

***Helicobacter pylori* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 7**

Catalog No. NR-19483

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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-19483 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 7, NR-19483.”

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.

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 7 (ZHPAG)¹

Strain	Clone	Well Position	Locus ID	Description	ORF Length	Accession Number ²	Average Depth of Coverage
26695	58446	A01	HP1519	hypothetical protein	787	NP_208310.1	3.831
26695	58451	A02	HP0230	CTP:CMP-3-deoxy-D-manno-octulosonate-cytidylyl-transferase	766	NP_207028.1	2.6867
26695	58456	A03	HP1395	outer membrane protein	763	NP_208186.1	1.7392
26695	58459	A04	HP1182	conserved hypothetical protein	796	NP_207973.1	2
26695	58462	A05	HP0561	3-ketoacyl-acyl carrier protein reductase	778	NP_207356.1	1.9949
26695	58467	A06	HP1171	glutamine ABC transporter, ATP-binding protein	781	NP_207962.1	2
26695	58470	A07	HP0956	conserved hypothetical protein	763	NP_207748.1	2
26695	58474	A08	HP0777	uridine 5'-monophosphate (UMP) kinase	757	NP_207570.1	1.9947
26695	58479	A09	HP0318	conserved hypothetical protein	790	NP_207116.1	2
26695	58482	A10	HP0014	hypothetical protein	862	NP_206816.1	1.5174
26695	58486	A11	HP1030	fliY protein	898	NP_207820.1	2
26695	58491	A12	HP1316	ribosomal protein L2	865	NP_208108.1	2
26695	58494	B01	HP0185	hypothetical protein	838	NP_206984.1	2.5143
26695	58499	B02	HP1431	16S rRNA (adenosine-N6,N6-)-dimethyltransferase	850	NP_208222.1	2
26695	58503	B03	HP1277	tryptophan synthase, alpha subunit	823	NP_208069.1	1.9903
26695	58507	B04	HP0152	hypothetical protein	898	NP_206951.1	2
26695	58510	B05	HP0301	dipeptide ABC transporter, ATP-binding protein	898	NP_207099.1	2
26695	58515	B06	HP0111	hypothetical protein	865	NP_206911.1	1.7572
26695	58519	B07	HP0679	lipopolysaccharide biosynthesis protein	904	NP_207473.1	1.8429
26695	58522	B08	HP0130	hypothetical protein	895	NP_206930.1	1.9911
26695	58526	B09	HP1139	SpoOJ regulator	829	NP_207930.1	2.2967
26695	58531	B10	HP0766	hypothetical protein	859	NP_207559.1	1.9942
26695	58534	B11	HP0803	hypothetical protein	874	NP_207596.1	2
26695	58538	B12	HP0552	conserved hypothetical protein	898	NP_207347.1	2.343
26695	58542	C01	HP0955	prolipoprotein diacylglycerol transferase	889	NP_207747.1	1.8391
26695	58547	C02	HP0331	cell division inhibitor	841	NP_207129.1	2
26695	58552	C03	HP0300	dipeptide ABC transporter, permease protein	892	NP_207098.1	2.1502

Strain	Clone	Well Position	Locus ID	Description	ORF Length	Accession Number ²	Average Depth of Coverage
26695	58554	C04	HP0532	cag pathogenicity island protein	877	NP_207328.1	1.5336
26695	58559	C05	HP1397	hypothetical protein	850	NP_208188.1	1.9906
26695	58566	C06	HP1554	ribosomal protein S2	829	NP_208345.1	2
26695	58573	C07	HP0381	HemK family methylase, putative	865	NP_207179.1	2.1642
26695	58580	C08	HP0492	lipoprotein, putative	871	NP_207289.1	2.1447
26695	58583	C09	HP0333	DNA processing chain A	847	NP_207131.1	1.9976
26695	58586	C10	HP0671	outer membrane protein	847	NP_207465.1	1.9693
26695	58594	C11	HP0226	conserved hypothetical integral membrane protein	868	NP_207024.1	3.0876
26695	58598	C12	HP1113	outer membrane protein	868	NP_207904.1	2
26695	58602	D01	HP1341	siderophore-mediated iron transport protein	892	NP_208133.1	2.3789
26695	58610	D02	HP1443	conserved hypothetical protein	841	NP_208234.1	1.9964
26695	58614	D03	HP0749	cell division membrane protein	841	NP_207542.1	1.9952
26695	58618	D04	HP1056	hypothetical protein	889	NP_207847.1	2
26695	58626	D05	HP0006	pantoate-beta-alanine ligase	865	NP_206808.1	1.9468
26695	58631	D06	HP1481	hypothetical protein	832	NP_208272.1	2
26695	58634	D07	HP1415	tRNA delta(2)-isopentenylpyrophosphate transferase	835	NP_208206.1	1.9952
26695	58639	D08	HP1582	pyridoxal phosphate biosynthetic protein J	823	NP_208373.1	2
26695	58644	D09	HP0548	DNA helicase, putative, authentic point mutation	862	N/A	2.1462
26695	58646	D10	HP0983	conserved hypothetical integral membrane protein	859	NP_207774.1	3.78
26695	58650	D11	HP1092	flagellar basal-body rod protein	844	NP_207883.1	2
26695	58654	D12	HP0646	UDP-glucose pyrophosphorylase	856	NP_207440.1	3.7407
26695	58659	E01	HP0543	cag pathogenicity island protein	841	NP_207339.1	1.9524
26695	58662	E02	HP0555	hypothetical protein	856	NP_207350.1	2
26695	58666	E03	HP0151	conserved hypothetical membrane protein	847	NP_206950.1	2
26695	58670	E04	HP0059	hypothetical protein	889	NP_206859.1	1.9944
26695	58675	E05	HP1355	nicotinate-nucleotide pyrophosphorylase	856	NP_208147.1	2
26695	58679	E06	HP0930	stationary-phase survival protein	838	NP_207722.1	1.9952
26695	58683	E07	HP1172	glutamine ABC transporter, periplasmic glutamine-binding protein	868	NP_207963.1	2
26695	58686	E08	HP0067	urease accessory protein	832	NP_206867.1	2
26695	58694	E09	HP0479	hypothetical protein	883	NP_207277.1	2
26695	58698	E10	HP1058	3-methyl-2-oxobutanoate hydroxymethyltransferase	847	NP_207849.1	2
26695	58702	E11	HP1249	shikimate 5-dehydrogenase	826	NP_208041.1	2
26695	58706	E12	HP0796	outer membrane protein	871	NP_207589.1	1.9954
26695	58710	F01	HP1375	UDP-N-acetylglucosamine acyltransferase	847	NP_208166.1	2
26695	58714	F02	HP0400	penicillin tolerance protein	859	NP_207198.1	1.9942
26695	58718	F03	HP0519	conserved hypothetical protein	865	NP_207316.1	2
26695	58722	F04	HP0003	3-deoxy-d-manno-octulosonic acid 8-phosphate synthetase	865	NP_206805.1	3.1306
26695	58730	F05	HP1564	outer membrane protein	850	NP_208355.1	1.8388

