

Resource Summary Report

Generated by T1D on Aug 3, 2026

NGSmethDB

RRID:SCR_012847

Type: Tool

Proper Citation

NGSmethDB (RRID:SCR_012847)

Resource Information

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

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Description: A dedicated database for the storage, browsing and data mining of whole-genome, single-base-pair resolution methylomes.

Abbreviations: NGSmethDB

Synonyms: NGSmethDB - A database for NGS single-cytosine-resolution DNA methylation data

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

Defining Citation: [PMID:20965971](#)

Keywords: bio.tools

Resource Name: NGSmethDB

Resource ID: SCR_012847

Alternate IDs: OMICS_01844, biotools:ngsmethdb

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

Record Creation Time: 20220129T080312+0000

Record Last Update: 20260803T040609+0000

Ratings and Alerts

No rating or validation information has been found for NGSmethDB.

No alerts have been found for NGSmethDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Erraji H, et al. (2025) Leveraging epigenetic aberrations in the pathogenesis of endometriosis: from DNA methylation to non-coding RNAs. *Frontiers in genetics*, 16, 1597287.

Uroshlev LA, et al. (2020) A Method for Identification of the Methylation Level of CpG Islands From NGS Data. *Scientific reports*, 10(1), 8635.

Ye P, et al. (2017) MethSMRT: an integrative database for DNA N6-methyladenine and N4-methylcytosine generated by single-molecular real-time sequencing. *Nucleic acids research*, 45(D1), D85.

Lebr??n R, et al. (2017) NGSmethDB 2017: enhanced methylomes and differential methylation. *Nucleic acids research*, 45(D1), D97.

Nalabothula N, et al. (2015) Genome-Wide Profiling of PARP1 Reveals an Interplay with Gene Regulatory Regions and DNA Methylation. *PloS one*, 10(8), e0135410.

Mugal CF, et al. (2015) Evolutionary consequences of DNA methylation on the GC content in vertebrate genomes. *G3 (Bethesda, Md.)*, 5(3), 441.

Wang S, et al. (2015) MethyRAD: a simple and scalable method for genome-wide DNA methylation profiling using methylation-dependent restriction enzymes. *Open biology*, 5(11).

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

Chuang TJ, et al. (2014) Impacts of pretranscriptional DNA methylation, transcriptional transcription factor, and posttranscriptional microRNA regulations on protein evolutionary rate. *Genome biology and evolution*, 6(6), 1530.