

Resource Summary Report

Generated by [nidm-terms](#) on Jul 29, 2026

Encode

RRID:SCR_015482

Type: Tool

Proper Citation

Encode (RRID:SCR_015482)

Resource Information

URL: <https://www.encodeproject.org/>

Proper Citation: Encode (RRID:SCR_015482)

Description: Consortium to build comprehensive parts list of functional elements in human genome. This includes elements that act at protein and RNA levels, and regulatory elements that control cells and circumstances in which gene is active. Data from 2012-present.

Synonyms: ENCODE Project

Resource Type: data set, data or information resource, organization portal, consortium, portal

Defining Citation: [PMID:15499007](#)

Keywords: genome, sequencing, protein, rna, dna, consortium

Funding: NHGRI HG006992

Availability: Free, Freely available

Resource Name: Encode

Resource ID: SCR_015482

Record Creation Time: 20220129T080326+0000

Record Last Update: 20260729T044351+0000

Ratings and Alerts

No rating or validation information has been found for Encode.

No alerts have been found for Encode.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1244 mentions in open access literature.

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

Lee D, et al. (2025) Increased local DNA methylation disorder in AMLs with DNMT3A-destabilizing variants and its clinical implication. *Nature communications*, 16(1), 560.

Rohm D, et al. (2025) Activation of the imprinted Prader-Willi syndrome locus by CRISPR-based epigenome editing. *Cell genomics*, 5(2), 100770.

Chen W, et al. (2025) OCT4 translationally promotes AKT signaling as an RNA-binding protein in stressed pluripotent stem cells. *Stem cell research & therapy*, 16(1), 84.

Mathios D, et al. (2025) Detection of Brain Cancer Using Genome-wide Cell-free DNA Fragmentomes. *Cancer discovery*, 15(8), 1593.

Irastorza-Azcarate I, et al. (2025) Extensive folding variability between homologous chromosomes in mammalian cells. *Molecular systems biology*, 21(7), 735.

Li T, et al. (2025) Cancer-associated fibroblast derived CXCL14 drives cisplatin chemoresistance by enhancing nucleotide excision repair in bladder cancer. *Journal of experimental & clinical cancer research : CR*, 44(1), 265.

Huang Y, et al. (2025) Short tandem repeats in populations of the Qinghai-Tibet Plateau and adjacent regions provide insights into high-altitude adaptation. *Science advances*, 11(42), eadx1590.

Luo J, et al. (2025) Targeting histone H2B acetylated enhanceosomes via p300/CBP degradation in prostate cancer. *Nature genetics*, 57(10), 2468.

Wang M, et al. (2025) Integrative analysis of non-small cell lung cancer identifies Jumonji domain-containing 6/ETS homologous factor axis as a target to overcome radioresistance. *Signal transduction and targeted therapy*, 10(1), 391.

Song X, et al. (2025) Excessive MYC Orchestrates Macrophages induced Chromatin Remodeling to Sustain Micropapillary-Patterned Malignancy in Lung Adenocarcinoma. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(12), e2403851.

Raymond JH, et al. (2025) Targeting GRPR for sex hormone-dependent cancer after loss of E-cadherin. *Nature*, 643(8072), 801.

Miranda AMA, et al. (2025) Selective remodelling of the adipose niche in obesity and weight loss. *Nature*, 644(8077), 769.

Zhang X, et al. (2025) Long non-coding RNA NORAD serves as a promoter of oncogenesis and inhibits ferroptosis via miR-144-3p-mTOR-ferritinophagy axis in cancer. *European journal of medical research*, 30(1), 704.

Sun L, et al. (2025) Disruption of YY1-mediated super-enhancer-promoter looping drives transcriptomic changes during mammalian stem-cell aging. *Research square*.

Chen F, et al. (2025) Global DNA methylation differences involving germline structural variation impact gene expression in pediatric brain tumors. *Nature communications*, 16(1), 4713.

Kosicki M, et al. (2025) Massively parallel reporter assays and mouse transgenic assays provide correlated and complementary information about neuronal enhancer activity. *Nature communications*, 16(1), 4786.

Zhang Y, et al. (2025) OncoSplicing 3.0: an updated database for identifying RBPs regulating alternative splicing events in cancers. *Nucleic acids research*, 53(D1), D1460.

Bjune JI, et al. (2025) IRX3 controls a SUMOylation-dependent differentiation switch in adipocyte precursor cells. *Nature communications*, 16(1), 7248.

Barker HR, et al. (2025) TFBSFootprinter: a multiomics tool for prediction of transcription factor binding sites in vertebrate species. *Transcription*, 16(2-3), 204.

Paramo MI, et al. (2025) Simultaneous measurement of intrinsic promoter and enhancer potential reveals principles of functional duality and regulatory reciprocity. *Research square*.