Resource Summary Report

Generated by RRID on Sep 3, 2026

Human CRISPRa sgRNA library Calabrese in backbone XPR_502 (P65 HSF), Set A

RRID:Addgene_92379
Type: Plasmid

Proper Citation

RRID:Addgene_92379

Plasmid Information

URL: http://www.addgene.org/92379

Proper Citation: RRID:Addgene_92379

Bacterial Resistance: Ampicillin

Defining Citation: PMID:30575746

Vector Backbone Description: Vector Backbone:XPR_502; Vector Types:Lentiviral; Bacterial Resistance:Ampicillin

Plasmid Name: Human CRISPRa sgRNA library Calabrese in backbone XPR_502 (P65 HSF), Set A

Record Creation Time: 20220422T222625+0000

Record Last Update: 20260902T050528+0000

Ratings and Alerts

No rating or validation information has been found for Human CRISPRa sgRNA library Calabrese in backbone XPR_502 (P65 HSF), Set A.

No alerts have been found for Human CRISPRa sgRNA library Calabrese in backbone XPR_502 (P65 HSF), Set A.

Data and Source Information

Source: Addgene

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Rathore U, et al. (2026) Systematic discovery of pro- and anti-HIV host factors in primary human CD4+ T cells. Cell, 189(12), 3651.

Moura F, et al. (2026) Enhancing gene therapy vectors manufacturing: CEBPA as a master regulator of rAAV biogenesis. Journal of biological engineering, 20(1), 24.

Ma X, et al. (2025) Soluble MFGE8 mediates cell entry of Crimean-Congo hemorrhagic fever virus. mBio, 16(10), e0161725.

Liang Z, et al. (2025) Cytotoxicity of activator expression in CRISPR-based transcriptional activation systems. Nature communications, 16(1), 8071.

Würth R, et al. (2025) Circulating tumor cell plasticity determines breast cancer therapy resistance via neuregulin 1-HER3 signaling. Nature cancer, 6(1), 67.

Allen TP, et al. (2025) dFLASH; dual FLuorescent transcription factor activity sensor for histone integrated live-cell reporting and high-content screening. Nature communications, 16(1), 3298.

Ramberger E, et al. (2024) The proteogenomic landscape of multiple myeloma reveals insights into disease biology and therapeutic opportunities. Nature cancer, 5(8), 1267.

Maddineni A, et al. (2024) Cytotoxicity of Activator Expression in CRISPR-based Transcriptional Activation Systems. bioRxiv : the preprint server for biology.

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

Loo L, et al. (2023) Fibroblast-expressed LRRC15 is a receptor for SARS-CoV-2 spike and controls antiviral and antifibrotic transcriptional programs. PLoS biology, 21(2), e3001967.

Liang D, et al. (2023) Ferroptosis surveillance independent of GPX4 and differentially regulated by sex hormones. Cell, 186(13), 2748.

Trimarco JD, et al. (2022) Cellular glycan modification by B3GAT1 broadly restricts influenza virus infection. Nature communications, 13(1), 6456.

Schmidt R, et al. (2022) CRISPR activation and interference screens decode stimulation responses in primary human T cells. Science (New York, N.Y.), 375(6580), eabj4008.

Biering SB, et al. (2022) Genome-wide bidirectional CRISPR screens identify mucins as host factors modulating SARS-CoV-2 infection. Nature genetics, 54(8), 1078.

Fujihara KM, et al. (2022) Eprenetapopt triggers ferroptosis, inhibits NFS1 cysteine desulfurase, and synergizes with serine and glycine dietary restriction. Science advances, 8(37), eabm9427.

Zhu X, et al. (2022) ZBTB7A promotes virus-host homeostasis during human coronavirus 229E infection. Cell reports, 41(4), 111540.

Clements KE, et al. (2020) Identification of regulators of poly-ADP-ribose polymerase inhibitor response through complementary CRISPR knockout and activation screens. Nature communications, 11(1), 6118.

Schleicher EM, et al. (2020) Dual genome-wide CRISPR knockout and CRISPR activation screens identify mechanisms that regulate the resistance to multiple ATR inhibitors. PLoS genetics, 16(11), e1009176.