:
    - `md5sum file1 file2 ... fileN` on Linux
    - `md5 file1 file2 ... fileN` on Mac
    - `certutil -hashfile <file> MD5` on Windows
2. Upload your data file(s) to our FTP server at **ftp-private-2.ebi.ac.uk/m6ul21u1-1jv8iyj8vkl0i/** using the following credentials: user **aexpress**, password **aexpress1**
3. Paste file names and MD5 hashes into the area below, one file per line. Recognized formats:
    - `filename.ext cc43eddbea164ff18047c5e49ec4d61c`
    - `cc43eddbea164ff18047c5e49ec4d61c filename.ext`
    - `MD5 (filename.ext) = cc43eddbea164ff18047c5e49ec4d61c`

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('_', '-', '.', '#')

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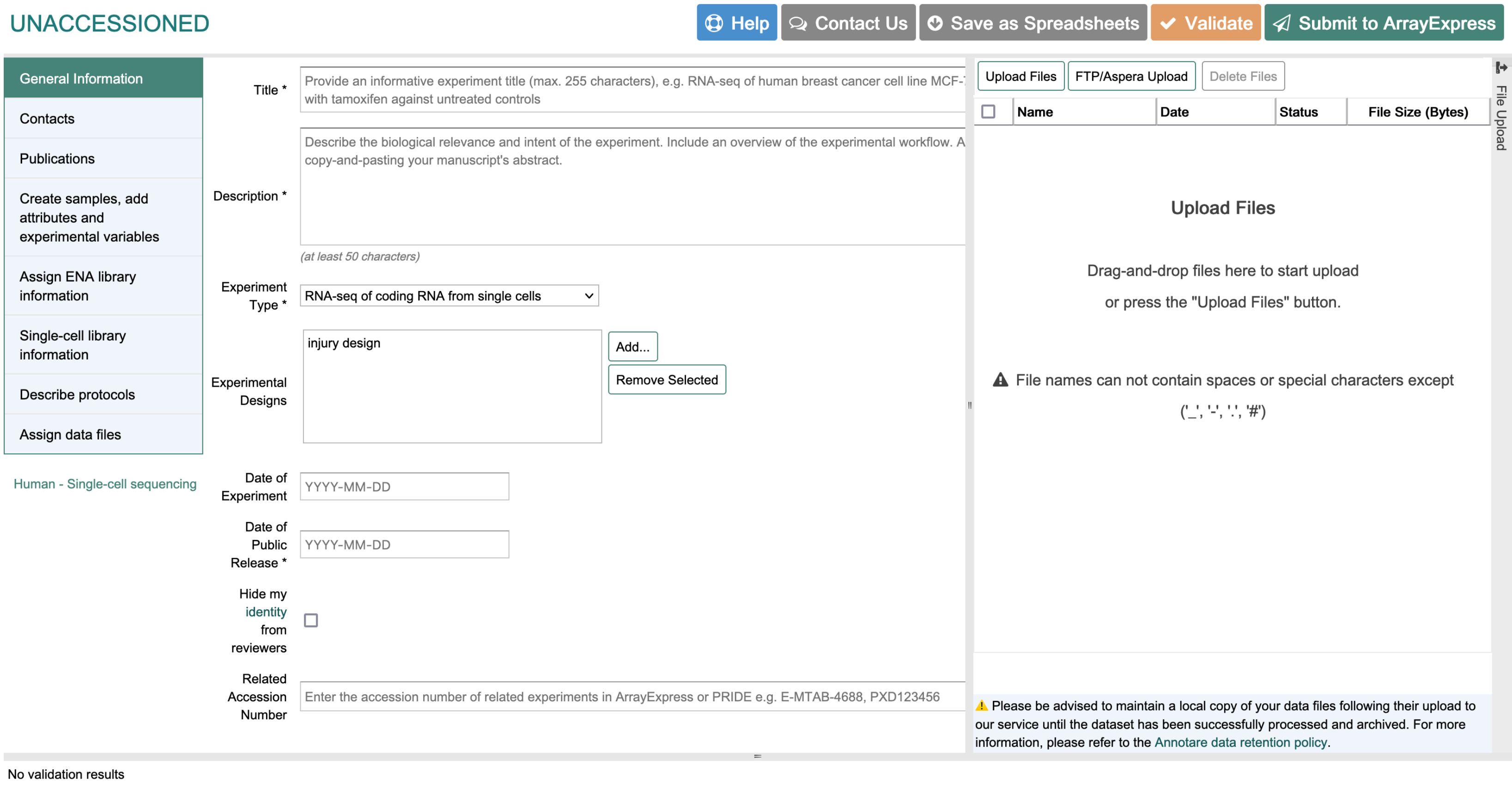
Using Annotare



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copy-and-pasting your manuscript's abstract.

(at least 50 characters)

Experiment Type * RNA-seq of coding RNA from single cells

Experimental Designs: injury design

Date of Experiment: YYYY-MM-DD

Date of Public Release *: YYYY-MM-DD

Hide my identity from reviewers ☐

Related Accession Number: Enter the accession number of related experiments in ArrayExpress or PRIDE e.g. E-MTAB-4688, PXD123456

☐	Name	Date	Status	File Size (Bytes)

Upload Files

Drag-and-drop files here to start upload

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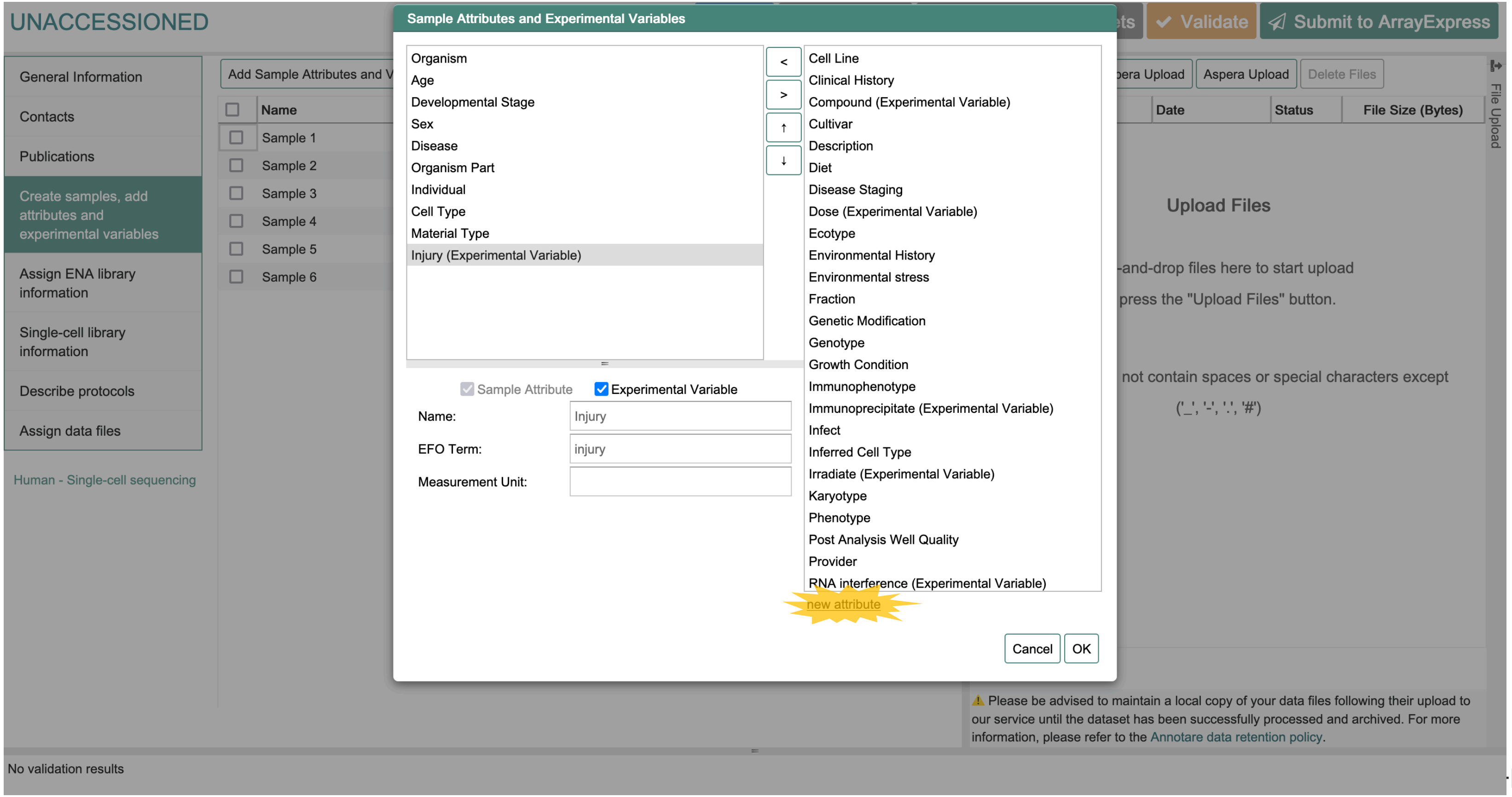
No validation results

Using Annotare – sample attributes and variables



Sample Attributes and Experimental Variables

Organism
Age
Developmental Stage
Sex
Disease
Organism Part
Individual
Cell Type
Material Type
Injury (Experimental Variable)

Cell Line
Clinical History
Compound (Experimental Variable)
Cultivar
Description
Diet
Disease Staging
Dose (Experimental Variable)
Ecotype
Environmental History
Environmental stress
Fraction
Genetic Modification
Genotype
Growth Condition
Immunophenotype
Immunoprecipitate (Experimental Variable)
Infect
Inferred Cell Type
Irradiate (Experimental Variable)
Karyotype
Phenotype
Post Analysis Well Quality
Provider
RNA interference (Experimental Variable)

