

***Mycobacterium tuberculosis* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 36**

Catalog No. NR-19672

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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-19672.

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-19672 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 36, NR-19672.”

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 36 (ZMTLZ)¹

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
10132	A01	1456	Rv0290	transmembrane protein	NP_214804.1	6.192994505
10193	A02	1456	Rv0777	adenylosuccinate lyase	NP_215291.1	1.333791209
10268	A03	1456	Rv3195	hypothetical protein Rv3195	NP_217711.1	7.090659341
10310	A04	1456	Rv1182	polyketide synthase associated protein PapA3	NP_215698.1	7.06456044
10254	A05	1456	Rv1477	invasion protein	NP_215993.1	5.460164835
10235	A06	1456	Rv3087	hypothetical protein Rv3087	NP_217603.1	1.343406593
10201	A07	1459	Rv2247	acetyl/propionyl-CoA carboxylase beta subunit AccD6	NP_216763.1	1.32830706
10457	A08	1459	Rv1193	acyl-CoA synthetase	NP_215709.1	1.419465387
10343	A10	1462	Rv3225c	transferase	NP_217742.1	1.358413133
10330	A11	1462	Rv3088	hypothetical protein Rv3088	NP_217604.1	7.432968536
10428	A12	1462	Rv0465c	transcriptional regulatory protein	NP_214979.1	6.645690834
10334	B01	1465	Rv0157	NAD(P) transhydrogenase subunit beta	NP_214671.1	7.521501706
10452	B02	1465	Rv1378c	hypothetical protein Rv1378c	NP_215894.1	7.434812287
10507	B03	1468	Rv3685c	cytochrome P450 137	NP_218202.1	1.360354223
10418	B04	1468	Rv2320c	cationic amino acid transport integral membrane protein RocE	NP_216836.1	7.271117166
10375	B05	1468	Rv1746	anchored-membrane serine/threonine-protein kinase PKNF (protein kinase F) (STPK F)	NP_216262.1	6.669618529
10388	B06	1471	Rv0537c	integral membrane protein	NP_215051.1	7.407205982
10491	B07	1471	Rv2920c	ammonium transporter	NP_217436.1	6.571040109
10326	B08	1474	Rv2220	glutamine synthetase GLNA1 (glutamine synthase) (GS-I)	NP_216736.1	7.379918589
10344	B09	1477	Rv2440c	GTPase ObgE	NP_216956.1	6.532836831
10454	B10	1477	Rv3539	PPE family protein	YP_177987.1	6.970886933
10332	B11	1477	Rv0341	isoniazid inducible gene protein INIB	NP_214855.1	7.280297901
10486	B12	1477	Rv0697	dehydrogenase	NP_215211.1	7.260663507
10352	C01	1477	Rv1843c	inosine 5-monophosphate dehydrogenase	NP_216359.1	6.773188896
10405	C02	1477	Rv2650c	phage protein		1.373053487
10339	C03	1480	Rv2997	alanine rich dehydrogenase	NP_217513.1	1.383783784
10508	C04	1480	Rv0486	mannosyltransferase	NP_215000.1	7.252702703
10407	C05	1480	Rv3585	DNA repair protein RadA	NP_218102.1	7.080405405
10358	C07	1480	Rv2205c	hypothetical protein Rv2205c	NP_216721.2	7.07972973
10394	C08	1483	Rv1630	30S ribosomal protein S1	NP_216146.1	7.484828051
10432	C09	1486	Rv1148c	hypothetical protein Rv1148c	NP_215664.1	6.664199192
10410	C10	1486	Rv0235c	transmembrane protein	NP_214749.1	7.345222073
10439	C11	1492	Rv2363	amidase	NP_216879.1	7.105227882
10480	C12	1495	Rv1623c	integral membrane cytochrome D ubiquinol oxidase (subunit I) cydA (cytochrome bd-I oxidase subunit I)	YP_177824.1	6.802675585
10378	D01	1498	Rv2155c	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	NP_216671.1	7.315754339
10380	D02	1498	Rv1310	F0F1 ATP synthase subunit beta	NP_215826.1	6.335781041
10350	D03	1498	Rv0565c	monooxygenase	NP_215079.1	7.452603471
10356	D04	1501	Rv2075c	hypothetical protein Rv2075c	NP_216591.1	7.38107928
10336	D05	1501	Rv0346c	L-asparagine ABC transporter permease	YP_177718.1	7.43637575

