

Resource Summary Report

Generated by [nidm-terms](#) on Sep 18, 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: 20260912T091518+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 [nidm-terms](#) .

McKenna JK, et al. (2025) The ubiquitin ligase HUWE1 enhances WNT signaling by antagonizing destruction complex-mediated β -catenin degradation and through a mechanism independent of changes in β -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 β -catenin degradation and through a mechanism independent of β -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 α -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.