Resource Summary Report

Generated by dkNET on Apr 26, 2025

Simpleaffy

RRID:SCR_001302
Type: Tool

Proper Citation

Simpleaffy (RRID:SCR_001302)

Resource Information

URL: http://www.bioconductor.org/packages/release/bioc/html/simpleaffy.html

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Description: Software package that provides high level functions for reading Affy .CEL files, phenotypic data, and then computing simple things with it, such as t-tests, fold changes and the like. It makes heavy use of the affy library. It also has some basic scatter plot functions and mechanisms for generating high resolution journal figures.

Abbreviations: Simpleaffy

Synonyms: Simpleaffy - Very simple high level analysis of Affymetrix data

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

Defining Citation: PMID:16076888

Keywords: affymetrix, annotation, data import, differential expression, microarray, one channel, preprocessing, quality control, report writing, transcription, visualization

Funding:

Availability: GNU General Public License, v2 or newer

Resource Name: Simpleaffy

Resource ID: SCR_001302

Alternate IDs: OMICS_02034

Record Creation Time: 20220129T080206+0000

Record Last Update: 20250426T055438+0000

Ratings and Alerts

No rating or validation information has been found for Simpleaffy.

No alerts have been found for Simpleaffy.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 84 mentions in open access literature.

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

Peng B, et al. (2024) Comprehensive landscape of m6A regulator-related gene patterns and tumor microenvironment infiltration characterization in gastric cancer. Scientific reports, 14(1), 16404.

He Y, et al. (2024) LINC00998 Modulating M2 Macrophage Activation in Allergic Rhinitis by Stabilizing BOB.1 mRNA. Journal of inflammation research, 17, 2309.

Chen B, et al. (2023) m6A and m5C modification of GPX4 facilitates anticancer immunity via STING activation. Cell death & disease, 14(12), 809.

Wang Q, et al. (2023) A compendium of mitochondrial molecular characteristics provides novel perspectives on the treatment of rheumatoid arthritis patients. Journal of translational medicine, 21(1), 561.

Alaskar A, et al. (2023) Inhibition of signaling downstream of beta-2 adrenoceptor by propranolol in prostate cancer cells. The Prostate, 83(3), 237.

Zhang B, et al. (2022) The chromatin remodeler CHD6 promotes colorectal cancer development by regulating TMEM65-mediated mitochondrial dynamics via EGF and Wnt signaling. Cell discovery, 8(1), 130.

Zhou J, et al. (2022) Pyroptosis patterns of colon cancer could aid to estimate prognosis, microenvironment and immunotherapy: evidence from multi-omics analysis. Aging, 14(18), 7547.

Nie X, et al. (2022) N6-methyladenosine-related lncRNAs is a potential marker for predicting prognosis and immunotherapy in ovarian cancer. Hereditas, 159(1), 17.

Li F, et al. (2021) m5C Regulator-Mediated Methylation Modification Patterns and Tumor Microenvironment Infiltration Characterization in Papillary Thyroid Carcinoma. Frontiers in oncology, 11, 729887.

Jin Y, et al. (2021) Analysis of Ferroptosis-Mediated Modification Patterns and Tumor Immune Microenvironment Characterization in Uveal Melanoma. Frontiers in cell and developmental biology, 9, 685120.

Jiang Y, et al. (2021) Deciphering potential pharmacological mechanism of Sha-Shen-Mai-Dong decoction on primary Sjogren's syndrome. BMC complementary medicine and therapies, 21(1), 79.

Zhang W, et al. (2021) Molecular subtypes based on ferroptosis-related genes and tumor microenvironment infiltration characterization in lung adenocarcinoma. Oncoimmunology, 10(1), 1959977.

Gözen D, et al. (2021) Transcriptome profiles associated with selenium-deficiency-dependent oxidative stress identify potential diagnostic and therapeutic targets in liver cancer cells. Turkish journal of biology = Turk biyoloji dergisi, 45(2), 149.

Dom G, et al. (2021) Transcriptomic Signature of Human Embryonic Thyroid Reveals Transition From Differentiation to Functional Maturation. Frontiers in cell and developmental biology, 9, 669354.

Marzec J, et al. (2021) The Transcriptomic Landscape of Prostate Cancer Development and Progression: An Integrative Analysis. Cancers, 13(2).

Jin Y, et al. (2021) Analysis of m6A-Related Signatures in the Tumor Immune Microenvironment and Identification of Clinical Prognostic Regulators in Adrenocortical Carcinoma. Frontiers in immunology, 12, 637933.

Zhang B, et al. (2020) m6A regulator-mediated methylation modification patterns and tumor microenvironment infiltration characterization in gastric cancer. Molecular cancer, 19(1), 53.

Liu D, et al. (2020) Association of an anaplastic lymphoma kinase pathway signature with cell de-differentiation, neoadjuvant chemotherapy response, and recurrence risk in breast cancer. Cancer communications (London, England), 40(9), 422.

Bil P, et al. (2020) Circuits Regulating Superoxide and Nitric Oxide Production and Neutralization in Different Cell Types: Expression of Participating Genes and Changes Induced by Ionizing Radiation. Antioxidants (Basel, Switzerland), 9(8).

Pathak RK, et al. (2020) Computational analysis of microarray data of Arabidopsis thaliana challenged with Alternaria brassicicola for identification of key genes in Brassica. Journal, genetic engineering & biotechnology, 18(1), 17.