

Resource Summary Report

Generated by [RRID](#) on Aug 21, 2026

[pKDsgRNA-ack](#)

RRID:Addgene_62654

Type: Plasmid

Proper Citation

RRID:Addgene_62654

Plasmid Information

URL: <http://www.addgene.org/62654>

Proper Citation: RRID:Addgene_62654

Insert Name: exo, beta, gam, sgRNA

Bacterial Resistance: Spectinomycin

Defining Citation: [PMID:26463009](#)

Vector Backbone Description: Vector Backbone:pKD46; Vector Types:Bacterial Expression; Bacterial Resistance:Spectinomycin

Plasmid Name: pKDsgRNA-ack

Record Creation Time: 20220422T222358+0000

Record Last Update: 20260815T081754+0000

Ratings and Alerts

No rating or validation information has been found for pKDsgRNA-ack.

No alerts have been found for pKDsgRNA-ack.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

van Roosmalen RN, et al. (2026) A Stereospecific Lactic Acid Exclusion Biosensor for Grass Silage Fed Green Biorefinery. *Microbial biotechnology*, 19(5), e70374.

Yadav D, et al. (2025) Chaperone Dependency during Primary Protein Biogenesis Does Not Correlate with Chaperone Dependency during in vitro Refolding. *bioRxiv : the preprint server for biology*.

Liu YA, et al. (2025) Heterologous synthesis of a simplified nitrogenase analog in *Escherichia coli*. *Science advances*, 11(18), eadw6785.

Vignolini T, et al. (2024) Highly inclined light sheet allows volumetric super-resolution imaging of efflux pumps distribution in bacterial biofilms. *Scientific reports*, 14(1), 12902.

Song J, et al. (2023) Phage Engineering for Targeted Multidrug-Resistant *Escherichia coli*. *International journal of molecular sciences*, 24(3).

Hills E, et al. (2022) Comprehensive Mutational Analysis of the Lasso Peptide Klebsidin. *ACS chemical biology*, 17(4), 998.

Gupta M, et al. (2022) Isobutanol production by combined in vivo and in vitro metabolic engineering. *Metabolic engineering communications*, 15, e00210.

Gregor C, et al. (2022) Generation of bright autoluminescent bacteria by chromosomal integration of the improved lux operon ilux2. *Scientific reports*, 12(1), 19039.

Ellington AJ, et al. (2022) Generating Single Nucleotide Point Mutations in *E. coli* with the No-SCAR System. *Methods in molecular biology (Clifton, N.J.)*, 2479, 119.

D'Souza R, et al. (2021) Role of AmpG in the resistance to β -lactam agents, including cephalosporins and carbapenems: candidate for a novel antimicrobial target. *Annals of clinical microbiology and antimicrobials*, 20(1), 45.

Wang CY, et al. (2021) Metabolome and proteome analyses reveal transcriptional misregulation in glycolysis of engineered *E. coli*. *Nature communications*, 12(1), 4929.

Yu Q, et al. (2021) Mutability of demographic noise in microbial range expansions. *The ISME journal*, 15(9), 2643.

Gray MJ, et al. (2020) Interactions between DksA and Stress-Responsive Alternative Sigma Factors Control Inorganic Polyphosphate Accumulation in *Escherichia coli*. *Journal of bacteriology*, 202(14).

Sander T, et al. (2019) Allosteric Feedback Inhibition Enables Robust Amino Acid Biosynthesis in *E. coli* by Enforcing Enzyme Overabundance. *Cell systems*, 8(1), 66.

Hegde S, et al. (2019) CRISPR/Cas9-mediated gene deletion of the *ompA* gene in symbiotic *Cedecia neteri* impairs biofilm formation and reduces gut colonization of *Aedes aegypti* mosquitoes. *PLoS neglected tropical diseases*, 13(12), e0007883.

Li P, et al. (2019) Screening of Polyvalent Phage-Resistant *Escherichia coli* Strains Based on Phage Receptor Analysis. *Frontiers in microbiology*, 10, 850.

Li M, et al. (2018) Comparative genomics analysis of pTEM-2262, an MDR plasmid from *Citrobacter freundii*, harboring two unclassified replicons. *Future microbiology*, 13, 1657.

Li P, et al. (2018) vB_EcoS_IME347 a novel T1-like *Escherichia coli* bacteriophage. *Journal of basic microbiology*, 58(11), 968.

Erian AM, et al. (2018) Engineered *E. coli* W enables efficient 2,3-butanediol production from glucose and sugar beet molasses using defined minimal medium as economic basis. *Microbial cell factories*, 17(1), 190.

Reisch CR, et al. (2017) Scarless Cas9 Assisted Recombineering (no-SCAR) in *Escherichia coli*, an Easy-to-Use System for Genome Editing. *Current protocols in molecular biology*, 117, 31.8.1.