

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 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 [PRECISE-TBI](#) .

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.

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.

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.

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.

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.