# Resource Summary Report

Generated by RRID on Sep 2, 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:** 20260902T042002+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 RRID .


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.