

Selecting Items

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Introduction

Most objects in the IGB display can be selected by clicking on them. These include annotations, graphs, results from search sequence, and entire tracks.

When an item is selected, IGB draws a red box around it.

IGB also supports selecting and deselecting more than one item at once.

How to select an item (or items) in IGB

To select items, click the pointer icon to activate the selection tool:



The following are ways to select items in the **Main View** window using the selection tool; selections are outlined in red.

To do this:	Do this:
Select a single annotation or feature.	Click it.
Select a multi-exon gene model	Click a line connecting exons or on the label (if active).
Select a single-exon gene model	Click an exon, right-click and choose Select parent .
Add to the current selection	SHIFT-click to add individual items or shift and drag to add multiple items.
Select multiple items in the display	Click-drag the mouse over all items you wish to select. Start the drag in an empty area. SHIFT-click or SHIFT-drag to add to current selection. <div style="border: 1px solid #ccc; padding: 5px; margin-top: 10px;"><p> Click-dragging selects entire annotations rather than individual parts.</p></div> <div style="border: 1px solid #ccc; padding: 5px; margin-top: 10px;"><p> IGB reports the number of selected items in the Selection Info box. Use this to count aligned sequences in an alignments track.</p></div>
Deselect 1 item from a group selection.	Type SHIFT+CNTRL and click the item you want to de-select
Select a sequence region.	Click-drag over the sequence bases you want to select. To select residues, begin dragging in the axis tier.
Deselect everything.	Click an empty region anywhere in the main view.
Select a floating graph.	Click its handle - the rectangle at the left inside the data display area
Select an entire annotation track.	Click its track label in the left-hand panel.

Selecting items activates edge matching

When you select items in the display, the edges of the selected item and all other items with identical edges are highlighted.

This feature helps in comparing splice variation, exon length, read location, etc.

You can change the edge match color or turn it off. See [Other Options](#).