

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 7, 2026

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: 20260905T133107+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 [PRECISE-TBI](#) .

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.