

Resource Summary Report

Generated by [dkNET](#) on Aug 16, 2026

pLenti-FNLS-P2A-Puro

RRID:Addgene_110841

Type: Plasmid

Proper Citation

RRID:Addgene_110841

Plasmid Information

URL: <http://www.addgene.org/110841>

Proper Citation: RRID:Addgene_110841

Insert Name: BE3RA-FNLS

Organism: Synthetic

Bacterial Resistance: Ampicillin

Defining Citation: [PMID:29969439](#)

Vector Backbone Description: Backbone Size:6296; Vector Backbone:Adapted from lentiCRISPRv1; Vector Types:Lentiviral; Bacterial Resistance:Ampicillin

Plasmid Name: pLenti-FNLS-P2A-Puro

Relevant Mutation: D10A and NLS sequence at the N-terminus

Record Creation Time: 20220422T221539+0000

Record Last Update: 20260815T080144+0000

Ratings and Alerts

No rating or validation information has been found for pLenti-FNLS-P2A-Puro.

No alerts have been found for pLenti-FNLS-P2A-Puro.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Alonso S, et al. (2026) Concurrent genetic and non-genetic resistance mechanisms to KRAS inhibition in colorectal cancer. *Cancer cell*, 44(7), 1368.

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.

Zhao N, et al. (2024) Evolved cytidine and adenine base editors with high precision and minimized off-target activity by a continuous directed evolution system in mammalian cells. *Nature communications*, 15(1), 8140.

Meitinger F, et al. (2024) Control of cell proliferation by memories of mitosis. *Science (New York, N.Y.)*, 383(6690), 1441.

Prasad K, et al. (2024) Precise correction of a spectrum of β -thalassemia mutations in coding and non-coding regions by base editors. *Molecular therapy. Nucleic acids*, 35(2), 102205.

Amistadi S, et al. (2023) Functional restoration of a CFTR splicing mutation through RNA delivery of CRISPR adenine base editor. *Molecular therapy : the journal of the American Society of Gene Therapy*, 31(6), 1647.

Morris JA, et al. (2023) Discovery of target genes and pathways at GWAS loci by pooled single-cell CRISPR screens. *Science (New York, N.Y.)*, 380(6646), eadh7699.

Ghobashi AH, et al. (2023) Activation of AKT induces EZH2-mediated β -catenin trimethylation in colorectal cancer. *iScience*, 26(9), 107630.

Sánchez-Rivera FJ, et al. (2022) Base editing sensor libraries for high-throughput engineering and functional analysis of cancer-associated single nucleotide variants. *Nature biotechnology*, 40(6), 862.

Nie J, et al. (2022) CHD7 regulates otic lineage specification and hair cell differentiation in human inner ear organoids. *Nature communications*, 13(1), 7053.

Pallaseni A, et al. (2022) Predicting base editing outcomes using position-specific sequence determinants. *Nucleic acids research*, 50(6), 3551.

Cheng W, et al. (2022) Parallel functional assessment of m6A sites in human endodermal differentiation with base editor screens. *Nature communications*, 13(1), 478.

Ravi NS, et al. (2022) Identification of novel HPFH-like mutations by CRISPR base editing that elevate the expression of fetal hemoglobin. *eLife*, 11.

Berríos KN, et al. (2021) Controllable genome editing with split-engineered base editors. *Nature chemical biology*, 17(12), 1262.

Billon P, et al. (2020) Detection of Marker-Free Precision Genome Editing and Genetic Variation through the Capture of Genomic Signatures. *Cell reports*, 30(10), 3280.

Zuo E, et al. (2020) A rationally engineered cytosine base editor retains high on-target activity while reducing both DNA and RNA off-target effects. *Nature methods*, 17(6), 600.

Erwood S, et al. (2019) Modeling Niemann-Pick disease type C in a human haploid cell line allows for patient variant characterization and clinical interpretation. *Genome research*, 29(12), 2010.