

Right-click (context) menus

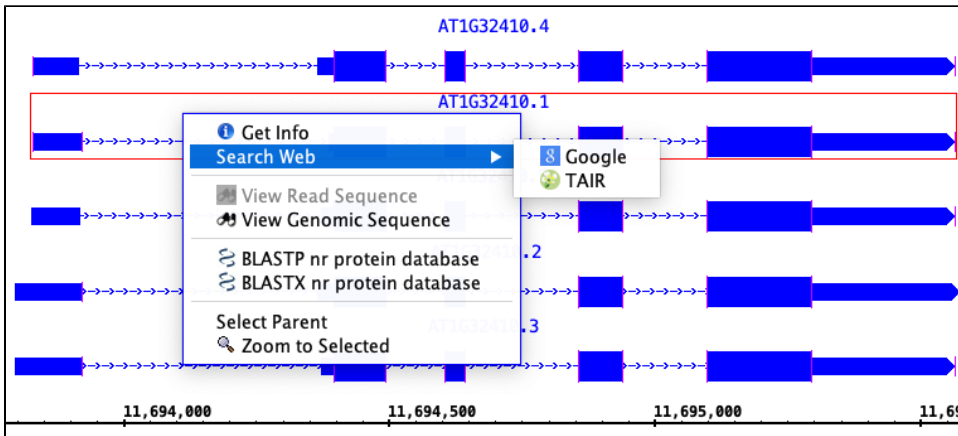
IGB displays context menus when you right-click track labels or items in the data display area. These menus are called "context menus" because the menu options you'll see depend on what you clicked.

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Right-clicking annotations

When you right-click an annotation, you'll see a context menu with the following options:

- **Get Info** displays the **Selection Info** panel containing information relevant to your selection.
- **Search Web** opens your web browser to Web pages that have more information about the selected model.
- **View Genomic Sequence** loads genomic sequence (if not already loaded) and displays it in a new **Sequence Viewer** window.
- **BLASTP nr protein database** searches a non-redundant **protein** database using a **protein** query.
- **BLASTX nr protein database** searches a non-redundant **protein** database using a **translated nucleotide** query.
- **Select Parent** selects the feature of which the right-clicked item is a part. For example, if you right-click an exon and choose **Select Parent**, the entire gene model is selected.
- **Zoom to Selected** zooms to the right-clicked item. Choosing this option is the same as double-clicking.

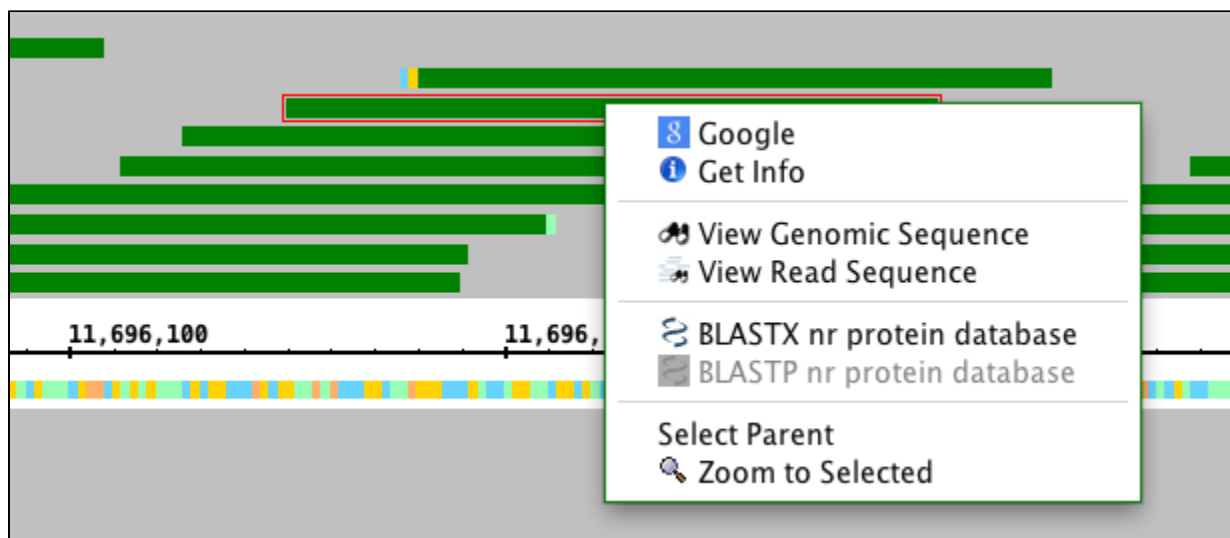


Right-clicking alignments

When you right-click an alignment, you'll see the same options as in the preceding section plus new options specific to alignments. Context menu items for alignments include:

View Read Sequence opens the aligned sequence in the **Sequence Viewer**.

