

Resource Summary Report

Generated by [RRID](#) on Aug 27, 2026

[pCAG-scFvGCN4sfGFPTET1CD](#)

RRID:Addgene_82561

Type: Plasmid

Proper Citation

RRID:Addgene_82561

Plasmid Information

URL: <http://www.addgene.org/82561>

Proper Citation: RRID:Addgene_82561

Insert Name: scFvGCN4sfGFPTET1CD

Bacterial Resistance: Kanamycin

Defining Citation: [PMID:27571369](#)

Vector Backbone Description: Vector Backbone:pCAG; Vector Types:Mammalian Expression; Bacterial Resistance:Kanamycin

Plasmid Name: pCAG-scFvGCN4sfGFPTET1CD

Record Creation Time: 20220422T222535+0000

Record Last Update: 20260815T082057+0000

Ratings and Alerts

No rating or validation information has been found for pCAG-scFvGCN4sfGFPTET1CD.

No alerts have been found for pCAG-scFvGCN4sfGFPTET1CD.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Susa T, et al. (2026) Androgen Signaling Represses Homeobox C9, an Inhibitor of Androgen Receptor, in Prostate Cancer Cells. *International journal of molecular sciences*, 27(4).

Albrecht C, et al. (2024) Locus-Specific and Stable DNA Demethylation at the H19/IGF2 ICR1 by Epigenome Editing Using a dCas9-SunTag System and the Catalytic Domain of TET1. *Genes*, 15(1).

Kojima S, et al. (2022) Epigenome editing reveals core DNA methylation for imprinting control in the Dlk1-Dio3 imprinted domain. *Nucleic acids research*, 50(9), 5080.

Singh K, et al. (2022) Genome-wide DNA hypermethylation opposes healing in patients with chronic wounds by impairing epithelial-mesenchymal transition. *The Journal of clinical investigation*, 132(17).

Kobayashi N, et al. (2022) The microRNA cluster C19MC confers differentiation potential into trophoblast lineages upon human pluripotent stem cells. *Nature communications*, 13(1), 3071.

Taghbalout A, et al. (2022) TALE.Sense: A Versatile DNA Sensor Platform for Live Mammalian Cells. *ACS synthetic biology*, 11(1), 116.

Chan WF, et al. (2022) Activation of stably silenced genes by recruitment of a synthetic de-methylating module. *Nature communications*, 13(1), 5582.

Horii T, et al. (2020) Successful generation of epigenetic disease model mice by targeted demethylation of the epigenome. *Genome biology*, 21(1), 77.

Le Berre G, et al. (2019) Repression of TERRA Expression by Subtelomeric DNA Methylation Is Dependent on NRF1 Binding. *International journal of molecular sciences*, 20(11).

Taghbalout A, et al. (2019) Enhanced CRISPR-based DNA demethylation by Casilio-ME-mediated RNA-guided coupling of methylcytosine oxidation and DNA repair pathways. *Nature communications*, 10(1), 4296.

Morita S, et al. (2018) Editing of DNA Methylation Using dCas9-Peptide Repeat and scFv-TET1 Catalytic Domain Fusions. *Methods in molecular biology (Clifton, N.J.)*, 1767, 419.

Tong Y, et al. (2018) MICMIC: identification of DNA methylation of distal regulatory regions with causal effects on tumorigenesis. *Genome biology*, 19(1), 73.

Marx N, et al. (2018) CRISPR-Based Targeted Epigenetic Editing Enables Gene Expression Modulation of the Silenced Beta-Galactoside Alpha-2,6-Sialyltransferase 1 in CHO Cells. *Biotechnology journal*, 13(10), e1700217.

Ji L, et al. (2018) TET-mediated epimutagenesis of the Arabidopsis thaliana methylome. *Nature communications*, 9(1), 895.