

Resource Summary Report

Generated by [NIF](#) on Jul 28, 2026

pSAM_AraC

RRID:Addgene_91569

Type: Plasmid

Proper Citation

RRID:Addgene_91569

Plasmid Information

URL: <http://www.addgene.org/91569>

Proper Citation: RRID:Addgene_91569

Insert Name: AraC/PBAD

Organism: E. coli

Bacterial Resistance: Ampicillin and Kanamycin

Defining Citation: [PMID:28614382](#)

Vector Backbone Description: Backbone Marker:N/A; Backbone Size:4559; Vector Backbone:pSAM_Ec; Vector Types:Bacterial Expression; Bacterial Resistance:Ampicillin and Kanamycin

Comments: Mariner himar1C9 transposase driven by an arabinose promoter on an R6K gamma suicide plasmid. The transposon allows identification of fitness factors by Illumina sequencing. This transposon will randomly insert a kanamycin resistance cassette into genomic TA sites. Ampicillin resistance is contained on the plasmid backbone. For further background, see: Goodman, Andrew L., Meng Wu, and Jeffrey I. Gordon. "Identifying Microbial Fitness Determinants by Insertion Sequencing (INSeq) Using Genome-Wide Transposon Mutant Libraries." Nature Protocols 6.12 (2011): 1969–1980. PMC. Web. 11 Apr. 2017. Wiles, Travis J. et al. "Combining Quantitative Genetic Footprinting and Trait Enrichment Analysis to Identify Fitness Determinants of a Bacterial Pathogen." Ed. Danielle A. Garsin. PLoS Genetics 9.8 (2013): e1003716. PMC. Web. 11 Apr. 2017.

Plasmid Name: pSAM_AraC

Record Creation Time: 20220422T222619+0000

Record Last Update: 20260725T075355+0000

Ratings and Alerts

No rating or validation information has been found for pSAM_AraC.

No alerts have been found for pSAM_AraC.

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Hwang J, et al. (2025) Integrated Tn-seq and MAGE-assisted rapid genome engineering targeting in Escherichia coli. Trends in biotechnology.

English MA, et al. (2023) A self-propagating, barcoded transposon system for the dynamic rewiring of genomic networks. Molecular systems biology, 19(6), e11398.

Pearson MM, et al. (2022) Construction of an Ordered Transposon Library for Uropathogenic Proteus mirabilis HI4320. Microbiology spectrum, 10(6), e0314222.

Ishizawa H, et al. (2022) Genome-wide identification of bacterial colonization and fitness determinants on the floating macrophyte, duckweed. Communications biology, 5(1), 68.

Forsyth VS, et al. (2019) Transposon Insertion Site Sequencing in a Urinary Tract Model. Methods in molecular biology (Clifton, N.J.), 2021, 297.