

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>

Proper Citation: ChAMP (RRID:SCR_012891)

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: 20260905T132729+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 791 mentions in open access literature.

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

Tosi M, et al. (2026) A multi-omics study on monozygotic twins discordant for amyotrophic lateral sclerosis and literature review underline a potential role for innate immunity and epigenetic dysregulation in disease mechanisms. *Neurological sciences : official journal of the Italian Neurological Society and of the Italian Society of Clinical Neurophysiology*, 47(3), 230.

Solomon CU, et al. (2026) Integrative functional genomics analysis identifies pleiotropic genes for vascular diseases. *Nature communications*, 17(1).

Weinstein S, et al. (2026) Distinct epigenetic aging in sporadic and hereditary neuroendocrine neoplasms. *Clinical epigenetics*, 18(1).

You C, et al. (2026) Single-Nucleus Multi-Omics Reveals Hypoxia-Driven Angiogenic Programs and Their Epigenetic Control in Sinonasal Squamous Cell Carcinoma. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(12), e10302.

Tlais D, et al. (2026) Pediatric H3 G34-mutant diffuse hemispheric glioma: clinical, imaging and molecular prognostic factors, MGMT expression, and temozolomide response. *Acta neuropathologica*, 151(1).

Christian H, et al. (2026) Compositional movement behaviours and preschool children's social-emotional development. *The international journal of behavioral nutrition and physical activity*, 23(1).

Park SJ, et al. (2026) Development and validation of a digital PCR assay targeting plasma FAR1 methylation for early detection of hepatocellular carcinoma. *Epigenetics*, 21(1), 2653956.

William W, et al. (2026) Adaptive quadtree-based segmentation of nucleus and cytoplasm in pap-smear images: a lightweight and interpretable approach for automated cytology. *Frontiers in artificial intelligence*, 9, 1834763.

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.

Santella B, et al. (2026) Epigenetic alterations of AKT1 orchestrate a metabolic reprogramming in advanced lipedema: translational insights from an integrated multi-omics study. *Journal of translational medicine*, 24(1), 265.

Obrezanenko VS, et al. (2026) Analysis of HERV-K (HML2) Expression in Colorectal Cancer Samples. *Epigenomes*, 10(1).

Xia C, et al. (2026) Reduced Maintenance DNA Methylation Thresholds Enable Sensitive Reporter Assays for UHRF1 and DNMT1 Inhibition. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(32), e19080.

Matías-García PR, et al. (2026) DNAm landscape up to 4 months post SARS-CoV-2 infection: insights from four population-based cohorts. *Clinical epigenetics*, 18(1).

Toubon G, et al. (2026) Gut microbiome composition and functional potential associate with incident type 2 diabetes in 4,685 adults from a Swedish prospective cohort. *Cell reports. Medicine*, 7(6), 102835.

Zheng J, et al. (2026) Prognostic value of PRAME gene promoter methylation and expression in hepatocellular carcinoma. *Clinical epigenetics*, 18(1).

Bunse L, et al. (2026) IDH1-mutant vaccine in newly diagnosed astrocytoma: final analysis of the multicenter, single-arm, open-label, first-in-human phase 1 NOA16 trial. *Nature cancer*.

Ma J, et al. (2026) DNA methylation analysis of the epigenome in oral squamous cell carcinoma. *Human genomics*, 20(1), 30.

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.

Li Y, et al. (2026) Integrated multi-omics analysis reveals comprehensive metabolism-driven tumor heterogeneity and immune microenvironment in hepatocellular carcinomas. *Scientific reports*, 16(1).

Diani LM, et al. (2026) The epigenetic role of ADRB3 DNA methylation in post-bariatric energy expenditure for women with obesity: a longitudinal observational study. *Scientific reports*, 16(1).