

***Helicobacter pylori* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 1**

Catalog No. NR-19477

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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-19477 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 1, NR-19477.”

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.

Disclaimers:

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

- Jungblut, P. R., et al. "Comparative Proteome Analysis of *Helicobacter pylori*." *Mol. Microbiol.* 36 (2000): 710-725. PubMed: 10844659.
- Tomb, J. F., et al. "The Complete Genome Sequence of the Gastric Pathogen *Helicobacter pylori*." *Nature* 388 (1997): 539-547. PubMed: 9252185.

References:

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

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Table 1: *Helicobacter pylori* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 1 (ZHPAA)¹

Strain	Clone	Well Position	Locus ID	Description	ORF Length	Accession Number ²	Average Depth of Coverage
26695	55794	A01	HP1389	hypothetical protein	217	NP_208180.1	-
26695	55798	A02	HP1264	hypothetical protein	265	NP_208056.1	-
26695	55802	A03	HP0135	lipoprotein, putative	169	NP_206935.1	-
26695	55806	A04	HP0385	hypothetical protein	265	NP_207183.1	2
26695	55810	A05	HP1308	ribosomal protein L24	256	NP_208100.1	2
26695	55814	A06	HP1306	ribosomal protein S14	220	NP_208098.1	2
26695	55818	A07	HP0007	hypothetical protein	106	-	-
26695	55822	A08	HP1176	hypothetical protein	139	NP_207967.1	2
26695	55830	A09	HP0146	cbb3-type cytochrome c oxidase subunit Q	256	NP_206945.1	2
26695	55834	A10	HP0562	ribosomal protein S21	247	NP_207357.1	2
26695	55838	A11	HP0491	ribosomal protein L28	223	NP_207288.1	-
26695	55842	A12	HP0200	ribosomal protein L32	181	NP_206999.1	2
26695	55846	B01	HP0511	lipoprotein, putative	151	NP_207308.1	-
26695	55850	B02	HP0551	ribosomal protein L31	238	NP_207346.1	2
26695	55854	B03	HP0341	hypothetical protein	130	NP_207139.1	-
26695	55858	B04	HP0881	hypothetical protein	130	NP_207675.1	2
26695	55870	B05	HP0008	hypothetical protein	118	NP_206810.1	2
26695	55875	B06	HP0335	hypothetical protein	223	NP_207133.1	-
26695	55878	B07	HP1073	copper ion binding protein	235	NP_207864.1	2
26695	55882	B08	HP0046	hypothetical protein	172	NP_206847.1	2
26695	55886	B09	HP0924	4-oxalocrotonate tautomerase	241	NP_207716.1	2
26695	55890	B10	HP0057	lipoprotein, putative	244	NP_206858.1	2
26695	55894	B11	HP0873	hypothetical protein	250	NP_207667.1	2
26695	55898	B12	HP0789	hypothetical protein	181	NP_207582.1	2
26695	55902	C01	HP0365	hypothetical protein	127	NP_207163.1	-
26695	55914	C02	HP1405	hypothetical protein	139	NP_208196.1	-
26695	55918	C03	HP1442	carbon storage regulator	265	NP_208233.1	2
26695	55923	C04	HP0085	hypothetical protein	223	NP_206885.1	2
26695	55926	C05	HP0784	hypothetical protein	169	NP_207577.1	2
26695	55930	C06	HP1311	ribosomal protein L29	235	NP_208103.1	2
26695	55934	C07	HP1528	hypothetical protein	112	NP_208318.1	2
26695	55942	C08	HP1297	ribosomal protein L36	148	NP_208089.1	2
26695	55946	C09	HP1239	hypothetical protein	124	NP_208031.1	-

