# 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.

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.