

Pipeline management

The Pipeline management page allows users to view and manage the pipelines within a Partek Flow instance. To access the page, click the avatar on the top right corner, choose **Settings**, then select **Pipelines** on the left. This page can be accessed by administrative and non-administrative users. The table (Figure 1) shows a list of pipelines with their description, creation date, and the display name of the owner (the user who created or imported the pipeline). Non-administrative users can see pipelines created by other Partek Flow users in the table if the pipeline has been shared by the user. Administrative users can see all details.

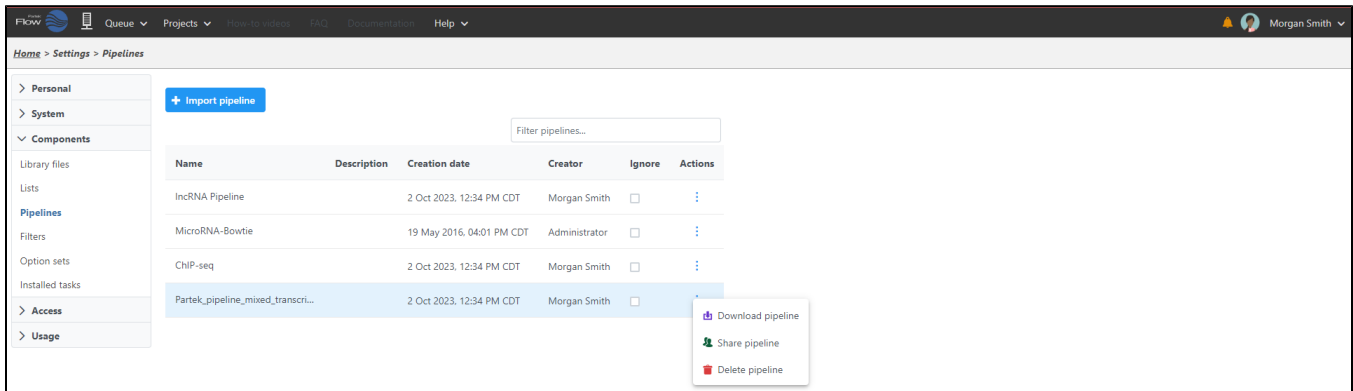



Figure 1. Pipeline Management Page view of an administrative user. The view for non-administrative users will not have the 'Enable by default' column and,


Hiding Pipelines

All pipelines that have been created or imported within the same Partek Flow instance can be shared by all users. The pipeline manager allows each user to choose the pipelines that appear on their Task Menu. To hide a pipeline, select the corresponding checkbox in the *Ignore* column (Figure 1).

Downloading a pipeline

To download a pipeline, click the  **Download pipeline** in the Actions column. A file with the extension *.pipeline will be download to the default download directory of your local computer.

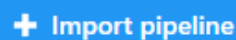
Deleting a pipeline

Pipelines can be deleted by the owner (as listed in the Creator column) or by a user with admin privileges. Clicking  **Delete pipeline** in the Actions column will delete the pipeline and it will no longer be available to any Partek Flow user. Note that deleting a pipeline affects all users of the same Partek Flow instance.

Importing a Pipeline

Within the Pipeline management page, you can upload a pipeline from your local computer or import a pre-built pipeline directly from the Partek website. You can import a pipeline even before you create or open a project within Partek Flow.

From My Computer



1. To import a .pipeline file from your local machine, click on the **Import pipeline** button
2. By default, the **My computer** option at the top of the *Import pipeline* page should already be selected. Click the **Choose** button (Figure 2)
3. Browse to the location of the .pipeline file on your local machine and select it for upload. The selected file name will be displayed next to the *Choose pipeline* button
4. If you wish to give the pipeline a new name, type a new name into the *Rename pipeline* box and click **Import**

My computer

Hosted pipelines

Pipeline file

+ Choose

Task section

Pipelines

Rename pipeline

Import

Cancel

Figure 2. Importing a pipeline from your local machine

From Partek Website

+ Import pipeline

1. To download a pipeline from the Partek website, click on the **Import pipeline** button
2. Select **Hosted pipelines** (Figure 3). This will display all available pre-built pipelines from the Partek website.
3. Click the **Import pipeline** button next to the pipeline you wish to import (Figure 3). Alternatively, click **Import all pipelines** at the bottom of the page to import all pipelines displayed.

My computer

Hosted pipelines

Lexogen QuantSeq Pipeline

This pipeline works with unaligned reads generated by the Lexogen QuantSeq library prep kit. It performs adapter trimming and quality trimming, aligns data to a reference genome, and quantifies read counts with a transcriptome model. This pipeline works with Partek Flow 6.0.17.0903 and later.

Note: This pipeline requires a fasta file of adapter sequences for the adapter trimming step. Please contact support@partek.com to obtain this file.

Import pipeline

Lexogen QuantSeq FWD-UMI Pipeline

This QuantSeq FWD-UMI Data Analysis Pipeline works with unaligned reads generated by the Lexogen QuantSeq Library Prep Kit that contain Unique Molecular Identifiers (UMIs) in Read 1. It performs adapter trimming and quality trimming, aligns data to a reference genome, deduplicates read counts based on identical read location and UMI criteria, and quantifies read counts with a transcriptome model. This pipeline works with Partek Flow 8.0.19.0508 and later.

Note: The pipeline requires Lexogen QuantSeq FWD-UMI prep kit, which can be downloaded to the Library File Management.

Import pipeline

Dolomite Bio Drop-Seq Pipeline

This pipeline is suitable for analyzing Drop-Seq data from single-cells that have been processed on a Dolomite Bio Nadia instrument. Starting with paired scRNA-Seq fastq files, the UMI & cell barcodes are trimmed and the reads are aligned to a reference genome. Pre- and post-alignment QA/QC reports are produced in addition to a coverage report. Finally, the UMIs are deduplicated. The 'knee' plot can be inspected and used to filter high-quality cell barcodes for downstream analysis (e.g. Quantify to barcodes, single cell QA/QC etc).

Import pipeline

Figure 3. Pre-built pipelines that can be imported from the Partek website. To preview a pipeline to see more detail, click the pipeline image

For additional information, visit the [Pipelines](#) documentation page.

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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