Strain	Clone	Well Position	Locus ID	Description	ORF Length	Accession Number ²	Average Depth of Coverage
26695	55950	C10	HP0720	hypothetical protein	196	NP_207514.1	-
26695	55954	C11	HP1427	histidine-rich, metal binding polypeptide	217	NP_208218.1	2
26695	55958	C12	HP1163	hypothetical protein	226	NP_207954.1	2
26695	55967	D01	HP1242	conserved hypothetical protein	265	NP_208034.1	-
26695	55974	D02	HP0999	hypothetical protein	220	NP_207790.1	-
26695	55978	D03	HP0767	hypothetical protein	109	NP_207560.1	-
26695	55982	D04	HP1093	hypothetical protein	121	NP_207884.1	2
26695	55987	D05	HP1203.5	preprotein translocase, SecE subunit	214	NP_207995.1	-
26695	55995	D06	HP1515	hypothetical protein	127	NP_208306.1	-
26695	55998	D07	HP0594	hypothetical protein	199	NP_207389.1	2
26695	56002	D08	HP1432	histidine and glutamine-rich protein	253	NP_208223.1	2
26695	56006	D09	HP0560	hypothetical protein	115	-	1.98261
26695	56010	D10	HP1219	hypothetical protein	226	NP_208011.1	2
26695	56014	D11	HP0148	hypothetical protein	241	NP_206947.1	2
26695	56018	D12	HP0188	hypothetical protein	136	NP_206987.1	2
26695	56023	E01	HP0314	hypothetical protein	154	NP_207112.1	2
26695	56027	E02	HP0533	hypothetical protein	124	-	-
26695	56034	E03	HP0222	hypothetical protein	256	NP_207020.1	2
26695	56038	E04	HP0225	hypothetical protein	103	NP_207023.1	2
26695	56042	E05	HP1194	hypothetical protein	121	NP_207985.1	-
26695	56047	E06	HP1298	translation initiation factor EF-1	253	NP_208090.1	2
26695	56054	E07	HP0125	ribosomal protein L35	229	NP_206925.1	2
26695	56058	E08	HP0564	hypothetical protein	205	NP_207359.1	2
26695	56062	E09	HP0131	hypothetical protein	136	NP_206931.1	2
26695	56066	E10	HP0704	hypothetical protein	145	NP_207498.1	2
26695	56070	E11	HP0901	hypothetical protein	160	NP_207694.1	1.9875
26695	56075	E12	HP0461	hypothetical protein	127	NP_207259.1	2
26695	56086	F01	HP0445	hypothetical protein	220	NP_207243.1	2
26695	56090	F02	HP0504	hypothetical protein	184	NP_207301.1	2
26695	56094	F03	HP0756	hypothetical protein	181	NP_207549.1	2
26695	56103	F04	HP0698	hypothetical protein	124	NP_207492.1	-
26695	56106	F05	HP0081	hypothetical protein	157	NP_206881.1	2
26695	56110	F06	HP1204	ribosomal protein L33	193	NP_207996.1	-
26695	56118	F07	HP0801	molybdopterin converting factor, subunit 1	259	NP_207594.1	2
26695	56122	F08	HP0122	lipoprotein, putative	166	NP_206922.1	2
26695	56126	F09	HP0128	hypothetical protein	160	NP_206928.1	-
26695	56134	F10	HP0641	hypothetical protein	262	NP_207435.1	2
26695	56138	F11	HP0161	hypothetical protein	145	NP_206960.1	2
26695	56142	F12	HP0917	hypothetical protein	106	NP_207709.1	-
26695	56146	G01	HP1151	ribosomal protein S16	265	NP_207942.1	2
26695	56150	G02	HP1536	hypothetical protein	91	NP_208327.1	-
26695	56155	G03	HP1590	hypothetical protein	154	NP_208381.1	-
26695	56158	G04	HP1425	hypothetical protein	262	NP_208216.1	2
26695	56167	G05	HP1097	hypothetical protein	130	NP_207888.1	-
26695	56170	G06	HP0023	hypothetical protein	154	NP_206825.1	2
26695	56178	G07	HP1449	conserved hypothetical protein	388	NP_208240.1	1.98969
26695	56182	G08	HP0588	ferrodoxin-like protein	376	NP_207383.1	2
26695	56186	G09	HP1408	hypothetical protein	370	NP_208199.1	2

Strain	Clone	Well Position	Locus ID	Description	ORF Length	Accession Number ²	Average Depth of Coverage
26695	56190	G10	HP1199	ribosomal protein L7/L12	412	NP_207990.1	1.76699
26695	56195	G11	HP0584	flagellar switch protein	406	NP_207379.1	-
26695	56198	G12	HP0261	hypothetical protein	433	NP_207059.1	2
26695	56202	H01	HP1414	conserved hypothetical protein	376	NP_208205.1	2
26695	56206	H02	HP1212	ATP synthase F0, subunit c	352	NP_208004.1	1.96023
26695	56210	H03	HP0535	cag pathogenicity island protein	415	NP_207331.1	2
26695	56214	H04	HP1150	hypothetical protein	382	NP_207941.1	1.98953
26695	56218	H05	HP0448	hypothetical protein	421	NP_207246.1	1.9905
26695	56222	H06	HP0808	holo-acp synthase	394	NP_207601.1	1.98477
26695	56226	H07	HP0981	exonuclease VII-like protein	400	NP_207772.1	1.99
26695	56230	H08	HP0083	ribosomal protein S9	424	NP_206883.1	2
26695	56234	H09	HP0316	hypothetical protein	427	NP_207114.1	1.91569
26695	56238	H10	HP1094	hypothetical protein	391	NP_207885.1	1.89003
26695	56243	H11	HP0520	cag pathogenicity island protein	382	NP_207317.1	-
26695	56246	H12	HP1586	hypothetical protein	373	NP_208377.1	1.93834

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

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