Helicobacter pylori Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 17

Catalog No. NR-19493

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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 *att*B substrate (*att*B-PCR product or a linearized *att*B expression clone) with an *att*P substrate (pDONR™221) to create an *att*L-containing entry clone. The entry clone contains recombinational cloning sites, *att*L1 and *att*L2 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-19493 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 17, NR-19493."

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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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 17 (ZHPAR)[1]

Strain	Clone	Well Position	Locus ID	Description	ORF Length	Accession Number[2]	Average Depth of Coverage
26695	62170	A01	HP0632	quinone-reactive Ni/Fe hydrogenase, large subunit	1771	NP_207426.1	3.8345567
26695	62175	A02	HP0486	hypothetical protein	1621	NP_207283.1	4.3109192
26695	62186	A03	HP0351	flagellar basal-body M-ring protein	1738	NP_207149.1	4.4654776
26695	62190	A04	HP1489	lipase-like protein	1567	NP_208280.1	3.8021698
26695	62195	A05	HP0529	cag pathogenicity island protein	1642	NP_207325.1	3.7052375
26695	62199	A06	HP0912	outer membrane protein	1582	NP_207704.1	4.3761062
26695	62202	A07	HP0908	flagellar hook	1852	NP_207700.1	3.3882289
26695	62207	A08	HP1017	amino acid permease	1594	NP_207807.1	4.651192
26695	62210	A09	HP1532	glucosamine fructose-6-phosphate aminotransferase (isomerizing)	1828	NP_208322.1	4.2253829
26695	62218	A10	HP0010	chaperone and heat shock protein	1675	NP_206812.1	4.6429851
26695	62222	A11	HP0409	GMP synthase	1561	NP_207207.1	3.5887252
26695	62226	A12	HP0104	2',3'-cyclic-nucleotide 2'-phosphodiesterase	1780	NP_206904.1	3.9938202
26695	62230	B01	HP0286	cell division protein	1687	NP_207084.1	3.9490219
26695	62238	B02	HP0079	outer membrane protein	1822	NP_206879.1	2.9906696
26695	62247	B03	HP0915	iron-regulated outer membrane protein	1723	NP_207707.1	3.5066744
26695	62250	B04	HP1282	anthranilate synthase component I	1537	NP_208074.1	3.504229
26695	62258	B05	HP0348	single-stranded-DNA-specific exonuclease	1585	NP_207146.1	4.7318612
26695	62263	B06	HP0140	L-lactate permease	1684	NP_206940.1	4.25
26695	62266	B07	HP0349	CTP synthetase	1651	NP_207147.1	3.9848577
26695	62271	B08	HP0617	aspartyl-tRNA synthetase	1768	NP_207412.1	3.6023756
26695	62274	B09	HP0875	catalase	1552	NP_207669.1	4.7551546
26695	62278	B10	HP0103	methyl-accepting chemotaxis protein	1732	NP_206903.1	3.98903
26695	62282	B11	HP0600	multidrug resistance protein	1816	NP_207395.1	2.9162996
26695	62286	B12	HP0914	hypothetical protein	1579	NP_207706.1	4.4268524
26695	62293	C01	HP0141	L-lactate permease	1690	NP_206941.1	3.6266272
26695	62297	C02	HP1119	flagellar hook-associated protein 1 (HAP1)	1855	NP_207910.1	2.793531
26695	62299	C03	HP0397	phosphoglycerate dehydrogenase	1609	NP_207195.1	4.4108142

