Resource Summary Report

Generated by NIF on Apr 21, 2025

beadarray

RRID:SCR_001314
Type: Tool

Proper Citation

beadarray (RRID:SCR_001314)

Resource Information

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

Proper Citation: beadarray (RRID:SCR_001314)

Description: Software package to read bead-level data (raw TIFFs and text files) output by BeadScan as well as bead-summary data from BeadStudio. Methods for quality assessment and low-level analysis are provided.

Abbreviations: beadarray

Synonyms: beadarray - Quality assessment and low-level analysis for Illumina BeadArray data

Resource Type: software resource

Defining Citation: PMID:17586828

Keywords: microarray, quality control, one channel, preprocessing, bio.tools

Funding:

Availability: GNU General Public License, v2

Resource Name: beadarray

Resource ID: SCR_001314

Alternate IDs: OMICS_02021, biotools:beadarray

Alternate URLs: https://bio.tools/beadarray

Record Creation Time: 20220129T080206+0000

Record Last Update: 20250420T014026+0000

Ratings and Alerts

No rating or validation information has been found for beadarray.

No alerts have been found for beadarray.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 116 mentions in open access literature.

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

Danielewicz H, et al. (2024) Cord blood methylation at TNFRSF17 is associated with early allergic phenotypes. Immunologic research, 72(6), 1259.

Cendrowski J, et al. (2024) NF?B and JNK pathways mediate metabolic adaptation upon ESCRT-I deficiency. Cellular and molecular life sciences : CMLS, 81(1), 458.

Lee HS, et al. (2024) The association between sleep quality and accelerated epigenetic aging with metabolic syndrome in Korean adults. Clinical epigenetics, 16(1), 92.

DeSouza-Vieira T, et al. (2024) Functional plasticity shapes neutrophil response to Leishmania major infection in susceptible and resistant strains of mice. PLoS pathogens, 20(10), e1012592.

Lucas-Herald AK, et al. (2024) Gonadal Function in Boys with Bilateral Undescended Testes. Journal of the Endocrine Society, 8(2), bvad153.

Krieger N, et al. (2024) Epigenetic Aging and Racialized, Economic, and Environmental Injustice: NIMHD Social Epigenomics Program. JAMA network open, 7(7), e2421832.

Alexander J, et al. (2024) Pathway-based signatures predict patient outcome, chemotherapy benefit and synthetic lethal dependencies in invasive lobular breast cancer. British journal of cancer, 130(11), 1828.

Ladd-Acosta C, et al. (2023) Analysis of Pregnancy Complications and Epigenetic Gestational Age of Newborns. JAMA network open, 6(2), e230672.

Krieger N, et al. (2023) Epigenetic aging & embodying injustice: US My Body My Story and Multi-Ethnic Atherosclerosis Study. medRxiv : the preprint server for health sciences.

Farmaki E, et al. (2023) ONC201/TIC10 enhances durability of mTOR inhibitor everolimus in metastatic ER+ breast cancer. eLife, 12.

Wang C, et al. (2022) Short- and intermediate-term exposure to ambient fine particulate elements and leukocyte epigenome-wide DNA methylation in older men: the Normative Aging Study. Environment international, 158, 106955.

Huang H, et al. (2021) Piwil1 Regulates Glioma Stem Cell Maintenance and Glioblastoma Progression. Cell reports, 34(1), 108522.

Ntunzwenimana JC, et al. (2021) Functional screen of inflammatory bowel disease genes reveals key epithelial functions. Genome medicine, 13(1), 181.

Balzano-Nogueira L, et al. (2021) Integrative analyses of TEDDY Omics data reveal lipid metabolism abnormalities, increased intracellular ROS and heightened inflammation prior to autoimmunity for type 1 diabetes. Genome biology, 22(1), 39.

Bakulski KM, et al. (2021) Prenatal Particulate Matter Exposure Is Associated with Saliva DNA Methylation at Age 15: Applying Cumulative DNA Methylation Scores as an Exposure Biomarker. Toxics, 9(10).

Turpín-Sevilla MDC, et al. (2021) Global Methylome Scores Correlate with Histological Subtypes of Colorectal Carcinoma and Show Different Associations with Common Clinical and Molecular Features. Cancers, 13(20).

Grieshober L, et al. (2021) Pre-diagnosis neutrophil-to-lymphocyte ratio and mortality in individuals who develop lung cancer. Cancer causes & control : CCC, 32(11), 1227.

Morotti M, et al. (2021) Increased expression of glutamine transporter SNAT2/SLC38A2 promotes glutamine dependence and oxidative stress resistance, and is associated with worse prognosis in triple-negative breast cancer. British journal of cancer, 124(2), 494.

Tran MGB, et al. (2020) Independence of HIF1a and androgen signaling pathways in prostate cancer. BMC cancer, 20(1), 469.

Hu W, et al. (2020) Genome-wide association mapping revealed syntenic loci QFhb-4AL and QFhb-5DL for Fusarium head blight resistance in common wheat (Triticum aestivum L.). BMC plant biology, 20(1), 29.