

***Bacillus anthracis* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 7**

**Catalog No. NR-19731**

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**Contributor:**

Pathogen Functional Genomics Resource Center at the J. Craig Venter Institute

**Manufacturer:**

BEI Resources

**Product Description:**

Clone plates are replicated using a BioMek® FX robot. 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 only confirms the clone plate orientation and viability of randomly picked clones. BEI Resources does not confirm or validate individual clone identities provided by the contributor.

The *Bacillus anthracis* (*B. anthracis*) Gateway® clone set consists of 58 plates which contain 5341 sequence validated clones from *B. anthracis*, strains Ames (5139 clones), Sterne (107 clones; contains plasmid pXO1 only) and A2012 (95 clones; contains plasmid pXO2 only) cloned in *Escherichia coli* (*E. coli*) DH10B-T1 cells. Each open reading frame was constructed in vector pDONR™221 (Invitrogen™) with an ATG start codon and no stop codon. The library was independently cloned and sequence verified by the [Harvard Institute of Proteomics](#). 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 a Harvard-modified *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-19731.

**Material Provided:**

Each inoculated well of the 96-well plate contains approximately 60 µL of *E. coli* culture (strain DH10B-T1) in Luria Bertani (LB) broth containing 50 µg/mL kanamycin supplemented with 15% glycerol.

**Packaging/Storage:**

NR-19731 was packaged aseptically in 96-well plates. 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 containing 50 µg/mL kanamycin

LB 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 24 hours.

**Citation:**

Acknowledgment for publications should read "The following reagent was obtained through BEI Resources, NIAID, NIH: *Bacillus anthracis* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 7, NR-19731."

**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).

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**References:**

1. Read, T. D., et al. "The Genome Sequence of *Bacillus anthracis* Ames and Comparison to Closely Related Bacteria." *Nature* 423 (2003): 81-86. PubMed: 12721629.
2. Read, T. D., et al. "Comparative Genome Sequencing for Discovery of Novel Polymorphisms in *Bacillus anthracis*." *Science* 296 (2002): 2028-2033. PubMed: 12004073.

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**Table 1: *Bacillus anthracis*, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 7 (QMG002848)<sup>1</sup>**

Clone	Well Position	Locus ID	Description	Source	Accession Number	FLEX CloneID
50340	A02	BA1463	ribosomal protein L5 domain protein	Chromosome (NC_003997)	NP_843918.1	241045
50599	A03	BA3798	hypothetical protein	Chromosome (NC_003997)	NP_846051.1	241059
48452	A04	BA3795	hypothetical protein	Chromosome (NC_003997)	NP_846049.1	241068
51237	A05	BA3807	hypothetical protein	Chromosome (NC_003997)	NP_846060.1	241077
48916	A06	BA3834	transcriptional repressor GlnR	Chromosome (NC_003997)	NP_846085.1	241086
51670	A07	BA1450	proton/glutamate symporter family protein	Chromosome (NC_003997)	NP_843906.1	241095
49530	A08	BA3850	hypothetical protein	Chromosome (NC_003997)	NP_846100.1	241108
47725	A09	BA0892	hypothetical protein	Chromosome (NC_003997)	NP_843403.1	240400
50695	A10	BA2787	glycine betaine/L-proline ABC transporter, glycine betaine/L-pr	Chromosome (NC_003997)	NP_845136.1	240419
51047	A11	BA0912	oligopeptide ABC transporter, ATP-binding protein	Chromosome (NC_003997)	NP_843420.1	240429
48724	A12	BA2812	hypothetical protein	Chromosome (NC_003997)	NP_845159.1	240438
50005	B01	BA1454	PspA/IM30 family protein	Chromosome (NC_003997)	NP_843910.1	241033
48163	B02	BA3836	hypothetical protein	Chromosome (NC_003997)	NP_846087.1	241046
48319	B03	BA1413	hypothetical protein	Chromosome (NC_003997)	NP_843870.1	241060
51008	B04	BA3839	stage V sporulation protein K	Chromosome (NC_003997)	NP_846090.1	241069
48666	B05	BA3800	hypothetical protein	Chromosome (NC_003997)	NP_846053.1	241078
51584	B06	BA3786	hypothetical protein	Chromosome (NC_003997)	NP_846042.1	241087
49072	B07	BA3830	prophage LambdaBa01, repressor protein, putative	Chromosome (NC_003997)	NP_846082.1	241096
49633	B08	BA3804	hypothetical protein	Chromosome (NC_003997)	NP_846057.1	241110
47828	B09	BA0900	hypothetical protein	Chromosome (NC_003997)	NP_843411.1	240406
48157	B10	BA2804	hypothetical protein	Chromosome (NC_003997)	NP_845153.1	240420
48583	B11	BA2782	cpsH domain protein	Chromosome (NC_003997)	NP_845131.1	240430
51163	B12	BA2811	membrane protein, putative	Chromosome (NC_003997)	NP_845158.1	240439
48009	C01	BA3825	hypothetical protein	Chromosome (NC_003997)	NP_846077.1	241034
48222	C02	BA3842	host factor-I protein	Chromosome (NC_003997)	NP_846093.1	241048
50612	C03	BA3818	hypothetical protein	Chromosome (NC_003997)	NP_846070.2	241061
48470	C04	BA3811	hypothetical protein	Chromosome (NC_003997)	NP_846063.1	241070
51267	C05	BA1456	sensor histidine kinase	Chromosome (NC_003997)	NP_843912.1	241079
48982	C06	BA1411	hypothetical protein	Chromosome (NC_003997)	NP_843868.1	241088
51758	C07	BA1452	Na <sup>+</sup> /H <sup>+</sup> antiporter family protein	Chromosome (NC_003997)	NP_843908.1	241097
47622	C08	BA0913	hypothetical protein	Chromosome (NC_003997)	NP_843421.1	240394

