

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

Availability: Free, Available for download, Freely available

Resource Name: EpiFactors

Resource ID: SCR_016956

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260829T183034+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 24 mentions in open access literature.

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

Xie J, et al. (2026) Critical Biological Functions and Clinical Implications of Epigenetic-Related Candidate Biomarkers in Chronic Obstructive Pulmonary Disease: Integrated Machine Learning Screening and Basic Experimental Validation. International journal of chronic obstructive pulmonary disease, 21, 592045.

Chen S, et al. (2026) Diversity-triggered 2-naphthoic acid exudation recruits keystone microbial taxa to promote soybean drought tolerance. Cell host & microbe, 34(5), 844.

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.

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.

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

Li X, et al. (2024) Development and validation of epigenetic modification-related signals for the diagnosis and prognosis of colorectal cancer. BMC genomics, 25(1), 51.

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.

Fasano C, et al. (2023) The chromatin remodeling factors EP300 and TRRAP are novel SMYD3 interactors involved in the emerging 'nonmutational epigenetic reprogramming' cancer hallmark. Computational and structural biotechnology journal, 21, 5240.

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

Hu Y, et al. (2023) An immune and epigenetics-related scoring model and drug candidate prediction for hepatic carcinogenesis via dynamic network biomarker analysis and connectivity mapping. *Computational and structural biotechnology journal*, 21, 4619.

Gawriyski L, et al. (2023) Comprehensive characterization of the embryonic factor LEUTX. *iScience*, 26(3), 106172.

Wang C, et al. (2022) Identification and verification of a novel epigenetic-related gene signature for predicting the prognosis of hepatocellular carcinoma. *Frontiers in genetics*, 13, 897123.

Cerutti C, et al. (2022) Computational identification of new potential transcriptional partners of ERR α in breast cancer cells: specific partners for specific targets. *Scientific reports*, 12(1), 3826.

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

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

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.

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

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