

# Adding Aligner Indexes Based on an Annotation Model

Note that this task is for adding indexes for alignment to a subset of the genome (e.g. the transcriptome). If you want to align to the whole genome, see [Adding Reference Aligner Indexes](#).

On the [library file management page](#), click the **green plus (+)** icon next to the *Annotation models* section header and choose **Aligner index** from the Library type drop-down list in the dialog (Figure 1). Alternatively, click the **Add library file** button, and choose **Aligner index** from the [Library type drop-down list](#).

Choose the aligner you wish to use from the *Aligners* drop-down list (Figure 1). All aligners are available for indexing to an annotation model.

The annotation model(s) that have already been associated with an assembly will appear at the top of the *Index to* drop-down list. Choose the annotation model you wish to index to, select the **Build index** radio button and click **Create** (Figure 1). To build an aligner index based on an annotation model, a [reference sequence](#) file must already be associated with the assembly.

If you are using an assembly supported by Partek (e.g. human), annotation models from a variety of commonly used sources will appear in the *Index to* drop-down list in addition to the ones that have already been associated with the assembly. If you choose an annotation model that has not already been associated, it will automatically be downloaded prior to building the index.

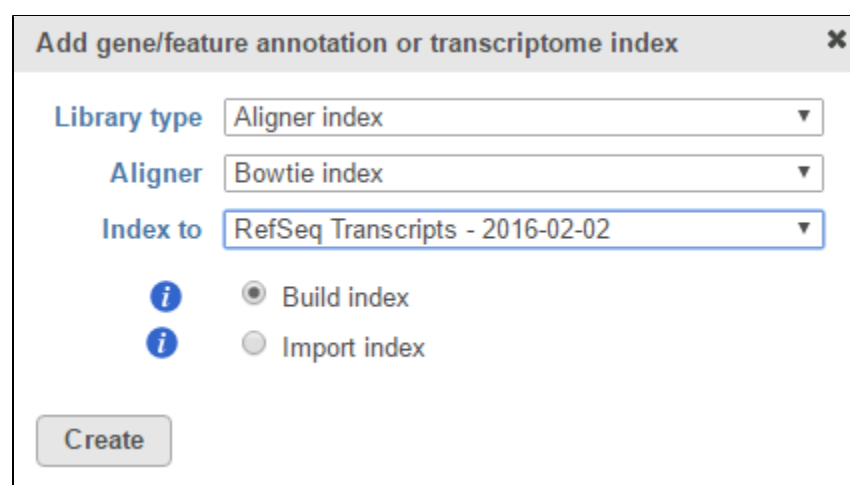


Figure 1. Building an aligner index for an annotation model

## 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 an Annotation Model](#) [Adding Library Files from Within a Project](#) »



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