

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 19, 2026

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

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: 20260912T195701+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 [PRECISE-TBI](#) .

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.