Resource Summary Report

Generated by NIF on Apr 9, 2025

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

Funding:

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: 20250409T061007+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 NIF.

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.