Resource Summary Report

Generated by RRID on Aug 19, 2026

3xFLAG-dCas9/pCMV-7.1

RRID:Addgene_47948
Type: Plasmid

Proper Citation

RRID:Addgene_47948

Plasmid Information

URL: http://www.addgene.org/47948

Proper Citation: RRID:Addgene_47948

Insert Name: 3xFLAG-dCas9

Bacterial Resistance: Ampicillin

Defining Citation: PMID:23942116

Vector Backbone Description: Backbone Marker:Sigma-Aldrich; Backbone Size:4636; Vector Backbone:pCMV-7.1; Vector Types:Mammalian Expression, CRISPR; Bacterial Resistance:Ampicillin

Comments: This plasmid can be used to isolate specific genomic regions of interest using a catalytically inactive Cas9 fused with a tag(s). Purify: locus-specific chromatin immunoprecipitation (enChIP) This system is compatible with gRNA_cloning_vector (www.addgene.org/41824) from the Church lab. Additional information and protocols can be found at: http://www.med.hirosaki-u.ac.jp/~bgb/iChIP_protocols/index_e.html

Plasmid Name: 3xFLAG-dCas9/pCMV-7.1

Relevant Mutation: human codon-optimized, D10A + H840A (catalytically inactive)

Record Creation Time: 20220422T222246+0000

Record Last Update: 20260815T081546+0000

Ratings and Alerts

No rating or validation information has been found for 3xFLAG-dCas9/pCMV-7.1.

No alerts have been found for 3xFLAG-dCas9/pCMV-7.1.

Data and Source Information

Source: Addgene

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Teague AG, et al. (2023) A polycistronic transgene design for combinatorial genetic perturbations from a single transcript in Drosophila. PLoS genetics, 19(6), e1010792.

Kwak Y, et al. (2022) Dynamic and widespread control of poly(A) tail length during macrophage activation. RNA (New York, N.Y.), 28(7), 947.

Siadous FA, et al. (2021) Coxiella effector protein CvpF subverts RAB26-dependent autophagy to promote vacuole biogenesis and virulence. Autophagy, 17(3), 706.

Li K, et al. (2020) Interrogation of enhancer function by enhancer-targeting CRISPR epigenetic editing. Nature communications, 11(1), 485.

Huang Y, et al. (2020) Mass spectrometry-based proteomic capture of proteins bound to the MACC1 promoter in colon cancer. Clinical & experimental metastasis, 37(4), 477.

Gonz??lez-Rico FJ, et al. (2020) Alu retrotransposons modulate Nanog expression through dynamic changes in regional chromatin conformation via aryl hydrocarbon receptor. Epigenetics & chromatin, 13(1), 15.

Sher F, et al. (2019) Rational targeting of a NuRD subcomplex guided by comprehensive in situ mutagenesis. Nature genetics, 51(7), 1149.

Hamidian A, et al. (2018) Promoter-associated proteins of EPAS1 identified by enChIP-MS - A putative role of HDX as a negative regulator. Biochemical and biophysical research communications, 499(2), 291.

Fujita T, et al. (2018) enChIP systems using different CRISPR orthologues and epitope tags. BMC research notes, 11(1), 154.

Zuin J, et al. (2017) Regulation of the cohesin-loading factor NIPBL: Role of the lncRNA NIPBL-AS1 and identification of a distal enhancer element. PLoS genetics, 13(12), e1007137.

Fujii H, et al. (2015) Isolation of Specific Genomic Regions and Identification of Their Associated Molecules by Engineered DNA-Binding Molecule-Mediated Chromatin Immunoprecipitation (enChIP) Using the CRISPR System and TAL Proteins. International journal of molecular sciences, 16(9), 21802.

Fujita T, et al. (2015) Isolation of specific genomic regions and identification of associated molecules by engineered DNA-binding molecule-mediated chromatin immunoprecipitation (enChIP) using CRISPR. Methods in molecular biology (Clifton, N.J.), 1288, 43.