

# Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

## Cancer Methylome System

RRID:SCR\_012013

Type: Tool

### Proper Citation

Cancer Methylome System (RRID:SCR\_012013)

### Resource Information

**URL:** <http://cbbiweb.uthscsa.edu/KMethylomes/>

**Proper Citation:** Cancer Methylome System (RRID:SCR\_012013)

**Description:** Database and web-based system for visualization and analysis of genome-wide methylation data of human cancers.

**Abbreviations:** CMS

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

**Defining Citation:** [PMID:22035855](#)

**Keywords:** gene, methylation, visualization

**Related Condition:** Cancer, Normal

**Funding:** NCI

**Availability:** Acknowledgement requested

**Resource Name:** Cancer Methylome System

**Resource ID:** SCR\_012013

**Alternate IDs:** OMICS\_01836

**Record Creation Time:** 20220129T080308+0000

**Record Last Update:** 20260904T000329+0000

### Ratings and Alerts

No rating or validation information has been found for Cancer Methylome System.

No alerts have been found for Cancer Methylome System.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 8 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

Kusi M, et al. (2022) 2-Hydroxyglutarate destabilizes chromatin regulatory landscape and lineage fidelity to promote cellular heterogeneity. Cell reports, 38(2), 110220.

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.

Buchegger K, et al. (2017) Reprimo, a Potential p53-Dependent Tumor Suppressor Gene, Is Frequently Hypermethylated in Estrogen Receptor ??-Positive Breast Cancer. International journal of molecular sciences, 18(8).

Trimarchi MP, et al. (2017) Identification of endometrial cancer methylation features using combined methylation analysis methods. PloS one, 12(3), e0173242.

Buchegger K, et al. (2016) Reprimo as a modulator of cell migration and invasion in the MDA-MB-231 breast cancer cell line. Biological research, 49, 5.

Mao Z, et al. (2014) BIMMER: a novel algorithm for detecting differential DNA methylation regions from MBDCap-seq data. BMC bioinformatics, 15 Suppl 12(Suppl 12), S6.

Gu F, et al. (2013) CMS: a web-based system for visualization and analysis of genome-wide methylation data of human cancers. PloS one, 8(4), e60980.

Rao X, et al. (2013) CpG island shore methylation regulates caveolin-1 expression in breast cancer. Oncogene, 32(38), 4519.