

# Resource Summary Report

Generated by [RRID](#) on Aug 4, 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 toolkit, software resource

**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:** 20260803T040906+0000

### Ratings and Alerts

No rating or validation information has been found for MethylSig.

No alerts have been found for MethylSig.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

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

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<sup>+</sup> chronic myeloid leukemia. *Leukemia*, 30(9), 1861.