Resource Summary Report

Generated by RRID on Aug 24, 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.

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.

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.

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.