Resource Summary Report

Generated by NIF on Aug 11, 2026

ENCODE

RRID:SCR_006793
Type: Tool

Proper Citation

ENCODE (RRID:SCR_006793)

Resource Information

URL: http://genome.ucsc.edu/ENCODE

Proper Citation: ENCODE (RRID:SCR_006793)

Description: Encyclopedia of DNA elements consisting of list of functional elements in human genome, including elements that act at protein and RNA levels, and regulatory elements that control cells and circumstances in which gene is active. Enables scientific and medical communities to interpret role of human genome in biology and disease. Provides identification of common cell types to facilitate integrative analysis and new experimental technologies based on high-throughput sequencing. Genome Browser containing ENCODE and Epigenomics Roadmap data. Data are available for entire human genome.

Synonyms: ENCODE - Encyclopedia of DNA Elements, ENCODE + Epigenomics Roadmap Combined Data Browser, Encyclopedia of DNA Elements, Encyclopedia of DNA Elements (ENCODE)

Resource Type: data or information resource, analysis service resource, data repository, production service resource, database, service resource, data analysis service, storage service resource

Defining Citation: PMID:21526222

Keywords: Encyclopedia, DNA, element, functional, human, genome, protein, RNA, level, regulatory, gene, active, disease, analysis

Funding: NHGRI

Availability: Free, Freely available

Resource Name: ENCODE

Resource ID: SCR_006793

Alternate IDs: nif-0000-02797, r3d100013051, SCR_017493, OMICS_00532

Alternate URLs: http://encodeproject.org/ENCODE/, https://www.genome.gov/Funded-Programs-Projects/ENCODE-Project-ENCyclopedia-Of-DNA-Elements, https://www.encodeproject.org/, https://doi.org/10.17616/R31NJMKB

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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 4206 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF .

Gadad SS, et al. (2026) X-linked cancer-associated polypeptide (XCP) from lncRNA1456 modulates PHF8 histone demethylase activity to regulate the epigenome, gene expression, and cellular pathways in breast cancer. Oncogene, 45(17), 1557.

Song SJ, et al. (2026) Arid1a deficiency promotes metabolic dysfunction-associated steatohepatitis and hepatocellular carcinoma by disrupting the FXR-gut microbiota-bile acid axis. Cancer letters, 652, 218567.

Kempynck N, et al. (2026) CREsted: modeling genomic and synthetic cell-type-specific enhancers across tissues and species. Nature methods, 23(5), 946.

López-Fuentes E, et al. (2026) Epigenetic and Transcriptional Programs Define Osteosarcoma Subtypes and Establish Targetable Vulnerabilities. Cancer discovery, 16(2), 296.

Bisht D, et al. (2026) Liquid biopsy-based diagnostic evaluation of hypermethylated CpG sites for ovarian cancer diagnosis. Molecular oncology.

Vuong TT, et al. (2026) DNA Methyltransferase Inhibition Prevents Platinum-Induced Ovarian Cancer Stem Cell Enrichment. Cancer research communications, 6(7), 1721.

Zhang Y, et al. (2026) Architectural and evolutionary features of TE-derived TSSs shape tissue-specific promoter activity in the human genome. Nature communications, 17(1).

Wu TZ, et al. (2026) Molecular divergence of TRPA1 in cetaceans supports lineage-specific adaptation to aquatic life. Zoological research, 47(1), 117.

Wang L, et al. (2026) Comprehensive analysis of mRNA-microRNA-lncRNA expression profiles in post-traumatic elbow heterotopic ossification using RNA sequencing and experimental validation. Annals of medicine, 58(1), 2611612.

Shankar A, et al. (2026) In vivo CRISPR screening identifies SAGA complex members as key regulators of hematopoiesis. Nature communications, 17(1), 1756.

Yu Z, et al. (2026) ChromBERT: A foundation model for learning interpretable representations for context-specific transcriptional regulatory networks. Cell genomics, 6(4), 101130.

Zhao LN, et al. (2026) FOXM1 influences DNA methylation to augment TACC3 alternative splicing directed by KAT2A in hepatocellular carcinoma. Clinical and molecular hepatology, 32(2), 808.

Holmes ME, et al. (2026) Interdependent Regulation of Alternative Splicing by Serine/Arginine-Rich and Heterogeneous Nuclear Ribonucleoprotein Splicing Factors. Genes, 17(1).

Ao Y, et al. (2026) Multi-omics profiling reveals intrathymic triggers and novel biomarkers in thymoma-associated myasthenia gravis. Biomarker research, 14(1), 26.

Tan J, et al. (2026) Potential regulators and metabolic networks of muscle fatty infiltration: genomic and radiomics investigation based on 33 300 participants. International journal of surgery (London, England), 112(1), 472.

Mauksch C, et al. (2026) FACT depletion demonstrates a role for nucleosome organization in TAD formation. Molecular systems biology, 22(1), 119.

Mu Z, et al. (2026) Impact of disease-associated chromatin accessibility QTLs across immune cell types and contexts. Cell genomics, 6(1), 101061.

Islam KMT, et al. (2026) SIRT7 as a context-dependent biomarker and therapeutic target: Insights from a pan-cancer study. PloS one, 21(2), e0342269.

Lim PSL, et al. (2026) Distinct roles for SET? and SET? in early cell fate decisions. Nucleic acids research, 54(4).

Reisman SJ, et al. (2026) Mismatch tolerance of a gRNA for CRISPR-based gene activation confers broad activity critical for cell reprogramming. bioRxiv : the preprint server for biology.