

***Mycobacterium tuberculosis* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 4**

**Catalog No. NR-19640**

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

**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-19640.

**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-19640 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 18 to 24 hours.

**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 4, NR-19640."

**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/bmb15/index.htm](http://www.cdc.gov/biosafety/publications/bmb15/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 4 (ZMTDD)**

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
73090	A01	865	Rv2957	glycosyl transferase	NP_217473.1	4.04277457
73154	A02	868	Rv0153c	phosphotyrosine protein phosphatase PTPB (protein-tyrosine-phosphatase) (PTPase) (ptbB)	NP_214667.1	1.73041475
72826	A03	868	Rv2136c	undecaprenyl pyrophosphate phosphatase (uppP)	NP_216652.1	3.29608295
72860	A04	868	Rv2938	daunorubicin-DIM-transport integral membrane protein ABC transporter DrrC (drrC)	NP_217454.1	2
72841	A05	871	Rv3487c	esterase/lipase LipF (lipF)	NP_218004.1	3.05740528
72874	A06	874	Rv1460	transcriptional regulatory protein	NP_215976.2	1.49084668
73097	A07	874	Rv2119	hypothetical protein Rv2119	NP_216635.1	3.03546911
72854	A08	877	Rv2409c	hypothetical protein Rv2409c	NP_216925.1	3.26567845
72971	A09	880	Rv3243c	hypothetical protein Rv3243c	NP_217760.1	3.43977273
72936	A10	880	Rv3438	hypothetical protein Rv3438	NP_217955.1	1.9625
73046	A11	880	Rv3783	O-antigen/lipopolysaccharide transport integral membrane protein ABC transporter RfbD (rfbD)	NP_218300.1	3.92840909
72911	A12	880	Rv3878	hypothetical protein Rv3878	NP_218395.1	3.08977273
73014	B01	883	Rv2605c	acyl-CoA thioesterase II (tesB2)	NP_217121.1	2.93318233
72926	B02	883	Rv3333c	hypothetical protein Rv3333c	NP_217850.1	1.66591166
73131	B03	886	Rv1978	hypothetical protein Rv1978	NP_216494.1	3.87358916
72922	B04	892	Rv2313c	hypothetical protein Rv2313c	NP_216829.1	1.72309417
72879	B05	892	Rv3435c	transmembrane protein	NP_217952.1	3.55605381
72810	B06	892	Rv3810	exported repetitive protein precursor PirG (cell surface protein) (EXP53) (pirG)	NP_218327.1	1.70852018
72961	B07	895	Rv1062	hypothetical protein Rv1062	NP_215578.1	2.87932961
73037	B08	895	Rv1472	enoyl-CoA hydratase (echA12)	NP_215988.1	2.95642458
72801	B09	898	Rv0375c	carbon monoxide dehydrogenase medium subunit	NP_214889.1	3.04565702
72994	B10	898	Rv0436c	CDP-diacylglycerol--serine O-phosphatidyltransferase (pssA)	NP_214950.1	3.80400891
73141	B11	898	Rv1118c	hypothetical protein Rv1118c	NP_215634.1	2.97772829
72990	B12	898	Rv1244	lipoprotein LpqZ (lpqZ)	NP_215760.1	1.29064588
73034	C01	901	Rv0470c	hypothetical protein Rv0470A	YP_177622.1	2.88346282
72938	C02	901	Rv1455	hypothetical protein Rv1455	NP_215971.1	1.32297447
73073	C03	901	Rv1920	hypothetical protein Rv1920	NP_216436.1	2.98224195
73027	C04	901	Rv2877c	integral membrane protein	YP_177912.1	3.24750277
73049	C05	901	Rv3057c	short chain dehydrogenase	NP_217573.1	3.02219756
73082	C06	904	Rv0881	rRNA methyltransferase	NP_215396.1	1.67035398
73087	C07	904	Rv2161c	hypothetical protein Rv2161c	NP_216677.1	3.20685841
73101	C08	907	Rv2275	hypothetical protein Rv2275	NP_216791.1	2.98235943
73022	C09	907	Rv2924c	formamidopyrimidine-DNA glycosylase (fpg)	NP_217440.1	2.73980154
72951	C10	907	Rv2937	daunorubicin-DIM-transport integral membrane protein ABC transporter DrrB (drrB)	NP_217453.1	1.22601985

