

***Mycobacterium tuberculosis* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 35**

Catalog No. NR-19671

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For research use only. Not for human use.

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-19671.

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-19671 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 35, NR-19671."

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](#). 5th ed. Washington, DC: U.S. Government Printing Office, 2009; 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 35 (ZMTLY)¹

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
44080	A01	1369	Rv0878c	PPE family protein	YP_177764.1	4.042366691
44083	A02	1372	Rv1313c	transposase	NP_215829.1	4.352769679
44085	A03	1372	Rv3798	transposase	NP_218315.1	4.331632653
44084	A04	1372	Rv2382c	polyketide synthetase MBTC (polyketide synthase)	NP_216898.1	4.344752187
44091	A05	1375	Rv3150	NADH dehydrogenase I chain F	NP_217666.1	3.794181818
44090	A06	1375	Rv2994	integral membrane protein	NP_217510.1	4.344
44098	A08	1378	Rv1923	lipase LIPD	NP_216439.1	4.314949202
44099	A09	1378	Rv2222c	glutamine synthetase	NP_216738.1	4.335994194
44096	A10	1378	Rv1592c	hypothetical protein Rv1592c	NP_216108.1	4.375181422
44097	A11	1378	Rv1774	oxidoreductase	NP_216290.1	4.377358491
44095	A12	1378	Rv1307	F0F1 ATP synthase subunit delta	NP_215823.1	1.945573295
44106	B01	1381	Rv1293	diaminopimelate decarboxylase LysA	NP_215809.1	2.640115858
44107	B02	1381	Rv3197	ABC transporter ATP-binding protein	NP_217713.1	4.310644461
44109	B03	1384	Rv0729	D-xylulose kinase XylB	NP_215243.1	4.265895954
44110	B04	1384	Rv2141c	hypothetical protein Rv2141c	YP_177864.1	4.26300578
44112	B05	1384	Rv3170	flavin-containing monoamine oxidase	NP_217686.1	1.836705202
44113	B06	1384	Rv3262	F420-0--gamma-glutamyl ligase	NP_217779.1	3.998554913
44108	B07	1384	Rv0026	hypothetical protein Rv0026	NP_214540.1	4.302745665
44114	B08	1384	Rv3441c	phospho-sugar mutase / MRSA protein	NP_217958.1	4
44115	B09	1384	Rv3740c	hypothetical protein Rv3740c	NP_218257.1	2.831647399
44117	B10	1387	Rv0161	oxidoreductase	NP_214675.1	1.902667628
44120	B11	1387	Rv0541c	integral membrane protein	NP_215055.1	3.775054074
44123	B12	1387	Rv3290c	L-lysine aminotransferase	NP_217807.1	4.218457102
44125	C01	1387	Rv3476c	dicarboxylic acid transport integral membrane protein KgtP	NP_217993.1	3.7444051911
44122	C02	1387	Rv2962c	glycosyl transferase	NP_217478.1	4.281903389
44121	C03	1387	Rv2589	4-aminobutyrate aminotransferase	NP_217105.1	4.211968277
44124	C04	1387	Rv3340	O-acetylhomoserine aminocarboxypropyltransferase	NP_217857.1	4.187454939
44118	C05	1387	Rv0327c	cytochrome P450 135A1	NP_214841.1	4.226387888
44128	C06	1390	Rv1878	glutamine synthetase	NP_216394.1	4.248920863
44133	C07	1390	Rv3227	3-phosphoshikimate 1-carboxyvinyltransferase	NP_217744.1	4.158273381
44129	C08	1390	Rv2386c	salicylate synthase MbtI	YP_177877.1	4.285611511
44138	C09	1393	Rv3496c	MCE-family protein MCE4D	NP_218013.1	4.312993539
44139	C10	1393	Rv3689	transmembrane protein	NP_218206.1	4.274946159
44137	C11	1393	Rv1128c	hypothetical protein Rv1128c	NP_215644.1	3.765254846
44134	C12	1393	Rv0483	lipoprotein LprQ	NP_214997.1	4.231155779
44141	D01	1396	Rv3593	lipoprotein LpqF	NP_218110.1	4.246418338
44140	D02	1396	Rv2559c	recombination factor protein RarA	NP_217075.1	3.53008596
10085	D03	1396	Rv2097c	hypothetical protein Rv2097c	NP_216613.1	1.377507163
10095	D04	1396	Rv0180c	transmembrane protein	NP_214694.1	1.388968481
10049	D05	1402	Rv1945	hypothetical protein Rv1945	NP_216461.1	7.45149786
10088	D06	1402	Rv3734c	hypothetical protein Rv3734c	NP_218251.1	7.538516405
10028	D07	1402	Rv0242c	3-ketoacyl-(acyl-carrier-protein) reductase	NP_214756.1	6.813837375
10058	D08	1402	Rv0169	MCE-family protein MCE1A	YP_177701.1	6.44721826

