

***Rickettsia prowazekii*, Strain Madrid E, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 7**

**Catalog No. NR-19455**

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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-19455.

**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-19455 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 7, NR-19455.”

**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 7 (ZRPAG)<sup>1</sup>**

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
46726	A01	RP018	190 kDa antigen precursor	1078	NP_220413.1	1.735622
46782	A02	RP338	hypothetical protein RP338	1078	NP_220721.1	1.752319
46599	A03	RP267	putative monovalent cation/H+ antiporter subunit B	1081	NP_220652.1	3.130435
46526	A04	RP243	multidrug resistance protein A (emrA)	1087	NP_220628.1	1.716651
46491	A05	RP417	phenylalanyl-tRNA synthetase subunit alpha	1087	NP_220798.1	1.661454
46811	A06	RP109	phosphate acetyltransferase	1090	NP_220501.1	1.76151
46650	A07	RP630	putative permease PerM	1090	NP_220995.1	1.644954
46666	A08	RP198	hypothetical protein RP198	1102	NP_220586.1	3.050817
46770	A09	RP529	peptide chain release factor 1	1102	NP_220902.1	4.279492
46747	A10	RP012	hypothetical protein RP012	1108	NP_220407.1	3.113718
46742	A11	RP212	putative ATPase N2B (n2B)	1108	NP_220598.1	1.674524
46823	A12	RP045	hypothetical protein RP045	1111	NP_220439.1	2.36241
46635	B01	RP306	tRNA-specific 2-thiouridylase MnmA	1111	NP_220690.1	3.114311
46839	B02	RP161	hypothetical protein RP161	1114	NP_220551.1	3.156194
46531	B03	RP029	recombination protein F	1117	NP_220423.1	2.417189
46778	B04	RP871	hypothetical protein RP871	1117	NP_221219.1	4.409132
46539	B05	RP595	phospho-N-acetylmuramoyl-pentapeptide-transferase	1120	NP_220963.1	1.7375
46654	B06	RP721	queuine tRNA-ribosyltransferase	1120	NP_221076.1	1.633929
46682	B07	RP769	hypothetical protein RP769	1123	NP_221121.1	1.632235
46519	B08	RP604	GTP-dependent nucleic acid-binding protein EngD	1132	NP_220972.1	1.60689
46795	B09	RP165	hypothetical protein RP165	1141	NP_220555.1	1.499562
46546	B10	RP274	peptide chain release factor 2	1145	-	4.300437
46542	B11	RP184	chaperone protein DnaJ	1147	NP_220573.1	4.761116
46807	B12	RP278	hypothetical protein RP278	1150	NP_220662.1	1.555652
46706	C01	RP748	hypothetical protein RP748	1150	NP_221100.1	2.97302
46703	C02	RP335	hypothetical protein RP335	1156	NP_220718.1	3.026817
46731	C03	RP760	hypothetical protein RP760	1156	NP_221112.1	3.722318
46759	C04	RP334	putative UDP-N-acetylglucosamine 2-epimerase (rfe)	1165	NP_220717.1	1.663519
46855	C05	RP487	NifS protein	1165	NP_220864.1	4.681545
46631	C06	RP411	cell division protein FTSW (ftsW)	1168	NP_220792.1	2.895548
46607	C07	RP678	hypothetical protein RP678	1174	NP_221039.1	3.68569
46523	C08	RP321	lipid-A-disaccharide synthase	1177	NP_220704.1	2.846285

