Resource Summary Report

Generated by nidm-terms on Jul 28, 2026

MethylSig

RRID:SCR_025849
Type: Tool

Proper Citation

MethylSig (RRID:SCR_025849)

Resource Information

URL: https://www.bioconductor.org/packages/release/bioc/html/methylSig.html

Proper Citation: MethylSig (RRID:SCR_025849)

Description: Software R package as whole genome DNA methylation analysis pipeline. Used for testing differentially methylated cytosines or regions in whole-genome bisulfite sequencing or reduced representation bisulfite sequencing experiments. Several options exist for either site-specific or sliding window tests, and variance estimation.

Resource Type: software resource, software toolkit

Defining Citation: PMID:24836530

Keywords: whole genome DNA methylation analysis, whole genome DNA, DNA methylation, testing differentially methylated cytosines, whole-genome bisulfite sequencing, reduced representation bisulfite sequencing,

Funding: NCI R01CA158286;
NIEHS P30 ES017885

Availability: Free, Available for download, Freely available

Resource Name: MethylSig

Resource ID: SCR_025849

License: GNU GPL v3

Record Creation Time: 20241005T053245+0000

Record Last Update: 20260725T191511+0000

Ratings and Alerts

No rating or validation information has been found for MethylSig.

No alerts have been found for MethylSig.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Lu H, et al. (2024) Dissecting the Impact of Maternal Androgen Exposure on Developmental Programming through Targeting the Androgen Receptor. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(36), e2309429.

Grunert M, et al. (2020) The Needle in the Haystack-Searching for Genetic and Epigenetic Differences in Monozygotic Twins Discordant for Tetralogy of Fallot. Journal of cardiovascular development and disease, 7(4).

Heller G, et al. (2016) Next-generation sequencing identifies major DNA methylation changes during progression of Ph+ chronic myeloid leukemia. Leukemia, 30(9), 1861.