

***Rickettsia prowazekii*, Strain Madrid E, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 4**

**Catalog No. NR-19452**

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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:**

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 *Rickettsia prowazekii* (*R. prowazekii*), strain Madrid E, Gateway® clone set consists of approximately 750 sequence validated clones from *R. prowazekii*, strain Madrid E, 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 sequence was validated by full length sequencing of each 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-19452.

**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-19452 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: *E. coli*, strain DH10B-T1 clones should be grown at 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: *Rickettsia prowazekii*, Strain Madrid E, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 4, NR-19452."

**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](http://www.cdc.gov/biosafety/publications/bmbL5/index.htm).

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**References:**

1. Andersson, S. G., et al. "The Genome Sequence of *Rickettsia prowazekii* and the Origin of Mitochondria." *Nature* 396 (1998): 133-140. PubMed: 9823893.

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**Table 1: *Rickettsia prowazekii*, Strain Madrid E, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 4 (ZRPAD)<sup>1</sup>**

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
45638	A01	RP461	hypothetical protein RP461	553	NP_220841.1	1.992767
45466	A02	RP501	tRNA pseudouridine synthase B	553	NP_220877.1	2.985507
45534	A03	RP437	hypothetical protein RP437	556	NP_220818.1	2
45503	A04	RP566	hypothetical protein RP566	556	NP_220938.1	1.992806
45395	A05	RP162	transcription antitermination protein NusB	559	NP_220552.1	1.987478
45363	A06	RP356	NADH dehydrogenase subunit B	559	NP_220740.1	1.989267
45542	A07	RP208	peptide deformylase	562	NP_220596.1	2
45603	A08	RP253	cytochrome C (cycM)	562	NP_220638.1	2
45378	A09	RP642	30S ribosomal protein S5	562	NP_221006.1	1.998221
45447	A10	RP270	cytochrome B6-F complex IRON-sulfur subunit (petA)	568	NP_220655.1	1.987676
45343	A11	RP353	NADH dehydrogenase subunit E	568	NP_220737.1	1.989437
45674	A12	RP644	50S ribosomal protein L6	568	NP_221008.1	1.991197
45622	B01	RP190	ubiquinone biosynthesis protein COQ7 (coq7)	571	NP_220579.1	1.992995
45414	B02	RP304	cytochrome C oxidase assembly protein	571	NP_220688.1	2
45670	B03	RP629	heat shock protein GrpE	571	NP_220994.1	-
45358	B04	RP647	50S ribosomal protein L5	574	NP_221011.1	1.989547
45678	B05	RP392	intracellular septation protein A	577	NP_220773.1	1.989601
45338	B06	RP741	putative metalloprotease	577	NP_221093.1	2
45470	B07	RP788	hypothetical protein RP787	577	NP_221138.1	1.991334
45478	B08	RP049	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (pgsA)	580	NP_220443.1	2
45514	B09	RP573	hypothetical protein RP573	580	NP_220945.1	2
45462	B10	RP319	ATP-dependent protease peptidase subunit	583	NP_220702.1	1.993139
45555	B11	RP693	ribosomal-protein-alanine acetyltransferase (rimJ)	586	NP_221054.1	2
45510	B12	RP264	hypothetical protein RP264	589	NP_220649.1	-
45531	C01	RP516	hypothetical protein RP516	592	NP_220892.1	1.988176
45687	C02	RP605	peptidyl-tRNA hydrolase	592	NP_220973.1	1.989865
45350	C03	RP073	hypothetical protein RP073	595	NP_220467.1	2
45631	C04	RP154	ribosome recycling factor	595	NP_220545.1	2
45418	C05	RP069	deoxycytidine triphosphate deaminase	601	NP_220463.1	1.991681
45458	C06	RP238	elongation factor P	601	NP_220623.1	4.259136

