

Resource Summary Report

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VISTA Enhancer Browser

RRID:SCR_007973

Type: Tool

Proper Citation

VISTA Enhancer Browser (RRID:SCR_007973)

Resource Information

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

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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 repository, data or information resource, database, storage service resource, 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 ;
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: 20260804T043337+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 233 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

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

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.

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

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.

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

- 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.
- Batool F, et al. (2025) The combinatorial binding syntax of transcription factors in forebrain-specific enhancers. *Biology open*, 14(2).
- Kagda MS, et al. (2025) Data navigation on the ENCODE portal. *Nature communications*, 16(1), 9592.
- Trigila AP, et al. (2025) Comparative genomics sheds light on mammalian and avian gene regulation and phenotypic evolution. *Nature communications*, 16(1), 9111.
- Nielsen T, et al. (2025) Functional analysis across model systems implicates ribosomal proteins in growth and proliferation defects associated with hypoplastic left heart syndrome. *eLife*, 14.
- Mannens CCA, et al. (2025) Chromatin accessibility during human first-trimester neurodevelopment. *Nature*, 647(8088), 179.
- 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).
- 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.
- Darbellay F, et al. (2024) Pre-hypertrophic chondrogenic enhancer landscape of limb and axial skeleton development. *Nature communications*, 15(1), 4820.
- 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.