Mycobacterium tuberculosis Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 21

Catalog No. NR-19657

This reagent is the tangible property of the U.S. Government.

For research use only. Not for use in humans.

Contributor:

Pathogen Functional Genomics Resource Center at the J. Craig Venter Institute

Manufacturer:

BEI Resources

Product Description:

Production in the 96-well format has increased risk of cross-contamination between adjacent wells. Individual clones should be purified (e.g., single colony isolation and purification using good microbiological practices) and sequence-verified prior to use. BEI Resources does not confirm or validate individual mutants provided by the contributor.

The *Mycobacterium tuberculosis (M. tuberculosis)* Gateway® clone set consists of 42 plates which contain 3724 sequence validated clones [3294 *M. tuberculosis,* strain H37Rv clones supplemented with 430 unique open reading frames (ORF) from *M. tuberculosis*, strain CDC1551] cloned in *Escherichia coli (E. coli)* DH10B-T1 cells. Each ORF was recombined in vector pDONR™221 with an ATG start codon and no stop codon. The sequence was validated by full-length sequencing of each entry clone with greater than 1X coverage and a mutation rate of less than 0.2%. Detailed information about each clone is shown in Table 1.

Information related to the use of Gateway® Clones can be obtained from Invitrogen™. Recombination was facilitated through an *att*B substrate (*att*B-PCR product or a linearized *att*B expression clone) with an *att*P substrate (pDONR™221) to create an *att*L-containing entry clone. The entry clone contains recombinational cloning sites, *att*L1 and *att*L2 to facilitate gene transfer into a destination vector, M13 forward and reverse priming sites for sequencing and a kanamycin resistance gene for selection. Please refer to the Invitrogen™ Gateway® Technology Manual for additional details.

Plate orientation and viability were confirmed for NR-19657.

Material Provided:

Each inoculated well of the 96-well plate contains approximately 60 µL of culture in Luria Bertani (LB) broth containing 50 µg/mL kanamycin supplemented with 15% glycerol.

Packaging/Storage:

NR-19657 was packaged aseptically in a 96-well plate. The product is provided frozen and should be stored at -80°C or colder immediately upon arrival. For long-term storage, the vapor phase of a liquid nitrogen freezer is recommended. Freeze-thaw cycles should be avoided.

Growth Conditions:

Media:
LB broth or agar containing 50 µg/mL kanamycin
Incubation:
Temperature: 37°C
Atmosphere: Aerobic
Propagation:

1. Scrape top of frozen well with a pipette tip and streak onto agar plate.
2. Incubate the plates at 37°C for 1 day.

Citation:

Acknowledgment for publications should read “The following reagent was obtained through BEI Resources, NIAID, NIH: *Mycobacterium tuberculosis* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 21, NR-19657.”

Biosafety Level: 1

Appropriate safety procedures should always be used with this material. Laboratory safety is discussed in the following publication: U.S. Department of Health and Human Services, Public Health Service, Centers for Disease Control and Prevention, and National Institutes of Health. Biosafety in Microbiological and Biomedical Laboratories (BMBL). 6th ed. Washington, DC: U.S. Government Printing Office, 2020.

Disclaimers:

You are authorized to use this product for research use only. It is not intended for human use.

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References:

1. Cole, S. T., et al. "Deciphering the Biology of *Mycobacterium tuberculosis* from the Complete Genome Sequence." Nature 393 (1998): 537-544. PubMed: 9634230.
2. Camus, J. C., et al. "Re-Annotation of the Genome Sequence of *Mycobacterium tuberculosis* H37Rv." Microbiology 148 (2002): 2967-2973. PubMed: 12368430.

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Table 1: *Mycobacterium tuberculosis* Gateway® Clones, Plate 21 (ZMTLK)[1]

