Resource Summary Report

Generated by dkNET on Aug 1, 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: 20260801T075928+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 16 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET .

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.

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

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

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 ?-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.

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

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

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.