

***Mycobacterium tuberculosis* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 3**

Catalog No. NR-19639

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-19639.

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-19639 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 3, NR-19639."

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:

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 3 (ZMTDC)¹

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
72677	A01	700	Rv0085	hydrogenase HycP (hycP)	NP_214599.1	2
72733	A02	700	Rv0540	hypothetical protein Rv0540	NP_215054.1	1.93
72473	A03	700	Rv1362c	hypothetical protein Rv1362c	NP_215878.1	2
72714	A04	703	Rv3323c	MOAD-MOAE fusion protein MOAX (moaX)	YP_177959.1	1.87339972
72741	A05	712	Rv0649	malonyl CoA-acyl carrier protein transacylase (fabD2)	YP_177744.1	1.09410112
72754	A06	712	Rv0962c	lipoprotein LprP (lprP)	NP_215477.1	-
72616	A07	712	Rv2014	transposase	NP_216530.2	1.99157303
72580	A08	712	Rv2607	pyridoxamine 5'-phosphate Oxidase (pdxH)	NP_217123.1	1.99157303
72458	A09	718	Rv0229c	hypothetical protein Rv0229c	NP_214743.1	1.99860724
72689	A10	718	Rv1016c	lipoprotein LpqT (lpqT)	NP_215532.1	2.96657382
72409	A11	718	Rv1570	dithiobiotin synthetase (bioD)	NP_216086.1	1.60724234
72717	A12	727	Rv3268	hypothetical protein Rv3268	NP_217785.1	1.75240715
72481	B01	730	Rv0059	hypothetical protein Rv0059	NP_214573.1	1.99726027
72761	B02	730	Rv1566c	inv protein	NP_216082.1	1.75068493
72533	B03	733	Rv1710	hypothetical protein Rv1710	NP_216226.1	2
72746	B04	736	Rv0013	para-aminobenzoate synthase component II (trpG)	YP_177615.1	2.74592391
72585	B05	739	Rv2227	hypothetical protein Rv2227	NP_216743.1	2
72515	B06	742	Rv2013	transposase	NP_216529.2	2
72659	B07	742	Rv3765c	two component transcriptional regulatory protein	NP_218282.1	1.96361186
72618	B08	748	Rv2135c	hypothetical protein Rv2135c	NP_216651.1	1.97593583
72472	B09	748	Rv3519	hypothetical protein Rv3519	NP_218036.1	2
72653	B10	754	Rv0308	integral membrane protein	NP_214822.1	2
72485	B11	754	Rv0639	transcription antitermination protein NusG (nusG)	NP_215153.1	2
72421	B12	760	Rv1078	proline-rich antigen (pra)	NP_215594.1	1.98815789
72433	C01	760	Rv2525c	hypothetical protein Rv2525c	NP_217041.1	3.08552632
72729	C02	763	Rv0275c	TetR family transcriptional regulator	YP_177706.1	1.70249017
72695	C03	766	Rv3287c	anti-sigma factor rsbW (sigma negative effector) (rsbW)	NP_217804.2	3.02610966
72725	C04	769	Rv1748	hypothetical protein Rv1748	NP_216264.1	3.11053316
72547	C05	772	Rv0387c	PPE family protein	NP_214901.1	2.02720207
72441	C06	775	Rv1603	phosphoribosyl isomerase A (hisA)	NP_216119.1	1.8916129
72529	C07	778	Rv0625c	transmembrane protein	NP_215139.1	1.83547558
72402	C08	778	Rv1164	respiratory nitrate reductase subunit gamma NarI (narI)	NP_215680.1	1.8496144
72621	C09	778	Rv2573	2-dehydropantoate 2-reductase	NP_217089.2	1.30719794
72541	C10	778	Rv3653	PE-PGRS family-related protein (PE_PGRS61)	YP_178002.1	1.46272494
72766	C11	781	Rv0606	hypothetical protein Rv0606	NP_215120.1	1.9346991
72510	C12	781	Rv0757	two component system response transcriptional positive regulator PHOP (phoP)	NP_215271.1	2
72527	D01	781	Rv1350	3-ketoacyl-(acyl-carrier-protein) reductase (fabG)	NP_215866.1	2.30985915
72667	D02	781	Rv1553	fumarate reductase iron-sulfur subunit FrdB (frdB)	NP_216069.1	2.48015365
72641	D03	781	Rv3451	cutinase precursor CUT3 (cut3)	NP_217968.2	2.29961588
72625	D04	781	Rv3550	enoyl-CoA hydratase (echA20)	NP_218067.1	2.03072983
72705	D05	784	Rv0247c	fumarate reductase iron-sulfur subunit	NP_214761.1	1.83290816
72771	D06	784	Rv0769	short chain dehydrogenase	NP_215283.1	2.10714286
72597	D07	787	Rv0184	hypothetical protein Rv0184	NP_214698.1	1.85387548

