

Resource Summary Report

Generated by [NIF](#) on Jul 28, 2026

PCR4-Shh::lacZ-H11

RRID:Addgene_139098

Type: Plasmid

Proper Citation

RRID:Addgene_139098

Plasmid Information

URL: <http://www.addgene.org/139098>

Proper Citation: RRID:Addgene_139098

Bacterial Resistance: Ampicillin and Kanamycin

Defining Citation: [PMID:32169219](#)

Vector Backbone Description: Backbone Marker:Invitrogen; Backbone Size:3956; Vector Backbone:PCR4-TOPO; Vector Types:Mammalian Expression, Mouse Targeting, CRISPR; Bacterial Resistance:Ampicillin and Kanamycin

Comments: Please note that there are minor differences between the Addgene verified result and the depositor's reference sequence (under the supplemental documents section). Please refer to the Addgene NGS result for more accurate sequence information. These differences do not affect the plasmid function.

Plasmid Name: PCR4-Shh::lacZ-H11

Record Creation Time: 20220422T221805+0000

Record Last Update: 20260725T073923+0000

Ratings and Alerts

No rating or validation information has been found for PCR4-Shh::lacZ-H11.

No alerts have been found for PCR4-Shh::lacZ-H11.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Xu X, et al. (2025) Auricular malformations are driven by copy number variations in a hierarchical enhancer cluster and a dominant enhancer recapitulates human pathogenesis. *Nature communications*, 16(1), 4598.

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*.

Britton JC, et al. (2025) Evidence for Fgf and Wnt regulation of Lhx2 during limb development via two limb-specific Lhx2-associated cis-regulatory modules. *Frontiers in cell and developmental biology*, 13, 1552716.

Xie Z, et al. (2025) DNA-guided transcription factor interactions extend human gene regulatory code. *Nature*, 641(8065), 1329.

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.

Bower G, et al. (2025) Range extender mediates long-distance enhancer activity. *Nature*, 643(8072), 830.

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

Kosicki M, et al. (2024) Mutagenesis Sensitivity Mapping of Human Enhancers In Vivo. *bioRxiv : the preprint server for biology*.

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

Ding X, et al. (2024) Scalable and Efficient Generation of Mouse Primordial Germ Cell-like Cells. *bioRxiv : the preprint server for biology*.

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*.

Bower G, et al. (2024) Conserved Cis-Acting Range Extender Element Mediates Extreme Long-Range Enhancer Activity in Mammals. *bioRxiv : the preprint server for biology*.

Shin T, et al. (2024) Rare variation in non-coding regions with evolutionary signatures contributes to autism spectrum disorder risk. *Cell genomics*, 4(8), 100609.

Xue JR, et al. (2023) The functional and evolutionary impacts of human-specific deletions in conserved elements. *Science (New York, N.Y.)*, 380(6643), eabn2253.

Rajderkar SS, et al. (2023) Cell Type- and Tissue-specific Enhancers in Craniofacial Development. bioRxiv : the preprint server for biology.

Rajderkar S, et al. (2023) Topologically associating domain boundaries are required for normal genome function. Communications biology, 6(1), 435.

Osterwalder M, et al. (2022) Characterization of Mammalian In Vivo Enhancers Using Mouse Transgenesis and CRISPR Genome Editing. Methods in molecular biology (Clifton, N.J.), 2403, 147.

Snetkova V, et al. (2021) Ultraconserved enhancer function does not require perfect sequence conservation. Nature genetics, 53(4), 521.