☑ Sample Attribute ☑ Experimental Variable

Name: Injury
EFO Term: injury
Measurement Unit:

Upload Files

-and-drop files here to start upload

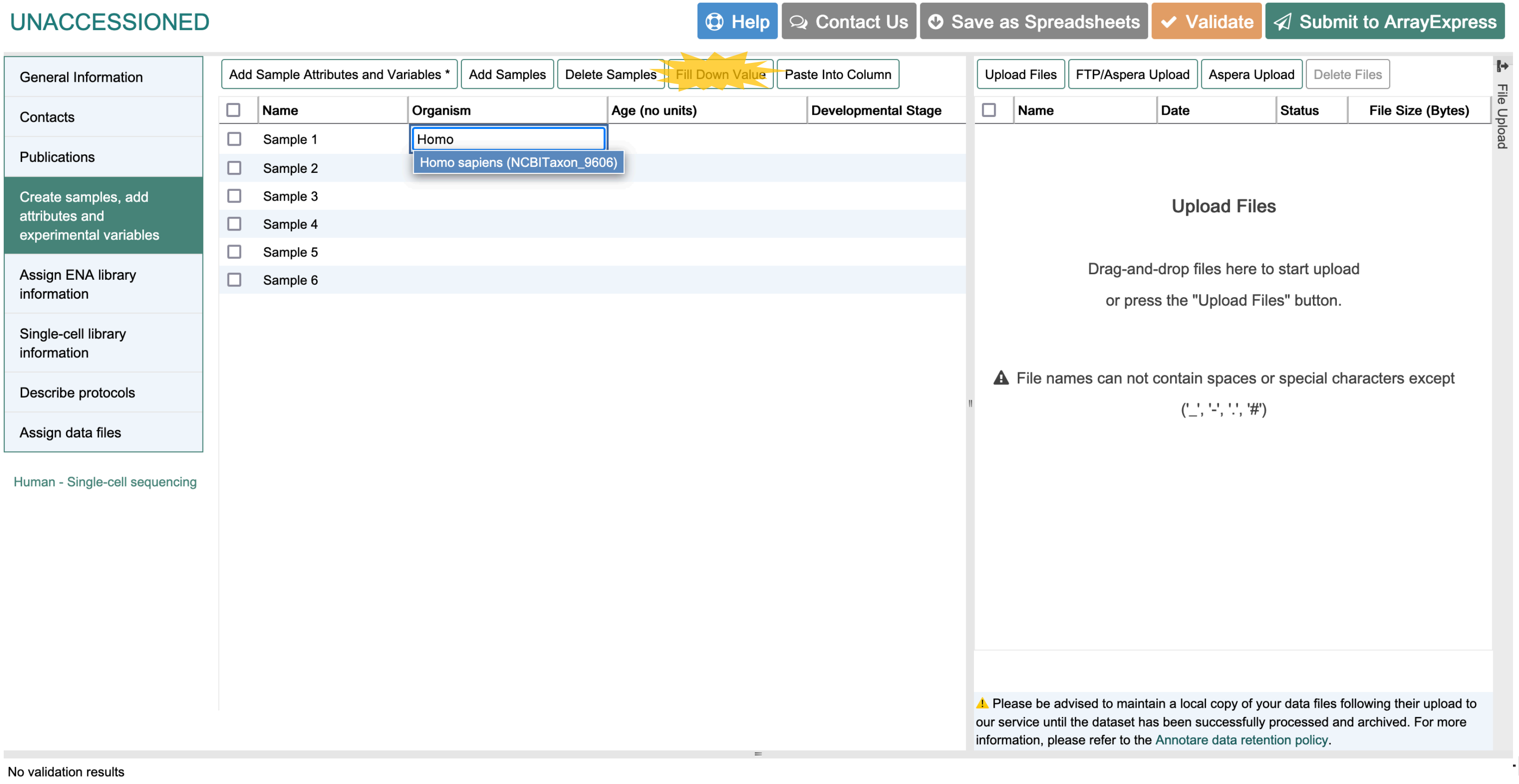
press the "Upload Files" button.

not contain spaces or special characters except ('_', '-', '.', '#')

⚠ Please be advised to maintain a local copy of your data files following their upload to our service until the dataset has been successfully processed and archived. For more information, please refer to the Annotare data retention policy.

No validation results

Using Annotare – ontology terms



UNACCESSIONED

☐	Name	Organism	Age (no units)	Developmental Stage
☐	Sample 1	Homo		
☐	Sample 2			
☐	Sample 3			
☐	Sample 4			
☐	Sample 5			
☐	Sample 6			

Homo sapiens (NCBITaxon_9606)

Upload Files

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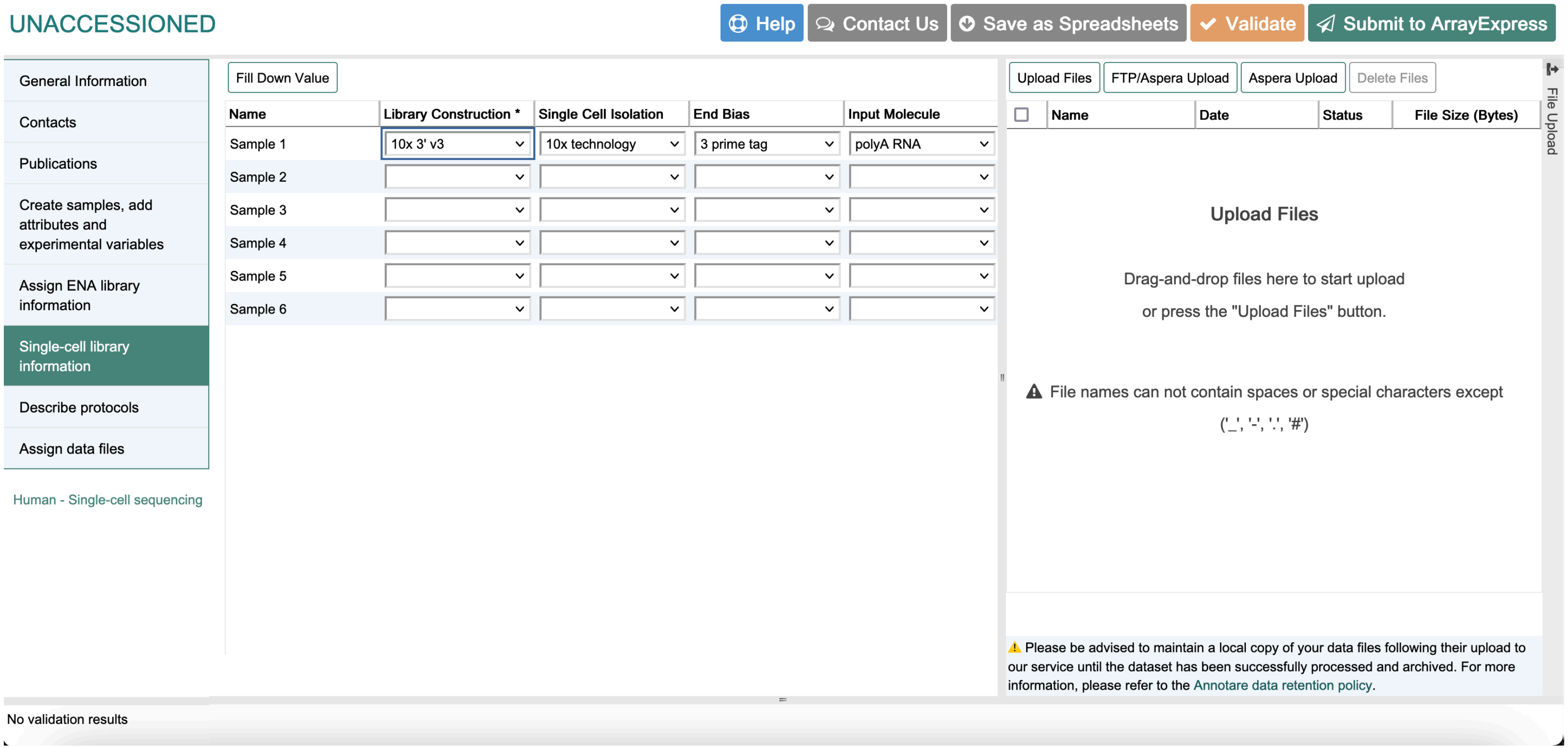
Human - Single-cell sequencing

No validation results

Using Annotare – drop-downs and pre-fills



Name	Library Construction *	Single Cell Isolation	End Bias	Input Molecule
Sample 1	10x 3' v3	10x technology	3 prime tag	polyA RNA
Sample 2				
Sample 3				
Sample 4				
Sample 5				
Sample 6				

☐	Name	Date	Status	File Size (Bytes)

Upload Files

Drag-and-drop files here to start upload or press the "Upload Files" button.