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
72757	D08	787	Rv0494	GntR family transcriptional regulator	NP_215008.2	1.88437103
72390	D09	787	Rv2208	cobalamin synthase (cobS)	NP_216724.1	2.57814485
72681	D10	790	Rv1144	short-chain type dehydrogenase/reductase	NP_215660.1	1.91265823
72633	D11	790	Rv2516c	hypothetical protein Rv2516c	NP_217032.2	1.94050633
72591	D12	793	Rv0116c	hypothetical protein Rv0116c	NP_214630.1	2.50189155
72685	E01	793	Rv2403c	lipoprotein LppR (lppR)	NP_216919.1	1.89281211
72569	E02	796	Rv1491c	hypothetical protein Rv1491c	NP_216007.1	1.97613065
72648	E03	796	Rv2667	ATP-dependent protease ATP-binding subunit ClpC2 (clpC2)	YP_177897.1	2
72557	E04	796	Rv2686c	antibiotic ABC transporter transmembrane protein	NP_217202.1	1.55778894
72956	E05	799	Rv1424c	hypothetical protein Rv1424c	NP_215940.1	2
72780	E06	802	Rv1056	hypothetical protein Rv1056	NP_215572.1	1.99625935
73123	E07	805	Rv0091	bifunctional 5'-methylthioadenosine nucleosidase/S-adenosylhomocysteine nucleosidase (mtn)	NP_214605.1	2.7068323
73002	E08	805	Rv2237	hypothetical protein Rv2237	NP_216753.1	2.94782609
72959	E09	805	Rv3297	endonuclease VIII (nei)	NP_217814.1	3.08447205
73116	E10	808	Rv0446c	transmembrane protein	NP_214960.1	2
73029	E11	808	Rv2486	enoyl-CoA hydratase (echA14)	NP_217002.1	1.94554455
73135	E12	808	Rv3455c	tRNA pseudouridine synthase A (truA)	NP_217972.2	2.9009901
73005	F01	808	Rv3662c	hypothetical protein Rv3662c	NP_218179.1	1.50371287
73055	F02	811	Rv2189c	hypothetical protein Rv2189c	NP_216705.1	2.37731196
73139	F03	814	Rv3839	hypothetical protein Rv3839	NP_218356.1	1.47788698
72818	F04	823	Rv2928	thioesterase TESA (tesA)	NP_217444.1	1.87970838
72884	F05	823	Rv3286c	RNA polymerase sigma factor SigF (sigF)	NP_217803.1	2
73146	F06	826	Rv1086	short (C15) chain Z-isoprenyl diphosphate synthase (Z-FPP synthase) (Z-farnesyl diphosphate synthase) (Z-FPP synthetase) (Z-farnesyl diphosphate synthetase) (geranyltranstransferase) (farnesyl pyrophosphate synthetase)	NP_215602.1	2.60290557
72835	F07	826	Rv3559c	short chain dehydrogenase	NP_218076.1	2.0472155
72918	F08	829	Rv3516	enoyl-CoA hydratase (echA19)	NP_218033.1	2.51507841
72872	F09	829	Rv3833	AraC family transcriptional regulator	NP_218350.1	1.95778046
72813	F10	832	Rv0466	hypothetical protein Rv0466	NP_214980.1	1.90024039
72890	F11	832	Rv1008	deoxyribonuclease TatD (YijV protein) (tatD)	NP_215524.1	1.88221154
72979	F12	832	Rv3351c	hypothetical protein Rv3351c	NP_217868.1	2.37980769
72929	G01	835	Rv1964	integral membrane protein YrbE3A (yrbE3A)	NP_216480.1	1.97844311
73009	G02	835	Rv2362c	DNA repair protein RecO (recO)	NP_216878.1	1.62994012
72916	G03	835	Rv2702	polyphosphate glucokinase PPGK (polyphosphate-glucose phosphotransferase) (ppgK)	NP_217218.1	1.99281437
73079	G04	838	Rv3213c	SOJ/PARA-like protein	NP_217729.1	2.87350835
72966	G05	839	Rv2631	hypothetical protein Rv2631	NP_217147.2	2.81883194
72832	G06	841	Rv2131c	monophosphatase CysQ (cysQ)	NP_216647.1	1.90249703
72799	G07	844	Rv1141c	enoyl-CoA hydratase (echA11)	NP_215657.1	3.08530806
72839	G08	844	Rv2464c	DNA glycosylase	NP_216980.1	3.08649289
72942	G09	844	Rv3307	purine nucleoside phosphorylase (deoD)	NP_217824.1	2.32701422
72885	G10	847	Rv0971c	enoyl-CoA hydratase (echA7)	NP_215486.1	1.97048406
72976	G11	850	Rv0839	hypothetical protein Rv0839	NP_215354.1	2
73094	G12	850	Rv1613	tryptophan synthase subunit alpha (trpA)	NP_216129.1	1.81882353
73149	H01	850	Rv2813	hypothetical protein Rv2813	NP_217329.1	2.73882353
73067	H02	856	Rv1718	hypothetical protein Rv1718	NP_216234.1	3.27336449
73105	H03	856	Rv3600c	pantothenate kinase	NP_218117.1	2.99649533
72898	H04	859	Rv0079	hypothetical protein Rv0079	NP_214593.1	3.13853318
72782	H05	859	Rv0249c	succinate dehydrogenase membrane anchor subunit	NP_214763.1	1.65308498
72981	H06	859	Rv1339	hypothetical protein Rv1339	NP_215855.1	2.18044237
73042	H07	859	Rv2622	methyltransferase (methylase)	NP_217138.1	1.774156
72807	H08	862	Rv1403c	putative methyltransferase	NP_215919.1	3.54060325
72885	G10	847	Rv0971c	enoyl-CoA hydratase (echA7)	NP_215486.1	1.97048406
72976	G11	850	Rv0839	hypothetical protein Rv0839	NP_215354.1	2

