

Resource Summary Report

Generated by [NIF](#) on Sep 17, 2026

CROP-seq-opti

RRID:Addgene_106280

Type: Plasmid

Proper Citation

RRID:Addgene_106280

Plasmid Information

URL: <http://www.addgene.org/106280>

Proper Citation: RRID:Addgene_106280

Insert Name: EF1a-Puro-WPRE-hU6-gRNA

Organism: Synthetic

Bacterial Resistance: Ampicillin

Defining Citation: [PMID:29457792](#)

Vector Backbone Description: Backbone Marker:Feng Zhang Lab; Vector Backbone:lentiGuide-puro; Vector Types:Mammalian Expression, Lentiviral, CRISPR; Bacterial Resistance:Ampicillin

Plasmid Name: CROP-seq-opti

Record Creation Time: 20220422T221516+0000

Record Last Update: 20260912T091424+0000

Ratings and Alerts

No rating or validation information has been found for CROP-seq-opti.

No alerts have been found for CROP-seq-opti.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 27 mentions in open access literature.

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

Shi L, et al. (2026) Mapping kinase-dependent tumor immune adaptation with multiplexed single-cell CRISPR screens. *bioRxiv : the preprint server for biology*.

Porter DF, et al. (2025) Disease-linked regulatory DNA variants and homeostatic transcription factors in epidermis. *Nature communications*, 16(1), 8387.

Ho CH, et al. (2025) Genetic and epigenetic screens in primary human T cells link candidate causal autoimmune variants to T cell networks. *Nature genetics*, 57(10), 2536.

Zhao K, et al. (2025) Endogenous fine-mapping and prioritization of functional regulatory elements in complex genetic loci. *Cell genomics*, 100982.

Kaushik K, et al. (2025) Requirements for the neurodevelopmental disorder-associated gene ZNF292 in human cortical interneuron development and function. *Cell reports*, 44(5), 115597.

Vartiainen E, et al. (2025) Astrocytic-supplied cholesterol drives synaptic gene expression programs in developing neurons and downstream astrocytic transcriptional programs. *bioRxiv : the preprint server for biology*.

Liu M, et al. (2025) Genome-coverage single-cell histone modifications for embryo lineage tracing. *Nature*, 640(8059), 828.

Xu Z, et al. (2024) Dissecting key regulators of transcriptome kinetics through scalable single-cell RNA profiling of pooled CRISPR screens. *Nature biotechnology*, 42(8), 1218.

Karbassi E, et al. (2024) Targeted CRISPR activation is functional in engineered human pluripotent stem cells but undergoes silencing after differentiation into cardiomyocytes and endothelium. *Cellular and molecular life sciences : CMLS*, 81(1), 95.

Edenhofer FC, et al. (2024) Generation and characterization of inducible KRAB-dCas9 iPSCs from primates for cross-species CRISPRi. *iScience*, 27(6), 110090.

Tegtmeyer M, et al. (2024) High-dimensional phenotyping to define the genetic basis of cellular morphology. *Nature communications*, 15(1), 347.

Zhang L, et al. (2024) Genome Engineering of Primary and Pluripotent Stem Cell-Derived Hepatocytes for Modeling Liver Tumor Formation. *Biology*, 13(9).

Chapman G, et al. (2024) Defining cis-regulatory elements and transcription factors that control human cortical interneuron development. *iScience*, 27(6), 109967.

Schnitzler GR, et al. (2024) Convergence of coronary artery disease genes onto endothelial cell programs. *Nature*, 626(8000), 799.

McFaline-Figueroa JL, et al. (2024) Multiplex single-cell chemical genomics reveals the kinase dependence of the response to targeted therapy. *Cell genomics*, 4(2), 100487.

McFaline-Figueroa JL, et al. (2023) Multiplex single-cell chemical genomics reveals the kinase dependence of the response to targeted therapy. *bioRxiv : the preprint server for biology*.

Yang X, et al. (2023) Functional characterization of Alzheimer's disease genetic variants in microglia. *Nature genetics*, 55(10), 1735.

Alborzinia H, et al. (2023) LRP8-mediated selenocysteine uptake is a targetable vulnerability in MYCN-amplified neuroblastoma. *EMBO molecular medicine*, 15(8), e18014.

Yao D, et al. (2023) Compressed Perturb-seq: highly efficient screens for regulatory circuits using random composite perturbations. *bioRxiv : the preprint server for biology*.

Bielczyk-Maczynska E, et al. (2023) A single-cell CRISPRi platform for characterizing candidate genes relevant to metabolic disorders in human adipocytes. *American journal of physiology. Cell physiology*, 325(3), C648.