

Resource Summary Report

Generated by [dkNET](#) on Jul 30, 2026

gRNA_Cloning Vector

RRID:Addgene_41824

Type: Plasmid

Proper Citation

RRID:Addgene_41824

Plasmid Information

URL: <http://www.addgene.org/41824>

Proper Citation: RRID:Addgene_41824

Bacterial Resistance: Kanamycin

Defining Citation: [PMID:23287722](#)

Vector Backbone Description: Backbone Marker:Invitrogen; Vector Backbone:pCR-Blunt II-TOPO; Vector Types:Mammalian Expression, CRISPR; Bacterial Resistance:Kanamycin

Plasmid Name: gRNA_Cloning Vector

Record Creation Time: 20220422T222216+0000

Record Last Update: 20260725T074655+0000

Ratings and Alerts

No rating or validation information has been found for gRNA_Cloning Vector.

No alerts have been found for gRNA_Cloning Vector.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 370 mentions in open access literature.

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

Tobias IC, et al. (2025) A Sox2 enhancer cluster regulates region-specific neural fates from mouse embryonic stem cells. *G3* (Bethesda, Md.), 15(4).

El Boujnouni N, et al. (2025) Repeat length as a key determinant for disease severity and antisense oligonucleotide activity in myotonic dystrophy type 1. *Molecular therapy. Methods & clinical development*, 33(3), 101502.

Nakamura J, et al. (2025) Development of programmable RNA imaging with RNA-guided GFP via click chemistry. *Nucleic acids research*, 53(20).

Ogawa Y, et al. (2025) GATA4 binding to the Sox9 enhancer mXYSRa/Enh13 is critical for testis differentiation in mouse. *Communications biology*, 8(1), 81.

Pulgarin DV, et al. (2025) Light-induced expression of gRNA allows for optogenetic gene editing of T lymphocytes in vivo. *Nucleic acids research*, 53(6).

Mladenov E, et al. (2025) CRISPR/Cas9 generated DSB clusters mimic complex lesions induced by high-LET radiation and shift repair from c-NHEJ to mutagenic repair pathways. *Scientific reports*, 15(1), 36480.

Dunn J, et al. (2025) Transcription Factor-Wide Association Studies to Identify Functional SNPs in Alzheimer's Disease. *The Journal of neuroscience : the official journal of the Society for Neuroscience*, 45(2).

Hirose J, et al. (2025) Targeted in vivo gene integration of a secretion-enabled GLP-1 receptor agonist reverses diet-induced non-genetic obesity and pre-diabetes. *Communications medicine*, 5(1), 269.

Chou PC, et al. (2025) Phase separation of TTBK2 and CEP164 is necessary for ciliogenesis. *Cell reports*, 44(6), 115810.

Azeroglu B, et al. (2025) Conserved and unique features of terminal telomeric sequences in ALT-positive cancer cells. *eLife*, 14.

Tsukamura A, et al. (2025) KNTC1 introduces segmental heterogeneity to mitochondria. *Disease models & mechanisms*, 18(3).

Yamada H, et al. (2025) Dual-directional epi-genotoxicity assay for assessing chemically induced epigenetic effects utilizing the housekeeping TK gene. *Scientific reports*, 15(1), 7780.

Dias M, et al. (2025) Beyond Trypanosoma cruzi: LINE-1 Activation as a Driver of Chronic Inflammation in Chagas Disease. *International journal of molecular sciences*, 26(10).

Natsumoto B, et al. (2025) Identification of Potential Therapeutic Agents for Type I Interferonopathy Using iPSC-Based Disease Modeling. *Journal of clinical immunology*, 45(1), 140.

Hara S, et al. (2025) Identification of maternal allele sequences of IG-DMR that are essential for neonatal viability. *PloS one*, 20(5), e0324882.

Lueg GA, et al. (2025) MYC deregulation sensitizes cancer cells to N-myristoyltransferase inhibition. *Cell reports*, 44(9), 116180.

Shock LS, et al. (2025) Cytosine methylase and hydroxymethylase activity in mammalian mitochondria. *Frontiers in cell and developmental biology*, 13, 1677402.

Zhang YL, et al. (2025) Loop engineering of AtCas9 for effective and broad genome editing. *Cell insight*, 4(6), 100286.

Zhang Z, et al. (2024) Fluorogenic CRISPR for genomic DNA imaging. *Nature communications*, 15(1), 934.

Weischedel J, et al. (2024) Modular cytosine base editing promotes epigenomic and genomic modifications. *Nucleic acids research*, 52(2), e8.