Resource Summary Report

Generated by dkNET on Aug 29, 2026

pML107

RRID:Addgene_67639
Type: Plasmid

Proper Citation

RRID:Addgene_67639

Plasmid Information

URL: http://www.addgene.org/67639

Proper Citation: RRID:Addgene_67639

Insert Name: Cas9

Organism: Saccharomyces cerevisiae

Bacterial Resistance: Ampicillin

Defining Citation: PMID:26305040

Vector Backbone Description: Backbone Size:6841; Vector Backbone:pRSII425; Vector Types:Yeast Expression, CRISPR; Bacterial Resistance:Ampicillin

Plasmid Name: pML107

Record Creation Time: 20220422T222422+0000

Record Last Update: 20260829T080910+0000

Ratings and Alerts

No rating or validation information has been found for pML107.

No alerts have been found for pML107.

Data and Source Information

Source: Addgene

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

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

Acharya N, et al. (2025) STI1 domain dynamically engages transient helices in disordered regions to drive self-association and phase separation of yeast ubiquilin Dsk2. bioRxiv : the preprint server for biology.

Namjilsuren S, et al. (2025) The Glc7/PP1 phosphatase triggers Paf1C dissociation from RNA polymerase II to enable transcription termination. bioRxiv : the preprint server for biology.

Waite KA, et al. (2024) Proteasome condensate formation is driven by multivalent interactions with shuttle factors and ubiquitin chains. Proceedings of the National Academy of Sciences of the United States of America, 121(10), e2310756121.

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.

Collins MA, et al. (2022) Variation in ubiquitin system genes creates substrate-specific effects on proteasomal protein degradation. eLife, 11.

Singh R, et al. (2022) Easy efficient HDR-based targeted knock-in in Saccharomyces cerevisiae genome using CRISPR-Cas9 system. Bioengineered, 13(6), 14857.

Xue T, et al. (2018) Improved bioethanol production using CRISPR/Cas9 to disrupt the ADH2 gene in Saccharomyces cerevisiae. World journal of microbiology & biotechnology, 34(10), 154.