Resource Summary Report

Generated by NIF on Aug 21, 2026

HMCan

RRID:SCR_010858
Type: Tool

Proper Citation

HMCan (RRID:SCR_010858)

Resource Information

URL: http://www.cbrc.kaust.edu.sa/hmcan/

Proper Citation: HMCan (RRID:SCR_010858)

Description: A Hidden Markov Model based software tool that is developed to detect histone modification in cancer ChIP-seq data.

Abbreviations: HMCan

Synonyms: Histone Modification in Cancer

Resource Type: software resource

Defining Citation: PMID:24021381

Keywords: bio.tools

Resource Name: HMCan

Resource ID: SCR_010858

Alternate IDs: biotools:hmcan, OMICS_00443

Alternate URLs: https://bio.tools/hmcan

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260815T182414+0000

Ratings and Alerts

No rating or validation information has been found for HMCan.

No alerts have been found for HMCan.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF .

Gautier M, et al. (2026) A regulatory circuitry driving a noradrenergic to mesenchymal transition highlights YAP/TAZ as critical players in neuroblastoma plasticity. Cell reports, 45(5), 117351.

Zamuner FT, et al. (2025) Epigenetic profiling reveals key super-enhancer networks driving oncogenesis in HPV-positive HNSCC. iScience, 28(11), 113911.

Jin J, et al. (2025) ICMC: An Interpretable Cross-domain Multi-modal Classification model for grading teaching plan. PloS one, 20(9), e0330684.

Mondal S, et al. (2025) The Super Enhancer-Driven Long Noncoding RNA PRKCQ-AS1 Promotes Neuroblastoma Tumorigenesis by Interacting With MSI2 Protein and Is Targetable by Small Molecule Compounds. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(18), e2412520.

Thirant C, et al. (2023) Reversible transitions between noradrenergic and mesenchymal tumor identities define cell plasticity in neuroblastoma. Nature communications, 14(1), 2575.

Mohammed Ismail W, et al. (2023) MacroH2A histone variants modulate enhancer activity to repress oncogenic programs and cellular reprogramming. Communications biology, 6(1), 215.

Jdeed S, et al. (2022) The Role of ARID1A in the Nonestrogenic Modulation of IGF-1 Signaling. Molecular cancer research : MCR, 20(7), 1071.

Gregoricchio S, et al. (2022) HDAC1 and PRC2 mediate combinatorial control in SPI1/PU.1-dependent gene repression in murine erythroleukaemia. Nucleic acids research, 50(14), 7938.

Liehrmann A, et al. (2021) Increased peak detection accuracy in over-dispersed ChIP-seq data with supervised segmentation models. BMC bioinformatics, 22(1), 323.

Jarroux J, et al. (2021) HOTAIR lncRNA promotes epithelial-mesenchymal transition by redistributing LSD1 at regulatory chromatin regions. EMBO reports, 22(7), e50193.

Kaukonen D, et al. (2020) Analysis of H3K4me3 and H3K27me3 bivalent promotors in HER2+ breast cancer cell lines reveals variations depending on estrogen receptor status and significantly correlates with gene expression. BMC medical genomics, 13(1), 92.

Erd??s E, et al. (2020) NR2F2 Orphan Nuclear Receptor is Involved in Estrogen Receptor Alpha-Mediated Transcriptional Regulation in Luminal A Breast Cancer Cells. International journal of molecular sciences, 21(6).

Lopez-Delisle L, et al. (2018) Activated ALK signals through the ERK-ETV5-RET pathway to drive neuroblastoma oncogenesis. Oncogene, 37(11), 1417.

Ashoor H, et al. (2017) HMCan-diff: a method to detect changes in histone modifications in cells with different genetic characteristics. Nucleic acids research, 45(8), e58.