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
10500	D06	1501	Rv0223c	aldehyde dehydrogenase	NP_214737.1	7.299133911
10512	D07	1501	Rv2447c	folylpolyglutamate synthase protein FolC	NP_216963.1	7.033977348
10423	D08	1501	Rv1817	hypothetical protein Rv1817	NP_216333.1	6.995336442
10440	D09	1504	Rv3858c	glutamate synthase subunit beta	NP_218375.1	7.229388298
10371	D10	1504	Rv0086	possible hydrogenase HycQ		1.311170213
10367	D11	1504	Rv1180	polyketide beta-ketoacyl synthase PKS3	NP_215696.1	1.325797872
10408	D12	1507	Rv2268c	cytochrome P450 128	NP_216784.1	7.092236231
10346	E01	1507	Rv1371	hypothetical protein Rv1371	NP_215887.1	7.378898474
10434	E02	1507	Rv0768	aldehyde dehydrogenase NAD dependent AldA	NP_215282.1	7.171201062
10488	E03	1510	Rv0888	hypothetical protein Rv0888	NP_215403.1	7.223178808
10427	E04	1510	Rv3060c	GntR family transcriptional regulator	NP_217576.1	1.228476821
10402	E05	1510	Rv1127c	pyruvate phosphate dikinase	NP_215643.1	7.103311258
10464	E06	1510	Rv2992c	glutamyl-tRNA synthetase	YP_177915.1	7.151655629
10364	E07	1513	Rv2443	C4-dicarboxylate-transport transmembrane protein DctA	NP_216959.1	7.208856576
10470	E08	1513	Rv0016c	penicillin-binding protein PbpA	NP_214530.1	6.77461996
10448	E09	1513	Rv2484c	hypothetical protein Rv2484c	NP_217000.1	7.36483807
10443	E10	1516	Rv0210	hypothetical protein Rv0210	NP_214724.1	1.309366755
10463	E11	1519	Rv2852c	malate:quinone oxidoreductase	NP_217368.1	6.900592495
10528	E12	1525	Rv0892	monooxygenase	NP_215407.1	6.36
10702	F02	1525	Rv1018c	UDP-N-acetylglucosamine pyrophosphorylase glmU	NP_215534.1	7.203934426
10578	F03	1525	Rv3895c	hypothetical protein Rv3895c	NP_218412.1	7.300327869
10616	F04	1528	Rv2947c	polyketide synthase PKS15	NP_217463.1	7.152486911
10663	F05	1528	Rv1317c	bifunctional methylated-DNA--protein-cysteine methyltransferase/O-6-methylguanine-DNA transcription regulator	NP_215833.1	6.352748691
10570	F06	1534	Rv2643	arsenic-transport integral membrane protein ArsC	NP_217159.1	7.099739244
10623	F07	1534	Rv3267	hypothetical protein Rv3267	NP_217784.1	6.245110821
10682	F08	1534	Rv0419	lipoprotein peptidase LpqM	NP_214933.1	6.9726206
10640	F09	1537	Rv0794c	oxidoreductase	YP_177756.1	7.316851008
10706	F10	1540	Rv0418	lipoprotein aminopeptidase LpqL	NP_214932.1	8.116883117
10544	F11	1543	Rv3377c	cyclase	NP_217894.1	8.259235256
10686	F12	1543	Rv0654	dioxygenase	NP_215168.1	8.15683733
10609	G01	1543	Rv3220c	two component sensor kinase	NP_217736.1	1.259883344
10691	G02	1546	Rv1663	polyketide synthase pks17	NP_216179.1	5.598318241
10525	G03	1546	Rv0160c	PE family protein	YP_177698.1	1.309184994
10520	G04	1546	Rv0913c	dioxygenase	NP_215428.1	8.118369987
10633	G05	1546	Rv3506	acyl-CoA synthetase	NP_218023.1	1.307891332
10538	G06	1546	Rv1760	hypothetical protein Rv1760	NP_216276.1	7.714747736
10692	G07	1549	Rv2897c	hypothetical protein Rv2897c	NP_217413.1	8.143963848
10537	G08	1549	Rv1795	hypothetical protein Rv1795	NP_216311.1	1.293092318
10548	G09	1549	Rv0515	13E12 repeat family protein	NP_215029.1	7.487411233
10612	G10	1549	Rv1002c	hypothetical protein Rv1002c	NP_215518.1	7.834086507
10648	G11	1552	Rv0104	hypothetical protein Rv0104	NP_214618.1	7.428479381
10552	G12	1552	Rv3812	PE-PGRS family protein	YP_178019.1	7.326675258
10678	H01	1552	Rv0846c	oxidase	NP_215361.1	8.007087629
10656	H02	1555	Rv3598c	lysyl-tRNA synthetase	NP_218115.1	8.11318328
10518	H03	1555	Rv2315c	hypothetical protein Rv2315c	NP_216831.1	8.030868167
10606	H04	1558	Rv1782	hypothetical protein Rv1782	NP_216298.1	7.840179718
10564	H05	1561	Rv0458	aldehyde dehydrogenase	NP_214972.1	8.123638693
10638	H06	1561	Rv0001	chromosomal replication initiation protein	NP_214515.1	8.060858424
10615	H07	1564	Rv2349c	phospholipase C 3 PLCC	NP_216865.1	5.710358056
10522	H08	1567	Rv1032c	two component sensor histidine kinase TRCS	NP_215548.1	7.767070836
10593	H09	1567	Rv1330c	nicotinate phosphoribosyltransferase	NP_215846.2	1.25909381
10694	H10	1570	Rv0753c	methylmalonate-semialdehyde dehydrogenase	NP_215267.1	6.902547771
10660	H11	1573	Rv3824c	polyketide synthase associated protein	NP_218341.1	7.268277177
10566	H12	1573	Rv3877	transmembrane protein	NP_218394.1	6.262555626

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