

Resource Summary Report

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pFastBac cloning vector with BioBrick PolyPromoter LIC Subcloning (438-A)

RRID:Addgene_55218

Type: Plasmid

Proper Citation

RRID:Addgene_55218

Plasmid Information

URL: <http://www.addgene.org/55218>

Proper Citation: RRID:Addgene_55218

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-A is an untagged pFastBac LIC Subcloning vector. The 438 vectors use the LICvBac Forward primer and the LICv1 Reverse primer. LICvBacF - 5'-TACTTCCAATCCAATCG-3' (Note: ATG must be added to ORF) 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/>

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Record Creation Time: 20220422T222323+0000

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Ratings and Alerts

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

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

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

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.

Jagannatha P, et al. (2026) Large-scale tethered screen of RNA-binding proteins reveals novel regulators of poly(A) site selection. Molecular cell, 86(14), 2811.

Huang L, et al. (2025) Molecular basis for the recognition of low-frequency polyadenylation signals by mPSF. Nucleic acids research, 53(17).

Sala FA, et al. (2025) Structural basis of Nipah virus RNA synthesis. Nature communications, 16(1), 2261.

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.

Braxton JR, et al. (2023) The p97/VCP adapter UBXD1 drives AAA+ remodeling and ring opening through multi-domain tethered interactions. bioRxiv : the preprint server for biology.

Qin Y, et al. (2023) Structural Basis of the Transcriptional Elongation Factor Paf1 Core Complex from Saccharomyces eubayanus. International journal of molecular sciences, 24(10).

Huang J, et al. (2023) An examination of the metal ion content in the active sites of human endonucleases CPSF73 and INTS11. The Journal of biological chemistry, 299(4), 103047.

Hasanova Z, et al. (2023) Human senataxin is a bona fide R-loop resolving enzyme and transcription termination factor. Nucleic acids research, 51(6), 2818.

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

Farnung L, et al. (2021) Structural basis of nucleosome transcription mediated by Chd1 and FACT. *Nature structural & molecular biology*, 28(4), 382.

Aibara S, et al. (2021) Structures of mammalian RNA polymerase II pre-initiation complexes. *Nature*, 594(7861), 124.

Rengachari S, et al. (2021) Structure of the human Mediator-RNA polymerase II pre-initiation complex. *Nature*, 594(7861), 129.

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.

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. (2018) Structure of activated transcription complex Pol II-DSIF-PAF-SPT6. *Nature*, 560(7720), 607.