Local Quickload

General Function Checklist

This page tests local QuickLoads using relative file paths.

(To test absolute file paths see QuickLoad Saver release testing documentation)

Add files to your computer

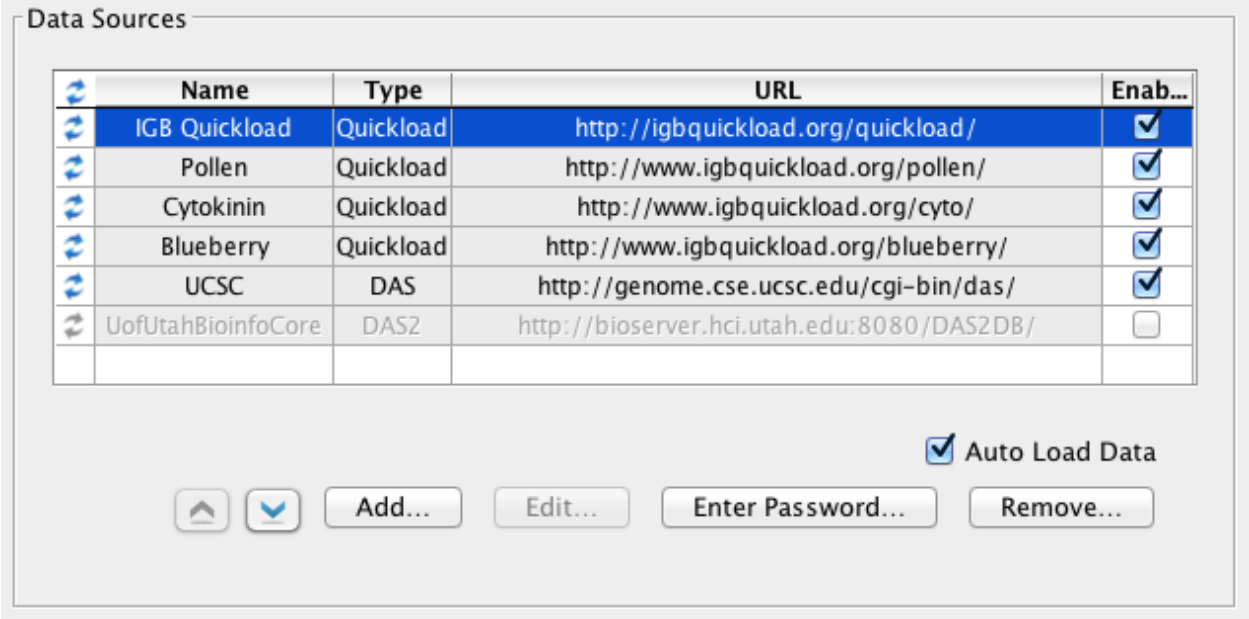
1. Download the following file: relative space.zip
2. Extract it to where you would like your local QuickLoad to be stored. (Desktop, C drive, etc.)

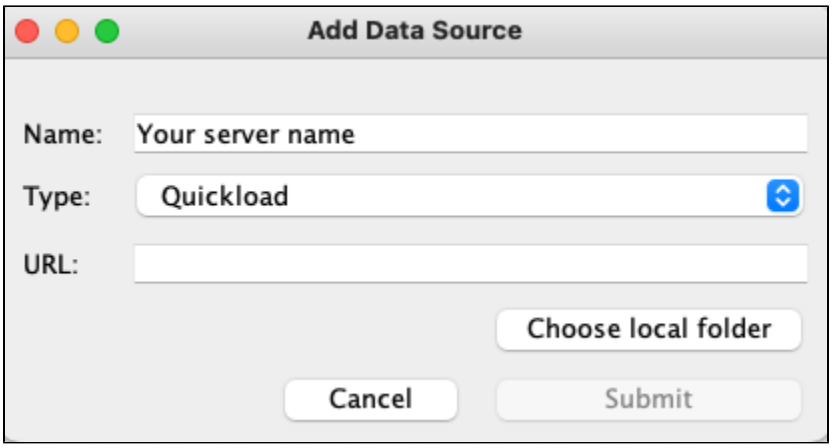
- Files were extracted to local machine:

