

Resource Summary Report

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ChAMP

RRID:SCR_012891

Type: Tool

Proper Citation

ChAMP (RRID:SCR_012891)

Resource Information

URL: <http://www.bioconductor.org/packages/2.13/bioc/html/ChAMP.html>

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Description: Software package that includes quality control metrics, a selection of normalization methods and novel methods to identify differentially methylated regions and to highlight copy number aberrations.

Abbreviations: ChAMP

Synonyms: ChAMP - Chip Analysis Methylation Pipeline for Illumina HumanMethylation450

Resource Type: software resource

Availability: Free

Resource Name: ChAMP

Resource ID: SCR_012891

Alternate IDs: OMICS_01796

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260725T190740+0000

Ratings and Alerts

No rating or validation information has been found for ChAMP.

No alerts have been found for ChAMP.

Data and Source Information

Usage and Citation Metrics

We found 734 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Mareckova K, et al. (2026) Functional Impact Score of Mitochondrial Variants and Its Relationship With Functional Connectivity of the Brain: Potential Origins of Premature Aging in Young Adulthood. *Human brain mapping*, 47(1), e70447.

Gu Y, et al. (2026) Multi-omics analyses identify potential epigenetic loci associated with survival in amyotrophic lateral sclerosis across diverse populations. *EBioMedicine*, 123, 106071.

Wick W, et al. (2025) Molecularly matched targeted therapies plus radiotherapy in glioblastoma: the phase 1/2a N2M2 umbrella trial. *Nature medicine*.

Peng T, et al. (2025) Individualized patient tumor organoids faithfully preserve human brain tumor ecosystems and predict patient response to therapy. *Cell stem cell*, 32(4), 652.

Li P, et al. (2025) Peripheral blood mononuclear cell DNA methylation biomarkers for prognostic stratification in Chinese lung adenocarcinoma: a genome-wide epigenetic profiling study. *Clinical epigenetics*, 17(1), 177.

Leoni Z, et al. (2025) Mucinous cystic neoplasms of the pancreas and liver share a similar DNA methylation profile with mucinous ovarian tumors. *The Journal of pathology*, 267(1), 10.

Taryma-Le?niak O, et al. (2025) Changes of methylation at enhancers appear to be essential for HIV infection progression. *Clinical epigenetics*, 17(1), 104.

Avila Martins CC, et al. (2025) Differential methylation in blood pressure control genes is associated to essential hypertension in African Brazilian populations. *Epigenetics*, 20(1), 2477850.

Ye Z, et al. (2025) Multimodal diagnostic models and subtype analysis for neoadjuvant therapy in breast cancer. *Frontiers in immunology*, 16, 1559200.

Barrett JE, et al. (2025) Epigenetic signatures in surrogate tissues are able to assess cancer risk and indicate the efficacy of preventive measures. *Communications medicine*, 5(1), 97.

Du Y, et al. (2025) Multiomics analysis of umbilical cord hematopoietic stem cells from a multiethnic cohort of Hawaii reveals the intergenerational effect of maternal prepregnancy obesity and risks for cancers. *GigaScience*, 14.

Wu N, et al. (2025) A diagnostic model for non-invasive urothelial cancer early detection based on methylation of urinary tumor DNA. *Cancer cell international*, 25(1), 148.

Rahman ML, et al. (2025) Epigenome-wide association study of household air pollution exposure in an area with high lung cancer incidence. medRxiv : the preprint server for health sciences.

Petersson A, et al. (2025) Reliable on-treatment prognostication and target identification with a customized assay for circulating tumor DNA in patients with newly diagnosed pancreatic cancer. Scientific reports, 15(1), 34481.

Picaud JC, et al. (2025) Partially hydrolyzed, whey-based infant formula with six human milk oligosaccharides, B. infantis LMG11588, and B. lactis CNCM I-3446 is safe, well tolerated, and improves gut health: a staged analysis of a randomized trial. Frontiers in nutrition, 12, 1628847.

Yang M, et al. (2025) BTLA promoter hypomethylation correlates with enhanced immune cell infiltration, favorable prognosis, and immunotherapy response in melanoma. Journal for immunotherapy of cancer, 13(3).

Chitta P, et al. (2025) Blood-based biomarkers derived from tumor-informed DNA methylation analysis for lung adenocarcinoma. Heliyon, 11(4), e42581.

Noble AJ, et al. (2025) Prenatal cannabis exposure is associated with alterations in offspring DNA methylation at genes involved in neurodevelopment, across the life course. Molecular psychiatry, 30(4), 1418.

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

Li X, et al. (2025) Constructing methylation-driven ceRNA networks unveil tumor heterogeneity and predict patient prognosis. Human molecular genetics, 34(3), 251.