Resource Summary Report

Generated by NIF on May 15, 2025

Aroma.affymetrix

RRID:SCR_010919
Type: Tool

Proper Citation

Aroma.affymetrix (RRID:SCR_010919)

Resource Information

URL: http://aroma-project.org/

Proper Citation: Aroma.affymetrix (RRID:SCR_010919)

Description: An R package for analyzing large Affymetrix data sets.

Abbreviations: Aroma.affymetrix

Resource Type: software resource

Keywords: bio.tools

Funding:

Resource Name: Aroma.affymetrix

Resource ID: SCR_010919

Alternate IDs: OMICS_00703, biotools:aroma.affymetrix

Alternate URLs: https://bio.tools/aroma.affymetrix

Record Creation Time: 20220129T080301+0000

Record Last Update: 20250420T014515+0000

Ratings and Alerts

No rating or validation information has been found for Aroma.affymetrix.

No alerts have been found for Aroma.affymetrix.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 32 mentions in open access literature.

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

Köferle A, et al. (2022) Interrogation of cancer gene dependencies reveals paralog interactions of autosome and sex chromosome-encoded genes. Cell reports, 39(2), 110636.

Hanna BS, et al. (2021) Interleukin-10 receptor signaling promotes the maintenance of a PD-1int TCF-1+ CD8+ T cell population that sustains anti-tumor immunity. Immunity, 54(12), 2825.

Ortiz-Estévez M, et al. (2021) Integrative multi-omics identifies high risk multiple myeloma subgroup associated with significant DNA loss and dysregulated DNA repair and cell cycle pathways. BMC medical genomics, 14(1), 295.

Guyon C, et al. (2020) Aire-dependent genes undergo Clp1-mediated 3'UTR shortening associated with higher transcript stability in the thymus. eLife, 9.

Li Z, et al. (2020) Comprehensive identification and characterization of somatic copy number alterations in triple?negative breast cancer. International journal of oncology, 56(2), 522.

Del Carmen S, et al. (2020) Prognostic implications of EGFR protein expression in sporadic colorectal tumors: Correlation with copy number status, mRNA levels and miRNA regulation. Scientific reports, 10(1), 4662.

Marin E, et al. (2019) Human Tolerogenic Dendritic Cells Regulate Immune Responses through Lactate Synthesis. Cell metabolism, 30(6), 1075.

Bhutta MF, et al. (2019) Transcript Analysis Reveals a Hypoxic Inflammatory Environment in Human Chronic Otitis Media With Effusion. Frontiers in genetics, 10, 1327.

Pellinen T, et al. (2018) ITGB1-dependent upregulation of Caveolin-1 switches TGF? signalling from tumour-suppressive to oncogenic in prostate cancer. Scientific reports, 8(1), 2338.

Gracio F, et al. (2017) Splicing imbalances in basal-like breast cancer underpin perturbation of cell surface and oncogenic pathways and are associated with patients' survival. Scientific reports, 7, 40177.

Abbuehl JP, et al. (2017) Long-Term Engraftment of Primary Bone Marrow Stromal Cells Repairs Niche Damage and Improves Hematopoietic Stem Cell Transplantation. Cell stem cell, 21(2), 241.

Böttcher R, et al. (2016) Human PDE4D isoform composition is deregulated in primary prostate cancer and indicative for disease progression and development of distant metastases. Oncotarget, 7(43), 70669.

Liu K, et al. (2015) Overexpression of FGFR2 contributes to inherent resistance to MET inhibitors in MET-amplified patient-derived gastric cancer xenografts. Oncology letters, 10(4), 2003.

Bosch PJ, et al. (2015) mRNA and microRNA analysis reveals modulation of biochemical pathways related to addiction in the ventral tegmental area of methamphetamine self-administering rats. BMC neuroscience, 16, 43.

Böttcher R, et al. (2015) Novel long non-coding RNAs are specific diagnostic and prognostic markers for prostate cancer. Oncotarget, 6(6), 4036.

Van der Goten J, et al. (2014) Integrated miRNA and mRNA expression profiling in inflamed colon of patients with ulcerative colitis. PloS one, 9(12), e116117.

Lee W, et al. (2014) PRC2 is recurrently inactivated through EED or SUZ12 loss in malignant peripheral nerve sheath tumors. Nature genetics, 46(11), 1227.

Rodrigo-Domingo M, et al. (2014) Reproducible probe-level analysis of the Affymetrix Exon 1.0 ST array with R/Bioconductor. Briefings in bioinformatics, 15(4), 519.

Katsogiannou M, et al. (2014) The functional landscape of Hsp27 reveals new cellular processes such as DNA repair and alternative splicing and proposes novel anticancer targets. Molecular & cellular proteomics : MCP, 13(12), 3585.

de Rinaldis E, et al. (2013) Integrated genomic analysis of triple-negative breast cancers reveals novel microRNAs associated with clinical and molecular phenotypes and sheds light on the pathways they control. BMC genomics, 14, 643.