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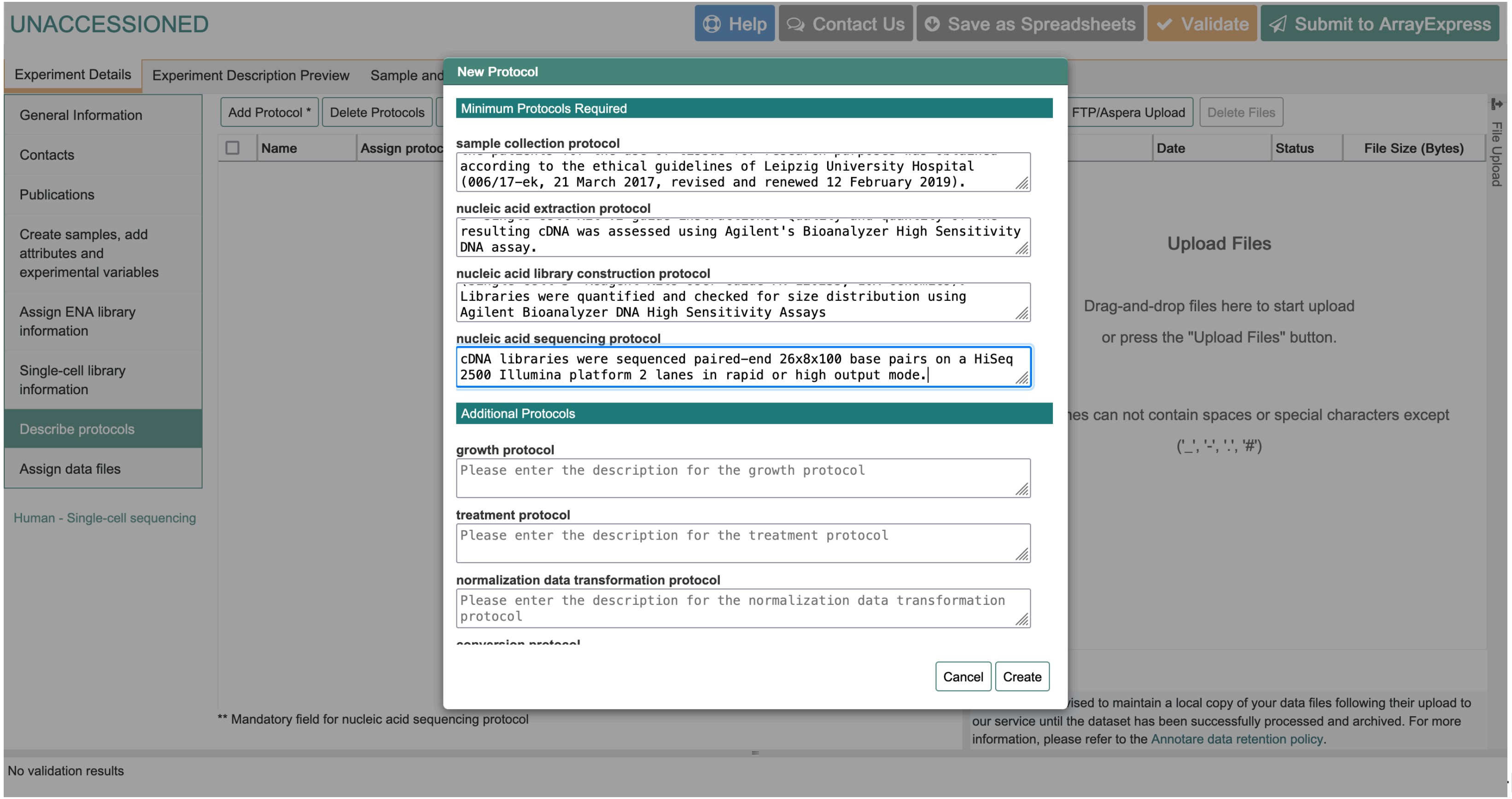
No validation results

Using Annotare – protocols



New Protocol

Minimum Protocols Required

sample collection protocol

according to the ethical guidelines of Leipzig University Hospital (006/17-ek, 21 March 2017, revised and renewed 12 February 2019).

nucleic acid extraction protocol

resulting cDNA was assessed using Agilent's Bioanalyzer High Sensitivity DNA assay.

nucleic acid library construction protocol

Libraries were quantified and checked for size distribution using Agilent Bioanalyzer DNA High Sensitivity Assays

nucleic acid sequencing protocol

cDNA libraries were sequenced paired-end 26x8x100 base pairs on a HiSeq 2500 Illumina platform 2 lanes in rapid or high output mode.

Additional Protocols

growth protocol

Please enter the description for the growth protocol

treatment protocol

Please enter the description for the treatment protocol

normalization data transformation protocol

Please enter the description for the normalization data transformation protocol

conversion protocol

Drag-and-drop files here to start upload or press the "Upload Files" button.

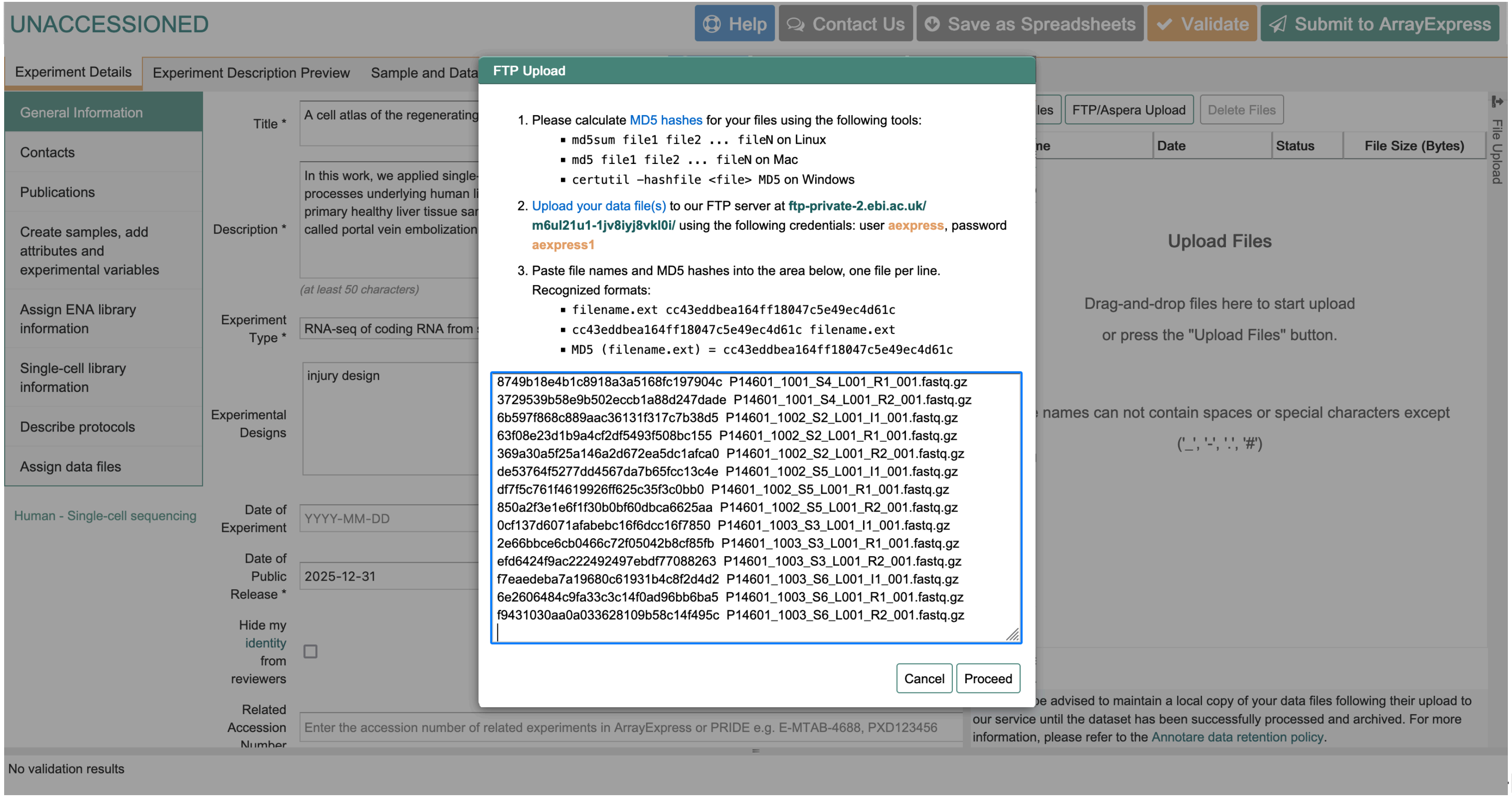
es can not contain spaces or special characters except ('_', '-', '.', '#')

** Mandatory field for nucleic acid sequencing protocol

ised to maintain a local copy of your data files following their upload to our service until the dataset has been successfully processed and archived. For more information, please refer to the Annotare data retention policy.

No validation results

Using Annotare – register and assign data files



Title * A cell atlas of the regenerating

Description * In this work, we applied single- processes underlying human li primary healthy liver tissue sar called portal vein embolization

(at least 50 characters)

Experiment Type * RNA-seq of coding RNA from

Experimental Designs injury design

Date of Experiment YYYY-MM-DD

Date of Public Release * 2025-12-31

Hide my identity from reviewers ☐

Related Accession Number Enter the accession number of related experiments in ArrayExpress or PRIDE e.g. E-MTAB-4688, PXD123456

FTP Upload

1. Please calculate MD5 hashes for your files using the following tools:
    - `md5sum file1 file2 ... fileN` on Linux
    - `md5 file1 file2 ... fileN` on Mac
    - `certutil -hashfile <file> MD5` on Windows
2. Upload your data file(s) to our FTP server at **ftp-private-2.ebi.ac.uk/m6ul21u1-1jv8iyj8vkl0i/** using the following credentials: user **aexpress**, password **aexpress1**
3. Paste file names and MD5 hashes into the area below, one file per line.
   Recognized formats:
    - `filename.ext cc43eddbea164ff18047c5e49ec4d61c`
    - `cc43eddbea164ff18047c5e49ec4d61c filename.ext`
    - `MD5 (filename.ext) = cc43eddbea164ff18047c5e49ec4d61c`

```
8749b18e4b1c8918a3a5168fc197904c  P14601_1001_S4_L001_R1_001.fastq.gz
3729539b58e9b502eccb1a88d247dade  P14601_1001_S4_L001_R2_001.fastq.gz
6b597f868c889aac36131f317c7b38d5  P14601_1002_S2_L001_I1_001.fastq.gz
63f08e23d1b9a4cf2df5493f508bc155  P14601_1002_S2_L001_R1_001.fastq.gz
369a30a5f25a146a2d672ea5dc1afca0  P14601_1002_S2_L001_R2_001.fastq.gz
de53764f5277dd4567da7b65fcc13c4e  P14601_1002_S5_L001_I1_001.fastq.gz
df7f5c761f4619926ff625c35f3c0bb0  P14601_1002_S5_L001_R1_001.fastq.gz
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efd6424f9ac222492497ebdf77088263  P14601_1003_S3_L001_R2_001.fastq.gz
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6e2606484c9fa33c3c14f0ad96bb6ba5  P14601_1003_S6_L001_R1_001.fastq.gz
f9431030aa0a033628109b58c14f495c  P14601_1003_S6_L001_R2_001.fastq.gz
```

Drag-and-drop files here to start upload or press the "Upload Files" button.

