

***Helicobacter pylori* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 9**

Catalog No. NR-19485

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Contributor:

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

Manufacturer:

BEI Resources

Product Description:

Clone plates are replicated using a BioMek® FX robot. 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 only confirms the clone plate orientation and viability of randomly picked clones. BEI Resources does not confirm or validate individual clone identities provided by the contributor.

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.

Plate orientation and viability were confirmed for NR-19485.

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.

Packaging/Storage:

NR-19485 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 9, NR-19485.”

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 9 (ZHPAI)¹

Strain	Clone	Well Position	Locus ID	Description	ORF Length	Accession Number ²	Average Depth of Coverage
26695	59376	A01	HP0246	flagellar basal-body P-ring protein	1063	NP_207044.1	2.402634
26695	59378	A02	HP0196	UDP-3-0-(3-hydroxymyristoyl) glucosamine N-acyltransferase	1045	NP_206995.1	1.885167
26695	59382	A03	HP1226	oxygen-independent coproporphyrinogen III oxidase, putative	1093	NP_208018.1	4.129003
26695	59386	A04	HP0738	D-alanine:D-alanine ligase A	1078	NP_207532.1	4.481447
26695	59390	A05	HP0483	cytosine specific DNA methyltransferase, authentic point mutation	1081	-	4.20259
26695	59397	A06	HP1562	iron(III) ABC transporter, periplasmic iron-binding protein	1036	NP_208353.1	2.148649
26695	59410	A07	HP1155	transferase, peptidoglycan synthesis	1096	NP_207946.1	3.989051
26695	59418	A09	HP0036	hypothetical protein	1039	NP_206838.1	1.710298
26695	59427	A10	HP1284	conserved hypothetical protein	1075	NP_208076.1	3.876279
26695	59430	A11	HP0812	hypothetical protein	1045	NP_207605.1	3.957895
26695	59435	A12	HP0364	ribonucleoside diphosphate reductase, beta subunit	1060	NP_207162.1	4.14717
26695	59438	B01	HP0376	ferrochelataase	1039	NP_207174.1	1.873917
26695	59444	B02	HP1373	rod shape-determining protein	1078	NP_208164.1	2.115955
26695	59448	B03	HP0567	membrane protein	1081	NP_207362.1	2.122109
26695	59455	B04	HP0258	conserved hypothetical integral membrane protein	1081	NP_207056.1	4.06938
26695	59459	B05	HP0201	fatty acid/phospholipid synthesis protein	1051	NP_207000.1	4.203616
26695	59464	B06	HP1267	NADH-ubiquinone oxidoreductase, NQO8 subunit	1024	NP_208059.1	1.775391
26695	59472	B07	HP0052	hypothetical protein	1027	NP_206853.1	1.895813
26695	59475	B08	HP0360	UDP-glucose 4-epimerase	1069	NP_207158.1	4.015903
26695	59478	B09	HP0499	phospholipase A1 precursor	1102	NP_207296.1	1.590744
26695	59490	B10	HP0699	hypothetical protein	1063	NP_207493.1	1.82032
26695	59498	B11	HP1428	conserved hypothetical protein	1108	NP_208219.1	3.541516
26695	59503	B12	HP1031	flagellar motor switch protein	1099	NP_207821.1	3.761601

Strain	Clone	Well Position	Locus ID	Description	ORF Length	Accession Number ²	Average Depth of Coverage
26695	59511	C01	HP0804	GTP cyclohydrolase II/3,4-dihydroxy-2-butanone 4-phosphate synthase	1069	NP_207597.1	3.803555
26695	59526	C02	HP0859	ADP-L-glycero-D-mannoheptose-6-epimerase	1027	NP_207653.1	1.703019
26695	59531	C03	HP0051	cytosine specific DNA methyltransferase	1102	NP_206852.1	3.987296
26695	59534	C04	HP0518	conserved hypothetical secreted protein	1027	NP_207315.1	1.747809
26695	59540	C05	HP0352	flagellar motor switch protein	1066	NP_207150.1	3.032833
26695	59542	C06	HP0294	aliphatic amidase	1054	NP_207092.1	1.755218
26695	59549	C07	HP0728	tRNA(Ile)-lysidine synthetase	1045	NP_207522.1	3.179904
26695	59554	C09	HP1280	anthranilate synthase component II	1042	NP_208072.1	2.981766
26695	59560	C10	HP1062	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	1072	NP_207853.1	2.844216
26695	59563	C11	HP0013	hypothetical protein	1087	NP_206815.1	4.127875
26695	59566	C12	HP0235	conserved hypothetical secreted protein	1102	NP_207033.1	4.34029
26695	59570	D01	HP1208	ulcer associated adenine specific DNA methyltransferase	1024	NP_208000.1	1.878906
26695	59574	D02	HP0840	flaA1 protein	1036	NP_207633.1	2.683398
26695	59578	D03	HP0604	uroporphyrinogen decarboxylase	1057	NP_207399.1	1.787133
26695	59586	D04	HP0153	recombinase	1078	NP_206952.1	3.62616
26695	59590	D05	HP1104	cinnamyl-alcohol dehydrogenase ELI3-2	1081	NP_207895.1	3.954672
26695	59594	D06	HP0047	hydrogenase expression/formation protein	1033	NP_206848.1	1.849952
26695	59598	D07	HP1042	hypothetical protein	1081	NP_207832.1	2.881591
26695	59602	D08	HP1429	polysialic acid capsule expression protein	1024	NP_208220.1	1.880859
26695	59606	D09	HP1068	ribosomal protein L11 methyltransferase	1036	NP_207859.1	1.782819
26695	59610	D10	HP0525	virB11 homolog	1027	NP_207321.1	1.860759
26695	59619	D11	HP0418	hypothetical protein	1042	NP_207216.1	3.869482
26695	59626	D12	HP1328	cation efflux system protein	1051	NP_208120.1	1.842055
26695	59630	E01	HP0037	NADH-ubiquinone oxidoreductase subunit	1090	NP_206839.1	4.937615
26695	59639	E02	HP0540	cag pathogenicity island protein	1180	NP_207336.1	3.351695
26695	59644	E03	HP0654	conserved hypothetical protein	1117	NP_207448.1	2.26231
26695	59647	E04	HP0421	type 1 capsular polysaccharide biosynthesis protein J	1204	NP_207219.1	3.966777
26695	59650	E05	HP0171	peptide chain release factor RF-2	1126	NP_206970.1	1.706039
26695	59654	E06	HP1507	conserved hypothetical ATP-binding protein	1192	NP_208298.1	1.562919
26695	59658	E07	HP0580	hypothetical protein	1153	NP_207374.1	1.562012
26695	59662	E08	HP0923	outer membrane protein	1144	NP_207715.1	1.736888
26695	59667	E09	HP0736	phosphoserine aminotransferase	1144	NP_207530.1	4.071678
26695	59670	E10	HP1321	conserved hypothetical ATP-binding protein	1168	NP_208113.1	3.947774
26695	59675	E11	HP0856	hypothetical protein	1129	NP_207650.1	4.070859
26695	59678	E12	HP1416	lipopolysaccharide 1,2-glucosyltransferase	1138	NP_208207.1	1.463093