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
72986	C11	907	Rv3335c	integral membrane protein	NP_217852.1	1.52701213
72865	C12	907	Rv3555c	hypothetical protein Rv3555c	NP_218072.1	2.94928335
73161	D01	910	Rv1189	RNA polymerase sigma factor SigI (sigI)	NP_215705.1	1.58571429
73234	D02	911	Rv1282c	oligopeptide-transport integral membrane protein ABC transporter OppC (oppC)	NP_215798.1	3.54226125
73369	D03	913	Rv2911	D-alanyl-D-alanine carboxypeptidase (dacB2)	YP_177914.1	1.59255203
73518	D04	916	Rv0534c	1,4-dihydroxy-2-naphthoate octaprenyltransferase (menA)	NP_215048.1	1.38209607
73285	D05	922	Rv1369c	transposase	NP_215885.1	1.54121475
73215	D06	922	Rv2026c	hypothetical protein Rv2026c	NP_216542.1	1.78308026
73390	D07	922	Rv3395c	hypothetical protein Rv3395A	YP_177969.1	3.57375271
73210	D08	925	Rv0289	hypothetical protein Rv0289	NP_214803.1	1.3372973
73457	D09	925	Rv2886c	resolvase	NP_217402.1	1.47459459
73424	D10	925	Rv3232c	transcriptional regulatory protein PvdS (pvdS)	NP_217749.1	1.70054054
73381	D11	928	Rv0495c	hypothetical protein Rv0495c	NP_215009.1	1.5700431
73329	D12	928	Rv2751	hypothetical protein Rv2751	NP_217267.1	3.72198276
73522	E01	931	Rv1076	lipase LipU (lipU)	NP_215592.1	1.4650913
73313	E02	931	Rv2415c	hypothetical protein Rv2415c	NP_216931.1	1.58539205
73326	E03	934	Rv2793c	tRNA pseudouridine synthase B (truB)	NP_217309.1	3.25481799
73380	E04	943	Rv0936	phosphate ABC transporter transmembrane protein (pstA2)	NP_215451.1	1.8388123
73373	E05	946	Rv0281	hypothetical protein Rv0281	NP_214795.1	1.42494715
73396	E06	946	Rv0428c	hypothetical protein Rv0428c	NP_214942.1	1.86786469
73441	E07	946	Rv0650	sugar kinase	NP_215164.1	2.83192389
73481	E08	946	Rv1486c	hypothetical protein Rv1486c	NP_216002.2	3.54862579
73525	E09	946	Rv2458	homocysteine methyltransferase (mmuM)	NP_216974.1	3.77484144
73505	E10	949	Rv2835c	sn-glycerol-3-phosphate transport integral membrane protein ABC transporter UGPA (ugpA)	NP_217351.1	1.46786091
73297	E11	952	Rv1111c	hypothetical protein Rv1111c	NP_215627.2	1.52521008
73409	E12	952	Rv1324	thioredoxin	NP_215840.1	1.51365546
73229	F01	952	Rv3298c	esterase lipoprotein LpqC (lpqC)	NP_217815.1	3.3802521
73406	F02	955	Rv0930	phosphate ABC transporter transmembrane protein (pstA1)	NP_215445.2	1.41884817
73266	F03	964	Rv0142	hypothetical protein Rv0142	NP_214656.1	1.48858921
73264	F04	964	Rv3665c	peptide ABC transporter transmembrane protein (dppB)	NP_218182.1	1.5
73366	F05	967	Rv2252	diacylglycerol kinase	NP_216768.1	2.44984488
73358	F06	967	Rv2776c	oxidoreductase	NP_217292.1	1.48293692
73480	F07	970	Rv2334	cysteine synthase A CysK1 (cysK1)	YP_177868.1	1.79484536
73172	F08	970	Rv3695	hypothetical protein Rv3695	NP_218212.1	1.81237113
73454	F09	976	Rv1092c	pantothenate kinase (coaA)	NP_215608.1	1.85553279
73207	F10	976	Rv2282c	LysR family transcriptional regulator	NP_216798.1	2.57172131
73302	F11	979	Rv0796	transposase IS6110	NP_215311.1	1.46067416
73431	F12	982	Rv0233	ribonucleotide-diphosphate reductase subunit beta (nrdB)	NP_214747.1	2.59775967
73339	G01	982	Rv2727c	tRNA delta(2)-isopentenylpyrophosphate transferase (miaA)	NP_217243.1	1.88289206
73356	G02	982	Rv2824c	hypothetical protein Rv2824c	NP_217340.1	1.74541752
73228	G03	982	Rv2905	alanine rich lipoprotein LppW (lppW)	NP_217421.1	1.43584521
73220	G04	982	Rv3485c	short chain dehydrogenase	NP_218002.1	1.79327902
73433	G05	982	Rv3767c	hypothetical protein Rv3767c	NP_218284.1	2.59063136
73474	G06	988	Rv0604	lipoprotein lppO (lpqO)	NP_215118.1	2.52732794
73534	G07	988	Rv1296	homoserine kinase (thrB)	NP_215812.1	2.53846154
73203	G08	988	Rv1845c	hypothetical protein Rv1845c	NP_216361.1	1.6417004
73180	G09	988	Rv2413c	hypothetical protein Rv2413c	NP_216929.1	1.79149798

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
73183	G10	991	Rv1201c	transferase	NP_215717.1	1.23713421
73426	G11	991	Rv2985	hydrolase MutT1 (mutT1)	NP_217501.1	2.65489405
73485	G12	994	Rv3176c	epoxide hydrolase MesT (mesT)	YP_177938.1	2.46177062
73258	H01	997	Rv0787	hypothetical protein Rv0787	NP_215301.1	1.37311936
73495	H02	997	Rv1399c	lipase LipH (lipH)	NP_215915.1	2.45135406
73467	H03	997	Rv3683	hypothetical protein Rv3683	NP_218200.1	2.23570712
73397	H04	1000	Rv1400c	lipase LipI (lipI)	NP_215916.1	2.391
73513	H05	1000	Rv1949c	hypothetical protein Rv1949c	NP_216465.1	1.483
73173	H06	1009	Rv1336	cysteine synthase B CysM (cysM)	NP_215852.1	1.40336967
73197	H07	1009	Rv3625c	cell cycle protein MESJ (mesJ)	NP_218142.1	1.52923687
73501	H08	1015	Rv2893	oxidoreductase	NP_217409.1	1.34679803
73449	H09	1018	Rv1538c	L-aperaginase ansA (ansA)	NP_216054.1	1.35265226
73401	H10	1027	Rv1188	proline dehydrogenase	NP_215704.1	1.39240506
73537	H11	1027	Rv2649	transposase IS6110	NP_217165.1	2.3962999
73241	H12	1027	Rv3382c	LYTB-like protein LYTB1 (lytB1)	YP_177967.1	1.42161636

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