

***Mycobacterium tuberculosis* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 12**

Catalog No. NR-19648

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 *attB* substrate (*attB*-PCR product or a linearized *attB* expression clone) with an *attP* substrate (pDONR™221) to create an *attL*-containing entry clone. The entry clone contains recombinational cloning sites, *attL1* and *attL2* 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-19648.

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-19648 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 12, NR-19648.”

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](#). 6th ed. Washington, DC: U.S. Government Printing Office, 2020; see www.cdc.gov/biosafety/publications/bmbl5/index.htm.

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.

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Table 1: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 12 (ZMTLB)¹

Clone	Well Position	ORF Length	Locus ID	Description	Accession Number	Average Depth of Coverage
40120	A01	286	Rv1741	hypothetical protein	NP_216257.1	2
40128	A02	289	Rv2517c	hypothetical protein	NP_217033.1	2
40126	A03	289	Rv1960c	hypothetical protein	NP_216476.1	2
40127	A04	289	Rv2076c	hypothetical protein	NP_216592.1	2
40129	A05	289	Rv3112	molybdenum cofactor biosynthesis protein D	YP_177928.1	1.626297578
10046	A06	289	Rv2094c	twin arginine translocase protein A	NP_216610.1	4.166089965
9950	A07	289	Rv0634A	hypothetical protein	YP_177629.1	1.775086505
40131	A08	292	Rv0623	hypothetical protein	NP_215137.1	2
40130	A09	292	Rv0055	30S ribosomal protein S18	YP_177688.1	2
40134	A10	292	Rv2104c	hypothetical protein	NP_216620.1	2
40139	A11	292	Rv3219	transcriptional regulatory protein WHIB-like WHIB1	NP_217735.1	2
40136	B01	292	Rv2664	hypothetical protein Rv2664	NP_217180.1	2.284246575
9952	B02	292	Rv3198A	ATP-dependent DNA helicase II UVRD2	NP_217714.1	2.657534247
10092	B03	292	Rv0590A	MCE family-like protein	YP_177627.1	2.366438356
40146	B04	295	Rv1107c	exodeoxyribonuclease VII small subunit	NP_215623.1	2
40162	B05	295	Rv3358	hypothetical protein	NP_217875.1	2
40159	B06	295	Rv2871	hypothetical protein	NP_217387.1	2.379661017
40150	B07	295	Rv1831	hypothetical protein	NP_216347.1	1.983050847
40156	B08	295	Rv2706c	hypothetical protein	NP_217222.1	2.644067797
40143	B09	295	Rv0596c	hypothetical protein	NP_215110.1	1.610169492
40157	B10	295	Rv2808	hypothetical protein	NP_217324.1	2
40161	B12	295	Rv3346c	hypothetical protein	NP_217863.1	2.613559322
10122	C01	295	Rv1638A	hypothetical protein	YP_177650.1	2.762711864
40167	C02	298	Rv2657c	phiRv2 prophage protein	NP_217173.1	2
40163	C03	298	Rv0626	hypothetical protein	NP_215141.1	2
40165	C04	298	Rv2412	30S ribosomal protein S20	NP_216928.1	2
40164	C05	298	Rv1241	hypothetical protein	NP_215757.1	2
40166	C06	298	Rv2441c	50S ribosomal protein L27	NP_216957.1	2
40173	C07	301	Rv2866	hypothetical protein	NP_217382.1	2
40169	C08	301	Rv0476	transmembrane protein	NP_214990.1	2
40170	C09	301	Rv0898c	hypothetical protein	NP_215413.1	3.485049834
40172	C10	301	Rv1839c	hypothetical protein	NP_216355.1	2
40168	C11	301	Rv0033	acyl carrier protein AcpA	NP_214547.1	2
40177	C12	304	Rv1083	hypothetical protein	NP_215599.1	3.289473684
40178	D01	304	Rv2055c	30S ribosomal protein S18	NP_216571.1	2
40174	D02	304	Rv0550c	hypothetical protein	NP_215064.1	2
40175	D03	304	Rv0569	hypothetical protein	NP_215083.1	2
40176	D04	304	Rv0616c	hypothetical protein	NP_215130.1	2
40179	D05	304	Rv2758c	hypothetical protein	NP_217274.1	1.644736842
9946	D06	304	Rv3566A	hypothetical protein	YP_177990.1	3.161184211
40185	D07	307	Rv3260c	transcriptional regulatory protein WHIB-like WHIB2	NP_217777.1	2
40181	D08	307	Rv1519	hypothetical protein	NP_216035.1	2
40182	D09	307	Rv2312	hypothetical protein	NP_216828.1	2

