

Resource Summary Report

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pFastBac His6 MBP Asn10 TEV cloning vector with BioBrick PolyPromoter LIC Subcloning (438-C)

RRID:Addgene_55220

Type: Plasmid

Proper Citation

RRID:Addgene_55220

Plasmid Information

URL: <http://www.addgene.org/55220>

Proper Citation: RRID:Addgene_55220

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-C has a TEV cleavable His6-MBP N10 at the N-terminus. MBP can improve expression and solubility of the target protein. The 438-C 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/>

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Ratings and Alerts

No rating or validation information has been found for pFastBac His6 MBP Asn10 TEV cloning vector with BioBrick PolyPromoter LIC Subcloning (438-C).

No alerts have been found for pFastBac His6 MBP Asn10 TEV cloning vector with BioBrick PolyPromoter LIC Subcloning (438-C).

Data and Source Information

Source: [Addgene](#)

Usage and Citation Metrics

We found 25 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.

Tsukamoto Y, et al. (2025) Condensation-dependent interactome of a chromatin remodeler underlies tumor suppressor activities. Nature communications, 16(1), 9599.

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.

Antonicka H, et al. (2025) FASTKD5 processes mitochondrial pre-mRNAs at noncanonical cleavage sites. Nucleic acids research, 53(13).

Zhang L, et al. (2025) Structure of a transcribing Pol II-DSIF-SPT6-U1 snRNP complex. Nature communications, 16(1), 5823.

Huang Y, et al. (2024) DSS1 restrains BRCA2's engagement with dsDNA for homologous recombination, replication fork protection, and R-loop homeostasis. Nature communications, 15(1), 7081.

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

Wang J, et al. (2024) ARF alters PAF1 complex integrity to selectively repress oncogenic transcription programs upon p53 loss. Molecular cell, 84(23), 4538.

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

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.

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).

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

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

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

Fianu I, et al. (2021) Cryo-EM structure of mammalian RNA polymerase II in complex with human RPAP2. *Communications biology*, 4(1), 606.

Wang H, et al. (2020) Structure of H3K36-methylated nucleosome-PWWP complex reveals multivalent cross-gyre binding. *Nature structural & molecular biology*, 27(1), 8.

Farnung L, et al. (2020) Nucleosome-CHD4 chromatin remodeler structure maps human disease mutations. *eLife*, 9.

Hillen HS, et al. (2020) Structure of replicating SARS-CoV-2 polymerase. *Nature*, 584(7819), 154.

Kroupova A, et al. (2019) Structural basis for acceptor RNA substrate selectivity of the 3' terminal uridylyl transferase Tailor. *Nucleic acids research*, 47(2), 1030.