

***Helicobacter pylori* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 16**

**Catalog No. NR-19492**

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**Contributor:**

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

**Manufacturer:**

BEI Resources

**Product Description:**

The *Helicobacter pylori* (*H. pylori*) Gateway® clone set consists of approximately 1600 sequence validated clones from *H. pylori*, strain 26695 and strain J99 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.

**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.

**Note:** 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 cannot confirm or validate any clone not identified on the plate information table.

**Packaging/Storage:**

NR-19492 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: *Helicobacter pylori* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 16, NR-19492.”

**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. Alm, R. A., et al. "Genomic-Sequence Comparison of

Two Unrelated Isolates of the Human Gastric Pathogen *Helicobacter pylori*." *Nature* 397 (1999): 176-180. PubMed: 9923682.

2. Jungblut, P. R., et al. "Comparative Proteome Analysis of *Helicobacter pylori*." *Mol. Microbiol.* 36 (2000): 710-725. PubMed: 10844659.

3. Tomb, J. F., et al. "The Complete Genome Sequence of the Gastric Pathogen *Helicobacter pylori*." *Nature* 388 (1997): 539-547. PubMed: 9252185.

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**Table 1: *Helicobacter pylori* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 16 (ZHPAQ)<sup>1</sup>**

Strain	Clone	Well Position	Locus ID	Description	ORF Length	Accession Number <sup>2</sup>	Average Depth of Coverage
26695	61578	A01	HP0306	glutamate-1-semialdehyde 2,1-aminomutase	1327	<a href="#">NP_207104.1</a>	1.28937
26695	61582	A02	HP1366	type IIS restriction enzyme R protein	1306	<a href="#">NP_208158.1</a>	1.38055
26695	61587	A03	HP1143	hypothetical protein	1336	<a href="#">NP_207934.1</a>	1.26722
26695	61594	A04	HP1179	phosphopentomutase	1276	<a href="#">NP_207970.1</a>	1.42555
26695	61598	A05	HP1506	glutamate permease	1261	<a href="#">NP_208297.1</a>	1.37748
26695	61602	A06	HP0714	RNA polymerase sigma-54 factor	1279	<a href="#">NP_207508.1</a>	4.34715
26695	61607	A07	HP0619	lipopolysaccharide biosynthesis glycosyl transferase, degenerate	1287	-	4.35587
26695	61615	A08	HP0659	hypothetical protein	1279	<a href="#">NP_207453.1</a>	1.37764
26695	61619	A09	HP0169	collagenase	1303	<a href="#">NP_206968.1</a>	1.31389
26695	61623	A10	HP1361	competence locus E	1288	<a href="#">NP_208153.1</a>	1.41382
26695	61630	A11	HP1392	fibronectin/fibrinogen-binding protein	1342	<a href="#">NP_208183.1</a>	1.29657
26695	61635	A12	HP0438	IS605 transposase	1318	<a href="#">NP_207236.1</a>	1.34219
26695	61638	B01	HP1105	LPS biosynthesis protein	1330	<a href="#">NP_207896.1</a>	2.64211
26695	61646	B02	HP1364	signal-transducing protein, histidine kinase	1228	<a href="#">NP_208156.1</a>	2.75244
26695	61650	B03	HP0471	glutathione-regulated potassium-efflux system protein	1285	<a href="#">NP_207269.1</a>	3.78054
26695	61659	B04	HP0648	UDP-N-acetylglucosamine enolpyruvyl transferase	1303	<a href="#">NP_207442.1</a>	1.17498
26695	61662	B05	HP1420	flagellar export protein ATP synthase	1339	<a href="#">NP_208211.1</a>	3.19343
26695	61667	B06	HP0020	carboxynorspermidine decarboxylase	1252	<a href="#">NP_206822.1</a>	1.46805
26695	61670	B07	HP1023	hypothetical protein	1285	<a href="#">NP_207813.1</a>	4.41089
26695	61678	B08	HP1020	conserved hypothetical protein	1255	<a href="#">NP_207810.1</a>	3.34582
26695	61683	B09	HP1520	hypothetical protein	1327	<a href="#">NP_208311.1</a>	1.16202
26695	61687	B10	HP0027	isocitrate dehydrogenase	1312	<a href="#">NP_206829.1</a>	1.37271
26695	61690	B11	HP1218	glycinamide ribonucleotide synthetase	1309	<a href="#">NP_208010.1</a>	4.00535
26695	61695	B12	HP0673	hypothetical protein	1315	<a href="#">NP_207467.1</a>	3.09734
26695	61698	C01	HP0759	conserved hypothetical integral membrane protein	1288	<a href="#">NP_207552.1</a>	1.3028
26695	61702	C02	HP1534	IS605 transposase	1318	<a href="#">NP_208324.1</a>	1.45979
26695	61715	C03	HP1263	NADH-ubiquinone oxidoreductase, NQO4 subunit	1264	<a href="#">NP_208055.1</a>	1.38845

