

Resource Summary Report

Generated by [dkNET](#) on Sep 6, 2026

pCMV-T7-ABEmax(7.10)-SpG-P2A-EGFP (RTW4562)

RRID:Addgene_140002

Type: Plasmid

Proper Citation

RRID:Addgene_140002

Plasmid Information

URL: <http://www.addgene.org/140002>

Proper Citation: RRID:Addgene_140002

Insert Name: human codon optimized ABEmax(7.10) SpCas9 variant named SpG with P2A-EGFP

Organism: Synthetic

Bacterial Resistance: Ampicillin

Defining Citation: [PMID:32217751](#)

Vector Backbone Description: Backbone Marker:David Liu (Addgene Plasmid 112101); Vector Backbone:pCMV_ABEmax_P2A_GFP; Vector Types:Mammalian Expression, CRISPR, in vitro transcription; T7 promoter; Bacterial Resistance:Ampicillin

Comments: The depositing laboratory has released the equivalent ABE8e versions of this enzyme, which they have found to show much higher editing efficiency. See <https://www.addgene.org/browse/article/28228617/> for the plasmids.

Plasmid Name: pCMV-T7-ABEmax(7.10)-SpG-P2A-EGFP (RTW4562)

Relevant Mutation: nSpCas9=D10A;
SpG=D1135L/S1136W/G1218K/E1219Q/R1335Q/T1337R

Record Creation Time: 20220422T221809+0000

Record Last Update: 20260905T074850+0000

Ratings and Alerts

No rating or validation information has been found for pCMV-T7-ABEmax(7.10)-SpG-P2A-EGFP (RTW4562).

No alerts have been found for pCMV-T7-ABEmax(7.10)-SpG-P2A-EGFP (RTW4562).

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#).

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

Naiisseh B, et al. (2024) Context base editing for splice correction of IVSI-110 ??-thalassemia. *Molecular therapy. Nucleic acids*, 35(2), 102183.

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

Bao K, et al. (2024) A di-acetyl-decorated chromatin signature couples liquid condensation to suppress DNA end synapsis. *Molecular cell*.

Jin M, et al. (2024) Correction of human nonsense mutation via adenine base editing for Duchenne muscular dystrophy treatment in mouse. *Molecular therapy. Nucleic acids*, 35(2), 102165.

Wang P, et al. (2023) Correction of DMD in human iPSC-derived cardiomyocytes by base-editing-induced exon skipping. *Molecular therapy. Methods & clinical development*, 28, 40.

Chen X, et al. (2023) The FXR1 network acts as signaling scaffold for actomyosin remodeling. *bioRxiv : the preprint server for biology*.

Schene IF, et al. (2022) Mutation-specific reporter for optimization and enrichment of prime editing. *Nature communications*, 13(1), 1028.

Erwood S, et al. (2022) Saturation variant interpretation using CRISPR prime editing. *Nature biotechnology*, 40(6), 885.