

***Helicobacter pylori* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 4**

Catalog No. NR-19480

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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-19480 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 4, NR-19480.”

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 4 (ZHPAD)¹

Strain	Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
26695	57142	A01	HP0783	hypothetical protein	532	NP_207576.1	2
26695	57147	A02	HP0028	conserved hypothetical secreted protein	568	NP_206830.1	2
26695	57151	A03	HP0383	hypothetical protein	559	NP_207181.1	2
26695	57155	A04	HP1200	ribosomal protein L10	529	NP_207991.1	2
26695	57159	A05	HP1125	peptidoglycan associated lipoprotein precursor	574	NP_207916.1	2
26695	57162	A06	HP1307	ribosomal protein L5	580	NP_208099.1	2
26695	57167	A07	HP1173	hypothetical protein	586	NP_207964.1	2
26695	57171	A08	HP1358	hypothetical protein	541	NP_208150.1	2
26695	57174	A09	HP0327	flagellar protein G	577	NP_207125.1	1.925476603
26695	57179	A10	HP0249	hypothetical protein	574	NP_207047.1	2
26695	57183	A11	HP1135	ATP synthase F1, subunit delta	577	NP_207926.1	2
26695	57187	A12	HP1516	hypothetical protein	574	NP_208307.1	2
26695	57191	B01	HP1028	hypothetical protein	532	NP_207818.1	2
26695	57195	B02	HP1209	ulcer-associated gene restriction endonuclease	553	NP_208001.1	2
26695	57198	B03	HP1159	cell filamentation protein	568	NP_207950.1	2
26695	57203	B04	HP0866	transcription elongation factor GreA	529	NP_207660.1	2
26695	57206	B05	HP1339	biopolymer transport protein	535	NP_208131.1	2
26695	57211	B06	HP0611	hypothetical protein	535	NP_207406.1	2
26695	57214	B07	HP1161	flavodoxin	529	NP_207952.1	2
26695	57219	B08	HP0218	hypothetical protein	586	NP_207016.1	-
26695	57223	B09	HP0653	nonheme iron-containing ferritin	538	NP_207447.1	2
26695	57230	B10	HP0469	conserved hypothetical protein	523	NP_207267.1	2.145315488
26695	57235	B11	HP0697	hypothetical protein	541	NP_207491.1	2
26695	57238	B12	HP0676	methylated-DNA--protein-cysteine methyltransferase	541	NP_207470.1	2
26695	57242	C01	HP1036	7, 8-dihydro-6-hydroxymethylpterin-pyrophosphokinase	526	NP_207826.1	2
26695	57246	C02	HP0681	hypothetical protein	541	NP_207475.1	2
26695	57251	C03	HP0523	cag pathogenicity island protein	544	NP_207319.1	2
26695	57258	C04	HP1210	serine acetyltransferase	550	NP_208002.1	1.78
26695	57263	C05	HP1546	hypothetical protein	547	NP_208337.1	2
26695	57267	C06	HP0799	molybdopterin biosynthesis protein	565	NP_207592.1	2