Clone	Well Position	ORF Length	Locus ID	Description	Accession Number	Average Depth of Coverage
41614	A01	679	Rv3373	enoyl-CoA hydratase	NP_217890.1	2
41609	A02	679	Rv2036	hypothetical protein Rv2036	NP_216552.1	2
41616	A03	682	Rv0356c	hypothetical protein Rv0356c	NP_214870.1	2
41627	A04	682	Rv3247c	thymidylate kinase	NP_217764.1	3.850439883
41629	A05	682	Rv3338	hypothetical protein Rv3338	NP_217855.1	2
41617	A06	682	Rv0835	lipoprotein LpqQ	NP_215350.1	2
41620	A07	682	Rv2197c	transmembrane protein	NP_216713.1	2
41633	A08	682	Rv3705c	proline rich protein	YP_178006.1	2.19941349
41626	A09	682	Rv3241c	hypothetical protein Rv3241c	NP_217758.1	2
41631	A10	682	Rv3368c	oxidoreductase	NP_217885.1	2.394428152
41621	A11	682	Rv2460c	ATP-dependent Clp protease proteolytic subunit	NP_216976.1	2
41615	A12	682	Rv0158	TetR family transcriptional regulator	NP_214672.1	2
41647	B02	685	Rv2825c	hypothetical protein Rv2825c	NP_217341.1	4.081751825
41638	B03	685	Rv1015c	50S ribosomal protein L25/general stress protein Ctc	NP_215531.1	3.861313869
41646	B04	685	Rv2511	oligoribonuclease	NP_217027.1	3.835036496
41649	B05	688	Rv0844c	nitrate/nitrite response transcriptional regulatory protein NarL	NP_215359.1	2
41654	B06	688	Rv3223c	RNA polymerase sigma factor RpoE	NP_217739.1	2
41656	B07	688	Rv3855	transcriptional regulatory repressor protein (TETR-family) ETHR	NP_218372.1	2
41653	B08	688	Rv3058c	TetR family transcriptional regulator	NP_217574.1	2
41655	B09	688	Rv3624c	hypoxanthine-guanine phosphoribosyltransferase	NP_218141.1	2
41652	B10	688	Rv2700	secreted alanine rich protein	NP_217216.1	2
41648	B11	688	Rv0526	thioredoxin protein	NP_215040.1	2
41664	B12	691	Rv1301	hypothetical protein Rv1301	NP_215817.1	2
41659	C01	691	Rv0413	7,8-dihydro-8-oxoguanine-triphosphatase	NP_214927.1	3.269175109
41668	C02	691	Rv1984c	cutinase precursor CFP21	NP_216500.1	2
41663	C03	691	Rv0836c	hypothetical protein Rv0836c	NP_215351.1	2
41675	C04	691	Rv3133c	two component transcriptional regulatory protein DevR	NP_217649.1	2
41679	C05	691	Rv3690	hypothetical protein Rv3690	NP_218207.1	2
41667	C06	691	Rv1667c	macrolide-transport ATP-binding protein ABC transporter	NP_216183.1	2
41676	C07	691	Rv3376	hypothetical protein Rv3376	NP_217893.1	2
41674	C08	691	Rv2720	LexA repressor	NP_217236.1	2
41671	C09	691	Rv2474c	hypothetical protein Rv2474c	NP_216990.1	2
41661	C10	691	Rv0434	hypothetical protein Rv0434	NP_214948.1	2
41662	C11	691	Rv0701	50S ribosomal protein L3	NP_215215.1	2
41693	C12	694	Rv3013	hypothetical protein Rv3013	NP_217529.1	2
41690	D01	694	Rv2503c	succinyl-CoA:3-ketoacid-coenzyme A transferase subunit beta ScoB	NP_217019.1	3.005763689
41695	D02	694	Rv3850	hypothetical protein Rv3850	NP_218367.1	2
41689	D03	694	Rv2046	lipoprotein lppI	NP_216562.1	2.061959654
41694	D04	694	Rv3513c	fatty-acid-CoA ligase	NP_218030.1	2
41684	D05	694	Rv0990c	hypothetical protein Rv0990c	NP_215505.1	2