Strain	Clone	Well Position	Locus ID	Description	ORF Length	Accession Number ²	Average Depth of Coverage
26695	59682	F01	HP0212	succinyl-diaminopimelate desuccinylase	1186	NP_207010.1	1.664418
26695	59686	F02	HP1560	cell division protein	1201	NP_208351.1	1.543714
26695	59690	F03	HP0569	GTP-binding protein	1135	NP_207364.1	1.625551
26695	59694	F04	HP1333	hypothetical protein	1183	NP_208125.1	2.851226
26695	59710	F05	HP1185	conserved hypothetical integral membrane protein	1210	NP_207976.1	4.055372
26695	59714	F06	HP1278	tryptophan synthase, beta subunit	1216	NP_208070.1	3.754112
26695	59722	F07	HP0248	conserved hypothetical protein	1123	NP_207046.1	4.324132
26695	59726	F08	HP1237	carbamoyl-phosphate synthetase	1162	NP_208029.1	1.489673
26695	59730	F09	HP1349	hypothetical protein	1198	NP_208141.1	4.237062
26695	59734	F10	HP0672	solute-binding signature and mitochondrial signature protein	1207	NP_207466.1	1.589064
26695	59738	F11	HP0477	outer membrane protein	1138	NP_207275.1	1.579086
26695	59742	F12	HP0663	chorismate synthase	1132	NP_207457.1	1.740283
26695	59746	G01	HP0957	3-deoxy-d-manno-octulosonic-acid transferase	1216	NP_207749.1	4.749178
26695	59750	G02	HP0743	rod shape-determining protein	1180	NP_207537.1	1.634746
26695	59754	G03	HP1352	adenine specific DNA methyltransferase	1114	NP_208144.1	1.745063
26695	59758	G04	HP1232	dihydropteroate synthase	1177	NP_208024.1	4.246389
26695	59773	G05	HP0439	hypothetical protein	1135	NP_207237.1	2.907489
26695	59774	G06	HP0303	GTP-binding protein	1117	NP_207101.1	3.953447
26695	59778	G07	HP1002	lipoprotein, putative	1219	NP_207793.1	1.589828
26695	59786	G08	HP1335	conserved hypothetical protein	1117	NP_208127.2	1.699194
26695	59790	G09	HP0589	ferredoxin oxidoreductase, alpha subunit	1162	NP_207384.1	3.63253
26695	59796	G10	HP0313	nitrite extrusion protein	1180	NP_207111.1	2.65678
26695	59798	G11	HP1572	regulatory protein DniR	1153	NP_208363.1	1.653079
26695	59802	G12	HP0500	DNA polymerase III beta-subunit	1159	NP_207297.1	1.661777
26695	59807	H01	HP0224	peptide methionine sulfoxide reductase	1114	NP_207022.1	3.201077
26695	59818	H02	HP0266	dihydroorotase	1171	NP_207064.1	1.664389
26695	59822	H03	HP1183	NA+/H+ antiporter	1186	NP_207974.1	1.672007
26695	59826	H04	HP0598	8-amino-7-oxononanoate synthase	1156	NP_207393.1	4.829585
26695	59830	H05	HP0541	cag pathogenicity island protein	1147	NP_207337.1	3.839582
26695	59838	H06	HP0773	hypothetical protein	1126	NP_207566.1	1.636767
26695	59842	H07	HP0941	alanine racemase, biosynthetic	1168	NP_207733.1	4.547945
26695	59846	H08	HP1486	conserved hypothetical integral membrane protein	1165	NP_208277.1	4.057511
26695	59850	H09	HP0675	integrase/recombinase	1123	NP_207469.1	1.612645
26695	59855	H10	HP0044	GDP-D-mannose dehydratase	1180	NP_206845.1	3.719492
26695	59858	H11	HP0703	response regulator	1180	NP_207497.1	4.345763
26695	59862	H12	HP0159	lipopolysaccharide 1,2-glucosyltransferase	1153	NP_206958.1	1.638335

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).