Resource Summary Report

Generated by dkNET on May 18, 2025

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

Funding:

Availability: GNU General Public License, v3

Resource Name: wateRmelon

Resource ID: SCR_001296

Alternate IDs: OMICS_02039, biotools:watermelon

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

Record Creation Time: 20220129T080206+0000

Record Last Update: 20250420T014025+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 265 mentions in open access literature.

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

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

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

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

Brempou D, et al. (2024) Using parenclitic networks on phaeochromocytoma and paraganglioma tumours provides novel insights on global DNA methylation. Scientific reports, 14(1), 29958.

Murthy M, et al. (2024) DNA methylation patterns in the frontal lobe white matter of multiple system atrophy, Parkinson's disease, and progressive supranuclear palsy: a cross-comparative investigation. Acta neuropathologica, 148(1), 4.

Smith RG, et al. (2024) Blood DNA methylomic signatures associated with CSF biomarkers of Alzheimer's disease in the EMIF-AD study. Alzheimer's & dementia : the journal of the Alzheimer's Association, 20(10), 6722.

Koetsier J, et al. (2024) Blood-based multivariate methylation risk score for cognitive impairment and dementia. Alzheimer's & dementia : the journal of the Alzheimer's Association, 20(10), 6682.

Carbonneau M, et al. (2024) Epigenetic Age Mediates the Association of Life's Essential 8 With Cardiovascular Disease and Mortality. Journal of the American Heart Association, 13(11), e032743.

Panitch R, et al. (2024) APOE genotype-specific methylation patterns are linked to Alzheimer disease pathology and estrogen response. Translational psychiatry, 14(1), 129.

Wortinger LA, et al. (2024) Divergent epigenetic responses to perinatal asphyxia in severe mental disorders. Translational psychiatry, 14(1), 16.

Neumann M, et al. (2024) Molecular subgroups of T-cell acute lymphoblastic leukemia in adults treated according to pediatric-based GMALL protocols. Leukemia, 38(6), 1213.

Shastri GG, et al. (2024) Examining epigenetic aging in the post-mortem brain in attention deficit hyperactivity disorder. Frontiers in genetics, 15, 1480761.

Zhou J, et al. (2024) Attenuated sex-related DNA methylation differences in cancer highlight the magnitude bias mediating existing disparities. Biology of sex differences, 15(1), 106.

Lê BM, et al. (2024) Characterizing epigenetic aging in an adult sickle cell disease cohort. Blood advances, 8(1), 47.

Bourassa KJ, et al. (2024) Posttraumatic stress disorder, trauma, and accelerated biological aging among post-9/11 veterans. Translational psychiatry, 14(1), 4.

Zhang Z, et al. (2024) Synthetic DNA barcodes identify singlets in scRNA-seq datasets and evaluate doublet algorithms. Cell genomics, 4(7), 100592.

Jacquin N, et al. (2024) Metastatic renal cell carcinoma with occult primary: a multicenter prospective cohort. NPJ precision oncology, 8(1), 147.

Auvinen P, et al. (2024) Genome-wide DNA methylation and gene expression in human placentas derived from assisted reproductive technology. Communications medicine, 4(1), 267.

Bonham L, et al. (2024) DNA methylation age from peripheral blood predicts progression to Alzheimer's disease, white matter disease burden, and cortical atrophy. Research square.

Mckinnon K, et al. (2024) Epigenetic scores derived in saliva are associated with gestational age at birth. Clinical epigenetics, 16(1), 84.