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
46819	C09	RP255	hypothetical protein RP255	1180	NP_220640.1	1.448305
46767	C10	RP419	DNA polymerase III subunit beta	1180	NP_220800.1	1.499574
46851	C11	RP064	deoxyguanosinetriphosphate triphosphohydrolase-like protein	1186	NP_220458.1	2.910624
46751	C12	RP213	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	1186	NP_220599.1	1.626476
46786	D01	RP280	rod shape-determining protein RODA (rodA)	1186	NP_220664.1	1.586003
46815	D02	RP863	alanine dehydrogenase PntAa	1186	NP_221211.1	4.74199
46575	D03	RP874	succinyl-diaminopimelate desuccinylase	1186	NP_221221.1	2.939292
46514	D04	RP110	acetate kinase (ackA)	1192	NP_220502.1	2.822987
46691	D05	RP412	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	1192	NP_220793.1	1.578859
46586	D06	RP364	hypothetical protein RP364	1195	NP_220747.1	4.009205
46619	D07	RP433	succinyl-CoA synthetase subunit beta	1195	NP_220814.1	1.442678
46755	D08	RP015	poly(A) polymerase (pcnB)	1198	NP_220410.1	3.887866
46555	D09	RP037	putative DNA-binding/iron metalloprotein/AP endonuclease	1198	NP_220431.1	2.678631
46735	D10	RP047	hypothetical protein RP047	1201	NP_220441.1	4.633639
46871	D11	RP344	CAPM protein (capM1)	1204	NP_220727.1	4.548173
46834	D12	RP439	hypothetical protein RP439	1210	NP_220820.1	1.529752
46798	E01	RP698	bicyclomycin resistance protein (bcr2)	1210	NP_221058.1	4.624793
46698	E02	RP737	acetyl-CoA acetyltransferase	1213	NP_221089.1	1.546579
46803	E03	RP661	elongation factor Tu	1219	NP_221025.1	1.518458
46566	E04	RP038	acyl-CoA desaturase 1 (aco1)	1222	NP_220432.1	1.51964
46695	E05	RP223	hypothetical protein RP223	1231	NP_220609.1	1.559708
46594	E06	RP271	cytochrome B (petB)	1231	NP_220656.1	1.501219
46507	E07	RP175	coproporphyrinogen III oxidase	1234	NP_220565.1	3.623987
46830	E08	RP179	dihydrolipoamide succinyltransferase	1240	NP_220569.1	4.748382
46570	E09	RP337	hypothetical protein RP337	1246	NP_220720.1	1.421348
46610	E10	RP095	alanine racemase	1249	NP_220488.1	2.6672
46679	E11	RP375	proline/betaine transporter (proP3)	1255	NP_220758.1	3.172112
46722	E12	RP246	hypothetical protein RP246	1258	NP_220631.1	2.72496
46858	F01	RP336	hypothetical protein RP336	1258	NP_220719.1	1.461722
46791	F02	RP603	bicyclomycin resistance protein (bcr1)	1258	NP_220971.1	1.510334
46739	F03	RP669	putative ATP-dependent RNA helicase RHLE (rhIE)	1258	NP_221031.1	4.507154
46579	F04	RP668	muropeptide permease AmpG	1261	NP_221030.1	2.691515
46847	F05	RP486	cysteine desulfurase	1267	NP_220863.1	1.43015
46774	F06	RP556	tyrosyl-tRNA synthetase	1270	NP_220928.1	1.389764
46866	F07	RP091	aspartate aminotransferase	1273	NP_220484.1	1.357199
46510	F08	RP219	protease	1273	NP_220605.1	1.455617
46559	F09	RP259	penicillin-binding protein 4* (pbpE)	1279	NP_220644.1	1.352619
46762	F10	RP841	5-aminolevulinic acid synthase	1279	NP_221189.1	3.366693
46646	F11	RP232	hypothetical protein RP232	1282	NP_220618.1	2.655226
46827	F12	RP699	hypothetical protein RP699	1282	NP_221059.1	2.076443
46583	G01	RP852	proline/betaine transporter (proP6)	1282	NP_221200.1	1.438378
46662	G02	RP308	histidyl-tRNA synthetase	1285	NP_220692.1	1.442802
46495	G03	RP077	proline/betaine transporter (proP1)	1291	NP_220471.1	2.011619
46603	G04	RP579	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	1294	NP_220950.1	2.559073

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
46842	G05	RP743	serine hydroxymethyltransferase	1297	NP_221095.1	1.377024
46671	G06	RP115	NADH dehydrogenase I subunit F	1300	NP_220507.1	4.432308
46675	G07	RP416	hypothetical protein RP416	1300	NP_220797.1	1.304615
47026	G08	RP781	hypothetical protein RP780	1300	NP_221131.1	3.479231
47142	G09	RP681	hypothetical protein RP681	1306	NP_221042.1	1.405054
47015	G10	RP881	proline/betaine transporter (proP7)	1306	NP_221227.1	2.585758
47160	G11	RP702	hypothetical protein RP702	1309	NP_221062.1	4.576012
47075	G12	RP783	hypothetical protein RP782	1312	NP_221133.1	2.495427
46891	H01	RP690	hypothetical protein RP690	1315	NP_221051.1	3.870722
47134	H02	RP755	proline/betaine transporter (proP5)	1315	NP_221107.1	4.474525
46987	H03	RP764	3-oxoacyl-(acyl carrier protein) synthase II	1315	NP_221116.1	4.525475
47030	H04	RP054	glycerol-3-phosphate transporter (glpT)	1324	NP_220448.1	4.481118
47006	H05	RP483	putrescine-ornithine antiporter (potE)	1324	NP_220860.1	3.033208
47050	H06	RP284	putative monovalent cation/H <sup>+</sup> antiporter subunit D	1333	NP_220668.1	2.469617
47154	H07	RP384	prolyl-tRNA synthetase	1333	NP_220765.1	3.452363
47042	H08	RP536	folylpolyglutamate synthase (folC)	1336	NP_220909.1	3.497006
47171	H09	RP779	DNA polymerase III subunit alpha	1339	NP_221129.1	2.595967
47175	H10	RP844	type II citrate synthase	1345	NP_221192.1	2.441636
46963	H11	RP426	osmolarity sensor protein ENVZ (envZ)	1348	NP_220807.1	2.557864
47179	H12	RP685	proline/betaine transporter (proP4)	1351	NP_221046.1	1.431532

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