

Resource Summary Report

Generated by [dkNET](#) on Aug 26, 2026

DBCAT

RRID:SCR_012014

Type: Tool

Proper Citation

DBCAT (RRID:SCR_012014)

Resource Information

URL: <http://dbcat.cgm.ntu.edu.tw/>

Proper Citation: DBCAT (RRID:SCR_012014)

Description: A database of CpG islands and analytical tools for identifying comprehensive methylation profiles in cancer cells.

Abbreviations: DBCAT

Resource Type: data or information resource, database

Defining Citation: [PMID:21214365](#)

Related Condition: Cancer

Resource Name: DBCAT

Resource ID: SCR_012014

Alternate IDs: OMICS_01837

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260821T193937+0000

Ratings and Alerts

No rating or validation information has been found for DBCAT.

No alerts have been found for DBCAT.

Data and Source Information

Usage and Citation Metrics

We found 48 mentions in open access literature.

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

Guo Z, et al. (2026) RASGEF1B suppresses hepatocellular carcinoma through the ALDH7A1/Betaine/SNAI1 metabolic?epigenetic axis. Journal of translational medicine, 24(1).

Sankar S, et al. (2025) Role of DNA methylation in regulating inflammatory cytokine expression in neonates with late-onset sepsis. Frontiers in immunology, 16, 1613333.

Momajadi L, et al. (2024) Designing a multi-epitope influenza vaccine: an immunoinformatics approach. Scientific reports, 14(1), 25382.

Mondal I, et al. (2024) ALDH5A1/miR-210 axis plays a key role in reprogramming cellular metabolism and has a significant correlation with glioblastoma patient survival. Cancer cell international, 24(1), 259.

Atsbeha G, et al. (2024) Analysis of promoter region and regulatory elements of Rhizobium giardinii DNA-binding response regulator A3AY_RS01 genes. Journal, genetic engineering & biotechnology, 22(3), 100397.

Tang Z, et al. (2023) Combined inhibition of histone deacetylase and cytidine deaminase improves epigenetic potency of decitabine in colorectal adenocarcinomas. Clinical epigenetics, 15(1), 89.

Shen CH, et al. (2023) Epigenetic regulation of human WIF1 and DNA methylation situation of WIF1 and GSTM5 in urothelial carcinoma. Heliyon, 9(5), e16004.

Henry S, et al. (2023) Polycomb protein RYBP activates transcription factor Plagl1 during in vitro cardiac differentiation of mouse embryonic stem cells. Open biology, 13(2), 220305.

Gardner CC, et al. (2023) Common as well as unique methylation-sensitive DNA regulatory elements in three mammalian SLC9C1 genes. bioRxiv : the preprint server for biology.

Worku D, et al. (2023) Genetic variation in promoter region of the bovine LAP3 gene associated with estimated breeding values of milk production traits and clinical mastitis in dairy cattle. PloS one, 18(5), e0277156.

Assem M, et al. (2023) Promoter methylation might shift the balance of Galectin-3 & 12 expression in de novo adult acute myeloid leukemia patients. Frontiers in genetics, 14, 1122864.

Luo HL, et al. (2023) VCAN Hypomethylation and Expression as Predictive Biomarkers of Drug Sensitivity in Upper Urinary Tract Urothelial Carcinoma. International journal of

molecular sciences, 24(8).

Mohanad M, et al. (2022) Epigenetic inactivation of DNA repair genes as promising prognostic and predictive biomarkers in urothelial bladder carcinoma patients. *Molecular genetics and genomics* : MGG, 297(6), 1671.

Hamde F, et al. (2022) In silico analysis of promoter regions to identify regulatory elements in TetR family transcriptional regulatory genes of *Mycobacterium colombiense* CECT 3035. *Journal, genetic engineering & biotechnology*, 20(1), 53.

Abera B, et al. (2022) MAGE genes encoding for embryonic development in cattle is mainly regulated by zinc finger transcription factor family and slightly by CpG Islands. *BMC genomic data*, 23(1), 19.

Sutus E, et al. (2022) RYBP regulates Pax6 during in vitro neural differentiation of mouse embryonic stem cells. *Scientific reports*, 12(1), 2364.

Shi Z, et al. (2022) Hypomethylation status of miR-657 promoter region as biomarker for diagnosis of hepatocellular carcinoma: a retrospective study. *Translational cancer research*, 11(5), 1112.

Dibbisa D, et al. (2022) In Silico Study of Mercury Resistance Genes Extracted from *Pseudomonas* spp. Involved in Bioremediation: Understanding the Promoter Regions and Regulatory Elements. *International journal of genomics*, 2022, 6185615.

Sánchez-Navarro A, et al. (2021) Vegfa promoter gene hypermethylation at HIF1 α binding site is an early contributor to CKD progression after renal ischemia. *Scientific reports*, 11(1), 8769.

Senbeta D, et al. (2021) Investigation of promoter regions, motifs, and CpG islands in the regulation of gene expression in *Trametes hirsuta* strain 072. *Journal, genetic engineering & biotechnology*, 19(1), 160.