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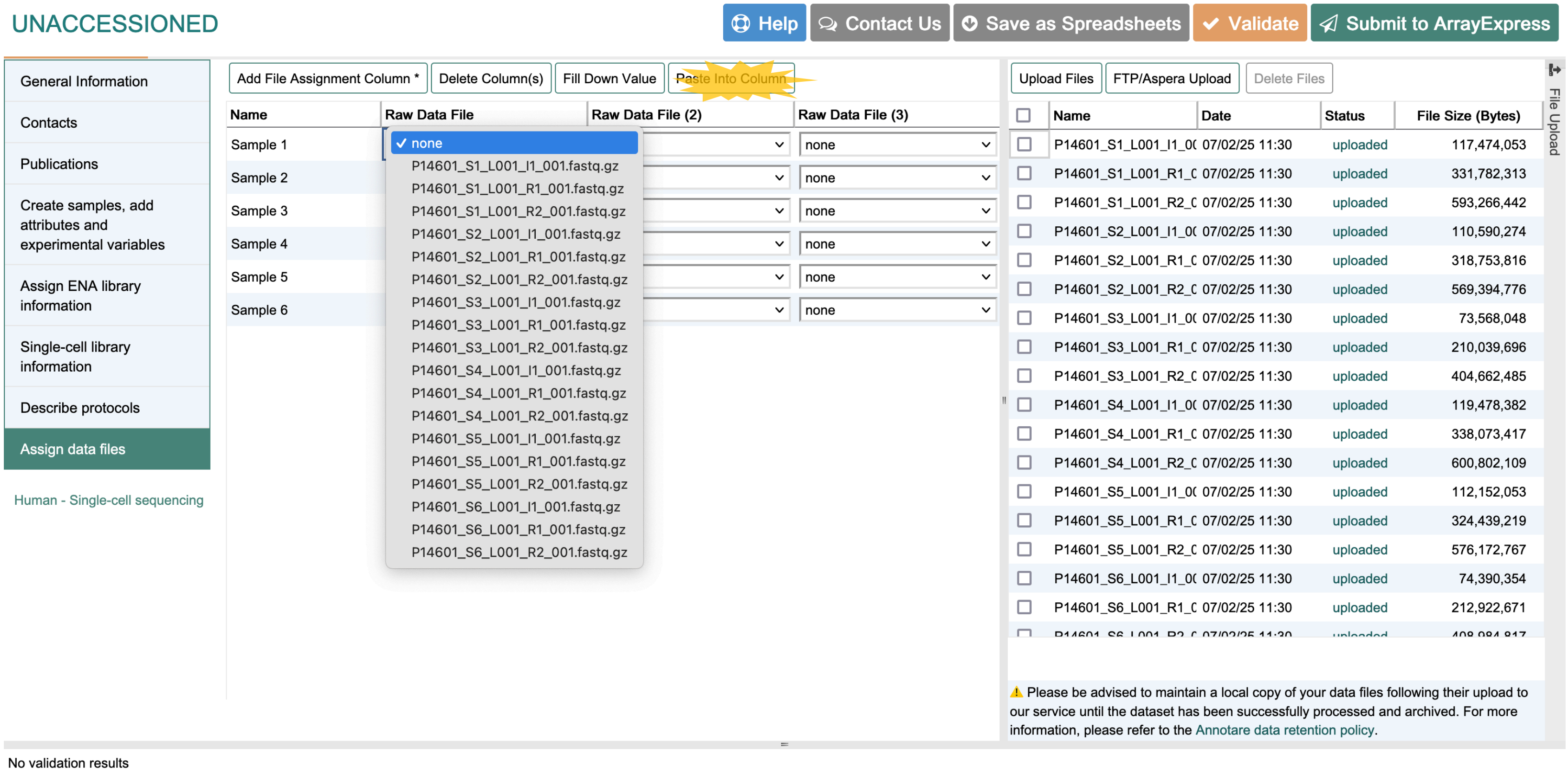
Using Annotare – register and assign data files



Name	Raw Data File	Raw Data File (2)	Raw Data File (3)
Sample 1	✓ none		none
Sample 2			none
Sample 3			none
Sample 4			none
Sample 5			none
Sample 6			none

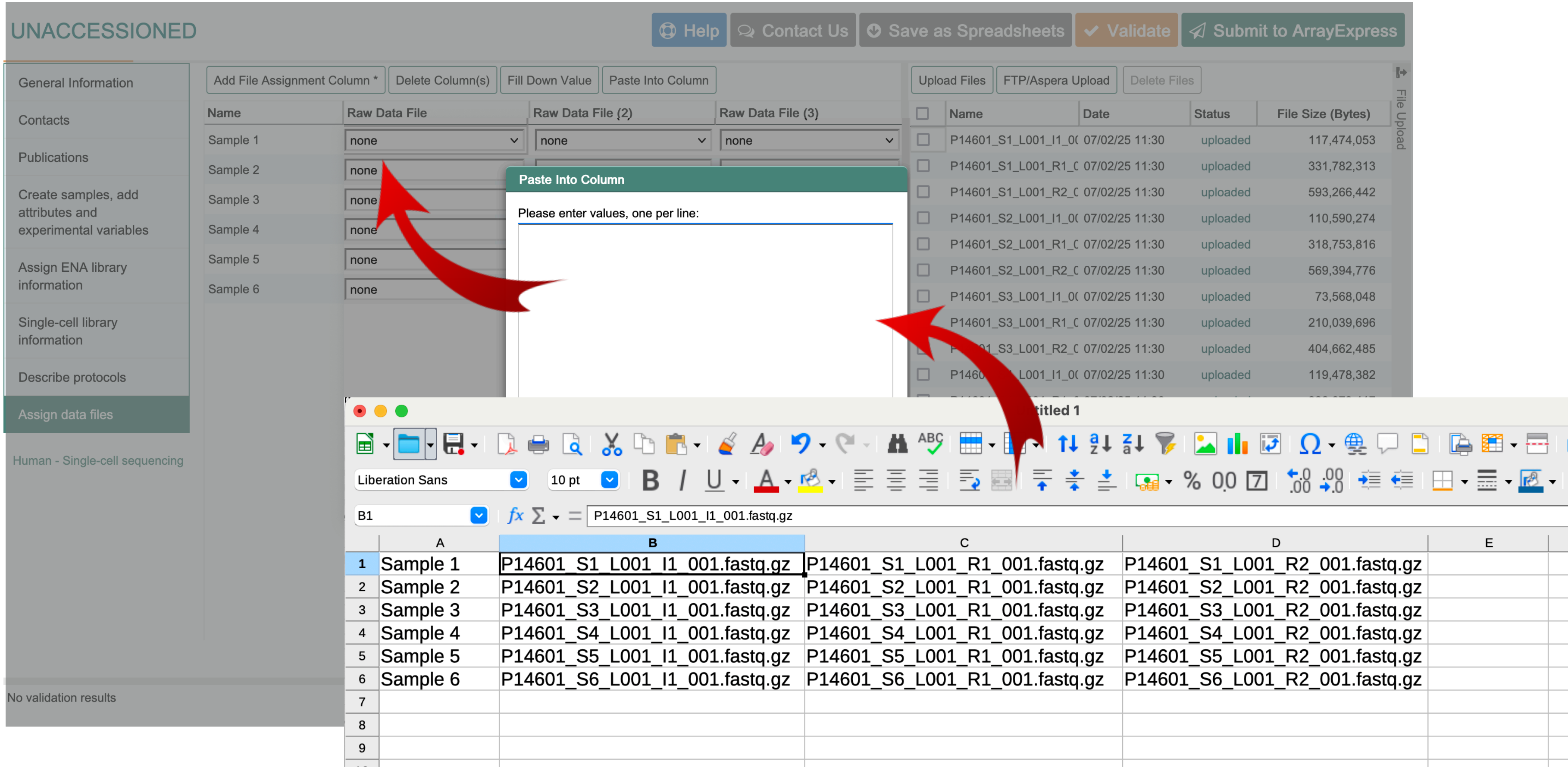
- ✓ none
- P14601_S1_L001_I1_001.fastq.gz
- P14601_S1_L001_R1_001.fastq.gz
- P14601_S1_L001_R2_001.fastq.gz
- P14601_S2_L001_I1_001.fastq.gz
- P14601_S2_L001_R1_001.fastq.gz
- P14601_S2_L001_R2_001.fastq.gz
- P14601_S3_L001_I1_001.fastq.gz
- P14601_S3_L001_R1_001.fastq.gz
- P14601_S3_L001_R2_001.fastq.gz
- P14601_S4_L001_I1_001.fastq.gz
- P14601_S4_L001_R1_001.fastq.gz
- P14601_S4_L001_R2_001.fastq.gz
- P14601_S5_L001_I1_001.fastq.gz
- P14601_S5_L001_R1_001.fastq.gz
- P14601_S5_L001_R2_001.fastq.gz
- P14601_S6_L001_I1_001.fastq.gz
- P14601_S6_L001_R1_001.fastq.gz
- P14601_S6_L001_R2_001.fastq.gz

