

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 19, 2026

Methylumi

RRID:SCR_012831

Type: Tool

Proper Citation

Methylumi (RRID:SCR_012831)

Resource Information

URL: <http://www.bioconductor.org/packages/release/bioc/html/methylumi.html>

Proper Citation: Methylumi (RRID:SCR_012831)

Description: Software package that provides classes for holding and manipulating Illumina methylation data.

Abbreviations: Methylumi

Resource Type: software resource

Resource Name: Methylumi

Resource ID: SCR_012831

Alternate IDs: OMICS_00798

Record Creation Time: 20220129T080312+0000

Record Last Update: 20260919T195233+0000

Ratings and Alerts

No rating or validation information has been found for Methylumi.

No alerts have been found for Methylumi.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Berezovsky A, et al. (2025) Impact of developmental state, p53 status, and interferon signaling on glioblastoma cell response to radiation and temozolomide treatment. PloS one, 20(2), e0315171.

García-Calzón S, et al. (2025) Epigenetic biomarkers predict macrovascular events in individuals with type 2 diabetes. Cell reports. Medicine, 6(8), 102290.

Wilker S, et al. (2023) Epigenetics of traumatic stress: The association of NR3C1 methylation and posttraumatic stress disorder symptom changes in response to narrative exposure therapy. Translational psychiatry, 13(1), 14.

Mizuno M, et al. (2021) Transplantation of human autologous synovial mesenchymal stem cells with trisomy 7 into the knee joint and 5 years of follow-up. Stem cells translational medicine, 10(11), 1530.

Han L, et al. (2019) Changes in DNA methylation from pre- to post-adolescence are associated with pubertal exposures. Clinical epigenetics, 11(1), 176.

Zadel M, et al. (2018) DNA Methylation Profiles in Whole Blood of Huntington's Disease Patients. Frontiers in neurology, 9, 655.

Philibert R, et al. (2018) Dose Response and Prediction Characteristics of a Methylation Sensitive Digital PCR Assay for Cigarette Consumption in Adults. Frontiers in genetics, 9, 137.

Shen J, et al. (2018) Integrated analysis of the gene expression profile and DNA methylation profile of obese patients with type 2 diabetes. Molecular medicine reports, 17(6), 7636.

Kebir O, et al. (2018) Epigenetic variability in conversion to psychosis: novel findings from an innovative longitudinal methylomic analysis. Translational psychiatry, 8(1), 93.

Spiers H, et al. (2017) 5-hydroxymethylcytosine is highly dynamic across human fetal brain development. BMC genomics, 18(1), 738.

Khuc E, et al. (2017) Comprehensive characterization of DNA methylation changes in Fuchs endothelial corneal dystrophy. PloS one, 12(4), e0175112.

Cazaly E, et al. (2016) Comparison of pre-processing methodologies for Illumina 450k methylation array data in familial analyses. Clinical epigenetics, 8, 75.

Mok A, et al. (2016) Genome-wide profiling identifies associations between lupus nephritis and differential methylation of genes regulating tissue hypoxia and type 1 interferon responses. Lupus science & medicine, 3(1), e000183.

Lim AM, et al. (2016) Genome-scale methylation assessment did not identify prognostic biomarkers in oral tongue carcinomas. Clinical epigenetics, 8, 74.

Hao JJ, et al. (2016) Spatial intratumoral heterogeneity and temporal clonal evolution in esophageal squamous cell carcinoma. *Nature genetics*, 48(12), 1500.

Spiers H, et al. (2015) Methylomic trajectories across human fetal brain development. *Genome research*, 25(3), 338.

Miao Z, et al. (2015) Analysis of the transcriptional regulation of cancer-related genes by aberrant DNA methylation of the cis-regulation sites in the promoter region during hepatocyte carcinogenesis caused by arsenic. *Oncotarget*, 6(25), 21493.

Jones MR, et al. (2015) Systems Genetics Reveals the Functional Context of PCOS Loci and Identifies Genetic and Molecular Mechanisms of Disease Heterogeneity. *PLoS genetics*, 11(8), e1005455.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. *Database : the journal of biological databases and curation*, 2015.

Moore JB, et al. (2015) Epigenetic reprogramming and re-differentiation of a Ewing sarcoma cell line. *Frontiers in cell and developmental biology*, 3, 15.