Resource Summary Report

Generated by RRID on Apr 17, 2025

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

Funding:

Availability: Free, Freely available

Resource Name: Shiny

Resource ID: SCR_001626

Alternate IDs: nlx_153894

Record Creation Time: 20220129T080208+0000

Record Last Update: 20250412T054629+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

Source: SciCrunch Registry

Usage and Citation Metrics

We found 411 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

González 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.

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

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.

Biar CG, et al. (2025) Curated loci prime editing (cliPE) for accessible multiplexed assays of variant effect (MAVEs). ArXiv.

Wei S, et al. (2025) Establishment and validation of predictive model of ARDS in critically ill patients. Journal of translational medicine, 23(1), 64.

He C, et al. (2025) BbGSD: Black-boned Sheep Genome SNP Database. Database : the journal of biological databases and curation, 2025.

Ge X, et al. (2025) Spatiotemporal transcriptome and metabolome landscapes of cotton somatic embryos. Nature communications, 16(1), 859.

Yoosefzadeh Najafabadi M, et al. (2025) Machine learning-enhanced multi-trait genomic prediction for optimizing cannabinoid profiles in cannabis. The Plant journal : for cell and molecular biology, 121(1), e17164.

Koh H, et al. (2025) MiCML: a causal machine learning cloud platform for the analysis of treatment effects using microbiome profiles. BioData mining, 18(1), 10.

König LM, et al. (2025) Umbrella review of social inequality in digital interventions targeting dietary and physical activity behaviors. NPJ digital medicine, 8(1), 11.

Steiner IM, et al. (2024) Mapping from SIBDQ to EQ-5D-5L for patients with inflammatory bowel disease. The European journal of health economics : HEPAC : health economics in prevention and care, 25(3), 539.

Wang H, et al. (2024) NYUS.2: an automated machine learning prediction model for the large-scale real-time simulation of grapevine freezing tolerance in North America. Horticulture research, 11(2), uhad286.

Wanichthanarak K, et al. (2024) Data processing solutions to render metabolomics more quantitative: case studies in food and clinical metabolomics using Metabox 2.0. GigaScience, 13.

Gerault MA, et al. (2024) IMPRINTS.CETSA and IMPRINTS.CETSA.app: an R package and a Shiny application for the analysis and interpretation of IMPRINTS-CETSA data. Briefings in bioinformatics, 25(3).

Bassetto CC, et al. (2024) Revisiting anthelmintic resistance in sheep flocks from São Paulo State, Brazil. International journal for parasitology. Drugs and drug resistance, 24, 100527.

Lattanzi P, et al. (2024) Bridging the gap in fishing effort mapping: a spatially-explicit fisheries dataset for Campanian MPAs, Italy. Scientific data, 11(1), 54.

Salihoglu R, et al. (2024) Cat-E: A comprehensive web tool for exploring cancer targeting strategies. Computational and structural biotechnology journal, 23, 1376.

Radde N, et al. (2024) Measuring the burden of hundreds of BioBricks defines an evolutionary limit on constructability in synthetic biology. bioRxiv : the preprint server for biology.

Fifer S, et al. (2024) Understanding the experience, treatment preferences and goals of people living with chronic lymphocytic leukemia (CLL) in Australia. BMC cancer, 24(1), 831.

Gray SM, et al. (2024) Mouse adaptation of human inflammatory bowel diseases microbiota enhances colonization efficiency and alters microbiome aggressiveness depending on the recipient colonic inflammatory environment. Microbiome, 12(1), 147.