

***Mycobacterium tuberculosis* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 7**

Catalog No. NR-19643

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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-19643.

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-19643 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 7, NR-19643.”

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/bmlb5/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 7 (ZMTDG)¹

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
74787	A01	1534	Rv2004c	hypothetical protein	NP_216520.1	3.322685789
74777	A02	1540	Rv3490	alpha,alpha-trehalose-phosphate synthase	NP_218007.1	3.507142857
74918	A03	1549	Rv0336	13E12 repeat family protein	NP_214850.1	2.276307295
74957	A04	1555	Rv0895	hypothetical protein	NP_215410.1	3.427652733
74903	A05	1558	Rv0147	aldehyde dehydrogenase	NP_214661.1	3.486521181
74866	A06	1561	Rv3062	ATP-dependent DNA ligase	NP_217578.1	3.624599616
74906	A07	1561	Rv3561	acyl-CoA synthetase	NP_218078.1	2.864189622
75055	A08	1564	Rv0592	MCE-family protein MCE2D	NP_215106.1	4.098465473
74893	A09	1567	Rv3698	hypothetical protein	NP_218215.1	5.124441608
74971	A10	1567	Rv3887c	transmembrane protein	NP_218404.1	4.257817486
74921	A11	1573	Rv0234c	succinic semialdehyde dehydrogenase	NP_216247.2	4.27972028
74810	A12	1576	Rv2209	integral membrane protein	NP_216725.1	3.556472081
74897	B01	1576	Rv2733c	hypothetical protein	NP_217249.1	3.277284264
74697	B02	1582	Rv2414c	hypothetical protein	NP_216930.1	5.06573957
75046	B03	1585	Rv0171	MCE-family protein MCE1C	NP_214685.1	2.998107256
75041	B04	1585	Rv2213	leucyl aminopeptidase	NP_216729.1	5.203154574
74833	B05	1585	Rv2329c	nitrite extrusion protein 1 NarK1	NP_216845.1	3.013249211
74994	B06	1585	Rv3509c	hypothetical protein	NP_218026.1	3.176656151
75037	B07	1588	Rv2174	integral membrane protein	NP_216690.1	4.08186398
74737	B08	1594	Rv0453	PPE family protein	YP_177727.1	2.640526976
74938	B09	1597	Rv3776	hypothetical protein	NP_218293.1	3.046963056
74758	B10	1600	Rv2223c	exported protease	NP_216739.1	3.515
75058	B11	1603	Rv1345	long-chain-fatty-acid--	NP_215861.1	3.670617592
74769	B12	1612	Rv2154c	FtsW-like protein FtsW	NP_216670.1	4.265508685
74849	C01	1612	Rv3049c	monooxygenase	NP_217565.1	2.905086849
74713	C02	1621	Rv3211	ATP-dependent RNA helicase RhlE	NP_217727.1	3.312152992
74927	C03	1624	Rv2672	secreted protease	NP_217188.1	3.253694581
74935	C04	1627	Rv2502c	acetyl-/propionyl-CoA carboxylase subunit beta	NP_217018.1	3.525507068
74981	C05	1627	Rv3737	transmembrane protein	NP_218254.1	4.163491088
74855	C06	1636	Rv0806c	UDP-glucose-4-epimerase CpsY	NP_215321.1	3.647310513
74989	C07	1642	Rv3308	phosphomannomutase	NP_217825.1	3.950669915
75069	C08	1645	Rv0897c	oxidoreductase	NP_215412.1	4.145896657
74838	C09	1648	Rv3379c	1-deoxy-D-xylulose-5-phosphate synthase	NP_217896.1	3.52973301
74843	C10	1651	Rv3885c	hypothetical protein	NP_218402.1	4.235614779
75035	C11	1654	Rv1186c	hypothetical protein	NP_215702.1	3.477629988
74953	C12	1657	Rv3811	hypothetical protein	YP_178018.1	3.02051901
74883	D01	1666	Rv0672	acyl-CoA dehydrogenase FADE8	NP_215186.1	3.662665066
74998	D02	1672	Rv1013	acyl-CoA synthetase	NP_215529.1	3.003588517