For more information about alignments, see [Visualizing read alignments](#).

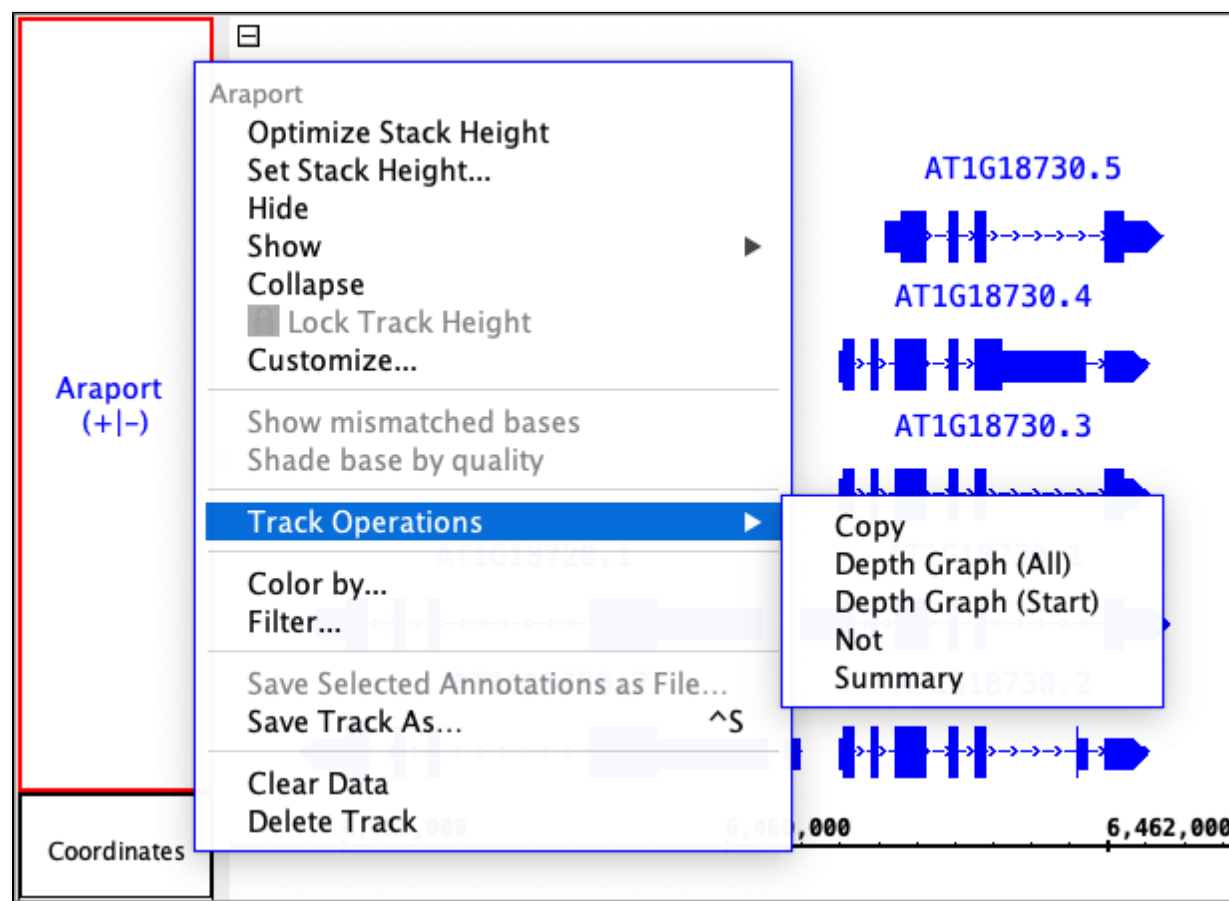


Track labels

Right click a track label to view options and operations.

The menu you see will vary depending on the track type.

