

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

BMIQ

RRID:SCR_003446

Type: Tool

Proper Citation

BMIQ (RRID:SCR_003446)

Resource Information

URL: <https://code.google.com/p/bmiq/>

Proper Citation: BMIQ (RRID:SCR_003446)

Description: Software using a beta-mixture quantile normalization method for correcting probe design bias in Illumina Infinium 450 k DNA methylation data.

Abbreviations: BMIQ

Synonyms: bmiq - Beta Mixture Quantile Model, Beta Mixture Quantile dilation

Resource Type: software resource

Defining Citation: [PMID:23175756](#)

Keywords: illumina infinium 450k, dna methylation, probe design, normalization

Availability: Free, Available for download, Freely available

Resource Name: BMIQ

Resource ID: SCR_003446

Alternate IDs: OMICS_02304

Alternate URLs: <https://aeteschendorff-lab.github.io/software/BMIQ/>

Record Creation Time: 20220129T080219+0000

Record Last Update: 20260905T132503+0000

Ratings and Alerts

No rating or validation information has been found for BMIQ.

No alerts have been found for BMIQ.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 133 mentions in open access literature.

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

Li H, et al. (2026) Accelerated epigenetic aging as a modifier of homocysteine-associated cognitive decline: Findings from NHANES. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 22(4), e71349.

Mahmoud NM, et al. (2026) Integrating DNA methylation biomarkers for breast cancer risk prediction using artificial intelligence. *Scientific reports*, 16(1).

Guo X, et al. (2026) Guidelines on optimizing DNA methylation reference panels for cell-type deconvolution. *Communications biology*, 9(1).

Ravaei A, et al. (2026) Epigenome-wide DNA methylation patterns associated with disease activity in systemic lupus erythematosus. *Scientific reports*, 16(1).

Ferrier K, et al. (2026) Epigenome-wide association study meta-analysis of BMI in African Americans. *HGG advances*, 7(1), 100552.

Zhu M, et al. (2026) Integrative analysis of DNA methylation and inflammatory protein biomarkers in hypertension. *Frontiers in immunology*, 17, 1671540.

Kashiwagi T, et al. (2025) Variation of Gene Expression and Methylation Profiling in Gingival and Tongue Cancers. *Cancer science*, 116(12), 3459.

Bozack AK, et al. (2025) Dietary fatty acids and epigenetic aging in US adults: results from the National Health and Nutrition Examination Survey. *npj aging*, 12(1), 3.

Li P, et al. (2025) Peripheral blood mononuclear cell DNA methylation biomarkers for prognostic stratification in Chinese lung adenocarcinoma: a genome-wide epigenetic profiling study. *Clinical epigenetics*, 17(1), 177.

Jiang X, et al. (2025) Identification of blood-derived DNA methylation biomarkers of glaucoma and intraocular pressure measurements in three European ancestry cohorts including the Canadian longitudinal study on aging. *Epigenetics*, 20(1), 2566496.

Jiang T, et al. (2025) Associations of Epigenetic Age Acceleration with Motor Impairment: Evidence from the PPMI Cohort. *medRxiv : the preprint server for health sciences*.

Qin M, et al. (2025) DNA methylation predicts adverse outcomes of coronary artery disease. *Nature communications*, 16(1), 11396.

Bozack A, et al. (2025) Dietary Fatty Acids and Epigenetic Aging in US Adults: Results from the National Health and Nutrition Examination Survey. medRxiv : the preprint server for health sciences.

Tang X, et al. (2025) Causality-driven candidate identification for reliable DNA methylation biomarker discovery. Nature communications, 16(1), 680.

Chen H, et al. (2025) Prognostic value of LPAR1 expression and methylation in low-grade gliomas: a meta-analysis of TCGA and CGGA datasets and functional validation. BMC cancer, 26(1), 161.

Chernoff M, et al. (2025) Differential DNA Methylation in the Benign and Cancerous Prostate Tissue of African American and European American Men. Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology, 34(3), 428.

Kuznetsov DV, et al. (2025) Genetic and environmental contributions to epigenetic aging across adolescence and young adulthood. Clinical epigenetics, 17(1), 78.

Wall??n E, et al. (2025) Effects of alcohol on the transcriptome, methylome and metabolome of in vitro gastrulating human embryonic cells. Disease models & mechanisms, 18(6).

Guo X, et al. (2025) Variations in Innate Immune Cell Subtypes Correlate with Epigenetic Clocks, Inflammaging and Health Outcomes. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(43), e05922.

Zelenova E, et al. (2025) Multi-omics study of molecular and genetic bases of orthostatic hypotension. Clinical epigenetics, 17(1), 202.