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

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 analysis service, data or information resource, data repository, storage service resource, database, service resource, production service resource, analysis 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 3681 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

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.

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

Li A, et al. (2026) Hi-Enhancer: a two-stage framework for prediction and localization of enhancers based on Blending-KAN and Stacking-Auto models. Bioinformatics (Oxford, England), 42(1).

Yeki S, et al. (2026) Sex-Specific doublesex Regulation Targeting the Color-Patterning Gene h Underlies the Evolution of Wing Sexual Dimorphism in the Harlequin Ladybug Harmonia axyridis. Evolution & development, 28(1), e70028.

Sankar V, et al. (2026) Genetic elements promote retention of extrachromosomal DNA in cancer cells. Nature, 649(8095), 152.

Martinez-Salas E, et al. (2026) GEMIN5 and neurodevelopmental diseases: From functional insights to disease perception. Neural regeneration research, 21(1), 187.

Xiong Z, et al. (2026) C/EBP??-induced alternative splicing of RCAN1 generates a potent TCR-T target in mesenchymal glioblastoma. Cellular & molecular immunology, 23(1), 94.

Leban T, et al. (2026) Multiomics Data Synthesis of FAM83H in Amelogenesis Imperfecta. International dental journal, 76(1), 109293.

Esposito DV, et al. (2026) A non-coding ABO regulatory variant associated with VWF levels, thrombosis risk, and COVID-19 severity is topologically linked to ADAMTS13 in endothelial cells. HGG advances, 7(1), 100550.

Banno A, et al. (2026) A simple, efficient, and scalable method to generate oocyte-like cells in vitro. Life science alliance, 9(2).

Telonis AG, et al. (2026) Synergistic intragenic epigenetic deregulation by IDH2 and SRSF2 mutations causes mis-splicing of key transcriptional regulators. Science advances, 12(1), eadu8292.

Luzadder MM, et al. (2025) The Distinct Roles of NEIL1 and XPA in Limiting Aflatoxin B1-Induced Mutagenesis in Mice. Molecular cancer research : MCR, 23(1), 46.

Renatino Canevarolo R, et al. (2025) Epigenetic Plasticity Drives Carcinogenesis and Multi-Therapy Resistance in Multiple Myeloma. Research square.

Zhao Y, et al. (2025) Sodium-glucose exchanger 2 inhibitor canagliflozin promotes mitochondrial metabolism and alleviates salt-induced cardiac hypertrophy via preserving SIRT3 expression. Journal of advanced research, 70, 255.

Jin C, et al. (2025) Molecular and genetic insights into human ovarian aging from single-nuclei multi-omics analyses. Nature aging, 5(2), 275.

Lei T, et al. (2025) Genetic Influence of the Brain on Muscle Structure: A Mendelian Randomization Study of Sarcopenia. Journal of cachexia, sarcopenia and muscle, 16(1), e13647.

Perez MF, et al. (2025) CelEst: a unified gene regulatory network for estimating transcription factor activities in C. elegans. Genetics, 229(3).

Lombardi O, et al. (2025) Conserved patterns of transcriptional dysregulation, heterogeneity, and cell states in clear cell kidney cancer. Cell reports, 44(1), 115169.

Gur ER, et al. (2025) scATAC-seq generates more accurate and complete regulatory maps than bulk ATAC-seq. Scientific reports, 15(1), 3665.

Xiang RR, et al. (2025) CRISPR screening identifies regulators of enhancer-mediated androgen receptor transcription in advanced prostate cancer. Cell reports, 44(2), 115312.