

# Resource Summary Report

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## 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:** consortium, data or information resource, data set, organization portal, 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:** 20260829T182513+0000

### Ratings and Alerts

No rating or validation information has been found for Encode.

No alerts have been found for Encode.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 1293 mentions in open access literature.

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

Bruckner I, et al. (2026) Extrachromosomal microDNA Signature as a Candidate Biomarker in Pediatric Acute Lymphoblastic Leukemia. Cancer research communications, 6(1), 143.

Chen H, et al. (2026) Genome-wide rotational and translational phasing of nucleosomes with human transcription factors. Molecular cell, 86(14), 2722.

van de Grift YBC, et al. (2026) GRHL and PGR control WNT4 expression via 3D looping of conserved and species-specific enhancers. Cell reports, 45(7), 117575.

Grammatikakis I, et al. (2026) Intron Retention Controls Localization of lncRNAs PURPL and MALAT1 to Promote Cell Proliferation and Migration. bioRxiv : the preprint server for biology.

Sain R, et al. (2026) Genetic and genomic approaches to explore roles for the conserved 3'-5' exoribonuclease EXOSC10 in normal and malignant cells. RNA (New York, N.Y.), 32(6), 789.

Rudnizky S, et al. (2026) Chromatin boundary permeability is controlled by CTCF conformational ensembles. bioRxiv : the preprint server for biology.

Ren X, et al. (2026) CRISPR tiling deletion screens reveal functional enhancers and allelic compensation effects (ACE) on SIN3A transcription. Nature communications, 17(1).

MacKenzie TMG, et al. (2026) In Depth Characterization of the Promoter Proximal Proteome of Single Copy Locus FOXP2. Molecular & cellular proteomics : MCP, 25(6), 101570.

Borges RL, et al. (2026) Unbalanced chromatin binding of Polycomb complexes drives neurodevelopmental disorders. Molecular cell, 86(4), 604.

Grover A, et al. (2026) UniversalEPI: robust prediction of cell type-specific and differential chromatin interactions from DNA sequence and chromatin accessibility. Nucleic acids research, 54(10).

Zhu X, et al. (2026) Bioinformatic analysis and experimental validation of the function of mitogen-activated protein kinase in esophageal cancer. Discover oncology, 17(1).

Kar R, et al. (2026) A distinct subset of stem-cell memory is poised for the cytotoxicity program in CD4+ T cells in humans. Science advances, 12(2), eady6423.

Ota M, et al. (2026) Causal modelling of gene effects from regulators to programs to traits. *Nature*, 650(8101), 399.

Hallast P, et al. (2026) Population-scale Y chromosome assemblies reveal recurrent remodeling within constrained architectures. *bioRxiv : the preprint server for biology*.

Qin M, et al. (2026) SLC13A2-transported citrate remodels transcriptional regulation through protein acetylation to suppress tumor growth. *Science advances*, 12(15), eaec4368.

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.

Liang Q, et al. (2025) Topology entropy: Enhancing graph partitioning for TAD identification and single-cell clustering. *Computational and structural biotechnology journal*, 27, 1864.

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

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.

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