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
9998	D09	1402	Rv1702c	hypothetical protein Rv1702c	NP_216218.1	6.728245364
10306	D10	1405	Rv3449	membrane-anchored mycosin	NP_217966.1	7.392882562
10244	D11	1405	Rv0127	hypothetical protein Rv0127	NP_214641.1	6.985765125
10169	D12	1405	Rv2858c	aldehyde dehydrogenase	NP_217374.1	1.471886121
10212	E01	1405	Rv1842c	hypothetical protein Rv1842c	NP_216358.1	7.257651246
10202	E02	1408	Rv3106	NADPH:adrenodoxin oxidoreductase FPRA (NADPH-ferredoxin reductase)	NP_217622.1	7.219460227
10184	E03	1408	Rv1288	hypothetical protein Rv1288	NP_215804.1	6.966619318
10221	E04	1408	Rv0473	transmembrane protein	NP_214987.1	1.365056818
10240	E05	1411	Rv2848c	cobyrinic acid a,c-diamide synthase	NP_217364.1	6.936924167
10180	E06	1411	Rv2860c	glutamine synthetase	NP_217376.1	7.055988661
10161	E07	1411	Rv1407	Fmu protein (SUN protein)	NP_215923.1	1.429482636
10288	E08	1414	Rv1005c	aminodeoxychorismate synthase component I	NP_215521.1	6.465346535
10298	E09	1417	Rv2280	dehydrogenase	NP_216796.1	6.2900494
10198	E10	1417	Rv1425	hypothetical protein Rv1425	NP_215941.1	7.028934368
10174	E11	1417	Rv2978c	transposase	NP_217494.1	7.607621736
10167	E12	1417	Rv2855	mycothione reductase	YP_177910.1	6.310515173
10230	F01	1417	Rv0958	magnesium chelatase	NP_215473.1	7.330275229
10280	F02	1420	Rv3432c	glutamate decarboxylase GadB	NP_217949.1	7.152816901
10247	F03	1420	Rv1751	hypothetical protein Rv1751	NP_216267.1	1.29084507
10150	F04	1420	Rv2885c	transposase	NP_217401.1	7.199295775
10290	F05	1420	Rv0362	Mg ²⁺ transport transmembrane protein MgtE	NP_214876.1	7.507042254
10258	F06	1423	Rv3627c	hypothetical protein Rv3627c	NP_218144.1	7.134926212
10190	F07	1423	Rv0291	membrane-anchored mycosin	NP_214805.1	7.359803233
10292	F08	1423	Rv3790	oxidoreductase	NP_218307.1	7.361911455
10250	F10	1423	Rv0069c	L-serine dehydratase SdaA	NP_214583.1	6.817287421
10285	F11	1423	Rv1394c	cytochrome P450 132	YP_177807.1	7.027406887
10243	F12	1426	Rv1263	amidase	NP_215779.1	1.368863955
10300	G01	1426	Rv2178c	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase AroG	NP_216694.1	7.389200561
10314	G02	1426	Rv3254	hypothetical protein Rv3254	NP_217771.1	7.292426367
10318	G03	1426	Rv3882c	hypothetical protein Rv3882c	NP_218399.1	7.561009818
10282	G04	1426	Rv0524	glutamate-1-semialdehyde aminotransferase	NP_215038.1	7.312061711
10294	G05	1429	Rv3130c	triacylglycerol synthase	NP_217646.1	7.501049685
10214	G06	1429	Rv1854c	NADH dehydrogenase	NP_216370.1	7.491252624
10262	G07	1429	Rv0267	integral membrane nitrite extrusion protein NarU	NP_214781.1	7.405878237
10153	G08	1429	Rv2357c	glycyl-tRNA synthetase	NP_216873.1	1.371588523
10159	G09	1429	Rv1713	GTP-binding protein EngA	NP_216229.1	1.417074878
10279	G10	1432	Rv0462	dihydrolipoamide dehydrogenase	NP_214976.1	6.314944134
10178	G11	1444	Rv0509	glutamyl-tRNA reductase	NP_215023.1	6.808864266
10146	G12	1444	Rv3139	acyl-CoA dehydrogenase FADE24	NP_217655.1	5.709141274
10260	H01	1444	Rv0159c	PE family protein	YP_177697.1	6.263850416
10316	H02	1444	Rv1235	sugar-binding lipoprotein LpqY	NP_215751.1	7.493074792
10210	H03	1444	Rv1809	PPE family protein	YP_177845.1	6.844875346
10312	H04	1444	Rv2713	soluble pyridine nucleotide transhydrogenase	NP_217229.1	5.906509695
10188	H05	1447	Rv1586c	phiRv1 integrase	NP_216102.1	7.09813407
10305	H06	1447	Rv0017c	cell division protein RodA	NP_214531.1	6.451278507
10137	H07	1450	Rv1659	argininosuccinate lyase	NP_216175.1	6.547586207
10182	H08	1450	Rv3719	hypothetical protein Rv3719	NP_218236.1	6.151034483
10248	H09	1450	Rv0696	membrane sugar transferase	NP_215210.1	6.937241379
10272	H10	1450	Rv1146	transmembrane transport protein MmpL13B	NP_215662.1	5.846896552
10216	H11	1453	Rv1634	drug efflux membrane protein	NP_216150.1	7.052993806
10177	H12	1453	Rv1582c	probable phiRv1 phage protein	NP_216098.1	7.152787337

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