

Resource Summary Report

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DiseaseMeth

RRID:SCR_005942

Type: Tool

Proper Citation

DiseaseMeth (RRID:SCR_005942)

Resource Information

URL: <http://bio-bigdata.hrbmu.edu.cn/diseasemeth/>

Proper Citation: DiseaseMeth (RRID:SCR_005942)

Description: Human disease methylation database. DiseaseMeth version 2.0 is focused on aberrant methylomes of human diseases. Used for understanding of DNA methylation driven human diseases.

Synonyms: , Disease Meth-The Human Disease Methylation Database, DiseaseMeth database, DiseaseMeth version 2.0

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

Defining Citation: [PMID:22135302](#), [PMID:27899673](#)

Keywords: disease, methylation, dna methylation, genome, gene, epigenetics, epigenomics, methylome, bio.tools

Funding: National Natural Science Foundation of China ;
Natural Science Foundation of Heilongjiang Province ;
State Key Laboratory of Urban Water Resource and Environment ;
Scientific Research Fund of Heilongjiang Provincial Education Department

Availability: Free, Freely available

Resource Name: DiseaseMeth

Resource ID: SCR_005942

Alternate IDs: OMICS_01838, nlx_151289, biotools:diseasemeth, SCR_017488

Alternate URLs: <http://bioinfo.hrbmu.edu.cn/diseasemeth>, <https://bio.tools/diseasemeth>

Old URLs: <http://202.97.205.78/diseasemeth/>

Record Creation Time: 20220129T080233+0000

Record Last Update: 20260808T185850+0000

Ratings and Alerts

No rating or validation information has been found for DiseaseMeth.

No alerts have been found for DiseaseMeth.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 44 mentions in open access literature.

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

Han Y, et al. (2026) RASSF2 promoter hypermethylation determines malignant and microenvironmental features in lung cancer. Genes and immunity.

Fan L, et al. (2025) Comprehensive analysis of ceRNA Networks in UCEC: Prognostic and therapeutic implications. PloS one, 20(1), e0314314.

Hu X, et al. (2025) The role of lnc[?]MAPKAPK5[?]AS1 in immune cell infiltration in hepatocellular carcinoma: Bioinformatics analysis and validation. Oncology letters, 29(3), 141.

Shi C, et al. (2025) Novel DNA methylation biomarkers in urine for non-invasive diagnosis of bladder urothelial carcinoma. Clinical epigenetics, 17(1), 204.

Wang R, et al. (2025) RNA adenosine modification writers define characteristics of immunity and prognosis in head and neck squamous cell carcinoma. Discover oncology, 16(1), 1909.

Lan M, et al. (2025) The SLC26A4-AS1/NTRK2 axis in breast cancer: insights into the ceRNA network and implications for prognosis and immune microenvironment. Discover oncology, 16(1), 329.

Bi L, et al. (2024) Blood-based HYAL2 methylation as a potential marker for the preclinical detection of coronary heart disease and stroke. Clinical epigenetics, 16(1), 130.

Pei L, et al. (2024) USP43 impairs cisplatin sensitivity in epithelial ovarian cancer through HDAC2-dependent regulation of Wnt/[?]-catenin signaling pathway. Apoptosis : an international journal on programmed cell death, 29(1-2), 210.

Zhang M, et al. (2024) Integration of single-cell and bulk RNA sequencing data reveals that CYTOR is a potential prognostic and immunotherapeutic response marker for skin cutaneous melanoma. *Journal of Cancer*, 15(12), 3890.

Zeng F, et al. (2023) Integrated analysis of SKA1-related ceRNA network and SKA1 immunoassays in HCC: A study based on bioinformatic. *Medicine*, 102(38), e34826.

Xu ZJ, et al. (2023) Pan-cancer analysis identifies CD300 molecules as potential immune regulators and promising therapeutic targets in acute myeloid leukemia. *Cancer medicine*, 12(1), 789.

Pan Y, et al. (2023) Construction of a Novel Cuproptosis-Related ceRNA Network-SNHG3/miR-1306-5p/PDHA1 and Identification of SNHG3 as a Prognostic Biomarker in Hepatocellular Carcinoma. *ACS omega*, 8(41), 38690.

Wei H, et al. (2023) BAIAP2L2 is a novel prognostic biomarker related to migration and invasion of HCC and associated with cuproptosis. *Scientific reports*, 13(1), 8692.

Han J, et al. (2023) Pyroptosis-Related Genes as Markers for Identifying Prognosis and Microenvironment in Low-Grade Glioma. *Journal of healthcare engineering*, 2023, 6603151.

Guenther M, et al. (2023) TPX2 expression as a negative predictor of gemcitabine efficacy in pancreatic cancer. *British journal of cancer*, 129(1), 175.

Liu Y, et al. (2023) Caveolin-1 promotes glioma progression and maintains its mitochondrial inhibition resistance. *Discover. Oncology*, 14(1), 161.

Dai L, et al. (2023) Multi-omics analyses of CD276 in pan-cancer reveals its clinical prognostic value in glioblastoma and other major cancer types. *BMC cancer*, 23(1), 102.

Leng D, et al. (2023) Comprehensive Analysis of Tumor Microenvironment Reveals Prognostic ceRNA Network Related to Immune Infiltration in Sarcoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 29(19), 3986.

Li L, et al. (2022) Serum Exosomal lncRNA AC007099.1 Regulates the Expression of Neuropeptide-Related FAP, as a Potential Biomarker for Hepatocarcinogenesis. *Disease markers*, 2022, 9501008.

Li G, et al. (2022) The RIPK family: expression profile and prognostic value in lung adenocarcinoma. *Aging*, 14(14), 5946.