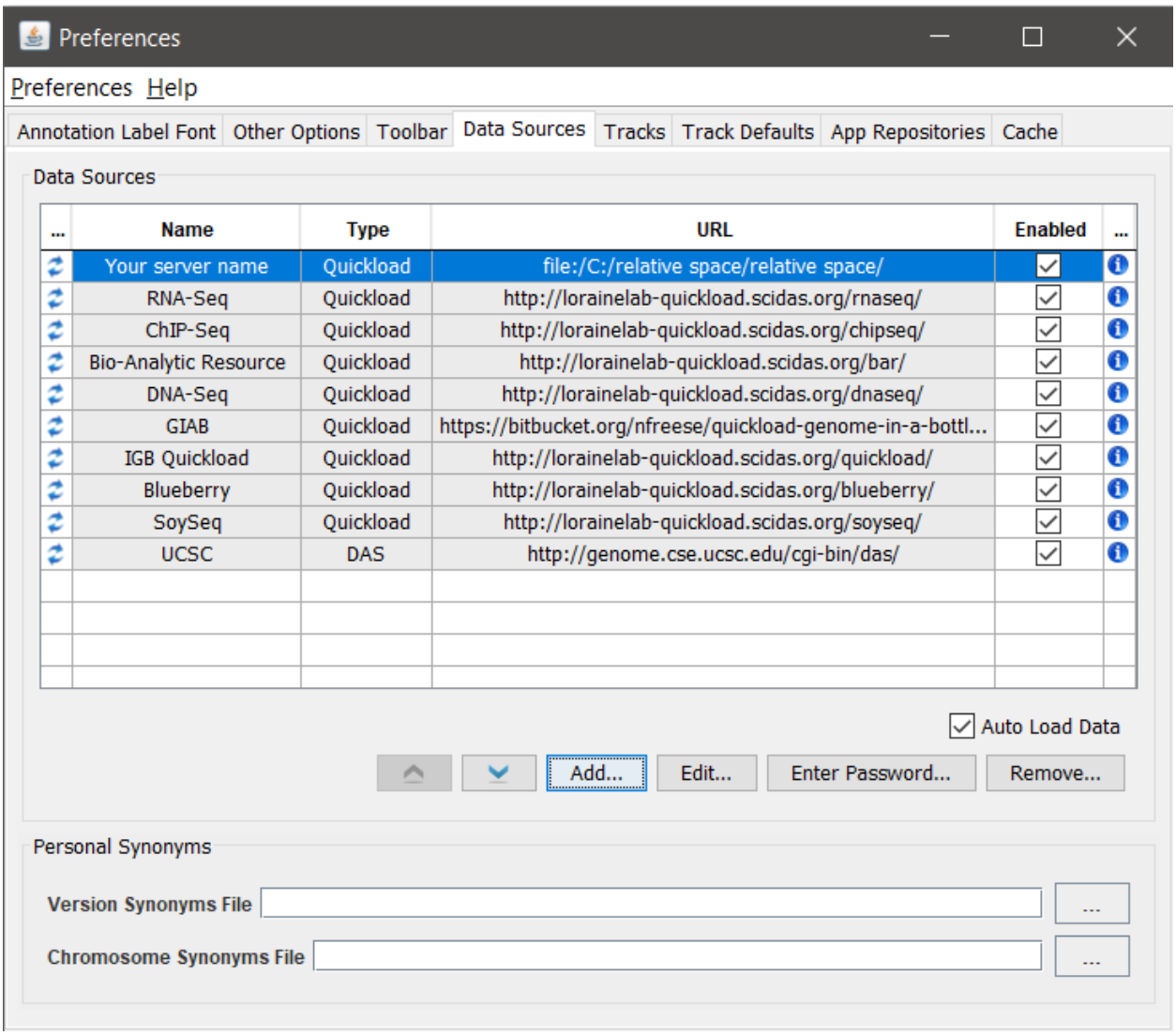
- [ ] mac
- [ ] linux
- [ ] windows

Add the QuickLoad to IGB

1. Open the **Data Sources** tab in **Preferences**.
2. Click **Add…** to open the **Add Data Source** window.
3. Click **Choose local folder**.
4. Choose the unzipped QuickLoad folder “relative space”.
5. Click **Submit**.







- The data on your QuickLoad is reachable by IGB and not highlighted in Red, Yellow, or Greyed out.

