

# Importing Feature Barcoding Data

- [Create a new Project](#)
- [Import data](#)

## Create a new Project

Let's start by creating a new project.

- On the *Home page*, click **New project** (Figure 1)
- Give the project a name
- Click **Create project**

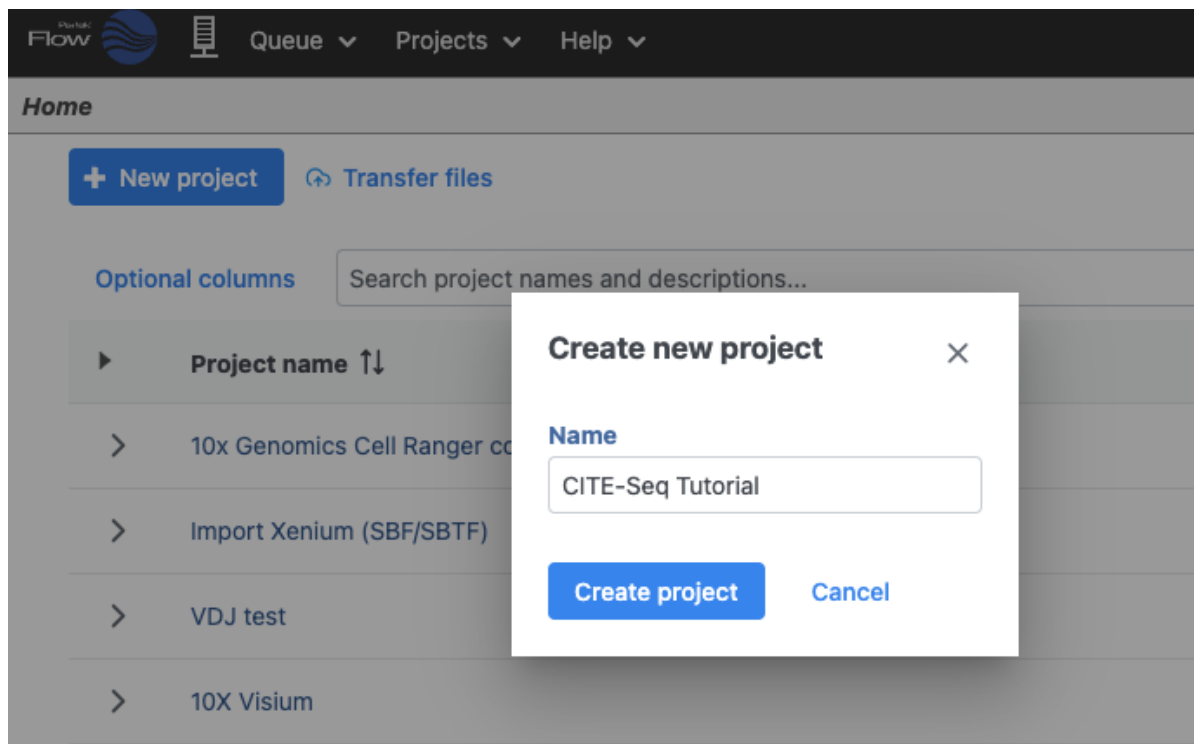


Figure 5. Create a new project and give it a meaningful name (e.g. CITE-Seq tutorial)

## Import data

- In the Analyses tab, click **Add data**
- Click **10x Genomics Cell Ranger counts h5** (Figure 2)
- Choose the filtered HDF5 file for the MALT sample produced by Cell Ranger

Single cell
Bulk
Other

scRNA-Seq
Spatial transcriptomics
scATAC-Seq
V(D)J
Flow/Mass Cytometry

Select the format

☐ Import scRNA count feature-barcode-mtx  
This sparse matrix output is common for 10x Genomics, Fluent Biosciences and Parse Biosciences. Each sample has 3 files (two .csv with one .mtx or two .tsv with one .mtx for each sample).

☒ 10x Genomics Cell Ranger counts h5  
This compressed binary format is preferred for 10x Genomics Cell Ranger output. There is 1 filtered .h5 file per sample and multiple files can be selected

☐ Full count matrix  
This rectangular cell-by-feature count matrix is common for BD Rhapsody. There is one file for one or more samples (txt, csv, tsv, txt.gz, csv.gz, tsv.gz)

☐ Seurat Rds  
This R object is for data processed by Seurat (.rds)

☐ h5ad  
This AnnData object in the h5ad file format is for data processed by Scanpy

☐ fastq  
The fastq format is used for unaligned reads. Acceptable file types are fastq, fastq.gz, fastq.bz2, fq, fq.gz, fq.bz2

Back
Next

Figure 6. Import options for CITE-Seq tutorial data

Move the .h5 file to where Partek Flow is installed using , then browse to its location.

File select

Transfer files to the server

Current directory ⓘ

/home/flow/FlowData/CITE-Seq Goto

CITE-Seq
CR\_h5\_scRNA
Generic\_count
library\_files
library\_files\_local
Parse\_f-b-m\_format
Parse\_res

Don't see your folder? [Refresh folder list](#)

1 files selected

<input checked="" type="checkbox"/>	Name	Size
<input checked="" type="checkbox"/>	malt_10k_protein_v3_filtered_feature_bc_matrix.h5	18.75 MB

Valid files are: txt, csv, tsv, .h5, .loom, fcs or gz

Back
Next

Figure 7. Import options for CITE-Seq tutorial data

Note that Partek Flow also supports the feature-barcode matrix output (barcodes.tsv, features.tsv, matrix.mtx) from Cell Ranger. The import steps for a feature-barcode matrix are identical to this tutorial.

- Click **Next**
- Name the sample **MALT** (the default is the file name)
- Specify the annotation used for the gene expression data (here, we choose **Homo sapiens (human) - hg38** and **Ensembl Transcripts release 109**). If Ensembl 109 is not available from the drop-down list, choose **Add annotation** and download it.
- Check **Features with non-zero values across all samples** in the *Report* section
- Click **Finish** (Figure 3)

### Sample names

<input checked="" type="checkbox"/>	Sample name	Files	Cells	Features
<input checked="" type="checkbox"/>	MALT	malt_10k_protein_v3_filtered_feature_bc_matrix.h5	8412	33555

### Feature annotation

#### ☒ Use annotation file

Select the file that has been used to generate the feature counts (e.g. gene or protein information).

#### Assembly

Homo sapiens (human) - hg38 ▾

#### Annotation model

Ensembl Transcripts release 109 (Matt Luberti) ▾

#### Primary feature identifier

- ☒ Feature name (Values: MIR1302-2HG, FAM138A, OR4F5, AL627309.1, AL627309....)  
☐ Feature ID (Values: ENSG00000243485, ENSG00000237613, ENSG00000186092,...)

#### Deduplication method

If the feature ID is not unique, the feature will be summarized by the selected method.

- ☒ Mean ☐ Maximum ☐ Sum

### Count value format

- ☒ Raw count ☐ Normalized count with log base None ▾

### Report

- ☐ All features ☒ Features with non-zero values across all samples

#### ☒ Cells with total read count at least

A low total read count threshold will result in a large number of cells which might take a long time to import

400

Back

Finish

Figure 8. File format options for MALT data set

A *Single cell counts* data node will be created under the *Analyses* tab after the file has been imported. We can move on to processing the data.

« Analyzing CITE-Seq Data Data Processing »

## Additional Assistance

If you need additional assistance, please visit [our support page](#) to submit a help ticket or find phone numbers for regional support.



Your Rating:  Results:  7 rates