

Resource Summary Report

Generated by [NIF](#) on Aug 4, 2026

pHRdSV40-scFv-GCN4-sfGFP-VP64-GB1-NLS

RRID:Addgene_60904

Type: Plasmid

Proper Citation

RRID:Addgene_60904

Plasmid Information

URL: <http://www.addgene.org/60904>

Proper Citation: RRID:Addgene_60904

Insert Name: scFv-GCN4

Bacterial Resistance: Ampicillin

Defining Citation: [PMID:25307933](#)

Vector Backbone Description: Vector Backbone:pHR; Vector Types:Mammalian Expression, Lentiviral; Bacterial Resistance:Ampicillin

Comments: For more information, visit <https://valelab4.ucsf.edu/external/research/suntag.html> Note this plasmid was used with the CRISPRa library, as described in Gilbert et al. Cell 2014 PubMed ID: 25307932.

Plasmid Name: pHRdSV40-scFv-GCN4-sfGFP-VP64-GB1-NLS

Record Creation Time: 20220422T222350+0000

Record Last Update: 20260801T081548+0000

Ratings and Alerts

No rating or validation information has been found for pHRdSV40-scFv-GCN4-sfGFP-VP64-GB1-NLS.

No alerts have been found for pHRdSV40-scFv-GCN4-sfGFP-VP64-GB1-NLS.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 57 mentions in open access literature.

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

Xiao N, et al. (2025) Type A cholesterol-dependent cytolysins translocate to the trans-Golgi network for NLRP3 inflammasome activation. *Nature immunology*, 26(10), 1673.

Liu J, et al. (2025) SunTag-PE: a modular prime editing system enables versatile and efficient genome editing. *Communications biology*, 8(1), 452.

Zhao T, et al. (2025) Derepressing nuclear pyruvate dehydrogenase induces therapeutic cancer cell reprogramming. *Cell metabolism*, 37(8), 1667.

Liu J, et al. (2024) Involvement of ribosomal protein L17 and Y-box binding protein 1 in the assembly of hepatitis C virus potentially via their interaction with the 3' untranslated region of the viral genome. *Journal of virology*, 98(7), e0052224.

Mu S, et al. (2024) Enhancing prime editor flexibility with coiled-coil heterodimers. *Genome biology*, 25(1), 108.

Arriaga JM, et al. (2024) In vivo genome-wide CRISPR screening identifies CITED2 as a driver of prostate cancer bone metastasis. *Oncogene*, 43(17), 1303.

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.

Conger KO, et al. (2024) ASCT2 is a major contributor to serine uptake in cancer cells. *Cell reports*, 43(8), 114552.

Jung P, et al. (2023) CRISPR Activation/Interference Screen to Identify Genetic Networks in HDAC-Inhibitor-Resistant Cells. *Methods in molecular biology (Clifton, N.J.)*, 2589, 429.

Peng H, et al. (2023) Epigenome-wide association study identifies novel genes associated with ischemic stroke. *Clinical epigenetics*, 15(1), 106.

Conger KO, et al. (2023) ASCT2 is the primary serine transporter in cancer cells. *bioRxiv : the preprint server for biology*.

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*.

Liu X, et al. (2023) IMPDH inhibition activates TLR-VCAM1 pathway and suppresses the development of MLL-fusion leukemia. *EMBO molecular medicine*, 15(1), e15631.

Yabushita T, et al. (2023) Mitotic perturbation is a key mechanism of action of decitabine in myeloid tumor treatment. *Cell reports*, 42(9), 113098.

Liu X, et al. (2022) G-quadruplex-guided RNA engineering to modulate CRISPR-based genomic regulation. *Nucleic acids research*, 50(19), 11387.

Danziger O, et al. (2022) Inducible CRISPR activation screen for interferon-stimulated genes identifies OAS1 as a SARS-CoV-2 restriction factor. *PLoS pathogens*, 18(4), e1010464.

Wood RK, et al. (2022) Secretory defects in pediatric osteosarcoma result from downregulation of selective COPII coatomer proteins. *iScience*, 25(4), 104100.

Manj??n AG, et al. (2022) Unexpected gene activation following CRISPR-Cas9-mediated genome editing. *EMBO reports*, 23(2), e53902.

Wang K, et al. (2022) Systematic comparison of CRISPR-based transcriptional activators uncovers gene-regulatory features of enhancer-promoter interactions. *Nucleic acids research*, 50(14), 7842.

Tang WWC, et al. (2022) Sequential enhancer state remodelling defines human germline competence and specification. *Nature cell biology*, 24(4), 448.