

Resource Summary Report

Generated by [RRID](#) on Aug 23, 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: 20260815T080100+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 [RRID](#) .

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.

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

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.

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.

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

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

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.