

Resource Summary Report

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SeSAmE

RRID:SCR_027388

Type: Tool

Proper Citation

SeSAmE (RRID:SCR_027388)

Resource Information

URL: <https://www.bioconductor.org/packages/release/bioc/html/sesame.html>

Proper Citation: SeSAmE (RRID:SCR_027388)

Description: Software R package for reducing artifactual detection of DNA methylation by Infinium BeadChips in genomic deletions.

Abbreviations: SeSAmE

Synonyms: SEnsible Step-wise Analysis of DNA MEthylation

Resource Type: software toolkit, software resource

Defining Citation: [PMID:30085201](#)

Keywords: reducing artifactual detection, DNA methylation, Infinium BeadChips, genomic deletions,

Funding: NCI U24 CA143882;
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Ovarian Cancer Research Fund Grant ;
Michelle Lunn Hope Foundation ;
Van Andel Research Institute

Availability: Free, Available for download, Freely available,

Resource Name: SeSAmE

Resource ID: SCR_027388

Record Creation Time: 20250903T063617+0000

Record Last Update: 20260803T040941+0000

Ratings and Alerts

No rating or validation information has been found for SeSAmE.

No alerts have been found for SeSAmE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Chambers TL, et al. (2025) Methylome-proteome integration after late-life voluntary exercise training reveals regulation and target information for improved skeletal muscle health. *The Journal of physiology*, 603(1), 211.

Zhang G, et al. (2025) Integrative analysis of RNA expression signatures and recurrent genomic alterations before treatment: link to menopausal status, short-term endocrine therapy response and disease-free survival in luminal breast cancer. *ESMO open*, 10(12), 105913.

Goldberg DC, et al. (2025) Scalable screening of ternary-code DNA methylation dynamics associated with human traits. *Cell genomics*, 5(9), 100929.

Mulligan CJ, et al. (2025) Epigenetic signatures of intergenerational exposure to violence in three generations of Syrian refugees. *Scientific reports*, 15(1), 5945.

Rayner JG, et al. (2025) Sex differences in DNA methylation in bats. *Annals of the New York Academy of Sciences*, 1551(1), 115.

Denault WRP, et al. (2025) fSuSiE enables fine-mapping of QTLs from genome-scale molecular profiles. *bioRxiv : the preprint server for biology*.

Foong YH, et al. (2024) TET1 displays catalytic and non-catalytic functions in the adult mouse cortex. *Epigenetics*, 19(1), 2374979.

Gaugel J, et al. (2024) Picalm, a novel regulator of GLUT4-trafficking in adipose tissue. *Molecular metabolism*, 88, 102014.

Nirgude S, et al. (2024) Cancer predisposition signaling in Beckwith-Wiedemann Syndrome drives Wilms tumor development. *British journal of cancer*, 130(4), 638.

Xu H, et al. (2024) A novel method for cell deconvolution using DNA methylation in PCA space. *BMC genomics*, 25(1), 798.

Zhang W, et al. (2024) Critical evaluation of the reliability of DNA methylation probes on the Illumina MethylationEPIC v1.0 BeadChip microarrays. *Epigenetics*, 19(1), 2333660.

Blanchett R, et al. (2024) Homeobox and Polycomb target gene methylation in human solid tumors. *Scientific reports*, 14(1), 13912.

Li T, et al. (2023) Unveiling targeted cell-free DNA methylation regions through paired methylome analysis of tumor and normal tissues. *bioRxiv : the preprint server for biology*.

Hill EB, et al. (2023) The Microbiome, Epigenome, and Diet in Adults with Obesity during Behavioral Weight Loss. *Nutrients*, 15(16).

Bagheri M, et al. (2023) Alteration of DNMT1/DNMT3A by eribulin elicits global DNA methylation changes with potential therapeutic implications for triple-negative breast cancer. *bioRxiv : the preprint server for biology*.

Schmidt M, et al. (2020) Deconvolution of cellular subsets in human tissue based on targeted DNA methylation analysis at individual CpG sites. *BMC biology*, 18(1), 178.

Johnson RK, et al. (2020) Longitudinal DNA methylation differences precede type 1 diabetes. *Scientific reports*, 10(1), 3721.

Vaughan RM, et al. (2019) The finger loop of the SRA domain in the E3 ligase UHRF1 is a regulator of ubiquitin targeting and is required for the maintenance of DNA methylation. *The Journal of biological chemistry*, 294(43), 15724.