Strain	Clone	Well Position	Locus ID	Description	ORF Length	Accession Number <sup>2</sup>	Average Depth of Coverage
26695	61718	C04	HP0657	processing protease	1333	<a href="#">NP_207451.1</a>	1.43886
26695	61723	C05	HP0558	beta ketoacyl-acyl carrier protein synthase II	1273	<a href="#">NP_207353.1</a>	1.42262
26695	61726	C06	HP1126	colicin tolerance-like protein	1288	<a href="#">NP_207917.1</a>	1.35559
26695	61735	C07	HP1494	UDP-MurNac-tripeptide synthetase	1378	<a href="#">NP_208285.1</a>	1.29608
26695	61743	C08	HP0209	hypothetical protein	1387	<a href="#">NP_207007.1</a>	3.3057
26695	61747	C09	HP0223	ATP-dependent protease	1405	<a href="#">NP_207021.1</a>	3.55089
26695	61751	C10	HP0239	glutamyl-tRNA reductase	1384	<a href="#">NP_207037.1</a>	3.63006
26695	61762	C11	HP1279	anthranilate isomerase	1393	<a href="#">NP_208071.1</a>	1.28428
26695	61774	C12	HP1363	conserved hypothetical integral membrane protein	1435	<a href="#">NP_208155.1</a>	3.45087
26695	61779	D01	HP0724	anaerobic C4-dicarboxylate transport protein	1366	<a href="#">NP_207518.1</a>	1.39092
26695	61782	D02	HP1190	histidyl-tRNA synthetase	1363	<a href="#">NP_207981.1</a>	1.38958
26695	61787	D03	HP0623	UDP-N-acetylmuramate-alanine ligase	1384	<a href="#">NP_207417.1</a>	4.1922
26695	61790	D04	HP0229	outer membrane protein	1486	<a href="#">NP_207027.1</a>	3.6568
26695	61799	D05	HP0132	L-serine deaminase	1402	<a href="#">NP_206932.1</a>	1.36448
26695	61802	D06	HP0252	outer membrane protein	1498	<a href="#">NP_207050.1</a>	3.79439
26695	61809	D07	HP0087	lipoprotein, putative	1408	<a href="#">NP_206887.1</a>	2.93395
26695	61823	D08	HP0643	glutamyl-tRNA synthetase	1354	<a href="#">NP_207437.1</a>	1.32792
26695	61827	D09	HP1325	fumarase	1426	<a href="#">NP_208117.1</a>	1.07433
26695	61839	D10	HP0370	biotin carboxylase	1411	<a href="#">NP_207168.1</a>	1.17647
26695	61846	D11	HP1529	chromosomal replication initiator protein	1408	<a href="#">NP_208319.1</a>	4.15767
26695	61850	D12	HP0834	GTP-binding protein homologue	1411	<a href="#">NP_207627.1</a>	1.28207
26695	61862	E01	HP0508	hypothetical protein	1393	<a href="#">NP_207305.1</a>	1.30581
26695	61866	E02	HP0693	conserved hypothetical integral membrane protein	1399	<a href="#">NP_207487.1</a>	3.99571
26695	61871	E03	HP0885	virulence factor mviN protein	1495	<a href="#">NP_207678.1</a>	2.4495
26695	61875	E04	HP0670	hypothetical protein	1384	<a href="#">NP_207464.1</a>	1.20303
26695	61878	E05	HP1273	NADH-ubiquinone oxidoreductase, NQO14 subunit	1507	<a href="#">NP_208065.1</a>	3.61845
26695	61894	E06	HP0134	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase	1384	<a href="#">NP_206934.1</a>	1.35549
26695	61898	E07	HP1527	hypothetical protein	1474	<a href="#">NP_208317.1</a>	1.25984
26695	61906	E08	HP0487	hypothetical protein	1477	<a href="#">NP_207284.1</a>	2.96073
26695	61910	E09	HP1490	conserved hypothetical protein	1384	<a href="#">NP_208281.1</a>	3.54118
26695	61915	E10	HP1152	signal recognition particle protein	1381	<a href="#">NP_207943.1</a>	1.27806
26695	61919	E11	HP1283	hypothetical protein	1492	<a href="#">NP_208075.1</a>	3.78954
26695	61923	E12	HP0977	conserved hypothetical secreted protein	1498	<a href="#">NP_207768.1</a>	3.91055
26695	61927	F01	HP0075	urease protein	1372	<a href="#">NP_206875.1</a>	1.25219
26695	61930	F02	HP0405	nifS-like protein	1357	<a href="#">NP_207203.1</a>	1.3552
26695	61934	F03	HP0795	trigger factor	1390	<a href="#">NP_207588.1</a>	3.2295
26695	61954	F04	HP0098	threonine synthase	1495	<a href="#">NP_206898.1</a>	1.18127
26695	61959	F05	HP0978	cell division protein (ftsA) protein	1513	<a href="#">NP_207769.1</a>	1.00925
26695	61962	F06	HP0522	cag pathogenicity island protein	1480	<a href="#">NP_207318.1</a>	4.18716
26695	61971	F07	HP1181	multidrug-efflux transporter	1366	<a href="#">NP_207972.1</a>	4.29502
26695	61983	F08	HP0086	conserved hypothetical protein	1387	<a href="#">NP_206886.1</a>	1.27397
26695	61986	F09	HP1012	protease	1369	<a href="#">NP_207802.1</a>	1.3645

