

Resource Summary Report

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pFastBac His6 TEV cloning vector with BioBrick PolyPromoter LIC Subcloning (438-B)

RRID:Addgene_55219

Type: Plasmid

Proper Citation

RRID:Addgene_55219

Plasmid Information

URL: <http://www.addgene.org/55219>

Proper Citation: RRID:Addgene_55219

Bacterial Resistance: Ampicillin

Defining Citation: [PMID:28668116](#)

Vector Backbone Description: Vector Backbone:pFastBac; Vector Types:Insect Expression; Bacterial Resistance:Ampicillin

Comments: In order to increase the efficiency of subcloning with the Series-11 MacroBac plasmids we developed a new strategy the uses LIC (Ligation Independent Cloning). The problem with the Series-11 ligation mediated subcloning was that when the plasmid size approached or exceeded 20 kb we had to screen many colonies to find a positive. We developed a strategy to use LIC for subcloning. Because this method uses no ligase, the cloning background associated with re-ligation of the empty plasmid are eliminated. 438-B has a TEV cleavable His6 at the N-terminus. The 438-B vector use the LICv1 Forward and Reverse primers. LICv1Forward - 5'-TACTTCCAATCCAATGCA-3' LICv1 Reverse - 5'-TTATCCACTTCCAATGTTATTA-3' As the target plasmid size gets >20kb you may have to increase the amount of DNA you anneal and/or transform. We have found this method gives no background colonies at all and 100% of the colonies we pick are positive. The cells we transform into are XL1Blues with a competency $\sim 6 \times 10^7$ cfu/ul. For more information, please see our website: <http://qb3.berkeley.edu/qb3/macrolab/>

Plasmid Name: pFastBac His6 TEV cloning vector with BioBrick PolyPromoter LIC Subcloning (438-B)

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Ratings and Alerts

No rating or validation information has been found for pFastBac His6 TEV cloning vector with BioBrick PolyPromoter LIC Subcloning (438-B).

No alerts have been found for pFastBac His6 TEV cloning vector with BioBrick PolyPromoter LIC Subcloning (438-B).

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Klapstova V, et al. (2026) Distinct mechanisms of recognition of phosphorylated RNAPII C-terminal domain by BRCT repeats of the BRCA1-BARD1 complex. *The Journal of biological chemistry*, 302(1), 111010.

Bhatta A, et al. (2025) Molecular basis of human nuclear and mitochondrial tRNA 3' processing. *Nature structural & molecular biology*, 32(4), 613.

Fianu I, et al. (2024) Structural basis of Integrator-dependent RNA polymerase II termination. *Nature*, 629(8010), 219.

Mevissen TET, et al. (2024) STK19 positions TFIIH for cell-free transcription-coupled DNA repair. *Cell*, 187(25), 7091.

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.

Li W, et al. (2023) Structure of histone deacetylase complex Rpd3S bound to nucleosome. *Nature structural & molecular biology*, 30(12), 1893.

Kroupova A, et al. (2021) Molecular architecture of the human tRNA ligase complex. *eLife*, 10.

Kokic G, et al. (2021) Structural basis of human transcription-DNA repair coupling. *Nature*, 598(7880), 368.

Asanovi? I, et al. (2021) The oxidoreductase PYROXD1 uses NAD(P)⁺ as an antioxidant to sustain tRNA ligase activity in pre-tRNA splicing and unfolded protein response. *Molecular cell*, 81(12), 2520.

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.

Kokic G, et al. (2019) Structural basis of TFIIH activation for nucleotide excision repair. *Nature communications*, 10(1), 2885.

Parker MW, et al. (2019) A new class of disordered elements controls DNA replication through initiator self-assembly. *eLife*, 8.

Clerici M, et al. (2018) Structural basis of AAUAAA polyadenylation signal recognition by the human CPSF complex. *Nature structural & molecular biology*, 25(2), 135.

Vos SM, et al. (2016) Architecture and RNA binding of the human negative elongation factor. *eLife*, 5.