

Resource Summary Report

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Plotly

RRID:SCR_013991

Type: Tool

Proper Citation

Plotly (RRID:SCR_013991)

Resource Information

URL: <https://plot.ly>

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Description: Web application to collaboratively create interactive graphs and share them with others. JavaScript toolbox plotly.js enables users with little to no web development skills to make scientific charts.

Resource Type: collaboration tool, software resource

Keywords: collaboration, interactive, tool, graph, plot, chart

Funding: CNRC-NRC ;
MHS Capital ;
RealVentures ;
Rho ;
Siemens ;
Silicon Valley Bank

Availability: Restricted

Resource Name: Plotly

Resource ID: SCR_013991

Alternate URLs: <https://plot.ly/product/enterprise/>, <https://github.com/plotly>

License URLs: <https://plot.ly/terms-of-service/>, <https://plot.ly/privacy/>

Record Creation Time: 20220129T080318+0000

Record Last Update: 20260821T193959+0000

Ratings and Alerts

No rating or validation information has been found for Plotly.

No alerts have been found for Plotly.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 503 mentions in open access literature.

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

Yu ZM, et al. (2026) scVMAP: a comprehensive platform for integrating single-cell chromatin accessibility regions with causal variants. Nucleic acids research, 54(D1), D1270.

Wang FQ, et al. (2026) DisCP-Atlas: a comprehensive resource mapping cellular processes to complex diseases. Nucleic acids research, 54(D1), D1376.

See SB, et al. (2026) Dominant intragraft plasma cells targeting bilirubin implicate local heme catabolism in human cardiac allograft vasculopathy. The Journal of clinical investigation, 136(3).

Brodrick AJ, et al. (2026) The C-terminus of infectious bursal disease virus VP3 encodes a predicted intrinsically disordered region, which promotes the formation of cytoplasmic puncta and modulates their physical properties. mBio, 17(2), e0310725.

Qi Q, et al. (2026) scSuperAnnotator: a platform for benchmarking comparison and visualizing automated cellular annotation methods for scRNA-seq data. Nucleic acids research, 54(1).

Sun P, et al. (2026) ArGD: An Integrated Database and Analysis Platform for Artocarpus Genomics and Transcriptomics. Genes, 17(1).

Malsagova KA, et al. (2026) Changes in the proteomic profile of athletes' plasma associated with exercise intensity. Scientific reports, 16(1).

Fornace ME, et al. (2026) NUPACK: Computational Nucleic Acid Analysis and Design. ACS synthetic biology, 15(4), 1426.

Meuret L, et al. (2026) ARNy plotter: A comprehensive web server for RNA ensemble structural analysis and visualization. PLoS computational biology, 22(3), e1013873.

Ahmadi A, et al. (2026) Genomic diversity and virulence of Pasteurella multocida in Norwegian calves. Microbial genomics, 12(6).

Groeneweg R, et al. (2026) Quality-adjusted life years in the presence and absence of organized mammographic screening using data from BreastScreen Norway. International

journal of cancer, 158(10), 2537.

Jumutc V, et al. (2026) Multispectral imaging and autofluorescence photobleaching combined in a multi-head neural network for skin cancer classification. *Frontiers in medicine*, 13, 1763105.

Branscom GA, et al. (2026) Long non-coding RNA profiling of hypertrophic cardiomyopathy in mice. *Scientific data*, 13(1).

Popova M, et al. (2026) *Aedes aegypti* Mosquitoes from Central Vietnam Feature Specific Viromic Profiles Linked to Dengue Virus Coinfection. *Viruses*, 18(4).

Seo D, et al. (2026) Treatment Patterns and Outcomes of Anti-MuSK Antibody-Positive Myasthenia Gravis: A Retrospective Single-Center Study. *Journal of Korean medical science*, 41(20), e151.

Kaddoura MJ, et al. (2026) Characterization of bacterial endophytes isolated from *Cannabis sativa* L. and *Chelidonium majus* L. for their application as biostimulants and biocontrol agents. *Frontiers in microbiomes*, 5, 1780965.

Lui M, et al. (2026) Environmental Pollutant PCB 153 Is Associated with Candidate Alternative Splicing Alterations in Intellectual Disability-Associated Genes: An Exploratory RNA-Seq Splicing Analysis in a Neuronal Model. *Genes*, 17(6).

Del Campo AO, et al. (2026) Automated abstraction of clinical parameters of multiple myeloma from real-world clinical notes using large language models. *BMC medical informatics and decision making*, 26(1).

Hafner A, et al. (2026) Modular Adaptive Processing Infrastructure (MAPI): a blueprint for interconnecting generic workflows with modern interfaces. *Journal of synchrotron radiation*, 33(Pt 1), 106.

Fuchs R, et al. (2026) The evolutionary dynamics between viral mimics and host proteins. *Molecular systems biology*, 22(6), 902.