

Resource Summary Report

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pdCas9-DNMT3A-EGFP

RRID:Addgene_71666

Type: Plasmid

Proper Citation

RRID:Addgene_71666

Plasmid Information

URL: <http://www.addgene.org/71666>

Proper Citation: RRID:Addgene_71666

Insert Name: S. pyogenes dCas9 fused with the catalytic domain of human DNMT3A (amino acids P602-V912) and T2A-EGFP

Organism: Homo sapiens

Bacterial Resistance: Ampicillin

Defining Citation: [PMID:26969735](#)

Vector Backbone Description: Backbone Size:4246; Vector Backbone:PX462; Vector Types:Mammalian Expression, CRISPR; Bacterial Resistance:Ampicillin

Comments: The catalytic domain of human DNMT3A (amino acids P602-V912) was derived from the plasmid pcDNA3/Myc-DNMT3A (Addgene, plasmid #35521) (Chen et al., 2005, J Cell Biochem 95: 902-917). Undesired BbsI restriction site was removed by site-directed mutagenesis, without affecting the amino acid sequence. Plasmid pSpCas9n(BB)-2A-Puro (PX462) (Addgene, plasmid #48141) (Ran et al., 2013, Nat Protoc 8: 2281-2308) was used as a backbone. Additional H840A mutation was introduced into Cas9n D10A nickase. T2A-PuroR EcoRI fragment was replaced with T2A-EGFP fragment from pSpCas9n(BB)-2A-GFP (PX461) (Addgene, plasmid #48140) (Ran et al., 2013, Nat Protoc 8: 2281-2308).

Plasmid Name: pdCas9-DNMT3A-EGFP

Relevant Mutation: D10A and H840A in S.pyogenes Cas9

Record Creation Time: 20220422T222441+0000

Record Last Update: 20260829T080945+0000

Ratings and Alerts

No rating or validation information has been found for pdCas9-DNMT3A-EGFP.

No alerts have been found for pdCas9-DNMT3A-EGFP.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 28 mentions in open access literature.

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

Brown ME, et al. (2025) Pancreatic islet β -cell subtypes are derived from biochemically-distinct and nutritionally-regulated islet progenitors. *Nature communications*, 16(1), 5758.

Brane A, et al. (2025) p21 Promoter Methylation Is Vital for the Anticancer Activity of Withaferin A. *International journal of molecular sciences*, 26(3).

Hosseininia Z, et al. (2025) PRAME-AS lncRNA, regulated by MZF1, modulates PRAME expression and cell stemness. *PloS one*, 20(9), e0331190.

Regan SB, et al. (2025) Megabase-scale loss of heterozygosity provoked by CRISPR-Cas9 DNA double-strand breaks. *Molecular cell*, 85(22), 4119.

Gu G, et al. (2024) Endocrine islet β -cell subtypes with differential function are derived from biochemically distinct embryonic endocrine islet progenitors that are regulated by maternal nutrients. *Research square*.

Han SH, et al. (2024) VIM-AS1, which is regulated by CpG methylation, cooperates with IGF2BP1 to inhibit tumor aggressiveness via EPHA3 degradation in hepatocellular carcinoma. *Experimental & molecular medicine*, 56(12), 2617.

Zhang C, et al. (2024) The dCas9-based genome editing in *Plasmodium yoelii*. *mSphere*, 9(3), e0009524.

Roberts JB, et al. (2024) Specific isoforms of the ubiquitin ligase gene WWP2 are targets of osteoarthritis genetic risk via a differentially methylated DNA sequence. *Arthritis research & therapy*, 26(1), 78.

Rahman MM, et al. (2024) dCas9-HDAC8-EGFP fusion enables epigenetic editing of breast cancer cells by H3K9 deacetylation. *European journal of cell biology*, 103(4), 151463.

Kehayova YS, et al. (2023) Mediation of the Same Epigenetic and Transcriptional Effect by Independent Osteoarthritis Risk-Confering Alleles on a Shared Target Gene, COLGALT2. *Arthritis & rheumatology (Hoboken, N.J.)*, 75(6), 910.

- Alvizi L, et al. (2023) Neural crest E-cadherin loss drives cleft lip/palate by epigenetic modulation via pro-inflammatory gene-environment interaction. *Nature communications*, 14(1), 2868.
- 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).
- Yu H, et al. (2022) Dynamic reprogramming of H3K9me3 at hominoid-specific retrotransposons during human preimplantation development. *Cell stem cell*, 29(7), 1031.
- Koike Y, et al. (2021) Age-related demethylation of the TDP-43 autoregulatory region in the human motor cortex. *Communications biology*, 4(1), 1107.
- Li M, et al. (2021) Regulation of MYB by distal enhancer elements in human myeloid leukemia. *Cell death & disease*, 12(2), 223.
- Kehayova YS, et al. (2021) Genetic and Epigenetic Interplay Within a COLGALT2 Enhancer Associated With Osteoarthritis. *Arthritis & rheumatology (Hoboken, N.J.)*, 73(10), 1856.
- Vizoso M, et al. (2021) Diverse transcriptional regulation and functional effects revealed by CRISPR/Cas9-directed epigenetic editing. *Oncotarget*, 12(17), 1651.
- Dahlet T, et al. (2020) Genome-wide analysis in the mouse embryo reveals the importance of DNA methylation for transcription integrity. *Nature communications*, 11(1), 3153.
- Deng M, et al. (2020) Locus-Specific Regulation of Xist Expression Using the CRISPR-Cas9-Based System. *DNA and cell biology*, 39(4), 572.
- Liu J, et al. (2019) Neurog3-Independent Methylation Is the Earliest Detectable Mark Distinguishing Pancreatic Progenitor Identity. *Developmental cell*, 48(1), 49.