Resource Summary Report

Generated by SPARC SAWG on Sep 6, 2026

pCMV_ABEmax_P2A_GFP

RRID:Addgene_112101
Type: Plasmid

Proper Citation

RRID:Addgene_112101

Plasmid Information

URL: http://www.addgene.org/112101

Proper Citation: RRID:Addgene_112101

Insert Name: ABEmax_P2A_GFP

Organism: Homo sapiens

Bacterial Resistance: Ampicillin

Defining Citation: PMID:29813047

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

Plasmid Name: pCMV_ABEmax_P2A_GFP

Record Creation Time: 20220422T221546+0000

Record Last Update: 20260905T074428+0000

Ratings and Alerts

No rating or validation information has been found for pCMV_ABEmax_P2A_GFP.

No alerts have been found for pCMV_ABEmax_P2A_GFP.

Data and Source Information

Source: Addgene

Usage and Citation Metrics

We found 44 mentions in open access literature.

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

McKenna JK, et al. (2025) The ubiquitin ligase HUWE1 enhances WNT signaling by antagonizing destruction complex-mediated ?-catenin degradation and through a mechanism independent of changes in ?-catenin abundance. PLoS genetics, 21(5), e1011677.

Fontana L, et al. (2025) Multiplex base editing of BCL11A regulatory elements to treat sickle cell disease. Cell reports. Medicine, 102376.

Chey YCJ, et al. (2025) Optimal SpCas9- and SaCas9-mediated gene editing by enhancing gRNA transcript levels through scaffold poly-T tract reduction. BMC genomics, 26(1), 138.

Vasquez CA, et al. (2025) Precision genome editing and in-cell measurements of oxidative DNA damage repair enable functional and mechanistic characterization of cancer-associated MUTYH variants. Nucleic acids research, 53(6).

Buchert R, et al. (2025) Bi-allelic KICS2 mutations impair KICSTOR complex-mediated mTORC1 regulation, causing intellectual disability and epilepsy. American journal of human genetics, 112(2), 374.

Liu J, et al. (2025) Enhanced genome editing with a Streptococcus equinus Cas9. Communications biology, 8(1), 196.

Liu Y, et al. (2025) Massively parallel interrogation of human functional variants modulating cancer immunosurveillance. Signal transduction and targeted therapy, 10(1), 88.

Kim HS, et al. (2024) Direct measurement of engineered cancer mutations and their transcriptional phenotypes in single cells. Nature biotechnology, 42(8), 1254.

Selgrade DF, et al. (2024) Susceptibility to innate immune activation in genetically mediated myocarditis. The Journal of clinical investigation, 134(13).

Takeda Y, et al. (2024) A de novo dominant-negative variant is associated with OTULIN-related autoinflammatory syndrome. The Journal of experimental medicine, 221(6).

McKenna JK, et al. (2024) The ubiquitin ligase HUWE1 enhances WNT signaling by antagonizing destruction complex-mediated ?-catenin degradation and through a mechanism independent of ?-catenin stability. bioRxiv : the preprint server for biology.

Veronese M, et al. (2024) ERLIN1/2 scaffolds bridge TMUB1 and RNF170 and restrict cholesterol esterification to regulate the secretory pathway. Life science alliance, 7(8).

Shafaei Pishabad Z, et al. (2024) The Y49H cytochrome c variant enhances megakaryocytic maturation of K-562 cells. Biochimica et biophysica acta. Molecular basis of disease, 1870(5), 167134.

Christensen CL, et al. (2024) Base editing rescues acid ?-glucosidase function in infantile-onset Pompe disease patient-derived cells. Molecular therapy. Nucleic acids, 35(2), 102220.

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

Pan Q, et al. (2024) Mapping functional elements of the DNA damage response through base editor screens. Cell reports, 43(12), 115047.

Rha AK, et al. (2024) Base editing of the GLB1 gene is therapeutic in GM1 gangliosidosis patient-derived cells. Molecular genetics and metabolism, 143(1-2), 108568.

Zhang C, et al. (2023) Prediction of base editor off-targets by deep learning. Nature communications, 14(1), 5358.

Geurts MH, et al. (2023) One-step generation of tumor models by base editor multiplexing in adult stem cell-derived organoids. Nature communications, 14(1), 4998.

Ranzau BL, et al. (2023) The Wild-Type tRNA Adenosine Deaminase Enzyme TadA Is Capable of Sequence-Specific DNA Base Editing. Chembiochem : a European journal of chemical biology, 24(16), e202200788.