

Resource Summary Report

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Shiny

RRID:SCR_001626

Type: Tool

Proper Citation

Shiny (RRID:SCR_001626)

Resource Information

URL: <http://www.rstudio.com/shiny/>

Proper Citation: Shiny (RRID:SCR_001626)

Description: Open source R package that provides web framework for building web applications using R. Used to create interactive web apps in native R, without needing to use HTML, CSS, or JavaScript.

Resource Type: software toolkit, software resource

Defining Citation: [PMID:34642739](#), [PMID:26225240](#)

Keywords: R, analysis, interactive, web, application

Availability: Free, Available for download, Freely available

Resource Name: Shiny

Resource ID: SCR_001626

Alternate IDs: nlx_153894

Record Creation Time: 20220129T080208+0000

Record Last Update: 20260803T040312+0000

Ratings and Alerts

No rating or validation information has been found for Shiny.

No alerts have been found for Shiny.

Data and Source Information

Usage and Citation Metrics

We found 522 mentions in open access literature.

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

Macleod BM, et al. (2026) Integration of machine learning and viscoelastic testing to improve survival prediction in horses experiencing acute abdominal pain at a veterinary teaching hospital. *Equine veterinary journal*, 58(1), 105.

Trinh XT, et al. (2026) OmicsQ: a user-friendly platform for interactive quantitative omics data analysis. *Bioinformatics (Oxford, England)*, 42(1).

Sun T, et al. (2026) Conserved spatial patterning of gene expression in independent lineages of C4 plants. *The New phytologist*, 249(1), 24.

Aponte Ribero V, et al. (2026) Development and validation of the CARE-DM model to predict the cardiovascular risk in older persons with type 2 diabetes. *European journal of preventive cardiology*, 33(1), 44.

Kirwan R, et al. (2026) Resting energy expenditure of women with and without polycystic ovary syndrome: a systematic review and meta-analysis. *medRxiv : the preprint server for health sciences*.

Bennett S, et al. (2025) Bioacoustics as a Measure of Population Size and Breeding Success of European Storm Petrels *Hydrobates pelagicus*. *Ecology and evolution*, 15(8), e71893.

Gonzalez F, et al. (2025) Introducing CHiDO-A No Code Genomic Prediction software implementation for the characterization and integration of driven omics. *The plant genome*, 18(1), e20519.

Chotsiri P, et al. (2025) Pharmacometric and statistical considerations for dose optimization. *CPT: pharmacometrics & systems pharmacology*, 14(2), 279.

Coyle MG, et al. (2025) Prediction of site-specific pharmacologic therapy among newborns with neonatal opioid withdrawal syndrome. *Journal of perinatology : official journal of the California Perinatal Association*, 45(4), 465.

Ni P, et al. (2025) Construction of a nomogram prediction model for the pathological complete response after neoadjuvant chemotherapy in breast cancer: a study based on ultrasound and clinicopathological features. *Frontiers in oncology*, 15, 1459914.

Tursi AR, et al. (2025) CytoPheno: Automated descriptive cell type naming in flow and mass cytometry. *bioRxiv : the preprint server for biology*.

Karlsson L, et al. (2025) Eco Friendly and Budget Smart: An Economic and Environmental Evaluation of Alternative PD-1 and PD-L1 Inhibitor Dosing Regimens. *PharmacoEconomics*, 43(12), 1433.

Xu C, et al. (2025) Development and validation of a machine learning model for cardiovascular disease risk prediction in type 2 diabetes patients. *Scientific reports*, 15(1), 32818.

Pan R, et al. (2025) BestopCloud: an integrated one-stop solution for single-cell RNA sequencing data analysis. *BMC genomics*, 26(1), 905.

Xiao H, et al. (2025) Covariation MS uncovers a protein that controls cysteine catabolism. *Nature*.

Xu H, et al. (2025) Multi-center real-world data-driven web calculator for predicting outcomes in IDH-mutant gliomas: Integrating molecular subtypes and treatment modalities. *Neuro-oncology advances*, 7(1), vdae221.

Sun X, et al. (2025) Spatiotemporal transcriptome and metabolome landscapes of cotton fiber during initiation and early development. *Nature communications*, 16(1), 858.

Jansma A, et al. (2025) High order expression dependencies finely resolve cryptic states and subtypes in single cell data. *Molecular systems biology*, 21(2), 173.

Kroll F, et al. (2025) Behavioural pharmacology predicts disrupted signalling pathways and candidate therapeutics from zebrafish mutants of Alzheimer's disease risk genes. *eLife*, 13.

Chen J, et al. (2025) A systematic analysis and prediction of the disease burden of ischemic heart disease caused by hyperglycemia. *Journal of diabetes investigation*, 16(6), 1065.