☐	Name	Date	Status	File Size (Bytes)
☐	P14601_S1_L001_I1_0	07/02/25 11:30	uploaded	117,474,053
☐	P14601_S1_L001_R1_	07/02/25 11:30	uploaded	331,782,313
☐	P14601_S1_L001_R2_	07/02/25 11:30	uploaded	593,266,442
☐	P14601_S2_L001_I1_0	07/02/25 11:30	uploaded	110,590,274
☐	P14601_S2_L001_R1_	07/02/25 11:30	uploaded	318,753,816
☐	P14601_S2_L001_R2_	07/02/25 11:30	uploaded	569,394,776
☐	P14601_S3_L001_I1_0	07/02/25 11:30	uploaded	73,568,048
☐	P14601_S3_L001_R1_	07/02/25 11:30	uploaded	210,039,696
☐	P14601_S3_L001_R2_	07/02/25 11:30	uploaded	404,662,485
☐	P14601_S4_L001_I1_0	07/02/25 11:30	uploaded	119,478,382
☐	P14601_S4_L001_R1_	07/02/25 11:30	uploaded	338,073,417
☐	P14601_S4_L001_R2_	07/02/25 11:30	uploaded	600,802,109
☐	P14601_S5_L001_I1_0	07/02/25 11:30	uploaded	112,152,053
☐	P14601_S5_L001_R1_	07/02/25 11:30	uploaded	324,439,219
☐	P14601_S5_L001_R2_	07/02/25 11:30	uploaded	576,172,767
☐	P14601_S6_L001_I1_0	07/02/25 11:30	uploaded	74,390,354
☐	P14601_S6_L001_R1_	07/02/25 11:30	uploaded	212,922,671
☐	P14601_S6_L001_R2_	07/02/25 11:30	uploaded	408,984,817

⚠ Please be advised to maintain a local copy of your data files following their upload to our service until the dataset has been successfully processed and archived. For more information, please refer to the Annotare data retention policy.

No validation results

Using Annotare – bulk assign data files



Name	Raw Data File	Raw Data File (2)	Raw Data File (3)
Sample 1	none	none	none
Sample 2	none		
Sample 3	none		
Sample 4	none		
Sample 5	none		
Sample 6	none		

Paste Into Column

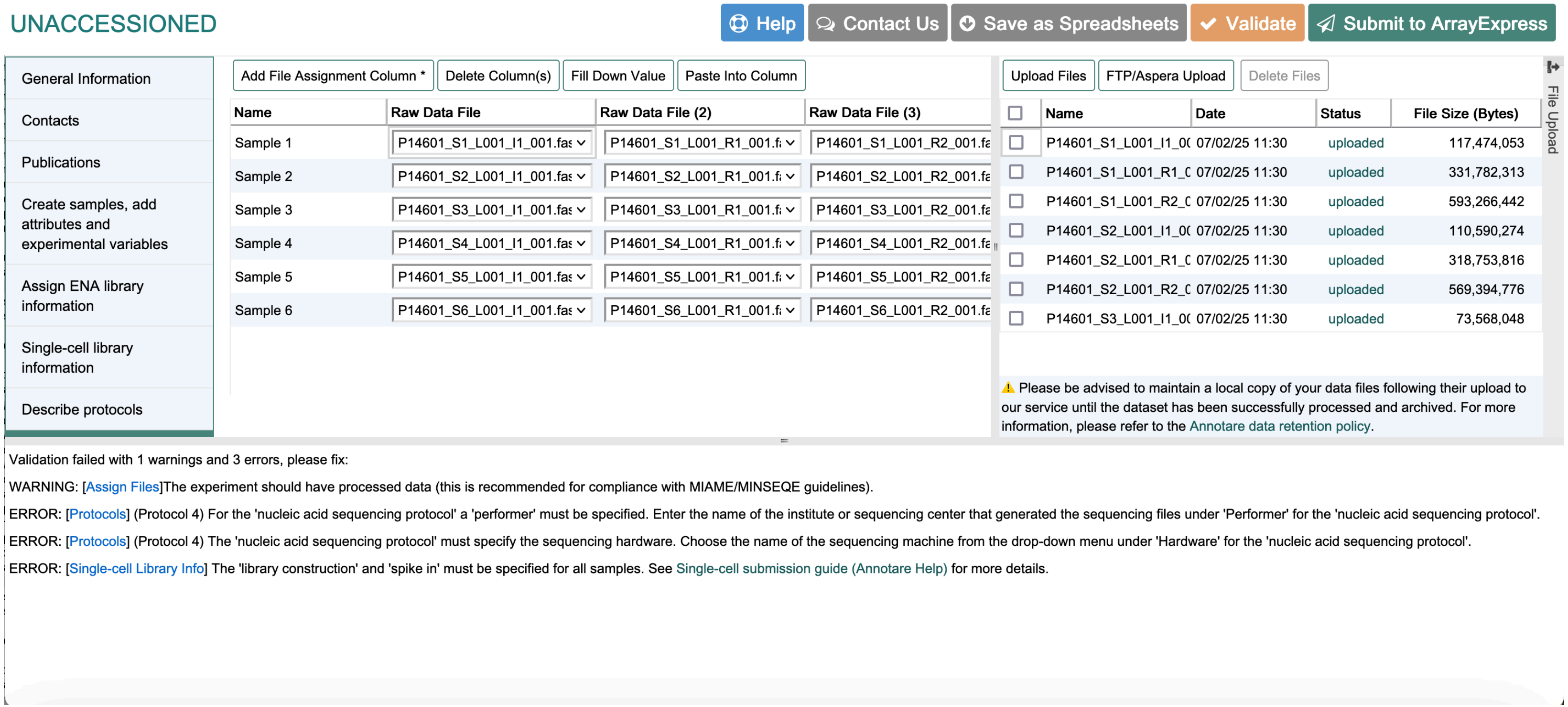
Please enter values, one per line:

☐	Name	Date	Status	File Size (Bytes)
☐	P14601_S1_L001_I1_0(	07/02/25 11:30	uploaded	117,474,053
☐	P14601_S1_L001_R1_C	07/02/25 11:30	uploaded	331,782,313
☐	P14601_S1_L001_R2_C	07/02/25 11:30	uploaded	593,266,442
☐	P14601_S2_L001_I1_0(	07/02/25 11:30	uploaded	110,590,274
☐	P14601_S2_L001_R1_C	07/02/25 11:30	uploaded	318,753,816
☐	P14601_S2_L001_R2_C	07/02/25 11:30	uploaded	569,394,776
☐	P14601_S3_L001_I1_0(	07/02/25 11:30	uploaded	73,568,048
	P14601_S3_L001_R1_C	07/02/25 11:30	uploaded	210,039,696
	1_S3_L001_R2_C	07/02/25 11:30	uploaded	404,662,485
☐	P1460 L001_I1_0(	07/02/25 11:30	uploaded	119,478,382

B1 fx P14601_S1_L001_I1_001.fastq.gz

	A	B	C	D	E
1	Sample 1	P14601_S1_L001_I1_001.fastq.gz	P14601_S1_L001_R1_001.fastq.gz	P14601_S1_L001_R2_001.fastq.gz	
2	Sample 2	P14601_S2_L001_I1_001.fastq.gz	P14601_S2_L001_R1_001.fastq.gz	P14601_S2_L001_R2_001.fastq.gz	
3	Sample 3	P14601_S3_L001_I1_001.fastq.gz	P14601_S3_L001_R1_001.fastq.gz	P14601_S3_L001_R2_001.fastq.gz	
4	Sample 4	P14601_S4_L001_I1_001.fastq.gz	P14601_S4_L001_R1_001.fastq.gz	P14601_S4_L001_R2_001.fastq.gz	
5	Sample 5	P14601_S5_L001_I1_001.fastq.gz	P14601_S5_L001_R1_001.fastq.gz	P14601_S5_L001_R2_001.fastq.gz	
6	Sample 6	P14601_S6_L001_I1_001.fastq.gz	P14601_S6_L001_R1_001.fastq.gz	P14601_S6_L001_R2_001.fastq.gz	
7					
8					
9					

Using Annotare – metadata validation



Name	Raw Data File	Raw Data File (2)	Raw Data File (3)
Sample 1	P14601_S1_L001_I1_001.fas	P14601_S1_L001_R1_001.f	P14601_S1_L001_R2_001.fa
Sample 2	P14601_S2_L001_I1_001.fas	P14601_S2_L001_R1_001.f	P14601_S2_L001_R2_001.fa
Sample 3	P14601_S3_L001_I1_001.fas	P14601_S3_L001_R1_001.f	P14601_S3_L001_R2_001.fa
Sample 4	P14601_S4_L001_I1_001.fas	P14601_S4_L001_R1_001.f	P14601_S4_L001_R2_001.fa
Sample 5	P14601_S5_L001_I1_001.fas	P14601_S5_L001_R1_001.f	P14601_S5_L001_R2_001.fa
Sample 6	P14601_S6_L001_I1_001.fas	P14601_S6_L001_R1_001.f	P14601_S6_L001_R2_001.fa

☐	Name	Date	Status	File Size (Bytes)
☐	P14601_S1_L001_I1_0	07/02/25 11:30	uploaded	117,474,053
☐	P14601_S1_L001_R1_	07/02/25 11:30	uploaded	331,782,313
☐	P14601_S1_L001_R2_	07/02/25 11:30	uploaded	593,266,442
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☐	P14601_S2_L001_R2_	07/02/25 11:30	uploaded	569,394,776
☐	P14601_S3_L001_I1_0	07/02/25 11:30	uploaded	73,568,048

⚠ Please be advised to maintain a local copy of your data files following their upload to our service until the dataset has been successfully processed and archived. For more information, please refer to the Annotare data retention policy.

