

***Mycobacterium tuberculosis* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 37**

Catalog No. NR-19673

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-19673.

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-19673 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 37, NR-19673."

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.

Disclaimers:

You are authorized to use this product for research use only. It is not intended for human use.

Use of this product is subject to the terms and conditions of the BEI Resources Material Transfer Agreement (MTA). The MTA is available on our Web site at www.beiresources.org.

While BEI Resources uses reasonable efforts to include accurate and up-to-date information on this product sheet, neither ATCC® nor the U.S. Government makes any warranties or representations as to its accuracy. Citations from scientific literature and patents are provided for informational purposes only. Neither ATCC® nor the U.S. Government warrants that such information has been confirmed to be accurate.

This product is sent with the condition that you are responsible for its safe storage, handling, use and disposal. ATCC® and the U.S. Government are not liable for any damages or injuries arising from receipt and/or use of this product. While reasonable effort is made to ensure authenticity and reliability of materials on deposit, the U.S. Government, ATCC®, their suppliers and contributors to BEI Resources are not liable for

damages arising from the misidentification or misrepresentation of products.

Use Restrictions:

This material is distributed for internal research, non-commercial purposes only. This material, its product or its derivatives may not be distributed to third parties. Except as performed under a U.S. Government contract, individuals contemplating commercial use of the material, its products or its derivatives must contact the contributor to determine if a license is required. U.S. Government contractors may need a license before first commercial sale.

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.

ATCC® is a trademark of the American Type Culture Collection.



Table 1: *Mycobacterium tuberculosis*, Gateway® Clones, Plate 37 (ZMTMA)¹

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
10583	A01	1573	Rv2045c	carboxylesterase LipT	NP_216561.1	6.824539097
10602	A02	1576	Rv3484	hypothetical protein Rv3484	NP_218001.1	7.066624365
10670	A03	1576	Rv2351c	membrane-associated phospholipase C	NP_216867.1	7.310913706
10658	A04	1576	Rv2350c	membrane-associated phospholipase C	NP_216866.1	7.871192893
10550	A05	1576	Rv0773c	bifunctional cephalosporin acylase/gamma-glutamyltranspeptidase	NP_215287.1	7.068527919
10586	A06	1579	Rv2226	hypothetical protein Rv2226	NP_216742.1	6.872070931
10624	A07	1585	Rv2024c	hypothetical protein Rv2024c	NP_216540.1	7.137539432
10654	A08	1588	Rv2249c	glycerol-3-phosphate dehydrogenase	NP_216765.1	6.569899244
10516	A09	1588	Rv3818	hypothetical protein Rv3818	NP_218335.1	6.304156171
10652	A10	1588	Rv0594	MCE-family protein MCE2F	NP_215108.1	5.493073048
10590	A11	1591	Rv1730c	penicillin-binding protein	NP_216246.1	5.525455688
10676	A12	1591	Rv3696c	glycerol kinase	NP_218213.1	6.325581395
10674	B01	1594	Rv1410c	aminoglycosides/tetracycline-transport integral membrane protein	NP_215926.1	7.215809285
10650	B02	1597	Rv1007c	methionyl-tRNA synthetase	NP_215523.1	6.381340013
10794	B03	1603	Rv1290c	hypothetical protein Rv1290A	YP_177642.1	7.149719276
10867	B04	1609	Rv0957	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	NP_215472.1	5.625233064
10734	B05	1615	Rv2916c	signal recognition particle protein	NP_217432.1	7.064396285
10724	B06	1615	Rv3396c	GMP synthase	NP_217913.1	4.575851393
10888	B07	1618	Rv3031	hypothetical protein Rv3031	NP_217547.1	6.247218789
10821	B08	1618	Rv1130	hypothetical protein Rv1130	NP_215646.1	7.576019778
10841	B09	1621	Rv1595	L-aspartate oxidase	NP_216111.1	7.256631709
10714	B10	1621	Rv0808	amidophosphoribosyltransferase	NP_215323.1	6.906230722
10861	B11	1621	Rv3394c	hypothetical protein Rv3394c	NP_217911.1	6.072794571
10762	B12	1624	Rv1279	dehydrogenase FAD flavoprotein GMC oxidoreductase	NP_215795.1	6.594211823
10712	C01	1624	Rv2996c	D-3-phosphoglycerate dehydrogenase	YP_177916.1	6.891009852
10834	C02	1624	Rv1430	PE family protein	YP_177810.1	7.334359606
10854	C03	1627	Rv3411c	inosine 5'-monophosphate dehydrogenase	NP_217928.1	7.105716042
10742	C04	1627	Rv0974c	acetyl-/propionyl-CoA carboxylase subunit beta	NP_215489.1	7.371850031
10709	C05	1630	Rv0172	MCE-family protein MCE1D	NP_214686.1	5.662576687
10878	C06	1630	Rv2846c	integral membrane efflux protein EfpA	NP_217362.1	7.155828221
10837	C07	1636	Rv1750c	acyl-CoA synthetase	NP_216266.1	1.216381418
10824	C08	1639	Rv3403c	hypothetical protein Rv3403c	NP_217920.1	6.796217206
10850	C09	1642	Rv2052c	hypothetical protein Rv2052c	NP_216568.1	7.851400731
10726	C10	1642	Rv0552	hypothetical protein Rv0552	NP_215066.1	6.891595615
10862	C11	1645	Rv1319c	adenylate cyclase	NP_215835.1	6.900911854

