Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 11, 2025

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: Datbase 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: 20250410T070227+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.

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 FDI Lab - SciCrunch.org.

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.