Clone	Well Position	ORF Length	Locus ID	Description	Accession Number	Average Depth of Coverage
40180	D10	307	Rv1247c	hypothetical protein	NP_215763.1	1.993485342
40184	D11	307	Rv2785c	30S ribosomal protein S15	NP_217301.1	2
40183	D12	307	Rv2760c	hypothetical protein	NP_217276.1	2
40186	E01	310	Rv0664	hypothetical protein	NP_215178.1	2.396774194
40192	E02	310	Rv3904c	hypothetical protein	NP_218421.1	2
40191	E03	310	Rv3769	hypothetical protein	NP_218286.1	2
40190	E04	310	Rv2662	hypothetical protein	NP_217178.1	2
40189	E05	310	Rv2422	hypothetical protein	NP_216938.1	2
40187	E06	310	Rv1580c	phiRv1 phage protein	NP_216096.1	2
40188	E07	310	Rv1993c	hypothetical protein	NP_216509.1	2
10007	E08	310	Rv3208A	hypothetical protein	YP_177943.1	-
40194	E09	313	Rv0879c	transmembrane protein	NP_215394.1	3.083067093
40195	E10	313	Rv1053c	hypothetical protein	NP_215569.1	3.562300319
40193	E11	313	Rv0424c	hypothetical protein	NP_214938.1	2
40198	E12	313	Rv3357	hypothetical protein	NP_217874.1	2
40197	F01	313	Rv2755c	type I restriction/modification system specificity determinant HsdS	YP_177904.1	2
40200	F02	316	Rv0544c	transmembrane protein	NP_215058.1	2.379746835
40202	F03	316	Rv0942	hypothetical protein	NP_215457.1	2
40203	F04	316	Rv2545	hypothetical protein	NP_217061.1	2
40201	F05	316	Rv0868c	molybdenum cofactor biosynthesis protein D	NP_215383.1	2
9985	F06	316	Rv2438A	hypothetical protein	YP_177671.1	-
9964	F07	316	Rv3197A	transcriptional regulatory protein WHIB-like WHIB7	YP_177940.1	3.155063291
40213	F08	319	Rv2865	hypothetical protein	NP_217381.1	2
40205	F09	319	Rv0705	30S ribosomal protein S19	NP_215219.1	2
40210	F10	319	Rv2632c	hypothetical protein	NP_217148.1	2
40206	F11	319	Rv0863	hypothetical protein	NP_215378.1	2
40214	F12	319	Rv3269	hypothetical protein	NP_217786.1	2
40207	G01	319	Rv1335	9.5 kDa culture filtrate antigen CFP10A	NP_215851.1	2
40209	G02	319	Rv2122c	phosphoribosyl-ATP pyrophosphatase	YP_177860.1	2.344827586
40204	G03	319	Rv0011c	putative septation inhibitor protein	NP_214525.1	2.482758621
9959	G04	319	Rv2922A	acylphosphatase	YP_177679.1	2
40222	G05	322	Rv1793	putative ESAT-6 like protein ESXN (ESAT-6 like protein 5)	YP_177838.1	2
40220	G06	322	Rv1567c	hypothetical protein	NP_216083.1	2
40221	G07	322	Rv1738	hypothetical protein	NP_216254.1	2
40219	G08	322	Rv1198	putative ESAT-6 like protein ESXL (ESAT-6 like protein 4)	NP_215714.1	2
40216	G09	322	Rv0105c	50S ribosomal protein L28	YP_177691.1	1.605590062
10056	G10	322	Rv1159A	pterin-4-alpha-carbinolamine dehydratase	YP_177641.1	4.335403727
10090	G11	325	Rv2309A	hypothetical protein	YP_177668.1	4.033846154
9954	G12	325	Rv2601A	hypothetical protein	YP_177673.1	2.593846154
10100	H01	337	Rv2077A	transmembrane protein	NP_216593.1	2.584569733
10130	H02	343	Rv3221A	putative acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	NP_217737.1	3.174927114
40328	H03	349	Rv1574	phiRV1 phage related protein	NP_216090.1	2
10080	H04	349	Rv3312A	secreted protein antigen	YP_177957.1	3.277936963
40342	H05	352	Rv0741	transposase	NP_215255.1	2
40350	H06	352	Rv3126c	hypothetical protein	NP_217642.1	2
40349	H07	352	Rv2876	transmembrane protein	NP_217392.1	2
40344	H08	352	Rv1849	urease subunit beta	NP_216365.1	2
40348	H09	352	Rv2749	hypothetical protein	NP_217265.1	2
40347	H10	352	Rv2442c	50S ribosomal protein L21	NP_216958.1	2
40346	H11	352	Rv2078	hypothetical protein	NP_216594.1	2
40343	H12	352	Rv1579c	phiRv1 phage protein	NP_216095.1	2

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