Resource Summary Report

Generated by PRECISE-TBI on Aug 9, 2026

pCMV-PEmax-P2A-GFP

RRID:Addgene_180020
Type: Plasmid

Proper Citation

RRID:Addgene_180020

Plasmid Information

URL: http://www.addgene.org/180020

Proper Citation: RRID:Addgene_180020

Insert Name: PEmax-P2A-EGFP

Organism: Synthetic

Bacterial Resistance: Ampicillin

Defining Citation: PMID:34653350

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

Plasmid Name: pCMV-PEmax-P2A-GFP

Relevant Mutation: Detailed in manuscript

Record Creation Time: 20220422T222033+0000

Record Last Update: 20260808T081329+0000

Ratings and Alerts

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

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

Data and Source Information

Source: Addgene

Usage and Citation Metrics

We found 12 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Vrathasha V, et al. (2026) Variant-to-gene mapping identifies ARHGEF12 as a primary open-angle glaucoma effector gene operating within retinal ganglion cells. bioRxiv : the preprint server for biology.

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.

Yu W, et al. (2025) A single non-coding SNP in FPGS modulates folate drug efficacy in acute lymphoblastic leukemia: data-driven exploration and experimental validation. Molecular biomedicine, 6(1), 114.

Biar CG, et al. (2025) Protocol to perform multiplexed assays of variant effect using curated loci prime editing. STAR protocols, 6(2), 103851.

Liu Z, et al. (2025) Precise Correction of the Pde6b-L659P Mutation Causing Retinal Degeneration with Minimum Bystander Editing by Advanced Genome Editing Tools. Research (Washington, D.C.), 8, 0770.

Netsawang C, et al. (2025) Precise correction of G6PD Viangchan mutation in iPSCs by prime editing strategy. Scientific reports, 15(1), 30192.

Cerqua M, et al. (2025) The integrated stress response drives MET oncogene overexpression in cancers. The EMBO journal, 44(4), 1107.

Binder S, et al. (2024) Prime-Editing of human ACTB in induced pluripotent stem cells to model human ACTB Loss-of-Function diseases and compensatory mechanisms. Stem cell research, 75, 103304.

Chen X, et al. (2024) The FXR1 network acts as a signaling scaffold for actomyosin remodeling. Cell, 187(18), 5048.

Biar CG, et al. (2024) Multimodal framework to resolve variants of uncertain significance in TSC2. bioRxiv : the preprint server for biology.

Hwang HY, et al. (2024) Precise editing of pathogenic nucleotide repeat expansions in iPSCs using paired prime editor. Nucleic acids research, 52(10), 5792.

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.