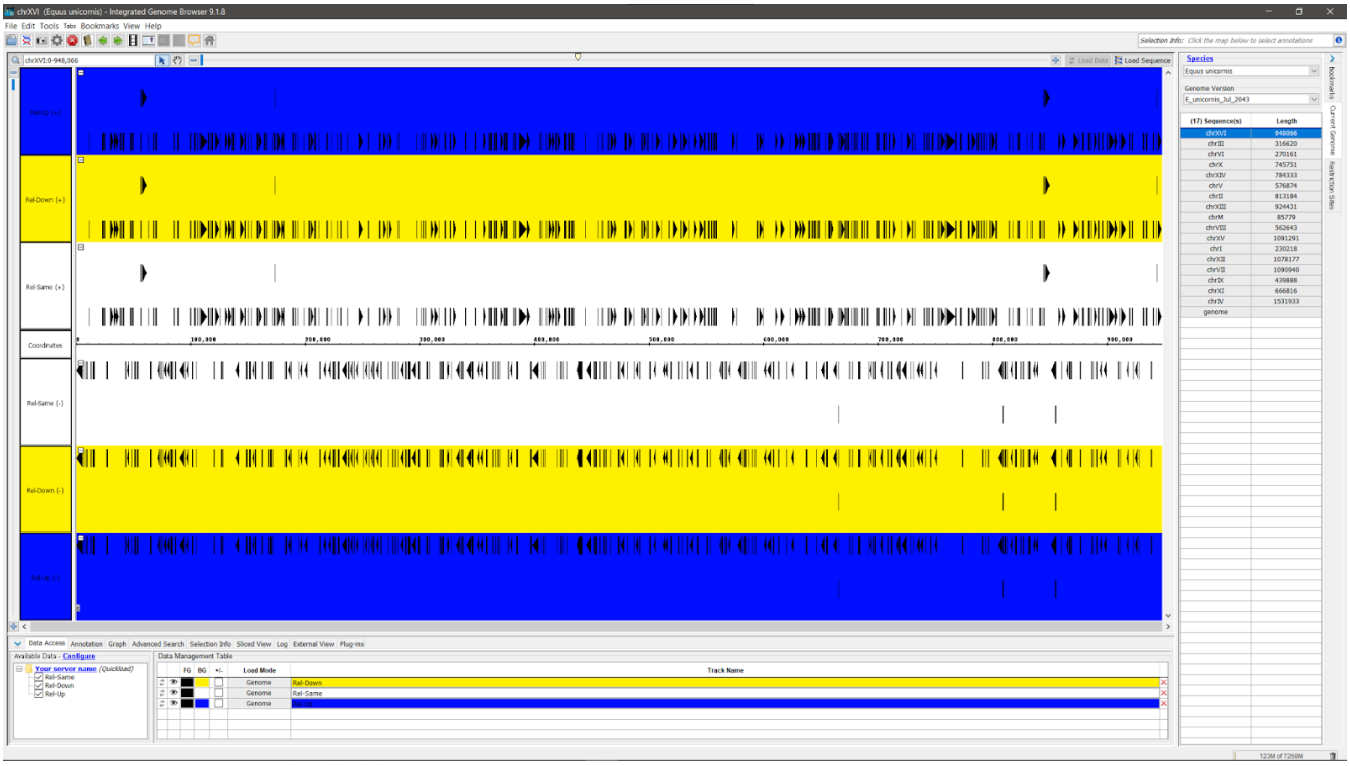
- [ ] mac
- [ ] linux
- [ ] windows

Access local QuickLoad data

1. Close the **Preferences** window.
2. Open the **E_unicornis_Jul_2043** genome.

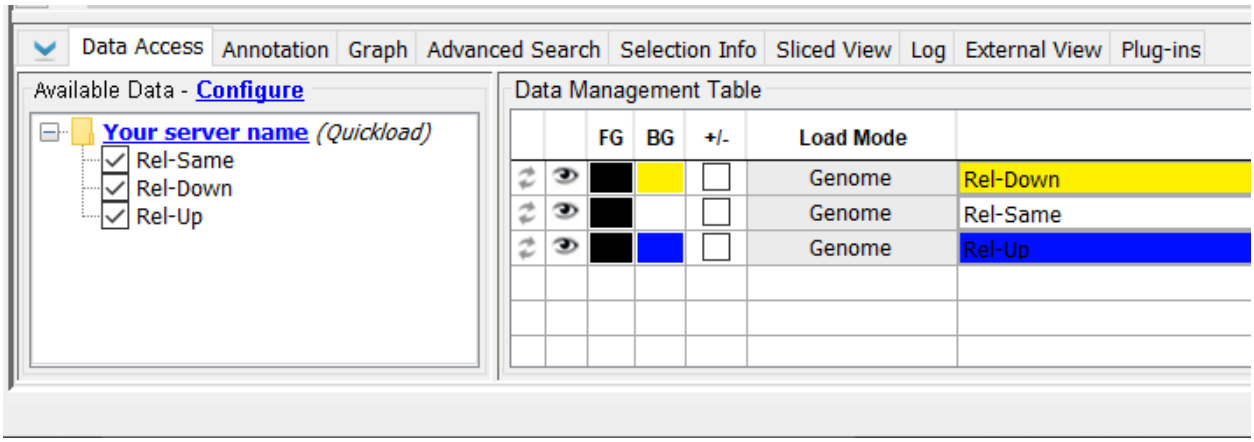
- The correct **Species** (E_unicornis) and **Genome Version** (Jul_2043) loaded.

