

Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](https://fdi-lab.sci-crunch.org) on May 2, 2025

p426-SNR52p-gRNA.CAN1.Y-SUP4t

RRID:Addgene_43803

Type: Plasmid

Proper Citation

RRID:Addgene_43803

Plasmid Information

URL: <http://www.addgene.org/43803>

Proper Citation: RRID:Addgene_43803

Insert Name: CAN1.y gRNA

Organism: *Saccharomyces cerevisiae*

Bacterial Resistance: Ampicillin

Defining Citation: [PMID:23460208](https://pubmed.ncbi.nlm.nih.gov/23460208/)

Vector Backbone Description: Backbone Size:5886; Vector Backbone:p426; Vector Types:Yeast Expression, CRISPR; Bacterial Resistance:Ampicillin

Comments: For more information on Church Lab CRISPR Plasmids please refer to: <http://www.addgene.org/crispr/church/> gRNA target sequence GATACGTTCTCTATGGAGGA

Plasmid Name: p426-SNR52p-gRNA.CAN1.Y-SUP4t

Record Creation Time: 20220422T222227+0000

Record Last Update: 20220422T224105+0000

Ratings and Alerts

No rating or validation information has been found for p426-SNR52p-gRNA.CAN1.Y-SUP4t.

No alerts have been found for p426-SNR52p-gRNA.CAN1.Y-SUP4t.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Ruta GV, et al. (2024) Eukaryotic-driven directed evolution of Cas9 nucleases. *Genome biology*, 25(1), 79.

Gourgues G, et al. (2024) A toolbox for manipulating the genome of the major goat pathogen, *Mycoplasma capricolum* subsp. *capripneumoniae*. *Microbiology (Reading, England)*, 170(1).

Liu P, et al. (2024) Transposase-assisted target-site integration for efficient plant genome engineering. *Nature*, 631(8021), 593.

Fasken MB, et al. (2024) A biallelic variant of the RNA exosome gene, EXOSC4, associated with neurodevelopmental defects impairs RNA exosome function and translation. *The Journal of biological chemistry*, 300(8), 107571.

Nishimura A, et al. (2024) Longevity control by supersulfide-mediated mitochondrial respiration and regulation of protein quality. *Redox biology*, 69, 103018.

Fujii H, et al. (2022) An enChIP system for the analysis of genome functions in budding yeast. *Biology methods & protocols*, 7(1), bpac025.

Schubert OT, et al. (2022) Genome-wide base editor screen identifies regulators of protein abundance in yeast. *eLife*, 11.