Strain	Clone	Well Position	Locus ID	Description	ORF Length	Accession Number ²	Average Depth of Coverage
26695	58734	F06	HP1585	flagellar basal-body rod protein	823	NP_208376.1	3.1677
26695	58738	F07	HP1459	conserved hypothetical protein	823	NP_208250.1	2
26695	58746	F08	HP1357	phosphatidylserine decarboxylase proenzyme	838	NP_208149.1	1.9988
26695	58750	F09	HP0475	molybdenum ABC transporter, ATP-binding protein	832	NP_207273.1	1.7752
26695	58754	F10	HP1464	conserved hypothetical secreted protein	850	NP_208255.1	2.8506
26695	58760	F11	HP0092	type II restriction enzyme M protein	868	NP_206892.1	1.4654
26695	58763	F12	HP1368	type IIS restriction enzyme M2 protein	898	NP_208160.1	2
26695	58767	G01	HP1380	prephenate dehydrogenase	832	NP_208171.1	2
26695	58770	G02	HP0826	lipooligosaccharide 5G8 epitope biosynthesis-associated protein	856	NP_207619.1	1.993
26695	58774	G03	HP1451	hypothetical protein	829	NP_208242.1	2
26695	58778	G04	HP0845	thiamin phosphate pyrophosphorylase/hydroxyethylthiazole kinase	856	NP_207638.1	2
26695	58782	G05	HP0215	CDP-diglyceride synthetase	835	NP_207013.1	1.6731
26695	58786	G06	HP0805	lipooligosaccharide 5G8 epitope biosynthesis-associated protein	889	NP_207598.1	2
26695	58791	G07	HP0127	outer membrane protein	895	NP_206927.1	1.9844
26695	58794	G08	HP0091	type II restriction enzyme R protein	868	NP_206891.1	2
26695	58798	G09	HP1087	riboflavin biosynthesis regulatory protein	877	NP_207878.1	2
26695	58810	G10	HP1509	conserved hypothetical integral membrane protein	823	NP_208300.1	2
26695	58814	G11	HP0706	outer membrane protein	856	NP_207500.1	1.9965
26695	58818	G12	HP0844	thiamine biosynthesis protein	847	NP_207637.1	1.9008
26695	58822	H01	HP1024	co-chaperone-curved DNA binding protein A	901	NP_207814.1	1.8846
26695	58826	H02	HP1004	hypothetical protein	856	NP_207795.1	2
26695	58830	H03	HP1406	biotin synthetase	883	NP_208197.1	2
26695	58834	H04	HP0302	dipeptide ABC transporter, ATP-binding protein	841	NP_207100.1	2
26695	58838	H05	HP0937	hypothetical protein	829	NP_207729.1	2
26695	58844	H06	HP0195	enoyl-(acyl-carrier-protein) reductase (NADH)	862	NP_206994.1	1.5255
26695	58846	H07	HP1022	hypothetical protein	871	NP_207812.1	1.9644
26695	58852	H08	HP1394	conserved hypothetical protein	889	NP_208185.1	2.0664
26695	58855	H09	HP0231	hypothetical protein	832	NP_207029.1	2
26695	58858	H10	HP1538	ubiquinol cytochrome c oxidoreductase, cytochrome c1 subunit	892	NP_208329.1	2.7197
26695	58863	H11	HP1074	hypothetical protein	823	NP_207865.1	2
26695	58866	H12	HP0309	conserved hypothetical protein	913	NP_207107.1	1.9934

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).