Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 8, 2025

Anno-J

RRID:SCR_008192
Type: Tool

Proper Citation

Anno-J (RRID:SCR_008192)

Resource Information

URL: http://www.annoj.org/

Proper Citation: Anno-J (RRID:SCR_008192)

Description: A REST-based web application designed for visualizing deep sequencing data and other genome annotation data.

Abbreviations: Anno-J

Resource Type: source code, data access protocol, software resource, web service

Funding:

Availability: Creative Commons Attribution-NonCommercial-ShareAlike License, v3

Resource Name: Anno-J

Resource ID: SCR_008192

Alternate IDs: OMICS_00901

Record Creation Time: 20220129T080246+0000

Record Last Update: 20250407T215702+0000

Ratings and Alerts

No rating or validation information has been found for Anno-J.

No alerts have been found for Anno-J.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Zhang TY, et al. (2018) Environmental enrichment increases transcriptional and epigenetic differentiation between mouse dorsal and ventral dentate gyrus. Nature communications, 9(1), 298.

Narsai R, et al. (2017) Extensive transcriptomic and epigenomic remodelling occurs during Arabidopsis thaliana germination. Genome biology, 18(1), 172.

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

Pak TR, et al. (2013) ChromoZoom: a flexible, fluid, web-based genome browser. Bioinformatics (Oxford, England), 29(3), 384.

Li F, et al. (2012) Global analysis of RNA secondary structure in two metazoans. Cell reports, 1(1), 69.

Sen TZ, et al. (2010) Choosing a genome browser for a Model Organism Database: surveying the maize community. Database : the journal of biological databases and curation, 2010, baq007.

Zheng Q, et al. (2010) Genome-wide double-stranded RNA sequencing reveals the functional significance of base-paired RNAs in Arabidopsis. PLoS genetics, 6(9), e1001141.

Matsushima A, et al. (2009) OmicBrowse: a Flash-based high-performance graphics interface for genomic resources. Nucleic acids research, 37(Web Server issue), W57.

Lister R, et al. (2008) Highly integrated single-base resolution maps of the epigenome in Arabidopsis. Cell, 133(3), 523.