

Resource Summary Report

Generated by [dkNET](#) on Sep 5, 2026

pET co-transformation cloning vector (13S-A)

RRID:Addgene_48323

Type: Plasmid

Proper Citation

RRID:Addgene_48323

Plasmid Information

URL: <http://www.addgene.org/48323>

Proper Citation: RRID:Addgene_48323

Bacterial Resistance: Spectinomycin

Vector Backbone Description: Backbone Size:3566; Vector Backbone:pET; Vector Types:Bacterial Expression; Bacterial Resistance:Spectinomycin

Comments: This plasmid is an empty vector to be used with a LIC cloning protocol. It has a Spec resistance. To clone into this vector, add LICv2 fusion tags to the 5' end of your PCR primers. LICv2 Forward - 5'TTTAAGAAGGAGATATAGATC3' LICv2 Reverse - 5'TTATGGAGTTGGGATCTTATTA3' Linearize the plasmid with EcoRV and gel purify. When digesting the DNA with T4 polymerase for LIC, use dCTP for insert and dGTP for vector. The 13-series vectors were designed to enable rapid cloning for a co-expression system. Vectors are based on Novagen's Duet system. Each gene is expressed on its own vector, which has been optimized so that each gene expresses at approximately equal levels. The 13-series vectors are all compatible with 2-series transfer vectors, so if cotransformation fails, there is a readily available backup in polycistronic expression. 13S CDF origin SpecR13K ColA origin KanR2-series transfer ColE1 origin AmpR13S vectors must be cotransformed with a 2-series vector for optimal expression (that is, the presence of an empty 2A-T vector enhances expression of a gene in 13S). For triple expressions, the proteins all seem to express at approximately equal levels. Genes in the CDF vector consistently express at very slightly lower levels, so if you're trying to pull down stoichiometric complexes, it's probably best to put His6-fusion protein in this vector. More information on this vector can be found through <http://qb3.berkeley.edu/qb3/macrolab/>

Plasmid Name: pET co-transformation cloning vector (13S-A)

Record Creation Time: 20220422T222248+0000

Record Last Update: 20260905T075720+0000

Ratings and Alerts

No rating or validation information has been found for pET co-transformation cloning vector (13S-A).

No alerts have been found for pET co-transformation cloning vector (13S-A).

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Glasner DR, et al. (2025) The IFIT2-IFIT3 antiviral complex targets short 5' untranslated regions on viral mRNAs for translation inhibition. *Nature microbiology*, 10(11), 2934.

Yang J, et al. (2025) Insights into the compact CRISPR-Cas9d system. *Nature communications*, 16(1), 2462.

Glasner DR, et al. (2025) Short 5' UTRs serve as a marker for viral mRNA translation inhibition by the IFIT2-IFIT3 antiviral complex. *bioRxiv : the preprint server for biology*.

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

Pradhan B, et al. (2024) Loop extrusion-mediated plasmid DNA cleavage by the bacterial SMC Wadjet complex. *bioRxiv : the preprint server for biology*.

Deep A, et al. (2024) Architecture and infection-sensing mechanism of the bacterial PARIS defense system. *bioRxiv : the preprint server for biology*.

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

Wang X, et al. (2022) Target RNA-guided protease activity in type III-E CRISPR-Cas system. *Nucleic acids research*, 50(22), 12913.

Yu G, et al. (2022) Structure and function of a bacterial type III-E CRISPR-Cas7-11 complex. *Nature microbiology*, 7(12), 2078.

Kim S, et al. (2020) Selective loading and processing of prespacers for precise CRISPR adaptation. *Nature*, 579(7797), 141.