Resource Summary Report

Generated by nidm-terms on Aug 9, 2026

pCMV-PE2-P2A-GFP

RRID:Addgene_132776
Type: Plasmid

Proper Citation

RRID:Addgene_132776

Plasmid Information

URL: http://www.addgene.org/132776

Proper Citation: RRID:Addgene_132776

Insert Name: PE2-P2A-GFP

Organism: Synthetic

Bacterial Resistance: Ampicillin

Defining Citation: PMID:31634902

Vector Backbone Description: Vector Backbone:pCMV; Vector Types:Mammalian Expression; Bacterial Resistance:Ampicillin

Comments: Please note that this plasmid may run as a dimer.

Plasmid Name: pCMV-PE2-P2A-GFP

Relevant Mutation: See manuscript

Record Creation Time: 20220422T221736+0000

Record Last Update: 20260808T080804+0000

Ratings and Alerts

No rating or validation information has been found for pCMV-PE2-P2A-GFP.

No alerts have been found for pCMV-PE2-P2A-GFP.

Data and Source Information

Source: Addgene

Usage and Citation Metrics

We found 26 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Komatsu-Hirota S, et al. (2026) Phosphorylation tunes p62 condensates to drive autophagic degradation of ubiquitinated proteins. The EMBO journal, 45(12), 4061.

Takada S, et al. (2025) KEAP1 retention in phase-separated p62 bodies drives liver damage under autophagy-deficient conditions. EMBO reports, 26(13), 3384.

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.

Chen YT, et al. (2025) ATRX silences Cartpt expression in osteoblastic cells during skeletal development. The Journal of clinical investigation, 135(1).

Couly S, et al. (2024) Benzomorphan and non-benzomorphan agonists differentially alter sigma-1 receptor quaternary structure, as does types of cellular stress. Cellular and molecular life sciences : CMLS, 81(1), 14.

Van Scoyk AN, et al. (2024) Bioluminescence assay of lysine deacylase sirtuin activity. Cell chemical biology, 31(11), 2002.

Fernandez MM, et al. (2024) Engineering Oncogenic Hotspot Mutations on SF3B1 via CRISPR-Directed PRECIS Mutagenesis. Cancer research communications, 4(9), 2498.

Busquets O, et al. (2024) iSCORE-PD: an isogenic stem cell collection to research Parkinson's Disease. bioRxiv : the preprint server for biology.

Li J, et al. (2024) Modeling the atrioventricular conduction axis using human pluripotent stem cell-derived cardiac assembloids. Cell stem cell, 31(11), 1667.

Lee KE, et al. (2024) Prime editing-mediated correction of the leptin receptor in muscle cells of db/db mice. Biotechnology journal, 19(5), e2300676.

Madaan V, et al. (2024) ISGylation enhances dsRNA-induced interferon response and NF??B signaling in fallopian tube epithelial cells. The Journal of biological chemistry, 300(9), 107686.

Hasan MN, et al. (2023) Flow cytometry-based quantification of genome editing efficiency in human cell lines using the L1CAM gene. PloS one, 18(11), e0294146.

Fong JHC, et al. (2023) Parallel engineering and activity profiling of a base editor system. Cell systems, 14(5), 392.

Dirkx N, et al. (2023) Increased prime edit rates in KCNQ2 and SCN1A via single nicking all-in-one plasmids. BMC biology, 21(1), 156.

Van Scoyk AN, et al. (2023) Bioluminescence Assay of Lysine Deacylase Sirtuin Activity. bioRxiv : the preprint server for biology.

Koeppel J, et al. (2023) Prediction of prime editing insertion efficiencies using sequence features and DNA repair determinants. Nature biotechnology, 41(10), 1446.

Monda JK, et al. (2023) HAPSTR1 localizes HUWE1 to the nucleus to limit stress signaling pathways. Cell reports, 42(5), 112496.

Zhou T, et al. (2022) Lupus enhancer risk variant causes dysregulation of IRF8 through cooperative lncRNA and DNA methylation machinery. Nature communications, 13(1), 1855.

Nishiyama T, et al. (2022) Precise genomic editing of pathogenic mutations in RBM20 rescues dilated cardiomyopathy. Science translational medicine, 14(672), eade1633.

Hou Y, et al. (2022) Challenges in Gene Therapy for Somatic Reverted Mosaicism in X-Linked Combined Immunodeficiency by CRISPR/Cas9 and Prime Editing. Genes, 13(12).