Resource Summary Report

Generated by NIF on Apr 8, 2025

JBrowse

RRID:SCR_001004
Type: Tool

Proper Citation

JBrowse (RRID:SCR_001004)

Resource Information

URL: http://jbrowse.org/

Proper Citation: JBrowse (RRID:SCR_001004)

Description: A high-performance visualization tool for interactive exploration of large, integrated genomic datasets written primarily in JavaScript. It supports a wide variety of data types, including array-based and next-generation sequence data, and genomic annotations.

Abbreviations: JBrowse

Resource Type: software resource

Defining Citation: PMID:22517427, PMID:21221095

Keywords: genome

Funding: NHGRI 5R01HG004483-09

Availability: GNU Lesser General Public License, Account required

Resource Name: JBrowse

Resource ID: SCR_001004

Alternate IDs: OMICS_00918

Alternate URLs: https://sources.debian.org/src/jbrowse/

Record Creation Time: 20220129T080205+0000

Record Last Update: 20250214T182931+0000

Ratings and Alerts

No rating or validation information has been found for JBrowse.

No alerts have been found for JBrowse.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 29 mentions in open access literature.

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

Mansueto L, et al. (2024) Building a community-driven bioinformatics platform to facilitate Cannabis sativa multi-omics research. GigaByte (Hong Kong, China), 2024, gigabyte137.

Miller J, et al. (2022) Chromosome-level genome and the identification of sex chromosomes in Uloborus diversus. GigaScience, 12.

Barros CP, et al. (2022) A new haplotype-resolved turkey genome to enable turkey genetics and genomics research. GigaScience, 12.

Kim HS, et al. (2022) KOREF_S1: phased, parental trio-binned Korean reference genome using long reads and Hi-C sequencing methods. GigaScience, 11.

Machado AM, et al. (2022) A genome assembly of the Atlantic chub mackerel (Scomber colias): a valuable teleost fishing resource. GigaByte (Hong Kong, China), 2022, gigabyte40.

Kim HS, et al. (2022) LT1, an ONT long-read-based assembly scaffolded with Hi-C data and polished with short reads. GigaByte (Hong Kong, China), 2022, gigabyte51.

Vosburg C, et al. (2021) Utilizing a chromosomal-length genome assembly to annotate the Wnt signaling pathway in the Asian citrus psyllid, Diaphorina citri. GigaByte (Hong Kong, China), 2021, gigabyte21.

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

Cubry P, et al. (2018) The Rise and Fall of African Rice Cultivation Revealed by Analysis of 246 New Genomes. Current biology : CB, 28(14), 2274.

Mao F, et al. (2018) EpiDenovo: a platform for linking regulatory de novo mutations to developmental epigenetics and diseases. Nucleic acids research, 46(D1), D92.

Shi J, et al. (2017) JNSViewer-A JavaScript-based Nucleotide Sequence Viewer for DNA/RNA secondary structures. PloS one, 12(6), e0179040.

Blake JA, et al. (2017) Mouse Genome Database (MGD)-2017: community knowledge resource for the laboratory mouse. Nucleic acids research, 45(D1), D723.

Canaguier A, et al. (2017) A new version of the grapevine reference genome assembly (12X.v2) and of its annotation (VCost.v3). Genomics data, 14, 56.

Foley SW, et al. (2017) A Global View of RNA-Protein Interactions Identifies Post-transcriptional Regulators of Root Hair Cell Fate. Developmental cell, 41(2), 204.

Cemel IA, et al. (2017) The coding and noncoding transcriptome of Neurospora crassa. BMC genomics, 18(1), 978.

Mao F, et al. (2016) RBP-Var: a database of functional variants involved in regulation mediated by RNA-binding proteins. Nucleic acids research, 44(D1), D154.

Buels R, et al. (2016) JBrowse: a dynamic web platform for genome visualization and analysis. Genome biology, 17, 66.

Edwards JD, et al. (2016) Ricebase: a breeding and genetics platform for rice, integrating individual molecular markers, pedigrees and whole-genome-based data. Database : the journal of biological databases and curation, 2016.

Liu Q, et al. (2016) PoplarGene: poplar gene network and resource for mining functional information for genes from woody plants. Scientific reports, 6, 31356.

Bult CJ, et al. (2016) Mouse genome database 2016. Nucleic acids research, 44(D1), D840.