

Resource Summary Report

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ENCODE

RRID:SCR_006793

Type: Tool

Proper Citation

ENCODE (RRID:SCR_006793)

Resource Information

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

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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: analysis service resource, data analysis service, data or information resource, data repository, database, production service resource, service resource, 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>

Record Creation Time: 20220129T080238+0000

Record Last Update: 20260821T193814+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 4206 mentions in open access literature.

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

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.

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

- Starble RM, et al. (2026) Epigenetic priming promotes tyrosine kinase inhibitor resistance and oncogene amplification. *Nature structural & molecular biology*, 33(1), 7.
- Mauksch C, et al. (2026) FACT depletion demonstrates a role for nucleosome organization in TAD formation. *Molecular systems biology*, 22(1), 119.
- 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.
- Liu CS, et al. (2026) isoSeQL: comparing long-read isoforms across multiple datasets. *Bioinformatics (Oxford, England)*, 42(1).
- Wei Y, et al. (2026) Transformer-based InsightGWAS improves GERD genetic discovery via pretraining on GWAS for major depressive disorder. *Communications biology*, 9(1), 2.
- Lim PSL, et al. (2026) Distinct roles for SET γ and SET δ in early cell fate decisions. *Nucleic acids research*, 54(4).
- Shankar A, et al. (2026) In vivo CRISPR screening identifies SAGA complex members as key regulators of hematopoiesis. *Nature communications*, 17(1), 1756.
- Pal VK, et al. (2026) HIV-1 Integration Site Determines the Transcriptional Fate and Persistence of Integrated Proviruses. *bioRxiv : the preprint server for biology*.
- Goovaerts S, et al. (2026) The craniofacial shape of modern humans embodies genomic signatures of evolution, diversity, and clinical conditions. *bioRxiv : the preprint server for biology*.
- 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.
- Kong H, et al. (2026) Functional characterization of a multi-cancer risk locus on chromosome band 2q33.1 near CASP8. *bioRxiv : the preprint server for biology*.
- 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).
- Ao Y, et al. (2026) Multi-omics profiling reveals intrathymic triggers and novel biomarkers in thymoma-associated myasthenia gravis. *Biomarker research*, 14(1), 26.