

Resource Summary Report

Generated by [RRID](#) on Aug 19, 2026

PB-TRE-dCas9-VPR

RRID:Addgene_63800

Type: Plasmid

Proper Citation

RRID:Addgene_63800

Plasmid Information

URL: <http://www.addgene.org/63800>

Proper Citation: RRID:Addgene_63800

Insert Name: dCas9-VPR

Organism: Homo sapiens

Bacterial Resistance: Ampicillin

Defining Citation: [PMID:25730490](#)

Vector Backbone Description: Vector Backbone:PB-TRE; Vector Types:Mammalian Expression, CRISPR, Synthetic Biology, Piggybac; Bacterial Resistance:Ampicillin

Plasmid Name: PB-TRE-dCas9-VPR

Record Creation Time: 20220422T222405+0000

Record Last Update: 20260815T081805+0000

Ratings and Alerts

No rating or validation information has been found for PB-TRE-dCas9-VPR.

No alerts have been found for PB-TRE-dCas9-VPR.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 41 mentions in open access literature.

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

Malcher A, et al. (2025) TKTL1: a new candidate gene in non-obstructive azoospermia. Reproductive biomedicine online, 51(3), 104895.

Gu S, et al. (2025) Elucidating the genetic mechanisms governing cytosine base editing outcomes through CRISPRi screens. Nature communications, 16(1), 4685.

Lodewijk GA, et al. (2025) Self-organization of mouse embryonic stem cells into reproducible pre-gastrulation embryo models via CRISPRa programming. Cell stem cell, 32(6), 895.

Chen H, et al. (2025) PARP7 Inhibitors and AHR Agonists Act Synergistically across a Wide Range of Cancer Models. Molecular cancer therapeutics, 24(1), 56.

Love KS, et al. (2025) Model-guided design of microRNA-based gene circuits supports precise dosage of transgenic cargoes into diverse primary cells. Cell systems, 16(6), 101269.

Lodewijk GA, et al. (2025) Application of CRISPR-Based Epigenome Editing Tools for Engineering Programmable Embryo Models. Methods in molecular biology (Clifton, N.J.).

Li J, et al. (2025) CRISPR-based screening identifies the role of KRAB-containing transcription factors ZIM3 and ZNF394 in human major zygotic genome activation. Cell reports, 44(8), 116015.

Ching RW, et al. (2025) Forced expression of MSR repeat transcripts above a threshold limit breaks heterochromatin organisation. Nature communications, 16(1), 6420.

Ding Y, et al. (2025) ETV2 Overexpression Promotes Efficient Differentiation of Pluripotent Stem Cells to Endothelial Cells. Biotechnology and bioengineering, 122(7), 1914.

Kabrani E, et al. (2025) RIF1 integrates DNA repair and transcriptional requirements during the establishment of humoral immune responses. Nature communications, 16(1), 777.

Lodewijk GA, et al. (2024) Self-organization of embryonic stem cells into a reproducible embryo model through epigenome editing. bioRxiv : the preprint server for biology.

Nadalin F, et al. (2024) Multi-omic lineage tracing predicts the transcriptional, epigenetic and genetic determinants of cancer evolution. Nature communications, 15(1), 7609.

Ozturk K, et al. (2024) Interface-guided phenotyping of coding variants in the transcription factor RUNX1. Cell reports, 43(7), 114436.

Chang CH, et al. (2024) The pRb/RBL2-E2F1/4-GCN5 axis regulates cancer stem cell formation and G0 phase entry/exit by paracrine mechanisms. Nature communications, 15(1), 3580.

Vega-Sendino M, et al. (2024) The homeobox transcription factor DUXBL controls exit from totipotency. *Nature genetics*, 56(4), 697.

Malcher A, et al. (2023) ESX1 gene as a potential candidate responsible for male infertility in nonobstructive azoospermia. *Scientific reports*, 13(1), 16563.

Madrigal P, et al. (2023) Epigenetic and transcriptional regulations prime cell fate before division during human pluripotent stem cell differentiation. *Nature communications*, 14(1), 405.

Pilat JM, et al. (2023) SELENOP modifies sporadic colorectal carcinogenesis and WNT signaling activity through LRP5/6 interactions. *The Journal of clinical investigation*, 133(13).

Nagasaki SC, et al. (2023) Enhancement of Vivid-based photo-activatable Gal4 transcription factor in mammalian cells. *Cell structure and function*, 48(1), 31.

Nikolic A, et al. (2023) macroH2A2 antagonizes epigenetic programs of stemness in glioblastoma. *Nature communications*, 14(1), 3062.