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 or information resource, service resource, analysis service resource, data analysis service, data repository, production service resource, database, 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, 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/

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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 3147 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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

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.

Chen C, et al. (2025) Comprehensive characterization of the transcriptional landscape in Alzheimer's disease (AD) brains. Science advances, 11(1), eadn1927.

Lusby R, et al. (2025) Pan-cancer drivers of metastasis. Molecular cancer, 24(1), 2.

Cyr Y, et al. (2025) lncRNA CARINH regulates expression and function of innate immune transcription factor IRF1 in macrophages. Life science alliance, 8(3).

Saelens W, et al. (2025) ChromatinHD connects single-cell DNA accessibility and

conformation to gene expression through scale-adaptive machine learning. Nature communications, 16(1), 317.

Wang S, et al. (2025) Ferroptosis-related genes participate in the microglia-induced neuroinflammation of spinal cord injury via NF-?B signaling: evidence from integrated single-cell and spatial transcriptomic analysis. Journal of translational medicine, 23(1), 43.

Wen Z, et al. (2025) Nucleosome wrapping states encode principles of 3D genome organization. Nature communications, 16(1), 352.

Liao JY, et al. (2025) RBPWorld for exploring functions and disease associations of RNA-binding proteins across species. Nucleic acids research, 53(D1), D220.

Segert JA, et al. (2025) Histone H4 lysine 20 monomethylation is not a mark of transcriptional silencers. bioRxiv : the preprint server for biology.

Zou X, et al. (2025) Impact of rare non-coding variants on human diseases through alternative polyadenylation outliers. Nature communications, 16(1), 682.

Pampari A, et al. (2025) ChromBPNet: bias factorized, base-resolution deep learning models of chromatin accessibility reveal cis-regulatory sequence syntax, transcription factor footprints and regulatory variants. bioRxiv : the preprint server for biology.

Zhang Y, et al. (2025) OncoSplicing 3.0: an updated database for identifying RBPs regulating alternative splicing events in cancers. Nucleic acids research, 53(D1), D1460.

Xu J, et al. (2025) miRStart 2.0: enhancing miRNA regulatory insights through deep learning-based TSS identification. Nucleic acids research, 53(D1), D138.

Rose JC, et al. (2025) Disparate Pathways for Extrachromosomal DNA Biogenesis and Genomic DNA Repair. Cancer discovery, 15(1), 69.

Wang G, et al. (2025) CRISPRoffT: comprehensive database of CRISPR/Cas off-targets. Nucleic acids research, 53(D1), D914.

Boileau E, et al. (2025) Sci-ModoM: a quantitative database of transcriptome-wide high-throughput RNA modification sites. Nucleic acids research, 53(D1), D310.

Zhou X, et al. (2025) Transethnic analysis identifies SORL1 variants and haplotypes protective against Alzheimer's disease. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(1), e14214.

Dong Z, et al. (2025) A KSHV-targeted small molecule efficiently blocks SARS-CoV-2 infection via inhibiting expression of EGFR and Cyclin A2. Emerging microbes & infections, 14(1), 2440490.

Fu X, et al. (2025) A foundation model of transcription across human cell types. Nature, 637(8047), 965.