Clone	Well Position	Locus ID	Description	Source	Accession Number	FLEX CloneID
50591	C09	BA2783	hypothetical protein	Chromosome (NC_003997)	NP_845132.1	240409
48333	C10	BA0930	hypothetical protein	Chromosome (NC_003997)	NP_843436.1	240422
51063	C11	BA0902	ornithine cyclodeaminase/mu-crystallin family protein	Chromosome (NC_003997)	NP_843413.1	240431
48867	C12	BA2808	hypothetical protein	Chromosome (NC_003997)	NP_845156.1	240440
48073	D01	BA3796	hypothetical protein	Chromosome (NC_003997)	NP_846050.1	241038
48229	D02	BA1469	hypothetical protein	Chromosome (NC_003997)	NP_843924.1	241050
48382	D03	BA3823	hypothetical protein	Chromosome (NC_003997)	NP_846075.1	241062
51032	D04	BA3840	site-specific recombinase, phage integrase family	Chromosome (NC_003997)	NP_846091.1	241071
48762	D05	BA1453	hypothetical protein	Chromosome (NC_003997)	NP_843909.1	241080
51610	D06	BA1408	proton/glutamate symporter family protein	Chromosome (NC_003997)	NP_843865.1	241089
49316	D07	BA3822	hypothetical protein	Chromosome (NC_003997)	NP_846074.1	241098
50260	D08	BA5114	DNA binding protein, DksA/TraR family	Chromosome (NC_003997)	NP_847300.1	240395
47913	D09	BA2784	hypothetical protein	Chromosome (NC_003997)	NP_845133.1	240410
50972	D10	BA5125	L-lactate dehydrogenase	Chromosome (NC_003997)	NP_847311.1	240423
48634	D11	BA0932	hypothetical protein	Chromosome (NC_003997)	NP_843438.1	240432
51218	D12	BA0891	hypothetical protein	Chromosome (NC_003997)	NP_843402.1	240441
50198	E01	BA3827	hypothetical protein	Chromosome (NC_003997)	NP_846079.1	241039
50356	E02	BA3813	prophage LambdaBa01, thymidylate synthase-complementing protein	Chromosome (NC_003997)	NP_846065.1	241051
50872	E03	BA3847	1-phosphofructokinase	Chromosome (NC_003997)	NP_846098.1	241063
48642	E04	BA3824	hypothetical protein	Chromosome (NC_003997)	NP_846076.1	241072
51337	E05	BA1465	membrane protein, putative	Chromosome (NC_003997)	NP_843920.1	241081
49008	E06	BA3829	hypothetical protein	Chromosome (NC_003997)	NP_846081.1	241090
49386	E07	BA3803	prophage LambdaBa01, positive control factor Xpf, putative	Chromosome (NC_003997)	NP_846056.1	241100
47682	E08	BA5124	hypothetical protein	Chromosome (NC_003997)	NP_847310.1	240396
50634	E09	BA2785	glycine betaine/L-proline ABC transporter, permease protein	Chromosome (NC_003997)	NP_845134.1	240411
50982	E10	BA0909	oligopeptide ABC transporter, permease protein	Chromosome (NC_003997)	NP_843418.1	240425
48664	E11	BA2813	hypothetical protein	Chromosome (NC_003997)	NP_845160.1	240434
48874	E12	BA2780	hypothetical protein	Chromosome (NC_003997)	NP_845129.1	240442
48092	F01	BA3828	hypothetical protein	Chromosome (NC_003997)	NP_846080.1	241040
48291	F02	BA3809	hypothetical protein	Chromosome (NC_003997)	NP_846061.1	241052
48397	F03	BA3826	hypothetical protein	Chromosome (NC_003997)	NP_846078.1	241064
48641	F04	BA3810	hypothetical protein	Chromosome (NC_003997)	NP_846062.1	241074
48845	F05	BA3788	hypothetical protein	Chromosome (NC_003997)	NP_846044.1	241082
49050	F06	BA3792	hypothetical protein	Chromosome (NC_003997)	NP_846047.1	241092
51796	F07	BA1409	potassium uptake protein, TrkH family	Chromosome (NC_003997)	NP_843866.1	241101
50300	F08	BA0931	transcriptional regulator, MerR family	Chromosome (NC_003997)	NP_843437.1	240397
50662	F09	BA2778	oxidoreductase, short-chain dehydrogenase/reductase family	Chromosome (NC_003997)	NP_845127.1	240413
48396	F10	BA2790	ferredoxin	Chromosome (NC_003997)	NP_845139.1	240426
51119	F11	BA5128	hypothetical protein	Chromosome (NC_003997)	NP_847314.1	240435

