Resource Summary Report

Generated by NIF on Apr 28, 2025

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

Funding:

Availability: Free

Resource Name: ChAMP

Resource ID: SCR_012891

Alternate IDs: OMICS_01796

Record Creation Time: 20220129T080313+0000

Record Last Update: 20250420T014623+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

Source: SciCrunch Registry

Usage and Citation Metrics

We found 624 mentions in open access literature.

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

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

Tejedor JR, et al. (2025) Integration of multi-omics layers empowers precision diagnosis through unveiling pathogenic mechanisms on maple syrup urine disease. Journal of inherited metabolic disease, 48(1), e12829.

Dao B, et al. (2025) Crosstalk between genomic variants and DNA methylation in FLT3 mutant acute myeloid leukemia. Briefings in functional genomics, 24.

Qian Q, et al. (2025) CVD Atlas: a multi-omics database of cardiovascular disease. Nucleic acids research, 53(D1), D1348.

Ganguli P, et al. (2025) Context-dependent effects of CDKN2A and other 9p21 gene losses during the evolution of esophageal cancer. Nature cancer, 6(1), 158.

Paz-López G, et al. (2025) Pre-operative DNA methylation marks as predictors of weight loss outcomes after sleeve gastrectomy. Molecular metabolism, 92, 102087.

Lu X, et al. (2025) Stratification system with dual human endogenous retroviruses for predicting immunotherapy efficacy in metastatic clear-cell renal cell carcinoma. Journal for immunotherapy of cancer, 13(1).

Tang X, et al. (2025) Causality-driven candidate identification for reliable DNA methylation biomarker discovery. Nature communications, 16(1), 680.

Gianno F, et al. (2025) MicroRNAs Expression Profile in MN1-Altered Astroblastoma. Biomedicines, 13(1).

English KA, et al. (2025) Calcium sensing receptor expression is downregulated in gastroenteropancreatic neuroendocrine tumours via epigenetic mechanisms. International journal of cancer, 156(5), 980.

Kuroiwa T, et al. (2025) DNA methylation of bone morphogenetic protein 7 in leukocytes as a possible biomarker for hand osteoarthritis: A pilot study. Journal of orthopaedic research : official publication of the Orthopaedic Research Society, 43(1), 84.

Shorey-Kendrick LE, et al. (2024) Improvements in lung function following vitamin C supplementation to pregnant smokers are associated with buccal DNA methylation at 5 years of age. Clinical epigenetics, 16(1), 35.

Kibe Y, et al. (2024) Pediatric-type high-grade gliomas with PDGFRA amplification in adult patients with Li-Fraumeni syndrome: clinical and molecular characterization of three cases. Acta neuropathologica communications, 12(1), 57.

Park PH, et al. (2024) Association between gut microbiota and CpG island methylator phenotype in colorectal cancer. Gut microbes, 16(1), 2363012.

Alegrete J, et al. (2024) Effectiveness of the KC@H programme compared with clinic-based rehabilitation in patients recovering from ACL reconstruction: a study protocol for a single-centre, two-arm, single-blinded, randomised controlled superiority trial. BMJ open sport & exercise medicine, 10(1), e001868.

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

Zheng Y, et al. (2024) Multi-omics data integration using ratio-based quantitative profiling with Quartet reference materials. Nature biotechnology, 42(7), 1133.

Wang C, et al. (2024) A multidimensional atlas of human glioblastoma-like organoids reveals highly coordinated molecular networks and effective drugs. NPJ precision oncology, 8(1), 19.

Win PW, et al. (2024) Simultaneous assessment of mitochondrial DNA copy number and nuclear epigenetic age towards predictive models of development and aging. BMC research notes, 17(1), 21.

Lin Z, et al. (2024) Identification of a CpG-based signature coupled with gene expression as prognostic indicators for melanoma: a preliminary study. Scientific reports, 14(1), 5302.