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Strain	Clone	Well Position	Locus ID	Description	ORF Length	Accession Number[2]	Average Depth of Coverage
26695	62303	C04	HP1118	gamma-glutamyltranspeptidase	1738	NP_207909.1	3.646145
26695	62314	C05	HP0818	osmoprotection protein	1696	NP_207611.1	4.2134434
26695	62318	C06	HP0355	GTP-binding membrane protein	1843	NP_207153.1	3.9788388
26695	62327	C07	HP0731	hypothetical protein	1756	NP_207525.1	3.8872437
26695	62330	C08	HP0740	UDP-MurNac-pentapeptide presynthetase	1516	NP_207534.1	2.6484169
26695	62335	C09	HP0913	outer membrane protein	1624	NP_207705.1	3.8485222
26695	62338	C10	HP1393	DNA repair protein	1609	NP_208184.1	4.0435053
26695	62349	C11	HP0468	conserved hypothetical protein	1522	NP_207266.1	2.8863338
26695	62350	C12	HP0946	conserved hypothetical integral membrane protein	1525	NP_207738.1	2.6472131
26695	62355	D01	HP0063	hypothetical protein	1525	NP_206863.1	3.0465574
26695	62358	D02	HP0645	soluble lytic murein transglycosylase	1717	NP_207439.1	4.2550961
26695	62362	D03	HP0452	conserved hypothetical protein	1591	NP_207250.1	3.8170962
26695	62366	D04	HP0966	conserved hypothetical protein	1684	NP_207758.1	4.4667458
26695	62370	D05	HP0399	ribosomal protein S1	1705	NP_207197.1	4.5958944
26695	62375	D06	HP1417	conserved hypothetical protein, authentic frameshift	1704	-	3.508216
26695	62379	D07	HP1491	phosphate permease	1636	NP_208282.1	4.1668704
26695	62382	D08	HP0905	phosphotransacetylase, degenerate	1581	NP_207697.1	4.8640101
26695	62389	D09	HP0470	oligoendopeptidase F	1771	NP_207268.1	3.4618859
26695	62390	D10	HP0190	conserved hypothetical secreted protein	1543	NP_206989.1	4.0758263
26695	62394	D11	HP0853	ABC transporter, ATP-binding protein	1636	NP_207647.1	3.6338631
26695	62398	D12	HP0055	proline permease	1525	NP_206856.1	3.1659016
26695	62403	E01	HP0717	DNA polymerase III gamma and tau subunits	1771	NP_207511.1	4.0801807
26695	62410	E02	HP0322	poly E-rich protein	1552	NP_207120.1	3.1726804
26695	62414	E03	HP0293	para-aminobenzoate synthetase	1714	NP_207091.1	3.5315053
26695	62418	E04	HP0012	DNA primase	1714	NP_206814.1	4.6931155
26695	62422	E05	HP1166	glucose-6-phosphate isomerase	1672	NP_207957.1	3.7834928
26695	62434	E06	HP1252	oligopeptide ABC transporter, periplasmic oligopeptide-binding protein	1819	NP_208044.1	4.0186916
26695	62449	E07	HP0182	lysyl-tRNA synthetase	1540	NP_206981.1	3.6987013
26695	62450	E08	HP0850	type I restriction enzyme M protein	1618	NP_207641.1	4.9524104
26695	62454	E09	HP0072	urease beta subunit (urea amidohydrolase)	1744	NP_206872.1	3.2815367
26695	62463	E10	HP1450	60 kDa inner-membrane protein	1678	NP_208241.1	4.6644815
26695	62467	E11	HP1134	ATP synthase F1, subunit alpha	1546	NP_207925.1	1.0614489
26695	62470	E12	HP0906	hypothetical protein	1618	NP_207698.1	4.2533993
26695	62474	F01	HP0528	cag pathogenicity island protein	1603	NP_207324.1	4.2495321
26695	62479	F02	HP0601	flagellin A	1567	NP_207396.1	4.7766433
26695	62482	F03	HP0284	conserved hypothetical integral membrane protein	1606	NP_207082.1	4.1457036
26695	62487	F04	HP0238	prolyl-tRNA synthetase	1768	NP_207036.1	3.3947964
26695	62491	F05	HP1082	multidrug resistance protein	1690	NP_207873.1	4.7349112
26695	62494	F06	HP0480	GTP-binding protein, fusA-homolog	1834	NP_207278.1	3.5550709
26695	62501	F07	HP0686	iron(III) dicitrate transport protein	2338	NP_207480.1	3.4452524
26695	62502	F08	HP0109	chaperone and heat shock protein 70	1897	NP_206909.1	2.7385345

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Strain	Clone	Well Position	Locus ID	Description	ORF Length	Accession Number[2]	Average Depth of Coverage
26695	62508	F09	HP1430	conserved hypothetical ATP-binding protein	2104	NP_208221.1	3.8355513
26695	62510	F10	HP0116	DNA topoisomerase I	2245	NP_206916.1	4.0681514
26695	62515	F11	HP0054	adenine/cytosine DNA methyltransferase	2506	NP_206855.1	3.5199521
26695	62526	F12	HP1114	excinuclease ABC subunit B	2011	NP_207905.1	3.1387369
26695	62531	G01	HP1010	polyphosphate kinase	2062	NP_207800.1	3.9941804
26695	62534	G02	HP0396	conserved hypothetical protein	1885	NP_207194.1	4.3188329
26695	62543	G03	HP0210	chaperone and heat shock protein C62.5	1900	NP_207008.1	3.2126316
26695	62546	G04	HP1248	virulence associated protein homolog	1969	NP_208040.1	3.8283393
26695	62550	G05	HP1069	cell division protein	1933	NP_207860.1	4.2793585
26695	62557	G06	HP1041	flagellar biosynthesis protein	2236	NP_207831.1	3.5845259
26695	62558	G07	HP0227	outer membrane protein	2110	NP_207025.1	3.8137441
26695	62565	G08	HP0775	penta-phosphate guanosine-3'-pyrophosphohydrolase	2362	NP_207568.1	2.599492
26695	62570	G09	HP0415	conserved hypothetical integral membrane protein	1906	NP_207213.1	2.8147954
26695	62576	G10	HP0066	conserved hypothetical ATP-binding protein	2530	NP_206866.1	2.9533597
26695	62578	G11	HP1453	conserved hypothetical protein	2275	NP_208244.1	3.3854945
26695	62582	G12	HP0422	arginine decarboxylase	1882	NP_207220.1	3.3910733
26695	62589	H01	HP0373	conserved hypothetical protein	2137	NP_207171.1	3.5577913
26695	62590	H02	HP0009	outer membrane protein	1939	NP_206811.1	3.2676637
26695	62594	H03	HP1411	hypothetical protein	1894	NP_208202.1	3.6948258
26695	62607	H04	HP0114	hypothetical protein	1921	NP_206914.1	2.8807913
26695	62611	H05	HP0876	iron-regulated outer membrane protein	2410	NP_207670.1	3.2228216
26695	62618	H06	HP0972	glycyl-tRNA synthetase, beta subunit	2140	NP_207763.1	3.521028
26695	62622	H07	HP0424	hypothetical protein	1894	NP_207222.1	3.9197466
26695	62631	H08	HP0621	DNA mismatch repair protein	2323	NP_207415.1	3.7421438
26695	62642	H09	HP1342	outer membrane protein	2110	NP_208134.1	3.6919431
26695	62647	H10	HP0402	phenylalanyl-tRNA synthetase, beta subunit	2329	NP_207200.1	3.6977243
26695	62663	H11	HP0465	conserved hypothetical protein	1930	NP_207263.1	3.6917098
26695	62671	H12	HP0578	hypothetical protein	2071	NP_207372.1	3.8952197

[1]All information in this table was provided by J. Craig Venter Institute at the time of deposition.
[2]Not all genes were annotated at the time this document was produced (NA – gene accession number not available).

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