

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

**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:** 20260804T043258+0000

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## Ratings and Alerts

No rating or validation information has been found for DiseaseMeth.

No alerts have been found for DiseaseMeth.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 34 mentions in open access literature.

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

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

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

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.

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.

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

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

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.

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.

- Liu Y, et al. (2023) Caveolin-1 promotes glioma progression and maintains its mitochondrial inhibition resistance. *Discover. Oncology*, 14(1), 161.
- 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.
- Wei H, et al. (2023) BAIAP2L2 is a novel prognostic biomarker related to migration and invasion of HCC and associated with cuprotoxis. *Scientific reports*, 13(1), 8692.
- Guenther M, et al. (2023) TPX2 expression as a negative predictor of gemcitabine efficacy in pancreatic cancer. *British journal of cancer*, 129(1), 175.
- 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 G, et al. (2022) The RIPK family: expression profile and prognostic value in lung adenocarcinoma. *Aging*, 14(14), 5946.
- Guo Z, et al. (2022) Comprehensive analysis to identify noncoding RNAs mediated upregulation of maternal embryonic leucine zipper kinase (MELK) correlated with poor prognosis in hepatocellular carcinoma. *Aging*, 14(9), 3973.
- Liang J, et al. (2022) PRLR and CACNA2D1 Impact the Prognosis of Breast Cancer by Regulating Tumor Immunity. *Journal of personalized medicine*, 12(12).
- Cai L, et al. (2022) PLP1 may serve as a potential diagnostic biomarker of uterine fibroids. *Frontiers in genetics*, 13, 1045395.
- Xiao H, et al. (2021) Expression of MAP9 in Epstein-Barr virus-associated gastric carcinoma. *Virus research*, 293, 198253.
- Wu J, et al. (2021) Long non-coding RNA LINC01296 acts as a migration and invasion promoter in head and neck squamous cell carcinoma and predicts poor prognosis. *Bioengineered*, 12(1), 5607.
- Villalba GC, et al. (2021) Fantastic databases and where to find them: Web applications for researchers in a rush. *Genetics and molecular biology*, 44(2), e20200203.