

Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

MethBase

RRID:SCR_017487

Type: Tool

Proper Citation

MethBase (RRID:SCR_017487)

Resource Information

URL: <http://smithlabresearch.org/software/methbase/>

Proper Citation: MethBase (RRID:SCR_017487)

Description: Central reference methylome database created from public BS-seq datasets. Provides methylation level at individual sites, regions of allele specific methylation, hypo- or hyper-methylated regions, partially methylated regions, and detailed meta data and summary statistics.

Synonyms: MethBase: a reference methylome database

Resource Type: database, data or information resource, service resource

Keywords: Methylome, database, public, BSseq, dataset, methylation, site, region, allele, specific, metadata, statistics, bio.tools

Availability: Free, Freely available

Resource Name: MethBase

Resource ID: SCR_017487

Alternate IDs: BioTools:MethBase, biotools:Methbase

Alternate URLs: <https://bio.tools/MethBase>, <https://bio.tools/MethBase>, <https://bio.tools/MethBase>

Record Creation Time: 20220129T080335+0000

Record Last Update: 20260808T190440+0000

Ratings and Alerts

No rating or validation information has been found for MethBase.

No alerts have been found for MethBase.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Ehrlich M, et al. (2024) Epigenetics of Genes Preferentially Expressed in Dissimilar Cell Populations: Myoblasts and Cerebellum. Epigenomes, 8(1).