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
45642	C07	RP032	hypothetical protein RP032	604	NP_220426.1	1.991722
45355	C08	RP541	aromatic acid decarboxylase	604	NP_220914.1	1.860927
45482	C09	RP383	GTP cyclohydrolase I	607	NP_220764.1	1.99341
45486	C10	RP667	hypothetical protein RP667	607	NP_221029.1	2
45574	C11	RP031	SCO2 protein precursor (sco2)	610	NP_220425.1	2
45434	C12	RP057	16S rRNA methyltransferase GidB	610	NP_220451.1	2
45390	D01	RP135	transcription antitermination protein NusG	613	NP_220526.1	2
45582	D02	RP050	hypothetical protein RP050	616	NP_220444.1	2
45550	D03	RP202	ribonuclease HII	616	NP_220590.1	2
45490	D04	RP187	hypothetical protein RP187	619	NP_220576.1	2
45586	D05	RP324	hypothetical protein RP324	619	NP_220707.1	2
45523	D06	RP408	lipoprotein signal peptidase	619	NP_220789.1	1.990307
45540	D07	RP355	NADH dehydrogenase subunit C	628	NP_220739.1	3.504777
45571	D08	RP765	guanylate kinase	628	NP_221117.1	1.990446
45566	D09	RP794	cytochrome c biogenesis protein CcmA	628	NP_221144.1	1.993631
45411	D10	RP094	hypothetical protein RP094	634	NP_220487.1	1.992114
45659	D11	RP385	Holliday junction DNA helicase RuvA	634	NP_220766.1	-
45442	D12	RP327	thioredoxin peroxidase 1 (tdpX1)	637	NP_220710.1	2
45374	E01	RP026	hypothetical protein RP026	640	NP_220420.1	1.992188
45654	E02	RP506	hypothetical protein RP506	640	NP_220882.1	2
45690	E03	RP520	ATP-dependent Clp protease proteolytic subunit	640	NP_220894.1	2
45651	E04	RP750	phosphatidylglycerophosphatase A (pgpA)	640	NP_221102.1	1.99375
45595	E05	RP422	hypothetical protein RP422	646	NP_220803.1	1.993808
45406	E06	RP606	50S ribosomal protein L25/general stress protein Ctc	646	NP_220974.1	2
45714	E07	RP616	hypothetical protein RP616	646	NP_220983.1	2
45682	E08	RP684	thymidylate kinase	646	NP_221045.1	1.993808
45518	E09	RP592	hypothetical protein RP592	649	NP_220961.1	2
45507	E10	RP860	hypothetical protein RP860	649	NP_221208.1	1.998459
45626	E11	RP345	30S ribosomal protein S4	652	NP_220728.1	1.993865
45498	E12	RP587	SCO2 protein precursor (sco2)	652	NP_220956.1	1.949387
45474	F01	RP790	NADH dehydrogenase subunit J	652	NP_221140.1	2
45702	F02	RP819	hypothetical protein RP819	652	NP_221168.1	1.993865
45422	F03	RP193	hypothetical protein RP193	658	NP_220582.1	2
45398	F04	RP658	50S ribosomal protein L4	658	NP_221022.1	-
45382	F05	RP396	hypothetical protein RP396	661	NP_220777.1	1.993949
45430	F06	RP535	superoxide dismutase (sodB)	664	NP_220908.1	2
45662	F07	RP851	hypothetical protein RP851	664	NP_221199.1	2
45546	F08	RP300	outer membrane antigenic lipoprotein B precursor (nlpD)	667	NP_220684.1	2.991004
45371	F09	RP434	hypothetical protein RP434	673	NP_220815.1	1.995542
45710	F10	RP854	hypothetical protein RP854	673	NP_221202.1	1.991085
45610	F11	RP391	hypothetical protein RP391	676	NP_220772.1	1.994083
45386	F12	RP638	adenylate kinase	676	NP_221002.1	2
45526	G01	RP864	hypothetical protein RP864	676	NP_221212.1	1.994083
45647	G02	RP102	ribosome biogenesis GTP-binding protein YsxC	679	NP_220494.1	2
45635	G03	RP744	hypothetical protein RP744	682	NP_221096.1	1.991202
45494	G04	RP659	50S ribosomal protein L3	685	NP_221023.1	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
45699	G05	RP351	3-methyladenine DNA glycosylase	688	NP_220734.1	1.994186
45347	G06	RP653	30S ribosomal protein S3	688	NP_221017.1	1.988372
45450	G07	RP033	hypothetical protein RP033	691	NP_220427.1	1.994211
45427	G08	RP090	hypothetical protein RP090	691	NP_220483.1	1.991317
45707	G09	RP129	putative glutamine transport system permease protein GLNP (glnP)	691	NP_220521.1	3.98987
45562	G10	RP363	hypothetical protein RP363	691	NP_220746.1	1.994211
45366	G11	RP030	hypothetical protein RP030	694	NP_220424.1	1.994236
45454	G12	RP413	hypothetical protein RP413	694	NP_220794.1	1.994236
45615	H01	RP522	cytidylate kinase	694	NP_220896.1	1.991354
45619	H02	RP231	hypothetical protein RP231	697	NP_220617.1	4
45719	H03	RP870	hypothetical protein RP870	697	NP_221218.1	3.929699
45578	H04	RP397	thiol:disulfide interchange protein TLPA (tlpA)	700	NP_220778.1	2
45439	H05	RP631	hypothetical protein RP631	700	NP_220996.1	1.994286
45694	H06	RP700	glutamine transport ATP-binding protein GLNQ (glnQ1)	700	NP_221060.1	1.994286
45599	H07	RP066	hypothetical protein RP066	703	NP_220460.1	1.99431
45558	H08	RP490	hypothetical protein RP490	703	NP_220867.1	1.99431
45727	H09	RP815	Maf-like protein	703	NP_221164.1	2
45894	H10	RP828	hypothetical protein RP828	703	NP_221177.1	3.607397
45859	H11	RP242	CDP-diacylglycerol--serine O-phosphatidyltransferase (pssA)	709	NP_220627.1	1.991537
45863	H12	RP117	ribonuclease III	712	NP_220509.1	2

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