

# GBrowse 2.20

## Fast, Friendly and Sociable



Anthony deCatanzaro<sup>1</sup>, Christopher Vandeveld<sup>1</sup>, Peter Ruzanov<sup>2</sup>, Ian Davies<sup>1</sup>, Scott Cain<sup>2</sup>, Lincoln Stein<sup>2</sup>  
<sup>1</sup>University of Waterloo, Waterloo, ON, Canada <sup>2</sup>Ontario Institute for Cancer Research, Toronto, ON, Canada

The Generic Genome Browser (GBrowse) is a free, open source, web-based browser for displaying and navigating genome features. It is part of the Generic Model Organism Database (GMOD) project which aims to provide reusable components for working with genomic data, and is in use by hundreds of organizations around the world. Since January 2010, GBrowse has averaged over 200 reported installations each month, and has been used to represent the genomes of over 150 diverse species. GBrowse has been used to visualize very large data sets, including modENCODE (<http://www.modencode.org/>) which features more than 1300 data tracks.

GBrowse version 2.20 adds numerous improvements to both the user interface and the back end architecture. User interface improvements include the ability to share tracks with the public or selected individuals, the ability to organize tracks into subtracks, instantaneous side-to-side track-panning, extensive support for customizing public and private tracks using a graphical interface, and a general interface to download data from any track in the most suitable format. Back end improvements include VISTA plot support for ChIP-chip and ChIP-seq display, faster track rendering, stable user accounts using passwords or OpenID, an upload manager that allows tracks to be shared selectively or publicly, and the ability to display next generation sequencing data in SAM or BAM formats. GBrowse is available from CPAN or from the GMOD website, <http://gmod.org/>.

### Community Tracks

Share uploaded tracks with specific users, groups, or everyone. A graphical user interface makes it easy to choose who can see each track.



### Improved Rendering Speed

Improvements to rendering efficiency mean track images load in less time.

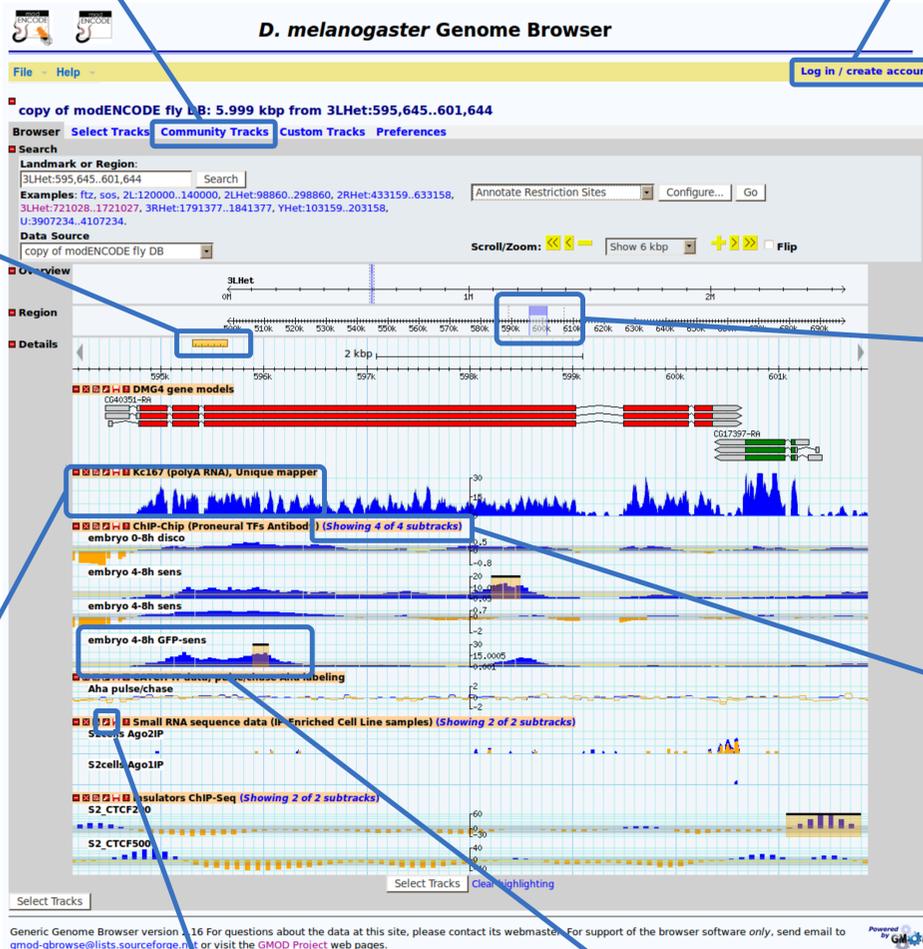
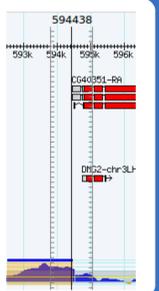
### User Accounts

GBrowse 2.20 includes support for user accounts and OpenID login.



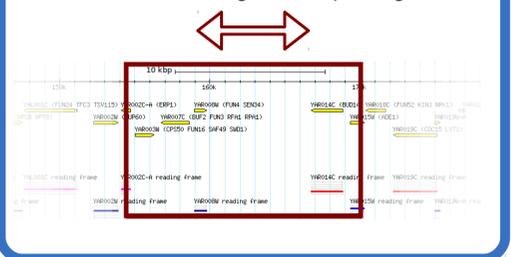
### Ruler

Used to line up data, and can be repositioned as needed. Useful when viewing a large number of tracks at once.



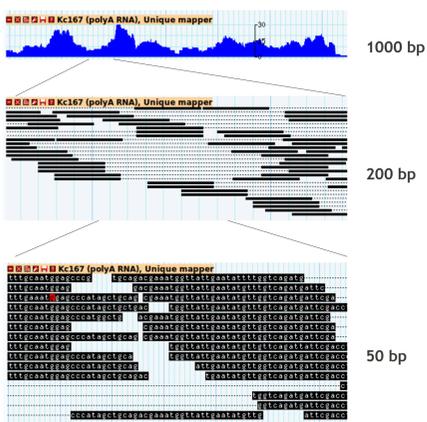
### Fast Track Panning

Track images are partially preloaded, so they can be instantly panned left or right. Also introduces mouse drag-and-drop navigation.

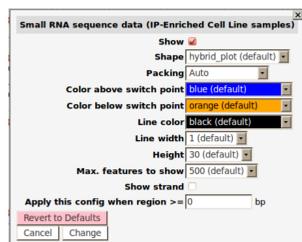


### SAM and BAM support

GBrowse 2.20 can display next-generation sequencing data in SAM and BAM formats.

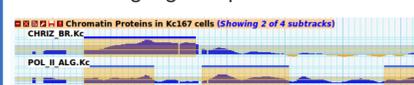


### Graphical Interface for Track Customization



### Vista Plot

This glyph superimposes quantitative data with highlighted peaks.



### Subtracks

Organize multiple related datasets in one track with subtracks. You can select which subtracks should appear by default and in what order.



GBrowse is a free, open-source application. It is available from CPAN or from the GMOD website, <http://gmod.org/>.

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