Resource Summary Report

Generated by T1D on Aug 1, 2026

seqbias

RRID:SCR_006832
Type: Tool

Proper Citation

seqbias (RRID:SCR_006832)

Resource Information

URL: http://bioconductor.org/packages/2.12/bioc/html/seqbias.html

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Description: Software package that implements a model of per-position sequencing bias in high-throughput sequencing data using a simple Bayesian network, the structure and parameters of which are trained on a set of aligned reads and a reference genome sequence.

Abbreviations: seqbias

Synonyms: seqbias - Estimation of per-position bias in high-throughput sequencing data

Resource Type: software resource

Keywords: bio.tools

Availability: GNU Lesser General Public License

Resource Name: seqbias

Resource ID: SCR_006832

Alternate IDs: OMICS_01237, biotools:seqbias, BioTools:seqbias

Alternate URLs: https://bio.tools/seqbias, https://bio.tools/seqbias, https://bio.tools/seqbias

Record Creation Time: 20220129T080238+0000

Record Last Update: 20260725T190629+0000

Ratings and Alerts

No rating or validation information has been found for seqbias.

No alerts have been found for seqbias.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 30 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Ham DJ, et al. (2025) Muscle fiber Myc is dispensable for muscle growth and its forced expression severely perturbs homeostasis. Nature communications, 16(1), 3190.

Giordano G, et al. (2025) The cGAS-STING pathway is a master regulator of OCT4 expression in persistent sarcoma cells and enhances cellular immunotherapy with NK and CIK lymphocytes. Cancer immunology, immunotherapy : CII, 74(10), 312.

Ham AS, et al. (2025) Single-nuclei sequencing of skeletal muscle reveals subsynaptic-specific transcripts involved in neuromuscular junction maintenance. Nature communications, 16(1), 2220.

Hoof V, et al. (2025) Brain region-specific and systemic transcriptomic alterations in a human alpha-synuclein overexpressing rat model. Aging, 17(10), 2598.

Clark TC, et al. (2025) Immune cell-resolved transcriptomics provides insights into the basis for variations of fish genetic resistance to viral disease. BMC biology, 23(1), 348.

Crain AT, et al. (2024) Drosophila melanogaster Set8 and L(3)mbt function in gene expression independently of histone H4 lysine 20 methylation. Genes & development, 38(9-10), 455.

Heim TE, et al. (2024) RNA-sequencing predicts a role of androgen receptor and aldehyde dehydrogenase 1A1 in osteosarcoma lung metastases. Oncogene, 43(14), 1007.

Sutherland L, et al. (2024) Secondary Analysis of Human Bulk RNA-Seq Dataset Suggests Potential Mechanisms for Letrozole Resistance in Estrogen-Positive (ER+) Breast Cancer. Current issues in molecular biology, 46(7), 7114.

Bajželj M, et al. (2024) Deregulation in adult IgA vasculitis skin as the basis for the discovery of novel serum biomarkers. Arthritis research & therapy, 26(1), 85.

Giannoukakos S, et al. (2024) Assessing the complementary information from an increased number of biologically relevant features in liquid biopsy-derived RNA-Seq data. Heliyon, 10(6), e27360.

Hansen SSK, et al. (2024) Pulmonary maternal immune activation does not cross the placenta but leads to fetal metabolic adaptation. Nature communications, 15(1), 4711.

Morita K, et al. (2023) Rat Deconvolution as Knowledge Miner for Immune Cell Trafficking from Toxicogenomics Databases. Toxicological sciences : an official journal of the Society of Toxicology, 197(2), 121.

Kilzheimer A, et al. (2023) Failure of diet-induced transcriptional adaptations in alpha-synuclein transgenic mice. Human molecular genetics, 32(3), 450.

Gómez-Pascual A, et al. (2023) Polyglucosan body density in the aged mouse hippocampus is controlled by a novel modifier locus on chromosome 1. bioRxiv : the preprint server for biology.

Ragu S, et al. (2023) A noncanonical response to replication stress protects genome stability through ROS production, in an adaptive manner. Cell death and differentiation, 30(5), 1349.

Davidson NR, et al. (2023) Molecular subtypes of high-grade serous ovarian cancer across racial groups and gene expression platforms. bioRxiv : the preprint server for biology.

Brezovec N, et al. (2022) Molecular and Cellular Markers in Chlorhexidine-Induced Peritoneal Fibrosis in Mice. Biomedicines, 10(11).

Lenehan PJ, et al. (2021) Type 2 immunity is maintained during cancer-associated adipose tissue wasting. Immunotherapy advances, 1(1), ltab011.

Baranowski BJ, et al. (2021) Cerebrovascular insufficiency and amyloidogenic signaling in Ossabaw swine with cardiometabolic heart failure. JCI insight, 6(10).

Priedigkeit N, et al. (2021) Acquired mutations and transcriptional remodeling in long-term estrogen-deprived locoregional breast cancer recurrences. Breast cancer research : BCR, 23(1), 1.