Resource Summary Report

Generated by NIF on Sep 10, 2026

phU6-gRNA

RRID:Addgene_53188
Type: Plasmid

Proper Citation

RRID:Addgene_53188

Plasmid Information

URL: http://www.addgene.org/53188

Proper Citation: RRID:Addgene_53188

Bacterial Resistance: Kanamycin

Defining Citation: PMID:25122746

Vector Backbone Description: Backbone Size:3515; Vector Backbone:pzDonor; Vector Types:Mammalian Expression, CRISPR; Bacterial Resistance:Kanamycin

Plasmid Name: phU6-gRNA

Record Creation Time: 20220422T222312+0000

Record Last Update: 20260905T075758+0000

Ratings and Alerts

No rating or validation information has been found for phU6-gRNA.

No alerts have been found for phU6-gRNA.

Data and Source Information

Source: Addgene

Usage and Citation Metrics

We found 49 mentions in open access literature.

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

Mirizio G, et al. (2026) Combinatorial pioneer transcription factor binding reinforces bivalent epigenetic states to preserve lineage fidelity. bioRxiv : the preprint server for biology.

Matsui S, et al. (2026) MAPK/ERK signaling regulates H3K9me3 heterochromatin reorganization to confer mesendoderm developmental competence. Nucleic acids research, 54(12).

Stankevi?ius V, et al. (2026) Catalytic footprints of DNMT1 dynamics during mammalian cell state transitions. Cell reports, 45(6), 117435.

Venhuizen AJ, et al. (2026) Hepatocellular carcinoma-linked AXIN1 mutations drive low Wnt/?-catenin activity enabling niche-independent growth and YAP/TAZ signaling. iScience, 29(1), 114501.

Yu H, et al. (2025) H3K4me3 amplifies transcription at intergenic active regulatory elements. Genes & development, 39(21-22), 1290.

El Bouazzaoui L, et al. (2025) BRAFV600E augments WNT signaling in colorectal cancer via aberrant DNA methylation. iScience, 28(7), 112708.

Gong JN, et al. (2025) Re-appraising assays on permeabilized blood cancer cells testing venetoclax or other BH3 mimetic agents selectively targeting pro-survival BCL2 proteins. Cell death and differentiation, 32(8), 1382.

Valcárcel G, et al. (2025) Modulating immune cell fate and inflammation through CRISPR-mediated DNA methylation editing. Science advances, 11(29), eadt1644.

El Bouazzaoui L, et al. (2025) BRAFV600E maintains the CpG island methylator phenotype, and DNA methylation of PRC2 targets genes in colon cancer. iScience, 28(7), 112905.

Nelson HM, et al. (2024) Transfer of miR-100 and miR-125b increases 3D growth and invasiveness in recipient cancer cells. Extracellular vesicles and circulating nucleic acids, 5(3), 397.

Ma Y, et al. (2024) Exchange of subtelomeric regions between chromosomes 4q and 10q reverts the FSHD genotype and phenotype. Science advances, 10(18), eadl1922.

Matsui S, et al. (2024) Pioneer and PRDM transcription factors coordinate bivalent epigenetic states to safeguard cell fate. Molecular cell, 84(3), 476.

Matsui S, et al. (2024) Protocol for establishing inducible CRISPR interference system for multiple-gene silencing in human pluripotent stem cells. STAR protocols, 5(3), 103221.

Huang S, et al. (2024) Extended replicative lifespan of primary resting T cells by CRISPR/dCas9-based epigenetic modifiers and transcriptional activators. Cellular and molecular life sciences : CMLS, 81(1), 407.

Cai H, et al. (2024) CRISPR/Cas9 model of prostate cancer identifies Kmt2c deficiency as a metastatic driver by Odam/Cabs1 gene cluster expression. Nature communications,

15(1), 2088.

Sifri C, et al. (2023) An AlphaFold2 map of the 53BP1 pathway identifies a direct SHLD3-RIF1 interaction critical for shieldin activity. EMBO reports, 24(8), e56834.

Canoy RJ, et al. (2023) Easy and robust electrotransfection protocol for efficient ectopic gene expression and genome editing in human B cells. Gene therapy, 30(1-2), 167.

Morimoto M, et al. (2023) Bi-allelic ATG4D variants are associated with a neurodevelopmental disorder characterized by speech and motor impairment. NPJ genomic medicine, 8(1), 4.

Loftus D, et al. (2023) Allelic chromatin structure primes imprinted expression of Kcnk9 during neurogenesis. bioRxiv : the preprint server for biology.

Grosch M, et al. (2023) Striated muscle-specific base editing enables correction of mutations causing dilated cardiomyopathy. Nature communications, 14(1), 3714.