- [ ] mac
- [ ] linux
- [ ] windows



- Data loads automatically and appears the same as the above image.

- [ ] mac
- [ ] linux
- [ ] windows

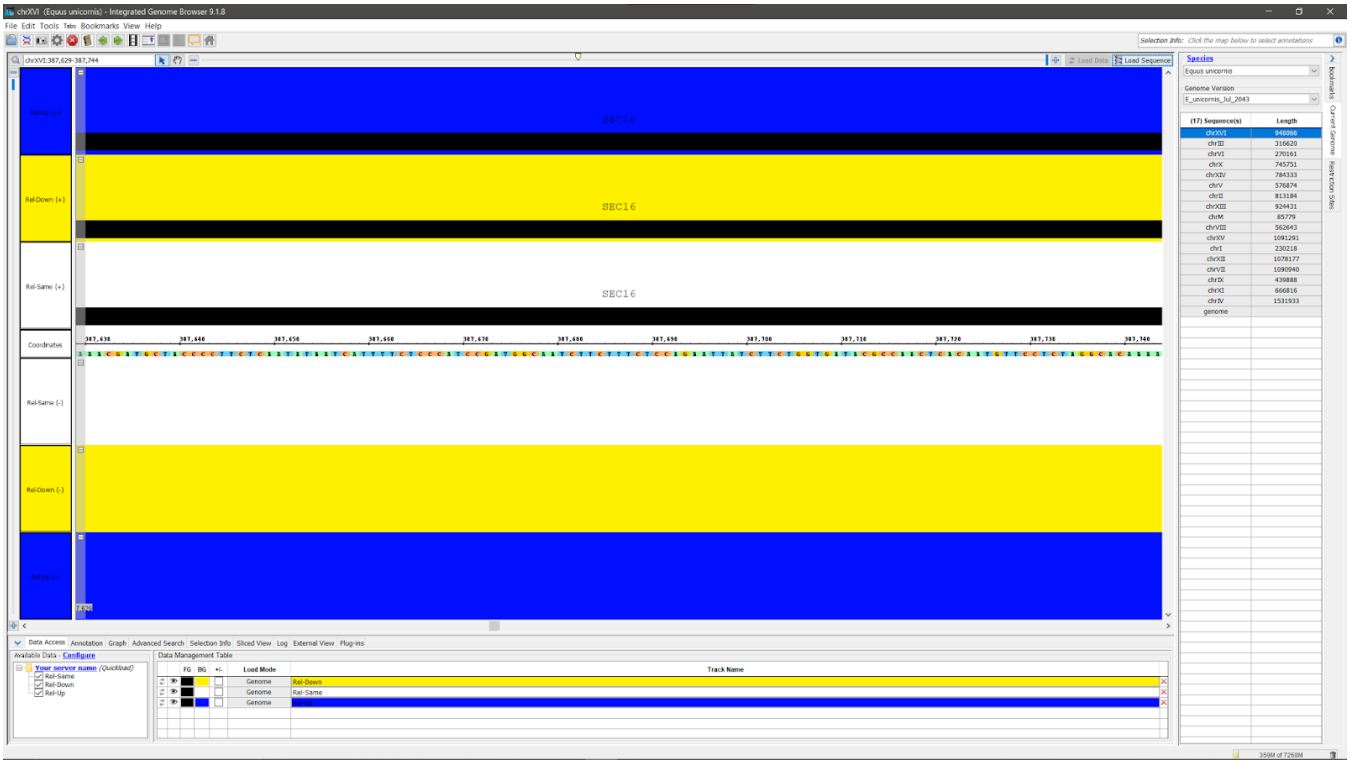


- Your QuickLoad appears in the **Available Data** section.

- [ ] mac

- [ ] linux
- [ ] windows

Zoom to the following coordinates, then click **Load Sequence**: **chrXVI:387,629-387,744**



- The sequence data loads along the coordinates track.

- [ ] mac
- [ ] linux
- [ ] windows