Strain	Clone	Well Position	Locus ID	Description	ORF Length	Accession Number <sup>2</sup>	Average Depth of Coverage
26695	61990	F10	HP0144	cytochrome c oxidase, heme b and copper-binding subunit, membrane-bound	1501	<a href="#">NP_206943.1</a>	3.36376
26695	61999	F11	HP0974	phosphoglycerate mutase	1510	<a href="#">NP_207765.1</a>	3.32119
26695	62006	F12	HP0143	2-oxoglutarate/malate translocator, authentic frameshift	1485	-	3.98316
26695	62015	G01	HP0758	conserved hypothetical integral membrane protein	1348	<a href="#">NP_207551.1</a>	1.34941
26695	62018	G02	HP0512	glutamine synthetase	1480	<a href="#">NP_207309.1</a>	4.0527
26695	62038	G03	HP0498	sodium- and chloride-dependent transporter	1363	<a href="#">NP_207295.1</a>	2.8628
26695	62043	G04	HP0282	hypothetical protein	1477	<a href="#">NP_207080.1</a>	3.44414
26695	62062	G05	HP0138	conserved hypothetical iron-sulfur protein	1480	<a href="#">NP_206938.1</a>	1.27027
26695	62066	G06	HP0269	conserved hypothetical ATP-binding protein	1348	<a href="#">NP_207067.1</a>	1.33531
26695	62070	G07	HP0509	glycolate oxidase subunit	1414	<a href="#">NP_207306.1</a>	3.33098
26695	62079	G08	HP1035	flagellar biosynthesis protein	1414	<a href="#">NP_207825.1</a>	2.58911
26695	62087	G09	HP0516	heat shock protein (hslU) ORF1	1366	<a href="#">NP_207313.1</a>	3.7123
26695	62090	G10	HP0380	glutamate dehydrogenase	1381	<a href="#">NP_207178.1</a>	1.28313
26695	62094	G11	HP0550	transcription termination factor Rho	1351	<a href="#">NP_207345.1</a>	3.97557
26695	62106	G12	HP0772	N-acetylmuramoyl-L-alanine amidase	1357	<a href="#">NP_207565.1</a>	1.2675
26695	62114	H01	HP0996	hypothetical protein	1837	<a href="#">NP_207787.1</a>	3.59499
26695	62119	H02	HP0444	hypothetical protein	1558	<a href="#">NP_207242.1</a>	3.99551
26695	62131	H03	HP0358	hypothetical protein	1570	<a href="#">NP_207156.1</a>	3.75732
26695	62134	H04	HP0115	flagellin B	1579	<a href="#">NP_206915.1</a>	4.37302
26695	62139	H05	HP0030	hypothetical protein	1816	<a href="#">NP_206832.1</a>	3.07159
26695	62142	H06	HP0733	hypothetical protein	1600	<a href="#">NP_207527.1</a>	3.76125
26695	62146	H07	HP0821	excinuclease ABC subunit C	1819	<a href="#">NP_207614.1</a>	4.11435
26695	62150	H08	HP0319	arginyl-tRNA synthetase	1660	<a href="#">NP_207117.1</a>	4.66867
26695	62154	H09	HP0855	alginate O-acetylation protein	1618	<a href="#">NP_207649.1</a>	3.9759
26695	62158	H10	HP0593	adenine specific DNA methyltransferase	1831	<a href="#">NP_207388.1</a>	3.70453
26695	62162	H11	HP1272	NADH-ubiquinone oxidoreductase, NQO13 subunit	1573	<a href="#">NP_208064.1</a>	3.58487
26695	62167	H12	HP1206	multidrug resistance protein	1771	<a href="#">NP_207998.1</a>	3.91869

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

<sup>2</sup>Not all genes were annotated at the time this document was produced (NA – gene accession number not available).