

Resource Summary Report

Generated by PRECISE-TBI on Sep 7, 2026

MethylExtract

RRID:SCR_005446

Type: Tool

Proper Citation

MethylExtract (RRID:SCR_005446)

Resource Information

URL: <http://bioinfo2.ugr.es/MethylExtract/>

Proper Citation: MethylExtract (RRID:SCR_005446)

Description: A user friendly software tool to generate i) high quality, whole genome methylation maps and ii) to detect sequence variation within the same sample preparation.

Abbreviations: MethylExtract

Synonyms: High-Quality methylation maps and SNV calling from BS-Seq experiments

Resource Type: software resource

Keywords: bisulfite sequencing, methylation map, methylation, sequence variation, bio.tools

Availability: Acknowledgement requested

Resource Name: MethylExtract

Resource ID: SCR_005446

Alternate IDs: biotools:methylextract, OMICS_00605

Alternate URLs: <https://bio.tools/methylextract>

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260905T132535+0000

Ratings and Alerts

No rating or validation information has been found for MethylExtract.

No alerts have been found for MethylExtract.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Peng Y, et al. (2025) The genomic and epigenomic landscapes of hemizygous genes across crops with contrasting reproductive systems. *Proceedings of the National Academy of Sciences of the United States of America*, 122(6), e2422487122.

Gawra J, et al. (2023) Epigenetic variations are more substantial than genetic variations in rapid adaptation of oyster to Pacific oyster mortality syndrome. *Science advances*, 9(36), eadh8990.

Zhang K, et al. (2023) The lack of negative association between TE load and subgenome dominance in synthesized Brassica allotetraploids. *Proceedings of the National Academy of Sciences of the United States of America*, 120(42), e2305208120.

Wibowo AT, et al. (2022) Predictable and stable epimutations induced during clonal plant propagation with embryonic transcription factor. *PLoS genetics*, 18(11), e1010479.

Lee HY, et al. (2021) Identifying molecular targets for reverse aging using integrated network analysis of transcriptomic and epigenomic changes during aging. *Scientific reports*, 11(1), 12317.

Gómez-Martín C, et al. (2021) geno5mC: A Database to Explore the Association between Genetic Variation (SNPs) and CpG Methylation in the Human Genome. *Journal of molecular biology*, 433(11), 166709.

Lewis SH, et al. (2020) -----Widespread conservation and lineage-specific diversification of genome-wide DNA methylation patterns across arthropods. *PLoS genetics*, 16(6), e1008864.

Bhak Y, et al. (2019) Depression and suicide risk prediction models using blood-derived multi-omics data. *Translational psychiatry*, 9(1), 262.

Ito T, et al. (2019) Seasonal Stability and Dynamics of DNA Methylation in Plants in a Natural Environment. *Genes*, 10(7).

Rošić S, et al. (2018) Evolutionary analysis indicates that DNA alkylation damage is a byproduct of cytosine DNA methyltransferase activity. *Nature genetics*, 50(3), 452.

Rondon R, et al. (2017) Effects of a parental exposure to diuron on Pacific oyster spat methylome. *Environmental epigenetics*, 3(1), dvx004.

Geisen S, et al. (2014) NGSmethDB: an updated genome resource for high quality, single-cytosine resolution methylomes. *Nucleic acids research*, 42(Database issue), D53.

Barturen G, et al. (2013) CpGislandEVO: a database and genome browser for comparative evolutionary genomics of CpG islands. *BioMed research international*, 2013, 709042.

Barturen G, et al. (2013) MethylExtract: High-Quality methylation maps and SNV calling from whole genome bisulfite sequencing data. *F1000Research*, 2, 217.