Resource Summary Report

Generated by dkNET on Apr 25, 2025

minfi

RRID:SCR_012830
Type: Tool

Proper Citation

minfi (RRID:SCR_012830)

Resource Information

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

Proper Citation: minfi (RRID:SCR_012830)

Description: Software tools for analyzing and visualizing Illumina''s 450k array data.

Abbreviations: minfi

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

Defining Citation: PMID:28035024

Keywords: Illumina, array data, Analyze Illumina Infinium DNA methylation arrays, DNA methylation array, bio.tools

Funding:

Availability: Free, Available for download, Freely available

Resource Name: minfi

Resource ID: SCR_012830

Alternate IDs: biotools:minfi, OMICS_00799, BioTools:minfi

Alternate URLs: https://bio.tools/minfi, https://bio.tools/minfi, https://bio.tools/minfi

Record Creation Time: 20220129T080312+0000

Record Last Update: 20250425T055923+0000

Ratings and Alerts

No rating or validation information has been found for minfi.

No alerts have been found for minfi.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 342 mentions in open access literature.

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

Walker A, et al. (2025) Deep learning-based classifier for carcinoma of unknown primary using methylation quantitative trait loci. Journal of neuropathology and experimental neurology, 84(2), 147.

Kasan M, et al. (2025) Genomic and phenotypic stability of fusion-driven pediatric sarcoma cell lines. Nature communications, 16(1), 380.

Noble A, et al. (2025) Epigenetic age acceleration and methylation differences in IgG4-related cholangitis and primary sclerosing cholangitis. Clinical epigenetics, 17(1), 6.

Zhou J, et al. (2025) Deep learning predicts DNA methylation regulatory variants in specific brain cell types and enhances fine mapping for brain disorders. Science advances, 11(1), eadn1870.

Tomczak K, et al. (2025) Plasma DNA Methylation-Based Biomarkers for MPNST Detection in Patients With Neurofibromatosis Type 1. Molecular carcinogenesis, 64(1), 44.

Lee E, et al. (2024) Exploring the effects of Dasatinib, Quercetin, and Fisetin on DNA methylation clocks: a longitudinal study on senolytic interventions. Aging, 16(4), 3088.

Hannon ER, et al. (2024) Transcriptome- and DNA methylation-based cell-type deconvolutions produce similar estimates of differential gene expression and differential methylation. Research square.

Mohazzab-Hosseinian S, et al. (2024) Effect of parental adverse childhood experiences on intergenerational DNA methylation signatures from peripheral blood mononuclear cells and buccal mucosa. Translational psychiatry, 14(1), 89.

Martino D, et al. (2024) Respiratory infection- and asthma-prone, low vaccine responder children demonstrate distinct mononuclear cell DNA methylation pathways. Clinical epigenetics, 16(1), 85.

Lai TJ, et al. (2024) Epigenetic Induction of Cancer-Testis Antigens and Endogenous Retroviruses at Single-Cell Level Enhances Immune Recognition and Response in Glioma. Cancer research communications, 4(7), 1834.

Martino D, et al. (2024) DNA Methylation signatures underpinning blood neutrophil to lymphocyte ratio during first week of human life. Nature communications, 15(1), 8167.

Hjort L, et al. (2024) Epigenetics of the non-coding RNA nc886 across blood, adipose tissue and skeletal muscle in offspring exposed to diabetes in pregnancy. Clinical epigenetics, 16(1), 61.

Liao Y, et al. (2024) Differences in the DNA methylome of T cells in adults with asthma of varying severity. Clinical epigenetics, 16(1), 139.

Yamaguchi J, et al. (2024) Dual phenotypes in recurrent astrocytoma, IDH-mutant; coexistence of IDH-mutant and IDH-wildtype components: a case report with genetic and epigenetic analysis. Acta neuropathologica communications, 12(1), 169.

Ferrier ST, et al. (2024) Azacytidine treatment affects the methylation pattern of genomic and cell-free DNA in uveal melanoma cell lines. BMC cancer, 24(1), 1299.

Kibe Y, et al. (2024) Pediatric-type high-grade gliomas with PDGFRA amplification in adult patients with Li-Fraumeni syndrome: clinical and molecular characterization of three cases. Acta neuropathologica communications, 12(1), 57.

Liang M, et al. (2024) A homozygous stop codon in HORMAD2 in a patient with recurrent digynic triploid miscarriage. Molecular genetics & genomic medicine, 12(2), e2402.

Lariviere D, et al. (2024) Methylation profiles at birth linked to early childhood obesity. medRxiv : the preprint server for health sciences.

Berglund A, et al. (2024) Integration of long-read sequencing, DNA methylation and gene expression reveals heterogeneity in Y chromosome segment lengths in phenotypic males with 46,XX testicular disorder/difference of sex development. Biology of sex differences, 15(1), 77.

Pahlevan Kakhki M, et al. (2024) A genetic-epigenetic interplay at 1q21.1 locus underlies CHD1L-mediated vulnerability to primary progressive multiple sclerosis. Nature communications, 15(1), 6419.