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
10798	C12	1645	Rv1427c	acyl-CoA synthetase	NP_215943.1	6.490577508
10890	D01	1648	Rv3829c	dehydrogenase	NP_218346.1	7.466626214
10884	D03	1651	Rv0214	acyl-CoA synthetase	NP_214728.1	6.520896426
10772	D04	1651	Rv2333c	integral membrane transport protein	NP_216849.1	7.611144761
10784	D05	1654	Rv0283	hypothetical protein Rv0283	NP_214797.1	6.974002418
10730	D06	1657	Rv3417c	chaperonin GroEL	NP_217934.1	6.754375377
10817	D07	1660	Rv0440	chaperonin GroEL	NP_214954.1	7.677710843
10828	D08	1660	Rv0099	acyl-CoA synthetase	NP_214613.1	7.294578313
10783	D09	1660	Rv2756c	type I restriction/modification system DNA methylase HsdM	NP_217272.1	5.535542169
10768	D10	1660	Rv0783c	multidrug resistance integral membrane efflux protein EmrB	NP_215297.1	6.559036145
10729	D11	1663	Rv3666c	periplasmic dipeptide-binding lipoprotein DppA	NP_218183.1	7.12808178
10770	D12	1663	Rv1318c	adenylate cyclase	NP_215834.1	7.288634997
10710	E01	1666	Rv1473	macrolide ABC transporter ATP-binding protein	NP_215989.1	5.456782713
10864	E02	1669	Rv1187	pyrroline-5-carboxylate dehydrogenase ROCA	NP_215703.1	6.738765728
10806	E03	1669	Rv1058	acyl-CoA synthetase	NP_215574.1	6.039544638
10746	E05	1681	Rv3068c	phosphoglucosyltransferase	NP_217584.1	7.715645449
10858	E06	1681	Rv0423c	thiamine biosynthesis protein ThiC	NP_214937.1	7.769185009
10886	E07	1684	Rv3663c	peptide ABC transporter ATP-binding protein	NP_218180.1	7.793349169
10789	E08	1684	Rv3515c	acyl-CoA synthetase	YP_177983.1	1.119952494
10856	E09	1684	Rv3280	propionyl-CoA carboxylase beta chain	NP_217797.1	7.361638955
10786	E10	1687	Rv2196	ubiquinol-cytochrome C reductase QcrB (cytochrome B subunit)	NP_216712.1	7.622406639
10810	E11	1687	Rv3645	probable conserved transmembrane protein		7.502667457
10766	E12	1687	Rv1223	serine protease HtrA	NP_215739.2	6.819798459
10898	F01	1687	Rv1308	F0F1 ATP synthase subunit alpha	NP_215824.1	6.39122703
10740	F02	1690	Rv0922	transposase	NP_215437.1	7.205325444
10797	F03	1690	Rv1292	arginyl-tRNA synthetase	NP_215808.1	7.641420118
10716	F04	1690	Rv3886c	alanine and proline rich membrane-anchored mycosin	NP_218403.1	7.605325444
10920	F05	1693	Rv2411c	hypothetical protein Rv2411c	NP_216927.1	5.064382753
10993	F07	1696	Rv3470c	acetolactate synthase large subunit	NP_217987.1	1.188679245
10978	F08	1696	Rv3558	PPE family protein	YP_177988.1	7.102004717
