

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: 20260905T132742+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 [Kravitz](#) .

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 intra-graft 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.