

Resource Summary Report

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NCBI Epigenomics

RRID:SCR_006151

Type: Tool

Proper Citation

NCBI Epigenomics (RRID:SCR_006151)

Resource Information

URL: <https://www.ncbi.nlm.nih.gov/geo/>

Proper Citation: NCBI Epigenomics (RRID:SCR_006151)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on January 19, 2022.

Abbreviations: Epigenomics

Synonyms: NCBI Epigenomic Gateway, National Center for Biotechnology Information Epigenomics, NCBI Epigenomic Hub

Resource Type: data or information resource, database

Keywords: genome-wide map, dna, histone, modification, epigenomic, genome, gold standard, gene mapping, gene amplification, genetic code, gene library, dna fingerprinting, chromatin, histone modification, dna methylation, dnaase footprinting, genome wide association study, gene expression

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: NCBI Epigenomics

Resource ID: SCR_006151

Alternate IDs: nlx_151643, OMICS_01848, r3d100010782

Alternate URLs: <https://doi.org/10.17616/R34K7J>

Old URLs: <http://www.ncbi.nlm.nih.gov/epigenomics>

Record Creation Time: 20220129T080234+0000

Record Last Update: 20260919T195656+0000

Ratings and Alerts

No rating or validation information has been found for NCBI Epigenomics.

No alerts have been found for NCBI Epigenomics.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14631 mentions in open access literature.

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

Guo Y, et al. (2026) Comprehensive analysis of COLGALT1 in tumor microenvironment regulation and prognosis of clear cell renal cell carcinoma. Clinical and experimental medicine, 26(1), 127.

Tang B, et al. (2026) Identification and validation of NETs-related biomarkers in hepatocellular carcinoma through bioinformatics analysis and machine learning algorithms. Discover oncology, 17(1).

Jia X, et al. (2026) Identification and characterization of tryptophan metabolism-related genes in carotid artery plaques. PloS one, 21(2), e0341122.

Zhang Y, et al. (2026) Arginase 2 Promotes Colorectal Cancer Metastasis via PI3K/AKT Pathway Activation and Regulates Tumor Immune Infiltration. Cancer medicine, 15(2), e71567.

Huang L, et al. (2026) Integrative single-cell analysis uncovers distinct tumour??microenvironment ecotypes and immune evasion across skin cancers. Clinical and translational medicine, 16(2), e70611.

Liu Q, et al. (2026) Integrative bioinformatics analyses of mitochondrial dysfunction-related genes in human non-obstructive azoospermia. Scientific reports, 16(1).

Wang Z, et al. (2026) Association of ANXA3 methylation with clinical outcomes of glucocorticoid therapy in patients with hepatitis B virus-related acute-on-chronic liver failure. Scientific reports, 16(1).

Li X, et al. (2026) SDHA Deficiency in Hepatocellular Carcinoma Promotes Tumor Progression through Succinate-Induced M2 Macrophage Polarization. Oncology research, 34(2), 25.

Martinez-Martinez YB, et al. (2026) HIV impairs and exploits pulmonary Th17 and Th22 cell-mediated immune responses to Mycobacterium tuberculosis. PLoS pathogens, 22(1), e1013897.

Xu L, et al. (2026) CEP55 promotes prostate cancer progression via TPX2-dependent activation of AURKA-PI3K-AKT signaling and inhibition of ferroptosis. *The Journal of biological chemistry*, 302(3), 111218.

Lang H, et al. (2026) An exploratory microarray analysis of estrogen-mediated gene expression in central pathways that control energy balance in female rats (*Rattus norvegicus*). *BMC research notes*, 19(1).

Li Q, et al. (2026) Th17-related genes PGAP1 and TMBIM1 serve as potential diagnostic and predictive biomarkers in systemic sclerosis: bioinformatic identification and murine model validation. *Clinical rheumatology*, 45(3), 1721.

Choi W, et al. (2026) Oxidative stress-associated genes TPPP3 and VEGFA in COPD revealed by bulk and single-cell sequencing analysis. *Scientific reports*, 16(1), 6801.

Zhang D, et al. (2026) ACACA modulates R-loop homeostasis to enhance lipid metabolism and microenvironmental interactions in ccRCC. *NPJ precision oncology*, 10(1).

Silvey S, et al. (2026) Sample size requirements for machine learning classification of binary outcomes in bulk RNA-Seq data. *BMC bioinformatics*, 27(1).

Ren G, et al. (2026) Targeting Wnt3a and Loxl2 Synergistically Induces Ferroptosis in Liver Cancer Stem Cells and Suppresses Tumorigenesis. *Cancer science*, 117(4), 972.

Liang W, et al. (2026) Recognition of immunogenomic signature and prognostic value of the subtype of epithelial-mesenchymal transition in breast cancer. *Biochemistry and biophysics reports*, 45, 102456.

Cui C, et al. (2026) Diagnostic and prognostic value of deregulated miR-6822-3p in patients with severe pneumonia. *BMC immunology*, 27(1), 14.

Xiong J, et al. (2026) A Meta-Analysis of the Effects of Chronic Stress on the Prefrontal Transcriptome in Animal Models and Convergence With Existing Human Data. *Brain and behavior*, 16(1), e71197.

Wang C, et al. (2026) Neutrophil extracellular traps as biomarkers for predicting prognosis and chemotherapy response in colorectal cancer. *Scientific reports*, 16(1), 3074.