

Resource Summary Report

Generated by [NIF](#) on Aug 19, 2026

[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: software application, software resource, data analysis software, data processing software, data visualization software

Defining Citation: [PMID:28035024](#)

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

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: 20260819T044333+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 417 mentions in open access literature.

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

Jeong D, et al. (2026) Multidimensional profiling of heterogeneity in supratentorial ependymomas. *Nature*, 652(8111), 1016.

Zhu I, et al. (2026) IFN signaling is associated with radiotherapy response in malignant peripheral nerve sheath tumors. *The Journal of clinical investigation*, 136(5).

Pahlevan Kakhki M, et al. (2026) Comprehensive profiling of CRISPR/dCas9 epigenome editors indicates a complex link between on and off target effects. *Genome biology*, 27(1).

Jensen D, et al. (2026) Adolescent White Matter Maturation Mediates Epigenetic Associations With Cognitive Development. *Developmental neurobiology*, 86(1), e70000.

Maas SLN, et al. (2026) A microenvironment-determined risk continuum refines subtyping in meningioma and reveals determinants of machine learning-based tumor classification. *Nature genetics*, 58(2), 341.

Humaloja L, et al. (2026) Longitudinal association of circulating inflammatory biomarkers with epigenetic ageing in the Young Finns Study. *Scientific reports*, 16(1).

Wang Z, et al. (2026) Estimating population structure using epigenome-wide methylation data. *Briefings in bioinformatics*, 27(2).

Grant OA, et al. (2026) Systematic investigation of interindividual variation of DNA methylation in human whole blood. *Genome biology*, 27(1).

Sueyoshi H, et al. (2026) Histological grade 2 and non-contrast-enhancing phenotype provide prognostic information complementary to DNA methylation classification in TERTp-mutant molecular glioblastomas. *Acta neuropathologica communications*, 14(1).

Kordowitzki P, et al. (2026) SYTL4 May Serve as a New Predictive Biomarker for Survival and Trastuzumab Treatment Responsiveness in HER2-Positive Breast Cancer. *International journal of molecular sciences*, 27(10).

Thursby SJ, et al. (2026) Epigenetic Instability-Based Metrics in Cell-Free DNA for Early Cancer Detection. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(8), 1528.

Basrai S, et al. (2026) Blood-based epigenetic instability linked to human aging and disease. *Nature communications*, 17(1).

Kwiatkowska KM, et al. (2026) DNA methylation signatures of treatment response in medication-overuse headache. *The journal of headache and pain*, 27(1).

Williams JS, et al. (2026) Patient-derived pediatric brain tumor orthotopic xenografts and tumor organoids faithfully recapitulate primary tumors. *Science advances*, 12(16), eaea4966.

Avolio M, et al. (2026) The Molecular and Functional Landscape of Resistance to FOLFIRI Chemotherapy in Metastatic Colorectal Cancer. *Cancer discovery*, 16(2), 270.

Kasamoto J, et al. (2026) DNA Methylation Signatures of Cellular Senescence Are Not Reversed by Senolytic Treatment. *Aging cell*, 25(3), e70430.

Tallaksen HBL, et al. (2026) DNA hypomethylation at specific CG-sites within TRAK1 is linked to the neurocognitive profile in Klinefelter syndrome. *Molecular psychiatry*, 31(3), 1409.

Kwiatkowska KM, et al. (2026) Whole blood DNA methylation signature of epigenetic aging in medication overuse headache. *The journal of headache and pain*, 27(1).

Li Y, et al. (2026) Integrated multi-omics analysis reveals comprehensive metabolism-driven tumor heterogeneity and immune microenvironment in hepatocellular carcinomas. *Scientific reports*, 16(1).

Foong YH, et al. (2026) Molecular profiling of sacral chordomas through methylation, spatial transcriptomics and multiplexed immunofluorescence. *ESMO rare cancers*, 5.