Analyzing CITE-Seq Data

- Importing Feature Barcoding Data
- Data Processing
- Dimensionality Reduction and Clustering
- Classifying Cells
- Differentially Expressed Proteins and Genes

This tutorial presents an outline of the basic series of steps for analyzing a 10x Genomics Gene Expression with Feature Barcoding (antibody) data set in Partek Flow starting with the output of Cell Ranger.

If you have Cell Hashing data, please see our documentation on Hashtag demultiplexing.

This tutorial includes only one sample, but the same steps will be followed when analyzing multiple samples. For notes on a few aspects specific to a multi-sample analysis, please see our Single Cell RNA-Seq Analysis (Multiple Samples) tutorial.

If you are new to Partek Flow, please see Getting Started with Your Partek Flow Hosted Trial for information about data transfer and import and Creating and Analyzing a Project for information about the Partek Flow user interface.

Data set

The data set for this tutorial is a demonstration data set from 10x Genomics. The sample includes cells from a dissociated Extranodal Marginal Zone B-Cell Tumor (MALT: Mucosa-Associated Lymphoid Tissue) stained with BioLegend TotalSeq-B antibodies. We are starting with the Feature / cell matrix HDF5 (filtered) produced by Cell Ranger. Prior to beginning, transfer this file to your Partek Flow using the **Transfer files** button on the homepage.

Additional Assistance

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

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