

Resource Summary Report

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proc

RRID:SCR_024286

Type: Tool

Proper Citation

proc (RRID:SCR_024286)

Resource Information

URL: <https://cran.r-project.org/package=pROC>

Proper Citation: proc (RRID:SCR_024286)

Description: Software R tools for visualizing, smoothing and comparing receiver operating characteristic. Partial area under curve AUC can be compared with statistical tests based on U-statistics or bootstrap. Confidence intervals can be computed for (p)AUC or ROC curves.

Resource Type: software resource, software toolkit

Keywords: visualizing, smoothing and comparing receiver operating characteristic,

Availability: Free, Available for download, Freely available,

Resource Name: proc

Resource ID: SCR_024286

Alternate IDs: OMICS_17528

Alternate URLs: <https://sources.debian.org/src/r-cran-proc/>

License: GPL (? 3)

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260919T195622+0000

Ratings and Alerts

No rating or validation information has been found for proc.

No alerts have been found for proc.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 56 mentions in open access literature.

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

Tang Y, et al. (2026) Association of lifestyle and demographic variables with hepatitis risk: Evidence from machine learning and cross-sectional study. *SAGE open medicine*, 14, 20503121261442016.

Chen F, et al. (2026) CCL3+ Neutrophil Signature Predicts Response to Neoadjuvant Toripalimab plus Chemotherapy in Patients with Hypopharyngeal Squamous Cell Carcinoma: A Phase II Trial. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(11), 2166.

Andersen L, et al. (2026) Cell-Free DNA-Derived Immune Cell Ratios Uncover Cancer-Associated Systemic Changes. *Cancer research communications*, 6(4), 811.

Tang F, et al. (2026) Identification and preliminary clinical validation of type 2 diabetes signature genes through machine learning analysis of scRNA-seq data. *Frontiers in medicine*, 13, 1801737.

Thursby SJ, et al. (2026) Epigenetic Instability-Based Metrics in Cell-Free DNA for Early Cancer Detection. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(8), 1528.

Chang LJ, et al. (2026) Assessment of Circulating Tumor DNA for Early Detection of Hepatocellular Carcinoma in Alpha-Fetoprotein-Negative Patients With Cirrhotic Nodules. *JGH open : an open access journal of gastroenterology and hepatology*, 10(1), e70331.

Yin Q, et al. (2026) Neurocognitive Processing of Facial Emotion Recognition in Individuals With Depression and Suicidal Ideation: An Eye-Tracking and EEG Study. *Alpha psychiatry*, 27(1), 44992.

Li N, et al. (2026) Diagnostic significance of the checkpoint kinase 1 gene in high-grade gastroenteropancreatic neuroendocrine neoplasms. *Experimental and therapeutic medicine*, 31(1), 6.

Wang M, et al. (2026) T Cell Exhaustion and Dendritic Cell-Mediated Tertiary Lymphoid Structures (TLSs) Modulation Affect Response to Neoadjuvant Chemoradiotherapy in Microsatellite Stable Rectal Cancer. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(4), e14332.

L??tsch J, et al. (2026) Resolving Interpretation Challenges in Machine Learning Feature Selection With an Iterative Approach in Biomedical Pain Data. *European journal of pain (London, England)*, 30(2), e70221.

Wu B, et al. (2026) Proteomic profiling of single extracellular vesicles as a promising new approach for the diagnosis and treatment modality of advanced ovarian cancer. *NPJ precision oncology*, 10(1), 65.

Ali M, et al. (2026) Large-scale CSF and plasma proteomics reveal immune, synaptic, and extracellular matrix disruptions across neurodegenerative diseases. *Neuron*, 114(14), 2549.

Pham FK, et al. (2026) Melanoma cell states shape spatial tumor-immune ecosystems to dictate the efficacy of anti-PD1 immunotherapy. *Journal for immunotherapy of cancer*, 14(6).

Ghoochani A, et al. (2026) Cell-type resolved protein atlas of brain lysosomes identifies SLC45A1-associated disease as a lysosomal disorder. *Cell*, 189(3), 765.

Ikegami M, et al. (2026) Germline Pathogenic Variant Prediction Model for Tumor-Only Sequencing Based on Japanese Clinicogenomic Database. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(4), 770.

Zeng Q, et al. (2026) Intratumoral Tertiary Lymphoid Structures Characterized by a B Cell-Related Signature Elicit Antitumor Effect through HAPLN3 in Hepatocellular Carcinoma. *Cancer immunology research*, 14(5), 771.

Hu Q, et al. (2025) Circulating tumor DNA monitoring detects minimal residual disease and predicts outcomes in patients with esophageal adenocarcinoma or squamous cell carcinoma after esophagectomy. *BJC reports*, 3(1), 52.

Sun M, et al. (2025) Elevated SGO2 expression in lung adenocarcinoma promotes migration and invasion via MAD2 and correlates with poor prognosis. *Scientific reports*, 15(1), 25642.

Ye F, et al. (2025) Characteristics and filtering of low-frequency artificial short deletion variations based on nanopore sequencing. *GigaScience*, 14.

Geng S, et al. (2025) A Cost-Effective Two-Step Approach for Multi-Cancer Early Detection in High-Risk Populations. *Cancer research communications*, 5(1), 150.