Resource Summary Report

Generated by NIF on Sep 22, 2026

pCMV-ABE7.10

RRID:Addgene_102919
Type: Plasmid

Proper Citation

RRID:Addgene_102919

Plasmid Information

URL: http://www.addgene.org/102919

Proper Citation: RRID:Addgene_102919

Insert Name: ABE7.10

Organism: Synthetic

Bacterial Resistance: Ampicillin

Defining Citation: PMID:29160308

Vector Backbone Description: Backbone Marker:Liu lab; Backbone Size:3388; Vector Backbone:pBR322/CMV; Vector Types:Mammalian Expression; Bacterial Resistance:Ampicillin

Plasmid Name: pCMV-ABE7.10

Relevant Mutation: see manuscript

Record Creation Time: 20220422T221458+0000

Record Last Update: 20260919T090409+0000

Ratings and Alerts

No rating or validation information has been found for pCMV-ABE7.10.

No alerts have been found for pCMV-ABE7.10.

Data and Source Information

Source: Addgene

Usage and Citation Metrics

We found 40 mentions in open access literature.

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

Djamshidi M, et al. (2026) Protocol for enhancing CRISPR-Cas9 genome editing using histone deacetylase inhibition and engineered virus-like particle delivery. STAR protocols, 7(2), 104493.

Tachida Y, et al. (2025) Systematic empirical evaluation of individual base editing targets: Validating therapeutic targets in USH2A and comparison of methods. Molecular therapy : the journal of the American Society of Gene Therapy, 33(4), 1466.

Djamshidi M, et al. (2025) FAME-CRISPR improves CRISPR-Cas9 genome editing via HDAC inhibition and engineered virus-like particle delivery. Cell reports methods, 101248.

Yuan K, et al. (2025) Selict-seq profiles genome-wide off-target effects in adenosine base editing. Nucleic acids research, 53(7).

Roman A, et al. (2025) Prime editing corrects the dilated cardiomyopathy causing RBM20-P633L-mutation in human cardiomyocytes. Molecular therapy. Nucleic acids, 36(4), 102734.

Sun Y, et al. (2025) Deep learning models simultaneously trained on multiple datasets improve base-editing activity prediction. Nature communications, 16(1), 9821.

Luo X, et al. (2024) Primate Model Carrying LMNA Mutation Develops Dilated Cardiomyopathy. JACC. Basic to translational science, 9(3), 380.

Mention K, et al. (2023) Use of adenine base editing and homology-independent targeted integration strategies to correct the cystic fibrosis causing variant, W1282X. Human molecular genetics, 32(23), 3237.

Jing Q, et al. (2023) Highly Efficient A-to-G Editing in PFFs via Multiple ABEs. Genes, 14(4).

Mengiste AA, et al. (2023) Expanded MutaT7 toolkit efficiently and simultaneously accesses all possible transition mutations in bacteria. Nucleic acids research, 51(6), e31.

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.

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.

Ambrosini C, et al. (2022) Translational enhancement by base editing of the Kozak sequence rescues haploinsufficiency. Nucleic acids research, 50(18), 10756.

Rovai A, et al. (2022) In vivo adenine base editing reverts C282Y and improves iron metabolism in hemochromatosis mice. Nature communications, 13(1), 5215.

Sankar A, et al. (2022) Histone editing elucidates the functional roles of H3K27 methylation and acetylation in mammals. Nature genetics, 54(6), 754.

Zhao D, et al. (2022) Highly efficient A-to-G base editing by ABE8.17 in rabbits. Molecular therapy. Nucleic acids, 27, 1156.

Yuan Q, et al. (2022) Multiplex base- and prime-editing with drive-and-process CRISPR arrays. Nature communications, 13(1), 2771.

Mori H, et al. (2022) A framework to efficiently describe and share reproducible DNA materials and construction protocols. Nature communications, 13(1), 2894.

Lee NE, et al. (2021) One-step genotyping method in CRISPR based on short inner primer-assisted, tetra primer-paired amplifications. Molecular and cellular probes, 55, 101675.

Eggenschwiler R, et al. (2021) A selectable all-in-one CRISPR prime editing piggyBac transposon allows for highly efficient gene editing in human cell lines. Scientific reports, 11(1), 22154.