Clone	Well Position	Locus ID	Description	Source	Accession Number	FLEX CloneID
51230	F12	BA5121	glycogen biosynthesis protein GlgD	Chromosome (NC_003997)	NP_847307.1	240443
50285	G01	BA1455	hypothetical protein	Chromosome (NC_003997)	NP_843911.1	241041
50430	G02	BA1462	methlytransferase, UbiE/COQ5 family	Chromosome (NC_003997)	NP_843917.1	241053
48423	G03	BA3820	hypothetical protein	Chromosome (NC_003997)	NP_846072.1	241066
51279	G04	BA3837	GTP-binding protein	Chromosome (NC_003997)	NP_846088.2	241075
51426	G05	BA1441	sulfate adenylyltransferase	Chromosome (NC_003997)	NP_843897.1	241083
51673	G06	BA3835	hypothetical protein	Chromosome (NC_003997)	NP_846086.1	241093
51814	G07	BA1459	branched-chain amino acid transport system II carrier protein	Chromosome (NC_003997)	NP_843915.1	241103
47708	G08	BA5126	hypothetical protein	Chromosome (NC_003997)	NP_847312.1	240398
50675	G09	BA0910	oligopeptide ABC transporter, permease protein	Chromosome (NC_003997)	NP_843419.1	240415
51000	G10	BA5113	1,4-dihydroxy-2-naphthoate octaprenyltransferase, putative	Chromosome (NC_003997)	NP_847299.1	240427
48687	G11	BA0929	hypothetical protein	Chromosome (NC_003997)	NP_843435.1	240436
48894	G12	BA5148	comA operon protein, putative	Chromosome (NC_003997)	NP_847334.1	240444
50334	H01	BA3848	transcriptional regulator, DeoR family	Chromosome (NC_003997)	NP_846099.1	241043
48307	H02	BA3844	hypothetical protein	Chromosome (NC_003997)	NP_846095.1	241056
50968	H03	BA3843	tRNA delta(2)-isopentenylpyrophosphate transferase	Chromosome (NC_003997)	NP_846094.1	241067
48649	H04	BA1458	hypothetical protein	Chromosome (NC_003997)	NP_843914.1	241076
48839	H05	BA1410	hypothetical protein	Chromosome (NC_003997)	NP_843867.1	241084
49058	H06	BA3793	hypothetical protein	Chromosome (NC_003997)	NP_846048.1	241094
49451	H07	BA1451	hypothetical protein	Chromosome (NC_003997)	NP_843907.1	241106
50435	H08	BA2809	hypothetical protein	Chromosome (NC_003997)	NP_845157.1	240399
50686	H09	BA0899	hypothetical protein	Chromosome (NC_003997)	NP_843410.1	240417
48549	H10	BA0895	hypothetical protein	Chromosome (NC_003997)	NP_843406.1	240428
51126	H11	BA2776	TPP-dependent acetoin dehydrogenase E1 alpha-subunit	Chromosome (NC_003997)	NP_845125.1	240437

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