

# Resource Summary Report

Generated by T1D on Sep 5, 2026

## MethyCancer

RRID:SCR\_013399

Type: Tool

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### Proper Citation

MethyCancer (RRID:SCR\_013399)

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### Resource Information

**URL:** <http://methycancer.psych.ac.cn/>

**Proper Citation:** MethyCancer (RRID:SCR\_013399)

**Description:** Database to study interplay of DNA methylation, gene expression and cancer that hosts both highly integrated data of DNA methylation, cancer-related gene, mutation and cancer information from public resources, and the CpG Island (CGI) clones derived from our large-scale sequencing. Interconnections between different data types were analyzed and presented. Search tool and graphical MethyView are developed to help users access all the data and data connections and view DNA methylation in context of genomics and genetics data. The search tool and graphical MethyView are developed to help users access all the data and data connections and view DNA methylation in context of genomics and genetics data. As part of the Cancer Epigenomics Project in China, MethyCancer serves as a platform for sharing data and analytical results from the Cancer Genome/Epigenome Project in China with colleagues all over the world.

**Abbreviations:** MethyCancer

**Synonyms:** database of human DNA Methylation and Cancer

**Resource Type:** data or information resource, database

**Defining Citation:** [PMID:17890243](#)

**Keywords:** dna methylation, gene expression, cancer

**Related Condition:** Cancer

**Resource Name:** MethyCancer

**Resource ID:** SCR\_013399

**Alternate IDs:** OMICS\_01842, nif-0000-03120

**Old URLs:** <http://methycancer.genomics.org.cn>

**Record Creation Time:** 20220129T080315+0000

**Record Last Update:** 20260904T000309+0000

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## Ratings and Alerts

No rating or validation information has been found for MethyCancer.

No alerts have been found for MethyCancer.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Liu Y, et al. (2024) DNA methylation analysis of the SDC2, SEPT9 and VIM genes in fecal DNA for colorectal cancer diagnosis. BMC cancer, 24(1), 1205.

Khan AT, et al. (2022) A computational and bioinformatic analysis of ACE2: an elucidation of its dual role in COVID-19 pathology and finding its associated partners as potential therapeutic targets. Journal of biomolecular structure & dynamics, 40(4), 1813.

Pradhan S, et al. (2021) dbGENVOC: database of GENomic Variants of Oral Cancer, with special reference to India. Database : the journal of biological databases and curation, 2021.

Pawar G, et al. (2019) In Silico Toxicology Data Resources to Support Read-Across and (Q)SAR. Frontiers in pharmacology, 10, 561.

Singh AN, et al. (2017) Identification of key pathways and genes with aberrant methylation in prostate cancer using bioinformatics analysis. OncoTargets and therapy, 10, 4925.

Han Y, et al. (2016) Integrating Epigenomics into the Understanding of Biomedical Insight. Bioinformatics and biology insights, 10, 267.

Shukla A, et al. (2016) DREMECELS: A Curated Database for Base Excision and Mismatch Repair Mechanisms Associated Human Malignancies. PloS one, 11(6), e0157031.

Yang Y, et al. (2015) Databases and web tools for cancer genomics study. Genomics, proteomics & bioinformatics, 13(1), 46.

Pavlopoulou A, et al. (2015) Human cancer databases (review). *Oncology reports*, 33(1), 3.

Zou D, et al. (2015) Biological databases for human research. *Genomics, proteomics & bioinformatics*, 13(1), 55.

Milanowska K, et al. (2011) Databases and bioinformatics tools for the study of DNA repair. *Molecular biology international*, 2011, 475718.