

Resource Summary Report

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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 processing software, data analysis software, software resource, software application, 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: 20260805T044305+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 390 mentions in open access literature.

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

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

Dragic D, et al. (2025) Alcohol consumption and DNA methylation: an epigenome-wide association study within the French E3N cohort. *Clinical epigenetics*, 17(1), 118.

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.

Sharma-Oates A, et al. (2025) Ethnicity-specific patterns of epigenetic age acceleration in rheumatoid arthritis. *GeroScience*, 47(3), 3965.

Tokairin K, et al. (2025) Genome-Wide DNA Methylation Profiling Reveals Low Methylation Variability in Moyamoya Disease. *Translational stroke research*, 16(4), 1198.

Dawson KL, et al. (2025) Epigenetic aging and DNA methylation biomarker changes following ketamine treatment in patients with MDD and PTSD: a pilot study. *Translational psychiatry*, 15(1), 452.

Terradas M, et al. (2025) Constitutional epimutations in LTBP4, a component of the TGF- β signaling, and in BRCA1, as potential drivers of early-onset colorectal cancer. *Clinical epigenetics*, 17(1), 183.

Rubens M, et al. (2025) A Pilot Epigenome-Wide Study of Posttraumatic Growth: Identifying Novel Candidates for Future Research. *Epigenomes*, 9(4).

Doherty T, et al. (2025) Analysis of blood-based DNA methylation signatures of aging and disease progression in inflammatory bowel disease. *Human genetics*, 144(11-12), 1079.

Vestin H, et al. (2025) Patients with systemic lupus erythematosus (SLE) have an increased bisphenol A methylation score linked to SLE risk genes and selected clinical subphenotypes. *RMD open*, 11(3).

Kemda Ngueta C, et al. (2025) One-sample missing DNA-methylation value imputation. *BMC bioinformatics*, 26(1), 143.

Corbett RJ, et al. (2025) Germline pathogenic variation impacts somatic alterations and patient outcomes in pediatric central nervous system tumors. *Nature communications*,

16(1), 10282.

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

Skinner CM, et al. (2025) DNA methylation clocks struggle to distinguish inflammaging from healthy aging, but feature rectification improves coherence and enhances detection of inflammaging. *GeroScience*, 47(3), 3043.

Vlasac IM, et al. (2025) DNA-based cell typing in menstrual effluent identifies cell type variation by sample collection method: toward noninvasive biomarker development for women's health. *Epigenetics*, 20(1), 2453275.

Cui X, et al. (2025) DNA Methylation Algorithms of Aging and Incident Cardiovascular Disease: A Prospective Cohort Study. *Journal of the American Heart Association*, 14(23), e045545.

Krech M, et al. (2025) Outcome-associated factors in a molecularly defined cohort of central neurocytoma. *Acta neuropathologica*, 149(1), 61.

Chitta P, et al. (2025) Exploring DNA methylation age and the influence of physical performance, and hypertension on frailty in elderly women. *Scientific reports*, 15(1), 28043.

Andersen MS, et al. (2025) Establishment of a patient-derived 3D in vitro meningioma model in xeno-free hydrogel for clinical applications. *Acta neuropathologica communications*, 13(1), 81.

Tauziède-Espariat A, et al. (2025) CIC/ATXN1-rearranged tumors in the central nervous system are mainly represented by sarcomas: A comprehensive clinicopathological and epigenetic series. *Brain pathology (Zurich, Switzerland)*, 35(2), e13303.