Resource Summary Report

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pLKO.1-puro U6 sgRNA BfuAI large stuffer

RRID:Addgene_52628
Type: Plasmid

Proper Citation

RRID:Addgene_52628

Plasmid Information

URL: http://www.addgene.org/52628

Proper Citation: RRID:Addgene_52628

Insert Name: Kanamycin cassette

Organism: Bacterial origin

Bacterial Resistance: Ampicillin and Kanamycin

Vector Backbone Description: Backbone Size:7145; Vector Backbone:pLKO.1; Vector Types:Mammalian Expression, Lentiviral, CRISPR; Bacterial Resistance:Ampicillin and Kanamycin

Comments: This is a second generation plasmid that increases the efficiency of sgRNA guide cloning over the original "pLKO.1-puro U6 sgRNA BspMI stuffer" vector. "pLKO.1-puro U6 sgRNA BfuAI large stuffer" was created to simplify the cloning of the sgRNA guide cassette into pLKO.1-puro U6 sgRNA BspMI stuffer vector originally described in the manuscript “Kearns, NA, etal. Development 2014, 141(1):219-23”. The original vector has a small intervening sequence that presents two problems: 1) the efficiency of excision by BfuAI is moderate, and 2) the size of this spacer is similar to the guide sequence, which makes distinguishing positive clones from reclosures challenging. Consequently, we have inserted a Kanamycin cassette between these sites at a unique Bcl1 site. This element is more efficiently excised by BfuAI and makes distinguishing vectors containing the desired guide sequence easy to distinguish from the parent vector. The excision of the Kan cassette by BfuAI cuts this cassette into 3 fragments due to two internal BfuAI sites within the Kan cassette. Otherwise the cloning of the guides is carried out as described in the manuscript.

Plasmid Name: pLKO.1-puro U6 sgRNA BfuAI large stuffer

Record Creation Time: 20220422T222309+0000

Record Last Update: 20260829T080651+0000

Ratings and Alerts

No rating or validation information has been found for pLKO.1-puro U6 sgRNA BfuAI large stuffer.

No alerts have been found for pLKO.1-puro U6 sgRNA BfuAI large stuffer.

Data and Source Information

Source: Addgene

Usage and Citation Metrics

We found 23 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Guia S, et al. (2025) Genome-wide CRISPR/Cas9 screen reveals factors that influence the susceptibility of tumor cells to NK cell-mediated killing. Journal for immunotherapy of cancer, 13(3).

Roy S, et al. (2025) BLIMP1 negatively regulates IL-2 signaling in T cells. Science advances, 11(29), eadx8105.

Liu D, et al. (2024) BMP-ACVR1 Axis is Critical for Efficacy of PRC2 Inhibitors in B-Cell Lymphoma. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(12), e2306499.

Choi J, et al. (2024) Molecular targets of glucocorticoids that elucidate their therapeutic efficacy in aggressive lymphomas. Cancer cell, 42(5), 833.

Phelan JD, et al. (2024) Response to Bruton's tyrosine kinase inhibitors in aggressive lymphomas linked to chronic selective autophagy. Cancer cell, 42(2), 238.

Bolatkan A, et al. (2022) Downregulation of METTL6 mitigates cell progression, migration, invasion and adhesion in hepatocellular carcinoma by inhibiting cell adhesion molecules. International journal of oncology, 60(1).

Machino H, et al. (2022) The metabolic stress-activated checkpoint LKB1-MARK3 axis acts as a tumor suppressor in high-grade serous ovarian carcinoma. Communications biology, 5(1), 39.

Mazor G, et al. (2021) TP73-AS1 is induced by YY1 during TMZ treatment and highly expressed in the aging brain. Aging, 13(11), 14843.

Li J, et al. (2021) Therapeutic targeting of the PLK1-PRC1-axis triggers cell death in genomically silent childhood cancer. Nature communications, 12(1), 5356.

Dersh D, et al. (2021) Genome-wide Screens Identify Lineage- and Tumor-Specific Genes Modulating MHC-I- and MHC-II-Restricted Immunosurveillance of Human Lymphomas.

Immunity, 54(1), 116.

Tsagkaraki E, et al. (2021) CRISPR-enhanced human adipocyte browning as cell therapy for metabolic disease. Nature communications, 12(1), 6931.

Woods S, et al. (2020) microRNA-seq of cartilage reveals an overabundance of miR-140-3p which contains functional isomiRs. RNA (New York, N.Y.), 26(11), 1575.

Mazor G, et al. (2019) The lncRNA TP73-AS1 is linked to aggressiveness in glioblastoma and promotes temozolomide resistance in glioblastoma cancer stem cells. Cell death & disease, 10(3), 246.

Kim S, et al. (2019) Deregulation of the Histone Lysine-Specific Demethylase 1 Is Involved in Human Hepatocellular Carcinoma. Biomolecules, 9(12).

Moran JD, et al. (2019) SOX4 regulates invasion of bladder cancer cells via repression of WNT5a. International journal of oncology, 55(2), 359.

Musa J, et al. (2019) Cooperation of cancer drivers with regulatory germline variants shapes clinical outcomes. Nature communications, 10(1), 4128.

Palstra RJ, et al. (2018) Allele-specific long-distance regulation dictates IL-32 isoform switching and mediates susceptibility to HIV-1. Science advances, 4(2), e1701729.

Phelan JD, et al. (2018) A multiprotein supercomplex controlling oncogenic signalling in lymphoma. Nature, 560(7718), 387.

Amrani N, et al. (2018) NmeCas9 is an intrinsically high-fidelity genome-editing platform. Genome biology, 19(1), 214.

De Jaime-Soguero A, et al. (2017) Wnt/Tcf1 pathway restricts embryonic stem cell cycle through activation of the Ink4/Arf locus. PLoS genetics, 13(3), e1006682.