Validation failed with 1 warnings and 3 errors, please fix:

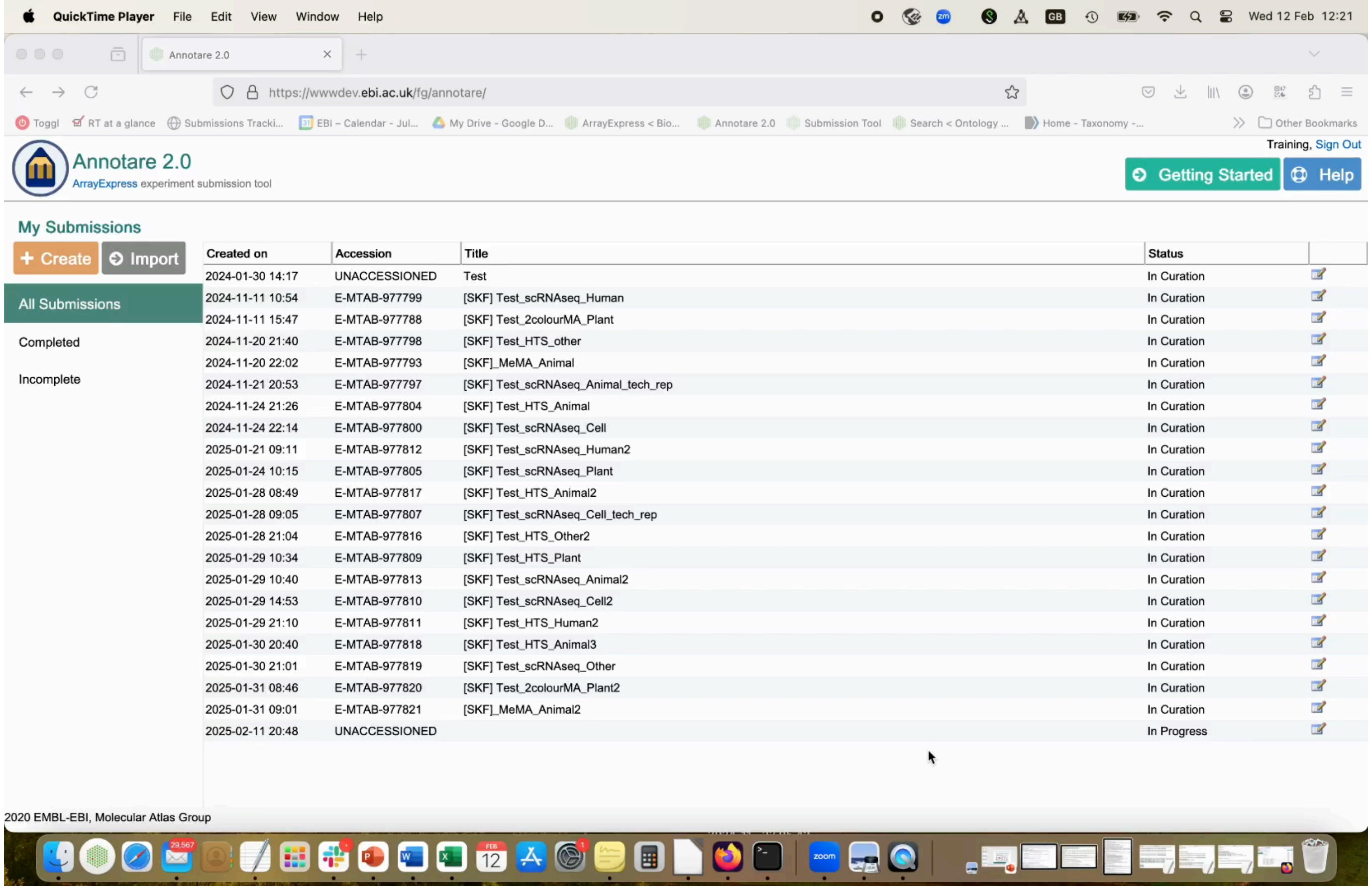
WARNING: [Assign Files]The experiment should have processed data (this is recommended for compliance with MIAME/MINSEQE guidelines).

ERROR: [Protocols] (Protocol 4) For the 'nucleic acid sequencing protocol' a 'performer' must be specified. Enter the name of the institute or sequencing center that generated the sequencing files under 'Performer' for the 'nucleic acid sequencing protocol'.

ERROR: [Protocols] (Protocol 4) The 'nucleic acid sequencing protocol' must specify the sequencing hardware. Choose the name of the sequencing machine from the drop-down menu under 'Hardware' for the 'nucleic acid sequencing protocol'.

ERROR: [Single-cell Library Info] The 'library construction' and 'spike in' must be specified for all samples. See Single-cell submission guide (Annotare Help) for more details.

