

Resource Summary Report

Generated by [RRID](#) on Sep 2, 2026

pCAG-CBE4max-SpRY-P2A-EGFP (RTW5133)

RRID:Addgene_139999

Type: Plasmid

Proper Citation

RRID:Addgene_139999

Plasmid Information

URL: <http://www.addgene.org/139999>

Proper Citation: RRID:Addgene_139999

Insert Name: human codon optimized CBE4max SpCas9 variant named SpRY with P2A-EGFP

Organism: Synthetic

Bacterial Resistance: Ampicillin

Defining Citation: [PMID:32217751](#)

Vector Backbone Description: Backbone Marker:Ketih Joung; Vector Backbone:pRZ33 ; Vector Types:Mammalian Expression, CRISPR; Bacterial Resistance:Ampicillin

Plasmid Name: pCAG-CBE4max-SpRY-P2A-EGFP (RTW5133)

Relevant Mutation: nSpCas9=D10A;

SpRY=A61R/L1111R/D1135L/S1136W/G1218K/E1219Q/N1317R/A1322R/R1333P/R1335Q/T1337

Record Creation Time: 20220422T221809+0000

Record Last Update: 20260902T042002+0000

Ratings and Alerts

No rating or validation information has been found for pCAG-CBE4max-SpRY-P2A-EGFP (RTW5133).

No alerts have been found for pCAG-CBE4max-SpRY-P2A-EGFP (RTW5133).

Data and Source Information

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Huang Z, et al. (2026) Base editing of Artemis mutations ex vivo sheds light on gene therapy for Artemis-deficient SCID. *Advanced biotechnology*, 4(2).

Carrozzo I, et al. (2025) Functional rescue of F508del-CFTR through revertant mutations introduced by CRISPR base editing. *Molecular therapy : the journal of the American Society of Gene Therapy*, 33(3), 970.

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.

Loret C, et al. (2024) CRISPR Base Editing to Create Potential Charcot-Marie-Tooth Disease Models with High Editing Efficiency: Human Induced Pluripotent Stem Cell Harboring SH3TC2 Variants. *Biomedicines*, 12(7).

Baudrier L, et al. (2024) One-pot DTECT enables rapid and efficient capture of genetic signatures for precision genome editing and clinical diagnostics. *Cell reports methods*, 4(2), 100698.

Zhao L, et al. (2023) PAM-flexible genome editing with an engineered chimeric Cas9. *Nature communications*, 14(1), 6175.

Yuan Q, et al. (2022) Multiplex base- and prime-editing with drive-and-process CRISPR arrays. *Nature communications*, 13(1), 2771.

Rosello M, et al. (2022) Disease modeling by efficient genome editing using a near PAM-less base editor in vivo. *Nature communications*, 13(1), 3435.

Wang H, et al. (2022) LMNA Co-Regulated Gene Expression as a Suitable Readout after Precise Gene Correction. *International journal of molecular sciences*, 23(24).

Lau CH, et al. (2022) PAM-flexible dual base editor-mediated random mutagenesis and self-activation strategies to improve CRISPRa potency. *Molecular therapy. Methods & clinical development*, 26, 26.

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

Hu S, et al. (2022) Transcription factor antagonism regulates heterogeneity in embryonic stem cell states. *Molecular cell*, 82(23), 4410.

Zhao T, et al. (2021) Small-molecule compounds boost genome-editing efficiency of cytosine base editor. *Nucleic acids research*, 49(15), 8974.