Resource Summary Report

Generated by dkNET on Apr 28, 2025

NGSmethDB

RRID:SCR_012847
Type: Tool

Proper Citation

NGSmethDB (RRID:SCR_012847)

Resource Information

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

Proper Citation: NGSmethDB (RRID:SCR_012847)

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 repository, service resource, storage service resource, database, data or information resource

Defining Citation: PMID:20965971

Keywords: bio.tools

Funding:

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: 20250428T053723+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 8 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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

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

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.

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) MethylRAD: 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.