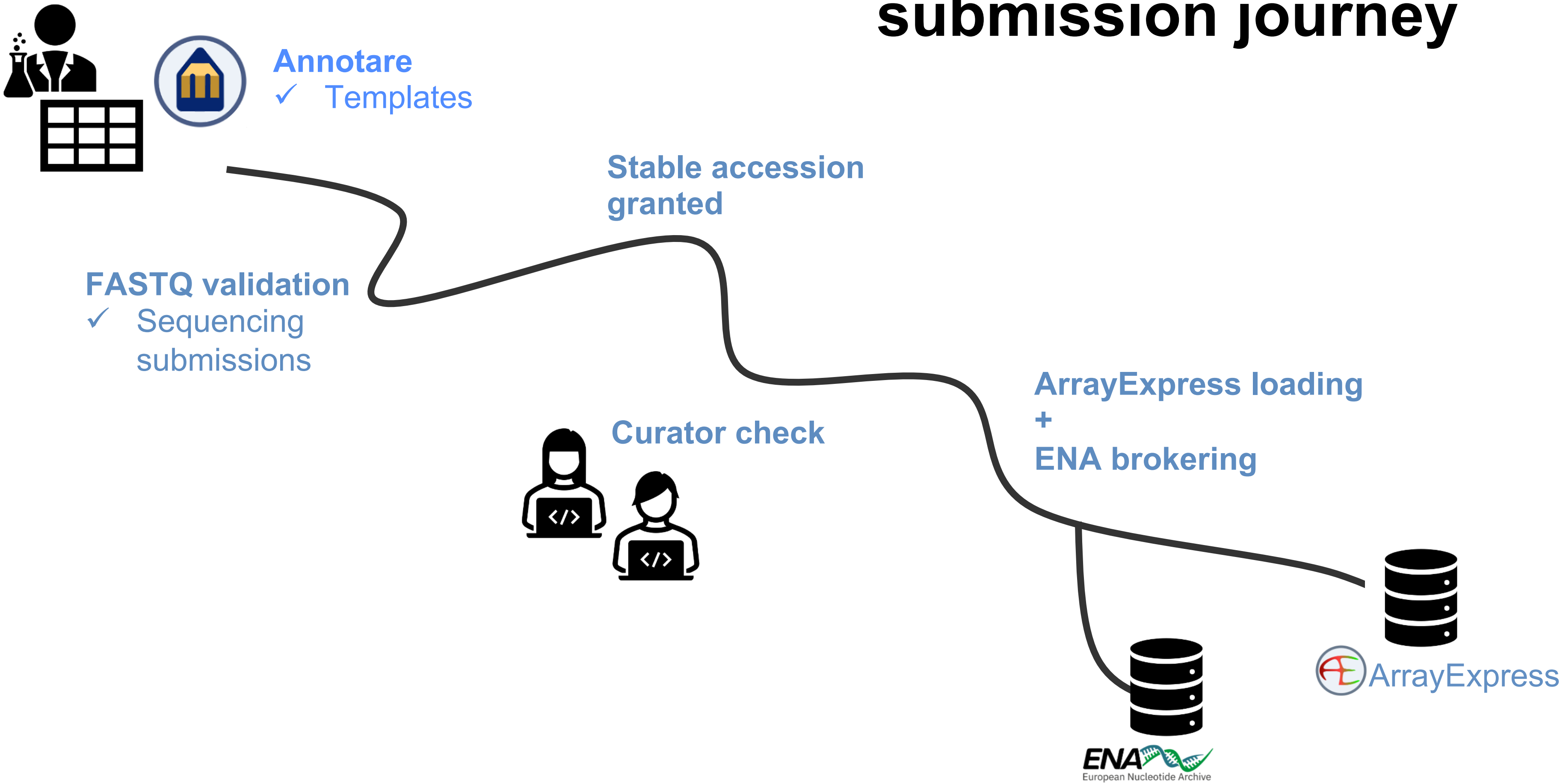
Using Annotare – demo



Created on	Accession	Title	Status
2024-01-30 14:17	UNACCESSIONED	Test	In Curation
2024-11-11 10:54	E-MTAB-977799	[SKF] Test_scRNAseq_Human	In Curation
2024-11-11 15:47	E-MTAB-977788	[SKF] Test_2colourMA_Plant	In Curation
2024-11-20 21:40	E-MTAB-977798	[SKF] Test_HTS_other	In Curation
2024-11-20 22:02	E-MTAB-977793	[SKF]_MeMA_Animal	In Curation
2024-11-21 20:53	E-MTAB-977797	[SKF] Test_scRNAseq_Animal_tech_rep	In Curation
2024-11-24 21:26	E-MTAB-977804	[SKF] Test_HTS_Animal	In Curation
2024-11-24 22:14	E-MTAB-977800	[SKF] Test_scRNAseq_Cell	In Curation
2025-01-21 09:11	E-MTAB-977812	[SKF] Test_scRNAseq_Human2	In Curation
2025-01-24 10:15	E-MTAB-977805	[SKF] Test_scRNAseq_Plant	In Curation
2025-01-28 08:49	E-MTAB-977817	[SKF] Test_HTS_Animal2	In Curation
2025-01-28 09:05	E-MTAB-977807	[SKF] Test_scRNAseq_Cell_tech_rep	In Curation
2025-01-28 21:04	E-MTAB-977816	[SKF] Test_HTS_Other2	In Curation
2025-01-29 10:34	E-MTAB-977809	[SKF] Test_HTS_Plant	In Curation
2025-01-29 10:40	E-MTAB-977813	[SKF] Test_scRNAseq_Animal2	In Curation
2025-01-29 14:53	E-MTAB-977810	[SKF] Test_scRNAseq_Cell2	In Curation
2025-01-29 21:10	E-MTAB-977811	[SKF] Test_HTS_Human2	In Curation
2025-01-30 20:40	E-MTAB-977818	[SKF] Test_HTS_Animal3	In Curation
2025-01-30 21:01	E-MTAB-977819	[SKF] Test_scRNAseq_Other	In Curation
2025-01-31 08:46	E-MTAB-977820	[SKF] Test_2colourMA_Plant2	In Curation
2025-01-31 09:01	E-MTAB-977821	[SKF]_MeMA_Animal2	In Curation
2025-02-11 20:48	UNACCESSIONED		In Progress

Submitted – what happens next?

submission journey



Annotare
- ✓ Templates

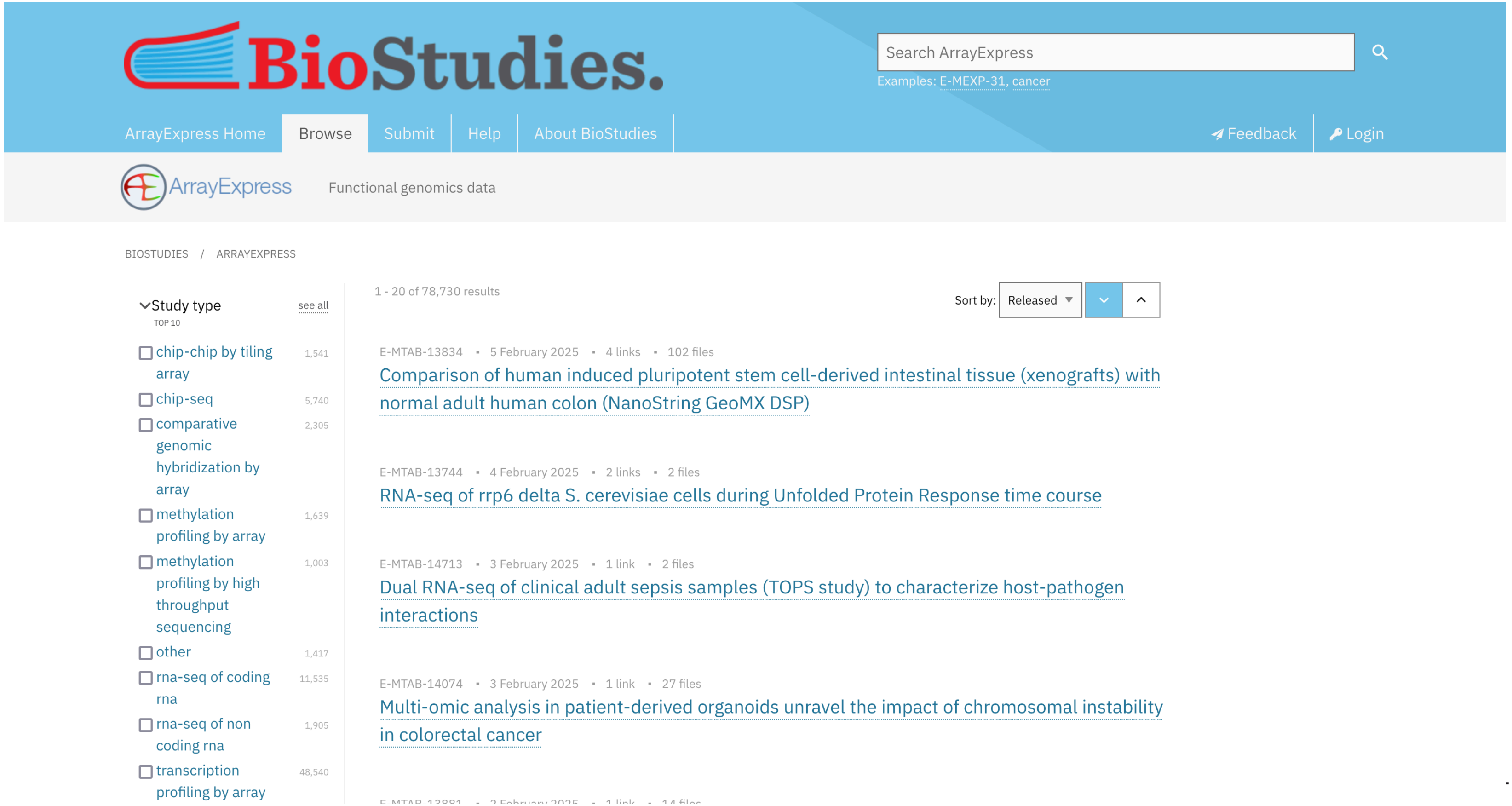
FASTQ validation
- ✓ Sequencing submissions

Stable accession granted

Curator check

ArrayExpress loading
+
ENA brokering

End result: experiment in BST/ArrayExpress



1 - 20 of 78,730 results

Study type see all

TOP 10

☐ chip-chip by tiling array	1,541
☐ chip-seq	5,740
☐ comparative genomic hybridization by array	2,305
☐ methylation profiling by array	1,639
☐ methylation profiling by high throughput sequencing	1,003
☐ other	1,417
☐ rna-seq of coding rna	11,535
☐ rna-seq of non coding rna	1,905
☐ transcription profiling by array	48,540

E-MTAB-13834 • 5 February 2025 • 4 links • 102 files
Comparison of human induced pluripotent stem cell-derived intestinal tissue (xenografts) with normal adult human colon (NanoString GeoMX DSP)

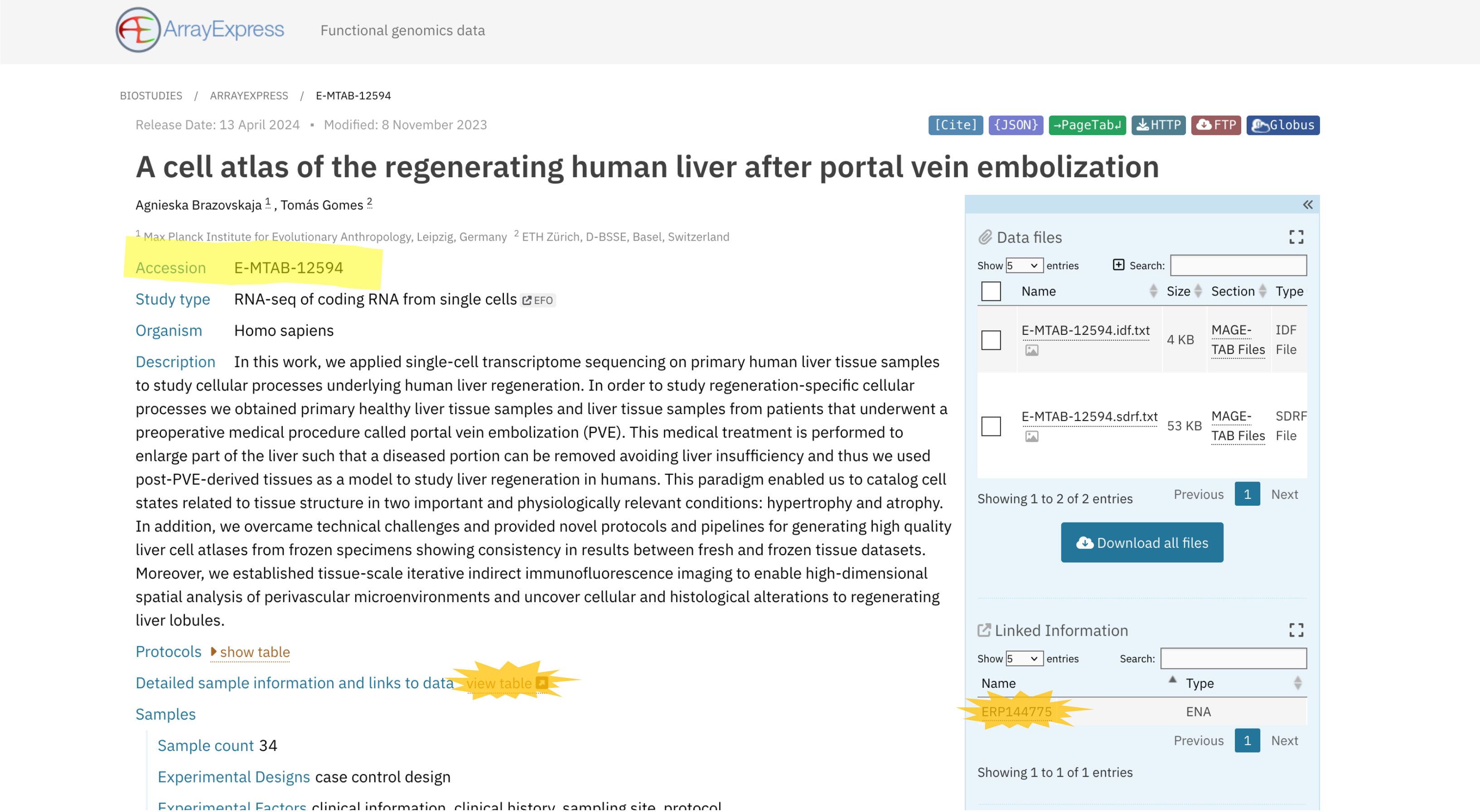
E-MTAB-13744 • 4 February 2025 • 2 links • 2 files
RNA-seq of rrp6 delta S. cerevisiae cells during Unfolded Protein Response time course