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
73094	G12	850	Rv1613	tryptophan synthase subunit alpha (trpA)	NP_216129.1	1.81882353
73149	H01	850	Rv2813	hypothetical protein Rv2813	NP_217329.1	2.73882353
73067	H02	856	Rv1718	hypothetical protein Rv1718	NP_216234.1	3.27336449
73105	H03	856	Rv3600c	pantothenate kinase	NP_218117.1	2.99649533
72898	H04	859	Rv0079	hypothetical protein Rv0079	NP_214593.1	3.13853318
72782	H05	859	Rv0249c	succinate dehydrogenase membrane anchor subunit	NP_214763.1	1.65308498
72981	H06	859	Rv1339	hypothetical protein Rv1339	NP_215855.1	2.18044237
73042	H07	859	Rv2622	methyltransferase (methylase)	NP_217138.1	1.774156
72807	H08	862	Rv1403c	putative methyltransferase	NP_215919.1	3.54060325
73125	H09	862	Rv3030	hypothetical protein Rv3030	NP_217546.1	2.16589327
72852	H10	865	Rv0687	3-ketoacyl-(acyl-carrier-protein) reductase (fabG)	NP_215201.1	2
73110	H11	865	Rv1040c	PE family protein (PE8)	YP_177779.1	2.67630058
72861	H12	865	Rv2769c	PE family protein (PE27)	YP_177907.1	1.63468208

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