

Resource Summary Report

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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: 20260725T190741+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.

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.

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.

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.