E-MTAB-14713 • 3 February 2025 • 1 link • 2 files
Dual RNA-seq of clinical adult sepsis samples (TOPS study) to characterize host-pathogen interactions

E-MTAB-14074 • 3 February 2025 • 1 link • 27 files
Multi-omic analysis in patient-derived organoids unravel the impact of chromosomal instability in colorectal cancer

E-MTAB-13881 • 2 February 2025 • 1 link • 14 files

End result: experiment in BST/ArrayExpress



Release Date: 13 April 2024 • Modified: 8 November 2023

A cell atlas of the regenerating human liver after portal vein embolization

Agnieszka Brazovskaja [1] , Tomás Gomes [2]

[1] Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany [2] ETH Zürich, D-BSSE, Basel, Switzerland

Accession E-MTAB-12594

Study type RNA-seq of coding RNA from single cells EFO

Organism Homo sapiens

Description In this work, we applied single-cell transcriptome sequencing on primary human liver tissue samples to study cellular processes underlying human liver regeneration. In order to study regeneration-specific cellular processes we obtained primary healthy liver tissue samples and liver tissue samples from patients that underwent a preoperative medical procedure called portal vein embolization (PVE). This medical treatment is performed to enlarge part of the liver such that a diseased portion can be removed avoiding liver insufficiency and thus we used post-PVE-derived tissues as a model to study liver regeneration in humans. This paradigm enabled us to catalog cell states related to tissue structure in two important and physiologically relevant conditions: hypertrophy and atrophy. In addition, we overcame technical challenges and provided novel protocols and pipelines for generating high quality liver cell atlases from frozen specimens showing consistency in results between fresh and frozen tissue datasets. Moreover, we established tissue-scale iterative indirect immunofluorescence imaging to enable high-dimensional spatial analysis of perivascular microenvironments and uncover cellular and histological alterations to regenerating liver lobules.

Protocols ▸ show table

Detailed sample information and links to data view table

Samples

- Sample count 34
- Experimental Designs case control design
- Experimental Factors clinical information, clinical history, sampling site, protocol

Data files

Show 5 entries Search:

☐	Name	Size	Section	Type
☐	E-MTAB-12594.idf.txt	4 KB	MAGE-TAB Files	IDF File
☐	E-MTAB-12594.sdrf.txt	53 KB	MAGE-TAB Files	SDRF File

Showing 1 to 2 of 2 entries Previous 1 Next

Download all files

Linked Information

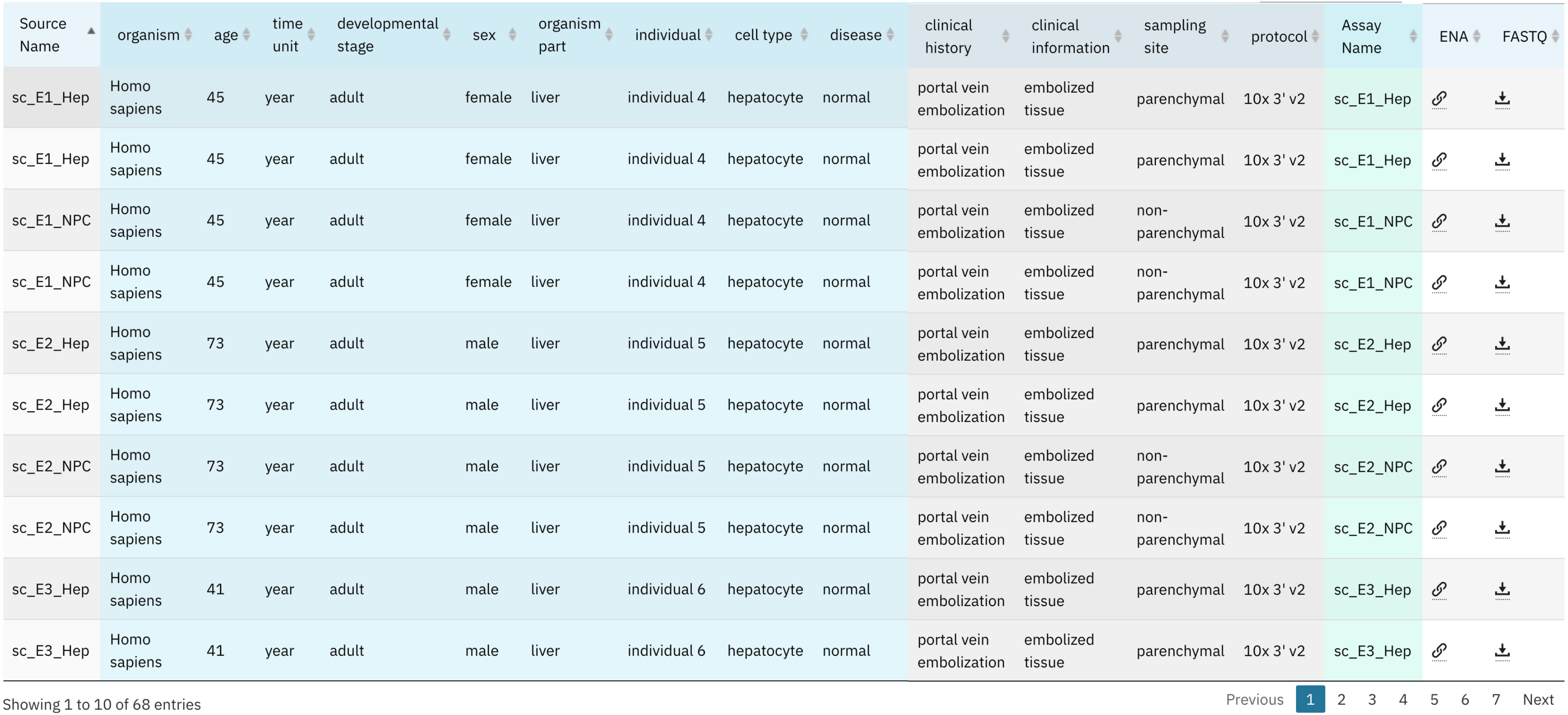
Show 5 entries Search:

Name	Type
ERP144775	ENA

Previous 1 Next

Showing 1 to 1 of 1 entries

End result: experiment in BST/ArrayExpress



Source Name	organism	age	time unit	developmental stage	sex	organism part	individual	cell type	disease	clinical history	clinical information	sampling site	protocol	Assay Name	ENA	FASTQ
sc_E1_Hep	Homo sapiens	45	year	adult	female	liver	individual 4	hepatocyte	normal	portal vein embolization	embolized tissue	parenchymal	10x 3' v2	sc_E1_Hep	🔗	⬇
sc_E1_Hep	Homo sapiens	45	year	adult	female	liver	individual 4	hepatocyte	normal	portal vein embolization	embolized tissue	parenchymal	10x 3' v2	sc_E1_Hep	🔗	⬇
sc_E1_NPC	Homo sapiens	45	year	adult	female	liver	individual 4	hepatocyte	normal	portal vein embolization	embolized tissue	non-parenchymal	10x 3' v2	sc_E1_NPC	🔗	⬇
sc_E1_NPC	Homo sapiens	45	year	adult	female	liver	individual 4	hepatocyte	normal	portal vein embolization	embolized tissue	non-parenchymal	10x 3' v2	sc_E1_NPC	🔗	⬇
sc_E2_Hep	Homo sapiens	73	year	adult	male	liver	individual 5	hepatocyte	normal	portal vein embolization	embolized tissue	parenchymal	10x 3' v2	sc_E2_Hep	🔗	⬇
sc_E2_Hep	Homo sapiens	73	year	adult	male	liver	individual 5	hepatocyte	normal	portal vein embolization	embolized tissue	parenchymal	10x 3' v2	sc_E2_Hep	🔗	⬇
sc_E2_NPC	Homo sapiens	73	year	adult	male	liver	individual 5	hepatocyte	normal	portal vein embolization	embolized tissue	non-parenchymal	10x 3' v2	sc_E2_NPC	🔗	⬇
sc_E2_NPC	Homo sapiens	73	year	adult	male	liver	individual 5	hepatocyte	normal	portal vein embolization	embolized tissue	non-parenchymal	10x 3' v2	sc_E2_NPC	🔗	⬇
sc_E3_Hep	Homo sapiens	41	year	adult	male	liver	individual 6	hepatocyte	normal	portal vein embolization	embolized tissue	parenchymal	10x 3' v2	sc_E3_Hep	🔗	⬇
sc_E3_Hep	Homo sapiens	41	year	adult	male	liver	individual 6	hepatocyte	normal	portal vein embolization	embolized tissue	parenchymal	10x 3' v2	sc_E3_Hep	🔗	⬇

Showing 1 to 10 of 68 entries

EMBL-EBI

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Pedro Madrigal

Iris Diana Yu

Anil Shantilal Thanki

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Jose Carlos Marugan

Liora Vilmovsky

Sandeep Reddy Kurri

Software Development

Karoly Erdos

Lingyun Zhao

Upendra Kumbham

Questions?

Dr Silvie Korena Fexova

Submissions Project Lead
Functional Genomics Team

EMBL-EBI