

Resource Summary Report

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wateRmelon

RRID:SCR_001296

Type: Tool

Proper Citation

wateRmelon (RRID:SCR_001296)

Resource Information

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

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Description: Software package for Illumina 450 methylation array normalization and metrics including 15 flavors of betas and three performance metrics, with methods for objects produced by methylumi, minfi and IMA packages.

Abbreviations: wateRmelon

Resource Type: software resource

Defining Citation: [PMID:23631413](#)

Keywords: dna methylation, microarray, preprocessing, quality control, two channel, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: wateRmelon

Resource ID: SCR_001296

Alternate IDs: OMICS_02039, biotools:watermelon

Alternate URLs: <https://bio.tools/watermelon>

License: GNU General Public License, v4

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260829T182040+0000

Ratings and Alerts

No rating or validation information has been found for wateRmelon.

No alerts have been found for wateRmelon.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 314 mentions in open access literature.

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

Laroche VT, et al. (2026) Epigenomic subtypes of late-onset Alzheimer's disease reveal distinct microglial signatures. *Acta neuropathologica*, 151(1).

O'Shea DM, et al. (2026) Development and validation of MethylCog, a blood DNA methylation proxy for cognition. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 22(5), e71421.

Ofori JK, et al. (2026) Cell-specific DNA methylation in human alpha and beta cells regulates gene expression in type 2 diabetes. *Nature metabolism*, 8(4), 957.

Lin A, et al. (2026) DeepStrataAge: an interpretable deep-learning clock that reveals stage- and sex-divergent DNA methylation aging dynamics. *npj aging*, 12(1).

Janssen FW, et al. (2026) Identification and validation of liquid biopsy-based methylation biomarkers for germ cell tumor subtypes. *Communications medicine*, 6(1).

Lukacsovich D, et al. (2026) Longitudinal Blood DNA Methylation Changes During Weight-Loss Intervention and Dementia Progression Risk. *Research square*.

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

Tallaksen HBL, et al. (2026) DNA hypomethylation at specific CG-sites within TRAK1 is linked to the neurocognitive profile in Klinefelter syndrome. *Molecular psychiatry*, 31(3), 1409.

Renner M, et al. (2026) Multi-layered molecular profiling informs the diagnosis and targeted therapy of desmoplastic small round cell tumor. *Nature communications*, 17(1).

Willott T, et al. (2026) Modeling medulloblastoma pathogenesis and treatment in human cerebellar organoids. *Genes & development*, 40(11-12), 936.

Hansknecht A, et al. (2026) NSD1 governs H3K36me2-mediated DNA methylation and drives endo-mesodermal differentiation of human iPSCs. *Clinical epigenetics*, 18(1).

Yoshida K, et al. (2026) Epigenetic Alterations Beyond CpG Islands in Periodontitis: In Silico Study of DNA Methylation Data. *Clinical and experimental dental research*, 12(2), e70312.

Kim M, et al. (2026) Ontology-aware DNA methylation classification with a curated atlas of human tissues and cell types. *Cell reports methods*, 6(3), 101328.

Wang Z, et al. (2026) Estimating population structure using epigenome-wide methylation data. *Briefings in bioinformatics*, 27(2).

Liu T, et al. (2026) The association of epigenetic age acceleration with internal smoking dose, risk of lung cancer, and all-cause mortality in cigarette smokers: the Multiethnic Cohort study. *Clinical epigenetics*, 18(1).

Kordowitzki P, et al. (2026) SYTL4 May Serve as a New Predictive Biomarker for Survival and Trastuzumab Treatment Responsiveness in HER2-Positive Breast Cancer. *International journal of molecular sciences*, 27(10).

Van Dijck E, et al. (2025) Gradual DNA methylation changes reveal transcription factors implicated in metabolic dysfunction-associated steatotic liver disease progression and epigenetic age acceleration. *Clinical epigenetics*, 17(1), 138.

Beach SRH, et al. (2025) Elevated Alcohol Consumption and Chronic Inflammation Predict Cardiovascular Risk Among Black Americans: Examination of a Dual-Risk Model Using Epigenetic Risk Markers. *Epigenomes*, 9(4).

Perez RF, et al. (2025) Epigenetic signatures, age acceleration, and injury risk in elite female and male soccer players. *Scientific reports*, 15(1), 41826.

Walker EM, et al. (2025) Guidance for the design and analysis of cell-type-specific DNA methylation epidemiology studies. *Briefings in bioinformatics*, 26(4).