

# Quick start

If you are new to IGB, use this **Quick Start Guide** get started.

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## Step 1: Get and start IGB

- Go to [BioViz.org](#) and click the **Download** button
- Select and download the installer for your platform

If you have trouble starting IGB, visit the [help page on BioViz.org](#) for assistance.

## Step 2: Choose species and genome version

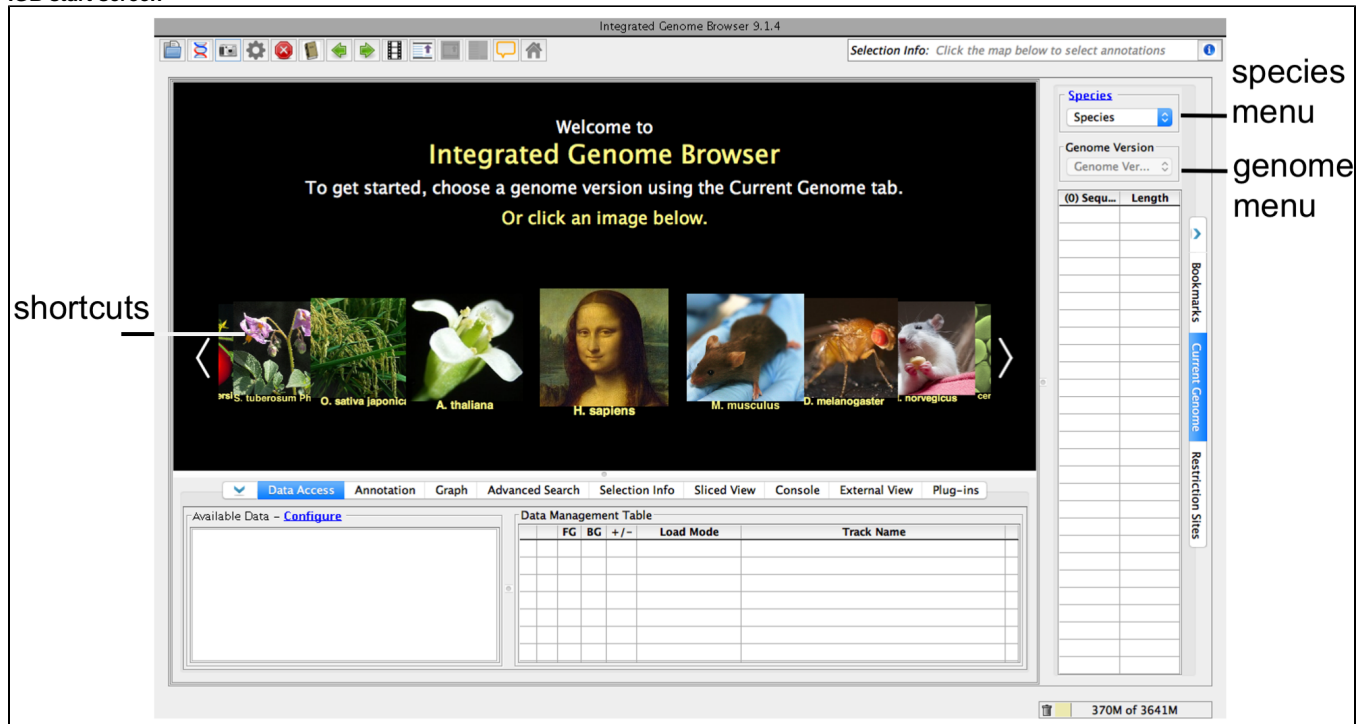
To choose a species and genome version

- Click a shortcut image (loads most recent genome)

or

- Choose **Species** and **Genome Version** using the **Current Genome** tab.

IGB start screen



If your species or genome version is not listed, you can view it if you have a fasta or 2bit file with sequence data. See [Custom Genomes](#)

## Step 3. Open data sets

Open data sets from remote data sources (**Data Access** tab) or by opening local files.

To open a data set from an IGB Quickload data source (see [About IGB Quickload](#))

1. Select **Data Access**

2. Select data sets in the **Available Data** section

To open local files on your computer

1. Select **File > Open File...** or **File > Open URL...**
2. Enter file name or URL

When you select a data sets or a file, IGB adds a new empty track to the main view and lists it in the **Data Management** table. Empty regions in the new track that do not have data loaded are gray.

#### IGB window after opening human genome RNA-Seq coverage graphs from Adrenal Gland, Kidney, and Thymus data sets

The screenshot shows the IGB interface with the following components:

- new tracks:** Points to the top of the main view where new tracks are added.
- gene model tracks:** Points to the 'RefSeq Curated (+)' and 'RefSeq Curated (-)' tracks.
- data sets:** Points to the 'RNA-Seq (Quickload)' section in the 'Data Access' panel.
- new tracks:** Points to the 'Adrenal gland scaled coverage', 'Kidney scaled coverage', and 'Thymus scaled coverage' tracks in the 'Data Management Table'.

## Step 4: Zoom in

Because many data files contain too much data to view all at once, IGB does not load data into the viewer until you click the **Load Data** button.

Before loading data, zoom in to a region.

1. Click a location in the main view
2. Drag the horizontal zoom slider or use plus and minus buttons

#### IGB horizontal zooming controls

The screenshot shows the zoom controls at the bottom of the IGB window. The 'horizontal zoom slider' is a horizontal line with a vertical bar in the center. The 'zoom out' button is a minus sign, and the 'zoom in' button is a plus sign. The 'Load Data' and 'Load Sequence' buttons are located to the right of the zoom controls.

## Other ways to zoom

Other ways to zoom include

- Search for a gene by name or keyword (For example, **TBATA** or **thymus**)
- Double-click an exon or gene model to zoom in on it
- Click-drag the coordinate axis to zoom in on a region

See also:

- [Zooming](#)
- [Panning the display](#)

## Step 5: Load data

To load data, click **Load Data** button. Regions with loaded data show the selected background color; areas without loaded data appear darker.

IGB after loading data

The screenshot shows the IGB interface for Chromosome 10 (Homo sapiens). The main display area shows a genomic track with a coordinate scale from 66,000,000 to 74,000,000. A track labeled 'region with data loaded' is highlighted in orange. A track labeled 'region with no data loaded' is dark grey. The 'Load Data' button is visible in the top right. The 'gene model tracks' section on the left includes 'RefSeq Curated (+)', 'Coordinates', and 'RefSeq Curated (-)'. The 'Data Management Table' at the bottom shows the loaded data tracks and their settings.

	FG	BG	+/-	Load Mode	Track Name
				Genome	RefSeq Curated
				Manual	Adrenal gland scaled coverage
				Manual	Kidney scaled coverage
				Manual	Thymus scaled coverage

See also:

- [Main View](#)
- [Loading Data](#)

## Step 6: Configure tracks

You can reorder the tracks by dragging the **Track Label** (the **Data Management Table** reflect changes).

To change style elements of a track, click the track label and use the **Annotation** or **Graph** tab to change to change color, track height, annotation label, amount of data shown (stack height), and other options.

See also:

- [Customizing tracks](#)
- [Preferences](#)
- [Annotation tab](#)
- [Graph Tab](#)