

Resource Summary Report

Generated by T1D on Aug 5, 2026

BioJS

RRID:SCR_003119

Type: Tool

Proper Citation

BioJS (RRID:SCR_003119)

Resource Information

URL: <https://github.com/biojs>

Proper Citation: BioJS (RRID:SCR_003119)

Description: An open source JavaScript library of components for visualisation of biological data on the web.

Abbreviations: BioJS

Resource Type: data processing software, software resource, software application, software library, data visualization software, software toolkit

Defining Citation: [PMID:23435069](https://pubmed.ncbi.nlm.nih.gov/23435069/)

Keywords: javascript, bio.tools

Funding: BBSRC ;
NHLBI HHSN268201000035C;
European Union PSIMEx FP7-HEALTH-2007-223411

Availability: Free, Freely available

Resource Name: BioJS

Resource ID: SCR_003119

Alternate IDs: biotools:biojs, nlx_156742

Alternate URLs: <http://www.ebi.ac.uk/Tools/biojs/registry/>, <https://bio.tools/biojs>

Old URLs: <http://www.tgac.ac.uk/tools-resources/biojs/>

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260805T044049+0000

Ratings and Alerts

No rating or validation information has been found for BioJS.

No alerts have been found for BioJS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 22 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Lin G, et al. (2025) Cell-death pathways and tau-associated neuronal vulnerability in Alzheimer's disease. *Cell reports*, 44(6), 115758.

Tourasse NJ, et al. (2021) T1TAdb: the database of type I toxin-antitoxin systems. *RNA* (New York, N.Y.), 27(12), 1471.

Barik A, et al. (2020) DEPICTER: Intrinsic Disorder and Disorder Function Prediction Server. *Journal of molecular biology*, 432(11), 3379.

Dagan-Wiener A, et al. (2019) BitterDB: taste ligands and receptors database in 2019. *Nucleic acids research*, 47(D1), D1179.

Helfrich EJN, et al. (2019) Automated structure prediction of trans-acyltransferase polyketide synthase products. *Nature chemical biology*, 15(8), 813.

Pecrix Y, et al. (2019) Sunflower resistance to multiple downy mildew pathotypes revealed by recognition of conserved effectors of the oomycete *Plasmopara halstedii*. *The Plant journal : for cell and molecular biology*, 97(4), 730.

Téletchéa S, et al. (2019) Repository of Enriched Structures of Proteins Involved in the Red Blood Cell Environment (RESPIRE). *PloS one*, 14(2), e0211043.

Lo Giudice C, et al. (2018) REDIdb 3.0: A Comprehensive Collection of RNA Editing Events in Plant Organellar Genomes. *Frontiers in plant science*, 9, 482.

Blanco-Míguez A, et al. (2018) BlasterJS: A novel interactive JavaScript visualisation component for BLAST alignment results. *PloS one*, 13(10), e0205286.

Hirsh L, et al. (2018) RepeatsDB-lite: a web server for unit annotation of tandem repeat proteins. *Nucleic acids research*, 46(W1), W402.

Segura J, et al. (2017) 3DBIONOTES v2.0: a web server for the automatic annotation of macromolecular structures. *Bioinformatics (Oxford, England)*, 33(22), 3655.

Mirdita M, et al. (2017) Uniclust databases of clustered and deeply annotated protein sequences and alignments. *Nucleic acids research*, 45(D1), D170.

Tessé S, et al. (2017) Asy2/Mer2: an evolutionarily conserved mediator of meiotic recombination, pairing, and global chromosome compaction. *Genes & development*, 31(18), 1880.

Horro C, et al. (2017) BioCIDER: a Contextualisation InDEX for biological Resources discovery. *Bioinformatics (Oxford, England)*, 33(16), 2607.

Andrés-León E, et al. (2016) DDRprot: a database of DNA damage response-related proteins. *Database : the journal of biological databases and curation*, 2016.

Stanley CE, et al. (2016) flyDIVaS: A Comparative Genomics Resource for Drosophila Divergence and Selection. *G3 (Bethesda, Md.)*, 6(8), 2355.

Draizen EJ, et al. (2016) HistoneDB 2.0: a histone database with variants--an integrated resource to explore histones and their variants. *Database : the journal of biological databases and curation*, 2016.

Rohart F, et al. (2016) A molecular classification of human mesenchymal stromal cells. *PeerJ*, 4, e1845.

Younesy H, et al. (2015) VisRseq: R-based visual framework for analysis of sequencing data. *BMC bioinformatics*, 16 Suppl 11(Suppl 11), S2.

Neugebauer T, et al. (2015) DNA Data Visualization (DDV): Software for Generating Web-Based Interfaces Supporting Navigation and Analysis of DNA Sequence Data of Entire Genomes. *PloS one*, 10(12), e0143615.