

Resource Summary Report

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EpiFactors

RRID:SCR_016956

Type: Tool

Proper Citation

EpiFactors (RRID:SCR_016956)

Resource Information

URL: <http://epifactors.autosome.ru/>

Proper Citation: EpiFactors (RRID:SCR_016956)

Description: Manually curated collection of human epigenetic factors, their complexes, corresponding genes and products.

Resource Type: data or information resource, database

Defining Citation: [PMID:26153137](#)

Keywords: manually, curated, collection, human, epigenetic, factor, complex, corresponding, gene, target, product

Funding: Russian Fund For Basic Research ;
Ministerio de Economia Y Competividad ;
Spain ;
Åke Olsson's foundation ;
Swedish Cancer foundation ;
Swedish Childhood cancer foundation ;
Dynasty Foundation Fellowship ;
Japanese Ministry of Education ;
Culture ;
Sports ;
Science and Technology ;
Norwegian University of Science and Technology

Availability: Free, Available for download, Freely available

Resource Name: EpiFactors

Resource ID: SCR_016956

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260801T191017+0000

Ratings and Alerts

No rating or validation information has been found for EpiFactors .

No alerts have been found for EpiFactors .

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Na Z, et al. (2025) Research on biliary atresia and epigenetic factors from the perspective of transcriptomics: identification of key genes and experimental validation. *Frontiers in pediatrics*, 13, 1624671.

Wang N, et al. (2025) Integration of multi-omics profiling reveals an epigenetic-based molecular classification of lung adenocarcinoma: implications for drug sensitivity and immunotherapy response prediction. *Frontiers in pharmacology*, 16, 1540477.

Lukauskas S, et al. (2024) Decoding chromatin states by proteomic profiling of nucleosome readers. *Nature*, 627(8004), 671.

Giannoudis A, et al. (2024) ENO1 as a Biomarker of Breast Cancer Progression and Metastasis: A Bioinformatic Approach Using Available Databases. *Breast cancer : basic and clinical research*, 18, 11782234241285648.

Sun W, et al. (2023) Epigenetic regulation of human-specific gene expression in the prefrontal cortex. *BMC biology*, 21(1), 123.

Sorek M, et al. (2022) Impaired activation of transposable elements in SARS-CoV-2 infection. *EMBO reports*, 23(9), e55101.

Das M, et al. (2022) The role of CPT1A as a biomarker of breast cancer progression: a bioinformatic approach. *Scientific reports*, 12(1), 16441.

Farhana A, et al. (2021) Nanoparticle-Encapsulated Camptothecin: Epigenetic Modulation in DNA Repair Mechanisms in Colon Cancer Cells. *Molecules (Basel, Switzerland)*, 26(17).

Wang Z, et al. (2021) Development and validation of a novel epigenetic-related prognostic signature and candidate drugs for patients with lung adenocarcinoma. *Aging*, 13(14),

18701.

Yomtoubian S, et al. (2020) Inhibition of EZH2 Catalytic Activity Selectively Targets a Metastatic Subpopulation in Triple-Negative Breast Cancer. *Cell reports*, 30(3), 755.

de Lima RMS, et al. (2020) Amygdala 5-HTT Gene Network Moderates the Effects of Postnatal Adversity on Attention Problems: Anatomo-Functional Correlation and Epigenetic Changes. *Frontiers in neuroscience*, 14, 198.

Ohsawa S, et al. (2020) Network and Evolutionary Analysis of Human Epigenetic Regulators to Unravel Disease Associations. *Genes*, 11(12).

Barili V, et al. (2020) Targeting p53 and histone methyltransferases restores exhausted CD8+ T cells in HCV infection. *Nature communications*, 11(1), 604.

Wang J, et al. (2020) Development and validation of a nomogram with an epigenetic signature for predicting survival in patients with lung adenocarcinoma. *Aging*, 12(22), 23200.

Poojan S, et al. (2020) Cancer cells undergoing epigenetic transition show short-term resistance and are transformed into cells with medium-term resistance by drug treatment. *Experimental & molecular medicine*, 52(7), 1102.

Yi G, et al. (2019) Chromatin-Based Classification of Genetically Heterogeneous AMLs into Two Distinct Subtypes with Diverse Stemness Phenotypes. *Cell reports*, 26(4), 1059.