Strain	Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
26695	57271	C07	HP0070	urease accessory protein	547	NP_206870.1	2
26695	57274	C08	HP1146	hypothetical protein	544	NP_207937.1	2
26695	57279	C09	HP0928	GTP cyclohydrolase I	577	NP_207720.1	2
26695	57282	C10	HP0688	hypothetical protein	535	NP_207482.1	1.992523364
26695	57287	C11	HP0408	hypothetical protein	523	NP_207206.1	2
26695	57291	C12	HP0184	hypothetical protein	577	NP_206983.1	2
26695	57294	D01	HP1448	ribonuclease P, protein component	520	NP_208239.1	2
26695	57298	D02	HP1337	conserved hypothetical protein	559	NP_208129.1	1.98568873
26695	57303	D03	HP0095	hypothetical protein	565	NP_206895.1	-
26695	57306	D04	HP1076	hypothetical protein	550	NP_207867.1	2
26695	57310	D05	HP0620	inorganic pyrophosphatase	556	NP_207414.1	2
26695	57315	D06	HP1496	general stress protein	571	NP_208287.1	2
26695	57318	D07	HP1203	transcription termination factor NusG	565	NP_207994.1	2
26695	57323	D08	HP1390	hypothetical protein	535	NP_208181.1	2
26695	57327	D09	HP0515	heat shock protein	577	NP_207312.1	2
26695	57330	D10	HP1250	hypothetical protein	613	NP_208042.1	2
26695	57334	D11	HP0909	hypothetical protein	640	NP_207701.1	2
26695	57339	D12	HP0857	phosphoheptose isomerase	613	NP_207651.1	-
26695	57343	E01	HP1533	conserved hypothetical protein	661	NP_208323.1	1.993948563
26695	57347	E02	HP0785	conserved hypothetical secreted protein	589	NP_207578.1	1.808149406
26695	57350	E03	HP1493	hypothetical protein	646	NP_208284.1	2
26695	57355	E04	HP0406	hypothetical protein	625	NP_207204.1	2
26695	57359	E05	HP0262	hypothetical protein	637	NP_207060.1	2
26695	57363	E06	HP1457	hypothetical protein	667	NP_208248.1	2
26695	57367	E07	HP0879	hypothetical protein	643	NP_207673.1	1.888024883
26695	57370	E08	HP0435	hypothetical protein	610	NP_207233.1	1.921311475
26695	57374	E09	HP1476	phenylacrylic acid decarboxylase	598	NP_208267.1	-
26695	57378	E10	HP0951	hypothetical protein	652	NP_207743.1	-
26695	57382	E11	HP0156	hypothetical protein	637	NP_206955.1	1.954474097
26695	57386	E12	HP0110	co-chaperone and heat shock protein	604	NP_206910.1	1.983443709
26695	57391	F01	HP0831	conserved hypothetical ATP binding protein	625	NP_207624.1	-
26695	57399	F02	HP1569	hypothetical protein	628	NP_208360.1	2
26695	57402	F03	HP1257	orotate phosphoribosyltransferase	640	NP_208049.1	2
26695	57411	F04	HP0650	hypothetical protein	625	NP_207444.1	2
26695	57414	F05	HP0149	hypothetical protein	619	NP_206948.1	1.95638126
26695	57419	F06	HP0596	lipoprotein, putative	613	NP_207391.1	2
26695	57423	F07	HP1291	conserved hypothetical protein	649	NP_208083.1	1.993836672
26695	57427	F08	HP1099	2-keto-3-deoxy-6-phosphogluconate aldolase	661	NP_207890.1	2.104387292
26695	57430	F09	HP1563	alkyl hydroperoxide reductase	631	NP_208354.1	1.993660856
26695	57435	F10	HP0150	hypothetical protein	625	NP_206949.1	1.9936
26695	57439	F11	HP0367	hypothetical protein	643	NP_207165.1	1.948678072
26695	57442	F12	HP1567	conserved hypothetical GTP-binding protein	661	NP_208358.1	2
26695	57450	G01	HP0526	cag pathogenicity island protein	634	NP_207322.1	2
26695	57454	G02	HP1589	conserved hypothetical protein	658	NP_208380.1	2
26695	57458	G03	HP0321	5'-guanylate kinase	655	NP_207119.1	-
26695	57462	G04	HP0071	urease accessory protein	622	NP_206871.1	2
26695	57467	G05	HP0953	hypothetical protein	601	NP_207745.1	1.762063228

Strain	Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
26695	57470	G06	HP0021	hypothetical protein	607	NP_206823.1	2
26695	57474	G07	HP0108	hypothetical protein	595	NP_206908.1	2
26695	57479	G08	HP0838	lipoprotein, putative	652	NP_207631.1	2
26695	57482	G09	HP0925	recombinational DNA repair protein	616	NP_207717.1	-
26695	57486	G10	HP0603	hypothetical protein	604	NP_207398.1	2
26695	57490	G11	HP1294	ribosomal protein S4	661	NP_208086.1	-
26695	57495	G12	HP1240	conserved hypothetical protein	607	NP_208032.1	1.774299835
26695	57499	H01	HP0810	conserved hypothetical protein	637	NP_207603.1	2
26695	57502	H02	HP1149	conserved hypothetical protein	589	NP_207940.1	1.983022071
26695	57507	H03	HP1255	protein translocation protein, low temperature	640	NP_208047.1	1.90625
26695	57510	H04	HP1081	lipoprotein, putative	658	NP_207872.1	1.990881459
26695	57514	H05	HP0618	adenylate kinase	610	NP_207413.1	2
26695	57518	H06	HP0762	lipoprotein, putative	592	NP_207555.1	1.983108108
26695	57522	H07	HP1322	hypothetical protein	640	NP_208114.1	-
26695	57526	H08	HP1080	conserved hypothetical integral membrane protein	604	NP_207871.1	1.993377483
26695	57530	H09	HP1319	ribosomal protein L3	610	NP_208111.1	1.983606557
26695	57534	H10	HP1162	conserved hypothetical integral membrane protein	649	NP_207953.1	-
26695	57538	H11	HP0591	ferredoxin oxidoreductase, gamma subunit	595	NP_207386.1	2
26695	57542	H12	HP0571	conserved hypothetical integral membrane protein	613	NP_207366.1	1.993474715

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