

Resource Summary Report

Generated by [RRID](#) on Aug 22, 2026

[pwtCas9-bacteria](#)

RRID:Addgene_44250

Type: Plasmid

Proper Citation

RRID:Addgene_44250

Plasmid Information

URL: <http://www.addgene.org/44250>

Proper Citation: RRID:Addgene_44250

Insert Name: wild-type Cas9

Organism: S .pyogenes

Bacterial Resistance: Ampicillin

Defining Citation: [PMID:23452860](#)

Vector Backbone Description: Vector Backbone:pUC19; Vector Types:Bacterial Expression, CRISPR; Bacterial Resistance:Ampicillin

Plasmid Name: pwtCas9-bacteria

Record Creation Time: 20220422T222229+0000

Record Last Update: 20260815T081513+0000

Ratings and Alerts

No rating or validation information has been found for pwtCas9-bacteria.

No alerts have been found for pwtCas9-bacteria.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Herring-Nicholas A, et al. (2024) Selection of extended CRISPR RNAs with enhanced targeting and specificity. *Communications biology*, 7(1), 86.

Burian J, et al. (2023) High-throughput retrieval of target sequences from complex clone libraries using CRISPRi. *Nature biotechnology*, 41(5), 626.

Zhu Y, et al. (2023) Inhibition of CXorf56 promotes PARP inhibitor-induced cytotoxicity in triple-negative breast cancer. *NPJ breast cancer*, 9(1), 34.

Herring-Nicholas A, et al. (2023) Selection of Extended CRISPR RNAs with Enhanced Targeting and Specificity. *bioRxiv : the preprint server for biology*.

Huszár K, et al. (2023) Position-dependent sequence motif preferences of SpCas9 are largely determined by scaffold-complementary spacer motifs. *Nucleic acids research*.

Tsuji A, et al. (2022) Establishment of genetic tools for genomic DNA engineering of *Halomonas* sp. KM-1, a bacterium with potential for biochemical production. *Microbial cell factories*, 21(1), 122.

Liu X, et al. (2022) The Involvement of Thiamine Uptake in the Virulence of *Edwardsiella piscicida*. *Pathogens (Basel, Switzerland)*, 11(4).

Contreras-Llano LE, et al. (2020) Holistic engineering of cell-free systems through proteome-reprogramming synthetic circuits. *Nature communications*, 11(1), 3138.

Audibert S, et al. (2020) Addressing the role of centromere sites in activation of ParB proteins for partition complex assembly. *PloS one*, 15(5), e0226472.

Hamamoto K, et al. (2020) Characterization of blaCTX-M-14 transposition from plasmid to chromosome in *Escherichia coli* experimental strain. *International journal of medical microbiology : IJMM*, 310(2), 151395.

Dong H, et al. (2019) Exploiting a conjugative CRISPR/Cas9 system to eliminate plasmid harbouring the mcr-1 gene from *Escherichia coli*. *International journal of antimicrobial agents*, 53(1), 1.

Mehrer CR, et al. (2018) Anaerobic production of medium-chain fatty alcohols via a γ -reduction pathway. *Metabolic engineering*, 48, 63.

Zheng K, et al. (2018) Highly efficient base editing in bacteria using a Cas9-cytidine deaminase fusion. *Communications biology*, 1, 32.

Liu F, et al. (2018) Capping-RACE: a simple, accurate, and sensitive 5' RACE method for use in prokaryotes. *Nucleic acids research*, 46(21), e129.

Zhang K, et al. (2016) Multigene disruption in undomesticated *Bacillus subtilis* ATCC 6051a using the CRISPR/Cas9 system. *Scientific reports*, 6, 27943.

Su T, et al. (2016) A CRISPR-Cas9 Assisted Non-Homologous End-Joining Strategy for One-step Engineering of Bacterial Genome. *Scientific reports*, 6, 37895.

Briner AE, et al. (2014) Guide RNA functional modules direct Cas9 activity and orthogonality. *Molecular cell*, 56(2), 333.