Resource Summary Report

Generated by RRID on Aug 27, 2026

pET28-MKH8SUMO

RRID:Addgene_79526
Type: Plasmid

Proper Citation

RRID:Addgene_79526

Plasmid Information

URL: http://www.addgene.org/79526

Proper Citation: RRID:Addgene_79526

Bacterial Resistance: Kanamycin

Vector Backbone Description: Backbone Marker:SGC; Backbone Size:7649; Vector Backbone:pET28-MKH8SUMO; Vector Types:Bacterial Expression; Bacterial Resistance:Kanamycin

Comments: Please see http://www.thesgc.org/sites/default/files/toronto_vectors/pET28-MKH8SUMO.pdf for more information. The pET28-MKH8SUMO vector was derived from expression plasmid pET28a-LIC (SGC). It is used for T7 promoter driven expression of recombinant proteins with the addition of an N-terminal fusion tag containing 8X His followed by a thrombin cleavage site, a SUMO, and a TEV cleavage site. Two lysines were encoded after the Met start site. Two stop codons are included in the vector at the downstream cloning site. Insertion of DNA sequence into the cloning/expression region is performed using ClonTech In-Fusion enzyme mediated directional recombination between complementary 15 nucleotide DNA sequences at the ends of the insert (PCR product) and BseRI/BsaI linearized vector. Insertion of target sequence involves replacement of a SacB gene stuffer sequence, which provides for negative selection of the original plasmid on 5% sucrose.The 15-bp primer extensions are compatible with those for pET28-MHL, such that the PCR inserts prepared for pET28-MHL can be directly used for cloning into pET28-MKH8SUMO.

Plasmid Name: pET28-MKH8SUMO

Record Creation Time: 20220422T222521+0000

Record Last Update: 20260815T082031+0000

Ratings and Alerts

No rating or validation information has been found for pET28-MKH8SUMO.

No alerts have been found for pET28-MKH8SUMO.

Data and Source Information

Source: Addgene

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID .

Xiao R, et al. (2025) Structural basis of RNA-guided transcription by a dCas12f-??E-RNAP complex. bioRxiv : the preprint server for biology.

Yang Z, et al. (2025) Identification of a non-inhibitory aptameric ligand to CRL2ZYG11B E3 ligase for targeted protein degradation. Nature communications, 16(1), 2494.

Liu Z, et al. (2025) Molecular mechanism of the type 2 defense-associated reverse transcriptase. Nucleic acids research, 53(20).

Yan X, et al. (2024) Molecular basis of SAP05-mediated ubiquitin-independent proteasomal degradation of transcription factors. Nature communications, 15(1), 1170.

Zhou M, et al. (2024) Molecular insights into degron recognition by CRL5ASB7 ubiquitin ligase. Nature communications, 15(1), 6177.

Wang X, et al. (2023) Recognition of an Ala-rich C-degron by the E3 ligase Pirh2. Nature communications, 14(1), 2474.

Li Y, et al. (2022) CRL2ZER1/ZYG11B recognizes small N-terminal residues for degradation. Nature communications, 13(1), 7636.

Ru Y, et al. (2022) C-terminal glutamine acts as a C-degron targeted by E3 ubiquitin ligase TRIM7. Proceedings of the National Academy of Sciences of the United States of America, 119(30), e2203218119.

Zhang B, et al. (2022) Structural insights into ORF10 recognition by ZYG11B. Biochemical and biophysical research communications, 616, 14.

Xiao R, et al. (2021) Structural basis of target DNA recognition by CRISPR-Cas12k for RNA-guided DNA transposition. Molecular cell, 81(21), 4457.

Yan X, et al. (2021) Molecular basis for recognition of Gly/N-degrons by CRL2ZYG11B and CRL2ZER1. Molecular cell, 81(16), 3262.