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
75005	D03	1684	Rv1217c	tetronasin-transport integral membrane protein ABC transporter	NP_215733.1	3.866983373
75074	D04	1687	Rv2800	hydrolase	NP_217316.1	3.462359218
75065	D05	1690	Rv2100	hypothetical protein	NP_216616.1	3.956213018
74789	D06	1696	Rv0782	oligopeptidase B	NP_215295.2	4.264150943
74914	D07	1699	Rv0946c	glucose-6-phosphate isomerase	NP_215461.1	3.380812243
74782	D08	1702	Rv0166	acyl-CoA synthetase	NP_214680.1	3.456521739
75449	D09	1708	Rv0256c	PPE family protein	YP_177704.1	4.266978923
75125	D10	1729	Rv1754c	hypothetical protein	NP_216270.1	4.053209948
75323	D11	1741	Rv3245c	two component sensory transduction histidine kinase MTRB	NP_217762.1	3.998276852
75289	D12	1753	Rv1550	fatty-acid-CoA ligase	NP_216066.1	4.19965773
75182	E01	1768	Rv0226c	transmembrane protein	NP_214740.1	3.182126697
75393	E02	1774	Rv1185c	acyl-CoA synthetase	NP_215701.1	4.117249154
75317	E03	1786	Rv3533c	PPE family protein	YP_177985.1	3.555431131
75110	E04	1789	Rv2565	hypothetical protein	NP_217081.1	3.474007826
75142	E05	1792	Rv3590c	PE-PGRS family protein	YP_177993.1	1.938616071
75129	E06	1807	Rv2088	transmembrane serine/threonine-protein kinase J	NP_216604.1	4.122302158
75453	E07	1813	Rv1280c	periplasmic oligopeptide-binding lipoprotein OppA	NP_215796.1	4.079426365
75275	E08	1813	Rv3635	transmembrane protein	NP_218152.1	3.237727523
75262	E09	1828	Rv2572c	aspartyl-tRNA synthetase	NP_217088.1	2.791575492
75410	E10	1843	Rv0126	trehalose synthase TRES	NP_214640.1	2.295713511
75265	E11	1846	Rv1297	transcription termination factor Rho	NP_215813.1	2.908992416
75145	E12	1867	Rv2115c	ATPase	NP_216631.1	4.086234601
75330	F01	1873	Rv0244c	acyl-CoA dehydrogenase FADE5	NP_214758.1	2.849973305
75097	F02	1876	Rv1281c	oligopeptide-transport ATP-binding protein ABC transporter OppD	NP_215797.1	4.065565032
75351	F03	1885	Rv1492	methylmalonyl-CoA mutase small subunit	NP_216008.1	4.187798408
75083	F04	1885	Rv2356c	PPE family protein	YP_177872.1	3.975066313
75339	F05	1894	Rv1768	PE-PGRS family protein	YP_177832.1	2.343189018
75191	F06	1897	Rv3884c	CBXX/CFQX family protein	NP_218401.1	4.112282551
75375	F07	1900	Rv1925	acyl-CoA synthetase	NP_216441.1	3.796315789
75345	F08	1903	Rv1551	glycerol-3-phosphate acyltransferase	NP_216067.1	3.280084078
75137	F09	1933	Rv0282	hypothetical protein	NP_214796.1	3.829280911
75238	F10	1933	Rv1272c	drugs-transport transmembrane ATP-binding protein ABC transporter	NP_215788.1	3.167615106
75206	F11	1951	Rv3801c	acyl-CoA synthetase	NP_218318.1	3.150691953
75253	F12	1951	Rv3808c	bifunctional UDP-galactofuranosyl transferase GLFT	NP_218325.1	3.897488467
75333	G01	1954	Rv2682c	1-deoxy-D-xylulose-5-phosphate synthase	YP_177898.1	3.217502559
75305	G02	1972	Rv3710	2-isopropylmalate synthase	NP_218227.2	3.303245436
75113	G03	1978	Rv0248c	succinate dehydrogenase flavoprotein subunit	NP_214762.1	3.364509606
75219	G04	1978	Rv1420	excinuclease ABC subunit C	NP_215936.1	4.003538928
75367	G05	1981	Rv2299c	heat shock protein 90	NP_216815.1	3.467945482
75193	G06	1993	Rv3667	acetyl-CoA synthetase	NP_218184.1	3.538384345
75327	G07	2008	Rv2079	hypothetical protein	NP_216595.1	3.840139442
75170	G08	2020	Rv3743c	cation transporter P-type ATPase CtpJ	NP_218260.1	2.593069307
75159	G09	2023	Rv0102	integral membrane protein	NP_214616.1	3.739495798
75163	G10	2032	Rv0931c	transmembrane serine/threonine-protein kinase D PKND (protein kinase D) (STPK D)	NP_215446.1	3.758366142
75117	G11	2038	Rv3779	transmembrane protein alanine and leucine rich	NP_218296.1	4.407752699
75443	G12	2041	Rv2395	integral membrane protein	NP_216911.1	4.24399804
75242	H01	2059	Rv0457c	peptidase	NP_214971.1	3.639630889
75437	H02	2059	Rv1084	hypothetical protein	NP_215600.1	4.066537154

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
75249	H03	2071	Rv1836c	hypothetical protein	NP_216352.1	4.142926123
75593	H04	2101	Rv1877	integral membrane protein	NP_216393.1	4.360780581
75691	H05	2131	Rv2326c	transmembrane ATP-binding protein ABC transporter	NP_216842.1	3.916001877
75765	H06	2182	Rv0120c	elongation factor G	NP_214634.1	4.250229148
75579	H07	2203	Rv1564c	maltooligosyltrehalose synthase TreX	YP_177821.1	3.860190649
75622	H08	2212	Rv1781c	4-alpha-glucanotransferase MalQ	NP_216297.1	3.775768535
75697	H09	2266	Rv2984	polyphosphate kinase	NP_217500.1	7.053398058
75799	H10	2317	Rv0938	ATP-dependent DNA ligase	NP_215453.1	3.981009927
75702	H11	2350	Rv0969	metal cation transporter P-type ATPase CtpV	NP_215484.1	3.098297872
75843	H12	2353	Rv0949	ATP-dependent DNA helicase II UVRD1	YP_177772.1	3.552911177

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