## **Resource Summary Report**

Generated by <u>NIF</u> on May 17, 2025

# 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:** service resource, database, data or information resource, storage service resource, data repository

#### 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 ;

NIDCR ; NHLBI HL066681; NHGRI HG003988; DOE contract DE-AC02-05CH11231; NINDS NS062859; DOE DE020060

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: 20250517T055844+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 217 mentions in open access literature.

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

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

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.

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.

Wilderman A, et al. (2024) A distant global control region is essential for normal expression of anterior HOXA genes during mouse and human craniofacial development. Nature communications, 15(1), 136.

Pratt HE, et al. (2024) Using a comprehensive atlas and predictive models to reveal the complexity and evolution of brain-active regulatory elements. Science advances, 10(21), eadj4452.

Darbellay F, et al. (2024) Pre-hypertrophic chondrogenic enhancer landscape of limb and axial skeleton development. Nature communications, 15(1), 4820.

Tritto V, et al. (2024) Genetic/epigenetic effects in NF1 microdeletion syndrome: beyond the haploinsufficiency, looking at the contribution of not deleted genes. Human genetics, 143(6), 775.

Xiao T, et al. (2024) The Myc-associated zinc finger protein epigenetically controls expression of interferon-?-stimulated genes by recruiting STAT1 to chromatin. Proceedings of the National Academy of Sciences of the United States of America, 121(17), e2320938121.

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.

Aurigemma I, et al. (2024) Endothelial gene regulatory elements associated with cardiopharyngeal lineage differentiation. Communications biology, 7(1), 351.

Rajderkar SS, et al. (2024) Dynamic enhancer landscapes in human craniofacial development. Nature communications, 15(1), 2030.

Hu W, et al. (2024) A deep learning model for DNA enhancer prediction based on nucleotide position aware feature encoding. iScience, 27(6), 110030.

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.

Deng Y, et al. (2024) SCAN: Spatiotemporal Cloud Atlas for Neural cells. Nucleic acids research, 52(D1), D998.

Dvoretskova E, et al. (2024) Spatial enhancer activation influences inhibitory neuron identity during mouse embryonic development. Nature neuroscience, 27(5), 862.

Lee AS, et al. (2024) A cell type-aware framework for nominating non-coding variants in Mendelian regulatory disorders. Nature communications, 15(1), 8268.

Bosone C, et al. (2024) A polarized FGF8 source specifies frontotemporal signatures in spatially oriented cell populations of cortical assembloids. Nature methods, 21(11), 2147.

Makino Y, et al. (2023) STAT3 is Activated by CTGF-mediated Tumor-stroma Cross Talk to Promote HCC Progression. Cellular and molecular gastroenterology and hepatology, 15(1), 99.

Kocher AA, et al. (2023) CpG island turnover events predict evolutionary changes in enhancer activity. bioRxiv : the preprint server for biology.

Li Y, et al. (2023) Combined genome-wide association study of 136 quantitative ear morphology traits in multiple populations reveal 8 novel loci. PLoS genetics, 19(7), e1010786.