

Resource Summary Report

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[affy](#)

RRID:SCR_012835

Type: Tool

Proper Citation

affy (RRID:SCR_012835)

Resource Information

URL: <http://www.bioconductor.org/packages/release/bioc/html/affy.html>

Proper Citation: affy (RRID:SCR_012835)

Description: Software R package of functions and classes for the analysis of oligonucleotide arrays manufactured by Affymetrix. Used to process probe level data and for exploratory oligonucleotide array analysis.

Abbreviations: Affy

Synonyms: Affymetrix, analysis of Affymetrix GeneChip data at the probe level, analysis of Affymetrix GeneChip data

Resource Type: software application, software resource, data processing software, data analysis software

Defining Citation: [PMID:14960456](#)

Keywords: analysis, oligonucleotide, array, Affymetrix, process, probe, data, function, bio.tools

Funding: Danish Biotechnology Instrument Center

Availability: Free, Available for download, Freely available

Resource Name: affy

Resource ID: SCR_012835

Alternate IDs: BioTools:affy, OMICS_00740, biotools:affy

Alternate URLs: <https://bio.tools/affy>, <https://sources.debian.org/src/r-bioc-affy/>

License: GPL

Record Creation Time: 20220129T080312+0000

Record Last Update: 20260728T043417+0000

Ratings and Alerts

No rating or validation information has been found for affy.

No alerts have been found for affy.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2996 mentions in open access literature.

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

Huang Y, et al. (2026) Integration of Single-cell and Bulk Transcriptome Analyses Unravels a Macrophage-based Gene Signature for Prognostication and Treatment in Triple-negative Breast Cancer. International journal of medical sciences, 23(1), 253.

Li LI, et al. (2026) Augmenter of Liver Regeneration Enhances Hepatocellular Carcinoma Cell Growth Through COX-2-associated Signaling. Cancer genomics & proteomics, 23(1), 109.

Liharska LE, et al. (2026) A study of gene expression in the living human brain. Molecular psychiatry, 31(1), 137.

Wang S, et al. (2025) Ferroptosis-related genes participate in the microglia-induced neuroinflammation of spinal cord injury via NF- κ B signaling: evidence from integrated single-cell and spatial transcriptomic analysis. Journal of translational medicine, 23(1), 43.

Geng J, et al. (2025) Moderate-intensity interval exercise exacerbates cardiac lipotoxicity in high-fat, high-calories diet-fed mice. Nature communications, 16(1), 613.

Zhang K, et al. (2025) Development of a Novel Mitochondrial Dysfunction-Related Alzheimer's Disease Diagnostic Model Using Bioinformatics and Machine Learning. Current Alzheimer research, 22(1), 19.

Zhan J, et al. (2025) Immunomodulatory insights of monoterpene glycosides in endometriosis: immune infiltration and target pathways analysis. Hereditas, 162(1), 1.

Qiao Y, et al. (2025) Multi-Target Mechanism of Compound Qingdai Capsule for Treatment of Psoriasis: Multi-Omics Analysis and Experimental Verification. Drug design, development and therapy, 19, 5209.

Fu Y, et al. (2025) LARS2 DNA methylation predicts the prognosis in colon cancer. *Scientific reports*, 15(1), 26542.

Gao X, et al. (2025) Integrative analysis of ubiquitination-related genes identifies HSPA1A as a critical regulator in colorectal cancer progression. *Medical oncology (Northwood, London, England)*, 42(4), 123.

Liu X, et al. (2025) Identification of the Hub Gene LDB3 in Stanford Type A Aortic Dissection Based on Comprehensive Bioinformatics Analysis. *Journal of cellular and molecular medicine*, 29(6), e70471.

Gao YX, et al. (2025) Targeting LHPP in neoadjuvant chemotherapy resistance of gastric cancer: insights from single-cell and multi-omics data on tumor immune microenvironment and stemness characteristics. *Cell death & disease*, 16(1), 306.

Xing Q, et al. (2025) Construction and validation of a predictive model for the efficacy of valproic acid monotherapy in epilepsy based on Lasso-logistic regression. *Clinics (Sao Paulo, Brazil)*, 80, 100684.

Li Y, et al. (2025) Identification and validation of NEIL2 as a prognostic biomarker and potential therapeutic target in cervical cancer. *Discover oncology*, 16(1), 1194.

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.

Jalali P, et al. (2025) Bioinformatics analysis reveals shared molecular pathways for relationship between ulcerative colitis and primary sclerosing cholangitis. *Genomics & informatics*, 23(1), 12.

Liu Q, et al. (2025) Prognostic value of natural killer T cell related genes in acute myeloid leukemia. *Cancer cell international*, 25(1), 143.

Khalaj M, et al. (2025) High-Throughput Screening on Primary Tumor-Associated Microglia and Macrophages Identifies HDAC Inhibitors as Enhancers of Phagocytosis and Potent Partners for Immunotherapy in Glioblastoma. *bioRxiv : the preprint server for biology*.

Khayer N, et al. (2025) A dynamic co-expression approach reveals Gins2 as a potential upstream modulator of HNSCC metastasis. *Scientific reports*, 15(1), 3322.

Elghaish RA, et al. (2025) A computational framework for identifying cytoskeletal genes associated with age-related diseases. *Scientific reports*, 15(1), 14590.