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: production service resource, data or information resource, database, data repository, service resource, storage service resource, data analysis service, 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 ASWG .

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

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.

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.

Mannion BJ, et al. (2025) Uncovering hidden enhancers through unbiased in vivo testing. Nature communications, 16(1), 7313.

Wei Y, et al. (2025) Screening, identification, and experimental validation of SUMOylation biomarkers in Parkinson's disease. Hereditas, 162(1), 154.

Li J, et al. (2025) Unveiling the Temporal Dynamics and Molecular Regulation Profiles of Neutrophil Extracellular Traps Following Spinal Cord Injury. Journal of inflammation research, 18, 10585.

Sahinyan K, et al. (2025) REST/NRSF Preserves muscle stem cell identity by repressing alternate cell fate. Nature communications, 16(1), 7487.

Salnikov P, et al. (2025) Direction and modality of transcription changes caused by TAD boundary disruption in Slc29a3/Unc5b locus depends on tissue-specific epigenetic context. Epigenetics & chromatin, 18(1), 55.

Vasconcelos AG, et al. (2025) Methylation profile of individuals with sickle cell trait. Epigenetics, 20(1), 2539234.