

Resource Summary Report

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preprocesscore

RRID:SCR_024254

Type: Tool

Proper Citation

preprocesscore (RRID:SCR_024254)

Resource Information

URL: <https://bioconductor.org/packages/preprocessCore/>

Proper Citation: preprocesscore (RRID:SCR_024254)

Description: Software library of core preprocessing routines.

Resource Type: software toolkit, software resource

Keywords: core preprocessing routines,

Availability: Free, Available for download, Freely available,

Resource Name: preprocesscore

Resource ID: SCR_024254

Alternate URLs: <https://sources.debian.org/src/r-bioc-preprocesscore/>

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260729T044604+0000

Ratings and Alerts

No rating or validation information has been found for preprocesscore.

No alerts have been found for preprocesscore.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 57 mentions in open access literature.

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

Zhang J, et al. (2025) Integrated Analysis of Volatile Metabolites in Rose Varieties: Effects of Cultivar Differences and Drying Temperatures on Flavor Profiles. *Metabolites*, 15(5).

Arthur TD, et al. (2025) IFN γ activates an immune-like regulatory network in the cardiac vascular endothelium. *Journal of molecular and cellular cardiology plus*, 11, 100289.

Dordevic N, et al. (2025) Extensive modulation of the circulating blood proteome by hormonal contraceptive use across two population studies. *Communications medicine*, 5(1), 131.

Schmidt L, et al. (2025) Protocol for generating protein profiles and distance-based network analysis of murine tissue slices. *STAR protocols*, 6(1), 103578.

Desterke C, et al. (2025) Single-Cell RNA Sequencing Reveals LEF1-Driven Wnt Pathway Activation as a Shared Oncogenic Program in Hepatoblastoma and Medulloblastoma. *Current oncology (Toronto, Ont.)*, 32(1).

Xiao X, et al. (2025) Exploring the impact of neutrophils on lung adenocarcinoma using Mendelian randomization and transcriptomic study. *Scientific reports*, 15(1), 23835.

Jothi D, et al. (2025) GTEx pro enables accurate multi-tissue gene expression analysis using robust normalization and batch correction. *Scientific reports*, 15(1), 32684.

Hermelo I, et al. (2025) Unsupervised clustering reveals noncanonical myeloid cell subsets in the brain tumor microenvironment. *Cancer immunology, immunotherapy : CII*, 74(2), 63.

Lin Z, et al. (2025) Identification of regulatory cell death-related genes during MASH progression using bioinformatics analysis and machine learning strategies. *Frontiers in immunology*, 16, 1542524.

Nadendla EK, et al. (2025) HCK regulates NLRP12-mediated PANoptosis. *Proceedings of the National Academy of Sciences of the United States of America*, 122(21), e2422079122.

Huang T, et al. (2025) Heat shock protein family H member 1 HSPH1 expression correlates with progression and prognosis of hepatocellular carcinoma. *Scientific reports*, 15(1), 31151.

Li LN, et al. (2025) Purine metabolism-associated key genes depict the immune landscape in gout patients. *Discover oncology*, 16(1), 193.

Wang D, et al. (2025) Deciphering the epigenomic regulatory variations reveals function diversity in adipose lineage among different adipose depots of pigs. *Cell & bioscience*, 15(1), 170.

Wang L, et al. (2024) Potential diagnostic markers shared between non-alcoholic fatty liver disease and atherosclerosis determined by machine learning and bioinformatic analysis.

Frontiers in medicine, 11, 1322102.

Yang M, et al. (2024) Develop a Novel Signature to Predict the Survival and Affect the Immune Microenvironment of Osteosarcoma Patients: Anoikis-Related Genes. Journal of immunology research, 2024, 6595252.

Chen J, et al. (2024) Sialylation-associated long non-coding RNA signature predicts the prognosis, tumor microenvironment, and immunotherapy and chemotherapy options in uterine corpus endometrial carcinoma. Cancer cell international, 24(1), 314.

Hu J, et al. (2024) Construction of the porcine genome mobile element variations and investigation of its role in population diversity and gene expression. Journal of animal science and biotechnology, 15(1), 162.

Han JH, et al. (2024) NINJ1 mediates inflammatory cell death, PANoptosis, and lethality during infection conditions and heat stress. Nature communications, 15(1), 1739.

Lou Y, et al. (2024) ITGAM-mediated macrophages contribute to basement membrane damage in diabetic nephropathy and atherosclerosis. BMC nephrology, 25(1), 72.

Dong YM, et al. (2024) CD27 as a Diagnostic Biomarker and Its Role in Immune Heterogeneity and Predicting Clinical Drug Responses in Hashimoto's Thyroiditis. Pharmacogenomics and personalized medicine, 17, 535.