

Sharing data using QuickLoad sites

About IGB QuickLoad

Use IGB QuickLoad (QL) to share data files on-line using a Web site or cloud storage service like Dropbox. Using IGB QuickLoad, you can set up and configure data sets so that they'll be listed in the IGB **Data Access** panel, making it easy for lab members, collaborators, and members of the public to browse and load your data as new tracks in IGB.

QuickLoad sites can be local or remote. Typically, you'll create a QuickLoad site on your local computer, test it there, and once you're happy with how the data look when loaded into IGB, you'll transfer it to a Web site.

How to set up an IGB QuickLoad site

First, find out if your genome is already supported by the [main IGB QuickLoad site](#).

If your genome is already there, then you should make a satellite QuickLoad site. A satellite site should not contain sequence data or gene models annotations as these are already available from the main IGB QuickLoad site.

To find out if your genome is already supported, look for it in the the main IGB QuickLoad site's [contents.txt](#) file.

| IGB genome version names | contents.txt |
|--------------------------|---|
| H_sapiens_Dec_2013 | Homo sapiens (Dec 2013) human being (GRCh38/hg38) |
| H_sapiens_Feb_2009 | Homo sapiens (Feb 2009) human being (GRCh37/hg19) |
| H_sapiens_Mar_2006 | Homo sapiens (Mar 2006) human being (NCBI36/hg18) |
| H_sapiens_May_2004 | Homo sapiens (May 2004) human being (NCBI35/hg17) |
| G_gallus_Nov_2011 | Gallus gallus (Nov 2011) chicken (galGal4/ICGC Gallus-gallus-4.0) |
| G_max_Aug_2010 | Glycine max Glymal |
| G_max_Jan_2014 | Glycine max Gmax 275_v2.0 |

These appear in the "genome version" menu in the IGB **Current Sequence** tab

descriptions, including commonly used synonyms IGB displays this text in the title bar of the main IGB window.

If your genome is listed, go to: [Create a satellite IGB QuickLoad site for genomes already supported in the main IGB QuickLoad](#).

If your genome is **not** listed, go to: [Sharing data for a new or custom genome **not** already part of IGB QuickLoad](#).