

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

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 resource, software toolkit

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: 20260905T133106+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 63 mentions in open access literature.

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

Zhong Y, et al. (2026) MT2A-Mediated Regulation of Cuproptosis in Human Dental Pulp Cells Modulates Macrophage M1 Polarization in Pulpitis. *International dental journal*, 76(3), 109506.

Sarropoulos I, et al. (2026) The evolution of gene regulation in mammalian cerebellum development. *Science (New York, N.Y.)*, 391(6784), eadw9154.

Wang X, et al. (2026) Genomics meets metabolomics: decoding *Arnebia tschimganica* and the shikonin biosynthesis pathway. *Horticulture research*, 13(6), uhag077.

Maier AD, et al. (2026) Novel insights into meningioma brain invasion with spatial transcriptomic profiling. *Acta neuropathologica communications*, 14(1), 32.

Liu H, et al. (2026) C9orf72 hexanucleotide repeat RNA drives transcriptional dysregulation through genome-wide DNA:RNA hybrid G-quadruplexes. *Neuron*, 114(6), 1045.

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).

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).

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.

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.

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.

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

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.

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.

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.

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.