Resource Summary Report

Generated by kravitz2 on Jul 31, 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/

Proper Citation: Argo Genome Browser (RRID:SCR_011763)

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: 20260731T042839+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 kravitz2 .

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 Rhodosporidium toruloides. Nature communications, 3, 1112.

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