Resource Summary Report

Generated by RRID on Aug 25, 2026

pBA904

RRID:Addgene_122238
Type: Plasmid

Proper Citation

RRID:Addgene_122238

Plasmid Information

URL: http://www.addgene.org/122238

Proper Citation: RRID:Addgene_122238

Insert Name: sgRNA with cs1 in stem loop 2 of the constant region

Organism: Synthetic

Bacterial Resistance: Ampicillin

Defining Citation: PMID:32231336

Vector Backbone Description: Vector Backbone:pU6-sgRNA EF1Alpha-puro-T2A-BFP (Addgene, #60955); Vector Types:Mammalian Expression, Lentiviral, CRISPR; Bacterial Resistance:Ampicillin

Plasmid Name: pBA904

Record Creation Time: 20220422T221639+0000

Record Last Update: 20260815T080342+0000

Ratings and Alerts

No rating or validation information has been found for pBA904.

No alerts have been found for pBA904.

Data and Source Information

Source: Addgene

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Nan J, et al. (2026) Single-cell perturbations decipher ribosomal stress-surveillance regulators in type 2 diabetes. Nature metabolism.

Ramste M, et al. (2025) Enhancer-targeting CRISPR screens at coronary artery disease loci suggest shared mechanisms of disease risk. medRxiv : the preprint server for health sciences.

Wang L, et al. (2024) Charting Single Cell Lineage Dynamics and Mutation Networks via Homing CRISPR. bioRxiv : the preprint server for biology.

Liu SJ, et al. (2024) Epigenetic reprogramming shapes the cellular landscape of schwannoma. Nature communications, 15(1), 476.

Southard KM, et al. (2024) Comprehensive transcription factor perturbations recapitulate fibroblast transcriptional states. bioRxiv : the preprint server for biology.

Saliba-Gustafsson P, et al. (2024) A functional genomic framework to elucidate novel causal non-alcoholic fatty liver disease genes. medRxiv : the preprint server for health sciences.

Shin T, et al. (2024) Rare variation in non-coding regions with evolutionary signatures contributes to autism spectrum disorder risk. Cell genomics, 4(8), 100609.

Chen Y, et al. (2024) MicroRNA-focused CRISPR/Cas9 screen identifies miR-142 as a key regulator of Epstein-Barr virus reactivation. PLoS pathogens, 20(6), e1011970.

Tidball AM, et al. (2023) Genome-wide CRISPRi Screen in Human iNeurons to Identify Novel Focal Cortical Dysplasia Genes. bioRxiv : the preprint server for biology.

Shin T, et al. (2023) Rare variation in noncoding regions with evolutionary signatures contributes to autism spectrum disorder risk. medRxiv : the preprint server for health sciences.

Claude-Taupin A, et al. (2023) The AMPK-Sirtuin 1-YAP axis is regulated by fluid flow intensity and controls autophagy flux in kidney epithelial cells. Nature communications, 14(1), 8056.