

***Rickettsia prowazekii*, Strain Madrid E, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 5**

**Catalog No. NR-19453**

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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-19453.

**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-19453 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 5, NR-19453."

**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. 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 5 (ZRPAE)<sup>1</sup>**

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
45815	A01	RP427	PETR protein (ompR)	712	NP_220808.1	1.994382
46102	A02	RP425	hypothetical protein RP425	715	NP_220806.1	3.986014
45746	A03	RP459	hypothetical protein RP459	715	NP_220839.1	1.538462
45899	A04	RP163	cell division protein FTSJ (ftsJ)	718	NP_220553.1	2.995822
45807	A05	RP694	hypothetical protein RP694	718	NP_221055.1	1.994429
46079	A06	RP277	hypothetical protein RP277	721	NP_220661.1	1.998613
45754	A07	RP424	phosphatidate cytidyltransferase (cdsA)	721	NP_220805.1	1.535368
45742	A08	RP732	DNA polymerase III subunit epsilon	724	NP_221085.1	2
46072	A09	RP830	HEME exporter protein C (ccmC)	727	NP_221179.1	4.22696
45874	A10	RP241	phosphatidylserine decarboxylase	730	NP_220626.1	2
45974	A11	RP473	hypothetical protein RP473	730	NP_220852.1	2
46010	A12	RP493	hypothetical protein RP493	730	NP_220869.1	2
45986	B01	RP867	hypothetical protein RP867	730	NP_221215.1	2
45943	B02	RP834	iron ABC transporter ATP-binding protein	736	NP_221183.1	1.990489
45763	B03	RP111	tRNA (guanine-N(1)-)-methyltransferase	739	NP_220503.1	1.987821
45946	B04	RP607	hypothetical protein RP607	739	NP_220975.1	1.928281
45995	B05	RP544	hypothetical protein RP544	742	NP_220917.1	1.994609
45827	B06	RP220	phosphoribosylaminoimidazole-succinocarboxamide synthase	745	NP_220606.1	1.836242
46006	B07	RP545	hypothetical protein RP545	745	NP_220918.1	1.994631
46063	B08	RP471	hypothetical protein RP471	751	NP_220850.1	2
45795	B09	RP148	dihydrodipicolinate reductase	754	NP_220539.1	1.994695
45750	B10	RP494	hypothetical protein RP494	757	NP_220870.1	1.993395
45790	B11	RP628	ribonuclease PH	757	NP_220993.1	2
46026	B12	RP868	glutamine transport ATP-binding protein GLNQ (glnQ2)	757	NP_221216.1	2
45979	C01	RP035	acetoacetyl-CoA reductase	760	NP_220429.1	2
45835	C02	RP150	amino-acid ABC transporter binding protein (yqiX)	760	NP_220541.1	1.986842
45970	C03	RP309	TOLQ protein (tolQ)	760	NP_220693.1	2
45851	C04	RP762	3-ketoacyl-(acyl-carrier-protein) reductase	760	NP_221114.1	3.967105
46022	C05	RP023	F0F1 ATP synthase subunit A	763	NP_220417.1	2
46098	C06	RP155	uridylylate kinase	763	NP_220546.1	3.994758

