

Resource Summary Report

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Preprocessing tools for oligonucleotide arrays

RRID:SCR_023726

Type: Tool

Proper Citation

Preprocessing tools for oligonucleotide arrays (RRID:SCR_023726)

Resource Information

URL: <https://bioconductor.org/packages/release/bioc/html/oligo.html>

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Description: Software R package to analyze oligonucleotide arrays at probe level. Supports Affymetrix (CEL files) and NimbleGen arrays (XYS files). Used for annotation of Affymetrix Gene Array data.

Synonyms: affycoretools

Resource Type: software toolkit, software resource

Defining Citation: [PMID:20688976](#)

Keywords: analyze oligonucleotide arrays, Affymetrix Gene Array, NimbleGen array, Affymetrix Gene Array data annotation,

Funding: Brazilian Funding Agency CAPES ;
NCRR R01 RR021967;
NHGRI P41 HG004059

Availability: Free, Available for download, Freely available

Resource Name: Preprocessing tools for oligonucleotide arrays

Resource ID: SCR_023726

License: LGPL

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Ratings and Alerts

No rating or validation information has been found for Preprocessing tools for oligonucleotide arrays.

No alerts have been found for Preprocessing tools for oligonucleotide arrays.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

González-Gualda E, et al. (2026) Treatment resistance to platinum-based chemotherapy in lung and ovarian cancer is driven by a targetable TGF β senescent secretome. *Nature aging*, 6(2), 368.

Huang F, et al. (2025) Inhalation of 1-bromopropane alters hippocampal expression of pathways related to immune system/inflammation and insulin signaling in experimental rats. *Scientific reports*, 16(1), 2341.

Swenson H, et al. (2025) Integrative analysis of epigenetic and transcriptional interrelations identifies histotype-specific biomarkers in early-stage ovarian carcinoma. *Journal of ovarian research*, 18(1), 103.

Zimmermann S, et al. (2025) Association of Lifestyle-Induced Weight Loss With Gene Expression in Subcutaneous Adipose Tissue in Metabolic Syndrome. *Journal of diabetes*, 17(4), e70083.

Wu Y, et al. (2024) Flu-CED: A comparative transcriptomics database of influenza virus-infected human and animal models. *Animal models and experimental medicine*, 7(6), 881.

Gómez-Bañuelos E, et al. (2024) Uncoupling interferons and the interferon signature explains clinical and transcriptional subsets in SLE. *Cell reports. Medicine*, 5(5), 101569.

Ferrarese L, et al. (2024) Inflammatory Mediators Suppress FGFR2 Expression in Human Keratinocytes to Promote Inflammation. *Molecular and cellular biology*, 44(11), 489.

Mikhael S, et al. (2024) Evaluating synergistic effects of metformin and simvastatin on ovarian cancer cells. *PloS one*, 19(3), e0298127.

Cabrera-Aldana EE, et al. (2023) Administration of Tamoxifen Can Regulate Changes in Gene Expression during the Acute Phase of Traumatic Spinal Cord Injury. *Current issues in molecular biology*, 45(9), 7476.

Moreno-Molina M, et al. (2021) Genomic analyses of *Mycobacterium tuberculosis* from human lung resections reveal a high frequency of polyclonal infections. *Nature communications*, 12(1), 2716.

Youlten SE, et al. (2021) Osteocyte transcriptome mapping identifies a molecular landscape controlling skeletal homeostasis and susceptibility to skeletal disease. *Nature communications*, 12(1), 2444.

Fisch U, et al. (2020) Neonatal hypoxia-ischemia in rat elicits a region-specific neurotrophic response in SVZ microglia. *Journal of neuroinflammation*, 17(1), 26.

Biemann R, et al. (2020) Gene expression profile of CD14⁺ blood monocytes following lifestyle-induced weight loss in individuals with metabolic syndrome. *Scientific reports*, 10(1), 17855.

Cáceres M, et al. (2020) Pancreatic duct ligation reduces premalignant pancreatic lesions in a Kras model of pancreatic adenocarcinoma in mice. *Scientific reports*, 10(1), 18344.

Wiehle L, et al. (2017) mIDH-associated DNA hypermethylation in acute myeloid leukemia reflects differentiation blockage rather than inhibition of TET-mediated demethylation. *Cell stress*, 1(1), 55.