

Adding a Reference Sequence

Click the **green plus (+)** icon next to the *Reference Files* section header and choose **Reference sequence** from the *Library type* drop-down list in the *Add reference sequence* dialog (Figure 1). Alternatively, click the **Add library file** button and choose *Reference sequence* from the *Library type* drop-down list. If a cytoband file is already associated with an assembly, *Reference sequence* will be the only option available in the *Add reference sequence* dialog and will not appear in a drop-down list (Figure 1).

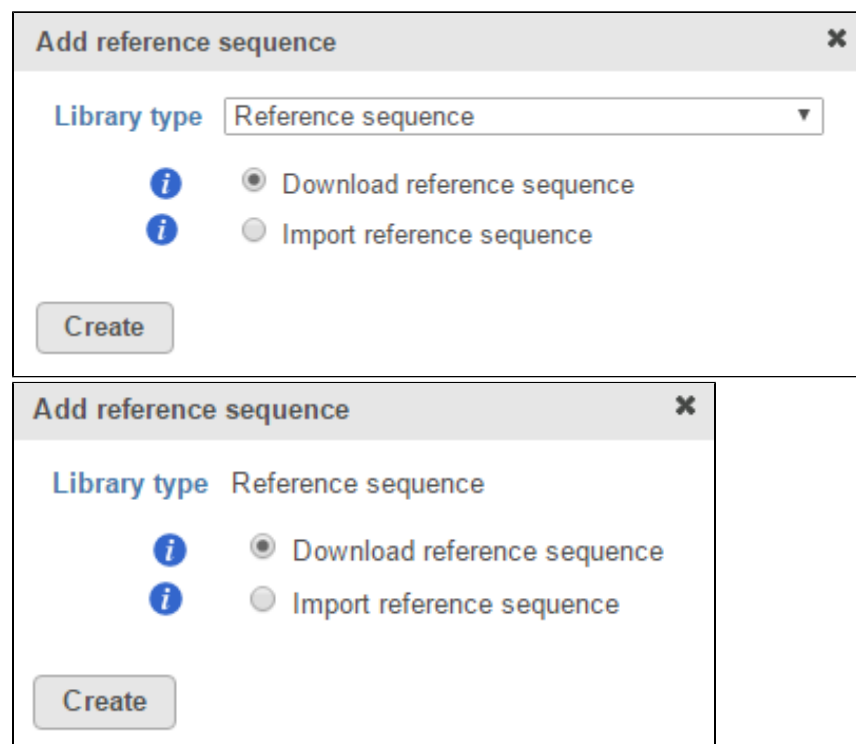


Figure 1. Add reference sequence dialog. If the reference sequence and cytoband files have not been added yet, both options will appear in the Library type drop-down list (left). If one is missing, it will appear as the only option (right). For many model organisms, automatic downloads are available from the Partek repository.

If you are using an assembly supported by Partek (e.g. human), there are two radio button options: *Download reference sequence* and *Import reference sequence* (Figure 1). Select **Download reference sequence** and click **Create** to get the reference sequence from the Partek repository. Alternatively, select **Import reference sequence** and click **Create** to add the reference sequence from another source.

If you are using a custom assembly (e.g. for a non-model organism), only the *Import reference sequence* radio button will be available (Figure 2).

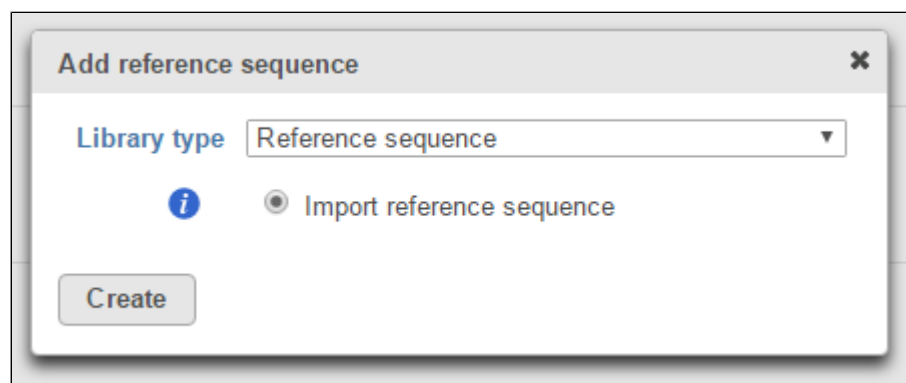


Figure 2. For custom assemblies, automatic downloads are not available so the reference sequence has to be imported from another source

The *Import reference sequence* option allows you to add a reference sequence from the *Partek Flow Server*, *My Computer* or a *URL* download link (Figure 3).

Figure 3. A reference sequence can be added from multiple sources

To add a reference sequence from the Partek Flow server, select **Partek Flow Server**, click **Browse** and navigate to the directory storing the reference sequence file(s) (Figure 4). Only files with the correct file extensions (.fa, .2bit or any compressed format) will be displayed in the file browser. Select the checkbox next to the file name(s) you wish to import and click **Continue** (Figure 4). Click **Finish** to add the selected reference sequence file(s) (Figure 3).

	Name	Size
☐	Example_reference_sequence.2bit	237.53 MB
☒	Example_reference_sequence.fa	795.49 MB
☐	Example_reference_sequence.fa.bz2	196.40 MB
☐	Example_reference_sequence.fa.gz	212.05 MB
☐	Example_reference_sequence.fa.tar	212.05 MB
☐	Example_reference_sequence.fa.zip	212.05 MB

Figure 4. Add a reference sequence file(s) from the Partek Flow Server

To upload a reference sequence from your local computer select **My computer**, click **Choose file** and navigate to the location of the file(s) on your local machine (Figure 5). It is not advisable to upload large files through the web browser, as this will likely result in an error (e.g. an upload timeout). Administrative users are able to set a limit on the upload file size via [System preferences](#). The default file size limit is 500 MB. Please note that only one file can be uploaded at a time. Click **Finish** to add the selected reference sequence file(s) (Figure 5).

Figure 5. Upload a reference sequence file from your local computer through the browser

To download a reference sequence (e.g. from a public repository such as ENSEMBL), select **URL** and input the URL address (Figure 6). Make sure to include the full URL address, starting with the transfer protocol (e.g. `http://` or `ftp://`) and ending with the file name. It is advisable to find the download link address, copy it to the clipboard and paste it into the *Input URL* box. Click **Finish** to add the selected reference sequence file(s) (Figure 6).

Figure 6. Download a reference sequence from the internet

Note that you can specify multiple fasta files (e.g. one file per chromosome) and Partek Flow will concatenate them. If a fasta file is imported, a 2bit version of the file will automatically be created and vice-versa. Partek Flow will also accept a range of compressed file formats (gzip, bzip2, zip, tar). If a compressed file is imported, it will automatically be uncompressed and processed.

Additional Assistance

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

« [Adding Library Files on the Library File Management Page](#) [Adding a Cytoband](#) »



Your Rating: ☆☆☆☆☆ Results: ★★★★★ 42 rates

