

Adding Reference Aligner Indexes

Note that this task is for adding indexes for alignment to the whole genome. If you want to align to the transcriptome or another set of genomic features, see [Adding Aligner Indexes Based on an Annotation Model](#).

Click the **green plus (+)** icon next to *Reference aligner indexes* section header on the [library file management page](#). Alternatively, click the **Add library file** button, choose **Aligner index** from the *Library type* drop-down list and **whole genome** from the *Index to* drop-down list. If an aligner index is already associated with an assembly, it will not appear in the *Aligner* drop-down list. If all but one of the possible aligner indexes have been added, the remaining aligner index will be the only option and will not appear in a drop-down list (Figure 1).

The figure displays two instances of the 'Add aligner index' dialog box. The top dialog shows the 'Aligner' dropdown menu set to 'Bowtie index'. Below this, there are three radio button options: 'Download index' (which is selected), 'Build index', and 'Import index'. Each option is preceded by an information icon (i). At the bottom of the dialog is a 'Create' button. The bottom dialog shows the 'Aligner' dropdown menu set to 'Isaac 2 index'. It also has three radio button options: 'Download index' (selected), 'Build Isaac 2 index', and 'Import index', each with an information icon. A 'Create' button is also present at the bottom.

Figure 1. Add aligner index dialog. If more than one aligner index has not been added to an assembly, the missing aligner indexes will appear in the drop-down list (left). If only one aligner index remains to be added, it will be the only option (right). For many model organisms, automatic downloads are available from the Partek repository

Choose the aligner index you wish to add from the drop-down list in the *Add aligner index* dialog (Figure 1). The following indexes can be added:

- Bowtie
- Bowtie colorspace
- Bowtie 2
- TMAP
- BWA
- SHRIMP 2
- SHRIMP 2 colorspace
- Isaac 2
- STAR
- STAR 2.4 1d
- GSNAP
- GSNAP v8

If you are using an assembly supported by Partek (e.g. human), there are three radio button options: *Download index*, *Build index* or *Import index* (Figure 1). Certain aligner indexes may not be available for automatic download because the file sizes are too large to download efficiently.

If available, select **Download index** and click **Create** to get the chosen reference aligner index from the Partek repository.

Alternatively, select **Import index** and click **Create** to add an aligner index from another source. An aligner index can be added from the *Partek Flow Server*, *My Computer* or a *URL* download link. The behavior of each option is similar to when importing a reference sequence (see [Adding a Reference Sequence](#)). When browsing for files on the Partek Flow server, only the files with relevant file extensions will be visible. This will vary for each aligner.

Add aligner index

Library type

Aligner index

Aligner

Bowtie index

i

☒ Build index

i

☐ Import index

Create

Additional Assistance

« Adding a Cytoband Adding a Gene Set »