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
46046	C07	RP289	hypothetical protein RP289	766	NP_220673.1	1.994778
45731	C08	RP469	1-acyl-SN-glycerol-3-phosphate acyltransferase	766	NP_220848.1	3.792428
45903	C09	RP733	surfeit locus protein 1 (surf1)	769	NP_221086.1	1.992198
45982	C10	RP239	extragenic suppressor protein SUHB (suhB)	772	NP_220624.1	2
45854	C11	RP125	hypothetical protein RP125	778	NP_220517.1	2
45810	C12	RP287	VirB8	778	NP_220671.1	2
46035	D01	RP401	hypothetical protein RP401	778	NP_220782.1	2
46038	D02	RP591	hypothetical protein RP591	781	NP_220960.1	2
45962	D03	RP664	hypothetical protein RP664	781	NP_221026.1	2
46054	D04	RP827	hypothetical protein RP827	781	NP_221176.1	2
45934	D05	RP454	UDP-N-acetylglucosamine pyrophosphorylase (glmU)	784	NP_220834.1	1.994898
45830	D06	RP869	hypothetical protein RP869	784	NP_221217.1	1.994898
45938	D07	RP028	hypothetical protein RP028	787	NP_220422.1	3.947903
45926	D08	RP230	hypothetical protein RP230	787	NP_220616.1	1.994917
45722	D09	RP093	VACJ lipoprotein precursor (vacJ)	790	NP_220486.1	2
45759	D10	RP183	hypothetical protein RP183	790	NP_220572.1	1.916456
45891	D11	RP782	muropeptide permease AmpG	790	NP_221132.1	1.994937
46050	D12	RP003	O-antigen export system ATP-binding protein RFBE (rfbE)	793	NP_220399.1	2
45914	E01	RP027	hypothetical protein RP027	793	NP_220421.1	1.994956
46058	E02	RP097	ribonucleotide ABC transporter ATP-binding protein	793	NP_220490.1	2
45923	E03	RP343	hypothetical protein RP343	793	NP_220726.1	1.994956
45866	E04	RP455	hypothetical protein RP455	793	NP_220835.1	2
46031	E05	RP622	3-demethylubiquinone-9 3-methyltransferase	793	NP_220989.1	2.839849
46082	E06	RP272	cytochrome C1, HEME protein precursor (fbch)	796	NP_220657.1	1.993719
45911	E07	RP621	hypothetical protein RP621	796	NP_220988.1	2
45844	E08	RP857	tRNA pseudouridine synthase A	796	NP_221205.1	4.180905
45818	E09	RP508	ABC transporter ATP-binding protein	799	NP_220884.1	1.993742
45798	E10	RP440	inorganic polyphosphate/ATP-NAD kinase	802	NP_220821.1	1.995012
45774	E11	RP845	hypothetical protein RP845	811	NP_221193.1	2
45931	E12	RP096	hypothetical protein RP096	814	NP_220489.1	3.895577
45870	F01	RP824	methionine aminopeptidase	814	NP_221173.1	2
46042	F02	RP044	succinate dehydrogenase iron-sulfur subunit	820	NP_220438.1	1.993902
46020	F03	RP260	exodeoxyribonuclease III (xthA1)	820	NP_220645.1	4.179268
45998	F04	RP365	enoyl-(acyl carrier protein) reductase	820	NP_220748.1	1.995122
46075	F05	RP297	3'-phosphoadenosine-5'-phosphosulfate (PAPS) 3'-phosphatase	823	NP_220681.1	2
45779	F06	RP007	UDP-N-acetylglucosamine acyltransferase	829	NP_220403.1	1.992762
46002	F07	RP116	signal peptidase I (lepB)	829	NP_220508.1	1.995175
45738	F08	RP143	hypothetical protein RP143	829	NP_220534.1	1.993969
45734	F09	RP680	ubiquinone/menaquinone biosynthesis methyltransferase	832	NP_221041.1	1.995192
45847	F10	RP075	hypothetical protein RP075	838	NP_220469.1	1.995227
45990	F11	RP250	cell division protein FTSQ (ftsQ)	838	NP_220635.1	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
45918	F12	RP046	prolipoprotein diacylglyceryl transferase	841	NP_220440.1	2
45906	G01	RP533	biotin--protein ligase	841	NP_220906.1	2
46014	G02	RP672	dimethyladenosine transferase	841	NP_221033.1	2
45959	G03	RP172	DNA polymerase III subunit delta'	844	NP_220562.1	1.994076
45887	G04	RP474	hypothetical protein RP474	844	NP_220853.1	2.809242
45879	G05	RP676	exodeoxyribonuclease III (xthA2)	844	NP_221037.1	1.991706
45787	G06	RP415	diaminopimelate epimerase	847	NP_220796.1	2.819362
45955	G07	RP730	hypothetical protein RP730	847	NP_221083.1	3.034238
45770	G08	RP025	hypothetical protein RP025	853	NP_220419.1	3.118406
45883	G09	RP001	hypothetical protein RP001	856	NP_220397.1	1.991822
45803	G10	RP072	7-cyano-7-deazaguanine reductase	856	NP_220466.1	4.01986
46094	G11	RP656	50S ribosomal protein L2	856	NP_221020.1	3.535589
45950	G12	RP837	hypothetical protein RP837	856	NP_221186.1	3.165888
45782	H01	RP194	2,3,4,5-tetrahydropyridine-2,6-carboxylate N-succinyltransferase	859	NP_220583.1	3.777648
46086	H02	RP296	hypothetical protein RP296	859	NP_220680.1	2
46090	H03	RP062	2-dehydro-3-deoxyphosphooctonate aldolase	862	NP_220456.1	1.975638
45839	H04	RP463	hypothetical protein RP463	865	NP_220843.1	3.574566
46211	H05	RP495	hypothetical protein RP495	865	NP_220871.1	1.927168
46387	H06	RP191	cytochrome C oxidase polypeptide III (coxC)	871	NP_220580.1	1.95178
46275	H07	RP882	coproporphyrinogen III oxidase	874	NP_221228.1	1.994279
46115	H08	RP368	hypothetical protein RP368	877	NP_220751.1	3.868871
46139	H09	RP446	glycosyl transferase (IgtD)	877	NP_220827.1	2
46162	H10	RP747	hypothetical protein RP747	877	NP_221099.1	2.141391
46330	H11	RP404	hypothetical protein RP404	880	NP_220785.1	2.15
46455	H12	RP462	ribonuclease D (RND)	880	NP_220842.1	3.743182

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