Clone	Well Position	ORF Length	Locus ID	Description	Accession Number	Average Depth of Coverage
41683	D06	694	Rv0802c	hypothetical protein Rv0802c	NP_215317.1	2
41682	D07	694	Rv0727c	L-fuculose-phosphate aldolase	NP_215241.1	2
41687	D08	694	Rv1674c	transcriptional regulatory protein	NP_216190.1	2
41697	D09	697	Rv0349	hypothetical protein Rv0349	NP_214863.1	2
41699	D10	697	Rv2250c	transcriptional regulator	NP_216766.2	2.444763271
41696	D11	697	Rv0199	hypothetical protein Rv0199	NP_214713.1	2
41708	D12	700	Rv0187	O-methyltransferase	NP_214701.1	2
41710	E02	700	Rv0320	hypothetical protein Rv0320	NP_214834.1	3.837142857
41714	E03	700	Rv0721	30S ribosomal protein S5	NP_215235.1	2
41721	E04	700	Rv3483c	hypothetical protein Rv3483c	NP_218000.1	2
41717	E05	700	Rv2544	lipoprotein LppB	NP_217060.1	4.26
41709	E06	700	Rv0314c	hypothetical protein Rv0314c	NP_214828.1	2
41720	E07	700	Rv2873	cell surface lipoprotein mpt83 (lipoprotein P23)	NP_217389.1	2
41719	E08	700	Rv2692	TRK system potassium uptake protein CEOC	YP_177901.1	2.39
41725	E09	703	Rv1815	hypothetical protein Rv1815	NP_216331.1	4.226173542
41722	E10	703	Rv0448c	hypothetical protein Rv0448c	NP_214962.1	3.20625889
41731	E11	703	Rv3295	TetR family transcriptional regulator	NP_217812.1	4.105263158
41727	E12	703	Rv1975	hypothetical protein Rv1975	NP_216491.1	-
41728	F01	703	Rv2177c	transposase	NP_216693.1	4.216216216
41732	F02	703	Rv3301c	phosphate transporter PhoU	NP_217818.1	1.992887624
41723	F03	703	Rv1505c	hypothetical protein Rv1505c	NP_216021.1	1.991465149
41730	F04	703	Rv2322c	ornithine aminotransferase	NP_216838.1	2.691322902
41724	F05	703	Rv1591	hypothetical protein Rv1591	NP_216107.1	1.991465149
41736	F06	706	Rv0414c	thiamine-phosphate pyrophosphorylase	NP_214928.1	4
41735	F07	706	Rv0319	pyrrolidone-carboxylate peptidase	NP_214833.1	3.827195467
41742	F08	706	Rv3113	phosphatase	NP_217629.1	2
41737	F09	706	Rv1588c	REP13E12 repeat-containing protein	NP_216104.1	1.994334278
41744	F10	706	Rv3282	Maf-like protein	NP_217799.1	1.992917847
41745	F11	706	Rv3466	hypothetical protein Rv3466	NP_217983.1	2
41741	F12	706	Rv2469c	hypothetical protein Rv2469c	NP_216985.1	2.253541076
41743	G01	706	Rv3271c	integral membrane protein	NP_217788.1	1.992917847
41753	G02	709	Rv2419c	phosphoglycerate mutase (phosphoglyceromutase)	NP_216935.1	1.992947814
41750	G03	709	Rv0323c	hypothetical protein Rv0323c	NP_214837.1	4.235543018
41756	G04	709	Rv2693c	integral membrane alanine and leucine rich protein	NP_217209.1	2
41752	G05	709	Rv0702	50S ribosomal protein L4	NP_215216.1	4.231311707
41749	G06	709	Rv0306	putative oxidoreductase	NP_214820.1	2.047954866
41754	G07	709	Rv2584c	adenine phosphoribosyltransferase	NP_217100.1	4.221438646
41765	G08	712	Rv1852	urease accessory protein ureG	NP_216368.1	2
41771	G09	712	Rv2621c	transcriptional regulatory protein	NP_217137.1	3.233146067
41768	G10	712	Rv2581c	glyoxalase II	NP_217097.1	1.990168539
41761	G11	712	Rv0788	phosphoribosylformylglycinamidine synthase I	NP_215303.1	1.992977528
41775	G12	712	Rv3741c	oxidoreductase	NP_218258.1	1.992977528
41758	H02	712	Rv0478	deoxyribose-phosphate aldolase	NP_214992.1	2
41764	H03	712	Rv1216c	integral membrane protein	NP_215732.1	2
41772	H04	712	Rv3203	lipase LipV	NP_217719.1	3.231741573
41757	H05	712	Rv0088	hypothetical protein Rv0088	NP_214602.1	2
41776	H06	712	Rv3919c	16S rRNA methyltransferase GidB	NP_218436.1	4.247191011
41783	H07	715	Rv2636	hypothetical protein Rv2636	NP_217152.1	3.620979021
41781	H08	715	Rv1856c	short chain dehydrogenase	NP_216372.1	3.586013986
41780	H09	715	Rv1830	hypothetical protein Rv1830	NP_216346.1	1.993006993
41784	H10	715	Rv3387	transposase	NP_217904.1	2
41782	H11	715	Rv2618	hypothetical protein Rv2618	NP_217134.1	1.991608392
41791	H12	718	Rv1027c		NP_215543.1	1.991643454

[1] All information in this table was provided by the J. Craig Venter Institute at the time of deposition.