

Resource Summary Report

Generated by [RRID](#) on Sep 3, 2026

pET28-MHL

RRID:Addgene_26096

Type: Plasmid

Proper Citation

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Plasmid Information

URL: <http://www.addgene.org/26096>

Proper Citation: RRID:Addgene_26096

Bacterial Resistance: Kanamycin

Vector Backbone Description: Backbone Marker:Structural Genomics Consortium; Backbone Size:7325; Vector Backbone:pET28-MHL; Vector Types:Bacterial Expression; Bacterial Resistance:Kanamycin

Comments: The pET28-MHL vector (GenBank accession EF456735) was derived from expression plasmid pET28a-LIC (SGC). It is used for T7 promoter driven expression of recombinant proteins with the addition of an 18 amino acid N-terminal fusion tag containing 6X His followed by a TEV cleavage site. The GSS residues after the Met start site were removed to reduce N-terminal gluconoylation via preventing N-terminal Met excision. Two stop codons are included in the vector at the C-terminal cloning site. Insertion of DNA sequence into the cloning/expression region is performed using BD-Biosciences Infusion enzyme mediated directional recombination between complementary 15 nucleotide DNA sequences at the ends of the insert (PCR product) and BseRI 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. <http://www.sgc.utoronto.ca/SGC-WebPages/toronto-vectors.php>

Plasmid Name: pET28-MHL

Record Creation Time: 20220422T222116+0000

Record Last Update: 20260902T045133+0000

Ratings and Alerts

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

No alerts have been found for pET28-MHL.

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](#) .

Bagdadi N, et al. (2024) Stable GDP-tubulin islands rescue dynamic microtubules. The Journal of cell biology, 223(8).

Lei K, et al. (2024) Endosome-microautophagy targeting chimera (eMIATAC) for targeted proteins degradation and enhance CAR-T cell anti-tumor therapy. Theranostics, 14(11), 4481.

Nie DY, et al. (2024) Recruitment of FBXO22 for targeted degradation of NSD2. Nature chemical biology, 20(12), 1597.

Wang X, et al. (2024) The ATAC complex represses the transcriptional program of the autophagy-lysosome pathway via its E3 ubiquitin ligase activity. Cell reports, 43(12), 115033.

He Q, et al. (2023) Nucleic Acid Detection through RNA-Guided Protease Activity in Type III-E CRISPR-Cas Systems. Chembiochem : a European journal of chemical biology, 24(22), e202300401.

Nie DY, et al. (2023) Recruitment of FBXO22 for Targeted Degradation of NSD2. bioRxiv : the preprint server for biology.

Wei Y, et al. (2022) The MYC oncoprotein directly interacts with its chromatin cofactor PNUTS to recruit PP1 phosphatase. Nucleic acids research, 50(6), 3505.

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

Fukuda Y, et al. (2021) Binding and transport of SFPQ-RNA granules by KIF5A/KLC1 motors promotes axon survival. The Journal of cell biology, 220(1).

Guegueniat J, et al. (2021) The human pseudouridine synthase PUS7 recognizes RNA with an extended multi-domain binding surface. Nucleic acids research, 49(20), 11810.

Gurzau AD, et al. (2021) SMCHD1's ubiquitin-like domain is required for N-terminal dimerization and chromatin localization. The Biochemical journal, 478(13), 2555.

Dong C, et al. (2020) Structural Basis for the Binding Selectivity of Human CDY Chromodomains. Cell chemical biology, 27(7), 827.

Guo Q, et al. (2019) Structural insights into SETD3-mediated histidine methylation on ??-actin. *eLife*, 8.

Lewis R, et al. (2019) Global Reduction of H3K4me3 Improves Chemotherapeutic Efficacy for Pediatric Ependymomas. *Neoplasia* (New York, N.Y.), 21(6), 505.

Heinkel F, et al. (2018) Biophysical Characterization of the Tandem FHA Domain Regulatory Module from the Mycobacterium tuberculosis ABC Transporter Rv1747. *Structure* (London, England : 1993), 26(7), 972.

Xu C, et al. (2018) DNA Sequence Recognition of Human CXXC Domains and Their Structural Determinants. *Structure* (London, England : 1993), 26(1), 85.

Shrestha R, et al. (2017) Mechanistic Insights into Dye-Decolorizing Peroxidase Revealed by Solvent Isotope and Viscosity Effects. *ACS catalysis*, 7(9), 6352.

Perez-Borrajero C, et al. (2016) Structural and Dynamics Studies of Pax5 Reveal Asymmetry in Stability and DNA Binding by the Paired Domain. *Journal of molecular biology*, 428(11), 2372.

Jia K, et al. (2016) Study of Class I and Class III Polyhydroxyalkanoate (PHA) Synthases with Substrates Containing a Modified Side Chain. *Biomacromolecules*, 17(4), 1477.

Blazer LL, et al. (2016) PR Domain-containing Protein 7 (PRDM7) Is a Histone 3 Lysine 4 Trimethyltransferase. *The Journal of biological chemistry*, 291(26), 13509.