

Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 28, 2026

[stats](#)

RRID:SCR_025968

Type: Tool

Proper Citation

stats (RRID:SCR_025968)

Resource Information

URL: <https://stat.ethz.ch/R-manual/R-devel/library/stats/html/00Index.html>

Proper Citation: stats (RRID:SCR_025968)

Description: Software package contains functions for statistical calculations and random number generation.

Resource Type: software application, software resource

Keywords: functions, statistical calculations, random number generation,

Availability: Free, Freely available

Resource Name: stats

Resource ID: SCR_025968

Record Creation Time: 20241024T053301+0000

Record Last Update: 20260727T040840+0000

Ratings and Alerts

No rating or validation information has been found for stats.

No alerts have been found for stats.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Licona Angeles J, et al. (2025) Community Composition of Epibiont Hydroids of the Naturalized Alien Macroalga *Acanthophora spicifera* in Pichilingue, Mexico. *Biology*, 14(1).

Shafer AM, et al. (2025) Immunocompetent Murine Models Recapitulate the Heterogeneous Tumor-Immune Microenvironment of Human Liposarcoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(23), 5078.

García-Ruiz S, et al. (2025) Splicing accuracy varies across human introns, tissues, age and disease. *Nature communications*, 16(1), 1068.

van Velthoven CTJ, et al. (2025) Transcriptomic and spatial organization of telencephalic GABAergic neurons. *Nature*, 647(8088), 143.

Alves da Quinta D, et al. (2025) Genetic Ancestry, Intrinsic Tumor Subtypes, and Breast Cancer Survival in Latin American Women. *Cancer research communications*, 5(7), 1070.

Bensberg M, et al. (2025) Exposing the DNA methylation-responsive compartment of the leukaemic genome in T-ALL cell lines support its potential as a novel therapeutic target in T-ALL. *Clinical epigenetics*, 17(1), 114.

Kisakol B, et al. (2025) High-Resolution Spatial Proteomics Characterises Colorectal Cancer Consensus Molecular Subtypes. *bioRxiv : the preprint server for biology*.

Mier-Quesada Z, et al. (2025) Micro and macro structural brain plastic changes induced by sexual experience in male rats. *PloS one*, 20(10), e0334959.

Levé M, et al. (2025) Metabolomics and metagenomics in mice reveal the role of the gut microbiota in tryptophan metabolism. *iScience*, 28(11), 113751.

Menozzi E, et al. (2025) Exploring the relationship between GBA1 host genotype and gut microbiome in the GBA1 L444P/WT mouse model: implications for Parkinson's disease pathogenesis. *Frontiers in neuroscience*, 19, 1546203.

Gemünd I, et al. (2025) Characterization of human CMV-specific CD8+ T cells using multi-layer single-cell omics. *Cell reports methods*, 5(7), 101085.

Zhou Z, et al. (2025) A plasma metabolite-based test to detect minimal residual disease in post-surgery patients with colorectal cancer. *iScience*, 28(9), 113138.

Shirai Y, et al. (2024) Characteristics of and changes in the cardiometabolic measures of Japanese workers grouped according to their vegetables and salt intake through workplace cafeteria meals. *Public health nutrition*, 27(1), 1.

Tu J, et al. (2024) Lignin accumulation in cell wall plays a role in clubroot resistance. *Frontiers in plant science*, 15, 1401265.

Sawhney SS, et al. (2023) Diagnostic and commensal *Staphylococcus pseudintermedius* genomes reveal niche adaptation through parallel selection of defense mechanisms. *Nature communications*, 14(1), 7065.

Ru B, et al. (2023) Predicting Measles Outbreaks in the United States: Evaluation of Machine Learning Approaches. *JMIR formative research*, 7, e42832.

Beasley DE, et al. (2022) The bacterial community of childcare centers: potential implications for microbial dispersal and child exposure. *Environmental microbiome*, 17(1), 8.

Li S, et al. (2022) Identification of co-expression hub genes for ferroptosis in kidney renal clear cell carcinoma based on weighted gene co-expression network analysis and The Cancer Genome Atlas clinical data. *Scientific reports*, 12(1), 4821.

Lin N, et al. (2021) Demographic history and local adaptation of *Myriophyllum dioica* (Asteraceae) provide insight on plant evolution in northern China flora. *Ecology and evolution*, 11(12), 8000.

Min JJ, et al. (2021) Remodelling of femoral head deformity after hip reconstructive surgery in patients with cerebral palsy. *The bone & joint journal*, 103-B(1), 198.