

Resource Summary Report

Generated by [RRID](#) on Aug 25, 2026

[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](#)

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

Comments: gRNA target sequence GATACGTTCTCTATGGAGGA

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

Record Creation Time: 20220422T222227+0000

Record Last Update: 20260815T081509+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 61 mentions in open access literature.

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

Pillalamarri V, et al. (2026) TOR-dependent regulation of the yeast homolog of the juvenile Batten Disease-associated gene CLN3. *Microbial cell* (Graz, Austria), 13, 131.

Zha H, et al. (2026) Development of a CRISPR/Cas12a genome editing toolbox in *Kluyveromyces marxianus* and its application in succinic acid biosynthesis. *Synthetic and systems biotechnology*, 11, 193.

Vedova CD, et al. (2025) Combining face-to-face laboratory sessions and a computer simulation effectively teaches gene editing and DNA sequencing to undergraduate genetics students. *Biochemistry and molecular biology education : a bimonthly publication of the International Union of Biochemistry and Molecular Biology*, 53(3), 286.

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).

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

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.

Zhao Y, et al. (2023) CREEPY: CRISPR-mediated editing of synthetic episomes in yeast. *Nucleic acids research*, 51(13), e72.

Fasken MB, et al. (2023) A Biallelic Variant of the RNA Exosome Gene EXOSC4 Causes Translational Defects Associated with a Neurodevelopmental Disorder. *medRxiv : the preprint server for health sciences*.

Mendoza BJ, et al. (2023) Potency of CRISPR-Cas Antifungals Is Enhanced by Cotargeting DNA Repair and Growth Regulatory Machinery at the Genetic Level. *ACS infectious diseases*, 9(12), 2494.

Sterrett MC, et al. (2023) Comparative analyses of disease-linked missense mutations in the RNA exosome modeled in budding yeast reveal distinct functional consequences in translation. *bioRxiv : the preprint server for biology*.

Park JH, et al. (2023) Design of Four Small-Molecule-Inducible Systems in the Yeast Chromosome, Applied to Optimize Terpene Biosynthesis. *ACS synthetic biology*, 12(4),

1119.

Žun G, et al. (2023) Construction and evaluation of gRNA arrays for multiplex CRISPR-Cas9. *Yeast* (Chichester, England), 40(1), 32.

Souffriau B, et al. (2022) Polygenic Analysis of Tolerance to Carbon Dioxide Inhibition of Isoamyl Acetate "Banana" Flavor Production in Yeast Reveals MDS3 as Major Causative Gene. *Applied and environmental microbiology*, 88(18), e0081422.

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.

Li A, et al. (2022) Cytosine base editing systems with minimized off-target effect and molecular size. *Nature communications*, 13(1), 4531.

Xu L, et al. (2022) Metabolic engineering of *Saccharomyces cerevisiae* for gram-scale diosgenin production. *Metabolic engineering*, 70, 115.

Vos PD, et al. (2022) Computationally designed hyperactive Cas9 enzymes. *Nature communications*, 13(1), 3023.