

Resource Summary Report

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RUVSeq

RRID:SCR_006263

Type: Tool

Proper Citation

RUVSeq (RRID:SCR_006263)

Resource Information

URL: <http://www.bioconductor.org/packages/devel/bioc/html/RUVSeq.html>

Proper Citation: RUVSeq (RRID:SCR_006263)

Description: Software package that implements the remove unwanted variation (RUV) methods for the normalization of RNA-Seq read counts between samples.

Synonyms: RUVSeq: Remove Unwanted Variation from RNA-Seq Data

Resource Type: software resource

Defining Citation: [PMID:25150836](#)

Keywords: software package, unix/linux, mac os x, windows, r, differential expression, preprocessing, rna-seq

Availability: Artistic License, v2

Resource Name: RUVSeq

Resource ID: SCR_006263

Alternate IDs: OMICS_05652

Record Creation Time: 20220129T080235+0000

Record Last Update: 20260725T190620+0000

Ratings and Alerts

No rating or validation information has been found for RUVSeq.

No alerts have been found for RUVSeq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 449 mentions in open access literature.

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

Darlington KC, et al. (2026) Myeloid Cell Adhesion Molecule 1 (CADM1) Promotes Proinflammatory Signaling in Human Inflammatory Bowel Diseases. Cellular and molecular gastroenterology and hepatology, 20(1), 101618.

Areesawangkit P, et al. (2026) A dual diacylglycerol kinase (DGK) alpha/zeta inhibitor augments the activity of human tumor infiltrating lymphocytes in in vivo and ex vivo models. Oncoimmunology, 15(1), 2608439.

Liu JF, et al. (2025) Decoding m6Am by simultaneous transcription-start mapping and methylation quantification. eLife, 13.

Yang R, et al. (2025) Perturbations in the microbiota-gut-brain axis shaped by social status loss. Communications biology, 8(1), 401.

Shilikbay T, et al. (2025) RNA helicase MOV10 suppresses fear memory and dendritic arborization and regulates microtubule dynamics in hippocampal neurons. BMC biology, 23(1), 36.

Coul??e M, et al. (2025) Chromatin environment-dependent effects of DOT1L on gene expression in male germ cells. Communications biology, 8(1), 138.

Wu W, et al. (2025) Glycolysis Induces Abnormal Transcription Through Histone Lactylation in T-cell Acute Lymphoblastic Leukemia. Genomics, proteomics & bioinformatics, 23(2).

Plummer R, et al. (2025) TIMEPOINT, a phase 1 study combining MTL-CEBPA with pembrolizumab, supports the immunomodulatory effect of MTL-CEBPA in solid tumors. Cell reports. Medicine, 6(4), 102041.

Chen KA, et al. (2025) Post-operative Crohn's Disease Recurrence and Infectious Complications: A Transcriptomic Analysis. Digestive diseases and sciences, 70(1), 203.

Lapehn S, et al. (2025) A transcriptomic comparison of in vitro models of the human placenta. Placenta, 159, 52.

Mejia-Trujillo R, et al. (2025) RNA Pol I activity maintains chromatin condensation and the H3K4me3 gradient essential for oogenesis, independent of ribosome production. bioRxiv : the preprint server for biology.

Bodmer NK, et al. (2025) Latent transforming growth factor binding protein-2 (LTBP2), an IPF biomarker of clinical decline, promotes TGF-beta signaling and lung fibrosis in mice.

bioRxiv : the preprint server for biology.

Aron L, et al. (2025) Lithium deficiency and the onset of Alzheimer's disease. *Nature*, 645(8081), 712.

Zhang H, et al. (2025) Fosl2 facilitates chromatin accessibility to determine developmental events during follicular maturation. *Nature communications*, 16(1), 8955.

Shin JH, et al. (2025) Distinct spatial transcriptomic patterns of substantia Nigra in Parkinson disease and Parkinsonian subtype of multiple system atrophy. *Acta neuropathologica communications*, 13(1), 193.

Falcucci S, et al. (2025) Transcriptome analysis of HPV16-positive cells expressing intrabodies targeting E6 and E7 oncoproteins to unravel intrabody antitumor activity. *Journal of translational medicine*, 23(1), 1095.

Sonn JY, et al. (2025) MeCP2 interacts with the super elongation complex to regulate transcription. *Science advances*, 11(48), eadt5937.

Chambers TL, et al. (2025) At the Nexus Between Epigenetics and Senescence: The Effects of Senolytic (BI01) Administration on DNA Methylation Clock Age and the Methylome in Aged and Regenerated Skeletal Muscle. *Aging cell*, 24(7), e70068.

Musillo C, et al. (2025) Maternal stressors disrupt mouse placental proteome and fetal brain development in a sex-specific fashion through inflammation and oxidative stress. *Molecular psychiatry*, 30(11), 5072.

Sosnowska D, et al. (2025) Tumor microenvironments with an active type I IFN response are sensitive to inhibitors of heme degradation. *JCI insight*, 10(16).