

Resource Summary Report

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pET His6 Sumo TEV LIC cloning vector (1S)

RRID:Addgene_29659

Type: Plasmid

Proper Citation

RRID:Addgene_29659

Plasmid Information

URL: <http://www.addgene.org/29659>

Proper Citation: RRID:Addgene_29659

Insert Name: None

Bacterial Resistance: Kanamycin

Vector Backbone Description: Backbone Size:5661; 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 His6 fusion tag on its N-terminus. Sumo can enhance the expression and solubility of your protein of interest. 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 His6 Sumo TEV LIC cloning vector (1S)

Record Creation Time: 20220422T222131+0000

Record Last Update: 20260725T074534+0000

Ratings and Alerts

No rating or validation information has been found for pET His6 Sumo TEV LIC cloning vector (1S).

No alerts have been found for pET His6 Sumo TEV LIC cloning vector (1S).

Data and Source Information

Usage and Citation Metrics

We found 34 mentions in open access literature.

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

Finocchio G, et al. (2025) Structural basis of TnsC oligomerization and transposase recruitment in type I-B CRISPR-associated transposons. *Nucleic acids research*, 53(5).

Kim Y, et al. (2025) LOPAC library screening identifies suramin as a TRIM21 binder with a unique binding mode revealed by crystal structure. *Acta crystallographica. Section F, Structural biology communications*, 81(Pt 3), 101.

Okada H, et al. (2025) Bni5 regulates and coordinates septin architecture and myosin-II functions at the cell division site. *The Journal of cell biology*, 224(12).

Schmidheini L, et al. (2024) Continuous directed evolution of a compact CjCas9 variant with broad PAM compatibility. *Nature chemical biology*, 20(3), 333.

Louder RK, et al. (2024) Molecular basis of global promoter sensing and nucleosome capture by the SWR1 chromatin remodeler. *Cell*, 187(24), 6849.

Xu Y, et al. (2024) Partial closure of the γ -tubulin ring complex by CDK5RAP2 activates microtubule nucleation. *Developmental cell*, 59(23), 3161.

Sharma PK, et al. (2024) Role of the leucine-rich repeat protein kinase 2 C-terminal tail in domain cross-talk. *The Biochemical journal*, 481(4), 313.

Wu M, et al. (2024) Structure Characterization of Zinc Finger Motif 1 and 2 of GLI1 DNA Binding Region. *International journal of molecular sciences*, 25(24).

Marquardt J, et al. (2024) Reciprocal regulation by Elm1 and Gin4 controls septin hourglass assembly and remodeling. *The Journal of cell biology*, 223(5).

Maker A, et al. (2022) Reconstitution of the full transmembrane cadherin-catenin complex. *Protein expression and purification*, 193, 106056.

Kuo YW, et al. (2022) The force required to remove tubulin from the microtubule lattice by pulling on its γ -tubulin C-terminal tail. *Nature communications*, 13(1), 3651.

Jeong H, et al. (2022) TRIP13 Participates in Immediate-Early Sensing of DNA Strand Breaks and ATM Signaling Amplification through MRE11. *Cells*, 11(24).

Ravalin M, et al. (2022) A single-component luminescent biosensor for the SARS-CoV-2 spike protein. *bioRxiv : the preprint server for biology*.

Tanaka Y, et al. (2022) Identification and characterization of a serine racemase in the silkworm *Bombyx mori*. *Journal of biochemistry*, 172(1), 17.

Payliss BJ, et al. (2022) Phosphorylation of the DNA repair scaffold SLX4 drives folding of the SAP domain and activation of the MUS81-EME1 endonuclease. *Cell reports*, 41(4), 111537.

Liu TY, et al. (2021) Accelerated RNA detection using tandem CRISPR nucleases. *Nature chemical biology*, 17(9), 982.

Gabel C, et al. (2021) Structural basis for inhibition of the type I-F CRISPR-Cas surveillance complex by AcrIF4, AcrIF7 and AcrIF14. *Nucleic acids research*, 49(1), 584.

Imaide S, et al. (2021) Trivalent PROTACs enhance protein degradation via combined avidity and cooperativity. *Nature chemical biology*, 17(11), 1157.

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

Van Orden MJ, et al. (2020) CRISPR type II-A subgroups exhibit phylogenetically distinct mechanisms for prespacer insertion. *The Journal of biological chemistry*, 295(32), 10956.