

Resource Summary Report

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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: data or information resource, database

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: 20260729T044143+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 43 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

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).

Pal A, et al. (2024) Defining the contribution of microRNA-specific Argonautes with slicer capability in animals. Nucleic acids research, 52(9), 5002.

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.

Skorupa M, et al. (2021) Salt stress and salt shock differently affect DNA methylation in salt-responsive genes in sugar beet and its wild, halophytic ancestor. PloS one, 16(5), e0251675.

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

- Michaud P, et al. (2021) The RabGAP TBC-11 controls Argonaute localization for proper microRNA function in *C. elegans*. *PLoS genetics*, 17(4), e1009511.
- Michaelides M, et al. (2020) Striatal Rgs4 regulates feeding and susceptibility to diet-induced obesity. *Molecular psychiatry*, 25(9), 2058.
- Samy JKA, et al. (2020) ForageGrassBase: molecular resource for the forage grass meadow fescue (*Festuca pratensis* Huds.). *Database : the journal of biological databases and curation*, 2020.
- 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.
- 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.
- Sempéré G, et al. (2019) Gigwa v2-Extended and improved genotype investigator. *GigaScience*, 8(5).
- Jasrotia RS, et al. (2019) VigSatDB: genome-wide microsatellite DNA marker database of three species of *Vigna* for germplasm characterization and improvement. *Database : the journal of biological databases and curation*, 2019.
- 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.
- Wakisaka KT, et al. (2018) Association of zygotic piRNAs derived from paternal P elements with hybrid dysgenesis in *Drosophila melanogaster*. *Mobile DNA*, 9, 7.
- Iwasaka H, et al. (2018) A Possible Trifunctional β -Carotene Synthase Gene Identified in the Draft Genome of *Aurantiochytrium* sp. Strain KH105. *Genes*, 9(4).
- Shoguchi E, et al. (2018) Two divergent *Symbiodinium* genomes reveal conservation of a gene cluster for sunscreen biosynthesis and recently lost genes. *BMC genomics*, 19(1), 458.
- 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.
- Lorgen M, et al. (2017) NFAT5 genes are part of the osmotic regulatory system in Atlantic salmon (*Salmo salar*). *Marine genomics*, 31, 25.