10930	F09	1699	Rv3157	NADH dehydrogenase subunit M	NP_217673.1	7.260153031
11010	F10	1699	Rv3263	DNA methylase (modification methylase) (methyltransferase)	NP_217780.1	6.965862272
10917	F11	1708	Rv1635c	transmembrane protein	NP_216151.1	1.159836066
11023	F12	1708	Rv1704c	D-serine/alanine/glycine transporter protein CycA	NP_216220.1	7.6264637
10902	G01	1714	Rv2477c	putative ABC transporter ATP-binding protein	NP_216993.1	7.779463244
11046	G02	1714	Rv1162	respiratory nitrate reductase subunit beta NarH	NP_215678.1	5.457992999
10927	G03	1714	Rv2752c	hypothetical protein Rv2752c	NP_217268.1	1.168028005
10988	G04	1714	Rv1983	PE-PGRS family protein	YP_177854.1	7.694865811
10994	G05	1720	Rv0853c	pyruvate or indole-3-pyruvate decarboxylase pdc	NP_215368.1	6.439534884
11021	G06	1720	Rv1739c	sulphate-transport transmembrane protein ABC transporter	NP_216255.1	7.074418605
11014	G07	1720	Rv0976c	hypothetical protein Rv0976c	NP_215491.1	6.597674419
10961	G08	1720	Rv0270	acyl-CoA synthetase	NP_214784.1	1.080232558
11038	G09	1726	Rv0035	fatty-acid-CoA ligase	YP_177686.1	6.582271147
11012	G10	1726	Rv2797c	hypothetical protein Rv2797c	NP_217313.1	7.629779838
10972	G11	1726	Rv1204c	hypothetical protein Rv1204c	NP_215720.1	7.281575898
11074	G12	1729	Rv1253	cold-shock DEAD-box protein A	NP_215769.1	7.322151533
10912	H01	1729	Rv2391	ferredoxin-dependent nitrite reductase NIRA	NP_216907.1	7.326778485
11002	H02	1729	Rv3537	3-ketosteroid-delta-1-dehydrogenase	NP_218054.1	7.360902256

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
11066	H03	1738	Rv0785	putative FAD-binding dehydrogenase	NP_215299.1	7.445914845
10964	H04	1744	Rv0231	acyl-CoA dehydrogenase FADE4	NP_214745.1	7.514908257
10928	H05	1750	Rv3327	transposase	NP_217844.1	6.885142857
11042	H06	1753	Rv1029	potassium-transporting ATPase subunit A	NP_215545.1	6.938391329
11072	H07	1759	Rv3868	hypothetical protein Rv3868	NP_218385.1	6.683342808
10947	H08	1759	Rv2587c	preprotein translocase subunit SecD	NP_217103.1	7.198976691
11052	H09	1765	Rv0886	NADPH:adrenodoxin oxidoreductase FprB	NP_215401.1	7.128045326
11000	H10	1768	Rv1132	hypothetical protein Rv1132	NP_215648.1	6.846719457
10940	H11	1771	Rv1850	urease subunit alpha	NP_216366.1	7.451722191
11082	H12	1774	Rv3721c	DNA polymerase III (subunit gamma/tau) dnaZ/X	NP_218238.1	6.896279594

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