

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.

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.

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.

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.