

Resource Summary Report

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pET His6 GST TEV LIC cloning vector (2G-T)

RRID:Addgene_29707

Type: Plasmid

Proper Citation

RRID:Addgene_29707

Plasmid Information

URL: <http://www.addgene.org/29707>

Proper Citation: RRID:Addgene_29707

Insert Name: None

Bacterial Resistance: Ampicillin

Vector Backbone Description: Backbone Size:5458; Vector Backbone:pET; Vector Types:Bacterial Expression; Bacterial Resistance:Ampicillin

Comments: This plasmid is an empty vector. Your gene can be inserted with a LIC cloning protocol. All 2-series vectors work as single-expression vectors, as well as transfer vectors for our polycistronic system. The LIC cloning site is flanked by 5 pairs of restriction sites, so that your gene can easily be subcloned into our polycistronic destination vectors (2D, 2E, or 2Z). 2G-T has a TEV-cleavable N-terminal His6-GST fusion tag. GST can improve the expression and solubility of your target protein. To clone into this vector, add LIC v1 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/qb3/macrolab/>

Plasmid Name: pET His6 GST TEV LIC cloning vector (2G-T)

Record Creation Time: 20220422T222131+0000

Record Last Update: 20260815T081320+0000

Ratings and Alerts

No rating or validation information has been found for pET His6 GST TEV LIC cloning vector (2G-T).

No alerts have been found for pET His6 GST TEV LIC cloning vector (2G-T).

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

Gybe? T, et al. (2024) Splice variants of CK1? and CK1?-like: Comparative analysis of subcellular localization, kinase activity, and function in the Wnt signaling pathway. The Journal of biological chemistry, 300(7), 107407.

Lin L, et al. (2022) Calmodulin Modulation of Insect Ryanodine Receptors. Journal of agricultural and food chemistry, 70(51), 16156.

Muckenfuss LM, et al. (2022) Fip1 is a multivalent interaction scaffold for processing factors in human mRNA 3' end biogenesis. eLife, 11.

Peters CE, et al. (2022) Structure-function analysis of enterovirus protease 2A in complex with its essential host factor SETD3. Nature communications, 13(1), 5282.

Boyd RJ, et al. (2022) Characterization and computational simulation of human Syx, a RhoGEF implicated in glioblastoma. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 36(7), e22378.

Kim J, et al. (2021) FOXO4 Transactivation Domain Interaction with Forkhead DNA Binding Domain and Effect on Selective DNA Recognition for Transcription Initiation. Journal of molecular biology, 433(4), 166808.

Lee D, et al. (2020) Regulation of reactive oxygen species during plant immunity through phosphorylation and ubiquitination of RBOHD. Nature communications, 11(1), 1838.

Lal NK, et al. (2020) Phytopathogen Effectors Use Multiple Mechanisms to Manipulate Plant Autophagy. Cell host & microbe, 28(4), 558.

Boneberg FM, et al. (2019) Molecular mechanism of the RNA helicase DHX37 and its activation by UTP14A in ribosome biogenesis. RNA (New York, N.Y.), 25(6), 685.

Li F, et al. (2019) Deleting nebulin's C-terminus reveals its importance to sarcomeric structure and function and is sufficient to invoke nemaline myopathy. Human molecular genetics, 28(10), 1709.

Zhang Y, et al. (2019) TurboID-based proximity labeling reveals that UBR7 is a regulator of NLR immune receptor-mediated immunity. *Nature communications*, 10(1), 3252.

Zhang M, et al. (2018) The MAP4 Kinase SIK1 Ensures Robust Extracellular ROS Burst and Antibacterial Immunity in Plants. *Cell host & microbe*, 24(3), 379.

Ding B, et al. (2018) Dissecting Substrate Specificities of the Mitochondrial AFG3L2 Protease. *Biochemistry*, 57(28), 4225.

Wang L, et al. (2017) LIN28 Zinc Knuckle Domain Is Required and Sufficient to Induce let-7 Oligouridylation. *Cell reports*, 18(11), 2664.

Rampello AJ, et al. (2017) Identification of a Degradation Signal Sequence within Substrates of the Mitochondrial i-AAA Protease. *Journal of molecular biology*, 429(6), 873.

Clerici M, et al. (2017) Structural insights into the assembly and polyA signal recognition mechanism of the human CPSF complex. *eLife*, 6.

Philip F, et al. (2017) Measuring Phospholipase D Enzymatic Activity Through Biochemical and Imaging Methods. *Methods in enzymology*, 583, 309.

Lebedev I, et al. (2016) A Novel In Vitro CypD-Mediated p53 Aggregation Assay Suggests a Model for Mitochondrial Permeability Transition by Chaperone Systems. *Journal of molecular biology*, 428(20), 4154.

Shi H, et al. (2016) Engineered AAA+ proteases reveal principles of proteolysis at the mitochondrial inner membrane. *Nature communications*, 7, 13301.