Mycobacterium tuberculosis Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 20

Catalog No. NR-19656

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-19656.

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-19656 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 20, NR-19656."

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:

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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.

Support Provided by NIAID

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Table 1: *Mycobacterium tuberculosis* Gateway® Clones, Plate 20 (ZMTLJ)[1]

Clone	Well Position	ORF Length	Locus ID	Description	Accession Number	Average Depth of Coverage
41456	A01	643	Rv0078	transcriptional regulatory protein	NP_214592.1	2
41471	A02	643	Rv1911c	lipoprotein LppC	NP_216427.1	3.833592535
41479	A03	646	Rv0525	hypothetical protein	NP_215039.1	4.27244582
41490	A04	646	Rv3609c	GTP cyclohydrolase I	NP_218126.1	2
41484	A05	646	Rv1539	lipoprotein signal peptidase	NP_216055.1	2
41481	A06	646	Rv1252c	lipoprotein LprE	NP_215768.1	2
41485	A07	646	Rv1556	regulatory protein	NP_216072.1	4.255417957
41482	A08	646	Rv1255c	transcriptional regulatory protein	NP_215771.1	2
41483	A09	646	Rv1435c	proline, glycine, valine-rich secreted protein	NP_215951.1	2
41489	A10	646	Rv3465	dTDP-4-dehydrorhamnose 3,5-epimerase RmlC	NP_217982.1	2
41487	A11	646	Rv2811	hypothetical protein	NP_217327.1	2
41480	A12	646	Rv0605	resolvase	NP_215119.1	2
41488	B01	646	Rv3066	DeoR family transcriptional regulator	NP_217582.1	2
41498	B02	649	Rv1890c	hypothetical protein	NP_216406.1	2
41495	B03	649	Rv1688	3-methyladenine DNA glycosylase	NP_216204.1	2
41501	B04	649	Rv3715c	recombination protein RecR	NP_218232.1	2
41492	B05	649	Rv0698	hypothetical protein	NP_215212.1	4.235747304
41502	B06	649	Rv3828c	resolvase	NP_218345.1	2
41500	B07	649	Rv3214	acid phosphatase	YP_177944.1	2
41499	B08	649	Rv2193	cytochrome C oxidase subunit III	NP_216709.1	2
41497	B09	649	Rv1745c	isopentenyl-diphosphate delta-isomerase	NP_216261.1	3.1201849
41510	B10	652	Rv2732c	transmembrane protein	NP_217248.1	2
41504	B11	652	Rv0238	TetR family transcriptional regulator	NP_214752.1	4.225460123
41509	B12	652	Rv1958c	hypothetical protein	NP_216474.1	2
41508	C01	652	Rv1341	putative deoxyribonucleotide triphosphate pyrophosphatase	NP_215857.1	3.685582822
41505	C02	652	Rv0316	muconolactone isomerase	NP_214830.1	2
41515	C03	652	Rv3322c	methyltransferase	YP_177958.1	2
41511	C04	652	Rv3007c	oxidoreductase	NP_217523.1	4.306748466
41518	C05	655	Rv1626	two-component system transcriptional regulator	NP_216142.1	2
41517	C06	655	Rv1498c	hypothetical protein	YP_177647.1	3.838167939
41524	C07	658	Rv2597	hypothetical protein	NP_217113.1	1.995440729
41523	C08	658	Rv2170	hypothetical protein	NP_216686.1	2
41522	C09	658	Rv1602	imidazole glycerol phosphate synthase subunit HisH	NP_216118.1	2
41519	C10	658	Rv0273c	transcriptional regulatory protein	NP_214787.1	2
41542	C11	661	Rv3588c	carbonic anhydrase	NP_218105.1	3.838124054
41539	C12	661	Rv3008	hypothetical protein	NP_217524.1	2
41527	D01	661	Rv0600c	two component sensor kinase	NP_215114.2	2
41533	D02	661	Rv2114	hypothetical protein	NP_216630.1	2
41537	D03	661	Rv2849c	cob(I)yrinic acid a,c-diamide adenosyltransferase	YP_177908.1	4.220877458
41534	D04	661	Rv2466c	hypothetical protein	NP_216982.1	2
41540	D05	661	Rv3309c	uracil phosphoribosyltransferase	NP_217826.1	4.248108926
41532	D06	661	Rv1700	hypothetical protein	NP_216216.1	2

