

Resource Summary Report

Generated by [ASWG](#) on Aug 2, 2026

ABrowse

RRID:SCR_000345

Type: Tool

Proper Citation

ABrowse (RRID:SCR_000345)

Resource Information

URL: <http://www.abrowse.org/>

Proper Citation: ABrowse (RRID:SCR_000345)

Description: A genome browser framework which gives an open browsing experience, open data access, collaborative work support, and a framework to import annotations. Multiple data access approaches are supported for external platforms to retrieve data from ABrowse. This resource also contains an online user-space in which users can create, store and share comments, annotations and landmarks.

Resource Type: software resource

Defining Citation: [PMID:22222089](#)

Keywords: genome browser, collaborative work, open data access, collaborative work support, framework, import annotation

Availability: Free, Available for download, Freely available

Resource Name: ABrowse

Resource ID: SCR_000345

Alternate IDs: OMICS_00899

License: GNU Lesser General Public License v3

Record Creation Time: 20220129T080201+0000

Record Last Update: 20260801T190111+0000

Ratings and Alerts

No rating or validation information has been found for ABrowse.

No alerts have been found for ABrowse.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Yang Y, et al. (2015) CyanOmics: an integrated database of omics for the model cyanobacterium *Synechococcus* sp. PCC 7002. Database : the journal of biological databases and curation, 2015.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. Database : the journal of biological databases and curation, 2015.

Pavlopoulos GA, et al. (2015) Visualizing genome and systems biology: technologies, tools, implementation techniques and trends, past, present and future. GigaScience, 4, 38.

Kong L, et al. (2012) ABrowse--a customizable next-generation genome browser framework. BMC bioinformatics, 13, 2.