Resource Summary Report

Generated by NIF on Aug 26, 2026

VISTA Enhancer Browser

RRID:SCR_007973
Type: Tool

Proper Citation

VISTA Enhancer Browser (RRID:SCR_007973)

Resource Information

URL: http://enhancer.lbl.gov/

Proper Citation: VISTA Enhancer Browser (RRID:SCR_007973)

Description: Resource for experimentally validated human and mouse noncoding fragments with gene enhancer activity as assessed in transgenic mice. Most of these noncoding elements were selected for testing based on their extreme conservation in other vertebrates or epigenomic evidence (ChIP-Seq) of putative enhancer marks. Central public database of experimentally validated human and mouse noncoding fragments with gene enhancer activity as assessed in transgenic mice. Users can retrieve elements near single genes of interest, search for enhancers that target reporter gene expression to particular tissue, or download entire collections of enhancers with defined tissue specificity or conservation depth.

Abbreviations: VISTA Enhancer Browser

Resource Type: data or information resource, data repository, database, service resource, storage service resource

Defining Citation: PMID:17130149

Keywords: human, noncoding fragment, mutant mouse strain, molecular neuroanatomy resource, image, telencephalon, development, genome, enhancer, dna fragment, embryo, embryonic mouse, brain, neural tube, eye, ear, heart, tail, limb, nose, cranial nerve, trigeminal, dorsal root ganglia, face, branchial arch, gene expression, annotation, vector, transgenic embryo, lacz reporter vector, lacz, biomaterial supply resource, in vivo, image collection, transcriptional enhancer, chip-seq, bio.tools, FASEB list

Funding: American Heart Association ;
DOE contract DE-AC02-05CH11231;
DOE DE020060;
NHGRI HG003988;
NHLBI HL066681;

NIDCR ;
NINDS NS062859

Availability: Free, Freely available

Resource Name: VISTA Enhancer Browser

Resource ID: SCR_007973

Alternate IDs: nif-0000-03637, OMICS_01568, biotools:vista_enhancer_browser

Alternate URLs: https://bio.tools/vista_enhancer_browser

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260821T193831+0000

Ratings and Alerts

No rating or validation information has been found for VISTA Enhancer Browser.

No alerts have been found for VISTA Enhancer Browser.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 249 mentions in open access literature.

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

Bisht V, et al. (2026) Functional annotation of non-coding variants identifies a novel enhancer with activity in neural crest cell-derived lineages. Research square.

Jin L, et al. (2026) Computational identification of lineage-committed precursors in mammalian organogenesis reveals a novel hematopoietic enhancer regulating Bhlhe41 expression. Briefings in bioinformatics, 27(2).

Shen X, et al. (2026) A foundation model for nucleotide sequences. Nucleic acids research, 54(6).

Liang X, et al. (2026) Predicting enhancer-gene links from single-cell multi-omics data by integrating prior Hi-C information. Nucleic acids research, 54(9).

Maurya S, et al. (2026) ePerturbDB: enhancer's experimental perturbation database. Database : the journal of biological databases and curation, 2026.

Roland V, et al. (2025) Functional architecture of cardiac TF regulatory landscapes in control of mammalian heart development. bioRxiv : the preprint server for biology.

Kosicki M, et al. (2025) Massively parallel reporter assays and mouse transgenic assays provide correlated and complementary information about neuronal enhancer activity. Nature communications, 16(1), 4786.

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

Kosicki M, et al. (2025) VISTA Enhancer browser: an updated database of tissue-specific developmental enhancers. Nucleic acids research, 53(D1), D324.

Wang Y, et al. (2025) Whole-genome sequencing reveals individual and cohort level insights into chromosome 9p syndromes. Genome medicine, 17(1), 129.

Widmayer SJ, et al. (2025) Low-coverage whole-genome sequencing facilitates accurate and cost-effective haplotype reconstruction in complex mouse crosses. Mammalian genome : official journal of the International Mammalian Genome Society.

Hong D, et al. (2025) Divergent combinations of enhancers encode spatial gene expression. Nature communications, 16(1), 5091.

Kosugi S, et al. (2025) TRsv: simultaneous detection of tandem repeat variations, structural variations, and short indels using long read sequencing data. Genome biology, 26(1), 246.

Mannens CCA, et al. (2025) Chromatin accessibility during human first-trimester neurodevelopment. Nature, 647(8088), 179.

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 S, et al. (2025) A MGMT Enhancer Variant is Associated with Glioma Susceptibility and Progression. Cellular and molecular neurobiology, 45(1), 88.

Tedja MS, et al. (2025) A genome-wide scan of non-coding RNAs and enhancers for refractive error and myopia. Human genetics, 144(1), 67.

Wonkam A, et al. (2025) FLT1 and other candidate fetal haemoglobin modifying loci in sickle cell disease in African ancestries. Nature communications, 16(1), 2092.

Malkmus J, et al. (2025) WNT signaling coordinately controls mouse limb bud outgrowth and establishment of the digit-interdigit pattern. Development (Cambridge, England), 152(11).

Batool F, et al. (2025) The combinatorial binding syntax of transcription factors in forebrain-specific enhancers. Biology open, 14(2).