# Resource Summary Report

Generated by RRID on Apr 11, 2025

# 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

**Funding:**

**Availability:** GNU General Public License, v2

**Resource Name:** BMIQ

**Resource ID:** SCR_003446

**Alternate IDs:** OMICS_02304

**Record Creation Time:** 20220129T080219+0000

**Record Last Update:** 20250410T065007+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 114 mentions in open access literature.

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

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

Wen B, et al. (2024) Causal impact of DNA methylation on refracture in elderly individuals with osteoporosis - a prospective cohort study. BMC musculoskeletal disorders, 25(1), 432.

Lee HS, et al. (2024) Genome- and epigenome-wide association studies identify susceptibility of CpG sites and regions for metabolic syndrome in a Korean population. Clinical epigenetics, 16(1), 60.

Chen JQ, et al. (2024) Matched analysis of detailed peripheral blood and tumor immune microenvironment profiles in bladder cancer. Epigenomics, 16(1), 41.

Martínez-Montoro JI, et al. (2024) Interactions between the gut microbiome and DNA methylation patterns in blood and visceral adipose tissue in subjects with different metabolic characteristics. Journal of translational medicine, 22(1), 1089.

Tong H, et al. (2024) Quantifying the stochastic component of epigenetic aging. Nature aging, 4(6), 886.

Juran BD, et al. (2024) Epigenetic disease markers in primary sclerosing cholangitis and primary biliary cholangitis-methylomics of cholestatic liver disease. Hepatology communications, 8(8).

Tong H, et al. (2024) Cell-type specific epigenetic clocks to quantify biological age at cell-type resolution. Aging, 16(22), 13452.

Zhu T, et al. (2024) An improved epigenetic counter to track mitotic age in normal and precancerous tissues. Nature communications, 15(1), 4211.

Liu X, et al. (2024) DNA methylation and whole-genome transcription analysis in CD4+ T

cells from systemic lupus erythematosus patients with or without renal damage. Clinical epigenetics, 16(1), 98.

Ko YK, et al. (2024) Epigenome-wide Association Study for Tic Disorders in Children: A Preliminary Study in Korean Population. Clinical psychopharmacology and neuroscience : the official scientific journal of the Korean College of Neuropsychopharmacology, 22(2), 295.

Halama A, et al. (2024) A roadmap to the molecular human linking multiomics with population traits and diabetes subtypes. Nature communications, 15(1), 7111.

Monjé N, et al. (2024) AHRR and SFRP2 in primary versus recurrent high-grade serous ovarian carcinoma and their prognostic implication. British journal of cancer.

Haefliger S, et al. (2024) Epigenetic age acceleration is a distinctive trait of epithelioid sarcoma with potential therapeutic implications. GeroScience, 46(5), 5203.

Carlund O, et al. (2023) DNA methylation variations and epigenetic aging in telomere biology disorders. Scientific reports, 13(1), 7955.

Kitaba NT, et al. (2023) Fathers' preconception smoking and offspring DNA methylation. Clinical epigenetics, 15(1), 131.

Liao X, et al. (2023) Effect of mechanical unloading on genome-wide DNA methylation profile of the failing human heart. JCI insight, 8(4).

Westin IM, et al. (2023) DNA methylation changes and increased mRNA expression of coagulation proteins, factor V and thrombomodulin in Fuchs endothelial corneal dystrophy. Cellular and molecular life sciences : CMLS, 80(3), 62.

Santamarina-Ojeda P, et al. (2023) Multi-omic integration of DNA methylation and gene expression data reveals molecular vulnerabilities in glioblastoma. Molecular oncology, 17(9), 1726.

Ruiz-Arenas C, et al. (2023) Epimutation detection in the clinical context: guidelines and a use case from a new Bioconductor package. Epigenetics, 18(1), 2230670.