

Resource Summary Report

Generated by [NIF](#) on Aug 3, 2026

pCMV-BE3

RRID:Addgene_73021

Type: Plasmid

Proper Citation

RRID:Addgene_73021

Plasmid Information

URL: <http://www.addgene.org/73021>

Proper Citation: RRID:Addgene_73021

Insert Name: BE3

Organism: Rattus norvegicus

Bacterial Resistance: Ampicillin

Defining Citation: [PMID:27096365](https://pubmed.ncbi.nlm.nih.gov/27096365/)

Vector Backbone Description: Backbone Marker:origene; Backbone Size:3399; Vector Backbone:CMV; Vector Types:Mammalian Expression; Bacterial Resistance:Ampicillin

Plasmid Name: pCMV-BE3

Record Creation Time: 20220422T222448+0000

Record Last Update: 20260801T081747+0000

Ratings and Alerts

No rating or validation information has been found for pCMV-BE3.

No alerts have been found for pCMV-BE3.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 78 mentions in open access literature.

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

Chen Q, et al. (2025) Engineering of Peptide-Inserted Base Editors with Enhanced Accuracy and Security. *Small* (Weinheim an der Bergstrasse, Germany), 21(14), e2411583.

Ha TY, et al. (2025) SOX9 haploinsufficiency reveals SOX9-Noggin interaction in BMP-SMAD signaling pathway in chondrogenesis. *Cellular and molecular life sciences : CMLS*, 82(1), 99.

Morito T, et al. (2025) Human MAPT knockin mouse models of frontotemporal dementia for the neurodegenerative research community. *Cell reports methods*, 5(4), 101024.

Flisikowska T, et al. (2025) Perinatal death in pig models of hypertrophic cardiomyopathy carrying sarcomere pathogenic variants. *Journal of molecular and cellular cardiology plus*, 12, 100457.

Song X, et al. (2024) RNA splicing analysis deciphers developmental hierarchies and reveals therapeutic targets in adult glioma. *The Journal of clinical investigation*, 134(11).

Berríos KN, et al. (2024) Cooperativity between Cas9 and hyperactive AID establishes broad and diversifying mutational footprints in base editors. *Nucleic acids research*, 52(4), 2078.

Park JC, et al. (2024) Enhancing genome editing in hPSCs through dual inhibition of DNA damage response and repair pathways. *Nature communications*, 15(1), 4002.

Pérez-Gómez A, et al. (2024) PPAR γ is dispensable for bovine embryo development up to tubular stages†. *Biology of reproduction*, 111(3), 557.

Yang Q, et al. (2024) T4 DNA polymerase prevents deleterious on-target DNA damage and enhances precise CRISPR editing. *The EMBO journal*, 43(17), 3733.

He Y, et al. (2024) Protocol to use protein language models predicting and following experimental validation of function-enhancing variants of thymine-N-glycosylase. *STAR protocols*, 5(3), 103188.

Li Q, et al. (2023) Base editing-mediated one-step inactivation of the Dnmt gene family reveals critical roles of DNA methylation during mouse gastrulation. *Nature communications*, 14(1), 2922.

Ruan X, et al. (2023) PIE-seq: identifying RNA-binding protein targets by dual RNA-deaminase editing and sequencing. *Nature communications*, 14(1), 3275.

Duo T, et al. (2023) Single-base editing in IGF2 improves meat production and intramuscular fat deposition in Liang Guang Small Spotted pigs. *Journal of animal science and biotechnology*, 14(1), 141.

Xu C, et al. (2023) Mutation of S461, in the GOLGA3 phosphorylation site, does not affect mouse spermatogenesis. *PeerJ*, 11, e15133.

Rieffer AE, et al. (2023) APOBEC Reporter Systems for Evaluating diNucleotide Editing Levels. *The CRISPR journal*, 6(5), 430.

Luo L, et al. (2022) Base editing in bovine embryos reveals a species-specific role of SOX2 in regulation of pluripotency. *PLoS genetics*, 18(7), e1010307.

Lau CH, et al. (2022) PAM-flexible dual base editor-mediated random mutagenesis and self-activation strategies to improve CRISPRa potency. *Molecular therapy. Methods & clinical development*, 26, 26.

Tao J, et al. (2022) Frequency and mechanisms of LINE-1 retrotransposon insertions at CRISPR/Cas9 sites. *Nature communications*, 13(1), 3685.

Zhou J, et al. (2022) Eliminating predictable DNA off-target effects of cytosine base editor by using dual guiders including sgRNA and TALE. *Molecular therapy : the journal of the American Society of Gene Therapy*, 30(7), 2443.

Schubert OT, et al. (2022) Genome-wide base editor screen identifies regulators of protein abundance in yeast. *eLife*, 11.