

Resource Summary Report

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[waterRmelon](#)

RRID:SCR_001296

Type: Tool

Proper Citation

waterRmelon (RRID:SCR_001296)

Resource Information

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

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: waterRmelon

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: 20260725T190502+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 296 mentions in open access literature.

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

Hüls A, et al. (2025) Epigenome-wide association study of cerebrospinal fluid-based biomarkers of Alzheimer's disease in cognitively normal individuals. medRxiv : the preprint server for health sciences.

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.

Perlstein TA, et al. (2025) Alcohol and aging: Next-generation epigenetic clocks predict biological age acceleration in individuals with alcohol use disorder. Alcohol, clinical & experimental research, 49(4), 829.

Cui X, et al. (2025) Associations of DNA Methylation Algorithms of Aging With Cardiovascular Disease and Mortality Risk Among US Older Adults. Journal of the American Heart Association, 14(9), e040374.

Lemaire M, et al. (2025) Meta-analysis examining fetal sex-specific placental DNA methylation intensities and estimated cell composition post IVF. Molecular human reproduction, 31(3).

Palmer AS, et al. (2025) Integrated fibre-specific methylome and proteome profiling of human skeletal muscle across males and females with fibre-type deconvolution. Skeletal muscle, 15(1), 28.

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

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).

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

Noble A, et al. (2025) Epigenetic age acceleration and methylation differences in IgG4-related cholangitis and primary sclerosing cholangitis. Clinical epigenetics, 17(1), 6.

Lim H, et al. (2025) DNA Methylation Profile in Buffy Coat Identifies Methylation Differences Between Cirrhosis with and Without Hepatocellular Carcinoma. *Cancers*, 17(2).

Ryan B, et al. (2025) An integrative network approach for longitudinal stratification in Parkinson's disease. *PLoS computational biology*, 21(3), e1012857.

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.

Eulalio T, et al. (2025) regionalpcs improve discovery of DNA methylation associations with complex traits. *Nature communications*, 16(1), 368.

Kouhsar M, et al. (2025) A brain DNA co-methylation network analysis of psychosis in Alzheimer's disease. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 21(2), e14501.

Zhang W, et al. (2025) DNA methylation signature of a lifestyle-based resilience index for cognitive health. *Alzheimer's research & therapy*, 17(1), 88.

Butler AA, et al. (2025) Measuring technical variability in illumina DNA methylation microarrays. *PloS one*, 20(7), e0326337.

Wallén 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).

Harvey J, et al. (2025) Interrogating DNA methylation associated with Lewy body pathology in a cross brain-region and multi-cohort study. *medRxiv : the preprint server for health sciences*.

Laroche VT, et al. (2025) Epigenomic subtypes of late-onset Alzheimer's disease reveal distinct microglial signatures. *Research square*.