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

Source: Addgene

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.

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.

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).

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.