Resource Summary Report

Generated by RRID on May 19, 2025

GBrowse

RRID:SCR_006829
Type: Tool

Proper Citation

GBrowse (RRID:SCR_006829)

Resource Information

URL: http://gbrowse.org/

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Description: A database and interactive web site for manipulating and displaying annotations on genomes. Features include: detailed views of the genome; use of a variety of premade or personally made glyphs ; customizable order and appearance of tracks by administrators and end-users; search by annotation ID, name, or comment; support of third party annotation using GFF formats; DNA and GFF dumps; connectivity to different databases, including BioSQL and Chado; and a customizable plug-in architecture (e.g. run BLAST, find oligonucleotides, design primers, etc.). GBrowse is distributed as source code for Macintosh OS X, UNIX and Linux platforms, and as pre-packaged binaries for Windows machines. It can be installed using the standard Perl module build procedure, or automated using a network-based install script. In order to use the net installer, you will need to have Perl 5.8.6 or higher and the Apache web server installed. The wiki portion accepts data submissions.

Abbreviations: GBrowse

Synonyms: Generic Genome Browser

Resource Type: database, data or information resource

Defining Citation: PMID:19957275, PMID:18428797, PMID:12368253, PMID:21400697, PMID:20194461, PMID:19357095, DOI:10.1002/0471250953.bi0909s28

Keywords: genome, annotation, database, perl, virus, dna, protein, reference sequence, chromosome, visualization, bio.tools

Funding: Howard Hughes Medical Institute ;

NHGRI HG00739;
NHGRI P41HG02223

Availability: The community can contribute to this resource, Requires Perl 5.8.6 or higher and the Apache web server

Resource Name: GBrowse

Resource ID: SCR_006829

Alternate IDs: OMICS_00910, biotools:gbrowse, nif-0000-30597

Alternate URLs: http://gmod.org/wiki/GBrowse, https://bio.tools/gbrowse, https://sources.debian.org/src/gbrowse/

License: Artistic License (software), Apache License v2 (web server)

Record Creation Time: 20220129T080238+0000

Record Last Update: 20250519T204713+0000

Ratings and Alerts

No rating or validation information has been found for GBrowse.

No alerts have been found for GBrowse.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 26 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Qian X, et al. (2025) The Potassium Utilization Gene Network in Brassica napus and Functional Validation of BnaZSHAK5.2 Gene in Response to Potassium Deficiency. International journal of molecular sciences, 26(2).

Oblessuc PR, et al. (2022) Pseudomonas phaseolicola preferentially modulates genes encoding leucine-rich repeat and malectin domains in the bean landrace G2333. Planta, 256(2), 25.

Song JM, et al. (2021) BnPIR: Brassica napus pan-genome information resource for 1689 accessions. Plant biotechnology journal, 19(3), 412.

Wang Y, et al. (2019) A distinct class of eukaryotic MT-A70 methyltransferases maintain symmetric DNA N6-adenine methylation at the ApT dinucleotides as an epigenetic mark associated with transcription. Nucleic acids research, 47(22), 11771.

Sempéré G, et al. (2019) Gigwa v2-Extended and improved genotype investigator. GigaScience, 8(5).

Botwright NA, et al. (2019) Greenlip Abalone (Haliotis laevigata) Genome and Protein Analysis Provides Insights into Maturation and Spawning. G3 (Bethesda, Md.), 9(10), 3067.

Huylmans AK, et al. (2019) Sex-Biased Gene Expression and Dosage Compensation on the Artemia franciscana Z-Chromosome. Genome biology and evolution, 11(4), 1033.

Jenjaroenpun P, et al. (2017) R-loopDB: a database for R-loop forming sequences (RLFS) and R-loops. Nucleic acids research, 45(D1), D119.

Blitz IL, et al. (2017) A catalog of Xenopus tropicalis transcription factors and their regional expression in the early gastrula stage embryo. Developmental biology, 426(2), 409.

Sheng X, et al. (2017) MTD: a mammalian transcriptomic database to explore gene expression and regulation. Briefings in bioinformatics, 18(1), 28.

Sato K, et al. (2016) Improvement of barley genome annotations by deciphering the Haruna Nijo genome. DNA research : an international journal for rapid publication of reports on genes and genomes, 23(1), 21.

Wang Y, et al. (2016) Comparative analysis of the terpenoid biosynthesis pathway in Azadirachta indica and Melia azedarach by RNA-seq. SpringerPlus, 5(1), 819.

Xiong J, et al. (2016) Dissecting relative contributions of cis- and trans-determinants to nucleosome distribution by comparing Tetrahymena macronuclear and micronuclear chromatin. Nucleic acids research, 44(21), 10091.

Edwards-Jones B, et al. (2015) Translational arrest due to cytoplasmic redox stress delays adaptation to growth on methanol and heterologous protein expression in a typical fed-batch culture of Pichia pastoris. PloS one, 10(3), e0119637.

Mbandi SK, et al. (2014) A glance at quality score: implication for de novo transcriptome reconstruction of Illumina reads. Frontiers in genetics, 5, 17.

Xiong J, et al. (2013) Tetrahymena functional genomics database (TetraFGD): an integrated resource for Tetrahymena functional genomics. Database : the journal of biological databases and curation, 2013, bat008.

Abraham MC, et al. (2013) Natural variation identifies multiple loci controlling petal shape and size in Arabidopsis thaliana. PloS one, 8(2), e56743.

Wang Q, et al. (2012) Community annotation and bioinformatics workforce development in concert--Little Skate Genome Annotation Workshops and Jamborees. Database : the journal of biological databases and curation, 2012, bar064.

Stano M, et al. (2011) phiGENOME: an integrative navigation throughout bacteriophage genomes. Genomics, 98(5), 376.

Baev V, et al. (2011) Implementation of a de novo genome-wide computational approach for updating Brachypodium miRNAs. Genomics, 97(5), 282.