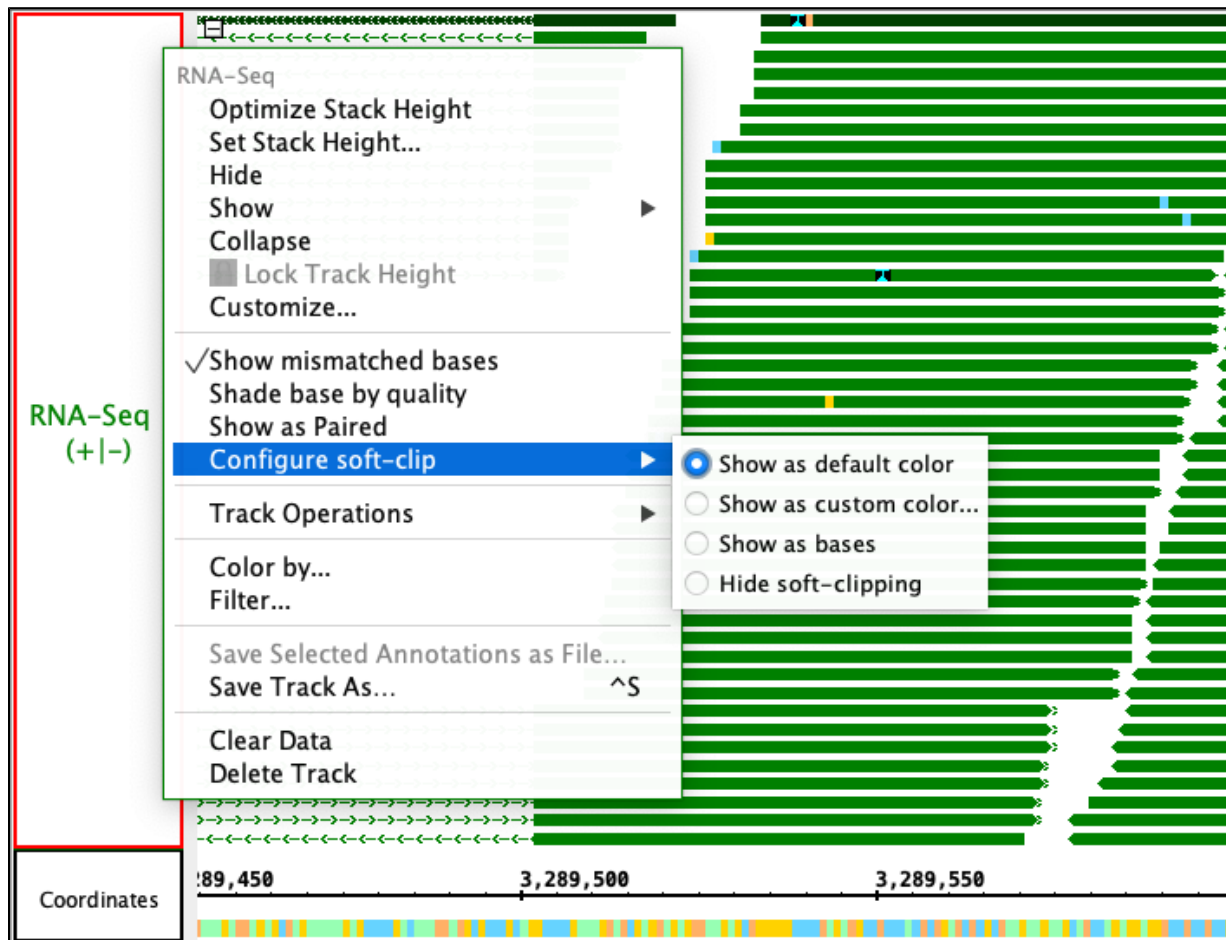
Annotation track right-click menu



- **Optimize Stack Height** sets the stack height so that all available annotations in the currently visible region are shown.
- **Set Stack Height...** opens a window that allows you to set the stack height.
- **Hide** hides the track.

- **Show** shows hidden tracks.
- **Collapse** compresses the track so that all annotations occupy a single row.
- **Lock Track Height** locks the track at its current height.
- **Customize...** opens the **Preferences > Tracks** tab window. See [Tracks](#)
- **Track Operations** performs operations on a track. See [Annotation track operations](#)
- **Color by...** changes annotation color depending on annotation attributes. See [Customize annotation colors using Color By](#)
- **Filter...** filters annotations based on their attributes. See [Filter annotation data](#)
- **Save Selected Annotations as File...** saves selected annotations to a file.
- **Save Track As...** saves all the data in the track as a file.
- **Clear Data** removes all data from the current sequence for the selected tracks.
- **Delete Track** deletes the selected track.

Short read (alignment) track right-click menu



- **Show mismatches** highlights bases that do not match the corresponding base in the reference sequence.
- **Shade base by quality** highlights bases based on quality score.
- **Show as Paired** connects paired reads by a thin black line and colors reads by strand. See [Paired-end reads](#)
- **Configure Soft-clip** configures the way soft-clipping is displayed. See [Soft-clipped reads](#)
- **Track Operations** performs operations on a track. See [Creating graph tracks from annotations tracks](#)

Graph track right-click menu