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Clone	Well Position	ORF Length	Locus ID	Description	Accession Number	Average Depth of Coverage
41538	D07	661	Rv2926c	hypothetical protein	NP_217442.1	2
41544	D08	661	Rv3846	superoxide dismutase	NP_218363.1	2.515885023
41529	D09	661	Rv1044	hypothetical protein	NP_215560.1	2
41528	D10	661	Rv0775	hypothetical protein	NP_215289.1	2
41535	D11	661	Rv2491	hypothetical protein	NP_217007.1	2
41545	D12	664	Rv0042c	MarR family transcriptional regulator	NP_214556.1	2
41546	E01	664	Rv0329c	hypothetical protein	NP_214843.1	2
41553	E02	664	Rv2652c	phiRv2 prophage protein	NP_217168.1	2
41554	E03	664	Rv3167c	TetR family transcriptional regulator	NP_217683.1	2
41551	E04	664	Rv2065	precorrin-8X methylmutase	NP_216581.1	2
41548	E05	664	Rv1389	guanylate kinase	NP_215905.1	3.826807229
41549	E06	664	Rv1853	urease accessory protein ureD	NP_216369.1	3.832831325
41552	E07	664	Rv2306c	hypothetical protein	NP_216823.1	2
10033	E08	664	Rv3395A	hypothetical protein	NP_217912.2	2
41558	E09	667	Rv1822	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	NP_216338.1	2
41563	E10	667	Rv3016	lipoprotein LpqA	NP_217532.1	2
41555	E12	667	Rv0421c	hypothetical protein	NP_214935.1	2
41559	F01	667	Rv2746c	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	NP_217262.1	2
41562	F02	667	Rv2804c	hypothetical protein	NP_217320.1	4.24137931
41560	F03	667	Rv2799	hypothetical protein	NP_217315.1	2
41564	F04	667	Rv3830c	transcriptional regulatory protein TetR-family	NP_218347.1	4.217391304
41572	F05	670	Rv1601	imidazoleglycerol-phosphate dehydratase	NP_216117.1	2
41565	F06	670	Rv0264c	hypothetical protein	NP_214778.1	2
41578	F07	670	Rv3897c	hypothetical protein	NP_218414.1	2
41567	F08	670	Rv0539	dolichyl-phosphate sugar synthase	NP_215053.1	2
41577	F09	670	Rv2968c	integral membrane protein	NP_217484.1	2
41574	F10	670	Rv1733c	transmembrane protein	NP_216249.1	4.219402985
41566	F11	670	Rv0302	TetR/ACRR family transcriptional regulator	NP_214816.1	2
41570	F12	670	Rv1289	hypothetical protein	NP_215805.1	2
41569	G01	670	Rv0970	integral membrane protein	NP_215485.1	4.228358209
41571	G02	670	Rv1347c	hypothetical protein	NP_215863.1	2
41584	G03	673	Rv2421c	nicotinic acid mononucleotide adenylyltransferase	NP_216937.1	3.50371471
41583	G04	673	Rv2260	hypothetical protein	NP_216776.1	1.891530461
41590	G05	673	Rv3421c	hypothetical protein	NP_217938.1	2
41591	G06	673	Rv3641c	cell filamentation protein FIC	NP_218158.1	2
41581	G07	673	Rv1870c	hypothetical protein	NP_216386.1	2
41580	G08	673	Rv1851	urease accessory protein uref	NP_216367.1	2
41579	G09	673	Rv0195	two component transcriptional regulatory protein	NP_214709.1	-
41588	G10	673	Rv3249c	TetR family transcriptional regulator	NP_217766.1	2
41596	G12	676	Rv1377c	putative transferase	NP_215893.1	2.044378698
41593	H01	676	Rv1109c	hypothetical protein	NP_215625.1	2.221893491
41597	H02	676	Rv2295	hypothetical protein	NP_216811.1	3.125739645
41594	H03	676	Rv1219c	transcriptional regulatory protein	NP_215735.1	2
41600	H04	676	Rv3414c	RNA polymerase sigma factor SigD	NP_217931.1	2.202662722
41610	H05	679	Rv3160c	TetR family transcriptional regulator	NP_217676.1	2
41603	H06	679	Rv0398c	hypothetical protein	NP_214912.1	2
41604	H07	679	Rv0767c	hypothetical protein	NP_215281.1	4.762886598
41606	H08	679	Rv0821c	phosphate transport regulator	NP_215336.1	2
41607	H09	679	Rv0825c	hypothetical protein	NP_215340.1	2
41613	H10	679	Rv3242c	hypothetical protein	NP_217759.1	2.223858616
41611	H11	679	Rv3235	hypothetical protein	NP_217752.1	3.430044183
41608	H12	679	Rv1154c	hypothetical protein	NP_215670.1	2

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

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