Resource Summary Report

Generated by NIF on Apr 22, 2025

Encode

RRID:SCR_015482
Type: Tool

Proper Citation

Encode (RRID:SCR_015482)

Resource Information

URL: https://www.encodeproject.org/

Proper Citation: Encode (RRID:SCR_015482)

Description: Consortium to build comprehensive parts list of functional elements in human genome. This includes elements that act at protein and RNA levels, and regulatory elements that control cells and circumstances in which gene is active. Data from 2012-present.

Synonyms: ENCODE Project

Resource Type: consortium, portal, data or information resource, organization portal, data set

Defining Citation: PMID:15499007

Keywords: genome, sequencing, protein, rna, dna, consortium

Funding: NHGRI HG006992

Availability: Free, Freely available

Resource Name: Encode

Resource ID: SCR_015482

Record Creation Time: 20220129T080326+0000

Record Last Update: 20250422T055901+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 1207 mentions in open access literature.

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

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.

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.

Parag RR, et al. (2025) Novel Isoforms of Adhesion G Protein-Coupled Receptor B1 (ADGRB1/BAI1) Generated from an Alternative Promoter in Intron 17. Molecular neurobiology, 62(1), 900.

Lee D, et al. (2025) Increased local DNA methylation disorder in AMLs with DNMT3A-destabilizing variants and its clinical implication. Nature communications, 16(1), 560.

Hariprakash JM, et al. (2024) Leveraging Tissue-Specific Enhancer-Target Gene Regulatory Networks Identifies Enhancer Somatic Mutations That Functionally Impact Lung Cancer. Cancer research, 84(1), 133.

Huang LC, et al. (2024) BRCA1 and ELK-1 regulate neural progenitor cell fate in the optic tectum in response to visual experience in Xenopus laevis tadpoles. Proceedings of the National Academy of Sciences of the United States of America, 121(3), e2316542121.

Kosicki M, et al. (2024) Massively parallel reporter assays and mouse transgenic assays provide complementary information about neuronal enhancer activity. bioRxiv : the preprint server for biology.

Deng L, et al. (2024) Atlas of cardiac endothelial cell enhancer elements linking the mineralocorticoid receptor to pathological gene expression. Science advances, 10(10), eadj5101.

Xiao F, et al. (2024) Functional dissection of human cardiac enhancers and noncoding de novo variants in congenital heart disease. Nature genetics, 56(3), 420.

Moqri M, et al. (2024) PRC2-AgeIndex as a universal biomarker of aging and rejuvenation. Nature communications, 15(1), 5956.

Meulebrouck S, et al. (2024) Functional genetics reveals the contribution of delta opioid receptor to type 2 diabetes and beta-cell function. Nature communications, 15(1), 6627.

Hawkins S, et al. (2024) ePRINT: exonuclease assisted mapping of protein-RNA interactions. Genome biology, 25(1), 140.

Chuah CW, et al. (2024) GMean-a semi-supervised GRU and K-mean model for predicting the TF binding site. Scientific reports, 14(1), 2539.

Parolia A, et al. (2024) NSD2 is a requisite subunit of the AR/FOXA1 neo-enhanceosome in promoting prostate tumorigenesis. Nature genetics, 56(10), 2132.

Abassah-Oppong S, et al. (2024) A gene desert required for regulatory control of pleiotropic Shox2 expression and embryonic survival. Nature communications, 15(1), 8793.

Wahbeh MH, et al. (2024) A functional schizophrenia-associated genetic variant near the TSNARE1 and ADGRB1 genes. HGG advances, 5(3), 100303.

Brümmer A, et al. (2024) Disentangling genetic effects on transcriptional and post-transcriptional gene regulation through integrating exon and intron expression QTLs. Nature communications, 15(1), 3786.

Mu W, et al. (2024) Machine learning methods for predicting guide RNA effects in CRISPR epigenome editing experiments. bioRxiv : the preprint server for biology.

Ai G, et al. (2024) Dissecting the molecular basis of spike traits by integrating gene regulatory networks and genetic variation in wheat. Plant communications, 5(5), 100879.

McCallum-Loudeac J, et al. (2024) Deletion of a conserved genomic region associated with adolescent idiopathic scoliosis leads to vertebral rotation in mice. Human molecular genetics, 33(9), 787.