

Resource Summary Report

Generated by [RRID](#) on Aug 24, 2026

[pML104](#)

RRID:Addgene_67638

Type: Plasmid

Proper Citation

RRID:Addgene_67638

Plasmid Information

URL: <http://www.addgene.org/67638>

Proper Citation: RRID:Addgene_67638

Insert Name: Cas9

Organism: Saccharomyces cerevisiae

Bacterial Resistance: Ampicillin

Defining Citation: [PMID:26305040](#)

Vector Backbone Description: Backbone Size:5718; Vector Backbone:pRSII426; Vector Types:Yeast Expression, CRISPR; Bacterial Resistance:Ampicillin

Plasmid Name: pML104

Record Creation Time: 20220422T222422+0000

Record Last Update: 20260815T081837+0000

Ratings and Alerts

No rating or validation information has been found for pML104.

No alerts have been found for pML104.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 31 mentions in open access literature.

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

Batté A, et al. (2026) The modifiers that cause changes in gene essentiality. *Cell systems*, 17(4), 101515.

Kotz J, et al. (2026) Physical interactions within the SIR heterochromatin complex potentiate inter-subunit communication and gene repression. *Cell reports*, 45(7), 117564.

Demeshkina NA, et al. (2026) Cytoplasmic circular dsDNA is a key constituent of stress granules. *eLife*, 15.

Lichauco C, et al. (2025) Sir2 and Fun30 regulate ribosomal DNA replication timing via MCM helicase positioning and nucleosome occupancy. *eLife*, 13.

Jiang W, et al. (2025) Sensitive, high-throughput, metabolic analysis by molecular sensors on the membrane surface of mother yeast cells. *Nature communications*, 16(1), 8908.

Lichauco C, et al. (2024) Sir2 and Fun30 regulate ribosomal DNA replication timing via MCM helicase positioning and nucleosome occupancy. *bioRxiv : the preprint server for biology*.

Pomp W, et al. (2024) Transcription factor exchange enables prolonged transcriptional bursts. *Molecular cell*, 84(6), 1036.

Jeon Y, et al. (2024) RNA-mediated double-strand break repair by end-joining mechanisms. *Nature communications*, 15(1), 7935.

Cleere MM, et al. (2024) Optogenetic control of phosphate-responsive genes using single component fusion proteins in *Saccharomyces cerevisiae*. *bioRxiv : the preprint server for biology*.

Duveau F, et al. (2024) Yeast cell responses and survival during periodic osmotic stress are controlled by glucose availability. *eLife*, 12.

Martin R, et al. (2024) Template switching between the leading and lagging strands at replication forks generates inverted copy number variants through hairpin-capped extrachromosomal DNA. *PLoS genetics*, 20(1), e1010850.

Cleere MM, et al. (2024) Optogenetic Control of Phosphate-Responsive Genes Using Single-Component Fusion Proteins in *Saccharomyces cerevisiae*. *ACS synthetic biology*, 13(12), 4085.

Shortt C, et al. (2023) A simple and accessible CRISPR genome editing laboratory exercise using yeast. *microPublication biology*, 2023.

Agrotis A, et al. (2023) Multiple phosphorylation of the Cdc48/p97 cofactor protein Shp1/p47 occurs upon cell stress in budding yeast. *Life science alliance*, 6(4).

Stanton DA, et al. (2023) The importance of proteasome grip depends on substrate stability. *Biochemical and biophysical research communications*, 677, 162.

Carminati M, et al. (2023) A direct interaction between CPF and RNA Pol II links RNA 3' end processing to transcription. *Molecular cell*, 83(24), 4461.

Martínez AA, et al. (2023) Long-Term Adaptation to Galactose as a Sole Carbon Source Selects for Mutations Outside the Canonical GAL Pathway. *Journal of molecular evolution*, 91(1), 46.

Aggeli D, et al. (2022) Overdominant and partially dominant mutations drive clonal adaptation in diploid *Saccharomyces cerevisiae*. *Genetics*, 221(2).

McDonnell L, et al. (2022) CRISPR in Your Kitchen: an At-Home CRISPR Kit to Edit Genes in *Saccharomyces cerevisiae* Used during a Remote Lab Course. *Journal of microbiology & biology education*, 23(1).

van Breugel ME, et al. (2022) Epi-Decoder: Decoding the Local Proteome of a Genomic Locus by Massive Parallel Chromatin Immunoprecipitation Combined with DNA-Barcode Sequencing. *Methods in molecular biology* (Clifton, N.J.), 2458, 123.