

Resource Summary Report

Generated by SPARC SAWG on Aug 10, 2026

Argo Genome Browser

RRID:SCR_011763

Type: Tool

Proper Citation

Argo Genome Browser (RRID:SCR_011763)

Resource Information

URL: <http://www.broadinstitute.org/annotation/argo/>

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Description: A tool for visualizing and manually annotating whole genomes that can be run as Applet or Webstart application as well as standalone application.

Abbreviations: Argo Genome Browser

Resource Type: data or information resource, software resource, data set

Availability: Open unspecified license, Free

Resource Name: Argo Genome Browser

Resource ID: SCR_011763

Alternate IDs: OMICS_00902

Record Creation Time: 20220129T080306+0000

Record Last Update: 20260808T190316+0000

Ratings and Alerts

No rating or validation information has been found for Argo Genome Browser.

No alerts have been found for Argo Genome Browser.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Lv GY, et al. (2017) Molecular Characterization, Gene Evolution, and Expression Analysis of the Fructose-1, 6-bisphosphate Aldolase (FBA) Gene Family in Wheat (*Triticum aestivum* L.). *Frontiers in plant science*, 8, 1030.

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

Zhao Y, et al. (2014) Genome-wide identification, evolution and expression analysis of mTERF gene family in maize. *PloS one*, 9(4), e94126.

Zhu Z, et al. (2012) A multi-omic map of the lipid-producing yeast *Rhodospiridium toruloides*. *Nature communications*, 3, 1112.

Wawrzyn GT, et al. (2012) Discovery and characterization of terpenoid biosynthetic pathways of fungi. *Methods in enzymology*, 515, 83.