Resource Summary Report

Generated by kravitz2 on Aug 3, 2026

pET StrepII TEV LIC cloning vector (1R)

RRID:Addgene_29664
Type: Plasmid

Proper Citation

RRID:Addgene_29664

Plasmid Information

URL: http://www.addgene.org/29664

Proper Citation: RRID:Addgene_29664

Insert Name: None

Bacterial Resistance: Kanamycin

Vector Backbone Description: Backbone Size:5352; Vector Backbone:pET; Vector Types:Bacterial Expression; Bacterial Resistance:Kanamycin

Comments: This plasmid is an empty vector to be used with a LIC cloning protocol. It has a TEV-cleavable Strep II fusion tag on its N-terminus. To clone into this vector, add LIC fusion tags to the 5' end of your PCR primers. Forward - 5'TACTTCCAATCCAATGCA3' Reverse - 5'TTATCCACTTCCAATGTTATTA3' Linearize the plasmid with SspI and gel purify. When digesting the DNA with T4 polymerase, use dCTP for insert and dGTP for vector. More information on this vector can be found through http://qb3.berkeley.edu/macrolab/

Plasmid Name: pET StrepII TEV LIC cloning vector (1R)

Record Creation Time: 20220422T222131+0000

Record Last Update: 20260801T081119+0000

Ratings and Alerts

No rating or validation information has been found for pET StrepII TEV LIC cloning vector (1R).

No alerts have been found for pET StrepII TEV LIC cloning vector (1R).

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 kravitz2 .

Alsina FC, et al. (2024) The RNA-binding protein EIF4A3 promotes axon development by direct control of the cytoskeleton. Cell reports, 43(9), 114666.

Schmitz M, et al. (2022) Structural basis for the assembly of the type V CRISPR-associated transposon complex. Cell, 185(26), 4999.

Querques I, et al. (2021) Target site selection and remodelling by type V CRISPR-transposon systems. Nature, 599(7885), 497.

Nimkar S, et al. (2020) Cas3/I-C mediated target DNA recognition and cleavage during CRISPR interference are independent of the composition and architecture of Cascade surveillance complex. Nucleic acids research, 48(5), 2486.

Yoganand KN, et al. (2019) Fidelity of prespacer capture and processing is governed by the PAM-mediated interactions of Cas1-2 adaptation complex in CRISPR-Cas type I-E system. The Journal of biological chemistry, 294(52), 20039.

Sharma H, et al. (2019) Ribosome assembly defects subvert initiation Factor3 mediated scrutiny of bona fide start signal. Nucleic acids research, 47(21), 11368.

Yoganand KN, et al. (2017) Asymmetric positioning of Cas1-2 complex and Integration Host Factor induced DNA bending guide the unidirectional homing of protospacer in CRISPR-Cas type I-E system. Nucleic acids research, 45(1), 367.

Tosi L, et al. (2017) Long-adapter single-strand oligonucleotide probes for the massively multiplexed cloning of kilobase genome regions. Nature biomedical engineering, 1.